Inference of Macromolecular Assemblies from Crystalli

Journal of Molecular Biology

372, 774-797

DOI: 10.1016/j.jmb.2007.05.022

Citation Report

#	ARTICLE	IF	CITATIONS
25	Protein Databases on the Internet. Current Protocols in Molecular Biology, 2004, 68, Unit 19.4.	2.9	11
26	Structure of PlcR: Insights into virulence regulation and evolution of quorum sensing in Gram-positive bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18490-18495.	3.3	132
27	A Structural Overview of the Vertebrate Prion Proteins. Prion, 2007, 1, 185-197.	0.9	32
28	Structural Basis for Light-dependent Signaling in the Dimeric LOV Domain of the Photosensor YtvA. Journal of Molecular Biology, 2007, 373, 112-126.	2.0	211
29	Crystal Structures of the Staphylococcal Toxin SSL5 in Complex with Sialyl Lewis X Reveal a Conserved Binding Site that Shares Common Features with Viral and Bacterial Sialic Acid Binding Proteins. Journal of Molecular Biology, 2007, 374, 1298-1308.	2.0	62
30	Preliminary X-ray crystallographic studies of a tetrameric phospholipase A2formed by two isoforms of crotoxin B fromCrotalus durissus terrificusvenom. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 1067-1069.	0.7	6
31	Dimerization of inositol monophosphatase Mycobacterium tuberculosis SuhB is not constitutive, but induced by binding of the activator Mg2+. BMC Structural Biology, 2007, 7, 55.	2.3	15
32	PiQSi: Protein Quaternary Structure Investigation. Structure, 2007, 15, 1364-1367.	1.6	105
33	Characterization of substrate binding and catalysis in the potential antibacterial target <i>N</i>â€acetylglucosamineâ€1â€phosphate uridyltransferase (GlmU). Protein Science, 2007, 16, 2657-2666.	3.1	40
34	The leucine-rich repeat structure. Cellular and Molecular Life Sciences, 2008, 65, 2307-2333.	2.4	392
35	Relating Macromolecular Function and Association: The Structural Basis of Proteinâ€“DNA and RNA Recognition. Cellular and Molecular Bioengineering, 2008, 1, 327-338.	1.0	11
36	The befores and afters of molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 17-24.	2.5	11
37	Structure of wild-type Plk-1 kinase domain in complex with a selective DARPin. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 339-353.	2.5	34
38	Structure of the C-terminal domain of the arginine repressor protein fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 950-956.	2.5	8
39	Structure of HsaD, a steroid-degrading hydrolase, from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 2-7.	0.7	31
40	Structures of an alanine racemase from<i>Bacillus anthracis</i>(BA0252) in the presence and absence of (<i>R</i>)-1-aminoethylphosphonic acid (<scp>L</scp>-Ala-P). Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 327-333.	0.7	16
41	Structure of<i>Staphylococcus aureus</i>5â€²-methylthioadenosine/<i>S</i>-adenosylhomocysteine nucleosidase. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 343-350.	0.7	33
42	Dimerization effect of sucrose octasulfate on rat FGF1. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 448-452.	0.7	7

#	ARTICLE	IF	CITATIONS
43	Structure ofDeinococcus radioduranstunicamycin-resistance protein (TmrD), a phosphotransferase. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 479-486.	0.7	7
44	A covalent Sâ€F heterodimer of leucotoxin reveals molecular plasticity of Î²â€barrel poreâ€forming toxins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 485-496.	1.5	28
45	Insights into the role of oligomeric state on the biological activities of crotoxin: Crystal structure of a tetrameric phospholipase A₂formed by two isoforms of crotoxin B from<i>Crotalus durissus terrificus</i>venom. Proteins: Structure, Function and Bioinformatics, 2008, 72, 883-891.	1.5	55
46	Crystal structure of an ADPâ€ribosylated protein with a cytidine deaminaseâ€like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1546-1552.	1.5	6
47	Crystal structure of YagE, a putative DHDPSâ€like protein from <i>Escherichia coli K12</i>. Proteins: Structure, Function and Bioinformatics, 2008, 71, 2102-2108.	1.5	5
48	Crystal structure of an alkaline serine protease from <i>Nesterenkonia</i> sp. defines a novel family of secreted bacterial proteases. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1072-1075.	1.5	3
49	Identification of Pharmacological Chaperones for Gaucher Disease and Characterization of Their Effects on Î²â€Glucocerebrosidase by Hydrogen/Deuterium Exchange Mass Spectrometry. ChemBioChem, 2008, 9, 2650-2662.	1.3	74
50	Crystallographic structure and substrate-binding interactions of the molybdate-binding protein of the phytopathogen Xanthomonas axonopodis pv. citri. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 393-399.	1.1	25
51	Crystal structure of Mycobacterium tuberculosis Rv0760c at 1.50ÂÃ… resolution, a structural homolog of Î”5-3-ketosteroid isomerase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1625-1632.	1.1	9
52	Biochemical and Structural Insights of the Early Glycosylation Steps in Calicheamicin Biosynthesis. Chemistry and Biology, 2008, 15, 842-853.	6.2	51
53	The structure of an archaeal homodimeric ligase which has RNA circularization activity. Protein Science, 2008, 17, 1336-1345.	3.1	28
54	Structural evidence for substrateâ€induced synergism and halfâ€sites reactivity in biotin carboxylase. Protein Science, 2008, 17, 1706-1718.	3.1	67
55	Crystal structure of LpxC from <i>Pseudomonas aeruginosa</i> complexed with the potent BBâ€78485 inhibitor. Protein Science, 2008, 17, 450-457.	3.1	51
56	Crystallographic and biochemical studies revealing the structural basis for antizyme inhibitor function. Protein Science, 2008, 17, 793-802.	3.1	41
57	High Affinity Interaction between a Bivalve C-type Lectin and a Biantennary Complex-type N-Glycan Revealed by Crystallography and Microcalorimetry. Journal of Biological Chemistry, 2008, 283, 30112-30120.	1.6	35
58	Structure of Vps26B and Mapping of its Interaction with the Retromer Protein Complex. Traffic, 2008, 9, 366-379.	1.3	104
59	Crystal structures of <i>Drosophila</i> mutant translin and characterization of translin variants reveal the structural plasticity of translin proteins. FEBS Journal, 2008, 275, 4235-4249.	2.2	12
60	Structural and functional studies on a mesophilic stationary phase survival protein (Sur E) from <i>Salmonellaâ€ƒtyphimurium</i>. FEBS Journal, 2008, 275, 5855-5864.	2.2	10

#	ARTICLE	IF	CITATIONS
61	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. Nature, 2008, 456, 107-111.	13.7	150
62	Crystal structure of the ZP-N domain of ZP3 reveals the core fold of animal egg coats. Nature, 2008, 456, 653-657.	13.7	120
63	More complicated than it looks: assembly of Notch pathway transcription complexes. Oncogene, 2008, 27, 5099-5109.	2.6	139
64	Understanding the molecular machinery of genetics through 3D structures. Nature Reviews Genetics, 2008, 9, 141-151.	7.7	69
65	Structure and functional properties of the <i>Bacillus subtilis</i> transcriptional repressor Rex. Molecular Microbiology, 2008, 69, 466-478.	1.2	134
66	Comprehensive inventory of protein complexes in the Protein Data Bank from consistent classification of interfaces. BMC Bioinformatics, 2008, 9, 234.	1.2	26
67	Crystal structure of the ternary FimCâ€“FimF_tâ€“FimD_N complex indicates conserved pilus chaperoneâ€“subunit complex recognition by the usher FimD. FEBS Letters, 2008, 582, 651-655.	1.3	42
68	Xâ€•ray structure of the metalâ€•sensor CnrX in both the apoâ€•and copperâ€•bound forms. FEBS Letters, 2008, 582, 3954-3958.	1.3	20
69	A selective blocker of Kv1.2 and Kv1.3 potassium channels from the venom of the scorpion Centruroides suffusus suffusus. Biochemical Pharmacology, 2008, 76, 1142-1154.	2.0	46
70	A double mutation of MBP83â€“99 peptide induces IL-4 responses and antagonizes IFN-Î³ responses. Journal of Neuroimmunology, 2008, 200, 77-89.	1.1	34
71	Crystal structures of Toxoplasma gondii pterin-4a-carbinolamine dehydratase and comparisons with mammalian and parasite orthologues. Molecular and Biochemical Parasitology, 2008, 158, 131-138.	0.5	5
72	Crystal packing of a bacteriophage MS2 coat protein mutant corresponds to octahedral particles. Protein Science, 2008, 17, 1731-1739.	3.1	17
73	Thioredoxin as a fusion tag for carrierâ€•driven crystallization. Protein Science, 2008, 17, 2070-2079.	3.1	33
74	Proteinâ€“protein interaction and quaternary structure. Quarterly Reviews of Biophysics, 2008, 41, 133-180.	2.4	354
75	The leptospiral antigen Lp49 is a two-domain protein with putative protein binding function. Journal of Structural Biology, 2008, 163, 53-60.	1.3	11
76	Amyloid-Î²â€“Anti-Amyloid-Î² Complex Structure Reveals an Extended Conformation in the Immunodominant B-Cell Epitope. Journal of Molecular Biology, 2008, 377, 181-192.	2.0	49
77	Crystal Structures of the Clock Protein EA4 from the Silkworm Bombyx mori. Journal of Molecular Biology, 2008, 377, 630-635.	2.0	26
78	Structural Insights into Rice BGlu1 Î²-Glucosidase Oligosaccharide Hydrolysis and Transglycosylation. Journal of Molecular Biology, 2008, 377, 1200-1215.	2.0	77

#	ARTICLE	IF	CITATIONS
79	The Crystal Structure of Î²-Alanine Synthase from Drosophila melanogaster Reveals a Homooctameric Helical Turn-Like Assembly. Journal of Molecular Biology, 2008, 377, 1544-1559.	2.0	35
80	The Crystal Structure of DehI Reveals a New Î±-Haloacid Dehalogenase Fold and Active-Site Mechanism. Journal of Molecular Biology, 2008, 378, 284-294.	2.0	48
81	Crystal Structure of the Peptidoglycan Recognition Protein at 1.8ÂÃ… Resolution Reveals Dual Strategy to Combat Infection Through Two Independent Functional Homodimers. Journal of Molecular Biology, 2008, 378, 923-932.	2.0	14
82	Snapshots of a Y-Family DNA Polymerase in Replication: Substrate-induced Conformational Transitions and Implications for Fidelity of Dpo4. Journal of Molecular Biology, 2008, 379, 317-330.	2.0	86
83	Structural Analysis of the Saf Pilus by Electron Microscopy and Image Processing. Journal of Molecular Biology, 2008, 379, 174-187.	2.0	31
84	A Putative Î±-Helical Porin from Corynebacterium glutamicum. Journal of Molecular Biology, 2008, 379, 482-491.	2.0	31
85	Structure of an Fabâ€“Protease Complex Reveals a Highly Specific Non-canonical Mechanism of Inhibition. Journal of Molecular Biology, 2008, 380, 351-360.	2.0	55
86	Structure and Mode of Action of a Mosquitocidal Holotoxin. Journal of Molecular Biology, 2008, 381, 150-159.	2.0	39
87	Statistical Analysis of Interface Similarity in Crystals of Homologous Proteins. Journal of Molecular Biology, 2008, 381, 487-507.	2.0	102
88	Dissecting NGF Interactions with TrkA and p75 Receptors by Structural and Functional Studies of an Anti-NGF Neutralizing Antibody. Journal of Molecular Biology, 2008, 381, 881-896.	2.0	43
89	The Crystal Structure of CHIR-AB1: A Primordial Avian Classical Fc Receptor. Journal of Molecular Biology, 2008, 381, 1012-1024.	2.0	30
90	Structural and Kinetic Properties of a Î²-Hydroxyacid Dehydrogenase Involved in Nicotinate Fermentation. Journal of Molecular Biology, 2008, 382, 802-811.	2.0	11
91	Crystal Structure of the Ig1 Domain of the Neural Cell Adhesion Molecule NCAM2 Displays Domain Swapping. Journal of Molecular Biology, 2008, 382, 1113-1120.	2.0	7
92	C4-Dicarboxylates Sensing Mechanism Revealed by the Crystal Structures of DctB Sensor Domain. Journal of Molecular Biology, 2008, 383, 49-61.	2.0	75
93	Structure of Staphylococcus aureus EsxA Suggests a Contribution to Virulence by Action as a Transport Chaperone and/or Adaptor Protein. Journal of Molecular Biology, 2008, 383, 603-614.	2.0	70
94	The Crystal Structure of Enamidase: A Bifunctional Enzyme of the Nicotinate Catabolism. Journal of Molecular Biology, 2008, 384, 837-847.	2.0	7
95	Three-dimensional Structures of Pseudomonas aeruginosa PvcA and PvcB, Two Proteins Involved in the Synthesis of 2-Isocyano-6,7-dihydroxycoumarin. Journal of Molecular Biology, 2008, 384, 193-205.	2.0	34
96	Crystal Structure of the Arginine Repressor Protein in Complex with the DNA Operator from Mycobacterium tuberculosis. Journal of Molecular Biology, 2008, 384, 1330-1340.	2.0	17

#	Article	IF	Citations
97	Specificity and Reactivity in Menaquinone Biosynthesis: The Structure of Escherichia coli MenD (2-Succinyl-5-Enolpyruvyl-6-Hydroxy-3-Cyclohexadiene-1-Carboxylate Synthase). Journal of Molecular Biology, 2008, 384, 1353-1368.	2.0	39
98	A Fence-like Coat for the Nuclear Pore Membrane. Molecular Cell, 2008, 32, 815-826.	4.5	117
99	Mannosylation of mutated MBP83â€"99 peptides diverts immune responses from Th1 to Th2. Molecular Immunology, 2008, 45, 3661-3670.	1.0	32
100	A Bony Fish Immunological Receptor of the NITR Multigene Family Mediates Allogeneic Recognition. Immunity, 2008, 29, 228-237.	6.6	42
101	Implications for Kinetochore-Microtubule Attachment from the Structure of an Engineered Ndc80 Complex. Cell, 2008, 133, 427-439.	13.5	479
102	Dissecting proteinâ€"RNA recognition sites. Nucleic Acids Research, 2008, 36, 2705-2716.	6.5	108
103	Role of a Conserved Glutamine Residue in Tuning the Catalytic Activity of <i>Escherichia coli</i> Cytochrome <i>c</i> Nitrite Reductase. Biochemistry, 2008, 47, 3789-3799.	1.2	36
104	Crystallography and proteinâ€"protein interactions: biological interfaces and crystal contacts. Biochemical Society Transactions, 2008, 36, 1438-1441.	1.6	61
105	The Protein Data Bank (PDB), Its Related Services and Software Tools as Key Components for In Silico Guided Drug Discovery. Journal of Medicinal Chemistry, 2008, 51, 7021-7040.	2.9	91
106	Regulation of Protein Function: Crystal Packing Interfaces and Conformational Dimerization. Biochemistry, 2008, 47, 6583-6589.	1.2	20
107	Designed Protein-Protein Association. Science, 2008, 319, 206-209.	6.0	127
108	Changes at the KinA PAS-A Dimerization Interface Influence Histidine Kinase Function[,]. Biochemistry, 2008, 47, 4051-4064.	1.2	59
109	Structural and Functional Characterization of the C-Terminal Domain of the Ecdysteroid Phosphate Phosphatase from <i>Bombyx mori</i> Reveals a New Enzymatic Activity. Biochemistry, 2008, 47, 12135-12145.	1.2	14
110	Changes in Quaternary Structure in the Signaling Mechanisms of PAS Domains[,]. Biochemistry, 2008, 47, 12078-12086.	1.2	45
111	A Covalent Linker Allows for Membrane Targeting of an Oxylipin Biosynthetic Complex. Biochemistry, 2008, 47, 10665-10676.	1.2	13
112	The Structure of FSTL3Â·Activin A Complex. Journal of Biological Chemistry, 2008, 283, 32831-32838.	1.6	63
113	Crystal Structure of Fosfomycin Resistance Kinase FomA from Streptomyces wedmorensis. Journal of Biological Chemistry, 2008, 283, 28518-28526.	1.6	23
114	PilF Is an Outer Membrane Lipoprotein Required for Multimerization and Localization of the<i>Pseudomonas aeruginosa</i>Type IV Pilus Secretin. Journal of Bacteriology, 2008, 190, 6961-6969.	1.0	97

#	Article	IF	Citations
115	Binding to DNA of the RNA-polymerase II C-terminal domain allows discrimination between Cdk7 and Cdk9 phosphorylation. Nucleic Acids Research, 2008, 37, 1260-1268.	6.5	18
116	Crystal Structure of the FeS Clusterâ€"Containing Nucleotide Excision Repair Helicase XPD. PLoS Biology, 2008, 6, e149.	2.6	195
117	Crystal Structures of F420-dependent Glucose-6-phosphate Dehydrogenase FGD1 Involved in the Activation of the Anti-tuberculosis Drug Candidate PA-824 Reveal the Basis of Coenzyme and Substrate Binding. Journal of Biological Chemistry, 2008, 283, 17531-17541.	1.6	79
118	A survey of available tools and web servers for analysis of protein-protein interactions and interfaces. Briefings in Bioinformatics, 2008, 10, 217-232.	3.2	140
119	Crystal Structure of Human Liver Î"4-3-Ketosteroid 5Î²-Reductase (AKR1D1) and Implications for Substrate Binding and Catalysis. Journal of Biological Chemistry, 2008, 283, 16830-16839.	1.6	67
120	The Crystal Structure of the Human Toll-like Receptor 10 Cytoplasmic Domain Reveals a Putative Signaling Dimer. Journal of Biological Chemistry, 2008, 283, 11861-11865.	1.6	171
121	Structural Basis of Human Triosephosphate Isomerase Deficiency. Journal of Biological Chemistry, 2008, 283, 23254-23263.	1.6	68
122	Identification of Noncollagenous Sites Encoding Specific Interactions and Quaternary Assembly of Î±3Î±4Î±5(IV) Collagen. Journal of Biological Chemistry, 2008, 283, 35070-35077.	1.6	13
123	Structure and Evolution of a Novel Dimeric Enzyme from a Clinically Important Bacterial Pathogen. Journal of Biological Chemistry, 2008, 283, 27598-27603.	1.6	85
124	Crystal Structure of Human Plasma Platelet-activating Factor Acetylhydrolase. Journal of Biological Chemistry, 2008, 283, 31617-31624.	1.6	77
125	Structure and Function of Sedoheptulose-7-phosphate Isomerase, a Critical Enzyme for Lipopolysaccharide Biosynthesis and a Target for Antibiotic Adjuvants. Journal of Biological Chemistry, 2008, 283, 2835-2845.	1.6	63
126	Structural Insight into Bioremediation of Triphenylmethane Dyes by Citrobacter sp. Triphenylmethane Reductase. Journal of Biological Chemistry, 2008, 283, 31981-31990.	1.6	36
127	Structural and functional analysis of AsbF: Origin of the stealth 3,4-dihydroxybenzoic acid subunit for petrobactin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17133-17138.	3.3	58
128	Structural Analysis of a Periplasmic Binding Protein in the Tripartite ATP-independent Transporter Family Reveals a Tetrameric Assembly That May Have a Role in Ligand Transport. Journal of Biological Chemistry, 2008, 283, 32812-32820.	1.6	27
129	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological proteinâ€"protein interactions. Bioinformatics, 2008, 24, 652-658.	1.8	83
130	The Cysteine-Rich Interdomain Region from the Highly Variable Plasmodium falciparum Erythrocyte Membrane Protein-1 Exhibits a Conserved Structure. PLoS Pathogens, 2008, 4, e1000147.	2.1	46
131	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2â€"Like Fold but Have Evolved to Inhibit NF-Î°B rather than Apoptosis. PLoS Pathogens, 2008, 4, e1000128.	2.1	136
132	FutA2 Is a Ferric Binding Protein from Synechocystis PCC 6803. Journal of Biological Chemistry, 2008, 283, 12520-12527.	1.6	56

#	ARTICLE	IF	CITATIONS
133	Structure of the DNA Repair Helicase Hel308 Reveals DNA Binding and Autoinhibitory Domains. Journal of Biological Chemistry, 2008, 283, 5118-5126.	1.6	81
134	The C-terminal region of Ge-1 presents conserved structural features required for P-body localization. Rna, 2008, 14, 1991-1998.	1.6	30
135	Crystal structure and kinetic study of dihydrodipicolinate synthase from <i>Mycobacterium tuberculosis</i>. Biochemical Journal, 2008, 411, 351-360.	1.7	74
136	The Crystal Structure of the Periplasmic Domain of the Escherichia coli Membrane Protein Insertase YidC Contains a Substrate Binding Cleft. Journal of Biological Chemistry, 2008, 283, 9350-9358.	1.6	55
137	Insights into the Catalytic Mechanism of Tyrosine Phenol-lyase from X-ray Structures of Quinonoid Intermediates. Journal of Biological Chemistry, 2008, 283, 29206-29214.	1.6	31
138	Crystal Structure of the Avian Reovirus Inner Capsid Protein ÏƒA. Journal of Virology, 2008, 82, 11208-11216.	1.5	20
139	PixE promotes dark oligomerization of the BLUF photoreceptor PixD. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11715-11719.	3.3	62
140	Molecular Dynamics Characterization of Protein Crystal Contacts in Aqueous Solutions. Physical Review Letters, 2008, 101, 248102.	2.9	38
141	Crystal Structure and Carbohydrate Analysis of Nipah Virus Attachment Glycoprotein: a Template for Antiviral and Vaccine Design. Journal of Virology, 2008, 82, 11628-11636.	1.5	109
142	Discrimination between biological interfaces and crystal-packing contacts. Advances and Applications in Bioinformatics and Chemistry, 2008, 1, 99.	1.6	23
143	Computational Structural Analysis: Multiple Proteins Bound to DNA. PLoS ONE, 2008, 3, e3243.	1.1	10
144	Mycobacterium tuberculosis Glucosyl-3-Phosphoglycerate Synthase: Structure of a Key Enzyme in Methylglucose Lipopolysaccharide Biosynthesis. PLoS ONE, 2008, 3, e3748.	1.1	21
145	Intervening with Urinary Tract Infections Using Anti-Adhesives Based on the Crystal Structure of the FimHâ€“Oligomannose-3 Complex. PLoS ONE, 2008, 3, e2040.	1.1	202
147	Optimized Null Model for Protein Structure Networks. PLoS ONE, 2009, 4, e5967.	1.1	34
148	The Crystal Structure of the Escherichia coli Autoinducer-2 Processing Protein LsrF. PLoS ONE, 2009, 4, e6820.	1.1	14
149	Bioinformatics and Structural Characterization of a Hypothetical Protein from Streptococcus mutans: Implication of Antibiotic Resistance. PLoS ONE, 2009, 4, e7245.	1.1	16
150	Dual roles of Lys57 at the dimer interface of human mitochondrial NAD(P)+-dependent malic enzyme. Biochemical Journal, 2009, 420, 201-209.	1.7	8
151	Structural and Biochemical Characterization of the Wild Type PCSK9-EGF(AB) Complex and Natural Familial Hypercholesterolemia Mutants. Journal of Biological Chemistry, 2009, 284, 1313-1323.	1.6	112

#	Article	IF	Citations
152	Chaperones of F1-ATPase. Journal of Biological Chemistry, 2009, 284, 17138-17146.	1.6	28
153	An Asymmetric Model for Na+-translocating Glutaconyl-CoA Decarboxylases. Journal of Biological Chemistry, 2009, 284, 28401-28409.	1.6	12
154	High-Affinity IgE Recognition of a Conformational Epitope of the Major Respiratory Allergen Phl p 2 As Revealed by X-Ray Crystallography. Journal of Immunology, 2009, 182, 2141-2151.	0.4	104
155	Crystal Structure and Function of a DARPin Neutralizing Inhibitor of Lactococcal Phage TP901-1. Journal of Biological Chemistry, 2009, 284, 30718-30726.	1.6	55
156	Identification and structural analysis of type I collagen sites in complex with fibronectin fragments. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4195-4200.	3.3	77
157	Crystal structure of the catalytic domain of the tumor-associated human carbonic anhydrase IX. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16233-16238.	3.3	451
158	Structure of the vesicular stomatitis virus nucleocapsid in complex with the nucleocapsid-binding domain of the small polymerase cofactor, P. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11713-11718.	3.3	107
159	Complex Structure of Bacillus subtilis RibG. Journal of Biological Chemistry, 2009, 284, 1725-1731.	1.6	13
160	Structural Insight into the Activation Mechanism of Human Pancreatic Prophospholipase A2. Journal of Biological Chemistry, 2009, 284, 16659-16666.	1.6	25
161	Crystal Structure of Procaspase-1 Zymogen Domain Reveals Insight into Inflammatory Caspase Autoactivation. Journal of Biological Chemistry, 2009, 284, 6546-6553.	1.6	74
162	Molecular Mimicry in Innate Immunity. Journal of Biological Chemistry, 2009, 284, 21386-21392.	1.6	75
163	The structure of CrgA from Neisseria meningitidis reveals a new octameric assembly state for LysR transcriptional regulators. Nucleic Acids Research, 2009, 37, 4545-4558.	6.5	64
164	Model for eukaryotic tail-anchored protein binding based on the structure of Get3. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14849-14854.	3.3	82
165	Crystal structure of KorA bound to operator DNA: insight into repressor cooperation in RP4 gene regulation. Nucleic Acids Research, 2009, 37, 1915-1924.	6.5	21
166	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. Journal of Virology, 2009, 83, 12895-12906.	1.5	115
167	Architectural Nucleoporins Nup157/170 and Nup133 Are Structurally Related and Descend from a Second Ancestral Element. Journal of Biological Chemistry, 2009, 284, 28442-28452.	1.6	75
168	Dimerization and Protein Binding Specificity of the U2AF Homology Motif of the Splicing Factor Puf60. Journal of Biological Chemistry, 2009, 284, 630-639.	1.6	59
169	Crystal packing analysis of murine VDAC1 crystals in a lipidic environment reveals novel insights on oligomerization and orientation. Channels, 2009, 3, 167-170.	1.5	42

#	ARTICLE	IF	CITATIONS
170	The nature of the TRAPâ€“Anti-TRAP complex. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2176-2181.	3.3	27
171	Intrinsic Disorder in Protein Interactions: Insights From a Comprehensive Structural Analysis. PLoS Computational Biology, 2009, 5, e1000316.	1.5	104
172	ATP and MO25Î± Regulate the Conformational State of the STRADÎ± Pseudokinase and Activation of the LKB1 Tumour Suppressor. PLoS Biology, 2009, 7, e1000126.	2.6	118
173	Dimerization of Hepatitis E Virus Capsid Protein E2s Domain Is Essential for Virusâ€“Host Interaction. PLoS Pathogens, 2009, 5, e1000537.	2.1	123
174	Crystal structure of native RPE65, the retinoid isomerase of the visual cycle. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17325-17330.	3.3	140
175	Heme uptake across the outer membrane as revealed by crystal structures of the receptorâ€“hemophore complex. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1045-1050.	3.3	149
176	Extensive DNA mimicry by the ArdA anti-restriction protein and its role in the spread of antibiotic resistance. Nucleic Acids Research, 2009, 37, 4887-4897.	6.5	117
177	Crystal Structure of a Mammalian CTP: Phosphocholine Cytidylyltransferase Catalytic Domain Reveals Novel Active Site Residues within a Highly Conserved Nucleotidyltransferase Fold. Journal of Biological Chemistry, 2009, 284, 33535-33548.	1.6	51
178	Crystal Structures of YkuI and Its Complex with Second Messenger Cyclic Di-GMP Suggest Catalytic Mechanism of Phosphodiester Bond Cleavage by EAL Domains. Journal of Biological Chemistry, 2009, 284, 13174-13184.	1.6	96
179	Crystal structure and assembly of the functional Nanoarchaeum equitans tRNA splicing endonuclease. Nucleic Acids Research, 2009, 37, 5793-5802.	6.5	25
180	Crystal Structure of the N-terminal Domain of Anaphase-promoting Complex Subunit 7. Journal of Biological Chemistry, 2009, 284, 15137-15146.	1.6	20
181	The sequenceâ€“structure relationship and protein function prediction. Current Opinion in Structural Biology, 2009, 19, 357-362.	2.6	99
182	Fold space unlimited. Current Opinion in Structural Biology, 2009, 19, 312-320.	2.6	20
183	Structural and Biophysical Studies of the Human IL-7/IL-7RÎ± Complex. Structure, 2009, 17, 54-65.	1.6	77
184	Structural Analysis of the GGDEF-EAL Domain-Containing c-di-GMP Receptor FimX. Structure, 2009, 17, 1104-1116.	1.6	161
185	Structural Plasticity of Eph Receptor A4 Facilitates Cross-Class Ephrin Signaling. Structure, 2009, 17, 1386-1397.	1.6	86
186	Predicting protein-protein binding sites in membrane proteins. BMC Bioinformatics, 2009, 10, 312.	1.2	31
187	Crystal structure of a soluble decoy receptor ILâ€22BP bound to interleukinâ€22. FEBS Letters, 2009, 583, 1072-1077.	1.3	50

#	ARTICLE	IF	CITATIONS
188	The crystal structure of a hyperthermoactive exopolygalacturonase from <i>Thermotoga maritima</i> reveals a unique tetramer. FEBS Letters, 2009, 583, 3665-3670.	1.3	27
189	Metalâ€Mediated Selfâ€Assembly of a Î²â€Sandwich Protein. Chemistry - A European Journal, 2009, 15, 12672-12680.	1.7	7
190	Structural modeling and biochemical studies reveal insights into the molecular basis of the recognition of <i>Î²</i>â€2â€microglobulin by antibody BBM.1. Journal of Molecular Recognition, 2009, 22, 465-473.	1.1	3
191	Domainâ€"ligand mapping for enzymes. Journal of Molecular Recognition, 2010, 23, 194-208.	1.1	6
192	Modification of protein crystal packing by systematic mutations of surface residues: Implications on biotemplating and crystal porosity. Biotechnology and Bioengineering, 2009, 104, 444-457.	1.7	13
193	X-Ray crystal structure of GarRâ€"tartronate semialdehyde reductase from SalmonellaÂtyphimurium. Journal of Structural and Functional Genomics, 2009, 10, 249-253.	1.2	12
194	The three-dimensional structure of diaminopimelate decarboxylase from Mycobacterium tuberculosis reveals a tetrameric enzyme organisation. Journal of Structural and Functional Genomics, 2009, 10, 209-217.	1.2	14
195	Data Deposition and Annotation at the Worldwide Protein Data Bank. Molecular Biotechnology, 2009, 42, 1-13.	1.3	113
196	Structural insight into function and regulation of carnitine palmitoyltransferase. Cellular and Molecular Life Sciences, 2009, 66, 2489-2501.	2.4	59
197	The ATP-binding cassette family: a structural perspective. Cellular and Molecular Life Sciences, 2009, 66, 3111-3126.	2.4	92
198	The crystal structure of the protein YhaK from <i>Escherichia coli</i> reveals a new subclass of redox sensitive enterobacterial bicupins. Proteins: Structure, Function and Bioinformatics, 2009, 74, 18-31.	1.5	20
199	Crystal structure of the DUF54 family protein PH1010 from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> OT3. Proteins: Structure, Function and Bioinformatics, 2009, 74, 256-260.	1.5	1
200	Defining and characterizing protein surface using alpha shapes. Proteins: Structure, Function and Bioinformatics, 2009, 76, 1-12.	1.5	66
201	An unusually small dimer interface is observed in all available crystal structures of cytosolic sulfotransferases. Proteins: Structure, Function and Bioinformatics, 2009, 75, 289-295.	1.5	19
202	Crystal structure of a novel Smâ€like protein of putative cyanophage origin at 2.60 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2009, 75, 296-307.	1.5	18
203	Xâ€ray structure of <i>Danio rerio</i> secretagogin: A hexaâ€EFâ€hand calcium sensor. Proteins: Structure, Function and Bioinformatics, 2009, 76, 477-483.	1.5	22
204	Crystal structure of the <i>Bacillus anthracis</i> nucleoside diphosphate kinase and its characterization reveals an enzyme adapted to perform under stress conditions. Proteins: Structure, Function and Bioinformatics, 2009, 76, 496-506.	1.5	13
205	Crystal structure of TTHA1264, a putative M16â€family zinc peptidase from <i>Thermus thermophilus</i> HB8 that is homologous to the Î² subunit of mitochondrial processing peptidase. Proteins: Structure, Function and Bioinformatics, 2009, 75, 774-780.	1.5	13

#	Article	IF	Citations
206	Crystal structure of KaiCâ€like protein PH0186 from hyperthermophilic archaea <i>Pyrococcus horikoshii</i> OT3. Proteins: Structure, Function and Bioinformatics, 2009, 75, 1035-1039.	1.5	14
207	Combining interface core and whole interface descriptors in postscan processing of proteinâ€protein docking models. Proteins: Structure, Function and Bioinformatics, 2009, 77, 297-318.	1.5	16
208	Xâ€ray crystallographic studies of RNase A variants engineered at the most destabilizing positions of the main hydrophobic core: Further insight into protein stability. Proteins: Structure, Function and Bioinformatics, 2009, 77, 658-669.	1.5	7
209	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from <i>Ruminococcus flavefaciens</i>. Proteins: Structure, Function and Bioinformatics, 2009, 77, 699-709.	1.5	16
210	Assessment of ligand binding residue predictions in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 138-146.	1.5	36
211	The dimeric structure of <i>Sulfolobus solfataricus</i> thioredoxin A2 and the basis of its thermostability. Proteins: Structure, Function and Bioinformatics, 2009, 77, 1004-1008.	1.5	5
212	Mutations of key hydrophobic surface residues of 11Î²â€hydroxysteroid dehydrogenase type 1 increase solubility and monodispersity in a bacterial expression system. Protein Science, 2009, 18, 1552-1563.	3.1	10
213	Structure and electrostatic property of cytoplasmic domain of ZntB transporter. Protein Science, 2009, 18, 2043-2052.	3.1	15
214	Crystal structure of a 3B3 variantâ€"A broadly neutralizing HIVâ€1 scFv antibody. Protein Science, 2009, 18, 2429-2441.	3.1	16
215	The crystal structures of macrophage migration inhibitory factor from <i>Plasmodium falciparum</i> and <i>Plasmodium berghei</i>. Protein Science, 2009, 18, 2578-2591.	3.1	30
216	Structure and function of GlmU from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 275-283.	2.5	54
217	Structure of<i>Thermotoga maritima</i>TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn²⁺-binding FCD domains. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 356-365.	2.5	31
218	The F4 fimbrial chaperone FaeE is stable as a monomer that does not require self-capping of its pilin-interactive surfaces. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 411-420.	2.5	5
219	Structure of SRP14 from the<i>Schizosaccharomyces pombe</i>signal recognition particle. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 421-433.	2.5	10
220	Structure of the sporulation histidine kinase inhibitor Sda fromBacillus subtilisand insights into its solution state. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 574-581.	2.5	11
221	Structure of the C-terminal domain of nsp4 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 839-846.	2.5	23
222	Structure of the Calx-Î² domain of the integrin Î²4 subunit: insights into function and cation-independent stability. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 858-871.	2.5	33
223	Structure of the single-stranded DNA-binding protein fromStreptomyces coelicolor. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 974-979.	2.5	5

#	ARTICLE	IF	CITATIONS
224	The effect of a proline residue on the rate of growth and the space group of Î±-spectrin SH3-domain crystals. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1247-1252.	2.5	7
225	Structure of the X (ADRP) domain of nsp3 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1292-1300.	2.5	16
226	Structures of the apo and holo forms of formate dehydrogenase from the bacterium<i>Moraxella</i>sp. C-1: towards understanding the mechanism of the closure of the interdomain cleft. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1315-1325.	2.5	32
227	Structures of restriction endonuclease<i>Hin</i>dIII in complex with its cognate DNA and divalent cations. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1326-1333.	2.5	13
228	Structure of the twin-arginine signal-binding protein DmsD from<i>Escherichia coli</i>. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 746-750.	0.7	18
229	Crystallization and preliminary X-ray analysis of mannosyl-3-phosphoglycerate synthase from<i>Thermus thermophilus</i>HB27. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1014-1017.	0.7	5
230	Crystallization and preliminary X-ray diffraction analysis of crotoxin B from<i>Crotalus durissus collilineatus</i>venom. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1011-1013.	0.7	8
231	The high-resolution structure of the extracellular domain of human CD69 using a novel polymer. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1258-1260.	0.7	15
232	Structure of the first PDZ domain of human PSD-93. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1254-1257.	0.7	9
233	Structure of hypothetical Mo-cofactor biosynthesis protein B (ST2315) fromSulfolobus tokodaii. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1200-1203.	0.7	2
234	Structure of SurE protein fromAquifex aeolicusVF5 at 1.5â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1204-1208.	0.7	6
235	The structure of an archaeal ribose-5-phosphate isomerase from<i>Methanocaldococcus jannaschii</i>(MJ1603). Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1214-1217.	0.7	5
236	Structural and phylogenetic analysis of a conserved actinobacteria-specific protein (ASP1; SCO1997) from Streptomyces coelicolor. BMC Structural Biology, 2009, 9, 40.	2.3	10
237	Biochemical and structural characterization of alanine racemase from Bacillus anthracis (Ames). BMC Structural Biology, 2009, 9, 53.	2.3	32
238	The crystal structure of Haloferax volcanii proliferating cell nuclear antigen reveals unique surface charge characteristics due to halophilic adaptation. BMC Structural Biology, 2009, 9, 55.	2.3	40
239	Initial insight into the function of the lysosomal 66.3 kDa protein from mouse by means of X-ray crystallography. BMC Structural Biology, 2009, 9, 56.	2.3	16
240	Structural insight into the essential PB1â€“PB2 subunit contact of the influenza virus RNA polymerase. EMBO Journal, 2009, 28, 1803-1811.	3.5	167
241	Structure and function of a complex between chorismate mutase and DAHP synthase: efficiency boost for the junior partner. EMBO Journal, 2009, 28, 2128-2142.	3.5	52

#	ARTICLE	IF	CITATIONS
242	The structure of myostatin:follistatin 288: insights into receptor utilization and heparin binding. EMBO Journal, 2009, 28, 2662-2676.	3.5	148
243	The structure of an integrin/talin complex reveals the basis of inside-out signal transduction. EMBO Journal, 2009, 28, 3623-3632.	3.5	287
244	The structure of a cytolytic Î±-helical toxin pore reveals its assembly mechanism. Nature, 2009, 459, 726-730.	13.7	303
245	AcsD catalyzes enantioselective citrate desymmetrization in siderophore biosynthesis. Nature Chemical Biology, 2009, 5, 174-182.	3.9	67
246	Protein structure homology modeling using SWISS-MODEL workspace. Nature Protocols, 2009, 4, 1-13.	5.5	1,092
247	Molecular architecture of the Nup84â€"Nup145Câ€"Sec13 edge element in the nuclear pore complex lattice. Nature Structural and Molecular Biology, 2009, 16, 1173-1177.	3.6	79
248	Substitution of residues at the double dimer interface affects the stability and oligomerization of goose Î´â€crystallin. FEBS Journal, 2009, 276, 5126-5136.	2.2	2
249	A single intersubunit salt bridge affects oligomerization and catalytic activity in a bacterial quinone reductase. FEBS Journal, 2009, 276, 5263-5274.	2.2	35
250	Uneven twins: Comparison of two enantiocomplementary hydroxynitrile lyases with Î±/Î²-hydrolase fold. Journal of Biotechnology, 2009, 141, 166-173.	1.9	54
251	The 1.4ÂÃ… crystal structure of the large and cold-active Vibrio sp. alkaline phosphatase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 297-308.	1.1	48
252	Structural organization of WrbA in apo- and holoprotein crystals. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1288-1298.	1.1	13
253	Cloning and characterisation of dihydrodipicolinate synthase from the pathogen Neisseria meningitidis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1168-1174.	1.1	32
254	Crystal structure of a phospholipase A2 homolog complexed with p-bromophenacyl bromide reveals important structural changes associated with the inhibition of myotoxic activity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1583-1590.	1.1	33
255	Structural Redesign of Lipase B from Candida antarctica by Circular Permutation and Incremental Truncation. Journal of Molecular Biology, 2009, 393, 191-201.	2.0	61
256	Structure and Inhibition of Human Diamine Oxidase. Biochemistry, 2009, 48, 9810-9822.	1.2	95
257	Structure and Function of Bacillus subtilis YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif,. Biochemistry, 2009, 48, 8664-8671.	1.2	37
258	Dihydroorotase from the Hyperthermophile <i>Aquifiex aeolicus</i> Is Activated by Stoichiometric Association with Aspartate Transcarbamoylase and Forms a One-Pot Reactor for Pyrimidine Biosynthesis. Biochemistry, 2009, 48, 766-778.	1.2	36
259	Macrophage Scavenger Receptor A Mediates Adhesion to Apolipoproteins A-I and E. Biochemistry, 2009, 48, 11858-11871.	1.2	48

#	ARTICLE	IF	CITATIONS
260	The Structure of the UbcH8â[^]'Ubiquitin Complex Shows a Unique Ubiquitin Interaction Site. Biochemistry, 2009, 48, 12169-12179.	1.2	46
261	Structural Artifacts in Proteinâ[^]'Ligand X-ray Structures: Implications for the Development of Docking Scoring Functions. Journal of Medicinal Chemistry, 2009, 52, 5673-5684.	2.9	49
262	Ring1B Contains a Ubiquitin-Like Docking Module for Interaction with Cbx Proteins[,]. Biochemistry, 2009, 48, 10542-10548.	1.2	37
263	Impaired Protofibril Formation in Fibrinogen Î³N308K Is Due to Altered D:D and â€œA:aâ€•Interactions,. Biochemistry, 2009, 48, 8656-8663.	1.2	12
264	Control of Protein Oligomerization Symmetry by Metal Coordination: <i>C</i>₂ and <i>C</i>₃ Symmetrical Assemblies through Cu^{II} and Ni^{II} Coordination. Inorganic Chemistry, 2009, 48, 2726-2728.	1.9	73
265	Folding and Association of Thermophilic Dimeric and Trimeric DsrEFH Proteins: Tm0979 and Mth1491. Biochemistry, 2009, 48, 2891-2906.	1.2	12
266	Crystal Structure of Baeyerâ[^]'Villiger Monooxygenase MtmOIV, the Key Enzyme of the Mithramycin Biosynthetic Pathway,. Biochemistry, 2009, 48, 4476-4487.	1.2	75
267	Identification of continuous interaction sites in PLA2-based protein complexes by peptide arrays. Biochimie, 2009, 91, 1482-1492.	1.3	18
268	Structures of Asymmetric ClpX Hexamers Reveal Nucleotide-Dependent Motions in a AAA+ Protein-Unfolding Machine. Cell, 2009, 139, 744-756.	13.5	231
269	Openâ€“closed conformational change revealed by the crystal structures of 3-keto-l-gulonate 6-phosphate decarboxylase from Streptococcus mutans. Biochemical and Biophysical Research Communications, 2009, 381, 429-433.	1.0	1
270	The quaternary structure of Escherichia coli N-acetylneuraminate lyase is essential for functional expression. Biochemical and Biophysical Research Communications, 2009, 388, 107-111.	1.0	11
271	Structure of the Enterococcus faecalis EIIAgnt PTS component. Biochemical and Biophysical Research Communications, 2009, 388, 626-629.	1.0	5
272	Structureâ€“function relationships of the outer membrane translocon Wza investigated by cryo-electron microscopy and mutagenesis. Journal of Structural Biology, 2009, 166, 172-182.	1.3	15
273	Comparative structural studies on Lys49-phospholipases A2 from Bothrops genus reveal their myotoxic site. Journal of Structural Biology, 2009, 167, 106-116.	1.3	60
274	The dimer formed by the periplasmic domain of EpsL from the Type 2 Secretion System of Vibrio parahaemolyticus. Journal of Structural Biology, 2009, 168, 313-322.	1.3	44
275	Crystal Structure of the Resuscitation-Promoting Factor Î”DUFRpfB from M. tuberculosis. Journal of Molecular Biology, 2009, 385, 153-162.	2.0	72
276	Vancomycin Forms Ligand-Mediated Supramolecular Complexes. Journal of Molecular Biology, 2009, 385, 200-211.	2.0	38
277	Structure and Action of the Myxobacterial Chondrochloren Halogenase CndH: A New Variant of FAD-dependent Halogenases. Journal of Molecular Biology, 2009, 385, 520-530.	2.0	60

#	ARTICLE	IF	CITATIONS
278	Crystal Structure of SpoVT, the Final Modulator of Gene Expression during Spore Development in Bacillus subtilis. Journal of Molecular Biology, 2009, 386, 962-975.	2.0	18
279	Structural Base for Enzymatic Cyclodextrin Hydrolysis. Journal of Molecular Biology, 2009, 385, 606-617.	2.0	32
280	The Crystal Structure of ATP-bound Phosphofructokinase from Trypanosoma brucei Reveals Conformational Transitions Different from those of Other Phosphofructokinases. Journal of Molecular Biology, 2009, 385, 1519-1533.	2.0	38
281	Domain Organization in Clostridium botulinum Neurotoxin Type E Is Unique: Its Implication in Faster Translocation. Journal of Molecular Biology, 2009, 386, 233-245.	2.0	161
282	Conformations of NhaA, the Na/H Exchanger from Escherichia coli, in the pH-Activated and Ion-Translocating States. Journal of Molecular Biology, 2009, 386, 351-365.	2.0	40
283	Crystal Structures of Mite Allergens Der f 1 and Der p 1 Reveal Differences in Surface-Exposed Residues that May Influence Antibody Binding. Journal of Molecular Biology, 2009, 386, 520-530.	2.0	79
284	Crystal Structure of the IrrE Protein, a Central Regulator of DNA Damage Repair in Deinococcaceae. Journal of Molecular Biology, 2009, 386, 704-716.	2.0	70
285	Solution Structure of Human Î¶-COP: Direct Evidences for Structural Similarity between COP I and Clathrin-Adaptor Coats. Journal of Molecular Biology, 2009, 386, 903-912.	2.0	22
286	Structural and Functional Studies of the Biotin Protein Ligase from Aquifex aeolicus Reveal a Critical Role for a Conserved Residue in Target Specificity. Journal of Molecular Biology, 2009, 387, 129-146.	2.0	39
287	Structural Basis for Catalysis of a Tetrameric Class IIa Fructose 1,6-Bisphosphate Aldolase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2009, 386, 1038-1053.	2.0	38
288	Crystal Structures of Limulus SAP-Like Pentraxin Reveal Two Molecular Aggregations. Journal of Molecular Biology, 2009, 386, 1240-1254.	2.0	17
289	The Oligomeric Assembly of the Novel Haem-Degrading Protein HbpS Is Essential for Interaction with Its Cognate Two-Component Sensor Kinase. Journal of Molecular Biology, 2009, 386, 1108-1122.	2.0	22
290	First Inactive Conformation of CK2Î±, the Catalytic Subunit of Protein Kinase CK2. Journal of Molecular Biology, 2009, 386, 1212-1221.	2.0	30
291	Crystal Structure of the Full-Length Sorbitol Operon Regulator SorC from Klebsiella pneumoniae: Structural Evidence for a Novel Transcriptional Regulation Mechanism. Journal of Molecular Biology, 2009, 387, 759-770.	2.0	13
292	Crystal Structure of LipL32, the Most Abundant Surface Protein of Pathogenic Leptospira spp.. Journal of Molecular Biology, 2009, 387, 1229-1238.	2.0	53
293	The Structure of the Arginine Repressor from Mycobacterium tuberculosis Bound with its DNA Operator and Co-repressor, L-Arginine. Journal of Molecular Biology, 2009, 388, 85-97.	2.0	15
294	Erratum to â€œConformations of NhaA, the Na+/H+ Exchanger from Escherichia coli, in the pH-Activated and Ion-Translocating Statesâ€•[J. Mol. Biol. 386 (2009) 351â€“385]. Journal of Molecular Biology, 2009, 388, 659-672.	2.0	39
295	Insights into Positive and Negative Requirements for Proteinâ€“Protein Interactions by Crystallographic Analysis of the Î²-Lactamase Inhibitory Proteins BLIP, BLIP-I, and BLP. Journal of Molecular Biology, 2009, 389, 289-305.	2.0	35

#	ARTICLE	IF	CITATIONS
296	Structures of Glycinamide Ribonucleotide Transformylase (PurN) from Mycobacterium tuberculosis Reveal a Novel Dimer with Relevance to Drug Discovery. Journal of Molecular Biology, 2009, 389, 722-733.	2.0	15
297	An Ion-channel Modulator from the Saliva of the Brown Ear Tick has a Highly Modified Kunitz/BPTI Structure. Journal of Molecular Biology, 2009, 389, 734-747.	2.0	42
298	The Three-dimensional Structure of a Mycobacterial DapD Provides Insights into DapD Diversity and Reveals Unexpected Particulars about the Enzymatic Mechanism. Journal of Molecular Biology, 2009, 389, 863-879.	2.0	23
299	Contributions of Interfacial Residues of Human Interleukin15 to the Specificity and Affinity for Its Private Î±-Receptor. Journal of Molecular Biology, 2009, 389, 880-894.	2.0	19
300	The X-Ray Crystal Structure of the Phage Î» Tail Terminator Protein Reveals the Biologically Relevant Hexameric Ring Structure and Demonstrates a Conserved Mechanism of Tail Termination among Diverse Long-Tailed Phages. Journal of Molecular Biology, 2009, 389, 938-951.	2.0	55
301	Structure and Calcium-Binding Activity of LipL32, the Major Surface Antigen of Pathogenic Leptospira sp.. Journal of Molecular Biology, 2009, 390, 722-736.	2.0	41
302	The Crystal Structures of Human S100A12 in Apo Form and in Complex with Zinc: New Insights into S100A12 Oligomerisation. Journal of Molecular Biology, 2009, 391, 536-551.	2.0	90
303	Intermodular Linker Flexibility Revealed from Crystal Structures of Adjacent Cellulosomal Cohesins of Acetivibrio cellulolyticus. Journal of Molecular Biology, 2009, 391, 86-97.	2.0	23
304	Dimer Interface Migration in a Viral Sulfhydryl Oxidase. Journal of Molecular Biology, 2009, 391, 758-768.	2.0	26
305	Crystal Structure of Miner1: The Redox-active 2Fe-2S Protein Causative in Wolfram Syndrome 2. Journal of Molecular Biology, 2009, 392, 143-153.	2.0	110
306	The Structural Basis of Î²-Peptide-Specific Cleavage by the Serine Protease Cyanophycinase. Journal of Molecular Biology, 2009, 392, 393-404.	2.0	22
307	Structure and Function of the FeoB G-Domain from Methanococcus jannaschii. Journal of Molecular Biology, 2009, 392, 405-419.	2.0	27
308	Crystal Structure of the Frizzled-Like Cysteine-Rich Domain of the Receptor Tyrosine Kinase MuSK. Journal of Molecular Biology, 2009, 393, 1-9.	2.0	63
309	Crystal Structure of the Hexameric Catabolic Ornithine Transcarbamylase from Lactobacillus hilgardii: Structural Insights into the Oligomeric Assembly and Metal Binding. Journal of Molecular Biology, 2009, 393, 425-434.	2.0	17
310	Determinants for the Activation and Autoinhibition of the Diguanylate Cyclase Response Regulator WspR. Journal of Molecular Biology, 2009, 393, 619-633.	2.0	129
311	Structure of the Mature Streptococcal Cysteine Protease Exotoxin mSpeB in Its Active Dimeric Form. Journal of Molecular Biology, 2009, 393, 693-703.	2.0	15
312	Crystal Structure of the Antitoxinâ€“Toxin Protein Complex RelBâ€“RelE from Methanococcus jannaschii. Journal of Molecular Biology, 2009, 393, 898-908.	2.0	39
313	Periplasmic Domains of Pseudomonas aeruginosa PilN and PilO Form a Stable Heterodimeric Complex. Journal of Molecular Biology, 2009, 394, 143-159.	2.0	72

#	ARTICLE	IF	CITATIONS
314	Crystal Structures of the Histidine Acid Phosphatase from Francisella tularensis Provide Insight into Substrate Recognition. Journal of Molecular Biology, 2009, 394, 893-904.	2.0	12
315	Structure of the Yeast DEAD Box Protein Mss116p Reveals Two Wedges that Crimp RNA. Molecular Cell, 2009, 35, 598-609.	4.5	125
316	Analysis of B-cell epitopes from the allergen Hev b 6.02 revealed by using blocking antibodies. Molecular Immunology, 2009, 46, 668-676.	1.0	11
317	The Î²Î³-Crystallin Superfamily Contains a Universal Motif for Binding Calcium[,]. Biochemistry, 2009, 48, 12180-12190.	1.2	63
319	Genome and proteome annotation: organization, interpretation and integration. Journal of the Royal Society Interface, 2009, 6, 129-147.	1.5	45
320	Structural insights into tail-anchored protein binding and membrane insertion by Get3. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21131-21136.	3.3	92
321	From Protein Structure to Function with Bioinformatics. , 2009, , .		29
322	High-Affinity Recognition of Lanthanide(III) Chelate Complexes by a Reprogrammed Human Lipocalin 2. Journal of the American Chemical Society, 2009, 131, 3565-3576.	6.6	59
323	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. Molecular BioSystems, 2009, 5, 1456.	2.9	8
324	Biomedical Informatics. Methods in Molecular Biology, 2009, 569, v.	0.4	1
325	The structure of CDK4/cyclin D3 has implications for models of CDK activation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4171-4176.	3.3	102
326	Structural Analysis of a Multifunctional, Tandemly Repeated Inositol Polyphosphatase. Journal of Molecular Biology, 2009, 392, 75-86.	2.0	15
327	Structure of the Notch1-negative regulatory region: implications for normal activation and pathogenic signaling in T-ALL. Blood, 2009, 113, 4381-4390.	0.6	154
328	Crystal structure of protein Zâ€“dependent inhibitor complex shows how protein Z functions as a cofactor in the membrane inhibition of factor X. Blood, 2009, 114, 3662-3667.	0.6	44
329	Crystal Structure of Bucain, a Three-Fingered Toxin from the Venom of the Malayan Krait (Bungarus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	7
330	Influence of Quaternary Conformation on the Biological Activities of the Asp49-phospholipases A2s from Snake Venoms. Protein and Peptide Letters, 2009, 16, 852-859.	0.4	15
331	The Intriguing Phospholipases A2 Homologues: Relevant Structural Features on Myotoxicity and Catalytic Inactivity. Protein and Peptide Letters, 2009, 16, 887-893.	0.4	25
332	Role of a PA14 domain in determining substrate specificity of a glycoside hydrolase family 3 Î²-glucosidase from <i>Kluyveromyces marxianus</i>. Biochemical Journal, 2010, 431, 39-49.	1.7	102

#	ARTICLE	IF	CITATIONS
333	Structure of an Ebf1:DNA complex reveals unusual DNA recognition and structural homology with Rel proteins. Genes and Development, 2010, 24, 2270-2275.	2.7	47
334	Crystal structure and collagen-binding site of immune inhibitory receptor LAIR-1: unexpected implications for collagen binding by platelet receptor GPVI. Blood, 2010, 115, 1364-1373.	0.6	62
335	Crystal structure of the human transcription elongation factor DSIF hSpt4 subunit in complex with the hSpt5 dimerization interface. Biochemical Journal, 2010, 425, 373-380.	1.7	23
336	RING domain dimerization is essential for RNF4 function. Biochemical Journal, 2010, 431, 23-29.	1.7	80
337	Structure at 1.0 Ã… resolution of a high-potential ironâ€"sulfur protein involved in the aerobic respiratory chain of Rhodothermus marinus. Journal of Biological Inorganic Chemistry, 2010, 15, 303-313.	1.1	20
338	Protein subunit interfaces: a statistical analysis of hot spots in Sm proteins. Journal of Molecular Modeling, 2010, 16, 1743-1751.	0.8	6
339	Cloning, Overexpression, Purification and Preliminary Characterization of Human Septin 8. Protein Journal, 2010, 29, 328-335.	0.7	2
340	Structure of Trypanosoma brucei glutathione synthetase: Domain and loop alterations in the catalytic cycle of a highly conserved enzyme. Molecular and Biochemical Parasitology, 2010, 170, 93-99.	0.5	11
341	Crystal Structure of the APOBEC3G Catalytic Domain Reveals Potential Oligomerization Interfaces. Structure, 2010, 18, 28-38.	1.6	116
342	A TNF-like Trimeric Lectin Domain from Burkholderia cenocepacia with Specificity for Fucosylated Human Histo-Blood Group Antigens. Structure, 2010, 18, 59-72.	1.6	76
343	AlgK Is a TPR-Containing Protein and the Periplasmic Component of a Novel Exopolysaccharide Secretin. Structure, 2010, 18, 265-273.	1.6	98
344	Structure of the GLD-1 Homodimerization Domain: Insights into STAR Protein-Mediated Translational Regulation. Structure, 2010, 18, 377-389.	1.6	23
345	Molecular Basis for Shared Cytokine Recognition Revealed in the Structure of an Unusually High Affinity Complex between IL-13 and IL-13RÎ±2. Structure, 2010, 18, 332-342.	1.6	121
346	A Single Mutation Promotes Amyloidogenicity through a Highly Promiscuous Dimer Interface. Structure, 2010, 18, 563-570.	1.6	42
347	Crystal Structure of an Intracellular Subtilisin Reveals Novel Structural Features Unique to this Subtilisin Family. Structure, 2010, 18, 744-755.	1.6	20
348	Molecular Basis for the Association of Human E4B U Box Ubiquitin Ligase with E2-Conjugating Enzymes UbcH5c and Ubc4. Structure, 2010, 18, 955-965.	1.6	45
349	Crystal Structures of Phd-Doc, HigA, and YeeU Establish Multiple Evolutionary Links between Microbial Growth-Regulating Toxin-Antitoxin Systems. Structure, 2010, 18, 996-1010.	1.6	65
350	Structure and Cellular Roles of the RMI Core Complex from the Bloom Syndrome Dissolvasome. Structure, 2010, 18, 1149-1158.	1.6	33

#	Article	IF	Citations
351	Folding, DNA Recognition, and Function of GIY-YIG Endonucleases: Crystal Structures of R.Eco29kI. Structure, 2010, 18, 1321-1331.	1.6	37
352	Crystal Structure of Group II Chaperonin in the Open State. Structure, 2010, 18, 1270-1279.	1.6	38
353	MoDEL (Molecular Dynamics Extended Library): AÂDatabase of Atomistic Molecular Dynamics Trajectories. Structure, 2010, 18, 1399-1409.	1.6	123
354	WD40 proteins propel cellular networks. Trends in Biochemical Sciences, 2010, 35, 565-574.	3.7	518
355	ATP-dependent MurE ligase in Mycobacterium tuberculosis: Biochemical and structural characterisation. Tuberculosis, 2010, 90, 16-24.	0.8	49
356	Structural characterization of a family of cytochromes c7 involved in Fe(III) respiration by Geobacter sulfurreducens. Biochimica Et Biophysica Acta - Bioenergetics, 2010, 1797, 222-232.	0.5	59
357	Structure of the GTPase and GDI domains of FeoB, the ferrous iron transporter of <i>Legionella pneumophila</i>. FEBS Letters, 2010, 584, 733-738.	1.3	25
358	Structure of translation initiation factor 1 from <i>Mycobacterium tuberculosis</i> and inferred binding to the 30S ribosomal subunit. FEBS Letters, 2010, 584, 1011-1015.	1.3	11
359	A disulfide driven domain swap switches off the activity of <i>Shigella</i> IpaH9.8 E3 ligase. FEBS Letters, 2010, 584, 4163-4168.	1.3	31
360	Crystal contacts as nature's docking solutions. Journal of Computational Chemistry, 2010, 31, 133-143.	1.5	282
361	Biocatalysis with Thermostable Enzymes: Structure and Properties of a Thermophilic â€˜eneâ€™â€Reductase related to Old Yellow Enzyme. ChemBioChem, 2010, 11, 197-207.	1.3	110
362	Recent developments in cyclin-dependent kinase biochemical and structural studies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 511-519.	1.1	96
363	Structure and catalytic mechanism of the Î²-carbonic anhydrases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 362-373.	1.1	138
364	Structural Characterization of Acylimine-Containing Blue and Red Chromophores in mTagBFP and TagRFP Fluorescent Proteins. Chemistry and Biology, 2010, 17, 333-341.	6.2	98
365	Structural and Mechanistic Studies on Î³-Butyrobetaine Hydroxylase. Chemistry and Biology, 2010, 17, 1316-1324.	6.2	78
366	<i>AMINONET</i>â€" a tool to construct and visualize amino acid networks, and to calculate topological parameters. Journal of Applied Crystallography, 2010, 43, 367-369.	1.9	13
367	Structure of a family 3bâ€² carbohydrate-binding module from the Cel9V glycoside hydrolase from<i>Clostridium thermocellum</i>: structural diversity and implications for carbohydrate binding. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 33-43.	2.5	18
368	Structure of theMethanothermobacter thermautotrophicusexosome RNase PH ring. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 522-528.	2.5	7

#	ARTICLE	IF	CITATIONS
369	Structure of dehaloperoxidase B at 1.58â€…Ã… resolution and structural characterization of the AB dimer from<i>Amphitrite ornata</i>. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 529-538.	2.5	31
370	Structure determination of the minimal complex between Tfb5 and Tfb2, two subunits of the yeast transcription/DNA-repair factor TFIIH: a retrospective study. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 745-755.	2.5	4
371	The high-resolution structure of pig heart succinyl-CoA:3-oxoacid coenzyme A transferase. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 797-805.	2.5	8
372	Structure of the<i>Escherichia coli</i>RNA polymerase Î± subunit C-terminal domain. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 806-812.	2.5	10
373	Structures of apo and GTP-bound molybdenum cofactor biosynthesis protein MoaC from<i>Thermus thermophilus</i>HB8. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 821-833.	2.5	22
374	Structure of<i>Staphylococcus aureus</i>adenylosuccinate lyase (PurB) and assessment of its potential as a target for structure-based inhibitor discovery. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 881-888.	2.5	17
375	Structural and functional analysis of Rv0554 from<i>Mycobacterium tuberculosis</i>: testing a putative role in menaquinone biosynthesis. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 909-917.	2.5	12
376	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 979-987.	2.5	12
377	Crystallization of small proteins assisted by green fluorescent protein. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1059-1066.	2.5	31
378	Structural and biochemical analyses reveal a monomeric state of the bacterial lipocalin Blc. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1308-1315.	2.5	18
379	Conformational changes associated with the binding of zinc acetate at the putative active site ofXcTcmJ, a cupin fromXanthomonas campestrispv.campestris. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1347-1353.	0.7	5
380	Structure of an essential bacterial protein YeaZ (TM0874) from<i>Thermotoga maritima</i>at 2.5â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1230-1236.	0.7	17
381	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1211-1217.	0.7	10
382	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1205-1210.	0.7	3
383	The structure of Jann_2411 (DUF1470) from<i>Jannaschia</i>sp. at 1.45â€…Ã… resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1198-1204.	0.7	9
384	Structure of the first representative of Pfam family PF09410 (DUF2006) reveals a structural signature of the calycin superfamily that suggests a role in lipid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1153-1159.	0.7	18
385	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1245-1253.	0.7	8
386	Structures of the first representatives of Pfam family PF06938 (DUF1285) reveal a new fold with repeated structural motifs and possible involvement in signal transduction. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1218-1225.	0.7	8

#	Article	IF	Citations
387	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of theBacilluschorismate mutase fold and suggest a role in amino-acid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1182-1189.	0.7	3
388	A new crystal form of human diamine oxidase. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 137-142.	0.7	10
389	The structure of DinB from<i>Geobacillus stearothermophilus</i>: a representative of a unique four-helix-bundle superfamily. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 219-224.	0.7	14
390	A triclinic crystal form of<i>Escherichia coli</i>4-diphosphocytidyl-2<i>C</i>-methyl-<scp>D</scp>-erythritol kinase and reassessment of the quaternary structure. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 237-241.	0.7	11
391	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1160-1166.	0.7	20
392	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1167-1173.	0.7	3
393	Dramatic improvement of crystal quality for low-temperature-grown rabbit muscle aldolase. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 595-600.	0.7	1
394	The structure of PhaZ7 at atomic (1.2â€…Ã…) resolution reveals details of the active site and suggests a substrate-binding mode. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 648-654.	0.7	13
395	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved Î±+Î² core domain and an auxiliary C-terminal treble-clef zinc finger. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1335-1346.	0.7	8
396	Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 fromExiguobacterium sibiricum255-15. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1237-1244.	0.7	2
397	Near-atomic resolution analysis of BipD, a component of the type III secretion system of<i>Burkholderia pseudomallei</i>. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 990-993.	0.7	8
398	Structure of<i>Bacteroides thetaiotaomicron</i>BT2081 at 2.05â€…Ã… resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1287-1296.	0.7	2
399	High-resolution structure of an Î±-spectrin SH3-domain mutant with a redesigned hydrophobic core. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1023-1027.	0.7	3
400	Structural analysis of<i>Bacillus pumilus</i>phenolic acid decarboxylase, a lipocalin-fold enzyme. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1407-1414.	0.7	26
401	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1274-1280.	0.7	11
402	The homodimeric GBS1074 fromStreptococcus agalactiae. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1421-1425.	0.7	16
403	Structure of Hsp33/YOR391Cp from the yeastSaccharomyces cerevisiae. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1557-1561.	0.7	5
404	A biophysical elucidation for less toxicity of Agglutinin than Abrin-a from the Seeds of Abrus Precatorius in consequence of crystal structure. Journal of Biomedical Science, 2010, 17, 34.	2.6	23

#	ARTICLE	IF	CITATIONS
405	Evidence for alternative quaternary structure in a bacterial Type III secretion system chaperone. BMC Structural Biology, 2010, 10, 21.	2.3	18
406	Thermodynamic and structural insights into CSLâ€DNA complexes. Protein Science, 2010, 19, 34-46.	3.1	43
407	Structure of the catalytic domain of the human mitochondrial Lon protease: Proposed relation of oligomer formation and activity. Protein Science, 2010, 19, 987-999.	3.1	45
408	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. Protein Science, 2010, 19, 1031-1043.	3.1	264
409	The shortâ€chain oxidoreductase Q9HYA2 from <i>Pseudomonas aeruginosa</i> PAO1 contains an atypical catalytic center. Protein Science, 2010, 19, 1097-1103.	3.1	1
410	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. Protein Science, 2010, 19, 1439-1443.	3.1	12
411	The crystal structure of the <i>mycobacterium tuberculosis</i> Rv3019câ€Rv3020c ESX complex reveals a domainâ€swapped heterotetramer. Protein Science, 2010, 19, 1692-1703.	3.1	27
412	Crystal structure of human thioredoxin revealing an unraveled helix and exposed <i>Sâ€</i>nitrosation site. Protein Science, 2010, 19, 1801-1806.	3.1	24
413	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp23.1, a putative chaperone. Protein Science, 2010, 19, 1812-1816.	3.1	11
414	The crystal structure of a bacterial Sufuâ€like protein defines a novel group of bacterial proteins that are similar to the Nâ€terminal domain of human Sufu. Protein Science, 2010, 19, 2131-2140.	3.1	12
415	The structure and NO binding properties of the nitrophorinâ€like hemeâ€binding protein from <i>Arabidopsis thaliana</i> gene locus At1g79260.1. Proteins: Structure, Function and Bioinformatics, 2010, 78, 917-931.	1.5	49
416	Heterologous quaternary structure of CXCL12 and its relationship to the CC chemokine family. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1331-1337.	1.5	40
417	Amino acid substitutions at proteinâ€“protein interfaces that modulate the oligomeric state. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1563-1574.	1.5	12
418	Structure of human CLIC3 at 2 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1594-1600.	1.5	25
419	<i>p</i>â€Coumaric acid decarboxylase from <i>Lactobacillus plantarum</i>: Structural insights into the active site and decarboxylation catalytic mechanism. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1662-1676.	1.5	52
420	Structural investigation of transcriptional regulator HlyIIR: Influence of a disordered region on protein fold and dimerization. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1870-1877.	1.5	2
421	Crystal structure of an eIF4Gâ€like protein from <i>Danio rerio</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1803-1806.	1.5	2
422	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1992-1998.	1.5	13

#	ARTICLE	IF	CITATIONS
423	Crystal structures of holo and Cuâ€deficient Cu/Znâ€SOD from the silkworm <i>Bombyx mori</i> and the implications in amyotrophic lateral sclerosis. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1999-2004.	1.5	11
424	Structure and oligomerization of the PilC type IV pilus biogenesis protein from <i>Thermus thermophilus</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2049-2057.	1.5	49
425	Self-association of TPR domains: Lessons learned from a designed, consensus-based TPR oligomer. Proteins: Structure, Function and Bioinformatics, 2010, 78, NA-NA.	1.5	41
426	Structure of fullâ€length class I chitinase from rice revealed by Xâ€ray crystallography and smallâ€angle Xâ€ray scattering. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2295-2305.	1.5	48
427	CRK: An evolutionary approach for distinguishing biologically relevant interfaces from crystal contacts. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2707-2713.	1.5	27
428	Sideâ€chain rotamer transitions at proteinâ€protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	1.5	15
429	Structure of FocB â€“ a member of a family of transcription factors regulating fimbrial adhesin expression in uropathogenic <i>Escherichiaâ€ƒcoli</i>. FEBS Journal, 2010, 277, 3368-3381.	2.2	7
430	A coleopteran triosephosphate isomerase: Xâ€ray structure and phylogenetic impact of insect sequences. Insect Molecular Biology, 2010, 19, 35-48.	1.0	7
431	Structural studies on the fullâ€length LysRâ€<i>type</i> regulator TsaR from <i>Comamonas testosteroni</i> Tâ€2 reveal a novel open conformation of the tetrameric LTTR fold. Molecular Microbiology, 2010, 75, 1199-1214.	1.2	72
432	Structural basis of respiratory syncytial virus neutralization by motavizumab. Nature Structural and Molecular Biology, 2010, 17, 248-250.	3.6	156
433	The structure of the catalytic subunit FANCL of the Fanconi anemia core complex. Nature Structural and Molecular Biology, 2010, 17, 294-298.	3.6	65
434	How baculovirus polyhedra fit square pegs into round holes to robustly package viruses. EMBO Journal, 2010, 29, 505-514.	3.5	90
435	Structural basis for the function of DEAH helicases. EMBO Reports, 2010, 11, 180-186.	2.0	104
436	Structural basis for receptor recognition of vitamin-B12â€“intrinsic factor complexes. Nature, 2010, 464, 445-448.	13.7	100
437	Structural basis of semaphorinâ€“plexin signalling. Nature, 2010, 467, 1118-1122.	13.7	211
438	Visualization of macromolecular structures. Nature Methods, 2010, 7, S42-S55.	9.0	137
439	Phenotypic variability, neurological outcome and genetics background of 6â€pyruvoylâ€tetrahydropterin synthase deficiency. Clinical Genetics, 2010, 77, 249-257.	1.0	59
440	The Minimal Autoinhibited Unit of the Guanine Nucleotide Exchange Factor Intersectin. PLoS ONE, 2010, 5, e11291.	1.1	22

#	Article	IF	Citations
441	Crystal Structure of the RNA Recognition Motif of Yeast Translation Initiation Factor eIF3b Reveals Differences to Human eIF3b. PLoS ONE, 2010, 5, e12784.	1.1	11
442	Comparative Structural Analysis of Human DEAD-Box RNA Helicases. PLoS ONE, 2010, 5, e12791.	1.1	101
443	Structural profiling of endogenous S-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein S-nitrosylation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16958-16963.	3.3	236
444	Functional Differences of Invariant and Highly Conserved Residues in the Extracellular Domain of the Glycoprotein Hormone Receptors. Journal of Biological Chemistry, 2010, 285, 34813-34827.	1.6	15
445	Structure of the FoxM1 DNA-recognition domain bound to a promoter sequence. Nucleic Acids Research, 2010, 38, 4527-4538.	6.5	109
446	The mechanism and control of DNA transfer by the conjugative relaxase of resistance plasmid pCU1. Nucleic Acids Research, 2010, 38, 5929-5943.	6.5	25
447	Plastid-associated Porphobilinogen Synthase from Toxoplasma gondii. Journal of Biological Chemistry, 2010, 285, 22122-22131.	1.6	30
448	Implications of the HIV-1 Rev dimer structure at 3.2Ââ„« resolution for multimeric binding to the Rev response element. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5810-5814.	3.3	124
449	Identification, subcellular localization, biochemical properties, and high-resolution crystal structure of Trypanosoma brucei UDP-glucose pyrophosphorylase. Glycobiology, 2010, 20, 1619-1630.	1.3	30
450	Drug resistance against HCV NS3/4A inhibitors is defined by the balance of substrate recognition versus inhibitor binding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20986-20991.	3.3	176
451	Structural basis for substrate activation and regulation by cystathionine beta-synthase (CBS) domains in cystathionine Î²-synthase. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20958-20963.	3.3	341
452	High-Resolution X-Ray Structure and Functional Analysis of the Murine Norovirus 1 Capsid Protein Protruding Domain. Journal of Virology, 2010, 84, 5695-5705.	1.5	78
453	Structural and Kinetic Analysis of Free Methionine-R-sulfoxide Reductase from Staphylococcus aureus. Journal of Biological Chemistry, 2010, 285, 25044-25052.	1.6	13
454	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2010, 38, D308-D317.	6.5	108
455	Structural and functional characterization of the transcriptional repressor CsoR from Thermus thermophilus HB8. Microbiology (United Kingdom), 2010, 156, 1993-2005.	0.7	51
456	ZBP1 recognition of Î²-actin zipcode induces RNA looping. Genes and Development, 2010, 24, 148-158.	2.7	161
457	Crystallographic Structure of Porcine Adenovirus Type 4 Fiber Head and Galectin Domains. Journal of Virology, 2010, 84, 10558-10568.	1.5	19
458	Structure of the Nucleoprotein Binding Domain of Mokola Virus Phosphoprotein. Journal of Virology, 2010, 84, 1089-1096.	1.5	27

#	Article	IF	Citations
459	H-NS forms a superhelical protein scaffold for DNA condensation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15728-15732.	3.3	165
460	Structural Determination of Functional Domains in Early B-cell Factor (EBF) Family of Transcription Factors Reveals Similarities to Rel DNA-binding Proteins and a Novel Dimerization Motif. Journal of Biological Chemistry, 2010, 285, 25875-25879.	1.6	26
461	Global Conformational Change Associated with the Two-step Reaction Catalyzed by Escherichia coli Lipoate-Protein Ligase A. Journal of Biological Chemistry, 2010, 285, 9971-9980.	1.6	36
462	Structural Characterization of Apical Membrane Antigen 1 (AMA1) from Toxoplasma gondii. Journal of Biological Chemistry, 2010, 285, 15644-15652.	1.6	46
463	The N Domain of Human Angiotensin-I-converting Enzyme. Journal of Biological Chemistry, 2010, 285, 35685-35693.	1.6	76
464	Neuroplastinâ€55 binds to and signals through the fibroblast growth factor receptor. FASEB Journal, 2010, 24, 1139-1150.	0.2	48
465	Quality assessment of protein model-structures using evolutionary conservation. Bioinformatics, 2010, 26, 1299-1307.	1.8	46
466	Symmetry versus Asymmetry in the Molecules of Life: Homomeric Protein Assemblies. Symmetry, 2010, 2, 884-906.	1.1	19
467	ComSin: database of protein structures in bound (complex) and unbound (single) states in relation to their intrinsic disorder. Nucleic Acids Research, 2010, 38, D283-D287.	6.5	31
468	Crystal structure of the P2 C-repressor: a binder of non-palindromic direct DNA repeats. Nucleic Acids Research, 2010, 38, 7778-7790.	6.5	10
469	PyETV: a PyMOL evolutionary trace viewer to analyze functional site predictions in protein complexes. Bioinformatics, 2010, 26, 2981-2982.	1.8	46
470	Shedding of Large Functionally Active CD11/CD18 Integrin Complexes from Leukocyte Membranes during Synovial Inflammation Distinguishes Three Types of Arthritis through Differential Epitope Exposure. Journal of Immunology, 2010, 185, 4154-4168.	0.4	45
471	Metal templated design of protein interfaces. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1827-1832.	3.3	125
472	The Coxsackievirusâ€"Adenovirus Receptor Reveals Complex Homophilic and Heterophilic Interactions on Neural Cells. Journal of Neuroscience, 2010, 30, 2897-2910.	1.7	60
473	ANCHOR: a web server and database for analysis of protein-protein interaction binding pockets for drug discovery. Nucleic Acids Research, 2010, 38, W407-W411.	6.5	102
474	Structural and Functional Characterization of an RNase HI Domain from the Bifunctional Protein Rv2228c from <i>Mycobacterium tuberculosis</i>. Journal of Bacteriology, 2010, 192, 2878-2886.	1.0	39
475	Structure and folding of a designed knotted protein. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20732-20737.	3.3	123
476	Evolution of New Enzymatic Function by Structural Modulation of Cysteine Reactivity in Pseudomonas fluorescens Isocyanide Hydratase. Journal of Biological Chemistry, 2010, 285, 29651-29661.	1.6	35

#	Article	IF	Citations
477	Implications for Collagen Binding from the Crystallographic Structure of Fibronectin 6FnI1â€“2FnII7FnI. Journal of Biological Chemistry, 2010, 285, 33764-33770.	1.6	30
478	Ferredoxin:NADPH oxidoreductase is recruited to thylakoids by binding to a polyproline type II helix in a pH-dependent manner. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19260-19265.	3.3	54
479	Dimeric Architecture of the Hendra Virus Attachment Glycoprotein: Evidence for a Conserved Mode of Assembly. Journal of Virology, 2010, 84, 6208-6217.	1.5	90
480	Mutational Analyses Reveal that the Staphylococcal Immune Evasion Molecule Sbi and Complement Receptor 2 (CR2) Share Overlapping Contact Residues on C3d: Implications for the Controversy Regarding the CR2/C3d Cocrystal Structure. Journal of Immunology, 2010, 184, 1946-1955.	0.4	35
481	Structural Basis for the Blockage of IL-2 Signaling by Therapeutic Antibody Basiliximab. Journal of Immunology, 2010, 184, 1361-1368.	0.4	34
482	Structural and Kinetic Analysis of Schwanniomyces occidentalis Invertase Reveals a New Oligomerization Pattern and the Role of Its Supplementary Domain in Substrate Binding. Journal of Biological Chemistry, 2010, 285, 13930-13941.	1.6	71
483	Inferred Biomolecular Interaction Serverâ€"a web server to analyze and predict protein interacting partners and binding sites. Nucleic Acids Research, 2010, 38, D518-D524.	6.5	75
484	Structure and biochemical analysis of the heparin-induced E1 dimer of the amyloid precursor protein. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5381-5386.	3.3	104
485	The Multifunctional Protein in Peroxisomal Î²-Oxidation. Journal of Biological Chemistry, 2010, 285, 24066-24077.	1.6	43
486	Crystal Structure of Leishmania major Oligopeptidase B Gives Insight into the Enzymatic Properties of a Trypanosomatid Virulence Factor. Journal of Biological Chemistry, 2010, 285, 39249-39259.	1.6	53
487	Crystal Structure of CCM3, a Cerebral Cavernous Malformation Protein Critical for Vascular Integrity. Journal of Biological Chemistry, 2010, 285, 24099-24107.	1.6	75
488	Crystal Structure of Aminomethyltransferase in Complex with Dihydrolipoyl-H-Protein of the Glycine Cleavage System. Journal of Biological Chemistry, 2010, 285, 18684-18692.	1.6	32
489	Structural and Kinetic Characterization of 4-Hydroxy-4-methyl-2-oxoglutarate/4-Carboxy-4-hydroxy-2-oxoadipate Aldolase, a Protocatechuate Degradation Enzyme Evolutionarily Convergent with the HpaI and DmpG Pyruvate Aldolases. Journal of Biological Chemistry, 2010, 285, 36608-36615.	1.6	28
490	Structural and Biochemical Characterization of Peroxiredoxin QÎ² from Xylella fastidiosa. Journal of Biological Chemistry, 2010, 285, 16051-16065.	1.6	50
491	An Antibody as Surrogate Receptor Reveals Determinants of Activity of an Innate Immune Peptide Antibiotic. Journal of Biological Chemistry, 2010, 285, 35750-35758.	1.6	6
492	Structural Basis for Substrate Selectivity in Human Maltase-Glucoamylase and Sucrase-Isomaltase N-terminal Domains. Journal of Biological Chemistry, 2010, 285, 17763-17770.	1.6	173
493	Functional Hybrid Rubisco Enzymes with Plant Small Subunits and Algal Large Subunits. Journal of Biological Chemistry, 2010, 285, 19833-19841.	1.6	121
494	Structural Basis for the Interaction between the Growth Factor-binding Protein GRB10 and the E3 Ubiquitin Ligase NEDD4. Journal of Biological Chemistry, 2010, 285, 42130-42139.	1.6	25

#	ARTICLE	IF	CITATIONS
495	Structural and Mechanistic Studies on Klebsiella pneumoniae 2-Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline Decarboxylase. Journal of Biological Chemistry, 2010, 285, 35446-35454.	1.6	19
496	Substrate-mediated Stabilization of a Tetrameric Drug Target Reveals Achilles Heel in Anthrax. Journal of Biological Chemistry, 2010, 285, 5188-5195.	1.6	44
497	Structural Analysis of Thermus thermophilus HB27 Mannosyl-3-phosphoglycerate Synthase Provides Evidence for a Second Catalytic Metal Ion and New Insight into the Retaining Mechanism of Glycosyltransferases. Journal of Biological Chemistry, 2010, 285, 17857-17868.	1.6	14
498	Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1 Â. Plant Physiology, 2010, 153, 1706-1715.	2.3	159
499	Molecular Basis for Association of PIPKIÎ³-p90 with Clathrin Adaptor AP-2. Journal of Biological Chemistry, 2010, 285, 2734-2749.	1.6	27
500	A Conserved Protein Interaction Interface on the Type 5 G Protein Î² Subunit Controls Proteolytic Stability and Activity of R7 Family Regulator of G Protein Signaling Proteins. Journal of Biological Chemistry, 2010, 285, 41100-41112.	1.6	15
501	Structural Insights into the Catalytic Mechanism of Bacterial Guanosine-diphospho-d-mannose Pyrophosphorylase and Its Regulation by Divalent Ions. Journal of Biological Chemistry, 2010, 285, 27468-27476.	1.6	33
502	Structure of lactococcal phage p2 baseplate and its mechanism of activation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6852-6857.	3.3	143
503	Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2908-2913.	3.3	60
504	The structural and energetic basis for high selectivity in a high-affinity protein-protein interaction. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10080-10085.	3.3	112
505	tRNA ^{His} guanylyltransferase (THG1), a unique 3â€²-5â€² nucleotidyl transferase, shares unexpected structural homology with canonical 5â€²-3â€² DNA polymerases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20305-20310.	3.3	47
506	Interaction of Decay-Accelerating Factor with Echovirus 7. Journal of Virology, 2010, 84, 12665-12674.	1.5	38
507	Structural basis of immunosuppression by the therapeutic antibody daclizumab. Cell Research, 2010, 20, 1361-1371.	5.7	31
508	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. Rna, 2010, 16, 1205-1216.	1.6	18
509	Structural Basis of Cell Wall Cleavage by a Staphylococcal Autolysin. PLoS Pathogens, 2010, 6, e1000807.	2.1	78
510	A computational analysis of the antigenic properties of haemagglutinin in influenza A H3N2. Bioinformatics, 2010, 26, 1403-1408.	1.8	43
511	Adaptive Divergence of Ancient Gene Duplicates in the Avian MHC Class II Â. Molecular Biology and Evolution, 2010, 27, 2360-2374.	3.5	66
512	Unloading RNAs in the cytoplasm. Nucleus, 2010, 1, 139-143.	0.6	8

#	ARTICLE	IF	CITATIONS
513	Structure of a Major Antigenic Site on the Respiratory Syncytial Virus Fusion Glycoprotein in Complex with Neutralizing Antibody 101F. Journal of Virology, 2010, 84, 12236-12244.	1.5	105
514	The Structure of the Poxvirus A33 Protein Reveals a Dimer of Unique C-Type Lectin-Like Domains. Journal of Virology, 2010, 84, 2502-2510.	1.5	34
515	Crystal Structure and Functional Insights of Hemopexin Fold Protein from Grass Pea Â Â. Plant Physiology, 2010, 152, 1842-1850.	2.3	24
516	Structural and Functional Characterization of a Novel Homodimeric Three-finger Neurotoxin from the Venom of Ophiophagus hannah (King Cobra). Journal of Biological Chemistry, 2010, 285, 8302-8315.	1.6	77
517	Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20352-20357.	3.3	160
518	Homodimeric Enzymes as Drug Targets. Current Medicinal Chemistry, 2010, 17, 826-846.	1.2	45
519	Visualizing the Metal-Binding Versatility of Copper Trafficking Sites,. Biochemistry, 2010, 49, 7798-7810.	1.2	27
520	Pressure Perturbation Calorimetry and the Thermodynamics of Noncovalent Interactions in Water: Comparison of Proteinâˆ’Protein, Proteinâˆ’Ligand, and Cyclodextrinâˆ’Adamantane Complexes. Journal of Physical Chemistry B, 2010, 114, 16228-16235.	1.2	40
521	The Crystal Structure of the Human Nascent Polypeptide-Associated Complex Domain Reveals a Nucleic Acid-Binding Region on the NACA Subunit,. Biochemistry, 2010, 49, 2890-2896.	1.2	27
522	Structural studies of BmooMPÎ±-I, a non-hemorrhagic metalloproteinase from Bothrops moojeni venom. Toxicon, 2010, 55, 361-368.	0.8	37
523	Intermolecular Interactions in a 44 kDa Interferonâˆ’Receptor Complex Detected by Asymmetric Reverse-Protonation and Two-Dimensional NOESY. Biochemistry, 2010, 49, 5117-5133.	1.2	21
524	Conformational Selection in the Recognition of the Snurportin Importin Î² Binding Domain by Importin Î². Biochemistry, 2010, 49, 5042-5047.	1.2	19
525	Domain Organization in <i>Candida glabrata</i> THI6, a Bifunctional Enzyme Required for Thiamin Biosynthesis in Eukaryotes,. Biochemistry, 2010, 49, 9922-9934.	1.2	15
526	Identification of Carbonic Anhydrase I Immunodominant Epitopes Recognized by Specific Autoantibodies Which Indicate an Improved Prognosis in Patients with Malignancy after Autologous Stem Cell Transplantation. Journal of Proteome Research, 2010, 9, 5171-5179.	1.8	12
527	Structure of the bacteriophage T4 long tail fiber receptor-binding tip. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20287-20292.	3.3	159
528	Crystal Structure of Arginase from <i>Plasmodium falciparum</i> and Implications for <scp>l</scp>-Arginine Depletion in Malarial Infection,. Biochemistry, 2010, 49, 5600-5608.	1.2	39
529	Î”¹²-Prostaglandin J₂ as a Product and Ligand of Human Serum Albumin: Formation of an Unusual Covalent Adduct at His146. Journal of the American Chemical Society, 2010, 132, 824-832.	6.6	62
530	Reversible Phase Transitions in Self-Assembled Monolayers at the Liquidâˆ’Solid Interface: Temperature-Controlled Opening and Closing of Nanopores. Journal of the American Chemical Society, 2010, 132, 5084-5090.	6.6	223

#	ARTICLE	IF	CITATIONS
531	Are Scoring Functions in Proteinâˆ'Protein Docking Ready To Predict Interactomes? Clues from a Novel Binding Affinity Benchmark. Journal of Proteome Research, 2010, 9, 2216-2225.	1.8	224
532	X-ray Study of Proteinâ€"Protein Complexes and Analysis of Interfaces. , 2010, , 1-24.		1
533	Crystal Structure of the Cofactor-Independent Monooxygenase SnoaB from Streptomyces nogalater: Implications for the Reaction Mechanism. Biochemistry, 2010, 49, 934-944.	1.2	34
534	Insights into the Specificity of Thioredoxin Reductaseâˆ'Thioredoxin Interactions. A Structural and Functional Investigation of the Yeast Thioredoxin System. Biochemistry, 2010, 49, 3317-3326.	1.2	66
535	Mutation of Archaeal Isopentenyl Phosphate Kinase Highlights Mechanism and Guides Phosphorylation of Additional Isoprenoid Monophosphates. ACS Chemical Biology, 2010, 5, 589-601.	1.6	30
536	Crystallographic and Nuclear Magnetic Resonance Evaluation of the Impact of Peptide Binding to the Second PDZ Domain of Protein Tyrosine Phosphatase 1E. Biochemistry, 2010, 49, 9280-9291.	1.2	64
537	X-ray Structures of Isopentenyl Phosphate Kinase. ACS Chemical Biology, 2010, 5, 517-527.	1.6	28
538	Structural insights into substrate specificity and solvent tolerance in alcohol dehydrogenase ADH-â€˜Aâ€™ from Rhodococcus ruber DSM 44541. Chemical Communications, 2010, 46, 6314.	2.2	65
539	Mutational Analysis of VIM-2 Reveals an Essential Determinant for Metallo-Î²-Lactamase Stability and Folding. Antimicrobial Agents and Chemotherapy, 2010, 54, 3197-3204.	1.4	53
540	The Mechanism of Prion Inhibition by HET-S. Molecular Cell, 2010, 38, 889-899.	4.5	86
541	Exploring peptide mimics for the production of antibodies against discontinuous protein epitopes. Molecular Immunology, 2010, 47, 1137-1148.	1.0	30
542	Comparative structural studies of two natural isoforms of ammodytoxin, phospholipases A2 from Vipera ammodytes ammodytes which differ in neurotoxicity and anticoagulant activityâ˜†. Journal of Structural Biology, 2010, 169, 360-369.	1.3	41
543	Structure of dihydropyrimidinase from Sinorhizobium meliloti CECT4114: New features in an amidohydrolase family member. Journal of Structural Biology, 2010, 169, 200-208.	1.3	28
544	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from Thermoplasma acidophilum. Journal of Structural Biology, 2010, 169, 304-311.	1.3	13
545	Inhibition of Toll-like receptors TLR4 and 7 signaling pathways by SIGIRR: A computational approach. Journal of Structural Biology, 2010, 169, 323-330.	1.3	63
546	The crystal structure of Escherichia coli spermidine synthase SpeE reveals a unique substrate-binding pocket. Journal of Structural Biology, 2010, 169, 277-285.	1.3	20
547	Bacillus licheniformis Anti-TRAP can assemble into two types of dodecameric particles with the same symmetry but inverted orientation of trimers. Journal of Structural Biology, 2010, 170, 127-133.	1.3	4
548	Atomic structure of vimentin coil 2. Journal of Structural Biology, 2010, 170, 369-376.	1.3	97

#	Article	IF	Citations
549	Crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase from the hyperthermophile Thermotoga maritima for insights into the coordination of conformational changes and an inhibitor binding. Journal of Structural Biology, 2010, 170, 532-539.	1.3	24
550	Comparison between apo and complexed structures of bothropstoxin-I reveals the role of Lys122 and Ca2+-binding loop region for the catalytically inactive Lys49-PLA2s. Journal of Structural Biology, 2010, 171, 31-43.	1.3	46
551	The structure of tryptophanyl-tRNA synthetase from Giardia lamblia reveals divergence from eukaryotic homologs. Journal of Structural Biology, 2010, 171, 238-243.	1.3	12
552	The Crystal Structure of the Novobiocin Biosynthetic Enzyme NovP: The First Representative Structure for the TylF O-Methyltransferase Superfamily. Journal of Molecular Biology, 2010, 395, 390-407.	2.0	29
553	Evolution of Protein Binding Modes in Homooligomers. Journal of Molecular Biology, 2010, 395, 860-870.	2.0	61
554	Crystal Structure of the ATPPase Subunit and Its Substrate-Dependent Association with the GATase Subunit: A Novel Regulatory Mechanism for a Two-Subunit-Type GMP Synthetase from Pyrococcus horikoshii OT3. Journal of Molecular Biology, 2010, 395, 417-429.	2.0	21
555	Ligand-Mediated Dimerization of the Met Receptor Tyrosine Kinase by the Bacterial Invasion Protein InlB. Journal of Molecular Biology, 2010, 395, 522-532.	2.0	43
556	A Single Mutation at the Sheet Switch Region Results in Conformational Changes Favoring Î»6 Light-Chain Fibrillogenesis. Journal of Molecular Biology, 2010, 396, 280-292.	2.0	43
557	Binding of S-Methyl-5â€²-Thioadenosine and S-Adenosyl-l-Methionine to Protein MJ0100 Triggers an Open-to-Closed Conformational Change in Its CBS Motif Pair. Journal of Molecular Biology, 2010, 396, 800-820.	2.0	42
558	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. Journal of Molecular Biology, 2010, 396, 1244-1259.	2.0	16
559	Structural Basis of Substrate Binding in WsaF, a Rhamnosyltransferase from Geobacillus stearothermophilus. Journal of Molecular Biology, 2010, 397, 436-447.	2.0	22
560	Crystal Structure of the First Eubacterial Mre11 Nuclease Reveals Novel Features that May Discriminate Substrates During DNA Repair. Journal of Molecular Biology, 2010, 397, 647-663.	2.0	41
561	A Single-Domain Llama Antibody Potently Inhibits the Enzymatic Activity of Botulinum Neurotoxin by Binding to the Non-Catalytic Î±-Exosite Binding Region. Journal of Molecular Biology, 2010, 397, 1106-1118.	2.0	78
562	Structural and Functional Analyses of Î²-Glucosidase 3B from Thermotoga neapolitana: A Thermostable Three-Domain Representative of Glycoside Hydrolase 3. Journal of Molecular Biology, 2010, 397, 724-739.	2.0	117
563	Structure of Bacteriophage T4 Endonuclease II Mutant E118A, a Tetrameric GIY-YIG Enzyme. Journal of Molecular Biology, 2010, 397, 1003-1016.	2.0	6
564	The Subunit Interfaces of Weakly Associated Homodimeric Proteins. Journal of Molecular Biology, 2010, 398, 146-160.	2.0	107
565	The X-ray Crystal Structure of the First RNA Recognition Motif and Site-Directed Mutagenesis Suggest a Possible HuR Redox Sensing Mechanism. Journal of Molecular Biology, 2010, 397, 1231-1244.	2.0	40
566	Nonantibiotic Properties of Tetracyclines: Structural Basis for Inhibition of Secretory Phospholipase A2. Journal of Molecular Biology, 2010, 398, 83-96.	2.0	27

#	ARTICLE	IF	CITATIONS
567	Crystal Structure of Sulfide:Quinone Oxidoreductase from Acidithiobacillus ferrooxidans: Insights into Sulfidotrophic Respiration and Detoxification. Journal of Molecular Biology, 2010, 398, 292-305.	2.0	84
568	Crystal Structures of the CBS and DRTGG Domains of the Regulatory Region of Clostridium perfringens Pyrophosphatase Complexed with the Inhibitor, AMP, and Activator, Diadenosine Tetraphosphate. Journal of Molecular Biology, 2010, 398, 400-413.	2.0	35
569	The Crystal Structure of Protein MJ1225 from Methanocaldococcus jannaschii Shows Strong Conservation of Key Structural Features Seen in the Eukaryal Î³-AMPK. Journal of Molecular Biology, 2010, 399, 53-70.	2.0	27
570	Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. Journal of Molecular Biology, 2010, 399, 196-206.	2.0	39
571	Crystal Structure of the Intermediate Complex of the Arginine Repressor from Mycobacterium tuberculosis Bound with Its DNA Operator Reveals Detailed Mechanism of Arginine Repression. Journal of Molecular Biology, 2010, 399, 240-254.	2.0	12
572	Geometric Similarities of Proteinâ€"Protein Interfaces at Atomic Resolution Are Only Observed within Homologous Families: An Exhaustive Structural Classification Study. Journal of Molecular Biology, 2010, 399, 526-540.	2.0	17
573	Structural and Biochemical Characterization of a Halophilic Archaeal Alkaline Phosphatase. Journal of Molecular Biology, 2010, 400, 52-62.	2.0	22
574	Oligomeric State in the Crystal Structure of Modular FAD Synthetase Provides Insights into Its Sequential Catalysis in Prokaryotes. Journal of Molecular Biology, 2010, 400, 218-230.	2.0	40
575	Crystal Structure of Human RNA Helicase A (DHX9): Structural Basis for Unselective Nucleotide Base Binding in a DEAD-Box Variant Protein. Journal of Molecular Biology, 2010, 400, 768-782.	2.0	36
576	Crystal Structure of the 2-Oxoglutarate- and Fe(II)-Dependent Lysyl Hydroxylase JMJD6. Journal of Molecular Biology, 2010, 401, 211-222.	2.0	85
577	P. aeruginosa PilT Structures with and without Nucleotide Reveal a Dynamic Type IV Pilus Retraction Motor. Journal of Molecular Biology, 2010, 400, 1011-1021.	2.0	77
578	The Structure of the FnIII Tandem A77-A78 Points to a Periodically Conserved Architecture in the Myosin-Binding Region of Titin. Journal of Molecular Biology, 2010, 401, 843-853.	2.0	31
579	Structure and Reactivity of Bacillus subtilis MenD Catalyzing the First Committed Step in Menaquinone Biosynthesis. Journal of Molecular Biology, 2010, 401, 253-264.	2.0	36
580	Structure and Function of P19, a High-Affinity Iron Transporter of the Human Pathogen Campylobacter jejuni. Journal of Molecular Biology, 2010, 401, 590-604.	2.0	35
581	Structure-Based Annotation of a Novel Sugar Isomerase from the Pathogenic E. coli O157:H7. Journal of Molecular Biology, 2010, 401, 866-881.	2.0	29
582	Crystal Structure of Glyceraldehyde-3-Phosphate Dehydrogenase 1 from Methicillin-Resistant Staphylococcus aureus MRSA252 Provides Novel Insights into Substrate Binding and Catalytic Mechanism. Journal of Molecular Biology, 2010, 401, 949-968.	2.0	42
583	Molecular Basis for Complement Recognition and Inhibition Determined by Crystallographic Studies of the Staphylococcal Complement Inhibitor (SCIN) Bound to C3c and C3b. Journal of Molecular Biology, 2010, 402, 17-29.	2.0	39
584	Structural Conservation of Components in the Amino Acid Sensing Branch of the TOR Pathway in Yeast and Mammals. Journal of Molecular Biology, 2010, 402, 388-398.	2.0	51

#	Article	IF	Citations
585	Computational Design of a Chain-Specific Tetracycline Repressor Heterodimer. Journal of Molecular Biology, 2010, 403, 371-385.	2.0	7
586	Crystal Structure of Zebrafish Hatching Enzyme 1 from the Zebrafish Danio rerio. Journal of Molecular Biology, 2010, 402, 865-878.	2.0	39
587	Diversity of Bisubstrate Binding Modes of Adenosine Analogueâ€"Oligoarginine Conjugates in Protein Kinase A and Implications for Protein Substrate Interactions. Journal of Molecular Biology, 2010, 403, 66-77.	2.0	27
588	Crystal Structure of Î³-Hexachlorocyclohexane Dehydrochlorinase LinA from Sphingobium japonicum UT26. Journal of Molecular Biology, 2010, 403, 260-269.	2.0	38
589	TolA Modulates the Oligomeric Status of YbgF in the Bacterial Periplasm. Journal of Molecular Biology, 2010, 403, 270-285.	2.0	34
590	Full-Length Structures of BenM and Two Variants Reveal Different Oligomerization Schemes for LysR-Type Transcriptional Regulators. Journal of Molecular Biology, 2010, 404, 568-586.	2.0	55
591	Gradual Adaptive Changes of a Protein Facing High Salt Concentrations. Journal of Molecular Biology, 2010, 404, 493-505.	2.0	40
592	Crystal Structure of Human Interferon-Î»1 in Complex with Its High-Affinity Receptor Interferon-Î»R1. Journal of Molecular Biology, 2010, 404, 650-664.	2.0	76
593	Microcin J25 triggers cytochrome c release through irreversible damage of mitochondrial proteins and lipids. International Journal of Biochemistry and Cell Biology, 2010, 42, 273-281.	1.2	21
594	Bioinformatics and molecular modelling approaches to GPCR oligomerization. Current Opinion in Pharmacology, 2010, 10, 30-37.	1.7	61
595	Sorting of the Alzheimer's Disease Amyloid Precursor Protein Mediated by the AP-4 Complex. Developmental Cell, 2010, 18, 425-436.	3.1	228
596	In vitro receptor binding properties of a â€œpainlessâ€• NGF mutein, linked to hereditary sensory autonomic neuropathy type V. Biochemical and Biophysical Research Communications, 2010, 391, 824-829.	1.0	47
597	A Large-Scale Conformational Change Couples Membrane Recruitment to Cargo Binding in the AP2 Clathrin Adaptor Complex. Cell, 2010, 141, 1220-1229.	13.5	305
598	Insights into Egg Coat Assembly and Egg-Sperm Interaction from the X-Ray Structure of Full-Length ZP3. Cell, 2010, 143, 404-415.	13.5	132
599	Crotoxin: Novel activities for a classic Î²-neurotoxin. Toxicon, 2010, 55, 1045-1060.	0.8	110
600	Exploring the dihydrodipicolinate synthase tetramer: How resilient is the dimerâ€"dimer interface?. Archives of Biochemistry and Biophysics, 2010, 494, 58-63.	1.4	30
601	Disruption of quaternary structure in Escherichia coli dihydrodipicolinate synthase (DHDPS) generates a functional monomer that is no longer inhibited by lysine. Archives of Biochemistry and Biophysics, 2010, 503, 202-206.	1.4	12
602	Directed Evolution of a Thermostable Quorum-quenching Lactonase from the Amidohydrolase Superfamily. Journal of Biological Chemistry, 2010, 285, 40911-40920.	1.6	77

#	Article	IF	Citations
603	Crystal structure of the aspartyl-tRNA synthetase from Entamoeba histolytica. Molecular and Biochemical Parasitology, 2010, 169, 95-100.	0.5	14
604	Homomeric protein complexes: evolution and assembly. Biochemical Society Transactions, 2010, 38, 879-882.	1.6	25
605	Catalysis and Inhibition of <i>Mycobacterium tuberculosis</i> Methionine Aminopeptidase. Journal of Medicinal Chemistry, 2010, 53, 1329-1337.	2.9	37
607	Biochemical Characterization of the Transcriptional Regulator BzdR from Azoarcus sp. CIB. Journal of Biological Chemistry, 2010, 285, 35694-35705.	1.6	33
608	Intrinsic disorder and protein multibinding in domain, terminal, and linker regions. Molecular BioSystems, 2010, 6, 1821.	2.9	20
609	Position 552 in a FMRFamide-Gated Na⁺Channel Affects the Gating Properties and the Potency of FMRFamide. Zoological Science, 2010, 27, 440-448.	0.3	9
610	Structural Analysis of Saccharomyces cerevisiae Î±-Galactosidase and Its Complexes with Natural Substrates Reveals New Insights into Substrate Specificity of GH27 Glycosidases. Journal of Biological Chemistry, 2010, 285, 28020-28033.	1.6	36
611	Crystal Structure of Bacteriophage SPP1 Distal Tail Protein (gp19.1). Journal of Biological Chemistry, 2010, 285, 36666-36673.	1.6	70
612	Structural Determinants Underlying Photoprotection in the Photoactive Orange Carotenoid Protein of Cyanobacteria. Journal of Biological Chemistry, 2010, 285, 18364-18375.	1.6	152
613	An accurate classification of native and non-native protein-protein interactions using supervised and semi-supervised learning approaches. , 2010, , .		0
614	Regioselective deacetylation based on teicoplanin-complexed Orf2* crystal structures. Molecular BioSystems, 2011, 7, 1224.	2.9	22
615	EspR, a key regulator of <i>Mycobacterium tuberculosis</i> virulence, adopts a unique dimeric structure among helix-turn-helix proteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13450-13455.	3.3	33
616	Identification of cytoplasmic and membrane-associated complexes in human embryonic stem cells using blue native PAGE. Molecular BioSystems, 2011, 7, 2688.	2.9	7
617	Structural basis for the neutralization and genotype specificity of hepatitis E virus. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10266-10271.	3.3	109
618	Heterogeneous and homogeneous crystal nucleation in colloidal hard-sphere like microgels at low metastabilities. Soft Matter, 2011, 7, 11267.	1.2	29
619	Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon. Nature, 2011, 478, 412-416.	13.7	91
620	Dehaloperoxidase-Hemoglobin from <i>Amphitrite ornata</i> Is Primarily a Monomer in Solution. Journal of Physical Chemistry B, 2011, 115, 4266-4272.	1.2	13
621	The Crystal Structure of <i>Escherichia coli</i> Group 4 Capsule Protein GfcC Reveals a Domain Organization Resembling That of Wza. Biochemistry, 2011, 50, 5465-5476.	1.2	31

#	Article	IF	Citations
622	Modular mechanism of Wnt signaling inhibition by Wnt inhibitory factor 1. Nature Structural and Molecular Biology, 2011, 18, 886-893.	3.6	135
623	Molecular Modeling and Molecular Dynamics Simulation Studies of Delta-Notch Complex. Journal of Biomolecular Structure and Dynamics, 2011, 29, 297-310.	2.0	3
624	Broad Distribution of Energetically Important Contacts across an Extended Protein Interface. Journal of the American Chemical Society, 2011, 133, 10038-10041.	6.6	39
625	The Crystal Structure of Necrosis- and Ethylene-Inducing Protein 2 from the Causal Agent of Cacaoâ€™s Witchesâ€™ Broom Disease Reveals Key Elements for Its Activity. Biochemistry, 2011, 50, 9901-9910.	1.2	31
626	Evidence of the Participation of Remote Residues in the Catalytic Activity of Co-Type Nitrile Hydratase from <i>Pseudomonas putida</i>. Biochemistry, 2011, 50, 4923-4935.	1.2	48
627	Three Clusters of Conformational States in P450cam Reveal a Multistep Pathway for Closing of the Substrate Access Channel,. Biochemistry, 2011, 50, 693-703.	1.2	53
628	Flavin-Induced Oligomerization in <i>Escherichia coli</i> Adaptive Response Protein AidB. Biochemistry, 2011, 50, 10159-10169.	1.2	9
629	The protein common interface database (ProtCID)--a comprehensive database of interactions of homologous proteins in multiple crystal forms. Nucleic Acids Research, 2011, 39, D761-D770.	6.5	79
630	Structure of the USP15 N-Terminal Domains: A Î²-Hairpin Mediates Close Association between the DUSP and UBL Domains. Biochemistry, 2011, 50, 7995-8004.	1.2	25
631	Molecular Basis of the Thermostability and Thermophilicity of Laminarinases: X-ray Structure of the Hyperthermostable Laminarinase from <i>Rhodothermus marinus</i> and Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2011, 115, 7940-7949.	1.2	26
632	Stabilization of a Protein Nanocage through the Plugging of a Proteinâ€"Protein Interfacial Water Pocket. Biochemistry, 2011, 50, 4029-4037.	1.2	27
633	The Chp1â€"Tas3 core is a multifunctional platform critical for gene silencing by RITS. Nature Structural and Molecular Biology, 2011, 18, 1351-1357.	3.6	38
634	Systematic computational prediction of protein interaction networks. Physical Biology, 2011, 8, 035008.	0.8	35
635	Structure and Activity ofAspergillus nidulansCopper Amine Oxidase. Biochemistry, 2011, 50, 5718-5730.	1.2	21
636	Automated Protein Structure Modeling with SWISS-MODEL Workspace and the Protein Model Portal. Methods in Molecular Biology, 2011, 857, 107-136.	0.4	124
637	Three-Dimensional Structure of Mannosyl-3-phosphoglycerate Phosphatase from <i>Thermus thermophilus</i> HB27: A New Member of the Haloalcanoic Acid Dehalogenase Superfamily. Biochemistry, 2011, 50, 9551-9567.	1.2	9
638	Crystal structures of a halophilic archaeal malate synthase from Haloferax volcanii and comparisons with isoforms A and G. BMC Structural Biology, 2011, 11, 23.	2.3	15
639	Thermodynamic Characterization of the Binding Interaction between the Histone Demethylase LSD1/KDM1 and CoREST. Biochemistry, 2011, 50, 546-557.	1.2	20

#	ARTICLE	IF	CITATIONS
640	Fragment Growing Induces Conformational Changes in Acetylcholine-Binding Protein: A Structural and Thermodynamic Analysis. Journal of the American Chemical Society, 2011, 133, 5363-5371.	6.6	72
641	Glutathione Transferases of Phanerochaete chrysosporium. Journal of Biological Chemistry, 2011, 286, 9162-9173.	1.6	38
642	Stability of domain structures in multi-domain proteins. Scientific Reports, 2011, 1, 40.	1.6	96
643	Focused Evolution of HIV-1 Neutralizing Antibodies Revealed by Structures and Deep Sequencing. Science, 2011, 333, 1593-1602.	6.0	788
644	Host Cell Invasion by Apicomplexan Parasites: Insights from the Co-Structure of AMA1 with a RON2 Peptide. Science, 2011, 333, 463-467.	6.0	168
645	Observation of Intermolecular Interactions in Large Protein Complexes by 2D-Double Difference Nuclear Overhauser Enhancement Spectroscopy: Application to the 44 kDa Interferonâ€"Receptor Complex. Journal of the American Chemical Society, 2011, 133, 14755-14764.	6.6	14
646	Mutational and Structural Studies of the PixD BLUF Output Signal That Affects Light-Regulated Interactions with PixE. Biochemistry, 2011, 50, 6365-6375.	1.2	37
647	Crystallographic Proof for an Extended Hydrogen-Bonding Network in Small Prolyl Isomerases. Journal of the American Chemical Society, 2011, 133, 20096-20099.	6.6	30
648	Amphiphilic nanotubes in the crystal structure of a biosurfactant protein hydrophobin HFBII. Chemical Communications, 2011, 47, 9843.	2.2	6
649	The crystal structure of an oxygen-tolerant hydrogenase uncovers a novel iron-sulphur centre. Nature, 2011, 479, 249-252.	13.7	342
650	Crystal structure determination and dynamic studies of Mycobacterium tuberculosis Cytidine deaminase in complex with products. Archives of Biochemistry and Biophysics, 2011, 509, 108-115.	1.4	6
651	Crystal structure and immunogenicity of the class C acid phosphatase from Pasteurella multocida. Archives of Biochemistry and Biophysics, 2011, 509, 76-81.	1.4	4
652	The crystal structure of rice (Oryza sativa L.) Os4BGlu12, an oligosaccharide and tuberonic acid glucoside-hydrolyzing Î²-glucosidase with significant thioglucohydrolase activity. Archives of Biochemistry and Biophysics, 2011, 510, 62-72.	1.4	28
653	A tetrameric structure is not essential for activity in dihydrodipicolinate synthase (DHDPS) from Mycobacterium tuberculosis. Archives of Biochemistry and Biophysics, 2011, 512, 154-159.	1.4	16
654	Structure of Candida albicans methionine synthase determined by employing surface residue mutagenesis. Archives of Biochemistry and Biophysics, 2011, 513, 19-26.	1.4	8
655	Structural Basis of the 9-Fold Symmetry of Centrioles. Cell, 2011, 144, 364-375.	13.5	317
656	The Mechanism of Linkage-Specific Ubiquitin Chain Elongation by a Single-Subunit E2. Cell, 2011, 144, 769-781.	13.5	241
657	Structural Linkage between Ligand Discrimination and Receptor Activation by Type I Interferons. Cell, 2011, 146, 621-632.	13.5	310

#	Article	IF	Citations
658	Molecular Architecture of the Transport Channel of the Nuclear Pore Complex. Cell, 2011, 147, 590-602.	13.5	98
659	The Molecular Basis of CRL4DDB2/CSA Ubiquitin Ligase Architecture, Targeting, and Activation. Cell, 2011, 147, 1024-1039.	13.5	372
660	The Molecular Basis for the Endocytosis of Small R-SNAREs by the Clathrin Adaptor CALM. Cell, 2011, 147, 1118-1131.	13.5	172
661	Crystal structure of the cysteine protease inhibitor 2 from Entamoeba histolytica: Functional convergence of a common protein fold. Gene, 2011, 471, 45-52.	1.0	15
662	Crystal structure of Bn IV in complex with myristic acid: A Lys49 myotoxic phospholipase A2 from Bothrops neuwiedi venom. Biochimie, 2011, 93, 513-518.	1.3	22
663	Structure of Leishmania major methionyl-tRNA synthetase in complex with intermediate products methionyladenylate and pyrophosphate. Biochimie, 2011, 93, 570-582.	1.3	50
664	Tight association of N-terminal and catalytic subunits of rabbit 12/15-lipoxygenase is important for protein stability and catalytic activity. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2011, 1811, 1001-1010.	1.2	19
665	Molecular evolution and selection pressure in alpha-class carbonic anhydrase family members. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1854-1861.	1.1	6
666	Structure of a novel class II phospholipase D: Catalytic cleft is modified by a disulphide bridge. Biochemical and Biophysical Research Communications, 2011, 409, 622-627.	1.0	49
667	Inverted repeats in the promoter as an autoregulatory sequence for TcrX in Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2011, 415, 17-23.	1.0	20
668	Structural Analyses of a Purine Biosynthetic Enzyme from Mycobacterium tuberculosis Reveal a Novel Bound Nucleotide. Journal of Biological Chemistry, 2011, 286, 40706-40716.	1.6	15
669	Structural and functional analysis of three Î²-glucosidases from bacterium Clostridium cellulovorans, fungus Trichoderma reesei and termite Neotermes koshunensis. Journal of Structural Biology, 2011, 173, 46-56.	1.3	161
670	Structures of a key interaction protein from the Trypanosoma brucei editosome in complex with single domain antibodies. Journal of Structural Biology, 2011, 174, 124-136.	1.3	27
671	Crystal structure of Salmonella typhimurium 2-methylcitrate synthase: Insights on domain movement and substrate specificity. Journal of Structural Biology, 2011, 174, 58-68.	1.3	9
672	The crystal structure of the leptospiral hypothetical protein LIC12922 reveals homology with the periplasmic chaperone SurA. Journal of Structural Biology, 2011, 173, 312-322.	1.3	9
673	Structural basis for pH dependent monomerâ€"dimer transition of 3,4-dihydroxy 2-butanone-4-phosphate synthase domain from Mycobacterium tuberculosis. Journal of Structural Biology, 2011, 174, 374-384.	1.3	8
674	Designed ankyrin repeat protein binders for the crystallization of AcrB: Plasticity of the dominant interface. Journal of Structural Biology, 2011, 174, 269-281.	1.3	21
675	A novel heterotetrameric structure of the crenarchaeal PCNA2â€"PCNA3 complex. Journal of Structural Biology, 2011, 174, 443-450.	1.3	13

#	ARTICLE	IF	CITATIONS
676	Crystal structure of the 30 K protein from the silkworm Bombyx mori reveals a new member of the Î²-trefoil superfamily. Journal of Structural Biology, 2011, 175, 97-103.	1.3	29
677	Molecular architecture of mouse activating NKR-P1 receptors. Journal of Structural Biology, 2011, 175, 434-441.	1.3	34
678	Crystal structures of Pseudomonas aeruginosa guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. Journal of Structural Biology, 2011, 175, 329-338.	1.3	15
679	The unusual extended C-terminal helix of the peroxisomal Î±/Î²-hydrolase Lpx1 is involved in dimer contacts but dispensable for dimerization. Journal of Structural Biology, 2011, 175, 362-371.	1.3	19
680	Crystal structure of the TL29 protein from Arabidopsis thaliana: An APX homolog without peroxidase activity. Journal of Structural Biology, 2011, 176, 24-31.	1.3	16
681	Binding site and interlobe interactions of the ionotropic glutamate receptor GluK3 ligand binding domain revealed by high resolution crystal structure in complex with (S)-glutamate. Journal of Structural Biology, 2011, 176, 307-314.	1.3	26
682	Structural Characterization of HBXIP: The Protein That Interacts with the Anti-Apoptotic Protein Survivin and the Oncogenic Viral Protein HBx. Journal of Molecular Biology, 2011, 405, 331-340.	2.0	28
683	Specific Inhibition of the Aspartate Aminotransferase of Plasmodium falciparum. Journal of Molecular Biology, 2011, 405, 956-971.	2.0	42
684	The Structure of the CRISPR-Associated Protein Csa3 Provides Insight into the Regulation of the CRISPR/Cas System. Journal of Molecular Biology, 2011, 405, 939-955.	2.0	87
685	The Structure of Physarum polycephalum Hemagglutinin I Suggests a Minimal Carbohydrate Recognition Domain of Legume Lectin Fold. Journal of Molecular Biology, 2011, 405, 560-569.	2.0	4
686	The Filamentous Phages fd and IF1 Use Different Mechanisms to Infect Escherichia coli. Journal of Molecular Biology, 2011, 405, 989-1003.	2.0	23
687	Crystal Structure of Arrestin-3 Reveals the Basis of the Difference in Receptor Binding Between Two Non-visual Subtypes. Journal of Molecular Biology, 2011, 406, 467-478.	2.0	185
688	A Product Analog Bound Form of 3-Oxoadipate-enol-Lactonase (PcaD) Reveals a Multifunctional Role for the Divergent Cap Domain. Journal of Molecular Biology, 2011, 406, 649-658.	2.0	35
689	The Crystal Structure of l-Sorbose Reductase from Gluconobacter frateurii Complexed with NADPH and l-Sorbose. Journal of Molecular Biology, 2011, 407, 543-555.	2.0	17
690	Ligand Bound Structures of a Glycosyl Hydrolase Family 30 Glucuronoxylan Xylanohydrolase. Journal of Molecular Biology, 2011, 407, 92-109.	2.0	72
691	Energetics of SecA Dimerization. Journal of Molecular Biology, 2011, 408, 87-98.	2.0	29
692	Interaction between Nucleosome Assembly Protein 1-like Family Members. Journal of Molecular Biology, 2011, 407, 647-660.	2.0	35
693	Crystal Structure of R120G Disease Mutant of Human Î±B-Crystallin Domain Dimer Shows Closure of a Groove. Journal of Molecular Biology, 2011, 408, 118-134.	2.0	106

#	Article	IF	Citations
694	Simultaneous Formation of Right- and Left-handed Anti-parallel Coiled-coil Interfaces by a Coil2 Fragment of Human Lamin A. Journal of Molecular Biology, 2011, 408, 135-146.	2.0	32
695	The Double-Length Tyrosyl-tRNA Synthetase from the Eukaryote Leishmania major Forms an Intrinsically Asymmetric Pseudo-Dimer. Journal of Molecular Biology, 2011, 409, 159-176.	2.0	40
696	Structural Analysis of a Novel Class of Râ€"M Controller Proteins: C.Csp231I from Citrobacter sp. RFL231. Journal of Molecular Biology, 2011, 409, 177-188.	2.0	12
697	The Crystal Structure of Death Receptor 6 (DR6): A Potential Receptor of the Amyloid Precursor Protein (APP). Journal of Molecular Biology, 2011, 409, 189-201.	2.0	22
698	The Extra-Membranous Domains of the Competence Protein HofQ Show DNA Binding, Flexibility and a Shared Fold with Type I KH Domains. Journal of Molecular Biology, 2011, 409, 642-653.	2.0	20
699	Probing Dimerization and Structural Flexibility of Mammalian Lipoxygenases by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2011, 409, 654-668.	2.0	37
700	Structural Analysis of a Putative Aminoglycoside N-Acetyltransferase from Bacillus anthracis. Journal of Molecular Biology, 2011, 410, 411-423.	2.0	17
701	Structure and Organisation of SinR, the Master Regulator of Biofilm Formation in Bacillus subtilis. Journal of Molecular Biology, 2011, 411, 597-613.	2.0	37
702	The Crystal Structure of Zebrafish S100Z: Implications for Calcium-Promoted S100 Protein Oligomerisation. Journal of Molecular Biology, 2011, 411, 1072-1082.	2.0	8
703	The Structure of BRMS1 Nuclear Export Signal and SNX6 Interacting Region Reveals a Hexamer Formed by Antiparallel Coiled Coils. Journal of Molecular Biology, 2011, 411, 1114-1127.	2.0	13
704	The Dimeric Structure of the Cpn60.2 Chaperonin of Mycobacterium tuberculosis at 2.8ÂÃ… Reveals Possible Modes of Function. Journal of Molecular Biology, 2011, 412, 192-203.	2.0	25
705	Crystal Structure of Crotoxin Reveals Key Residues Involved in the Stability and Toxicity of This Potent Heterodimeric Î²-Neurotoxin. Journal of Molecular Biology, 2011, 412, 176-191.	2.0	88
706	Structure of the Food-Poisoning Clostridium perfringens Enterotoxin Reveals Similarity to the Aerolysin-Like Pore-Forming Toxins. Journal of Molecular Biology, 2011, 413, 138-149.	2.0	76
707	The Structures of Thermoplasma volcanium Phosphoribosyl Pyrophosphate Synthetase Bound to Ribose-5-Phosphate and ATP Analogs. Journal of Molecular Biology, 2011, 413, 844-856.	2.0	21
708	High-Throughput Genetic Identification of Functionally Important Regions of the Yeast DEAD-Box Protein Mss116p. Journal of Molecular Biology, 2011, 413, 952-972.	2.0	15
709	Crystal Structure of the Passenger Domain of the Escherichia coli Autotransporter EspP. Journal of Molecular Biology, 2011, 413, 985-1000.	2.0	49
710	A Disulfide-Free Single-Domain VL Intrabody with Blocking Activity towards Huntingtin Reveals a Novel Mode of Epitope Recognition. Journal of Molecular Biology, 2011, 414, 337-355.	2.0	33
711	Structure of the Escherichia coli Phosphonate Binding Protein PhnD and Rationally Optimized Phosphonate Biosensors. Journal of Molecular Biology, 2011, 414, 356-369.	2.0	60

#	ARTICLE	IF	CITATIONS
712	The Crystal Structure of Odorant Binding Protein 7 from Anopheles gambiae Exhibits an Outstanding Adaptability of Its Binding Site. Journal of Molecular Biology, 2011, 414, 401-412.	2.0	76
713	Structure and Dynamics of a Stabilized Coiled-Coil Domain in the P-TEFb Regulator Hexim1. Journal of Molecular Biology, 2011, 414, 639-653.	2.0	12
714	Molecular Mechanisms of Viral and Host Cell Substrate Recognition by Hepatitis C Virus NS3/4A Protease. Journal of Virology, 2011, 85, 6106-6116.	1.5	45
715	Accelerated Macromolecular Solution Structure Recovery. Nature Precedings, 2011, , .	0.1	0
716	Modulation of the Pharmacological Activities of Secretory Phospholipase A2 from Crotalus durissus cascavella Induced by Naringin. Molecules, 2011, 16, 738-761.	1.7	5
717	Co-Crystal Structures of Inhibitors with MRCKÎ², a Key Regulator of Tumor Cell Invasion. PLoS ONE, 2011, 6, e24825.	1.1	43
718	Identification of Amino Acids that Account for Long-Range Interactions in Two Triosephosphate Isomerases from Pathogenic Trypanosomes. PLoS ONE, 2011, 6, e18791.	1.1	15
719	Crystal Structure of the Heteromolecular Chaperone, AscE-AscG, from the Type III Secretion System in Aeromonas hydrophila. PLoS ONE, 2011, 6, e19208.	1.1	13
720	Critical Factors Governing the Difference in Antizyme-Binding Affinities between Human Ornithine Decarboxylase and Antizyme Inhibitor. PLoS ONE, 2011, 6, e19253.	1.1	19
721	Identification of the Allosteric Regulatory Site of Insulysin. PLoS ONE, 2011, 6, e20864.	1.1	34
722	Structural and Sequence Analysis of Imelysin-Like Proteins Implicated in Bacterial Iron Uptake. PLoS ONE, 2011, 6, e21875.	1.1	17
723	An Inserted Î±/Î² Subdomain Shapes the Catalytic Pocket of Lactobacillus johnsonii Cinnamoyl Esterase. PLoS ONE, 2011, 6, e23269.	1.1	46
724	An Angiotensin I-Converting Enzyme Mutation (Y465D) Causes a Dramatic Increase in Blood ACE via Accelerated ACE Shedding. PLoS ONE, 2011, 6, e25952.	1.1	37
725	Crystal Structure of Thrombin in Complex with S-Variegin: Insights of a Novel Mechanism of Inhibition and Design of Tunable Thrombin Inhibitors. PLoS ONE, 2011, 6, e26367.	1.1	40
726	A Novel N-Acetylglutamate Synthase Architecture Revealed by the Crystal Structure of the Bifunctional Enzyme from Maricaulis maris. PLoS ONE, 2011, 6, e28825.	1.1	14
727	X-ray structural studies of the entire extracellular region of the serine/threonine kinase PrkC from Staphylococcus aureus. Biochemical Journal, 2011, 435, 33-41.	1.7	48
728	Crystal structure of a novel type of odorant-binding protein from <i>Anopheles gambiae</i>, belonging to the C-plus class. Biochemical Journal, 2011, 437, 423-430.	1.7	52
729	Structure of the leukemia oncogene LMO2: implications for the assembly of a hematopoietic transcription factor complex. Blood, 2011, 117, 2146-2156.	0.6	59

#	ARTICLE	IF	CITATIONS
730	The P2â€² residue is a key determinant of mesotrypsin specificity: engineering a high-affinity inhibitor with anticancer activity. Biochemical Journal, 2011, 440, 95-105.	1.7	37
731	Archaeal RNA polymerase: the influence of the protruding stalk in crystal packing and preliminary biophysical analysis of the Rpo13 subunit. Biochemical Society Transactions, 2011, 39, 25-30.	1.6	10
732	Functional and structural characterization of a novel mannosylâ€3â€phosphoglycerate synthase from <i>Rubrobacter xylanophilus</i> reveals its dual substrate specificity. Molecular Microbiology, 2011, 79, 76-93.	1.2	18
733	Atypical DNA recognition mechanism used by the EspR virulence regulator of <i>Mycobacterium tuberculosis</i>. Molecular Microbiology, 2011, 82, 251-264.	1.2	22
734	Crystal structure of an ascomycete fungal laccase from <i>Thielaviaâ€ƒarenaria</i>â€ƒâ€"â€ƒcommon structural features of ascoâ€laccases. FEBS Journal, 2011, 278, 2283-2295.	2.2	71
735	Insights into the Rrf2 repressor familyâ€ƒâ€"â€ƒthe structure of CymR, the global cysteine regulator of <i>Bacillusâ€ƒsubtilis</i>. FEBS Journal, 2011, 278, 2689-2701.	2.2	45
736	Quaternary structure, conformational variability and global motions of phosphoglucosamine mutase. FEBS Journal, 2011, 278, 3298-3307.	2.2	10
737	Characterization of an oxidoreductase from the arylamine <i>N</i>â€acetyltransferase operon in <i>Mycobacteriumâ€ƒsmegmatis</i>. FEBS Journal, 2011, 278, 4824-4832.	2.2	4
738	Regulation and structure of YahD, a copper-inducible Î±/Î² serine hydrolase of Lactococcus lactis IL1403. FEMS Microbiology Letters, 2011, 314, 57-66.	0.7	5
739	Structural basis for MOF and MSL3 recruitment into the dosage compensation complex by MSL1. Nature Structural and Molecular Biology, 2011, 18, 142-149.	3.6	98
740	Structural basis of substrate discrimination and integrin binding by autotaxin. Nature Structural and Molecular Biology, 2011, 18, 198-204.	3.6	247
741	Three-dimensional structure of a viral genome-delivery portal vertex. Nature Structural and Molecular Biology, 2011, 18, 597-603.	3.6	142
742	Conformational changes in IgE contribute to its uniquely slow dissociation rate from receptor FcÉ›RI. Nature Structural and Molecular Biology, 2011, 18, 571-576.	3.6	105
743	Structure of Importin13-Ubc9 complex: nuclear import and release of a key regulator of sumoylation. EMBO Journal, 2011, 30, 427-438.	3.5	37
744	Substrate recognition by complement convertases revealed in the C5-cobra venom factor complex. EMBO Journal, 2011, 30, 606-616.	3.5	87
745	Structure of the HECT:ubiquitin complex and its role in ubiquitin chain elongation. EMBO Reports, 2011, 12, 342-349.	2.0	146
746	Structural Characterization of the Multidomain Regulatory Protein Rv1364c from Mycobacterium tuberculosis. Structure, 2011, 19, 56-69.	1.6	19
747	Realizing the Allosteric Potential of the Tetrameric Protein Kinase A RIÎ± Holoenzyme. Structure, 2011, 19, 265-276.	1.6	42

#	ARTICLE	IF	CITATIONS
748	Interferon-Inducible Protein 16: Insight into the Interaction with Tumor Suppressor p53. Structure, 2011, 19, 418-429.	1.6	82
749	Combining Bayes Classification and Point Group Symmetry under Boolean Framework for Enhanced Protein Quaternary Structure Inference. Structure, 2011, 19, 304-312.	1.6	30
750	Structure and Activity of a Novel Archaeal Î²-CASP Protein with N-Terminal KH Domains. Structure, 2011, 19, 622-632.	1.6	30
751	Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding. Structure, 2011, 19, 859-867.	1.6	174
752	The Crystal Structure of the Î±-Neurexin-1 Extracellular Region Reveals a Hinge Point for Mediating Synaptic Adhesion and Function. Structure, 2011, 19, 767-778.	1.6	56
753	The Structure of Neurexin 1Î± Reveals Features Promoting a Role as Synaptic Organizer. Structure, 2011, 19, 779-789.	1.6	60
754	Insights into the Evolution of a Complex Virus from the Crystal Structure of Vaccinia Virus D13. Structure, 2011, 19, 1011-1020.	1.6	78
755	Crystal Structure of cGMP-Dependent Protein Kinase Reveals Novel Site of Interchain Communication. Structure, 2011, 19, 1317-1327.	1.6	57
756	Structural Basis for Complex Formation between Human IRSp53 and the Translocated Intimin Receptor Tir of Enterohemorrhagic E. coli. Structure, 2011, 19, 1294-1306.	1.6	30
757	Unusual, Dual Endo- and Exonuclease Activity in the Degradosome Explained by Crystal Structure Analysis of RNase J1. Structure, 2011, 19, 1241-1251.	1.6	53
758	Phosphorylation in Protein-Protein Binding: Effect on Stability and Function. Structure, 2011, 19, 1807-1815.	1.6	246
759	Phosphorylation at the Interface. Structure, 2011, 19, 1726-1727.	1.6	5
760	Evolving specificity from variability for protein interaction domains. Trends in Biochemical Sciences, 2011, 36, 183-190.	3.7	39
761	Characterization of a new phosphatase from Plasmodium. Molecular and Biochemical Parasitology, 2011, 179, 69-79.	0.5	21
762	A structural basis for Staphylococcal complement subversion: X-ray structure of the complement-binding domain of Staphylococcus aureus protein Sbi in complex with ligand C3d. Molecular Immunology, 2011, 48, 452-462.	1.0	32
763	CD4-binding site alterations in CCR5-using HIV-1 envelopes influencing gp120â€“CD4 interactions and fusogenicity. Virology, 2011, 410, 418-428.	1.1	26
764	Exploiting the high-resolution crystal structure of Staphylococcus aureus MenH to gain insight into enzyme activity. BMC Structural Biology, 2011, 11, 19.	2.3	13
765	Structural characterization of a ribose-5-phosphate isomerase B from the pathogenic fungus Coccidioides immitis. BMC Structural Biology, 2011, 11, 39.	2.3	7

#	ARTICLE	IF	CITATIONS
766	Crystal structures of LacD from<i>Staphylococcus aureus</i>and LacD.1 from<i>Streptococcus pyogenes</i>: Insights into substrate specificity and virulence gene regulation. FEBS Letters, 2011, 585, 307-312.	1.3	6
767	Structural basis for a new tetracycline resistance mechanism relying on the TetX monooxygenase. FEBS Letters, 2011, 585, 1061-1066.	1.3	87
768	MEMO associated with an ErbB2 receptor phosphopeptide reveals a new phosphotyrosine motif. FEBS Letters, 2011, 585, 2688-2692.	1.3	7
769	Structural basis of coagulation factor V recognition for cleavage by RVV-V. FEBS Letters, 2011, 585, 3020-3025.	1.3	31
770	Hell's Gate globin I: An acid and thermostable bacterial hemoglobin resembling mammalian neuroglobin. FEBS Letters, 2011, 585, 3250-3258.	1.3	29
771	Glycolipids that Elicit IFN-Î³-Biased Responses from Natural Killer T Cells. Chemistry and Biology, 2011, 18, 1620-1630.	6.2	37
772	Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. Physical Biology, 2011, 8, 035007.	0.8	94
773	Prediction of proteinâ€“protein interactions: unifying evolution and structure at protein interfaces. Physical Biology, 2011, 8, 035006.	0.8	58
774	The nucleotide-binding domain 2 of the human transporter protein MRP6. Journal of Bioenergetics and Biomembranes, 2011, 43, 465-471.	1.0	17
775	Nine Crystal Structures Determine the Substrate Envelope of the MDR HIV-1 Protease. Protein Journal, 2011, 30, 173-183.	0.7	24
776	Protein structure reports in JIMD â€•an important enhancement of journal scope. Journal of Inherited Metabolic Disease, 2011, 34, 563-564.	1.7	0
777	Crystal structure of tarocystatinâ€“papain complex: implications for the inhibition property of group-2 phytocystatins. Planta, 2011, 234, 243-254.	1.6	38
778	ISC-like [2Feâ€“2S] ferredoxin (FdxB) dimer from Pseudomonas putida JCM 20004: structural and electronâ€“nuclear double resonance characterization. Journal of Biological Inorganic Chemistry, 2011, 16, 923-935.	1.1	12
779	dockYardâ€“a repository to assist modeling of protein-protein docking. Journal of Molecular Modeling, 2011, 17, 599-606.	0.8	2
780	Kinetic and structural evidence of the alkenal/one reductase specificity of human Î¶-crystallin. Cellular and Molecular Life Sciences, 2011, 68, 1065-1077.	2.4	17
781	The crystal structure of an esterase from the hyperthermophilic microorganism Pyrobaculum calidifontis VA1 explains its enantioselectivity. Applied Microbiology and Biotechnology, 2011, 91, 1061-1072.	1.7	64
782	Protein Structure Databases. Molecular Biotechnology, 2011, 48, 183-198.	1.3	6
783	Crystal structures of Burkholderia cenocepacia dihydropteroate synthase in the apo-form and complexed with the product 7,8-dihydropteroate. BMC Structural Biology, 2011, 11, 21.	2.3	31

#	ARTICLE	IF	CITATIONS
784	Structural comparison of tRNA m1A58 methyltransferases revealed different molecular strategies to maintain their oligomeric architecture under extreme conditions. BMC Structural Biology, 2011, 11, 48.	2.3	18
785	Large-scale experimental studies show unexpected amino acid effects on protein expression and solubility in vivo in E. coli. Microbial Informatics and Experimentation, 2011, 1, 6.	7.6	30
786	Diffusion of hydrophobin proteins in solution and interactions with a graphite surface. BMC Biophysics, 2011, 4, 9.	4.4	17
787	Novel approach to controlled protein crystallization through ligandation of yttrium cations. Journal of Applied Crystallography, 2011, 44, 755-762.	1.9	57
788	The Protein Data Bank in Europe (PDBe): bringing structure to biology. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 324-330.	2.5	27
789	Overview of the<i>CCP</i>4 suite and current developments. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 235-242.	2.5	11,098
790	Structure of the effector-binding domain of the LysR-type transcription factor RovM from<i>Yersinia pseudotuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 81-90.	2.5	13
791	Structural characterization of CalO1: a putative orsellinic acid methyltransferase in the calicheamicin-biosynthetic pathway. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 197-203.	2.5	16
792	Structure of the sortase AcSrtC-1 from<i>Actinomyces oris</i>. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 212-217.	2.5	23
793	Macromolecular complexes in crystals and solutions. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 376-385.	2.5	54
794	Presenting your structures: the<i>CCP</i>4<i>mg</i>molecular-graphics software. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 386-394.	2.5	1,133
795	Scaffoldin-borne family 3b carbohydrate-binding module from the cellulosome of<i>Bacteroides cellulosolvens</i>: structural diversity and significance of calcium for carbohydrate binding. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 506-515.	2.5	18
796	Crystallographic determination of the disease-associated T1184R variant of complement regulator factor H. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 593-600.	2.5	7
797	High-resolution X-ray structure of the rabbit histidine triad nucleotide-binding protein 1 (rHINT1)â€“adenosine complex at 1.10â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 601-607.	2.5	6
798	Structure of 2-oxo-3-deoxygalactonate kinase from<i>Klebsiella pneumoniae</i>. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 678-689.	2.5	4
799	Structural features of peroxisomal catalase from the yeast<i>Hansenula polymorpha</i>. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 690-698.	2.5	10
800	High-resolution structure of a retroviral protease folded as a monomer. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 907-914.	2.5	22
801	The structure of<i>Serratia marcescens</i>Lip, a membrane-bound component of the type VI secretion system. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 1065-1072.	2.5	27

#	Article	IF	Citations
802	Deriving the ultrastructure of Î±-crustacyanin usingÂlower-resolution structural and biophysical methods. Journal of Synchrotron Radiation, 2011, 18, 79-83.	1.0	12
803	Structure of the dimeric form of CTP synthase from<i>Sulfolobus solfataricus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 201-208.	0.7	20
804	Pentapeptide-repeat proteins that act as topoisomerase poison resistance factors have a common dimer interface. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 296-302.	0.7	30
805	Structure of the extended-spectrum Î²-lactamase TEM-72 inhibited by citrate. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 303-306.	0.7	14
806	Crystallization and preliminary X-ray analysis of mannosyl-3-phosphoglycerate phosphatase from<i>Thermus thermophilus</i>HB27. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 390-396.	0.7	1
807	BrabA.11339.a: anomalous diffraction and ligand binding guide towards the elucidation of the function of a `putative Î²-lactamase-like protein' from<i>Brucella melitensis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1106-1112.	0.7	5
808	Structure of nitrilotriacetate monooxygenase component B from<i>Mycobacterium thermoresistibile</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1100-1105.	0.7	14
809	Structure of thymidylate kinase fromEhrlichia chaffeensis. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1090-1094.	0.7	2
810	Structure of theDrosophila melanogasterRab6 GTPase at 1.4â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 744-748.	0.7	3
811	Crystallization and preliminary X-ray analysis of a putative sensor histidine kinase domain: the C-terminal domain of HksP4 fromAquifex aeolicusVF5. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 803-807.	0.7	1
812	Structure of triosephosphate isomerase from<i>Cryptosporidium parvum</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1095-1099.	0.7	3
813	Structure of fructose bisphosphate aldolase from<i>Encephalitozoon cuniculi</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1055-1059.	0.7	4
814	Structure of filamin A immunoglobulin-like repeat 10 from<i>Homo sapiens</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 871-876.	0.7	14
815	Structure of fumarate hydratase from<i>Rickettsia prowazekii</i>, the agent of typhus and suspected relative of the mitochondria. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1123-1128.	0.7	3
816	Structures of respiratory syncytial virus nucleocapsid protein from two crystal forms: details of potential packing interactions in the native helical form. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1179-1183.	0.7	17
817	Structure of 3-ketoacyl-(acyl-carrier-protein) reductase from<i>Rickettsia prowazekii</i>at 2.25â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1118-1122.	0.7	10
818	Purification, crystallization and diffraction studies of the methyltransferases BT_2972 and BVU_3255 from antibiotic-resistant pathogens of the genusBacteroidesfrom the human intestine. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1359-1362.	0.7	0
819	Structure of cellobiose phosphorylase from<i>Clostridium thermocellum</i>in complex with phosphate. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1345-1349.	0.7	25

#	Article	IF	Citations
820	Crystallographic analysis of the C-terminal domain of the<i>Escherichia coli</i>lipoprotein BamC. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1350-1358.	0.7	20
821	Structure of hyperthermophilic Î²-glucosidase from <i>Pyrococcus furiosus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1473-1479.	0.7	29
822	Structure of the H107R variant of the extracellular domain of mouse NKR-P1A at 2.3â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1519-1523.	0.7	7
823	Comprehensive, atomic-level characterization of structurally characterized protein-protein interactions: the PICCOLO database. BMC Bioinformatics, 2011, 12, 313.	1.2	56
824	The UlaG protein family defines novel structural and functional motifs grafted on an ancient RNase fold. BMC Evolutionary Biology, 2011, 11, 273.	3.2	7
825	The crystal structure of alanine racemase from Streptococcus pneumoniae, a target for structure-based drug design. BMC Microbiology, 2011, 11, 116.	1.3	30
826	Structural studies on the enzyme complex isopropylmalate isomerase (LeuCD) from <i>Mycobacterium tuberculosis</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 35-49.	1.5	26
827	Structural, functional, and bioinformatics studies reveal a new snake venom homologue phospholipase A₂ class. Proteins: Structure, Function and Bioinformatics, 2011, 79, 61-78.	1.5	44
828	Crystal structure of isoamyl acetateâ€hydrolyzing esterase from <i>Saccharomyces cerevisiae</i> reveals a novel active site architecture and the basis of substrate specificity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 662-668.	1.5	16
829	Crystal structure of curcuminoid synthase CUS from <i>Oryza sativa</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 669-673.	1.5	8
830	Insights into <i>Mycoplasma genitalium</i> metabolism revealed by the structure of MG289, an extracytoplasmic thiamine binding lipoprotein. Proteins: Structure, Function and Bioinformatics, 2011, 79, 528-536.	1.5	10
831	Structures of parasitic CDPK domains point to a common mechanism of activation. Proteins: Structure, Function and Bioinformatics, 2011, 79, 803-820.	1.5	74
832	Structure of the Câ€terminal hemeâ€binding domain of THAP domain containing protein 4 from <i>Homo sapiens</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1337-1341.	1.5	28
833	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1215-1229.	1.5	29
834	Structural basis for a ribofuranosyl binding protein: Insights into the furanose specific transport. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1352-1357.	1.5	4
835	Crystal structure of the GAFâ€B domain from human phosphodiesterase 5. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1682-1687.	1.5	4
836	Structure of an archaealâ€type phosphoenolpyruvate carboxylase sensitive to inhibition by aspartate. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1820-1829.	1.5	6
837	The structure of a <scp>D</scp>â€lyxose isomerase from the Ïƒ^B regulon of <i>Bacillus subtilis</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2015-2019.	1.5	12

#	ARTICLE	IF	CITATIONS
838	Crystal structure of a metalâ€dependent phosphoesterase (YP_910028.1) from <i>Bifidobacterium adolescentis</i>: Computational prediction and experimental validation of phosphoesterase activity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2146-2160.	1.5	11
839	Cover and spacer insertions: Small nonhydrophobic accessories that assist protein oligomerization. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2372-2379.	1.5	11
840	Structure of the catalytic domain of glucuronoyl esterase Cip2 from <i>Hypocrea jecorina</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2588-2592.	1.5	50
841	Docking and free energy simulations to predict conformational domains involved in hCGâ€“LH receptor interactions using recombinant antibodies. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3108-3122.	1.5	7
842	Assessment of ligandâ€binding residue predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 126-136.	1.5	72
843	Assessment of template based protein structure predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 37-58.	1.5	152
844	The crystal structures of the <i>Salmonella</i> type III secretion system tip protein SipD in complex with deoxycholate and chenodeoxycholate. Protein Science, 2011, 20, 75-86.	3.1	62
845	Crystal structure of the sensory domain of <i>Escherichia coli</i> CadC, a member of the ToxRâ€like protein family. Protein Science, 2011, 20, 656-669.	3.1	26
846	Selfâ€association studies of the bifunctional <i>N</i>â€acetylglucosamineâ€1â€phosphate uridyltransferase from <i>Escherichia coli</i>. Protein Science, 2011, 20, 745-752.	3.1	3
847	Crystal structure of New Delhi metalloâ€î²â€lactamase reveals molecular basis for antibiotic resistance. Protein Science, 2011, 20, 1484-1491.	3.1	175
848	Crystal structure of Nâ€domain of FKBP22 from <i>Shewanella</i> sp. SIB1: Dimer dissociation by disruption of Valâ€Leu knot. Protein Science, 2011, 20, 1755-1764.	3.1	13
849	Rational disruption of the oligomerization of the miniâ€ferritin <i>E. coli</i> DPS through proteinâ€protein interface mutation. Protein Science, 2011, 20, 1907-1917.	3.1	24
850	Featureâ€based classification of native and nonâ€native proteinâ€“protein interactions: Comparing supervised and semiâ€supervised learning approaches. Proteomics, 2011, 11, 4321-4330.	1.3	13
851	Contribution of Nonâ€Canonical Interactions to the Stability of Sm/LSm Oligomeric Assemblies. Molecular Informatics, 2011, 30, 430-442.	1.4	5
852	Using correlated parameters for improved ranking of proteinâ€“protein docking decoys. Journal of Computational Chemistry, 2011, 32, 787-796.	1.5	15
853	Crystal structure of an arthritogenic anticollagen immune complex. Arthritis and Rheumatism, 2011, 63, 3740-3748.	6.7	25
854	Small angle Xâ€ray scattering as a complementary tool for highâ€throughput structural studies. Biopolymers, 2011, 95, 517-530.	1.2	69
855	Reâ€structuring protein crystals porosity for biotemplating by chemical modification of lysine residues. Biotechnology and Bioengineering, 2011, 108, 1-11.	1.7	10

#	Article	IF	Citations
856	Tolerance of Î²â€diketone hydrolases as representatives of the crotonase superfamily towards organic solvents. Biotechnology and Bioengineering, 2011, 108, 2815-2822.	1.7	7
857	Inter-subunit interactions in erythroid and non-erythroid spectrins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 420-427.	1.1	5
858	The lipoproteins of cyanobacterial photosystem II. Journal of Photochemistry and Photobiology B: Biology, 2011, 104, 191-203.	1.7	49
859	Non-covalent interactions across subunit interfaces in Sm proteins. Journal of Theoretical Biology, 2011, 271, 18-26.	0.8	5
860	Protein Modifications Giving Rise to Homo-oligomers. Progress in Molecular Biology and Translational Science, 2011, 103, 187-229.	0.9	0
861	Novel Pentameric Structure of the Diarrhea-Inducing Region of the Rotavirus Enterotoxigenic Protein NSP4. Journal of Virology, 2011, 85, 12721-12732.	1.5	23
862	Crystal structure of the human astrovirus capsid spike. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12681-12686.	3.3	77
863	COCOMAPS: a web application to analyze and visualize contacts at the interface of biomolecular complexes. Bioinformatics, 2011, 27, 2915-2916.	1.8	253
864	Structural and Immunologic Characterization of Ara h 1, a Major Peanut Allergen. Journal of Biological Chemistry, 2011, 286, 39318-39327.	1.6	89
865	Structural Basis for Antiviral Inhibition of the Main Protease, 3C, from Human Enterovirus 93. Journal of Virology, 2011, 85, 10764-10773.	1.5	20
866	Kinked Î²-strands mediate high-affinity recognition of mRNA targets by the germ-cell regulator DAZL. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18266-18271.	3.3	58
867	The RCSB Protein Data Bank: redesigned web site and web services. Nucleic Acids Research, 2011, 39, D392-D401.	6.5	549
868	A Structural Model of the Sgt2 Protein and Its Interactions with Chaperones and the Get4/Get5 Complex. Journal of Biological Chemistry, 2011, 286, 34325-34334.	1.6	58
869	PCNA directs type 2 RNase H activity on DNA replication and repair substrates. Nucleic Acids Research, 2011, 39, 3652-3666.	6.5	112
870	Structure of QnrB1, a Plasmid-mediated Fluoroquinolone Resistance Factor. Journal of Biological Chemistry, 2011, 286, 25265-25273.	1.6	72
871	Structural basis for the role of the Sir3 AAA⁺ domain in silencing: interaction with Sir4 and unmethylated histone H3K79. Genes and Development, 2011, 25, 1835-1846.	2.7	40
872	Structural insights into cis element recognition of non-polyadenylated RNAs by the Nab3-RRM. Nucleic Acids Research, 2011, 39, 337-346.	6.5	33
873	A prominent Â-hairpin structure in the winged-helix domain of RECQ1 is required for DNA unwinding and oligomer formation. Nucleic Acids Research, 2011, 39, 1703-1717.	6.5	52

#	Article	IF	Citations
874	The E3 Ubiquitin Ligase- and Protein Phosphatase 2A (PP2A)-binding Domains of the Alpha4 Protein Are Both Required for Alpha4 to Inhibit PP2A Degradation. Journal of Biological Chemistry, 2011, 286, 17665-17671.	1.6	40
875	Crystal structures of two active proliferating cell nuclear antigens (PCNAs) encoded by <i>Thermococcus kodakaraensis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2711-2716.	3.3	29
876	Structural basis for complement factor I control and its disease-associated sequence polymorphisms. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12839-12844.	3.3	118
877	Structural Basis for Two-component System Inhibition and Pilus Sensing by the Auxiliary CpxP Protein. Journal of Biological Chemistry, 2011, 286, 9805-9814.	1.6	59
878	Characterization of the Interactions between the Nucleoprotein and the Phosphoprotein of Henipavirus. Journal of Biological Chemistry, 2011, 286, 13583-13602.	1.6	65
879	Adaptive evolution of threonine deaminase in plant defense against insect herbivores. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5897-5902.	3.3	75
880	High-resolution structural insights on the sugar-recognition and fusion tag properties of a versatile Î²-trefoil lectin domain from the mushroom Laetiporus sulphureus. Glycobiology, 2011, 21, 1349-1361.	1.3	34
881	A Dimeric Rep Protein Initiates Replication of a Linear Archaeal Virus Genome: Implications for the Rep Mechanism and Viral Replication. Journal of Virology, 2011, 85, 925-931.	1.5	36
882	Molecular Rearrangements Involved in the Capsid Shell Maturation of Bacteriophage T7. Journal of Biological Chemistry, 2011, 286, 234-242.	1.6	55
883	Structure of the PilM-PilN Inner Membrane Type IV Pilus Biogenesis Complex from Thermus thermophilus. Journal of Biological Chemistry, 2011, 286, 24434-24442.	1.6	72
884	M-ORBIS: Mapping of mOleculaR Binding sItes and Surfaces. Nucleic Acids Research, 2011, 39, 30-43.	6.5	15
885	Structural Basis of Neutralization of the Major Toxic Component from the Scorpion Centruroides noxius Hoffmann by a Human-derived Single-chain Antibody Fragment. Journal of Biological Chemistry, 2011, 286, 20892-20900.	1.6	19
886	HIV-1 Escape from the CCR5 Antagonist Maraviroc Associated with an Altered and Less-Efficient Mechanism of gp120-CCR5 Engagement That Attenuates Macrophage Tropism. Journal of Virology, 2011, 85, 4330-4342.	1.5	70
887	Structure and binding analysis of Polyporus squamosus lectin in complex with the Neu5AcÎ±2-6GalÎ²1-4GlcNAc human-type influenza receptor. Glycobiology, 2011, 21, 973-984.	1.3	53
888	BISC: Binary SubComplexes in proteins database. Nucleic Acids Research, 2011, 39, D705-D711.	6.5	4
889	PKA Phosphorylation of NDE1 Is DISC1/PDE4 Dependent and Modulates Its Interaction with LIS1 and NDEL1. Journal of Neuroscience, 2011, 31, 9043-9054.	1.7	72
890	Structure of Burkholderia cepacia UDP-Glucose Dehydrogenase (UGD) BceC and Role of Tyr10 in Final Hydrolysis of UGD Thioester Intermediate. Journal of Bacteriology, 2011, 193, 3978-3987.	1.0	25
891	Structure of the Periplasmic Stress Response Protein CpxP. Journal of Bacteriology, 2011, 193, 2149-2157.	1.0	41

#	ARTICLE	IF	CITATIONS
892	Crystal Structure of Archaeoglobus fulgidus CTP:Inositol-1-Phosphate Cytidylyltransferase, a Key Enzyme for Di-myo-Inositol-Phosphate Synthesis in (Hyper)Thermophiles. Journal of Bacteriology, 2011, 193, 2177-2185.	1.0	16
893	Temperature-Sensitive Mutants of RNase E in Salmonella enterica. Journal of Bacteriology, 2011, 193, 6639-6650.	1.0	7
894	SDM--a server for predicting effects of mutations on protein stability and malfunction. Nucleic Acids Research, 2011, 39, W215-W222.	6.5	453
895	Structure-Activity Analysis of Cathepsin K/Chondroitin 4-Sulfate Interactions. Journal of Biological Chemistry, 2011, 286, 8988-8998.	1.6	33
896	Defining a Structural and Kinetic Rationale for Paralogous Copies of Phenylacetate-CoA Ligases from the Cystic Fibrosis Pathogen Burkholderia cenocepacia J2315. Journal of Biological Chemistry, 2011, 286, 15577-15585.	1.6	28
897	Structure of Human C8 Protein Provides Mechanistic Insight into Membrane Pore Formation by Complement. Journal of Biological Chemistry, 2011, 286, 17585-17592.	1.6	94
898	Characterization of a Dipartite Iron Uptake System from Uropathogenic Escherichia coli Strain F11. Journal of Biological Chemistry, 2011, 286, 25317-25330.	1.6	34
899	Mapping the Îº B Kinase Î² (IKKÎ²)-binding Interface of the B14 Protein, a Vaccinia Virus Inhibitor of IKKÎ²-mediated Activation of Nuclear Factor ÎºB. Journal of Biological Chemistry, 2011, 286, 20727-20735.	1.6	48
900	Molecular Basis for the Unique Role of the AAA+ Chaperone ClpV in Type VI Protein Secretion. Journal of Biological Chemistry, 2011, 286, 30010-30021.	1.6	95
901	Î±-Galactosidase/Sucrose Kinase (AgaSK), a Novel Bifunctional Enzyme from the Human Microbiome Coupling Galactosidase and Kinase Activities. Journal of Biological Chemistry, 2011, 286, 40814-40823.	1.6	32
902	Molecular Recognition of Leucine-Aspartate Repeat (LD) Motifs by the Focal Adhesion Targeting Homology Domain of Cerebral Cavernous Malformation 3 (CCM3). Journal of Biological Chemistry, 2011, 286, 26138-26147.	1.6	35
903	Molecular Analysis of the Interaction of the Snake Venom Rhodocytin with the Platelet Receptor CLEC-2. Toxins, 2011, 3, 991-1003.	1.5	10
904	Compensated pathogenic deviations. Biomolecular Concepts, 2011, 2, 281-292.	1.0	7
905	Toward the estimation of the absolute quality of individual protein structure models. Bioinformatics, 2011, 27, 343-350.	1.8	1,855
906	Crystal structure of human natural cytotoxicity receptor NKp30 and identification of its ligand binding site. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6223-6228.	3.3	60
907	Molecular Recognition of Chymotrypsin by the Serine Protease Inhibitor Ecotin from Yersinia pestis. Journal of Biological Chemistry, 2011, 286, 24015-24022.	1.6	15
908	New Insights into the Mechanism of Odorant Detection by the Malaria-transmitting Mosquito Anopheles gambiae. Journal of Biological Chemistry, 2011, 286, 34175-34183.	1.6	28
909	Atomic Structure of Bacteriophage Sf6 Tail Needle Knob. Journal of Biological Chemistry, 2011, 286, 30867-30877.	1.6	33

#	ARTICLE	IF	CITATIONS
910	Structures of Phytophthora RXLR Effector Proteins. Journal of Biological Chemistry, 2011, 286, 35834-35842.	1.6	178
911	The Crystal Structure and Mechanism of an Unusual Oxidoreductase, GilR, Involved in Gilvocarcin V Biosynthesis. Journal of Biological Chemistry, 2011, 286, 23533-23543.	1.6	21
912	The Structure of the Plakin Domain of Plectin Reveals a Non-canonical SH3 Domain Interacting with Its Fourth Spectrin Repeat. Journal of Biological Chemistry, 2011, 286, 12429-12438.	1.6	43
913	Crystal Structure of the cis-Dimer of Nectin-1. Journal of Biological Chemistry, 2011, 286, 12659-12669.	1.6	45
914	Structural and Biological Properties of the Drosophila Insulin-like Peptide 5 Show Evolutionary Conservation. Journal of Biological Chemistry, 2011, 286, 661-673.	1.6	61
915	Novel Folding and Stability Defects Cause a Deficiency of Human Glutathione Transferase Omega 1. Journal of Biological Chemistry, 2011, 286, 4271-4279.	1.6	24
916	Insights into Association of the NuRD Complex with FOG-1 from the Crystal Structure of an RbAp48Â·FOG-1 Complex. Journal of Biological Chemistry, 2011, 286, 1196-1203.	1.6	89
917	Structural Basis of Tumor Suppressor in Lung Cancer 1 (TSLC1) Binding to Differentially Expressed in Adenocarcinoma of the Lung (DAL-1/4.1B). Journal of Biological Chemistry, 2011, 286, 4511-4516.	1.6	22
918	TCRs Used in Cancer Gene Therapy Cross-React with MART-1/Melan-A Tumor Antigens via Distinct Mechanisms. Journal of Immunology, 2011, 187, 2453-2463.	0.4	120
919	Idas, a Novel Phylogenetically Conserved Geminin-related Protein, Binds to Geminin and Is Required for Cell Cycle Progression. Journal of Biological Chemistry, 2011, 286, 23234-23246.	1.6	43
920	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. Nature, 2011, 480, 336-343.	13.7	794
921	Computational design of a symmetric homodimer using Î²-strand assembly. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20562-20567.	3.3	71
922	Crystal Structure of Bacillus anthracis Phosphoglucosamine Mutase, an Enzyme in the Peptidoglycan Biosynthetic Pathway. Journal of Bacteriology, 2011, 193, 4081-4087.	1.0	39
923	The Leishmania donovani UMP Synthase Is Essential for Promastigote Viability and Has an Unusual Tetrameric Structure That Exhibits Substrate-controlled Oligomerization. Journal of Biological Chemistry, 2011, 286, 20930-20941.	1.6	38
924	Unexpected Diversity of Chlorite Dismutases: a Catalytically Efficient Dimeric Enzyme from Nitrobacter winogradskyi. Journal of Bacteriology, 2011, 193, 2408-2417.	1.0	76
925	The Virulence Factor PEB4 (Cj0596) and the Periplasmic Protein Cj1289 Are Two Structurally Related SurA-like Chaperones in the Human Pathogen Campylobacter jejuni. Journal of Biological Chemistry, 2011, 286, 21254-21265.	1.6	33
926	X-Ray Structure and Site-Directed Mutagenesis Analysis of the<i>Escherichia coli</i>Colicin M Immunity Protein. Journal of Bacteriology, 2011, 193, 205-214.	1.0	21
927	Ligand-induced Conformational Changes within a Hexameric Acyl-CoA Thioesterase. Journal of Biological Chemistry, 2011, 286, 35643-35649.	1.6	11

#	ARTICLE	IF	CITATIONS
928	Crystal Structures of Staphylococcus epidermidis Mevalonate Diphosphate Decarboxylase Bound to Inhibitory Analogs Reveal New Insight into Substrate Binding and Catalysis. Journal of Biological Chemistry, 2011, 286, 23900-23910.	1.6	29
929	The Structure of the Kinesin-1 Motor-Tail Complex Reveals the Mechanism of Autoinhibition. Science, 2011, 333, 883-885.	6.0	159
930	Structural and Functional Analysis of a New Subfamily of Glycosyltransferases Required for Glycosylation of Serine-rich Streptococcal Adhesins. Journal of Biological Chemistry, 2011, 286, 27048-27057.	1.6	26
931	Remote control of regioselectivity in acyl-acyl carrier protein-desaturases. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16594-16599.	3.3	59
932	Molecular Basis of 1,6-Anhydro Bond Cleavage and Phosphoryl Transfer by Pseudomonas aeruginosa 1,6-Anhydro-N-acetylmuramic Acid Kinase. Journal of Biological Chemistry, 2011, 286, 12283-12291.	1.6	24
933	Structure and Mechanism of the Lipooligosaccharide Sialyltransferase from Neisseria meningitidis. Journal of Biological Chemistry, 2011, 286, 37237-37248.	1.6	36
934	Crystal Structure of Î²-Barrel Assembly Machinery BamCD Protein Complex. Journal of Biological Chemistry, 2011, 286, 39116-39121.	1.6	71
935	Crystal Structure of Uronate Dehydrogenase from Agrobacterium tumefaciens. Journal of Biological Chemistry, 2011, 286, 27294-27300.	1.6	25
936	Crystal Structure of Heterodimeric Hexaprenyl Diphosphate Synthase from Micrococcus luteus B-P 26 Reveals That the Small Subunit Is Directly Involved in the Product Chain Length Regulation. Journal of Biological Chemistry, 2011, 286, 3729-3740.	1.6	23
937	Crystal Structure of the Pseudomonas aeruginosa Virulence Factor Regulator. Journal of Bacteriology, 2011, 193, 4069-4074.	1.0	14
938	Conformational Flexibility of the Ligand-Binding Domain Dimer in Kainate Receptor Gating and Desensitization. Journal of Neuroscience, 2011, 31, 2916-2924.	1.7	27
939	Mechanism of ubiquitylation by dimeric RING ligase RNF4. Nature Structural and Molecular Biology, 2011, 18, 1052-1059.	3.6	157
940	Mechanism of actin filament nucleation by the bacterial effector VopL. Nature Structural and Molecular Biology, 2011, 18, 1068-1074.	3.6	56
941	Structures of SAS-6 Suggest Its Organization in Centrioles. Science, 2011, 331, 1196-1199.	6.0	284
942	Structural basis for the removal of ubiquitin and interferon-stimulated gene 15 by a viral ovarian tumor domain-containing protease. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2222-2227.	3.3	90
943	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2011, 39, D402-D410.	6.5	64
944	Crystal structure of Toll-like receptor adaptor MAL/TIRAP reveals the molecular basis for signal transduction and disease protection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14879-14884.	3.3	123
945	Proteinâ€“protein binding affinity prediction on a diverse set of structures. Bioinformatics, 2011, 27, 3002-3009.	1.8	103

#	Article	IF	Citations
946	The ancestral role of ATP hydrolysis in type II topoisomerases: prevention of DNA double-strand breaks. Nucleic Acids Research, 2011, 39, 6327-6339.	6.5	62
947	Structure-based approach to rationally design a chimeric protein for an effective vaccine against Group B <i>Streptococcus</i> infections. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10278-10283.	3.3	132
948	Changes in Dynamics upon Oligomerization Regulate Substrate Binding and Allostery in Amino Acid Kinase Family Members. PLoS Computational Biology, 2011, 7, e1002201.	1.5	49
949	Structural and Functional Studies on the Interaction of GspC and GspD in the Type II Secretion System. PLoS Pathogens, 2011, 7, e1002228.	2.1	83
950	Towards a Structural Comprehension of Bacterial Type VI Secretion Systems: Characterization of the TssJ-TssM Complex of an Escherichia coli Pathovar. PLoS Pathogens, 2011, 7, e1002386.	2.1	132
951	Structural insights into quinolone antibiotic resistance mediated by pentapeptide repeat proteins: conserved surface loops direct the activity of a Qnr protein from a Gram-negative bacterium. Nucleic Acids Research, 2011, 39, 3917-3927.	6.5	74
952	The crystal structure of the ubiquitin-like (UbL) domain of human homologue A of Rad23 (hHR23A) protein. Protein Engineering, Design and Selection, 2011, 24, 131-138.	1.0	4
953	Xwalk: computing and visualizing distances in cross-linking experiments. Bioinformatics, 2011, 27, 2163-2164.	1.8	130
954	Architecture of the flagellar rotor. EMBO Journal, 2011, 30, 2962-2971.	3.5	91
955	Crystal structures of an archaeal class II DNA photolyase and its complex with UV-damaged duplex DNA. EMBO Journal, 2011, 30, 4437-4449.	3.5	82
956	The Binding of Triclosan to SmeT, the Repressor of the Multidrug Efflux Pump SmeDEF, Induces Antibiotic Resistance in Stenotrophomonas maltophilia. PLoS Pathogens, 2011, 7, e1002103.	2.1	94
957	Membrane Remodeling by the Double-Barrel Scaffolding Protein of Poxvirus. PLoS Pathogens, 2011, 7, e1002239.	2.1	44
958	Molecular Recognition of the Tes LIM2â€"3 Domains by the Actin-related Protein Arp7A. Journal of Biological Chemistry, 2011, 286, 11543-11554.	1.6	36
959	Structural basis for cell surface patterning through NetrinG-NGL interactions. EMBO Journal, 2011, 30, 4479-4488.	3.5	58
960	Structural Basis for Partial Redundancy in a Class of Transcription Factors, the LIM Homeodomain Proteins, in Neural Cell Type Specification. Journal of Biological Chemistry, 2011, 286, 42971-42980.	1.6	35
961	Structure of a Light-Activated LOV Protein Dimer That Regulates Transcription. Science Signaling, 2011, 4, ra50.	1.6	108
962	A conserved lysine residue of plant Whirly proteins is necessary for higher order protein assembly and protection against DNA damage. Nucleic Acids Research, 2012, 40, 258-269.	6.5	48
963	Functional comparison of <i>Deinococcus radiodurans</i> Dps proteins suggests distinct <i>in vivo</i> roles. Biochemical Journal, 2012, 447, 381-391.	1.7	26

#	ARTICLE	IF	CITATIONS
964	A flexible brace maintains the assembly of a hexameric replicative helicase during DNA unwinding. Nucleic Acids Research, 2012, 40, 2271-2283.	6.5	12
965	Assessing the range of kinase autoinhibition mechanisms in the insulin receptor family. Biochemical Journal, 2012, 448, 213-220.	1.7	75
966	Insights into Chi recognition from the structure of an AddAB-type helicase-nuclease complex. EMBO Journal, 2012, 31, 1568-1578.	3.5	56
967	Biochemical identification and crystal structure of kynurenine formamidase from <i>Drosophila melanogaster</i>. Biochemical Journal, 2012, 446, 253-260.	1.7	27
968	Insights into ubiquitin-conjugating enzyme/ co-activator interactions from the structure of the Pex4p:Pex22p complex. EMBO Journal, 2012, 31, 391-402.	3.5	52
969	A stomatin dimer modulates the activity of acid-sensing ion channels. EMBO Journal, 2012, 31, 3635-3646.	3.5	72
970	The substrate/product-binding modes of a novel GH120 Î²-xylosidase (XylC) from <i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485. Biochemical Journal, 2012, 448, 401-407.	1.7	16
971	MpaA is a murein-tripeptide-specific zinc carboxypeptidase that functions as part of a catabolic pathway for peptidoglycan-derived peptides in Î³-proteobacteria. Biochemical Journal, 2012, 448, 329-341.	1.7	12
972	Tail-anchor targeting by a Get3 tetramer: the structure of an archaeal homologue. EMBO Journal, 2012, 31, 707-719.	3.5	37
973	Novel Clostridium thermocellum Type I Cohesin-Dockerin Complexes Reveal a Single Binding Mode. Journal of Biological Chemistry, 2012, 287, 44394-44405.	1.6	27
974	Structural Basis for Paxillin Binding and Focal Adhesion Targeting of Î²-Parvin. Journal of Biological Chemistry, 2012, 287, 32566-32577.	1.6	33
975	Mutational and Structural Analysis of l - N -Carbamoylase Reveals New Insights into a Peptidase M20/M25/M40 Family Member. Journal of Bacteriology, 2012, 194, 5759-5768.	1.0	23
976	Substrate Recognition Mechanism and Substrate-Dependent Conformational Changes of an ROK Family Glucokinase from Streptomyces griseus. Journal of Bacteriology, 2012, 194, 607-616.	1.0	28
977	Crystal Structure of the VgrG1 Actin Cross-linking Domain of the Vibrio cholerae Type VI Secretion System. Journal of Biological Chemistry, 2012, 287, 38190-38199.	1.6	60
978	Cloning, Baeyer-Villiger Biooxidations, and Structures of the Camphor Pathway 2-Oxo-Î” ³ -4,5,5-Trimethylcyclopentenylacetyl-Coenzyme A Monooxygenase of Pseudomonas putida ATCC 17453. Applied and Environmental Microbiology, 2012, 78, 2200-2212.	1.4	51
979	IBIS (Inferred Biomolecular Interaction Server) reports, predicts and integrates multiple types of conserved interactions for proteins. Nucleic Acids Research, 2012, 40, D834-D840.	6.5	88
980	Structure and mechanism of the polynucleotide kinase component of the bacterial Pnkp-Hen1 RNA repair system. Rna, 2012, 18, 2277-2286.	1.6	18
981	Structural Mechanism of ATP-induced Polymerization of the Partition Factor ParF. Journal of Biological Chemistry, 2012, 287, 26146-26154.	1.6	31

#	Article	IF	Citations
982	Protein Databases on the Internet. Current Protocols in Molecular Biology, 2012, 97, Unit 19.4..	2.9	6
983	Crystal Structure of Escherichia coli Diaminopropionate Ammonia-lyase Reveals Mechanism of Enzyme Activation and Catalysis. Journal of Biological Chemistry, 2012, 287, 20369-20381.	1.6	15
984	Characterization of a Phanerochaete chrysosporium Glutathione Transferase Reveals a Novel Structural and Functional Class with Ligandin Properties. Journal of Biological Chemistry, 2012, 287, 39001-39011.	1.6	33
985	Dissecting the proteinâ€"RNA interface: the role of protein surface shapes and RNA secondary structures in proteinâ€"RNA recognition. Nucleic Acids Research, 2012, 40, 3299-3306.	6.5	50
986	Structural Insights into the Catalytic Mechanism of Escherichia coli Selenophosphate Synthetase. Journal of Bacteriology, 2012, 194, 499-508.	1.0	21
987	Structural and Functional Characterization of VanG d-Ala:d-Ser Ligase Associated with Vancomycin Resistance in Enterococcus faecalis. Journal of Biological Chemistry, 2012, 287, 37583-37592.	1.6	23
988	Crystal structure of the DNA-bound VapBC2 antitoxin/toxin pair from Rickettsia felis. Nucleic Acids Research, 2012, 40, 3245-3258.	6.5	51
989	Structure of the Cytoplasmic Region of PelD, a Degenerate Diguanylate Cyclase Receptor That Regulates Exopolysaccharide Production in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2012, 287, 23582-23593.	1.6	101
990	Invariant Gly Residue Is Important for Î±-Defensin Folding, Dimerization, and Function. Journal of Biological Chemistry, 2012, 287, 18900-18912.	1.6	30
991	Interactions of Isolated C-terminal Fragments of Neural Wiskott-Aldrich Syndrome Protein (N-WASP) with Actin and Arp2/3 Complex. Journal of Biological Chemistry, 2012, 287, 34646-34659.	1.6	38
992	Crystal structure of the human PRMT5:MEP50 complex. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17960-17965.	3.3	261
993	Design of Meningococcal Factor H Binding Protein Mutant Vaccines That Do Not Bind Human Complement Factor H. Infection and Immunity, 2012, 80, 2667-2677.	1.0	24
994	Assignment of protein sequences to existing domain and family classification systems: Pfam and the PDB. Bioinformatics, 2012, 28, 2763-2772.	1.8	56
995	Wzy-Dependent Bacterial Capsules as Potential Drug Targets. Current Drug Targets, 2012, 13, 1421-1431.	1.0	13
996	Bioinformatics of Protein-Protein Interfaces and Small Molecule Effectors. Current Bioinformatics, 2012, 7, 159-172.	0.7	1
997	Structural study of TTR-52 reveals the mechanism by which a bridging molecule mediates apoptotic cell engulfment. Genes and Development, 2012, 26, 1339-1350.	2.7	15
998	Identification of Key Residues for the Binding of Glucagon to the N-Terminal Domain of its Receptor: An Alanine Scan and Modeling Study. Hormone and Metabolic Research, 2012, 44, 804-809.	0.7	6
999	Crystal structure of ISG54 reveals a novel RNA binding structure and potential functional mechanisms. Cell Research, 2012, 22, 1328-1338.	5.7	76

#	Article	IF	Citations
1000	Structural analysis of an eIF3 subcomplex reveals conserved interactions required for a stable and proper translation pre-initiation complex assembly. Nucleic Acids Research, 2012, 40, 2294-2311.	6.5	64
1002	Biochemical and Structural Characterization of the <i>Arabidopsis</i> Bifunctional Enzyme Dethiobiotin Synthetaseâ€"Diaminopelargonic Acid Aminotransferase: Evidence for Substrate Channeling in Biotin Synthesis. Plant Cell, 2012, 24, 1608-1625.	3.1	25
1003	Structural insight into how <i>Pseudomonas aeruginosa</i> peptidoglycanhydrolase Tse1 and its immunity protein Tsi1 function. Biochemical Journal, 2012, 448, 201-211.	1.7	22
1004	The binding of Varp to VAMP7 traps VAMP7 in a closed, fusogenically inactive conformation. Nature Structural and Molecular Biology, 2012, 19, 1300-1309.	3.6	68
1005	The First Structure of Polarity Suppression Protein, Psu from Enterobacteria Phage P4, Reveals a Novel Fold and a Knotted Dimer. Journal of Biological Chemistry, 2012, 287, 44667-44675.	1.6	19
1006	Crystal Structure of the N-terminal Domain of the Yeast General Corepressor Tup1p and Its Functional Implications. Journal of Biological Chemistry, 2012, 287, 26528-26538.	1.6	20
1007	Structural basis of coactivation of liver receptor homolog-1 by Î²-catenin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 143-148.	3.3	55
1008	Structure of Salmonella Effector Protein SopB N-terminal Domain in Complex with Host Rho GTPase Cdc42. Journal of Biological Chemistry, 2012, 287, 13348-13355.	1.6	20
1009	Structure and Mechanism of Human UDP-xylose Synthase. Journal of Biological Chemistry, 2012, 287, 31349-31358.	1.6	36
1010	Solution NMR Structure of the Ca2+-bound N-terminal Domain of CaBP7. Journal of Biological Chemistry, 2012, 287, 38231-38243.	1.6	7
1011	Structural Basis for Small G Protein Effector Interaction of Ras-related Protein 1 (Rap1) and Adaptor Protein Krev Interaction Trapped 1 (KRIT1). Journal of Biological Chemistry, 2012, 287, 22317-22327.	1.6	46
1012	Nucleoporin Nup50 Stabilizes Closed Conformation of Armadillo repeat 10 in Importin Î±5. Journal of Biological Chemistry, 2012, 287, 2022-2031.	1.6	22
1013	Extra-domain B in Oncofetal Fibronectin Structurally Promotes Fibrillar Head-to-tail Dimerization of Extracellular Matrix Protein. Journal of Biological Chemistry, 2012, 287, 17578-17588.	1.6	34
1014	Crystal Structures and Small-angle X-ray Scattering Analysis of UDP-galactopyranose Mutase from the Pathogenic Fungus Aspergillus fumigatus. Journal of Biological Chemistry, 2012, 287, 9041-9051.	1.6	33
1015	Structural Basis for Membrane Binding Specificity of the Bin/Amphiphysin/Rvs (BAR) Domain of Arfaptin-2 Determined by Arl1 GTPase. Journal of Biological Chemistry, 2012, 287, 25478-25489.	1.6	31
1016	Insights into Structural Network Responsible for Oligomerization and Activity of Bacterial Virulence Regulator Caseinolytic Protease P (ClpP) Protein. Journal of Biological Chemistry, 2012, 287, 9484-9494.	1.6	62
1017	Mouse Clr-g, a Ligand for NK Cell Activation Receptor NKR-P1F: Crystal Structure and Biophysical Properties. Journal of Immunology, 2012, 189, 4881-4889.	0.4	21
1018	Structural Basis for Morpheein-type Allosteric Regulation of Escherichia coli Glucosamine-6-phosphate Synthase. Journal of Biological Chemistry, 2012, 287, 34533-34546.	1.6	19

#	ARTICLE	IF	CITATIONS
1019	Mapping Ultra-weak Protein-Protein Interactions between Heme Transporters of Staphylococcus aureus. Journal of Biological Chemistry, 2012, 287, 16477-16487.	1.6	43
1020	Multiple Binding Sites on the Pyrin Domain of ASC Protein Allow Self-association and Interaction with NLRP3 Protein. Journal of Biological Chemistry, 2012, 287, 41732-41743.	1.6	146
1021	The Extracellular Protein Factor Epf from Streptococcus pyogenes Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. Journal of Biological Chemistry, 2012, 287, 38178-38189.	1.6	18
1022	Optimizing ring assembly reveals the strength of weak interactions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2348-2353.	3.3	41
1023	The molecular basis of ubiquitin-like protein NEDD8 deamidation by the bacterial effector protein Cif. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1830-E1838.	3.3	28
1024	Structure of a Calcium-dependent 11R-Lipoxygenase Suggests a Mechanism for Ca2+ Regulation. Journal of Biological Chemistry, 2012, 287, 22377-22386.	1.6	52
1025	Structure of the heterodimer of human NONO and paraspeckle protein component 1 and analysis of its role in subnuclear body formation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4846-4850.	3.3	132
1026	Structure of the Nuclear Factor ÎºB-inducing Kinase (NIK) Kinase Domain Reveals a Constitutively Active Conformation. Journal of Biological Chemistry, 2012, 287, 27326-27334.	1.6	44
1027	Mitochondrial localization and structure-based phosphate activation mechanism of Glutaminase C with implications for cancer metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1092-1097.	3.3	225
1028	Structure of the surface layer of the methanogenic archaean <i>Methanosarcina acetivorans</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11812-11817.	3.3	67
1029	Structural and functional analysis of phosphorylation-specific binders of the kinase ERK from designed ankyrin repeat protein libraries. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2248-57.	3.3	91
1030	Biophysical and computational fragment-based approaches to targeting proteinâ€"protein interactions: applications in structure-guided drug discovery. Quarterly Reviews of Biophysics, 2012, 45, 383-426.	2.4	90
1031	Structures of the PelD Cyclic Diguanylate Effector Involved in Pellicle Formation in Pseudomonas aeruginosa PAO1. Journal of Biological Chemistry, 2012, 287, 30191-30204.	1.6	37
1032	Crystal Structure of N-Glycosylated Human Glypican-1 Core Protein. Journal of Biological Chemistry, 2012, 287, 14040-14051.	1.6	54
1033	Diversity in the C3b Convertase Contact Residues and Tertiary Structures of the Staphylococcal Complement Inhibitor (SCIN) Protein Family. Journal of Biological Chemistry, 2012, 287, 628-640.	1.6	26
1034	Crystal Structures of N-Acetylmannosamine Kinase Provide Insights into Enzyme Activity and Inhibition. Journal of Biological Chemistry, 2012, 287, 13656-13665.	1.6	36
1035	The crystal structure of an intermediate dimer of aspergilloglutamic peptidase that mimics the enzyme-activation product complex produced upon autoproteolysis. Journal of Biochemistry, 2012, 152, 45-52.	0.9	9
1036	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2012, 40, D445-D452.	6.5	166

#	ARTICLE	IF	CITATIONS
1037	Crystal Structure of the Japanese Encephalitis Virus Envelope Protein. Journal of Virology, 2012, 86, 2337-2346.	1.5	184
1038	The structure of the yeast NADH dehydrogenase (Ndi1) reveals overlapping binding sites for water- and lipid-soluble substrates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15247-15252.	3.3	88
1039	Structural Characterization of Closely Related O-antigen Lipopolysaccharide (LPS) Chain Length Regulators. Journal of Biological Chemistry, 2012, 287, 15696-15705.	1.6	24
1040	Cdt1 and Geminin in DNA Replication Initiation. Sub-Cellular Biochemistry, 2012, 62, 71-87.	1.0	22
1041	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. Nucleic Acids Research, 2012, 40, 1828-1840.	6.5	35
1042	The Crystal Structure of Arabidopsis VSP1 Reveals the Plant Class C-Like Phosphatase Structure of the DDDD Superfamily of Phosphohydrolases. PLoS ONE, 2012, 7, e49421.	1.1	7
1043	PDBTM: Protein Data Bank of transmembrane proteins after 8 years. Nucleic Acids Research, 2012, 41, D524-D529.	6.5	245
1044	OPM database and PPM web server: resources for positioning of proteins in membranes. Nucleic Acids Research, 2012, 40, D370-D376.	6.5	1,572
1045	X-ray crystal structure of the streptococcal specific phage lysin PlyC. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12752-12757.	3.3	80
1046	Structural Basis for the Recognition of C20:2-Î±GalCer by the Invariant Natural Killer T Cell Receptor-like Antibody L363*. Journal of Biological Chemistry, 2012, 287, 1269-1278.	1.6	29
1047	Structural Characterization and Oligomerization of the TssL Protein, a Component Shared by Bacterial Type VI and Type IVb Secretion Systems. Journal of Biological Chemistry, 2012, 287, 14157-14168.	1.6	91
1048	Inhibiting Alternative Pathway Complement Activation by Targeting the Factor D Exosite. Journal of Biological Chemistry, 2012, 287, 12886-12892.	1.6	75
1049	Insights into Substrate Specificity and Metal Activation of Mammalian Tetrahedral Aspartyl Aminopeptidase. Journal of Biological Chemistry, 2012, 287, 13356-13370.	1.6	33
1050	Quantitative Analysis of Prenylated RhoA Interaction with Its Chaperone, RhoGDI. Journal of Biological Chemistry, 2012, 287, 26549-26562.	1.6	47
1051	Structural Insights into the Regulatory Mechanism of the Response Regulator RocR from Pseudomonas aeruginosa in Cyclic Di-GMP Signaling. Journal of Bacteriology, 2012, 194, 4837-4846.	1.0	57
1052	Structural Characterization of a Conserved, Calcium-Dependent Periplasmic Protease from Legionella pneumophila. Journal of Bacteriology, 2012, 194, 4415-4425.	1.0	48
1053	Crystal Structure of the Klebsiella pneumoniae NFeoB/FeoC Complex and Roles of FeoC in Regulation of Fe ²⁺ Transport by the Bacterial Feo System. Journal of Bacteriology, 2012, 194, 6518-6526.	1.0	38
1054	Crystal Structure of an Indole-3-Acetic Acid Amido Synthetase from Grapevine Involved in Auxin Homeostasis. Plant Cell, 2012, 24, 4525-4538.	3.1	70

#	Article	IF	Citations
1055	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. Nucleic Acids Research, 2012, 40, 4178-4192.	6.5	54
1056	InterEvol database: exploring the structure and evolution of protein complex interfaces. Nucleic Acids Research, 2012, 40, D847-D856.	6.5	47
1057	Structural Determinants of the Î²-Selectivity of a Bacterial Aminotransferase. Journal of Biological Chemistry, 2012, 287, 28495-28502.	1.6	30
1058	Furin-cleaved Proprotein Convertase Subtilisin/Kexin Type 9 (PCSK9) Is Active and Modulates Low Density Lipoprotein Receptor and Serum Cholesterol Levels. Journal of Biological Chemistry, 2012, 287, 43482-43491.	1.6	74
1059	On the Origin and Evolution of Thermophily: Reconstruction of Functional Precambrian Enzymes from Ancestors of Bacillus. Molecular Biology and Evolution, 2012, 29, 825-835.	3.5	83
1060	Protein-protein Docking and Hot-spot Prediction for Drug Discovery. Current Pharmaceutical Design, 2012, 18, 4607-4618.	0.9	41
1061	A human XRCC4â€“XLF complex bridges DNA. Nucleic Acids Research, 2012, 40, 1868-1878.	6.5	135
1062	Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from <i>Arabidopsis thaliana</i>. Biochemical Journal, 2012, 443, 427-437.	1.7	13
1064	Computational Drug Design Targeting Protein-Protein Interactions. Current Pharmaceutical Design, 2012, 18, 1240-1254.	0.9	64
1065	Computational Drug Design Targeting Protein-Protein Interactions. Current Drug Metabolism, 2012, 18, 1240-1254.	0.7	0
1066	Largeâ€scale mapping of human protein interactome using structural complexes. EMBO Reports, 2012, 13, 266-271.	2.0	43
1067	Getting personalized cancer genome analysis into the clinic: the challenges in bioinformatics. Genome Medicine, 2012, 13, 61.	3.6	23
1068	Roles of residues in the interface of transient protein-protein complexes before complexation. Scientific Reports, 2012, 2, 334.	1.6	30
1069	Structural and biochemical characterization of a trapped coenzyme A adduct of<i>Caenorhabditis elegans</i>glucosamine-6-phosphate<i>N</i>-acetyltransferase 1. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1019-1029.	2.5	14
1070	Structural features of the single-stranded DNA-binding protein MoSub1 from<i>Magnaporthe oryzae</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1071-1076.	2.5	10
1071	High-resolution structure of<i>Bombyx mori</i>lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1140-1151.	2.5	14
1072	The structure of augmenter of liver regeneration crystallized in the presence of 50â€…mMCdCl2reveals a novel Cd2Cl4O6cluster that aids in crystal packing. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1128-1133.	2.5	4
1073	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen<i>Giardia lamblia</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1194-1200.	2.5	9

#	ARTICLE	IF	CITATIONS
1074	Structure of theArchaeoglobus fulgidusorphan ORF AF1382 determined by sulfur SAD from a moderately diffracting crystal. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1242-1252.	2.5	5
1075	The structure of<i>Enterococcus faecalis</i>thymidylate synthase provides clues about folate bacterial metabolism. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1232-1241.	2.5	28
1076	Crystallization, dehydration and experimental phasing of WbdD, a bifunctional kinase and methyltransferase fromEscherichia coliO9a. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1371-1379.	2.5	5
1077	Structural polymorphism of c-di-GMP bound to an EAL domain and in complex with a type II PilZ-domain protein. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1380-1392.	2.5	42
1078	Crystallization and preliminary X-ray diffraction analysis of three myotoxic phospholipases A₂from<i>Bothrops brazili</i>venom. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 935-938.	0.7	1
1079	A new crystal form of human histidine triad nucleotide-binding protein 1 (hHINT1) in complex with adenosine 5â€²-monophosphate at 1.38â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 883-888.	0.7	13
1080	Structure of a UDP-glucose dehydrogenase from the hyperthermophilic archaeonPyrobaculum islandicum. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1003-1007.	0.7	3
1081	Structure of anabolic ornithine carbamoyltransferase fromCampylobacter jejuniat 2.7â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1018-1024.	0.7	4
1082	High-resolution structures of<i>Thermus thermophilus</i>enoyl-acyl carrier protein reductase in the apo form, in complex with NAD⁺and in complex with NAD⁺and triclosan. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1139-1148.	0.7	7
1083	Crystal structure of the glycosyltransferase SnogD from the biosynthetic pathway of nogalamycin in <i>Streptomycesâ€ƒnogalater</i>. FEBS Journal, 2012, 279, 3251-3263.	2.2	17
1084	<scp>X</scp>â€ray structure of a proteaseâ€resistant mutant form of human galectinâ€8 with two carbohydrate recognition domains. FEBS Journal, 2012, 279, 3937-3951.	2.2	34
1085	New secreted toxins and immunity proteins encoded within the <scp>T</scp>ype <scp>VI</scp> secretion system gene cluster of <i><scp>S</scp>erratia marcescens</i>. Molecular Microbiology, 2012, 86, 921-936.	1.2	121
1086	Structural Analysis of a Dengue Cross-Reactive Antibody Complexed with Envelope Domain III Reveals the Molecular Basis of Cross-Reactivity. Journal of Immunology, 2012, 188, 4971-4979.	0.4	82
1087	The Native GCN4 Leucine-Zipper Domain Does Not Uniquely Specify a Dimeric Oligomerization State. Biochemistry, 2012, 51, 9581-9591.	1.2	42
1088	Toward a Hepatitis C Virus Vaccine: the Structural Basis of Hepatitis C Virus Neutralization by AP33, a Broadly Neutralizing Antibody. Journal of Virology, 2012, 86, 12923-12932.	1.5	89
1089	RANKL Employs Distinct Binding Modes to Engage RANK and the Osteoprotegerin Decoy Receptor. Structure, 2012, 20, 1971-1982.	1.6	100
1090	Structure of a RING E3 ligase and ubiquitin-loaded E2 primed for catalysis. Nature, 2012, 489, 115-120.	13.7	437
1091	Inhibiting the Protein Ubiquitination Cascade by Ubiquitin-Mimicking Short Peptides. Organic Letters, 2012, 14, 5760-5763.	2.4	12

#	ARTICLE	IF	CITATIONS
1092	High Affinity Peptide Inhibitors of the Hepatitis C Virus NS3-4A Protease Refractory to Common Resistant Mutants. Journal of Biological Chemistry, 2012, 287, 39224-39232.	1.6	20
1093	Structure of NPP1, an Ectonucleotide Pyrophosphatase/Phosphodiesterase Involved in Tissue Calcification. Structure, 2012, 20, 1948-1959.	1.6	75
1094	Crystal Structure of the HLA-DMâ€“HLA-DR1 Complex Defines Mechanisms for Rapid Peptide Selection. Cell, 2012, 151, 1557-1568.	13.5	149
1095	Crystal Structure of Calmodulin Binding Domain of Orai1 in Complex with Ca2+â€¢Calmodulin Displays a Unique Binding Mode. Journal of Biological Chemistry, 2012, 287, 43030-43041.	1.6	58
1096	Analysis of Deltaâ€“Notch interaction by molecular modeling and molecular dynamic simulation studies. Journal of Biomolecular Structure and Dynamics, 2012, 30, 13-29.	2.0	0
1097	Atypical Reactive Center Kunitz-Type Inhibitor from the Sea Anemone Heteractis crispa. Marine Drugs, 2012, 10, 1545-1565.	2.2	22
1098	2P2Idb: a structural database dedicated to orthosteric modulation of proteinâ€“protein interactions. Nucleic Acids Research, 2012, 41, D824-D827.	6.5	133
1099	Structural and Functional Characterization of NikO, an Enolpyruvyl Transferase Essential in Nikkomycin Biosynthesis. Journal of Biological Chemistry, 2012, 287, 31427-31436.	1.6	14
1100	Architecture of the Atg17 Complex as a Scaffold for Autophagosome Biogenesis. Cell, 2012, 151, 1501-1512.	13.5	205
1101	Crystal structure of the conserved domain of the DC lysosomal associated membrane protein: implications for the lysosomal glycocalyx. BMC Biology, 2012, 10, 62.	1.7	82
1102	LpxI structures reveal how a lipid A precursor is synthesized. Nature Structural and Molecular Biology, 2012, 19, 1132-1138.	3.6	21
1103	The Last Piece in the Vitamin B1 Biosynthesis Puzzle. Journal of Biological Chemistry, 2012, 287, 42333-42343.	1.6	27
1104	Structure of a novel phosphotyrosine-binding domain in Hakai that targets E-cadherin. EMBO Journal, 2012, 31, 1308-1319.	3.5	56
1105	Identification and Characterization of a Multifunctional Dye Peroxidase from a Lignin-Reactive Bacterium. ACS Chemical Biology, 2012, 7, 2074-2081.	1.6	184
1106	Mechanistic and structural insight into the functional dichotomy between IL-2 and IL-15. Nature Immunology, 2012, 13, 1187-1195.	7.0	206
1107	Neuropilins lock secreted semaphorins onto plexins in a ternary signaling complex. Nature Structural and Molecular Biology, 2012, 19, 1293-1299.	3.6	160
1108	Unique motifs and hydrophobic interactions shape the binding of modified DNA ligands to protein targets. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19971-19976.	3.3	215
1109	The crystal structure of the Rv0301â€Rv0300 VapBCâ€3 toxinâ€”antitoxin complex from <i>M. tuberculosis</i> reveals a Mg²⁺ ion in the active site and a putative RNAâ€binding site. Protein Science, 2012, 21, 1754-1767.	3.1	54

#	ARTICLE	IF	CITATIONS
1110	Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from <i>Mycobacterium tuberculosis</i> at 2.0 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2799-2803.	1.5	9
1111	Structural basis for modification of flavonol and naphthol glucoconjugates by Nicotiana tabacum malonyltransferase (NtMaT1). Planta, 2012, 236, 781-793.	1.6	23
1112	Molecular simulation and docking studies of Gal1p and Gal3p proteins in the presence and absence of ligands ATP and galactose: implication for transcriptional activation of GAL genes. Journal of Computer-Aided Molecular Design, 2012, 26, 847-864.	1.3	7
1113	The crystal structures of the Î±-subunit of the Î±2Î²2 tetrameric Glycyl-tRNA synthetase. Journal of Structural and Functional Genomics, 2012, 13, 233-239.	1.2	11
1114	Crystal structure of mouse RhoA:GTPÎ³S complex in a centered lattice. Journal of Structural and Functional Genomics, 2012, 13, 241-245.	1.2	7
1115	Lowâ€resolution structure of <i>Drosophila</i> translin. FEBS Open Bio, 2012, 2, 37-46.	1.0	6
1116	Structural characterization of the PliG lysozyme inhibitor family. Journal of Structural Biology, 2012, 180, 235-242.	1.3	12
1117	How many packing contacts are observed in protein crystals?. Journal of Structural Biology, 2012, 180, 96-100.	1.3	24
1118	Explorations of linked editosome domains leading to the discovery of motifs defining conserved pockets in editosome OB-folds. Journal of Structural Biology, 2012, 180, 362-373.	1.3	6
1119	Structural insights into serine protease inhibition by a marine invertebrate BPTI Kunitz-type inhibitor. Journal of Structural Biology, 2012, 180, 271-279.	1.3	18
1120	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. Virology, 2012, 434, 257-264.	1.1	14
1121	Structural Basis for Broad Detection of Genogroup II Noroviruses by a Monoclonal Antibody That Binds to a Site Occluded in the Viral Particle. Journal of Virology, 2012, 86, 3635-3646.	1.5	75
1122	Structures of the Sgt2/SGTA Dimerization Domain with the Get5/UBL4A UBL Domain Reveal an Interaction that Forms a Conserved Dynamic Interface. Cell Reports, 2012, 2, 1620-1632.	2.9	52
1123	Mutational analysis of phenolic acid decarboxylase from Bacillus subtilis (BsPAD), which converts bio-derived phenolic acids to styrene derivatives. Catalysis Science and Technology, 2012, 2, 1568.	2.1	32
1124	Chemical and Structural Analysis of an Antibody Folding Intermediate Trapped during Glycan Biosynthesis. Journal of the American Chemical Society, 2012, 134, 17554-17563.	6.6	65
1125	Bifidobacterium longum subsp. infantis ATCC 15697 Î±-Fucosidases Are Active on Fucosylated Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2012, 78, 795-803.	1.4	204
1126	Crystal Structures of Glycoside Hydrolase Family 51 Î±-<scp>L</scp>-Arabinofuranosidase from<i>Thermotoga maritima</i>. Bioscience, Biotechnology and Biochemistry, 2012, 76, 423-428.	0.6	17
1127	An Ultra-specific Avian Antibody to Phosphorylated Tau Protein Reveals a Unique Mechanism for Phosphoepitope Recognition. Journal of Biological Chemistry, 2012, 287, 44425-44434.	1.6	53

#	ARTICLE	IF	CITATIONS
1128	fSUB: Normal Mode Analysis with Flexible Substructures. Journal of Physical Chemistry B, 2012, 116, 8636-8645.	1.2	5
1129	Proteinâ€“Protein Interactions and Substrate Channeling in Orthologous and Chimeric Aldolaseâ€“Dehydrogenase Complexes. Biochemistry, 2012, 51, 1942-1952.	1.2	19
1130	Competition between Anion Binding and Dimerization Modulates Staphylococcus aureus Phosphatidylinositol-specific Phospholipase C Enzymatic Activity. Journal of Biological Chemistry, 2012, 287, 40317-40327.	1.6	12
1131	The structure of the C-terminal domain of the largest editosome interaction protein and its role in promoting RNA binding by RNA-editing ligase L2. Nucleic Acids Research, 2012, 40, 6966-6977.	6.5	19
1132	Metal Binding at the <i>Deinococcus radiodurans</i> Dps-1 N-Terminal Metal Site Controls Dodecameric Assembly and DNA Binding. Biochemistry, 2012, 51, 6679-6689.	1.2	18
1133	The 2.8â€‰Å… crystal structure of the dynein motor domain. Nature, 2012, 484, 345-350.	13.7	235
1134	Structure of 2-Methylisoborneol Synthase from <i>Streptomyces coelicolor</i> and Implications for the Cyclization of a Noncanonical <i>C</i>-Methylated Monoterpenoid Substrate. Biochemistry, 2012, 51, 3011-3020.	1.2	42
1135	Impact of Quaternary Structure upon Bacterial Cytochrome <i>c</i> Peroxidases: Does Homodimerization Matter?. Biochemistry, 2012, 51, 10008-10016.	1.2	8
1136	Structural Insights into the Conformation and Oligomerization of E2â^¼Ubiquitin Conjugates. Biochemistry, 2012, 51, 4175-4187.	1.2	78
1137	Crystal Structures ofTrypanosoma cruziUDP-Galactopyranose Mutase Implicate Flexibility of the Histidine Loop in Enzyme Activation. Biochemistry, 2012, 51, 4968-4979.	1.2	23
1138	Crystal Structures of <i>Xanthomonas campestris</i> OleA Reveal Features That Promote Head-to-Head Condensation of Two Long-Chain Fatty Acids. Biochemistry, 2012, 51, 4138-4146.	1.2	26
1139	Distinct regions of the <i>Pseudomonas syringae</i> coiled-coil effector AvrRps4 are required for activation of immunity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16371-16376.	3.3	81
1140	Conservation of Oxidative Protein Stabilization in an Insect Homologue of Parkinsonism-Associated Protein DJ-1. Biochemistry, 2012, 51, 3799-3807.	1.2	28
1141	Structure of a Specialized Acyl Carrier Protein Essential for Lipid A Biosynthesis with Very Long-Chain Fatty Acids in Open and Closed Conformations. Biochemistry, 2012, 51, 7239-7249.	1.2	14
1142	Structure of Geranyl Diphosphate <i>C</i>-Methyltransferase from <i>Streptomyces coelicolor</i> and Implications for the Mechanism of Isoprenoid Modification. Biochemistry, 2012, 51, 3003-3010.	1.2	41
1143	Structural Investigation of the Thermostability and Product Specificity of Amylosucrase from the Bacterium Deinococcus geothermalis. Journal of Biological Chemistry, 2012, 287, 6642-6654.	1.6	55
1144	Structure of a Bacteriophytochrome and Light-Stimulated Protomer Swapping with a Gene Repressor. Structure, 2012, 20, 1436-1446.	1.6	88
1145	The C-terminal priming domain is strongly associated with the main body of bacteriophage Ï•6 RNA-dependent RNA polymerase. Virology, 2012, 432, 184-193.	1.1	9

#	ARTICLE	IF	CITATIONS
1146	Structural elements of primary CCR5-using HIV-1 gp120 proteins influencing sensitivity and resistance to the broadly neutralizing monoclonal antibody b12. Virology, 2012, 432, 394-404.	1.1	1
1147	Structural basis for RNA-duplex recognition and unwinding by the DEAD-box helicase Mss116p. Nature, 2012, 490, 121-125.	13.7	108
1148	Computational and Experimental Analysis of the Transmembrane Domain 4/5 Dimerization Interface of the Serotonin 5-HT_{1A} Receptor. Molecular Pharmacology, 2012, 82, 448-463.	1.0	47
1149	Structure-based prediction of proteinâ€"protein interactions on a genome-wide scale. Nature, 2012, 490, 556-560.	13.7	652
1150	Molecular Determinants for Antibody Binding on Group 1 House Dust Mite Allergens. Journal of Biological Chemistry, 2012, 287, 7388-7398.	1.6	75
1151	Structural Characterization of Binding Mode of Smoking Cessation Drugs to Nicotinic Acetylcholine Receptors through Study of Ligand Complexes with Acetylcholine-binding Protein. Journal of Biological Chemistry, 2012, 287, 23283-23293.	1.6	45
1152	The structural basis for the sensing and binding of cyclic di-GMP by STING. Nature Structural and Molecular Biology, 2012, 19, 728-730.	3.6	178
1153	Dynamic dissociating homo-oligomers and the control of protein function. Archives of Biochemistry and Biophysics, 2012, 519, 131-143.	1.4	100
1154	Structure of the Glycosyltransferase EryCIII in Complex with its Activating P450 Homologue EryCII. Journal of Molecular Biology, 2012, 415, 92-101.	2.0	29
1155	Intra-Chain 3D Segment Swapping Spawns the Evolution of New Multidomain Protein Architectures. Journal of Molecular Biology, 2012, 415, 221-235.	2.0	13
1156	Structure and Kinetic Stability of the p63 Tetramerization Domain. Journal of Molecular Biology, 2012, 415, 503-513.	2.0	31
1157	Structural Analysis of Chi1 Chitinase from Yen-Tc: The Multisubunit Insecticidal ABC Toxin Complex of Yersinia entomophaga. Journal of Molecular Biology, 2012, 415, 359-371.	2.0	61
1158	A Conserved Gluâ€"Arg Salt Bridge Connects Coevolved Motifs That Define the Eukaryotic Protein Kinase Fold. Journal of Molecular Biology, 2012, 415, 666-679.	2.0	39
1159	A Reverse Binding Motif That Contributes to Specific Protease Inhibition by Antibodies. Journal of Molecular Biology, 2012, 415, 699-715.	2.0	45
1160	Protein Kinase Domain of CTR1 from Arabidopsis thaliana Promotes Ethylene Receptor Cross Talk. Journal of Molecular Biology, 2012, 415, 768-779.	2.0	42
1161	Modulating Proteinâ€"Protein Interactions with Small Molecules: The Importance of Binding Hotspots. Journal of Molecular Biology, 2012, 415, 443-453.	2.0	61
1162	Metal Binding Dictates Conformation and Function of the Amyloid Precursor Protein (APP) E2 Domain. Journal of Molecular Biology, 2012, 416, 438-452.	2.0	88
1163	Structural, Bioinformatic, and In Vivo Analyses of Two Treponema pallidum Lipoproteins Reveal a Unique TRAP Transporter. Journal of Molecular Biology, 2012, 416, 678-696.	2.0	30

#	Article	IF	Citations
1164	Structure of the Ultra-High-Affinity Colicin E2 DNaseâ€“Im2 Complex. Journal of Molecular Biology, 2012, 417, 79-94.	2.0	54
1165	Structurally Similar but Functionally Diverse ZU5 Domains in Human Erythrocyte Ankyrin. Journal of Molecular Biology, 2012, 417, 336-350.	2.0	21
1166	Structural Basis for the Slow Dark Recovery of a Full-Length LOV Protein from Pseudomonas putida. Journal of Molecular Biology, 2012, 417, 362-374.	2.0	54
1167	Crystal Structure of Bifunctional Aldos-2-Ulose Dehydratase/Isomerase from Phanerochaete chrysosporium with the Reaction Intermediate Ascopyrone M. Journal of Molecular Biology, 2012, 417, 279-293.	2.0	5
1168	Structure-Based Inhibition of Norovirus RNA-Dependent RNA Polymerases. Journal of Molecular Biology, 2012, 419, 198-210.	2.0	86
1169	Crystal Structure of Bacillus subtilis Signal Peptide Peptidase A. Journal of Molecular Biology, 2012, 419, 347-358.	2.0	15
1170	Evolvability of Yeast Proteinâ€“Protein Interaction Interfaces. Journal of Molecular Biology, 2012, 419, 387-396.	2.0	4
1171	The Î²-Scaffold of the LOV Domain of the Brucella Light-Activated Histidine Kinase Is a Key Element for Signal Transduction. Journal of Molecular Biology, 2012, 420, 112-127.	2.0	27
1172	Structural and Functional Characterization of Microcin C Resistance Peptidase MccF from Bacillus anthracis. Journal of Molecular Biology, 2012, 420, 366-383.	2.0	22
1173	Structure and Catalytic Mechanism of a Cyclic Dipeptide Prenyltransferase with Broad Substrate Promiscuity. Journal of Molecular Biology, 2012, 422, 87-99.	2.0	66
1174	X-ray Crystal Structure and Specificity of the Plasmodium falciparum Malaria Aminopeptidase PfM18AAP. Journal of Molecular Biology, 2012, 422, 495-507.	2.0	33
1175	Crystal structure of Apis mellifera OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. Insect Biochemistry and Molecular Biology, 2012, 42, 41-50.	1.2	135
1176	Evaluation of three different formats of a neutralizing single chain human antibody against toxin Cn2: Neutralization capacity versus thermodynamic stability. Immunology Letters, 2012, 143, 152-160.	1.1	7
1177	Crystallographic and spectroscopic characterizations of Sulfolobus solfataricus TrxA1 provide insights into the determinants of thioredoxin fold stability. Journal of Structural Biology, 2012, 177, 506-512.	1.3	6
1178	The sensor region of the ubiquitous cytosolic sensor kinase, PdtaS, contains PAS and GAF domain sensing modules. Journal of Structural Biology, 2012, 177, 498-505.	1.3	18
1179	Structural basis of specificity in tetrameric Kluyveromyces lactis Î²-galactosidase. Journal of Structural Biology, 2012, 177, 392-401.	1.3	88
1180	Crystal structure of a mono- and diacylglycerol lipase from Malassezia globosa reveals a novel lid conformation and insights into the substrate specificity. Journal of Structural Biology, 2012, 178, 363-369.	1.3	59
1181	Structural basis for catalytic activity of a silkworm Delta-class glutathione transferase. Biochimica Et Biophysica Acta - General Subjects, 2012, 1820, 1469-1474.	1.1	23

#	ARTICLE	IF	CITATIONS
1182	Interaction of GAPR-1 with lipid bilayers is regulated by alternative homodimerization. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 2175-2183.	1.4	27
1183	Crystal structure of the Rasputin NTF2-like domain from Drosophila melanogaster. Biochemical and Biophysical Research Communications, 2012, 420, 188-192.	1.0	12
1184	Crystal structure of Plasmodium falciparum thioredoxin reductase, a validated drug target. Biochemical and Biophysical Research Communications, 2012, 425, 806-811.	1.0	25
1185	Structural Basis of the Intracellular Sorting of the SNARE VAMP7 by the AP3 Adaptor Complex. Developmental Cell, 2012, 22, 979-988.	3.1	55
1186	CENP-T-W-S-X Forms a Unique Centromeric Chromatin Structure with a Histone-like Fold. Cell, 2012, 148, 487-501.	13.5	229
1187	A novel dimerization interface of cyclic nucleotide binding domain, which is disrupted in presence of cAMP: implications for CNG channels gating. Journal of Molecular Modeling, 2012, 18, 4053-4060.	0.8	1
1188	Dynamic features of homodimer interfaces calculated by normalâ€mode analysis. Protein Science, 2012, 21, 1503-1513.	3.1	4
1189	Engineered variants of InlB with an additional leucineâ€rich repeat discriminate between physiologically relevant and packing contacts in crystal structures of the InlB:MET complex. Protein Science, 2012, 21, 1528-1539.	3.1	9
1190	Progressive dry-core-wet-rim hydration trend in a nested-ring topology of protein binding interfaces. BMC Bioinformatics, 2012, 13, 51.	1.2	7
1191	CONS-COCOMAPS: a novel tool to measure and visualize the conservation of inter-residue contacts in multiple docking solutions. BMC Bioinformatics, 2012, 13, S19.	1.2	32
1192	Crystal structure of the Yersinia enterocolitica type III secretion chaperone SycD in complex with a peptide of the minor translocator YopD. BMC Structural Biology, 2012, 12, 13.	2.3	23
1193	Integrative structural modeling with small angle X-ray scattering profiles. BMC Structural Biology, 2012, 12, 17.	2.3	92
1194	Structural and mechanistic investigations on Salmonella typhimurium acetate kinase (AckA): identification of a putative ligand binding pocket at the dimeric interface. BMC Structural Biology, 2012, 12, 24.	2.3	30
1195	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. BMC Structural Biology, 2012, 12, 6.	2.3	19
1196	Protein Databases on the Internet. Current Protocols in Protein Science, 2012, 70, Unit2.6.	2.8	11
1197	Structural insights into activation of antiviral <scp>NK</scp> cell responses. Immunological Reviews, 2012, 250, 239-257.	2.8	30
1198	Structure of the haptoglobinâ€"haemoglobin complex. Nature, 2012, 489, 456-459.	13.7	180
1199	Unusual carbon fixation gives rise to diverse polyketide extender units. Nature Chemical Biology, 2012, 8, 117-124.	3.9	63

#	ARTICLE	IF	CITATIONS
1200	Protein interface classification by evolutionary analysis. BMC Bioinformatics, 2012, 13, 334.	1.2	130
1201	The structural biochemistry of Zucchini implicates it as a nuclease in piRNA biogenesis. Nature, 2012, 491, 279-283.	13.7	276
1202	Structure of a force-conveying cadherin bond essential for inner-ear mechanotransduction. Nature, 2012, 492, 128-132.	13.7	157
1203	Exploiting a natural conformational switch to engineer an interleukin-2 â€˜superkineâ€™. Nature, 2012, 484, 529-533.	13.7	438
1204	A monomeric TIM-barrel structure fromPyrococcus furiosusis optimized for extreme temperatures. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1479-1487.	2.5	2
1205	Structure analysis of geranyl pyrophosphate methyltransferase and the proposed reaction mechanism of SAM-dependent<i>C</i>-methylation. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1558-1569.	2.5	16
1206	Structure of the corrinoid:coenzyme M methyltransferase MtaA from<i>Methanosarcina mazei</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1549-1557.	2.5	7
1207	Substrate channels revealed in the trimeric<i>Lactobacillus reuteri</i>bacterial microcompartment shell protein PduB. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1642-1652.	2.5	57
1208	Dimeric structure of the N-terminal domain of PriB protein fromThermoanaerobacter tengcongensissolvedab initio. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1680-1689.	2.5	1
1209	Influence of intermolecular contacts on the structure of recombinant prolidase from<i>Thermococcus sibiricus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1275-1278.	0.7	7
1210	Structure of ribose 5-phosphate isomerase from the probiotic bacterium<i>Lactobacillus salivarius</i>UCC118. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1427-1433.	0.7	8
1211	ATP-dependent DNA ligase fromThermococcussp. 1519 displays a new arrangement of the OB-fold domain. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1440-1447.	0.7	16
1212	On the roles of polyvalent binding in immune recognition: Perspectives in the nanoscience of immunology and the immune response to nanomedicines. Advanced Drug Delivery Reviews, 2012, 64, 1759-1781.	6.6	54
1213	Alternaria alternata allergen Alt a 1: A unique Î²-barrel protein dimer found exclusively in fungi. Journal of Allergy and Clinical Immunology, 2012, 130, 241-247.e9.	1.5	99
1214	Structural and biochemical studies of the open state of Lys48-linked diubiquitin. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 2046-2056.	1.9	40
1215	Crystal structures of triosephosphate isomerase from methicillin resistant Staphylococcus aureus MRSA252 provide structural insights into novel modes of ligand binding and unique conformations of catalytic loop. Biochimie, 2012, 94, 2532-2544.	1.3	9
1216	Structural insight into the molecular basis of polyextremophilicity of short-chain alcohol dehydrogenase from the hyperthermophilic archaeon Thermococcus sibiricus. Biochimie, 2012, 94, 2628-2638.	1.3	23
1217	The Crystal Structure of the Intact E.Âcoli RelBE Toxin-Antitoxin Complex Provides the Structural Basis for Conditional Cooperativity. Structure, 2012, 20, 1641-1648.	1.6	88

#	Article	IF	Citations
1218	Crystal Structure of the Yeast Vacuolar ATPase Heterotrimeric EGChead Peripheral Stalk Complex. Structure, 2012, 20, 1881-1892.	1.6	63
1219	Structure and Function of âˆ†1-Tetrahydrocannabinolic Acid (THCA) Synthase, the Enzyme Controlling the Psychoactivity of Cannabis sativa. Journal of Molecular Biology, 2012, 423, 96-105.	2.0	96
1220	Assembling of AcrB Trimer in Cell Membrane. Journal of Molecular Biology, 2012, 423, 123-134.	2.0	14
1221	Crystal Structures of Penicillin-Binding Protein 3 (PBP3) from Methicillin-Resistant Staphylococcus aureus in the Apo and Cefotaximeâ€Bound Forms. Journal of Molecular Biology, 2012, 423, 351-364.	2.0	48
1222	The Structural Domains of Pseudomonas aeruginosa Phosphorylcholine Phosphatase Cooperate in Substrate Hydrolysis: 3D Structure and Enzymatic Mechanism. Journal of Molecular Biology, 2012, 423, 503-514.	2.0	6
1223	Structural Basis for ASPP2 Recognition by the Tumor Suppressor p73. Journal of Molecular Biology, 2012, 423, 515-527.	2.0	20
1224	Conservation of Functionally Important Global Motions in an Enzyme Superfamily across Varying Quaternary Structures. Journal of Molecular Biology, 2012, 423, 831-846.	2.0	13
1225	Structural Analysis of the Quaking Homodimerization Interface. Journal of Molecular Biology, 2012, 423, 766-781.	2.0	26
1226	Structure and Catalytic Mechanism of Nicotinate (Vitamin B₃) Degradative Enzyme Maleamate Amidohydrolase from <i>Bordetella bronchiseptica</i> RB50. Biochemistry, 2012, 51, 545-554.	1.2	15
1227	Structures of Apo and Product-Bound Human <scp>l</scp>-Asparaginase: Insights into the Mechanism of Autoproteolysis and Substrate Hydrolysis. Biochemistry, 2012, 51, 6816-6826.	1.2	50
1228	Structure of a Novel Winged-Helix Like Domain from Human NFRKB Protein. PLoS ONE, 2012, 7, e43761.	1.1	5
1229	Broad and potent neutralization of HIV-1 by a gp41-specific human antibody. Nature, 2012, 491, 406-412.	13.7	753
1230	Functional Structural Motifs for Proteinâ€“Ligand, Proteinâ€“Protein, and Proteinâ€“Nucleic Acid Interactions and their Connection to Supersecondary Structures. Methods in Molecular Biology, 2012, 932, 295-315.	0.4	0
1231	The Crystal Structures of the Tryparedoxin-Tryparedoxin Peroxidase Couple Unveil the Structural Determinants of Leishmania Detoxification Pathway. PLoS Neglected Tropical Diseases, 2012, 6, e1781.	1.3	61
1232	The cloning, expression, purification, characterization and modeled structure of Caulobacter crescentus Î²-Xylosidase I. World Journal of Microbiology and Biotechnology, 2012, 28, 2879-2888.	1.7	22
1233	Detection of KCNJ11 Gene Mutations in a Family with Neonatal Diabetes Mellitus. Molecular Diagnosis and Therapy, 2012, 16, 109-114.	1.6	9
1234	Two Structures of a Thiazolinyl Imine Reductase from <i>Yersinia enterocolitica</i> Provide Insight into Catalysis and Binding to the Nonribosomal Peptide Synthetase Module of HMWP1. Biochemistry, 2012, 51, 9002-9013.	1.2	21
1235	Structural basis of evasion of cellular adaptive immunity by HIV-1 Nef. Nature Structural and Molecular Biology, 2012, 19, 701-706.	3.6	131

#	Article	IF	Citations
1236	Structure, Function, and Chemical Synthesis of <i>Vaejovis mexicanus</i> Peptide 24: A Novel Potent Blocker of Kv1.3 Potassium Channels of Human T Lymphocytes. Biochemistry, 2012, 51, 4049-4061.	1.2	51
1237	Structural Characterization of a Novel Chlamydia pneumoniae Type III Secretion-Associated Protein, Cpn0803. PLoS ONE, 2012, 7, e30220.	1.1	12
1238	Structural View of a Non Pfam Singleton and Crystal Packing Analysis. PLoS ONE, 2012, 7, e31673.	1.1	2
1239	Structural Characterisation of Tpx from Yersinia pseudotuberculosis Reveals Insights into the Binding of Salicylidene Acylhydrazide Compounds. PLoS ONE, 2012, 7, e32217.	1.1	17
1240	Macro-to-Micro Structural Proteomics: Native Source Proteins for High-Throughput Crystallization. PLoS ONE, 2012, 7, e32498.	1.1	36
1241	Insight on an Arginine Synthesis Metabolon from the Tetrameric Structure of Yeast Acetylglutamate Kinase. PLoS ONE, 2012, 7, e34734.	1.1	18
1242	M. tuberculosis Sliding Î²-Clamp Does Not Interact Directly with the NAD+ -Dependent DNA Ligase. PLoS ONE, 2012, 7, e35702.	1.1	17
1243	Linking Yeast Gcn5p Catalytic Function and Gene Regulation Using a Quantitative, Graded Dominant Mutant Approach. PLoS ONE, 2012, 7, e36193.	1.1	12
1244	Structural and Mutational Studies on Substrate Specificity and Catalysis of Salmonella typhimurium D-Cysteine Desulfhydrase. PLoS ONE, 2012, 7, e36267.	1.1	15
1245	Analysis of Domain-Swapped Oligomers Reveals Local Sequence Preferences and Structural Imprints at the Linker Regions and Swapped Interfaces. PLoS ONE, 2012, 7, e39305.	1.1	21
1246	The Crystal Structures of Dystrophin and Utrophin Spectrin Repeats: Implications for Domain Boundaries. PLoS ONE, 2012, 7, e40066.	1.1	23
1247	Characterisation of the First Enzymes Committed to Lysine Biosynthesis in Arabidopsis thaliana. PLoS ONE, 2012, 7, e40318.	1.1	45
1248	Structural Insights into the Effector â€“ Immunity System Tse1/Tsi1 from Pseudomonas aeruginosa. PLoS ONE, 2012, 7, e40453.	1.1	46
1249	Crystal Structure of a Monomeric Thiolase-Like Protein Type 1 (TLP1) from Mycobacterium smegmatis. PLoS ONE, 2012, 7, e41894.	1.1	4
1250	Crystal Structure of the Sema-PSI Extracellular Domain of Human RON Receptor Tyrosine Kinase. PLoS ONE, 2012, 7, e41912.	1.1	33
1251	13C NMR Reveals No Evidence of nâˆ'Ï€* Interactions in Proteins. PLoS ONE, 2012, 7, e42075.	1.1	16
1252	The â€œCPC Clip Motifâ€: A Conserved Structural Signature for Heparin-Binding Proteins. PLoS ONE, 2012, 7, e42692.	1.1	41
1253	Structures of Human DPP7 Reveal the Molecular Basis of Specific Inhibition and the Architectural Diversity of Proline-Specific Peptidases. PLoS ONE, 2012, 7, e43019.	1.1	23

#	ARTICLE	IF	CITATIONS
1254	Insights into Phosphate Cooperativity and Influence of Substrate Modifications on Binding and Catalysis of Hexameric Purine Nucleoside Phosphorylases. PLoS ONE, 2012, 7, e44282.	1.1	10
1255	A Green Fluorescent Protein Containing a QFG Tri-Peptide Chromophore: Optical Properties and X-Ray Crystal Structure. PLoS ONE, 2012, 7, e47331.	1.1	7
1256	Structural Insight into the Clostridium difficile Ethanolamine Utilisation Microcompartment. PLoS ONE, 2012, 7, e48360.	1.1	59
1257	Characterization of Arabidopsis FPS Isozymes and FPS Gene Expression Analysis Provide Insight into the Biosynthesis of Isoprenoid Precursors in Seeds. PLoS ONE, 2012, 7, e49109.	1.1	30
1258	Structural Insight into Inhibitor of Apoptosis Proteins Recognition by a Potent Divalent Smac-Mimetic. PLoS ONE, 2012, 7, e49527.	1.1	13
1259	Crystal Structure of the Hexachlorocyclohexane Dehydrochlorinase (LinA-Type2): Mutational Analysis, Thermostability and Enantioselectivity. PLoS ONE, 2012, 7, e50373.	1.1	15
1260	Molecular interaction analysis of cigarette smoke carcinogens NNK and NNAL with enzymes involved in DNA repair pathways: An in silico approach. Bioinformation, 2012, 8, 795-800.	0.2	13
1261	Mining Genomes of Marine Cyanobacteria for Elements of Zinc Homeostasis. Frontiers in Microbiology, 2012, 3, 142.	1.5	51
1262	Carbonic Anhydrase and Zinc in Plant Physiology. Chilean Journal of Agricultural Research, 2012, 72, 140-146.	0.4	42
1263	Structural features and kinetic characterization of alanine racemase from<i>Staphylococcus aureus</i>(Mu50). Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 82-92.	2.5	19
1264	Structure of the cytoplasmic domain of<i>Yersinia pestis</i>YscD, an essential component of the type III secretion system. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 201-209.	2.5	14
1265	High-resolution structures of complexes of plant<i>S</i>-adenosyl-<scp>L</scp>-homocysteine hydrolase (<i>Lupinus luteus</i>). Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 218-231.	2.5	19
1266	Structural insights into RipC, a putative citrate lyase Î² subunit from a<i>Yersinia pestis</i>virulence operon. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 2-7.	0.7	21
1267	Lysozyme contamination facilitates crystallization of a heterotrimeric cortactinâ€“Argâ€“lysozyme complex. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 154-158.	0.7	11
1268	Structureâ€“function relationship of assimilatory nitrite reductases from the leaf and root of tobacco based on highâ€resolution structures. Protein Science, 2012, 21, 383-395.	3.1	15
1269	Structural characterization of human Uch37. Proteins: Structure, Function and Bioinformatics, 2012, 80, 649-654.	1.5	34
1270	Computational protein design with explicit consideration of surface hydrophobic patches. Proteins: Structure, Function and Bioinformatics, 2012, 80, 825-838.	1.5	60
1271	Crystal structure of hypothetical protein TTHB210, controlled by the Ïƒ^E/antiâ€Ïƒ^E regulatory system in <i>Thermus thermophilus</i> HB8, reveals a novel homodecamer. Proteins: Structure, Function and Bioinformatics, 2012, 80, 958-962.	1.5	0

#	Article	IF	Citations
1272	Conformational dynamics of capping protein and interaction partners: Simulation studies. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1066-1077.	1.5	10
1273	Crystal structure and fluorescence studies reveal the role of helical dimeric interface of staphylococcal fabg1 in positive cooperativity for NADPH. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1250-1257.	1.5	29
1274	A structural mechanism for dimeric to tetrameric oligomer conversion in <i>Halomonas</i> sp. nucleoside diphosphate kinase. Protein Science, 2012, 21, 498-510.	3.1	17
1275	Functional and structural characterization of a thermostable acetyl esterase from <i>Thermotoga maritima</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1545-1559.	1.5	46
1276	Crystal structure and biochemical properties of putrescine carbamoyltransferase from <i>Enterococcus faecalis</i>: Assembly, active site, and allosteric regulation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1436-1447.	1.5	4
1277	Structural and biochemical characterization of native and recombinant single insulinâ€like growth factorâ€binding domain protein (SIBDâ€1) from the Central American Hunting Spider <i>Cupiennius salei (Ctenidae)</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2323-2329.	1.5	6
1278	Structural insights into catalysis by Î²Câ€S lyase from <i>Streptococcus anginosus</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2447-2458.	1.5	11
1279	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. Immunity, 2012, 36, 1073-1086.	6.6	282
1280	Structural and Biochemical Basis of Yos9 Protein Dimerization and Possible Contribution to Self-association of 3-Hydroxy-3-methylglutaryl-Coenzyme A Reductase Degradation Ubiquitin-Ligase Complex. Journal of Biological Chemistry, 2012, 287, 8633-8640.	1.6	13
1281	Matrix Metalloproteinase-10 (MMP-10) Interaction with Tissue Inhibitors of Metalloproteinases TIMP-1 and TIMP-2. Journal of Biological Chemistry, 2012, 287, 15935-15946.	1.6	88
1282	Protein camouflage in cytochrome câ€"calixarene complexes. Nature Chemistry, 2012, 4, 527-533.	6.6	189
1283	Quaternary Ammonium Oxidative Demethylation: X-ray Crystallographic, Resonance Raman, and UVâ€"Visible Spectroscopic Analysis of a Rieske-Type Demethylase. Journal of the American Chemical Society, 2012, 134, 2823-2834.	6.6	48
1284	G-protein-coupled receptor dynamics: dimerization and activation models compared with experiment. Biochemical Society Transactions, 2012, 40, 394-399.	1.6	13
1285	Quality control of disulfide bond formation in pilus subunits by the chaperone FimC. Nature Chemical Biology, 2012, 8, 707-713.	3.9	46
1286	Mapping a Neutralizing Epitope onto the Capsid of Adeno-Associated Virus Serotype 8. Journal of Virology, 2012, 86, 7739-7751.	1.5	86
1287	Computational study of ligand binding in lipid transfer proteins: Structures, interfaces, and free energies of proteinâ€lipid complexes. Journal of Computational Chemistry, 2012, 33, 1831-1844.	1.5	18
1288	Computational Design of Self-Assembling Protein Nanomaterials with Atomic Level Accuracy. Science, 2012, 336, 1171-1174.	6.0	588
1289	Structure of the receptor-binding carboxy-terminal domain of bacteriophage T7 tail fibers. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9390-9395.	3.3	95

#	ARTICLE	IF	CITATIONS
1290	Structural Basis of Wnt Recognition by Frizzled. Science, 2012, 337, 59-64.	6.0	711
1291	MMDB: 3D structures and macromolecular interactions. Nucleic Acids Research, 2012, 40, D461-D464.	6.5	96
1292	Monospecific Inhibitors Show That Both Mannan-binding Lectin-associated Serine Protease-1 (MASP-1) and -2 Are Essential for Lectin Pathway Activation and Reveal Structural Plasticity of MASP-2. Journal of Biological Chemistry, 2012, 287, 20290-20300.	1.6	69
1293	Dimeric Î±-Cobratoxin X-ray Structure. Journal of Biological Chemistry, 2012, 287, 6725-6734.	1.6	33
1294	Thermodynamic and structural description of allosterically regulated VEGFR-2 dimerization. Blood, 2012, 119, 1781-1788.	0.6	108
1295	The structure of a GH10 xylanase from<i>Fusarium oxysporum</i>reveals the presence of an extended loop on top of the catalytic cleft. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 735-742.	2.5	12
1296	Structural and Catalytic Characterization of <i>Pichia stipitis</i> OYE 2.6, a Useful Biocatalyst for Asymmetric Alkene Reductions. Advanced Synthesis and Catalysis, 2012, 354, 1949-1960.	2.1	31
1297	Tailoring a Stabilized Variant of Hydroxynitrile Lyase from <i>Arabidopsis thaliana</i>. ChemBioChem, 2012, 13, 797-802.	1.3	20
1298	Hydroxynitrile Lyases with Î±/Î²â€•Hydrolase Fold: Two Enzymes with Almost Identical 3D Structures but Opposite Enantioselectivities and Different Reaction Mechanisms. ChemBioChem, 2012, 13, 1932-1939.	1.3	25
1299	Allosteric antibody inhibition of human hepsin protease. Biochemical Journal, 2012, 442, 483-494.	1.7	29
1300	Structural Determinants of Protein Kinase CK2 Regulation by Autoinhibitory Polymerization. ACS Chemical Biology, 2012, 7, 1158-1163.	1.6	58
1301	Plant UVR8 Photoreceptor Senses UV-B by Tryptophan-Mediated Disruption of Cross-Dimer Salt Bridges. Science, 2012, 335, 1492-1496.	6.0	397
1302	Structural Studies on Molecular Interactions between Camel Peptidoglycan Recognition Protein, CPGRP-S, and Peptidoglycan Moieties N-Acetylglucosamine and N-Acetylmuramic Acid. Journal of Biological Chemistry, 2012, 287, 22153-22164.	1.6	7
1303	Crystal structure of a putative isochorismatase hydrolase from Oleispira antarctica. Journal of Structural and Functional Genomics, 2012, 13, 27-36.	1.2	22
1304	Crystal structures of putative phosphoglycerate kinases from B. anthracis and C. jejuni. Journal of Structural and Functional Genomics, 2012, 13, 15-26.	1.2	7
1305	Conformational changes in 2-trans-enoyl-ACP (CoA) reductase (InhA) from M. tuberculosis induced by an inorganic complex: a molecular dynamics simulation study. Journal of Molecular Modeling, 2012, 18, 1779-1790.	0.8	12
1306	The conjugation protein TcpC from <i>Clostridium perfringens</i> is structurally related to the type IV secretion system protein VirB8 from Gramâ€•negative bacteria. Molecular Microbiology, 2012, 83, 275-288.	1.2	68
1307	Inhibition mechanism of human galectinâ€•7 by a novel galactoseâ€•benzylphosphate inhibitor. FEBS Journal, 2012, 279, 193-202.	2.2	18

#	Article	IF	Citations
1308	Structure and activity of exoâ€1,3/1,4â€Î²â€glucanase from marine bacterium <i>Pseudoalteromonasâ€ƒ</i>sp. BB1 showing a novel Câ€terminal domain. FEBS Journal, 2012, 279, 464-478.	2.2	25
1309	Conservation of structure and mechanism within the transaldolase enzyme family. FEBS Journal, 2012, 279, 766-778.	2.2	14
1310	Dissecting Heterogeneous Molecular Chaperone Complexes Using a Mass Spectrum Deconvolution Approach. Chemistry and Biology, 2012, 19, 599-607.	6.2	70
1311	Breaking Down Order to Keep Cells Tidy. Chemistry and Biology, 2012, 19, 547-548.	6.2	0
1312	Accommodating variety in ironâ€responsive elements: Crystal structure of transferrin receptor 1 B IRE bound to iron regulatory protein 1. FEBS Letters, 2012, 586, 32-35.	1.3	23
1313	Crystal structure of cce_0566 from <i>Cyanothece 51142</i>, a protein associated with nitrogen fixation in the DUF269 family. FEBS Letters, 2012, 586, 350-355.	1.3	1
1314	Crystal structures of the Tudor domains of human PHF20 reveal novel structural variations on the Royal Family of proteins. FEBS Letters, 2012, 586, 859-865.	1.3	22
1315	The crystal structure of the MPN domain from the COP9 signalosome subunit CSN6. FEBS Letters, 2012, 586, 1147-1153.	1.3	20
1316	FolX from <i>Pseudomonas aeruginosa</i> is octameric in both crystal and solution. FEBS Letters, 2012, 586, 1160-1165.	1.3	3
1317	Hookworm SCP/TAPS protein structureâ€"A key to understanding hostâ€"parasite interactions and developing new interventions. Biotechnology Advances, 2012, 30, 652-657.	6.0	31
1318	Crystal structure of the native plasminogen reveals an activationâ€resistant compact conformation. Journal of Thrombosis and Haemostasis, 2012, 10, 1385-1396.	1.9	67
1319	Structural Basis of Highâ€Affinity Nuclear Localization Signal Interactions with Importinâ€Î±. Traffic, 2012, 13, 532-548.	1.3	91
1320	Structural analysis, enzymatic characterization, and catalytic mechanisms of Î²â€galactosidase from <i>Bacillusâ€ƒcirculans</i> sp. <i>alkalophilus</i>. FEBS Journal, 2012, 279, 1788-1798.	2.2	59
1321	Structural role of the activeâ€site metal in the conformation of <i>Trypanosomaâ€ƒbrucei</i> phosphoglycerate mutase. FEBS Journal, 2012, 279, 2012-2021.	2.2	18
1322	Structure and stability of a thermostable carboxylesterase from the thermoacidophilic archaeon <i>Sulfolobusâ€ƒtokodaii</i>. FEBS Journal, 2012, 279, 3071-3084.	2.2	41
1323	Structural analysis of trimeric phospholipase A₂ neurotoxin from the Australian taipan snake venom. FEBS Journal, 2012, 279, 3121-3135.	2.2	23
1324	Computational analysis of RNAâ€"protein interaction interfaces via the Voronoi diagram. Journal of Theoretical Biology, 2012, 293, 55-64.	0.8	4
1325	Saccharomyces Cerevisiae MHF Complex Structurally Resembles the Histones (H3-H4)2 Heterotetramer and Functions as a Heterotetramer. Structure, 2012, 20, 364-370.	1.6	20

#	ARTICLE	IF	CITATIONS
1326	Structure of the Human Obesity Receptor Leptin-Binding Domain Reveals the Mechanism of Leptin Antagonism by a Monoclonal Antibody. Structure, 2012, 20, 487-497.	1.6	65
1327	The Structure of Human Tripeptidyl Peptidase II as Determined by a Hybrid Approach. Structure, 2012, 20, 593-603.	1.6	19
1328	Crystal Structures of Aureochrome1 LOV Suggest New Design Strategies for Optogenetics. Structure, 2012, 20, 698-706.	1.6	67
1329	Complex Structures of the Abscisic Acid Receptor PYL3/RCAR13 Reveal a Unique Regulatory Mechanism. Structure, 2012, 20, 780-790.	1.6	71
1330	Crystal Structures of the Outer Membrane Domain of Intimin and Invasin from Enterohemorrhagic E. coli and Enteropathogenic Y. pseudotuberculosis. Structure, 2012, 20, 1233-1243.	1.6	82
1331	Chemical shift prediction for protein structure calculation and quality assessment using an optimally parameterized force field. Progress in Nuclear Magnetic Resonance Spectroscopy, 2012, 60, 1-28.	3.9	32
1332	Relationship between the structure and the enzymatic activity of crotoxin complex and its phospholipase A2 subunit: An in silico approach. Journal of Molecular Graphics and Modelling, 2012, 35, 36-42.	1.3	12
1333	The<i>Small Angle Scattering ToolBox</i>(<i>SASTBX</i>): an open-source software for biomolecular small-angle scattering. Journal of Applied Crystallography, 2012, 45, 587-593.	1.9	64
1334	Structure of phosphoserine aminotransferase from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 553-563.	2.5	11
1335	Structures of ternary complexes of aspartate-semialdehyde dehydrogenase (Rv3708c) from<i>Mycobacterium tuberculosis</i>H37Rv. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 671-679.	2.5	17
1336	Structures ofStaphylococcus aureuspeptide deformylase in complex with two classes of new inhibitors. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 784-793.	2.5	4
1337	Structure of a post-translationally processed heterodimeric double-headed Kunitz-type serine protease inhibitor from potato. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 794-799.	2.5	22
1338	In praise of impurity: 30S ribosomal S15 protein-assisted crystallization of turnip yellow mosaic virus proteinase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 486-490.	0.7	5
1339	Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from<i>Neisseria meningitidis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 730-737.	0.7	1
1340	Structure of the catalytic chain ofMethanococcus jannaschiiaspartate transcarbamoylase in a hexagonal crystal form: insights into the path of carbamoyl phosphate to the active site of the enzyme. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 527-534.	0.7	1
1341	The structure of an orthorhombic crystal form of a `forced reduced' thiol peroxidase reveals lattice formation aided by the presence of the affinity tag. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 522-526.	0.7	2
1342	Structure of a short-chain dehydrogenase/reductase from<i>Bacillus anthracis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 632-637.	0.7	3
1343	Structure of<i>Leishmania major</i>cysteine synthase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 738-743.	0.7	19

#	ARTICLE	IF	CITATIONS
1344	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 744-750.	0.7	11
1345	Identification of residues involved in NS2 homodimerization and elucidation of their impact on the HCV life cycle. Journal of Viral Hepatitis, 2012, 19, 189-198.	1.0	8
1346	Crystal structure of 6â€SST/6â€SFT from <i>Pachysandra terminalis</i>, a plant fructan biosynthesizing enzyme in complex with its acceptor substrate 6â€kestose. Plant Journal, 2012, 70, 205-219.	2.8	44
1347	Chromatography, mass spectrometry, and molecular modeling studies on ammodytoxins. Analytical and Bioanalytical Chemistry, 2012, 402, 2737-2748.	1.9	4
1348	Crystal structure and functional mapping of human ASMT, the last enzyme of the melatonin synthesis pathway. Journal of Pineal Research, 2013, 54, 46-57.	3.4	51
1349	INI1/hSNF5-interaction defective HIV-1 IN mutants exhibit impaired particle morphology, reverse transcription and integration in vivo. Retrovirology, 2013, 10, 66.	0.9	13
1350	Biophysical characterization and crystal structure of the Feline Immunodeficiency Virus p15 matrix protein. Retrovirology, 2013, 10, 64.	0.9	11
1351	Structure analysis of the extracellular domain reveals disulfide bond forming-protein properties of Mycobacterium tuberculosis Rv2969c. Protein and Cell, 2013, 4, 628-640.	4.8	9
1352	Crystal structures and biochemical studies of human lysophosphatidic acid phosphatase type 6. Protein and Cell, 2013, 4, 548-561.	4.8	9
1353	The nucleoprotein of severe fever with thrombocytopenia syndrome virus processes a stable hexameric ring to facilitate RNA encapsidation. Protein and Cell, 2013, 4, 445-455.	4.8	44
1354	Structural basis of bacterial defense against g-type lysozyme-based innate immunity. Cellular and Molecular Life Sciences, 2013, 70, 1113-1122.	2.4	26
1355	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from Salmonella Typhimurium. Journal of Structural and Functional Genomics, 2013, 14, 1-10.	1.2	4
1356	Structural, kinetic and computational investigation of Vitis vinifera DHDPS reveals new insight into the mechanism of lysine-mediated allosteric inhibition. Plant Molecular Biology, 2013, 81, 431-446.	2.0	30
1357	An InÂVivo Human-Plasmablast Enrichment Technique Allows Rapid Identification of Therapeutic Influenza A Antibodies. Cell Host and Microbe, 2013, 14, 93-103.	5.1	151
1358	Structural characterization of a D-isomer specific 2-hydroxyacid dehydrogenase from Lactobacillus delbrueckii ssp. bulgaricus. Journal of Structural Biology, 2013, 181, 179-184.	1.3	15
1359	Thrombin inhibition by the serpins. Journal of Thrombosis and Haemostasis, 2013, 11, 254-264.	1.9	60
1360	Full-Length Structure of a Sensor Histidine Kinase Pinpoints Coaxial Coiled Coils as Signal Transducers and Modulators. Structure, 2013, 21, 1127-1136.	1.6	165
1361	Structural Insights into the Mechanism of GTPase Activation in the GIMAP Family. Structure, 2013, 21, 550-559.	1.6	39

#	ARTICLE	IF	CITATIONS
1362	<i><scp>M</scp>edicagoÂtruncatula</i> histidineâ€containing phosphotransfer protein. FEBS Journal, 2013, 280, 3709-3720.	2.2	15
1363	Structure and Activity of NADPHâ€Dependent Reductase Q1EQE0 from <i>Streptomyces kanamyceticus</i>, which Catalyses the <i>R</i>â€Selective Reduction of an Imine Substrate. ChemBioChem, 2013, 14, 1372-1379.	1.3	90
1364	The structure of the D3 domain of Plasmodium falciparum myosin tail interacting protein MTIP in complex with a nanobody. Molecular and Biochemical Parasitology, 2013, 190, 87-91.	0.5	13
1365	The compact conformation of the Plasmodium knowlesi myosin tail interacting protein MTIP in complex with the C-terminal helix of myosin A. Molecular and Biochemical Parasitology, 2013, 190, 56-59.	0.5	5
1366	A dodecameric ring-like structure of the N0 domain of the type II secretin from enterotoxigenic Escherichia coli. Journal of Structural Biology, 2013, 183, 354-362.	1.3	19
1367	Combinatorial Design of an Anticalin Directed against the Extra-Domain B for the Specific Targeting of Oncofetal Fibronectin. Journal of Molecular Biology, 2013, 425, 780-802.	2.0	64
1368	Structural basis of <scp>FliG</scp>â€“<scp>FliM</scp> interaction in <i><scp>H</scp>elicobacter pylori</i>. Molecular Microbiology, 2013, 88, 798-812.	1.2	38
1369	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. Nature, 2013, 500, 350-353.	13.7	466
1370	Biocatalytic Asymmetric Alkene Reduction: Crystal Structure and Characterization of a Double Bond Reductase from <i>Nicotiana tabacum</i>. ACS Catalysis, 2013, 3, 370-379.	5.5	59
1371	The crystal structure of methenyltetrahydromethanopterin cyclohydrolase from Methanobrevibacter ruminantium. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2064-2070.	1.5	3
1372	The DNA binding mechanism of a SSB protein from Lactococcus lactis siphophage p2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1070-1076.	1.1	6
1373	Modeling Complexes of Transmembrane Proteins: Systematic Analysis of Proteinï£¿Protein Docking Tools. Molecular Informatics, 2013, 32, 717-733.	1.4	27
1374	Solvation Models and Computational Prediction of Orientations of Peptides and Proteins in Membranes. Methods in Molecular Biology, 2013, 1063, 125-142.	0.4	8
1376	ROCK: a resource for integrative breast cancer data analysis. Breast Cancer Research and Treatment, 2013, 139, 907-921.	1.1	30
1377	Structural Rearrangement of Ebola Virus VP40 Begets Multiple Functions in the Virus Life Cycle. Cell, 2013, 154, 763-774.	13.5	201
1378	Structure of the PilZâ€“FimXEALâ€“c-di-GMP Complex Responsible for the Regulation of Bacterial Type IV Pilus Biogenesis. Journal of Molecular Biology, 2013, 425, 2174-2197.	2.0	49
1379	Structural and Functional Analysis of Angucycline C-6 Ketoreductase LanV Involved in Landomycin Biosynthesis. Biochemistry, 2013, 52, 5304-5314.	1.2	15
1380	MgATP Regulates Allostery and Fiber Formation in IMPDHs. Structure, 2013, 21, 975-985.	1.6	72

#	Article	IF	Citations
1381	Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. Nature Communications, 2013, 4, 1613.	5.8	91
1382	Structural Basis for Regulation of Human Glucokinase by Glucokinase Regulatory Protein. Biochemistry, 2013, 52, 6232-6239.	1.2	41
1383	Structural characterization of <i>Staphylococcus aureus</i> biotin protein ligase and interaction partners: An antibiotic target. Protein Science, 2013, 22, 762-773.	3.1	32
1384	Putative conformations of the receptor-binding domain in S protein of hCoV-EMC in complex with its receptor dipeptidyl peptidase-4. Journal of Infection, 2013, 67, 156-158.	1.7	9
1385	Insights into the mechanism of drug resistance: X-ray structure analysis of multi-drug resistant HIV-1 protease ritonavir complex. Biochemical and Biophysical Research Communications, 2013, 431, 232-238.	1.0	6
1386	Structural templates for modeling homodimers. Protein Science, 2013, 22, 1655-1663.	3.1	16
1387	A structural modeling approach for the understanding of initiation and elongation of ALS-linked superoxide dismutase fibrils. Journal of Molecular Modeling, 2013, 19, 3695-3704.	0.8	4
1388	Computational structure analysis of biomacromolecule complexes by interface geometry. Computational Biology and Chemistry, 2013, 47, 16-23.	1.1	6
1389	Structural insights into the role of<i>Bacillus subtilis</i>YwfH (BacG) in tetrahydrotyrosine synthesis. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 324-332.	2.5	10
1390	Structural Basis for Signaling by Exclusive EDS1 Heteromeric Complexes with SAG101 or PAD4 in Plant Innate Immunity. Cell Host and Microbe, 2013, 14, 619-630.	5.1	227
1391	Structural bases for a complete myotoxic mechanism: Crystal structures of two non-catalytic phospholipases A2-like from Bothrops brazili venom. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2772-2781.	1.1	33
1392	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. Structure, 2013, 21, 1325-1337.	1.6	82
1393	Identification, characterization, and crystal structure of an aldoâ€“keto reductase (AKR2E4) from the silkworm Bombyx mori. Archives of Biochemistry and Biophysics, 2013, 538, 156-163.	1.4	16
1394	Functional site plasticity in domain superfamilies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 874-889.	1.1	31
1395	Structure and dynamics of human Nedd4-1 WW3 in complex with the Î±ENaC PY motif. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1632-1641.	1.1	26
1396	Structureâ€based engineering of streptavidin monomer with a reduced biotin dissociation rate. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1621-1633.	1.5	44
1397	Structural Basis for the Enzymatic Formation of the Key Strawberry Flavor Compound 4-Hydroxy-2,5-dimethyl-3(2H)-furanone. Journal of Biological Chemistry, 2013, 288, 16815-16826.	1.6	25
1398	Structural Basis for Kinesin-1:Cargo Recognition. Science, 2013, 340, 356-359.	6.0	85

#	ARTICLE	IF	CITATIONS
1399	Structure of a bifunctional alcohol dehydrogenase involved in bioethanol generation in<i>Geobacillus thermoglucosidasius</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2104-2115.	2.5	31
1400	The structure of the FnI-EGF-like tandem domain of coagulation factor XII solved using SIRAS. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 94-102.	0.7	12
1401	The diversity of microbial aldo/keto reductases from Escherichia coli K12. Chemico-Biological Interactions, 2013, 202, 168-177.	1.7	13
1402	Understanding specificity of the mycosin proteases in ESX/type VII secretion by structural and functional analysis. Journal of Structural Biology, 2013, 184, 115-128.	1.3	33
1403	Structural and biochemical characterization of Rv2140c, a phosphatidylethanolamineâ€binding protein from <i>Mycobacterium tuberculosis</i>. FEBS Letters, 2013, 587, 2936-2942.	1.3	11
1404	Structureâ€“Function Analysis of Arabidopsis thaliana Histidine Kinase AHK5 Bound to Its Cognate Phosphotransfer Protein AHP1. Molecular Plant, 2013, 6, 959-970.	3.9	38
1405	Design of a superior cytokine antagonist for topical ophthalmic use. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3913-3918.	3.3	49
1406	The X-ray crystal structure of PA1374 from Pseudomonas aeruginosa, a putative oxidative-stress sensing transcriptional regulator. Biochemical and Biophysical Research Communications, 2013, 431, 376-381.	1.0	8
1407	Modeling iron-catecholates binding to NGAL protein. Journal of Molecular Graphics and Modelling, 2013, 45, 111-121.	1.3	17
1408	Atomic Structure of Dual-Specificity Phosphatase 26, a Novel p53 Phosphatase. Biochemistry, 2013, 52, 938-948.	1.2	22
1409	Tryptophan-Accelerated Electron Flow Across a Proteinâ€“Protein Interface. Journal of the American Chemical Society, 2013, 135, 15515-15525.	6.6	43
1410	A cyclic GMP-dependent signalling pathway regulates bacterial phytopathogenesis. EMBO Journal, 2013, 32, 2430-2438.	3.5	46
1411	Structural study of interaction between brinzolamide and dorzolamide inhibition of human carbonic anhydrases. Bioorganic and Medicinal Chemistry, 2013, 21, 7210-7215.	1.4	98
1412	Functional Classification of Immune Regulatory Proteins. Structure, 2013, 21, 766-776.	1.6	23
1413	The crystal structure reveals the molecular mechanism of bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (Rv1415) fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1633-1644.	2.5	13
1414	RNA polymerase I structure and transcription regulation. Nature, 2013, 502, 650-655.	13.7	193
1415	Knowledge-Based Design of a Biosensor to Quantify Localized ERK Activation in Living Cells. Chemistry and Biology, 2013, 20, 847-856.	6.2	49
1416	Probing the amino acids critical for protein oligomerisation and proteinâ€“nucleotide interaction in Mycobacterium tuberculosis PII protein through integration of computational and experimental approaches. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2736-2749.	1.1	0

#	Article	IF	Citations
1417	Allophycocyanin and phycocyanin crystal structures reveal facets of phycobilisome assembly. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 311-318.	0.5	76
1418	Functional and Structural Study of the Dimeric Inner Membrane Protein SbmA. Journal of Bacteriology, 2013, 195, 5352-5361.	1.0	35
1419	Structural basis of preferential binding of fucose-containing saccharide by the Caenorhabditis elegans galectin LEC-6. Glycobiology, 2013, 23, 797-805.	1.3	11
1420	Structural and functional studies with mytoxin II from Bothrops moojeni reveal remarkable similarities and differences compared to other catalytically inactive phospholipases A2-like. Toxicon, 2013, 72, 52-63.	0.8	25
1421	A Model of the Membrane-bound Cytochrome b5-Cytochrome P450 Complex from NMR and Mutagenesis Data. Journal of Biological Chemistry, 2013, 288, 22080-22095.	1.6	105
1422	Wzi Is an Outer Membrane Lectin that Underpins Group 1 Capsule Assembly in Escherichia coli. Structure, 2013, 21, 844-853.	1.6	63
1423	The crystal structure of an extracellular catechol oxidase from the ascomycete fungus Aspergillus oryzae. Journal of Biological Inorganic Chemistry, 2013, 18, 917-929.	1.1	40
1424	The Molecular Basis of Iron-induced Oligomerization of Frataxin and the Role of the Ferroxidation Reaction in Oligomerization. Journal of Biological Chemistry, 2013, 288, 8156-8167.	1.6	21
1425	Structural Basis for the Recognition of Tyrosine-based Sorting Signals by the Î¼3A Subunit of the AP-3 Adaptor Complex. Journal of Biological Chemistry, 2013, 288, 9563-9571.	1.6	40
1426	Crystal Structure of an HSA/FcRn Complex Reveals Recycling by Competitive Mimicry of HSA Ligands at a pH-Dependent Hydrophobic Interface. Structure, 2013, 21, 1966-1978.	1.6	93
1427	Nucleotide-induced asymmetry within ATPase activator ring drives Ïƒ54â€“RNAP interaction and ATP hydrolysis. Genes and Development, 2013, 27, 2500-2511.	2.7	35
1428	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. Journal of Biological Chemistry, 2013, 288, 34131-34145.	1.6	29
1429	Structural Basis for Highly Effective HIV-1 Neutralization by CD4-Mimetic Miniproteins Revealed by 1.5ÂÃ… Cocrystal Structure of gp120 and M48U1. Structure, 2013, 21, 1018-1029.	1.6	29
1430	The crystal structure of the cell division amidase <scp>AmiC</scp> reveals the fold of the <scp>AMIN</scp> domain, a new peptidoglycan binding domain. Molecular Microbiology, 2013, 90, 267-277.	1.2	60
1431	Biochemical and structural characterisation of dehydroquinate synthase from the New Zealand kiwifruit Actinidia chinensis. Archives of Biochemistry and Biophysics, 2013, 537, 185-191.	1.4	18
1432	Computational Largeâ€Scale Mapping of Proteinâ€Protein Interactions Using Structural Complexes. Current Protocols in Protein Science, 2013, 73, 3.9.1-3.9.9.	2.8	2
1433	Outer Domain of HIV-1 gp120: Antigenic Optimization, Structural Malleability, and Crystal Structure with Antibody VRC-PG04. Journal of Virology, 2013, 87, 2294-2306.	1.5	34
1434	Hemoglobin Allostery: New Views on Old Players. Journal of Molecular Biology, 2013, 425, 1515-1526.	2.0	12

#	Article	IF	Citations
1435	Structure of the Sgt2/Get5 complex provides insights into GET-mediated targeting of tail-anchored membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1327-1332.	3.3	28
1436	Crystal structure of the Psb28 accessory factor of Thermosynechococcus elongatus photosystem II at 2.3Ââ„«. Photosynthesis Research, 2013, 117, 375-383.	1.6	10
1437	An analysis of oligomerization interfaces in transmembrane proteins. BMC Structural Biology, 2013, 13, 21.	2.3	29
1438	Antibacterial mechanisms identified through structural systems pharmacology. BMC Systems Biology, 2013, 7, 102.	3.0	23
1439	BioSuper: A web tool for the superimposition of biomolecules and assemblies with rotational symmetry. BMC Structural Biology, 2013, 13, 32.	2.3	8
1440	The crystal structure of sterol carrier protein 2 from Yarrowia lipolytica and the evolutionary conservation of a large, non-specific lipid-binding cavity. Journal of Structural and Functional Genomics, 2013, 14, 145-153.	1.2	10
1441	Effect of incorporating a thiophene tail in the scaffold of acetazolamide on the inhibition of human carbonic anhydrase isoforms I, II, IX and XII. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 5646-5649.	1.0	23
1442	Insights into the mechanism of pyrrole polymerization catalysed by porphobilinogen deaminase: high-resolution X-ray studies of the<i>Arabidopsis thaliana</i>enzyme. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 471-485.	2.5	21
1443	Crystal structure of peroxisomal targeting signal-2 bound to its receptor complex Pex7pâ€“Pex21p. Nature Structural and Molecular Biology, 2013, 20, 987-993.	3.6	56
1444	Mechanism of Transient Binding and Release of Substrate Protein during the Allosteric Cycle of the p97 Nanomachine. Journal of the American Chemical Society, 2013, 135, 14627-14636.	6.6	17
1445	Activation mechanism of claudin-4 by ephrin type-A receptor 2: a molecular dynamics approach. Molecular BioSystems, 2013, 9, 2627.	2.9	5
1446	Zinc Coordination Spheres in Protein Structures. Inorganic Chemistry, 2013, 52, 10983-10991.	1.9	205
1447	Buried and Accessible Surface Area Control Intrinsic Protein Flexibility. Journal of Molecular Biology, 2013, 425, 3250-3263.	2.0	62
1448	Crystal structures of interleukin 17A and its complex with IL-17 receptor A. Nature Communications, 2013, 4, 1888.	5.8	105
1449	A Large Solvent Isotope Effect on Protein Association Thermodynamics. Biochemistry, 2013, 52, 6595-6600.	1.2	10
1450	Structural and functional analysis of FIP2 binding to the endosome-localised Rab25 GTPase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2679-2690.	1.1	14
1451	Structural biology study of human TNF receptor associated factor 4 TRAF domain. Protein and Cell, 2013, 4, 687-694.	4.8	17
1452	An open conformation determined by a structural switch for 2A protease from coxsackievirus A16. Protein and Cell, 2013, 4, 782-792.	4.8	14

#	Article	IF	Citations
1453	Structural analysis of the <i><scp>R</scp>hizoctoniaÂsolani</i> agglutinin reveals a domainâ€swapping dimeric assembly. FEBS Journal, 2013, 280, 1750-1763.	2.2	19
1454	Spot14/Mig12 heterocomplex sequesters polymerization and restrains catalytic function of human acetylâ€CoA carboxylase 2. Journal of Molecular Recognition, 2013, 26, 679-688.	1.1	25
1455	Thermodynamic dissection of largeâ€scale domain motions coupled with ligand binding of enzyme I. Protein Science, 2013, 22, 1602-1611.	3.1	3
1456	Biochemical analysis and structure determination of <i><scp>P</scp>aucimonas lemoignei</i> poly(3â€hydroxybutyrate) (<scp>PHB</scp>) depolymerase <scp>PhaZ</scp>7 muteins reveal the <scp>PHB</scp> binding site and details of substrateâ€"enzyme interactions. Molecular Microbiology, 2013, 90, 649-664.	1.2	24
1457	Organophosphorus acid anhydrolase fromAlteromonas macleodii: structural study and functional relationship to prolidases. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 346-354.	0.7	19
1458	Structure of Signal Peptide Peptidase A with C-Termini Bound in the Active Sites: Insights into Specificity, Self-Processing, and Regulation. Biochemistry, 2013, 52, 8811-8822.	1.2	5
1459	Structure and assembly of an inner membrane platform for initiation of type IV pilus biogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4638-47.	3.3	57
1460	Structure and function of an insect Î±-carboxylesterase (Î± <i>Esterase</i> 7) associated with insecticide resistance. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10177-10182.	3.3	112
1461	Crystal structure of the dimeric coiled-coil domain of the cytosolic nucleic acid sensor LRRFIP1. Journal of Structural Biology, 2013, 181, 82-88.	1.3	13
1462	The Myosin Chaperone UNC-45 Is Organized in Tandem Modules to Support Myofilament Formation in C.Âelegans. Cell, 2013, 152, 183-195.	13.5	94
1463	Structure of a VP1-VP3 Complex Suggests How Birnaviruses Package the VP1 Polymerase. Journal of Virology, 2013, 87, 3229-3236.	1.5	15
1464	The structural basis of direct glucocorticoid-mediated transrepression. Nature Structural and Molecular Biology, 2013, 20, 53-58.	3.6	163
1465	Structure of a Dengue Virus Envelope Protein Late-Stage Fusion Intermediate. Journal of Virology, 2013, 87, 2287-2293.	1.5	114
1466	The Atomic Structure of the Virally Encoded Antifungal Protein, KP6. Journal of Molecular Biology, 2013, 425, 609-621.	2.0	13
1467	Light-Induced Subunit Dissociation by a Lightâ€"Oxygenâ€"Voltage Domain Photoreceptor from <i>Rhodobacter sphaeroides</i>. Biochemistry, 2013, 52, 378-391.	1.2	67
1468	ACAâ€specific RNA sequence recognition is acquired via the loop 2 region of MazF mRNA interferase. Proteins: Structure, Function and Bioinformatics, 2013, 81, 874-883.	1.5	8
1469	Crystal Structure of Rice Importin-Î± and Structural Basis of Its Interaction with Plant-Specific Nuclear Localization Signals. Plant Cell, 2013, 24, 5074-5088.	3.1	60
1470	Functional Genomics of Metalloregulators in Cyanobacteria. Advances in Botanical Research, 2013, , 107-156.	0.5	10

#	Article	IF	Citations
1471	Structure of the human ATG12~ATG5 conjugate required for LC3 lipidation in autophagy. Nature Structural and Molecular Biology, 2013, 20, 59-66.	3.6	336
1472	Evolution from the Prokaryotic to the Higher Plant Chloroplast Signal Recognition Particle: The Signal Recognition Particle RNA Is Conserved in Plastids of a Wide Range of Photosynthetic Organisms. Plant Cell, 2013, 24, 4819-4836.	3.1	37
1473	Natively Inhibited <i>Trypanosoma brucei</i> Cathepsin B Structure Determined by Using an X-ray Laser. Science, 2013, 339, 227-230.	6.0	393
1474	Structure of the St. Louis Encephalitis Virus Postfusion Envelope Trimer. Journal of Virology, 2013, 87, 818-828.	1.5	28
1475	Abstracting knowledge from the protein data bank. Biopolymers, 2013, 99, 183-188.	1.2	6
1476	A novel mechanism of ligand binding and release in the odorant binding protein 20 from the malaria mosquito <i>Anopheles gambiae</i>. Protein Science, 2013, 22, 11-21.	3.1	30
1477	Babesia divergensandNeospora caninumapical membrane antigen 1 structures reveal selectivity and plasticity in apicomplexan parasite host cell invasion. Protein Science, 2013, 22, 114-127.	3.1	35
1478	Crystal structure of the small GTPase Arl6/BBS3 from <i>Trypanosoma brucei</i>. Protein Science, 2013, 22, 196-203.	3.1	4
1479	Human C3a and C3a desArg anaphylatoxins have conserved structures, in contrast to C5a and C5a desArg. Protein Science, 2013, 22, 204-212.	3.1	51
1480	Prediction of phenotypes of missense mutations in human proteins from biological assemblies. Proteins: Structure, Function and Bioinformatics, 2013, 81, 199-213.	1.5	20
1481	S-linked protein homocysteinylation: identifying targets based on structural, physicochemical and proteinâ€“protein interactions of homocysteinylated proteins. Amino Acids, 2013, 44, 1307-1316.	1.2	7
1482	High-resolution crystal structure of the eukaryotic HMP-P synthase (THIC) from Arabidopsis thaliana. Journal of Structural Biology, 2013, 184, 438-444.	1.3	22
1483	Structures of CD200/CD200 Receptor Family and Implications for Topology, Regulation, and Evolution. Structure, 2013, 21, 820-832.	1.6	52
1484	Self-Assembly and Conformational Heterogeneity of the AXH Domain ofÂAtaxin-1: An Unusual Example of a Chameleon Fold. Biophysical Journal, 2013, 104, 1304-1313.	0.2	19
1485	Substrate Specificity and Oligomerization of Human GMP Synthetase. Journal of Molecular Biology, 2013, 425, 4323-4333.	2.0	31
1486	Structure of Stem Cell Growth Factor R-spondin 1 in Complex with the Ectodomain of Its Receptor LGR5. Cell Reports, 2013, 3, 1885-1892.	2.9	80
1487	The crystal structure of an activated Thermotoga maritima CheY with N-terminal region of FliM. International Journal of Biological Macromolecules, 2013, 54, 76-83.	3.6	17
1488	Structural peculiarities of the (MHF1â€“MHF2)₄ octamer provide a long DNA binding patch to anchor the MHFâ€“FANCM complex to chromatin: A solution SAXS study. FEBS Letters, 2013, 587, 2912-2917.	1.3	3

#	ARTICLE	IF	CITATIONS
1489	Structural Insights into the Mechanism and Inhibition of the Î²-Hydroxydecanoyl-Acyl Carrier Protein Dehydratase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2013, 425, 365-377.	2.0	30
1490	Identification of catalytically important amino acid residues for enzymatic reduction of glyoxylate in plants. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2663-2671.	1.1	11
1491	Rapid IgG heavy chain cleavage by the streptococcal IgG endopeptidase IdeS is mediated by IdeS monomers and is not due to enzyme dimerization. FEBS Letters, 2013, 587, 1818-1822.	1.3	26
1492	The Crystal Structure of the Lumenal Domain of Erv41p, a Protein Involved in Transport between the Endoplasmic Reticulum and Golgi Apparatus. Journal of Molecular Biology, 2013, 425, 2208-2218.	2.0	11
1493	The switch helix: A putative combinatorial relay for interprotomer communication in cGMP-dependent protein kinase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1346-1351.	1.1	10
1494	Calcium binding by the PKD1 domain regulates interdomain flexibility in <i>Vibrio cholerae</i> metalloprotease PrtV. FEBS Open Bio, 2013, 3, 263-270.	1.0	10
1495	Crystal Structure of the DNA Cytosine Deaminase APOBEC3F: The Catalytically Active and HIV-1 Vif-Binding Domain. Structure, 2013, 21, 1042-1050.	1.6	85
1496	X-Ray crystallographic structural characteristics of Arabidopsis hemoglobin I and their functional implications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1944-1956.	1.1	19
1497	In Human Pseudouridine Synthase 1 (hPus1), a C-Terminal Helical Insert Blocks tRNA from Binding in the Same Orientation as in the Pus1 Bacterial Homologue TruA, Consistent with Their Different Target Selectivities. Journal of Molecular Biology, 2013, 425, 3875-3887.	2.0	27
1498	RG7116, a Therapeutic Antibody That Binds the Inactive HER3 Receptor and Is Optimized for Immune Effector Activation. Cancer Research, 2013, 73, 5183-5194.	0.4	96
1499	DXP Synthaseâ€Catalyzed Cï£¿N Bond Formation: Nitroso Substrate Specificity Studies Guide Selective Inhibitor Design. ChemBioChem, 2013, 14, 1309-1315.	1.3	29
1500	<scp>X</scp>â€ray structure of a superinfection exclusion lipoprotein from phage <scp>TP</scp>â€<scp>J</scp>34 and identification of the tape measure protein as its target. Molecular Microbiology, 2013, 89, 152-165.	1.2	43
1501	Crystallographic study of multi-drug resistant HIV-1 protease lopinavir complex: Mechanism of drug recognition and resistance. Biochemical and Biophysical Research Communications, 2013, 437, 199-204.	1.0	8
1502	Structural Determinants of Oligomerization of Î”1-Pyrroline-5-Carboxylate Dehydrogenase: Identification of a Hexamerization Hot Spot. Journal of Molecular Biology, 2013, 425, 3106-3120.	2.0	24
1503	Conformational plasticity at the IgE-binding site of the B-cell receptor CD23. Molecular Immunology, 2013, 56, 693-697.	1.0	16
1504	CtpB Assembles a Gated Protease Tunnel Regulating Cell-Cell Signaling during Spore Formation in Bacillus subtilis. Cell, 2013, 155, 647-658.	13.5	31
1505	Conserved hydrogen bonds and water molecules in MDR HIV-1 protease substrate complexes. Biochemical and Biophysical Research Communications, 2013, 430, 1022-1027.	1.0	13
1506	Evidence for dimer/tetramer equilibrium in Trypanosoma brucei 6-phosphogluconate dehydrogenase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2647-2652.	1.1	16

#	Article	IF	Citations
1507	The crystal structure of a novel phosphopantothenate synthetase from the hyperthermophilic archaea, Thermococcus onnurineus NA1. Biochemical and Biophysical Research Communications, 2013, 439, 533-538.	1.0	4
1508	Salmonella enterica MTAN at 1.36ÂÃ… Resolution: A Structure-Based Design of Tailored Transition State Analogs. Structure, 2013, 21, 963-974.	1.6	17
1509	Structural determination of importin alpha in complex with beak and feather disease virus capsid nuclear localization signal. Biochemical and Biophysical Research Communications, 2013, 438, 680-685.	1.0	13
1510	Substrate binding to a GH131 Î²-glucanase catalytic domain from Podospora anserina. Biochemical and Biophysical Research Communications, 2013, 438, 193-197.	1.0	5
1511	Structural Basis of mRNA Recognition and Cleavage by Toxin MazF and Its Regulation by Antitoxin MazE in Bacillus subtilis. Molecular Cell, 2013, 52, 447-458.	4.5	77
1512	Structure Analysis of Archaeal AMP Phosphorylase Reveals Two Unique Modes of Dimerization. Journal of Molecular Biology, 2013, 425, 2709-2721.	2.0	9
1513	The structure of a novel glucuronoyl esterase from<i>Myceliophthora thermophila</i>gives new insights into its role as a potential biocatalyst. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 63-73.	2.5	38
1514	Structure of a C-terminal AHNAK peptide in a 1:2:2 complex with S100A10 and an acetylated N-terminal peptide of annexin A2. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 92-104.	2.5	24
1515	The AEROPATH project targetingPseudomonas aeruginosa: crystallographic studies for assessment of potential targets in early-stage drug discovery. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 25-34.	0.7	30
1516	A heterotetrameric alpha-amylase inhibitor from emmer (Triticum dicoccon Schrank) seeds. Phytochemistry, 2013, 88, 6-14.	1.4	25
1517	The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. Structure, 2013, 21, 595-603.	1.6	19
1518	Structural effect of phenyl ring compared to thiadiazole based adamantyl-sulfonamides on carbonic anhydrase inhibition. Bioorganic and Medicinal Chemistry, 2013, 21, 2314-2318.	1.4	20
1519	Crystal Structures of the Catalytic Domain of Human Soluble Guanylate Cyclase. PLoS ONE, 2013, 8, e57644.	1.1	78
1520	SOCS3 binds specific receptorâ€"JAK complexes to control cytokine signaling by direct kinase inhibition. Nature Structural and Molecular Biology, 2013, 20, 469-476.	3.6	229
1521	One Targetâ€"Two Different Binding Modes: Structural Insights into Gevokizumab and Canakinumab Interactions to Interleukin-1Î². Journal of Molecular Biology, 2013, 425, 94-111.	2.0	73
1522	Inhibition of <i>Yersinia pestis</i><scp>DNA</scp> adenine methyltransferase <i>in vitro</i> by a stibonic acid compound: identification of a potential novel class of antimicrobial agents. British Journal of Pharmacology, 2013, 168, 172-188.	2.7	11
1523	First structural evidence of sequestration of mRNA cap structures by type 1 ribosome inactivating protein from <i>Momordica balsamina</i>. Proteins: Structure, Function and Bioinformatics, 2013, 81, 896-905.	1.5	9
1524	Structure of<i>Ostertagia ostertagi</i>ASP-1: insights into disulfide-mediated cyclization and dimerization. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 493-503.	2.5	29

#	ARTICLE	IF	CITATIONS
1525	Structure of the PolIIIÎ±-Ï„c-DNA Complex Suggests an Atomic Model of the Replisome. Structure, 2013, 21, 658-664.	1.6	15
1526	Structure of Ldt_{Mt2}, an<scp>L</scp>,<scp>D</scp>-transpeptidase from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 432-441.	2.5	36
1527	Structural basis for the inhibition of<i>Mycobacterium tuberculosis</i><scp>L</scp>,<scp>D</scp>-transpeptidase by meropenem, a drug effective against extensively drug-resistant strains. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 420-431.	2.5	68
1528	Evolution of crystallins for a role in the vertebrate eye lens. Protein Science, 2013, 22, 367-380.	3.1	135
1529	Crystal structure of oligomeric Î²1-adrenergic G proteinâ€"coupled receptors in ligand-free basal state. Nature Structural and Molecular Biology, 2013, 20, 419-425.	3.6	235
1530	Limited conformational flexibility in the paratope may be responsible for degenerate specificity of HIV epitope recognition. International Immunology, 2013, 25, 77-90.	1.8	6
1531	Archaeal transcription: making up for lost time. Biochemical Society Transactions, 2013, 41, 356-361.	1.6	5
1532	A recurring motif for antibody recognition of the receptor-binding site of influenza hemagglutinin. Nature Structural and Molecular Biology, 2013, 20, 363-370.	3.6	141
1533	Structure of the Tubulin/FtsZ-Like Protein TubZ from Pseudomonas Bacteriophage Î¦KZ. Journal of Molecular Biology, 2013, 425, 2164-2173.	2.0	31
1534	Intertwined Associations in Structures of Homooligomeric Proteins. Structure, 2013, 21, 638-649.	1.6	27
1535	Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. Nature, 2013, 496, 469-476.	13.7	961
1536	Adaptation of Aminoacyl-tRNA Synthetase Catalytic Core to Carrier Protein Aminoacylation. Structure, 2013, 21, 614-626.	1.6	12
1537	Structure of the Trypanosoma cruzi protein tyrosine phosphatase TcPTP1, a potential therapeutic target for Chagasâ€™ disease. Molecular and Biochemical Parasitology, 2013, 187, 1-8.	0.5	7
1538	Oligomerisation status and evolutionary conservation of interfaces of protein structural domain superfamilies. Molecular BioSystems, 2013, 9, 1652.	2.9	72
1539	Biocatalytic and Structural Properties of a Highly Engineered Halohydrin Dehalogenase. ChemBioChem, 2013, 14, 870-881.	1.3	44
1540	Structure ofVibrio choleraeribosome hibernation promoting factor. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 228-236.	0.7	20
1541	Structural and functional characterization of a noncanonical nucleoside triphosphate pyrophosphatase from<i>Thermotoga maritima</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 184-193.	2.5	3
1542	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. Cell, 2013, 153, 461-470.	13.5	215

#	Article	IF	Citations
1543	Thermal inactivation and conformational lock studies on horse liver alcohol dehydrogenase: Structural mechanism. International Journal of Biological Macromolecules, 2013, 58, 66-72.	3.6	15
1544	The role of structural bioinformatics resources in the era of integrative structural biology. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 710-721.	2.5	17
1545	ORC1, ORC2 Mitochondrial Ornithine Carriers. , 2013, , 1807-1807.		0
1546	Crystal structure of human cytosolic aspartylâ€tRNA synthetase, a component of multiâ€tRNA synthetase complex. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1840-1846.	1.5	20
1547	Optical Tweezers. , 2013, , 1800-1807.		1
1548	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. Science, 2013, 340, 711-716.	6.0	680
1549	Evolutionary and molecular analysis of the emergent severe fever with thrombocytopenia syndrome virus. Epidemics, 2013, 5, 1-10.	1.5	84
1550	Crystal structure analysis of l-fuculose-1-phosphate aldolase from Thermus thermophilus HB8 and its catalytic action: as explained through in silico. Journal of Structural and Functional Genomics, 2013, 14, 59-70.	1.2	2
1551	Characterization of 14-3-3-Î¶ Interactions with Integrin Tails. Journal of Molecular Biology, 2013, 425, 3060-3072.	2.0	30
1552	Oriented-Sample NMR of Membrane Proteins: Sensitivity Enhancement and Spectroscopic Assignment. , 2013, , 1809-1813.		0
1553	Structure of Mycobacterial Î²-Oxidation Trifunctional Enzyme Reveals Its Altered Assembly and Putative Substrate Channeling Pathway. ACS Chemical Biology, 2013, 8, 1063-1073.	1.6	32
1554	Regulation of proteinâ€"protein binding by coupling between phosphorylation and intrinsic disorder: analysis of human protein complexes. Molecular BioSystems, 2013, 9, 1620.	2.9	60
1555	Structural, Evolutionary, and Assembly Principles of Protein Oligomerization. Progress in Molecular Biology and Translational Science, 2013, 117, 25-51.	0.9	107
1556	Evolutionary, Physicochemical, and Functional Mechanisms of Protein Homooligomerization. Progress in Molecular Biology and Translational Science, 2013, 117, 3-24.	0.9	34
1557	Crystal structures of Plasmodium falciparum cytosolic tryptophanyl-tRNA synthetase and its potential as a target for structure-guided drug design. Molecular and Biochemical Parasitology, 2013, 189, 26-32.	0.5	27
1558	Human UDP-Î±-<scp>d</scp>-xylose Synthase Forms a Catalytically Important Tetramer That Has Not Been Observed in Crystal Structures. Biochemistry, 2013, 52, 3888-3898.	1.2	6
1559	Antigenic Switching of Hepatitis B Virus by Alternative Dimerization of the Capsid Protein. Structure, 2013, 21, 133-142.	1.6	61
1560	Ligand-Dependent Activation and Deactivation of the Human Adenosine A2A Receptor. Journal of the American Chemical Society, 2013, 135, 8749-8759.	6.6	99

#	ARTICLE	IF	CITATIONS
1561	Crystal structure of arginase from Leishmania mexicana and implications for the inhibition of polyamine biosynthesis in parasitic infections. Archives of Biochemistry and Biophysics, 2013, 535, 163-176.	1.4	70
1562	Structural and Functional Characterization of MppR, an Enduracididine Biosynthetic Enzyme from <i>Streptomyces hygroscopicus</i>: Functional Diversity in the Acetoacetate Decarboxylase-like Superfamily. Biochemistry, 2013, 52, 4492-4506.	1.2	31
1563	The Dynamics of Lysozyme from Bacteriophage Lambda in Solution Probed by NMR and MD Simulations. ChemBioChem, 2013, 14, 1780-1788.	1.3	8
1564	A triclinic crystal structure of the carboxy-terminal domain of HIV-1 capsid protein with four molecules in the asymmetric unit reveals a novel packing interface. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 602-606.	0.7	8
1565	The human ITPA polymorphic variant P32T is destabilized by the unpacking of the hydrophobic core. Journal of Structural Biology, 2013, 182, 197-208.	1.3	15
1566	Bacteriophage P23-77 Capsid Protein Structures Reveal the Archetype of an Ancient Branch from a Major Virus Lineage. Structure, 2013, 21, 718-726.	1.6	38
1567	Crystal structures of glycoside hydrolase family 3 Î²-glucosidase 1 from <i>Aspergillus aculeatus</i>. Biochemical Journal, 2013, 452, 211-221.	1.7	77
1568	Structure, Dynamics, and Specificity of Endoglucanase D from Clostridium cellulovorans. Journal of Molecular Biology, 2013, 425, 4267-4285.	2.0	41
1569	Structure of SAICAR synthetase from Pyrococcus horikoshii OT3: Insights into thermal stability. International Journal of Biological Macromolecules, 2013, 53, 7-19.	3.6	6
1570	Systematic Optimization of Interface Interactions Increases the Thermostability of a Multimeric Enzyme. Angewandte Chemie - International Edition, 2013, 52, 9673-9676.	7.2	68
1571	Crystal and Solution Studies of the â€œPlus-Câ€• Odorant-binding Protein 48 from Anopheles gambiae. Journal of Biological Chemistry, 2013, 288, 33427-33438.	1.6	42
1572	Synthesis of Î±-Glucan in Mycobacteria Involves a Hetero-octameric Complex of Trehalose Synthase TreS and Maltokinase Pep2. ACS Chemical Biology, 2013, 8, 2245-2255.	1.6	27
1573	Filling out the structural map of the NTF2-like superfamily. BMC Bioinformatics, 2013, 14, 327.	1.2	74
1574	LUD, a new protein domain associated with lactate utilization. BMC Bioinformatics, 2013, 14, 341.	1.2	8
1575	Metal Binding Properties of <i>Escherichia coli</i> YjiA, a Member of the Metal Homeostasis-Associated COG0523 Family of GTPases. Biochemistry, 2013, 52, 1788-1801.	1.2	43
1576	Biochemical Characterization of Molybdenum Cofactor-free Nitrate Reductase from Neurospora crassa. Journal of Biological Chemistry, 2013, 288, 14657-14671.	1.6	20
1577	Structure of the Flavoprotein Tryptophan 2-Monooxygenase, a Key Enzyme in the Formation of Galls in Plants. Biochemistry, 2013, 52, 2620-2626.	1.2	26
1578	Specialized Dynamical Properties of Promiscuous Residues Revealed by Simulated Conformational Ensembles. Journal of Chemical Theory and Computation, 2013, 9, 5127-5147.	2.3	39

#	Article	IF	Citations
1579	Structure of the Bifunctional Acyltransferase/Decarboxylase LnmK from the Leinamycin Biosynthetic Pathway Revealing Novel Activity for a Double-Hot-Dog Fold. Biochemistry, 2013, 52, 902-911.	1.2	31
1580	Formiminoglutamase from<i>Trypanosoma Cruzi</i>Is An Arginase-Like Manganese Metalloenzyme. Biochemistry, 2013, 52, 9294-9309.	1.2	8
1581	High-resolution structure of an atypical Î±-phosphoglucomutase related to eukaryotic phosphomannomutases. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2008-2016.	2.5	4
1582	Structure of isochorismate synthase DhbC fromBacillus anthracis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 956-961.	0.7	2
1583	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. Molecular Immunology, 2013, 56, 794-803.	1.0	43
1584	Specificity of Processing Î±-Glucosidase I Is Guided by the Substrate Conformation. Journal of Biological Chemistry, 2013, 288, 13563-13574.	1.6	65
1585	Identification, Structure, and Function of a Novel Type VI Secretion Peptidoglycan Glycoside Hydrolase Effector-Immunity Pair. Journal of Biological Chemistry, 2013, 288, 26616-26624.	1.6	110
1586	A Structural Basis for the Regulation of the LIM-Homeodomain Protein Islet 1 (Isl1) by Intra- and Intermolecular Interactions. Journal of Biological Chemistry, 2013, 288, 21924-21935.	1.6	21
1587	The Structure of Allophanate Hydrolase from <i>Granulibacter bethesdensis</i> Provides Insights into Substrate Specificity in the Amidase Signature Family. Biochemistry, 2013, 52, 690-700.	1.2	15
1588	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant Staphylococcus aureus. Journal of Structural and Functional Genomics, 2013, 14, 97-108.	1.2	9
1589	On the binding affinity of macromolecular interactions: daring to ask why proteins interact. Journal of the Royal Society Interface, 2013, 10, 20120835.	1.5	353
1590	The crystal structures of the tri-functional Chloroflexus aurantiacus and bi-functional Rhodobacter sphaeroides malyl-CoA lyases and comparison with CitE-like superfamily enzymes and malate synthases. BMC Structural Biology, 2013, 13, 28.	2.3	11
1591	The structure of amylosucrase from<i>Deinococcus radiodurans</i>has an unusual open active-site topology. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 973-978.	0.7	23
1592	Landscape of neutralizing assessment of monoclonal antibodies against dengue virus. , 2013, , .		0
1593	Crystal structures of isoorotate decarboxylases reveal a novel catalytic mechanism of 5-carboxyl-uracil decarboxylation and shed light on the search for DNA decarboxylase. Cell Research, 2013, 23, 1296-1309.	5.7	50
1594	Deep mutational scanning of an RRM domain of the <i>Saccharomyces cerevisiae</i> poly(A)-binding protein. Rna, 2013, 19, 1537-1551.	1.6	207
1595	Problems of Protein Three-Dimensional Structures. , 2013, , .		0
1596	A Molecular Switch Governs the Interaction between the Human Complement Protease C1s and Its Substrate, Complement C4. Journal of Biological Chemistry, 2013, 288, 15821-15829.	1.6	29

#	Article	IF	Citations
1597	Increasing Affinity of Interferon-<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"><mml:mrow><mml:mi mathvariant="bold">Î³</mml:mi></mml:mrow></mml:math>Receptor 1 to Interferon-<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M2"><mml:mrow><mml:mi mathvariant="bold">Î³</mml:mi></mml:mrow></mml:math>by Computer-Aided Design. BioMed Research International, 2013, 2013, 1-12.	0.9	12
1598	Structural insights into the inhibition of typeÂVI effector Tae3 by its immunity protein Tai3. Biochemical Journal, 2013, 454, 59-68.	1.7	26
1599	IRAK-M mediates Toll-like receptor/IL-1R-induced NFÎºB activation and cytokine production. EMBO Journal, 2013, 32, 583-596.	3.5	103
1600	Structure of <i>Plasmodium falciparum</i> TRAP (thrombospondin-related anonymous protein) A domain highlights distinct features in apicomplexan von Willebrand factor A homologues. Biochemical Journal, 2013, 450, 469-476.	1.7	22
1601	Structure-guided optimization of protein kinase inhibitors reverses aminoglycoside antibiotic resistance. Biochemical Journal, 2013, 454, 191-200.	1.7	43
1602	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9054-9059.	3.3	59
1603	Post-translational modification in the archaea: structural characterization of multi-enzyme complex lipoylation. Biochemical Journal, 2013, 449, 415-425.	1.7	14
1604	Crystal Structure of the Gamma-2 Herpesvirus LANA DNA Binding Domain Identifies Charged Surface Residues Which Impact Viral Latency. PLoS Pathogens, 2013, 9, e1003673.	2.1	33
1605	Structural Units Important for Activity of a Novel-type Phosphoserine Phosphatase from Hydrogenobacter thermophilus TK-6 Revealed by Crystal Structure Analysis. Journal of Biological Chemistry, 2013, 288, 11448-11458.	1.6	18
1606	Putative Bioactive Motif of Tritrpticin Revealed by an Antibody with Biological Receptor-Like Properties. PLoS ONE, 2013, 8, e75582.	1.1	8
1607	Structural Insights into a Novel Interkingdom Signaling Circuit by Cartography of the Ligand-Binding Sites of the Homologous Quorum Sensing LuxR-Family. International Journal of Molecular Sciences, 2013, 14, 20578-20596.	1.8	18
1608	Crystal structure of hexanoyl-CoA bound to Î²-ketoacyl reductase FabG4 of <i>Mycobacterium tuberculosis</i>. Biochemical Journal, 2013, 450, 127-139.	1.7	34
1609	Structural and Functional Analysis of the CspB Protease Required for Clostridium Spore Germination. PLoS Pathogens, 2013, 9, e1003165.	2.1	99
1610	Broadly Neutralizing Antibody PGT121 Allosterically Modulates CD4 Binding via Recognition of the HIV-1 gp120 V3 Base and Multiple Surrounding Glycans. PLoS Pathogens, 2013, 9, e1003342.	2.1	267
1611	Peptide-binding dependent conformational changes regulate the transcriptional activity of the quorum-sensor NprR. Nucleic Acids Research, 2013, 41, 7920-7933.	6.5	57
1612	Dimerization of Sir3 via its C-terminal winged helix domain is essential for yeast heterochromatin formation. EMBO Journal, 2013, 32, 437-449.	3.5	29
1613	A structural basis for kinetochore recruitment of the Ndc80 complex via two distinct centromere receptors. EMBO Journal, 2013, 32, 409-423.	3.5	128
1614	Rezymogenation of active urokinase induced by an inhibitory antibody. Biochemical Journal, 2013, 449, 161-166.	1.7	25

#	ARTICLE	IF	CITATIONS
1615	Crystal structure of the capsular polysaccharide synthesizing protein CapE of Staphylococcus aureus. Bioscience Reports, 2013, 33, .	1.1	16
1616	A Compact Viral Processing Proteinase/Ubiquitin Hydrolase from the OTU Family. PLoS Pathogens, 2013, 9, e1003560.	2.1	28
1617	Crystal structures of SCP2-thiolases of Trypanosomatidae, human pathogens causing widespread tropical diseases: the importance for catalysis of the cysteine of the unique HDCF loop. Biochemical Journal, 2013, 455, 119-130.	1.7	20
1618	Structural and Functional Basis for Inhibition of Erythrocyte Invasion by Antibodies that Target Plasmodium falciparum EBA-175. PLoS Pathogens, 2013, 9, e1003390.	2.1	55
1619	Structural and molecular basis of ZNRF3/RNF43 transmembrane ubiquitin ligase inhibition by the Wnt agonist R-spondin. Nature Communications, 2013, 4, 2787.	5.8	161
1620	Structure of a dimeric crenarchaeal Cas6 enzyme with an atypical active site for CRISPR RNA processing. Biochemical Journal, 2013, 452, 223-230.	1.7	32
1621	Amino Acid Changes in Disease-Associated Variants Differ Radically from Variants Observed in the 1000 Genomes Project Dataset. PLoS Computational Biology, 2013, 9, e1003382.	1.5	54
1622	Structural Basis of HCV Neutralization by Human Monoclonal Antibodies Resistant to Viral Neutralization Escape. PLoS Pathogens, 2013, 9, e1003364.	2.1	86
1623	Structure-Based Function Prediction of Uncharacterized Protein Using Binding Sites Comparison. PLoS Computational Biology, 2013, 9, e1003341.	1.5	38
1624	Structural basis for endosomal trafficking of diverse transmembrane cargos by PX-FERM proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E643-52.	3.3	112
1625	GalaxyGemini: a web server for protein homo-oligomer structure prediction based on similarity. Bioinformatics, 2013, 29, 1078-1080.	1.8	38
1626	Phosphorylation-dependent conformational changes and domain rearrangements in <i>Staphylococcus aureus</i> VraR activation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8525-8530.	3.3	83
1627	The TP0796 Lipoprotein of Treponema pallidum Is a Bimetal-dependent FAD Pyrophosphatase with a Potential Role in Flavin Homeostasis. Journal of Biological Chemistry, 2013, 288, 11106-11121.	1.6	29
1628	Structure and Function of a Novel <scp>ld</scp> -Carboxypeptidase A Involved in Peptidoglycan Recycling. Journal of Bacteriology, 2013, 195, 5555-5566.	1.0	16
1629	Structural Basis for Cul3 Protein Assembly with the BTB-Kelch Family of E3 Ubiquitin Ligases. Journal of Biological Chemistry, 2013, 288, 7803-7814.	1.6	227
1630	1.2â€…Å… resolution crystal structure of<i>Escherichia coli</i>WrbA holoprotein. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1748-1757.	2.5	6
1631	Structural Basis of Subtilase Cytotoxin SubAB Assembly. Journal of Biological Chemistry, 2013, 288, 27505-27516.	1.6	21
1632	Structural and Functional Characterization of an Orphan ATP-Binding Cassette ATPase Involved in Manganese Utilization and Tolerance in Leptospira spp. Journal of Bacteriology, 2013, 195, 5583-5591.	1.0	5

#	Article	IF	Citations
1633	Characterization of Anopheles gambiae Transglutaminase 3 (AgTG3) and Its Native Substrate Plugin. Journal of Biological Chemistry, 2013, 288, 4844-4853.	1.6	14
1634	Nucleocapsid protein structures from orthobunyaviruses reveal insight into ribonucleoprotein architecture and RNA polymerization. Nucleic Acids Research, 2013, 41, 5912-5926.	6.5	69
1635	From Soil to Structure, a Novel Dimeric Î²-Glucosidase Belonging to Glycoside Hydrolase Family 3 Isolated from Compost Using Metagenomic Analysis. Journal of Biological Chemistry, 2013, 288, 14985-14992.	1.6	42
1636	Crystal Structure of the Avian Astrovirus Capsid Spike. Journal of Virology, 2013, 87, 7853-7863.	1.5	36
1637	Crystal structure of the FRP and identification of the active site for modulation of OCP-mediated photoprotection in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10022-10027.	3.3	102
1638	Evolutionary diversification of the multimeric states of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2821-8.	3.3	78
1639	Structure of the Repulsive Guidance Molecule (RGM)â€"Neogenin Signaling Hub. Science, 2013, 341, 77-80.	6.0	52
1640	Rv2969c, essential for optimal growth in<i>Mycobacterium tuberculosis</i>, is a DsbA-like enzyme that interacts with VKOR-derived peptides and has atypical features of DsbA-like disulfide oxidases. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1981-1994.	2.5	29
1641	Structure of ADP-aluminium fluoride-stabilized protochlorophyllide oxidoreductase complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2094-2098.	3.3	56
1642	Structural and biochemical studies of SLIP1â€"SLBP identify DBP5 and eIF3g as SLIP1-binding proteins. Nucleic Acids Research, 2013, 41, 7960-7971.	6.5	30
1643	Cross-Inhibition of Chikungunya Virus Fusion and Infection by Alphavirus E1 Domain III Proteins. Journal of Virology, 2013, 87, 7680-7687.	1.5	21
1644	Structures of Mycobacterium tuberculosis FadD10 Protein Reveal a New Type of Adenylate-forming Enzyme. Journal of Biological Chemistry, 2013, 288, 18473-18483.	1.6	35
1645	Structure of formaldehyde dehydrogenase from<i>Pseudomonas aeruginosa</i>: the binary complex with the cofactor NAD⁺. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 967-972.	0.7	11
1646	High-resolution structures of the IgM Fc domains reveal principles of its hexamer formation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10183-10188.	3.3	73
1647	The structure of the Mycobacterium smegmatis trehalose synthase reveals an unusual active site configuration and acarbose-binding mode. Glycobiology, 2013, 23, 1075-1083.	1.3	41
1648	Crystal structure analysis of a fatty acid double-bond hydratase from<i>Lactobacillus acidophilus</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 648-657.	2.5	46
1649	Structural features of antiviral DNA cytidine deaminases. Biological Chemistry, 2013, 394, 1357-1370.	1.2	38
1650	Heavy Chain-Only IgG2b Llama Antibody Effects Near-Pan HIV-1 Neutralization by Recognizing a CD4-Induced Epitope That Includes Elements of Coreceptor- and CD4-Binding Sites. Journal of Virology, 2013, 87, 10173-10181.	1.5	22

#	Article	IF	Citations
1651	Structural and functional characterization of HP0377, a thioredoxin-fold protein fromHelicobacter pylori. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 735-746.	2.5	8
1652	Computational Pharmacogenomics. , 2013, , 163-186.		0
1653	Crystal Structure of a Human IÎºB Kinase Î² Asymmetric Dimer. Journal of Biological Chemistry, 2013, 288, 22758-22767.	1.6	101
1654	Obstruction of Dengue Virus Maturation by Fab Fragments of the 2H2 Antibody. Journal of Virology, 2013, 87, 8909-8915.	1.5	24
1655	Structural insights into the functions of the FANCM-FAAP24 complex in DNA repair. Nucleic Acids Research, 2013, 41, 10573-10583.	6.5	13
1656	Crystal structure of the DdrB/ssDNA complex from Deinococcus radiodurans reveals a DNA binding surface involving higher-order oligomeric states. Nucleic Acids Research, 2013, 41, 9934-9944.	6.5	10
1657	Structures of enzymeâ€“intermediate complexes of yeast Nit2: insights into its catalytic mechanism and different substrate specificity compared with mammalian Nit2. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1470-1481.	2.5	16
1658	Structureâ€“function relationships of two paralogous single-stranded DNA-binding proteins from Streptomyces coelicolor: implication of SsbB in chromosome segregation during sporulation. Nucleic Acids Research, 2013, 41, 3659-3672.	6.5	17
1659	Structural and mechanistic basis of anti-termination of Rho-dependent transcription termination by bacteriophage P4 capsid protein Psu. Nucleic Acids Research, 2013, 41, 6839-6856.	6.5	17
1660	Structure, phosphorylation and U2AF65 binding of the N-terminal domain of splicing factor 1 during 3â€²-splice site recognition. Nucleic Acids Research, 2013, 41, 1343-1354.	6.5	61
1661	Functional convergence of structurally distinct thioesterases from cyanobacteria and plants involved in phylloquinone biosynthesis. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1876-1888.	2.5	8
1662	Structure of an outer surface lipoprotein BBA64 from the Lyme disease agent<i>Borrelia burgdorferi</i>which is critical to ensure infection after a tick bite. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1099-1107.	2.5	13
1663	Mutations inducing an active-site aperture inRhizobiumsp. sucrose isomerase confer hydrolytic activity. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 298-307.	2.5	11
1664	The structure of brazzein, a sweet-tasting protein from the wild African plantPentadiplandra brazzeana. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 642-647.	2.5	27
1665	The landscape of cytokinin binding by a plant nodulin. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2365-2380.	2.5	16
1666	Expression, purification, crystallization and X-ray crystallographic studies of different redox states of the active site of thioredoxin 1 from the whiteleg shrimp<i>Litopenaeus vannamei</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 488-493.	0.7	10
1667	Structure of the NS1 Protein N-Terminal Origin Recognition/Nickase Domain from the Emerging Human Bocavirus. Journal of Virology, 2013, 87, 11487-11493.	1.5	26
1668	Structural basis for the activation mechanism of the PlcR virulence regulator by the quorum-sensing signal peptide PapR. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1047-1052.	3.3	90

#	ARTICLE	IF	CITATIONS
1669	Structural and functional analysis of the yeast <i>N</i> -acetyltransferase Mpr1 involved in oxidative stress tolerance via proline metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11821-11826.	3.3	22
1670	X-ray structure of an AdoMet radical activase reveals an anaerobic solution for formylglycine posttranslational modification. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8519-8524.	3.3	113
1671	An Uncharacterized Member of the Ribokinase Family in Thermococcus kodakarensis Exhibits myo-Inositol Kinase Activity. Journal of Biological Chemistry, 2013, 288, 20856-20867.	1.6	9
1672	Structural Basis for Complement Evasion by Lyme Disease Pathogen Borrelia burgdorferi. Journal of Biological Chemistry, 2013, 288, 18685-18695.	1.6	50
1673	Crystal and Solution Studies Reveal That the Transcriptional Regulator AcnR of Corynebacterium glutamicum Is Regulated by Citrate-Mg2+ Binding to a Non-canonical Pocket. Journal of Biological Chemistry, 2013, 288, 15800-15812.	1.6	10
1674	Potential Regulatory Interactions of Escherichia coli RraA Protein with DEAD-box Helicases. Journal of Biological Chemistry, 2013, 288, 31919-31929.	1.6	13
1675	Dimeric Sfh3 has structural changes in its binding pocket that are associated with a dimerâ€"monomer state transformation induced by substrate binding. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 313-323.	2.5	12
1676	Novel c-di-GMP recognition modes of the mouse innate immune adaptor protein STING. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 352-366.	2.5	36
1677	GH1-family 6-P-Î²-glucosidases from human microbiome lactic acid bacteria. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 451-463.	2.5	19
1678	Proteinâ€"peptide complex crystallization: a case study on the ERK2 mitogen-activated protein kinase. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 486-489.	2.5	21
1679	Structural characterization of V57D and V57P mutants of human cystatin C, an amyloidogenic protein. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 577-586.	2.5	8
1680	Structural analysis of coniferyl alcohol 9-<i>O</i>-methyltransferase from<i>Linum nodiflorum</i>reveals a novel active-site environment. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 888-900.	2.5	8
1681	<i>S</i>-Adenosyl-<i>S</i>-carboxymethyl-<scp>L</scp>-homocysteine: a novel cofactor found in the putative tRNA-modifying enzyme CmoA. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1090-1098.	2.5	20
1682	Tying down the arm inBacillusdUTPase: structure and mechanism. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1367-1380.	2.5	12
1683	Anatomy of secretin binding to the<i>Dickeya dadantii</i>type II secretion system pilotin. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1381-1386.	2.5	21
1684	Catalysis product captured in lumazine synthase from the fungal pathogen<i>Candida glabrata</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1580-1586.	2.5	4
1685	Fine-tuning of prototype chicken galectins: structure of CG-2 and structureâ€"activity correlations. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1665-1676.	2.5	11
1686	Structural basis of high-order oligomerization of the cullin-3 adaptor SPOP. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1677-1684.	2.5	35

#	ARTICLE	IF	CITATIONS
1687	High-resolution structure of a papaya plant-defence barwin-like protein solved by in-house sulfur-SAD phasing. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2017-2026.	2.5	16
1688	Conformational changes in human prolyl-tRNA synthetase upon binding of the substrates proline and ATP and the inhibitor halofuginone. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2136-2145.	2.5	36
1689	Crystallographic identification of an unexpected protein complex in silkworm haemolymph. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2353-2364.	2.5	13
1690	The TLR signalling adaptor TRIF/TICAM-1 has an N-terminal helical domain with structural similarity to IFIT proteins. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2420-2430.	2.5	13
1691	Structural characterization of the ribonuclease H-like type ASKHA superfamily kinase MK0840 fromMethanopyrus kandleri. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2440-2450.	2.5	4
1692	Protein design by fusion: implications for protein structure prediction and evolution. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2451-2460.	2.5	3
1693	Structural basis for type VI secreted peptidoglycan<scp>DL</scp>-endopeptidase function, specificity and neutralization in<i>Serratia marcescens</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2468-2482.	2.5	37
1694	Improvements in the order, isotropy and electron density of glypican-1 crystals by controlled dehydration. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2524-2533.	2.5	11
1695	Structure of ALD1, a plant-specific homologue of the universal diaminopimelate aminotransferase enzyme of lysine biosynthesis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 84-89.	0.7	8
1696	Structure of glutaminyl cyclase from<i>Drosophila melanogaster</i>in space group<i>I</i>4. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 358-361.	0.7	2
1697	Deer mouse hemoglobin exhibits a lowered oxygen affinity owing to mobility of the E helix. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 393-398.	0.7	8
1698	Structure of an atypical FeoB G-domain reveals a putative domain-swapped dimer. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 399-404.	0.7	12
1699	Structure of diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase from<i>Acinetobacter baumannii</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 611-617.	0.7	4
1700	Structure of PatF from<i>Prochloron didemni</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 618-623.	0.7	27
1701	ErpC, a member of the complement regulator-acquiring family of surface proteins fromBorrelia burgdorferi, possesses an architecture previously unseen in this protein family. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 624-628.	0.7	12
1702	Conformational stability and crystal packing: polymorphism inNeurospora crassaCAT-3. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 753-758.	0.7	3
1703	The structure of substrate-free 1,5-anhydro-<scp>D</scp>-fructose reductase from<i>Sinorhizobium meliloti</i>1021 reveals an open enzyme conformation. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 844-849.	0.7	7
1704	Structure of CT584 fromChlamydia trachomatisrefined to 3.05â€…Å… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1196-1201.	0.7	8

#	Article	IF	Citations
1705	Two high-resolution structures of the human E3 ubiquitin ligase Siah1. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1339-1343.	0.7	9
1706	The Unique Structure of Haemophilus influenzae Protein E Reveals Multiple Binding Sites for Host Factors. Infection and Immunity, 2013, 81, 801-814.	1.0	46
1707	Capsid Antibodies to Different Adeno-Associated Virus Serotypes Bind Common Regions. Journal of Virology, 2013, 87, 9111-9124.	1.5	102
1708	SPACER: server for predicting allosteric communication and effects of regulation. Nucleic Acids Research, 2013, 41, W266-W272.	6.5	88
1709	Structural basis for Z-DNA binding and stabilization by the zebrafish Z-DNA dependent protein kinase PKZ. Nucleic Acids Research, 2013, 41, 9924-9933.	6.5	27
1710	Elastic and inelastic diffraction changes upon variation of the relative humidity environment of PurE crystals. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 194-212.	2.5	7
1711	Protein HP1028 from the human pathogen<i>Helicobacter pylori</i>belongs to the lipocalin family. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1387-1394.	2.5	3
1712	Putative dioxygen-binding sites and recognition of tigecycline and minocycline in the tetracycline-degrading monooxygenase TetX. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1758-1767.	2.5	28
1713	Analysis of the human cofilin 1 structure reveals conformational changes required for actin binding. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1780-1788.	2.5	23
1714	Structure of the prolyl-acyl carrier protein oxidase involved in the biosynthesis of the cyanotoxin anatoxin-a. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2340-2352.	2.5	11
1715	Further structural insights into the binding of complement factor H by complement regulator-acquiring surface protein 1 (CspA) of<i>Borrelia burgdorferi</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 629-633.	0.7	24
1716	Affinity of a galactoseâ€specific legume lectin from <i>Dolichos lablab</i> to adenine revealed by Xâ€ray cystallography. IUBMB Life, 2013, 65, 633-644.	1.5	14
1717	Analysis of periplasmic sensor domains from <i>Anaeromyxobacter dehalogenans</i> 2<scp>CP</scp>â€C: Structure of one sensor domain from a histidine kinase and another from a chemotaxis protein. MicrobiologyOpen, 2013, 2, 766-777.	1.2	7
1718	A broad specificity nucleoside kinase from <i>Thermoplasma acidophilum</i>. Proteins: Structure, Function and Bioinformatics, 2013, 81, 568-582.	1.5	10
1719	Biochemical phenotype of a common diseaseâ€causing mutation and a possible therapeutic approach for the phosphomannomutase 2â€associated disorder of glycosylation. Molecular Genetics & Genomic Medicine, 2013, 1, 32-44.	0.6	20
1720	Distinctive Conformation of Minor Siteâ€Specific Nuclear Localization Signals Bound to Importinâ€Î±. Traffic, 2013, 14, 1144-1154.	1.3	45
1721	Epistasis Among Adaptive Mutations in Deer Mouse Hemoglobin. Science, 2013, 340, 1324-1327.	6.0	174
1722	Insights into the oligomerization of <scp>CRMP</scp>s: crystal structure of human collapsin response mediator protein 5. Journal of Neurochemistry, 2013, 125, 855-868.	2.1	25

#	Article	IF	Citations
1723	Structure, biochemical characterization and analysis of the pleomorphism of carboxylesterase Cest-2923 from<i>LactobacillusÂplantarum</i>WCFS1. FEBS Journal, 2013, 280, 6658-6671.	2.2	32
1724	Structural and functional characterization of solute binding proteins for aromatic compounds derived from lignin: <i>p</i> -Coumaric acid and related aromatic acids. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1709-1726.	1.5	21
1725	Crystal structure of the protein from <i>Arabidopsis thaliana</i> gene At5g06450, a putative DnaQâ€like exonuclease domainâ€containing protein with homohexameric assembly. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1669-1675.	1.5	5
1726	Structural insights into the oligomerization mode of the human receptor for advanced glycation end-products. FEBS Journal, 2013, 280, 6556-6568.	2.2	63
1727	Structural Changes during Cysteine Desulfurase CsdA and Sulfur Acceptor CsdE Interactions Provide Insight into the trans-Persulfuration. Journal of Biological Chemistry, 2013, 288, 27172-27180.	1.6	40
1728	Crystal Structure of IL-17 Receptor B SEFIR Domain. Journal of Immunology, 2013, 190, 2320-2326.	0.4	30
1729	Structure and Function of the DUF2233 Domain in Bacteria and in the Human Mannose 6-Phosphate Uncovering Enzyme. Journal of Biological Chemistry, 2013, 288, 16789-16799.	1.6	7
1730	Structural Basis of the Interaction of MbtH-like Proteins, Putative Regulators of Nonribosomal Peptide Biosynthesis, with Adenylating Enzymes. Journal of Biological Chemistry, 2013, 288, 1991-2003.	1.6	86
1731	Structural Evaluation of a Mimicry-Recognizing Paratope: Plasticity in Antigenâ€"Antibody Interactions Manifests in Molecular Mimicry. Journal of Immunology, 2013, 191, 456-463.	0.4	20
1732	Structural Basis for Phosphorylated Autoinducer-2 Modulation of the Oligomerization State of the Global Transcription Regulator LsrR from Escherichia coli. Journal of Biological Chemistry, 2013, 288, 15878-15887.	1.6	13
1733	Architecture and Assembly of HIV Integrase Multimers in the Absence of DNA Substrates. Journal of Biological Chemistry, 2013, 288, 7373-7386.	1.6	29
1734	Dimerization of Bacterial Diaminopimelate Epimerase Is Essential for Catalysis. Journal of Biological Chemistry, 2013, 288, 9238-9248.	1.6	41
1735	Structural Analysis of Collagen Type I Interactions with Human Fibronectin Reveals a Cooperative Binding Mode. Journal of Biological Chemistry, 2013, 288, 17441-17450.	1.6	67
1736	Structure of the Ca2+-saturated C-terminal domain of scallop troponin C in complex with a troponin I fragment. Biological Chemistry, 2013, 394, 55-68.	1.2	7
1737	The Power of Two. Journal of Biological Chemistry, 2013, 288, 30862-30871.	1.6	19
1738	The 2.5 Å... Structure of the Enterococcus Conjugation Protein TraM resembles VirB8 Type IV Secretion Proteins. Journal of Biological Chemistry, 2013, 288, 2018-2028.	1.6	50
1739	Crystal structure and functional insights into uracil-DNA glycosylase inhibition by phage Ï•29 DNA mimic protein p56. Nucleic Acids Research, 2013, 41, 6761-6773.	6.5	23
1740	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12301-12306.	3.3	68

#	ARTICLE	IF	CITATIONS
1741	Quantitative Characterization of the Activation Steps of Mannan-binding Lectin (MBL)-associated Serine Proteases (MASPs) Points to the Central Role of MASP-1 in the Initiation of the Complement Lectin Pathway. Journal of Biological Chemistry, 2013, 288, 8922-8934.	1.6	64
1742	Biochemical Properties and Crystal Structure of a Î²-Phenylalanine Aminotransferase from Variovorax paradoxus. Applied and Environmental Microbiology, 2013, 79, 185-195.	1.4	29
1743	Structural Basis for Activity Regulation and Substrate Preference of Clostridial Collagenases G, H, and T. Journal of Biological Chemistry, 2013, 288, 20184-20194.	1.6	64
1744	Novel Insights into Eukaryotic Î³-Glutamyltranspeptidase 1 from the Crystal Structure of the Glutamate-bound Human Enzyme. Journal of Biological Chemistry, 2013, 288, 31902-31913.	1.6	66
1745	The Polybasic Insertion in Autotaxin Î± Confers Specific Binding to Heparin and Cell Surface Heparan Sulfate Proteoglycans. Journal of Biological Chemistry, 2013, 288, 510-519.	1.6	48
1746	Kinetics of Endophilin N-BAR Domain Dimerization and Membrane Interactions. Journal of Biological Chemistry, 2013, 288, 12533-12543.	1.6	39
1747	Structural and Biochemical Characterization of Plasmodium falciparum 12 (Pf12) Reveals a Unique Interdomain Organization and the Potential for an Antiparallel Arrangement with Pf41. Journal of Biological Chemistry, 2013, 288, 12805-12817.	1.6	63
1748	Monovalent antibody design and mechanism of action of onartuzumab, a MET antagonist with anti-tumor activity as a therapeutic agent. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2987-96.	3.3	206
1749	Interaction of local anesthetics with the K+channel pore domain. Channels, 2013, 7, 182-193.	1.5	7
1750	The Structure of the NTPase That Powers DNA Packaging into Sulfolobus Turreted Icosahedral Virus 2. Journal of Virology, 2013, 87, 8388-8398.	1.5	19
1751	Three-dimensional Structure of Saccharomyces Invertase. Journal of Biological Chemistry, 2013, 288, 9755-9766.	1.6	81
1752	Structure of an actin-related subcomplex of the SWI/SNF chromatin remodeler. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3345-3350.	3.3	81
1753	Structure of the archaeal Cascade subunit Csa5. RNA Biology, 2013, 10, 762-769.	1.5	24
1754	Personalized synthetic lethality induced by targeting RAD52 in leukemias identified by gene mutation and expression profile. Blood, 2013, 122, 1293-1304.	0.6	125
1756	The Structure of Glycerol Trinitrate Reductase NerA from <i>Agrobacterium radiobacter</i> Reveals the Molecular Reason for Nitroâ€•and Eneâ€Reductase Activity in OYE Homologues. ChemBioChem, 2013, 14, 836-845.	1.3	10
1757	Structure of the factor VIII C2 domain in a ternary complex with 2 inhibitor antibodies reveals classical and nonclassical epitopes. Blood, 2013, 122, 4270-4278.	0.6	25
1758	Crystal structure of SsfS6, the putative <i>C</i>â€glycosyltransferase involved in SF2575 biosynthesis. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1277-1282.	1.5	24
1760	Integron Gene Cassettes: A Repository of Novel Protein Folds with Distinct Interaction Sites. PLoS ONE, 2013, 8, e52934.	1.1	11

#	ARTICLE	IF	CITATIONS
1761	The Deinococcus radiodurans DR1245 Protein, a DdrB Partner Homologous to YbjN Proteins and Reminiscent of Type III Secretion System Chaperones. PLoS ONE, 2013, 8, e56558.	1.1	23
1762	Structural Characterization of the Self-Association of the Death Domain of p75NTR. PLoS ONE, 2013, 8, e57839.	1.1	11
1763	Determination of the Structure of the Catabolic N-Succinylornithine Transaminase (AstC) from Escherichia coli. PLoS ONE, 2013, 8, e58298.	1.1	17
1764	Kinetic and Structural Evidences on Human Prolidase Pathological Mutants Suggest Strategies for Enzyme Functional Rescue. PLoS ONE, 2013, 8, e58792.	1.1	21
1765	Beta Atomic Contacts: Identifying Critical Specific Contacts in Protein Binding Interfaces. PLoS ONE, 2013, 8, e59737.	1.1	6
1766	Evaluation and Use of In-Silico Structure-Based Epitope Prediction with Foot-and-Mouth Disease Virus. PLoS ONE, 2013, 8, e61122.	1.1	37
1767	Structural and Functional Insights into Saccharomyces cerevisiae Riboflavin Biosynthesis Reductase RIB7. PLoS ONE, 2013, 8, e61249.	1.1	4
1768	Two Crystal Structures of Bombyx mori Lipoprotein 3 - Structural Characterization of a New 30-kDa Lipoprotein Family Member. PLoS ONE, 2013, 8, e61303.	1.1	6
1769	Crystal Structures of a Plant Trypsin Inhibitor from Enterolobium contortisiliquum (EcTI) and of Its Complex with Bovine Trypsin. PLoS ONE, 2013, 8, e62252.	1.1	30
1770	Tetramerization Reinforces the Dimer Interface of MnSOD. PLoS ONE, 2013, 8, e62446.	1.1	15
1771	Structural Insights into the UbiD Protein Family from the Crystal Structure of PA0254 from Pseudomonas aeruginosa. PLoS ONE, 2013, 8, e63161.	1.1	33
1772	Crystal Structure of a Novel N-Substituted L-Amino Acid Dioxygenase from Burkholderia ambifaria AMMD. PLoS ONE, 2013, 8, e63996.	1.1	19
1773	Signal Transduction Pathways in the Pentameric Ligand-Gated Ion Channels. PLoS ONE, 2013, 8, e64326.	1.1	21
1774	Structural Insights into the Effector â€“ Immunity System Tae4/Tai4 from Salmonella typhimurium. PLoS ONE, 2013, 8, e67362.	1.1	26
1775	The Mode of Inhibitor Binding to Peptidyl-tRNA Hydrolase: Binding Studies and Structure Determination of Unbound and Bound Peptidyl-tRNA Hydrolase from Acinetobacter baumannii. PLoS ONE, 2013, 8, e67547.	1.1	21
1776	Crystal Structure of Pim1 Kinase in Complex with a Pyrido[4,3-D]Pyrimidine Derivative Suggests a Unique Binding Mode. PLoS ONE, 2013, 8, e70358.	1.1	11
1777	Toxoplasma gondii Sporozoites Invade Host Cells Using Two Novel Paralogues of RON2 and AMA1. PLoS ONE, 2013, 8, e70637.	1.1	48
1778	Structural Basis for the Interaction of the Adaptor Protein Grb14 with Activated Ras. PLoS ONE, 2013, 8, e72473.	1.1	23

#	ARTICLE	IF	CITATIONS
1779	Structure of the NheA Component of the Nhe Toxin from Bacillus cereus: Implications for Function. PLoS ONE, 2013, 8, e74748.	1.1	57
1780	Structural and Enzymatic Characterization of the Phosphotriesterase OPHC2 from Pseudomonas pseudoalcaligenes. PLoS ONE, 2013, 8, e77995.	1.1	50
1781	Crystal Structures of Trypanosoma brucei Oligopeptidase B Broaden the Paradigm of Catalytic Regulation in Prolyl Oligopeptidase Family Enzymes. PLoS ONE, 2013, 8, e79349.	1.1	31
1782	Novel Disulfide Bond-Mediated Dimerization of the CARD Domain Was Revealed by the Crystal Structure of CARMA1 CARD. PLoS ONE, 2013, 8, e79778.	1.1	13
1783	Crystal Structures of the Human G3BP1 NTF2-Like Domain Visualize FxFG Nup Repeat Specificity. PLoS ONE, 2013, 8, e80947.	1.1	43
1784	Heterologous Expression of Mycobacterial Esx Complexes in Escherichia coli for Structural Studies Is Facilitated by the Use of Maltose Binding Protein Fusions. PLoS ONE, 2013, 8, e81753.	1.1	21
1785	Structures of Wnt-Antagonist ZNRF3 and Its Complex with R-Spondin 1 and Implications for Signaling. PLoS ONE, 2013, 8, e83110.	1.1	58
1786	A monoclinic crystal form of casein kinase 1â€…Î´. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1077-1083.	0.7	7
1787	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge&#63;. Current Topics in Medicinal Chemistry, 2013, 13, 602-618.	1.0	23
1788	Unleashing the power of meta-threading for evolution/structure-based function inference of proteins. Frontiers in Genetics, 2013, 4, 118.	1.1	11
1789	Epitope Mapping of Metuximab on CD147 Using Phage Display and Molecular Docking. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-6.	0.7	15
1790	BmooMPÎ±-I (Bothrops moojeni). , 2013, , 1001-1005.		1
1791	Affinity Improvement of a Therapeutic Antibody by Structure-Based Computational Design: Generation of Electrostatic Interactions in the Transition State Stabilizes the Antibody-Antigen Complex. PLoS ONE, 2014, 9, e87099.	1.1	78
1792	CorA Is a Copper Repressible Surface-Associated Copper(I)-Binding Protein Produced in Methylomicrobium album BG8. PLoS ONE, 2014, 9, e87750.	1.1	18
1793	De Novo Structure Prediction of Globular Proteins Aided by Sequence Variation-Derived Contacts. PLoS ONE, 2014, 9, e92197.	1.1	98
1794	Esterase LpEst1 from Lactobacillus plantarum: A Novel and Atypical Member of the Î±Î² Hydrolase Superfamily of Enzymes. PLoS ONE, 2014, 9, e92257.	1.1	23
1795	Dimerization Interface of 3-Hydroxyacyl-CoA Dehydrogenase Tunes the Formation of Its Catalytic Intermediate. PLoS ONE, 2014, 9, e95965.	1.1	10
1796	Protein-Protein Interface Detection Using the Energy Centrality Relationship (ECR) Characteristic of Proteins. PLoS ONE, 2014, 9, e97115.	1.1	2

#	ARTICLE	IF	CITATIONS
1797	Structural Insight into the Tetramerization of an Iterative Ketoreductase SiaM through Aromatic Residues in the Interfaces. PLoS ONE, 2014, 9, e97996.	1.1	4
1798	B-Cell Epitopes in GroEL of Francisella tularensis. PLoS ONE, 2014, 9, e99847.	1.1	7
1799	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	1.1	13
1800	The Structure of the TFIIH p34 Subunit Reveals a Von Willebrand Factor A Like Fold. PLoS ONE, 2014, 9, e102389.	1.1	10
1801	The Structure of RdDddP from Roseobacter denitrificans Reveals That DMSP Lyases in the DddP-Family Are Metalloenzymes. PLoS ONE, 2014, 9, e103128.	1.1	22
1802	Identification of Polyketide Inhibitors Targeting 3-Dehydroquinate Dehydratase in the Shikimate Pathway of Enterococcus faecalis. PLoS ONE, 2014, 9, e103598.	1.1	7
1803	Structural and Biochemical Characterization of the Cop9 Signalosome CSN5/CSN6 Heterodimer. PLoS ONE, 2014, 9, e105688.	1.1	27
1804	Crystal Structure of Bombyx mori Lipoprotein 6: Comparative Structural Analysis of the 30-kDa Lipoprotein Family. PLoS ONE, 2014, 9, e108761.	1.1	11
1805	Structure of a Diguanylate Cyclase from Thermotoga maritima: Insights into Activation, Feedback Inhibition and Thermostability. PLoS ONE, 2014, 9, e110912.	1.1	22
1806	Structure of Putrescine Aminotransferase from Escherichia coli Provides Insights into the Substrate Specificity among Class III Aminotransferases. PLoS ONE, 2014, 9, e113212.	1.1	16
1807	Solution Structure of the SGTA Dimerisation Domain and Investigation of Its Interactions with the Ubiquitin-Like Domains of BAG6 and UBL4A. PLoS ONE, 2014, 9, e113281.	1.1	18
1808	RNA-directed remodeling of the HIV-1 protein Rev orchestrates assembly of the Revâ€"Rev response element complex. ELife, 2014, 3, e04120.	2.8	61
1809	Activation-triggered subunit exchange between CaMKII holoenzymes facilitates the spread of kinase activity. ELife, 2014, 3, e01610.	2.8	87
1810	Structural analysis of the endogenous glycoallergen Hev b 2 (endo-Î²-1,3-glucanase) from<i>Hevea brasiliensis</i>and its recognition by human basophils. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 329-341.	2.5	15
1811	Interactions of IgG1 CH2 and CH3 Domains with FcRn. Frontiers in Immunology, 2014, 5, 146.	2.2	33
1812	Crystallographic Studies Evidencing the High Energy Tolerance to Disrupting the Interface Disulfide Bond of Thioredoxin 1 from White Leg Shrimp Litopenaeus vannamei. Molecules, 2014, 19, 21113-21126.	1.7	5
1813	Multi-PAS domain-mediated protein oligomerization of PpsR from <i>Rhodobacter sphaeroides</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 863-876.	2.5	11
1814	Structural insight into activity enhancement and inhibition of H64A carbonic anhydrase II by imidazoles. IUCrJ, 2014, 1, 129-135.	1.0	31

#	ARTICLE	IF	CITATIONS
1815	The structure of cytomegalovirus immune modulator UL141 highlights structural Ig-fold versatility for receptor binding. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 851-862.	2.5	5
1816	Structure and Catalytic Mechanism of a Glycoside Hydrolase Family-127 Î²-L-Arabinofuranosidase (HypBA1). Journal of Bioprocessing & Biotechniques, 2014, 04, .	0.2	1
1817	Structural basis of nSH2 regulation and lipid binding in PI3KÎ±. Oncotarget, 2014, 5, 5198-5208.	0.8	62
1819	Structural insights into the substrate specificity and transglycosylation activity of a fungal glycoside hydrolase family 5 Î²-mannosidase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2970-2982.	2.5	27
1820	Structure-Function Analyses of Human Kallikrein-related Peptidase 2 Establish the 99-Loop as Master Regulator of Activity. Journal of Biological Chemistry, 2014, 289, 34267-34283.	1.6	28
1821	A Novel Structural Unit in the N-terminal Region of Filamins. Journal of Biological Chemistry, 2014, 289, 8588-8598.	1.6	18
1822	Structural insights into yeast histone chaperone Hif1: a scaffold protein recruiting protein complexes to core histones. Biochemical Journal, 2014, 462, 465-473.	1.7	14
1823	Structure and Function of a Decarboxylating <i>Agrobacterium tumefaciens</i> Keto-deoxy-<scp>d</scp>-galactarate Dehydratase. Biochemistry, 2014, 53, 8052-8060.	1.2	9
1824	Structural and enzymatic insights into Lambda glutathione transferases from <i>Populus trichocarpa</i>, monomeric enzymes constituting an early divergent class specific to terrestrial plants. Biochemical Journal, 2014, 462, 39-52.	1.7	46
1825	Investigation of Phycobilisome Subunit Interaction Interfaces by Coupled Cross-linking and Mass Spectrometry. Journal of Biological Chemistry, 2014, 289, 33084-33097.	1.6	18
1826	Targeting Î³-Herpesvirus 68 Bcl-2-mediated Down-regulation of Autophagy. Journal of Biological Chemistry, 2014, 289, 8029-8040.	1.6	41
1827	Structural and biochemical analyses of alanine racemase from the multidrug-resistantClostridium difficilestrain 630. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1922-1933.	2.5	16
1828	Discovery and characterization of olokizumab. MAbs, 2014, 6, 773-781.	2.6	66
1829	The structure of Rv2372c identifies an RsmE-like methyltransferase from <i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 821-832.	2.5	10
1830	Inhibition of Pore Formation by Blocking the Assembly of Staphylococcus aureus Î±-Hemolysin Through a Novel Peptide Inhibitor: an In Silco Approach. International Journal of Peptide Research and Therapeutics, 2014, 20, 575-583.	0.9	11
1831	Crystal Structure of the Dithiol Oxidase DsbA Enzyme from Proteus Mirabilis Bound Non-covalently to an Active Site Peptide Ligand. Journal of Biological Chemistry, 2014, 289, 19810-19822.	1.6	20
1832	A PDB-wide, evolution-based assessment of protein-protein interfaces. BMC Structural Biology, 2014, 14, 22.	2.3	54
1833	Stability-activity tradeoffs constrain the adaptive evolution of RubisCO. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2223-2228.	3.3	140

#	Article	IF	Citations
1834	Crystal Structure of the Nipah Virus Phosphoprotein Tetramerization Domain. Journal of Virology, 2014, 88, 758-762.	1.5	63
1835	Structure of the Acinetobacter baumannii Dithiol Oxidase DsbA Bound to Elongation Factor EF-Tu Reveals a Novel Protein Interaction Site. Journal of Biological Chemistry, 2014, 289, 19869-19880.	1.6	16
1836	Chronophin Dimerization Is Required for Proper Positioning of Its Substrate Specificity Loop. Journal of Biological Chemistry, 2014, 289, 3094-3103.	1.6	14
1837	Structural Insights into the Lipoprotein Outer Membrane Regulator of Penicillin-binding Protein 1B. Journal of Biological Chemistry, 2014, 289, 19245-19253.	1.6	17
1838	Stabilization of the Dimeric Birch Pollen Allergen Bet v 1 Impacts Its Immunological Properties. Journal of Biological Chemistry, 2014, 289, 540-551.	1.6	27
1839	Conformational Itinerary of Pseudomonas aeruginosa 1,6-Anhydro-N-acetylmuramic Acid Kinase during Its Catalytic Cycle. Journal of Biological Chemistry, 2014, 289, 4504-4514.	1.6	7
1840	Identification and Structural Analysis of an l-Asparaginase Enzyme from Guinea Pig with Putative Tumor Cell Killing Properties. Journal of Biological Chemistry, 2014, 289, 33175-33186.	1.6	48
1841	Structural and Functional Characterization of Ybr137wp Implicates Its Involvement in the Targeting of Tail-Anchored Proteins to Membranes. Molecular and Cellular Biology, 2014, 34, 4500-4512.	1.1	3
1842	Identification of Functionally Important Residues of the Silkmoth Pheromone Biosynthesis-activating Neuropeptide Receptor, an Insect Ortholog of the Vertebrate Neuromedin U Receptor. Journal of Biological Chemistry, 2014, 289, 19150-19163.	1.6	19
1843	Structural basis of IL-23 antagonism by an Alphabody protein scaffold. Nature Communications, 2014, 5, 5237.	5.8	54
1844	Structure and Mechanism of the Bifunctional CinA Enzyme from Thermus thermophilus. Journal of Biological Chemistry, 2014, 289, 33187-33197.	1.6	12
1845	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. Nature Communications, 2014, 5, 5701.	5.8	41
1846	Potent Neutralization of Vaccinia Virus by Divergent Murine Antibodies Targeting a Common Site of Vulnerability in L1 Protein. Journal of Virology, 2014, 88, 11339-11355.	1.5	40
1847	Nucleic Acid Ligands With Protein-like Side Chains: Modified Aptamers and Their Use as Diagnostic and Therapeutic Agents. Molecular Therapy - Nucleic Acids, 2014, 3, e201.	2.3	412
1848	Crystal Structure of the Human Fatty Acid Synthase Enoyl-Acyl Carrier Protein-Reductase Domain Complexed with Triclosan Reveals Allosteric Protein-Protein Interface Inhibition. Journal of Biological Chemistry, 2014, 289, 33287-33295.	1.6	21
1849	Specific binding of gibberellic acid by Cytokinin-Specific Binding Proteins: a new aspect of plant hormone-binding proteins with the PR-10 fold. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2032-2041.	2.5	27
1850	Molecular insights into the membrane-associated phosphatidylinositol 4-kinase IIÎ±. Nature Communications, 2014, 5, 3552.	5.8	52
1851	Identification of the Docking Site between a Type III Secretion System ATPase and a Chaperone for Effector Cargo. Journal of Biological Chemistry, 2014, 289, 23734-23744.	1.6	33

#	ARTICLE	IF	CITATIONS
1852	Structure of the epimerization domain of tyrocidine synthetase A. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1442-1452.	2.5	45
1853	Structural basis of recognition of interferon-Î± receptor by tyrosine kinase 2. Nature Structural and Molecular Biology, 2014, 21, 443-448.	3.6	127
1854	Structural basis for the auxin-induced transcriptional regulation by Aux/IAA17. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18613-18618.	3.3	69
1855	Potent Dengue Virus Neutralization by a Therapeutic Antibody with Low Monovalent Affinity Requires Bivalent Engagement. PLoS Pathogens, 2014, 10, e1004072.	2.1	51
1856	Host Cofactors and Pharmacologic Ligands Share an Essential Interface in HIV-1 Capsid That Is Lost upon Disassembly. PLoS Pathogens, 2014, 10, e1004459.	2.1	238
1857	Structures of the Inducer-Binding Domain of Pentachlorophenol-Degrading Gene Regulator PcpR from Sphingobium chlorophenolicum. International Journal of Molecular Sciences, 2014, 15, 20736-20752.	1.8	17
1858	The Structure and Regulation of Human Muscle Î±-Actinin. Cell, 2014, 159, 1447-1460.	13.5	178
1859	Exploring nicotinamide cofactor promiscuity in NAD(P)H-dependent flavin containing monooxygenases (FMOs) using natural variation within the phosphate binding loop. Structure and activity of FMOs from Cellvibrio sp. BR and Pseudomonas stutzeri NF13. Journal of Molecular Catalysis B: Enzymatic, 2014, 109, 191-198.	1.8	13
1860	Tracing the Evolution of the p53 Tetramerization Domain. Structure, 2014, 22, 1301-1310.	1.6	27
1861	Apo, Zn2+-bound and Mn2+-bound structures reveal ligand-binding properties of SitA from the pathogen <i>Staphylococcus pseudintermedius</i>. Bioscience Reports, 2014, 34, e00154.	1.1	30
1862	Dynamics of Gal80p in the Gal80pâ€"Gal3p complex differ significantly from the dynamics in the Gal80pâ€"Gal1p complex: implications for the higher specificity of Gal3p. Molecular BioSystems, 2014, 10, 3120-3129.	2.9	13
1863	Structure-based design and functional studies of novel noroviral 3C protease chimaeras offer insights into substrate specificity. Biochemical Journal, 2014, 464, 461-472.	1.7	10
1864	P. aeruginosa SGNH Hydrolase-Like Proteins AlgJ and AlgX Have Similar Topology but Separate and Distinct Roles in Alginate Acetylation. PLoS Pathogens, 2014, 10, e1004334.	2.1	54
1865	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. PLoS Computational Biology, 2014, 10, e1003791.	1.5	33
1866	Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. PLoS Computational Biology, 2014, 10, e1003889.	1.5	142
1867	Chromatin Insulator Factors Involved in Long-Range DNA Interactions and Their Role in the Folding of the Drosophila Genome. PLoS Genetics, 2014, 10, e1004544.	1.5	101
1868	Red Blood Cell Invasion by Plasmodium vivax: Structural Basis for DBP Engagement of DARC. PLoS Pathogens, 2014, 10, e1003869.	2.1	99
1869	Murine Anti-vaccinia Virus D8 Antibodies Target Different Epitopes and Differ in Their Ability to Block D8 Binding to CS-E. PLoS Pathogens, 2014, 10, e1004495.	2.1	17

#	Article	IF	Citations
1870	The TRIM-NHL Protein LIN-41 Controls the Onset of Developmental Plasticity in Caenorhabditis elegans. PLoS Genetics, 2014, 10, e1004533.	1.5	62
1871	Insights into the Initiation of JC Virus DNA Replication Derived from the Crystal Structure of the T-Antigen Origin Binding Domain. PLoS Pathogens, 2014, 10, e1003966.	2.1	12
1872	Crystal Structure of the Vaccinia Virus DNA Polymerase Holoenzyme Subunit D4 in Complex with the A20 N-Terminal Domain. PLoS Pathogens, 2014, 10, e1003978.	2.1	27
1873	Structural Insights into SraP-Mediated Staphylococcus aureus Adhesion to Host Cells. PLoS Pathogens, 2014, 10, e1004169.	2.1	85
1874	Crystal Structure of Cytomegalovirus IE1 Protein Reveals Targeting of TRIM Family Member PML via Coiled-Coil Interactions. PLoS Pathogens, 2014, 10, e1004512.	2.1	60
1875	Two TIR-like domain containing proteins in a newly emerging zoonotic Staphylococcus aureus strain sequence type 398 are potential virulence factors by impacting on the host innate immune response. Frontiers in Microbiology, 2014, 5, 662.	1.5	11
1876	Structural Data on the Periplasmic Aldehyde Oxidoreductase PaoABC from Escherichia coli: SAXS and Preliminary X-ray Crystallography Analysis. International Journal of Molecular Sciences, 2014, 15, 2223-2236.	1.8	13
1877	Structures of bacterial kynurenine formamidase reveal a crowded binuclear zinc catalytic site primed to generate a potent nucleophile. Biochemical Journal, 2014, 462, 581-589.	1.7	9
1878	Kinetic and Structural Characterization for Cofactor Preference of Succinic Semialdehyde Dehydrogenase from Streptococcus pyogenes. Molecules and Cells, 2014, 37, 719-726.	1.0	10
1879	Molecular basis for the fold organization and sarcomeric targeting of the muscle atrogin MuRF1. Open Biology, 2014, 4, 130172.	1.5	17
1880	Role of Îºâ†’Î» light-chain constant-domain switch in the structure and functionality of A17 reactibody. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 708-719.	2.5	22
1881	The crystal structure of wild-type human brain neuroglobin reveals flexibility of the disulfide bond that regulates oxygen affinity. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1005-1014.	2.5	51
1882	Functional Characterization and Categorization of Missense Mutations that Cause Methylmalonylâ€• <scp>C</scp> o <scp>A</scp> Mutase (<scp>MUT</scp>) Deficiency. Human Mutation, 2014, 35, 1449-1458.	1.1	40
1883	Structure of a three-dimensional domain-swapped dimer of the<i>Helicobacter pylori</i>type IV secretion system pilus protein CagL. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1391-1400.	2.5	19
1884	Calcium-induced conformational changes of the regulatory domain of human mitochondrial aspartate/glutamate carriers. Nature Communications, 2014, 5, 5491.	5.8	81
1885	Structural basis for the redox sensitivity of the<i>Mycobacterium tuberculosis</i>SigKâ€“RskA Ïƒâ€“anti-Ïƒ complex. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1026-1036.	2.5	35
1886	Evidence for henipavirus spillover into human populations in Africa. Nature Communications, 2014, 5, 5342.	5.8	143
1887	High-synconformation of uridine and asymmetry of the hexameric molecule revealed in the high-resolution structures ofShewanella oneidensisMR-1 uridine phosphorylase in the free form and in complex with uridine. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3310-3319.	2.5	13

#	ARTICLE	IF	CITATIONS
1888	Structural Basis for HIV-1 Neutralization by 2F5-Like Antibodies m66 and m66.6. Journal of Virology, 2014, 88, 2426-2441.	1.5	41
1889	Structural and Mutational Studies on the Unusual Substrate Specificity of <i>meso</i>â€Diaminopimelate Dehydrogenase from <i>Symbiobacterium thermophilum</i>. ChemBioChem, 2014, 15, 217-222.	1.3	29
1890	Full-length structure of a monomeric histidine kinase reveals basis for sensory regulation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17839-17844.	3.3	80
1891	Novel Prodrug-Like Fusion Toxin with Protease-Sensitive Bioorthogonal PEGylation for Tumor Targeting. Bioconjugate Chemistry, 2014, 25, 2144-2156.	1.8	19
1892	Affinity transfer to the archaeal extremophilic Sac7d protein by insertion of a CDR. Protein Engineering, Design and Selection, 2014, 27, 431-438.	1.0	16
1893	Hot-spot analysis to dissect the functional protein-protein interface of a tRNA-modifying enzyme. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2713-2732.	1.5	17
1894	Comparison of histidine recognition in human and trypanosomatid histidyl-tRNA synthetases. Biochimie, 2014, 106, 111-120.	1.3	11
1895	Crystal structure of human Ankyrin G death domain. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3476-3482.	1.5	3
1896	Discovery of protective <scp>B</scp>â€cell epitopes for development of antimicrobial vaccines and antibody therapeutics. Immunology, 2014, 142, 1-23.	2.0	49
1897	Crystal structure of a feruloyl esterase belonging to the tannase family: A disulfide bond near a catalytic triad. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2857-2867.	1.5	68
1898	Molecular Dynamics of Major Allergens from <i>Alternaria</i>, Birch Pollen and Peach. Molecular Informatics, 2014, 33, 682-694.	1.4	12
1899	Collapse of the native structure caused by a single amino acid exchange in human <scp>NAD</scp>(P)H:quinone oxidoreductase¹. FEBS Journal, 2014, 281, 4691-4704.	2.2	60
1900	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. Journal of Biological Chemistry, 2014, 289, 23403-23416.	1.6	62
1901	Structural basis for biomolecular recognition in overlapping binding sites in a diiron enzyme system. Nature Communications, 2014, 5, 5009.	5.8	24
1902	Structure of the effectorâ€binding domain of deoxyribonucleoside regulator DeoR from <i><scp>B</scp>acillusÂsubtilis</i>. FEBS Journal, 2014, 281, 4280-4292.	2.2	9
1903	Structural Identification of the Vps18 Î²-Propeller Reveals a Critical Role in the HOPS Complex Stability and Function. Journal of Biological Chemistry, 2014, 289, 33503-33512.	1.6	13
1904	The 2/2 hemoglobin from the cyanobacterium <i>Synechococcus</i> sp. PCC 7002 with covalently attached heme: Comparison of Xâ€ray and NMR structures. Proteins: Structure, Function and Bioinformatics, 2014, 82, 528-534.	1.5	18
1905	Polymorphisms and Interspecies Differences of the Activating and Inhibitory FcÎ³RII of <i>Macaca nemestrina</i> Influence the Binding of Human IgG Subclasses. Journal of Immunology, 2014, 192, 792-803.	0.4	41

#	Article	IF	Citations
1906	Conserved charged residues at the surface and interface of epithelial sodium channel subunitsÂâ€“Âroles in cell surface expression and the sodium selfâ€inhibition response. FEBS Journal, 2014, 281, 2097-2111.	2.2	19
1907	Duplication of Genes in an ATP-binding Cassette Transport System Increases Dynamic Range While Maintaining Ligand Specificity. Journal of Biological Chemistry, 2014, 289, 30090-30100.	1.6	14
1908	Crystal structure of the yeast <scp>TRAPP</scp>â€associated protein Tca17. FEBS Journal, 2014, 281, 4195-4206.	2.2	11
1909	Structure of the monofunctional heme catalase <scp>DR</scp>1998 from <i><scp>D</scp>einococcusÂradiodurans</i>. FEBS Journal, 2014, 281, 4138-4150.	2.2	16
1910	Natural single amino acid polymorphism (F19Y) in human galectinâ€8: detection of structural alterations and increased growthâ€regulatory activity on tumor cells. FEBS Journal, 2014, 281, 1446-1464.	2.2	40
1911	Structural and mutational analysis of substrate recognition in kojibiose phosphorylase. FEBS Journal, 2014, 281, 778-786.	2.2	17
1912	Structure of the pneumococcal <scp>l</scp>,<scp>d</scp>â€carboxypeptidase <scp>DacB</scp> and pathophysiological effects of disabled cell wall hydrolases <scp>DacA</scp> and <scp>DacB</scp>. Molecular Microbiology, 2014, 93, 1183-1206.	1.2	37
1913	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. Nucleic Acids Research, 2014, 42, D364-D373.	6.5	156
1914	Structure of human peptidylâ€prolyl <i>cisâ€“trans</i> isomerase FKBP22 containing two EFâ€hand motifs. Protein Science, 2014, 23, 67-75.	3.1	22
1915	The future of crystallography in drug discovery. Expert Opinion on Drug Discovery, 2014, 9, 125-137.	2.5	70
1916	Crystal structure of a putative quorum sensingâ€regulated protein (PA3611) from the Pseudomonasâ€specific DUF4146 family. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1086-1092.	1.5	7
1917	The structural comparison between membraneâ€associated human carbonic anhydrases provides insights into drug design of selective inhibitors. Biopolymers, 2014, 101, 769-778.	1.2	44
1918	The structural basis of the Tle4â€“Tli4 complex reveals the self-protection mechanism of H2-T6SS in<i>Pseudomonas aeruginosa</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3233-3243.	2.5	28
1919	Stapled HIV-1 peptides recapitulate antigenic structures and engage broadly neutralizing antibodies. Nature Structural and Molecular Biology, 2014, 21, 1058-1067.	3.6	69
1920	Computational design of protein antigens that interact with the CDR H3 loop of HIV broadly neutralizing antibody 2F5. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2770-2782.	1.5	16
1921	Crystal structure and immunological properties of the first annexin from <i>SchistosomaÂmansoni</i>: insights into the structural integrity of the schistosomal tegument. FEBS Journal, 2014, 281, 1209-1225.	2.2	21
1922	Structural and functional analysis show that the <i>Escherichia coli</i> uncharacterized protein <scp>Y</scp>jc<scp>S</scp> is likely an alkylsulfatase. Protein Science, 2014, 23, 1442-1450.	3.1	8
1923	Crystal structure of calpainâ€3 pentaâ€<scp>EF</scp>â€hand (<scp>PEF</scp>) domain â€“ a homodimerized <scp>PEF</scp> family member with calcium bound at the fifth <scp>EF</scp>â€hand. FEBS Journal, 2014, 281, 3138-3149.	2.2	26

#	ARTICLE	IF	CITATIONS
1924	RsaM: a transcriptional regulator of <i><scp>B</scp>urkholderia</i> spp. with novel fold. FEBS Journal, 2014, 281, 4293-4306.	2.2	14
1925	Structural basis for membrane targeting of the BBSome by ARL6. Nature Structural and Molecular Biology, 2014, 21, 1035-1041.	3.6	77
1926	Substrate-mediated control of the conformation of an ancillary domain delivers a competent catalytic site for N -acetylneuraminic acid synthase. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2054-2066.	1.5	2
1927	Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from<i>Methanocaldococcus jannaschii</i>. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1472-1479.	0.4	2
1928	Structural insight into the evolution of a new chemokine family from zebrafish. Proteins: Structure, Function and Bioinformatics, 2014, 82, 708-716.	1.5	5
1929	IRAK4 Dimerization and trans -Autophosphorylation Are Induced by Myddosome Assembly. Molecular Cell, 2014, 55, 891-903.	4.5	108
1930	Integrative Structureâ€"Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. Molecular and Cellular Proteomics, 2014, 13, 2911-2926.	2.5	67
1931	Structures of heterodimeric POZ domains of Miz1/BCL6 and Miz1/NAC1. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1591-1596.	0.4	25
1932	Unique Crystal Structure of a Novel Surfactant Protein from the Foam Nest of the Frog <i>Leptodactylus vastus</i>. ChemBioChem, 2014, 15, 393-398.	1.3	14
1933	Molecular Basis of the General Base Catalysis of an Î±/Î²-Hydrolase Catalytic Triad. Journal of Biological Chemistry, 2014, 289, 15867-15879.	1.6	21
1934	Mapping Post-translational Modifications of Mammalian Testicular Specific Histone Variant TH2B in Tetraploid and Haploid Germ Cells and Their Implications on the Dynamics of Nucleosome Structure. Journal of Proteome Research, 2014, 13, 5603-5617.	1.8	20
1935	Structural and Functional Characterization of Methicillin-Resistant <i>Staphylococcus aureusâ€™s</i> Class IIb Fructose 1,6-Bisphosphate Aldolase. Biochemistry, 2014, 53, 7604-7614.	1.2	13
1936	Xâ€ray structure of a novel <scp>l</scp>â€ribose isomerase acting on a nonâ€natural sugar <scp>l</scp>â€ribose as its ideal substrate. FEBS Journal, 2014, 281, 3150-3164.	2.2	14
1937	Molecular characterization of novel pyridoxalâ€5â€²â€phosphateâ€dependent enzymes from the human microbiome. Protein Science, 2014, 23, 1060-1076.	3.1	8
1939	Structures and binding specificity of galactose- and mannose-binding lectins from champedak: differences from jackfruit lectins. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 709-716.	0.4	10
1940	The crystal structure of BlmI as a model for nonribosomal peptide synthetase peptidyl carrier proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1210-1218.	1.5	33
1941	Structural dynamics of the two-component response regulator RstA in recognition of promoter DNA element. Nucleic Acids Research, 2014, 42, 8777-8788.	6.5	26
1942	Structure of the <scp><i>M</i></scp><i>ycobacterium tuberculosis</i> type <scp>VII</scp> secretion system chaperone <scp>EspG</scp>₅ in complex with <scp>PE</scp>25â€"<scp>PPE</scp>41 dimer. Molecular Microbiology, 2014, 94, 367-382.	1.2	83

#	Article	IF	Citations
1943	Structural characterization of MepB from <i>Staphylococcus aureus</i> reveals homology to endonucleases. Protein Science, 2014, 23, 594-602.	3.1	6
1944	Structural and mutational analyses of Aes, an inhibitor of MalT in<i>Escherichia coli</i>. Proteins: Structure, Function and Bioinformatics, 2014, 82, 268-277.	1.5	5
1945	Convergent Evolution in the Assembly of Polyubiquitin Degradation Signals by the Shigella flexneri IpaH9.8 Ligase. Journal of Biological Chemistry, 2014, 289, 34114-34128.	1.6	12
1946	A unique octameric structure of Axe2, an intracellular acetyl-xylooligosaccharide esterase from<i>Geobacillus stearothermophilus</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 261-278.	2.5	30
1947	Structural and functional analysis of MiD51, a dynamin receptor required for mitochondrial fission. Journal of Cell Biology, 2014, 204, 477-486.	2.3	91
1948	Structure and Mechanism of the Phycobiliprotein Lyase CpcT. Journal of Biological Chemistry, 2014, 289, 26677-26689.	1.6	33
1949	Evolutionary and Structural Analyses of Mammalian Haloacid Dehalogenase-type Phosphatases AUM and Chronophin Provide Insight into the Basis of Their Different Substrate Specificities. Journal of Biological Chemistry, 2014, 289, 3416-3431.	1.6	24
1950	Mutations in the ArsA ATPase that restore interaction with the ArsD metallochaperone. BioMetals, 2014, 27, 1263-1275.	1.8	5
1951	Crystal structure of a 4-thiouridine synthetaseâ€"RNA complex reveals specificity of tRNA U8 modification. Nucleic Acids Research, 2014, 42, 6673-6685.	6.5	46
1952	Characterization of the SAM domain of the PKD-related protein ANKS6 and its interaction with ANKS3. BMC Structural Biology, 2014, 14, 17.	2.3	37
1953	Evolutionary Origin of Bone Morphogenetic Protein 15 and Growth and Differentiation Factor 9 and Differential Selective Pressure Between Mono- and Polyovulating Species1. Biology of Reproduction, 2014, 91, 83.	1.2	24
1954	Crystal Structure of the Herpesvirus Inner Tegument Protein UL37 Supports Its Essential Role in Control of Viral Trafficking. Journal of Virology, 2014, 88, 5462-5473.	1.5	37
1955	Pathway of binding of the intrinsically disordered mitochondrial inhibitor protein to F ₁ -ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11305-11310.	3.3	75
1956	MP:PDâ€"a data base of internal packing densities, internal packing defects and internal waters of helical membrane proteins. Nucleic Acids Research, 2014, 42, D347-D351.	6.5	10
1957	How Periplasmic Thioredoxin TlpA Reduces Bacterial Copper Chaperone ScoI and Cytochrome Oxidase Subunit II (CoxB) Prior to Metallation*. Journal of Biological Chemistry, 2014, 289, 32431-32444.	1.6	32
1958	Structural and functional characterization of human and murine C5a anaphylatoxins. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1704-1717.	2.5	35
1959	MMDB and VAST+: tracking structural similarities between macromolecular complexes. Nucleic Acids Research, 2014, 42, D297-D303.	6.5	278
1960	Neutralizing antibodies can initiate genome release from human enterovirus 71. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2134-2139.	3.3	72

#	Article	IF	Citations
1961	Crystal structure of the essential transcription antiterminator M2-1 protein of human respiratory syncytial virus and implications of its phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1580-1585.	3.3	58
1962	Structure of transportin SR2, a karyopherin involved in human disease, in complex with Ran. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 723-729.	0.4	11
1963	A novel Î²-xylosidase structure fromGeobacillus thermoglucosidasius: the first crystal structure of a glycoside hydrolase family GH52 enzyme reveals unpredicted similarity to other glycoside hydrolase folds. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1366-1374.	2.5	17
1964	Activating killer cell immunoglobulin-like receptor 2DS2 binds to HLA-A*11. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2662-2667.	3.3	77
1965	Structureâ€“specificity relationships in Abp, a GH27 Î²-<scp>L</scp>-arabinopyranosidase from<i>Geobacillus stearothermophilus</i>T6. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2994-3012.	2.5	9
1966	Structure of the complete bacterial SRP Alu domain. Nucleic Acids Research, 2014, 42, 12284-12294.	6.5	18
1967	Crystallization and preliminary crystallographic analysis of human aquaporin 1 at a resolution of 3.28â€…Ã…. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1657-1663.	0.4	25
1968	Identifying functionally important <i>cis</i>â€peptide containing segments in proteins and their utility in molecular function annotation. FEBS Journal, 2014, 281, 5602-5621.	2.2	5
1969	Identification of promiscuous ene-reductase activity by mining structural databases using active site constellations. Nature Communications, 2014, 5, 4150.	5.8	67
1970	Structure and mechanism of a nonhaem-iron SAM-dependent<i>C</i>-methyltransferase and its engineering to a hydratase and an<i>O</i>-methyltransferase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1549-1560.	2.5	30
1971	Entrapment of DNA in an intersubunit tunnel system of a single-stranded DNA-binding protein. Nucleic Acids Research, 2014, 42, 6698-6708.	6.5	15
1972	Structural characteristics of alkaline phosphatase from the moderately halophilic bacterium <i>Halomonas</i> sp. 593. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 811-820.	2.5	13
1973	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2014, 42, D285-D291.	6.5	133
1974	Hydration of proteinâ€“RNA recognition sites. Nucleic Acids Research, 2014, 42, 10148-10160.	6.5	28
1975	The Crystal Structure of Giardia duodenalis 14-3-3 in the Apo Form: When Protein Post-Translational Modifications Make the Difference. PLoS ONE, 2014, 9, e92902.	1.1	12
1976	Molecular insights into replication initiation by QÎ² replicase using ribosomal protein S1. Nucleic Acids Research, 2014, 42, 10809-10822.	6.5	39
1977	Structural basis for the regulatory function of a complex zinc-binding domain in a replicative arterivirus helicase resembling a nonsense-mediated mRNA decay helicase. Nucleic Acids Research, 2014, 42, 3464-3477.	6.5	47
1978	Structure Prediction of Transmembrane Proteins. , 2014, , 199-221.		0

#	Article	IF	Citations
1979	Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from<i>Escherichia coli</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2848-2862.	2.5	47
1980	Structural insights into the dimerization of the response regulator ComE from Streptococcus pneumoniae. Nucleic Acids Research, 2014, 42, 5302-5313.	6.5	54
1981	Crystallographic and kinetic study of riboflavin synthase from<i>Brucella abortus</i>, a chemotherapeutic target with an enhanced intrinsic flexibility. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1419-1434.	2.5	8
1982	The bacterial antitoxin HipB establishes a ternary complex with operator DNA and phosphorylated toxin HipA to regulate bacterial persistence. Nucleic Acids Research, 2014, 42, 10134-10147.	6.5	45
1983	DAXX co-folds with H3.3/H4 using high local stability conferred by the H3.3 variant recognition residues. Nucleic Acids Research, 2014, 42, 4318-4331.	6.5	32
1984	The structured core domain of Î±B-crystallin can prevent amyloid fibrillation and associated toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1562-70.	3.3	181
1985	Homology model of human prothrombinase based on the crystal structure of Pseutarin C. Biological Chemistry, 2014, 395, 1233-1241.	1.2	15
1986	Large-Scale Analysis of B-Cell Epitopes on Influenza Virus Hemagglutinin â€“ Implications for Cross-Reactivity of Neutralizing Antibodies. Frontiers in Immunology, 2014, 5, 38.	2.2	12
1987	Interaction of the muscarinic acetylcholine receptor M2 subtype with G protein GÂi/o isotypes and GÂÂ subunits as studied with the maltose-binding protein-M2-GÂi/o fusion proteins expressed in Escherichia coli. Journal of Biochemistry, 2014, 156, 259-272.	0.9	1
1988	Ligand-dependent active-site closure revealed in the crystal structure of<i>Mycobacterium tuberculosis</i>MenB complexed with product analogues. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2959-2969.	2.5	3
1989	A new crystal form of a hyperthermophilic endocellulase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 878-883.	0.4	4
1990	Thermodynamic signatures in macromolecular interactions involving conformational flexibility. Biological Chemistry, 2014, 395, 905-911.	1.2	1
1991	Crystal structures of IspF from Plasmodium falciparum and Burkholderia cenocepacia: comparisons inform antimicrobial drug target assessment. BMC Structural Biology, 2014, 14, 1.	2.3	34
1992	Structural and functional features of Crl proteins and identification of conserved surface residues required for interaction with the RpoS/ÏƒS subunit of RNA polymerase. Biochemical Journal, 2014, 463, 215-224.	1.7	11
1993	The structure of the Slrpâ€“Trx1 complex sheds light on the autoinhibition mechanism of the typeÂIII secretion system effectors of the NEL family. Biochemical Journal, 2014, 464, 135-144.	1.7	28
1994	Crystal Structures of the Toll/Interleukin-1 Receptor (TIR) Domains from the Brucella Protein TcpB and Host Adaptor TIRAP Reveal Mechanisms of Molecular Mimicry. Journal of Biological Chemistry, 2014, 289, 669-679.	1.6	66
1995	Structures of Complexes of a Metal-independent Glycosyltransferase GT6 from Bacteroides ovatus with UDP-N-Acetylgalactosamine (UDP-GalNAc) and Its Hydrolysis Products. Journal of Biological Chemistry, 2014, 289, 8041-8050.	1.6	15
1996	Engagement of Nucleotide-binding Oligomerization Domain-containing Protein 1 (NOD1) by Receptor-interacting Protein 2 (RIP2) Is Insufficient for Signal Transduction. Journal of Biological Chemistry, 2014, 289, 22900-22914.	1.6	25

#	ARTICLE	IF	CITATIONS
1997	Insight into the Architecture of the NuRD Complex. Journal of Biological Chemistry, 2014, 289, 21844-21855.	1.6	75
1998	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. Journal of Biological Chemistry, 2014, 289, 24680-24690.	1.6	37
1999	Structural Basis for the Binding Specificity of Human Recepteur d'Origine Nantais (RON) Receptor Tyrosine Kinase to Macrophage-stimulating Protein. Journal of Biological Chemistry, 2014, 289, 29948-29960.	1.6	17
2000	Molecular evolution of protein-RNA mimicry as a mechanism for translational control. Nucleic Acids Research, 2014, 42, 3261-3271.	6.5	25
2001	BswR controls bacterial motility and biofilm formation in <i>Pseudomonas aeruginosa </i>through modulation of the small RNA <i>rsmZ</i>. Nucleic Acids Research, 2014, 42, 4563-4576.	6.5	38
2002	Crystal structure of the 5hmC specific endonuclease PvuRts1I. Nucleic Acids Research, 2014, 42, 5929-5936.	6.5	27
2003	The structure of hyperthermophilic Î²â€<i>N</i>â€acetylglucosaminidase reveals a novel dimer architecture associated with the active site. FEBS Journal, 2014, 281, 5092-5103.	2.2	3
2004	Potential for Reduction of Streptogramin A Resistance Revealed by Structural Analysis of Acetyltransferase VatA. Antimicrobial Agents and Chemotherapy, 2014, 58, 7083-7092.	1.4	19
2005	Structure determination of human Fas apoptosis inhibitory molecule and identification of the critical residues linking the interdomain interaction to the anti-apoptotic activity. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1812-1822.	2.5	7
2006	Crystal structure of human CRMP-4: correction of intensities for lattice-translocation disorder. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1680-1694.	2.5	20
2007	Â<scp>L</scp>-<i>allo</i>-Threonine aldolase with an H128Y/S292R mutation from<i>Aeromonas jandaei</i>DK-39 reveals the structural basis of changes in substrate stereoselectivity. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1695-1703.	2.5	19
2008	Structural and functional analysis of a novel haloalkane dehalogenase with two halide-binding sites. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1884-1897.	2.5	20
2009	Structures of the NLRP14 pyrin domain reveal a conformational switch mechanism regulating its molecular interactions. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2007-2018.	2.5	19
2010	Crystal structures and catalytic mechanism of the<i>C</i>-methyltransferase Coq5 provide insights into a key step of the yeast coenzyme Q synthesis pathway. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2085-2092.	2.5	22
2011	Structural and biophysical analysis of interactions between cod and human uracil-DNA<i>N</i>-glycosylase (UNG) and UNG inhibitor (Ugi). Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2093-2100.	2.5	6
2012	Structural insight into arginine methylation by the mouse protein arginine methyltransferase 7: a zinc finger freezes the mimic of the dimeric state into a single active site. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2401-2412.	2.5	32
2013	Structure of the 2,4â€²-dihydroxyacetophenone dioxygenase from<i>Alcaligenes</i>sp. 4HAP. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2444-2454.	2.5	12
2014	Structural basis for the substrate selectivity of PvuRts1I, a 5-hydroxymethylcytosine DNA restriction endonuclease. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2477-2486.	2.5	13

#	ARTICLE	IF	CITATIONS
2015	Structural analysis of arabinose-5-phosphate isomerase fromBacteroides fragilisand functional implications. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2640-2651.	2.5	0
2016	Structural insights into the human RyR2 N-terminal region involved in cardiac arrhythmias. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2897-2912.	2.5	25
2017	Effect of the L499M mutation of the ascomycetous<i>Botrytis aclada</i>laccase on redox potential and catalytic properties. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2913-2923.	2.5	31
2018	The structure of vanin 1: a key enzyme linking metabolic disease and inflammation. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3320-3329.	2.5	37
2019	<i>ACHESYM</i>: an algorithm and server for standardized placement of macromolecular models in the unit cell. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3290-3298.	2.5	57
2020	Structure of the carboxy-terminal domain of <i>Mycobacterium tuberculosis</i> CarD protein: an essential rRNA transcriptional regulator. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 160-165.	0.4	2
2021	A range of Câˆ Š3â€"Câˆ Š4 interdomain angles in IgE Fc accommodate binding to its receptor CD23. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 305-309.	0.4	12
2022	Structure of theReston ebolavirusVP30 C-terminal domain. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 457-460.	0.4	11
2023	Structure of 4-pyridoxolactonase fromMesorhizobium loti. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 424-432.	0.4	0
2024	Structural characterization of a novel autonomous cohesin from<i>Ruminococcus flavefaciens</i>. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 450-456.	0.4	3
2025	Comparison of four different crystal forms of the<i>Mycobacterium tuberculosis</i>ESX-1 secreted protein regulator EspR. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 433-437.	0.4	3
2026	Structure of nucleoside diphosphate kinase from pacific shrimp (<i>Litopenaeus vannamei</i>) in binary complexes with purine and pyrimidine nucleoside diphosphates. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1150-1154.	0.4	5
2027	The structure of alanine racemase fromAcinetobacter baumannii. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1199-1205.	0.4	4
2028	Enhancing ubiquitin crystallization through surface-entropy reduction. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1434-1442.	0.4	4
2029	The structure of the cyanobactin domain of unknown function from PatG in the patellamide gene cluster. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1597-1603.	0.4	15
2030	Longin and <scp>GAF</scp> Domains: Structural Evolution and Adaptation to the Subcellular Trafficking Machinery. Traffic, 2014, 15, 104-121.	1.3	40
2031	Structural Analysis of a Fungal Methionine Synthase with Substrates and Inhibitors. Journal of Molecular Biology, 2014, 426, 1839-1847.	2.0	10
2032	A unique insertion of low complexity amino acid sequence underlies protein-protein interaction in human malaria parasite orotate phosphoribosyltransferase and orotidine 5'-monophosphate decarboxylase. Asian Pacific Journal of Tropical Medicine, 2014, 7, 184-192.	0.4	7

#	ARTICLE	IF	CITATIONS
2033	Structures of a Bifunctional Cell Wall Hydrolase CwlT Containing a Novel Bacterial Lysozyme and an NlpC/P60 dl-Endopeptidase. Journal of Molecular Biology, 2014, 426, 169-184.	2.0	25
2034	Structure, Functional Characterization, and Evolution of the Dihydroorotase Domain of Human CAD. Structure, 2014, 22, 185-198.	1.6	60
2035	Structural Determinants of Unique Properties of Human IgG4-Fc. Journal of Molecular Biology, 2014, 426, 630-644.	2.0	96
2036	Applying Molecular Crowding Models to Simulations of Virus Capsid Assembly InÂVitro. Biophysical Journal, 2014, 106, 310-320.	0.2	31
2037	A computational tool to predict the evolutionarily conserved proteinâ€“protein interaction hotâ€spot residues from the structure of the unbound protein. FEBS Letters, 2014, 588, 326-333.	1.3	22
2038	Structural and mutagenetic analyses of a 1,3â€“1,4-Î²-glucanase from Paecilomyces thermophila. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 366-373.	1.1	20
2039	Structure and Function of the CSL-KyoT2 Corepressor Complex: A Negative Regulator of Notch Signaling. Structure, 2014, 22, 70-81.	1.6	56
2040	Structure-guided engineering of Anticalins with improved binding behavior and biochemical characteristics for application in radio-immuno imaging and/or therapy. Journal of Structural Biology, 2014, 185, 203-214.	1.3	24
2041	Structural and functional insights into the anti-BACE1 Fab fragment that recognizes the BACE1 exosite. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1421-1433.	2.0	8
2042	Structure of conjugated polyketone reductase from Candida parapsilosis IFO 0708 reveals conformational changes for substrate recognition upon NADPH binding. Applied Microbiology and Biotechnology, 2014, 98, 243-249.	1.7	21
2043	Dimeric structure of p300/CBP associated factor. BMC Structural Biology, 2014, 14, 2.	2.3	15
2044	New mini- zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. BMC Bioinformatics, 2014, 15, 1.	1.2	541
2045	Exploring the atomic structure and conformational flexibility of a 320â€…Ã… long engineered viral fiber using X-ray crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 342-353.	2.5	9
2046	Molecular basis for AUXIN RESPONSE FACTOR protein interaction and the control of auxin response repression. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5427-5432.	3.3	249
2047	Electrostatic charge at position 552 affects the activation and permeation of FMRFamide-gated Na+ channels. Journal of Physiological Sciences, 2014, 64, 141-150.	0.9	6
2048	Structures of Alcohol Dehydrogenases from Ralstonia and Sphingobium spp. Reveal the Molecular Basis for Their Recognition of â€˜Bulkyâ€“Bulkyâ€™ Ketones. Topics in Catalysis, 2014, 57, 356-365.	1.3	48
2049	Interactions and structural variability of Î²-carboxysomal shell protein CcmL. Photosynthesis Research, 2014, 121, 125-133.	1.6	21
2050	Crystal structures of the human Dysferlin inner DysF domain. BMC Structural Biology, 2014, 14, 3.	2.3	26

#	ARTICLE	IF	CITATIONS
2051	Functions of crystallins in and out of lens: Roles in elongated and post-mitotic cells. Progress in Biophysics and Molecular Biology, 2014, 115, 52-67.	1.4	71
2052	Structural and kinetic studies on adenylosuccinate lyase from <i>MycobacteriumÂsmegmatis</i> and <i>MycobacteriumÂtuberculosis</i> provide new insights on the catalytic residues of the enzyme. FEBS Journal, 2014, 281, 1642-1658.	2.2	14
2053	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. Science, 2014, 343, 1485-1489.	6.0	521
2054	Molecular basis underlying histone H3 lysineâ€“arginine methylation pattern readout by Spin/Ssty repeats of Spindlin1. Genes and Development, 2014, 28, 622-636.	2.7	101
2055	Structural basis for DNA recognition and nuclease processing by the Mre11 homologue SbcD in double-strand breaks repair. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 299-309.	2.5	7
2056	Cationâ€“Ï€, aminoâ€“Ï€, Ï€â€“Ï€, and Hâ€bond interactions stabilize antigenâ€“antibody interfaces. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1734-1746.	1.5	50
2057	Structure of the bacterial type <scp>II NADH</scp> dehydrogenase: a monotopic membrane protein with an essential role in energy generation. Molecular Microbiology, 2014, 91, 950-964.	1.2	103
2058	Crystal structure of <i>Mycobacterium tuberculosis</i> CarD, an essential RNA polymerase binding protein, reveals a quasidomainâ€swapped dimeric structural architecture. Proteins: Structure, Function and Bioinformatics, 2014, 82, 879-884.	1.5	21
2059	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. Science, 2014, 344, 299-303.	6.0	300
2060	Structural Stability of Influenza A(H1N1)pdm09 Virus Hemagglutinins. Journal of Virology, 2014, 88, 4828-4838.	1.5	51
2061	Crystallographic and Glycan Microarray Analysis of Human Polyomavirus 9 VP1 Identifies <i>N</i> -Glycolyl Neuraminic Acid as a Receptor Candidate. Journal of Virology, 2014, 88, 6100-6111.	1.5	36
2062	RipD (Rv1566c) from <i>Mycobacterium tuberculosis</i>: adaptation of an NlpC/p60 domain to a non-catalytic peptidoglycan-binding function. Biochemical Journal, 2014, 457, 33-41.	1.7	21
2063	The major cockroach allergen Bla g 4 binds tyramine and octopamine. Molecular Immunology, 2014, 60, 86-94.	1.0	22
2064	Different contribution of conserved amino acids to the global properties of triosephosphate isomerases. Proteins: Structure, Function and Bioinformatics, 2014, 82, 323-335.	1.5	15
2065	Cys139Ser mutation in dimeric nucleoside diphosphate kinase generates catalytically competent monomer. International Journal of Biological Macromolecules, 2014, 66, 66-73.	3.6	0
2066	Structural basis of Flavivirus NS1 assembly and antibody recognition. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4285-4290.	3.3	121
2067	The malaria parasite egress protease SUB1 is a calcium-dependent redox switch subtilisin. Nature Communications, 2014, 5, 3726.	5.8	43
2068	Functional and Structural Characterization of Vibrio cholerae Extracellular Serine Protease B, VesB. Journal of Biological Chemistry, 2014, 289, 8288-8298.	1.6	24

#	Article	IF	Citations
2069	Structural insights into the <scp>T</scp>6<scp>SS</scp> effector protein <scp>Tse</scp>3 and the <scp>Tse</scp>3â€"<scp>Tsi</scp>3 complex from <scp><i>P</i></scp><i>seudomonas aeruginosa</i> reveal a calciumâ€dependent membraneâ€binding mechanism. Molecular Microbiology, 2014, 92, 1092-1112.	1.2	29
2070	Insights into the Architecture of the eIF2BÎ±/Î²/Î´ Regulatory Subcomplex. Biochemistry, 2014, 53, 3432-3445.	1.2	32
2071	Structure of Dihydromethanopterin Reductase, a Cubic Protein Cage for Redox Transfer. Journal of Biological Chemistry, 2014, 289, 8852-8864.	1.6	11
2072	Flavivirus NS1 Structures Reveal Surfaces for Associations with Membranes and the Immune System. Science, 2014, 343, 881-885.	6.0	315
2073	Mechanism of Bacterial Interference with TLR4 Signaling by Brucella Toll/Interleukin-1 Receptor Domain-containing Protein TcpB. Journal of Biological Chemistry, 2014, 289, 654-668.	1.6	73
2074	Structural Change in FtsZ Induced by Intermolecular Interactions between Bound GTP and the T7 Loop. Journal of Biological Chemistry, 2014, 289, 3501-3509.	1.6	62
2075	Crystal Structure of the Bacteriophage QÎ² Coat Protein in Complex with the RNA Operator of the Replicase Gene. Journal of Molecular Biology, 2014, 426, 1039-1049.	2.0	29
2076	The structural analysis of shark IgNAR antibodies reveals evolutionary principles of immunoglobulins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8155-8160.	3.3	67
2077	Mechanism of Tc toxin action revealed in molecular detail. Nature, 2014, 508, 61-65.	13.7	149
2078	Structural basis for recognition of synaptic vesicle protein 2C by botulinum neurotoxin A. Nature, 2014, 505, 108-111.	13.7	103
2079	Multiscale modelling to understand the self-assembly mechanism of human Î²2-adrenergic receptor in lipid bilayer. Computational Biology and Chemistry, 2014, 48, 29-39.	1.1	28
2080	Molecular Dynamics Studies of the Proteinâ€"Protein Interactions in Inhibitor of ÎºB Kinase-Î². Journal of Chemical Information and Modeling, 2014, 54, 562-572.	2.5	13
2081	A Glutathione-independent Glyoxalase of the DJ-1 Superfamily Plays an Important Role in Managing Metabolically Generated Methylglyoxal in Candida albicans. Journal of Biological Chemistry, 2014, 289, 1662-1674.	1.6	75
2082	A sequence-specific DNA glycosylase mediates restriction-modification in Pyrococcus abyssi. Nature Communications, 2014, 5, 3178.	5.8	33
2083	Molecular Mechanism of Autophagic Membrane-Scaffold Assembly and Disassembly. Cell, 2014, 156, 469-481.	13.5	206
2084	The Oligomeric State of the Active Vps4 AAA ATPase. Journal of Molecular Biology, 2014, 426, 510-525.	2.0	51
2085	Role of the HIN Domain in Regulation of Innate Immune Responses. Molecular and Cellular Biology, 2014, 34, 2-15.	1.1	36
2086	An Antibody against the C-Terminal Domain of PCSK9 Lowers LDL Cholesterol Levels In Vivo. Journal of Molecular Biology, 2014, 426, 843-852.	2.0	31

#	ARTICLE	IF	CITATIONS
2087	Structure and Self-Assembly of the Calcium Binding Matrix Protein of Human Metapneumovirus. Structure, 2014, 22, 136-148.	1.6	44
2088	SH2B1Î² Interacts with STAT3 and Enhances Fibroblast Growth Factor 1-Induced Gene Expression during Neuronal Differentiation. Molecular and Cellular Biology, 2014, 34, 1003-1019.	1.1	17
2089	Active Form of the Protein Kinase CK2 Î±₂Î²₂ Holoenzyme Is a Strong Complex with Symmetric Architecture. ACS Chemical Biology, 2014, 9, 366-371.	1.6	29
2090	Insights into mitochondrial fatty acid synthesis from the structure of heterotetrameric 3-ketoacyl-ACP reductase/3R-hydroxyacyl-CoA dehydrogenase. Nature Communications, 2014, 5, 4805.	5.8	42
2091	Nonclassical Pathways of Protein Crystallization in the Presence of Multivalent Metal Ions. Crystal Growth and Design, 2014, 14, 6357-6366.	1.4	25
2092	Regulation of the NaV1.5 cytoplasmic domain by calmodulin. Nature Communications, 2014, 5, 5126.	5.8	72
2093	High-resolution structure of the M14-type cytosolic carboxypeptidase fromBurkholderia cenocepaciarefined exploitingPDB_REDOstrategies. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 279-289.	2.5	8
2094	The Active Form of E6-associated protein (E6AP)/UBE3A Ubiquitin Ligase Is an Oligomer. Journal of Biological Chemistry, 2014, 289, 1033-1048.	1.6	57
2095	Catalytic Mechanism of Retroviral Integrase for the Strand Transfer Reaction Explored by QM/MM Calculations. Journal of Chemical Theory and Computation, 2014, 10, 5458-5466.	2.3	6
2096	The Prophage-encoded Hyaluronate Lyase Has Broad Substrate Specificity and Is Regulated by the N-terminal Domain. Journal of Biological Chemistry, 2014, 289, 35225-35236.	1.6	15
2097	Structure and Dynamics of Apical Membrane Antigen 1 from <i>Plasmodium falciparum</i> FVO. Biochemistry, 2014, 53, 7310-7320.	1.2	23
2098	Structural basis of thymosin-Î²4/profilin exchange leading to actin filament polymerization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4596-605.	3.3	68
2099	An intramolecular lock facilitates folding and stabilizes the tertiary structure of <i>Streptococcus mutans</i> adhesin P1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15746-15751.	3.3	28
2100	Structure and Catalytic Mechanism of Î²-Carbonic Anhydrases. Sub-Cellular Biochemistry, 2014, 75, 53-76.	1.0	16
2101	Functional implications of large backbone amplitude motions of the glycoprotein 130â€binding epitope of interleukinâ€6. FEBS Journal, 2014, 281, 2471-2483.	2.2	7
2102	Crystal structures of <i>Entamoeba histolytica</i> lysylâ€tRNA synthetase reveal conformational changes upon lysine binding and a specific helix bundle domain. FEBS Letters, 2014, 588, 4478-4486.	1.3	3
2103	Crystal structure of the WOPR-DNA complex and implications for Wor1 function in white-opaque switching of Candida albicans. Cell Research, 2014, 24, 1108-1120.	5.7	15
2104	DockRank: Ranking docked conformations using partnerâ€specific sequence homologyâ€based protein interface prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 250-267.	1.5	28

#	Article	IF	Citations
2105	Understanding molecular recognition of promiscuity of thermophilic methionine adenosyltransferase s<scp>MAT</scp> from <i>SulfolobusÂsolfataricus</i>. FEBS Journal, 2014, 281, 4224-4239.	2.2	36
2106	Diverse modes of binding in structures of<i>Leishmania major</i><i>N</i>-myristoyltransferase with selective inhibitors. IUCrJ, 2014, 1, 250-260.	1.0	38
2107	A robust pipeline for rapid production of versatile nanobody repertoires. Nature Methods, 2014, 11, 1253-1260.	9.0	391
2108	Crystal Structure of Tryptophan Lyase (NosL): Evidence for Radical Formation at the Amino Group of Tryptophan. Angewandte Chemie - International Edition, 2014, 53, 11840-11844.	7.2	81
2109	Crystal structure of HlyU, the hemolysin gene transcription activator, from Vibrio cholerae N16961 and functional implications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2346-2354.	1.1	15
2110	The GSH- and GSSG-bound structures of glutaredoxin from Clostridium oremlandii. Archives of Biochemistry and Biophysics, 2014, 564, 20-25.	1.4	14
2111	Immunization with a functional protein complex required for erythrocyte invasion protects against lethal malaria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10311-10316.	3.3	92
2112	Enhanced Potency of a Broadly Neutralizing HIV-1 Antibody <i>In Vitro</i> Improves Protection against Lentiviral Infection <i>In Vivo</i>. Journal of Virology, 2014, 88, 12669-12682.	1.5	248
2113	Structural basis of PcsB-mediated cell separation in Streptococcus pneumoniae. Nature Communications, 2014, 5, 3842.	5.8	82
2114	Are hot-spots occluded from water?. Journal of Biomolecular Structure and Dynamics, 2014, 32, 186-197.	2.0	11
2115	Plasticity and redundancy among AMAâ€"RON pairs ensure host cell entry of Toxoplasma parasites. Nature Communications, 2014, 5, 4098.	5.8	138
2116	The Multidrug Resistance IncA/C Transferable Plasmid Encodes a Novel Domain-swapped Dimeric Protein-disulfide Isomerase. Journal of Biological Chemistry, 2014, 289, 2563-2576.	1.6	7
2117	Structural and functional insight into TAF1â€"TAF7, a subcomplex of transcription factor II D. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9103-9108.	3.3	42
2118	Crystal Structure of the Rab9A-RUTBC2 RBD Complex Reveals the Molecular Basis for the Binding Specificity of Rab9A with RUTBC2. Structure, 2014, 22, 1408-1420.	1.6	6
2119	Characterizing of functional human coding RNA editing from evolutionary, structural, and dynamic perspectives. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3117-3131.	1.5	15
2120	Structure and Proteinâ€"Protein Interactions of Methanol Dehydrogenase from <i>Methylococcus capsulatus</i> (Bath). Biochemistry, 2014, 53, 6211-6219.	1.2	52
2121	Structure of a new DNA-binding domain which regulates pathogenesis in a wide variety of fungi. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10404-10410.	3.3	18
2122	Comparative study of two <scp>GH</scp>19 chitinaseâ€like proteins from <i>HeveaÂbrasiliensis</i>, one exhibiting a novel carbohydrateâ€binding domain. FEBS Journal, 2014, 281, 4535-4554.	2.2	27

#	Article	IF	Citations
2123	Intrinsic Conformational Plasticity of Native EmrE Provides a Pathway for Multidrug Resistance. Journal of the American Chemical Society, 2014, 136, 8072-8080.	6.6	56
2124	Structure-Based Engineering of a Minimal Porin Reveals Loop-Independent Channel Closure. Biochemistry, 2014, 53, 4826-4838.	1.2	26
2125	Structural and functional analysis of the anti-malarial drug target prolyl-tRNA synthetase. Journal of Structural and Functional Genomics, 2014, 15, 181-190.	1.2	40
2126	Latent and active<i>ab</i>PPO4 mushroom tyrosinase cocrystallized with hexatungstotellurate(VI) in a single crystal. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2301-2315.	2.5	109
2127	Structure of<i>Rhodococcus equi</i>virulence-associated protein B (VapB) reveals an eight-stranded antiparallel Î²-barrel consisting of two Greek-key motifs. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 866-871.	0.4	17
2128	The structure of human interleukin-11 reveals receptor-binding site features and structural differences from interleukin-6. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2277-2285.	2.5	47
2129	Structural Investigations into the Stereochemistry and Activity of a Phenylalanine-2,3-aminomutase from <i>Taxus chinensis</i>. Biochemistry, 2014, 53, 3187-3198.	1.2	21
2130	Structural Plasticity of the Semliki Forest Virus Glycome upon Interspecies Transmission. Journal of Proteome Research, 2014, 13, 1702-1712.	1.8	26
2131	Mechanistic Basis for Functional Promiscuity in the TNF and TNF Receptor Superfamilies: Structure of the LIGHT:DcR3 Assembly. Structure, 2014, 22, 1252-1262.	1.6	27
2132	Structure of the eukaryotic translation initiation factor eIF4E in complex with 4EGI-1 reveals an allosteric mechanism for dissociating eIF4G. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3187-95.	3.3	72
2133	Structure of the LINGO-1â€"Anti-LINGO-1 Li81 Antibody Complex Provides Insights into the Biology of LINGO-1 and the Mechanism of Action of the Antibody Therapy. Journal of Pharmacology and Experimental Therapeutics, 2014, 350, 110-123.	1.3	19
2134	<i>trans</i> -Protease Activity and Structural Insights into the Active Form of the Alphavirus Capsid Protease. Journal of Virology, 2014, 88, 12242-12253.	1.5	24
2135	Conformational plasticity of the <scp>E</scp>bola virus matrix protein. Protein Science, 2014, 23, 1519-1527.	3.1	33
2136	Structural and functional characterization of ochratoxinase, a novel mycotoxin-degrading enzyme. Biochemical Journal, 2014, 462, 441-452.	1.7	62
2137	Crystal structures of three representatives of a new <scp>P</scp>fam family PF14869 (DUF4488) suggest they function in sugar binding/uptake. Protein Science, 2014, 23, 1380-1391.	3.1	3
2138	Intradimer/Intermolecular Interactions Suggest Autoinhibition Mechanism in Endophilin A1. Journal of the American Chemical Society, 2014, 136, 4557-4564.	6.6	22
2139	The crystal structure of archaeal serine hydroxymethyltransferase reveals idiosyncratic features likely required to withstand high temperatures. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3437-3449.	1.5	13
2140	Effective discrimination between biologically relevant contacts and crystal packing contacts using new determinants. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3090-3100.	1.5	13

#	Article	IF	Citations
2141	Dynamic Structure of NGF and proNGF Complexed with p75NTR: Pro-Peptide Effect. Journal of Chemical Information and Modeling, 2014, 54, 2051-2067.	2.5	4
2142	Structure and stability of an unusual zinc-binding protein from Bacteroides thetaiotaomicron. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2298-2305.	1.1	1
2143	Global analysis of protein structural changes in complex proteomes. Nature Biotechnology, 2014, 32, 1036-1044.	9.4	288
2144	X-ray structure of a CDP-alcohol phosphatidyltransferase membrane enzyme and insights into its catalytic mechanism. Nature Communications, 2014, 5, 4169.	5.8	39
2145	The structure of allophycocyanin B from<i>Synechocystis</i>PCC 6803 reveals the structural basis for the extreme redshift of the terminal emitter in phycobilisomes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2558-2569.	2.5	83
2146	Identification of Phe187 as a Crucial Dimerization Determinant Facilitates Crystallization of a Monomeric Retroviral Integrase Core Domain. Structure, 2014, 22, 1512-1519.	1.6	7
2147	Structure-Guided Functional Characterization of Enediyne Self-Sacrifice Resistance Proteins, CalU16 and CalU19. ACS Chemical Biology, 2014, 9, 2347-2358.	1.6	24
2148	Crystal structure of the full-length ATPase GspE from the Vibrio vulnificus type II secretion system in complex with the cytoplasmic domain of GspL. Journal of Structural Biology, 2014, 187, 223-235.	1.3	35
2149	Crystal Structure of <i>Escherichia coli</i> SsuE: Defining a General Catalytic Cycle for FMN Reductases of the Flavodoxin-like Superfamily. Biochemistry, 2014, 53, 3509-3519.	1.2	27
2150	Conserved aromatic residues of the hepatitis B virus Precore propeptide are involved in a switch between distinct dimeric conformations and essential in the formation of heterocapsids. Virology, 2014, 462-463, 273-282.	1.1	9
2151	Structure-Based Characterization of Multiprotein Complexes. Structure, 2014, 22, 1063-1070.	1.6	48
2152	Crystal structure of Clostridium acetobutylicum aspartate kinase (CaAk): An important allosteric enzyme for amino acids production. Biotechnology Reports (Amsterdam, Netherlands), 2014, 3, 73-85.	2.1	12
2153	Interactions of Protein Kinase C-Î± C1A and C1B Domains with Membranes: A Combined Computational and Experimental Study. Journal of the American Chemical Society, 2014, 136, 11757-11766.	6.6	31
2154	Trypanosomatid phosphoglycerate mutases have multiple conformational and oligomeric states. Biochemical and Biophysical Research Communications, 2014, 450, 936-941.	1.0	9
2155	Structural Insights into the Substrate Specificity of (S)-Ureidoglycolate Amidohydrolase and Its Comparison with Allantoate Amidohydrolase. Journal of Molecular Biology, 2014, 426, 3028-3040.	2.0	9
2156	Amiloride inhibits the initiation of Coxsackievirus and poliovirus RNA replication by inhibiting VPg uridylylation. Virology, 2014, 464-465, 87-97.	1.1	8
2157	Formation and structures of GroEL:GroES ₂ chaperonin footballs, the protein-folding functional form. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12775-12780.	3.3	69
2158	Probing the N-Terminal Î²-Sheet Conversion in the Crystal Structure of the Human Prion Protein Bound to a Nanobody. Journal of the American Chemical Society, 2014, 136, 937-944.	6.6	97

#	Article	IF	Citations
2159	Crystal Structure of the Ectoine Hydroxylase, a Snapshot of the Active Site. Journal of Biological Chemistry, 2014, 289, 29570-29583.	1.6	37
2160	Structure of a Sedoheptulose 7-Phosphate Cyclase: ValA from <i>Streptomyces hygroscopicus</i>. Biochemistry, 2014, 53, 4250-4260.	1.2	14
2161	Mechanism of actin filament pointed-end capping by tropomodulin. Science, 2014, 345, 463-467.	6.0	107
2162	Purification, crystal structure determination and functional characterization of type III antifreeze proteins from the European eelpout Zoarces viviparus. Cryobiology, 2014, 69, 163-168.	0.3	15
2163	Crystal structures of two tetrameric Î²â€•carbonic anhydrases from the filamentous ascomycete <i>SordariaÂmacrospora</i>. FEBS Journal, 2014, 281, 1759-1772.	2.2	40
2164	Binding mode analysis of a major <scp>T</scp>3<scp>SS</scp> translocator protein <scp>P</scp>op<scp>B</scp> with its chaperone <scp>P</scp>cr<scp>H</scp> from <i><scp>P</scp>seudomonas aeruginosa</i>. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3273-3285.	1.5	4
2165	Packing interface energetics in different crystal forms of the Î» Cro dimer. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1128-1141.	1.5	10
2166	Crystal structure of serine acetyl transferase from Brucella abortus and its complex with coenzyme A. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1741-1748.	1.1	13
2167	Prediction of proteinâ€“protein binding affinity using diverse proteinâ€“protein interface features. Chemometrics and Intelligent Laboratory Systems, 2014, 138, 7-13.	1.8	7
2168	Structure of Thermoplasma volcanium Ard1 belongs to N-acetyltransferase family member suggesting multiple ligand binding modes with acetyl coenzyme A and coenzyme A. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1790-1797.	1.1	14
2169	Structural characteristics of the nonallosteric human cytosolic malic enzyme. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1773-1783.	1.1	19
2170	Structure-Function Studies with the Unique Hexameric Form II Ribulose-1,5-bisphosphate Carboxylase/Oxygenase (Rubisco) from Rhodopseudomonas palustris. Journal of Biological Chemistry, 2014, 289, 21433-21450.	1.6	36
2171	Structure of the C.Âelegans ZYG-1 Cryptic Polo Box Suggests a Conserved Mechanism for Centriolar Docking of Plk4 Kinases. Structure, 2014, 22, 1090-1104.	1.6	45
2172	Directed Evolution Library Creation. Methods in Molecular Biology, 2014, , .	0.4	40
2173	Protein painting reveals solvent-excluded drug targets hidden within native proteinâ€“protein interfaces. Nature Communications, 2014, 5, 4413.	5.8	45
2174	Crystal Structure of the Chlamydomonas Starch Debranching Enzyme Isoamylase ISA1 Reveals Insights into the Mechanism of Branch Trimming and Complex Assembly. Journal of Biological Chemistry, 2014, 289, 22991-23003.	1.6	51
2175	Resistance through inhibition: Ectopic expression of serine protease inhibitor offers stress tolerance via delayed senescence in yeast cell. Biochemical and Biophysical Research Communications, 2014, 452, 361-368.	1.0	15
2176	Structure and Substrate Specificity of a Eukaryotic Fucosidase from Fusarium graminearum. Journal of Biological Chemistry, 2014, 289, 25624-25638.	1.6	33

#	ARTICLE	IF	CITATIONS
2177	Helical cyclic pentapeptides constrain HIV-1 Rev peptide forÂenhanced RNA binding. Tetrahedron, 2014, 70, 7645-7650.	1.0	5
2178	Structural Definition of an Antibody-Dependent Cellular Cytotoxicity Response Implicated in Reduced Risk for HIV-1 Infection. Journal of Virology, 2014, 88, 12895-12906.	1.5	108
2179	A novel Î²â€trefoil lectin from the parasol mushroom (<i>MacrolepiotaÂprocera</i>) is nematotoxic. FEBS Journal, 2014, 281, 3489-3506.	2.2	33
2180	Structural insights into RNA recognition properties of glyceraldehydeâ€3â€phosphate dehydrogenase 3 from <i>Saccharomyces cerevisiae</i>. IUBMB Life, 2014, 66, 631-638.	1.5	10
2181	Effective interactions in molecular dynamics simulations of lysozyme solutions. European Physical Journal B, 2014, 87, 1.	0.6	3
2182	Crystal structure of the lytic CHAPK domain of the endolysin LysK from Staphylococcus aureus bacteriophage K. Virology Journal, 2014, 11, 133.	1.4	47
2183	Gene Context Analysis Reveals Functional Divergence between Hypothetically Equivalent Enzymes of the Purineâ€"Ureide Pathway. Biochemistry, 2014, 53, 735-745.	1.2	7
2184	Insights into the Mechanism of Deubiquitination by JAMM Deubiquitinases from Cocrystal Structures of the Enzyme with the Substrate and Product. Biochemistry, 2014, 53, 3199-3217.	1.2	56
2185	Structure and Catalytic Regulatory Function of Ubiquitin Specific Protease 11 N-Terminal and Ubiquitin-like Domains. Biochemistry, 2014, 53, 2966-2978.	1.2	34
2186	Structure of the large ribosomal subunit from human mitochondria. Science, 2014, 346, 718-722.	6.0	260
2187	Crystal Structure of <i>Schistosoma mansoni</i> Arginase, a Potential Drug Target for the Treatment of Schistosomiasis. Biochemistry, 2014, 53, 4671-4684.	1.2	18
2188	An engineered Axl 'decoy receptor' effectively silences the Gas6-Axl signaling axis. Nature Chemical Biology, 2014, 10, 977-983.	3.9	117
2189	An improved method for specificity annotation shows a distinct evolutionary divergence among the microbial enzymes of the cholylglycine hydrolase family. Microbiology (United Kingdom), 2014, 160, 1162-1174.	0.7	22
2190	One motif to bind them: A small-XXX-small motif affects transmembrane domain 1 oligomerization, function, localization, and cross-talk between two yeast GPCRs. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 3036-3051.	1.4	16
2191	A functional feature analysis on diverse proteinâ€"protein interactions: application for the prediction of binding affinity. Journal of Computer-Aided Molecular Design, 2014, 28, 619-629.	1.3	22
2192	Structural insights into interactions of C/EBP transcriptional activators with the Taz2 domain of p300. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1914-1921.	2.5	21
2193	Structure of NADHâ€Dependent Carbonyl Reductase (CPCR2) from <i>Candida parapsilosis</i> Provides Insight into Mutations that Improve Catalytic Properties. ChemCatChem, 2014, 6, 1103-1111.	1.8	29
2194	Imparting Albumin-Binding Affinity to a Human Protein by Mimicking the Contact Surface of a Bacterial Binding Protein. ACS Chemical Biology, 2014, 9, 1052-1060.	1.6	2

#	ARTICLE	IF	CITATIONS
2195	Structure of the pseudokinase domain of BIR2, a regulator of BAK1-mediated immune signaling in Arabidopsis. Journal of Structural Biology, 2014, 186, 112-121.	1.3	53
2196	The Inner Membrane Complex Sub-compartment Proteins Critical for Replication of the Apicomplexan Parasite Toxoplasma gondii Adopt a Pleckstrin Homology Fold. Journal of Biological Chemistry, 2014, 289, 13962-13973.	1.6	14
2197	The Immunodominant Influenza A Virus M1_{58â€“66}Cytotoxic T Lymphocyte Epitope Exhibits Degenerate Class I Major Histocompatibility Complex Restriction in Humans. Journal of Virology, 2014, 88, 10613-10623.	1.5	30
2198	Effects of protein engineering and rational mutagenesis on crystal lattice of single chain antibody fragments. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1884-1895.	1.5	5
2199	Structure of the ubiquitin-activating enzyme loaded with two ubiquitin molecules. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1311-1320.	2.5	42
2200	Mechanism of the Rpn13-induced activation of Uch37. Protein and Cell, 2014, 5, 616-630.	4.8	27
2201	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. BMC Bioinformatics, 2014, 15, 75.	1.2	1
2202	High-resolution crystal structure of spin labelled (T21R1) azurin from Pseudomonas aeruginosa: a challenging structural benchmark for in silico spin labelling algorithms. BMC Structural Biology, 2014, 14, 16.	2.3	15
2203	Homooligomerization is needed for stability: a molecular modelling and solution study of <i>EscherichiaÂcoli</i> purine nucleoside phosphorylase. FEBS Journal, 2014, 281, 1860-1871.	2.2	14
2204	Edge strand engineering prevents nativeâ€like aggregation in <i><scp>S</scp>ulfolobusÂsolfataricus</i> acylphosphatase. FEBS Journal, 2014, 281, 4072-4084.	2.2	13
2205	Structure of the LCMV nucleoprotein provides a template for understanding arenavirus replication and immunosuppression. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1764-1769.	2.5	17
2206	Crystal Structure and Molecular Imaging of the Nav Channel Î²3 Subunit Indicates a Trimeric Assembly. Journal of Biological Chemistry, 2014, 289, 10797-10811.	1.6	67
2207	Rational Design, Preparation, and Characterization of a Therapeutic Enzyme Mutant with Improved Stability and Function for Cocaine Detoxification. ACS Chemical Biology, 2014, 9, 1764-1772.	1.6	37
2208	A G-quadruplexâ€“containing RNA activates fluorescence in a GFP-like fluorophore. Nature Chemical Biology, 2014, 10, 686-691.	3.9	277
2209	Structural Basis for Dimerization and Catalysis of a Novel Esterase from the GTSAG Motif Subfamily of the Bacterial Hormone-sensitive Lipase Family. Journal of Biological Chemistry, 2014, 289, 19031-19041.	1.6	57
2210	A structure-based proposal for a comprehensive myotoxic mechanism of phospholipase A2-like proteins from viperid snake venoms. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2265-2276.	1.1	73
2211	Modification and periplasmic translocation of the biofilm exopolysaccharide poly-Î²-1,6- <i>N</i> -acetyl- <scp>d</scp> -glucosamine. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11013-11018.	3.3	48
2212	Tetrameric c-di-GMP Mediates Effective Transcription Factor Dimerization to Control Streptomyces Development. Cell, 2014, 158, 1136-1147.	13.5	219

#	Article	IF	Citations
2213	Polymorphic Protein Crystal Growth: Influence of Hydration and Ions in Glucose Isomerase. Crystal Growth and Design, 2014, 14, 46-57.	1.4	17
2214	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in Streptococcus pyogenes. Journal of Biological Chemistry, 2014, 289, 18175-18188.	1.6	6
2215	Molecular Binding Sites Are Located Near the Interface of Intrinsic Dynamics Domains (IDDs). Journal of Chemical Information and Modeling, 2014, 54, 2275-2285.	2.5	23
2216	Is the bovine lysosomal phospholipase B-like protein an amidase?. Proteins: Structure, Function and Bioinformatics, 2014, 82, 300-311.	1.5	14
2217	Crystallographic Evidence of Drastic Conformational Changes in the Active Site of a Flavin-Dependent <i>N</i>-Hydroxylase. Biochemistry, 2014, 53, 6063-6077.	1.2	31
2218	Structural and mutational analysis of a monomeric and dimeric form of a single domain antibody with implications for protein misfolding. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3101-3116.	1.5	14
2219	Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. Nature Communications, 2014, 5, 4764.	5.8	86
2220	Crystal structure of PhoU from Pseudomonas aeruginosa, a negative regulator of the Pho regulon. Journal of Structural Biology, 2014, 188, 22-29.	1.3	11
2221	A dimerization interface mediated by functionally critical residues creates interfacial disulfide bonds and copper sites in CueP. Journal of Inorganic Biochemistry, 2014, 140, 199-201.	1.5	5
2222	Conformational Adaptation in the <i>E. coli</i> Sigma 32 Protein in Response to Heat Shock. Journal of Physical Chemistry B, 2014, 118, 4793-4802.	1.2	9
2223	Maturation of Rhizobium leguminosarum Hydrogenase in the Presence of Oxygen Requires the Interaction of the Chaperone HypC and the Scaffolding Protein HupK. Journal of Biological Chemistry, 2014, 289, 21217-21229.	1.6	7
2224	Structural biology of the ILâ€1 superfamily: Key cytokines in the regulation of immune and inflammatory responses. Protein Science, 2014, 23, 526-538.	3.1	67
2225	Sac1â€"Vps74 structure reveals a mechanism to terminate phosphoinositide signaling in the Golgi apparatus. Journal of Cell Biology, 2014, 206, 485-491.	2.3	40
2226	Crystal structure of FtsA from <i>Staphylococcus aureus</i>. FEBS Letters, 2014, 588, 1879-1885.	1.3	32
2227	The tripartite motif coiled-coil is an elongated antiparallel hairpin dimer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2494-2499.	3.3	158
2228	The structure of a farâ€red fluorescent protein, AQ143, shows evidence in support of reported redâ€shifting chromophore interactions. Protein Science, 2014, 23, 1148-1153.	3.1	3
2229	Antibody 8ANC195 Reveals a Site of Broad Vulnerability on the HIV-1 Envelope Spike. Cell Reports, 2014, 7, 785-795.	2.9	199
2230	Interferon regulatory factor-1 (IRF-1) interacts with regulated in development and DNA damage response 2 (REDD2) in the cytoplasm of mouse bone marrow cells. International Journal of Biological Macromolecules, 2014, 65, 41-50.	3.6	5

#	ARTICLE	IF	CITATIONS
2231	Structural Details of Human Tuba Recruitment by InlC of Listeria monocytogenes Elucidate Bacterial Cell-Cell Spreading. Structure, 2014, 22, 304-314.	1.6	25
2232	Synthesis of L-2,3-Diaminopropionic Acid, a Siderophore and Antibiotic Precursor. Chemistry and Biology, 2014, 21, 379-388.	6.2	60
2233	Characterization of hyaluronic acid specific hyaluronate lyase (HylP) from Streptococcus pyogenes. Biochimie, 2014, 102, 203-210.	1.3	12
2234	Development of a molecularly imprinted polymer for the recovery of lactoferrin. Food and Bioproducts Processing, 2014, 92, 226-232.	1.8	6
2235	Crystal structure and biochemical characterization of a manganese superoxide dismutase from Chaetomium thermophilum. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 422-429.	1.1	15
2236	The NreA Protein Functions as a Nitrate Receptor in the Staphylococcal Nitrate Regulation System. Journal of Molecular Biology, 2014, 426, 1539-1553.	2.0	40
2237	Structural Asymmetry in the Closed State of Mitochondrial Hsp90 (TRAP1) Supports a Two-Step ATP Hydrolysis Mechanism. Molecular Cell, 2014, 53, 330-343.	4.5	144
2238	Structure of the NADH-dependent thermostable alcohol dehydrogenase TADH from Thermus sp. ATN1 provides a platform for engineering specificity and improved compatibility with inorganic cofactor-regeneration catalysts. Journal of Molecular Catalysis B: Enzymatic, 2014, 105, 1-6.	1.8	10
2239	Structural evaluation of BTK and PKCÎ´ mediated phosphorylation of MAL at positions Tyr86 and Tyr106. Computational Biology and Chemistry, 2014, 51, 22-35.	1.1	13
2240	Crystal Structure of the Carbapenem Intrinsic Resistance Protein CarG. Journal of Molecular Biology, 2014, 426, 1958-1970.	2.0	6
2241	Destabilization of the Homotetrameric Assembly of 3-Deoxy-d-Arabino-Heptulosonate-7-Phosphate Synthase from the Hyperthermophile Pyrococcus furiosus Enhances Enzymatic Activity. Journal of Molecular Biology, 2014, 426, 656-673.	2.0	13
2242	Structure and Functional Analysis of YcfD, a Novel 2-Oxoglutarate/Fe2+-Dependent Oxygenase Involved in Translational Regulation in Escherichia coli. Journal of Molecular Biology, 2014, 426, 1898-1910.	2.0	13
2243	Structural basis for the substrate specificity and the absence of dehalogenation activity in 2-chloromuconate cycloisomerase from Rhodococcus opacus 1CP. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1541-1549.	1.1	2
2244	Coiled-Coil Helix Rotation Selects Repressing or Activating State of Transcriptional Regulator DhaR. Structure, 2014, 22, 478-487.	1.6	18
2245	Improvement of stability and enzymatic activity by site-directed mutagenesis of E. coli asparaginase II. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1219-1230.	1.1	32
2246	Purine nucleoside phosphorylase activity decline is linked to the decay of the trimeric form of the enzyme. Archives of Biochemistry and Biophysics, 2014, 549, 40-48.	1.4	7
2247	A Novel 8-nm Protein Cage Formed by Vibrio cholerae Acylphosphatase. Journal of Molecular Biology, 2014, 426, 36-38.	2.0	5
2248	Characterization of two homologous 2â€²-O-methyltransferases showing different specificities for their tRNA substrates. Rna, 2014, 20, 1257-1271.	1.6	69

#	ARTICLE	IF	CITATIONS
2249	Effect of CDR3 Sequences and Distal V Gene Residues in Regulating TCRâ€"MHC Contacts and Ligand Specificity. Journal of Immunology, 2014, 192, 6071-6082.	0.4	25
2250	Structural and functional analysis of the human spliceosomal DEAD-box helicase Prp28. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1622-1630.	2.5	18
2251	The first structure of a bacterial diterpene cyclase: CotB2. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1528-1537.	2.5	48
2252	Targeting Mycobacterium tuberculosis nucleoid-associated protein HU with structure-based inhibitors. Nature Communications, 2014, 5, 4124.	5.8	96
2253	A tale of tails: deciphering the contribution of terminal tails to the biochemical properties of two Dps proteins from Streptomyces coelicolor. Cellular and Molecular Life Sciences, 2014, 71, 4911-4926.	2.4	14
2254	Structural characterization of a Î²-hydroxyacid dehydrogenase from Geobacter sulfurreducens and Geobacter metallireducens with succinic semialdehyde reductase activity. Biochimie, 2014, 104, 61-69.	1.3	14
2255	Human immunoglobulin E flexes between acutely bent and extended conformations. Nature Structural and Molecular Biology, 2014, 21, 397-404.	3.6	52
2256	Intersubunit Salt Bridges with a Sulfate Anion Control Subunit Dissociation and Thermal Stabilization of <i>Bacillus</i> sp. TB-90 Urate Oxidase. Biochemistry, 2014, 53, 3879-3888.	1.2	15
2257	Sensor Domain of Histidine Kinase KinB of Pseudomonas. Journal of Biological Chemistry, 2014, 289, 12232-12244.	1.6	11
2258	High resolution crystal structure of<i>Clostridium propionicum</i>Î²-alanyl-CoA:ammonia lyase, a new member of the â€œhot dog foldâ€• protein superfamily. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2041-2053.	1.5	6
2259	Structure of the Proteus vulgaris HigB-(HigA)2-HigB Toxin-Antitoxin Complex. Journal of Biological Chemistry, 2014, 289, 1060-1070.	1.6	78
2260	Metals in Proteinâ€"Protein Interfaces. Annual Review of Biophysics, 2014, 43, 409-431.	4.5	63
2261	Structural Bioinformatics of the Interactome. Annual Review of Biophysics, 2014, 43, 193-210.	4.5	57
2262	Crystal structure of a human GABAA receptor. Nature, 2014, 512, 270-275.	13.7	623
2263	Atomic resolution crystal structure of VcLMWPTP-1 from Vibrio cholerae O395: Insights into a novel mode of dimerization in the low molecular weight protein tyrosine phosphatase family. Biochemical and Biophysical Research Communications, 2014, 450, 390-395.	1.0	9
2264	Improved catalytic efficiency of catalase from Bacillus subtilis by rational mutation of Lys114. Process Biochemistry, 2014, 49, 1497-1502.	1.8	14
2265	Glycan Specificity of the Vibrio vulnificus Hemolysin Lectin Outlines Evolutionary History of Membrane Targeting by a Toxin Family. Journal of Molecular Biology, 2014, 426, 2800-2812.	2.0	31
2266	The crystal structure of arginylâ€tRNA synthetase from <i>Homo sapiens</i>. FEBS Letters, 2014, 588, 2328-2334.	1.3	14

#	ARTICLE	IF	CITATIONS
2267	Structural aspects of dog allergies: The crystal structure of a dog dander allergen Can f 4. Molecular Immunology, 2014, 61, 7-15.	1.0	19
2268	Use of cysteineâ€•reactive crossâ€•linkers to probe conformational flexibility of human <scp>DJ</scp>â€•1 demonstrates that Glu18 mutations are dimers. Journal of Neurochemistry, 2014, 130, 839-853.	2.1	14
2269	ATP-Induced Dimerization of the F₀F₁ Îµ Subunit from <i>Bacillus</i> PS3: A Hydrogen Exchangeâ€"Mass Spectrometry Study. Biochemistry, 2014, 53, 4072-4080.	1.2	6
2270	Crystal structure of an efficacious gonococcal adherence inhibitor: An enolase from <i>Lactobacillus gasseri</i>. FEBS Letters, 2014, 588, 2212-2216.	1.3	9
2271	Prediction and redesign of proteinâ€"protein interactions. Progress in Biophysics and Molecular Biology, 2014, 116, 194-202.	1.4	25
2272	VARP Is Recruited on to Endosomes by Direct Interaction with Retromer, Where Together They Function in Export to the Cell Surface. Developmental Cell, 2014, 29, 591-606.	3.1	110
2273	Interaction of Circadian Clock Proteins CRY1 and PER2 Is Modulated by Zinc Binding and Disulfide Bond Formation. Cell, 2014, 157, 1203-1215.	13.5	162
2274	Structural insights into the cofactor-assisted substrate recognition of yeast methylglyoxal/isovaleraldehyde reductase Gre2. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1486-1492.	1.1	28
2275	PKA RIÎ± Homodimer Structure Reveals an Intermolecular Interface with Implications for Cooperative cAMP Binding and Carney Complex Disease. Structure, 2014, 22, 59-69.	1.6	37
2276	Structural Basis for Phosphorylation-Dependent Recruitment of Tel2 to Hsp90 by Pih1. Structure, 2014, 22, 805-818.	1.6	86
2277	DockTrina: Docking triangular protein trimers. Proteins: Structure, Function and Bioinformatics, 2014, 82, 34-44.	1.5	20
2278	Crystal structure of the N-terminal domain of EccA1 ATPase from the ESX-1 secretion system of Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2014, 82, 159-163.	1.5	26
2279	Effects of glycosylation and pH conditions in the dynamics of human arylsulfatase A. Journal of Biomolecular Structure and Dynamics, 2014, 32, 567-579.	2.0	6
2280	Neuroglobin as a regulator of mitochondrial-dependent apoptosis: A bioinformatics analysis. International Journal of Molecular Medicine, 2014, 33, 111-116.	1.8	30
2281	Use B-factor related features for accurate classification between protein binding interfaces and crystal packing contacts. BMC Bioinformatics, 2014, 15, S3.	1.2	56
2282	Comparative study of the molecular variation between â€˜centralâ€™ and â€˜peripheralâ€™ MUPs and significance for behavioural signalling. Biochemical Society Transactions, 2014, 42, 866-872.	1.6	30
2283	Structure of sulfamidase provides insight into the molecular pathology of mucopolysaccharidosis IIIA. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1321-1335.	2.5	29
2284	Structure and possible mechanism of the CcbJ methyltransferase from<i>Streptomyces caelestis</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 943-957.	2.5	11

#	Article	IF	Citations
2285	Structural characterization and comparison of the large subunits of IPM isomerase and homoaconitase from<i>Methanococcus jannaschii</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 922-931.	2.5	6
2287	Analysis of an industrial production suspension of<i>Bacillus lentus</i>subtilisin crystals by powder diffraction: a powerful quality-control tool. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1115-1123.	2.5	4
2288	The structure of a purple acid phosphatase involved in plant growth and pathogen defence exhibits a novel immunoglobulin-like fold. IUCrJ, 2014, 1, 101-109.	1.0	26
2289	Characterization of the proline-utilization pathway in<i>Mycobacterium tuberculosis</i>through structural and functional studies. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 968-980.	2.5	14
2290	Crystal structure and kinetic studies of a tetrameric type II Î²-carbonic anhydrase from the pathogenic bacterium<i>Vibrio cholerae</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2449-2456.	2.5	94
2291	EsxB, a secreted protein from <scp><i>B</i></scp><i>acillus anthracis</i> forms two distinct helical bundles. Protein Science, 2015, 24, 1389-1400.	3.1	12
2292	Structure of the response regulator RPA3017 involved in red-light signaling in <i>Rhodopseudomonas palustris</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1215-1222.	0.4	5
2293	Prediction of stability changes upon mutation in an icosahedral capsid. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1733-1741.	1.5	2
2294	Structure of the yeast Bre1 <scp>RING</scp> domain. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1185-1190.	1.5	21
2295	An enzyme captured in two conformational states: crystal structure of<i>S</i>-adenosyl-<scp>L</scp>-homocysteine hydrolase from<i>Bradyrhizobium elkanii</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2422-2432.	2.5	9
2296	Structure and function of <i>Caulobacter crescentus</i> aldoseâ€“aldose oxidoreductase. Biochemical Journal, 2015, 472, 297-307.	1.7	10
2297	Structure of human dipeptidyl peptidase 10 (DPPY): a modulator of neuronal Kv4 channels. Scientific Reports, 2015, 5, 8769.	1.6	24
2298	Structural transition in Bcl-xL and its potential association with mitochondrial calcium ion transport. Scientific Reports, 2015, 5, 10609.	1.6	17
2299	Extension of resolution and oligomerization-state studies of 2,4â€²-dihydroxyacetophenone dioxygenase from<i>Alcaligenes</i>sp. 4HAP. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1258-1263.	0.4	5
2300	Crystal structure of the catalytic subunit of magnesium chelatase. Nature Plants, 2015, 1, 15125.	4.7	46
2302	Structural basis for quinine-dependent antibody binding to platelet integrin Î±IIbÎ²3. Blood, 2015, 126, 2138-2145.	0.6	26
2304	Crystal structure analysis of c4763, a uropathogenicEscherichia coli-specific protein. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1042-1047.	0.4	1
2305	Specific GFP-binding artificial proteins (Î±Rep): a new tool for <i>inÂvitro</i> to live cell applications. Bioscience Reports, 2015, 35, .	1.1	27

#	ARTICLE	IF	CITATIONS
2306	Structural delineation of stem-loop RNA binding by human TAF15 protein. Scientific Reports, 2015, 5, 17298.	1.6	10
2307	High-resolution structures ofLactobacillus salivariustransketolase in the presence and absence of thiamine pyrophosphate. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1327-1334.	0.4	1
2308	Discovery and characterization of natural tropolones as inhibitors of the antibacterial target CapF from Staphylococcus aureus. Scientific Reports, 2015, 5, 15337.	1.6	22
2309	Structures of yeast peroxisomal Î”³,Î”²-enoyl-CoA isomerase complexed with acyl-CoA substrate analogues: the importance of hydrogen-bond networks for the reactivity of the catalytic base and the oxyanion hole. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2178-2191.	2.5	8
2310	Homotypic dimerization of a maltose kinase for molecular scaffolding. Scientific Reports, 2014, 4, 6418.	1.6	7
2311	Dimerization of lipocalin allergens. Scientific Reports, 2015, 5, 13841.	1.6	26
2312	Structural basis of Ornithine Decarboxylase inactivation and accelerated degradation by polyamine sensor Antizyme1. Scientific Reports, 2015, 5, 14738.	1.6	21
2313	In silico mechanistic analysis of IRF3 inactivation and high-risk HPV E6 species-dependent drug response. Scientific Reports, 2015, 5, 13446.	1.6	33
2314	Structural basis for Sfm1 functioning as a protein arginine methyltransferase. Cell Discovery, 2015, 1, 15037.	3.1	21
2315	The structural basis of an NADP+-independent dithiol oxidase in FK228 biosynthesis. Scientific Reports, 2015, 4, 4145.	1.6	11
2316	The structure of Legionella pneumophila LegK4 type four secretion system (T4SS) effector reveals a novel dimeric eukaryotic-like kinase. Scientific Reports, 2015, 5, 14602.	1.6	15
2317	Molecular docking to explore the possible binding mode of potential inhibitors of thioredoxin glutathione reductase. Molecular Medicine Reports, 2015, 12, 5787-5795.	1.1	13
2318	Crystal Structure and Atomic Level Analysis of Plasma PAF-AH. The Enzymes, 2015, 38, 95-116.	0.7	1
2319	Structural analysis of fungus-derived FAD glucose dehydrogenase. Scientific Reports, 2015, 5, 13498.	1.6	89
2320	Structure of human carbamoyl phosphate synthetase: deciphering the on/off switch of human ureagenesis. Scientific Reports, 2015, 5, 16950.	1.6	64
2321	Structural Characterisation of the Beta-Ketoacyl-Acyl Carrier Protein Synthases, FabF and FabH, of Yersinia pestis. Scientific Reports, 2015, 5, 14797.	1.6	19
2322	Structural analysis of Clostridium botulinum neurotoxin type D as a platform for the development of targeted secretion inhibitors. Scientific Reports, 2015, 5, 13397.	1.6	12
2323	PPCheck: A Webserver for the Quantitative Analysis of Protein-Protein Interfaces and Prediction of Residue Hotspots. Bioinformatics and Biology Insights, 2015, 9, BBI.S25928.	1.0	61

#	Article	IF	Citations
2324	Structure of human saposin A at lysosomal pH. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 895-900.	0.4	11
2325	Structures of<i>Pseudomonas aeruginosa</i>Î²-ketoacyl-(acyl-carrier-protein) synthase II (FabF) and a C164Q mutant provide templates for antibacterial drug discovery and identify a buried potassium ion and a ligand-binding site that is an artefact of the crystal form. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1020-1026.	0.4	4
2326	Discrete structural features among interface residue-level classes. BMC Bioinformatics, 2015, 16, S8.	1.2	11
2327	Structure of Slitrk2â€“PTPÎ´ complex reveals mechanisms for splicing-dependent trans-synaptic adhesion. Scientific Reports, 2015, 5, 9686.	1.6	46
2328	Crystal Structures of a Hyperthermophilic Archaeal Homoserine Dehydrogenase Suggest a Novel Cofactor Binding Mode for Oxidoreductases. Scientific Reports, 2015, 5, 11674.	1.6	14
2329	A structural dissection of large protein-protein crystal packing contacts. Scientific Reports, 2015, 5, 14214.	1.6	39
2330	Structural insights into YfiR sequestering by YfiB in Pseudomonas aeruginosa PAO1. Scientific Reports, 2015, 5, 16915.	1.6	16
2331	Crystallographic studies of two variants of<i>Pseudomonas aeruginosa</i>IMPDH with impaired allosteric regulation. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1890-1899.	2.5	19
2332	The structural basis of substrate promiscuity in UDP-hexose 4-epimeraseÂfrom the hyperthermophilic Eubacterium Thermotoga maritima. Archives of Biochemistry and Biophysics, 2015, 585, 39-51.	1.4	13
2333	Structure of the Helicase Domain of DNA Polymerase Theta Reveals a Possible Role in the Microhomology-Mediated End-Joining Pathway. Structure, 2015, 23, 2319-2330.	1.6	64
2334	Sequence specificity between interacting and non-interacting homologs identifies interface residues â€“ a homodimer and monomer use case. BMC Bioinformatics, 2015, 16, 325.	1.2	18
2335	Modeling of interaction between cytochrome c and the WD domains of Apaf-1: bifurcated salt bridges underlying apoptosome assembly. Biology Direct, 2015, 10, 29.	1.9	19
2336	Structural basis for suppression of hypernegative DNA supercoiling by<i>E. coli</i>topoisomerase I. Nucleic Acids Research, 2015, 43, 11031-11046.	6.5	52
2337	Structure of mitochondrial poly(A) RNA polymerase reveals the structural basis for dimerization, ATP selectivity and the SPAX4 disease phenotype. Nucleic Acids Research, 2015, 43, 9065-9075.	6.5	20
2338	Role of a non-canonical surface of Rad6 in ubiquitin conjugating activity. Nucleic Acids Research, 2015, 43, 9039-9050.	6.5	31
2339	Conformational dynamics of a short antigenic peptide in its free and antibody bound forms gives insight into the role of Î²â€•turns in peptide immunogenicity. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1352-1367.	1.5	6
2340	Crystal structure of the Zâ€•ring associated cell division protein ZapC from <i>Escherichia coli</i>. FEBS Letters, 2015, 589, 3822-3828.	1.3	13
2341	PDB-Explorer: a web-based interactive map of the protein data bank in shape space. BMC Bioinformatics, 2015, 16, 339.	1.2	31

#	ARTICLE	IF	CITATIONS
2342	Crystal structure of the fibre head domain of bovine adenovirus 4, a ruminant atadenovirus. Virology Journal, 2015, 12, 81.	1.4	6
2343	Structural insights into the mechanism defining substrate affinity in Arabidopsis thaliana dUTPase: the role of tryptophan 93 in ligand orientation. BMC Research Notes, 2015, 8, 784.	0.6	7
2344	Cofactorâ€induced reversible folding of <scp>F</scp>lavodoxinâ€4 from <scp><i>L</i></scp><i>actobacillus acidophilus</i>. Protein Science, 2015, 24, 1600-1608.	3.1	2
2345	Phosphate binding in the active centre of tomato multifunctional nuclease TBN1 and analysis of superhelix formation by the enzyme. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1408-1415.	0.4	2
2346	Structure of the N-terminal dimerization domain of CEACAM7. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1169-1175.	0.4	9
2347	Linking structural features of protein complexes and biological function. Protein Science, 2015, 24, 1486-1494.	3.1	33
2348	Structure of a thermophilic F₁â€<scp>ATP</scp>ase inhibited by an Îµâ€subunit: deeper insight into the Îµâ€inhibition mechanism. FEBS Journal, 2015, 282, 2895-2913.	2.2	73
2349	A novel <scp>NAD</scp>(P)Hâ€dependent carbonyl reductase specifically expressed in the thyroidectomized chicken fatty liver: catalytic properties and crystal structure. FEBS Journal, 2015, 282, 3918-3928.	2.2	6
2350	Dps from <i>Deinococcus radiodurans</i>: oligomeric forms of Dps1 with distinct cellular functions and Dps2 involved in metal storage. FEBS Journal, 2015, 282, 4307-4327.	2.2	30
2351	N463 Glycosylation Site on V5 Loop of a Mutant gp120 Regulates the Sensitivity of HIV-1 to Neutralizing Monoclonal Antibodies VRC01/03. Journal of Acquired Immune Deficiency Syndromes (1999), 2015, 69, 270-277.	0.9	17
2352	Prediction of proteinâ€“protein interaction sites from weakly homologous template structures using metaâ€threading and machine learning. Journal of Molecular Recognition, 2015, 28, 35-48.	1.1	22
2353	The three-dimensional structure of â€œLonely Guyâ€from<i>C</i><i>laviceps purpurea</i>provides insights into the phosphoribohydrolase function of Rossmann fold-containing lysine decarboxylase-like proteins. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1539-1546.	1.5	17
2354	Biochemical and biophysical characterisation of haloalkane dehalogenases <scp>DmrA</scp> and <scp>DmrB</scp> in <scp><i>M</i></scp><i>ycobacterium</i> strain <scp>JS</scp>60 and their role in growth on haloalkanes. Molecular Microbiology, 2015, 97, 439-453.	1.2	19
2355	Typeâ€<scp>II NADH</scp>:quinone oxidoreductase from S<i>taphylococcus aureus</i> has two distinct binding sites and is rate limited by quinone reduction. Molecular Microbiology, 2015, 98, 272-288.	1.2	39
2356	Acidâ€“Base Catalyst Discriminates between a Fructose 6â€Phosphate Aldolase and a Transaldolase. ChemCatChem, 2015, 7, 3140-3151.	1.8	17
2357	Bh3 induced conformational changes in <scp>B</scp>clâ€<scp>X</scp>_l revealed by crystal structure and comparative analysis. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1262-1272.	1.5	35
2358	Weak conservation of structural features in the interfaces of homologous transient proteinâ€“protein complexes. Protein Science, 2015, 24, 1856-1873.	3.1	7
2359	Structural analysis of Fc/FcÎ³R complexes: a blueprint for antibody design. Immunological Reviews, 2015, 268, 201-221.	2.8	68

#	ARTICLE	IF	CITATIONS
2360	The Heptameric SmAP1 and SmAP2 Proteins of the Crenarchaeon Sulfolobus Solfataricus Bind to Common and Distinct RNA Targets. Life, 2015, 5, 1264-1281.	1.1	19
2361	Î²-Carbonic Anhydrases: General Features and Medical Implications. , 2015, , 247-273.		1
2362	Exploring the stability of dimers through protein structure topology. Current Protein and Peptide Science, 2015, 17, 30-36.	0.7	18
2363	Structure and Biophysical Properties of a Triple-Stranded Beta-Helix Comprising the Central Spike of Bacteriophage T4. Viruses, 2015, 7, 4676-4706.	1.5	9
2364	Structure of the Receptor-Binding Carboxy-Terminal Domain of the Bacteriophage T5 L-Shaped Tail Fibre with and without Its Intra-Molecular Chaperone. Viruses, 2015, 7, 6424-6440.	1.5	46
2365	Quaternary Structure Analyses of an Essential Oligomeric Enzyme. Methods in Enzymology, 2015, 562, 205-223.	0.4	24
2366	Thermostable Carbonic Anhydrases in Biotechnological Applications. International Journal of Molecular Sciences, 2015, 16, 15456-15480.	1.8	66
2367	Globular and disorderedâ€"the non-identical twins in protein-protein interactions. Frontiers in Molecular Biosciences, 2015, 2, 40.	1.6	36
2368	Essential Role of the C-Terminal Helical Domain in Active Site Formation of Selenoprotein MsrA from Clostridium oremlandii. PLoS ONE, 2015, 10, e0117836.	1.1	2
2369	The Bactofilin Cytoskeleton Protein BacM of Myxococcus xanthus Forms an Extended Î²-Sheet Structure Likely Mediated by Hydrophobic Interactions. PLoS ONE, 2015, 10, e0121074.	1.1	18
2370	Crystal Structures of the Kinase Domain of the Sulfate-Activating Complex in Mycobacterium tuberculosis. PLoS ONE, 2015, 10, e0121494.	1.1	9
2371	Stability of the Octameric Structure Affects Plasminogen-Binding Capacity of Streptococcal Enolase. PLoS ONE, 2015, 10, e0121764.	1.1	14
2372	The Crystal Structure of D-Threonine Aldolase from Alcaligenes xylosoxidans Provides Insight into a Metal Ion Assisted PLP-Dependent Mechanism. PLoS ONE, 2015, 10, e0124056.	1.1	16
2373	The Structure of the T190M Mutant of Murine Î±-Dystroglycan at High Resolution: Insight into the Molecular Basis of a Primary Dystroglycanopathy. PLoS ONE, 2015, 10, e0124277.	1.1	13
2374	An Extended Surface Loop on Toxoplasma gondii Apical Membrane Antigen 1 (AMA1) Governs Ligand Binding Selectivity. PLoS ONE, 2015, 10, e0126206.	1.1	16
2375	The Structure of the RNA-Dependent RNA Polymerase of a Permutotetravirus Suggests a Link between Primer-Dependent and Primer-Independent Polymerases. PLoS Pathogens, 2015, 11, e1005265.	2.1	25
2376	Structural Characterisation of FabG from Yersinia pestis, a Key Component of Bacterial Fatty Acid Synthesis. PLoS ONE, 2015, 10, e0141543.	1.1	15
2377	An Integrated Framework Advancing Membrane Protein Modeling and Design. PLoS Computational Biology, 2015, 11, e1004398.	1.5	145

#	Article	IF	Citations
2378	DynaFace: Discrimination between Obligatory and Non-obligatory Protein-Protein Interactions Based on the Complexâ€™s Dynamics. PLoS Computational Biology, 2015, 11, e1004461.	1.5	9
2379	Cross Talk between KGF and KITLG Proteins Implicated with Ovarian Folliculogenesis in Buffalo Bubalus bubalis. PLoS ONE, 2015, 10, e0127993.	1.1	5
2380	Structural and Biochemical Characterization of the Francisella tularensis Pathogenicity Regulator, Macrophage Locus Protein A (MglA). PLoS ONE, 2015, 10, e0128225.	1.1	9
2381	Crystal Structure of Hcp from Acinetobacter baumannii: A Component of the Type VI Secretion System. PLoS ONE, 2015, 10, e0129691.	1.1	29
2382	Structural and Functional Analysis of Human HtrA3 Protease and Its Subdomains. PLoS ONE, 2015, 10, e0131142.	1.1	35
2383	Structural Basis for the Specificity of Human NUDT16 and Its Regulation by Inosine Monophosphate. PLoS ONE, 2015, 10, e0131507.	1.1	22
2384	Structure of the Glycosyltransferase Ktr4p from Saccharomyces cerevisiae. PLoS ONE, 2015, 10, e0136239.	1.1	7
2385	X-Ray Structure and Mutagenesis Studies of the N-Isopropylammelide Isopropylaminohydrolase, AtzC. PLoS ONE, 2015, 10, e0137700.	1.1	5
2386	Structure and Sialyllactose Binding of the Carboxy-Terminal Head Domain of the Fibre from a Siadenovirus, Turkey Adenovirus 3. PLoS ONE, 2015, 10, e0139339.	1.1	25
2387	Heterodimerization of Two Pathological Mutants Enhances the Activity of Human Phosphomannomutase2. PLoS ONE, 2015, 10, e0139882.	1.1	26
2388	Dimerization-Induced Allosteric Changes of the Oxyanion-Hole Loop Activate the Pseudorabies Virus Assemblin pUL26N, a Herpesvirus Serine Protease. PLoS Pathogens, 2015, 11, e1005045.	2.1	15
2389	Trichodysplasia spinulosa-Associated Polyomavirus Uses a Displaced Binding Site on VP1 to Engage Sialylated Glycolipids. PLoS Pathogens, 2015, 11, e1005112.	2.1	20
2390	Arenavirus Glycan Shield Promotes Neutralizing Antibody Evasion and Protracted Infection. PLoS Pathogens, 2015, 11, e1005276.	2.1	138
2391	Evolution of plant Î´1-pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. Frontiers in Plant Science, 2015, 6, 567.	1.7	21
2392	Electrostatic Interactions between Complement Regulator CD46(SCR1-2) and Adenovirus Ad11/Ad21 Fiber Protein Knob. Molecular Biology International, 2015, 2015, 1-15.	1.7	1
2393	Structure and inhibition of subunit I of the anthranilate synthase complex of <i>Mycobacterium tuberculosis</i> and expression of the active complex. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2297-2308.	2.5	17
2395	CCP4 Software Suite: history, evolution, content, challenges and future developments. Arbor, 2015, 191, a220.	0.1	4
2396	The structure of <i>Aquifex aeolicus</i> FtsH in the ADP-bound state reveals a <i>C</i>₂-symmetric hexamer. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1307-1318.	2.5	20

#	Article	IF	Citations
2397	Crystal structure of VmoLac, a tentative quorum quenching lactonase from the extremophilic crenarchaeon Vulcanisaeta moutnovskia. Scientific Reports, 2015, 5, 8372.	1.6	44
2398	Unique ATPase Site Architecture Triggers cis-Mediated Synchronized ATP Binding in Heptameric AAA+-ATPase Domain of Flagellar Regulatory Protein FlrC. Journal of Biological Chemistry, 2015, 290, 8734-8747.	1.6	15
2399	How pH Modulates the Dimer-Decamer Interconversion of 2-Cys Peroxiredoxins from the Prx1 Subfamily. Journal of Biological Chemistry, 2015, 290, 8582-8590.	1.6	43
2400	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. Journal of Biological Chemistry, 2015, 290, 3278-3292.	1.6	41
2401	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. Journal of Biological Chemistry, 2015, 290, 13191-13201.	1.6	33
2402	Evidence of Kinetic Cooperativity in Dimeric Ketopantoate Reductase from <i>Staphylococcus aureus</i>. Biochemistry, 2015, 54, 3360-3369.	1.2	14
2403	Structural Basis for the Stereochemical Control of Amine Installation in Nucleotide Sugar Aminotransferases. ACS Chemical Biology, 2015, 10, 2048-2056.	1.6	12
2404	The amino-terminal structure of human fragile X mental retardation protein obtained using precipitant-immobilized imprinted polymers. Nature Communications, 2015, 6, 6634.	5.8	40
2405	Structure of the MarR family protein Rv0880 fromMycobacterium tuberculosis. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 741-745.	0.4	4
2406	The structure of a contact-dependent growth-inhibition (CDI) immunity protein from<i>Neisseria meningitidis</i>MC58. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 702-709.	0.4	7
2407	Antibodies to Interleukin-2 Elicit Selective T Cell Subset Potentiation through Distinct Conformational Mechanisms. Immunity, 2015, 42, 815-825.	6.6	191
2408	Repulsive guidance molecule is a structural bridge between neogenin and bone morphogenetic protein. Nature Structural and Molecular Biology, 2015, 22, 458-465.	3.6	78
2409	Structural Basis for Competitive Inhibition of 3,4-Dihydroxy-2-butanone-4-phosphate Synthase from Vibrio cholerae. Journal of Biological Chemistry, 2015, 290, 11293-11308.	1.6	16
2410	Structure of the bovine COPI Î´ subunit Î¼ homology domain at 2.15â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1328-1334.	2.5	5
2411	Structure of a Single-Chain Fv Bound to the 17 N-Terminal Residues of Huntingtin Provides Insights into Pathogenic Amyloid Formation and Suppression. Journal of Molecular Biology, 2015, 427, 2166-2178.	2.0	21
2412	FlaF Is a Î²-Sandwich Protein that Anchors the Archaellum in the Archaeal Cell Envelope by Binding the S-Layer Protein. Structure, 2015, 23, 863-872.	1.6	60
2413	Structural analysis of Dis3l2, an exosome-independent exonuclease from <i>Schizosaccharomyces pombe</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1284-1294.	2.5	10
2414	Opioid receptors: Structural and mechanistic insights into pharmacology and signaling. European Journal of Pharmacology, 2015, 763, 206-213.	1.7	68

#	Article	IF	Citations
2415	Structure and Mechanism of the Siderophore-Interacting Protein from the Fuscachelin Gene Cluster of <i>Thermobifida fusca</i>. Biochemistry, 2015, 54, 3989-4000.	1.2	23
2416	Erythromelalgia Mutation Q875E Stabilizes the Activated State of Sodium Channel Nav1.7. Journal of Biological Chemistry, 2015, 290, 6316-6325.	1.6	23
2417	Structure of a bacterial toxin-activating acyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3058-66.	3.3	33
2418	An empirical energy function for structural assessment of protein transmembrane domains. Biochimie, 2015, 115, 155-161.	1.3	15
2419	Crystal structure of human persulfide dioxygenase: structural basis of ethylmalonic encephalopathy. Human Molecular Genetics, 2015, 24, 2458-2469.	1.4	48
2420	Crystal structure of the most catalytically effective carbonic anhydrase enzyme known, SazCA from the thermophilic bacterium Sulfurihydrogenibium azorense. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 2002-2006.	1.0	72
2421	Surface-Induced Dissociation of Homotetramers with D2 Symmetry Yields their Assembly Pathways and Characterizes the Effect of Ligand Binding. Chemistry and Biology, 2015, 22, 583-592.	6.2	62
2422	Structural, functional, and genetic analyses of the actinobacterial transcription factor RbpA. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7171-7176.	3.3	48
2423	Structural and biochemical characterization of novel bacterial Î±-galactosidases belonging to glycoside hydrolase family 31. Biochemical Journal, 2015, 469, 145-158.	1.7	26
2424	Crystal structure of caspase recruiting domain (CARD) of apoptosis repressor with CARD (ARC) and its implication in inhibition of apoptosis. Scientific Reports, 2015, 5, 9847.	1.6	17
2425	Structure and sequence analyses of Bacteroides proteins BVU_4064 and BF1687 reveal presence of two novel predominantly-beta domains, predicted to be involved in lipid and cell surface interactions. BMC Bioinformatics, 2015, 16, 7.	1.2	8
2426	Structural basis of cofactor-mediated stabilization and substrate recognition of the Î±-tubulin acetyltransferase Î±TAT1. Biochemical Journal, 2015, 467, 103-113.	1.7	5
2427	Dimeric c-di-GMP Is Required for Post-translational Regulation of Alginate Production in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2015, 290, 12451-12462.	1.6	75
2428	Structure of human dual-specificity phosphatase 7, a potential cancer drug target. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 650-656.	0.4	9
2429	Structural basis for the recognition of the scaffold protein Frmpd4/Preso1 by the TPR domain of the adaptor protein LGN. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 175-183.	0.4	8
2430	Anti-CD28 Antibody-Initiated Cytokine Storm in Canines. Transplantation Direct, 2015, 1, 1-11.	0.8	13
2431	Conformational toggling controls target site choice for the heteromeric transposase element Tn7. Nucleic Acids Research, 2015, 43, 10734-10745.	6.5	18
2432	Structural features of interfacial tyrosine residue in ROBO1 fibronectin domainâ€antibody complex: Crystallographic, thermodynamic, and molecular dynamic analyses. Protein Science, 2015, 24, 328-340.	3.1	19

#	ARTICLE	IF	CITATIONS
2433	A new suite of tnaA mutants suggests that Escherichia coli tryptophanase is regulated by intracellular sequestration and by occlusion of its active site. BMC Microbiology, 2015, 15, 14.	1.3	17
2434	Structural characterization of a mitochondrial 3-ketoacyl-CoA (T1)-like thiolase fromMycobacterium smegmatis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2479-2493.	2.5	5
2435	The Cell Shape-determining Csd6 Protein from Helicobacter pylori Constitutes a New Family of l,d-Carboxypeptidase. Journal of Biological Chemistry, 2015, 290, 25103-25117.	1.6	34
2436	The Structure of the Cyprinid herpesvirus 3 ORF112-ZÎ±Â·Z-DNA Complex Reveals a Mechanism of Nucleic Acids Recognition Conserved with E3L, a Poxvirus Inhibitor of Interferon Response. Journal of Biological Chemistry, 2015, 290, 30713-30725.	1.6	26
2437	mRNA maturation in giant viruses: variation on a theme. Nucleic Acids Research, 2015, 43, 3776-3788.	6.5	17
2438	Stock-based detection of protein oligomeric states in jsPISA. Nucleic Acids Research, 2015, 43, W314-W319.	6.5	226
2439	Functional significance of protein assemblies predicted by the crystal structure of the restriction endonuclease BsaWI. Nucleic Acids Research, 2015, 43, 8100-8110.	6.5	8
2440	Ankyrin-mediated self-protection during cell invasion by the bacterial predator Bdellovibrio bacteriovorus. Nature Communications, 2015, 6, 8884.	5.8	37
2441	Principles of assembly reveal a periodic table of protein complexes. Science, 2015, 350, aaa2245.	6.0	198
2442	Structure of recombinant prolidase from<i>Thermococcus sibiricus</i>in space group<i>P</i>2₁22₁. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 951-957.	0.4	4
2443	Protein Arginine Methyltransferase 8: Tetrameric Structure and Protein Substrate Specificity. Biochemistry, 2015, 54, 7514-7523.	1.2	24
2444	Stonefish toxin defines an ancient branch of the perforin-like superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15360-15365.	3.3	69
2445	Crystal Structure of the Human tRNA m1A58 Methyltransferaseâ€“tRNA3Lys Complex: Refolding of Substrate tRNA Allows Access to the Methylation Target. Journal of Molecular Biology, 2015, 427, 3862-3876.	2.0	48
2446	Structural basis of DNA gyrase inhibition by antibacterial QPT-1, anticancer drug etoposide and moxifloxacin. Nature Communications, 2015, 6, 10048.	5.8	100
2447	Structural basis of substrate recognition by a bacterial deubiquitinase important for dynamics of phagosome ubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15090-15095.	3.3	88
2448	The terminal phycobilisome emitter, L _{CM} : A light-harvesting pigment with a phytochrome chromophore. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15880-15885.	3.3	69
2449	Promoting protein self-association in non-glycosylated Thermomyces lanuginosus lipase based on crystal lattice contacts. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1914-1921.	1.1	3
2450	Structural Basis for Oxygen Activation at a Heterodinuclear Manganese/Iron Cofactor. Journal of Biological Chemistry, 2015, 290, 25254-25272.	1.6	29

#	Article	IF	Citations
2451	Carbon Dioxide â€œTrappedâ€• in a Î²-Carbonic Anhydrase. Biochemistry, 2015, 54, 6631-6638.	1.2	24
2452	Structural and Thermodynamic Basis of Epitope Binding by Neutralizing and Nonneutralizing Forms of the Anti-HIV-1 Antibody 4E10. Journal of Virology, 2015, 89, 11975-11989.	1.5	22
2453	Structure of a fungal form of aspartate semialdehyde dehydrogenase from<i>Cryptococcus neoformans</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1365-1371.	0.4	11
2454	Refining the Structural Model of a Heterohexameric Protein Complex: Surface Induced Dissociation and Ion Mobility Provide Key Connectivity and Topology Information. ACS Central Science, 2015, 1, 477-487.	5.3	57
2455	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. IUCrJ, 2015, 2, 207-217.	1.0	516
2456	Architecture of the Ubiquitylation Module of the Yeast Ccr4-Not Complex. Structure, 2015, 23, 921-928.	1.6	33
2457	Structureâ€"function relationships in Gan42B, an intracellular GH42 Î²-galactosidase from<i>Geobacillus stearothermophilus</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2433-2448.	2.5	19
2458	Structure-based approach to the identification of a novel group of selective glucosamine analogue inhibitors of Trypanosoma cruzi glucokinase. Molecular and Biochemical Parasitology, 2015, 204, 64-76.	0.5	18
2459	Calcium-controlled conformational choreography in the N-terminal half of adseverin. Nature Communications, 2015, 6, 8254.	5.8	13
2460	KSHV but not MHV-68 LANA induces a strong bend upon binding to terminal repeat viral DNA. Nucleic Acids Research, 2015, 43, gkv987.	6.5	15
2461	Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association. Proteins: Structure, Function and Bioinformatics, 2015, 83, 428-435.	1.5	30
2462	Molecular inhibition of telomerase recruitment using designer peptides: anin silicoapproach. Journal of Biomolecular Structure and Dynamics, 2015, 33, 1442-1459.	2.0	1
2463	Structures and binding studies of the complexes of phospholipase A2 with five inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 269-277.	1.1	24
2464	High-resolution structure of a new Tn antigen-binding lectin from Vatairea macrocarpa and a comparative analysis of Tn-binding legume lectins. International Journal of Biochemistry and Cell Biology, 2015, 59, 103-110.	1.2	25
2465	Crystal structure of the Locusta migratoria odorant binding protein. Biochemical and Biophysical Research Communications, 2015, 456, 737-742.	1.0	41
2466	Nanobody Binding to a Conserved Epitope Promotes Norovirus Particle Disassembly. Journal of Virology, 2015, 89, 2718-2730.	1.5	54
2467	A Flexible Extension of the Drosophila Ultrabithorax Homeodomain Defines a Novel Hox/PBC Interaction Mode. Structure, 2015, 23, 270-279.	1.6	27
2468	All-atom crystal simulations of DNA and RNA duplexes. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 1059-1071.	1.1	20

#	Article	IF	Citations
2469	The LisH Motif of Muskelin Is Crucial for Oligomerization and Governs Intracellular Localization. Structure, 2015, 23, 364-373.	1.6	29
2470	The Activator of Apoptosis Smac-DIABLO Acts as a Tetramer in Solution. Biophysical Journal, 2015, 108, 714-723.	0.2	12
2471	Models of proteinâ€"ligand crystal structures: trust, but verify. Journal of Computer-Aided Molecular Design, 2015, 29, 817-836.	1.3	70
2472	A Novel Phosphatidylinositol 4,5-Bisphosphate Binding Domain Mediates Plasma Membrane Localization of ExoU and Other Patatin-like Phospholipases. Journal of Biological Chemistry, 2015, 290, 2919-2937.	1.6	34
2473	Crystal structure of YwpF from <scp><i>S</i></scp><i>taphylococcus aureus</i> reveals its architecture comprised of a Î²â€barrel core domain resembling type VI secretion system proteins and a twoâ€helix pair. Proteins: Structure, Function and Bioinformatics, 2015, 83, 781-788.	1.5	0
2474	X-domain of peptide synthetases recruits oxygenases crucial for glycopeptide biosynthesis. Nature, 2015, 521, 105-109.	13.7	158
2475	Structural Basis for Replication Origin Unwinding by an Initiator Primase of Plasmid ColE2-P9. Journal of Biological Chemistry, 2015, 290, 3601-3611.	1.6	4
2476	The structure of the proteinaceous inhibitor PliI from<i>Aeromonas hydrophila</i>in complex with its target lysozyme. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 344-351.	2.5	6
2477	Oligomeric state and structural stability of two hyperthermophilic Î²-glucosidases from Thermotoga petrophila. Amino Acids, 2015, 47, 937-948.	1.2	16
2478	Structural basis for the interaction of protein S1 with the Escherichia coli ribosome. Nucleic Acids Research, 2015, 43, 661-673.	6.5	56
2479	Crystal structure analysis of peroxidase from the palm tree Chamaerops excelsa. Biochimie, 2015, 111, 58-69.	1.3	20
2480	Structure and biochemical characterization of bacteriophage phi92 endosialidase. Virology, 2015, 477, 133-143.	1.1	27
2481	Dissociation of glucocerebrosidase dimer in solution by its co-factor, saposin C. Biochemical and Biophysical Research Communications, 2015, 457, 561-566.	1.0	19
2482	The Conundrum of the High-Affinity NGF Binding Site Formation Unveiled?. Biophysical Journal, 2015, 108, 687-697.	0.2	20
2483	Limited effect of recombinant human mannose-binding lectin on the infection of novel influenza A (H7N9) virus inÂvitro. Biochemical and Biophysical Research Communications, 2015, 458, 77-81.	1.0	6
2484	The Amyloid Precursor Protein Shows a pH-Dependent Conformational Switch in Its E1 Domain. Journal of Molecular Biology, 2015, 427, 433-442.	2.0	25
2485	A computational design approach for virtual screening of peptide interactions across K + channel families. Computational and Structural Biotechnology Journal, 2015, 13, 85-94.	1.9	14
2486	The Cobalamin-Independent Methionine Synthase Enzyme Captured in a Substrate-Induced Closed Conformation. Journal of Molecular Biology, 2015, 427, 901-909.	2.0	3

#	ARTICLE	IF	CITATIONS
2487	How pyridoxal 5â€²â€phosphate differentially regulates human cytosolic and mitochondrial serine hydroxymethyltransferase oligomeric state. FEBS Journal, 2015, 282, 1225-1241.	2.2	78
2488	Structure-Function Analysis of VapB4 Antitoxin Identifies Critical Features of a Minimal VapC4 Toxin-Binding Module. Journal of Bacteriology, 2015, 197, 1197-1207.	1.0	12
2489	Crystal Structure of an Arginase-like Protein from <i>Trypanosoma brucei</i> That Evolved without a Binuclear Manganese Cluster. Biochemistry, 2015, 54, 458-471.	1.2	26
2490	X-ray Crystallographic Structure of BshC, a Unique Enzyme Involved in Bacillithiol Biosynthesis. Biochemistry, 2015, 54, 100-103.	1.2	6
2491	Dimerization of Matrix Protein Is Required for Budding of Respiratory Syncytial Virus. Journal of Virology, 2015, 89, 4624-4635.	1.5	56
2492	<i>Man oâ€™ War</i> Mutation in UDP-Î±-<scp>d</scp>-Xylose Synthase Favors the Abortive Catalytic Cycle and Uncovers a Latent Potential for Hexamer Formation. Biochemistry, 2015, 54, 807-819.	1.2	3
2493	Structure of the Human Autophagy Initiating Kinase ULK1 in Complex with Potent Inhibitors. ACS Chemical Biology, 2015, 10, 257-261.	1.6	132
2494	Structural characterization of a protective epitope spanning A(H1N1)pdm09 influenza virus neuraminidase monomers. Nature Communications, 2015, 6, 6114.	5.8	84
2495	Essentiality of tetramer formation of Cellulomonas parahominis L-ribose isomerase involved in novel L-ribose metabolic pathway. Applied Microbiology and Biotechnology, 2015, 99, 6303-6313.	1.7	13
2496	Minimalistic Predictor of Protein Binding Energy: Contribution of Solvation Factor to Protein Binding. Biophysical Journal, 2015, 108, 795-798.	0.2	17
2497	Flexibility in the Nâ€terminal actinâ€binding domain: Clues from <i>in silico</i> mutations and molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2015, 83, 696-710.	1.5	7
2498	Structural and Functional Characterization of a Ketosteroid Transcriptional Regulator of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2015, 290, 872-882.	1.6	29
2499	Insight into the structural flexibility and function of Mycobacterium tuberculosis isocitrate lyase. Biochimie, 2015, 110, 73-80.	1.3	21
2500	Epistasis Constrains Mutational Pathways of Hemoglobin Adaptation in High-Altitude Pikas. Molecular Biology and Evolution, 2015, 32, 287-298.	3.5	95
2501	Structure of a cupin protein Plu4264 from Photorhabdus luminescens subsp. laumondii TTO1 at 1.35 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2015, 83, 383-388.	1.5	2
2502	Vaccinia Virus Protein A49 Is an Unexpected Member of the B-cell Lymphoma (Bcl)-2 Protein Family. Journal of Biological Chemistry, 2015, 290, 5991-6002.	1.6	49
2503	Landscape of Intertwined Associations in Multi-Domain Homo-Oligomeric Proteins. Journal of Molecular Biology, 2015, 427, 350-370.	2.0	14
2504	Use of a â€œsilver bulletâ€•to resolve crystal lattice dislocation disorder: A cobalamin complex of Î”1-pyrroline-5-carboxylate dehydrogenase from Mycobacterium tuberculosis. Journal of Structural Biology, 2015, 189, 153-157.	1.3	1

#	Article	IF	Citations
2505	The Strength and Cooperativity of KIT Ectodomain Contacts Determine Normal Ligand-Dependent Stimulation or Oncogenic Activation in Cancer. Molecular Cell, 2015, 57, 191-201.	4.5	26
2506	Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67.	13.7	216
2507	Structural basis of DNA recognition by PCG2 reveals a novel DNA binding mode for winged helix-turn-helix domains. Nucleic Acids Research, 2015, 43, 1231-1240.	6.5	18
2508	Near-Atomic Resolution for One State of F-Actin. Structure, 2015, 23, 173-182.	1.6	121
2509	Crystal structure of a plant albumin from Cicer arietinum (chickpea) possessing hemopexin fold and hemagglutination activity. Planta, 2015, 241, 1061-1073.	1.6	9
2510	Structural and Molecular Basis for Resistance to Aminoglycoside Antibiotics by the Adenylyltransferase ANT(2â€³)-Ia. MBio, 2015, 6, .	1.8	49
2511	Structural basis for Notch1 engagement of Delta-like 4. Science, 2015, 347, 847-853.	6.0	222
2512	Structural insights into the broad substrate specificity of carboxypeptidase T from <i>ThermoactinomycesÂvulgaris</i>. FEBS Journal, 2015, 282, 1214-1224.	2.2	15
2513	NuProPlot: nucleic acid and protein interaction analysis and plotting program. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 667-674.	2.5	8
2514	Crystal Structure and Functional Characterization of Photosystem II-Associated Carbonic Anhydrase CAH3 in <i>Chlamydomonas reinhardtii</i>. Plant Physiology, 2015, 167, 950-962.	2.3	26
2515	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. Nature Communications, 2015, 6, 6337.	5.8	185
2516	Structure-Based Functional Characterization of Repressor of Toxin (Rot), a Central Regulator of Staphylococcus aureus Virulence. Journal of Bacteriology, 2015, 197, 188-200.	1.0	19
2517	Structure and function of a short LOV protein from the marine phototrophic bacterium Dinoroseobacter shibae. BMC Microbiology, 2015, 15, 30.	1.3	36
2518	Dysregulation of transition metal ion homeostasis is the molecular basis for cadmium toxicity in Streptococcus pneumoniae. Nature Communications, 2015, 6, 6418.	5.8	117
2519	Structure-Function Analysis of Heterodimer Formation, Oligomerization, and Receptor Binding of the Staphylococcus aureus Bi-component Toxin LukGH. Journal of Biological Chemistry, 2015, 290, 142-156.	1.6	54
2520	Crystal Structure of BamB Bound to a Periplasmic Domain Fragment of BamA, the Central Component of the Î²-Barrel Assembly Machine. Journal of Biological Chemistry, 2015, 290, 2126-2136.	1.6	49
2521	Site-directed Mutagenesis Reveals Regions Implicated in the Stability and Fiber Formation of Human Î»3r Light Chains. Journal of Biological Chemistry, 2015, 290, 2577-2592.	1.6	11
2522	Algorithmic approaches to protein-protein interaction site prediction. Algorithms for Molecular Biology, 2015, 10, 7.	0.3	62

#	Article	IF	Citations
2523	Structures of regulatory machinery reveal novel molecular mechanisms controlling <i>B. subtilis</i> nitrogen homeostasis. Genes and Development, 2015, 29, 451-464.	2.7	51
2524	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	13.5	216
2525	Structural basis for misfolding in myocilin-associated glaucoma. Human Molecular Genetics, 2015, 24, 2111-2124.	1.4	72
2526	Fully Human VH Single Domains That Rival the Stability and Cleft Recognition of Camelid Antibodies. Journal of Biological Chemistry, 2015, 290, 11905-11917.	1.6	59
2527	First Evidence for Substrate Channeling between Proline Catabolic Enzymes. Journal of Biological Chemistry, 2015, 290, 2225-2234.	1.6	37
2528	Structures of Human CCL18, CCL3, and CCL4 Reveal Molecular Determinants for Quaternary Structures and Sensitivity to Insulin-Degrading Enzyme. Journal of Molecular Biology, 2015, 427, 1345-1358.	2.0	21
2529	Structural basis for chemokine recognition and activation of a viral G proteinâ€"coupled receptor. Science, 2015, 347, 1113-1117.	6.0	261
2530	Evidence that phosphorylation of threonine in the GT motif triggers activation of PknA, a eukaryoticâ€type serine/threonine kinase from <i>MycobacteriumÂtuberculosis</i>. FEBS Journal, 2015, 282, 1419-1431.	2.2	20
2531	A series of PDB-related databanks for everyday needs. Nucleic Acids Research, 2015, 43, D364-D368.	6.5	757
2532	Structural characterization of the late competence protein ComFB from Bacillus subtilis. Bioscience Reports, 2015, 35, .	1.1	10
2533	Simulation of protein association: Kinetic pathways towards crystal contacts. Physical Review E, 2015, 91, 033311.	0.8	13
2534	Crystal Structure and Substrate Recognition of Cellobionic Acid Phosphorylase, Which Plays a Key Role in Oxidative Cellulose Degradation by Microbes. Journal of Biological Chemistry, 2015, 290, 18281-18292.	1.6	22
2535	Atomic Structure of GRK5 Reveals Distinct Structural Features Novel for G Protein-coupled Receptor Kinases. Journal of Biological Chemistry, 2015, 290, 20629-20647.	1.6	30
2536	Snapshots of ligand entry, malleable binding and induced helical movement in P-glycoprotein. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 732-741.	2.5	149
2537	Crystal Structure of Apo and Ligand Bound Vibrio cholerae Ribokinase (Vc-RK): Role of Monovalent Cation Induced Activation and Structural Flexibility in Sugar Phosphorylation. Advances in Experimental Medicine and Biology, 2015, 842, 293-307.	0.8	13
2538	Rgg protein structureâ€"function and inhibition by cyclic peptide compounds. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5177-5182.	3.3	57
2539	Structure of the eukaryotic MCM complex at 3.8 Ã…. Nature, 2015, 524, 186-191.	13.7	207
2540	Archaeal actin from a hyperthermophile forms a single-stranded filament. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9340-9345.	3.3	22

#	ARTICLE	IF	CITATIONS
2541	Comprehensive Structural and Biochemical Analysis of the Terminal Myxalamid Reductase Domain for the Engineered Production of Primary Alcohols. Chemistry and Biology, 2015, 22, 1018-1029.	6.2	56
2542	Crystal structure, biochemical and cellular activities demonstrate separate functions of MTH1 and MTH2. Nature Communications, 2015, 6, 7871.	5.8	96
2543	Crystallographic and solution studies of NAD+- and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from Escherichia coli provide insight into sequential enzymatic steps. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 1139-1152.	0.5	12
2544	Structural and biochemical properties of LuxF from Photobacterium leiognathi. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1466-1475.	1.1	13
2545	The Study of Carbamoyl Phosphate Synthetase 1 Deficiency Sheds Light on the Mechanism for Switching On/Off the Urea Cycle. Journal of Genetics and Genomics, 2015, 42, 249-260.	1.7	28
2546	The tuberculosis necrotizing toxin kills macrophages by hydrolyzing NAD. Nature Structural and Molecular Biology, 2015, 22, 672-678.	3.6	114
2547	Structure of human MDM2 complexed with RPL11 reveals the molecular basis of p53 activation. Genes and Development, 2015, 29, 1524-1534.	2.7	66
2548	The mammalian autophagy initiator complex contains 2 HORMA domain proteins. Autophagy, 2015, 11, 2300-2308.	4.3	26
2549	Cocrystal Structures of Antibody N60-i3 and Antibody JR4 in Complex with gp120 Define More Cluster A Epitopes Involved in Effective Antibody-Dependent Effector Function against HIV-1. Journal of Virology, 2015, 89, 8840-8854.	1.5	51
2550	Crystal structure of human POP1 and its distinct structural feature for PYD domain. Biochemical and Biophysical Research Communications, 2015, 460, 957-963.	1.0	6
2551	Structural basis for the substrate selectivity of a HAD phosphatase from Thermococcus onnurineus NA1. Biochemical and Biophysical Research Communications, 2015, 461, 122-127.	1.0	2
2552	Structural and functional studies of the<i>Mycobacterium tuberculosis</i>VapBC30 toxin-antitoxin system: implications for the design of novel antimicrobial peptides. Nucleic Acids Research, 2015, 43, 7624-7637.	6.5	68
2553	The crystal structure of Erwinia amylovora levansucrase provides a snapshot of the products of sucrose hydrolysis trapped into the active site. Journal of Structural Biology, 2015, 191, 290-298.	1.3	56
2554	The Crystal Structure of the Drosophila Germline Inducer Oskar Identifies Two Domains with Distinct Vasa Helicase- and RNA-Binding Activities. Cell Reports, 2015, 12, 587-598.	2.9	76
2555	Aldolases Utilize Different Oligomeric States To Preserve Their Functional Dynamics. Biochemistry, 2015, 54, 3543-3554.	1.2	12
2556	Domain-Swapping Switch Point in Ste20 Protein Kinase SPAK. Biochemistry, 2015, 54, 5063-5071.	1.2	19
2557	Crystal structure of the Ego1-Ego2-Ego3 complex and its role in promoting Rag GTPase-dependent TORC1 signaling. Cell Research, 2015, 25, 1043-1059.	5.7	71
2558	Reversibility and two state behaviour in the thermal unfolding of oligomeric TIM barrel proteins. Physical Chemistry Chemical Physics, 2015, 17, 20699-20714.	1.3	21

#	ARTICLE	IF	CITATIONS
2559	Protein cold adaptation: Role of physico-chemical parameters in adaptation of proteins to low temperatures. Journal of Theoretical Biology, 2015, 383, 130-137.	0.8	8
2560	Structural Insights into Ca2+-Calmodulin Regulation of Plectin 1a-Integrin Î²4 Interaction in Hemidesmosomes. Structure, 2015, 23, 558-570.	1.6	28
2561	The structure of FMNL2â€“Cdc42 yields insights into the mechanism of lamellipodia and filopodia formation. Nature Communications, 2015, 6, 7088.	5.8	63
2562	Structural insight into the thermostable NADP⁺-dependent<i>meso</i>-diaminopimelate dehydrogenase from<i>Ureibacillus thermosphaericus</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1136-1146.	2.5	12
2563	ABC transporter Cdr1p harbors charged residues in the intracellular loop and nucleotide-binding domain critical for protein trafficking and drug resistance. FEMS Yeast Research, 2015, 15, fov036.	1.1	7
2564	High-resolution Crystal Structure of Dimeric VP40 FromSudan ebolavirus. Journal of Infectious Diseases, 2015, 212, S167-S171.	1.9	7
2565	Structural asymmetry in a conserved signaling system that regulates division, replication, and virulence of an intracellular pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3709-18.	3.3	52
2566	Four crystal structures of human LLT1, a ligand of human NKR-P1, in varied glycosylation and oligomerization states. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 578-591.	2.5	20
2567	Structural basis for double cofactor specificity in a new formate dehydrogenase from the acidobacterium Granulicella mallensis MP5ACTX8. Applied Microbiology and Biotechnology, 2015, 99, 9541-9554.	1.7	39
2568	Universal allosteric mechanism for GÎ± activation by GPCRs. Nature, 2015, 524, 173-179.	13.7	291
2569	Structural basis for the RING-catalyzed synthesis of K63-linked ubiquitin chains. Nature Structural and Molecular Biology, 2015, 22, 597-602.	3.6	99
2570	Structural and Biochemical Characterization of AidC, a Quorum-Quenching Lactonase with Atypical Selectivity. Biochemistry, 2015, 54, 4342-4353.	1.2	19
2571	Quaternary organization in a bifunctional prokaryotic FAD synthetase: Involvement of an arginine at its adenylyltransferase module on the riboflavin kinase activity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 897-906.	1.1	18
2572	Structures of Orf Virus Chemokine Binding Protein in Complex with Host Chemokines Reveal Clues to Broad Binding Specificity. Structure, 2015, 23, 1199-1213.	1.6	28
2573	Structural analysis of DNA binding by C.Csp231I, a member of a novel class of R-M controller proteins regulating gene expression. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 398-407.	2.5	12
2574	Light Signaling Mechanism of Two Tandem Bacteriophytochromes. Structure, 2015, 23, 1179-1189.	1.6	42
2575	An intermolecular binding mechanism involving multiple LysM domains mediates carbohydrate recognition by an endopeptidase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 592-605.	2.5	34
2576	A Crystal Structure of the Dengue Virus NS5 Protein Reveals a Novel Inter-domain Interface Essential for Protein Flexibility and Virus Replication. PLoS Pathogens, 2015, 11, e1004682.	2.1	180

#	ARTICLE	IF	CITATIONS
2577	Characterization of the Mycobacterial Acyl-CoA Carboxylase Holo Complexes Reveals Their Functional Expansion into Amino Acid Catabolism. PLoS Pathogens, 2015, 11, e1004623.	2.1	19
2578	Crystal structure of a mirror-image L-RNA aptamer (Spiegelmer) in complex with the natural L-protein target CCL2. Nature Communications, 2015, 6, 6923.	5.8	77
2579	Hoefavidin: A dimeric bacterial avidin with a C-terminal binding tail. Journal of Structural Biology, 2015, 191, 139-148.	1.3	17
2580	Molecular mechanism of the dual activity of 4EGI-1: Dissociating eIF4G from eIF4E but stabilizing the binding of unphosphorylated 4E-BP1. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4036-45.	3.3	90
2581	Structure and Biophysical Characterization of the S-Adenosylmethionine-dependent O-Methyltransferase PaMTH1, a Putative Enzyme Accumulating during Senescence of Podospora anserina. Journal of Biological Chemistry, 2015, 290, 16415-16430.	1.6	20
2582	Structural Insights into the Distinct Binding Mode of Cyclic Di-AMP with <i>Sa</i>CpaA_RCK. Biochemistry, 2015, 54, 4936-4951.	1.2	48
2583	How release of phosphate from mammalian F ₁ -ATPase generates a rotary substep. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6009-6014.	3.3	51
2584	Elusive Structural, Functional, and Immunological Features of Act d 5, the Green Kiwifruit Kiwellin. Journal of Agricultural and Food Chemistry, 2015, 63, 6567-6576.	2.4	25
2585	Biogenesis and structure of a type VI secretion membrane core complex. Nature, 2015, 523, 555-560.	13.7	241
2586	Structure of human ST8SiaIII sialyltransferase provides insight into cell-surface polysialylation. Nature Structural and Molecular Biology, 2015, 22, 627-635.	3.6	62
2587	Structural Analysis of Der p 1â€"Antibody Complexes and Comparison with Complexes of Proteins or Peptides with Monoclonal Antibodies. Journal of Immunology, 2015, 195, 307-316.	0.4	23
2588	Controlled crystal dehydration triggers a space-group switch and shapes the tertiary structure of cytomegalovirus immediate-early 1 (IE1) protein. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1493-1504.	2.5	11
2589	An Unexpected Duo: Rubredoxin Binds Nine TPR Motifs to Form LapB, an Essential Regulator of Lipopolysaccharide Synthesis. Structure, 2015, 23, 1500-1506.	1.6	18
2590	Structural basis for the activation of the <i>C. elegans</i> noncanonical cytoplasmic poly(A)-polymerase GLD-2 by GLD-3. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8614-8619.	3.3	23
2591	Structure of Î³-conglutin: insight into the quaternary structure of 7S basic globulins from legumes. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 224-238.	2.5	31
2592	Snapshots of Conformational Changes Shed Light into the NtrX Receiver Domain Signal Transduction Mechanism. Journal of Molecular Biology, 2015, 427, 3258-3272.	2.0	16
2593	MemProtMD: Automated Insertion of Membrane Protein Structures into Explicit Lipid Membranes. Structure, 2015, 23, 1350-1361.	1.6	257
2594	The Anopheles-midgut APN1 structure reveals a new malaria transmissionâ€"blocking vaccine epitope. Nature Structural and Molecular Biology, 2015, 22, 532-539.	3.6	55

#	Article	IF	Citations
2595	The structure of the folded domain from the signature multifunctional protein ICP27 from herpes simplex virus-1 reveals an intertwined dimer. Scientific Reports, 2015, 5, 11234.	1.6	23
2596	Conserved Streptococcus pneumoniae Spirosomes Suggest a Single Type of Transformation Pilus in Competence. PLoS Pathogens, 2015, 11, e1004835.	2.1	26
2597	Kar1 binding to Sfi1 C-terminal regions anchors the SPB bridge to the nuclear envelope. Journal of Cell Biology, 2015, 209, 843-861.	2.3	25
2598	Structures of<i>Drosophila melanogaster</i>Rab2 and Rab3 bound to GMPPNP. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 34-40.	0.4	5
2599	High-resolution crystal structure of the leucine-rich repeat domain of the human tumour suppressor PP32A (ANP32A). Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 684-687.	0.4	4
2600	Molecular Characterization of LubX: Functional Divergence of the U-Box Fold by Legionella pneumophila. Structure, 2015, 23, 1459-1469.	1.6	34
2601	3-Sulfinopropionyl-coenzyme A (3SP-CoA) desulfinase from<i>Advenella mimigardefordensis</i>DPN7^T: crystal structure and function of a desulfinase with an acyl-CoA dehydrogenase fold. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1360-1372.	2.5	6
2602	Virulence Regulation with Venus Flytrap Domains: Structure and Function of the Periplasmic Moiety of the Sensor-Kinase BvgS. PLoS Pathogens, 2015, 11, e1004700.	2.1	51
2603	NMR Structure of the Myristylated Feline Immunodeficiency Virus Matrix Protein. Viruses, 2015, 7, 2210-2229.	1.5	21
2604	Standalone cohesin as a molecular shuttle in cellulosome assembly. FEBS Letters, 2015, 589, 1569-1576.	1.3	14
2605	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. PLoS Computational Biology, 2015, 11, e1004147.	1.5	59
2606	The Shear Stress of Host Cell Invasion: Exploring the Role of Biomolecular Complexes. PLoS Pathogens, 2015, 11, e1004539.	2.1	7
2607	The EBNA-2 N-Terminal Transactivation Domain Folds into a Dimeric Structure Required for Target Gene Activation. PLoS Pathogens, 2015, 11, e1004910.	2.1	10
2608	Structural characterization of substrate and inhibitor binding to farnesyl pyrophosphate synthase from<i>Pseudomonas aeruginosa</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 721-731.	2.5	17
2609	The structure of hookworm platelet inhibitor (HPI), a CAP superfamily member fromAncylostoma caninum. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 643-649.	0.4	14
2610	Structure of the catalytic domain of Mre11 from<i>Chaetomium thermophilum</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 752-757.	0.4	19
2611	Comparative structural analysis of the caspase family with other clan CD cysteine peptidases. Biochemical Journal, 2015, 466, 219-232.	1.7	74
2612	Structural Studies of Potassium Transport Protein KtrA Regulator of Conductance of K+ (RCK) C Domain in Complex with Cyclic Diadenosine Monophosphate (c-di-AMP). Journal of Biological Chemistry, 2015, 290, 16393-16402.	1.6	74

#	ARTICLE	IF	CITATIONS
2613	Structural and Kinetic Characterization of Thymidine Kinase from Leishmania major. PLoS Neglected Tropical Diseases, 2015, 9, e0003781.	1.3	13
2614	Structural Basis for Dodecameric Assembly States and Conformational Plasticity of the Full-Length AAA+ ATPases Rvb1Â·Rvb2. Structure, 2015, 23, 483-495.	1.6	39
2615	Structure of Halorhodopsin from Halobacterium salinarum in a new crystal form that imposes little restraint on the Eâ€“F loop. Journal of Structural Biology, 2015, 190, 373-378.	1.3	14
2616	Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4666-4671.	3.3	43
2617	Structural Analysis Reveals the Substrateâ€Binding Mechanism for the Expanded Substrate Specificity of Mutant <i>meso</i>â€Diaminopimelate Dehydrogenase. ChemBioChem, 2015, 16, 924-929.	1.3	14
2618	Collision Cross Sections for Structural Proteomics. Structure, 2015, 23, 791-799.	1.6	231
2619	Structural basis for carbohydrate binding properties of a plant chitinase-like agglutinin with conserved catalytic machinery. Journal of Structural Biology, 2015, 190, 115-121.	1.3	10
2620	Distinctive binding modes and inhibitory mechanisms of two peptidic inhibitors of urokinase-type plasminogen activator with isomeric P1 residues. International Journal of Biochemistry and Cell Biology, 2015, 62, 88-92.	1.2	2
2621	Structural and biophysical characterization of an epitope-specific engineered Fab fragment and complexation with membrane proteins: implications for co-crystallization. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 896-906.	2.5	13
2622	Structural and Enzymatic Analysis of TarM Glycosyltransferase from Staphylococcus aureus Reveals an Oligomeric Protein Specific for the Glycosylation of Wall Teichoic Acid. Journal of Biological Chemistry, 2015, 290, 9874-9885.	1.6	22
2623	A covalent adduct of MbtN, an acyl-ACP dehydrogenase from<i>Mycobacterium tuberculosis</i>, reveals an unusual acyl-binding pocket. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 862-872.	2.5	6
2624	Crystal structure and substrate-binding mode of GH63 mannosylglycerate hydrolase from Thermus thermophilus HB8. Journal of Structural Biology, 2015, 190, 21-30.	1.3	8
2625	Substrates Control Multimerization and Activation of the Multi-Domain ATPase Motor of Type VII Secretion. Cell, 2015, 161, 501-512.	13.5	124
2626	CyToStruct: Augmenting the Network Visualization of Cytoscape with the Power of Molecular Viewers. Structure, 2015, 23, 941-948.	1.6	20
2627	Characterization of the flexible lip regions in bacteriophage lambda lysozyme using MD simulations. European Biophysics Journal, 2015, 44, 235-247.	1.2	3
2628	Continuum electrostatic approach for evaluating positions and interactions of proteins in a bilayer membrane. Journal of Molecular Graphics and Modelling, 2015, 59, 81-91.	1.3	5
2629	Defining a Two-pronged Structural Model for PB1 (Phox/Bem1p) Domain Interaction in Plant Auxin Responses. Journal of Biological Chemistry, 2015, 290, 12868-12878.	1.6	31
2630	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. Cell, 2015, 161, 647-660.	13.5	482

#	Article	IF	Citations
2631	The bacteriocin AS-48 requires dimer dissociation followed by hydrophobic interactions with the membrane for antibacterial activity. Journal of Structural Biology, 2015, 190, 162-172.	1.3	40
2632	Structure of a complex of uridine phosphorylase from Yersinia pseudotuberculosis with the modified bacteriostatic antibacterial drug determined by X-ray crystallography and computer analysis. Crystallography Reports, 2015, 60, 217-226.	0.1	0
2633	High-resolution structure of a type IV pilin from the metal-reducing bacterium Shewanella oneidensis. BMC Structural Biology, 2015, 15, 4.	2.3	15
2634	Crystal structure of the DNA polymerase III Î² subunit (Î²-clamp) from the extremophile Deinococcus radiodurans. BMC Structural Biology, 2015, 15, 5.	2.3	7
2635	A novel inhibitor of Plasmodium falciparum spermidine synthase: a twist in the tail. Malaria Journal, 2015, 14, 54.	0.8	12
2636	Structural basis of multivalent galactoseâ€based dendrimer recognition by human galectinâ€7. FEBS Journal, 2015, 282, 372-387.	2.2	13
2637	Molecular dynamics of the asymmetric dimers of EGFR: Simulations on the active and inactive conformations of the kinase domain. Journal of Molecular Graphics and Modelling, 2015, 58, 16-29.	1.3	11
2638	Interaction of the amyloid precursor protein-like protein 1 (APLP1) E2 domain with heparan sulfate involves two distinct binding modes. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 494-504.	2.5	12
2639	Human DNA polymerase Î¸ grasps the primer terminus to mediate DNA repair. Nature Structural and Molecular Biology, 2015, 22, 304-311.	3.6	109
2640	Interdomain Hydrophobic Interactions Modulate the Thermostability of Microbial Esterases from the Hormone-Sensitive Lipase Family. Journal of Biological Chemistry, 2015, 290, 11188-11198.	1.6	56
2641	Molecular basis for mid-region amyloid-Î² capture by leading Alzheimer's disease immunotherapies. Scientific Reports, 2015, 5, 9649.	1.6	73
2642	Structural and functional analysis of betaine aldehyde dehydrogenase from<i>Staphylococcus aureus</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1159-1175.	2.5	16
2643	The structure of the giant haemoglobin from<i>Glossoscolex paulistus</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1257-1271.	2.5	12
2644	A Mimivirus Enzyme that Participates in Viral Entry. Structure, 2015, 23, 1058-1065.	1.6	22
2645	Molecular recognition of human ephrinB2 cell surface receptor by an emergent African henipavirus. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2156-65.	3.3	47
2646	A site of varicella-zoster virus vulnerability identified by structural studies of neutralizing antibodies bound to the glycoprotein complex gHgL. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6056-6061.	3.3	44
2647	Structures of C1q-like Proteins Reveal Unique Features among the C1q/TNF Superfamily. Structure, 2015, 23, 688-699.	1.6	56
2648	Active Site and Laminarin Binding in Glycoside Hydrolase Family 55. Journal of Biological Chemistry, 2015, 290, 11819-11832.	1.6	36

#	ARTICLE	IF	CITATIONS
2649	Insights into Herpesvirus Tegument Organization from Structural Analyses of the 970 Central Residues of HSV-1 UL36 Protein. Journal of Biological Chemistry, 2015, 290, 8820-8833.	1.6	15
2650	Structural and functional analysis of two universal stress proteins YdaA and YnaF from Salmonella typhimurium: possible roles in microbial stress tolerance. Journal of Structural Biology, 2015, 189, 238-250.	1.3	13
2651	Atomic structure of anthrax protective antigen pore elucidates toxin translocation. Nature, 2015, 521, 545-549.	13.7	217
2652	K2P channel gating mechanisms revealed by structures of TREK-2 and a complex with Prozac. Science, 2015, 347, 1256-1259.	6.0	255
2653	Crystal structure of Cry51Aa1: A potential novel insecticidal aerolysin-type Î²-pore-forming toxin from Bacillus thuringiensis. Biochemical and Biophysical Research Communications, 2015, 462, 184-189.	1.0	32
2654	Viral Receptor-Binding Site Antibodies with Diverse Germline Origins. Cell, 2015, 161, 1026-1034.	13.5	151
2655	Structures of theN-acetyltransferase domain ofXylella fastidiosaN-acetyl-L-glutamate synthase/kinase with and without a His tag bound toN-acetyl-L-glutamate. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 86-95.	0.4	3
2656	Atomic-resolution structure of the Â-galactosyl binding Lyophyllum decastes lectin reveals a new protein family found in both fungi and plants. Glycobiology, 2015, 25, 492-501.	1.3	14
2657	Crystal structure of the human mitochondrial chaperonin symmetrical football complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6044-6049.	3.3	92
2658	Three-dimensional Structure of a Kunitz-type Inhibitor in Complex with an Elastase-like Enzyme. Journal of Biological Chemistry, 2015, 290, 14154-14165.	1.6	17
2659	Structural and Functional Plasticity of Antibiotic Resistance Nucleotidylyltransferases Revealed by Molecular Characterization of Lincosamide Nucleotidylyltransferases Lnu(A) and Lnu(D). Journal of Molecular Biology, 2015, 427, 2229-2243.	2.0	7
2660	Structural insights into the binding of the human receptor for advanced glycation end products (RAGE) by S100B, as revealed by an S100Bâ€"RAGE-derived peptide complex. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1176-1183.	2.5	15
2661	Structure of a CutA1 divalent-cation tolerance protein from<i>Cryptosporidium parvum</i>, the protozoal parasite responsible for cryptosporidiosis. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 522-530.	0.4	1
2662	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. Nucleic Acids Research, 2015, 43, D345-D356.	6.5	461
2663	Atomic structures of a bactericidal contractile nanotube in its pre- and postcontraction states. Nature Structural and Molecular Biology, 2015, 22, 377-382.	3.6	134
2664	Structure of Prolyl-tRNA Synthetase-Halofuginone Complex Provides Basis for Development of Drugs against Malaria and Toxoplasmosis. Structure, 2015, 23, 819-829.	1.6	92
2665	The complete structure of the 55 <i>S</i> mammalian mitochondrial ribosome. Science, 2015, 348, 303-308.	6.0	344
2666	X-ray crystallographic validation of structure predictions used in computational design for protein stabilization. Proteins: Structure, Function and Bioinformatics, 2015, 83, 940-951.	1.5	17

#	Article	IF	Citations
2667	Crystal structure of a Xenopus laevis skin proto-type galectin, close to but distinct from galectin-1. Glycobiology, 2015, 25, 792-803.	1.3	10
2668	The dimeric crystal structure of the human fertility lipocalin glycodelin reveals a protein scaffold for the presentation of complex glycans. Biochemical Journal, 2015, 466, 95-104.	1.7	20
2669	Structural basis for the neutralization of hepatitis E virus by a cross-genotype antibody. Cell Research, 2015, 25, 604-620.	5.7	69
2670	Structure of p15PAFâ€“PCNA complex and implications for clamp sliding during DNA replication and repair. Nature Communications, 2015, 6, 6439.	5.8	65
2671	Structure and catalytic mechanism of the evolutionarily unique bacterial chalcone isomerase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 907-917.	2.5	21
2672	Expression, purification, crystallization and preliminary crystallographic analysis of a GH20 Î²-<i>N</i>-acetylglucosaminidase from the marine bacterium<i>Vibrio harveyi</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 427-433.	0.4	7
2673	Domains of Pyrococcus furiosus l-asparaginase fold sequentially and assemble through strong intersubunit associative forces. Extremophiles, 2015, 19, 681-691.	0.9	10
2674	CCM2â€“CCM3 interaction stabilizes their protein expression and permits endothelial network formation. Journal of Cell Biology, 2015, 208, 987-1001.	2.3	46
2675	Structural basis ofBacillus anthracisMoxXT disruption and the modulation of MoxT ribonuclease activity by rationally designed peptides. Journal of Biomolecular Structure and Dynamics, 2015, 33, 606-624.	2.0	12
2676	Structural characterization of metal binding to a cold-adapted frataxin. Journal of Biological Inorganic Chemistry, 2015, 20, 653-664.	1.1	9
2677	Structure of Liver Receptor Homolog-1 (NR5A2) with PIP3 hormone bound in the ligand binding pocket. Journal of Structural Biology, 2015, 192, 342-348.	1.3	44
2678	Structural and adhesive properties of the long polar fimbriae protein LpfD from adherent-invasiveEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1615-1626.	2.5	8
2679	Assembly of the Ebola Virus Nucleoprotein from a Chaperoned VP35 Complex. Cell Reports, 2015, 12, 140-149.	2.9	117
2680	Structural basis for gene regulation by a B12-dependent photoreceptor. Nature, 2015, 526, 536-541.	13.7	149
2681	Crystal structure and biophysical characterization of the nucleoside diphosphate kinase from Leishmania braziliensis. BMC Structural Biology, 2015, 15, 2.	2.3	7
2682	A conserved charged single Î±-helix with a putative steric role in paraspeckle formation. Rna, 2015, 21, 2023-2029.	1.6	13
2683	Molecular basis for the inhibition of Î²-hydroxyacyl-ACP dehydratase HadAB complex from Mycobacterium tuberculosis by flavonoid inhibitors. Protein and Cell, 2015, 6, 504-517.	4.8	28
2684	Proteinâ€“Protein Interfaces in Viral Capsids Are Structurally Unique. Journal of Molecular Biology, 2015, 427, 3613-3624.	2.0	5

#	Article	IF	Citations
2685	The REC domain mediated dimerization is critical for FleQ from Pseudomonas aeruginosa to function as a c-di-GMP receptor and flagella gene regulator. Journal of Structural Biology, 2015, 192, 1-13.	1.3	41
2686	Structural basis for the antipolymer activity of HbÎ¶2Î²s2trapped in a tense conformation. Journal of Molecular Structure, 2015, 1099, 99-107.	1.8	3
2687	A Structural Snapshot of Type II Pilus Formation in Streptococcus pneumoniae. Journal of Biological Chemistry, 2015, 290, 22581-22592.	1.6	17
2688	Loss of a Functionally and Structurally Distinct ld-Transpeptidase, LdtMt5, Compromises Cell Wall Integrity in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2015, 290, 25670-25685.	1.6	45
2689	Cryo-EM structures elucidate neutralizing mechanisms of anti-chikungunya human monoclonal antibodies with therapeutic activity. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13898-13903.	3.3	50
2690	Structure of the Ergothioneineâ€Biosynthesis Amidohydrolase EgtC. ChemBioChem, 2015, 16, 1490-1496.	1.3	32
2691	Binding of undamaged double stranded DNA to vaccinia virus uracil-DNA Glycosylase. BMC Structural Biology, 2015, 15, 10.	2.3	8
2692	Structural basis for catalytic activation by the human ZNF451 SUMO E3 ligase. Nature Structural and Molecular Biology, 2015, 22, 968-975.	3.6	101
2693	Structural analysis of an oxygen-regulated diguanylate cyclase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2158-2177.	2.5	40
2694	Structure and Sequence Analyses of Clustered Protocadherins Reveal Antiparallel Interactions that Mediate Homophilic Specificity. Structure, 2015, 23, 2087-2098.	1.6	65
2695	Structural Dissection of the Maltodextrin Disproportionation Cycle of the Arabidopsis Plastidial Disproportionating Enzyme 1 (DPE1). Journal of Biological Chemistry, 2015, 290, 29834-29853.	1.6	18
2696	Structure of the stationary phase survival protein YuiC from B.subtilis. BMC Structural Biology, 2015, 15, 12.	2.3	7
2697	Structure of Î±-carbonic anhydrase from the human pathogenHelicobacter pylori. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1005-1011.	0.4	8
2698	Efficient Cadmium Bioaccumulation by Displayed Hybrid CS3 Pili: Effect of Heavy Metal Binding Motif Insertion Site on Adsorption Capacity and Selectivity. Applied Biochemistry and Biotechnology, 2015, 177, 1729-1741.	1.4	3
2699	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. Nature, 2015, 527, 114-117.	13.7	145
2700	Illustration of SID-IM-SID (surface-induced dissociation-ion mobility-SID) mass spectrometry: homo and hetero model protein complexes. Analyst, The, 2015, 140, 7012-7019.	1.7	18
2701	Crystal Structure of the Michaelis Complex between Tissue-type Plasminogen Activator and Plasminogen Activators Inhibitor-1. Journal of Biological Chemistry, 2015, 290, 25795-25804.	1.6	41
2702	Structural analysis of the KRIT1 ankyrin repeat and FERM domains reveals a conformationally stable ARDâ€"FERM interface. Journal of Structural Biology, 2015, 192, 449-456.	1.3	12

#	ARTICLE	IF	CITATIONS
2703	Structures of the<i>T.â€‰brucei</i>kRNA editing factor MRB1590 reveal unique RNA-binding pore motif contained within an ABC-ATPase fold. Nucleic Acids Research, 2015, 43, 7096-7109.	6.5	12
2704	Mechanisms of splicing-dependent trans-synaptic adhesion by PTPÎ´â€“IL1RAPL1/IL-1RAcP for synaptic differentiation. Nature Communications, 2015, 6, 6926.	5.8	54
2705	Structure and Evolution of the Archaeal Lipid Synthesis Enzyme sn-Glycerol-1-phosphate Dehydrogenase. Journal of Biological Chemistry, 2015, 290, 21690-21704.	1.6	15
2706	Exploring the heat-induced structural changes of Î²-lactoglobulin -linoleic acid complex by fluorescence spectroscopy and molecular modeling techniques. Journal of Food Science and Technology, 2015, 52, 8095-8103.	1.4	10
2707	A Structural View of Negative Regulation of the Toll-like Receptor-Mediated Inflammatory Pathway. Biophysical Journal, 2015, 109, 1214-1226.	0.2	62
2708	Structure of Rab11â€“FIP3â€“Rabin8 reveals simultaneous binding of FIP3 and Rabin8 effectors to Rab11. Nature Structural and Molecular Biology, 2015, 22, 695-702.	3.6	40
2709	Crystal structures of the PsbS protein essential for photoprotection in plants. Nature Structural and Molecular Biology, 2015, 22, 729-735.	3.6	125
2710	The Substrate-free and -bound Crystal Structures of the Duplicated Taurocyamine Kinase from the Human Parasite Schistosoma mansoni. Journal of Biological Chemistry, 2015, 290, 12951-12963.	1.6	9
2711	Crystal Structure of Barley Limit Dextrinase-Limit Dextrinase Inhibitor (LD-LDI) Complex Reveals Insights into Mechanism and Diversity of Cereal Type Inhibitors. Journal of Biological Chemistry, 2015, 290, 12614-12629.	1.6	21
2712	Functional and structural diversity in <scp>GH</scp>62 Î±â€<scp>L</scp>â€arabinofuranosidases from the thermophilic fungus <scp><i>S</i></scp><i>cytalidium thermophilum</i>. Microbial Biotechnology, 2015, 8, 419-433.	2.0	31
2713	Complete catalytic cycle of cofactor-independent phosphoglycerate mutase involves a spring-loaded mechanism. FEBS Journal, 2015, 282, 1097-1110.	2.2	8
2714	Structure of ATP synthase from <i>Paracoccus denitrificans</i> determined by X-ray crystallography at 4.0 Ã… resolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13231-13236.	3.3	131
2715	Crystal structure of the bacteriophage P2 integrase catalytic domain. FEBS Letters, 2015, 589, 3556-3563.	1.3	3
2716	Mechanism of eIF6 release from the nascent 60S ribosomal subunit. Nature Structural and Molecular Biology, 2015, 22, 914-919.	3.6	168
2717	Sperm Lysozyme-Like Protein 1 (SLLP1), an intra-acrosomal oolemmal-binding sperm protein, reveals filamentous organization in protein crystal form. Andrology, 2015, 3, 756-771.	1.9	9
2718	Complement Evasion Mediated by Enhancement of Captured Factor H: Implications for Protection of Self-Surfaces from Complement. Journal of Immunology, 2015, 195, 4986-4998.	0.4	58
2719	<i>MEIS2</i> involvement in cardiac development, cleft palate, and intellectual disability. American Journal of Medical Genetics, Part A, 2015, 167, 1142-1146.	0.7	48
2720	STACâ€"A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. Journal of Molecular Biology, 2015, 427, 3327-3339.	2.0	17

#	ARTICLE	IF	CITATIONS
2721	The structure of Erb1-Ytm1 complex reveals the functional importance of a high-affinity binding between two Î²-propellers during the assembly of large ribosomal subunits in eukaryotes. Nucleic Acids Research, 2015, 43, 11017-11030.	6.5	18
2722	Evidence for cooperative tandem binding of hnRNP C RRMs in mRNA processing. Rna, 2015, 21, 1931-1942.	1.6	29
2723	Structure of AcrHâ€"AopB Chaperone-Translocator Complex Reveals a Role for Membrane Hairpins in Type III Secretion System Translocon Assembly. Structure, 2015, 23, 2022-2031.	1.6	43
2724	Structure-guided residence time optimization of a dabigatran reversal agent. MAbs, 2015, 7, 871-880.	2.6	11
2725	Structure and binding properties of a cameloid nanobody raised against KDM5B. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1235-1241.	0.4	6
2726	Structural and functional evidence for membrane docking and disruption sites on phospholipase A₂-like proteins revealed by complexation with the inhibitor suramin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2066-2078.	2.5	25
2727	Structure of the HECT domain of human WWP2. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1251-1257.	0.4	17
2728	Structures of the Apo and FADâ€Bound Forms of 2â€Hydroxybiphenyl 3â€monooxygenase (HbpA) Locate Activity Hotspots Identified by Using Directed Evolution. ChemBioChem, 2015, 16, 968-976.	1.3	11
2729	Structural and functional studies of a metallo-Î²-lactamase unveil a new type of structurally encoded nickel-containing heterodinuclear site. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2054-2065.	2.5	3
2730	Cryo-EM structure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. Science, 2015, 350, 404-409.	6.0	347
2731	Structural and Functional Characterization of the Hazelnut Allergen Cor a 8. Journal of Agricultural and Food Chemistry, 2015, 63, 9150-9158.	2.4	33
2732	Gating machinery of InsP3R channels revealed by electron cryomicroscopy. Nature, 2015, 527, 336-341.	13.7	199
2733	Structural basis for drug-induced allosteric changes to human Î²-cardiac myosin motor activity. Nature Communications, 2015, 6, 7974.	5.8	94
2734	The structure of human SFPQ reveals a coiled-coil mediated polymer essential for functional aggregation in gene regulation. Nucleic Acids Research, 2015, 43, 3826-3840.	6.5	115
2735	Structural Modeling of GR Interactions with the SWI/SNF Chromatin Remodeling Complex and C/EBP. Biophysical Journal, 2015, 109, 1227-1239.	0.2	31
2736	The non-detergent sulfobetaine-201 acts as a pharmacological chaperone to promote folding and crystallization of the type II TGF-Î² receptor extracellular domain. Protein Expression and Purification, 2015, 115, 19-25.	0.6	5
2737	The soluble Y115Eâ€"Y117E variant of human glutaminyl cyclase is a valid target for X-ray and NMR screening of inhibitors against Alzheimer disease. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 986-992.	0.4	6
2738	Congenital Cataract-Causing Mutation G129C in Î³C-Crystallin Promotes the Accumulation of Two Distinct Unfolding Intermediates That Form Highly Toxic Aggregates. Journal of Molecular Biology, 2015, 427, 2765-2781.	2.0	31

#	ARTICLE	IF	CITATIONS
2739	Polyhedra structures and the evolution of the insect viruses. Journal of Structural Biology, 2015, 192, 88-99.	1.3	25
2740	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. Structure, 2015, 23, 1858-1865.	1.6	50
2741	Dimerization of elongator protein 1 is essential for Elongator complex assembly. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10697-10702.	3.3	41
2742	Crystal Structure of the Vaccinia Virus Uracil-DNA Glycosylase in Complex with DNA. Journal of Biological Chemistry, 2015, 290, 17923-17934.	1.6	24
2743	<i>In Vivo</i> Formation of the Protein Disulfide Bond That Enhances the Thermostability of Diphosphomevalonate Decarboxylase, an Intracellular Enzyme from the Hyperthermophilic Archaeon Sulfolobus solfataricus. Journal of Bacteriology, 2015, 197, 3463-3471.	1.0	4
2744	Structural and biophysical characterization of the Î±-carbonic anhydrase from the gammaproteobacterium<i>Thiomicrospira crunogena</i>XCL-2: insights into engineering thermostable enzymes for CO₂sequestration. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1745-1756.	2.5	16
2745	The crystal structure of the thiocyanate-forming protein from Thlaspi arvense, a kelch protein involved in glucosinolate breakdown. Plant Molecular Biology, 2015, 89, 67-81.	2.0	17
2746	Structural and biochemical characterization of GTP cyclohydrolase II from Helicobacter pylori reveals its redox dependent catalytic activity. Journal of Structural Biology, 2015, 192, 100-115.	1.3	10
2747	Architecture of the synaptotagminâ€“SNARE machinery for neuronal exocytosis. Nature, 2015, 525, 62-67.	13.7	268
2748	Identification of a functional hotspot on ubiquitin required for stimulation of methyltransferase activity on chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10365-10370.	3.3	44
2749	Neuronal Calcium Sensor-1 Binds the D2 Dopamine Receptor and G-protein-coupled Receptor Kinase 1 (GRK1) Peptides Using Different Modes of Interactions. Journal of Biological Chemistry, 2015, 290, 18744-18756.	1.6	45
2750	Exploring Multimodularity in Plant Cell Wall Deconstruction. Journal of Biological Chemistry, 2015, 290, 17116-17130.	1.6	19
2751	The Landscape of Intertwined Associations in Homooligomeric Proteins. Biophysical Journal, 2015, 109, 1087-1100.	0.2	17
2752	Distinguishing Loss of Structure from Subunit Dissociation for Protein Complexes with Variable Temperature Ion Mobility Mass Spectrometry. Analytical Chemistry, 2015, 87, 6271-6279.	3.2	35
2753	On the predictability of the orientation of protein domains joined by a spanning alpha-helical linker. Protein Engineering, Design and Selection, 2015, 28, 491-500.	1.0	23
2754	IChemPIC: A Random Forest Classifier of Biological and Crystallographic Proteinâ€“Protein Interfaces. Journal of Chemical Information and Modeling, 2015, 55, 2005-2014.	2.5	26
2755	Structural Characterization of Bardet-Biedl Syndrome 9 Protein (BBS9). Journal of Biological Chemistry, 2015, 290, 19569-19583.	1.6	19
2756	Structural Basis for the ATP-dependent Configuration of Adenylation Active Site in Bacillus subtilis o-Succinylbenzoyl-CoA Synthetase. Journal of Biological Chemistry, 2015, 290, 23971-23983.	1.6	13

#	ARTICLE	IF	CITATIONS
2757	YehZYXW of <i>Escherichia coli</i> Is a Low-Affinity, Non-Osmoregulatory Betaine-Specific ABC Transporter. Biochemistry, 2015, 54, 5735-5747.	1.2	25
2758	Crystal Structure of Xanthomonas AvrRxo1-ORF1, a Type III Effector with a Polynucleotide Kinase Domain, and Its Interactor AvrRxo1-ORF2. Structure, 2015, 23, 1900-1909.	1.6	27
2759	Mechanistic Implications of the Unique Structural Features and Dimerization of the Cytoplasmic Domain of the <i>Pseudomonas</i> Sigma Regulator, PupR. Biochemistry, 2015, 54, 5867-5877.	1.2	6
2760	Allosteric activation of apicomplexan calcium-dependent protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4975-84.	3.3	51
2761	Structural basis for substrate recognition and processive cleavage mechanisms of the trimeric exonuclease PhoExo I. Nucleic Acids Research, 2015, 43, 7122-7136.	6.5	7
2762	Structures of plasmepsin II from<i>Plasmodium falciparum</i>in complex with two hydroxyethylamine-based inhibitors. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1531-1539.	0.4	14
2763	An extended dsRBD is required for post-transcriptional modification in human tRNAs. Nucleic Acids Research, 2015, 43, 9446-9456.	6.5	18
2764	SdsA polymorph isolation and improvement of their crystal quality using nonconventional crystallization techniques. Journal of Applied Crystallography, 2015, 48, 1551-1559.	1.9	5
2765	Structure of Spo0M, a sporulation-control protein fromBacillus subtilis. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1488-1497.	0.4	3
2766	Crystal structure of syndesmos and its interaction with Syndecan-4 proteoglycan. Biochemical and Biophysical Research Communications, 2015, 463, 762-767.	1.0	7
2767	A model for non-obligate oligomer formation in protein aggregration. Biochemical and Biophysical Research Communications, 2015, 465, 523-527.	1.0	5
2768	Transmembrane Complexes of DAP12 Crystallized in Lipid Membranes Provide Insights into Control of Oligomerization in Immunoreceptor Assembly. Cell Reports, 2015, 11, 1184-1192.	2.9	20
2769	Quaternary structure of <i>Dioclea grandiflora</i> lectin assessed by equilibrium sedimentation and crystallographic analysis of recombinant mutants. FEBS Letters, 2015, 589, 2290-2296.	1.3	9
2770	Structures of the Ultra-High-Affinity Proteinâ€"Protein Complexes of Pyocins S2 and AP41 and Their Cognate Immunity Proteins from Pseudomonas aeruginosa. Journal of Molecular Biology, 2015, 427, 2852-2866.	2.0	25
2771	A chimeric prokaryotic pentameric ligandâ€"gated channel reveals distinct pathways of activation. Journal of General Physiology, 2015, 146, 323-340.	0.9	14
2772	Translation elongation factor eEF1A1 is a novel partner of a multifunctional protein Sgt1. Biochimie, 2015, 119, 137-145.	1.3	13
2773	Identification of Noncompetitive Inhibitors of Cytosolic 5â€²-Nucleotidase II Using a Fragment-Based Approach. Journal of Medicinal Chemistry, 2015, 58, 9680-9696.	2.9	18
2774	Mechanistic basis of Nek7 activation through Nek9 binding and induced dimerization. Nature Communications, 2015, 6, 8771.	5.8	43

#	Article	IF	Citations
2775	Hen Eggâ€White Lysozyme Crystallisation: Protein Stacking and Structure Stability Enhanced by a Tellurium(VI)â€Centred Polyoxotungstate. ChemBioChem, 2015, 16, 233-241.	1.3	72
2776	Structure of the F-actinâ€"tropomyosin complex. Nature, 2015, 519, 114-117.	13.7	321
2777	Computational Electrostatics for Biological Applications. , 2015, , .		1
2778	Crystal structure of <scp><i>B</i></scp><i>acillus anthracis</i> virulence regulator <scp>AtxA</scp> and effects of phosphorylated histidines on multimerization and activity. Molecular Microbiology, 2015, 95, 426-441.	1.2	32
2779	Catalytic features and crystal structure of a tau class glutathione transferase from Glycine max specifically upregulated in response to soybean mosaic virus infections. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 166-177.	1.1	35
2780	Room temperature crystal structure of the fast switching M159T mutant of the fluorescent protein dronpa. Proteins: Structure, Function and Bioinformatics, 2015, 83, 397-402.	1.5	8
2781	Structures of citrate synthase and malate dehydrogenase of <scp><i>M</i></scp><i>ycobacterium tuberculosis</i>. Proteins: Structure, Function and Bioinformatics, 2015, 83, 389-394.	1.5	24
2782	Structural Basis of the Proteolytic and Chaperone Activity of Chlamydia trachomatis CT441. Journal of Bacteriology, 2015, 197, 211-218.	1.0	9
2783	Structural Flexibility of a Conserved Antigenic Region in Hepatitis C Virus Glycoprotein E2 Recognized by Broadly Neutralizing Antibodies. Journal of Virology, 2015, 89, 2170-2181.	1.5	96
2784	Structural and Functional Divergence of the Aldolase Fold in Toxoplasma gondii. Journal of Molecular Biology, 2015, 427, 840-852.	2.0	11
2785	Structural templates for comparative protein docking. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1563-1570.	1.5	25
2786	Crystal Structure of Snake Venom Acetylcholinesterase in Complex with Inhibitory Antibody Fragment Fab410 Bound at the Peripheral Site. Journal of Biological Chemistry, 2015, 290, 1522-1535.	1.6	20
2787	CRLI induces vascular smooth muscle relaxation and suggests a dual mechanism of eNOS activation by legume lectins via muscarinic receptors and shear stress. Archives of Biochemistry and Biophysics, 2015, 565, 32-39.	1.4	10
2788	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. Autophagy, 2015, 11, 75-87.	4.3	59
2789	Adeno-Associated Virus Serotype 1 (AAV1)- and AAV5-Antibody Complex Structures Reveal Evolutionary Commonalities in Parvovirus Antigenic Reactivity. Journal of Virology, 2015, 89, 1794-1808.	1.5	64
2790	Biochemical Roles of Eukaryotic Cell Surface Macromolecules. Advances in Experimental Medicine and Biology, 2015, , .	0.8	4
2791	Exploring alternate states and oligomerization preferences of coiledâ€coils by <i>de novo</i> structure modeling. Proteins: Structure, Function and Bioinformatics, 2015, 83, 235-247.	1.5	22
2792	Structural Details of Light Activation of the LOV2-based Photoswitch PA-Rac1. ACS Chemical Biology, 2015, 10, 502-509.	1.6	20

#	ARTICLE	IF	CITATIONS
2793	Bioinformatic Analysis of GJB2 Gene Missense Mutations. Cell Biochemistry and Biophysics, 2015, 71, 1623-1642.	0.9	16
2794	Insights into the potential function and membrane organization of the <scp>TP</scp>0435 (<scp>T</scp>p17) lipoprotein from <scp><i>T</i></scp><i>reponema pallidum</i> derived from structural and biophysical analyses. Protein Science, 2015, 24, 11-19.	3.1	15
2795	The Megavirus Chilensis Cu,Zn-Superoxide Dismutase: the First Viral Structure of a Typical Cellular Copper Chaperone-Independent Hyperstable Dimeric Enzyme. Journal of Virology, 2015, 89, 824-832.	1.5	27
2796	Structural insight into the conformational change of alcohol dehydrogenase from Arabidopsis thaliana L. during coenzyme binding. Biochimie, 2015, 108, 33-39.	1.3	15
2797	Thermal green protein, an extremely stable, nonaggregating fluorescent protein created by structureâ€guided surface engineering. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1225-1237.	1.5	18
2798	The multifaceted subunit interfaces of ionotropic glutamate receptors. Journal of Physiology, 2015, 593, 73-81.	1.3	10
2799	Engineering Bacterial Microcompartment Shells: Chimeric Shell Proteins and Chimeric Carboxysome Shells. ACS Synthetic Biology, 2015, 4, 444-453.	1.9	88
2800	Cloning, expression, purification, crystallization and X-ray diffraction analysis of dihydrodipicolinate synthase from the human pathogenic bacteriumBartonella henselaestrain Houston-1 at 2.1â€…Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 2-9.	0.4	5
2801	Crystal Structure of the N-Terminal RNA Recognition Motif of mRNA Decay Regulator AUF1. BioMed Research International, 2016, 2016, 1-9.	0.9	6
2802	PICI: A web server with a multi-parametric algorithm for identifying interaction sites within protein complexes. Bioinformation, 2016, 12, 78-81.	0.2	4
2803	Paulistineâ€"The Functional Duality of a Wasp Venom Peptide Toxin. Toxins, 2016, 8, 61.	1.5	5
2804	Structure and Function of the TIR Domain from the Grape NLR Protein RPV1. Frontiers in Plant Science, 2016, 7, 1850.	1.7	41
2805	Identification of Biomarkers for Resistance to Fusarium oxysporum f. sp. cubense Infection and in Silico Studies in Musa paradisiaca Cultivar Puttabale through Proteomic Approach. Proteomes, 2016, 4, 9.	1.7	7
2806	The structure and dynamics of secretory component and its interactions with polymeric immunoglobulins. ELife, 2016, 5, .	2.8	86
2807	Protein Structure and Folding. , 2016, , 47-48.		0
2808	Structural determinants of adhesion by Protocadherin-19 and implications for its role in epilepsy. ELife, 2016, 5, .	2.8	70
2809	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. BioMed Research International, 2016, 2016, 1-14.	0.9	7
2810	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. ELife, 2016, 5, .	2.8	19

#	Article	IF	Citations
2811	Structural basis for germline antibody recognition of HIV-1 immunogens. ELife, 2016, 5, .	2.8	68
2812	Genomic and expression analyses of Tursiops truncatus T cell receptor gamma (TRG) and alpha/delta (TRA/TRD) loci reveal a similar basic public Î³Î´ repertoire in dolphin and human. BMC Genomics, 2016, 17, 634.	1.2	32
2813	Structural snapshots of Xer recombination reveal activation by synaptic complex remodeling and DNA bending. ELife, 2016, 5, .	2.8	15
2814	Structure and Interactions of a Dimeric Variant of sHIP, a Novel Virulence Determinant of Streptococcus pyogenes. Frontiers in Microbiology, 2016, 7, 95.	1.5	0
2815	The Crystal Structure of the C-Terminal Domain of the Salmonella enterica PduO Protein: An Old Fold with a New Heme-Binding Mode. Frontiers in Microbiology, 2016, 7, 1010.	1.5	8
2816	Homology-Based Modeling of Universal Stress Protein from Listeria innocua Up-Regulated under Acid Stress Conditions. Frontiers in Microbiology, 2016, 7, 1998.	1.5	21
2817	Effects of a Mutation in the HSPE1 Gene Encoding the Mitochondrial Co-chaperonin HSP10 and Its Potential Association with a Neurological and Developmental Disorder. Frontiers in Molecular Biosciences, 2016, 3, 65.	1.6	38
2818	Structural Characterization of the Avidin Interactions with Fluorescent Pyrene-Conjugates: 1-Biotinylpyrene and 1-Desthiobiotinylpyrene. Molecules, 2016, 21, 1270.	1.7	7
2819	Crystal structure and DNA binding activity of a PadR family transcription regulator from hypervirulent Clostridium difficile R20291. BMC Microbiology, 2016, 16, 231.	1.3	13
2820	Identification of internalin-A-like virulent proteins in Leishmania donovani. Parasites and Vectors, 2016, 9, 557.	1.0	5
2821	Discovery and Characterization of a Thermostable and Highly Halotolerant GH5 Cellulase from an Icelandic Hot Spring Isolate. PLoS ONE, 2016, 11, e0146454.	1.1	61
2822	Deciphering Dimerization Modes of PAS Domains: Computational and Experimental Analyses of the AhR:ARNT Complex Reveal New Insights Into the Mechanisms of AhR Transformation. PLoS Computational Biology, 2016, 12, e1004981.	1.5	28
2823	Cholesterol Corrects Altered Conformation of MHC-II Protein in Leishmania donovani Infected Macrophages: Implication in Therapy. PLoS Neglected Tropical Diseases, 2016, 10, e0004710.	1.3	25
2824	Functional and Structural Analysis of a Î²-Glucosidase Involved in Î²-1,2-Glucan Metabolism in Listeria innocua. PLoS ONE, 2016, 11, e0148870.	1.1	36
2825	Crystal Structure of Alcohol Oxidase from Pichia pastoris. PLoS ONE, 2016, 11, e0149846.	1.1	39
2826	Structure-Based Analysis Reveals Cancer Missense Mutations Target Protein Interaction Interfaces. PLoS ONE, 2016, 11, e0152929.	1.1	80
2827	Crystal Structure of the FERM-SH2 Module of Human Jak2. PLoS ONE, 2016, 11, e0156218.	1.1	28
2828	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. PLoS ONE, 2016, 11, e0157070.	1.1	8

#	Article	IF	Citations
2829	Bending-Twisting Motions and Main Interactions in Nucleoplasmin Nuclear Import. PLoS ONE, 2016, 11, e0157162.	1.1	3
2830	The Panitumumab EGFR Complex Reveals a Binding Mechanism That Overcomes Cetuximab Induced Resistance. PLoS ONE, 2016, 11, e0163366.	1.1	55
2831	Crystal Structure of the Escherichia coli Fic Toxin-Like Protein in Complex with Its Cognate Antitoxin. PLoS ONE, 2016, 11, e0163654.	1.1	6
2832	The Structure of Treponema pallidum Tp0624 Reveals a Modular Assembly of Divergently Functionalized and Previously Uncharacterized Domains. PLoS ONE, 2016, 11, e0166274.	1.1	10
2833	Introducing a Clustering Step in a Consensus Approach for the Scoring of Protein-Protein Docking Models. PLoS ONE, 2016, 11, e0166460.	1.1	20
2834	Crystal Structure and Pyridoxal 5-Phosphate Binding Property of Lysine Decarboxylase from Selenomonas ruminantium. PLoS ONE, 2016, 11, e0166667.	1.1	15
2835	Using the Amino Acid Network to Modulate the Hydrolytic Activity of Î²-Glycosidases. PLoS ONE, 2016, 11, e0167978.	1.1	14
2836	Structural Based Analyses of the JC Virus T-Antigen F258L Mutant Provides Evidence for DNA Dependent Conformational Changes in the C-Termini of Polyomavirus Origin Binding Domains. PLoS Pathogens, 2016, 12, e1005362.	2.1	7
2837	Dengue Virus Nonstructural Protein 5 (NS5) Assembles into a Dimer with a Unique Methyltransferase and Polymerase Interface. PLoS Pathogens, 2016, 12, e1005451.	2.1	96
2838	Immunosuppressive Yersinia Effector YopM Binds DEAD Box Helicase DDX3 to Control Ribosomal S6 Kinase in the Nucleus of Host Cells. PLoS Pathogens, 2016, 12, e1005660.	2.1	31
2839	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. PLoS Pathogens, 2016, 12, e1005815.	2.1	104
2840	Ubiquitin-Dependent Modification of Skeletal Muscle by the Parasitic Nematode, Trichinella spiralis. PLoS Pathogens, 2016, 12, e1005977.	2.1	24
2841	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. PLoS Pathogens, 2016, 12, e1006079.	2.1	19
2842	Crystal Structure of Hyp-1, a Hypericum perforatum PR-10 Protein, in Complex with Melatonin. Frontiers in Plant Science, 2016, 7, 668.	1.7	35
2843	In-Silico Trials for Glucose Control in Hospitalized Patients with Type 2 Diabetes. Journal of Korean Medical Science, 2016, 31, 231.	1.1	2
2844	Blue light-induced LOV domain dimerization enhances the affinity of Aureochrome 1a for its target DNA sequence. ELife, 2016, 5, e11860.	2.8	76
2845	A single loop is essential for the octamerization of vanillyl alcohol oxidase. FEBS Journal, 2016, 283, 2546-2559.	2.2	13
2846	New Insights into Human 17Î²-Hydroxysteroid Dehydrogenase Type 14: First Crystal Structures in Complex with a Steroidal Ligand and with a Potent Nonsteroidal Inhibitor. Journal of Medicinal Chemistry, 2016, 59, 6961-6967.	2.9	12

#	Article	IF	Citations
2847	<i>Campylobacter jejuni</i> adenosine triphosphate phosphoribosyltransferase is an active hexamer that is allosterically controlled by the twisting of a regulatory tail. Protein Science, 2016, 25, 1492-1506.	3.1	15
2848	Exploring the unbinding of<i>L</i><i>eishmania</i>(<i>L</i>.)<i>amazonensis</i>CPB derived-epitopes from H2 MHC class I proteins. Proteins: Structure, Function and Bioinformatics, 2016, 84, 473-487.	1.5	14
2849	Biological function derived from predicted structures in CASP11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 370-391.	1.5	9
2850	Hybrid Structure of a Dynamic Single-Chain Carboxylase from Deinococcus radiodurans. Structure, 2016, 24, 1227-1236.	1.6	3
2851	The Structure of LiuC, a 3â€Hydroxyâ€3â€Methylglutaconyl CoA Dehydratase Involved in Isovalerylâ€CoA Biosynthesis in <i>Myxococcus xanthus</i>, Reveals Insights into Specificity and Catalysis. ChemBioChem, 2016, 17, 1658-1664.	1.3	9
2852	A Î²-Alanine Catabolism Pathway Containing a Highly Promiscuous Ï‰-Transaminase in the 12-Aminododecanate-Degrading Pseudomonas sp. Strain AAC. Applied and Environmental Microbiology, 2016, 82, 3846-3856.	1.4	21
2853	Crystal structures of the transpeptidase domain of the Mycobacterium tuberculosis penicillinâ€binding protein PonA1 reveal potential mechanisms of antibiotic resistance. FEBS Journal, 2016, 283, 2206-2218.	2.2	18
2854	Structure of the bacterial cell division determinant GpsB and its interaction with penicillinâ€binding proteins. Molecular Microbiology, 2016, 99, 978-998.	1.2	50
2855	Artificial domain duplication replicates evolutionary history of ketolâ€acid reductoisomerases. Protein Science, 2016, 25, 1241-1248.	3.1	4
2856	The SCP2-thiolase-like protein (SLP) of<i>Trypanosoma brucei</i>is an enzyme involved in lipid metabolism. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1075-1096.	1.5	5
2857	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	1.5	148
2858	SH3-like motif-containing C-terminal domain of staphylococcal teichoic acid transporter suggests possible function. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1328-1332.	1.5	5
2859	X-ray structures of the Pseudomonas cichorii D-tagatose 3-epimerase mutant form C66S recognizing deoxy sugars as substrates. Applied Microbiology and Biotechnology, 2016, 100, 10403-10415.	1.7	11
2860	Crystal structure of a putative exo-Î²-1,3-galactanase from<i>Bifidobacterium bifidum</i>S17. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 288-293.	0.4	3
2861	The extended structure of the periplasmic region of CdsD, a structural protein of the type III secretion system of <i>Chlamydia trachomatis</i>. Protein Science, 2016, 25, 987-998.	3.1	2
2862	Structural and functional studies of a large winged Zâ€<scp>DNA</scp>â€binding domain of <i>Danio rerio</i> protein kinase <scp>PKZ</scp>. FEBS Letters, 2016, 590, 2275-2285.	1.3	20
2863	Structural basis of substrate specificity in porcine <scp>RN</scp>ase 4. FEBS Journal, 2016, 283, 912-928.	2.2	6
2864	Elucidation of the molecular mechanisms of two nanobodies that inhibit thrombinâ€activatable fibrinolysis inhibitor activation and activated thrombinâ€activatable fibrinolysis inhibitor activity. Journal of Thrombosis and Haemostasis, 2016, 14, 1629-1638.	1.9	17

#	ARTICLE	IF	CITATIONS
2865	Structural, Functional, and Immunological Characterization of Profilin Panallergens Amb a 8, Art v 4, and Bet v 2. Journal of Biological Chemistry, 2016, 291, 15447-15459.	1.6	32
2866	Structural basis of thiol-based regulation of formaldehyde detoxification in<i>H. influenzae</i>by a MerR regulator with no sensor region. Nucleic Acids Research, 2016, 44, 6981-6993.	6.5	9
2867	Structural basis for dimer formation of the <scp>CRISPR</scp>â€associated protein Csm2 of <i>Thermotoga maritima</i>. FEBS Journal, 2016, 283, 694-703.	2.2	6
2868	Structure of AmtR, the global nitrogen regulator of <i>Corynebacterium glutamicum</i>, in free and <scp>DNA</scp>â€bound forms. FEBS Journal, 2016, 283, 1039-1059.	2.2	15
2869	CoDNaS 2.0: a comprehensive database of protein conformational diversity in the native state. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw038.	1.4	60
2870	Structural and histone binding ability characterization of the ARB2 domain of a histone deacetylase Hda1 from Saccharomyces cerevisiae. Scientific Reports, 2016, 6, 33905.	1.6	7
2871	Metal-coupled folding as the driving force for the extreme stability of Rad50 zinc hook dimer assembly. Scientific Reports, 2016, 6, 36346.	1.6	33
2872	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. Current Pharmaceutical Design, 2016, 22, 1-1.	0.9	2
2873	Identification, Characterization and X-ray Crystallographic Analysis of a Novel Type of Mannose-Specific Lectin CGL1 from the Pacific Oyster Crassostrea gigas. Scientific Reports, 2016, 6, 29135.	1.6	41
2874	Biochemical and Structural Analysis of a Novel Esterase from Caulobacter crescentus related to Penicillin-Binding Protein (PBP). Scientific Reports, 2016, 6, 37978.	1.6	16
2875	Structure of the host-recognition device of Staphylococcus aureus phage Ï•11. Scientific Reports, 2016, 6, 27581.	1.6	42
2876	Structural Characterization of H1N1 Nucleoprotein-Nucleozin Binding Sites. Scientific Reports, 2016, 6, 29684.	1.6	16
2877	The N14 anti-afamin antibody Fab: a rare VL1 CDR glycosylation, crystallographic re-sequencing, molecular plasticity and conservativeversusenthusiastic modelling. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1267-1280.	1.1	11
2878	Structural insights into the LCIB protein family reveals a new group of Î²-carbonic anhydrases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14716-14721.	3.3	61
2879	Structural analysis of the bright monomeric yellow-green fluorescent protein mNeonGreen obtained by directed evolution. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1298-1307.	1.1	41
2880	Discovery and structural characterisation of new fold type IV-transaminases exemplify the diversity of this enzyme fold. Scientific Reports, 2016, 6, 38183.	1.6	36
2881	Human antibody 3E1 targets the HA stem region of H1N1 and H5N6 influenza A viruses. Nature Communications, 2016, 7, 13577.	5.8	31
2882	ProtLID, a Residue-Based Pharmacophore Approach to Identify Cognate Protein Ligands in the Immunoglobulin Superfamily. Structure, 2016, 24, 2217-2226.	1.6	10

#	Article	IF	Citations
2883	<i>Neisseria meningitidis</i> factor H-binding protein bound to monoclonal antibody JAR5: implications for antibody synergy. Biochemical Journal, 2016, 473, 4699-4713.	1.7	21
2884	Regulators of complement activity mediate inhibitory mechanisms through a common C3bâ€binding mode. EMBO Journal, 2016, 35, 1133-1149.	3.5	123
2885	Construction of a hybrid Î²-hexosaminidase subunit capable of forming stable homodimers that hydrolyze GM2 ganglioside in vivo. Molecular Therapy - Methods and Clinical Development, 2016, 3, 15057.	1.8	39
2886	Crystal structures and inhibition of Trypanosoma brucei hypoxanthineâ€“guanine phosphoribosyltransferase. Scientific Reports, 2016, 6, 35894.	1.6	15
2887	Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD. BMC Biology, 2016, 14, 82.	1.7	26
2888	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. Scientific Reports, 2016, 6, 20915.	1.6	11
2889	Facilitating model reconstruction for single-particle scattering using small-angle X-ray scattering methods. Journal of Applied Crystallography, 2016, 49, 665-671.	1.9	4
2890	Crystal structure of AibC, a reductase involved in alternative<i>de novo</i>isovaleryl coenzyme A biosynthesis in<i>Myxococcus xanthus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 652-658.	0.4	3
2891	Biochemical and structural characterization of<i>Klebsiella pneumoniae</i>oxamate amidohydrolase in the uric acid degradation pathway. Acta Crystallographica Section D: Structural Biology, 2016, 72, 808-816.	1.1	3
2892	Structure of the RBM7â€“ZCCHC8 core of the NEXT complex reveals connections to splicing factors. Nature Communications, 2016, 7, 13573.	5.8	38
2893	Structure of the Dictyostelium Myosin-II Heavy Chain Kinase A (MHCK-A) Î±-kinase domain apoenzyme reveals a novel autoinhibited conformation. Scientific Reports, 2016, 6, 26634.	1.6	9
2894	A rationally engineered yeast pyruvyltransferase Pvg1p introduces sialylation-like properties in neo-human-type complex oligosaccharide. Scientific Reports, 2016, 6, 26349.	1.6	16
2895	The structure, kinetics and interactions of the Î²-carboxysomal Î²-carbonic anhydrase, CcaA. Biochemical Journal, 2016, 473, 4559-4572.	1.7	51
2896	A robust cosolvent-compatible halohydrin dehalogenase by computational library design. Protein Engineering, Design and Selection, 2017, 30, 173-187.	1.0	23
2897	Identification of an ATP-controlled allosteric switch that controls actin filament nucleation by Arp2/3 complex. Nature Communications, 2016, 7, 12226.	5.8	32
2898	Tetrameric structure of the restriction DNA glycosylase R.PabI in complex with nonspecific double-stranded DNA. Scientific Reports, 2016, 6, 35197.	1.6	8
2899	Biochemical and structural characterization of a novel halotolerant cellulase from soil metagenome. Scientific Reports, 2016, 6, 39634.	1.6	67
2900	The BR domain of PsrP interacts with extracellular DNA to promote bacterial aggregation; structural insights into pneumococcal biofilm formation. Scientific Reports, 2016, 6, 32371.	1.6	27

#	ARTICLE	IF	CITATIONS
2901	Toxin inhibition inC. crescentusVapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. Nucleic Acids Research, 2016, 45, gkw1266.	6.5	13
2902	Crystal structure of MytiLec, a galactose-binding lectin from the mussel Mytilus galloprovincialis with cytotoxicity against certain cancer cell types. Scientific Reports, 2016, 6, 28344.	1.6	39
2903	Molecular basis of cobalamin-dependent RNA modification. Nucleic Acids Research, 2016, 44, gkw806.	6.5	29
2904	Dimerization of the fungal defense lectin CCL2 is essential for its toxicity against nematodes. Glycobiology, 2016, 27, 486-500.	1.3	17
2905	Structural and functional analysis of the solute-binding protein UspC from <i>Mycobacterium tuberculosis</i> that is specific for amino sugars. Open Biology, 2016, 6, 160105.	1.5	27
2906	X-ray structures of uridine phosphorylase from Vibrio cholerae in complexes with uridine, thymidine, uracil, thymine, and phosphate anion: Substrate specificity of bacterial uridine phosphorylases. Crystallography Reports, 2016, 61, 954-973.	0.1	4
2907	Characterization and 1.57â€…Ã… resolution structure of the key fire blight phosphatase AmsI from<i>Erwinia amylovora</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 903-910.	0.4	8
2908	Near-atomic-resolution cryo-EM analysis of the Salmonella T3S injectisome basal body. Nature, 2016, 540, 597-601.	13.7	127
2909	Structural basis of myelin-associated glycoprotein adhesion and signalling. Nature Communications, 2016, 7, 13584.	5.8	94
2910	The Antiviral Mechanism of an Influenza A Virus Nucleoprotein-Specific Single-Domain Antibody Fragment. MBio, 2016, 7, .	1.8	28
2911	Crystal structure of the toxin Msmeg_6760, the structural homolog ofMycobacterium tuberculosisRv2035, a novel type II toxin involved in the hypoxic response. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 863-869.	0.4	5
2912	Restriction endonuclease AgeI is a monomer which dimerizes to cleave DNA. Nucleic Acids Research, 2016, 45, gkw1310.	6.5	11
2913	Insight into Coenzyme A cofactor binding and the mechanism of acyl-transfer in an acylating aldehyde dehydrogenase from Clostridium phytofermentans. Scientific Reports, 2016, 6, 22108.	1.6	18
2914	Structural basis of the high thermal stability of the histone-like HU protein from the mollicute Spiroplasma melliferum KC3. Scientific Reports, 2016, 6, 36366.	1.6	23
2915	MET-activating Residues in the B-repeat of the Listeria monocytogenes Invasion Protein InlB. Journal of Biological Chemistry, 2016, 291, 25567-25577.	1.6	8
2916	A Structural Investigation into Oct4 Regulation by Orphan Nuclear Receptors, Germ Cell Nuclear Factor (GCNF), and Liver Receptor Homolog-1 (LRH-1). Journal of Molecular Biology, 2016, 428, 4981-4992.	2.0	18
2917	Revisiting the mechanism of coagulation factor XIII activation and regulation from a structure/functional perspective. Scientific Reports, 2016, 6, 30105.	1.6	28
2918	Structural analysis of a phosphonate hydroxylase with an access tunnel at the back of the active site. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 362-368.	0.4	4

#	Article	IF	Citations
2919	Two common structural motifs for TCR recognition by staphylococcal enterotoxins. Scientific Reports, 2016, 6, 25796.	1.6	12
2920	Crystal structure of fuculose aldolase from the Antarctic psychrophilic yeast<i>Glaciozyma antarctica</i>PI12. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 831-839.	0.4	7
2921	Homology modeling and molecular dynamics provide structural insights into tospovirus nucleoprotein. BMC Bioinformatics, 2016, 17, 489.	1.2	11
2922	Distribution of singleâ€nucleotide variants on proteinâ€"protein interaction sites and its relationship with minor allele frequency. Protein Science, 2016, 25, 316-321.	3.1	14
2923	Structural and Kinetic Characterization of the 4-Carboxy-2-hydroxymuconate Hydratase from the Gallate and Protocatechuate 4,5-Cleavage Pathways of Pseudomonas putida KT2440. Journal of Biological Chemistry, 2016, 291, 7669-7686.	1.6	16
2924	A hybrid method for proteinâ€"protein interface prediction. Protein Science, 2016, 25, 159-165.	3.1	37
2925	Crystallographic studies of the complex of human HINT1 protein with a non-hydrolyzable analog of Ap4A. International Journal of Biological Macromolecules, 2016, 87, 62-69.	3.6	9
2926	The 2.2â€Angstrom resolution crystal structure of the carboxyâ€terminal region of ataxinâ€3. FEBS Open Bio, 2016, 6, 168-178.	1.0	12
2927	Paring Down HIV Env: Design and Crystal Structure of a Stabilized Inner Domain of HIV-1 gp120 Displaying a Major ADCC Target of the A32 Region. Structure, 2016, 24, 697-709.	1.6	46
2928	Structure-Function Relationships in l-Amino Acid Deaminase, a Flavoprotein Belonging to a Novel Class of Biotechnologically Relevant Enzymes. Journal of Biological Chemistry, 2016, 291, 10457-10475.	1.6	46
2929	The Quaternary Structure of a Glycoside Hydrolase Dictates Specificity toward Î²-Glucans. Journal of Biological Chemistry, 2016, 291, 7183-7194.	1.6	13
2930	Crystal structure of FhuD at 1.6â€…Ã… resolution: a ferrichrome-binding protein from the animal and human pathogen<i>Staphylococcus pseudintermedius</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 214-219.	0.4	2
2931	Structural and kinetic studies on RosA, the enzyme catalysing the methylation of 8â€demethylâ€8â€aminoâ€<scp>d</scp>â€riboflavin to the antibiotic roseoflavin. FEBS Journal, 2016, 283, 1531-1549.	2.2	13
2932	A Disease-Causing Variant in PCNA Disrupts a Promiscuous Protein Binding Site. Journal of Molecular Biology, 2016, 428, 1023-1040.	2.0	18
2933	Crystallographic and CD probing of ligand-induced conformational changes in a plant PR-10 protein. Journal of Structural Biology, 2016, 193, 55-66.	1.3	19
2934	Towards the molecular mechanism of the integration of peroxisomal membrane proteins. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 863-869.	1.9	18
2935	The Crystal Structure of <i>Burkholderia cenocepacia</i> DfsA Provides Insights into Substrate Recognition and Quorum Sensing Fatty Acid Biosynthesis. Biochemistry, 2016, 55, 3241-3250.	1.2	8
2936	An extended loop in CE7 carbohydrate esterase family is dispensable for oligomerization but required for activity and thermostability. Journal of Structural Biology, 2016, 194, 434-445.	1.3	12

#	Article	IF	Citations
2937	Structural and Functional Characterization of the LPS Transporter LptDE from Gram-Negative Pathogens. Structure, 2016, 24, 965-976.	1.6	110
2938	Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352.	13.7	231
2939	Broadly neutralizing epitopes in the <i>Plasmodium vivax</i> vaccine candidate Duffy Binding Protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6277-6282.	3.3	92
2940	Structure of the Membrane-intrinsic Nitric Oxide Reductase from Roseobacter denitrificans. Biochemistry, 2016, 55, 3198-3203.	1.2	13
2941	Bacterial Î²-Kdo glycosyltransferases represent a new glycosyltransferase family (GT99). Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3120-9.	3.3	43
2942	Divergent Evolution of Nuclear Localization Signal Sequences in Herpesvirus Terminase Subunits. Journal of Biological Chemistry, 2016, 291, 11420-11433.	1.6	22
2943	Structural diversity in a human antibody germline library. MAbs, 2016, 8, 1045-1063.	2.6	51
2944	Structural insights into chaperone-activity enhancement by a K354E mutation in tomato acidic leucine aminopeptidase. Acta Crystallographica Section D: Structural Biology, 2016, 72, 694-702.	1.1	4
2945	Energetic Coupling between Ligand Binding and Dimerization in <i>Escherichia coli</i> Phosphoglycerate Mutase. Biochemistry, 2016, 55, 1711-1723.	1.2	6
2946	A structured interdomain linker directs self-polymerization of human uromodulin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1552-1557.	3.3	85
2947	Structure of the Regulator of G Protein Signaling 8 (RGS8)-GÎ±q Complex. Journal of Biological Chemistry, 2016, 291, 5138-5145.	1.6	31
2948	<i>Anabaena</i>sp. DyP-type peroxidase is a tetramer consisting of two asymmetric dimers. Proteins: Structure, Function and Bioinformatics, 2016, 84, 31-42.	1.5	14
2949	Stability strengths and weaknesses in protein structures detected by statistical potentials: Application to bovine seminal ribonuclease. Proteins: Structure, Function and Bioinformatics, 2016, 84, 143-158.	1.5	16
2950	Crystal structure analysis of C-phycoerythrin from marine cyanobacterium Phormidium sp. A09DM. Photosynthesis Research, 2016, 129, 17-28.	1.6	15
2951	<i>Burkholderia glumae</i> ToxA Is a Dual-Specificity Methyltransferase That Catalyzes the Last Two Steps of Toxoflavin Biosynthesis. Biochemistry, 2016, 55, 2748-2759.	1.2	13
2952	Predicting Proteinâ€"Protein Interactions from the Molecular to the Proteome Level. Chemical Reviews, 2016, 116, 4884-4909.	23.0	289
2953	Binding interface change and cryptic variation in the evolution of protein-protein interactions. BMC Evolutionary Biology, 2016, 16, 40.	3.2	7
2954	Fasciola hepatica calcium-binding protein FhCaBP2: structure of the dynein light chain-like domain. Parasitology Research, 2016, 115, 2879-2886.	0.6	7

#	ARTICLE	IF	CITATIONS
2955	Made to measure â€“ keeping Rho kinase at a distance. Small GTPases, 2016, 7, 82-92.	0.7	22
2956	Structural insight into the cooperation of chloroplast chaperonin subunits. BMC Biology, 2016, 14, 29.	1.7	21
2957	Structural Analysis of the Phenol-Responsive Sensory Domain of the Transcription Activator PoxR. Structure, 2016, 24, 624-630.	1.6	15
2958	Computational study of pH-dependent oligomerization and ligand binding in Alt a 1, a highly allergenic protein with a unique fold. Journal of Computer-Aided Molecular Design, 2016, 30, 365-379.	1.3	8
2959	Structural Basis for the Functional Coupling of the Alternative Splicing Factors Smu1 and RED. Structure, 2016, 24, 762-773.	1.6	25
2960	Structure of a thermostable methionine adenosyltransferase from Thermus thermophilus HB27 reveals a novel fold of the flexible loop. RSC Advances, 2016, 6, 41743-41750.	1.7	2
2961	Structural insight for substrate tolerance to 2-deoxyribose-5-phosphate aldolase from the pathogen Streptococcus suis. Journal of Microbiology, 2016, 54, 311-321.	1.3	6
2962	Dimerization of Bacterial Diaminopimelate Decarboxylase Is Essential for Catalysis. Journal of Biological Chemistry, 2016, 291, 9785-9795.	1.6	31
2963	Molecular basis of PRC1 targeting to Polycomb response elements by PhoRC. Genes and Development, 2016, 30, 1116-1127.	2.7	78
2964	Human Pyruvate Dehydrogenase Complex E2 and E3BP Core Subunits: New Models and Insights from Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2016, 120, 4399-4409.	1.2	14
2965	RRM domain of human RBM7: purification, crystallization and structure determination. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 397-402.	0.4	6
2966	Functional Evolution in Orthologous Cell-encoded RNA-dependent RNA Polymerases. Journal of Biological Chemistry, 2016, 291, 9295-9309.	1.6	13
2967	Crystal structures of a group II intron maturase reveal a missing link in spliceosome evolution. Nature Structural and Molecular Biology, 2016, 23, 558-565.	3.6	79
2968	Structural Studies of Medicago truncatula Histidinol Phosphate Phosphatase from Inositol Monophosphatase Superfamily Reveal Details of Penultimate Step of Histidine Biosynthesis in Plants. Journal of Biological Chemistry, 2016, 291, 9960-9973.	1.6	19
2969	Protein Structure Databases. Methods in Molecular Biology, 2016, 1415, 31-53.	0.4	3
2970	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. Methods in Molecular Biology, 2016, 1415, 91-105.	0.4	4
2971	Exploring the structure of glutamate racemase from <i>Mycobacterium tuberculosis</i> as a template for anti-mycobacterial drug discovery. Biochemical Journal, 2016, 473, 1267-1280.	1.7	17
2972	Noncanonical DNA-binding mode of repressor and its disassembly by antirepressor. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2480-8.	3.3	14

#	ARTICLE	IF	CITATIONS
2973	Structure-based design and confirmation of peptide ligands for neuronal polo-like kinase to promote neuroregeneration. Computational Biology and Chemistry, 2016, 61, 238-244.	1.1	2
2974	DARPin-Based Crystallization Chaperones Exploit Molecular Geometry as a Screening Dimension in Protein Crystallography. Journal of Molecular Biology, 2016, 428, 1574-1588.	2.0	30
2975	Divergent non-heme iron enzymes in the nogalamycin biosynthetic pathway. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5251-5256.	3.3	44
2976	A Novel Fic (Filamentation Induced by cAMP) Protein from Clostridium difficile Reveals an Inhibitory Motif-independent Adenylylation/AMPylation Mechanism. Journal of Biological Chemistry, 2016, 291, 13286-13300.	1.6	14
2977	Structure of the Full-Length Bacteriophytochrome from the Plant Pathogen Xanthomonas campestris Provides Clues to its Long-Range Signaling Mechanism. Journal of Molecular Biology, 2016, 428, 3702-3720.	2.0	73
2978	Conformational features of the Staphylococcus aureus AgrA-promoter interactions rationalize quorum-sensing triggered gene expression. Biochemistry and Biophysics Reports, 2016, 6, 124-134.	0.7	25
2979	A small protein inhibits proliferating cell nuclear antigen by breaking the DNA clamp. Nucleic Acids Research, 2016, 44, 6232-6241.	6.5	11
2980	Crystal structure of bile salt hydrolase from<i>Lactobacillus salivarius</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 376-381.	0.4	26
2981	Structures of type IV pilins from Thermus thermophilus demonstrate similarities with type II secretion system pseudopilins. Journal of Structural Biology, 2016, 196, 375-384.	1.3	12
2982	Adhesive Dimerization of Human P-Cadherin Catalyzed by a Chaperone-like Mechanism. Structure, 2016, 24, 1523-1536.	1.6	20
2983	Circulatory zinc transport is controlled by distinct interdomain sites on mammalian albumins. Chemical Science, 2016, 7, 6635-6648.	3.7	67
2984	Architecture of the Human Mitochondrial Iron-Sulfur Cluster Assembly Machinery. Journal of Biological Chemistry, 2016, 291, 21296-21321.	1.6	24
2985	Structural and Functional Studies of Pavine N-Methyltransferase from Thalictrum flavum Reveal Novel Insights into Substrate Recognition and Catalytic Mechanism. Journal of Biological Chemistry, 2016, 291, 23403-23415.	1.6	34
2986	The Structure of the Periplasmic Sensor Domain of the Histidine Kinase CusS Shows Unusual Metal Ion Coordination at the Dimeric Interface. Biochemistry, 2016, 55, 5296-5306.	1.2	27
2987	T-to-R switch of muscle fructose-1,6-bisphosphatase involves fundamental changes of secondary and quaternary structure. Acta Crystallographica Section D: Structural Biology, 2016, 72, 536-550.	1.1	25
2988	Specific Recognition of a Single-Stranded RNA Sequence by a Synthetic Antibody Fragment. Journal of Molecular Biology, 2016, 428, 4100-4114.	2.0	11
2989	PilN Binding Modulates the Structure and Binding Partners of the Pseudomonas aeruginosa Type IVa Pilus Protein PilM. Journal of Biological Chemistry, 2016, 291, 11003-11015.	1.6	53
2990	Structural evidence of intramolecular propeptide inhibition of the aspzincin metalloendopeptidase AsaP1. FEBS Letters, 2016, 590, 3280-3294.	1.3	3

#	ARTICLE	IF	CITATIONS
2991	Rv2074 is a novel F 420 H 2 â€dependent biliverdin reductase in Mycobacterium tuberculosis. Protein Science, 2016, 25, 1692-1709.	3.1	31
2992	WD40 domain of Apc1 is critical for the coactivator-induced allosteric transition that stimulates APC/C catalytic activity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10547-10552.	3.3	16
2993	The Sampling of Conformational Dynamics in Ambient-Temperature Crystal Structures of Arginine Kinase. Structure, 2016, 24, 1658-1667.	1.6	5
2994	Structures of a Nonribosomal Peptide Synthetase Module Bound to MbtH-like Proteins Support a Highly Dynamic Domain Architecture. Journal of Biological Chemistry, 2016, 291, 22559-22571.	1.6	97
2995	Structural Basis for Interactions Between Contactin Family Members and Protein-tyrosine Phosphatase Receptor Type G in Neural Tissues. Journal of Biological Chemistry, 2016, 291, 21335-21349.	1.6	32
2996	Structure and Mechanism of the Sphingopyxinâ€…I Lasso Peptide Isopeptidase. Angewandte Chemie - International Edition, 2016, 55, 12717-12721.	7.2	27
2997	Structure of AP205 Coat Protein Reveals Circular Permutation in ssRNA Bacteriophages. Journal of Molecular Biology, 2016, 428, 4267-4279.	2.0	45
2998	Structural characterization of the novel aminoglycoside phosphotransferase AphVIII from Streptomyces rimosus with enzymatic activity modulated by phosphorylation. Biochemical and Biophysical Research Communications, 2016, 477, 595-601.	1.0	9
2999	Structure of an Inward Proton-Transporting Anabaena Sensory Rhodopsin Mutant: Mechanistic Insights. Biophysical Journal, 2016, 111, 963-972.	0.2	14
3000	1,2-Propanediol Dehydration in Roseburia inulinivorans. Journal of Biological Chemistry, 2016, 291, 15515-15526.	1.6	24
3001	2.4â€…Ã… resolution crystal structure of human TRAP1_{NM}, the Hsp90 paralog in the mitochondrial matrix. Acta Crystallographica Section D: Structural Biology, 2016, 72, 904-911.	1.1	16
3002	Structural analysis of point mutations at the<i>Vaccinia virus</i>A20/D4 interface. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 687-691.	0.4	7
3003	Structure of the Single-lobe Myosin Light Chain C in Complex with the Light Chain-binding Domains of Myosin-1C Provides Insights into Divergent IQ Motif Recognition. Journal of Biological Chemistry, 2016, 291, 19607-19617.	1.6	10
3004	Actin-Induced Structure in the Beta-Thymosin Family of Intrinsically Disordered Proteins. Vitamins and Hormones, 2016, 102, 55-71.	0.7	7
3005	Combination of Whole Genome Sequencing, Linkage, and Functional Studies Implicates a Missense Mutation in Titin as a Cause of Autosomal Dominant Cardiomyopathy With Features of Left Ventricular Noncompaction. Circulation: Cardiovascular Genetics, 2016, 9, 426-435.	5.1	67
3007	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from Burkholderia pseudomallei. Journal of Biological Chemistry, 2016, 291, 19387-19400.	1.6	28
3008	Crystal structure of Î²1â†'6â€galactosidase from <i>Bifidobacterium bifidum</i> S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by Î±â€galactose. FEBS Journal, 2016, 283, 4097-4112.	2.2	22
3009	X-ray structure of the human Î±4Î²2 nicotinic receptor. Nature, 2016, 538, 411-415.	13.7	352

#	ARTICLE	IF	CITATIONS
3010	Enzymatic hydrolysis by transition-metal-dependent nucleophilic aromatic substitution. Nature Chemical Biology, 2016, 12, 1031-1036.	3.9	12
3011	Circumventing the stability-function trade-off in an engineered FN3 domain. Protein Engineering, Design and Selection, 2016, 29, 541-550.	1.0	17
3012	Wnt Signalosome Assembly by DEP Domain Swapping of Dishevelled. Molecular Cell, 2016, 64, 92-104.	4.5	125
3013	Effects of interface mutations on the dimerization of alanine glyoxylate aminotransferase and implications in the mistargeting of the pathogenic variants F152I and I244T. Biochimie, 2016, 131, 137-148.	1.3	17
3014	Protein Dynamics and Contact Topology Reveal Proteinâ€"DNA Binding Orientation. Journal of Chemical Theory and Computation, 2016, 12, 5269-5277.	2.3	9
3015	Structure of Escherichia coli Flavodiiron Nitric Oxide Reductase. Journal of Molecular Biology, 2016, 428, 4686-4707.	2.0	30
3016	Osteocalcin and Sex Hormone Binding Globulin Compete on a Specific Binding Site of GPRC6A. Endocrinology, 2016, 157, 4473-4486.	1.4	43
3017	Structure and Function of the RING Domains of RNF20 and RNF40, Dimeric E3 Ligases that Monoubiquitylate Histone H2B. Journal of Molecular Biology, 2016, 428, 4073-4086.	2.0	23
3018	The methanogenic CO ₂ reducing-and-fixing enzyme is bifunctional and contains 46 [4Fe-4S] clusters. Science, 2016, 354, 114-117.	6.0	124
3019	Structural similarities and differences in Hâ€<scp>NS</scp> family proteins revealed by the Nâ€terminal structure of TurB in <i>Pseudomonas putida </i><scp>KT</scp>2440. FEBS Letters, 2016, 590, 3583-3594.	1.3	12
3020	Processing of A-form ssDNA by cryptic RNase H fold exonuclease PF2046. Archives of Biochemistry and Biophysics, 2016, 606, 143-150.	1.4	1
3021	Molecular Architecture of SF3b and Structural Consequences of Its Cancer-Related Mutations. Molecular Cell, 2016, 64, 307-319.	4.5	197
3022	Cyclic Purine and Pyrimidine Nucleotides Bind to the HCN2 Ion Channel and Variably Promote C-Terminal Domain Interactions and Opening. Structure, 2016, 24, 1629-1642.	1.6	16
3023	Ubiquitin Ligase COP1 Controls Hepatic Fat Metabolism by Targeting ATGL for Degradation. Diabetes, 2016, 65, 3561-3572.	0.3	49
3024	Structure of the second Single Stranded DNA Binding protein (SSBb) from Mycobacterium smegmatis. Journal of Structural Biology, 2016, 196, 448-454.	1.3	6
3025	Common Evolutionary Origin of Procapsid Proteases, Phage Tail Tubes, and Tubes of Bacterial Type VI Secretion Systems. Structure, 2016, 24, 1928-1935.	1.6	33
3026	Structural exploration of acid sphingomyelinase at different physiological pH through molecular dynamics and docking studies. RSC Advances, 2016, 6, 74859-74873.	1.7	9
3027	Context matters: The importance of dimerization-induced conformation of the LukGH leukocidin of<i>Staphylococcus aureus</i>for the generation of neutralizing antibodies. MAbs, 2016, 8, 1347-1360.	2.6	44

#	ARTICLE	IF	CITATIONS
3028	Mechanism of arginine sensing by CASTOR1 upstream of mTORC1. Nature, 2016, 536, 229-233.	13.7	224
3029	The Structure and Catalytic Mechanism of <i>Sorghum bicolor</i> Caffeoyl-CoA <i>O</i>-Methyltransferase. Plant Physiology, 2016, 172, 78-92.	2.3	46
3030	Divergence in Ubiquitin Interaction and Catalysis among the Ubiquitin-Specific Protease Family Deubiquitinating Enzymes. Biochemistry, 2016, 55, 4708-4719.	1.2	15
3031	Crystal structure of the Epithiospecifier Protein, ESP from Arabidopsis thaliana provides insights into its product specificity. Biochemical and Biophysical Research Communications, 2016, 478, 746-751.	1.0	12
3032	Tankyrase Requires SAM Domain-Dependent Polymerization to Support Wnt-Î²-Catenin Signaling. Molecular Cell, 2016, 63, 498-513.	4.5	72
3033	Crystal structure analysis of phycocyanin from chromatically adapted Phormidium rubidum A09DM. RSC Advances, 2016, 6, 77898-77907.	1.7	11
3034	Crystal structures of spleen tyrosine kinase in complex with novel inhibitors: structural insights for design of anticancer drugs. FEBS Journal, 2016, 283, 3613-3625.	2.2	10
3035	The dopamine D2 receptor dimer and its interaction with homobivalent antagonists: homology modeling, docking and molecular dynamics. Journal of Molecular Modeling, 2016, 22, 203.	0.8	28
3036	Crystal structure of <i>Arabidopsis thaliana</i> calmodulin7 and insight into its mode of <scp>DNA</scp> binding. FEBS Letters, 2016, 590, 3029-3039.	1.3	25
3037	Ferroceneâ€“Biotin Conjugates: Synthesis, Structure, Cytotoxic Activity and Interaction with Avidin. ChemPlusChem, 2016, 81, 1191-1201.	1.3	9
3038	HU histone-like DNA-binding protein from Thermus thermophilus: structural and evolutionary analyses. Extremophiles, 2016, 20, 695-709.	0.9	21
3039	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Enediyne Antitumor Antibiotic C-1027 in <i>Streptomyces globisporus</i>. Biochemistry, 2016, 55, 5142-5154.	1.2	18
3040	Structures of the activator of <i>K. pneumonia</i> biofilm formation, MrkH, indicates PilZ domains involved in c-di-GMP and DNA binding. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10067-10072.	3.3	45
3041	Structural Insights into the M-Channel Proximal C-Terminus/Calmodulin Complex. Biochemistry, 2016, 55, 5353-5365.	1.2	26
3042	Two distinct mechanisms of transcriptional regulation by the redox sensor YodB. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5202-11.	3.3	19
3043	The Crystal Structures of the N-terminal Photosensory Core Module of Agrobacterium Phytochrome Agp1 as Parallel and Anti-parallel Dimers. Journal of Biological Chemistry, 2016, 291, 20674-20691.	1.6	41
3044	Dynamic phosphorylation of RelA on Ser42 and Ser45 in response to TNFÎ± stimulation regulates DNA binding and transcription. Open Biology, 2016, 6, 160055.	1.5	19
3045	Structure of an acetylating aldehyde dehydrogenase from the thermophilic ethanologen <i>Geobacillus thermoglucosidasius</i>. Protein Science, 2016, 25, 2045-2053.	3.1	7

#	ARTICLE	IF	CITATIONS
3046	Near-Atomic Resolution Structure of a Highly Neutralizing Fab Bound to Canine Parvovirus. Journal of Virology, 2016, 90, 9733-9742.	1.5	27
3047	Interaction mode between catalytic and regulatory subunits in glucosidase II involved in ER glycoprotein quality control. Protein Science, 2016, 25, 2095-2101.	3.1	16
3048	The Structure of the Antibiotic Deactivating, N-hydroxylating Rifampicin Monooxygenase. Journal of Biological Chemistry, 2016, 291, 21553-21562.	1.6	36
3049	Crystal structure of<i>Plasmodium falciparum</i>proplasmepsin IV: the plasticity of proplasmepsins. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 659-666.	0.4	4
3050	Crystal structure of a human neuronal nAChR extracellular domain in pentameric assembly: Ligand-bound Î±2 homopentamer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9635-9640.	3.3	51
3051	Structural and functional insights into the stationary-phase survival protein SurE, an important virulence factor ofBrucella abortus. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 386-396.	0.4	0
3052	Crystal structure of truncated aspartate transcarbamoylase fromPlasmodium falciparum. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 523-533.	0.4	12
3053	The Structure of a High-Affinity Kainate Receptor: GluK4 Ligand-Binding Domain Crystallized with Kainate. Structure, 2016, 24, 1582-1589.	1.6	10
3054	Discovery and Evaluation of PRL Trimer Disruptors for Novel Anticancer Agents. Methods in Molecular Biology, 2016, 1447, 121-138.	0.4	0
3055	Mouse MORC3 is a GHKL ATPase that localizes to H3K4me3 marked chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5108-16.	3.3	41
3056	Structureâ€"Activity Studies of Î²-Hairpin Peptide Inhibitors of the Plasmodium falciparum AMA1â€"RON2 Interaction. Journal of Molecular Biology, 2016, 428, 3986-3998.	2.0	22
3057	Cryoannealing-induced space-group transition of crystals of the carbonic anhydrase psCA3. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 573-577.	0.4	5
3058	Characterization of a Cyanobacterial Haloperoxidase and Evaluation of its Biocatalytic Halogenation Potential. ChemBioChem, 2016, 17, 2028-2032.	1.3	42
3059	Extrinsic Functions of Lectin Domains in O-N-Acetylgalactosamine Glycan Biosynthesis. Journal of Biological Chemistry, 2016, 291, 25339-25350.	1.6	10
3060	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of Anabaena Alkaline Invertase InvA Reveals a Novel Glucosidase. Journal of Biological Chemistry, 2016, 291, 25667-25677.	1.6	24
3061	The IQGAP1 N-Terminus Forms Dimers, and the Dimer Interface Is Required for Binding F-Actin and Calcium-Bound Calmodulin. Biochemistry, 2016, 55, 6433-6444.	1.2	16
3062	Crystal Structure of a Histone Deacetylase Homologue from <i>Pseudomonas aeruginosa</i>. Biochemistry, 2016, 55, 6858-6868.	1.2	8
3063	Natively glycosylated HIV-1 Env structure reveals new mode for antibody recognition of the CD4-binding site. Nature Structural and Molecular Biology, 2016, 23, 906-915.	3.6	188

#	ARTICLE	IF	CITATIONS
3064	The centrosomal Deubiquitylase USP21 regulates Gli1 transcriptional activity and stability.. Journal of Cell Science, 2016, 129, 4001-4013.	1.2	30
3065	Crystal structure of dihydropyrimidinase from Pseudomonas aeruginosa PAO1: Insights into the molecular basis of formation of a dimer. Biochemical and Biophysical Research Communications, 2016, 478, 1449-1455.	1.0	21
3066	Structure of <i>Arabidopsis thaliana</i> FUT1 Reveals a Variant of the GT-B Class Fold and Provides Insight into Xyloglucan Fucosylation. Plant Cell, 2016, 28, 2352-2364.	3.1	33
3067	Structural insight into the role of the Ton complex in energy transduction. Nature, 2016, 538, 60-65.	13.7	142
3068	Structure and Substrate Recognition of the Bottromycin Maturation Enzyme BotP. ChemBioChem, 2016, 17, 2286-2292.	1.3	15
3069	A conserved two-step binding for the UAF1 regulator to the USP12 deubiquitinating enzyme. Journal of Structural Biology, 2016, 196, 437-447.	1.3	27
3070	Structure and Mechanism of the Sphingopyxinâ€…I Lasso Peptide Isopeptidase. Angewandte Chemie, 2016, 128, 12909-12913.	1.6	2
3071	Structural insights into the interaction of p97 N-terminus domain and VBM in rhomboid protease, RHBDL4. Biochemical Journal, 2016, 473, 2863-2880.	1.7	20
3072	Structural and biophysical analysis of nuclease protein antibiotics. Biochemical Journal, 2016, 473, 2799-2812.	1.7	12
3073	Structural Insights into the Association of Hif1 with Histones H2A-H2B Dimer and H3-H4 Tetramer. Structure, 2016, 24, 1810-1820.	1.6	14
3074	Signaling States of a Short Blue-Light Photoreceptor Protein PpSB1-LOV Revealed from Crystal Structures and Solution NMR Spectroscopy. Journal of Molecular Biology, 2016, 428, 3721-3736.	2.0	31
3075	A Structural, Functional, and Computational Analysis of BshA, the First Enzyme in the Bacillithiol Biosynthesis Pathway. Biochemistry, 2016, 55, 4654-4665.	1.2	12
3076	Sensing and signaling of oxidative stress in chloroplasts by inactivation of the SAL1 phosphoadenosine phosphatase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4567-76.	3.3	147
3077	Unusual Reversible Oligomerization of Unfolded Dengue Envelope Protein Domain 3 at High Temperatures and Its Abolition by a Point Mutation. Biochemistry, 2016, 55, 4469-4475.	1.2	20
3078	Structural basis of Smoothened regulation by its extracellular domains. Nature, 2016, 535, 517-522.	13.7	300
3079	EssC: domain structures inform on the elusive translocation channel in the TypeÂVII secretion system. Biochemical Journal, 2016, 473, 1941-1952.	1.7	48
3080	Accurate design of megadalton-scale two-component icosahedral protein complexes. Science, 2016, 353, 389-394.	6.0	466
3081	Cell cycle regulation and novel structural features of thymidine kinase, an essential enzyme in <i>Trypanosoma brucei</i>. Molecular Microbiology, 2016, 102, 365-385.	1.2	11

#	ARTICLE	IF	CITATIONS
3082	Development of a proteinâ€“ligand-binding site prediction method based on interaction energy and sequence conservation. Journal of Structural and Functional Genomics, 2016, 17, 39-49.	1.2	15
3083	Biocatalytic Properties and Structural Analysis of Eugenol Oxidase from <i>Rhodococcus jostii</i> RHA1: A Versatile Oxidative Biocatalyst. ChemBioChem, 2016, 17, 1359-1366.	1.3	29
3084	Structural basis for integration of GluD receptors within synaptic organizer complexes. Science, 2016, 353, 295-299.	6.0	128
3085	Structural mapping of Kelch13 mutations associated with artemisinin resistanceÂin malaria. Journal of Structural and Functional Genomics, 2016, 17, 51-56.	1.2	17
3086	Regulating levels of the neuromodulator <scp>d</scp>â€serine in human brain: structural insight into pLG72 and <scp>d</scp>â€amino acid oxidase interaction. FEBS Journal, 2016, 283, 3353-3370.	2.2	15
3087	Six independent fucose-binding sites in the crystal structure of Aspergillus oryzae lectin. Biochemical and Biophysical Research Communications, 2016, 477, 477-482.	1.0	16
3088	Structure of the Catalytic Domain of the Class I Polyhydroxybutyrate Synthase from Cupriavidus necator. Journal of Biological Chemistry, 2016, 291, 25264-25277.	1.6	69
3089	Crystal structure of a crustacean hyperglycemic hormone (<scp>CHH</scp>) precursor suggests structural variety in the Câ€terminal regions of <scp>CHH</scp> superfamily members. FEBS Journal, 2016, 283, 4325-4339.	2.2	14
3090	Crystal structure of human aldehyde dehydrogenase 1A3 complexed with NAD+ and retinoic acid. Scientific Reports, 2016, 6, 35710.	1.6	58
3091	Mechanistic Insights from the Crystal Structure of <i>Bacillus subtilis</i> <i>o</i>-Succinylbenzoyl-CoA Synthetase Complexed with the Adenylate Intermediate. Biochemistry, 2016, 55, 6685-6695.	1.2	8
3092	Reader domain specificity and lysine demethylase-4 family function. Nature Communications, 2016, 7, 13387.	5.8	45
3093	Structure and inhibition of <i>N</i>â€acetylneuraminate lyase from methicillinâ€resistant <i>Staphylococcus aureus</i>. FEBS Letters, 2016, 590, 4414-4428.	1.3	18
3094	Rational Design of Thermodynamic and Kinetic Binding Profiles by Optimizing Surface Water Networks Coating Protein-Bound Ligands. Journal of Medicinal Chemistry, 2016, 59, 10530-10548.	2.9	64
3095	Unique coenzyme binding mode of hyperthermophilic archaealsn-glycerol-1-phosphate dehydrogenase fromPyrobaculum calidifontis. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1786-1796.	1.5	1
3096	BMI1 regulates PRC1 architecture and activity through homo- and hetero-oligomerization. Nature Communications, 2016, 7, 13343.	5.8	52
3097	Rigid-Docking Approaches to Explore Proteinâ€“Protein Interaction Space. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 33-55.	0.6	5
3098	Sleeping Beauty transposase structure allows rational design of hyperactive variants for genetic engineering. Nature Communications, 2016, 7, 11126.	5.8	51
3099	The second messenger c-di-AMP inhibits the osmolyte uptake system OpuC in <i>Staphylococcus aureus</i>. Science Signaling, 2016, 9, ra81.	1.6	87

#	Article	IF	Citations
3100	Crystal structure of raptor adenovirus 1 fibre head and role of the beta-hairpin in siadenovirus fibre head domains. Virology Journal, 2016, 13, 106.	1.4	6
3101	Structural insights of ZIP4 extracellular domain critical for optimal zinc transport. Nature Communications, 2016, 7, 11979.	5.8	65
3102	Crystal structures of APOBEC3G N-domain alone and its complex with DNA. Nature Communications, 2016, 7, 12193.	5.8	80
3103	Binding site elucidation and structure guided design of macrocyclic IL-17A antagonists. Scientific Reports, 2016, 6, 30859.	1.6	36
3104	Structural insights into the IgE mediated responses induced by the allergens Hev b 8 and Zea m 12 in their dimeric forms. Scientific Reports, 2016, 6, 32552.	1.6	22
3105	Isolation, Co-Crystallization and Structure-Based Characterization of Anabaenopeptins as Highly Potent Inhibitors of Activated Thrombin Activatable Fibrinolysis Inhibitor (TAFIa). Scientific Reports, 2016, 6, 32958.	1.6	30
3106	High-resolution crystal structure of the therapeutic antibody pembrolizumab bound to the human PD-1. Scientific Reports, 2016, 6, 35297.	1.6	77
3107	Structural basis of allosteric and synergistic activation of AMPK by furan-2-phosphonic derivative C2 binding. Nature Communications, 2016, 7, 10912.	5.8	69
3108	Structural basis for cytokinin production by LOG from Corynebacterium glutamicum. Scientific Reports, 2016, 6, 31390.	1.6	23
3109	The Structure of the RAGE:S100A6 Complex Reveals a Unique Mode of Homodimerization for S100 Proteins. Structure, 2016, 24, 2043-2052.	1.6	39
3110	Computationally designed peptides for self-assembly of nanostructured lattices. Science Advances, 2016, 2, e1600307.	4.7	58
3111	Mass spectrometry locates local and allosteric conformational changes that occur on cofactor binding. Nature Communications, 2016, 7, 12163.	5.8	53
3112	Structures of Proline Utilization A (PutA) Reveal the Fold and Functions of the Aldehyde Dehydrogenase Superfamily Domain of Unknown Function. Journal of Biological Chemistry, 2016, 291, 24065-24075.	1.6	27
3113	Downsizing the BAD BH3 peptide to small constrained Î±-helices with improved ligand efficiency. Organic and Biomolecular Chemistry, 2016, 14, 10939-10945.	1.5	16
3114	Structural analysis of X-linked retinoschisis mutations reveals distinct classes which differentially effect retinoschisin function. Human Molecular Genetics, 2016, 25, ddw345.	1.4	16
3115	Dirigent Protein Mode of Action Revealed by the Crystal Structure of AtDIR6. Plant Physiology, 2016, 172, 2165-2175.	2.3	58
3116	An Atypical Î±/Î²-Hydrolase Fold Revealed in the Crystal Structure of Pimeloyl-Acyl Carrier Protein Methyl Esterase BioG from <i>Haemophilus influenzae</i>. Biochemistry, 2016, 55, 6705-6717.	1.2	19
3117	Structural Insights into the <i>Drosophila melanogaster</i> Retinol Dehydrogenase, a Member of the Short-Chain Dehydrogenase/Reductase Family. Biochemistry, 2016, 55, 6545-6557.	1.2	19

#	ARTICLE	IF	CITATIONS
3118	Substrate complexes of human dipeptidyl peptidase III reveal the mechanism of enzyme inhibition. Scientific Reports, 2016, 6, 23787.	1.6	41
3119	Crystal Structures and Binding Dynamics of Odorant-Binding Protein 3 from two aphid species Megoura viciae and Nasonovia ribisnigri. Scientific Reports, 2016, 6, 24739.	1.6	79
3120	â€˜ANDâ€™ logic gates at work: Crystal structure of Rad53 bound to Dbf4 and Cdc7. Scientific Reports, 2016, 6, 34237.	1.6	17
3121	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12856-12861.	3.3	105
3122	Structure of human Aichi virus and implications for receptor binding. Nature Microbiology, 2016, 1, 16150.	5.9	36
3123	Direct and indirect mechanisms of KLK4 inhibition revealed by structure and dynamics. Scientific Reports, 2016, 6, 35385.	1.6	28
3124	Structural basis of omalizumab therapy and omalizumab-mediated IgE exchange. Nature Communications, 2016, 7, 11610.	5.8	86
3125	Haem-dependent dimerization of PGRMC1/Sigma-2 receptor facilitates cancer proliferation and chemoresistance. Nature Communications, 2016, 7, 11030.	5.8	153
3126	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nature Communications, 2016, 7, 13047.	5.8	35
3127	GalaxyRefineComplex: Refinement of protein-protein complex model structures driven by interface repacking. Scientific Reports, 2016, 6, 32153.	1.6	94
3128	Structural and functional studies of the glycoside hydrolase family 3 Î²-glucosidase Cel3A from the moderately thermophilic fungus<i>Rasamsonia emersonii</i>. Acta Crystallographica Section D: Structural Biology, 2016, 72, 860-870.	1.1	28
3129	Structure of the cyanobactin oxidase ThcOx from<i>Cyanothece</i>sp. PCC 7425, the first structure to be solved at Diamond Light Source beamline I23 by means of S-SAD. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1174-1180.	1.1	26
3130	Structural Insights into the Tetrameric State of Aspartate-Î²-semialdehyde Dehydrogenases from Fungal Species. Scientific Reports, 2016, 6, 21067.	1.6	9
3131	Structural basis for the specific inhibition of glycoprotein IbÎ± shedding by an inhibitory antibody. Scientific Reports, 2016, 6, 24789.	1.6	12
3132	Abundance and Temperature Dependency of Protein-Protein Interaction Revealed by Interface Structure Analysis and Stability Evolution. Scientific Reports, 2016, 6, 26737.	1.6	13
3133	Diverse architectural properties of Sso10a proteins: Evidence for a role in chromatin compaction and organization. Scientific Reports, 2016, 6, 29422.	1.6	14
3134	Oligomeric interface modulation causes misregulation of purine 5Â´-nucleotidase in relapsed leukemia. BMC Biology, 2016, 14, 91.	1.7	9
3135	How the oxygen tolerance of a [NiFe]-hydrogenase depends on quaternary structure. Journal of Biological Inorganic Chemistry, 2016, 21, 121-134.	1.1	26

#	Article	IF	Citations
3136	Crystal structure of human S100A8 in complex with zinc and calcium. BMC Structural Biology, 2016, 16, 8.	2.3	22
3137	Structural dynamics of a methionine Î³-lyase for calicheamicin biosynthesis: Rotation of the conserved tyrosine stacking with pyridoxal phosphate. Structural Dynamics, 2016, 3, 034702.	0.9	4
3138	Crystal structure of ketopantoate reductase from<i>Thermococcus kodakarensis</i>complexed with NADP⁺. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 369-375.	0.4	3
3139	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. Journal of Biological Chemistry, 2016, 291, 14430-14446.	1.6	16
3141	Structural basis for inhibition of the deadenylase activity of human <scp>CNOT</scp>6L. FEBS Letters, 2016, 590, 1270-1279.	1.3	9
3142	Nanoarchitectonics for Dynamic Functional Materials from Atomicâ€/Molecularâ€Level Manipulation to Macroscopic Action. Advanced Materials, 2016, 28, 1251-1286.	11.1	441
3143	Hydrolysis of synthetic polyesters by <i>Clostridium botulinum</i> esterases. Biotechnology and Bioengineering, 2016, 113, 1024-1034.	1.7	65
3144	Crystal Structure of the HMGâ€CoA Synthase MvaS from the Gramâ€Negative Bacterium <i>Myxococcus xanthus</i>. ChemBioChem, 2016, 17, 1257-1262.	1.3	9
3145	Structural analysis of Î²-prism lectin from Colocasia esculenta (L.) S chott. International Journal of Biological Macromolecules, 2016, 91, 518-523.	3.6	8
3146	Structural database resources for biological macromolecules. Briefings in Bioinformatics, 2017, 18, bbw049.	3.2	13
3147	Crystal structure of the TK2203 protein fromThermococcus kodakarensis, a putative extradiol dioxygenase. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 427-433.	0.4	3
3148	Structural and Functional Characterization of Aerobactin Synthetase IucA from a Hypervirulent Pathotype of <i>Klebsiella pneumoniae</i>. Biochemistry, 2016, 55, 3559-3570.	1.2	21
3149	Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26.	3.0	46
3150	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. Nucleic Acids Research, 2016, 44, W344-W350.	6.5	2,395
3151	Structural basis for the antagonistic roles of RNP-8 and GLD-3 in GLD-2 poly(A)-polymerase activity. Rna, 2016, 22, 1139-1145.	1.6	8
3152	Structure of a phleboviral envelope glycoprotein reveals a consolidated model of membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7154-7159.	3.3	87
3153	Structural Basis for the Specific Recognition of RhoA by the Dual GTPase-activating Protein ARAP3. Journal of Biological Chemistry, 2016, 291, 16709-16719.	1.6	12
3154	The first crystal structure of human RNase 6 reveals a novel substrate-binding and cleavage site arrangement. Biochemical Journal, 2016, 473, 1523-1536.	1.7	44

#	Article	IF	Citations
3155	AraPPISite: a database of fine-grained proteinâ€"protein interaction site annotations for Arabidopsis thaliana. Plant Molecular Biology, 2016, 92, 105-116.	2.0	11
3156	Molecular dynamics simulations and structure-based network analysis reveal structural and functional aspects of G-protein coupled receptor dimer interactions. Journal of Computer-Aided Molecular Design, 2016, 30, 489-512.	1.3	26
3157	Interleukin-11: A Multifunctional Cytokine with Intrinsically Disordered Regions. Cell Biochemistry and Biophysics, 2016, 74, 285-296.	0.9	14
3158	Structural basis of potent Zikaâ€"dengue virus antibody cross-neutralization. Nature, 2016, 536, 48-53.	13.7	465
3159	Structure-based Epitope Mapping of Mycobacterium tuberculosis Secretary Antigen MTC28. Journal of Biological Chemistry, 2016, 291, 13943-13954.	1.6	8
3160	A complex water network contributes to high-affinity binding in an antibodyâ€"antigen interface. Data in Brief, 2016, 6, 394-397.	0.5	5
3161	Structural and mutational analysis of the interaction between the Middle-East respiratory syndrome coronavirus (MERS-CoV) papain-like protease and human ubiquitin. Virologica Sinica, 2016, 31, 288-299.	1.2	30
3162	Impact of the crystallization condition on importin-Î² conformation. Acta Crystallographica Section D: Structural Biology, 2016, 72, 705-717.	1.1	12
3163	In Streptomyces coelicolor SigR, methionine at the -35 element interacting region 4 confers the -31â€²-adenine base selectivity. Biochemical and Biophysical Research Communications, 2016, 470, 257-262.	1.0	6
3164	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. Structure, 2016, 24, 851-861.	1.6	21
3165	Molecular mechanism underlying promiscuous polyamine recognition by spermidine acetyltransferase. International Journal of Biochemistry and Cell Biology, 2016, 76, 87-97.	1.2	9
3166	Genome and network visualization facilitates the analyses of the effects of drugs and mutations on protein-protein and drug-protein networks. BMC Bioinformatics, 2016, 17, 54.	1.2	4
3167	Structures of EccB1 and EccD1 from the core complex of the mycobacterial ESX-1 type VII secretion system. BMC Structural Biology, 2016, 16, 5.	2.3	27
3168	Myristoylation drives dimerization of matrix protein from mouse mammary tumor virus. Retrovirology, 2016, 13, 2.	0.9	6
3169	The C-Terminal Arm of the Human Papillomavirus Major Capsid Protein Is Immunogenic and Involved in Virus-Host Interaction. Structure, 2016, 24, 874-885.	1.6	24
3170	Transcription of lncRNA prt, clustered prt RNA sites for Mmi1 binding, and RNA polymerase II CTD phospho-sites govern the repression of pho1 gene expression under phosphate-replete conditions in fission yeast. Rna, 2016, 22, 1011-1025.	1.6	47
3171	Tyrosine binding and promiscuity in the arginine repressor from the pathogenic bacterium Corynebacterium pseudotuberculosis. Biochemical and Biophysical Research Communications, 2016, 475, 350-355.	1.0	4
3172	Interdomain and Intermodule Organization in Epimerization Domain Containing Nonribosomal Peptide Synthetases. ACS Chemical Biology, 2016, 11, 2293-2303.	1.6	67

#	Article	IF	Citations
3173	Cross-class metallo-Î²-lactamase inhibition by bisthiazolidines reveals multiple binding modes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3745-54.	3.3	122
3174	Identification of a Functionally Relevant Adeno-Associated Virus Rep68 Oligomeric Interface. Journal of Virology, 2016, 90, 6612-6624.	1.5	7
3175	The immunity-related GTPase Irga6 dimerizes in a parallel head-to-head fashion. BMC Biology, 2016, 14, 14.	1.7	19
3176	Structural Basis for Eculizumab-Mediated Inhibition of the Complement Terminal Pathway. Journal of Immunology, 2016, 197, 337-344.	0.4	76
3177	Structural insights and membrane binding properties of <scp>MGD</scp>1, the major galactolipid synthase in plants. Plant Journal, 2016, 85, 622-633.	2.8	22
3178	Structure of a Cytoplasmic 11-Subunit RNA Exosome Complex. Molecular Cell, 2016, 63, 125-134.	4.5	72
3179	Structural and Functional Characterization of Hirudin P6 Derived Novel Bivalent Thrombin Inhibitors â€“ Studying the Effect of Linker Length and Glycosylation on Their Function. Chemical Biology and Drug Design, 2016, 88, 129-141.	1.5	9
3180	Structure of sm<scp>AKAP</scp> and its regulation by <scp>PKA</scp>â€mediated phosphorylation. FEBS Journal, 2016, 283, 2132-2148.	2.2	19
3181	Deciphering the Substrate Specificity of SbnA, the Enzyme Catalyzing the First Step in Staphyloferrin B Biosynthesis. Biochemistry, 2016, 55, 927-939.	1.2	22
3182	Novel S -enantioselective lipase TALipB from Trichosporon asahii MSR54: Heterologous expression, characterization, conformational stability and homology modeling. Enzyme and Microbial Technology, 2016, 83, 29-39.	1.6	11
3183	Nuclear Protein-Only Ribonuclease P2 Structure and Biochemical Characterization Provide Insight into the Conserved Properties of tRNA 5â€² End Processing Enzymes. Journal of Molecular Biology, 2016, 428, 26-40.	2.0	31
3184	Structural basis and function of XRN2 binding by XTB domains. Nature Structural and Molecular Biology, 2016, 23, 164-171.	3.6	17
3185	Structural Evolution of the Emerging 2014-2015 GII.17 Noroviruses. Journal of Virology, 2016, 90, 2710-2715.	1.5	35
3186	Structural Plasticity of the Protein Plug That Traps Newly Packaged Genomes in Podoviridae Virions. Journal of Biological Chemistry, 2016, 291, 215-226.	1.6	14
3187	Insights from the Structure of Mycobacterium tuberculosis Topoisomerase I with a Novel Protein Fold. Journal of Molecular Biology, 2016, 428, 182-193.	2.0	36
3188	Solution-Binding and Molecular Docking Approaches Combine to Provide an Expanded View of Multidrug Recognition in the MDR Gene Regulator BmrR. Journal of Chemical Information and Modeling, 2016, 56, 377-389.	2.5	4
3189	Structural and functional insight into the different oxidation states of SAV1875 from Staphylococcus aureus. Biochemical Journal, 2016, 473, 55-66.	1.7	6
3190	Sulfonamide inhibition studies of the Î±-carbonic anhydrase from the gammaproteobacterium Thiomicrospira crunogena XCL-2, TcruCA. Bioorganic and Medicinal Chemistry Letters, 2016, 26, 401-405.	1.0	2

#	Article	IF	Citations
3191	Structure of the polyisoprenyl-phosphate glycosyltransferase GtrB and insights into the mechanism of catalysis. Nature Communications, 2016, 7, 10175.	5.8	33
3192	Crystal structure of Rv2258c from Mycobacterium tuberculosis H37Rv, an S -adenosyl- l -methionine-dependent methyltransferase. Journal of Structural Biology, 2016, 193, 172-180.	1.3	3
3193	The Structure of a BamA-BamD Fusion Illuminates the Architecture of the Î²-Barrel Assembly Machine Core. Structure, 2016, 24, 243-251.	1.6	30
3194	Structural and Functional Analyses Reveal Insights into the Molecular Properties of the Escherichia coli Z Ring Stabilizing Protein, ZapC. Journal of Biological Chemistry, 2016, 291, 2485-2498.	1.6	10
3195	Structure of a Native-like Aureochrome 1a LOV Domain Dimer from Phaeodactylum tricornutum. Structure, 2016, 24, 171-178.	1.6	47
3196	Hyperstabilization of Tetrameric <i>Bacillus</i> sp. TB-90 Urate Oxidase by Introducing Disulfide Bonds through Structural Plasticity. Biochemistry, 2016, 55, 724-732.	1.2	29
3197	Phylogenetic and molecular analyses of human parainfluenza type 3 virus in Buenos Aires, Argentina, between 2009 and 2013: The emergence of new genetic lineages. Infection, Genetics and Evolution, 2016, 39, 85-91.	1.0	15
3198	Structural studies on tobacco streak virus coat protein: Insights into the pleomorphic nature of ilarviruses. Journal of Structural Biology, 2016, 193, 95-105.	1.3	3
3199	Structure of NDP-forming Acetyl-CoA synthetase ACD1 reveals a large rearrangement for phosphoryl transfer. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E519-28.	3.3	26
3200	Structural and functional insights into the fly microRNA biogenesis factor Loquacious. Rna, 2016, 22, 383-396.	1.6	11
3201	Loop-to-helix transition in the structure of multidrug regulator AcrR at the entrance of the drug-binding cavity. Journal of Structural Biology, 2016, 194, 18-28.	1.3	12
3202	The Structural and Functional Characterization of Mammalian ADP-dependent Glucokinase. Journal of Biological Chemistry, 2016, 291, 3694-3704.	1.6	29
3203	Dissecting the Structural Elements for the Activation of Î²-Ketoacyl-(Acyl Carrier Protein) Reductase from Vibrio cholerae. Journal of Bacteriology, 2016, 198, 463-476.	1.0	14
3204	Crystal structure of HINT fromHelicobacter pylori. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 42-48.	0.4	2
3205	Unveiling the Catalytic Mechanism of NADP⁺-Dependent Isocitrate Dehydrogenase with QM/MM Calculations. ACS Catalysis, 2016, 6, 357-368.	5.5	23
3206	Glycosyltransferase complexes in eukaryotes: long-known, prevalent but still unrecognized. Cellular and Molecular Life Sciences, 2016, 73, 305-325.	2.4	64
3207	Characterization of a poly(butylene adipate-co-terephthalate)-hydrolyzing lipase from Pelosinus fermentans. Applied Microbiology and Biotechnology, 2016, 100, 1753-1764.	1.7	75
3208	Structural analysis of a Dioclea sclerocarpa lectin: Study on the vasorelaxant properties of Dioclea lectins. International Journal of Biological Macromolecules, 2016, 82, 464-470.	3.6	15

#	ARTICLE	IF	CITATIONS
3209	Î²-Subunit Binding Is Sufficient for Ligands to Open the Integrin Î±IIbÎ²3 Headpiece. Journal of Biological Chemistry, 2016, 291, 4537-4546.	1.6	28
3210	PDBe: improved accessibility of macromolecular structure data from PDB and EMDB. Nucleic Acids Research, 2016, 44, D385-D395.	6.5	131
3211	The C-terminal region of the transcriptional regulator THAP11 forms a parallel coiled-coil domain involved in protein dimerization. Journal of Structural Biology, 2016, 194, 337-346.	1.3	10
3212	Analysis of two Schistosoma mansoni uridine phosphorylases isoforms suggests the emergence of a protein with a non-canonical function. Biochimie, 2016, 125, 12-22.	1.3	9
3213	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. Science, 2016, 351, 1458-1463.	6.0	382
3214	Structure and functional analysis of the siderophore periplasmic binding protein from the fuscachelin gene cluster of T hermobifida fusca. Proteins: Structure, Function and Bioinformatics, 2016, 84, 118-128.	1.5	2
3215	A Multivalent Marine Lectin from <i>Crenomytilus grayanus</i> Possesses Anti-cancer Activity through Recognizing Globotriose Gb3. Journal of the American Chemical Society, 2016, 138, 4787-4795.	6.6	51
3216	Biochemical characterization and structural analysis of a new cold-active and salt-tolerant esterase from the marine bacterium Thalassospira sp.. Extremophiles, 2016, 20, 323-336.	0.9	49
3217	A novel esterase subfamily with Î±/Î²â€hydrolase fold suggested by structures of two bacterial enzymes homologous to <scp>l</scp>â€homoserine <i>O</i>â€acetyl transferases. FEBS Letters, 2016, 590, 174-184.	1.3	5
3218	Structural basis of specific inhibition of tissue-type plasminogen activator by plasminogen activators inhibitor-1. Data in Brief, 2016, 6, 550-555.	0.5	2
3219	Mass Spectrometry Reveals Protein Kinase CK2 High-Order Oligomerization <i>via</i> the Circular and Linear Assembly. ACS Chemical Biology, 2016, 11, 1511-1517.	1.6	20
3220	Aurone synthase is a catechol oxidase with hydroxylase activity and provides insights into the mechanism of plant polyphenol oxidases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1806-15.	3.3	112
3221	Understanding the fabric of protein crystals: computational classification of biological interfaces and crystal contacts. Bioinformatics, 2016, 32, 481-489.	1.8	37
3222	Structural analysis of Centrolobium tomentosum seed lectin with inflammatory activity. Archives of Biochemistry and Biophysics, 2016, 596, 73-83.	1.4	27
3223	Evolution of Protein Quaternary Structure in Response to Selective Pressure for Increased Thermostability. Journal of Molecular Biology, 2016, 428, 2359-2371.	2.0	40
3224	Structural basis for therapeutic inhibition of complement C5. Nature Structural and Molecular Biology, 2016, 23, 378-386.	3.6	94
3225	PGL germ granule assembly protein is a base-specific, single-stranded RNase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1279-1284.	3.3	21
3226	An Esterase from Anaerobic <i>Clostridium hathewayi</i> Can Hydrolyze Aliphaticâ€“Aromatic Polyesters. Environmental Science & Technology, 2016, 50, 2899-2907.	4.6	39

#	ARTICLE	IF	CITATIONS
3227	Mechanism of a cytosolic <i>O</i> -glycosyltransferase essential for the synthesis of a bacterial adhesion protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1190-9.	3.3	36
3228	Characterization and Structural Insights into Selective E1-E2 Interactions in the Human and Plasmodium falciparum SUMO Conjugation Systems. Journal of Biological Chemistry, 2016, 291, 3860-3870.	1.6	15
3229	First structure of archaeal branched-chain amino acid aminotransferase from Thermoproteus uzoniensis specific for l-amino acids and R-amines. Extremophiles, 2016, 20, 215-225.	0.9	28
3230	Structural Decoding of the Netrin-1/UNC5 Interaction and its Therapeutical Implications in Cancers. Cancer Cell, 2016, 29, 173-185.	7.7	80
3231	Structural investigation of ribonuclease A conformational preferences using high pressure protein crystallography. Chemical Physics, 2016, 468, 53-62.	0.9	7
3232	Evolutionary Inference across Eukaryotes Identifies Specific Pressures Favoring Mitochondrial Gene Retention. Cell Systems, 2016, 2, 101-111.	2.9	131
3233	Structures of Xenopus Embryonic Epidermal Lectin Reveal a Conserved Mechanism of Microbial Glycan Recognition. Journal of Biological Chemistry, 2016, 291, 5596-5610.	1.6	33
3234	Structural investigation of the thymidine phosphorylase from<i>Salmonella typhimurium</i>in the unliganded state and its complexes with thymidine and uridine. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 224-233.	0.4	5
3235	Three-dimensional structures of two heavily N-glycosylated<i>Aspergillus</i>sp. family GH3 Î²-<scp>D</scp>-glucosidases. Acta Crystallographica Section D: Structural Biology, 2016, 72, 254-265.	1.1	38
3236	Identification of the Elusive Pyruvate Reductase of<i>Chlamydomonas reinhardtii</i>Chloroplasts. Plant and Cell Physiology, 2016, 57, 82-94.	1.5	23
3237	Structural Insights into the HWE Histidine Kinase Family: The Brucella Blue Light-Activated Histidine Kinase Domain. Journal of Molecular Biology, 2016, 428, 1165-1179.	2.0	18
3238	The Structure of the Toxin and Type Six Secretion System Substrate Tse2 in Complex with Its Immunity Protein. Structure, 2016, 24, 277-284.	1.6	25
3239	Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer. Nature, 2016, 531, 114-117.	13.7	453
3240	Structure-based analysis of the molecular interactions between acyltransferase and acyl carrier protein in vicenistatin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1802-1807.	3.3	69
3241	A glutamate/aspartate switch controls product specificity in a protein arginine methyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2068-2073.	3.3	44
3242	Hepatitis B Virus Capsids Have Diverse Structural Responses to Small-Molecule Ligands Bound to the Heteroaryldihydropyrimidine Pocket. Journal of Virology, 2016, 90, 3994-4004.	1.5	65
3243	Alba from Thermoplasma volcanium belongs to Î±-NAT's: An insight into the structural aspects of Tv Alba and its acetylation by Tv Ard1. Archives of Biochemistry and Biophysics, 2016, 590, 90-100.	1.4	3
3244	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i>-Aminosalicylic Acid Resistance. Biochemistry, 2016, 55, 1107-1119.	1.2	22

#	Article	IF	Citations
3245	How to Study Intermediate Filaments in Atomic Detail. Methods in Enzymology, 2016, 568, 3-33.	0.4	16
3246	Insights into Complex Oxidation during BE-7585A Biosynthesis: Structural Determination and Analysis of the Polyketide Monooxygenase BexE. ACS Chemical Biology, 2016, 11, 1137-1147.	1.6	10
3247	The Atomic Structure of the Phage Tuc2009 Baseplate Tripod Suggests that Host Recognition Involves Two Different Carbohydrate Binding Modules. MBio, 2016, 7, e01781-15.	1.8	58
3248	Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. Journal of Molecular Biology, 2016, 428, 1130-1141.	2.0	10
3249	Glucose Isomerase Polymorphs Obtained Using an Ad Hoc Protein Crystallization Temperature Device and a Growth Cell Applying an Electric Field. Crystal Growth and Design, 2016, 16, 1679-1686.	1.4	18
3250	PqsBC, a Condensing Enzyme in the Biosynthesis of the Pseudomonas aeruginosa Quinolone Signal. Journal of Biological Chemistry, 2016, 291, 6610-6624.	1.6	59
3251	Arm-in-Arm Response Regulator Dimers Promote Intermolecular Signal Transduction. Journal of Bacteriology, 2016, 198, 1218-1229.	1.0	7
3252	Expression, crystallization and structure elucidation of Î³-terpinene synthase fromThymus vulgaris. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 16-23.	0.4	19
3253	Structural characterization of GASDALIE Fc bound to the activating Fc receptor FcÎ³RIIIa. Journal of Structural Biology, 2016, 194, 78-89.	1.3	44
3254	Identification of LACTB2, a metallo-Î²-lactamase protein, as a human mitochondrial endoribonuclease. Nucleic Acids Research, 2016, 44, 1813-1832.	6.5	37
3255	Investigating the structural impact of S311C mutation in DRD2 receptor by molecular dynamics & docking studies. Biochimie, 2016, 123, 52-64.	1.3	10
3256	Structural transition of ETS1 from an auto-inhibited to functional state upon association with the p16INK4anative and mutated promoter region. RSC Advances, 2016, 6, 15960-15975.	1.7	4
3257	Concerted action of two subunits of the functional dimer ofShewanella oneidensisMR-1 uridine phosphorylase derived from a comparison of the C212S mutant and the wild-type enzyme. Acta Crystallographica Section D: Structural Biology, 2016, 72, 203-210.	1.1	3
3258	<scp>l</scp> -Hydroxyproline and <scp>d</scp> -Proline Catabolism in Sinorhizobium meliloti. Journal of Bacteriology, 2016, 198, 1171-1181.	1.0	20
3259	KatB, a cyanobacterial Mn-catalase with unique active site configuration: Implications for enzyme function. Free Radical Biology and Medicine, 2016, 93, 118-129.	1.3	21
3260	Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases. Nature, 2016, 531, 533-537.	13.7	70
3261	Structural basis of lenalidomide-induced CK1Î± degradation by the CRL4CRBN ubiquitin ligase. Nature, 2016, 532, 127-130.	13.7	426
3262	Directed evolution of Tau class glutathione transferases reveals a site that regulates catalytic efficiency and masks co-operativity. Biochemical Journal, 2016, 473, 559-570.	1.7	31

#	ARTICLE	IF	CITATIONS
3263	Molecular Insights into Toluene Sensing in the TodS/TodT Signal Transduction System. Journal of Biological Chemistry, 2016, 291, 8575-8590.	1.6	24
3264	Crystal structure of the homocysteine methyltransferase MmuM from <i>Escherichia coli</i>. Biochemical Journal, 2016, 473, 277-284.	1.7	9
3265	Crystal structure of the Saccharomyces cerevisiae monoglyceride lipase Yju3p. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 462-470.	1.2	25
3266	Crystal structure of a lipoxygenase from Cyanothece sp. may reveal novel features for substrate acquisition. Journal of Lipid Research, 2016, 57, 276-287.	2.0	30
3267	Crystal structure of human GDF11. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 160-164.	0.4	25
3268	Mapping Antigenic Epitopes on the Human Bocavirus Capsid. Journal of Virology, 2016, 90, 4670-4680.	1.5	28
3269	Structural basis of H2A.Z recognition by SRCAP chromatin-remodeling subunit YL1. Nature Structural and Molecular Biology, 2016, 23, 317-323.	3.6	70
3270	The Structure of the Transcriptional Repressor KstR in Complex with CoA Thioester Cholesterol Metabolites Sheds Light on the Regulation of Cholesterol Catabolism in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2016, 291, 7256-7266.	1.6	32
3271	Structurally conserved erythrocyte-binding domain in <i>Plasmodium</i> provides a versatile scaffold for alternate receptor engagement. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E191-200.	3.3	43
3272	The STAS domain of mammalian SLC26A5 prestin harbours an anion-binding site. Biochemical Journal, 2016, 473, 365-370.	1.7	24
3273	Insight into Structure-Function Relationships and Inhibition of the Fatty Acyl-AMP Ligase (FadD32) Orthologs from Mycobacteria. Journal of Biological Chemistry, 2016, 291, 7973-7989.	1.6	22
3274	Crystal structure of maize serine racemase with pyridoxal 5â€²-phosphate. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 165-171.	0.4	6
3275	Mitochondrial Hsp90 is a ligand-activated molecular chaperone coupling ATP binding to dimer closure through a coiled-coil intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2952-2957.	3.3	42
3276	Elongation of the Poly-Î³-glutamate Tail of F420 Requires Both Domains of the F420:Î³-Glutamyl Ligase (FbiB) of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2016, 291, 6882-6894.	1.6	24
3277	Antibody Response to Hypervariable Region 1 Interferes with Broadly Neutralizing Antibodies to Hepatitis C Virus. Journal of Virology, 2016, 90, 3112-3122.	1.5	59
3278	Molecular association of glucose-6-phosphate isomerase and pyruvate kinase M2 with glyceraldehyde-3-phosphate dehydrogenase in cancer cells. BMC Cancer, 2016, 16, 152.	1.1	25
3279	Crystal structure of a hypothetical protein, TTHA0829 from Thermus thermophilus HB8, composed of cystathionine-Î²-synthase (CBS) and aspartate-kinase chorismate-mutase tyrA (ACT) domains. Extremophiles, 2016, 20, 275-282.	0.9	4
3280	Intermolecular Interactions of Cardiac Transcription Factors NKX2.5 and TBX5. Biochemistry, 2016, 55, 1702-1710.	1.2	24

#	Article	IF	Citations
3281	Reply to â€œThe Broadly Neutralizing, Anti-HIV Antibody 4E10: an Open and Shut Case?â€• Journal of Virology, 2016, 90, 3276-3277.	1.5	2
3282	In Silico Analysis of FMR1 Gene Missense SNPs. Cell Biochemistry and Biophysics, 2016, 74, 109-127.	0.9	10
3283	Structural and Functional Significance of the N- and C-Terminal Appendages in <i>Arabidopsis</i> Truncated Hemoglobin. Biochemistry, 2016, 55, 1724-1740.	1.2	8
3284	Perchlorate Reductase Is Distinguished by Active Site Aromatic Gate Residues. Journal of Biological Chemistry, 2016, 291, 9190-9202.	1.6	71
3285	Crystal structure of truncated FlgD from the human pathogen Helicobacter pylori. Journal of Structural Biology, 2016, 194, 147-155.	1.3	7
3286	Architecture of the Yeast Mitochondrial Iron-Sulfur Cluster Assembly Machinery. Journal of Biological Chemistry, 2016, 291, 10378-10398.	1.6	17
3287	Quaternary Structure of Fur Proteins, a New Subfamily of Tetrameric Proteins. Biochemistry, 2016, 55, 1503-1515.	1.2	22
3288	Crystal Structure and Biochemical Characterization of a Mycobacterium smegmatis AAA-Type Nucleoside Triphosphatase Phosphohydrolase (Msm0858). Journal of Bacteriology, 2016, 198, 1521-1533.	1.0	8
3289	Optimal Neutralization of Centruroides noxius Venom Is Understood through a Structural Complex between Two Antibody Fragments and the Cn2 Toxin. Journal of Biological Chemistry, 2016, 291, 1619-1630.	1.6	19
3290	Structure of a TCR-Mimic Antibody with Target Predicts Pharmacogenetics. Journal of Molecular Biology, 2016, 428, 194-205.	2.0	48
3291	Crystal Structure of the Measles Virus Nucleoprotein Core in Complex with an N-Terminal Region of Phosphoprotein. Journal of Virology, 2016, 90, 2849-2857.	1.5	69
3292	Secondary ubiquitin-RING docking enhances Arkadia and Ark2C E3 ligase activity. Nature Structural and Molecular Biology, 2016, 23, 45-52.	3.6	46
3293	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of Î²-Aryl Ether Bonds in Lignin. Journal of Biological Chemistry, 2016, 291, 5234-5246.	1.6	40
3294	<i>Bacillus licheniformis</i>trehalose-6-phosphate hydrolase structures suggest keys to substrate specificity. Acta Crystallographica Section D: Structural Biology, 2016, 72, 59-70.	1.1	12
3295	Structure of an Actinobacterial-Type [NiFe]-Hydrogenase Reveals Insight into O 2 -Tolerant H 2 Oxidation. Structure, 2016, 24, 285-292.	1.6	43
3296	The structure of VgrG1 from<i>Pseudomonas aeruginosa</i>, the needle tip of the bacterial type VI secretion system. Acta Crystallographica Section D: Structural Biology, 2016, 72, 22-33.	1.1	37
3297	The structure of the Î²-barrel assembly machinery complex. Science, 2016, 351, 180-186.	6.0	209
3298	Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses. Acta Crystallographica Section D: Structural Biology, 2016, 72, 49-58.	1.1	14

#	ARTICLE	IF	CITATIONS
3299	A Structural Study of CESA1 Catalytic Domain of Arabidopsis Cellulose Synthesis Complex: Evidence for CESA Trimers. Plant Physiology, 2016, 170, 123-135.	2.3	104
3300	Reactive Center Loop (RCL) Peptides Derived from Serpins Display Independent Coagulation and Immune Modulating Activities. Journal of Biological Chemistry, 2016, 291, 2874-2887.	1.6	39
3301	Structural basis for leucine sensing by the Sestrin2-mTORC1 pathway. Science, 2016, 351, 53-58.	6.0	340
3302	New insights into the structural basis of DNA recognition by HINa and HINb domains of IFI16. Journal of Molecular Cell Biology, 2016, 8, 51-61.	1.5	48
3303	The activity of CouR, a MarR family transcriptional regulator, is modulated through a novel molecular mechanism. Nucleic Acids Research, 2016, 44, 595-607.	6.5	44
3304	Structural Insights into KCTD Protein Assembly and Cullin3 Recognition. Journal of Molecular Biology, 2016, 428, 92-107.	2.0	47
3305	Role of iso-receptors in receptor-receptor interactions with a focus on dopamine iso-receptor complexes. Reviews in the Neurosciences, 2016, 27, 1-25.	1.4	25
3306	Human dihydrofolate reductase and thymidylate synthase form a complex in vitro and co-localize in normal and cancer cells. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1474-1490.	2.0	16
3307	Role of sequence evolution and conformational dynamics in the substrate specificity and oligomerization mode of thymidylate kinases. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2136-2154.	2.0	1
3308	Methionine sulfoxide reductase A deficiency exacerbates acute liver injury induced by acetaminophen. Biochemical and Biophysical Research Communications, 2017, 484, 189-194.	1.0	22
3309	Binding and processing of Î²â€‘lactam antibiotics by the transpeptidase Ldt_{Mt2} from <i>Mycobacterium tuberculosis</i>. FEBS Journal, 2017, 284, 725-741.	2.2	35
3310	Structure of the <i>Arabidopsis thaliana </i><scp>NADPH</scp>â€‘cytochrome P450 reductase 2 (ATR2) provides insight into its function. FEBS Journal, 2017, 284, 754-765.	2.2	25
3311	High-resolution cryo-EM structure of the proteasome in complex with ADP-AlFx. Cell Research, 2017, 27, 373-385.	5.7	54
3312	MFN1 structures reveal nucleotide-triggered dimerization critical for mitochondrial fusion. Nature, 2017, 542, 372-376.	13.7	234
3313	The HhoA protease from Synechocystis sp. PCC 6803 â€“ Novel insights into structure and activity regulation. Journal of Structural Biology, 2017, 198, 147-153.	1.3	4
3314	Room temperature structure of human IgG4-Fc from crystals analysed in situ. Molecular Immunology, 2017, 81, 85-91.	1.0	7
3315	Crystal structure of a putrescine aminotransferase fromPseudomonassp. strain AAC. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 29-35.	0.4	3
3316	Structural studies of substrate and product complexes of 5-aminolaevulinic acid dehydratase from humans,<i>Escherichia coli</i>and the hyperthermophile<i>Pyrobaculum calidifontis</i>. Acta Crystallographica Section D: Structural Biology, 2017, 73, 9-21.	1.1	25

#	Article	IF	Citations
3317	Molecular dynamics simulations reveal structural insights into inhibitor binding modes and functionality in human Group IIA phospholipase A2. Proteins: Structure, Function and Bioinformatics, 2017, 85, 827-842.	1.5	3
3318	Disruption of cell adhesion by an antibody targeting the cell-adhesive intermediate (X-dimer) of human P-cadherin. Scientific Reports, 2017, 7, 39518.	1.6	18
3319	Structural and functional insights into asymmetric enzymatic dehydration of alkenols. Nature Chemical Biology, 2017, 13, 275-281.	3.9	30
3320	Crystal structure of the ATPase-C domain of the chromatin remodeller Fun30 from<i>Saccharomyces cerevisiae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 9-15.	0.4	2
3321	Xâ€ray crystal structure of the Nâ€terminal region of <scp>M</scp>oloney murine leukemia virus integrase and its implications for viral DNA recognition. Proteins: Structure, Function and Bioinformatics, 2017, 85, 647-656.	1.5	9
3322	Structural characterisation of the fatty acid biosynthesis enzyme FabF from the pathogen Listeria monocytogenes. Scientific Reports, 2017, 7, 39277.	1.6	5
3323	Structure-based mutational studies of <i>O</i>-acetylserine sulfhydrylase reveal the reason for the loss of cysteine synthase complex formation in <i>Brucella abortus</i>. Biochemical Journal, 2017, 474, 1221-1239.	1.7	14
3324	Discovery of a junctional epitope antibody that stabilizes IL-6 and gp80 protein:protein interaction and modulates its downstream signaling. Scientific Reports, 2017, 7, 37716.	1.6	34
3325	Structure ofMethylobacterium extorquensmalyl-CoA lyase: CoA-substrate binding correlates with domain shift. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 79-85.	0.4	1
3326	Gene polymorphism linked to increased asthma and IBD risk alters gasdermin-B structure, a sulfatide and phosphoinositide binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1128-E1137.	3.3	135
3327	The structure of the yeast mitochondrial ribosome. Science, 2017, 355, 528-531.	6.0	161
3328	The role of interfacial lipids in stabilizing membrane protein oligomers. Nature, 2017, 541, 421-424.	13.7	344
3329	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. Nature, 2017, 541, 407-411.	13.7	188
3330	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. Bioinformatics, 2017, 33, 1479-1487.	1.8	66
3331	Carbohydrateâ€"Lectin Interactions: An Unexpected Contribution to Affinity. ChemBioChem, 2017, 18, 539-544.	1.3	11
3332	ChaC2, an Enzyme for Slow Turnover of Cytosolic Glutathione. Journal of Biological Chemistry, 2017, 292, 638-651.	1.6	56
3333	Rescore protein-protein docked ensembles with an interface contact statistics. Proteins: Structure, Function and Bioinformatics, 2017, 85, 235-241.	1.5	7
3334	Functional and structural studies on the <i>Neisseria gonorrhoeae</i> GmhA, the first enzyme in the <i>glyceroâ€manno</i>â€heptose biosynthesis pathways, demonstrate a critical role in lipooligosaccharide synthesis and gonococcal viability. MicrobiologyOpen, 2017, 6, e00432.	1.2	20

#	ARTICLE	IF	CITATIONS
3335	Three-Dimensional Structure of Full-Length NtrX, an Unusual Member of the NtrC Family of Response Regulators. Journal of Molecular Biology, 2017, 429, 1192-1212.	2.0	26
3336	Structure of the acetophenone carboxylase core complex: prototype of a new class of ATP-dependent carboxylases/hydrolases. Scientific Reports, 2017, 7, 39674.	1.6	23
3337	Oxidative Maturation and Structural Characterization of Prenylated FMN Binding by UbiD, a Decarboxylase Involved in Bacterial Ubiquinone Biosynthesis. Journal of Biological Chemistry, 2017, 292, 4623-4637.	1.6	42
3338	A single <scp>MIU</scp> motif of <scp>MINDY</scp> â€1 recognizes K48â€linked polyubiquitin chains. EMBO Reports, 2017, 18, 392-402.	2.0	51
3339	Insights into ligand binding to a glutathione S-transferase from mango: Structure, thermodynamics and kinetics. Biochimie, 2017, 135, 35-45.	1.3	20
3340	Whaddaya Know: A Guide to Uncertainty and Subjectivity in Structural Biology. Trends in Biochemical Sciences, 2017, 42, 155-167.	3.7	14
3341	Interference of the complex between NCS-1 and Ric8a with phenothiazines regulates synaptic function and is an approach for fragile X syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E999-E1008.	3.3	40
3342	Structural studies of a vasorelaxant lectin from Dioclea reflexa Hook seeds: Crystal structure, molecular docking and dynamics. International Journal of Biological Macromolecules, 2017, 98, 12-23.	3.6	27
3343	Binding of NADP+ triggers an open-to-closed transition in a mycobacterial FabG Î²-ketoacyl-ACP reductase. Biochemical Journal, 2017, 474, 907-921.	1.7	12
3344	Myroilysin Is a New Bacterial Member of the M12A Family of Metzincin Metallopeptidases and Is Activated by a Cysteine Switch Mechanism. Journal of Biological Chemistry, 2017, 292, 5195-5206.	1.6	11
3345	The crystal structures of native hydroquinone 1,2-dioxygenase from Sphingomonas sp. TTNP3 and of substrate and inhibitor complexes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 520-530.	1.1	4
3346	Functional and Structural Analysis of Programmed C-Methylation in the Biosynthesis of the Fungal Polyketide Citrinin. Cell Chemical Biology, 2017, 24, 316-325.	2.5	30
3347	Atomic structure of granulin determined from native nanocrystalline granulovirus using an X-ray free-electron laser. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2247-2252.	3.3	65
3348	Structural insights unravel the zymogenic mechanism of the virulence factor gingipain K from Porphyromonas gingivalis, a causative agent of gum disease from the human oral microbiome. Journal of Biological Chemistry, 2017, 292, 5724-5735.	1.6	8
3349	Structural features of Zika virus non-structural proteins 3 and -5 and its individual domains in solution as well as insights into NS3 inhibition. Antiviral Research, 2017, 141, 73-90.	1.9	24
3350	A key centriole assembly interaction interface between human Plk4 and STIL appears to not be conserved in flies. Biology Open, 2017, 6, 381-389.	0.6	14
3351	Quaternary contact in the initial interaction of CD4 with the HIV-1 envelope trimer. Nature Structural and Molecular Biology, 2017, 24, 370-378.	3.6	94
3352	Crystal structure of dibenzothiophene sulfone monooxygenase BdsA from <i>Bacillus subtilis</i> WUâ€S2B. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1171-1177.	1.5	17

#	ARTICLE	IF	CITATIONS
3353	Studies on suppressors of sav2/shade avoidance 2 revealed altered interaction at the interface of Î±Î²-tubulin intradimer affects microtubule dynamics. Plant Growth Regulation, 2017, 81, 71-79.	1.8	1
3354	Structure and Function of the Stressosome Signalling Hub. Sub-Cellular Biochemistry, 2017, 83, 1-41.	1.0	38
3355	Higher-Order Structure in Bacterial VapBC Toxin-Antitoxin Complexes. Sub-Cellular Biochemistry, 2017, 83, 381-412.	1.0	15
3356	Structural basis of homo- and heterotrimerization of collagen I. Nature Communications, 2017, 8, 14671.	5.8	79
3357	Structural and functional characterization of a ubiquitin variant engineered for tight and specific binding to an alphaâ€helical ubiquitin interacting motif. Protein Science, 2017, 26, 1060-1069.	3.1	20
3358	Surface induced dissociation as a tool to study membrane protein complexes. Chemical Communications, 2017, 53, 3106-3109.	2.2	34
3359	Catalytic competence, structure and stability of the cancerâ€associated R139W variant of the human <scp>NAD</scp>(P)H:quinone oxidoreductase 1 (<scp>NQO</scp>1). FEBS Journal, 2017, 284, 1233-1245.	2.2	30
3360	Structural insights into the coordination of plastid division by the ARC6â€“PDV2 complex. Nature Plants, 2017, 3, 17011.	4.7	29
3361	Structural analysis of ribosomal RACK1 and its role in translational control. Cellular Signalling, 2017, 35, 272-281.	1.7	47
3362	Crystal Structure of the Maturation Protein from Bacteriophage QÎ². Journal of Molecular Biology, 2017, 429, 688-696.	2.0	24
3363	Potent and broad HIV-neutralizing antibodies in memory B cells and plasma. Science Immunology, 2017, 2, .	5.6	119
3364	A universal computational model for predicting antigenic variants of influenza A virus based on conserved antigenic structures. Scientific Reports, 2017, 7, 42051.	1.6	22
3365	Structure of a fungal form of aspartate-semialdehyde dehydrogenase from<i>Aspergillus fumigatus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 36-44.	0.4	9
3366	Molecular mechanism of the allosteric regulation of the Î±Î³ heterodimer of human NAD-dependent isocitrate dehydrogenase. Scientific Reports, 2017, 7, 40921.	1.6	24
3367	Notch-Jagged complex structure implicates a catch bond in tuning ligand sensitivity. Science, 2017, 355, 1320-1324.	6.0	232
3368	Structure of the Z Ring-associated Protein, ZapD, Bound to the C-terminal Domain of the Tubulin-like Protein, FtsZ, Suggests Mechanism of Z Ring Stabilization through FtsZ Cross-linking. Journal of Biological Chemistry, 2017, 292, 3740-3750.	1.6	30
3369	Long-range allosteric signaling in red lightâ€“regulated diguanylyl cyclases. Science Advances, 2017, 3, e1602498.	4.7	87
3370	Water-Soluble Chlorophyll Protein (WSCP) Stably Binds Two or Four Chlorophylls. Biochemistry, 2017, 56, 1726-1736.	1.2	25

#	Article	IF	Citations
3371	Macromolecular Protein Complexes. Sub-Cellular Biochemistry, 2017, , .	1.0	5
3372	Accurate model annotation of a near-atomic resolution cryo-EM map. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3103-3108.	3.3	111
3373	Structural Insights into the Broad Substrate Specificity of a Novel Endoglycoceramidase I Belonging to a New Subfamily of GH5 Glycosidases. Journal of Biological Chemistry, 2017, 292, 4789-4800.	1.6	17
3374	Structural, mechanistic and functional insight into gliotoxin <i>bis</i> -thiomethylation in <i>Aspergillus fumigatus</i>. Open Biology, 2017, 7, 160292.	1.5	40
3375	Nmd3 is a structural mimic of <scp>eIF</scp> 5A, and activates the cp <scp>GTP</scp> ase Lsg1 during 60S ribosome biogenesis. EMBO Journal, 2017, 36, 854-868.	3.5	67
3376	A Transition Metal-Binding, Trimeric Î²Î³-Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanosaeta thermophila</i>. Biochemistry, 2017, 56, 1299-1310.	1.2	7
3377	Cyclin F/FBXO1 Interacts with HIV-1 Viral Infectivity Factor (Vif) and Restricts Progeny Virion Infectivity by Ubiquitination and Proteasomal Degradation of Vif Protein through SCFcyclin F E3 Ligase Machinery. Journal of Biological Chemistry, 2017, 292, 5349-5363.	1.6	22
3378	Benchmarking Quantum Mechanics/Molecular Mechanics (QM/MM) Methods on the Thymidylate Synthase-Catalyzed Hydride Transfer. Journal of Chemical Theory and Computation, 2017, 13, 1375-1388.	2.3	17
3379	Five Fatty Aldehyde Dehydrogenase Enzymes from Marinobacter and Acinetobacter spp. and Structural Insights into the Aldehyde Binding Pocket. Applied and Environmental Microbiology, 2017, 83, .	1.4	7
3380	Hybrid Mass Spectrometry Approaches to Determine How L-Histidine Feedback Regulates the Enzyzme MtATP-Phosphoribosyltransferase. Structure, 2017, 25, 730-738.e4.	1.6	22
3381	Crystal structures of the Arabidopsis thaliana organellar RNA editing factors MORF1 and MORF9. Nucleic Acids Research, 2017, 45, 4915-4928.	6.5	32
3382	A structural bioinformatics investigation on proteinâ€“DNA complexes delineates their modes of interaction. Molecular BioSystems, 2017, 13, 1010-1017.	2.9	8
3383	Vesicular stomatitis virus N proteinâ€specific singleâ€domain antibody fragments inhibit replication. EMBO Reports, 2017, 18, 1027-1037.	2.0	22
3384	Crystal structure of a bicupin protein HutD involved in histidine utilization in <i>Pseudomonas</i>. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1580-1588.	1.5	2
3385	X-Ray Crystallography and Electron Microscopy of Cross- and Multi-Module Nonribosomal Peptide Synthetase Proteins Reveal a Flexible Architecture. Structure, 2017, 25, 783-793.e4.	1.6	90
3386	Leishmania donovani tyrosyl-tRNA synthetase structure in complex with a tyrosyl adenylate analog and comparisons with human and protozoan counterparts. Biochimie, 2017, 138, 124-136.	1.3	13
3387	Small methyltransferase RlmH assembles a composite active site to methylate a ribosomal pseudouridine. Scientific Reports, 2017, 7, 969.	1.6	13
3388	The Lon protease-like domain in the bacterial RecA paralog RadA is required for DNA binding and repair. Journal of Biological Chemistry, 2017, 292, 9801-9814.	1.6	15

#	ARTICLE	IF	CITATIONS
3389	Chloroplast Preproteins Bind to the Dimer Interface of the Toc159 Receptor during Import. Plant Physiology, 2017, 173, 2148-2162.	2.3	7
3390	The Nup62 Coiled-Coil Motif Provides Plasticity for Triple-Helix Bundle Formation. Biochemistry, 2017, 56, 2803-2811.	1.2	15
3392	Crystal structure of Pseudomonas aeruginosa N-acetyltransferase PA4534. Biochemical and Biophysical Research Communications, 2017, 487, 236-240.	1.0	2
3393	Using the pimeloyl-CoA synthetase adenylation fold to synthesize fatty acid thioesters. Nature Chemical Biology, 2017, 13, 660-667.	3.9	21
3394	Intermolecular Interactions Between DMÎ± and DMÎ² Proteins in BuLA-DM Complex of Water Buffalo Bubalus bubalis. Journal of Cellular Biochemistry, 2017, 118, 4254-4266.	1.2	1
3395	Symmetry in normal modes and its strong dependence on symmetry in structure. Journal of Molecular Graphics and Modelling, 2017, 75, 32-41.	1.3	6
3396	Cytidine deaminase efficiency of the lentiviral viral restriction factor APOBEC3C correlates with dimerization. Nucleic Acids Research, 2017, 45, 3378-3394.	6.5	38
3397	Structure-function analysis of RBP-J-interacting and tubulin-associated (RITA) reveals regions critical for repression of Notch target genes. Journal of Biological Chemistry, 2017, 292, 10549-10563.	1.6	34
3398	Structure and Spectroscopy of Alkene-Cleaving Dioxygenases Containing an Atypically Coordinated Non-Heme Iron Center. Biochemistry, 2017, 56, 2836-2852.	1.2	23
3399	Investigation of Core Structure and Stability of Human Pyruvate Dehydrogenase Complex: A Coarse-Grained Approach. ACS Omega, 2017, 2, 1134-1145.	1.6	12
3400	Structure, biochemical and kinetic properties of recombinant Pst2p from Saccharomyces cerevisiae , a FMN-dependent NAD(P)H:quinone oxidoreductase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1046-1056.	1.1	12
3401	Structure of a LOV protein in apo-state and implications for construction of LOV-based optical tools. Scientific Reports, 2017, 7, 42971.	1.6	16
3402	AibA/AibB Induces an Intramolecular Decarboxylation in Isovalerate Biosynthesis by Myxococcus xanthus. Angewandte Chemie - International Edition, 2017, 56, 9986-9989.	7.2	11
3403	NewProt â€" a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	1.0	11
3404	Selectivity determinants of GPCRâ€"G-protein binding. Nature, 2017, 545, 317-322.	13.7	297
3405	Rational mutagenesis by engineering disulphide bonds improves Kluyveromyces lactis beta-galactosidase for high-temperature industrial applications. Scientific Reports, 2017, 7, 45535.	1.6	24
3406	Computational dissection of allosteric inhibition of the SH2 domain of Bcr-Abl kinase by the monobody inhibitor AS25. Journal of Molecular Modeling, 2017, 23, 183.	0.8	2
3407	Identification of the key interactions in structural transition pathway of FtsZ from Staphylococcus aureus. Journal of Structural Biology, 2017, 198, 65-73.	1.3	41

#	Article	IF	Citations
3408	Crystal structure of APOBEC3A bound to single-stranded DNA reveals structural basis for cytidine deamination and specificity. Nature Communications, 2017, 8, 15024.	5.8	130
3409	Carbohydrate recognition by the rhamnoseâ€binding lectin SULâ€I with a novel threeâ€domain structure isolated from the venom of globiferous pedicellariae of the flower sea urchin <i>Toxopneustes pileolus</i>. Protein Science, 2017, 26, 1574-1583.	3.1	22
3410	Subnanometre-resolution structure of the doublet microtubule reveals new classes of microtubule-associated proteins. Nature Communications, 2017, 8, 15035.	5.8	98
3411	Structural insights into the substrate recognition and reaction specificity of the PLP-dependent fold-type I isoleucine 2-epimerase from Lactobacillus buchneri. Biochimie, 2017, 137, 165-173.	1.3	9
3412	Iron Uptake Oxidoreductase (IruO) Uses a Flavin Adenine Dinucleotide Semiquinone Intermediate for Iron-Siderophore Reduction. ACS Chemical Biology, 2017, 12, 1778-1786.	1.6	20
3413	Crystal structure of the nitrile-specifier protein NSP1 from Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2017, 488, 147-152.	1.0	8
3414	Allosteric mechanism of action of the therapeutic anti-IgE antibody omalizumab. Journal of Biological Chemistry, 2017, 292, 9975-9987.	1.6	61
3415	Structural insights into the production of 3-hydroxypropionic acid by aldehyde dehydrogenase from Azospirillum brasilense. Scientific Reports, 2017, 7, 46005.	1.6	17
3416	The Production and Utilization of GDP-glucose in the Biosynthesis of Trehalose 6-Phosphate by Streptomyces venezuelae. Journal of Biological Chemistry, 2017, 292, 945-954.	1.6	13
3417	Structural insights into a family 39 glycoside hydrolase from the gut symbiont Bacteroides cellulosilyticus WH2. Journal of Structural Biology, 2017, 197, 227-235.	1.3	9
3418	Structural Basis of Egg Coat-Sperm Recognition at Fertilization. Cell, 2017, 169, 1315-1326.e17.	13.5	78
3419	Open and compressed conformations of <i>Francisella tularensis</i> ClpP. Proteins: Structure, Function and Bioinformatics, 2017, 85, 188-194.	1.5	7
3420	S-adenosyl-L-homocysteine hydrolase from a hyperthermophile (Thermotoga maritima) is expressed in Escherichia coli in inactive form â€“ Biochemical and structural studies. International Journal of Biological Macromolecules, 2017, 104, 584-596.	3.6	8
3421	<i>Streptococcus pyogenes</i> quinolinateâ€salvage pathwayâ€”structural and functional studies of quinolinate phosphoribosyl transferase and NH₃â€dependent NAD⁺ synthetase. FEBS Journal, 2017, 284, 2425-2441.	2.2	6
3422	Structural Characterization of a Eukaryotic Cyanase from <i>Tetranychus urticae</i>. Journal of Agricultural and Food Chemistry, 2017, 65, 5453-5462.	2.4	11
3423	Regulation of E2s: A Role for Additional Ubiquitin Binding Sites?. Journal of Molecular Biology, 2017, 429, 3430-3440.	2.0	17
3424	De novo non-synonymous TBL1XR1 mutation alters Wnt signaling activity. Scientific Reports, 2017, 7, 2887.	1.6	19
3425	Mechanistic insight into the substrate specificity of 1,2-Î²-oligoglucan phosphorylase from Lachnoclostridium phytofermentans. Scientific Reports, 2017, 7, 42671.	1.6	36

#	ARTICLE	IF	CITATIONS
3426	A Polymerization-Associated Structural Switch in FtsZ That Enables Treadmilling of Model Filaments. MBio, 2017, 8, .	1.8	91
3427	Heterotrimeric complex of p38 MAPK, PKCÎ´, and TIRAP is required for AP1 mediated inflammatory response. International Immunopharmacology, 2017, 48, 211-218.	1.7	12
3428	The origin and evolution of human glutaminases and their atypical C-terminal ankyrin repeats. Journal of Biological Chemistry, 2017, 292, 11572-11585.	1.6	19
3429	Architecture of the paracellular channels formed by claudins of the bloodâ€"brain barrier tight junctions. Annals of the New York Academy of Sciences, 2017, 1405, 131-146.	1.8	56
3430	Structure of CC Chemokine Receptor 5 with a Potent Chemokine Antagonist Reveals Mechanisms of Chemokine Recognition and Molecular Mimicry by HIV. Immunity, 2017, 46, 1005-1017.e5.	6.6	148
3431	Interactions between gut bacteria and bile in health and disease. Molecular Aspects of Medicine, 2017, 56, 54-65.	2.7	341
3432	Virtual screening of selective inhibitors of phosphopantetheine adenylyltransferase from Mycobacterium tuberculosis. Crystallography Reports, 2017, 62, 405-410.	0.1	1
3433	Molecular Mechanism of MDGA1: Regulation of Neuroligin 2:Neurexin Trans-synaptic Bridges. Neuron, 2017, 94, 1132-1141.e4.	3.8	52
3434	The maximum penalty criterion for ridge regression: application to the calibration of the force constant in elastic network models. Integrative Biology (United Kingdom), 2017, 9, 627-641.	0.6	13
3435	Insights into PGâ€binding, conformational change, and dimerization of the OmpA Câ€terminal domains from Salmonella enterica serovar Typhimurium and Borrelia burgdorferi. Protein Science, 2017, 26, 1738-1748.	3.1	8
3436	Structural and Enzymatic Characterization of a cAMP-Dependent Diguanylate Cyclase from Pathogenic Leptospira Species. Journal of Molecular Biology, 2017, 429, 2337-2352.	2.0	24
3437	Structural basis of HypK regulating N-terminal acetylation by the NatA complex. Nature Communications, 2017, 8, 15726.	5.8	44
3438	Functional details of the Mycobacterium tuberculosis VapBC26 toxin-antitoxin system based on a structural study: insights into unique binding and antibiotic peptides. Nucleic Acids Research, 2017, 45, 8564-8580.	6.5	44
3439	Conformational Flexibility in the Immunoglobulin-Like Domain of the Hepatitis C Virus Glycoprotein E2. MBio, 2017, 8, .	1.8	31
3440	Recognition of EGF-like domains by the Notch-modifying O-fucosyltransferase POFUT1. Nature Chemical Biology, 2017, 13, 757-763.	3.9	62
3441	Structural basis for a novel type of cytokinin-activating protein. Scientific Reports, 2017, 7, 45985.	1.6	28
3442	Crystallographic and biochemical characterization of the dimeric architecture of site-2 protease. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 1859-1871.	1.4	6
3443	Structure of a soluble epoxide hydrolase identified in Trichoderma reesei. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1039-1045.	1.1	10

#	Article	IF	Citations
3444	Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in Enterococcus faecalis. Journal of Molecular Biology, 2017, 429, 2324-2336.	2.0	15
3445	Zinc and the iron donor frataxin regulate oligomerization of the scaffold protein to form new Feâ€"S cluster assembly centers. Metallomics, 2017, 9, 773-801.	1.0	6
3446	Molecular and functional characterization of a glycosylated Galactose-Binding lectin from Mytilus californianus. Fish and Shellfish Immunology, 2017, 66, 564-574.	1.6	27
3447	The LOTUS domain is a conserved DEAD-box RNA helicase regulator essential for the recruitment of Vasa to the germ plasm and nuage. Genes and Development, 2017, 31, 939-952.	2.7	61
3448	Discovery of novel inhibitors for Leishmania nucleoside diphosphatase kinase (NDK) based on its structural and functional characterization. Journal of Computer-Aided Molecular Design, 2017, 31, 547-562.	1.3	21
3449	The Crystal Structure of a Bacterial l-Arabinonate Dehydratase Contains a [2Fe-2S] Cluster. ACS Chemical Biology, 2017, 12, 1919-1927.	1.6	25
3450	A structural mechanism of flavonoids in inhibiting serine proteases. Food and Function, 2017, 8, 2437-2443.	2.1	46
3451	How an alloreactive T-cell receptor achieves peptide and MHC specificity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4792-E4801.	3.3	42
3452	The â€œSticky Patchâ€•Model of Crystallization and Modification of Proteins for Enhanced Crystallizability. Methods in Molecular Biology, 2017, 1607, 77-115.	0.4	17
3453	Tight Molecular Recognition of Benzo[<i>a</i>]pyrene by a Highâ€Affinity Antibody. Angewandte Chemie - International Edition, 2017, 56, 10592-10597.	7.2	9
3454	Structural Basis for Aryl Hydrocarbon Receptor-Mediated Gene Activation. Structure, 2017, 25, 1025-1033.e3.	1.6	95
3455	Insights into Hunter syndrome from the structure of iduronate-2-sulfatase. Nature Communications, 2017, 8, 15786.	5.8	68
3456	IgG Fc domains that bind C1q but not effector FcÎ³ receptors delineate the importance of complement-mediated effector functions. Nature Immunology, 2017, 18, 889-898.	7.0	122
3457	The Enzyme Activity and Substrate Specificity of Two Major Cinnamyl Alcohol Dehydrogenases in Sorghum (<i>Sorghum bicolor</i>), SbCAD2 and SbCAD4. Plant Physiology, 2017, 174, 2128-2145.	2.3	32
3458	Enge molekulare Erkennung von Benzo[<i>a</i>]pyren durch einen hochaffinen AntikÃ¶rper. Angewandte Chemie, 2017, 129, 10728-10733.	1.6	2
3459	Timing and Reset Mechanism of GTP Hydrolysis-Driven Conformational Changes of Atlastin. Structure, 2017, 25, 997-1010.e4.	1.6	27
3460	Structural studies of viperin, an antiviral radical SAM enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6806-6811.	3.3	69
3461	Crystal structure of the thioesterification conformation of Bacillus subtilis o-succinylbenzoyl-CoA synthetase reveals a distinct substrate-binding mode. Journal of Biological Chemistry, 2017, 292, 12296-12310.	1.6	6

#	ARTICLE	IF	CITATIONS
3462	Insight into the transition between the open and closed conformations of Thermus thermophilus carboxypeptidase. Biochemical and Biophysical Research Communications, 2017, 484, 787-793.	1.0	7
3463	Allosteric modulation of peroxisomal membrane protein recognition by farnesylation of the peroxisomal import receptor PEX19. Nature Communications, 2017, 8, 14635.	5.8	47
3464	The Structure of an Archaeal Î±-Glucosaminidase Provides Insight into Glycoside Hydrolase Evolution. Journal of Biological Chemistry, 2017, 292, 4996-5006.	1.6	8
3465	Hierarchical Assembly of Tough Bioelastomeric Egg Capsules is Mediated by a Bundling Protein. Biomacromolecules, 2017, 18, 931-942.	2.6	4
3466	Structural basis for redox sensitivity in Corynebacterium glutamicum diaminopimelate epimerase: an enzyme involved in l-lysine biosynthesis. Scientific Reports, 2017, 7, 42318.	1.6	19
3467	IgE binds asymmetrically to its B cell receptor CD23. Scientific Reports, 2017, 7, 45533.	1.6	25
3468	Is dimerization a common feature in thioredoxins? The case of thioredoxin from<i>Litopenaeus vannamei</i>. Acta Crystallographica Section D: Structural Biology, 2017, 73, 326-339.	1.1	11
3469	The structure and polymerase-recognition mechanism of the crucial adaptor protein AND-1 in the human replisome. Journal of Biological Chemistry, 2017, 292, 9627-9636.	1.6	33
3470	Unraveling self-assembly pathways of the 468-kDa proteolytic machine TET2. Science Advances, 2017, 3, e1601601.	4.7	28
3471	Structural Basis of Eco1-Mediated Cohesin Acetylation. Scientific Reports, 2017, 7, 44313.	1.6	10
3472	Structure of the WipA protein reveals a novel tyrosine protein phosphatase effector from Legionella pneumophila. Journal of Biological Chemistry, 2017, 292, 9240-9251.	1.6	12
3473	Human apo-SRP72 and SRP68/72 complex structures reveal the molecular basis of protein translocation. Journal of Molecular Cell Biology, 2017, 9, 220-230.	1.5	15
3474	Structure of the Cyanuric Acid Hydrolase TrzD Reveals Product Exit Channel. Scientific Reports, 2017, 7, 45277.	1.6	5
3475	Crystal structure of a small heat-shock protein from<i>Xylella fastidiosa</i>reveals a distinct high-order structure. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 222-227.	0.4	7
3476	Structural reconstruction of protein ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3897-3902.	3.3	12
3477	Kinetics and Structure of a Cold-Adapted Hetero-Octameric ATP Phosphoribosyltransferase. Biochemistry, 2017, 56, 793-803.	1.2	14
3478	Crystal structure of U2 snRNP SF3b components: Hsh49p in complex with Cus1p-binding domain. Rna, 2017, 23, 968-981.	1.6	10
3479	Structural basis of PROTAC cooperative recognition for selective protein degradation. Nature Chemical Biology, 2017, 13, 514-521.	3.9	758

#	ARTICLE	IF	CITATIONS
3480	Overall Shapes of the SMC-ScpAB Complex Are Determined by Balance between Constraint and Relaxation of Its Structural Parts. Structure, 2017, 25, 603-616.e4.	1.6	48
3481	Stilbene epoxidation and detoxification in a Photorhabdus luminescens-nematode symbiosis. Journal of Biological Chemistry, 2017, 292, 6680-6694.	1.6	20
3482	Crystal structure of the essential biotinâ€dependent carboxylase AccA3 from <i>Mycobacterium tuberculosis</i>. FEBS Open Bio, 2017, 7, 620-626.	1.0	3
3483	Structural insights into the Î³-lactamase activity and substrate enantioselectivity of an isochorismatase-like hydrolase from Microbacterium hydrocarbonoxydans. Scientific Reports, 2017, 7, 44542.	1.6	9
3484	Two alternative binding mechanisms connect the protein translocation Sec71-Sec72 complex with heat shock proteins. Journal of Biological Chemistry, 2017, 292, 8007-8018.	1.6	43
3485	Resolving the cofactor-binding site in the proline biosynthetic enzyme human pyrroline-5-carboxylate reductase 1. Journal of Biological Chemistry, 2017, 292, 7233-7243.	1.6	42
3486	Antibiotic Capture by Bacterial Lipocalins Uncovers an Extracellular Mechanism of Intrinsic Antibiotic Resistance. MBio, 2017, 8, .	1.8	31
3487	Structural basis of the day-night transition in a bacterial circadian clock. Science, 2017, 355, 1174-1180.	6.0	144
3488	Identification of C3b-Binding Small-Molecule Complement Inhibitors Using Cheminformatics. Journal of Immunology, 2017, 198, 3705-3718.	0.4	11
3489	Effect of Meso vs Macro Size of Hierarchical Porous Silica on the Adsorption and Activity of Immobilized Î²-Galactosidase. Langmuir, 2017, 33, 3333-3340.	1.6	26
3490	Discovery and characterization of an F420-dependent glucose-6-phosphate dehydrogenase (Rh-FGD1) from Rhodococcus jostii RHA1. Applied Microbiology and Biotechnology, 2017, 101, 2831-2842.	1.7	28
3491	Structure activity study of carbonic anhydrase IX: Selective inhibition with ureido-substituted benzenesulfonamides. European Journal of Medicinal Chemistry, 2017, 132, 184-191.	2.6	58
3492	Structures of human O-GlcNAcase and its complexes reveal a new substrate recognition mode. Nature Structural and Molecular Biology, 2017, 24, 362-369.	3.6	72
3493	Site-to-site interdomain communication may mediate different loss-of-function mechanisms in a cancer-associated NQO1 polymorphism. Scientific Reports, 2017, 7, 44532.	1.6	35
3494	The IFN-Î»-IFN-Î»R1-IL-10RÎ² Complex Reveals Structural Features Underlying Type III IFN Functional Plasticity. Immunity, 2017, 46, 379-392.	6.6	89
3495	Crystal Structure of the Extracellular Domain of the Human Dendritic Cell Surface Marker CD83. Journal of Molecular Biology, 2017, 429, 1227-1243.	2.0	11
3496	Insights into Rad3 kinase recruitment from the crystal structure of the DNA damage checkpoint protein Rad26. Journal of Biological Chemistry, 2017, 292, 8149-8157.	1.6	5
3497	Surface-Induced Dissociation of Protein Complexes in a Hybrid Fourier Transform Ion Cyclotron Resonance Mass Spectrometer. Analytical Chemistry, 2017, 89, 895-901.	3.2	22

#	Article	IF	Citations
3498	The structure of the mite allergen Blo t 1 explains the limited antibody cross-reactivity to Der p 1. Allergy: European Journal of Allergy and Clinical Immunology, 2017, 72, 665-670.	2.7	14
3499	The surge of flavonoids as novel, fine regulators of cardiovascular Cav channels. European Journal of Pharmacology, 2017, 796, 158-174.	1.7	45
3500	Cryo-electron Microscopy Study of the Genome Release of the Dicistrovirus Israeli Acute Bee Paralysis Virus. Journal of Virology, 2017, 91, .	1.5	10
3501	â€œTo Cross-Seed or Not To Cross-Seedâ€: A Pilot Study Using Metallo-Î²-lactamases. Crystal Growth and Design, 2017, 17, 913-924.	1.4	8
3502	Crystal structure of human chondroadherin: solving a difficult molecular-replacement problem using<i>de novo</i>models. Acta Crystallographica Section D: Structural Biology, 2017, 73, 53-63.	1.1	9
3503	Crystal structure of a phospholipase A2 from Bothrops asper venom: Insights into a new putative â€œmyotoxic clusterâ€. Biochimie, 2017, 133, 95-102.	1.3	18
3504	Structural Basis of the Oncogenic Interaction of Phosphatase PRL-1 with the Magnesium Transporter CNNM2. Journal of Biological Chemistry, 2017, 292, 786-801.	1.6	48
3505	Toward Closing the Gap: Quantum Mechanical Calculations and Experimentally Measured Chemical Shifts of a Microcrystalline Lectin. Journal of Physical Chemistry B, 2017, 121, 3574-3585.	1.2	9
3506	Identification of mouse cathepsin K structural elements that regulate the potency of odanacatib. Biochemical Journal, 2017, 474, 851-864.	1.7	24
3507	Architecture and mechanism of the late endosomal Rab7-like Ypt7 guanine nucleotide exchange factor complex Mon1â€“Ccz1. Nature Communications, 2017, 8, 14034.	5.8	59
3508	Mutational landscape of antibody variable domains reveals a switch modulating the interdomain conformational dynamics and antigen binding. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E486-E495.	3.3	72
3509	Short Carboxylic Acidâ€“Carboxylate Hydrogen Bonds Can Have Fully Localized Protons. Biochemistry, 2017, 56, 391-402.	1.2	41
3510	Binding of Myomesin to Obscurin-Like-1 at the Muscle M-Band Provides a Strategy for Isoform-Specific Mechanical Protection. Structure, 2017, 25, 107-120.	1.6	25
3511	Molecular insights into the enzyme promiscuity of an aromatic prenyltransferase. Nature Chemical Biology, 2017, 13, 226-234.	3.9	100
3512	The Methylerythritol Phosphate Pathway to Isoprenoids. Chemical Reviews, 2017, 117, 5675-5703.	23.0	129
3513	Structural basis of influenza virus fusion inhibition by the antiviral drug Arbidol. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 206-214.	3.3	340
3514	The tomato <i>I</i> gene for Fusarium wilt resistance encodes an atypical leucineâ€rich repeat receptorâ€like protein whose function is nevertheless dependent on <scp>SOBIR</scp>1 and <scp>SERK</scp>3/<scp>BAK</scp>1. Plant Journal, 2017, 89, 1195-1209.	2.8	103
3515	New additions to the <scp>C</scp>lus<scp>P</scp>ro server motivated by <scp>CAPRI</scp>. Proteins: Structure, Function and Bioinformatics, 2017, 85, 435-444.	1.5	395

#	ARTICLE	IF	CITATIONS
3516	Structural and Biochemical Characterization of Cinnamoyl-CoA Reductases. Plant Physiology, 2017, 173, 1031-1044.	2.3	29
3517	Proteome Bioinformatics. Methods in Molecular Biology, 2017, , .	0.4	5
3518	Bioinformatics Tools and Resources for Analyzing Protein Structures. Methods in Molecular Biology, 2017, 1549, 209-220.	0.4	21
3519	Reverse chemical ecology: Olfactory proteins from the giant panda and their interactions with putative pheromones and bamboo volatiles. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9802-E9810.	3.3	86
3520	Exploitation of an iron transporter for bacterial protein antibiotic import. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12051-12056.	3.3	76
3521	Norovirus Escape from Broadly Neutralizing Antibodies Is Limited to Allostery-Like Mechanisms. MSphere, 2017, 2, .	1.3	30
3522	Structural insights into GDP-mediated regulation of a bacterial acyl-CoA thioesterase. Journal of Biological Chemistry, 2017, 292, 20461-20471.	1.6	9
3523	Structure of a novel antibacterial toxin that exploits elongation factor Tu to cleave specific transfer RNAs. Nucleic Acids Research, 2017, 45, 10306-10320.	6.5	23
3524	Architecture of eukaryotic mRNA 3â€²-end processing machinery. Science, 2017, 358, 1056-1059.	6.0	124
3525	Functional and Structural Studies of a Multidomain Alginate Lyase from Persicobacter sp. CCB-QB2. Scientific Reports, 2017, 7, 13656.	1.6	52
3526	A unique surface on Pat1 C-terminal domain directly interacts with Dcp2 decapping enzyme and Xrn1 5â€²â€"3â€² mRNA exonuclease in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9493-E9501.	3.3	45
3527	The Crystal Structure and Conformations of an Unbranched Mixed Tri-Ubiquitin Chain Containing K48 and K63 Linkages. Journal of Molecular Biology, 2017, 429, 3801-3813.	2.0	3
3528	L-Asparaginase of Leishmania donovani: Metabolic target and its role in Amphotericin B resistance. International Journal for Parasitology: Drugs and Drug Resistance, 2017, 7, 337-349.	1.4	20
3529	Structure of a Reptilian Adenovirus Reveals a Phage Tailspike Fold Stabilizing a Vertebrate Virus Capsid. Structure, 2017, 25, 1562-1573.e5.	1.6	19
3530	Biophysical characterization and structure of the Fab fragment from the NIST reference antibody, RM 8671. Biologicals, 2017, 50, 27-34.	0.5	23
3531	Molecular basis of human CD22 function and therapeutic targeting. Nature Communications, 2017, 8, 764.	5.8	114
3532	Structural and Functional Characterization of a Short-Chain Flavodoxin Associated with a Noncanonical 1,2-Propanediol Utilization Bacterial Microcompartment. Biochemistry, 2017, 56, 5679-5690.	1.2	4
3533	Molecular architecture of the PBP2â€"MreC core bacterial cell wall synthesis complex. Nature Communications, 2017, 8, 776.	5.8	57

#	Article	IF	Citations
3534	Structural analyses of the MazEF4 toxin-antitoxin pair in Mycobacterium tuberculosis provide evidence for a unique extracellular death factor. Journal of Biological Chemistry, 2017, 292, 18832-18847.	1.6	25
3535	Proteinâ€"protein interactions leave evolutionary footprints: High molecular coevolution at the core of interfaces. Protein Science, 2017, 26, 2438-2444.	3.1	23
3536	Structural Basis for a Safety-Belt Mechanism That Anchors Condensin to Chromosomes. Cell, 2017, 171, 588-600.e24.	13.5	144
3537	Structure of SgK223 pseudokinase reveals novel mechanisms of homotypic and heterotypic association. Nature Communications, 2017, 8, 1157.	5.8	40
3538	Structural basis for the functional role of the Shu complex in homologous recombination. Nucleic Acids Research, 2017, 45, 13068-13079.	6.5	21
3539	Protocadherin <i>cis</i> -dimer architecture and recognition unit diversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9829-E9837.	3.3	55
3540	Procaspase-activating compound-1 induces apoptosis in Trypanosoma cruzi. Apoptosis: an International Journal on Programmed Cell Death, 2017, 22, 1564-1577.	2.2	11
3541	Structural insights into the interaction of the conserved mammalian proteins GAPR-1 and Beclin 1, a key autophagy protein. Acta Crystallographica Section D: Structural Biology, 2017, 73, 775-792.	1.1	14
3542	Structural basis for enzyme bifunctionality â€" the case of Gan1D from <i>GeobacillusÂstearothermophilus</i>. FEBS Journal, 2017, 284, 3931-3953.	2.2	9
3543	Toward Bayesian inference of the spatial distribution of proteins from three-cube FÃ¶rster resonance energy transfer data. Annals of Applied Statistics, 2017, 11, 1711-1737.	0.5	2
3544	Crystal structure and functional characterization of <scp>SF</scp>216 from <i>Shigella flexneri</i>. FEBS Letters, 2017, 591, 3692-3703.	1.3	1
3545	Selenoprotein MsrB1 deficiency exacerbates acetaminophen-induced hepatotoxicity via increased oxidative damage. Archives of Biochemistry and Biophysics, 2017, 634, 69-75.	1.4	13
3546	KLK5 induces shedding of DPP4 from circulatory Th17 cells in type 2 diabetes. Molecular Metabolism, 2017, 6, 1529-1539.	3.0	44
3547	Structural and Functional Implications of Human Transforming Growth Factor Î²-Induced Protein, TGFBIp, in Corneal Dystrophies. Structure, 2017, 25, 1740-1750.e2.	1.6	24
3548	Unraveling Binding Interactions between Human RANKL and Its Decoy Receptor Osteoprotegerin. Journal of Physical Chemistry B, 2017, 121, 9141-9148.	1.2	12
3549	Crystal structure of the <i>Legionella pneumophila</i> Lpg2936 in complex with the cofactor Sâ€adenosylâ€Lâ€methionine reveals novel insights into the mechanism of RsmE family methyltransferases. Protein Science, 2017, 26, 2381-2391.	3.1	9
3550	Cryo-EM structure of the extended type VI secretion system sheathâ€"tube complex. Nature Microbiology, 2017, 2, 1507-1512.	5.9	107
3551	Crystal Structures of Two Immune Complexes Identify Determinants for Viral Infectivity and Type-Specific Neutralization of Human Papillomavirus. MBio, 2017, 8, .	1.8	20

#	Article	IF	Citations
3552	Crystal structure of l -glutamate N -acetyltransferase ArgA from Mycobacterium tuberculosis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1800-1807.	1.1	6
3553	Structural analysis of Dioclea lasiocarpa lectin: A C6 cells apoptosis-inducing protein. International Journal of Biochemistry and Cell Biology, 2017, 92, 79-89.	1.2	12
3554	Crystal structure of a TAPBPRâ€"MHC I complex reveals the mechanism of peptide editing in antigen presentation. Science, 2017, 358, 1064-1068.	6.0	111
3555	Structural Basis of Mec1-Ddc2-RPA Assembly and Activation on Single-Stranded DNA at Sites of Damage. Molecular Cell, 2017, 68, 431-445.e5.	4.5	55
3556	A structural model of flagellar filament switching across multiple bacterial species. Nature Communications, 2017, 8, 960.	5.8	90
3557	Contributions and Future Directions for Structural Biology in the Study of Allergens. International Archives of Allergy and Immunology, 2017, 174, 57-66.	0.9	19
3558	APOBEC3H structure reveals an unusual mechanism of interaction with duplex RNA. Nature Communications, 2017, 8, 1021.	5.8	44
3559	Three-dimensional context rather than NLS amino acid sequence determines importin Î± subtype specificity for RCC1. Nature Communications, 2017, 8, 979.	5.8	54
3560	Molecular basis for inner kinetochore configuration through <scp>RWD</scp> domainâ€"peptide interactions. EMBO Journal, 2017, 36, 3458-3482.	3.5	34
3561	A General Strategy for Discovery of Inhibitors and Activators of RING and U-box E3 Ligases with Ubiquitin Variants. Molecular Cell, 2017, 68, 456-470.e10.	4.5	56
3562	Packing topology in crystals of proteins and small molecules: a comparison. Scientific Reports, 2017, 7, 13209.	1.6	31
3563	Structural Transitions of the Conserved and Metastable Hantaviral Glycoprotein Envelope. Journal of Virology, 2017, 91, .	1.5	38
3564	Distribution, Localization, and Structure of Plant Polyphenol Oxidases (PPOs). , 2017, , 11-32.		4
3565	Polyphenol Oxidases (PPOs) in Plants. , 2017, , .		21
3566	Structural Characterization of Acidic M17 Leucine Aminopeptidases from the TriTryps and Evaluation of Their Role in Nutrient Starvation in Trypanosoma brucei. MSphere, 2017, 2, .	1.3	15
3567	Tethering not required: the glucocorticoid receptor binds directly to activator protein-1 recognition motifs to repress inflammatory genes. Nucleic Acids Research, 2017, 45, 8596-8608.	6.5	69
3568	Crystal structures reveal metal-binding plasticity at the metallo-Î²-lactamase active site of PqqB from Pseudomonas putida. Journal of Biological Inorganic Chemistry, 2017, 22, 1089-1097.	1.1	10
3569	Structural analyses of the bacterial primosomal protein DnaB reveal that it is a tetramer and forms a complex with a primosomal re-initiation protein. Journal of Biological Chemistry, 2017, 292, 15744-15757.	1.6	8

#	ARTICLE	IF	CITATIONS
3570	Glucose-1-phosphate uridylyltransferase from Erwinia amylovora : Activity, structure and substrate specificity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1348-1357.	1.1	13
3571	Unitary Properties of AMPA Receptors with Reduced Desensitization. Biophysical Journal, 2017, 113, 2218-2235.	0.2	15
3572	Interaction of 2A proteinase of human rhinovirus genetic group A with eIF4E is required for eIF4G cleavage during infection. Virology, 2017, 511, 123-134.	1.1	16
3573	Structureâ€"function analysis of the <i>Fusarium oxysporum</i> Avr2 effector allows uncoupling of its immuneâ€suppressing activity from recognition. New Phytologist, 2017, 216, 897-914.	3.5	72
3574	Insights into the recognition and electron transfer steps in nitric oxide reductase from Marinobacter hydrocarbonoclasticus. Journal of Inorganic Biochemistry, 2017, 177, 402-411.	1.5	11
3575	Dissecting the CD93-Multimerin 2 interaction involved in cell adhesion and migration of the activated endothelium. Matrix Biology, 2017, 64, 112-127.	1.5	59
3576	IL-1 Family Cytokines Use Distinct Molecular Mechanisms to Signal through Their Shared Co-receptor. Immunity, 2017, 47, 510-523.e4.	6.6	48
3577	In silico modeling of the cryptic E2â^¼ubiquitinâ€"binding site of E6-associated protein (E6AP)/UBE3A reveals the mechanism of polyubiquitin chain assembly. Journal of Biological Chemistry, 2017, 292, 18006-18023.	1.6	18
3578	Atomic structures of Coxsackievirus A6 and its complex with a neutralizing antibody. Nature Communications, 2017, 8, 505.	5.8	61
3579	Structural characterization of CAS SH3 domain selectivity and regulation reveals new CAS interaction partners. Scientific Reports, 2017, 7, 8057.	1.6	14
3580	The human IL-17A/F heterodimer: a two-faced cytokine with unique receptor recognition properties. Scientific Reports, 2017, 7, 8906.	1.6	69
3581	Stabilizing an amyloidogenic Î»6 light chain variable domain. FEBS Journal, 2017, 284, 3702-3717.	2.2	9
3582	Crystal structure of a novel prolidase from <i>Deinococcus radiodurans</i> identifies new subfamily of bacterial prolidases. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2239-2251.	1.5	3
3583	Structure of an Insecticide Sequestering Carboxylesterase from the Disease Vector <i>Culex quinquefasciatus:</i> What Makes an Enzyme a Good Insecticide Sponge?. Biochemistry, 2017, 56, 5512-5525.	1.2	24
3584	Crystal structure of the human lysosomal mTORC1 scaffold complex and its impact on signaling. Science, 2017, 358, 377-381.	6.0	110
3585	A camelid single-domain antibody neutralizes botulinum neurotoxin A by blocking host receptor binding. Scientific Reports, 2017, 7, 7438.	1.6	16
3586	On the potential alternate binding change mechanism in a dimeric structure of Pyruvate Phosphate Dikinase. Scientific Reports, 2017, 7, 8020.	1.6	6
3587	Effect of amino acid mutations on the conformational dynamics of amyloidogenic immunoglobulin light-chains: A combined NMR and in silico study. Scientific Reports, 2017, 7, 10339.	1.6	4

#	ARTICLE	IF	CITATIONS
3588	Structures of Leishmania Fructose-1,6-Bisphosphatase Reveal Species-Specific Differences in the Mechanism of Allosteric Inhibition. Journal of Molecular Biology, 2017, 429, 3075-3089.	2.0	11
3589	Periplasmic Binding Protein Dimer Has a Second Allosteric Event Tied to Ligand Binding. Biochemistry, 2017, 56, 5328-5337.	1.2	14
3590	Structures of Medicago truncatula L-Histidinol Dehydrogenase Show Rearrangements Required for NAD+ Binding and the Cofactor Positioned to Accept a Hydride. Scientific Reports, 2017, 7, 10476.	1.6	11
3591	Structural and functional insights into the interaction between the Cas family scaffolding protein p130Cas and the focal adhesion-associated protein paxillin. Journal of Biological Chemistry, 2017, 292, 18281-18289.	1.6	16
3592	The fused SnoaL_2 domain in the Mycobacterium tuberculosis sigma factor ÏƒJ modulates promoter recognition. Nucleic Acids Research, 2017, 45, 9760-9772.	6.5	16
3593	The human cytomegalovirus nuclear egress complex unites multiple functions: Recruitment of effectors, nuclear envelope rearrangement, and docking to nuclear capsids. Reviews in Medical Virology, 2017, 27, e1934.	3.9	39
3594	Crystal structure of a Î²-fructofuranosidase with high transfructosylation activity from <i>Aspergillus kawachii</i>. Bioscience, Biotechnology and Biochemistry, 2017, 81, 1786-1795.	0.6	26
3595	Near-Atomic Resolution Structure of a Plant Geminivirus Determined by Electron Cryomicroscopy. Structure, 2017, 25, 1303-1309.e3.	1.6	35
3596	Cryo-EM structures of the ATP-bound Vps4E233Q hexamer and its complex with Vta1 at near-atomic resolution. Nature Communications, 2017, 8, 16064.	5.8	42
3597	Analysis and prediction of protein folding energy changes upon mutation by element specific persistent homology. Bioinformatics, 2017, 33, 3549-3557.	1.8	48
3598	Assessment of the protein interaction between coagulation factorÂXII and corn trypsin inhibitor by molecular docking and biochemical validation. Journal of Thrombosis and Haemostasis, 2017, 15, 1818-1828.	1.9	11
3599	Mechanism for G2 phase-specific nuclear export of the kinetochore protein CENP-F. Cell Cycle, 2017, 16, 1414-1429.	1.3	15
3600	Structure of the adenylation domain Thr1 involved in the biosynthesis of 4â€chlorothreonine in <i>Streptomyces</i> sp. <scp>OH</scp>â€5093â€”protein flexibility and molecular bases of substrate specificity. FEBS Journal, 2017, 284, 2981-2999.	2.2	13
3601	Biophysical investigation of type A PutAs reveals a conserved core oligomeric structure. FEBS Journal, 2017, 284, 3029-3049.	2.2	14
3602	Crystallographic and solution structure of the Nâ€terminal domain of the Rel protein from <i>Mycobacterium tuberculosis</i>. FEBS Letters, 2017, 591, 2323-2337.	1.3	27
3603	Insights into the Giardia intestinalis enolase and human plasminogen interaction. Molecular BioSystems, 2017, 13, 2015-2023.	2.9	9
3604	Use of a neutralizing antibody helps identify structural features critical for binding of Clostridium difficile toxin TcdA to the host cell surface. Journal of Biological Chemistry, 2017, 292, 14401-14412.	1.6	10
3605	Structure and evolution of <scp>ENTH</scp> and <scp>VHS</scp>/<scp>ENTH</scp>â€like domains in tepsin. Traffic, 2017, 18, 590-603.	1.3	9

#	ARTICLE	IF	CITATIONS
3606	Structural Insight into the Activation of PknI Kinase from M.Âtuberculosis via Dimerization of the Extracellular Sensor Domain. Structure, 2017, 25, 1286-1294.e4.	1.6	5
3607	Crystal structures of the isochorismatase domains from Vibrio anguillarum. Biochemical and Biophysical Research Communications, 2017, 490, 827-833.	1.0	3
3608	Structural bases of the altered catalytic properties of a pathogenic variant of apoptosis inducing factor. Biochemical and Biophysical Research Communications, 2017, 490, 1011-1017.	1.0	9
3609	Structure of thrombospondin type 3 repeats in bacterial outer membrane protein A reveals its intra-repeat disulfide bond-dependent calcium-binding capability. Cell Calcium, 2017, 66, 78-89.	1.1	7
3610	Structural Basis for Regulation of ESCRT-III Complexes by Lgd. Cell Reports, 2017, 19, 1750-1757.	2.9	17
3611	Structural insights into a high affinity nanobody:antigen complex by homology modelling. Journal of Molecular Graphics and Modelling, 2017, 76, 305-312.	1.3	12
3612	Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle. Molecular Cell, 2017, 67, 322-333.e6.	4.5	35
3613	Conformational variability of the stationary phase survival protein E from <i>Xylella fastidiosa</i> revealed by X-ray crystallography, small-angle X-ray scattering studies, and normal mode analysis. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1931-1943.	1.5	0
3614	Structural studies with BnSP-7 reveal an atypical oligomeric conformation compared to phospholipases A2-like toxins. Biochimie, 2017, 142, 11-21.	1.3	11
3615	The <i><scp>ALDH</scp>21</i> gene found in lower plants and some vascular plants codes for a <scp>NADP</scp>⁺â€dependent succinic semialdehyde dehydrogenase. Plant Journal, 2017, 92, 229-243.	2.8	10
3616	Crystal structure of master biofilm regulator CsgD regulatory domain reveals an atypical receiver domain. Protein Science, 2017, 26, 2073-2082.	3.1	11
3617	The trimer interface in the quaternary structure of the bifunctional prokaryotic FAD synthetase from Corynebacterium ammoniagenes. Scientific Reports, 2017, 7, 404.	1.6	16
3618	SnoN Stabilizes the SMAD3/SMAD4 Protein Complex. Scientific Reports, 2017, 7, 46370.	1.6	17
3619	Substrate specificity and reaction mechanism of human prolidase. FEBS Journal, 2017, 284, 2870-2885.	2.2	26
3620	OH1 from Orf Virus: A New Tyrosine Phosphatase that Displays Distinct Structural Features and Triple Substrate Specificity. Journal of Molecular Biology, 2017, 429, 2816-2824.	2.0	6
3621	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. Nature Structural and Molecular Biology, 2017, 24, 743-751.	3.6	140
3622	Structural basis for dolichylphosphate mannose biosynthesis. Nature Communications, 2017, 8, 120.	5.8	24
3623	Structural insights into a 20.8-kDa tegumental-allergen-like (TAL) protein from Clonorchis sinensis. Scientific Reports, 2017, 7, 1764.	1.6	9

#	ARTICLE	IF	CITATIONS
3624	An in-silico glimpse into the pH dependent structural changes of T7 RNA polymerase: a protein with simplicity. Scientific Reports, 2017, 7, 6290.	1.6	14
3625	Anthranilate phosphoribosyltransferase from the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> shows maximum activity with zinc and forms a unique dimeric structure. FEBS Open Bio, 2017, 7, 1217-1230.	1.0	11
3626	Structural analysis and evolution of specificity of the SUMO UFD E1-E2 interactions. Scientific Reports, 2017, 7, 41998.	1.6	9
3627	Crystal structure of Pisum arvense seed lectin (PAL) and characterization of its interaction with carbohydrates by molecularÂdocking and dynamics. Archives of Biochemistry and Biophysics, 2017, 630, 27-37.	1.4	9
3628	A PDZ-like domain mediates the dimerization of 11R-lipoxygenase. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2017, 1862, 1121-1128.	1.2	3
3629	Crystal structure of LysK, an enzyme catalyzing the last step of lysine biosynthesis in Thermus thermophilus, in complex with lysine: Insight into the mechanism for recognition of the amino-group carrier protein, LysW. Biochemical and Biophysical Research Communications, 2017, 491, 409-415.	1.0	7
3630	Structural and Functional Survey of Environmental Aminoglycoside Acetyltransferases Reveals Functionality of Resistance Enzymes. ACS Infectious Diseases, 2017, 3, 653-665.	1.8	9
3631	AibA/AibB induziert eine intramolekulare Decarboxylierung in der Deâ€novoâ€Biosynthese von Isovalerat aus Myxococcus xanthus. Angewandte Chemie, 2017, 129, 10118-10121.	1.6	3
3632	Computational evaluation of 2-amino-5-sulphonamido-1,3,4-thiadiazoles as human carbonic anhydrase-IX inhibitors: an insight into the structural requirement for the anticancer activity against HEK 293. Medicinal Chemistry Research, 2017, 26, 2272-2292.	1.1	2
3633	2â€²-Deoxyribosyltransferase from Leishmania mexicana, an efficient biocatalyst for one-pot, one-step synthesis of nucleosides from poorly soluble purine bases. Applied Microbiology and Biotechnology, 2017, 101, 7187-7200.	1.7	20
3634	Structural Basis of Catalysis in the Bacterial Monoterpene Synthases Linalool Synthase and 1,8-Cineole Synthase. ACS Catalysis, 2017, 7, 6268-6282.	5.5	47
3635	Catabolism of the Cholesterol Side Chain in <i>Mycobacterium tuberculosis</i> Is Controlled by a Redox-Sensitive Thiol Switch. ACS Infectious Diseases, 2017, 3, 666-675.	1.8	16
3636	Crystal structures of nematode (parasitic T. spiralis and free living C. elegans), compared to mammalian, thymidylate synthases (TS). Molecular docking and molecular dynamics simulations in search for nematode-specific inhibitors of TS. Journal of Molecular Graphics and Modelling, 2017, 77, 33-50.	1.3	2
3637	The primed SNAREâ€"complexinâ€"synaptotagmin complex for neuronal exocytosis. Nature, 2017, 548, 420-425.	13.7	229
3638	Immune evasion by a staphylococcal inhibitor of myeloperoxidase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9439-9444.	3.3	76
3639	Crystal structure of an engineered, HIV-specific recombinase for removal of integrated proviral DNA. Nucleic Acids Research, 2017, 45, 9726-9740.	6.5	8
3640	Structural Mechanism for Modulation of Synaptic Neuroligin-Neurexin Signaling by MDGA Proteins. Neuron, 2017, 95, 896-913.e10.	3.8	55
3641	Methanogenic heterodisulfide reductase (HdrABC-MvhAGD) uses two noncubane [4Fe-4S] clusters for reduction. Science, 2017, 357, 699-703.	6.0	162

#	ARTICLE	IF	CITATIONS
3642	Structures of the Nâ€•Terminal Domain of PqsA in Complex with Anthraniloylâ€•and 6â€•Fluoroanthraniloylâ€•AMP: Substrate Activation in <i>Pseudomonas</i> Quinolone Signal (PQS) Biosynthesis. ChemBioChem, 2017, 18, 2045-2055.	1.3	20
3643	Functional and structural characterization of synthetic cardosin B-derived rennet. Applied Microbiology and Biotechnology, 2017, 101, 6951-6968.	1.7	15
3644	Structural transitions in conserved, ordered Beclin 1 domains essential to regulating autophagy. Journal of Biological Chemistry, 2017, 292, 16235-16248.	1.6	10
3645	Crystal Structure and Substrate Specificity Modification of Acetyl Xylan Esterase from Aspergillus luchuensis. Applied and Environmental Microbiology, 2017, 83, .	1.4	25
3646	Catalytic Mechanism of the Hotdogâ€•Fold Thioesterase PA1618 Revealed by Xâ€•ray Structure Determination of a Substrateâ€•Bound Oxygen Ester Analogue Complex. ChemBioChem, 2017, 18, 1935-1943.	1.3	0
3647	Crystal Structure and Biochemical Characterization of an Aminopeptidase LapB from <i>Legionella pneumophila</i>. Journal of Agricultural and Food Chemistry, 2017, 65, 7569-7578.	2.4	11
3648	Structure of Chorismate Mutase-like Domain of DAHPS from Bacillus subtilis Complexed with Novel Inhibitor Reveals Conformational Plasticity of Active Site. Scientific Reports, 2017, 7, 6364.	1.6	12
3649	Acidic Environment Induces Dimerization and Ligand Binding Site Collapse in the Vps10p Domain of Sortilin. Structure, 2017, 25, 1809-1819.e3.	1.6	19
3650	Nucleotideâ€“ and Mal3-dependent changes in fission yeast microtubules suggest a structural plasticity view of dynamics. Nature Communications, 2017, 8, 2110.	5.8	31
3651	Structural basis of respiratory syncytial virus subtype-dependent neutralization by an antibody targeting the fusion glycoprotein. Nature Communications, 2017, 8, 1877.	5.8	53
3652	Structural basis for methylphosphonate biosynthesis. Science, 2017, 358, 1336-1339.	6.0	39
3653	Structural basis for GABAA receptor potentiation by neurosteroids. Nature Structural and Molecular Biology, 2017, 24, 986-992.	3.6	145
3654	TYK2-induced phosphorylation of Y640 suppresses STAT3 transcriptional activity. Scientific Reports, 2017, 7, 15919.	1.6	13
3655	Design and applications of a clamp for Green Fluorescent Protein with picomolar affinity. Scientific Reports, 2017, 7, 16292.	1.6	49
3656	Conservation of the Enzymeâ€“Coenzyme Interfaces in FAD and NADP Binding Adrenodoxin Reductaseâ€”A Ubiquitous Enzyme. Journal of Molecular Evolution, 2017, 85, 205-218.	0.8	25
3657	Structural and functional studies of SAV0551 from <i>Staphylococcus aureus</i> as a chaperone and glyoxalase III. Bioscience Reports, 2017, 37, .	1.1	6
3658	Structural and Functional Basis for Targeting <i>Campylobacter jejuni</i> Agmatine Deiminase To Overcome Antibiotic Resistance. Biochemistry, 2017, 56, 6734-6742.	1.2	6
3659	Structural Evidence for a Role of the Multi-functional Human Glycoprotein Afamin in Wnt Transport. Structure, 2017, 25, 1907-1915.e5.	1.6	29

#	ARTICLE	IF	CITATIONS
3660	Structural remodeling and oligomerization of human cathelicidin on membranes suggest fibril-like structures as active species. Scientific Reports, 2017, 7, 15371.	1.6	51
3661	Structural basis for the assembly of the Ragulator-Rag GTPase complex. Nature Communications, 2017, 8, 1625.	5.8	55
3662	Structural Basis for DNA Recognition of a Single-stranded DNA-binding Protein from Enterobacter Phage Enc34. Scientific Reports, 2017, 7, 15529.	1.6	15
3663	Unique architecture of thermophilic archaeal virus APBV1 and its genome packaging. Nature Communications, 2017, 8, 1436.	5.8	31
3664	Structural basis of arrestin-3 activation and signaling. Nature Communications, 2017, 8, 1427.	5.8	92
3665	Crystal Structure of Borrelia turicatae protein, BTA121, a differentially regulated Âgene in the tick-mammalian transmission cycle of relapsing fever spirochetes. Scientific Reports, 2017, 7, 15310.	1.6	2
3666	The computational prediction of protein assemblies. Current Opinion in Structural Biology, 2017, 46, 170-175.	2.6	4
3667	Crystal structure of tripartite-type ABC transporter MacB from Acinetobacter baumannii. Nature Communications, 2017, 8, 1336.	5.8	74
3668	The bacterial meta-cleavage hydrolase LigY belongs to the amidohydrolase superfamily, not to the Î±/Î²-hydrolase superfamily. Journal of Biological Chemistry, 2017, 292, 18290-18302.	1.6	11
3669	Coordination and redox stateâ€"dependent structural changes of the heme-based oxygen sensor AfGcHK associated with intraprotein signal transduction. Journal of Biological Chemistry, 2017, 292, 20921-20935.	1.6	19
3670	Evolution of Cytochrome c Oxidase in Hypoxia Tolerant Sculpins (Cottidae, Actinopterygii). Molecular Biology and Evolution, 2017, 34, 2153-2162.	3.5	27
3671	Frutapin, a lectin from <i>Artocarpus incisa</i> (breadfruit): cloning, expression and molecular insights. Bioscience Reports, 2017, 37, .	1.1	6
3672	Biochemical Characterization and Structural Basis of Reactivity and Regioselectivity Differences between <i>Burkholderia thailandensis</i> and <i>Burkholderia glumae</i> 1,6-Didesmethyltoxoflavin <i>N</i>-Methyltransferase. Biochemistry, 2017, 56, 3934-3944.	1.2	4
3673	A new approach for generating bispecific antibodies based on a common light chain format and the stable architecture of human immunoglobulin G1. Journal of Biological Chemistry, 2017, 292, 14706-14717.	1.6	70
3674	Antibody-induced uncoating of human rhinovirus B14. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8017-8022.	3.3	49
3675	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. Nature, 2017, 547, 360-363.	13.7	217
3676	Self-assembled Î±-Tocopherol Transfer Protein Nanoparticles Promote Vitamin E Delivery Across an Endothelial Barrier. Scientific Reports, 2017, 7, 4970.	1.6	21
3677	Ion- and water-binding sites inside an occluded hourglass pore of a trimeric intracellular cation (TRIC) channel. BMC Biology, 2017, 15, 31.	1.7	4

#	ARTICLE	IF	CITATIONS
3678	Modulation of the FMRFamide-gated Na+ channel by external Ca2+. Pflugers Archiv European Journal of Physiology, 2017, 469, 1335-1347.	1.3	4
3679	Biochemical and Structural Analyses of Two Cryptic Esterases in Bacteroides intestinalis and their Synergistic Activities with Cognate Xylanases. Journal of Molecular Biology, 2017, 429, 2509-2527.	2.0	25
3680	AlloSigMA: allosteric signaling and mutation analysis server. Bioinformatics, 2017, 33, 3996-3998.	1.8	116
3681	A novel function for globulin in sequestering plant hormone: Crystal structure of Wrightia tinctoria 11S globulin in complex with auxin. Scientific Reports, 2017, 7, 4705.	1.6	7
3682	X-ray structure of a protease-resistant mutant form of human galectin-9 having two carbohydrate recognition domains with a metal-binding site. Biochemical and Biophysical Research Communications, 2017, 490, 1287-1293.	1.0	5
3683	Functional characterization and crystal structure of thermostable amylase from Thermotoga petrophila , reveals high thermostability and an unusual form of dimerization. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1237-1245.	1.1	9
3684	Molecular modeling of biomolecules by paramagnetic NMR and computational hybrid methods. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1654-1663.	1.1	9
3685	Is the acid/base catalytic residue mutation in Î²- d -mannosidase Dt Man from Dictyoglomus thermophilum sufficient enough to provide thioglycoligase activity?. Biochimie, 2017, 137, 190-196.	1.3	11
3686	Phosphate steering by Flap Endonuclease 1 promotes 5â€²-flap specificity and incision to prevent genome instability. Nature Communications, 2017, 8, 15855.	5.8	81
3687	Crystal structure and DNA-binding property of the ATPase domain of bacterial mismatch repair endonuclease MutL from Aquifex aeolicus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1178-1187.	1.1	12
3688	Crystal structure of TAZ-TEAD complex reveals a distinct interaction mode from that of YAP-TEAD complex. Scientific Reports, 2017, 7, 2035.	1.6	76
3689	Convergent immunological solutions to Argentine hemorrhagic fever virus neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7031-7036.	3.3	31
3690	Interaction between the PH and START domains of ceramide transfer protein competes with phosphatidylinositol 4-phosphate binding by the PH domain. Journal of Biological Chemistry, 2017, 292, 14217-14228.	1.6	35
3691	The multidrug-resistance transporter MdfA from<i>Escherichia coli</i>: crystallization and X-ray diffraction analysis. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 423-430.	0.4	8
3692	From cheminformatics to structure-based design: Web services and desktop applications based on the NAOMI library. Journal of Biotechnology, 2017, 261, 207-214.	1.9	5
3693	Crystal Structure of Chicken Î³S-Crystallin Reveals Lattice Contacts with Implications for Function in the Lens and the Evolution of the Î²Î³-Crystallins. Structure, 2017, 25, 1068-1078.e2.	1.6	15
3694	Adenosine Monophosphate Binding Stabilizes the KTN Domain of the <i>Shewanella denitrificans</i> Kef Potassium Efflux System. Biochemistry, 2017, 56, 4219-4234.	1.2	9
3695	ProteinsPlus: a web portal for structure analysis of macromolecules. Nucleic Acids Research, 2017, 45, W337-W343.	6.5	158

#	Article	IF	Citations
3696	Crystal structure of the tricellulin Câ€terminal coiledâ€coil domain reveals a unique mode of dimerization. Annals of the New York Academy of Sciences, 2017, 1405, 147-159.	1.8	9
3697	Functional and dynamic polymerization of the ALS-linked protein TDP-43 antagonizes its pathologic aggregation. Nature Communications, 2017, 8, 45.	5.8	242
3698	Making Monomeric Aquaporin Z by Disrupting the Hydrophobic Tetramer Interface. ACS Omega, 2017, 2, 3017-3027.	1.6	17
3699	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 55-64.	1.1	13
3700	Crystal structure of <i>Ralstonia eutropha</i> polyhydroxyalkanoate synthase Câ€terminal domain and reaction mechanisms. Biotechnology Journal, 2017, 12, 1600648.	1.8	57
3701	Structural Insights into l -Tryptophan Dehydrogenase from a Photoautotrophic Cyanobacterium, Nostoc punctiforme. Applied and Environmental Microbiology, 2017, 83, .	1.4	5
3702	Structural and functional characterization of a cold adapted TPM-domain with ATPase/ADPase activity. Journal of Structural Biology, 2017, 197, 201-209.	1.3	4
3703	OmoMYC blunts promoter invasion by oncogenic MYC to inhibit gene expression characteristic of MYC-dependent tumors. Oncogene, 2017, 36, 1911-1924.	2.6	73
3704	A non-redundant protein-RNA docking benchmark version 2.0. Proteins: Structure, Function and Bioinformatics, 2017, 85, 256-267.	1.5	42
3705	Homogentisic acid induces aggregation and fibrillation of amyloidogenic proteins. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 135-146.	1.1	20
3706	ClusPro-DC: Dimer Classification by the Cluspro Server for Proteinâ€“Protein Docking. Journal of Molecular Biology, 2017, 429, 372-381.	2.0	36
3707	Structure and Function of a Câ€“C Bond Cleaving Oxygenase in Atypical Angucycline Biosynthesis. ACS Chemical Biology, 2017, 12, 142-152.	1.6	17
3708	Membrane skeletal association and postâ€translational allosteric regulation of <i>Toxoplasma gondii</i> GAPDH1. Molecular Microbiology, 2017, 103, 618-634.	1.2	18
3709	Deciphering metal ion preference and primary coordination sphere robustness of a designed zinc finger with highâ€resolution mass spectrometry. Protein Science, 2017, 26, 198-207.	3.1	0
3710	The macro domain as fusion tag for carrierâ€driven crystallization. Protein Science, 2017, 26, 365-374.	3.1	8
3711	Prediction of Protein Secondary Structure. Methods in Molecular Biology, 2017, , .	0.4	9
3712	Predicting Real-Valued Protein Residue Fluctuation Using FlexPred. Methods in Molecular Biology, 2017, 1484, 175-186.	0.4	4
3713	Structural and Biochemical Characterization of <i>Acinetobacter</i> spp. Aminoglycoside Acetyltransferases Highlights Functional and Evolutionary Variation among Antibiotic Resistance Enzymes. ACS Infectious Diseases, 2017, 3, 132-143.	1.8	17

#	Article	IF	Citations
3714	Inhibition of RAS function through targeting an allosteric regulatory site. Nature Chemical Biology, 2017, 13, 62-68.	3.9	237
3715	Functional and structural studies of a Phospholipase A2-like protein complexed to zinc ions: Insights on its myotoxicity and inhibition mechanism. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3199-3209.	1.1	24
3716	Structure of the Catalytic Domain of Î±-l-Arabinofuranosidase from Coprinopsis cinerea, CcAbf62A, Provides Insights into Structureâ€“Function Relationships in Glycoside Hydrolase Family 62. Applied Biochemistry and Biotechnology, 2017, 181, 511-525.	1.4	14
3717	High-resolution crystal structures of<i>Colocasia esculenta</i>tarin lectin. Glycobiology, 2017, 27, 50-56.	1.3	12
3718	Structure of the SLC4 transporter Bor1p in an inwardâ€facing conformation. Protein Science, 2017, 26, 130-145.	3.1	34
3719	Role of the Tyr270 residue in 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase from Mesorhizobium loti. Journal of Bioscience and Bioengineering, 2017, 123, 154-162.	1.1	5
3720	Structure of the magnetosomeâ€associated actinâ€like MamK filament at subnanometer resolution. Protein Science, 2017, 26, 93-102.	3.1	22
3721	Characterization of Class III Peroxidases from Switchgrass. Plant Physiology, 2017, 173, 417-433.	2.3	43
3722	Structural evaluation of a nanobody targeting complement receptor Vsig4 and its cross reactivity. Immunobiology, 2017, 222, 807-813.	0.8	23
3723	Molecular characterization of a single-chain antibody variable fragment (scFv) specific for PspA from Streptococcus pneumoniae. Biochemical and Biophysical Research Communications, 2017, 482, 141-146.	1.0	4
3724	Directed evolution of glutathione transferases towards a selective glutathione-binding site and improved oxidative stability. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3416-3428.	1.1	29
3725	Active-site plasticity revealed in the asymmetric dimer of AnPrx6 the 1-Cys peroxiredoxin and molecular chaperone from Anabaena sp. PCC 7120. Scientific Reports, 2017, 7, 17151.	1.6	6
3726	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. Scientific Reports, 2017, 7, 16809.	1.6	50
3727	The FOXP2 forkhead domain binds to a variety of DNA sequences with different rates and affinities. Journal of Biochemistry, 2017, 162, mvx003.	0.9	6
3728	The molecular basis of phosphite and hypophosphite recognition by ABC-transporters. Nature Communications, 2017, 8, 1746.	5.8	50
3729	Allosteric modulation of protein-protein interactions by individual lipid binding events. Nature Communications, 2017, 8, 2203.	5.8	65
3730	Structural dissection of human metapneumovirus phosphoprotein using small angle x-ray scattering. Scientific Reports, 2017, 7, 14865.	1.6	20
3731	Structures of human SRP72 complexes provide insights into SRP RNA remodeling and ribosome interaction. Nucleic Acids Research, 2017, 45, 470-481.	6.5	25

#	ARTICLE	IF	CITATIONS
3732	Structure of the <i>Bacillus anthracis</i> dTDP-<scp>L</scp>-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose reductase (RfbD). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 644-650.	0.4	6
3733	Nogo Receptor crystal structures with a native disulfide pattern suggest a novel mode of self-interaction. Acta Crystallographica Section D: Structural Biology, 2017, 73, 860-876.	1.1	3
3734	Structure and binding studies of proliferating cell nuclear antigen from Leishmania donovani. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 1395-1405.	1.1	3
3735	Crystal structure of a pyridoxal 5â€²-phosphate-dependent aspartate racemase derived from the bivalve mollusc Scapharca broughtonii. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 651-656.	0.4	4
3736	Bioinformatics comparisons of RNA-binding proteins of pathogenic and non-pathogenic Escherichia coli strains reveal novel virulence factors. BMC Genomics, 2017, 18, 658.	1.2	3
3737	Bivalent Llama Single-Domain Antibody Fragments against Tumor Necrosis Factor Have Picomolar Potencies due to Intramolecular Interactions. Frontiers in Immunology, 2017, 8, 867.	2.2	57
3738	Seeing but not believing: the structure of glycerol dehydrogenase initially assumed to be the structure of a survival protein from<i>Salmonella typhimurium</i>. Acta Crystallographica Section D: Structural Biology, 2017, 73, 609-617.	1.1	6
3739	Molecular Dynamics Simulations and Dynamic Network Analysis Reveal the Allosteric Unbinding of Monobody to H-Ras Triggered by R135K Mutation. International Journal of Molecular Sciences, 2017, 18, 2249.	1.8	23
3740	Prospecting Biotechnologically-Relevant Monooxygenases from Cold Sediment Metagenomes: An In Silico Approach. Marine Drugs, 2017, 15, 114.	2.2	13
3741	Binding Direction-Based Two-Dimensional Flattened Contact Area Computing Algorithm for Proteinâ€“Protein Interactions. Molecules, 2017, 22, 1722.	1.7	2
3742	Crystal Structure of the Full-Length Feline Immunodeficiency Virus Capsid Protein Shows an N-Terminal Î²-Hairpin in the Absence of N-Terminal Proline. Viruses, 2017, 9, 335.	1.5	10
3743	A conformational switch regulates the ubiquitin ligase HUWE1. ELife, 2017, 6, .	2.8	62
3744	Structural insights into RapZ-mediated regulation of bacterial amino-sugar metabolism. Nucleic Acids Research, 2017, 45, 10845-10860.	6.5	30
3745	Crystal structure of the N-terminal domain of VqsR fromPseudomonas aeruginosaat 2.1â€…Ã… resolution. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 431-436.	0.4	1
3746	Expression, Purification, Crystallization, and X-ray Structural Analysis of CRISPR-Associated Protein Cas6 from Methanocaldococcus jannaschii. Crystals, 2017, 7, 344.	1.0	3
3747	Effects of myosin variants on interacting-heads motif explain distinct hypertrophic and dilated cardiomyopathy phenotypes. ELife, 2017, 6, .	2.8	153
3748	Neutralization of Human Interleukin 23 by Multivalent Nanobodies Explained by the Structure of Cytokineâ€“Nanobody Complex. Frontiers in Immunology, 2017, 8, 884.	2.2	35
3749	Unveiling a Drift Resistant Cryptotope within Marburgvirus Nucleoprotein Recognized by Llama Single-Domain Antibodies. Frontiers in Immunology, 2017, 8, 1234.	2.2	15

#	Article	IF	Citations
3750	Ribonucleotide Reductases from Bifidobacteria Contain Multiple Conserved Indels Distinguishing Them from All Other Organisms: In Silico Analysis of the Possible Role of a 43 aa Bifidobacteria-Specific Insert in the Class III RNR Homolog. Frontiers in Microbiology, 2017, 8, 1409.	1.5	9
3751	The Negative Effects of KPN00353 on Glycerol Kinase and Microaerobic 1,3-Propanediol Production in Klebsiella pneumoniae. Frontiers in Microbiology, 2017, 8, 2441.	1.5	16
3752	Determining Complex Structures using Docking Method with Single Particle Scattering Data. Frontiers in Molecular Biosciences, 2017, 4, 23.	1.6	8
3753	Competitive Inhibitors Unveil Structure/Function Relationships in Human D-Amino Acid Oxidase. Frontiers in Molecular Biosciences, 2017, 4, 80.	1.6	23
3754	Fe65-PTB2 Dimerization Mimics Fe65-APP Interaction. Frontiers in Molecular Neuroscience, 2017, 10, 140.	1.4	10
3755	Structure of RNA polymerase bound to ribosomal 30S subunit. ELife, 2017, 6, .	2.8	87
3756	9Ã… structure of the COPI coat reveals that the Arf1 GTPase occupies two contrasting molecular environments. ELife, 2017, 6, .	2.8	103
3757	X-ray crystal structure of a malonate-semialdehyde dehydrogenase fromPseudomonassp. strain AAC. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 24-28.	0.4	2
3758	Biophysical and Computational Studies of the vCCI:vMIP-II Complex. International Journal of Molecular Sciences, 2017, 18, 1778.	1.8	4
3759	Improving protein-protein interaction prediction using evolutionary information from low-quality MSAs. PLoS ONE, 2017, 12, e0169356.	1.1	7
3760	Novel molecular, structural and evolutionary characteristics of the phosphoketolases from bifidobacteria and Coriobacteriales. PLoS ONE, 2017, 12, e0172176.	1.1	41
3761	Structural insights into the regulation of Bacillus subtilis SigW activity by anti-sigma RsiW. PLoS ONE, 2017, 12, e0174284.	1.1	19
3762	Alteration of the Î±1Î²2/Î±2Î²1 subunit interface contributes to the increased hemoglobin-oxygen affinity of high-altitude deer mice. PLoS ONE, 2017, 12, e0174921.	1.1	4
3763	Differential CLE peptide perception by plant receptors implicated from structural and functional analyses of TDIF-TDR interactions. PLoS ONE, 2017, 12, e0175317.	1.1	18
3764	Soaking suggests â€œalternative factsâ€: Only co-crystallization discloses major ligand-induced interface rearrangements of a homodimeric tRNA-binding protein indicating a novel mode-of-inhibition. PLoS ONE, 2017, 12, e0175723.	1.1	30
3765	Solution NMR structure of the TRIM21 B-box2 and identification of residues involved in its interaction with the RING domain. PLoS ONE, 2017, 12, e0181551.	1.1	9
3766	The N-terminal domains of FLASH and Lsm11 form a 2:1 heterotrimer for histone pre-mRNA 3â€™-end processing. PLoS ONE, 2017, 12, e0186034.	1.1	12
3767	Structural plasticity of the N-terminal capping helix of the TPR domain of kinesin light chain. PLoS ONE, 2017, 12, e0186354.	1.1	9

#	ARTICLE	IF	CITATIONS
3768	Crystal structure of a tripartite complex between C3dg, C-terminal domains of factor H and OspE of Borrelia burgdorferi. PLoS ONE, 2017, 12, e0188127.	1.1	13
3769	Potent and selective inhibition of pathogenic viruses by engineered ubiquitin variants. PLoS Pathogens, 2017, 13, e1006372.	2.1	48
3770	Convergent evolution involving dimeric and trimeric dUTPases in pathogenicity island mobilization. PLoS Pathogens, 2017, 13, e1006581.	2.1	9
3771	Structures of foot and mouth disease virus pentamers: Insight into capsid dissociation and unexpected pentamer reassociation. PLoS Pathogens, 2017, 13, e1006607.	2.1	21
3772	Complementarity determining regions and frameworks contribute to the disulfide bond independent folding of intrinsically stable scFv. PLoS ONE, 2017, 12, e0189964.	1.1	22
3773	Structure, activity and thermostability investigations of OXA-163, OXA-181 and OXA-245 using biochemical analysis, crystal structures and differential scanning calorimetry analysis. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 579-587.	0.4	12
3774	Molecular and functional characterization of ferredoxin NADP(H) oxidoreductase from Gracilaria chilensis and its complex with ferredoxin. Biological Research, 2017, 50, 39.	1.5	5
3775	Modeling of RAS complexes supports roles in cancer for less studied partners. BMC Biophysics, 2017, 10, 5.	4.4	10
3776	Crystal Structure of Colocasia esculenta Tuber Agglutinin at 1.74 Ã… Resolution and Its Quaternary Interactions. Journal of Glycobiology, 2017, 06, .	0.2	2
3777	Swit_4259, an acetoacetate decarboxylase-like enzyme from <i>Sphingomonas wittichii</i> RW1. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 672-681.	0.4	2
3778	Structural basis of the therapeutic anti-PD-L1 antibody atezolizumab. Oncotarget, 2017, 8, 90215-90224.	0.8	68
3779	Crystal structure of a Î²-aminopeptidase from an Australian<i>Burkholderia</i>sp.. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 386-392.	0.4	7
3782	Analysis of Evolutionarily Independent Protein-RNA Complexes Yields a Criterion to Evaluate the Relevance of Prebiotic Scenarios. Current Biology, 2018, 28, 526-537.e5.	1.8	39
3783	A potential substrate binding pocket of BdcA plays a critical role in NADPH recognition and biofilm dispersal. Biochemical and Biophysical Research Communications, 2018, 497, 863-868.	1.0	5
3784	The H-subunit of the restriction endonuclease CglI contains a prototype DEAD-Z1 helicase-like motor. Nucleic Acids Research, 2018, 46, 2560-2572.	6.5	1
3785	Structural and Mechanistic Analysis of the Choline Sulfatase from Sinorhizobium melliloti: A Class I Sulfatase Specific for an Alkyl Sulfate Ester. Journal of Molecular Biology, 2018, 430, 1004-1023.	2.0	18
3786	Escape of Hepatitis C Virus from Epitope I Neutralization Increases Sensitivity of Other Neutralization Epitopes. Journal of Virology, 2018, 92, .	1.5	20
3787	The 3.5-Ã… CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel. Molecular Cell, 2018, 69, 993-1004.e3.	4.5	103

#	ARTICLE	IF	CITATIONS
3788	Salvador has an extended SARAH domain that mediates binding to Hippo kinase. Journal of Biological Chemistry, 2018, 293, 5532-5543.	1.6	13
3789	Cryo-EM structure of the bacterial actin AlfA reveals unique assembly and ATP-binding interactions and the absence of a conserved subdomain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3356-3361.	3.3	7
3790	Grouper iridovirus GIV66 is a Bcl-2 protein that inhibits apoptosis by exclusively sequestering Bim. Journal of Biological Chemistry, 2018, 293, 5464-5477.	1.6	27
3791	Uncovering the mechanistic basis for specific recognition of monomethylated H3K4 by the CW domain of Arabidopsis histone methyltransferase SDG8. Journal of Biological Chemistry, 2018, 293, 6470-6481.	1.6	34
3792	A potent complement factor C3â€“specific nanobody inhibiting multiple functions in the alternative pathway of human and murine complement. Journal of Biological Chemistry, 2018, 293, 6269-6281.	1.6	47
3793	Virulence of the Melioidosis Pathogen Burkholderia pseudomallei Requires the Oxidoreductase Membrane Protein DsbB. Infection and Immunity, 2018, 86, .	1.0	13
3794	Crystal structure of heat shock protein 15 (Hsp15) from Vibrio cholerae: Novel mode of trimerization and nucleic acid binding properties. Biochemical and Biophysical Research Communications, 2018, 497, 1076-1081.	1.0	0
3795	Discovery of Selective Inhibitors of Imidazoleglycerol-Phosphate Dehydratase from Mycobacterium tuberculosis by Virtual Screening. Crystallography Reports, 2018, 63, 74-78.	0.1	3
3796	Snapshots of C-S Cleavage in Egt2 Reveals Substrate Specificity and Reaction Mechanism. Cell Chemical Biology, 2018, 25, 519-529.e4.	2.5	29
3797	The folate-binding module of<i>Thermus thermophilus</i>cobalamin-dependent methionine synthase displays a distinct variation of the classical TIM barrel: a TIM barrel with a `twist'. Acta Crystallographica Section D: Structural Biology, 2018, 74, 41-51.	1.1	5
3798	Domain swapping between FabGs deciphers the structural determinant for in-solution oligomerization and substrate binding. Biophysical Chemistry, 2018, 237, 9-21.	1.5	2
3799	Physiological temperatures reduce dimerization of dengue and Zika virus recombinant envelope proteins. Journal of Biological Chemistry, 2018, 293, 8922-8933.	1.6	22
3800	Interaction between Neisseria gonorrhoeae bacterial peroxidase and its electron donor, the lipidâ€modified azurin. FEBS Letters, 2018, 592, 1473-1483.	1.3	7
3801	Unusual Constriction Zones in the Major Porins OmpU and OmpT from Vibrio cholerae. Structure, 2018, 26, 708-721.e4.	1.6	22
3802	Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. Nature Communications, 2018, 9, 1549.	5.8	35
3803	Structural basis for the regulatory interaction of the methylglyoxal synthase MgsA with the carbon flux regulator Crh in. Journal of Biological Chemistry, 2018, 293, 5781-5792.	1.6	5
3804	Structural and kinetic basis for the selectivity of aducanumab for aggregated forms of amyloid-Î². Scientific Reports, 2018, 8, 6412.	1.6	182
3805	&lt;italic&gt;Legionella pneumophila&lt;/italic&gt; effector WipA, a bacterial PPP protein phosphatase with PTP activity. Acta Biochimica Et Biophysica Sinica, 2018, 50, 547-554.	0.9	3

#	Article	IF	Citations
3806	Insights into the pathogenesis of dominant retinitis pigmentosa associated with a D477G mutation in RPE65. Human Molecular Genetics, 2018, 27, 2225-2243.	1.4	26
3807	Structure of the activated Edc1-Dcp1-Dcp2-Edc3 mRNA decapping complex with substrate analog poised for catalysis. Nature Communications, 2018, 9, 1152.	5.8	38
3808	An Antibody Targeting the Fusion Machinery Neutralizes Dual-Tropic Infection and Defines a Site of Vulnerability on Epstein-Barr Virus. Immunity, 2018, 48, 799-811.e9.	6.6	104
3809	Structural and biochemical characterization of the type-II LOG protein from Streptomyces coelicolor A3. Biochemical and Biophysical Research Communications, 2018, 499, 577-583.	1.0	2
3810	Atomic Structure of the E2 Inner Core of Human Pyruvate Dehydrogenase Complex. Biochemistry, 2018, 57, 2325-2334.	1.2	28
3811	Crystal structure of exoâ€rhamnogalacturonan lyase from <i>Penicillium chrysogenum</i> as a member of polysaccharide lyase family 26. FEBS Letters, 2018, 592, 1378-1388.	1.3	16
3812	A new HIV-1 Rev structure optimizes interaction with target RNA (RRE) for nuclear export. Journal of Structural Biology, 2018, 203, 102-108.	1.3	13
3813	Inferring and Using Protein Quaternary Structure Information from Crystallographic Data. Methods in Molecular Biology, 2018, 1764, 357-375.	0.4	10
3814	Structural and enzymatic analysis of the cytochrome b5 reductase domain of Ulva prolifera nitrate reductase. International Journal of Biological Macromolecules, 2018, 111, 1175-1182.	3.6	5
3815	Structural and enzymatic analyses of <i>Anabaena</i> heterocystâ€specific alkaline invertase InvB. FEBS Letters, 2018, 592, 1589-1601.	1.3	12
3816	Structural basis for tumor necrosis factor blockade with the therapeutic antibody golimumab. Protein Science, 2018, 27, 1038-1046.	3.1	18
3817	Staphylopine, pseudopaline, and yersinopine dehydrogenases: A structural and kinetic analysis of a new functional class of opine dehydrogenase. Journal of Biological Chemistry, 2018, 293, 8009-8019.	1.6	34
3818	Proline hydroxylation in collagen supports integrin binding by two distinct mechanisms. Journal of Biological Chemistry, 2018, 293, 7645-7658.	1.6	57
3819	Structural and functional delineation of aerobactin biosynthesis in hypervirulent Klebsiella pneumoniae. Journal of Biological Chemistry, 2018, 293, 7841-7852.	1.6	33
3820	Cryptic glucocorticoid receptor-binding sites pervade genomic NF-ÎºB response elements. Nature Communications, 2018, 9, 1337.	5.8	90
3821	Substrate Recognition by a Colistin Resistance Enzyme from <i>Moraxella catarrhalis</i>. ACS Chemical Biology, 2018, 13, 1322-1332.	1.6	15
3822	The single berberine bridge enzyme homolog of <i>PhyscomitrellaÂpatens</i> is a cellobiose oxidase. FEBS Journal, 2018, 285, 1923-1943.	2.2	17
3823	Structure of a hyperthermostable carbonic anhydrase identified from an active hydrothermal vent chimney. Enzyme and Microbial Technology, 2018, 114, 48-54.	1.6	14

#	Article	IF	Citations
3824	Crystal structure and mechanism of human carboxypeptidase O: Insights into its specific activity for acidic residues. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3932-E3939.	3.3	15
3825	Discovery of Ubiquitin Deamidases in the Pathogenic Arsenal of Legionella pneumophila. Cell Reports, 2018, 23, 568-583.	2.9	43
3826	On the Trails of the Proteasome Fold: Structural and Functional Analysis of the Ancestral Î²-Subunit Protein Anbu. Journal of Molecular Biology, 2018, 430, 628-640.	2.0	4
3827	Quantitative characterization of all single amino acid variants of a viral capsid-based drug delivery vehicle. Nature Communications, 2018, 9, 1385.	5.8	43
3828	A novel Î²-glucosidase isolated from the microbial metagenome of Lake PoraquÃª (Amazon, Brazil). Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 569-579.	1.1	11
3829	Structural Characterization and Directed Evolution of a Novel Acetyl Xylan Esterase Reveals Thermostability Determinants of the Carbohydrate Esterase 7 Family. Applied and Environmental Microbiology, 2018, 84, .	1.4	18
3830	Structural snapshots along the reaction mechanism of the atypical poplar thioredoxinâ€like2.1. FEBS Letters, 2018, 592, 1030-1041.	1.3	13
3831	New tetrameric forms of the rotavirus NSP4 with antiparallel helices. Archives of Virology, 2018, 163, 1531-1547.	0.9	7
3832	Insights into the inhibitory mechanisms of NADH on the Î±Î³ heterodimer of human NAD-dependent isocitrate dehydrogenase. Scientific Reports, 2018, 8, 3146.	1.6	22
3833	Rox, a Rifamycin Resistance Enzyme with an Unprecedented Mechanism of Action. Cell Chemical Biology, 2018, 25, 403-412.e5.	2.5	48
3834	Molecular Interactions between a Fluoride Ion Channel and Synthetic Protein Blockers. Biochemistry, 2018, 57, 1212-1218.	1.2	9
3835	Divergent and parallel routes of biochemical adaptation in high-altitude passerine birds from the Qinghai-Tibet Plateau. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1865-1870.	3.3	74
3836	A complete structural characterization of the desferrioxamine E biosynthetic pathway from the fire blight pathogen Erwinia amylovora. Journal of Structural Biology, 2018, 202, 236-249.	1.3	26
3837	Structural and biochemical characterization of the plant type III polyketide synthases of the liverwort Marchantia paleacea. Plant Physiology and Biochemistry, 2018, 125, 95-105.	2.8	11
3838	Crystal Structures of Fungal Tectonin in Complex with O-Methylated Glycans Suggest Key Role in Innate Immune Defense. Structure, 2018, 26, 391-402.e4.	1.6	28
3839	Partner-Specific Prediction of Protein-Dimer Stability from Unbound Structure of Monomer. Journal of Chemical Information and Modeling, 2018, 58, 733-745.	2.5	5
3840	Structural basis of protein arginine rhamnosylation by glycosyltransferase EarP. Nature Chemical Biology, 2018, 14, 368-374.	3.9	22
3841	The Extracellular Domain of Pollen Receptor Kinase 3 is structurally similar to the SERK family of co-receptors. Scientific Reports, 2018, 8, 2796.	1.6	13

#	ARTICLE	IF	CITATIONS
3842	Cryo-EM reconstruction of AlfA from <i>Bacillus subtilis</i> reveals the structure of a simplified actin-like filament at 3.4-Ã… resolution. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3458-3463.	3.3	11
3843	Crystal structure of thebaine 6-O-demethylase from the morphine biosynthesis pathway. Journal of Structural Biology, 2018, 202, 229-235.	1.3	24
3844	Crystal structure of thermospermine synthase from <i>Medicago truncatula</i> and substrate discriminatory features of plant aminopropyltransferases. Biochemical Journal, 2018, 475, 787-802.	1.7	16
3845	Effects of Cross-Presentation, Antigen Processing, and Peptide Binding in HIV Evasion of T Cell Immunity. Journal of Immunology, 2018, 200, ji1701523.	0.4	11
3846	Crystal structure of the NADP+ and tartrate-bound complex of l-serine 3-dehydrogenase from the hyperthermophilic archaeon Pyrobaculum calidifontis. Extremophiles, 2018, 22, 395-405.	0.9	1
3847	Substrateâ€induced structural alterations of Mycobacterial mycothione reductase and critical residues involved. FEBS Letters, 2018, 592, 568-585.	1.3	4
3848	Retinoic acid prevents immunogenicity of milk lipocalin Bos d 5 through binding to its immunodominant T-cell epitope. Scientific Reports, 2018, 8, 1598.	1.6	48
3849	Structures and mechanism of dipeptidyl peptidases 8 and 9, important players in cellular homeostasis and cancer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1437-E1445.	3.3	58
3850	Unique Conformation in a Natural Interruption Sequence of Type XIX Collagen Revealed by Its High-Resolution Crystal Structure. Biochemistry, 2018, 57, 1087-1095.	1.2	7
3851	A presumed homologue of the regulatory subunits of eIF2B functions as ribose-1,5-bisphosphate isomerase in Pyrococcus horikoshii OT3. Scientific Reports, 2018, 8, 1891.	1.6	5
3852	Stu2 uses a 15-nm parallel coiled coil for kinetochore localization and concomitant regulation of the mitotic spindle. Molecular Biology of the Cell, 2018, 29, 285-294.	0.9	5
3853	Structures of Î²-klotho reveal a â€˜zip codeâ€™-like mechanism for endocrine FGF signalling. Nature, 2018, 553, 501-505.	13.7	160
3854	A Novel Ultra-Stable, Monomeric Green Fluorescent Protein For Direct Volumetric Imaging of Whole Organs Using CLARITY. Scientific Reports, 2018, 8, 667.	1.6	66
3855	Structural Basis for Activity and Specificity of an Anticoagulant Anti-FXIa Monoclonal Antibody and a Reversal Agent. Structure, 2018, 26, 187-198.e4.	1.6	8
3856	The mechanism of glycosphingolipid degradation revealed by a GALC-SapA complex structure. Nature Communications, 2018, 9, 151.	5.8	37
3857	Crystal structure reveals vaccine elicited bactericidal human antibody targeting a conserved epitope on meningococcal fHbp. Nature Communications, 2018, 9, 528.	5.8	18
3858	A Calmodulin C-Lobe Ca2+-Dependent Switch Governs Kv7 Channel Function. Neuron, 2018, 97, 836-852.e6.	3.8	63
3859	Identification of a staphylococcal complement inhibitor with broad host specificity in equid Staphylococcus aureus strains. Journal of Biological Chemistry, 2018, 293, 4468-4477.	1.6	34

#	Article	IF	Citations
3860	Structure and function of the bacillithiolâ€<i>S</i>â€transferase BstA from <i>Staphylococcus aureus</i>. Protein Science, 2018, 27, 898-902.	3.1	7
3861	Quaternary structure influences the peroxidase activity of peroxiredoxin 3. Biochemical and Biophysical Research Communications, 2018, 497, 558-563.	1.0	22
3862	Structural Study of the C-Terminal Domain of Nonstructural Protein 1 from Japanese Encephalitis Virus. Journal of Virology, 2018, 92, .	1.5	24
3863	Determination of protein oligomeric structure from smallâ€angle Xâ€ray scattering. Protein Science, 2018, 27, 814-824.	3.1	40
3864	The crystal structure of D-xylonate dehydratase reveals functional features of enzymes from the Ilv/ED dehydratase family. Scientific Reports, 2018, 8, 865.	1.6	21
3865	Crystal structure of cystathionine Î²-synthase from honeybee Apis mellifera. Journal of Structural Biology, 2018, 202, 82-93.	1.3	13
3866	Structure of the G119S Mutant Acetylcholinesterase of the Malaria Vector Anopheles gambiae Reveals Basis of Insecticide Resistance. Structure, 2018, 26, 130-136.e2.	1.6	44
3867	Structural characterization of a novel monotreme-specific protein with antimicrobial activity from the milk of the platypus. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 39-45.	0.4	10
3868	Computational analysis of the effect of polymerase acidic (PA) gene mutation F35L in the 2009 pandemic influenza A (H1N1) virus on binding aspects of mononucleotides in the endonuclease domain. Archives of Virology, 2018, 163, 1031-1036.	0.9	2
3869	Data on crystal organization in the structure of the Fab fragment from the NIST reference antibody, RM 8671. Data in Brief, 2018, 16, 29-36.	0.5	12
3870	Structural characterization of ribT from Bacillus subtilis reveals it as a GCN5-related N-acetyltransferase. Journal of Structural Biology, 2018, 202, 70-81.	1.3	8
3871	Diversity of Nicotinic Acetylcholine Receptor Positive Allosteric Modulators Revealed by Mutagenesis and a Revised Structural Model. Molecular Pharmacology, 2018, 93, 128-140.	1.0	39
3872	Molecular Mechanism of J-Domain-Triggered ATP Hydrolysis by Hsp70 Chaperones. Molecular Cell, 2018, 69, 227-237.e4.	4.5	201
3873	pH driven fibrillar aggregation of the super-sweet protein Y65R-MNEI: A step-by-step structural analysis. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 808-815.	1.1	13
3874	Glycine-rich loop encompassing active site at interface of hexameric M. tuberculosis Eis protein contributes to its structural stability and activity. International Journal of Biological Macromolecules, 2018, 109, 124-135.	3.6	5
3875	Structure of the Marine Siphovirus TW1: Evolution of Capsid-Stabilizing Proteins and Tail Spikes. Structure, 2018, 26, 238-248.e3.	1.6	32
3876	Structural basis for Ufm1 recognition by Uf<scp>SP</scp>. FEBS Letters, 2018, 592, 263-273.	1.3	7
3877	Structural basis for substrate specificity of meso-diaminopimelic acid decarboxylase from Corynebacterium glutamicum. Biochemical and Biophysical Research Communications, 2018, 495, 1815-1821.	1.0	6

#	Article	IF	Citations
3878	Crystal structure of UDP- N -acetylglucosamine-enolpyruvate reductase (MurB) from Mycobacterium tuberculosis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 397-406.	1.1	27
3879	Structures of the L27 Domain of Disc Large Homologue 1 Protein Illustrate a Self-Assembly Module. Biochemistry, 2018, 57, 1293-1305.	1.2	6
3880	Mutations in Escherichia coli Polyphosphate Kinase That Lead to Dramatically Increased <i>In Vivo</i> Polyphosphate Levels. Journal of Bacteriology, 2018, 200, .	1.0	37
3881	Conformational dynamism for DNA interaction in the Salmonella RcsB response regulator. Nucleic Acids Research, 2018, 46, 456-472.	6.5	17
3882	Engineered synthetic antibodies as probes to quantify the energetic contributions of ligand binding to conformational changes in proteins. Journal of Biological Chemistry, 2018, 293, 2815-2828.	1.6	26
3883	Structure and function of cytoplasmic serine hydroxymethyltransferase from Pichia pastoris. Biochemical and Biophysical Research Communications, 2018, 496, 753-757.	1.0	4
3884	Docking, thermodynamics and molecular dynamics (MD) studies of a non-canonical protease inhibitor, MP-4, from Mucuna pruriens. Scientific Reports, 2018, 8, 689.	1.6	9
3885	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. Biochemistry, 2018, 57, 963-977.	1.2	12
3886	Impact of intracellular ionic strength on dimer binding in the NF-ĸB Inducing kinase. Journal of Structural Biology, 2018, 202, 183-190.	1.3	0
3887	Structural Mechanism for the Temperature-Dependent Activation of the Hyperthermophilic Pf2001 Esterase. Structure, 2018, 26, 199-208.e3.	1.6	12
3888	A structurally dynamic N-terminal region drives function of the staphylococcal peroxidase inhibitor (SPIN). Journal of Biological Chemistry, 2018, 293, 2260-2271.	1.6	16
3889	Affinity maturation of a portable Fabâ€“RNA module for chaperone-assisted RNA crystallography. Nucleic Acids Research, 2018, 46, 2624-2635.	6.5	25
3890	Identifying functionally informative evolutionary sequence profiles. Bioinformatics, 2018, 34, 1278-1286.	1.8	7
3891	Structural Basis of Enhanced Crystallizability Induced by a Molecular Chaperone for Antibody Antigen-Binding Fragments. Journal of Molecular Biology, 2018, 430, 322-336.	2.0	39
3892	Crystal Structure of Bicc1 SAM Polymer and Mapping of Interactions between the Ciliopathy-Associated Proteins Bicc1, ANKS3, and ANKS6. Structure, 2018, 26, 209-224.e6.	1.6	18
3893	CDC42 binds PAK4 via an extended GTPase-effector interface. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 531-536.	3.3	29
3894	Self-protection of cytosolic malate dehydrogenase against oxidative stress in Arabidopsis. Journal of Experimental Botany, 2018, 69, 3491-3505.	2.4	48
3895	Comparative structural and enzymatic studies on Salmonella typhimurium diaminopropionate ammonia lyase reveal its unique features. Journal of Structural Biology, 2018, 202, 118-128.	1.3	5

#	Article	IF	Citations
3896	The protease GtgE from Salmonella exclusively targets inactive Rab GTPases. Nature Communications, 2018, 9, 44.	5.8	33
3897	Structure of the yeast oligosaccharyltransferase complex gives insight into eukaryotic N-glycosylation. Science, 2018, 359, 545-550.	6.0	157
3898	The structure of the Nâ€terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. Proteins: Structure, Function and Bioinformatics, 2018, 86, 912-923.	1.5	26
3899	Alternative dimerization interfaces in the glucocorticoid receptor-Î± ligand binding domain. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1810-1825.	1.1	18
3900	Structural insights into the CRISPR-Cas-associated ribonuclease activity of Staphylococcus epidermidis Csm3 and Csm6. Science Bulletin, 2018, 63, 691-699.	4.3	5
3901	Nuclear Receptor CAR Suppresses GADD45B-p38 MAPK Signaling to Promote Phenobarbital-induced Proliferation in Mouse Liver. Molecular Cancer Research, 2018, 16, 1309-1318.	1.5	12
3902	A Single Mutation Traps a Half-Sites Reactive Enzyme in Midstream, Explaining Asymmetry in Hydride Transfer. Biochemistry, 2018, 57, 2786-2795.	1.2	9
3903	Structural principles of distinct assemblies of the human Î±4Î²2 nicotinic receptor. Nature, 2018, 557, 261-265.	13.7	177
3904	An endogenous dAMP ligand in <i>Bacillus subtilis</i> class Ib RNR promotes assembly of a noncanonical dimer for regulation by dATP. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4594-E4603.	3.3	18
3905	Applying graph theory to protein structures: an Atlas of coiled coils. Bioinformatics, 2018, 34, 3316-3323.	1.8	17
3906	Structural basis of the bacteriophage <scp>TP</scp>901â€1 <scp>CI</scp> repressor dimerization and interaction with <scp>DNA</scp>. FEBS Letters, 2018, 592, 1738-1750.	1.3	5
3907	Crystal structure of the human 4-1BB/4-1BBL complex. Journal of Biological Chemistry, 2018, 293, 9880-9891.	1.6	16
3908	Crystal structure of pyrrolizidine alkaloid<i>N</i>-oxygenase from the grasshopper<i>Zonocerus variegatus</i>. Acta Crystallographica Section D: Structural Biology, 2018, 74, 422-432.	1.1	12
3909	The Structure of an Infectious Human Polyomavirus and Its Interactions with Cellular Receptors. Structure, 2018, 26, 839-847.e3.	1.6	29
3910	Chlamydial virulence factor TarP mimics talin to disrupt the talinâ€vinculin complex. FEBS Letters, 2018, 592, 1751-1760.	1.3	11
3911	The Molecular Basis of Polysaccharide Sulfatase Activity and a Nomenclature for Catalytic Subsites in this Class of Enzyme. Structure, 2018, 26, 747-758.e4.	1.6	30
3912	Ca2+-Triggered Synaptic Vesicle Fusion Initiated by Release of Inhibition. Trends in Cell Biology, 2018, 28, 631-645.	3.6	46
3913	Assembly of human C-terminal binding protein (CtBP) into tetramers. Journal of Biological Chemistry, 2018, 293, 9101-9112.	1.6	36

#	Article	IF	Citations
3914	Type II Secretion-Dependent Aminopeptidase LapA and Acyltransferase PlaC Are Redundant for Nutrient Acquisition during <i>Legionella pneumophila</i> Intracellular Infection of Amoebas. MBio, 2018, 9, .	1.8	27
3915	Structural characterization of a highly-potent V3-glycan broadly neutralizing antibody bound to natively-glycosylated HIV-1 envelope. Nature Communications, 2018, 9, 1251.	5.8	85
3916	First insights of peptidoglycan amidation in Gram-positive bacteria - the high-resolution crystal structure of Staphylococcus aureus glutamine amidotransferase GatD. Scientific Reports, 2018, 8, 5313.	1.6	12
3917	Atomic Structure of Type VI Contractile Sheath from Pseudomonas aeruginosa. Structure, 2018, 26, 329-336.e3.	1.6	29
3918	Proteinâ€"Protein Docking in Drug Design and Discovery. Methods in Molecular Biology, 2018, 1762, 285-305.	0.4	17
3919	AAV6 K531 serves a dual function in selective receptor and antibody ADK6 recognition. Virology, 2018, 518, 369-376.	1.1	20
3920	Structural and functional analysis of Erwinia amylovora SrlD. The first crystal structure of a sorbitol-6-phosphate 2-dehydrogenase. Journal of Structural Biology, 2018, 203, 109-119.	1.3	4
3921	A Pseudoisostructural Type II DAH7PS Enzyme from <i>Pseudomonas aeruginosa</i>: Alternative Evolutionary Strategies to Control Shikimate Pathway Flux. Biochemistry, 2018, 57, 2667-2678.	1.2	14
3922	A small-molecule fragment that emulates binding of receptor and broadly neutralizing antibodies to influenza A hemagglutinin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4240-4245.	3.3	25
3923	The crystal structure of the drug target<i>Mycobacterium tuberculosis</i>methionyl-tRNA synthetase in complex with a catalytic intermediate. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 245-254.	0.4	10
3924	A Neutralizing Antibody Recognizing Primarily N-Linked Glycan Targets the Silent Face of the HIV Envelope. Immunity, 2018, 48, 500-513.e6.	6.6	66
3925	Anticalins Reveal High Plasticity in the Mode of Complex Formation with a Common Tumor Antigen. Structure, 2018, 26, 649-656.e3.	1.6	8
3926	Biocatalytic Routes to Lactone Monomers for Polymer Production. Biochemistry, 2018, 57, 1997-2008.	1.2	33
3927	Systematic characterization of panâ€cancer mutation clusters. Molecular Systems Biology, 2018, 14, e7974.	3.2	39
3928	Crystal structure of an intramembranal phosphatase central to bacterial cell-wall peptidoglycan biosynthesis and lipid recycling. Nature Communications, 2018, 9, 1159.	5.8	43
3929	A structural dissection of proteinâ€"RNA interactions based on different RNA base areas of interfaces. RSC Advances, 2018, 8, 10582-10592.	1.7	9
3930	The invasin D protein from Yersinia pseudotuberculosis selectively binds the Fab region of host antibodies and affects colonization of the intestine. Journal of Biological Chemistry, 2018, 293, 8672-8690.	1.6	573
3931	Hydrophobic patches on SMAD2 and SMAD3 determine selective binding to cofactors. Science Signaling, 2018, 11, .	1.6	23

#	Article	IF	Citations
3932	Structural modelling of the DNAJB6 oligomeric chaperone shows a peptide-binding cleft lined with conserved S/T-residues at the dimer interface. Scientific Reports, 2018, 8, 5199.	1.6	43
3933	Structural and Functional Insights into Bacillus subtilis Sigma Factor Inhibitor, CsfB. Structure, 2018, 26, 640-648.e5.	1.6	12
3934	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in Mycobacterium smegmatis. Biochemical Journal, 2018, 475, 1295-1308.	1.7	13
3935	Complex Interplay between Epitope Specificity and Isotype Dictates the Biological Activity of Anti-human CD40 Antibodies. Cancer Cell, 2018, 33, 664-675.e4.	7.7	78
3936	Structural and functional analysis of the DOT1Lâ€“AF10 complex reveals mechanistic insights into MLL-AF10-associated leukemogenesis. Genes and Development, 2018, 32, 341-346.	2.7	17
3937	Assessing the Heterogeneity of the Fc-Glycan of a Therapeutic Antibody Using an engineered FcÎ³Receptor IIIa-Immobilized Column. Scientific Reports, 2018, 8, 3955.	1.6	48
3938	The structure of hydrogenase-2 from <i>Escherichia coli</i>: implications for H2-driven proton pumping. Biochemical Journal, 2018, 475, 1353-1370.	1.7	46
3939	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. Cell, 2018, 173, 208-220.e20.	13.5	51
3940	Crystal structure of DlyL, a mannose-specific lectin from Dioclea lasiophylla Mart. Ex Benth seeds that display cytotoxic effects against C6 glioma cells. International Journal of Biological Macromolecules, 2018, 114, 64-76.	3.6	25
3941	Structural basis of the Cope rearrangement and cyclization in hapalindole biogenesis. Nature Chemical Biology, 2018, 14, 345-351.	3.9	34
3942	Archaeal acetoacetyl-CoA thiolase/HMG-CoA synthase complex channels the intermediate via a fused CoA-binding site. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3380-3385.	3.3	44
3943	Crystal structure of a SFPQ/PSPC1 heterodimer provides insights into preferential heterodimerization of human DBHS family proteins. Journal of Biological Chemistry, 2018, 293, 6593-6602.	1.6	32
3944	An unexpected vestigial protein complex reveals the evolutionary origins of an s-triazine catabolic enzyme. Journal of Biological Chemistry, 2018, 293, 7880-7891.	1.6	18
3945	The first crystal structure of manganese superoxide dismutase from the genusStaphylococcus. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 135-142.	0.4	5
3946	Structure of the carboxypeptidase B complex with N-sulfamoyl-L-phenylalanine â€“ a transition state analog of non-specific substrate. Journal of Biomolecular Structure and Dynamics, 2018, 36, 956-965.	2.0	7
3947	Structural and antigenic properties of thermally treated gluten proteins. Food Chemistry, 2018, 267, 43-51.	4.2	41
3948	Crystal structure of acetylcholinesterase catalytic subunits of the malaria vector <i>Anopheles gambiae</i>. Insect Science, 2018, 25, 721-724.	1.5	20
3949	The proteinopathy of D169G and K263E mutants at the RNA Recognition Motif (RRM) domain of tar DNA-binding protein (tdp43) causing neurological disorders: A computational study. Journal of Biomolecular Structure and Dynamics, 2018, 36, 1075-1093.	2.0	31

#	Article	IF	Citations
3950	Thermal and chemical denaturation of Colocasia esculenta tuber agglutinin from Î±2Î²2 to unfolded state. Journal of Biomolecular Structure and Dynamics, 2018, 36, 2179-2193.	2.0	1
3951	IntPred: a structure-based predictor of proteinâ€"protein interaction sites. Bioinformatics, 2018, 34, 223-229.	1.8	59
3952	Proteinâ€"protein interaction specificity is captured by contact preferences and interface composition. Bioinformatics, 2018, 34, 459-468.	1.8	29
3953	Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. Environmental Microbiology, 2018, 20, 228-240.	1.8	20
3954	Assessment of protein assembly prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 247-256.	1.5	54
3955	<i>Rhodococcus erythropolis</i> Oleate Hydratase: a New Member in the Oleate Hydratase Family Treeâ€"Biochemical and Structural Studies. ChemCatChem, 2018, 10, 407-414.	1.8	29
3956	Applications of sequence coevolution in membrane protein biochemistry. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 895-908.	1.4	27
3957	Crystal structures of eukaryote glycosyltransferases reveal biologically relevant enzyme homooligomers. Cellular and Molecular Life Sciences, 2018, 75, 833-848.	2.4	18
3958	Forty years of collaborative computational crystallography. Protein Science, 2018, 27, 202-206.	3.1	2
3959	Modeling of protein complexes in CAPRI Round 37 using templateâ€based approach combined with model selection. Proteins: Structure, Function and Bioinformatics, 2018, 86, 292-301.	1.5	9
3960	Dockground: A comprehensive data resource for modeling of protein complexes. Protein Science, 2018, 27, 172-181.	3.1	70
3961	Effect of Phosphate Ion on the Structure of Lumazine Synthase, an Antigen Presentation System From Bacillus anthracis. Journal of Pharmaceutical Sciences, 2018, 107, 814-823.	1.6	9
3962	A 3.0-Angstrom Resolution Cryo-Electron Microscopy Structure and Antigenic Sites of Coxsackievirus A6-Like Particles. Journal of Virology, 2018, 92, .	1.5	14
3963	PDB-wide identification of biological assemblies from conserved quaternary structure geometry. Nature Methods, 2018, 15, 67-72.	9.0	69
3964	A neutralizing antibody that blocks delivery of the enzymatic cargo of Clostridium difficile toxin TcdB into host cells. Journal of Biological Chemistry, 2018, 293, 941-952.	1.6	27
3965	A hereditary spastic paraplegiaâ€"associated atlastin variant exhibits defective allosteric coupling in the catalytic core. Journal of Biological Chemistry, 2018, 293, 687-700.	1.6	16
3966	Inter-Enzyme Allosteric Regulation of Chorismate Mutase in <i>Corynebacterium glutamicum</i>: Structural Basis of Feedback Activation by Trp. Biochemistry, 2018, 57, 557-573.	1.2	23
3967	Crystal structure of native Î²â€<i>N</i>â€acetylhexosaminidase isolated from <i>AspergillusÂ oryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. FEBS Journal, 2018, 285, 580-598.	2.2	12

#	ARTICLE	IF	CITATIONS
3968	Diverse NADase effector families mediate interbacterial antagonism via the type VI secretion system. Journal of Biological Chemistry, 2018, 293, 1504-1514.	1.6	100
3969	Crystal Structure of Cleaved Serp-1, a Myxomavirus-Derived Immune Modulating Serpin: Structural Design of Serpin Reactive Center Loop Peptides with Improved Therapeutic Function. Biochemistry, 2018, 57, 1096-1107.	1.2	22
3970	Structural insights into ankyrin repeatâ€"mediated recognition of the kinesin motor protein KIF21A by KANK1, a scaffold protein in focal adhesion. Journal of Biological Chemistry, 2018, 293, 1944-1956.	1.6	25
3971	The dUTPase of white spot syndrome virus assembles its active sites in a noncanonical manner. Journal of Biological Chemistry, 2018, 293, 1088-1099.	1.6	9
3972	Biochemical and Structural Analysis of Substrate Specificity of a Phenylalanine Ammonia-Lyase. Plant Physiology, 2018, 176, 1452-1468.	2.3	99
3973	Structural insight into the substrate specificity of acyl-CoA oxidase1 from Yarrowia lipolytica for short-chain dicarboxylyl-CoAs. Biochemical and Biophysical Research Communications, 2018, 495, 1628-1634.	1.0	14
3974	Crystal structures of murine and human Histamine-Releasing Factor (HRF/TCTP) and a model for HRF dimerisation in mast cell activation. Molecular Immunology, 2018, 93, 216-222.	1.0	15
3975	The crystal structure of pseudokinase PEAK1 (Sugen kinase 269) reveals an unusual catalytic cleft and a novel mode of kinase fold dimerization. Journal of Biological Chemistry, 2018, 293, 1642-1650.	1.6	42
3976	Correlation between the molecular effects of mutations at the dimer interface of alanineâ€"glyoxylate aminotransferase leading to primary hyperoxaluria type I and the cellular response to vitamin B₆. Journal of Inherited Metabolic Disease, 2018, 41, 263-275.	1.7	18
3977	Introducing the new bacterial branch of the RNase A superfamily. RNA Biology, 2018, 15, 9-12.	1.5	12
3978	Insights into Biofilm Dispersal Regulation from the Crystal Structure of the PAS-GGDEF-EAL Region of RbdA from Pseudomonas aeruginosa. Journal of Bacteriology, 2018, 200, .	1.0	37
3979	The crystal structure and catalytic mechanism of hydroxynitrile lyase from passion fruit, <i>Passiflora edulis</i>. FEBS Journal, 2018, 285, 313-324.	2.2	12
3980	Structural and Functional Studies of the Daunorubicin Priming Ketosynthase DpsC. ACS Chemical Biology, 2018, 13, 141-151.	1.6	15
3981	Rare PfCSP C-terminal antibodies induced by live sporozoite vaccination are ineffective against malaria infection. Journal of Experimental Medicine, 2018, 215, 63-75.	4.2	79
3982	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensorâ€domain protein. Protein Science, 2018, 27, 568-572.	3.1	1
3983	The challenge of modeling protein assemblies: the CASP12â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	1.5	85
3984	Two intermediate states of the conformational switch in dual specificity phosphatase 13a. Pharmacological Research, 2018, 128, 211-219.	3.1	2
3985	Biochemical Characterization of Two Clinically-Relevant Human Fumarase Variants Defective for Oligomerization. The Open Biochemistry Journal, 2018, 12, 1-15.	0.3	15

#	Article	IF	Citations
3986	Study of the Behavior of Lysozyme Oligomers in Solutions by the Molecular Dynamics Method. Crystallography Reports, 2018, 63, 947-950.	0.1	14
3987	Crystal Structure of Bovine Alpha-Chymotrypsin in Space Group P65. Crystals, 2018, 8, 460.	1.0	4
3988	Mobile Loop in the Active Site of Metallocarboxypeptidases as an Underestimated Determinant of Substrate Specificity. Biochemistry (Moscow), 2018, 83, 1594-1602.	0.7	1
3989	Eisenaufnahme in Pilzen der Gattung <i>Aspergillus</i>: strukturelle und biochemische Einblicke in Siderophoresterasen. Angewandte Chemie, 2018, 130, 14834-14839.	1.6	0
3990	Structural analysis of activating mutants of YfiB from Pseudomonas aeruginosa PAO1. Biochemical and Biophysical Research Communications, 2018, 506, 997-1003.	1.0	2
3991	Analysis of the Binding of Aripiprazole to Human Serum Albumin: The Importance of a Chloro-Group in the Chemical Structure. ACS Omega, 2018, 3, 13790-13797.	1.6	26
3992	Structure of the 4-1BB/4-1BBL complex and distinct binding and functional properties of utomilumab and urelumab. Nature Communications, 2018, 9, 4679.	5.8	95
3993	Characterisation of a diazinon-metabolising glutathione S-transferase in the silkworm Bombyx mori by X-ray crystallography and genome editing analysis. Scientific Reports, 2018, 8, 16835.	1.6	12
3994	Large-scale conformational changes and redistribution of surface negative charge upon sugar binding dictate the fidelity of phosphorylation in Vibrio cholerae fructokinase. Scientific Reports, 2018, 8, 16925.	1.6	3
3995	Neuron-Subtype-Specific Expression, Interaction Affinities, and Specificity Determinants of DIP/Dpr Cell Recognition Proteins. Neuron, 2018, 100, 1385-1400.e6.	3.8	65
3996	The conserved mosaic prophage protein paratox inhibits the natural competence regulator ComR in Streptococcus. Scientific Reports, 2018, 8, 16535.	1.6	10
3997	A comparative structural analysis of the surface properties of asco-laccases. PLoS ONE, 2018, 13, e0206589.	1.1	18
3998	Individually double minimum-distance definition of proteinâ€“RNA binding residues and application to structure-based prediction. Journal of Computer-Aided Molecular Design, 2018, 32, 1363-1373.	1.3	5
3999	Structure and oligomerization of the periplasmic domain of GspL from the type II secretion system of Pseudomonas aeruginosa. Scientific Reports, 2018, 8, 16760.	1.6	12
4000	A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. Nature Structural and Molecular Biology, 2018, 25, 1093-1102.	3.6	31
4001	CDBâ€”a database for protein heterodimeric complexes. Protein Engineering, Design and Selection, 2018, 31, 361-365.	1.0	0
4002	Structural snapshots of OxyR reveal the peroxidatic mechanism of H ₂ O ₂ sensing. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11623-E11632.	3.3	42
4003	HCV Broadly Neutralizing Antibodies Use a CDRH3 Disulfide Motif to Recognize an E2 Glycoprotein Site that Can Be Targeted for Vaccine Design. Cell Host and Microbe, 2018, 24, 703-716.e3.	5.1	95

#	ARTICLE	IF	CITATIONS
4004	Structural insights into the function of type VI secretion system TssA subunits. Nature Communications, 2018, 9, 4765.	5.8	41
4005	Structural dissection of sterol glycosyltransferase UGT51 from Saccharomyces cerevisiae for substrate specificity. Journal of Structural Biology, 2018, 204, 371-379.	1.3	19
4006	The N-Terminal GTPase Domain of p190RhoGAP Proteins Is a PseudoGTPase. Structure, 2018, 26, 1451-1461.e4.	1.6	10
4007	Crystal Structure of the Human tRNA Guanine Transglycosylase Catalytic Subunit QTRT1. Biomolecules, 2018, 8, 81.	1.8	18
4008	Deciphering evolution of immune recognition in antibodies. BMC Structural Biology, 2018, 18, 19.	2.3	4
4009	Structural organization of a major neuronal G protein regulator, the RGS7-GÎ²5-R7BP complex. ELife, 2018, 7, .	2.8	18
4010	Structural Insights into the FtsQ/FtsB/FtsL Complex, a Key Component of the Divisome. Scientific Reports, 2018, 8, 18061.	1.6	28
4011	Novel regulatory mechanism of establishment genes of conjugative plasmids. Nucleic Acids Research, 2018, 46, 11910-11926.	6.5	8
4012	Deciphering the ATP-binding mechanism(s) in NLRP-NACHT 3D models using structural bioinformatics approaches. PLoS ONE, 2018, 13, e0209420.	1.1	28
4013	Structure of the type VI secretion system TssKâ€“TssFâ€“TssG baseplate subcomplex revealed by cryo-electron microscopy. Nature Communications, 2018, 9, 5385.	5.8	37
4014	Crystal Structure of the YAPâ€binding Domain of Human TEAD1. Bulletin of the Korean Chemical Society, 2019, 40, 74-77.	1.0	2
4015	Structure-function analysis of Sedolisins: evolution of tripeptidyl peptidase and endopeptidase subfamilies in fungi. BMC Bioinformatics, 2018, 19, 464.	1.2	2
4016	Elucidating Protein-protein Interactions Through Computational Approaches and Designing Small Molecule Inhibitors Against them for Various Diseases. Current Topics in Medicinal Chemistry, 2018, 18, 1719-1736.	1.0	9
4017	A Mechanically Weak Extracellular Membrane-Adjacent Domain Induces Dimerization of Protocadherin-15. Biophysical Journal, 2018, 115, 2368-2385.	0.2	27
4018	Stochastic protein multimerization, activity, and fitness. Physical Review E, 2018, 98, .	0.8	17
4019	Insights into the ZIKV NS1 Virology from Different Strains through a Fine Analysis of Physicochemical Properties. ACS Omega, 2018, 3, 16212-16229.	1.6	22
4020	Structural insight into substrate and product binding in an archaeal mevalonate kinase. PLoS ONE, 2018, 13, e0208419.	1.1	3
4021	A novel chlorination-induced ribonuclease YabJ from <i>Staphylococcus aureus</i>. Bioscience Reports, 2018, 38, .	1.1	12

#	ARTICLE	IF	CITATIONS
4022	Distinguishing crystallographic from biological interfaces in protein complexes: role of intermolecular contacts and energetics for classification. BMC Bioinformatics, 2018, 19, 438.	1.2	25
4023	A Gcn5-RelatedN-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibioticsin Vitro. Biochemistry, 2018, 57, 7011-7020.	1.2	11
4024	A novel decarboxylating amidohydrolase involved in avoiding metabolic dead ends during cyanuric acid catabolism in Pseudomonas sp. strain ADP. PLoS ONE, 2018, 13, e0206949.	1.1	11
4025	Design and implementation of structural bioinformatics projects for biological sciences undergraduate students. Biochemistry and Molecular Biology Education, 2018, 46, 547-554.	0.5	3
4026	Structural mechanism for HIV-1 TAR loop recognition by Tat and the super elongation complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12973-12978.	3.3	56
4027	Structure of native lens connexin 46/50 intercellular channels by cryo-EM. Nature, 2018, 564, 372-377.	13.7	107
4028	Molecular basis for the acid-initiated uncoating of human enterovirus D68. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12209-E12217.	3.3	38
4029	Structural characterization of geranylgeranyl pyrophosphate synthase GACE1337 from the hyperthermophilic archaeon Geoglobus acetivorans. Extremophiles, 2018, 22, 877-888.	0.9	7
4030	Structural characterization of 1-deoxy-D-xylulose 5-phosphate Reductoisomerase from Vibrio vulnificus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1209-1215.	1.1	1
4031	Biochemical and Structural Characterization of TesA, a Major Thioesterase Required for Outer-Envelope Lipid Biosynthesis in Mycobacterium tuberculosis. Journal of Molecular Biology, 2018, 430, 5120-5136.	2.0	22
4032	A multisubstrate reductase from Plantago major: structure-function in the short chain reductase superfamily. Scientific Reports, 2018, 8, 14796.	1.6	8
4033	Structural and functional characterisation of the entry point to pyocyanin biosynthesis in <i>Pseudomonas aeruginosa</i> defines a new 3-deoxy-<scp>d</scp>-arabino-heptulosonate 7-phosphate synthase subclass. Bioscience Reports, 2018, 38, .	1.1	14
4034	In Situ Random Microseeding and Streak Seeding Used for Growth of Crystals of Cold-Adapted Î²-d-Galactosidases: Crystal Structure of Î²DG from Arthrobacter sp. 32cB. Crystals, 2018, 8, 13.	1.0	5
4035	MBP-binding DARPins facilitate the crystallization of an MBP fusion protein. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 549-557.	0.4	4
4036	Structure and conformational stability of the triosephosphate isomerase from Zea mays. Comparison with the chemical unfolding pathways of other eukaryotic TIMs. Archives of Biochemistry and Biophysics, 2018, 658, 66-76.	1.4	4
4037	A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. Nature Communications, 2018, 9, 3932.	5.8	25
4038	Structural and biochemical characterization of the Cutibacterium acnes exo-Î²-1,4-mannosidase that targets the N-glycan core of host glycoproteins. PLoS ONE, 2018, 13, e0204703.	1.1	13
4039	Structure and function of<scp>L</scp>-threonine-3-dehydrogenase from the parasitic protozoan<i>Trypanosoma brucei</i>revealed by X-ray crystallography and geometric simulations. Acta Crystallographica Section D: Structural Biology, 2018, 74, 861-876.	1.1	8

#	ARTICLE	IF	CITATIONS
4040	Refining the macromolecular model â€" achieving the best agreement with the data from X-ray diffraction experiment. Crystallography Reviews, 2018, 24, 236-262.	0.4	43
4041	Structural properties of the peroxiredoxin AhpC2 from the hyperthermophilic eubacterium Aquifex aeolicus. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2797-2805.	1.1	4
4042	Salmonella Phage S16 Tail Fiber Adhesin Features a Rare Polyglycine Rich Domain for Host Recognition. Structure, 2018, 26, 1573-1582.e4.	1.6	69
4043	Structural basis for broad neutralization of ebolavirusesÂby an antibody targeting the glycoprotein fusion loop. Nature Communications, 2018, 9, 3934.	5.8	25
4044	<i>Tannerella forsythia</i> Tfo belongs to <i>Porphyromonas gingivalis</i> HmuY-like family of proteins but differs in heme-binding properties. Bioscience Reports, 2018, 38, .	1.1	24
4045	Structural basis for specific calcium binding by the polycystic-kidney-disease domain of Vibrio anguillarum protease Epp. Biochemical and Biophysical Research Communications, 2018, 505, 471-477.	1.0	0
4046	Structure-Based Engineering of <i>Phanerochaete chrysosporium</i> Alcohol Oxidase for Enhanced Oxidative Power toward Glycerol. Biochemistry, 2018, 57, 6209-6218.	1.2	25
4047	Structural insights into modulation and selectivity of transsynaptic neurexinâ€"LRRTM interaction. Nature Communications, 2018, 9, 3964.	5.8	29
4048	HIF-2Î±-pVHL complex reveals broad genotype-phenotype correlations in HIF-2Î±-driven disease. Nature Communications, 2018, 9, 3359.	5.8	26
4049	Restriction Enzyme Analysis of Double-Stranded DNA on Pristine Single-Walled Carbon Nanotubes. ACS Applied Materials & Interfaces, 2018, 10, 37386-37395.	4.0	15
4050	Identification, functional characterization, and crystal structure determination of bacterial levoglucosan dehydrogenase. Journal of Biological Chemistry, 2018, 293, 17375-17386.	1.6	16
4051	Comparative structure analysis of the ETSi domain of ERG3 and its complex with the E74 promoter DNA sequence. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 656-663.	0.4	3
4052	Crystal structure of a biliverdin-bound phycobiliprotein: Interdependence of oligomerization and chromophorylation. Journal of Structural Biology, 2018, 204, 519-522.	1.3	12
4053	A model for hydrophobic protrusions on peripheral membrane proteins. PLoS Computational Biology, 2018, 14, e1006325.	1.5	26
4054	A structural investigation of NRZ mediated apoptosis regulation in zebrafish. Cell Death and Disease, 2018, 9, 967.	2.7	8
4055	Structure of frequency-interacting RNA helicase from Neurospora crassa reveals high flexibility in a domain critical for circadian rhythm and RNA surveillance. PLoS ONE, 2018, 13, e0196642.	1.1	11
4056	A Viral Protein Restricts Drosophila RNAi Immunity by Regulating Argonaute Activity and Stability. Cell Host and Microbe, 2018, 24, 542-557.e9.	5.1	31
4057	Structural and Functional Basis of Difructose Anhydride III Hydrolase, Which Sequentially Converts Inulin Using the Same Catalytic Residue. ACS Catalysis, 2018, 8, 10683-10697.	5.5	12

#	Article	IF	Citations
4058	Characteristics of the essential pathogenicity factor Rv1828, a MerR family transcription regulator from <i>MycobacteriumÂtuberculosis</i>. FEBS Journal, 2018, 285, 4424-4444.	2.2	6
4059	Structure and dynamics of the yeast SWR1-nucleosome complex. Science, 2018, 362, .	6.0	131
4060	Structural Analysis of an Epitope Candidate of Triosephosphate Isomerase in Opisthorchis viverrini. Scientific Reports, 2018, 8, 15075.	1.6	5
4061	Structure of the Macrobrachium rosenbergii nodavirus: A new genus within the Nodaviridae?. PLoS Biology, 2018, 16, e3000038.	2.6	36
4062	Evolutionary Morphing of Tryptophan Synthase: Functional Mechanisms for the Enzymatic Channeling of Indole. Journal of Molecular Biology, 2018, 430, 5066-5079.	2.0	6
4063	Structural and kinetic analyses of penicillin-binding protein 4 (PBP4)-mediated antibiotic resistance in Staphylococcus aureus. Journal of Biological Chemistry, 2018, 293, 19854-19865.	1.6	44
4064	A single amino acid distorts the Fc Î³ receptor IIIb/CD16b structure upon binding immunoglobulin G1 and reduces affinity relative to CD16a. Journal of Biological Chemistry, 2018, 293, 19899-19908.	1.6	26
4065	Co-Evolution of Intrinsically Disordered Proteins with Folded Partners Witnessed by Evolutionary Couplings. International Journal of Molecular Sciences, 2018, 19, 3315.	1.8	23
4066	Structural delineation of potent transmission-blocking epitope I on malaria antigen Pfs48/45. Nature Communications, 2018, 9, 4458.	5.8	48
4067	Structural basis for activation of fluorogenic dyes by an RNA aptamer lacking a G-quadruplex motif. Nature Communications, 2018, 9, 4542.	5.8	37
4068	Identification and characterization of a large family of superbinding bacterial SH2 domains. Nature Communications, 2018, 9, 4549.	5.8	17
4069	New Thermophilic Î±/Î² Class Epoxide Hydrolases Found in Metagenomes From Hot Environments. Frontiers in Bioengineering and Biotechnology, 2018, 6, 144.	2.0	19
4070	Pathological macromolecular crystallographic data affected by twinning, partial-disorder and exhibiting multiple lattices for testing of data processing and refinement tools. Scientific Reports, 2018, 8, 14876.	1.6	11
4071	Structural Basis for S100B Interaction with its Target Proteins. Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research, 2018, 12, .	0.1	4
4072	Closed- and open-state models of human skeletal muscle sodium channel. Biochemical and Biophysical Research Communications, 2018, 506, 826-832.	1.0	0
4073	Impact of Dengue Virus Serotype 2 Strain Diversity on Serological Immune Responses to Dengue. ACS Infectious Diseases, 2018, 4, 1705-1717.	1.8	2
4074	CSGID Solves Structures and Identifies Phenotypes for Five Enzymes in Toxoplasma gondii. Frontiers in Cellular and Infection Microbiology, 2018, 8, 352.	1.8	14
4075	Changes of Cell Biochemical States Are Revealed in Protein Homomeric Complex Dynamics. Cell, 2018, 175, 1418-1429.e9.	13.5	36

#	ARTICLE	IF	CITATIONS
4076	Molecular mechanism of activation of the immunoregulatory amidase NAAA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10032-E10040.	3.3	36
4077	Structural insights into the electron/proton transfer pathways in the quinol:fumarate reductase from Desulfovibrio gigas. Scientific Reports, 2018, 8, 14935.	1.6	11
4078	Biogenesis and structure of a type VI secretion baseplate. Nature Microbiology, 2018, 3, 1404-1416.	5.9	76
4079	Transition-State Analogues of <i>Campylobacter jejuni</i> 5â€²-Methylthioadenosine Nucleosidase. ACS Chemical Biology, 2018, 13, 3173-3183.	1.6	11
4080	Structure of a glutamine donor mimicking inhibitory peptide shaped by the catalytic cleft of microbial transglutaminase. FEBS Journal, 2018, 285, 4684-4694.	2.2	11
4081	Structural, functional and biological insights into the role of<i>Mycobacterium tuberculosis</i>VapBC11 toxinâ€"antitoxin system: targeting a tRNase to tackle mycobacterial adaptation. Nucleic Acids Research, 2018, 46, 11639-11655.	6.5	37
4082	Structural basis forÂreceptor-regulated SMAD recognition by MAN1. Nucleic Acids Research, 2018, 46, 12139-12153.	6.5	16
4083	The structure of DcrB, a lipoprotein from Salmonella enterica, reveals flexibility in the N-terminal segment of the Mog1p/PsbP-like fold. Journal of Structural Biology, 2018, 204, 513-518.	1.3	4
4084	Spectral and structural analysis of large Stokes shift fluorescent protein dKeima570. Journal of Microbiology, 2018, 56, 822-827.	1.3	4
4085	Structure of glyoxysomal malate dehydrogenase (MDH3) from<i>Saccharomyces cerevisiae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 617-624.	0.4	10
4086	Two active site arginines are critical determinants of substrate binding and catalysis in MenD: a thiamine-dependent enzyme in menaquinone biosynthesis. Biochemical Journal, 2018, 475, 3651-3667.	1.7	11
4087	Active site complementation and hexameric arrangement in the GH family 29; a structureâ€"function study of Î±-l-fucosidase isoenzyme 1 from Paenibacillus thiaminolyticus. Glycobiology, 2019, 29, 59-73.	1.3	12
4088	Crystal structure of an Lrs14-like archaeal biofilm regulator from<i>Sulfolobus acidocaldarius</i>. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1105-1114.	1.1	4
4089	Structural Insights into Oxygen-Dependent Signal Transduction within Globin Coupled Sensors. Inorganic Chemistry, 2018, 57, 14386-14395.	1.9	17
4090	The molecular basis of protein toxin HicAâ€"dependent binding of the protein antitoxin HicB to DNA. Journal of Biological Chemistry, 2018, 293, 19429-19440.	1.6	10
4091	Engagement Rules That Underpin DBL-DARC Interactions for Ingress of Plasmodium knowlesi and Plasmodium vivax Into Human Erythrocytes. Frontiers in Molecular Biosciences, 2018, 5, 78.	1.6	4
4092	Unique Physicochemical Patterns of Residues in Proteinâ€"Protein Interfaces. Journal of Chemical Information and Modeling, 2018, 58, 2164-2173.	2.5	7
4093	Crystal structure of TcpK in complex with oriT DNA of the antibiotic resistance plasmid pCW3. Nature Communications, 2018, 9, 3732.	5.8	18

#	Article	IF	Citations
4094	Crystal structure of SSB complexed with inhibitor myricetin. Biochemical and Biophysical Research Communications, 2018, 504, 704-708.	1.0	15
4095	Structural basis of the arbitrium peptideâ€"AimR communication system in the phage lysisâ€"lysogeny decision. Nature Microbiology, 2018, 3, 1266-1273.	5.9	37
4096	KnowVolution Campaign of an Aryl Sulfotransferase Increases Activity toward Cellobiose. Chemistry - A European Journal, 2018, 24, 17117-17124.	1.7	18
4097	Structural Plasticity of Neurexin 1Î±: Implications for its Role as Synaptic Organizer. Journal of Molecular Biology, 2018, 430, 4325-4343.	2.0	10
4098	A conserved cation binding site in the DNA binding domain of forkhead box transcription factors regulates DNA binding by FOXP2. Archives of Biochemistry and Biophysics, 2018, 657, 56-64.	1.4	4
4099	Tc toxin activation requires unfolding and refolding of a Î²-propeller. Nature, 2018, 563, 209-213.	13.7	45
4100	DARPins recognizing mTFP1 as novel reagents for <i>in vitro</i> and <i>in vivo</i> protein manipulations. Biology Open, 2018, 7, .	0.6	7
4101	The quaternary structure of Thermus thermophilus aldehyde dehydrogenase is stabilized by an evolutionary distinct C-terminal arm extension. Scientific Reports, 2018, 8, 13327.	1.6	15
4102	Oxidative cyclization of N-methyl-dopa by a fungal flavoenzyme of the amine oxidase family. Journal of Biological Chemistry, 2018, 293, 17021-17032.	1.6	4
4103	How [Fe]â€Hydrogenase from Methanothermobacter is Protected Against Light and Oxidative Stress. Angewandte Chemie, 2018, 130, 15276-15279.	1.6	2
4104	How [Fe]â€Hydrogenase from Methanothermobacter is Protected Against Light and Oxidative Stress. Angewandte Chemie - International Edition, 2018, 57, 15056-15059.	7.2	2
4105	Crystal structure of p-nitrophenol 4-monooxygenase PnpA from Pseudomonas putida DLL-E4: The key enzyme involved in p-nitrophenol degradation. Biochemical and Biophysical Research Communications, 2018, 504, 715-720.	1.0	5
4106	Structural features of a bacterial cyclic Î±-maltosyl-(1â†'6)-maltose (CMM) hydrolase critical for CMM recognition and hydrolysis. Journal of Biological Chemistry, 2018, 293, 16874-16888.	1.6	7
4107	Crystal structure of the modification-dependent SRA-HNH endonuclease TagI. Nucleic Acids Research, 2018, 46, 10489-10503.	6.5	12
4108	Evolutionary shift toward protein-based architecture in trypanosomal mitochondrial ribosomes. Science, 2018, 362, .	6.0	107
4109	Structural determinants of Rab11 activation by the guanine nucleotide exchange factor SH3BP5. Nature Communications, 2018, 9, 3772.	5.8	29
4110	NAD⁺ promotes assembly of the active tetramer of aldehyde dehydrogenase 7A1. FEBS Letters, 2018, 592, 3229-3238.	1.3	11
4111	Structural basis for murine norovirus engagement of bile acids and the CD300lf receptor. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9201-E9210.	3.3	82

#	Article	IF	Citations
4112	Structure of Aspâ€bound peptidase E from Salmonella enterica : Active site at dimer interface illuminates Asp recognition. FEBS Letters, 2018, 592, 3346-3354.	1.3	7
4113	GEF mechanism revealed by the structure of SmgGDS-558 and farnesylated RhoA complex and its implication for a chaperone mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9563-9568.	3.3	25
4114	Unique N-terminal extension domain of human asparaginyl-tRNA synthetase elicits CCR3-mediated chemokine activity. International Journal of Biological Macromolecules, 2018, 120, 835-845.	3.6	12
4115	Diaminopelargonic acid transaminase from Psychrobacter cryohalolentis is active towards (S)-(-)-1-phenylethylamine, aldehydes and Î±-diketones. Applied Microbiology and Biotechnology, 2018, 102, 9621-9633.	1.7	6
4116	Discovery, Structural and Biochemical Studies of a rare Glu/Asp Specific M1 Class Aminopeptidase from Legionella pneumophila. International Journal of Biological Macromolecules, 2018, 120, 1111-1118.	3.6	2
4117	The nuclear actin-containing Arp8 module is a linker DNA sensor driving INO80 chromatin remodeling. Nature Structural and Molecular Biology, 2018, 25, 823-832.	3.6	63
4118	A speculation on the tandem fasciclin 1 repeat of FLA4 proteins in angiosperms. Plant Signaling and Behavior, 2018, 13, e1507403.	1.2	10
4119	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	45
4120	Structure of a Novel Dimeric SET Domain Methyltransferase that Regulates Cell Motility. Journal of Molecular Biology, 2018, 430, 4209-4229.	2.0	3
4121	Biochemical and Structural Characterization of TtnD, a Prenylated FMN-Dependent Decarboxylase from the Tautomycetin Biosynthetic Pathway. ACS Chemical Biology, 2018, 13, 2728-2738.	1.6	19
4122	Architecture of the native major royal jelly protein 1 oligomer. Nature Communications, 2018, 9, 3373.	5.8	47
4123	Structural aspects and physiological implications of the hemoglobin of green iguana (Iguana iguana). International Journal of Biological Macromolecules, 2018, 120, 1275-1285.	3.6	1
4124	PRISEs (progesterone 5Î²-reductase and/or iridoid synthase-like 1,4-enone reductases): Catalytic and substrate promiscuity allows for realization of multiple pathways in plant metabolism. Phytochemistry, 2018, 156, 9-19.	1.4	18
4125	Structural basis of cell wall peptidoglycan amidation by the GatD/MurT complex of Staphylococcus aureus. Scientific Reports, 2018, 8, 12953.	1.6	11
4126	Structure of a patient-derived antibody in complex with allergen reveals simultaneous conventional and superantigen-like recognition. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8707-E8716.	3.3	29
4127	The biological assembly of <scp>OXA</scp>â€48 reveals a dimer interface with high charge complementarity and very high affinity. FEBS Journal, 2018, 285, 4214-4228.	2.2	12
4128	Automated evaluation of quaternary structures from protein crystals. PLoS Computational Biology, 2018, 14, e1006104.	1.5	66
4129	Oligomeric interfaces as a tool in drug discovery: Specific interference with activity of malate dehydrogenase of Plasmodium falciparum in vitro. PLoS ONE, 2018, 13, e0195011.	1.1	15

#	Article	IF	Citations
4130	Investigation of protein quaternary structure via stoichiometry and symmetry Ä±nformation. PLoS ONE, 2018, 13, e0197176.	1.1	12
4131	Mechanism by which water and protein electrostatic interactions control proton transfer at the active site of channelrhodopsin. PLoS ONE, 2018, 13, e0201298.	1.1	19
4132	PDBe: towards reusable data delivery infrastructure at protein data bank in Europe. Nucleic Acids Research, 2018, 46, D486-D492.	6.5	76
4133	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. Structure, 2018, 26, 948-959.e5.	1.6	5
4134	Insights into the Substrate Specificity of Archaeal Entnerâ€"Doudoroff Aldolases: The Structures of <i>Picrophilus torridus</i> 2-Keto-3-deoxygluconate Aldolase and <i>Sulfolobus solfataricus</i> 2-Keto-3-deoxy-6-phosphogluconate Aldolase in Complex with 2-Keto-3-deoxy-6-phosphogluconate. Biochemistry, 2018, 57, 3797-3806.	1.2	3
4135	Structural basis for recognition of 53BP1 tandem Tudor domain by TIRR. Nature Communications, 2018, 9, 2123.	5.8	35
4136	Potent and selective antitumor activity of a T cell-engaging bispecific antibody targeting a membrane-proximal epitope of ROR1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5467-E5476.	3.3	60
4137	Molecular basis for the loss-of-function effects of the Alzheimer's diseaseâ€"associated R47H variant of the immune receptor TREM2. Journal of Biological Chemistry, 2018, 293, 12634-12646.	1.6	88
4138	Bio-knowledge-based filters improve residueâ€"residue contact prediction accuracy. Bioinformatics, 2018, 34, 3675-3683.	1.8	1
4139	Structural rearrangements occurring upon cofactor binding in the Mycobacterium smegmatis Î²-ketoacyl-acyl carrier protein reductase MabA. Acta Crystallographica Section D: Structural Biology, 2018, 74, 383-393.	1.1	6
4140	Product-oriented chemical surface modification of a levansucrase (SacB) <i>via</i> an ene-type reaction. Chemical Science, 2018, 9, 5312-5321.	3.7	19
4141	Structural and biochemical characterization of Siw14: A protein-tyrosine phosphatase fold that metabolizes inositol pyrophosphates. Journal of Biological Chemistry, 2018, 293, 6905-6914.	1.6	23
4142	Structural basis of ubiquitin modification by the Legionella effector SdeA. Nature, 2018, 557, 674-678.	13.7	69
4143	Functional and structural characterization of zebrafish ASC. FEBS Journal, 2018, 285, 2691-2707.	2.2	25
4144	Ad5NULL-A20: A Tropism-Modified, Î±vÎ²6 Integrin-Selective Oncolytic Adenovirus for Epithelial Ovarian Cancer Therapies. Clinical Cancer Research, 2018, 24, 4215-4224.	3.2	36
4145	Regulation of Shigella Effector Kinase OspG through Modulation of Its Dynamic Properties. Journal of Molecular Biology, 2018, 430, 2096-2112.	2.0	8
4146	Targeting G protein-coupled receptor signaling at the G protein level with a selective nanobody inhibitor. Nature Communications, 2018, 9, 1996.	5.8	65
4147	Structural Plasticity in the C-Terminal Region of Macrophage Migration Inhibitory Factor-2 Is Associated with an Induced Fit Mechanism for a Selective Inhibitor. Biochemistry, 2018, 57, 3599-3605.	1.2	17

#	ARTICLE	IF	CITATIONS
4148	Structural Characterization of the Hydratase-Aldolases, NahE and PhdJ: Implications for the Specificity, Catalysis, and <i>N</i>-Acetylneuraminate Lyase Subgroup of the Aldolase Superfamily. Biochemistry, 2018, 57, 3524-3536.	1.2	10
4149	Structural basis for the recognition of complex-type N-glycans by Endoglycosidase S. Nature Communications, 2018, 9, 1874.	5.8	38
4150	Structural Insights into Subunits Assembly and the Oxyester Splicing Mechanism of Neq pol Split Intein. Cell Chemical Biology, 2018, 25, 871-879.e2.	2.5	5
4151	Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. Structure, 2018, 26, 925-935.e8.	1.6	49
4152	Comparison of <i>Alicyclobacillus acidocaldarius</i> <i>o</i>-Succinylbenzoate Synthase to Its Promiscuous <i>N</i>-Succinylamino Acid Racemase/<i>o</i>-Succinylbenzoate Synthase Relatives. Biochemistry, 2018, 57, 3676-3689.	1.2	9
4153	Characterization and Structural Analysis of a Novel <i>exo</i>-Type Enzyme Acting on Î²-1,2-Glucooligosaccharides from <i>Parabacteroides distasonis</i>. Biochemistry, 2018, 57, 3849-3860.	1.2	14
4154	Gene cloning, expression, and X-ray crystallographic analysis of a Î²-mannanase from Eisenia fetida. Enzyme and Microbial Technology, 2018, 117, 15-22.	1.6	9
4155	Protein Engineering Allows for Mild Affinity-based Elution of Therapeutic Antibodies. Journal of Molecular Biology, 2018, 430, 3427-3438.	2.0	24
4156	Crystal Structure of the Dimerized N Terminus of Porcine Circovirus Type 2 Replicase Protein Reveals a Novel Antiviral Interface. Journal of Virology, 2018, 92, .	1.5	17
4157	Development of a new benchmark for assessing the scoring functions applicable to proteinâ€"protein interactions. Future Medicinal Chemistry, 2018, 10, 1555-1574.	1.1	9
4158	Integrating coâ€evolutionary signals and other properties of residue pairs to distinguish biological interfaces from crystal contacts. Protein Science, 2018, 27, 1723-1735.	3.1	11
4159	Structural characterization of<i>Porphyromonas gingivalis</i>enoyl-ACP reductase II (FabK). Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 105-112.	0.4	11
4160	Structure of a human synaptic GABAA receptor. Nature, 2018, 559, 67-72.	13.7	389
4161	Differences in substrate specificity of <i>V. cholerae</i> FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. FEBS Journal, 2018, 285, 2900-2921.	2.2	3
4162	Computational identification, characterization and validation of potential antigenic peptide vaccines from hrHPVs E6 proteins using immunoinformatics and computational systems biology approaches. PLoS ONE, 2018, 13, e0196484.	1.1	75
4163	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. ELife, 2018, 7, .	2.8	45
4164	Structureâ€Guided Engineering of Î±â€Keto Acid Decarboxylase for the Production of Higher Alcohols at Elevated Temperature. ChemSusChem, 2018, 11, 3335-3344.	3.6	13
4165	Structural basis of product inhibition by arabinose and xylose of the thermostable GH43 Î²-1,4-xylosidase from Geobacillus thermoleovorans IT-08. PLoS ONE, 2018, 13, e0196358.	1.1	25

#	Article	IF	Citations
4166	Structural Basis for MARK1 Kinase Autoinhibition by Its KA1 Domain. Structure, 2018, 26, 1137-1143.e3.	1.6	15
4167	A cylindrical assembly model and dynamics of the Ebola virus VP40 structural matrix. Scientific Reports, 2018, 8, 9776.	1.6	8
4168	A human anti-IL-2 antibody that potentiates regulatory T cells by a structure-based mechanism. Nature Medicine, 2018, 24, 1005-1014.	15.2	165
4169	Crystallization and X-ray analysis of all of the players in the autoregulation of the<i>ataRT</i>toxinâ€"antitoxin system. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 391-401.	0.4	5
4170	Trichomonas vaginalis metalloproteinase TvMP50 is a monomeric Aminopeptidase P-like enzyme. Molecular Biotechnology, 2018, 60, 563-575.	1.3	5
4171	Mechanism for remodelling of the cell cycle checkpoint protein MAD2 by the ATPase TRIP13. Nature, 2018, 559, 274-278.	13.7	109
4172	Structural and functional analysis of cystatin E reveals enzymologically relevant dimer and amyloid fibril states. Journal of Biological Chemistry, 2018, 293, 13151-13165.	1.6	25
4173	Crystal structures and kinetic analyses of<i>N</i>-acetylmannosamine-6-phosphate 2-epimerases from<i>Fusobacterium nucleatum</i>and<i>Vibrio cholerae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 431-440.	0.4	6
4174	Identification of a novel tRNA wobble uridine modifying activity in the biosynthesis of 5-methoxyuridine. Nucleic Acids Research, 2018, 46, 9160-9169.	6.5	13
4175	Crystal structures of the disease-causing D444V mutant and the relevant wild type human dihydrolipoamide dehydrogenase. Free Radical Biology and Medicine, 2018, 124, 214-220.	1.3	12
4176	Functional plasticity of antibacterial EndoU toxins. Molecular Microbiology, 2018, 109, 509-527.	1.2	25
4177	The crystallization additive hexatungstotellurate promotes the crystallization of the HSP70 nucleotide binding domain into two different crystal forms. PLoS ONE, 2018, 13, e0199639.	1.1	18
4178	Structural basis for the substrate recognition of peptidoglycan pentapeptides by Enterococcus faecalis VanYB. International Journal of Biological Macromolecules, 2018, 119, 335-344.	3.6	5
4179	TraN: A novel repressor of an Enterococcus conjugative type IV secretion system. Nucleic Acids Research, 2018, 46, 9201-9219.	6.5	11
4180	Cryo-EM of the dynamin polymer assembled on lipid membrane. Nature, 2018, 560, 258-262.	13.7	79
4181	Structural basis for selective inhibition of immunoglobulin E-receptor interactions by an anti-IgE antibody. Scientific Reports, 2018, 8, 11548.	1.6	22
4182	The structure of SALM5 suggests a dimeric assembly for the presynaptic RPTP ligand recognition. Protein Engineering, Design and Selection, 2018, 31, 147-157.	1.0	11
4183	Trehalose 6â€phosphate phosphatases of<i>Pseudomonas aeruginosa</i>. FASEB Journal, 2018, 32, 5470-5482.	0.2	9

#	ARTICLE	IF	CITATIONS
4184	Structural analyses reveal the mechanism of inhibition of influenza virus NS1 by two antiviral compounds. Journal of Biological Chemistry, 2018, 293, 14659-14668.	1.6	20
4185	Structural and Biochemical Characterization of AaL, a Quorum Quenching Lactonase with Unusual Kinetic Properties. Scientific Reports, 2018, 8, 11262.	1.6	38
4186	Structural insights into the mechanism of Type IVa pilus extension and retraction ATPase motors. FEBS Journal, 2018, 285, 3402-3421.	2.2	21
4187	Iron Scavenging in <i>Aspergillus</i> Species: Structural and Biochemical Insights into Fungal Siderophore Esterases. Angewandte Chemie - International Edition, 2018, 57, 14624-14629.	7.2	13
4188	Lactobacillus brevis CGMCC 1306 glutamate decarboxylase: Crystal structure and functional analysis. Biochemical and Biophysical Research Communications, 2018, 503, 1703-1709.	1.0	28
4189	Immunogenicity Testing of Lipidoids InÂVitro and In Silico: Modulating Lipidoid-Mediated TLR4 Activation by Nanoparticle Design. Molecular Therapy - Nucleic Acids, 2018, 11, 159-169.	2.3	27
4190	Structural and Functional Analysis of E.Âcoli Cyclopropane Fatty Acid Synthase. Structure, 2018, 26, 1251-1258.e3.	1.6	27
4191	Structure of the Î³â€“Îµ complex of cyanobacterial F1-ATPase reveals a suppression mechanism of the Î³ subunit on ATP hydrolysis in phototrophs. Biochemical Journal, 2018, 475, 2925-2939.	1.7	13
4192	Functional insights into theÂStreptococcus pneumoniae HicBA toxinâ€“antitoxin system based on a structural study. Nucleic Acids Research, 2018, 46, 6371-6386.	6.5	32
4193	A Structure-Based Strategy for Engineering Selective Ubiquitin Variant Inhibitors of Skp1-Cul1-F-Box Ubiquitin Ligases. Structure, 2018, 26, 1226-1236.e3.	1.6	27
4194	The crystal structure of the malic enzyme from<i>Candidatus</i>Phytoplasma reveals the minimal structural determinants for a malic enzyme. Acta Crystallographica Section D: Structural Biology, 2018, 74, 332-340.	1.1	5
4195	Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. Neuron, 2018, 99, 480-492.e5.	3.8	43
4196	Exploring Protein Structure: Principles and Practice. Learning Materials in Biosciences, 2018, , .	0.2	3
4197	Mechanistic and Structural Insights Into the Unique TetR-Dependent Regulation of a Drug Efflux Pump in Mycobacterium abscessus. Frontiers in Microbiology, 2018, 9, 649.	1.5	27
4198	2â€²-Deoxyribosyltransferase from Bacillus psychrosaccharolyticus: A Mesophilic-Like Biocatalyst for the Synthesis of Modified Nucleosides from a Psychrotolerant Bacterium. Catalysts, 2018, 8, 8.	1.6	18
4199	High-Resolution Crystal Structure of RpoS Fragment including a Partial Region 1.2 and Region 2 from the Intracellular Pathogen Legionella pneumophila. Crystals, 2018, 8, 54.	1.0	1
4200	Docking techniques in pharmacology: How much promising?. Computational Biology and Chemistry, 2018, 76, 210-217.	1.1	117
4201	Crystal structure and pH-dependent allosteric regulation of human Î²-ureidopropionase, an enzyme involved in anticancer drug metabolism. Biochemical Journal, 2018, 475, 2395-2416.	1.7	8

#	ARTICLE	IF	CITATIONS
4202	Structures of DNA-bound human ligase IV catalytic core reveal insights into substrate binding and catalysis. Nature Communications, 2018, 9, 2642.	5.8	37
4203	Structure of the flavocytochrome <i>c</i> sulfide dehydrogenase associated with the copper-binding protein CopC from the haloalkaliphilic sulfur-oxidizing bacterium <i>Thioalkalivibrio paradoxus</i>ARh 1. Acta Crystallographica Section D: Structural Biology, 2018, 74, 632-642.	1.1	9
4204	Insights into the Structures of Superoxide Reductases from the Symbionts <i>Ignicoccus hospitalis</i> and <i>Nanoarchaeum equitans</i>. Biochemistry, 2018, 57, 5271-5281.	1.2	5
4205	Computational Insights into the Interactions between Calmodulin and the c/nSH2 Domains of p85Î± Regulatory Subunit of PI3KÎ±: Implication for PI3KÎ± Activation by Calmodulin. International Journal of Molecular Sciences, 2018, 19, 151.	1.8	23
4206	Electrochemically-Driven Insertion of Biological Nanodiscs into Solid State Membrane Pores as a Basis for â€œPore-In-Poreâ€•Membranes. Nanomaterials, 2018, 8, 237.	1.9	7
4207	Crystal Structure of Botulinum Neurotoxin A2 in Complex with the Human Protein Receptor SV2C Reveals Plasticity in Receptor Binding. Toxins, 2018, 10, 153.	1.5	14
4208	A Novel ShK-Like Toxic Peptide from the Transcriptome of the Cnidarian Palythoa caribaeorum Displays Neuroprotection and Cardioprotection in Zebrafish. Toxins, 2018, 10, 238.	1.5	14
4209	Structure of an Acinetobacter Broad-Range Prophage Endolysin Reveals a C-Terminal Î±-Helix with the Proposed Role in Activity against Live Bacterial Cells. Viruses, 2018, 10, 309.	1.5	23
4210	Fatty Acyl-AMP Ligases as Mechanistic Variants of ANL Superfamily and Molecular Determinants Dictating Substrate Specificities. Journal of the Indian Institute of Science, 2018, 98, 261-272.	0.9	5
4211	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in Salmonella typhimurium. Journal of Molecular Biology, 2018, 430, 3170-3189.	2.0	29
4212	Capsid protein structure, self-assembly, and processing reveal morphogenesis of the marine virophage mavirus. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7332-7337.	3.3	18
4213	Structural and functional studies of the metalloregulator Fur identify a promoter-binding mechanism and itsÂrole in Francisella tularensis virulence. Communications Biology, 2018, 1, 93.	2.0	19
4214	Bent conformation of a backbone pilin N-terminal domain supports a three-stage pilus assembly mechanism. Communications Biology, 2018, 1, 94.	2.0	9
4215	MouR controls the expression of the Listeria monocytogenes Agr system and mediates virulence. Nucleic Acids Research, 2018, 46, 9338-9352.	6.5	26
4216	Crystal structure and substrate binding mode of ectonucleotide phosphodiesterase/pyrophosphatase-3 (NPP3). Scientific Reports, 2018, 8, 10874.	1.6	9
4217	A non-canonical GTPase interaction enables ORP1L-Rab7-RILP complex formation and late endosome positioning. Journal of Biological Chemistry, 2018, 293, 14155-14164.	1.6	25
4218	Investigating Proteins with Î²-Sheets. Learning Materials in Biosciences, 2018, , 197-226.	0.2	0
4219	Conformational and dynamical basis for cross-reactivity observed between anti HIV-1 protease antibody with protease and an epitope peptide from it. International Journal of Biological Macromolecules, 2018, 118, 1696-1707.	3.6	2

#	ARTICLE	IF	CITATIONS
4220	Crystal structures of two tandem malectin-like receptor kinases involved in plant reproduction. Acta Crystallographica Section D: Structural Biology, 2018, 74, 671-680.	1.1	49
4221	A positiveâ€charged patch and stabilized hydrophobic core are essential for avirulence function of AvrPib in the rice blast fungus. Plant Journal, 2018, 96, 133-146.	2.8	49
4222	Mechanistic Basis of the Fast Dark Recovery of the Short LOV Protein DsLOV from <i>Dinoroseobacter shibae</i>. Biochemistry, 2018, 57, 4833-4847.	1.2	17
4223	Custom-built electrostatics and supplementary bonding in the design of reinforced Collagen-g-P(methyl methacrylate-co-ethyl acrylate)/ nylon 66 core-shell fibers. Journal of the Mechanical Behavior of Biomedical Materials, 2018, 87, 19-29.	1.5	14
4224	Characterization of the binding mode of JNK-interacting protein 1 (JIP1) to kinesin-light chain 1 (KLC1). Journal of Biological Chemistry, 2018, 293, 13946-13960.	1.6	10
4225	Pseudomonas aeruginosa pyoverdine maturation enzyme PvdP has a noncanonical domain architecture and affords insight into a new subclass of tyrosinases. Journal of Biological Chemistry, 2018, 293, 14926-14936.	1.6	14
4226	Gluconeogenic precursor availability regulates flux through the glyoxylate shunt in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2018, 293, 14260-14269.	1.6	43
4227	Structure of the DNA-binding domain of human myelin-gene regulatory factor reveals its potential protein-DNA recognition mode. Journal of Structural Biology, 2018, 203, 170-178.	1.3	8
4228	Structural and functional determination of homologs of the Mycobacterium tuberculosis N-acetylglucosamine-6-phosphate deacetylase (NagA). Journal of Biological Chemistry, 2018, 293, 9770-9783.	1.6	27
4229	Atomic displacement parameters in structural biology. Amino Acids, 2018, 50, 775-786.	1.2	22
4230	Computational Resources for Predicting Proteinâ€“Protein Interactions. Advances in Protein Chemistry and Structural Biology, 2018, 110, 251-275.	1.0	11
4231	Contribution of the residue at position 4 within classical nuclear localization signals to modulating interaction with importins and nuclear targeting. Biochimica Et Biophysica Acta - Molecular Cell Research, 2018, 1865, 1114-1129.	1.9	22
4232	Identification and structural characterization of a histidinol phosphate phosphatase from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2018, 293, 10102-10118.	1.6	10
4233	Archaeal <scp>DNA</scp> on the histone merryâ€goâ€round. FEBS Journal, 2018, 285, 3168-3174.	2.2	13
4234	Identification and characterization of a calmodulin binding domain in the plasma membrane Ca 2+ -ATPase from Trypanosoma equiperdum. Molecular and Biochemical Parasitology, 2018, 222, 51-60.	0.5	5
4235	The protein kinase CK2 catalytic domain from Plasmodium falciparum: crystal structure, tyrosine kinase activity and inhibition. Scientific Reports, 2018, 8, 7365.	1.6	11
4236	Structural and kinetic insights into stimulation of RppH-dependent RNA degradation by the metabolic enzyme DapF. Nucleic Acids Research, 2018, 46, 6841-6856.	6.5	15
4237	Crystal structure of RecR, a member of the RecFOR DNA-repair pathway, from<i>Pseudomonas aeruginosa</i>PAO1. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 222-230.	0.4	7

#	ARTICLE	IF	CITATIONS
4238	Structural basis for nucleotide recognition by the ectoenzyme <scp>CD</scp>203c. FEBS Journal, 2018, 285, 2481-2494.	2.2	30
4239	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. Nature Communications, 2018, 9, 1820.	5.8	124
4240	A bipartite periplasmic receptorâ€“diguanylate cyclase pair (XAC2383â€“XAC2382) in the bacterium Xanthomonas citri. Journal of Biological Chemistry, 2018, 293, 10767-10781.	1.6	2
4241	Insights into degradation mechanism of N-end rule substrates by p62/SQSTM1 autophagy adapter. Nature Communications, 2018, 9, 3291.	5.8	62
4242	Structural and Mutagenesis Studies of the Thiamineâ€Dependent, Ketoneâ€Accepting YerE from <i>Pseudomonas protegens</i>. ChemBioChem, 2018, 19, 2283-2292.	1.3	8
4243	Lysine as a heme iron ligand: A property common to three truncated hemoglobins from Chlamydomonas reinhardtii. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2660-2673.	1.1	14
4244	Two Patched molecules engage distinct sites on Hedgehog yielding a signaling-competent complex. Science, 2018, 362, .	6.0	105
4245	Cryo-EM structure of infectious bronchitis coronavirus spike protein reveals structural and functional evolution of coronavirus spike proteins. PLoS Pathogens, 2018, 14, e1007009.	2.1	96
4246	Bonsai Gelsolin Survives Heat Induced Denaturation by Forming Î²-Amyloids which Leach Out Functional Monomer. Scientific Reports, 2018, 8, 12602.	1.6	14
4247	Structures of glycolate oxidase from Nicotiana benthamiana reveal a conserved pH sensor affecting the binding of FMN. Biochemical and Biophysical Research Communications, 2018, 503, 3050-3056.	1.0	6
4248	EPO does not promote interaction between the erythropoietin and beta-common receptors. Scientific Reports, 2018, 8, 12457.	1.6	21
4249	Structural insights into inhibitor binding to a fungal ortholog of aspartate semialdehyde dehydrogenase. Biochemical and Biophysical Research Communications, 2018, 503, 2848-2854.	1.0	9
4250	Structural rearrangements in the C-terminal domain homolog of Orange Carotenoid Protein are crucial for carotenoid transfer. Communications Biology, 2018, 1, 125.	2.0	39
4251	Structure of the GH9 glucosidase/glucosaminidase fromVibrio cholerae. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 512-523.	0.4	4
4252	4-Hydroxy-tetrahydrodipicolinate reductase from Neisseria gonorrhoeae â€“ structure and interactions with coenzymes and substrate analog. Biochemical and Biophysical Research Communications, 2018, 503, 1993-1999.	1.0	4
4253	Structures of Hepatitis B Virus Core- and e-Antigen Immune Complexes Suggest Multi-point Inhibition. Structure, 2018, 26, 1314-1326.e4.	1.6	15
4254	Activity and structure of EcoKMcrA. Nucleic Acids Research, 2018, 46, 9829-9841.	6.5	18
4255	Structural insight into molecular mechanism of cytokinin activating protein from <i>Pseudomonas aeruginosa</i> PAO1. Environmental Microbiology, 2018, 20, 3214-3223.	1.8	11

#	ARTICLE	IF	CITATIONS
4256	A new crystal form of Aspergillus oryzae catechol oxidase and evaluation of copper site structures in coupled binuclear copper enzymes. PLoS ONE, 2018, 13, e0196691.	1.1	8
4257	A Key Role for the Periplasmic PfeE Esterase in Iron Acquisition <i>via</i> the Siderophore Enterobactin in <i>Pseudomonas aeruginosa</i>. ACS Chemical Biology, 2018, 13, 2603-2614.	1.6	30
4258	Identification, Characterization, and X-ray Crystallographic Analysis of a Novel Type of Lectin AJLec from the Sea Anemone Anthopleura japonica. Scientific Reports, 2018, 8, 11516.	1.6	8
4259	Crystal structure of highly glycosylated human leukocyte elastase in complex with an S2â€² site binding inhibitor. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 480-489.	0.4	15
4260	Pathogen-derived HLA-E bound epitopes reveal broad primary anchor pocket tolerability and conformationally malleable peptide binding. Nature Communications, 2018, 9, 3137.	5.8	57
4261	Biochemical and structural features of diverse bacterial glucuronoyl esterases facilitating recalcitrant biomass conversion. Biotechnology for Biofuels, 2018, 11, 213.	6.2	35
4262	Modification of quaternary structure of Candida albicans GlcN-6-P synthase and its desensitization to inhibition by UDP-GlcNAc by site-directed mutagenesis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1181-1189.	1.1	5
4263	Supramolecular assembly of KAT2A with succinyl-CoA for histone succinylation. Cell Discovery, 2018, 4, 47.	3.1	23
4264	The structure of the ubiquitin-like modifier FAT10 reveals an alternative targeting mechanism for proteasomal degradation. Nature Communications, 2018, 9, 3321.	5.8	25
4265	Structural and Functional Analysis of Pyrimidine Nucleoside Phosphorylases of the NP-I and NP-II Families in Complexes with 6-Methyluracil. Crystallography Reports, 2018, 63, 418-427.	0.1	2
4266	Homodimer Architecture of QTRT2, the Noncatalytic Subunit of the Eukaryotic tRNA-Guanine Transglycosylase. Biochemistry, 2018, 57, 3953-3965.	1.2	8
4267	Combination of aptamer and drug for reversible anticoagulation in cardiopulmonary bypass. Nature Biotechnology, 2018, 36, 606-613.	9.4	52
4268	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. Nature Chemical Biology, 2018, 14, 730-737.	3.9	21
4269	An Alternative Homodimerization Interface of MnmG Reveals a Conformational Dynamics that Is Essential for Its tRNA Modification Function. Journal of Molecular Biology, 2018, 430, 2822-2842.	2.0	5
4270	Structural Basis of Proteinâ€"Protein Interactions between a <i>trans</i>-Acting Acyltransferase and Acyl Carrier Protein in Polyketide Disorazole Biosynthesis. Journal of the American Chemical Society, 2018, 140, 7970-7978.	6.6	40
4271	MyPMFs: a simple tool for creating statistical potentials to assess protein structural models. Biochimie, 2018, 151, 37-41.	1.3	4
4272	The archaeal ATPase PINA interacts with the helicase Hjm via its carboxyl terminal KH domain remodeling and processing replication fork and Holliday junction. Nucleic Acids Research, 2018, 46, 6627-6641.	6.5	19
4273	Noncatalytic Antioxidant Role for Helicobacter pylori Urease. Journal of Bacteriology, 2018, 200, .	1.0	27

#	ARTICLE	IF	CITATIONS
4274	Broadly Reactive Human Monoclonal Antibodies Elicited following Pandemic H1N1 Influenza Virus Exposure Protect Mice against Highly Pathogenic H5N1 Challenge. Journal of Virology, 2018, 92, .	1.5	33
4275	The crystal structure of monoacylglycerol lipase from M. tuberculosis reveals the basis for specific inhibition. Scientific Reports, 2018, 8, 8948.	1.6	23
4276	Crystal structure and insights into the oligomeric state of UDP-glucose pyrophosphorylase from sugarcane. PLoS ONE, 2018, 13, e0193667.	1.1	10
4277	Structural basis for recognition of the central conserved region of RSV G by neutralizing human antibodies. PLoS Pathogens, 2018, 14, e1006935.	2.1	50
4278	Domain swapping dissection in Thermotoga maritima arginine binding protein: How structural flexibility may compensate destabilization. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 952-962.	1.1	10
4279	Structural insight into the human mitochondrial tRNA purine N1-methyltransferase and ribonuclease P complexes. Journal of Biological Chemistry, 2018, 293, 12862-12876.	1.6	28
4280	Structures of the<i>Mycobacterium tuberculosis</i>GlpX protein (class II) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td (fructose-1,6-bis citrate inhibition. Acta Crystallographica Section D: Structural Biology, 2018, 74, 321-331.	1.1	8
4281	Plasticity in binding confers selectivity in ligand-induced protein degradation. Nature Chemical Biology, 2018, 14, 706-714.	3.9	391
4282	Structural basis for regulation of human acetyl-CoA carboxylase. Nature, 2018, 558, 470-474.	13.7	135
4283	Structural Basis for the Broad, Antibody-Mediated Neutralization of H5N1 Influenza Virus. Journal of Virology, 2018, 92, .	1.5	8
4284	Modeling the assembly order of multimeric heteroprotein complexes. PLoS Computational Biology, 2018, 14, e1005937.	1.5	30
4285	Cryo-EM structures of complex I from mouse heart mitochondria in two biochemically defined states. Nature Structural and Molecular Biology, 2018, 25, 548-556.	3.6	202
4286	Crystal structures of a [NiFe] hydrogenase large subunit HyhL in an immature state in complex with a Ni chaperone HypA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7045-7050.	3.3	27
4287	Structure-function study of two new middle-redox potential laccases from basidiomycetes Antrodiella faginea and Steccherinum murashkinskyi. International Journal of Biological Macromolecules, 2018, 118, 406-418.	3.6	21
4288	Structural and functional insights into the unique CBSâ€“CP12 fusion protein family in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7141-7146.	3.3	20
4289	Reversing allosteric communication: From detecting allosteric sites to inducing and tuning targeted allosteric response. PLoS Computational Biology, 2018, 14, e1006228.	1.5	66
4290	Protein Structure Databases. , 2019, , 460-471.		0
4291	Structure and specificity of several triclocarbanâ€binding single domain camelid antibody fragments. Journal of Molecular Recognition, 2019, 32, e2755.	1.1	21

#	ARTICLE	IF	CITATIONS
4292	Prediction of Protein-Protein Interactions: Looking Through the Kaleidoscope. , 2019, , 834-848.		1
4293	Compatibility of RUNX1/ETO fusion protein modules driving CD34+ human progenitor cell expansion. Oncogene, 2019, 38, 261-272.	2.6	6
4294	Structural Basis of Crossâ€Reactivity of Antiâ€“Citrullinated Protein Antibodies. Arthritis and Rheumatology, 2019, 71, 210-221.	2.9	64
4295	Binding and structural studies of the complexes of type 1 ribosome inactivating protein from <scp><i>Momordica balsamina</i></scp> with uracil and uridine. Proteins: Structure, Function and Bioinformatics, 2019, 87, 99-109.	1.5	1
4296	Regulation of phosphoribosyl ubiquitination by a calmodulin-dependent glutamylase. Nature, 2019, 572, 387-391.	13.7	91
4297	Structure functional insights into calcium binding during the activation of coagulation factor XIII A. Scientific Reports, 2019, 9, 11324.	1.6	52
4298	A strategy for the selection of monovalent antibodies that span protein dimer interfaces. Journal of Biological Chemistry, 2019, 294, 13876-13886.	1.6	16
4299	Structureâ€“function studies of tetrahydroprotoberberine N-methyltransferase reveal the molecular basis of stereoselective substrate recognition. Journal of Biological Chemistry, 2019, 294, 14482-14498.	1.6	19
4300	Cryo-EM structure of the activated RET signaling complex reveals the importance of its cysteine-rich domain. Science Advances, 2019, 5, eaau4202.	4.7	23
4301	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. Nature Communications, 2019, 10, 3629.	5.8	15
4302	ANO5 mutations in the Polish limb girdle muscular dystrophy patients: Effects on the protein structure. Scientific Reports, 2019, 9, 11533.	1.6	11
4303	T3S injectisome needle complex structures in four distinct states reveal the basis of membrane coupling and assembly. Nature Microbiology, 2019, 4, 2010-2019.	5.9	58
4304	Type 8 long QT syndrome: pathogenic variants in CACNA1C-encoded Cav1.2 cluster in STAC protein binding site. Europace, 2019, 21, 1725-1732.	0.7	15
4305	Structure and DNA damage-dependent derepression mechanism for the XRE family member DG-DdrO. Nucleic Acids Research, 2019, 47, 9925-9933.	6.5	28
4306	Molecular Origins of Functional Diversity in Benzylisoquinoline Alkaloid Methyltransferases. Frontiers in Plant Science, 2019, 10, 1058.	1.7	25
4307	The structure of a polygamous repressor reveals how phage-inducible chromosomal islands spread in nature. Nature Communications, 2019, 10, 3676.	5.8	11
4308	Diversity of oligomerization in Drosophila semaphorins suggests a mechanism of functional fine-tuning. Nature Communications, 2019, 10, 3691.	5.8	10
4309	The neuraminidase of A(H3N2) influenza viruses circulating since 2016 is antigenically distinct from the A/Hong Kong/4801/2014 vaccine strain. Nature Microbiology, 2019, 4, 2216-2225.	5.9	59

#	ARTICLE	IF	CITATIONS
4310	Structural and functional characterization of SiiA, an auxiliary protein from the SPI4â€encoded type 1 secretion system from <i>Salmonella enterica</i>. Molecular Microbiology, 2019, 112, 1403-1422.	1.2	9
4311	Structure and conformational plasticity of the intact <i>Thermus thermophilus</i> V/A-type ATPase. Science, 2019, 365, .	6.0	47
4312	Structural Basis of Glycerophosphodiester Recognition by the <i>Mycobacterium tuberculosis</i> Substrate-Binding Protein UgpB. ACS Chemical Biology, 2019, 14, 1879-1887.	1.6	13
4313	Crystal structure and biochemical characterization of O-acetylhomoserine acetyltransferase from Mycobacterium smegmatisÂATCC 19420. Biochemical and Biophysical Research Communications, 2019, 517, 399-406.	1.0	8
4314	Structural basis for broad substrate specificity of UDP-glucose 4-epimerase in the human milk oligosaccharide catabolic pathway of Bifidobacterium longum. Scientific Reports, 2019, 9, 11081.	1.6	17
4315	Distinct FcÎ± receptor N-glycans modulate the binding affinity to immunoglobulin A (IgA) antibodies. Journal of Biological Chemistry, 2019, 294, 13995-14008.	1.6	29
4316	Obtaining Soft Matter Models of Proteins and their Phase Behavior. Methods in Molecular Biology, 2019, 2039, 209-228.	0.4	3
4317	Atomic structures of an entire contractile injection system in both the extended and contracted states. Nature Microbiology, 2019, 4, 1885-1894.	5.9	45
4318	Structures of CENP-C cupin domains at regional centromeres reveal unique patterns of dimerization and recruitment functions for the inner pocket. Journal of Biological Chemistry, 2019, 294, 14119-14134.	1.6	18
4319	Toward Understanding the Impact of Dimerization Interfaces in Angiotensin II Type 1 Receptor. Journal of Chemical Information and Modeling, 2019, 59, 4314-4327.	2.5	13
4320	Perturbation of the interactions of calmodulin with GRK5 using a natural product chemical probe. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15895-15900.	3.3	18
4321	Phosphite binding by the HtxB periplasmic binding protein depends on the protonation state of the ligand. Scientific Reports, 2019, 9, 10231.	1.6	6
4322	Crystal structures of Moorella thermoacetica cyanuric acid hydrolase reveal conformational flexibility and asymmetry important for catalysis. PLoS ONE, 2019, 14, e0216979.	1.1	2
4323	Hydrophobic recognition allows the glycosyltransferase UGT76G1 to catalyze its substrate in two orientations. Nature Communications, 2019, 10, 3214.	5.8	47
4324	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. Structure, 2019, 27, 1427-1442.e4.	1.6	12
4325	Inactivating mutations and X-ray crystal structure of the tumor suppressor OPCML reveal cancer-associated functions. Nature Communications, 2019, 10, 3134.	5.8	9
4326	Predicting the Affinity of Peptides to Major Histocompatibility Complex Class II by Scoring Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2019, 59, 3464-3473.	2.5	34
4327	Identification, functional and structural characterization of novel aminoglycoside phosphotransferase APH(3â€³)-Id from Streptomyces rimosus subsp. rimosus ATCC 10970. Archives of Biochemistry and Biophysics, 2019, 671, 111-122.	1.4	7

#	ARTICLE	IF	CITATIONS
4328	Crystal Structure of <i>Aeromonas hydrophila</i> Cytoplasmic 5â€²-Methylthioadenosine/<i>S</i>-Adenosylhomocysteine Nucleosidase. Biochemistry, 2019, 58, 3136-3143.	1.2	0
4329	Distinct RNA-binding modules in a single PUF protein cooperate to determine RNA specificity. Nucleic Acids Research, 2019, 47, 8770-8784.	6.5	9
4330	Structural modeling of protein complexes: Current capabilities and challenges. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1222-1232.	1.5	12
4331	Structures of the Mitochondrial CDP-DAG Synthase Tam41 Suggest a Potential Lipid Substrate Pathway from Membrane to the Active Site. Structure, 2019, 27, 1258-1269.e4.	1.6	15
4332	Crystal Structure and Biochemical Characterization of Ketol-Acid Reductoisomerase from <i>Corynebacterium glutamicum</i>. Journal of Agricultural and Food Chemistry, 2019, 67, 8527-8535.	2.4	7
4333	Underestimated Noncovalent Interactions in Protein Data Bank. Journal of Chemical Information and Modeling, 2019, 59, 3389-3399.	2.5	25
4334	An Asymmetric Reductase That Intercepts Acyclic Imino Acids Produced <i>in Situ</i> by a Partner Oxidase. Journal of the American Chemical Society, 2019, 141, 12258-12267.	6.6	5
4335	Molecular basis of egg coat cross-linking sheds light on ZP1-associated female infertility. Nature Communications, 2019, 10, 3086.	5.8	43
4336	Structural underpinnings of Ric8A function as a G-protein Î±-subunit chaperone and guanine-nucleotide exchange factor. Nature Communications, 2019, 10, 3084.	5.8	22
4337	Characterization of two putative Dichelobacter nodosus footrot vaccine antigens identifies the first lysozyme inhibitor in the genus. Scientific Reports, 2019, 9, 10055.	1.6	3
4338	Structural basis of NKT cell inhibition using the T-cell receptor-blocking anti-CD1d antibody 1B1. Journal of Biological Chemistry, 2019, 294, 12947-12956.	1.6	0
4339	Crystal structures ofTrypanosoma bruceihypoxanthine â€" guanine â€" xanthine phosphoribosyltransferase in complex withIMP,GMPandXMP. FEBS Journal, 2019, 286, 4721-4736.	2.2	9
4340	Structures of singleâ€layer Î²â€sheet proteins evolved from Î²â€hairpin repeats. Protein Science, 2019, 28, 1676-1689.	3.1	4
4341	Structural Determinants for Substrate Selectivity in Guanine Deaminase Enzymes of the Amidohydrolase Superfamily. Biochemistry, 2019, 58, 3280-3292.	1.2	16
4342	Structural basis for the recognition of MucA by MucB and AlgU inPseudomonas aeruginosa. FEBS Journal, 2019, 286, 4982-4994.	2.2	27
4343	Alternative conformations of a major antigenic site on RSV F. PLoS Pathogens, 2019, 15, e1007944.	2.1	29
4344	Crystal Structure of Dihydro-Heme d1 Dehydrogenase NirN from Pseudomonas aeruginosa Reveals Amino Acid Residues Essential for Catalysis. Journal of Molecular Biology, 2019, 431, 3246-3260.	2.0	14
4345	Structure of the MORN4/Myo3a Tail Complex Reveals MORN Repeats as Protein Binding Modules. Structure, 2019, 27, 1366-1374.e3.	1.6	18

#	Article	IF	Citations
4346	Structural Basis for Recruitment of DAPK1 to the KLHL20 E3 Ligase. Structure, 2019, 27, 1395-1404.e4.	1.6	21
4347	Crystal structures of the closed form of<i>Mycobacterium tuberculosis</i>dihydrofolate reductase in complex with dihydrofolate and antifolates. Acta Crystallographica Section D: Structural Biology, 2019, 75, 682-693.	1.1	10
4348	Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1. Nature, 2019, 571, 429-433.	13.7	86
4349	Multiple Pleomorphic Tetramers of Thermostable Direct Hemolysin from Grimontia hollisae in Exerting Hemolysis and Membrane Binding. Scientific Reports, 2019, 9, 9833.	1.6	0
4350	In silico analysis of bacteriophage tail tubular proteins suggests a putative sugar binding site and a catalytic mechanism. Journal of Molecular Graphics and Modelling, 2019, 92, 8-16.	1.3	2
4351	Structural basis for stereoselective dehydration and hydrogen-bonding catalysis by the SAM-dependent pericyclase LepI. Nature Chemistry, 2019, 11, 812-820.	6.6	42
4352	Comparative structural and thermal stability studies of Cuc m 2.0101, Art v 4.0101 and other allergenic profilins. Molecular Immunology, 2019, 114, 19-29.	1.0	20
4353	The AAAâ€‰+â€‰ATPase TorsinA polymerizes into hollow helical tubes with 8.5 subunits per turn. Nature Communications, 2019, 10, 3262.	5.8	22
4354	Underlying molecular alterations in human dihydrolipoamide dehydrogenase deficiency revealed by structural analyses of disease-causing enzyme variants. Human Molecular Genetics, 2019, 28, 3339-3354.	1.4	19
4355	Detecting and Characterizing Protein Self-Assembly In Vivo by Flow Cytometry. Journal of Visualized Experiments, 2019, , .	0.2	11
4356	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. Cell, 2019, 178, 567-584.e19.	13.5	106
4357	Bile Salts Alter the Mouse Norovirus Capsid Conformation: Possible Implications for Cell Attachment and Immune Evasion. Journal of Virology, 2019, 93, .	1.5	39
4358	An Unprecedented Cyclization Mechanism in the Biosynthesis of Carbazole Alkaloids in <i>Streptomyces</i>. Angewandte Chemie - International Edition, 2019, 58, 13349-13353.	7.2	17
4359	Design and Characterization of Protein E-PilA, a Candidate Fusion Antigen for Nontypeable Haemophilus influenzae Vaccine. Infection and Immunity, 2019, 87, .	1.0	9
4360	Crystallization and Crystallographic Analysis of a Bradyrhizobium Elkanii USDA94 Haloalkane Dehalogenase Variant with an Eliminated Halide-Binding Site. Crystals, 2019, 9, 375.	1.0	3
4361	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. Journal of Molecular Biology, 2019, 431, 3718-3739.	2.0	67
4362	An Unprecedented Cyclization Mechanism in the Biosynthesis of Carbazole Alkaloids in Streptomyces. Angewandte Chemie, 2019, 131, 13483-13487.	1.6	2
4363	Inhibition of Plasmodium falciparum cysteine protease falcipain-2 by a human cross-class inhibitor serpinB3: A mechanistic insight. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 854-865.	1.1	7

#	ARTICLE	IF	CITATIONS
4364	The steroid side-chainâ€“cleaving aldolase Ltp2â€“ChsH2DUF35 is a thiolase superfamily member with a radically repurposed active site. Journal of Biological Chemistry, 2019, 294, 11934-11943.	1.6	18
4365	Predicting Specificities Under the Non-self Gametophytic Self-Incompatibility Recognition Model. Frontiers in Plant Science, 2019, 10, 879.	1.7	6
4366	Crystal structure of the aminoglycosides <i>N</i>â€acetyltransferase Eis2 from <i>MycobacteriumÂabscessus</i>. FEBS Journal, 2019, 286, 4342-4355.	2.2	14
4367	Structure Elucidation of Helical Aromatic Foldamerâ€“Protein Complexes with Large Contact Surface Areas. Chemistry - A European Journal, 2019, 25, 11042-11047.	1.7	15
4368	Chivosazole A Modulates Proteinâ€“Protein Interactions of Actin. Journal of Natural Products, 2019, 82, 1961-1970.	1.5	8
4369	BurkholderiaÂpseudomallei d â€alanineâ€•d â€alanine ligase; detailed characterisation and assessment of a potential antibiotic drug target. FEBS Journal, 2019, 286, 4509-4524.	2.2	4
4370	Abundant Perithecial Protein (APP) from Neurospora is a primitive functional analog of ocular crystallins. Biochemical and Biophysical Research Communications, 2019, 516, 796-800.	1.0	1
4371	Structural Basis of Tryptophan Reverse N-Prenylation Catalyzed by CymD. Biochemistry, 2019, 58, 3232-3242.	1.2	14
4372	Ambidextrous helical nanotubes from self-assembly of designed helical hairpin motifs. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14456-14464.	3.3	32
4374	Structural Basis of CD160:HVEM Recognition. Structure, 2019, 27, 1286-1295.e4.	1.6	33
4375	The CspC pseudoprotease regulates germination of Clostridioides difficile spores in response to multiple environmental signals. PLoS Genetics, 2019, 15, e1008224.	1.5	32
4376	Pricing and Incentive Strategy for Green Building Supply Chain with Incentive Mechanism. IOP Conference Series: Earth and Environmental Science, 2019, 304, 032111.	0.2	1
4377	Oligopeptidase B, a missing enzyme in mammals and a potential drug target for trypanosomatid diseases. Biochimie, 2019, 167, 207-216.	1.3	13
4378	Vibrio cholerae YaeO is a Structural Homologue of RNA Chaperone Hfq that Inhibits Rho-dependent Transcription Termination by Dissociating its Hexameric State. Journal of Molecular Biology, 2019, 431, 4749-4766.	2.0	8
4379	Cryo-EM Structure of Actin Filaments from <i>Zea mays</i> Pollen. Plant Cell, 2019, 31, 2855-2867.	3.1	18
4380	Structural Basis for Properdin Oligomerization and Convertase Stimulation in the Human Complement System. Frontiers in Immunology, 2019, 10, 2007.	2.2	47
4381	Staphylococcus aureus evasion proteins EapH1 and EapH2: Residue-level investigation of an alternative binding motif for human neutrophil elastase. Archives of Biochemistry and Biophysics, 2019, 676, 108140.	1.4	5
4382	Identification of an adhesive interface for the non-clustered Î´1 protocadherin-1 involved in respiratory diseases. Communications Biology, 2019, 2, 354.	2.0	17

#	ARTICLE	IF	CITATIONS
4383	Structureâ€“function relationships of the 5â€oxoprolinase subunit A: Guiding biological sciences students down the path less traveled. Biochemistry and Molecular Biology Education, 2019, 47, 620-631.	0.5	3
4384	Insights revealed by the coâ€crystal structure of the Saccharomyces cerevisiae histidine phosphotransfer protein Ypd1 and the receiver domain of its downstream response regulator Ssk1. Protein Science, 2019, 28, 2099-2111.	3.1	5
4385	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	1.5	99
4386	Crystal Structure of NADPH-Dependent Methylglyoxal Reductase Gre2 from Candida Albicans. Crystals, 2019, 9, 471.	1.0	3
4387	Structural Immunology. Advances in Experimental Medicine and Biology, 2019, , .	0.8	4
4388	Crystal Structure of Kluyveromyces lactis Glucokinase (KlGlk1). International Journal of Molecular Sciences, 2019, 20, 4821.	1.8	1
4389	The Crystal Structure of Dph2 in Complex with Elongation Factor 2 Reveals the Structural Basis for the First Step of Diphthamide Biosynthesis. Biochemistry, 2019, 58, 4343-4351.	1.2	7
4390	Recognition and processing of branched DNA substrates by Slx1â€“Slx4 nuclease. Nucleic Acids Research, 2019, 47, 11681-11690.	6.5	10
4391	Structural insights into the enzyme specificity of a novel Ï‰-transaminase from the thermophilic bacterium Sphaerobacter thermophilus. Journal of Structural Biology, 2019, 208, 107395.	1.3	4
4392	The Molecular Mechanism of Cellular Attachment for an Archaeal Virus. Structure, 2019, 27, 1634-1646.e3.	1.6	21
4393	Crystal structure of ErmE - 23S rRNA methyltransferase in macrolide resistance. Scientific Reports, 2019, 9, 14607.	1.6	9
4394	Deciphering the activation and recognition mechanisms of Staphylococcus aureus response regulator ArlR. Nucleic Acids Research, 2019, 47, 11418-11429.	6.5	15
4395	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. Molecular Cell, 2019, 76, 922-937.e7.	4.5	44
4396	Structural basis for substrate specificity and regulation of nucleotide sugar transporters in the lipid bilayer. Nature Communications, 2019, 10, 4657.	5.8	23
4397	The C-terminal region of human plasma fetuin-B is dispensable for the raised-elephant-trunk mechanism of inhibition of astacin metallopeptidases. Scientific Reports, 2019, 9, 14683.	1.6	6
4398	Structural Insights into Substrate Recognition and Activity Regulation of the Key Decarboxylase SbnH in Staphyloferrin B Biosynthesis. Journal of Molecular Biology, 2019, 431, 4868-4881.	2.0	7
4399	PRMT1 activates myogenin transcription via MyoD arginine methylation at R121. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 194442.	0.9	11
4400	Reprogramming Bacteriophage Host Range through Structure-Guided Design of Chimeric Receptor Binding Proteins. Cell Reports, 2019, 29, 1336-1350.e4.	2.9	135

#	Article	IF	Citations
4401	An aldo-keto reductase with 2-keto-l-gulonate reductase activity functions in l-tartaric acid biosynthesis from vitamin C in Vitis vinifera. Journal of Biological Chemistry, 2019, 294, 15932-15946.	1.6	14
4402	Crystal structure, epitope, and functional impact of an antibody against a superactive FVII a provide insights into allosteric mechanism. Research and Practice in Thrombosis and Haemostasis, 2019, 3, 412-419.	1.0	0
4403	Structural and Mechanistic Basis of an Oxepin-CoA Forming Isomerase in Bacterial Primary and Secondary Metabolism. ACS Chemical Biology, 2019, 14, 2876-2886.	1.6	8
4404	The non-swapped monomeric structure of the arginine-binding protein from <i>Thermotoga maritima</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 707-713.	0.4	5
4405	Streptococcal phosphotransferase system imports unsaturated hyaluronan disaccharide derived from host extracellular matrices. PLoS ONE, 2019, 14, e0224753.	1.1	10
4406	Common Mode of Remodeling AAA ATPases p97/CDC48 by Their Disassembling Cofactors ASPL/PUX1. Structure, 2019, 27, 1830-1841.e3.	1.6	13
4407	Atomic Structure of the Francisella T6SS Central Spike Reveals a Unique Î±-Helical Lid and a Putative Cargo. Structure, 2019, 27, 1811-1819.e6.	1.6	6
4408	A Potent Anti-SpuE Antibody Allosterically Inhibits Type III Secretion System and Attenuates Virulence of Pseudomonas Aeruginosa. Journal of Molecular Biology, 2019, 431, 4882-4896.	2.0	9
4409	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. Science, 2019, 366, .	6.0	172
4410	Biochemical and Structural Insights into Carbonic Anhydrase XII/Fab6A10 Complex. Journal of Molecular Biology, 2019, 431, 4910-4921.	2.0	23
4411	Structural mechanism for regulation of DNA binding of BpsR, a BordetellaÂregulator of biofilm formation, by 6-hydroxynicotinic acid. PLoS ONE, 2019, 14, e0223387.	1.1	5
4412	Structural and Functional Basis for LILRB Immune Checkpoint Receptor Recognition of HLA-G Isoforms. Journal of Immunology, 2019, 203, 3386-3394.	0.4	33
4413	â€˜Drcâ€™, a structurally novel ssDNA-binding transcription regulator of N4-related bacterial viruses. Nucleic Acids Research, 2020, 48, 445-459.	6.5	23
4414	An engineered antibody fragment targeting mutant Î²-catenin via major histocompatibility complex I neoantigen presentation. Journal of Biological Chemistry, 2019, 294, 19322-19334.	1.6	15
4415	Deciphering the Structural Basis of High Thermostability of Dehalogenase from Psychrophilic Bacterium Marinobacter sp. ELB17. Microorganisms, 2019, 7, 498.	1.6	18
4416	Molecular analysis of an enigmatic Streptococcus pneumoniae virulence factor: The raffinose-family oligosaccharide utilization system. Journal of Biological Chemistry, 2019, 294, 17197-17208.	1.6	6
4417	Crystallographic approaches to study the interaction modes of PD-1- and CTLA-4-blocking antibodies. Methods in Enzymology, 2019, 629, 383-399.	0.4	1
4418	Structural insights into a HECT-type E3 ligase AREL1 and its ubiquitination activities in vitro. Journal of Biological Chemistry, 2019, 294, 19934-19949.	1.6	14

#	ARTICLE	IF	CITATIONS
4419	Structure and Dynamics of a Site-Specific Labeled Fc Fragment with Altered Effector Functions. Pharmaceutics, 2019, 11, 546.	2.0	8
4420	Computational Analysis of Nonâ€covalent Interactions in Phycocyanin Subunit Interfaces. Molecular Informatics, 2019, 38, e1800145.	1.4	6
4421	Temperature-Dependent Interactions Explain Normal and Inverted Solubility in a Î³D-Crystallin Mutant. Biophysical Journal, 2019, 117, 930-937.	0.2	8
4422	Development of â€œPlug and Playâ€• Fiducial Marks for Structural Studies of GPCR Signaling Complexes by Single-Particle Cryo-EM. Structure, 2019, 27, 1862-1874.e7.	1.6	19
4423	Crystal structure of the catalytic unit of GH 87-type Î±-1,3-glucanase Agl-KA from Bacillus circulans. Scientific Reports, 2019, 9, 15295.	1.6	10
4424	Structural and functional aspects of mannuronic acidâ€"specific PL6 alginate lyase from the human gut microbe Bacteroides cellulosilyticus. Journal of Biological Chemistry, 2019, 294, 17915-17930.	1.6	40
4425	Hinge Region in DNA Packaging Terminase pUL15 of Herpes Simplex Virus: A Potential Allosteric Target for Antiviral Drugs. Biomolecules, 2019, 9, 603.	1.8	5
4426	Crystal Structure-Based Exploration of Arginine-Containing Peptide Binding in the ADP-Ribosyltransferase Domain of the Type III Effector XopAI Protein. International Journal of Molecular Sciences, 2019, 20, 5085.	1.8	4
4427	Crystal structure of the Siderophore-interacting protein SIP from Aeromonas hydrophila. Biochemical and Biophysical Research Communications, 2019, 519, 23-28.	1.0	2
4428	Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. Journal of Molecular Biology, 2019, 431, 3647-3661.	2.0	26
4429	How metal cofactors drive dimerâ€"dodecamer transition of the M42 aminopeptidase TmPep1050 of Thermotoga maritima. Journal of Biological Chemistry, 2019, 294, 17777-17789.	1.6	8
4430	Structural basis for the substrate recognition of aminoglycoside 7â€²â€²-phosphotransferase-la from <i>Streptomyces hygroscopicus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 599-607.	0.4	3
4431	Structural characterization of a prolyl aminodipeptidase (PepX) from <i>Lactobacillus helveticus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 625-633.	0.4	3
4432	Structure of a hyperthermostable dimeric archaeal Rubisco from<i>Hyperthermus butylicus</i>. Acta Crystallographica Section D: Structural Biology, 2019, 75, 536-544.	1.1	2
4433	ATP-specificity of succinyl-CoA synthetase from<i>Blastocystis hominis</i>. Acta Crystallographica Section D: Structural Biology, 2019, 75, 647-659.	1.1	3
4434	Structural and biochemical characterization of iminodiacetate oxidase from Chelativorans sp. BNC1. Molecular Microbiology, 2019, 112, 1863-1874.	1.2	1
4435	Structures of neurexophilinâ€"neurexin complexes reveal a regulatory mechanism of alternative splicing. EMBO Journal, 2019, 38, e101603.	3.5	19
4436	A revised order of subunits in mammalian septin complexes. Cytoskeleton, 2019, 76, 457-466.	1.0	69

#	Article	IF	Citations
4437	Mechanistic Insights into the cis- and trans-Acting DNase Activities of Cas12a. Molecular Cell, 2019, 73, 589-600.e4.	4.5	298
4438	<i>N</i>-(7-(1<i>H</i>-Imidazol-1-yl)-2,3-dioxo-6-(trifluoromethyl)-3,4-dihydroquinoxalin-1(2<i>H</i>)-yl)benzamide, a New Kainate Receptor Selective Antagonist and Analgesic: Synthesis, X-ray Crystallography, Structureâ€"Affinity Relationships, and in Vitro and in Vivo Pharmacology. ACS Chemical Neuroscience, 2019, 10, 4685-4695.	1.7	8
4439	Structural and functional insight into the Mycobacterium tuberculosis protein PrpR reveals a novel type of transcription factor. Nucleic Acids Research, 2019, 47, 9934-9949.	6.5	18
4440	Structure and mechanism of mitochondrial proton-translocating transhydrogenase. Nature, 2019, 573, 291-295.	13.7	55
4441	A new crystal structure and small-angle X-ray scattering analysis of the homodimer of human SFPQ. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 439-449.	0.4	10
4442	Structural and Functional Characterization of Dynamic Oligomerization in Burkholderia cenocepacia HMG-CoA Reductase. Biochemistry, 2019, 58, 3960-3970.	1.2	7
4443	Claudin-9 structures reveal mechanism for toxin-induced gut barrier breakdown. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17817-17824.	3.3	43
4444	Specific inter-domain interactions stabilize a compact HIV-1 Gag conformation. PLoS ONE, 2019, 14, e0221256.	1.1	2
4445	Role of flagellar hydrogen bonding in Salmonella motility and flagellar polymorphic transition. Molecular Microbiology, 2019, 112, 1519-1530.	1.2	6
4446	Crystal structure of BinAB toxin receptor (Cqm1) protein and molecular dynamics simulations reveal the role of unique Ca(II) ion. International Journal of Biological Macromolecules, 2019, 140, 1315-1325.	3.6	7
4447	Dynamic tuning of FRET in a green fluorescent protein biosensor. Science Advances, 2019, 5, eaaw4988.	4.7	28
4448	NAD ⁺ cleavage activity by animal and plant TIR domains in cell death pathways. Science, 2019, 365, 793-799.	6.0	357
4449	A head-to-toe dimerization has physiological relevance for ligand-induced inactivation of protein tyrosine receptor type Z. Journal of Biological Chemistry, 2019, 294, 14953-14965.	1.6	12
4450	Structure and Functional Binding Epitope of V-domain Ig Suppressor of T Cell Activation. Cell Reports, 2019, 28, 2509-2516.e5.	2.9	61
4451	Crystal structure of L-aspartate aminotransferase from Schizosaccharomyces pombe. PLoS ONE, 2019, 14, e0221975.	1.1	6
4452	Evolutionary plasticity in the allosteric regulator-binding site of pyruvate kinase isoform PykA from Pseudomonas aeruginosa. Journal of Biological Chemistry, 2019, 294, 15505-15516.	1.6	14
4453	Accurate Classification of Biological and non-Biological Interfaces in Protein Crystal Structures using Subtle Covariation Signals. Scientific Reports, 2019, 9, 12603.	1.6	6
4454	Structural and biochemical studies of an NB-ARC domain from a plant NLR immune receptor. PLoS ONE, 2019, 14, e0221226.	1.1	43

#	Article	IF	Citations
4455	Structural analysis of the recognition of the -35 promoter element by SigW from Bacillus subtilis. PLoS ONE, 2019, 14, e0221666.	1.1	5
4456	A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16.	13.5	108
4457	Comparative studies of <i>Aspergillus fumigatus</i> 2-methylcitrate synthase and human citrate synthase. Biological Chemistry, 2019, 400, 1567-1581.	1.2	3
4458	Structural and functional analyses of the lipase CinB from Enterobacter asburiae. Biochemical and Biophysical Research Communications, 2019, 519, 274-279.	1.0	4
4459	High-resolution crystal structure of arthropod Eiger TNF suggests a mode of receptor engagement and altered surface charge within endosomes. Communications Biology, 2019, 2, 293.	2.0	4
4460	Biochemical and structural analysis of the Klebsiella pneumoniae cytidine deaminase CDA. Biochemical and Biophysical Research Communications, 2019, 519, 280-286.	1.0	5
4461	The E. coli HicB Antitoxin Contains a Structurally Stable Helix-Turn-Helix DNA Binding Domain. Structure, 2019, 27, 1675-1685.e3.	1.6	23
4462	Structural basis for transcription activation by Crl through tethering of Ïƒ ^S and RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18923-18927.	3.3	21
4463	Structural insight into human N6amt1â€“Trm112 complex functioning as a protein methyltransferase. Cell Discovery, 2019, 5, 51.	3.1	26
4464	Structural modeling and role of HAX-1 as a positive allosteric modulator of human serine protease HtrA2. Biochemical Journal, 2019, 476, 2965-2980.	1.7	7
4465	Conservation of Atypical Allostery in <i>C. elegans</i> UDP-Glucose Dehydrogenase. ACS Omega, 2019, 4, 16318-16329.	1.6	5
4466	Structural basis of light-induced redox regulation in the Calvinâ€“Benson cycle in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20984-20990.	3.3	71
4467	Identification of Aethina tumida Kir Channels as Putative Targets of the Bee Venom Peptide Tertiapin Using Structure-Based Virtual Screening Methods. Toxins, 2019, 11, 546.	1.5	2
4468	Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. Cell Reports, 2019, 28, 3395-3405.e6.	2.9	63
4469	Potent antibody lineage against malaria transmission elicited by human vaccination with Pfs25. Nature Communications, 2019, 10, 4328.	5.8	37
4470	Arabidopsis immunity regulator EDS1 in a PAD4/SAG101-unbound form is a monomer with an inherently inactive conformation. Journal of Structural Biology, 2019, 208, 107390.	1.3	19
4471	Structure of tRNA methyltransferase complex of Trm7 and Trm734 reveals a novel binding interface for tRNA recognition. Nucleic Acids Research, 2019, 47, 10942-10955.	6.5	18
4472	New Functional Ingredients Based on Microencapsulation of Aqueous Anthocyanin-Rich Extracts Derived from Black Rice (Oryza sativa L.). Molecules, 2019, 24, 3389.	1.7	21

#	ARTICLE	IF	CITATIONS
4473	The interdimeric interface controls function and stability of Ureaplasma urealiticum methionine S-adenosyltransferase. Journal of Molecular Biology, 2019, 431, 4796-4816.	2.0	12
4474	Testosterone meets albumin â€" the molecular mechanism of sex hormone transport by serum albumins. Chemical Science, 2019, 10, 1607-1618.	3.7	38
4475	Crystal structure and biochemical characterization of malate dehydrogenase from Metallosphaera sedula. Biochemical and Biophysical Research Communications, 2019, 509, 833-838.	1.0	7
4476	Structural and Functional Studies of the RBPJ-SHARP Complex Reveal a Conserved Corepressor Binding Site. Cell Reports, 2019, 26, 845-854.e6.	2.9	38
4477	Biochemical Characterization of the Î±-<scp>l</scp>-Rhamnosidase <i>Dt</i>Rha from <i>Dictyoglomus thermophilum</i>: Application to the Selective Derhamnosylation of Natural Flavonoids. ACS Omega, 2019, 4, 1916-1922.	1.6	27
4478	PvdF of pyoverdin biosynthesis is a structurally unique N10-formyltetrahydrofolate-dependent formyltransferase. Archives of Biochemistry and Biophysics, 2019, 664, 40-50.	1.4	6
4479	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. Cell, 2019, 176, 1026-1039.e15.	13.5	558
4480	A 2.08â€‰Ã… resolution structure of HLB5, a novel cellulase from the anaerobic gut bacterium <i>Parabacteroides johnsonii DSM 18315</i>. Protein Science, 2019, 28, 794-799.	3.1	1
4481	Crystal structure of E. coli PRPP synthetase. BMC Structural Biology, 2019, 19, 1.	2.3	20
4482	Near-atomic structure of a giant virus. Nature Communications, 2019, 10, 388.	5.8	61
4483	Immunoinformatic and systems biology approaches to predict and validate peptide vaccines against Epsteinâ€"Barr virus (EBV). Scientific Reports, 2019, 9, 720.	1.6	37
4484	Structure and flexibility of the extracellular region of the PirB receptor. Journal of Biological Chemistry, 2019, 294, 4634-4643.	1.6	5
4485	Novel interactions of Selenium Binding Protein family with the PICOT containing proteins AtGRXS14 and AtGRXS16 in Arabidopsis thaliana. Plant Science, 2019, 281, 102-112.	1.7	8
4486	Illuminating the catalytic core of ectoine synthase through structural and biochemical analysis. Scientific Reports, 2019, 9, 364.	1.6	30
4487	Potent, multi-target serine protease inhibition achieved by a simplified Î²-sheet motif. PLoS ONE, 2019, 14, e0210842.	1.1	7
4488	Surface-Induced Dissociation of Noncovalent Protein Complexes in an Extended Mass Range Orbitrap Mass Spectrometer. Analytical Chemistry, 2019, 91, 3611-3618.	3.2	61
4489	Structural Analysis of the Hanks-Type Protein Kinase YabT From Bacillus subtilis Provides New Insights in its DNA-Dependent Activation. Frontiers in Microbiology, 2018, 9, 3014.	1.5	3
4490	Structure of a serine-type glutathione S-transferase of Ceriporiopsis subvermispora and identification of the enzymatically important non-canonical residues by functional mutagenesis. Biochemical and Biophysical Research Communications, 2019, 510, 177-183.	1.0	7

#	Article	IF	Citations
4491	Structure of the SLy1 SAM homodimer reveals a new interface for SAM domain self-association. Scientific Reports, 2019, 9, 54.	1.6	13
4492	Broad and Potent Neutralizing Antibodies Recognize the Silent Face of the HIV Envelope. Immunity, 2019, 50, 1513-1529.e9.	6.6	85
4493	Crystal structures of the c-di-AMPâ€“synthesizing enzyme CdaA. Journal of Biological Chemistry, 2019, 294, 10463-10470.	1.6	13
4494	Structural basis for neutralization of Plasmodium vivax by naturally acquired human antibodies that target DBP. Nature Microbiology, 2019, 4, 1486-1496.	5.9	52
4495	Decrypting protein surfaces by combining evolution, geometry, and molecular docking. Proteins: Structure, Function and Bioinformatics, 2019, 87, 952-965.	1.5	16
4496	The heme-sensitive regulator SbnI has a bifunctional role in staphyloferrin B production by Staphylococcus aureus. Journal of Biological Chemistry, 2019, 294, 11622-11636.	1.6	11
4497	A temporal thymic selection switch and ligand binding kinetics constrain neonatal Foxp3+ Treg cell development. Nature Immunology, 2019, 20, 1046-1058.	7.0	31
4498	Characterization of the pleiotropic LysR-type transcription regulator LeuO of Escherichia coli. Nucleic Acids Research, 2019, 47, 7363-7379.	6.5	13
4499	Crystal structure of the 65-kilodalton amino-terminal fragment of DNA topoisomerase I from the gram-positive model organism Streptococcus mutans. Biochemical and Biophysical Research Communications, 2019, 516, 333-338.	1.0	5
4500	Pyrimidine biosynthesis in pathogens â€“ Structures and analysis of dihydroorotases from Yersinia pestis and Vibrio cholerae. International Journal of Biological Macromolecules, 2019, 136, 1176-1187.	3.6	17
4501	Structural Basis of Protein Kinase R Autophosphorylation. Biochemistry, 2019, 58, 2967-2977.	1.2	22
4502	Sera Antibody Repertoire Analyses Reveal Mechanisms of Broad and Pandemic Strain Neutralizing Responses after Human Norovirus Vaccination. Immunity, 2019, 50, 1530-1541.e8.	6.6	71
4503	Cryo-EM structure of OSCA1.2 from <i>Oryza sativa</i> elucidates the mechanical basis of potential membrane hyperosmolality gating. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14309-14318.	3.3	71
4504	Structural basis for the homotypic fusion of chlamydial inclusions by the SNARE-like protein IncA. Nature Communications, 2019, 10, 2747.	5.8	16
4505	Studies of the oligomerisation mechanism of a cystatin-based engineered protein scaffold. Scientific Reports, 2019, 9, 9067.	1.6	2
4506	Structural basis of Type IV CRISPR RNA biogenesis by a Cas6 endoribonuclease. RNA Biology, 2019, 16, 1438-1447.	1.5	19
4507	Affinity Isolation and Mass Spectrometry Identification of Prostacyclin Synthase (PTGIS) Subinteractome. Biology, 2019, 8, 49.	1.3	10
4508	Analysis of the TP53 Deleterious Single Nucleotide Polymorphisms Impact on Estrogen Receptor Alpha-p53 Interaction: A Machine Learning Approach. International Journal of Molecular Sciences, 2019, 20, 2962.	1.8	8

#	ARTICLE	IF	CITATIONS
4509	Structural Characterization of Arabidopsis thaliana NAP1-Related Protein 2 (AtNRP2) and Comparison with its Homolog AtNRP1. Molecules, 2019, 24, 2258.	1.7	6
4510	Allosteric modulation of a human protein kinase with monobodies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13937-13942.	3.3	36
4511	Insights into real-time chemical processes in a calcium sensor protein-directed dynamic library. Nature Communications, 2019, 10, 2798.	5.8	16
4512	Residue Mutations in Murine Herpesvirus 68 Immunomodulatory Protein M3 Reveal Specific Modulation of Chemokine Binding. Frontiers in Cellular and Infection Microbiology, 2019, 9, 210.	1.8	3
4513	Crystal structure of pentameric shell protein CsoS4B of Halothiobacillus neapolitanus Î±-carboxysome. Biochemical and Biophysical Research Communications, 2019, 515, 510-515.	1.0	4
4514	A new crystal form of human acetylcholinesterase for exploratory room-temperature crystallography studies. Chemico-Biological Interactions, 2019, 309, 108698.	1.7	82
4515	Structural and biochemical analysis of a phosin from Streptomyces chartreusis reveals a combined polyphosphateâ€•and metalâ€•binding fold. FEBS Letters, 2019, 593, 2019-2029.	1.3	9
4516	The major secreted protein of the whipworm parasite tethers to matrix and inhibits interleukin-13 function. Nature Communications, 2019, 10, 2344.	5.8	48
4517	Spermidine Synthase (SPDS) Undergoes Concerted Structural Rearrangements Upon Ligand Binding â€“ A Case Study of the Two SPDS Isoforms From Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 555.	1.7	8
4518	Prediction of quaternary structure by analysis of hot spot residues in proteinâ€•protein interfaces: the case of anthranilate phosphoribosyltransferases. Proteins: Structure, Function and Bioinformatics, 2019, 87, 815-825.	1.5	18
4519	Genome-wide survey and crystallographic analysis suggests a role for both horizontal gene transfer and duplication in pantothenate biosynthesis pathways. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1547-1559.	1.1	8
4520	PRODIGY-crystal: a web-tool for classification of biological interfaces in protein complexes. Bioinformatics, 2019, 35, 4821-4823.	1.8	26
4521	Structural and biochemical characterization of Rv0187, an O-methyltransferase from Mycobacterium tuberculosis. Scientific Reports, 2019, 9, 8059.	1.6	17
4522	Structural basis for human coronavirus attachment to sialic acid receptors. Nature Structural and Molecular Biology, 2019, 26, 481-489.	3.6	475
4523	Structure of the super-elongation complex subunit AFF4 C-terminal homology domain reveals requirements for AFF homo- and heterodimerization. Journal of Biological Chemistry, 2019, 294, 10663-10673.	1.6	24
4524	Structural insights into the modulatory role of the accessory protein WYL1 in the Type VI-D CRISPR-Cas system. Nucleic Acids Research, 2019, 47, 5420-5428.	6.5	26
4525	Molecular Insights into the Substrate-Assisted Mechanism of Viral DNA 3â€²-End Processing in Intasome of Prototype Foamy Virus Integrase from Molecular Dynamic and QM/MM Studies. Journal of Chemical Information and Modeling, 2019, 59, 2995-3005.	2.5	3
4526	Crystal structure of a Y-box binding protein 1 (YB-1)â€“RNA complex reveals key features and residues interacting with RNA. Journal of Biological Chemistry, 2019, 294, 10998-11010.	1.6	47

#	ARTICLE	IF	CITATIONS
4527	A novel druggable interprotomer pocket in the capsid of rhino- and enteroviruses. PLoS Biology, 2019, 17, e3000281.	2.6	36
4528	New insights into the tetrameric family of the Fur metalloregulators. BioMetals, 2019, 32, 501-519.	1.8	14
4529	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. Cell Host and Microbe, 2019, 25, 873-883.e5.	5.1	42
4530	Structural mechanism for NEK7-licensed activation of NLRP3 inflammasome. Nature, 2019, 570, 338-343.	13.7	467
4531	Features and structure of a cold active N-acetylneuraminate lyase. PLoS ONE, 2019, 14, e0217713.	1.1	5
4532	Kistamicin biosynthesis reveals the biosynthetic requirements for production of highly crosslinked glycopeptide antibiotics. Nature Communications, 2019, 10, 2613.	5.8	48
4533	Structure and Properties of a Natural Competence-Associated Pilin Suggest a Unique Pilus Tip-Associated DNA Receptor. MBio, 2019, 10, .	1.8	23
4534	Structures of maintenance of carboxysome distribution Walker-box McdA and McdB adaptor homologs. Nucleic Acids Research, 2019, 47, 5950-5962.	6.5	13
4535	Structural insights into histone chaperone Chz1-mediated H2A.Z recognition and histone replacement. PLoS Biology, 2019, 17, e3000277.	2.6	18
4536	Structural and functional studies on <i>SalmonellaÂtyphimurium</i> pyridoxal kinase: the first structural evidence for the formation of Schiff base with the substrate. FEBS Journal, 2019, 286, 3684-3700.	2.2	8
4537	Disrupted apolipoprotein L1-miR193a axis dedifferentiates podocytes through autophagy blockade in an APOL1 risk milieu. American Journal of Physiology - Cell Physiology, 2019, 317, C209-C225.	2.1	21
4538	Crystal structure of CntK, the cofactor-independent histidine racemase in staphylopine-mediated metal acquisition of Staphylococcus aureus. International Journal of Biological Macromolecules, 2019, 135, 725-733.	3.6	11
4539	Structural and functional analyses of the N-terminal domain of the A subunit of a <i>Bacillus megaterium</i> spore germinant receptor. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11470-11479.	3.3	14
4540	Tumor suppression of novel antiâ€“PD-1 antibodies mediated through CD28 costimulatory pathway. Journal of Experimental Medicine, 2019, 216, 1525-1541.	4.2	23
4541	Asymmetry in catalysis by <i>Thermotoga maritima</i> membrane-bound pyrophosphatase demonstrated by a nonphosphorus allosteric inhibitor. Science Advances, 2019, 5, eaav7574.	4.7	16
4542	Structural basis for catalysis and substrate specificity of a 3C-like cysteine protease from a mosquito mesonivirus. Virology, 2019, 533, 21-33.	1.1	10
4543	An ultra-stable gold-coordinated protein cage displaying reversible assembly. Nature, 2019, 569, 438-442.	13.7	124
4544	Structural basis of substrate recognition by a novel thermostable (S)-enantioselective Ï‰-transaminase from Thermomicrobium roseum. Scientific Reports, 2019, 9, 6958.	1.6	7

#	ARTICLE	IF	CITATIONS
4545	Identification of conformation-selective nanobodies against the membrane protein insertase BamA by an integrated structural biology approach. Journal of Biomolecular NMR, 2019, 73, 375-384.	1.6	20
4546	Crystal structure of a xylulose 5-phosphate phosphoketolase. Insights into the substrate specificity for xylulose 5-phosphate. Journal of Structural Biology, 2019, 207, 85-102.	1.3	8
4547	Structural analysis of a Vibrio phospholipase reveals an unusual Serâ€“Hisâ€“chloride catalytic triad. Journal of Biological Chemistry, 2019, 294, 11391-11401.	1.6	25
4548	Conformational changes in glutaminyl-tRNA synthetases upon binding of the substratesÂand analogs using molecular docking and molecular dynamics approaches. Journal of Biomolecular Structure and Dynamics, 2020, 38, 1-15.	2.0	6
4549	Crystal structure of the multifunctional SAM-dependent enzyme LepI provides insights into its catalytic mechanism. Biochemical and Biophysical Research Communications, 2019, 515, 255-260.	1.0	5
4550	Geometric description of self-interaction potential in symmetric protein complexes. Scientific Data, 2019, 6, 64.	2.4	6
4551	Structural and functional insights into phosphomannose isomerase: the role of zinc and catalytic residues. Acta Crystallographica Section D: Structural Biology, 2019, 75, 475-487.	1.1	16
4552	Structural insights into a maleylpyruvate hydrolase from sphingobium sp. SYK-6, a bacterium degrading lignin-derived aryls. Biochemical and Biophysical Research Communications, 2019, 514, 765-771.	1.0	3
4553	Zika virus nonstructural protein 5 residue R681 is critical for dimer formation and enzymatic activity. FEBS Letters, 2019, 593, 1272-1291.	1.3	6
4554	TCRâ€induced alteration of primary MHC peptide anchor residue. European Journal of Immunology, 2019, 49, 1052-1066.	1.6	23
4555	Structural basis for the acetylation of histone H3K9 and H3K27 mediated by the histone chaperone Vps75 in Pneumocystis carinii. Signal Transduction and Targeted Therapy, 2019, 4, 14.	7.1	4
4556	DNA-guided DNA cleavage at moderate temperatures by Clostridium butyricum Argonaute. Nucleic Acids Research, 2019, 47, 5809-5821.	6.5	115
4557	Face-time with TAR: Portraits of an HIV-1 RNA with diverse modes of effector recognition relevant for drug discovery. Journal of Biological Chemistry, 2019, 294, 9326-9341.	1.6	34
4558	Adaptive Evolution within Gut Microbiomes of Healthy People. Cell Host and Microbe, 2019, 25, 656-667.e8.	5.1	289
4559	Structural Basis for YjbH Adaptor-Mediated Recognition of Transcription Factor Spx. Structure, 2019, 27, 923-936.e6.	1.6	16
4560	Characterization of the phosphotransacetylase-acetate kinase pathway for ATP production in<i>Porphyromonas gingivalis</i>. Journal of Oral Microbiology, 2019, 11, 1588086.	1.2	7
4561	Evidence of Destabilization of the Human Thymidylate Synthase (hTS) Dimeric Structure Induced by the Interface Mutation Q62R. Biomolecules, 2019, 9, 134.	1.8	3
4562	Crystal Structure and Directed Evolution of Specificity of NlaIV Restriction Endonuclease. Journal of Molecular Biology, 2019, 431, 2082-2094.	2.0	2

#	ARTICLE	IF	CITATIONS
4563	Revisiting SEPT7 and the slippage of Î²-strands in the septin family. Journal of Structural Biology, 2019, 207, 67-73.	1.3	14
4564	(p)ppGpp Regulates a Bacterial Nucleosidase by an Allosteric Two-Domain Switch. Molecular Cell, 2019, 74, 1239-1249.e4.	4.5	39
4565	High-symmetry protein assemblies: patterns and emerging applications. Current Opinion in Structural Biology, 2019, 55, 77-84.	2.6	41
4566	Impact of charge state on 193 nm ultraviolet photodissociation of protein complexes. Physical Chemistry Chemical Physics, 2019, 21, 9265-9276.	1.3	24
4567	Noncovalent structure of SENP1 in complex with SUMO2. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 332-339.	0.4	7
4568	Structural insights into the mechanism of single domain <scp>VHH</scp> antibody binding to cortisol. FEBS Letters, 2019, 593, 1248-1256.	1.3	20
4569	Structural basis for functional interactions in dimers of SLC26 transporters. Nature Communications, 2019, 10, 2032.	5.8	49
4570	Structural Insights into Bacteriophage GIL01 gp7 Inhibition of Host LexA Repressor. Structure, 2019, 27, 1094-1102.e4.	1.6	17
4571	Structure of a Therapeutic Full-Length Anti-NPRA IgG4 Antibody: Dissecting Conformational Diversity. Biophysical Journal, 2019, 116, 1637-1649.	0.2	17
4572	Fab Fragment of VHH-Based Antibody Netakimab: Crystal Structure and Modeling Interaction with Cytokine IL-17A. Crystals, 2019, 9, 177.	1.0	6
4573	Modeling of Proteinâ€"Protein Interactions in Cytokinin Signal Transduction. International Journal of Molecular Sciences, 2019, 20, 2096.	1.8	22
4574	The structure of (E)-biformene synthase provides insights into the biosynthesis of bacterial bicyclic labdane-related diterpenoids. Journal of Structural Biology, 2019, 207, 29-39.	1.3	7
4575	Structure of Sesquisabinene Synthase 1, a Terpenoid Cyclase That Generates a Strained [3.1.0] Bridged-Bicyclic Product. ACS Chemical Biology, 2019, 14, 1011-1019.	1.6	5
4576	Structural analyses of NudT16â€"ADP-ribose complexes direct rational design of mutants with improved processing of poly(ADP-ribosyl)ated proteins. Scientific Reports, 2019, 9, 5940.	1.6	15
4577	Structural Study of Agmatine Iminohydrolase From Medicago truncatula, the Second Enzyme of the Agmatine Route of Putrescine Biosynthesis in Plants. Frontiers in Plant Science, 2019, 10, 320.	1.7	8
4578	Structural Basis for <i>E. coli</i> Penicillin Binding Protein (PBP) 2 Inhibition, a Platform for Drug Design. Journal of Medicinal Chemistry, 2019, 62, 4742-4754.	2.9	31
4579	A systematic simulation-based meta-analytical framework for prediction of physiological biomarkers in alopecia. Journal of Biological Research, 2019, 26, 2.	2.2	31
4580	The Tumor Suppressor ING5 Is a Dimeric, Bivalent Recognition Molecule of the Histone H3K4me3 Mark. Journal of Molecular Biology, 2019, 431, 2298-2319.	2.0	18

#	Article	IF	Citations
4581	Multiple conformational states of the HPK1 kinase domain in complex with sunitinib reveal the structural changes accompanying HPK1 trans-regulation. Journal of Biological Chemistry, 2019, 294, 9029-9036.	1.6	19
4582	Engineering nanomolar peptide ligands that differentially modulate EphA2 receptor signaling. Journal of Biological Chemistry, 2019, 294, 8791-8805.	1.6	31
4583	Structure of the periplasmic domain of SflA involved in spatial regulation of the flagellar biogenesis of Vibrio reveals a TPR/SLR-like fold. Journal of Biochemistry, 2019, 166, 197-204.	0.9	9
4584	MM-131, a bispecific anti-Met/EpCAM mAb, inhibits HGF-dependent and HGF-independent Met signaling through concurrent binding to EpCAM. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7533-7542.	3.3	26
4585	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6800-6805.	3.3	33
4586	Bisubstrate analogues as structural tools to investigate m⁶A methyltransferase active sites. RNA Biology, 2019, 16, 798-808.	1.5	24
4587	Exploring designability of electrostatic complementarity at an antigen-antibody interface directed by mutagenesis, biophysical analysis, and molecular dynamics simulations. Scientific Reports, 2019, 9, 4482.	1.6	31
4588	Functional characterization of PLP fold type IV transaminase with a mixed type of activity from Haliangium ochraceum. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 575-585.	1.1	11
4589	Structural investigation of Rett-inducing MeCP2 mutations. Genes and Diseases, 2019, 6, 31-34.	1.5	5
4590	X-Ray Structure of Human Sulfide:Quinone Oxidoreductase: Insights into the Mechanism of Mitochondrial Hydrogen Sulfide Oxidation. Structure, 2019, 27, 794-805.e4.	1.6	31
4591	Structures of full-length plasma kallikrein bound to highly specific inhibitors describe a new mode of targeted inhibition. Journal of Structural Biology, 2019, 206, 170-182.	1.3	11
4592	The crystal structure of Rv2991 from Mycobacterium tuberculosis: An F420 binding protein with unknown function. Journal of Structural Biology, 2019, 206, 216-224.	1.3	0
4593	An ensemble of lipoxygenase structures reveals novel conformations of the Fe coordination sphere. Protein Science, 2019, 28, 920-927.	3.1	8
4594	Phage display derived therapeutic antibodies have enriched aliphatic content: Insights for developability issues. Proteins: Structure, Function and Bioinformatics, 2019, 87, 607-618.	1.5	22
4595	Structure and dynamics of Trichoderma harzianum Cel7B suggest molecular architecture adaptations required for a wide spectrum of activities on plant cell wall polysaccharides. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1015-1026.	1.1	12
4596	Structural Basis for Neutralization and Protection by a Zika Virus-Specific Human Antibody. Cell Reports, 2019, 26, 3360-3368.e5.	2.9	24
4597	Structure of the zebrafish galectin-1-L2 and model of its interaction with the infectious hematopoietic necrosis virus (IHNV) envelope glycoprotein. Glycobiology, 2019, 29, 419-430.	1.3	10
4598	Crystal structure of the yeast Rad7-Elc1 complex and assembly of the Rad7-Rad16-Elc1-Cul3 complex. DNA Repair, 2019, 77, 1-9.	1.3	4

#	ARTICLE	IF	CITATIONS
4599	FIP200 Claw Domain Binding to p62 Promotes Autophagosome Formation at Ubiquitin Condensates. Molecular Cell, 2019, 74, 330-346.e11.	4.5	223
4600	A small-molecule fusion inhibitor of influenza virus is orally active in mice. Science, 2019, 363, .	6.0	98
4601	Inhibitory Properties of ATP-Competitive Coumestrol and Boldine Are Correlated to Different Modulations of CK2 Flexibility. Journal of Natural Products, 2019, 82, 1014-1018.	1.5	4
4602	Eine peptidvermittelte Selbstspaltungsreaktion initiiert die Tyrosinaseaktivierung. Angewandte Chemie, 2019, 131, 7553-7557.	1.6	4
4603	A Peptideâ€Induced Selfâ€Cleavage Reaction Initiates the Activation of Tyrosinase. Angewandte Chemie - International Edition, 2019, 58, 7475-7479.	7.2	29
4604	Oligomeric protein interference validates druggability of aspartate interconversion in Plasmodium falciparum. MicrobiologyOpen, 2019, 8, e779.	1.2	4
4605	Molecular basis of cullin-3 (Cul3) ubiquitin ligase subversion by vaccinia virus protein A55. Journal of Biological Chemistry, 2019, 294, 6416-6429.	1.6	14
4606	Structural characterization of the Imm52 family protein TsiT in Pseudomonas aeruginosa. Protein Science, 2019, 28, 971-975.	3.1	2
4607	Crystal structure and epitope analysis of house dust mite allergen Der f 21. Scientific Reports, 2019, 9, 4933.	1.6	13
4608	Structural studies on dihydrouridine synthase A (DusA) from Pseudomonas aeruginosa. International Journal of Biological Macromolecules, 2019, 132, 254-264.	3.6	3
4609	In silico analyses of molecular interactions between groundnut bud necrosis virus and its vector, Thrips palmi. VirusDisease, 2019, 30, 245-251.	1.0	14
4610	Cryo-EM fibril structures from systemic AA amyloidosis reveal the species complementarity of pathological amyloids. Nature Communications, 2019, 10, 1104.	5.8	113
4611	Crystal structure and biochemical properties of msed_0281, the citrate synthase from Metallosphaera sedula. Biochemical and Biophysical Research Communications, 2019, 509, 722-727.	1.0	3
4612	Secondary hemostasis studies of crude venom and isolated proteins from the snake Crotalus durissus terrificus. International Journal of Biological Macromolecules, 2019, 131, 127-133.	3.6	17
4613	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea Geoglobus acetivorans and Archaeoglobus fulgidus: Biochemical and Structural Characterization. Frontiers in Bioengineering and Biotechnology, 2019, 7, 7.	2.0	26
4614	Structures of Class Id Ribonucleotide Reductase Catalytic Subunits Reveal a Minimal Architecture for Deoxynucleotide Biosynthesis. Biochemistry, 2019, 58, 1845-1860.	1.2	10
4615	Directed Assembly of Homopentameric Cholera Toxin B-Subunit Proteins into Higher-Order Structures Using Coiled-Coil Appendages. Journal of the American Chemical Society, 2019, 141, 5211-5219.	6.6	18
4616	Conservation of the structural and functional architecture of encapsulated ferritins in bacteria and archaea. Biochemical Journal, 2019, 476, 975-989.	1.7	23

#	Article	IF	Citations
4617	Crystal structure of chloramphenicol-metabolizing enzyme EstDL136 from a metagenome. PLoS ONE, 2019, 14, e0210298.	1.1	9
4618	CryoEM structure of adenovirus type 3 fibre with desmoglein 2 shows an unusual mode of receptor engagement. Nature Communications, 2019, 10, 1181.	5.8	24
4619	Disruption of APOL1-miR193a Axis Induces Disorganization of Podocyte Actin Cytoskeleton. Scientific Reports, 2019, 9, 3582.	1.6	22
4620	In Silico Screening to Identify Inhibitors of Growth Factor Receptor 2â€"Focal Adhesion Kinase Interaction for Therapeutic Treatment of Pathological Cardiac Hypertrophy. Assay and Drug Development Technologies, 2019, 17, 58-67.	0.6	3
4621	Metastable asymmetrical structure of a shaftless V ₁ motor. Science Advances, 2019, 5, eaau8149.	4.7	13
4622	Structural insights into the inhibition properties of archaeon citrate synthase from Metallosphaera sedula. PLoS ONE, 2019, 14, e0212807.	1.1	3
4623	The carbon monoxide dehydrogenase accessory protein CooJ is a histidine-rich multidomain dimer containing an unexpected Ni(II)-binding site. Journal of Biological Chemistry, 2019, 294, 7601-7614.	1.6	16
4624	<i>In situ</i> and highâ€resolution cryoâ€•<scp>EM</scp> structure of a bacterial type <scp>VI</scp> secretion system membrane complex. EMBO Journal, 2019, 38, .	3.5	72
4625	Drug Repositioning Inferred from E2F1-Coregulator Interactions Studies for the Prevention and Treatment of Metastatic Cancers. Theranostics, 2019, 9, 1490-1509.	4.6	15
4626	Single-molecule measurement and bioinformatics analysis suggest a preferred orientation of human coagulation factor VIII on hydrophobic interfaces. Biophysical Chemistry, 2019, 248, 9-15.	1.5	3
4627	Crystal structure of the TreS:Pep2 complex, initiating Î±-glucan synthesis in the GlgE pathway of mycobacteria. Journal of Biological Chemistry, 2019, 294, 7348-7359.	1.6	8
4628	Ca2+-dependent regulation of sodium channels NaV1.4 and NaV1.5 is controlled by the post-IQ motif. Nature Communications, 2019, 10, 1514.	5.8	30
4629	The putative polysaccharide deacetylase Ba0331: cloning, expression, crystallization and structure determination. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 312-320.	0.4	1
4630	Structure of a critical metabolic enzyme:<i>S</i>-adenosylmethionine synthetase from<i>Cryptosporidium parvum</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 290-298.	0.4	0
4631	The structure of lipopolysaccharide transport protein B (LptB) from <i>Burkholderia pseudomallei</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 227-232.	0.4	1
4632	Crystal structure and activation mechanism of DR3 death domain. FEBS Journal, 2019, 286, 2593-2610.	2.2	6
4633	Structural differences between the ectodomains of murine and human CD98hc. Proteins: Structure, Function and Bioinformatics, 2019, 87, 693-698.	1.5	8
4634	Rad54 Phosphorylation Promotes Homologous Recombination by Balancing Rad54 Mobility and DNA Binding. Biophysical Journal, 2019, 116, 1406-1419.	0.2	5

#	Article	IF	Citations
4635	Catalytic triad heterogeneity in S51 peptidase family: Structural basis for functional variability. Proteins: Structure, Function and Bioinformatics, 2019, 87, 679-692.	1.5	5
4636	Principles and characteristics of biological assemblies in experimentally determined protein structures. Current Opinion in Structural Biology, 2019, 55, 34-49.	2.6	16
4637	Increased versatility despite reduced molecular complexity: evolution, structure and function of metazoan splicing factor PRPF39. Nucleic Acids Research, 2019, 47, 5867-5879.	6.5	7
4638	A global map of the protein shape universe. PLoS Computational Biology, 2019, 15, e1006969.	1.5	24
4639	Structural basis for the Target <scp>DNA</scp> recognition and binding by the <scp>MYB</scp> domain of phosphate starvation response 1. FEBS Journal, 2019, 286, 2809-2821.	2.2	23
4640	A structural and functional analysis of the glycosyltransferase BshA from <scp><i>Staphylococcus aureus</i></scp>: Insights into the reaction mechanism and regulation of bacillithiol production. Protein Science, 2019, 28, 1083-1094.	3.1	15
4641	Binding of the regulatory domain of MutL to the sliding Î²-clamp is species specific. Nucleic Acids Research, 2019, 47, 4831-4842.	6.5	11
4642	Identification of key residues for activities of atypical glutathione S-transferase of Ceriporiopsis subvermispora, a selective degrader of lignin in woody biomass, by crystallography and functional mutagenesis. International Journal of Biological Macromolecules, 2019, 132, 222-229.	3.6	6
4643	Design of High-Affinity Metal-Controlled Protein Dimers. Biochemistry, 2019, 58, 2199-2207.	1.2	7
4644	Crystal Structure of VapBC-1 from Nontypeable Haemophilus influenzae and the Effect of PIN Domain Mutations on Survival during Infection. Journal of Bacteriology, 2019, 201, .	1.0	5
4645	Structural and functional characterisation of phosphoserine phosphatase, that plays critical role in the oxidative stress response in the parasite Entamoeba histolytica. Journal of Structural Biology, 2019, 206, 254-266.	1.3	7
4646	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. Cell, 2019, 177, 751-765.e15.	13.5	98
4647	Relative interfacial cleavage energetics of protein complexes revealed by surface collisions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8143-8148.	3.3	60
4648	Supramolecular arrangement of the full-length Zika virus NS5. PLoS Pathogens, 2019, 15, e1007656.	2.1	38
4649	Mutations in ILK, encoding integrin-linked kinase, are associated with arrhythmogenic cardiomyopathy. Translational Research, 2019, 208, 15-29.	2.2	33
4650	Novel Ca²⁺â€independent carbohydrate recognition of the Câ€type lectins, SPLâ€1 and SPLâ€2, from the bivalve <i>Saxidomus purpuratus</i>. Protein Science, 2019, 28, 766-778.	3.1	15
4651	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. Protein Science, 2019, 28, 848-856.	3.1	9
4652	Activation of the Endonuclease that Defines mRNA 3â€² Ends Requires Incorporation into an 8-Subunit Core Cleavage and Polyadenylation Factor Complex. Molecular Cell, 2019, 73, 1217-1231.e11.	4.5	70

#	ARTICLE	IF	CITATIONS
4653	3,17Î²-Bis-sulfamoyloxy-2-methoxyestra-1,3,5(10)-triene and Nonsteroidal Sulfamate Derivatives Inhibit Carbonic Anhydrase IX: Structureâ€“Activity Optimization for Isoform Selectivity. Journal of Medicinal Chemistry, 2019, 62, 2202-2212.	2.9	14
4654	Structure and function of the Ts2631 endolysin of Thermus scotoductus phage vB_Tsc2631 with unique N-terminal extension used for peptidoglycan binding. Scientific Reports, 2019, 9, 1261.	1.6	28
4655	The interplay of the metallosensor CueR with two distinct CopZ chaperones defines copper homeostasis in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2019, 294, 4934-4945.	1.6	27
4656	A subset of calciumâ€binding S100 proteins show preferential heterodimerization. FEBS Journal, 2019, 286, 1859-1876.	2.2	17
4657	Diversity within the adenovirus fiber knob hypervariable loops influences primary receptor interactions. Nature Communications, 2019, 10, 741.	5.8	46
4658	Reversible fold-switching controls the functional cycle of the antitermination factor RfaH. Nature Communications, 2019, 10, 702.	5.8	50
4659	Structural insights into chaperone addiction of toxin-antitoxin systems. Nature Communications, 2019, 10, 782.	5.8	15
4660	Tailoring the properties of (catalytically)-active inclusion bodies. Microbial Cell Factories, 2019, 18, 33.	1.9	34
4661	Breaking tolerance with engineered class I antigen-presenting molecules. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3136-3145.	3.3	5
4662	Spinnability of collagen as a biomimetic material: A review. International Journal of Biological Macromolecules, 2019, 129, 693-705.	3.6	72
4663	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. Journal of Molecular Biology, 2019, 431, 1160-1171.	2.0	6
4664	Structural Insights into Substrate Selectivity, Catalytic Mechanism, and Redox Regulation of Rice Photosystem II Core Phosphatase. Molecular Plant, 2019, 12, 86-98.	3.9	18
4665	Overall Structures of Mycobacterium tuberculosis DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. Structure, 2019, 27, 579-589.e5.	1.6	24
4666	Molecular Basis of Broad Spectrum <i>N</i>-Glycan Specificity and Processing of Therapeutic IgG Monoclonal Antibodies by Endoglycosidase S2. ACS Central Science, 2019, 5, 524-538.	5.3	27
4667	Molecular basis for AU-rich element recognition and dimerization by the HuR C-terminal RRM. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2935-2944.	3.3	69
4668	Structural basis of DSF recognition by its receptor RpfR and its regulatory interaction with the DSF synthase RpfF. PLoS Biology, 2019, 17, e3000123.	2.6	23
4669	Structural mechanism for versatile cargo recognition by the yeast class V myosin Myo2. Journal of Biological Chemistry, 2019, 294, 5896-5906.	1.6	13
4670	The macrocyclizing protease butelase 1 remains autocatalytic and reveals the structural basis for ligase activity. Plant Journal, 2019, 98, 988-999.	2.8	57

#	Article	IF	Citations
4671	Structural Analysis of Recent Allergen-Antibody Complexes and Future Directions. Current Allergy and Asthma Reports, 2019, 19, 17.	2.4	6
4672	Structural characterization of the Î±-N-acetylglucosaminidase, a key enzyme in the pathogenesis of Sanfilippo syndrome B. Journal of Structural Biology, 2019, 205, 65-71.	1.3	11
4673	The Plasticity of Molecular Interactions Governs Bacterial Microcompartment Shell Assembly. Structure, 2019, 27, 749-763.e4.	1.6	50
4674	Formylglycine-generating enzyme binds substrate directly at a mononuclear Cu(I) center to initiate O ₂ activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5370-5375.	3.3	38
4675	An efficient, step-economical strategy for the design of functional metalloproteins. Nature Chemistry, 2019, 11, 434-441.	6.6	57
4676	R pyocin tail fiber structure reveals a receptor-binding domain with a lectin fold. PLoS ONE, 2019, 14, e0211432.	1.1	21
4677	Manipulating intradiol dioxygenases by C-terminus truncation. Enzyme and Microbial Technology, 2019, 125, 21-28.	1.6	6
4678	Enzymatic and Structural Characterization of the <i>Naegleria fowleri</i> Glucokinase. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	21
4679	Crystal structure of the C-terminal domain of the primosomal DnaT protein: Insights into a new oligomerization mechanism. Biochemical and Biophysical Research Communications, 2019, 511, 1-6.	1.0	4
4680	Structural basis of ubiquitin recognition by the winged-helix domain of Cockayne syndrome group B protein. Nucleic Acids Research, 2019, 47, 3784-3794.	6.5	17
4681	Crystal structure of AlpK: An essential monooxygenase involved in the biosynthesis of kinamycin. Biochemical and Biophysical Research Communications, 2019, 510, 601-605.	1.0	2
4682	Crystal structure of MICU2 and comparison with MICU1 reveal insights into the uniporter gating mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3546-3555.	3.3	39
4683	Structure-Function Studies of the Bacillus subtilis Ric Proteins Identify the Fe-S Cluster-Ligating Residues and Their Roles in Development and RNA Processing. MBio, 2019, 10, .	1.8	12
4684	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25057-25067.	3.3	53
4685	Asymmetric opening of HIV-1 Env bound to CD4 and a coreceptor-mimicking antibody. Nature Structural and Molecular Biology, 2019, 26, 1167-1175.	3.6	43
4686	Molecular basis for the function of the Î±Î² heterodimer of human NAD-dependent isocitrate dehydrogenase. Journal of Biological Chemistry, 2019, 294, 16214-16227.	1.6	15
4687	Crystal structure determination of<i>Pseudomonas stutzeri</i>A1501 endoglucanase Cel5A: the search for a molecular basis for glycosynthesis in GH5_5 enzymes. Acta Crystallographica Section D: Structural Biology, 2019, 75, 605-615.	1.1	8
4688	Structures of major pilins in<i>Clostridium perfringens</i>demonstrate dynamic conformational change. Acta Crystallographica Section D: Structural Biology, 2019, 75, 718-732.	1.1	7

#	ARTICLE	IF	CITATIONS
4689	Comparison of a retroviral protease in monomeric and dimeric states. Acta Crystallographica Section D: Structural Biology, 2019, 75, 904-917.	1.1	2
4690	Structure and mechanism of piperideine-6-carboxylate dehydrogenase from<i>Streptomyces clavuligerus</i>. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1107-1118.	1.1	2
4691	The structure of CgnJ, a domain of unknown function protein from the crocagin gene cluster. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 205-211.	0.4	1
4692	Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryoâ€“electron microscopy. Science Advances, 2019, 5, eaax1803.	4.7	14
4693	A structure-based rationale for sialic acid independent host-cell entry of Sosuga virus. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21514-21520.	3.3	9
4694	Molecular basis for retinol binding by serum amyloid A during infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19077-19082.	3.3	21
4695	A Conserved Regulatory Circuit Controls Large Adhesins in Vibrio cholerae. MBio, 2019, 10, .	1.8	29
4696	Structural basis of binding of homodimers of the nuclear receptor NR4A2 to selective Nur-responsive DNA elements. Journal of Biological Chemistry, 2019, 294, 19795-19803.	1.6	23
4697	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. Scientific Reports, 2019, 9, 15481.	1.6	36
4698	Passenger sequences can promote interlaced dimers in a common variant of the maltose-binding protein. Scientific Reports, 2019, 9, 20396.	1.6	11
4699	The CCâ€² loop of IgV domains of the immune checkpoint receptors, plays a key role in receptor:ligand affinity modulation. Scientific Reports, 2019, 9, 19191.	1.6	15
4700	Crystal structures of p120RasGAP N-terminal SH2 domain in its apo form and in complex with a p190RhoGAP phosphotyrosine peptide. PLoS ONE, 2019, 14, e0226113.	1.1	13
4701	Elastic continuum stiffness of contractile tail sheaths from molecular dynamics simulations. Journal of Chemical Physics, 2019, 151, 185103.	1.2	1
4702	ATXN1 N-terminal region explains the binding differences of wild-type and expanded forms. BMC Medical Genomics, 2019, 12, 145.	0.7	6
4703	Structural comparisons of phosphoenolpyruvate carboxykinases reveal the evolutionary trajectories of these phosphodiester energy conversion enzymes. Journal of Biological Chemistry, 2019, 294, 19269-19278.	1.6	10
4704	The wild-type flagellar filament of the Firmicute Kurthia at 2.8â€‰Å… resolution in vivo. Scientific Reports, 2019, 9, 14948.	1.6	12
4705	Structure of Staphylococcal Enterotoxin N: Implications for Binding Properties to Its Cellular Proteins. International Journal of Molecular Sciences, 2019, 20, 5921.	1.8	4
4706	Characterization of Antigenic MHC-Class-I-Restricted T Cell Epitopes in the Glycoprotein of Ebolavirus. Cell Reports, 2019, 29, 2537-2545.e3.	2.9	7

#	ARTICLE	IF	CITATIONS
4707	Crystal Structure Of Photorespiratory Alanine:Glyoxylate Aminotransferase 1 (AGT1) From Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 1229.	1.7	9
4708	Structures of MERS-CoV spike glycoprotein in complex with sialoside attachment receptors. Nature Structural and Molecular Biology, 2019, 26, 1151-1157.	3.6	218
4709	Molecular characterization of a Trichinella spiralis enolase and its interaction with the hostâ€™s plasminogen. Veterinary Research, 2019, 50, 106.	1.1	14
4710	Structural Insights into the Intracellular Region of the Human Magnesium Transport Mediator CNNM4. International Journal of Molecular Sciences, 2019, 20, 6279.	1.8	13
4711	Changes in the allosteric site of human liver pyruvate kinase upon activator binding include the breakage of an intersubunit cationâ€“Ï€ bond. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 461-469.	0.4	12
4712	Structural evidence for the critical role of the prion protein hydrophobic region in forming an infectious prion. PLoS Pathogens, 2019, 15, e1008139.	2.1	22
4713	Structural analysis of mycobacterial homoserine transacetylases central to methionine biosynthesis reveals druggable active site. Scientific Reports, 2019, 9, 20267.	1.6	12
4714	Functional characterisation of two ferric-ion coordination modes of TtFbpA, the periplasmic subunit of an ABC-type iron transporter from <i>Thermus thermophilus</i> HB8. Metallomics, 2019, 11, 2078-2088.	1.0	5
4715	Structural and Biochemical Characterization of Aldehyde Dehydrogenase 12, the Last Enzyme of Proline Catabolism in Plants. Journal of Molecular Biology, 2019, 431, 576-592.	2.0	20
4716	Crystal structure of the DENR-MCT-1 complex revealed zinc-binding site essential for heterodimer formation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 528-533.	3.3	19
4717	Substrate specificities of aromatic ring-hydroxylating oxygenases of an uncultured gammaproteobacterium from chronically-polluted subantarctic sediments. International Biodeterioration and Biodegradation, 2019, 137, 127-136.	1.9	10
4718	Structural characterization of VapB46 antitoxin from Mycobacterium tuberculosis : insights into VapB46â€“ DNA binding. FEBS Journal, 2019, 286, 1174-1190.	2.2	4
4719	Structureâ€guided design combined with evolutionary diversity led to the discovery of the xyloseâ€releasing exoâ€xylanase activity in the glycoside hydrolase family 43. Biotechnology and Bioengineering, 2019, 116, 734-744.	1.7	15
4720	Structural and functional characterization of type three secretion system ATPase PscN and its regulator PscL from <i>Pseudomonas aeruginosa</i>. Proteins: Structure, Function and Bioinformatics, 2019, 87, 276-288.	1.5	10
4721	A comprehensive analysis of the protein-ligand interactions in crystal structures of Mycobacterium tuberculosis EthR. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 248-258.	1.1	11
4722	The Structure and Stability of the Disulfide-Linked Î³S-Crystallin Dimer Provide Insight into Oxidation Products Associated with Lens Cataract Formation. Journal of Molecular Biology, 2019, 431, 483-497.	2.0	35
4723	A novel cysteine carbamoyl-switch is responsible for the inhibition of formamidase, a nitrilase superfamily member. Archives of Biochemistry and Biophysics, 2019, 662, 151-159.	1.4	3
4724	GABAA receptor signalling mechanisms revealed by structural pharmacology. Nature, 2019, 565, 454-459.	13.7	386

#	Article	IF	Citations
4725	Cryo-EM structure of the human Î±1Î²3Î³2 GABAA receptor in a lipid bilayer. Nature, 2019, 565, 516-520.	13.7	264
4726	Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1- <i>O</i> -methyltransferase specific for 3- <i>O</i> -methylated mannosides. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 835-844.	3.3	7
4727	ParST is a widespread toxinâ€“antitoxin module that targets nucleotide metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 826-834.	3.3	24
4728	<i>Trypanosoma brucei</i> RRP44 is involved in an early stage of large ribosomal subunit RNA maturation. RNA Biology, 2019, 16, 133-143.	1.5	9
4729	Genetic and structural insights into broad neutralization of hepatitis C virus by human V _H 1-69 antibodies. Science Advances, 2019, 5, eaav1882.	4.7	77
4730	Structural insights into the substrate binding mechanism of novel ArgA from Mycobacterium tuberculosis. International Journal of Biological Macromolecules, 2019, 125, 970-978.	3.6	4
4731	Amine Transaminase from<i>Exophiala Xenobiotica</i>â€”Crystal Structure and Engineering of a Fold IV Transaminase that Naturally Converts Biaryl Ketones. ACS Catalysis, 2019, 9, 1140-1148.	5.5	34
4732	Structural basis for the specificity of renin-mediated angiotensinogen cleavage. Journal of Biological Chemistry, 2019, 294, 2353-2364.	1.6	21
4733	The crystal structure of glucokinase from Leishmania braziliensis. Molecular and Biochemical Parasitology, 2019, 227, 47-52.	0.5	5
4734	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. Nature, 2019, 565, 49-55.	13.7	264
4735	The peroxisomal zebrafish SCP2-thiolase (type-1) is a weak transient dimer as revealed by crystal structures and native mass spectrometry. Biochemical Journal, 2019, 476, 307-332.	1.7	12
4736	Crystal structures of <i>Hp</i>Sojâ€“DNA complexes and the nucleoid-adaptor complex formation in chromosome segregation. Nucleic Acids Research, 2019, 47, 2113-2129.	6.5	23
4737	<i>Arabidopsis</i> serylâ€‹<scp>tRNA</scp> synthetase: the first crystal structure and novel protein interactor of plant aminoacylâ€‹<scp>tRNA</scp> synthetase. FEBS Journal, 2019, 286, 536-554.	2.2	9
4738	Solution Structure, Self-Assembly, and Membrane Interactions of the Matrix Protein from Newcastle Disease Virus at Neutral and Acidic pH. Journal of Virology, 2019, 93, .	1.5	13
4739	Extended structure of pleiotropic DNA repairâ€promoting protein PprA from <i>Deinococcus radiodurans</i>. FASEB Journal, 2019, 33, 3647-3658.	0.2	7
4740	Surface-Induced Dissociation: An Effective Method for Characterization of Protein Quaternary Structure. Analytical Chemistry, 2019, 91, 190-209.	3.2	67
4741	The ribosomal maturation factor P from Mycobacterium smegmatis facilitates the ribosomal biogenesis by binding to the small ribosomal protein S12. Journal of Biological Chemistry, 2019, 294, 372-378.	1.6	13
4742	Heterohexamers Formed by CcmK3 and CcmK4 Increase the Complexity of Beta Carboxysome Shells. Plant Physiology, 2019, 179, 156-167.	2.3	61

#	ARTICLE	IF	CITATIONS
4743	Vibrio cholerae LMWPTP-2 display unique surface charge and grooves around the active site: Indicative of distinctive substrate specificity and scope to design specific inhibitor. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 114-124.	1.1	1
4744	Crystal structure and substrate recognition mechanism of Aspergillus oryzae isoprimeverose-producing enzyme. Journal of Structural Biology, 2019, 205, 84-90.	1.3	10
4745	Carboxypeptidase in prolyl oligopeptidase family: Unique enzyme activation and substrate-screening mechanisms. Journal of Biological Chemistry, 2019, 294, 89-100.	1.6	16
4746	Tri-arginine exosite patch of caspase-6 recruits substrates for hydrolysis. Journal of Biological Chemistry, 2019, 294, 71-88.	1.6	21
4747	The toxin from a ParDE toxinâ€antitoxin system found in <i>Pseudomonas aeruginosa</i> offers protection to cells challenged with antiâ€gyrase antibiotics. Molecular Microbiology, 2019, 111, 441-454.	1.2	36
4748	Unique mechanism of target recognition by PfoI restriction endonuclease of the CCGG-family. Nucleic Acids Research, 2019, 47, 997-1010.	6.5	3
4749	Predicting the ligand-binding properties of Borrelia burgdorferi s.s. Bmp proteins in light of the conserved features of related Borrelia proteins. Journal of Theoretical Biology, 2019, 462, 97-108.	0.8	5
4750	Structural identification of conserved RNA binding sites in herpesvirus ORF57 homologs: implications for PAN RNA recognition. Nucleic Acids Research, 2019, 47, 1987-2001.	6.5	4
4751	Cryo-Cooling Effect on DHFR Crystal Studied by Replica-Exchange Molecular Dynamics Simulations. Biophysical Journal, 2019, 116, 395-405.	0.2	3
4752	The crystal structure of amyloid precursorâ€like protein 2 E2 domain completes the amyloid precursor protein family. FASEB Journal, 2019, 33, 5076-5081.	0.2	7
4753	Characterization of a thermostable flavin-containing monooxygenase from Nitrincola lacisaponensis (NiFMO). Applied Microbiology and Biotechnology, 2019, 103, 1755-1764.	1.7	18
4754	Biochemical and structural insights into PLP fold type IV transaminase from Thermobaculum terrenum. Biochimie, 2019, 158, 130-138.	1.3	19
4755	Affinity Improvement of a Cancer-Targeted Antibody through Alanine-Induced Adjustment of Antigen-Antibody Interface. Structure, 2019, 27, 519-527.e5.	1.6	31
4756	Crystal Structure and Substrate Specificity of the 8-oxo-dGTP Hydrolase NUDT1 from <i>Arabidopsis thaliana</i>. Biochemistry, 2019, 58, 887-899.	1.2	7
4757	The small RbcS-like domains of the Î²-carboxysome structural protein CcmM bind RubisCO at a site distinct from that binding the RbcS subunit. Journal of Biological Chemistry, 2019, 294, 2593-5195.	1.6	44
4758	Comparison of the Levansucrase from the epiphyte Erwinia tasmaniensis vs its homologue from the phytopathogen Erwinia amylovora. International Journal of Biological Macromolecules, 2019, 127, 496-501.	3.6	13
4759	Insights into Thiotemplated Pyrrole Biosynthesis Gained from the Crystal Structure of Flavin-Dependent Oxidase in Complex with Carrier Protein. Biochemistry, 2019, 58, 918-929.	1.2	12
4760	N-glycan Utilization by Bifidobacterium Gut Symbionts Involves a Specialist Î²-Mannosidase. Journal of Molecular Biology, 2019, 431, 732-747.	2.0	18

#	Article	IF	Citations
4761	<i>N</i>1-Substituted Quinoxaline-2,3-diones as Kainate Receptor Antagonists: X-ray Crystallography, Structureâ€"Affinity Relationships, and in Vitro Pharmacology. ACS Chemical Neuroscience, 2019, 10, 1841-1853.	1.7	13
4762	Supercharging enables organized assembly of synthetic biomolecules. Nature Chemistry, 2019, 11, 204-212.	6.6	70
4763	Calicivirus VP2 forms a portal-like assembly following receptor engagement. Nature, 2019, 565, 377-381.	13.7	103
4764	Structural basis of a potent human monoclonal antibody against Zika virus targeting a quaternary epitope. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1591-1596.	3.3	53
4765	Structural mechanism of transcription inhibition by lasso peptides microcin J25 and capistruin. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1273-1278.	3.3	70
4766	Identification of an internal cavity in the PhoQ sensor domain for PhoQ activity and SafA-mediated control. Bioscience, Biotechnology and Biochemistry, 2019, 83, 684-694.	0.6	16
4767	A New Class of Phosphoribosyltransferases Involved in Cobamide Biosynthesis Is Found in Methanogenic Archaea and Cyanobacteria. Biochemistry, 2019, 58, 951-964.	1.2	10
4768	Structure, Mechanism, and Inhibition of <i>Aspergillus fumigatus</i> Thioredoxin Reductase. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	28
4769	Acetylation of CCAR2 Establishes a BET/BRD9 Acetyl Switch in Response to Combined Deacetylase and Bromodomain Inhibition. Cancer Research, 2019, 79, 918-927.	0.4	28
4770	High-Resolution Structural Characterization of a New Adeno-associated Virus Serotype 5 Antibody Epitope toward Engineering Antibody-Resistant Recombinant Gene Delivery Vectors. Journal of Virology, 2019, 93, .	1.5	37
4771	The RES domain toxins of RESâ€Xre toxinâ€antitoxin modules induce cell stasis by degrading NAD⁺. Molecular Microbiology, 2019, 111, 221-236.	1.2	46
4772	Structure and Catalytic Mechanism of a Bacterial Friedelâ€"Crafts Acylase. ChemBioChem, 2019, 20, 88-95.	1.3	27
4773	Rv3272 encodes a novel Family III CoA transferase that alters the cell wall lipid profile and protects mycobacteria from acidic and oxidative stress. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 317-330.	1.1	3
4774	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. Nature Microbiology, 2019, 4, 414-419.	5.9	73
4775	Structural basis for neutralization of cytotoxic abrin by monoclonal antibody D6F10. FEBS Journal, 2019, 286, 1003-1029.	2.2	3
4776	Crystal structure of the complex between venom toxin and serum inhibitor from Viperidae snake. Journal of Biological Chemistry, 2019, 294, 1250-1256.	1.6	11
4777	Structure and nucleotide-induced conformational dynamics of the Chlorobium tepidum Roco protein. Biochemical Journal, 2019, 476, 51-66.	1.7	21
4778	An engineered lipocalin that tightly complexes the plant poison colchicine for use as antidote and in bioanalytical applications. Biological Chemistry, 2019, 400, 351-366.	1.2	14

#	Article	IF	Citations
4779	Structural and functional characterization of an intradiol ring-cleavage dioxygenase from the polyphagous spider mite herbivore Tetranychus urticae Koch. Insect Biochemistry and Molecular Biology, 2019, 107, 19-30.	1.2	6
4780	Ligand binding to human prostaglandin E receptor EP4 at the lipid-bilayer interface. Nature Chemical Biology, 2019, 15, 18-26.	3.9	85
4781	Crystal structure of Kumaglobin: a hexacoordinated heme protein from an anhydrobiotic tardigrade, <i>Ramazzottius varieornatus</i>. FEBS Journal, 2019, 286, 1287-1304.	2.2	8
4782	Structural insights into the catalytic mechanism of 5-methylthioribose 1-phosphate isomerase. Journal of Structural Biology, 2019, 205, 67-77.	1.3	3
4783	Non-crystallographic symmetry in proteins: Jahnâ€"Teller-like and Butterfly-like effects?. Journal of Biological Inorganic Chemistry, 2019, 24, 91-101.	1.1	2
4784	Characterization of an RNase with two catalytic centers. Human RNase6 catalytic and phosphate-binding site arrangement favors the endonuclease cleavage of polymeric substrates. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 105-117.	1.1	23
4785	Heterozygous loss-of-function variants of MEIS2 cause a triad of palatal defects, congenital heart defects, and intellectual disability. European Journal of Human Genetics, 2019, 27, 278-290.	1.4	30
4786	Developing Hispolon-based novel anticancer therapeutics against human (NF-Î°Î²) using <i>in silico</i> approach of modelling, docking and protein dynamics. Journal of Biomolecular Structure and Dynamics, 2019, 37, 3947-3967.	2.0	14
4787	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. Briefings in Bioinformatics, 2019, 20, 1032-1056.	3.2	10
4788	Solution Structure and Dynamics of the Small Protein HVO_2922 from Haloferax volcanii. ChemBioChem, 2020, 21, 149-156.	1.3	9
4789	Structural and biochemical studies of phosphopantetheine adenylyltransferase from Acinetobacter baumannii with dephospho-coenzyme A and coenzyme A. International Journal of Biological Macromolecules, 2020, 142, 181-190.	3.6	1
4790	Structural and Functional Characterization of the Globin-Coupled Sensors ofAzotobacter vinelandiiandBordetella pertussis. Antioxidants and Redox Signaling, 2020, 32, 378-395.	2.5	4
4791	Structures in Tetrahydrofolate Methylation in Desulfitobacterial Glycine Betaine Metabolism at Atomic Resolution. ChemBioChem, 2020, 21, 776-779.	1.3	1
4792	Lateral A11 type tetramerization in lamins. Journal of Structural Biology, 2020, 209, 107404.	1.3	26
4793	Structural characterization of Î²â€ketoacyl ACP synthase I bound to platencin and fragment screening molecules at two substrate binding sites. Proteins: Structure, Function and Bioinformatics, 2020, 88, 47-56.	1.5	3
4794	Soft regions of protein surface are potent for stable dimer formation. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3587-3598.	2.0	5
4795	The Nâ€terminal peptide of the transglutaminaseâ€activating metalloprotease inhibitor from <i>StreptomycesÂmobaraensis</i> accommodates both inhibition and glutamine crossâ€linking sites. FEBS Journal, 2020, 287, 708-720.	2.2	6
4796	Potential complementation effects of two disease-associated mutations in tetrameric glutaryl-CoA dehydrogenase is due to inter subunit stability-activity counterbalance. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140269.	1.1	8

#	Article	IF	Citations
4797	Whole exome sequencing identifies a novel SCN1A mutation in genetic (idiopathic) generalized epilepsy and juvenile myoclonic epilepsy subtypes. Neurological Sciences, 2020, 41, 591-598.	0.9	6
4798	Dimerization of long hibernation promoting factor from Staphylococcus aureus: Structural analysis and biochemical characterization. Journal of Structural Biology, 2020, 209, 107408.	1.3	4
4799	Crystal structure of the complex of the interaction domains of Escherichia coli DnaB helicase and DnaC helicase loader: structural basis implying a distortion-accumulation mechanism for the DnaB ring opening caused by DnaC binding. Journal of Biochemistry, 2020, 167, 1-14.	0.9	13
4800	A comprehensive review and evaluation of computational methods for identifying protein complexes from proteinâ€“protein interaction networks. Briefings in Bioinformatics, 2020, 21, 1531-1548.	3.2	42
4801	Templateâ€based modeling of diverse protein interactions in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 939-947.	1.5	3
4802	Unique active site formation in a novel galactose 1â€phosphate uridylyltransferase from the hyperthermophilic archaeonPyrobaculum aerophilum. Proteins: Structure, Function and Bioinformatics, 2020, 88, 669-678.	1.5	0
4803	Crystal structure of a hypothetical T2SS effector Lpg0189 from Legionella pneumophila reveals a novel protein fold. Biochemical and Biophysical Research Communications, 2020, 521, 799-805.	1.0	2
4804	Unique surfaceâ€exposed hydrophobic residues in the C1 domain of factor VIII contribute to cofactor function and von Willebrand factor binding. Journal of Thrombosis and Haemostasis, 2020, 18, 364-372.	1.9	5
4805	Structures of MERS1, the 5â€² processing enzyme of mitochondrial mRNAs in <i>Trypanosoma brucei</i>. Rna, 2020, 26, 69-82.	1.6	3
4806	Structural insights into polysaccharide recognition by <i>FlavobacteriumÂ johnsoniae</i> dextranase, a member of glycoside hydrolase family 31. FEBS Journal, 2020, 287, 1195-1207.	2.2	17
4807	Reduced matrix metalloproteinase and collagen transcription mediated by the TGFâ€Î²/Smad pathway in passaged normal human dermal fibroblasts. Journal of Cosmetic Dermatology, 2020, 19, 1211-1218.	0.8	20
4808	Infant Respiratory Syncytial Virus Bronchiolitis and Subsequent Risk of Pneumonia, Otitis Media, and Antibiotic Utilization. Clinical Infectious Diseases, 2020, 71, 211-214.	2.9	8
4809	Biochemical and cellular mechanism of protein kinase CK2 inhibition by deceptive curcumin. FEBS Journal, 2020, 287, 1850-1864.	2.2	9
4810	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. Molecular Cell, 2020, 77, 723-733.e6.	4.5	148
4811	Broad Specificity of Amino Acid Chemoreceptor CtaA of <i>Pseudomonas fluorescens</i> Is Afforded by Plasticity of Its Amphipathic Ligand-Binding Pocket. Molecular Plant-Microbe Interactions, 2020, 33, 612-623.	1.4	12
4812	The Biosynthesis of the Benzoxazole in Nataxazole Proceeds via an Unstable Ester and has Synthetic Utility. Angewandte Chemie, 2020, 132, 6110-6117.	1.6	5
4813	Different ways to transport ammonia in human and Mycobacterium tuberculosis NAD+ synthetases. Nature Communications, 2020, 11, 16.	5.8	15
4814	Structural Basis of the Substrate Selectivity of Viperin. Biochemistry, 2020, 59, 652-662.	1.2	28

#	ARTICLE	IF	CITATIONS
4815	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. Nature Communications, 2020, 11, 38.	5.8	28
4816	The structure of <i>PlasmodiumÂfalciparum</i> hydroxymethyldihydropterin pyrophosphokinaseâ€dihydropteroate synthase reveals the basis of sulfa resistance. FEBS Journal, 2020, 287, 3273-3297.	2.2	24
4817	Catalytic mechanism and evolutionary characteristics of thioredoxin from <i>Halobacterium salinarum</i> NRC-1. Acta Crystallographica Section D: Structural Biology, 2020, 76, 73-84.	1.1	3
4818	Xâ€ray crystallographic structure of BshB, the zincâ€dependent deacetylase involved in bacillithiol biosynthesis. Protein Science, 2020, 29, 1021-1025.	3.1	4
4819	Structural insights into phosphopantetheinyl hydrolase PptH from Mycobacterium tuberculosis. Protein Science, 2020, 29, 744-757.	3.1	6
4820	Structural and mechanistic aspects of carotenoid cleavage dioxygenases (CCDs). Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2020, 1865, 158590.	1.2	29
4821	High resolution structure of Vibrio cholerae acylphosphatase (VcAcP) cage: Identification of drugs, location of its binding site and engineering to facilitate cage formation. Biochemical and Biophysical Research Communications, 2020, 523, 348-353.	1.0	2
4822	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. Journal of Molecular Biology, 2020, 432, 845-860.	2.0	26
4823	Redox Characterization of Electrode-Immobilized Bacterial Microcompartment Shell Proteins Engineered To Bind Metal Centers. ACS Applied Bio Materials, 2020, 3, 685-692.	2.3	9
4824	Catalytic Cycle of Glycoside Hydrolase BglX from <i>Pseudomonas aeruginosa</i> and Its Implications for Biofilm Formation. ACS Chemical Biology, 2020, 15, 189-196.	1.6	11
4825	An inhibitor of complement C5 provides structural insights into activation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 362-370.	3.3	27
4826	Molecular mechanism of two nanobodies that inhibit PAIâ€1 activity reveals a modulation at distinct stages of the PAIâ€1/plasminogen activator interaction. Journal of Thrombosis and Haemostasis, 2020, 18, 681-692.	1.9	12
4827	Structure of Urocanate Hydratase from the protozoan Trypanosoma cruzi. International Journal of Biological Macromolecules, 2020, 146, 716-724.	3.6	2
4828	Geneticsâ€™ Piece of the PI: Inferring the Origin of Complex Traits and Diseases from Proteomeâ€Wide Proteinâ€"Protein Interaction Dynamics. BioEssays, 2020, 42, 1900169.	1.2	0
4829	Alterations in plasma membrane ion channel structures stimulate NLRP3 inflammasome activation in APOL1 risk milieu. FEBS Journal, 2020, 287, 2000-2022.	2.2	16
4830	Cryo-EM Structure of Nucleotide-Bound Tel1ATM Unravels the Molecular Basis of Inhibition and Structural Rationale for Disease-Associated Mutations. Structure, 2020, 28, 96-104.e3.	1.6	28
4831	Near-Complete Structure and Model of Tel1ATM from Chaetomium thermophilum Reveals a Robust Autoinhibited ATP State. Structure, 2020, 28, 83-95.e5.	1.6	24
4832	Versatile and robust genome editing with <i>Streptococcus thermophilus</i> CRISPR1-Cas9. Genome Research, 2020, 30, 107-117.	2.4	51

#	ARTICLE	IF	CITATIONS
4833	A bipartite structural organization defines the SERINC family of HIV-1 restriction factors. Nature Structural and Molecular Biology, 2020, 27, 78-83.	3.6	50
4834	The gastrointestinal pathogen Campylobacter jejuni metabolizes sugars with potential help from commensal Bacteroides vulgatus. Communications Biology, 2020, 3, 2.	2.0	26
4835	The Biosynthesis of the Benzoxazole in Nataxazole Proceeds via an Unstable Ester and has Synthetic Utility. Angewandte Chemie - International Edition, 2020, 59, 6054-6061.	7.2	24
4836	The structure of the periplasmic FlaGâ€“FlaF complex and its essential role for archaellar swimming motility. Nature Microbiology, 2020, 5, 216-225.	5.9	32
4837	Structural basis for the dimerization of Gemin5 and its role in protein recruitment and translation control. Nucleic Acids Research, 2020, 48, 788-801.	6.5	19
4838	Molecular basis for <scp>GTP</scp> recognition by lightâ€activated guanylate cyclase Rh<scp>GC</scp>. FEBS Journal, 2020, 287, 2797-2807.	2.2	9
4839	Inhibition of Zea mays coniferyl aldehyde dehydrogenase by daidzin: A potential approach for the investigation of lignocellulose recalcitrance. Process Biochemistry, 2020, 90, 131-138.	1.8	30
4840	Structure and function of the two-component flavin-dependent methanesulfinate monooxygenase within bacterial sulfur assimilation. Biochemical and Biophysical Research Communications, 2020, 522, 107-112.	1.0	6
4841	Molecular and structural analysis of a mechanical transition of helices in the L. donovani coronin coiled-coil domain. International Journal of Biological Macromolecules, 2020, 143, 785-796.	3.6	3
4842	Characterization of novel lectins from Burkholderia pseudomallei and Chromobacterium violaceum with seven-bladed Î²-propeller fold. International Journal of Biological Macromolecules, 2020, 152, 1113-1124.	3.6	5
4843	Enhanced Characterization of Membrane Protein Complexes by Ultraviolet Photodissociation Mass Spectrometry. Analytical Chemistry, 2020, 92, 899-907.	3.2	21
4844	Extracellular micro<scp>RNA</scp> 130bâ€3p inhibits <scp>eCIRP</scp>â€induced inflammation. EMBO Reports, 2020, 21, e48075.	2.0	40
4845	Evolution-guided engineering of small-molecule biosensors. Nucleic Acids Research, 2020, 48, e3-e3.	6.5	92
4846	Structural insights into substrate recognition by the type VII secretion system. Protein and Cell, 2020, 11, 124-137.	4.8	25
4847	Structural and functional investigation of AerF, a NADPH-dependent alkenal double bond reductase participating in the biosynthesis of Choi moiety of aeruginosin. Journal of Structural Biology, 2020, 209, 107415.	1.3	5
4848	Structural and biochemical analysis of <i>BacillusÂanthracis</i> prephenate dehydrogenase reveals an unusual mode of inhibition by tyrosine via the ACT domain. FEBS Journal, 2020, 287, 2235-2255.	2.2	3
4849	Identification of Electrostatic Epitopes in Flavivirus by Computer Simulations: The PROCEEDpKa Method. Journal of Chemical Information and Modeling, 2020, 60, 944-963.	2.5	20
4850	Mechanism of conditional partner selectivity in MITF/TFE family transcription factors with a conserved coiled coil stammer motif. Nucleic Acids Research, 2020, 48, 934-948.	6.5	17

#	Article	IF	Citations
4851	Allosteric inhibition and kinetic characterization of Klebsiella pneumoniae CysE: An emerging drug target. International Journal of Biological Macromolecules, 2020, 151, 1240-1249.	3.6	7
4852	Synthetic Antibody Binding to a Preorganized RNA Domain of Hepatitis C Virus Internal Ribosome Entry Site Inhibits Translation. ACS Chemical Biology, 2020, 15, 205-216.	1.6	14
4853	Structural and functional characterization of three Type B and C chloramphenicol acetyltransferases from <i>Vibrio</i> species. Protein Science, 2020, 29, 695-710.	3.1	12
4854	Fulditoxin, representing a new class of dimeric snake toxins, defines novel pharmacology at nicotinic ACh receptors. British Journal of Pharmacology, 2020, 177, 1822-1840.	2.7	12
4855	GapR binds DNA through dynamic opening of its tetrameric interface. Nucleic Acids Research, 2020, 48, 9372-9386.	6.5	6
4856	Domain-Swap Dimerization ofAcanthamoeba castellaniiCYP51 and a Unique Mechanism of Inactivation by Isavuconazole. Molecular Pharmacology, 2020, 98, 770-780.	1.0	2
4857	The crystal structure of mycobacterial epoxide hydrolase A. Scientific Reports, 2020, 10, 16539.	1.6	4
4858	Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of V _o complex. Science Advances, 2020, 6, .	4.7	51
4859	Functional Recovery of a GCDH Variant Associated to Severe Deflavinylationâ€"Molecular Insights into Potential Beneficial Effects of Riboflavin Supplementation in Glutaric Aciduria-Type I Patients. International Journal of Molecular Sciences, 2020, 21, 7063.	1.8	4
4860	Structural features and development of an assay platform of the parasite target deoxyhypusine synthase of Brugia malayi and Leishmania major. PLoS Neglected Tropical Diseases, 2020, 14, e0008762.	1.3	4
4861	â€œThe structure of the Type III secretion system export gate with CdsO, an ATPase lever armâ€• PLoS Pathogens, 2020, 16, e1008923.	2.1	23
4862	<scp><i>Chlamydia trachomatis</i></scp> glyceraldehyde 3â€phosphate dehydrogenase: Enzyme kinetics, highâ€resolution crystal structure, and plasminogen binding. Protein Science, 2020, 29, 2446-2458.	3.1	5
4863	Characterization and functional insights into the Entamoeba histolytica pyridoxal kinase, an enzyme essential for its survival. Journal of Structural Biology, 2020, 212, 107645.	1.3	5
4864	Comparative docking studies to understand the binding affinity of nicotine with soluble ACE2 (sACE2)-SARS-CoV-2 complex over sACE2. Toxicology Reports, 2020, 7, 1366-1372.	1.6	9
4865	Structural Basis for the Inhibitor and Substrate Specificity of the Unique Fph Serine Hydrolases of <i>Staphylococcus aureus</i>. ACS Infectious Diseases, 2020, 6, 2771-2782.	1.8	14
4866	Trypanosomatid selenophosphate synthetase structure, function and interaction with selenocysteine lyase. PLoS Neglected Tropical Diseases, 2020, 14, e0008091.	1.3	5
4867	Structural and functional study of SaAcP, an acylphosphatase from Staphylococcus aureus. Biochemical and Biophysical Research Communications, 2020, 532, 173-178.	1.0	2
4868	Molecular Recognition at Septin Interfaces: The Switches Hold the Key. Journal of Molecular Biology, 2020, 432, 5784-5801.	2.0	24

#	ARTICLE	IF	CITATIONS
4869	Structural and functional modelling of SARS-CoV-2 entry in animal models. Scientific Reports, 2020, 10, 15917.	1.6	53
4870	Functional and structural characterization of an Î±-ĒŸ-arabinofuranosidase from Thermothielavioides terrestris and its exquisite domain-swapped Î²-propeller fold crystal packing. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140533.	1.1	5
4871	Structural basis for allosteric regulation of pyruvate kinase M2 by phosphorylation and acetylation. Journal of Biological Chemistry, 2020, 295, 17425-17440.	1.6	27
4872	High-resolution cryo-EM structure of urease from the pathogen Yersinia enterocolitica. Nature Communications, 2020, 11, 5101.	5.8	17
4873	Structural basis for CDK7 activation by MAT1 and Cyclin H. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26739-26748.	3.3	26
4874	A Therapeutic Non-self-reactive SARS-CoV-2 Antibody Protects from Lung Pathology in a COVID-19 Hamster Model. Cell, 2020, 183, 1058-1069.e19.	13.5	305
4875	Structural Basis of Nanomolar Inhibition of Tumor-Associated Carbonic Anhydrase IX: X-Ray Crystallographic and Inhibition Study of Lipophilic Inhibitors with Acetazolamide Backbone. Journal of Medicinal Chemistry, 2020, 63, 13064-13075.	2.9	26
4876	Crystal structure of caspase-11 CARD provides insights into caspase-11 activation. Cell Discovery, 2020, 6, 70.	3.1	14
4877	Dimerization regulates the human APC/C-associated ubiquitin-conjugating enzyme UBE2S. Science Signaling, 2020, 13, .	1.6	12
4878	Structural analysis of CACHE domain of the McpA chemoreceptor from Leptospira interrogans. Biochemical and Biophysical Research Communications, 2020, 533, 1323-1329.	1.0	2
4879	Bioinspired and Biomimetic Design of Multilayered and Multiscale Structures. , 2020, , 3-19.		1
4880	The Arabidopsis CRUMPLED LEAF protein, a homolog of the cyanobacterial bilin lyase, retains the bilinâ€binding pocket for a yet unknown function. Plant Journal, 2020, 104, 964-978.	2.8	3
4881	Promiscuous Binding of Microprotein Mozart1 to Î³-Tubulin Complex Mediates Specific Subcellular Targeting to Control Microtubule Array Formation. Cell Reports, 2020, 31, 107836.	2.9	15
4882	Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7â€"11ÂUncovers the Mannose 6-Phosphate Binding Site of Domain 9. Structure, 2020, 28, 1300-1312.e5.	1.6	8
4883	An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. Cell Reports, 2020, 33, 108274.	2.9	152
4884	Characterization of tau binding by gosuranemab. Neurobiology of Disease, 2020, 146, 105120.	2.1	36
4885	A Complement C3â€"Specific Nanobody for Modulation of the Alternative Cascade Identifies the C-Terminal Domain of C3b as Functional in C5 Convertase Activity. Journal of Immunology, 2020, 205, 2287-2300.	0.4	9
4886	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite Plasmodium falciparum. Cell Reports, 2020, 31, 107817.	2.9	23

#	ARTICLE	IF	CITATIONS
4887	Flowering Porationâ€”A Synergistic Multi-Mode Antibacterial Mechanism by a Bacteriocin Fold. IScience, 2020, 23, 101423.	1.9	16
4888	Bioinspired Design for Energy Storage Devices. , 2020, , 193-211.		0
4889	Structural characterization of the ICOS/ICOS-L immune complex reveals high molecular mimicry by therapeutic antibodies. Nature Communications, 2020, 11, 5066.	5.8	23
4890	Structural basis of BMPâ€2 and BMPâ€7 interactions with antagonists Gremlinâ€1 and Noggin in Glioblastoma tumors. Journal of Computational Chemistry, 2020, 41, 2544-2561.	1.5	5
4891	Structural basis of mammalian mucin processing by the human gut O-glycopeptidase OgpA from Akkermansia muciniphila. Nature Communications, 2020, 11, 4844.	5.8	57
4892	Structural role of essential light chains in the apicomplexan glideosome. Communications Biology, 2020, 3, 568.	2.0	10
4893	The L.donovani Hypoxanthine-guanine phosphoribosyl transferase (HGPRT) oligomer is distinct from the human homolog. Biochemical and Biophysical Research Communications, 2020, 532, 499-504.	1.0	4
4894	Bioinspired Underwater Propulsors. , 2020, , 113-139.		6
4895	Immunodominant proteins P1 and P40/P90 from human pathogen Mycoplasma pneumoniae. Nature Communications, 2020, 11, 5188.	5.8	22
4896	Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms. Science, 2020, 370, .	6.0	508
4897	Structural characterization of the C-terminal domain of SARS-CoV-2 nucleocapsid protein. Molecular Biomedicine, 2020, 1, 2.	1.7	76
4898	Binding Mechanism Elucidation of the Acute Respiratory Disease Causing Agent Adenovirus of Serotype 7 to Desmoglein-2. Viruses, 2020, 12, 1075.	1.5	7
4899	Structural Basis for Regulation of the Opposing (p)ppGpp Synthetase and Hydrolase within the Stringent Response Orchestrator Rel. Cell Reports, 2020, 32, 108157.	2.9	39
4900	Site mapping and small molecule blind docking reveal a possible target site on the SARS-CoV-2 main protease dimer interface. Computational Biology and Chemistry, 2020, 89, 107372.	1.1	30
4901	Crystal structure of the periplasmic sensor domain of histidine kinase VbrK suggests indirect sensing of Î²-lactam antibiotics. Journal of Structural Biology, 2020, 212, 107610.	1.3	7
4902	ppGpp Coordinates Nucleotide and Amino-Acid Synthesis in E. coli During Starvation. Molecular Cell, 2020, 80, 29-42.e10.	4.5	50
4903	Aquatic Animals Operating at High Reynolds Numbers. , 2020, , 235-270.		1
4904	Mutation of an atypical oxirane oxyanion hole improves regioselectivity of the Î±/Î²-fold epoxide hydrolase Alp1U. Journal of Biological Chemistry, 2020, 295, 16987-16997.	1.6	6

#	ARTICLE	IF	CITATIONS
4905	Higher-order oligomerization of a chimeric Î±Î²Î³ bifunctional diterpene synthase with prenyltransferase and class II cyclase activities is concentration-dependent. Journal of Structural Biology, 2020, 210, 107463.	1.3	11
4906	The discovery of a new antibody for BRIL-fused GPCR structure determination. Scientific Reports, 2020, 10, 11669.	1.6	21
4907	An influenza A hemagglutinin small-molecule fusion inhibitor identified by a new high-throughput fluorescence polarization screen. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18431-18438.	3.3	25
4908	Structural basis of a novel repressor, SghR, controlling Agrobacterium infection by cross-talking to plants. Journal of Biological Chemistry, 2020, 295, 12290-12304.	1.6	4
4909	The Cupin Protein Pac13 is Suggested by the Data to Be a Homodimer. Angewandte Chemie - International Edition, 2020, 59, 12580-12583.	7.2	4
4912	In crystallo-screening for discovery of human norovirus 3C-like protease inhibitors. Journal of Structural Biology: X, 2020, 4, 100031.	0.7	2
4913	Differential seminal plasma proteome signatures of boars with high and low resistance to hypothermic semen preservation at 5Â°C. Andrology, 2020, 8, 1907-1922.	1.9	5
4914	Highly Conserved Molecular Features in IgLONs Contrast Their Distinct Structural and Biological Outcomes. Journal of Molecular Biology, 2020, 432, 5287-5303.	2.0	13
4915	Glypicans shield the Wnt lipid moiety to enable signalling at a distance. Nature, 2020, 585, 85-90.	13.7	90
4916	Inactivation of the dimeric RappLS20 anti-repressor of the conjugation operon is mediated by peptide-induced tetramerization. Nucleic Acids Research, 2020, 48, 8113-8127.	6.5	4
4917	Structural basis of a shared antibody response to SARS-CoV-2. Science, 2020, 369, 1119-1123.	6.0	536
4918	Structural and Biochemical Analyses Reveal that Chlorogenic Acid Inhibits the Shikimate Pathway. Journal of Bacteriology, 2020, 202, .	1.0	12
4919	<scp>M42</scp> aminopeptidase catalytic site: the structural and functional role of a strictly conserved aspartate residue. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1639-1647.	1.5	2
4920	PE5â€"PPE4â€"EspG3 heterotrimer structure from mycobacterial ESX-3 secretion system gives insight into cognate substrate recognition by ESX systems. Journal of Biological Chemistry, 2020, 295, 12706-12715.	1.6	16
4921	New Structural insights into Kir channel gating from molecular simulations, HDX-MS and functional studies. Scientific Reports, 2020, 10, 8392.	1.6	10
4922	Insight into the sequence-structure relationship of TLR cytoplasmâ€™s Toll/Interleukin-1 receptor domain towards understanding the conserved functionality of TLR 2 heterodimer in mammals. Journal of Biomolecular Structure and Dynamics, 2021, 39, 5348-5357.	2.0	10
4923	Structure basis of the FERM domain of kindlin-3 in supporting integrin Î±IIbÎ²3 activation in platelets. Blood Advances, 2020, 4, 3128-3135.	2.5	20
4924	The RNA Polymerase Î± Subunit Recognizes the DNA Shape of the Upstream Promoter Element. Biochemistry, 2020, 59, 4523-4532.	1.2	12

#	ARTICLE	IF	CITATIONS
4925	Biophysical and Biochemical Characterization of TP0037, a <scp>d</scp> -Lactate Dehydrogenase, Supports an Acetogenic Energy Conservation Pathway in Treponema pallidum. MBio, 2020, 11, .	1.8	4
4926	Crystal Structure of Isoform CBd of the Basic Phospholipase A2 Subunit of Crotoxin: Description of the Structural Framework of CB for Interaction with Protein Targets. Molecules, 2020, 25, 5290.	1.7	7
4927	Multitask ATPases (NBDs) of bacterial ABC importers type I and their interspecies exchangeability. Scientific Reports, 2020, 10, 19564.	1.6	8
4928	Characterizing human Î±-1,6-fucosyltransferase (FUT8) substrate specificity and structural similarities with related fucosyltransferases. Journal of Biological Chemistry, 2020, 295, 17027-17045.	1.6	19
4929	Cross-Neutralization of a SARS-CoV-2 Antibody to a Functionally Conserved Site Is Mediated by Avidity. Immunity, 2020, 53, 1272-1280.e5.	6.6	185
4930	Controlling Protein Nanocage Assembly with Hydrostatic Pressure. Journal of the American Chemical Society, 2020, 142, 20640-20650.	6.6	17
4931	Bringing the Heavy Chain to Light: Creating a Symmetric, Bivalent IgG-Like Bispecific. Antibodies, 2020, 9, 62.	1.2	3
4932	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. Nature, 2020, 588, 327-330.	13.7	684
4933	SARS-CoV-2 neutralizing antibody structures inform therapeutic strategies. Nature, 2020, 588, 682-687.	13.7	1,346
4934	Succinic Semialdehyde Dehydrogenase Deficiency: In Vitro and In Silico Characterization of a Novel Pathogenic Missense Variant and Analysis of the Mutational Spectrum of ALDH5A1. International Journal of Molecular Sciences, 2020, 21, 8578.	1.8	5
4935	Ancestral L-amino acid oxidases for deracemization and stereoinversion of amino acids. Communications Chemistry, 2020, 3, .	2.0	21
4936	Turnip yellow mosaic virus protease binds ubiquitin suboptimally to fine-tune its deubiquitinase activity. Journal of Biological Chemistry, 2020, 295, 13769-13783.	1.6	8
4937	Post-translational Regulation of DNA Polymerase Î·, a Connection to Damage-Induced Cohesion in Saccharomyces cerevisiae. Genetics, 2020, 216, 1009-1022.	1.2	5
4938	The cryo-EM structure of a Î³-TuSC elucidates architecture and regulation of minimal microtubule nucleation systems. Nature Communications, 2020, 11, 5705.	5.8	7
4939	Phylogenetics-based identification and characterization of a superior 2,3-butanediol dehydrogenase for Zymomonas mobilis expression. Biotechnology for Biofuels, 2020, 13, 186.	6.2	5
4940	Structure of odorant binding proteins and chemosensory proteins determined by X-ray crystallography. Methods in Enzymology, 2020, 642, 151-167.	0.4	2
4941	NAP1-Related Protein 1 (NRP1) has multiple interaction modes for chaperoning histones H2A-H2B. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30391-30399.	3.3	13
4942	The antibiotic sorangicin A inhibits promoter DNA unwinding in a <i>Mycobacterium tuberculosis</i> rifampicin-resistant RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30423-30432.	3.3	25

#	ARTICLE	IF	CITATIONS
4943	Natural Killer Cell Activation Receptor NKp30 Oligomerization Depends on Its N-Glycosylation. Cancers, 2020, 12, 1998.	1.7	12
4944	The Cupin Protein Pac13 is Suggested by the Data to Be a Homodimer. Angewandte Chemie, 2020, 132, 12680-12683.	1.6	0
4945	Immunoinformatic construction of an adenovirus-based modular vaccine platform and its application in the design of a SARS-CoV-2 vaccine. Infection, Genetics and Evolution, 2020, 85, 104489.	1.0	4
4946	A monodomain class II terpene cyclase assembles complex isoprenoid scaffolds. Nature Chemistry, 2020, 12, 968-972.	6.6	24
4947	The Interaction of Bovine Î²-Lactoglobulin with Caffeic Acid: From Binding Mechanisms to Functional Complexes. Biomolecules, 2020, 10, 1096.	1.8	10
4948	Modulation of Light Energy Transfer from Chromophore to Protein in the Channelrhodopsin ReaChR. Biophysical Journal, 2020, 119, 705-716.	0.2	6
4949	Effect of Polyethylene Glycol-Induced Molecular Crowding on the Enzymatic Activity and Thermal Stability of Î²-Galactosidase from <i>Kluyveromyces lactis</i>. Journal of Agricultural and Food Chemistry, 2020, 68, 8875-8882.	2.4	9
4950	Transition-State Analogues of Phenylethanolamine <i>N</i>-Methyltransferase. Journal of the American Chemical Society, 2020, 142, 14222-14233.	6.6	16
4951	Securing SNAREs for assembly. Journal of Biological Chemistry, 2020, 295, 10136-10137.	1.6	3
4952	Crystal structures of the RNA triphosphatase from Trypanosoma cruzi provide insights into how it recognizes the 5â€²-end of the RNA substrate. Journal of Biological Chemistry, 2020, 295, 9076-9086.	1.6	5
4953	An International Multicenter Evaluation of Inheritance Patterns, Arrhythmic Risks, and Underlying Mechanisms of<i>CASQ2</i>-Catecholaminergic Polymorphic Ventricular Tachycardia. Circulation, 2020, 142, 932-947.	1.6	44
4954	Functional and Structural Characterization of a Potent C1q Inhibitor Targeting the Classical Pathway of the Complement System. Frontiers in Immunology, 2020, 11, 1504.	2.2	17
4955	Structural insights into the fungi-nematodes interaction mediated by fucose-specific lectin AofleA from Arthrobotrys oligospora. International Journal of Biological Macromolecules, 2020, 164, 783-793.	3.6	6
4956	Biochemical characterization of mouse d-aspartate oxidase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140472.	1.1	4
4957	Structure: Function Studies of the Cytosolic, Mo- and NAD+-Dependent Formate Dehydrogenase from Cupriavidus necator. Inorganics, 2020, 8, 41.	1.2	7
4958	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. Science Advances, 2020, 6, eabb5642.	4.7	26
4959	Antigen-Induced Allosteric Changes in a Human IgG1 Fc Increase Low-Affinity FcÎ³ Receptor Binding. Structure, 2020, 28, 516-527.e5.	1.6	23
4960	Recognition Patterns of the C1/C2 Epitopes Involved in Fc-Mediated Response in HIV-1 Natural Infection and the RV114 Vaccine Trial. MBio, 2020, 11, .	1.8	6

#	ARTICLE	IF	CITATIONS
4961	Biophysical Characterization of Cancer-Related Carbonic Anhydrase IX. International Journal of Molecular Sciences, 2020, 21, 5277.	1.8	4
4962	Structural analysis of the LDL receptorâ€“interacting FERM domain in the E3 ubiquitin ligase IDOL reveals an obscured substrate-binding site. Journal of Biological Chemistry, 2020, 295, 13570-13583.	1.6	7
4963	Orientation of immobilized antigens on common surfaces by a simple computational model: Exposition of SARS-CoV-2 Spike protein RBD epitopes. Biophysical Chemistry, 2020, 265, 106441.	1.5	9
4964	The variable oligomeric state of Amuc_1100 from Akkermansia muciniphila. Journal of Structural Biology, 2020, 212, 107593.	1.3	15
4965	Structural basis for carotenoid cleavage by an archaeal carotenoid dioxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19914-19925.	3.3	17
4966	Structural Characterization of an S-enantioselective Imine Reductase from Mycobacterium Smegmatis. Biomolecules, 2020, 10, 1130.	1.8	7
4967	Cyanobacterial Dihydroxyacid Dehydratases Are a Promising Growth Inhibition Target. ACS Chemical Biology, 2020, 15, 2281-2288.	1.6	10
4968	Direct Introduction of an Alkylsulfonamido Group on Câ€sites of Isomeric Dicarbaâ€<i>closo</i>â€dodecaboranes: The Influence of Stereochemistry on Inhibitory Activity against the Cancerâ€Associated Carbonic Anhydrase IX Isoenzyme. Chemistry - A European Journal, 2020, 26, 16541-16553.	1.7	4
4969	Intrinsic curvature of the HIV-1 CA hexamer underlies capsid topology and interaction with cyclophilin A. Nature Structural and Molecular Biology, 2020, 27, 855-862.	3.6	43
4970	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. Nature Structural and Molecular Biology, 2020, 27, 950-958.	3.6	268
4971	Structures of filamentous viruses infecting hyperthermophilic archaea explain DNA stabilization in extreme environments. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19643-19652.	3.3	29
4972	Structural and biochemical characterization of a glutathione transferase from the citrus canker pathogen<i>Xanthomonas</i>. Acta Crystallographica Section D: Structural Biology, 2020, 76, 778-789.	1.1	1
4973	Structure-Based Functional Modification Study of a Cyanobacterial Chloride Pump for Transporting Multiple Anions. Journal of Molecular Biology, 2020, 432, 5273-5286.	2.0	9
4974	Structural Characterization of Sphingomonas sp. KT-1 PahZ1-Catalyzed Biodegradation of Thermally Synthesized Poly(aspartic acid). ACS Sustainable Chemistry and Engineering, 2020, , .	3.2	1
4975	Mycobacterium tuberculosis FasR senses long fatty acyl-CoA through a tunnel and a hydrophobic transmission spine. Nature Communications, 2020, 11, 3703.	5.8	16
4976	Studying the Effects of ACE2 Mutations on the Stability, Dynamics, and Dissociation Process of SARS-CoV-2 S1/hACE2 Complexes. Journal of Proteome Research, 2020, 19, 4609-4623.	1.8	22
4977	The architecture and stabilisation of flagellotropic tailed bacteriophages. Nature Communications, 2020, 11, 3748.	5.8	28
4978	Specific targeting of IL-1Î² activity to CD8+ T cells allows for safe use as a vaccine adjuvant. Npj Vaccines, 2020, 5, 64.	2.9	15

#	ARTICLE	IF	CITATIONS
4979	On Monomeric and Multimeric Structures-Based Protein-Ligand Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 569-574.	1.9	1
4980	Revealing the mechanism of repressor inactivation during switching of a temperate bacteriophage. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20576-20585.	3.3	6
4981	The bacterial copper resistance protein CopG contains a cysteine-bridged tetranuclear copper cluster. Journal of Biological Chemistry, 2020, 295, 11364-11376.	1.6	17
4982	Structural Basis and Evolution of Glycan Receptor Specificities within the Polyomavirus Family. MBio, 2020, 11, .	1.8	9
4983	Structure-Guided Molecular Engineering of a Vascular Endothelial Growth Factor Antagonist to Treat Retinal Diseases. Cellular and Molecular Bioengineering, 2020, 13, 405-418.	1.0	2
4984	Molecular characterization of the RNA-protein complex directing â˜2/â˜1 programmed ribosomal frameshifting during arterivirus replicase expression. Journal of Biological Chemistry, 2020, 295, 17904-17921.	1.6	10
4985	Alpha-Carbonic Anhydrases from Hydrothermal Vent Sources as Potential Carbon Dioxide Sequestration Agents: In Silico Sequence, Structure and Dynamics Analyses. International Journal of Molecular Sciences, 2020, 21, 8066.	1.8	6
4986	Peptide Inhibitors of the Î±-Cobratoxinâ€"Nicotinic Acetylcholine Receptor Interaction. Journal of Medicinal Chemistry, 2020, 63, 13709-13718.	2.9	15
4987	Alternative conformation of the C-domain of the P140 protein from <i>Mycoplasma genitalium</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 508-516.	0.4	2
4988	X-ray structure analysis of a unique <scp>D</scp>-amino-acid oxidase from the thermophilic fungus <i>Rasamsonia emersonii</i> strain YA. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 517-523.	0.4	4
4989	The structural basis for monoclonal antibody 5D2 binding to the tryptophan-rich loop of lipoprotein lipase. Journal of Lipid Research, 2020, 61, 1347-1359.	2.0	11
4990	High-Resolution Crystal Structure of Chloroplastic Ribose-5-Phosphate Isomerase from Chlamydomonas reinhardtiiâ€"An Enzyme Involved in the Photosynthetic Calvin-Benson Cycle. International Journal of Molecular Sciences, 2020, 21, 7787.	1.8	5
4991	Structural and functional analysis of protective antibodies targeting the threefold plateau of enterovirus 71. Nature Communications, 2020, 11, 5253.	5.8	11
4992	Understanding the Pathogenesis of Spondyloarthritis. Biomolecules, 2020, 10, 1461.	1.8	54
4993	Structural and biochemical characterization of inorganic pyrophosphatase from Homo sapiens. Biochemical and Biophysical Research Communications, 2020, 533, 1115-1121.	1.0	6
4995	Bioinspired Design of Dental Functionally Graded Multilayer Structures. , 2020, , 140-166.		0
4996	Bionic Organs. , 2020, , 167-192.		1
4997	Bioinspired Design of Nanostructures. , 2020, , 212-232.		0

#	Article	IF	Citations
4998	Flying of Insects. , 2020, , 271-299.		5
4999	Bioinspired Building Envelopes. , 2020, , 343-354.		0
5001	A Key Glycine in Bacterial Steroid-Degrading Acyl-CoA Dehydrogenases Allows Flavin-Ring Repositioning and Modulates Substrate Side Chain Specificity. Biochemistry, 2020, 59, 4081-4092.	1.2	5
5002	Haptoglobin and the related haptoglobin protein: the N-terminus makes the difference. Journal of Biomolecular Structure and Dynamics, 2020, , 1-10.	2.0	2
5003	Crystal Structure of Mannose Specific IIA Subunit of Phosphotransferase System from Streptococcus pneumoniae. Molecules, 2020, 25, 4633.	1.7	3
5004	Identification and Structure of a Multidonor Class of Head-Directed Influenza-Neutralizing Antibodies Reveal the Mechanism for Its Recurrent Elicitation. Cell Reports, 2020, 32, 108088.	2.9	13
5005	The autoinhibited state of MKK4: Phosphorylation, putative dimerization and R134W mutant studied by molecular dynamics simulations. Computational and Structural Biotechnology Journal, 2020, 18, 2687-2698.	1.9	9
5006	Type III ATP synthase is a symmetry-deviated dimer that induces membrane curvature through tetramerization. Nature Communications, 2020, 11, 5342.	5.8	37
5007	Insight into human Miro1/2 domain organization based on the structure of its N-terminal GTPase. Journal of Structural Biology, 2020, 212, 107656.	1.3	17
5008	Antibiotic binding releases autoinhibition of the TipA multidrug-resistance transcriptional regulator. Journal of Biological Chemistry, 2020, 295, 17865-17876.	1.6	2
5009	Structural insights into the NAD+-dependent formate dehydrogenase mechanism revealed from the NADH complex and the formate NAD+ ternary complex of the Chaetomium thermophilum enzyme. Journal of Structural Biology, 2020, 212, 107657.	1.3	14
5010	Interaction of small molecules with the SARS-CoV-2 main protease in silico and in vitro validation of potential lead compounds using an enzyme-linked immunosorbent assay. Computational Biology and Chemistry, 2020, 89, 107408.	1.1	52
5011	Structural basis of heterotetrameric assembly and disease mutations in the human cis-prenyltransferase complex. Nature Communications, 2020, 11, 5273.	5.8	23
5012	Structure of Epstein-Barr virus tegument protein complex BBRF2-BSRF1 reveals its potential role in viral envelopment. Nature Communications, 2020, 11, 5405.	5.8	11
5013	The structure of a family 110 glycoside hydrolase provides insight into the hydrolysis of Î±-1,3-galactosidic linkages in Î»-carrageenan and blood group antigens. Journal of Biological Chemistry, 2020, 295, 18426-18435.	1.6	8
5014	Identification of a PGXPP degron motif in dishevelled and structural basis for its binding to the E3 ligase KLHL12. Open Biology, 2020, 10, 200041.	1.5	9
5015	Global distribution of single amino acid polymorphisms in <i>Plasmodium vivax</i> Duffy-binding-like domain and implications for vaccine development efforts. Open Biology, 2020, 10, 200180.	1.5	6
5016	Hexachlorobenzene Monooxygenase Substrate Selectivity and Catalysis: Structural and Biochemical Insights. Applied and Environmental Microbiology, 2020, 87, .	1.4	7

#	Article	IF	Citations
5017	Structural mechanism for replication origin binding and remodeling by a metazoan origin recognition complex and its co-loader Cdc6. Nature Communications, 2020, 11, 4263.	5.8	24
5018	Characterization of theÂCorynebacterium glutamicumÂdehydroshikimate dehydratase QsuB and its potential for microbial production of protocatechuic acid. PLoS ONE, 2020, 15, e0231560.	1.1	9
5019	Human Cortical Bone as a Structural Material. , 2020, , 20-44.		0
5020	Shared structural mechanisms of general anaesthetics and benzodiazepines. Nature, 2020, 585, 303-308.	13.7	195
5021	Three-dimensional structure of 22 uncultured ssRNA bacteriophages: Flexibility of the coat protein fold and variations in particle shapes. Science Advances, 2020, 6, .	4.7	6
5022	Symmetry breaking and structural polymorphism in a bacterial microcompartment shell protein for choline utilization. Protein Science, 2020, 29, 2201-2212.	3.1	11
5023	Structure of Arabidopsis HISTONE DEACETYLASE15. Plant Physiology, 2020, 184, 1585-1600.	2.3	13
5024	Recognition of an Î±-helical hairpin in P22 large terminase by a synthetic antibody fragment. Acta Crystallographica Section D: Structural Biology, 2020, 76, 876-888.	1.1	5
5025	X-ray crystallographic structural studies of Î±-amylase I from <i>Eisenia fetida</i>. Acta Crystallographica Section D: Structural Biology, 2020, 76, 834-844.	1.1	3
5026	Structure of a nucleotide pyrophosphatase/phosphodiesterase (NPP) from<i>Euphorbia characias</i>latex characterized by small-angle X-ray scattering: clues for the general organization of plant NPPs. Acta Crystallographica Section D: Structural Biology, 2020, 76, 857-867.	1.1	1
5027	Bamboo-Inspired Materials and Structures. , 2020, , 89-110.		5
5028	Designing Nature-Inspired Liquid-Repellent Surfaces. , 2020, , 300-319.		1
5030	Structure, Folding and Stability of Nucleoside Diphosphate Kinases. International Journal of Molecular Sciences, 2020, 21, 6779.	1.8	19
5031	Structure and function of bacteriophage CBA120 ORF211 (TSP2), the determinant of phage specificity towards E. coli O157:H7. Scientific Reports, 2020, 10, 15402.	1.6	15
5032	Structure and Function of the T4 Spackle Protein Gp61.3. Viruses, 2020, 12, 1070.	1.5	4
5034	The structural basis for the selectivity of sulfonamido dicarbaboranes toward cancer-associated carbonic anhydrase IX. Journal of Enzyme Inhibition and Medicinal Chemistry, 2020, 35, 1800-1810.	2.5	8
5035	Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. Cell, 2020, 183, 457-473.e20.	13.5	30
5036	Biomimetic and Soft Robotics. , 2020, , 320-342.		0

#	Article	IF	Citations
5037	Structural analysis and reaction mechanism of the disproportionating enzyme (Dâ€enzyme) from potato. Protein Science, 2020, 29, 2085-2100.	3.1	9
5038	Structural Basis for the Regulation of Biofilm Formation and Iron Uptake in <i>A. baumannii</i> by the Blue-Light-Using Photoreceptor, BlsA. ACS Infectious Diseases, 2020, 6, 2592-2603.	1.8	14
5039	Structure of an anti-PEG antibody reveals an open ring that captures highly flexible PEG polymers. Communications Chemistry, 2020, 3, .	2.0	40
5040	Targeting SARS-CoV-2 Nsp12/Nsp8 interaction interface with approved and investigational drugs: an <i>in silico</i> structure-based approach. Journal of Biomolecular Structure and Dynamics, 2022, 40, 918-930.	2.0	23
5041	The mechanism of activation of the actin binding protein EHBP1 by Rab8 family members. Nature Communications, 2020, 11, 4187.	5.8	18
5042	Ribosomal synthesis and de novo discovery of bioactive foldamer peptides containing cyclic Î²-amino acids. Nature Chemistry, 2020, 12, 1081-1088.	6.6	86
5043	Cryo-EM reveals the transition of Arp2/3 complex from inactive to nucleation-competent state. Nature Structural and Molecular Biology, 2020, 27, 1009-1016.	3.6	48
5044	Csx3 is a cyclic oligonucleotide phosphodiesterase associated with type III CRISPRâ€"Cas that degrades the second messenger cA4. Journal of Biological Chemistry, 2020, 295, 14963-14972.	1.6	10
5045	Side chain flexibility and the symmetry of protein homodimers. PLoS ONE, 2020, 15, e0235863.	1.1	5
5046	Flexible NAD+ Binding in Deoxyhypusine Synthase Reflects the Dynamic Hypusine Modification of Translation Factor IF5A. International Journal of Molecular Sciences, 2020, 21, 5509.	1.8	4
5047	Structural Insights into the Mechanism of a Nanobody That Stabilizes PAI-1 and Modulates Its Activity. International Journal of Molecular Sciences, 2020, 21, 5859.	1.8	8
5048	Calcium modulates the domain flexibility and function of an Î±-actinin similar to the ancestral Î±-actinin. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22101-22112.	3.3	10
5049	Distinct oligomeric structures of the YoeBâ€"YefM complex provide insights into the conditional cooperativity of type II toxinâ€"antitoxin system. Nucleic Acids Research, 2020, 48, 10527-10541.	6.5	16
5050	Molecular Packing of a Mutant of L-Asparaginase from Wolinella succinigenes in Two Crystal Modifications. Crystallography Reports, 2020, 65, 586-592.	0.1	2
5051	STXBP6, reciprocally regulated with autophagy, reduces triple negative breast cancer aggressiveness. Clinical and Translational Medicine, 2020, 10, e147.	1.7	3
5052	Metal-Mediated Proteinâ€"Cucurbituril Crystalline Architectures. Crystal Growth and Design, 2020, 20, 6983-6989.	1.4	12
5053	The cryoelectron microscopy structure of the human CDK-activating kinase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22849-22857.	3.3	42
5054	Structural characterization of anti-CCL5 activity of the tick salivary protein evasin-4. Journal of Biological Chemistry, 2020, 295, 14367-14378.	1.6	11

#	Article	IF	Citations
5055	DELTEX2 C-terminal domain recognizes and recruits ADP-ribosylated proteins for ubiquitination. Science Advances, 2020, 6, .	4.7	29
5056	Pharmacologic Properties and Preclinical Activity of Sasanlimab, A High-affinity Engineered Anti-Human PD-1 Antibody. Molecular Cancer Therapeutics, 2020, 19, 2105-2116.	1.9	10
5057	Novel bacterial clade reveals origin of form I Rubisco. Nature Plants, 2020, 6, 1158-1166.	4.7	46
5058	Structural insights of the enzymes from the chitin utilization locus of Flavobacterium johnsoniae. Scientific Reports, 2020, 10, 13775.	1.6	9
5059	Fibril structures of diabetes-related amylin variants reveal a basis for surface-templated assembly. Nature Structural and Molecular Biology, 2020, 27, 1048-1056.	3.6	71
5060	Cryo-EM structure of the entire mammalian F-type ATP synthase. Nature Structural and Molecular Biology, 2020, 27, 1077-1085.	3.6	122
5061	Loss-of-function maternal-effect mutations of PADI6 are associated with familial and sporadic Beckwith-Wiedemann syndrome with multi-locus imprinting disturbance. Clinical Epigenetics, 2020, 12, 139.	1.8	40
5062	Agonist Binding and G Protein Coupling in Histamine H2 Receptor: A Molecular Dynamics Study. International Journal of Molecular Sciences, 2020, 21, 6693.	1.8	10
5063	Tetherin downmodulation by SIVmac Nef lost with the H196Q escape variant is restored by an upstream variant. PLoS ONE, 2020, 15, e0225420.	1.1	3
5064	Improved therapeutic efficacy of quercetin-loaded polymeric nanoparticles on triple-negative breast cancer by inhibiting uPA. RSC Advances, 2020, 10, 34517-34526.	1.7	21
5065	Molecular basis of the potential interaction of SARS-CoV-2 spike protein to CD147 in COVID-19 associated-lymphopenia. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1109-1119.	2.0	62
5066	Berichtigung: Pac13 is a Small Dehydratase that Mediates the Formation of the 3â€²â€Deoxy Nucleoside of Pacidamycins. Angewandte Chemie, 2020, 132, 12673-12673.	1.6	1
5067	Bioinspired Design of Multilayered Composites. , 2020, , 45-88.		0
5068	Structural Aspects of the Allergen-Antibody Interaction. Frontiers in Immunology, 2020, 11, 2067.	2.2	29
5069	NME/NM23/NDPK and Histidine Phosphorylation. International Journal of Molecular Sciences, 2020, 21, 5848.	1.8	24
5070	The Structure of the Cysteine-Rich Domain of Plasmodium falciparum P113 Identifies the Location of the RH5 Binding Site. MBio, 2020, 11, .	1.8	7
5071	Allosteric regulation of lysosomal enzyme recognition by the cation-independent mannose 6-phosphate receptor. Communications Biology, 2020, 3, 498.	2.0	20
5072	Decoding the intricate network of molecular interactions of a hyperstable engineered biocatalyst. Chemical Science, 2020, 11, 11162-11178.	3.7	13

#	ARTICLE	IF	CITATIONS
5073	Comprehensive analysis of IncC plasmid conjugation identifies a crucial role for the transcriptional regulator AcaB. Nature Microbiology, 2020, 5, 1340-1348.	5.9	23
5074	BTN3A1 governs antitumor responses by coordinating Î±Î² and Î³Î´ T cells. Science, 2020, 369, 942-949.	6.0	83
5075	Binding of dipeptidyl peptidase III to the oxidative stress cell sensor Kelch-like ECH-associated protein 1 is a two-step process. Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-12.	2.0	7
5076	Structural basis for the multimerization of nonstructural protein nsp9 from SARS-CoV-2. Molecular Biomedicine, 2020, 1, 5.	1.7	21
5077	Structural basis for transcriptional coactivator recognition by SMAD2 in TGF-Î² signaling. Science Signaling, 2020, 13, .	1.6	6
5078	Assembly of the asymmetric human Î³-tubulin ring complex by RUVBL1-RUVBL2 AAA ATPase. Science Advances, 2020, 6, .	4.7	34
5079	Dissecting the Mechanism of (<i>R</i>)-3-Hydroxybutyrate Dehydrogenase by Kinetic Isotope Effects, Protein Crystallography, and Computational Chemistry. ACS Catalysis, 2020, 10, 15019-15032.	5.5	8
5080	Divergent architecture of the heterotrimeric NatC complex explains N-terminal acetylation of cognate substrates. Nature Communications, 2020, 11, 5506.	5.8	23
5081	Molecular basis for RNA polymerase-dependent transcription complex recycling by the helicase-like motor protein HelD. Nature Communications, 2020, 11, 6420.	5.8	29
5082	Structural Insight into the Contributions of the N-Terminus and Key Active-Site Residues to the Catalytic Efficiency of Glutamine Synthetase 2. Biomolecules, 2020, 10, 1671.	1.8	3
5083	<i>In silico</i> analysis of kiss2, expression studies and proteinâ€“protein interaction with gonadotropin-releasing hormone 2 (GnRH2) and luteinizing hormone beta (LHÎ²) in <i>Heteropneustes fossilis</i>. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4543-4557.	2.0	4
5084	Fermented Soy-Derived Bioactive Peptides Selected by a Molecular Docking Approach Show Antioxidant Properties Involving the Keap1/Nrf2 Pathway. Antioxidants, 2020, 9, 1306.	2.2	41
5085	Molecular Packing Interaction in DNA Crystals. Crystals, 2020, 10, 1093.	1.0	3
5086	Not Cleaving the His-tag of Thal Results in More Tightly Packed and Better-Diffracting Crystals. Crystals, 2020, 10, 1135.	1.0	1
5087	Structural Characterization of Glycerol Kinase from the Thermophilic Fungus Chaetomium thermophilum. International Journal of Molecular Sciences, 2020, 21, 9570.	1.8	8
5088	Structural bioinformatic survey of protein-small molecule interfaces delineates the role of glycine in surface pocket formation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	1.9	2
5089	A structurally unique Fusobacterium nucleatum tannase provides detoxicant activity against gallotannins and pathogen resistance. Microbial Biotechnology, 2020, , .	2.0	3
5090	Receptor-gated IL-2 delivery by an anti-human IL-2 antibody activates regulatory T cells in three different species. Science Translational Medicine, 2020, 12, .	5.8	49

#	Article	IF	Citations
5091	Fatal outcome after heart surgery in PMM2-CDG due to a rare homozygous gene variant with double effects. Molecular Genetics and Metabolism Reports, 2020, 25, 100673.	0.4	5
5092	Structural insights and evaluation of the potential impact of missense variants on the interactions of SLIT2 with ROBO1/4 in cancer progression. Scientific Reports, 2020, 10, 21909.	1.6	1
5093	HEPN-MNT Toxin-Antitoxin System: The HEPN Ribonuclease Is Neutralized by OligoAMPylation. Molecular Cell, 2020, 80, 955-970.e7.	4.5	19
5094	An improved fluorescent tag and its nanobodies for membrane protein expression, stability assay, and purification. Communications Biology, 2020, 3, 753.	2.0	20
5095	Structure and Characterization of Phosphoglucomutase 5 from Atlantic and Baltic Herringâ€"An Inactive Enzyme with Intact Substrate Binding. Biomolecules, 2020, 10, 1631.	1.8	4
5096	Protein Crystallization in the Presence of a Metastable Liquidâ€"Liquid Phase Separation. Crystal Growth and Design, 2020, 20, 7951-7962.	1.4	17
5097	The crystal structure of AjiA1 reveals a novel structural motion mechanism in the adenylate-forming enzyme family. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1201-1210.	1.1	2
5098	GAG-DB, the New Interface of the Three-Dimensional Landscape of Glycosaminoglycans. Biomolecules, 2020, 10, 1660.	1.8	16
5099	Modulation of Guanylate Cyclase Activating Protein 1 (GCAP1) Dimeric Assembly by Ca2+ or Mg2+: Hints to Understand Protein Activity. Biomolecules, 2020, 10, 1408.	1.8	11
5100	Functional Cross-Talk of MbtH-Like Proteins During Thaxtomin Biosynthesis in the Potato Common Scab Pathogen Streptomyces scabiei. Frontiers in Microbiology, 2020, 11, 585456.	1.5	2
5101	Identification and characterization of a rare variant in apolipoprotein A-IV, p.(V336M), and evaluation of HDL functionality in a Greek cohort with extreme HDL cholesterol levels. Archives of Biochemistry and Biophysics, 2020, 696, 108655.	1.4	1
5102	Structural Insight on Functional Regulation of Human MINERVA Protein. International Journal of Molecular Sciences, 2020, 21, 8186.	1.8	2
5103	Solution NMR structure of Se0862, a highly conserved cyanobacterial protein involved in biofilm formation. Protein Science, 2020, 29, 2274-2280.	3.1	8
5104	Thermodynamic Analysis of Point Mutations Inhibiting High-Temperature Reversible Oligomerization of PDZ3. Biophysical Journal, 2020, 119, 1391-1401.	0.2	6
5105	Examination of the Role of Mg²⁺ in the Mechanism of Nucleotide Binding to the Monomeric YME1L AAA+ Domain. Biochemistry, 2020, 59, 4303-4320.	1.2	3
5106	Translating the Concept of Bispecific Antibodies to Engineering Heterodimeric Phosphotriesterases with Broad Organophosphate Substrate Recognition. Biochemistry, 2020, 59, 4395-4406.	1.2	8
5107	Rings of Power: Enzymatic Routes to Î²-Lactones. , 2020, , 323-345.		3
5108	Structural and Functional Study of the <i>Klebsiella pneumoniae</i> VapBC Toxinâ€"Antitoxin System, Including the Development of an Inhibitor That Activates VapC. Journal of Medicinal Chemistry, 2020, 63, 13669-13679.	2.9	9

#	ARTICLE	IF	CITATIONS
5109	The New Dipeptide TSPO Ligands: Design, Synthesis and Structureâ€"Anxiolytic Activity Relationship. Molecules, 2020, 25, 5132.	1.7	8
5110	Two VHH Antibodies Neutralize Botulinum Neurotoxin E1 by Blocking Its Membrane Translocation in Host Cells. Toxins, 2020, 12, 616.	1.5	6
5111	Features of the Three Dimensional Structure of the Mutant Form of Wolinella succinogenes L-Asparaginase in Complexes with L-Aspartic and L-Glutamic Acids. Russian Journal of Bioorganic Chemistry, 2020, 46, 171-180.	0.3	4
5112	The Kalimantacin Polyketide Antibiotics Inhibit Fatty Acid Biosynthesis in <i>Staphylococcus aureus</i> by Targeting the Enoylâ€Acyl Carrier Protein Binding Site of FabI. Angewandte Chemie, 2020, 132, 10636-10643.	1.6	6
5113	Cryo-EM Structure of the Fork Protection Complex Bound to CMG at a Replication Fork. Molecular Cell, 2020, 78, 926-940.e13.	4.5	111
5114	Structure of P46, an immunodominant surface protein from<i>Mycoplasma hyopneumoniae</i>: interaction with a monoclonal antibody. Acta Crystallographica Section D: Structural Biology, 2020, 76, 418-427.	1.1	4
5115	Neutralization Mechanism of a Monoclonal Antibody Targeting a Porcine Circovirus Type 2 Cap Protein Conformational Epitope. Journal of Virology, 2020, 94, .	1.5	20
5116	Mutation-Associated Phenotypic Heterogeneity in Novel and Canonical PIK3CA Helical and Kinase Domain Mutants. Cells, 2020, 9, 1116.	1.8	6
5117	A terminal Î±3-galactose modification regulates an E3 ubiquitin ligase subunit in Toxoplasma gondii. Journal of Biological Chemistry, 2020, 295, 9223-9243.	1.6	6
5118	Exploring the Molecular Basis for Substrate Affinity and Structural Stability in Bacterial GH39 Î²-Xylosidases. Frontiers in Bioengineering and Biotechnology, 2020, 8, 419.	2.0	11
5119	Origin of complexity in haemoglobin evolution. Nature, 2020, 581, 480-485.	13.7	89
5120	CD95 Structure, Aggregation and Cell Signaling. Frontiers in Cell and Developmental Biology, 2020, 8, 314.	1.8	28
5121	HPV Infection Affects Human Sperm Functionality by Inhibition of Aquaporin-8. Cells, 2020, 9, 1241.	1.8	21
5122	Structural basis for the complex DNA binding behavior of the plant stem cell regulator WUSCHEL. Nature Communications, 2020, 11, 2223.	5.8	22
5123	Structural and functional insights into oligopeptide acquisition by the RagAB transporter from Porphyromonas gingivalis. Nature Microbiology, 2020, 5, 1016-1025.	5.9	46
5124	Crystal structure of gluconate 5-dehydrogenase from <i>Lentibacter algarum</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 228-234.	0.4	0
5125	AlloSigMA 2: paving the way to designing allosteric effectors and to exploring allosteric effects of mutations. Nucleic Acids Research, 2020, 48, W116-W124.	6.5	57
5126	In silico features of ADAMTS13 contributing to plasmatic ADAMTS13 levels in neonates with congenital heart disease. Thrombosis Research, 2020, 193, 66-76.	0.8	2

#	Article	IF	Citations
5127	X-ray structure of C-phycocyanin from Galdieria phlegrea: Determinants of thermostability and comparison with a C-phycocyanin in the entire phycobilisome. Biochimica Et Biophysica Acta - Bioenergetics, 2020, 1861, 148236.	0.5	18
5128	Structureâ€"Function Studies of the Antibiotic Target <scp>l</scp>,<scp>l</scp>-Diaminopimelate Aminotransferase from <i>Verrucomicrobium spinosum</i> Reveal an Unusual Oligomeric Structure. Biochemistry, 2020, 59, 2274-2288.	1.2	0
5129	Methionine-Rich Loop of Multicopper Oxidase McoA Follows Open-to-Close Transitions with a Role in Enzyme Catalysis. ACS Catalysis, 2020, 10, 7162-7176.	5.5	15
5130	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. Nature, 2020, 585, 293-297.	13.7	219
5131	Diversity in kinetics correlated with structure in nano body-stabilized LacY. PLoS ONE, 2020, 15, e0232846.	1.1	3
5132	Legionella effector MavC targets the Ube2N~Ub conjugate for noncanonical ubiquitination. Nature Communications, 2020, 11, 2365.	5.8	21
5133	Structural insight into tanapoxvirusâ€mediated inhibition of apoptosis. FEBS Journal, 2020, 287, 3733-3750.	2.2	11
5134	Crystal Structure and Active Site Engineering of a Halophilic Î³-Carbonic Anhydrase. Frontiers in Microbiology, 2020, 11, 742.	1.5	16
5135	Plant Proteomics. Methods in Molecular Biology, 2020, , .	0.4	4
5136	Structural Insights into the Mechanism of the Radical SAM Carbide Synthase NifB, a Key Nitrogenase Cofactor Maturating Enzyme. Journal of the American Chemical Society, 2020, 142, 11006-11012.	6.6	25
5137	International Union of Basic and Clinical Pharmacology. CVIII. Calcium-Sensing Receptor Nomenclature, Pharmacology, and Function. Pharmacological Reviews, 2020, 72, 558-604.	7.1	59
5138	These motors were made for walking. Protein Science, 2020, 29, 1707-1723.	3.1	17
5139	Structureâ€"function analysis of silkworm sucrose hydrolase uncovers the mechanism of substrate specificity in GH13 subfamily 17 exo-Î±-glucosidases. Journal of Biological Chemistry, 2020, 295, 8784-8797.	1.6	7
5140	Structural basis for membrane insertion by the human ER membrane protein complex. Science, 2020, 369, 433-436.	6.0	127
5141	Design of a surrogate Anticalin protein directed against <scp>CD98hc</scp> for preclinical studies in mice. Protein Science, 2020, 29, 1774-1783.	3.1	3
5142	Interaction of the prototypical Î±-ketoamide inhibitor with the SARS-CoV-2 main protease active site in silico: Molecular dynamic simulations highlight the stability of the ligand-protein complex. Computational Biology and Chemistry, 2020, 87, 107292.	1.1	64
5143	Principles of lipidâ€"enzyme interactions in the limbus region of the catalytic site of Candida antarctica Lipase B. International Journal of Biological Macromolecules, 2020, 158, 358-363.	3.6	19
5144	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. Nature Communications, 2020, 11, 2688.	5.8	304

#	Article	IF	Citations
5145	Structural basis for the binding of SNAREs to the multisubunit tethering complex Dsl1. Journal of Biological Chemistry, 2020, 295, 10125-10135.	1.6	18
5146	Structure and mechanism of the Nap adhesion complex from the human pathogen Mycoplasma genitalium. Nature Communications, 2020, 11, 2877.	5.8	19
5147	Structure and function of a flavin-dependent S-monooxygenase from garlic (Allium sativum). Journal of Biological Chemistry, 2020, 295, 11042-11055.	1.6	14
5148	Structural studies of geranylgeranylglyceryl phosphate synthase, a prenyltransferase found in thermophilic Euryarchaeota. Acta Crystallographica Section D: Structural Biology, 2020, 76, 542-557.	1.1	2
5149	Structural basis of prostate-specific membrane antigen recognition by the A9g RNA aptamer. Nucleic Acids Research, 2020, 48, 11130-11145.	6.5	15
5150	mRNA Interferase Bacillus cereus BC0266 Shows MazF-Like Characteristics Through Structural and Functional Study. Toxins, 2020, 12, 380.	1.5	4
5151	Identification of intermolecular bonds between human factor B and Cobra Venom Factor important for C3 convertase stability. Toxicon, 2020, 184, 68-77.	0.8	1
5152	Coiledâ€coil registry shifts in the <scp>F684I</scp> mutant of Bicaudal D result in cargoâ€independent activation of dynein motility. Traffic, 2020, 21, 463-478.	1.3	9
5153	Cryo-EM structures of NPC1L1 reveal mechanisms of cholesterol transport and ezetimibe inhibition. Science Advances, 2020, 6, eabb1989.	4.7	49
5154	Structural Characterization of TssL from Acinetobacter baumannii: a Key Component of the Type VI Secretion System. Journal of Bacteriology, 2020, 202, .	1.0	5
5155	Selective interactions between mimivirus uracil-DNA glycosylase and inhibitory proteins determined by a single amino acid. Journal of Structural Biology, 2020, 211, 107552.	1.3	3
5156	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. PLoS Pathogens, 2020, 16, e1008652.	2.1	44
5157	The key role of E418 carboxyl group in the formation of Nt.BspD6I nickase active site: Structural and functional properties of Nt.BspD6I E418A mutant. Journal of Structural Biology, 2020, 210, 107508.	1.3	1
5158	Crystal structure of the YoeBSa1-YefMSa1 complex from Staphylococcus aureus. Biochemical and Biophysical Research Communications, 2020, 527, 264-269.	1.0	1
5159	Rational design of a multi-valent human papillomavirus vaccine by capsomere-hybrid co-assembly of virus-like particles. Nature Communications, 2020, 11, 2841.	5.8	16
5160	A disulfide constrains the ToxR periplasmic domain structure, altering its interactions with ToxS and bile-salts. Scientific Reports, 2020, 10, 9002.	1.6	8
5161	T54R mutation destabilizes the dimer of superoxide dismutase 1^{T54R} by inducing steric clashes at the dimer interface. RSC Advances, 2020, 10, 10776-10788.	1.7	14
5162	Inactive dimeric structure of the protease domain of stomatin operon partner protein. Acta Crystallographica Section D: Structural Biology, 2020, 76, 515-520.	1.1	0

#	Article	IF	Citations
5163	SpeG polyamine acetyltransferase enzyme from Bacillus thuringiensis forms a dodecameric structure and exhibits high catalytic efficiency. Journal of Structural Biology, 2020, 210, 107506.	1.3	5
5164	Structural and functional evidence of bacterial antiphage protection by Thoeris defense system via NAD+ degradation. Nature Communications, 2020, 11, 2816.	5.8	68
5165	Structural Basis for Broad Substrate Selectivity of Alcohol Dehydrogenase YjgB from Escherichia coli. Molecules, 2020, 25, 2404.	1.7	2
5166	The Discovery of a Putative Allosteric Site in the SARS-CoV-2 Spike Protein Using an Integrated Structural/Dynamic Approach. Journal of Proteome Research, 2020, 19, 4576-4586.	1.8	66
5167	Neutralization of SARS-CoV-2 by Destruction of the Prefusion Spike. Cell Host and Microbe, 2020, 28, 445-454.e6.	5.1	298
5168	Human XPG nuclease structure, assembly, and activities with insights for neurodegeneration and cancer from pathogenic mutations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14127-14138.	3.3	37
5169	Structural and biochemical characterization of mitochondrial citrate synthase 4 from <i>Arabidopsis thaliana</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 109-115.	0.4	5
5170	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. Journal of Proteome Research, 2020, 19, 3478-3486.	1.8	19
5171	Uncovering the chemistry of Câ€“C bond formation in C-nucleoside biosynthesis: crystal structure of a C-glycoside synthase/PRPP complex. Chemical Communications, 2020, 56, 7617-7620.	2.2	15
5172	The structure of the extracellular domains of human interleukin 11Î± receptor reveals mechanisms of cytokine engagement. Journal of Biological Chemistry, 2020, 295, 8285-8301.	1.6	33
5173	CryoEM structures of human CMGâ€“ATPÎ³Sâ€“DNA and CMGâ€“AND-1 complexes. Nucleic Acids Research, 2020, 48, 6980-6995.	6.5	56
5174	Mechanism of effector capture and delivery by the type IV secretion system from Legionella pneumophila. Nature Communications, 2020, 11, 2864.	5.8	37
5175	Cellular and Structural Basis of Synthesis of the Unique Intermediate Dehydro-F ₄₂₀ -0 in Mycobacteria. MSystems, 2020, 5, .	1.7	9
5176	Crystal Structure of Flagellar Export Chaperone FliS in Complex With Flagellin and HP1076 of Helicobacter pylori. Frontiers in Microbiology, 2020, 11, 787.	1.5	6
5177	Molecular Mechanism of Regulation of the Purine Salvage Enzyme XPRT by the Alarmones pppGpp, ppGpp, and pGpp. Journal of Molecular Biology, 2020, 432, 4108-4126.	2.0	31
5178	Targeting epigenetic proteinâ€“protein interactions with small-molecule inhibitors. Future Medicinal Chemistry, 2020, 12, 1305-1326.	1.1	12
5179	Conformational changes in a Vernier zone region: Implications for antibody dual specificity. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1447-1457.	1.5	5
5180	The Structural Basis of T4 Phage Lysis Control: DNA as the Signal for Lysis Inhibition. Journal of Molecular Biology, 2020, 432, 4623-4636.	2.0	16

#	Article	IF	Citations
5181	Structural basis for loading and inhibition of a bacterial T6 <scp>SS</scp> phospholipase effector by the VgrG spike. EMBO Journal, 2020, 39, e104129.	3.5	31
5182	SjÃ¶gren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. Communications Biology, 2020, 3, 123.	2.0	5
5183	Structural and functional insights into a novel two-component endolysin encoded by a single gene in Enterococcus faecalis phage. PLoS Pathogens, 2020, 16, e1008394.	2.1	24
5184	Substrate Recognition and Catalytic Mechanism of the Phosphate Acyltransferase PlsX fromBacillus subtilis. ChemBioChem, 2020, 21, 2019-2028.	1.3	1
5185	Structural basis of cell-surface signaling by a conserved sigma regulator in Gram-negative bacteria. Journal of Biological Chemistry, 2020, 295, 5795-5806.	1.6	3
5186	Binding Options for the Small Subunit-Like Domain of Cyanobacteria to Rubisco. Frontiers in Microbiology, 2020, 11, 187.	1.5	2
5187	Structural Analysis Reveals that the Cytokine IL-17F Forms a Homodimeric Complex with Receptor IL-17RC to Drive IL-17RA-Independent Signaling. Immunity, 2020, 52, 499-512.e5.	6.6	55
5188	Structure of mouse coronavirus spike protein complexed with receptor reveals mechanism for viral entry. PLoS Pathogens, 2020, 16, e1008392.	2.1	126
5189	Involvement of the Î±-helical and Src homology 3 domains in the molecular assembly and enzymatic activity of human Î±1,6-fucosyltransferase, FUT8. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129596.	1.1	11
5190	Neighborhood Preference of Amino Acids in Protein Structures and its Applications in Protein Structure Assessment. Scientific Reports, 2020, 10, 4371.	1.6	6
5191	Stepwise Promoter Melting by Bacterial RNA Polymerase. Molecular Cell, 2020, 78, 275-288.e6.	4.5	88
5192	Insights into the stability and substrate specificity of the E. coli aerobic Î²-oxidation trifunctional enzyme complex. Journal of Structural Biology, 2020, 210, 107494.	1.3	10
5193	Structural elucidation of the <i>Clostridioides difficile</i> transferase toxin reveals a single-site binding mode for the enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6139-6144.	3.3	17
5194	ClusPro in rounds 38 to 45 of CAPRI: Toward combining templateâ€based methods with free docking. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1082-1090.	1.5	5
5195	Full-length human GLP-1 receptor structure without orthosteric ligands. Nature Communications, 2020, 11, 1272.	5.8	83
5196	A bifunctional O-antigen polymerase structure reveals a new glycosyltransferase family. Nature Chemical Biology, 2020, 16, 450-457.	3.9	26
5197	Drosophila OTK Is a Glycosaminoglycan-Binding Protein with High Conformational Flexibility. Structure, 2020, 28, 507-515.e5.	1.6	2
5198	The cryo-EM structure of the SNXâ€“BAR Mvp1 tetramer. Nature Communications, 2020, 11, 1506.	5.8	22

#	ARTICLE	IF	CITATIONS
5199	Molecular dissection of pheromone selectivity in the competence signaling system ComRS of streptococci. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7745-7754.	3.3	8
5200	Structural and mutational analyses of the bifunctional arginine dihydrolase and ornithine cyclodeaminase AgrE from the cyanobacterium Anabaena. Journal of Biological Chemistry, 2020, 295, 5751-5760.	1.6	7
5201	The Kalimantacin Polyketide Antibiotics Inhibit Fatty Acid Biosynthesis in Staphylococcus aureus by Targeting the Enoylâ€Acyl Carrier Protein Binding Site of FabI. Angewandte Chemie - International Edition, 2020, 59, 10549-10556.	7.2	20
5202	Synthetic antibodies against BRIL as universal fiducial marks for singleâˆ'particle cryoEM structure determination of membrane proteins. Nature Communications, 2020, 11, 1598.	5.8	57
5203	In silico analysis of the structural diversity and interactions between invertases and invertase inhibitors from potato (Solanum tuberosum L.). 3 Biotech, 2020, 10, 178.	1.1	7
5204	Identification of MLKL membrane translocation as a checkpoint in necroptotic cell death using Monobodies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8468-8475.	3.3	64
5205	A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. Science, 2020, 368, 630-633.	6.0	1,379
5206	A thermophilic phage uses a small terminase protein with a fixed helixâ€"turnâ€"helix geometry. Journal of Biological Chemistry, 2020, 295, 3783-3793.	1.6	7
5207	The basis for non-canonical ROK family function in the N-acetylmannosamine kinase from the pathogen Staphylococcus aureus. Journal of Biological Chemistry, 2020, 295, 3301-3315.	1.6	13
5208	The crystal structure of the tetrameric DABAâ€aminotransferase EctB, a rateâ€limiting enzyme in the ectoine biosynthesis pathway. FEBS Journal, 2020, 287, 4641-4658.	2.2	10
5209	A triclosanâ€resistance protein from the soil metagenome is a novel enoylâ€acyl carrier protein reductase: Structureâ€guided functional analysis. FEBS Journal, 2020, 287, 4710-4728.	2.2	6
5210	Biological vs. Crystallographic Protein Interfaces: An Overview of Computational Approaches for Their Classification. Crystals, 2020, 10, 114.	1.0	15
5211	Novel Genetically Encoded Bright Positive Calcium Indicator NCaMP7 Based on the mNeonGreen Fluorescent Protein. International Journal of Molecular Sciences, 2020, 21, 1644.	1.8	33
5212	N-terminal Backbone Pairing Shifts in CCL5-12AAA14 Dimer Interface: Structural Significance of the FAY Sequence. International Journal of Molecular Sciences, 2020, 21, 1689.	1.8	1
5213	ProNA2020 predicts proteinâ€"DNA, proteinâ€"RNA, and proteinâ€"protein binding proteins and residues from sequence. Journal of Molecular Biology, 2020, 432, 2428-2443.	2.0	67
5214	Conformational flexibility of coenzyme A and its impact on the postâ€translational modification of acyl carrier proteins by 4â€²â€phosphopantetheinyl transferases. FEBS Journal, 2020, 287, 4729-4746.	2.2	4
5215	The Dual PDZ Domain from Postsynaptic Density Protein 95 Forms a Scaffold with Peptide Ligand. Biophysical Journal, 2020, 119, 667-689.	0.2	9
5216	Structural basis of semaphorinâ€plexin <i>cis</i> interaction. EMBO Journal, 2020, 39, e102926.	3.5	17

#	Article	IF	Citations
5217	Recognition of Semaphorin Proteins by P.Âsordellii Lethal Toxin Reveals Principles of Receptor Specificity in Clostridial Toxins. Cell, 2020, 182, 345-356.e16.	13.5	29
5218	Structural basis for the hydrolytic dehalogenation of the fungicide chlorothalonil. Journal of Biological Chemistry, 2020, 295, 8668-8677.	1.6	4
5219	CoRNeA: A Pipeline to Decrypt the Inter-Protein Interfaces from Amino Acid Sequence Information. Biomolecules, 2020, 10, 938.	1.8	6
5220	Structure and Dynamics of a Thermostable Alcohol Dehydrogenase from the Antarctic Psychrophile <i>Moraxella</i> sp. TAE123. ACS Omega, 2020, 5, 14523-14534.	1.6	12
5221	Crystal structure of TEX101, a glycoprotein essential for male fertility, reveals the presence of tandemly arranged Ly6/uPAR domains. FEBS Letters, 2020, 594, 3020-3031.	1.3	4
5222	Larger active site in an ancestral hydroxynitrile lyase increases catalytically promiscuous esterase activity. PLoS ONE, 2020, 15, e0235341.	1.1	13
5223	Crystal structure and specific location of a germin-like protein with proteolytic activity from Thevetia peruviana. Plant Science, 2020, 298, 110590.	1.7	2
5224	Maturation of the functional mouse CRES amyloid from globular form. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16363-16372.	3.3	7
5225	Structural analysis of avibactam-mediated activation of the bla and mec divergons in methicillin-resistant Staphylococcus aureus. Journal of Biological Chemistry, 2020, 295, 10870-10884.	1.6	7
5226	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. Science Signaling, 2020, 13, .	1.6	12
5227	Addressing the Molecular Mechanism of Longitudinal Lamin Assembly Using Chimeric Fusions. Cells, 2020, 9, 1633.	1.8	10
5228	DiB-splits: nature-guided design of a novel fluorescent labeling split system. Scientific Reports, 2020, 10, 11049.	1.6	6
5229	Extensive sequence and structural evolution of Arginase 2 inhibitory antibodies enabled by an unbiased approach to affinity maturation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16949-16960.	3.3	10
5230	Structural and Functional Insights into the C-terminal Fragment of Insecticidal Vip3A Toxin of Bacillus thuringiensis. Toxins, 2020, 12, 438.	1.5	18
5231	Mechanism of Astragalus membranaceus in the treatment of laryngeal cancer based on gene co-expression network and molecular docking. Scientific Reports, 2020, 10, 11184.	1.6	9
5232	Atomic structure of the <i>Campylobacter jejuni</i> flagellar filament reveals how Îµ Proteobacteria escaped Toll-like receptor 5 surveillance. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16985-16991.	3.3	30
5233	Functional diversification in the <i>Nudix hydrolase</i> gene family drives sesquiterpene biosynthesis in <i>Rosa</i> Ã— <i>wichurana</i>. Plant Journal, 2020, 104, 185-199.	2.8	21
5234	Restriction of HIV-1 Escape by a Highly Broad and Potent Neutralizing Antibody. Cell, 2020, 180, 471-489.e22.	13.5	106

#	ARTICLE	IF	CITATIONS
5235	Structural Insights into RNA Dimerization: Motifs, Interfaces and Functions. Molecules, 2020, 25, 2881.	1.7	28
5236	Inhibition and Crystal Structure of the Human DHTKD1-Thiamin Diphosphate Complex. ACS Chemical Biology, 2020, 15, 2041-2047.	1.6	14
5237	Structural basis of human full-length kindlin-3 homotrimer in an auto-inhibited state. PLoS Biology, 2020, 18, e3000755.	2.6	26
5238	Evaluating the Potential for Cross-Interactions of Antitoxins in Type II TA Systems. Toxins, 2020, 12, 422.	1.5	7
5239	Homodimerization of a glycoside hydrolase family <scp>GH1</scp> Î²â€glucosidase suggests distinct activity of enzyme different states. Protein Science, 2020, 29, 1879-1889.	3.1	6
5240	Architecture and functional dynamics of the pentafunctional AROM complex. Nature Chemical Biology, 2020, 16, 973-978.	3.9	8
5241	Structural and biochemical characterization of novel carbonic anhydrases from<i>Phaeodactylum tricornutum</i>. Acta Crystallographica Section D: Structural Biology, 2020, 76, 676-686.	1.1	10
5242	Insight to the residue in P2 position prevents the peptide inhibitor from being hydrolyzed by serine proteases. Bioscience, Biotechnology and Biochemistry, 2020, 84, 1153-1159.	0.6	1
5243	Structures of human galectin-10/monosaccharide complexes demonstrate potential of monosaccharides as effectors in forming Charcot-Leyden crystals. Biochemical and Biophysical Research Communications, 2020, 525, 87-93.	1.0	6
5244	Cryo-EM structure of the Shigella type III needle complex. PLoS Pathogens, 2020, 16, e1008263.	2.1	36
5245	Structural Insights into Rational Design of Single-Domain Antibody-Based Antitoxins against Botulinum Neurotoxins. Cell Reports, 2020, 30, 2526-2539.e6.	2.9	24
5246	Fluorescence spectroscopy and molecular modeling of anthocyanins binding to bovine lactoferrin peptides. Food Chemistry, 2020, 318, 126508.	4.2	30
5247	Crystal Structure of the Chloroplastic Glutamine Phosphoribosylpyrophosphate Amidotransferase GPRAT2 From Arabidopsis thaliana. Frontiers in Plant Science, 2020, 11, 157.	1.7	5
5248	Model Reconstruction from Small-Angle X-Ray Scattering Data Using Deep Learning Methods. IScience, 2020, 23, 100906.	1.9	27
5249	Crystal structure of the translation recovery factor Trf from SulfolobusÂsolfataricus. FEBS Open Bio, 2020, 10, 221-228.	1.0	1
5250	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered Î´-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7.	2.9	35
5251	Multivalent interactions between CsoS2 and Rubisco mediate Î±-carboxysome formation. Nature Structural and Molecular Biology, 2020, 27, 281-287.	3.6	110
5252	Cryo-EM structures reveal translocational unfolding in the clostridial binary iota toxin complex. Nature Structural and Molecular Biology, 2020, 27, 288-296.	3.6	21

#	ARTICLE	IF	CITATIONS
5253	Structural analyses of the Group A flavin-dependent monooxygenase PieE reveal a sliding FAD cofactor conformation bridging OUT and IN conformations. Journal of Biological Chemistry, 2020, 295, 4709-4722.	1.6	9
5254	Restricted epitope specificity determined by variable region germline segment pairing in rodent antibody repertoires. MAbs, 2020, 12, 1722541.	2.6	6
5255	Structure-Function Analyses of a Keratin Heterotypic Complex Identify Specific Keratin Regions Involved in Intermediate Filament Assembly. Structure, 2020, 28, 355-362.e4.	1.6	19
5256	Carbohydrate-Binding Capability and Functional Conformational Changes of AbnE, an Arabino-oligosaccharide Binding Protein. Journal of Molecular Biology, 2020, 432, 2099-2120.	2.0	5
5257	The Catalytic Acidâ€“Base in GH109 Resides in a Conserved GGHGG Loop and Allows for Comparable Î±-Retaining and Î²-Inverting Activity in an <i>N</i>-Acetylgalactosaminidase from <i>Akkermansia muciniphila</i>. ACS Catalysis, 2020, 10, 3809-3819.	5.5	15
5258	Quaternary Structure of the Tryptophan Synthase Î±-Subunit Homolog BX1 from <i>Zea mays</i>. Journal of the American Society for Mass Spectrometry, 2020, 31, 227-233.	1.2	4
5259	Structural basis for disulphide-CoA inhibition of a butyryl-CoA hexameric thioesterase. Journal of Structural Biology, 2020, 210, 107477.	1.3	1
5260	Hydrogen molecules can modulate enzymatic activity and structural properties of pepsin in vitro. Colloids and Surfaces B: Biointerfaces, 2020, 189, 110856.	2.5	12
5261	Conditional Disorder in Small Heat-shock Proteins. Journal of Molecular Biology, 2020, 432, 3033-3049.	2.0	21
5262	The Molecular Mechanism of Polymer Formation of Farnesylated Human Guanylate-binding Protein 1. Journal of Molecular Biology, 2020, 432, 2164-2185.	2.0	23
5263	Massively parallel variant characterization identifies <i>NUDT15</i> alleles associated with thiopurine toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5394-5401.	3.3	95
5264	Trinuclear copper biocatalytic center forms an active site of thiocyanate dehydrogenase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5280-5290.	3.3	19
5265	Conformation-specific inhibitors of activated Ras GTPases reveal limited Ras dependency of patient-derived cancer organoids. Journal of Biological Chemistry, 2020, 295, 4526-4540.	1.6	19
5266	Structure-function analyses of alkylhydroperoxidase D from Streptococcus pneumoniae reveal an unusual three-cysteine active site architecture. Journal of Biological Chemistry, 2020, 295, 2984-2999.	1.6	4
5267	An Optogenetic Tool for Induced Protein Stabilization Based on the Phaeodactylum tricornutum Aureochrome 1a Lightâ€“Oxygenâ€“Voltage Domain. Journal of Molecular Biology, 2020, 432, 1880-1900.	2.0	22
5268	Crystal structure of Alr1298, a pentapeptide repeat protein from the cyanobacterium <i>Nostoc</i> sp. PCC 7120, determined at 2.1 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1143-1153.	1.5	7
5269	Thermodynamics, cooperativity and stability of the tetracycline repressor (TetR) upon tetracycline binding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140404.	1.1	8
5270	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. Current Research in Structural Biology, 2020, 2, 14-24.	1.1	18

#	ARTICLE	IF	CITATIONS
5271	Crystal Structure of the Mannose-6-Phosphate Uncovering Enzyme. Structure, 2020, 28, 426-436.e3.	1.6	6
5272	Mass spectrometry reveals the assembly pathway of encapsulated ferritins and highlights a dynamic ferroxidase interface. Chemical Communications, 2020, 56, 3417-3420.	2.2	14
5273	The recognition of proteasomal receptors by Plasmodium falciparum DSK2. Molecular and Biochemical Parasitology, 2020, 236, 111266.	0.5	1
5274	Structural and functional insights into the Asp1/2/3 complex mediated secretion of pneumococcal serine-rich repeat protein PsrP. Biochemical and Biophysical Research Communications, 2020, 524, 784-790.	1.0	1
5275	Beyond the heterodimer model for mineralocorticoid and glucocorticoid receptor interactions in nuclei and at DNA. PLoS ONE, 2020, 15, e0227520.	1.1	36
5276	Evolutionary Dynamics of Oropouche Virus in South America. Journal of Virology, 2020, 94, .	1.5	17
5277	Effect of pH on the structure and function of pyruvate dehydrogenase kinase 3: Combined spectroscopic and MD simulation studies. International Journal of Biological Macromolecules, 2020, 147, 768-777.	3.6	16
5278	The First Structure of an Active Mammalian dCTPase and its Complexes With Substrate Analogs and Products. Journal of Molecular Biology, 2020, 432, 1126-1142.	2.0	2
5280	Hup-Type Hydrogenases of Purple Bacteria: Homology Modeling and Computational Assessment of Biotechnological Potential. International Journal of Molecular Sciences, 2020, 21, 366.	1.8	4
5281	New variants of AADC deficiency expand the knowledge of enzymatic phenotypes. Archives of Biochemistry and Biophysics, 2020, 682, 108263.	1.4	19
5282	Consensus protein engineering on the thermostable histone-like bacterial protein HUs significantly improves stability and DNA binding affinity. Extremophiles, 2020, 24, 293-306.	0.9	6
5283	Unexpected CK2Î²-antagonistic functionality of bisubstrate inhibitors targeting protein kinase CK2. Bioorganic Chemistry, 2020, 96, 103608.	2.0	14
5284	Crystal Structure of Î±-Xylosidase from Aspergillus niger in Complex with a Hydrolyzed Xyloglucan Product and New Insights in Accurately Predicting Substrate Specificities of GH31 Family Glycosidases. ACS Sustainable Chemistry and Engineering, 2020, 8, 2540-2547.	3.2	12
5285	Structural basis of p62/SQSTM1 helical filaments and their role in cellular cargo uptake. Nature Communications, 2020, 11, 440.	5.8	71
5286	A Targeted Genetic Association Study of the Rare Type of Osteomyelitis. Journal of Dental Research, 2020, 99, 271-276.	2.5	5
5287	Structural Analyses on the Deamidation of N-Terminal Asn in the Human N-Degron Pathway. Biomolecules, 2020, 10, 163.	1.8	10
5288	Crystal structures of a Î²-trefoil lectin from Entamoeba histolytica in monomeric and a novel disulfide bond-mediated dimeric forms. Glycobiology, 2020, 30, 474-488.	1.3	5
5289	Robust Ï‰-Transaminases by Computational Stabilization of the Subunit Interface. ACS Catalysis, 2020, 10, 2915-2928.	5.5	52

#	ARTICLE	IF	CITATIONS
5291	The bacterial deubiquitinase Ceg23 regulates the association of Lys-63â€“linked polyubiquitin molecules on the Legionella phagosome. Journal of Biological Chemistry, 2020, 295, 1646-1657.	1.6	33
5292	Crystal structures of Triosephosphate Isomerases from Taenia solium and Schistosoma mansoni provide insights for vaccine rationale and drug design against helminth parasites. PLoS Neglected Tropical Diseases, 2020, 14, e0007815.	1.3	6
5293	Structural characterization of aminoglycoside 4â€²â€•O â€adenylyltransferase ANT(4â€²)â€Ib from Pseudomonas aeruginosa. Protein Science, 2020, 29, 758-767.	3.1	5
5294	Molecular mechanism for the recognition of sequence-divergent CIF peptides by the plant receptor kinases GSO1/SGN3 and GSO2. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2693-2703.	3.3	68
5295	Crystal structure of proteolyzed VapBC and DNAâ€bound VapBC from Salmonella enterica Typhimurium LT2 and VapC as a putative Ca 2+ â€dependent ribonuclease. FASEB Journal, 2020, 34, 3051-3068.	0.2	3
5296	Probing the mutational landscape of regulators of G protein signaling proteins in cancer. Science Signaling, 2020, 13, .	1.6	17
5297	Structural and Biophysical Analyses of Human N-Myc Downstream-Regulated Gene 3 (NDRG3) Protein. Biomolecules, 2020, 10, 90.	1.8	6
5298	ProtCID: a data resource for structural information on protein interactions. Nature Communications, 2020, 11, 711.	5.8	38
5299	Crystal structure of PMGL2 esterase from the hormone-sensitive lipase family with GCSAG motif around the catalytic serine. PLoS ONE, 2020, 15, e0226838.	1.1	10
5300	Identification of New Peptides from Fermented Milk Showing Antioxidant Properties: Mechanism of Action. Antioxidants, 2020, 9, 117.	2.2	66
5301	Differential Features of Fusion Activation within the Paramyxoviridae. Viruses, 2020, 12, 161.	1.5	26
5302	Posttranslational Modifications Mediate the Structural Diversity of Tauopathy Strains. Cell, 2020, 180, 633-644.e12.	13.5	300
5303	An Acetylation Switch of the NLRP3 Inflammasome Regulates Aging-Associated Chronic Inflammation and Insulin Resistance. Cell Metabolism, 2020, 31, 580-591.e5.	7.2	213
5304	FGCaMP7, an Improved Version of Fungi-Based Ratiometric Calcium Indicator for In Vivo Visualization of Neuronal Activity. International Journal of Molecular Sciences, 2020, 21, 3012.	1.8	17
5305	Nanogel receptors for high isoelectric point protein detection: influence of electrostatic and covalent polymerâ€“protein interactions. Chemical Communications, 2020, 56, 6141-6144.	2.2	12
5306	The DNA Sensor cGAS is Decorated by Acetylation and Phosphorylation Modifications in the Context of Immune Signaling. Molecular and Cellular Proteomics, 2020, 19, 1193-1208.	2.5	29
5307	Structural insights on binding mechanism of CAD complexes (CPSase, ATCase and DHOase). Journal of Biomolecular Structure and Dynamics, 2020, 39, 1-14.	2.0	2
5308	Boosting with AIDSVAX B/E Enhances Env Constant Region 1 and 2 Antibody-Dependent Cellular Cytotoxicity Breadth and Potency. Journal of Virology, 2020, 94, .	1.5	19

#	ARTICLE	IF	CITATIONS
5309	Structural Determination of a Filamentous Chaperone to Fabricate Electronically Conductive Metalloprotein Nanowires. ACS Nano, 2020, 14, 6559-6569.	7.3	20
5310	Snf5 and Swi3 subcomplex formation is required for SWI/SNF complex function in yeast. Biochemical and Biophysical Research Communications, 2020, 526, 934-940.	1.0	4
5311	A possible strategy to fight COVID-19: Interfering with spike glycoprotein trimerization. Biochemical and Biophysical Research Communications, 2020, 528, 35-38.	1.0	21
5312	DNA-Directed Protein Packing within Single Crystals. CheM, 2020, 6, 1007-1017.	5.8	17
5313	Structure of the Native Muscle-type Nicotinic Receptor and Inhibition by Snake Venom Toxins. Neuron, 2020, 106, 952-962.e5.	3.8	138
5314	Structural Basis for the Asymmetry of a 4-Oxalocrotonate Tautomerase Trimer. Biochemistry, 2020, 59, 1592-1603.	1.2	6
5315	Crystal structures of REF6 and its complex with DNA reveal diverse recognition mechanisms. Cell Discovery, 2020, 6, 17.	3.1	18
5316	Molecular basis of ALK1-mediated signalling by BMP9/BMP10 and their prodomain-bound forms. Nature Communications, 2020, 11, 1621.	5.8	43
5317	Structural basis for substrate and product recognition in human phosphoglucomutase-1 (PGM1) isoform 2, a member of the Î±-d-phosphohexomutase superfamily. Scientific Reports, 2020, 10, 5656.	1.6	9
5318	Human IgG1 Fc pH-dependent optimization from a constant pH molecular dynamics simulation analysis. RSC Advances, 2020, 10, 13066-13075.	1.7	3
5319	An integrated approach to unravel a crucial structural property required for the function of the insect steroidogenic Halloween protein Noppera-bo. Journal of Biological Chemistry, 2020, 295, 7154-7167.	1.6	14
5320	A knowledge-based scoring function to assess quaternary associations of proteins. Bioinformatics, 2020, 36, 3739-3748.	1.8	12
5321	MiR193a Modulation and Podocyte Phenotype. Cells, 2020, 9, 1004.	1.8	5
5322	Revisiting high-resolution crystal structure of Phormidium rubidum phycocyanin. Photosynthesis Research, 2020, 144, 349-360.	1.6	5
5323	RPTPÎ± phosphatase activity is allosterically regulated by the membrane-distal catalytic domain. Journal of Biological Chemistry, 2020, 295, 4923-4936.	1.6	18
5324	Comparative Structural Analysis of 20S Proteasome Ortholog Protein Complexes by Native Mass Spectrometry. ACS Central Science, 2020, 6, 573-588.	5.3	37
5325	Molecular basis for assembly of the shieldin complex and its implications for NHEJ. Nature Communications, 2020, 11, 1972.	5.8	35
5326	The structure of helical lipoprotein lipase reveals an unexpected twist in lipase storage. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10254-10264.	3.3	25

#	ARTICLE	IF	CITATIONS
5327	Evaluation of NHS-Acetate and DEPC labelling for determination of solvent accessible amino acid residues in protein complexes. Journal of Proteomics, 2020, 222, 103793.	1.2	5
5328	Recognition and Activation of the Plant AKT1 Potassium Channel by the Kinase CIPK23. Plant Physiology, 2020, 182, 2143-2153.	2.3	51
5329	Exploring the complex map of insulin polymorphism: a novel crystalline form in the presence of<i>m</i>-cresol. Acta Crystallographica Section D: Structural Biology, 2020, 76, 366-374.	1.1	2
5330	Half Way to Hypusineâ€"Structural Basis for Substrate Recognition by Human Deoxyhypusine Synthase. Biomolecules, 2020, 10, 522.	1.8	17
5331	High-resolution structure of a modular hyperthermostable endo-Î²-1,4-mannanase from Thermotoga petrophila: The ancillary immunoglobulin-like module is a thermostabilizing domain. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140437.	1.1	4
5332	Structural basis for Zika envelope domain III recognition by a germline version of a recurrent neutralizing antibody. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9865-9875.	3.3	7
5333	Xâ€ray crystal structure localizes the mechanism of inhibition of an <scp>ILâ€36R</scp> antagonist monoclonal antibody to interaction with Ig1 and Ig2 extra cellular domains. Protein Science, 2020, 29, 1679-1686.	3.1	3
5334	Crystal structure of Nsp15 endoribonuclease <scp>NendoU</scp> from <scp>SARSâ€CoV</scp>â€2. Protein Science, 2020, 29, 1596-1605.	3.1	294
5335	The quaternary assembly of KRas4B with Raf-1 at the membrane. Computational and Structural Biotechnology Journal, 2020, 18, 737-748.	1.9	50
5336	Structural basis for differentiation between two classes of thiolase: Degradative vs biosynthetic thiolase. Journal of Structural Biology: X, 2020, 4, 100018.	0.7	8
5337	NusA directly interacts with antitermination factor Q from phage Î». Scientific Reports, 2020, 10, 6607.	1.6	2
5338	Crystallographic and kinetic analyses of the FdsBG subcomplex of the cytosolic formate dehydrogenase FdsABG from Cupriavidus necator. Journal of Biological Chemistry, 2020, 295, 6570-6585.	1.6	16
5339	2.7 Ã… cryo-EM structure of rotavirus core protein VP3, a unique capping machine with a helicase activity. Science Advances, 2020, 6, eaay6410.	4.7	16
5340	Pyrethroid Carboxylesterase PytH from <i>Sphingobium faniae</i> JZ-2: Structure and Catalytic Mechanism. Applied and Environmental Microbiology, 2020, 86, .	1.4	25
5341	Crystal Packing of Phosphopantetheine Adenylyltransferase from Mycobacterium tuberculosis in Two Crystal Modifications. Crystallography Reports, 2020, 65, 84-90.	0.1	0
5342	Dynamics in the murine norovirus capsid revealed by high-resolution cryo-EM. PLoS Biology, 2020, 18, e3000649.	2.6	19
5343	Expression of quasi-equivalence and capsid dimorphism in the Hepadnaviridae. PLoS Computational Biology, 2020, 16, e1007782.	1.5	10
5344	From conservation to structure, studies of magnetosome associated cation diffusion facilitators (CDF) proteins in Proteobacteria. PLoS ONE, 2020, 15, e0231839.	1.1	4

#	Article	IF	Citations
5345	Crystal structure of thioredoxin 1 from Cryptococcus neoformans at 1.8ÂÃ… resolution shows unexpected plasticity of the loop preceding the catalytic site. Biochemistry and Biophysics Reports, 2020, 21, 100724.	0.7	2
5346	Crystal structure of NirF: insights into its role in heme <i>d</i>₁ biosynthesis. FEBS Journal, 2021, 288, 244-261.	2.2	3
5347	Crystal structures of human NSDHL and development of its novel inhibitor with the potential to suppress EGFR activity. Cellular and Molecular Life Sciences, 2021, 78, 207-225.	2.4	9
5348	The coâ€existence of cold activity and thermal stability in an Antarctic GH42 Î²â€galactosidase relies on its hexameric quaternary arrangement. FEBS Journal, 2021, 288, 546-565.	2.2	31
5349	Identification of quasi-stable water molecules near the Thr73â€"Lys13 catalytic diad of <i>Bacillus</i> sp. TB-90 urate oxidase by X-ray crystallography with controlled humidity. Journal of Biochemistry, 2021, 169, 15-23.	0.9	1
5350	Experimentally based structural model of Yih1 provides insight into its function in controlling the key translational regulator Gcn2. FEBS Letters, 2021, 595, 324-340.	1.3	1
5351	The ASK1 gene regulates the sensitivity of Fusarium graminearum to carbendazim, conidiation and sexual production by combining with Î²2-tubulin. Current Genetics, 2021, 67, 165-176.	0.8	1
5352	Heat inactivation of thermolabile polygalacturonase down to single molecule level. Systematic investigation and molecular modeling. LWT - Food Science and Technology, 2021, 137, 110385.	2.5	2
5353	Mechanism of auto-inhibition and activation of Mec1ATR checkpoint kinase. Nature Structural and Molecular Biology, 2021, 28, 50-61.	3.6	17
5354	Alkaline phosphatase dualâ€binding sites for collagen dictate cell migration and microvessel assembly in vitro. Journal of Cellular Biochemistry, 2021, 122, 116-129.	1.2	4
5355	Characterization of leftâ€handed beta helixâ€domains, and identification and functional annotation of proteins containing such domains. Proteins: Structure, Function and Bioinformatics, 2021, 89, 6-20.	1.5	1
5356	Dual specificity of a prokaryotic GTPaseâ€activating protein (GAP) to two small Rasâ€like GTPases in <i>Myxococcus xanthus</i>. FEBS Journal, 2021, 288, 1565-1585.	2.2	6
5357	Cowâ€™s milk protein Î²-lactoglobulin confers resilience against allergy by targeting complexed iron into immune cells. Journal of Allergy and Clinical Immunology, 2021, 147, 321-334.e4.	1.5	62
5358	Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. Biochemical and Biophysical Research Communications, 2021, 538, 192-203.	1.0	165
5359	Artificial intelligence based identification of the functional role of hirudin in diabetic erectile dysfunction treatment. Pharmacological Research, 2021, 163, 105244.	3.1	4
5360	Human galectin-16 has a pseudo ligand binding site and plays a role in regulating c-Rel-mediated lymphocyte activity. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129755.	1.1	17
5361	Characterization of the Pilotin-Secretin Complex from the Salmonella enterica Type III Secretion System Using Hybrid Structural Methods. Structure, 2021, 29, 125-138.e5.	1.6	9
5362	Involvement of subdomain II in the recognition of acetylâ€CoA revealed by the crystal structure of homocitrate synthase from Sulfolobus acidocaldarius. FEBS Journal, 2021, 288, 1975-1988.	2.2	1

#	ARTICLE	IF	CITATIONS
5363	Structural and Functional Impact of SRP54 Mutations Causing Severe Congenital Neutropenia. Structure, 2021, 29, 15-28.e7.	1.6	12
5364	Gas channel rerouting in a primordial enzyme: Structural insights of the carbon-monoxide dehydrogenase/acetyl-CoA synthase complex from the acetogen Clostridium autoethanogenum. Biochimica Et Biophysica Acta - Bioenergetics, 2021, 1862, 148330.	0.5	30
5365	Structure of the Extracellular Region of the Bacterial Type VIIb Secretion System Subunit EsaA. Structure, 2021, 29, 177-185.e6.	1.6	14
5366	Novel Î²â€Glucocerebrosidase Activators That Bind to a New Pocket at a Dimer Interface and Induce Dimerization. Angewandte Chemie - International Edition, 2021, 60, 5436-5442.	7.2	13
5367	Structure and Double-Stranded RNA-Binding Activity of the Birnavirus Drosophila X Virus VP3 Protein. Journal of Virology, 2021, 95, .	1.5	2
5368	A Novel Loss of Function Melanocortin-4-Receptor Mutation (MC4R-F313Sfs*29) in Morbid Obesity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 736-749.	1.8	4
5369	A FabG inhibitor targeting an allosteric binding site inhibits several orthologs from Gram-negative ESKAPE pathogens. Bioorganic and Medicinal Chemistry, 2021, 30, 115898.	1.4	12
5370	Aldosterone synthase inhibitors for cardiovascular diseases: A comprehensive review of preclinical, clinical and in silico data. Pharmacological Research, 2021, 163, 105332.	3.1	23
5371	Lipocalin Blc is a potential hemeâ€binding protein. FEBS Letters, 2021, 595, 206-219.	1.3	4
5372	PARCE: Protocol for Amino acid Refinement through Computational Evolution. Computer Physics Communications, 2021, 260, 107716.	3.0	12
5373	Crystal Structure of a Bivalent Antibody Fab Fragment. Journal of Molecular Biology, 2021, 433, 166714.	2.0	2
5374	Structural Basis for High-Affinity Trapping of the NaV1.7 Channel in Its Resting State by Tarantula Toxin. Molecular Cell, 2021, 81, 38-48.e4.	4.5	40
5375	Comparison of human poly-N-acetyl-lactosamine synthase structure with GT-A fold glycosyltransferases supports a modular assembly of catalytic subsites. Journal of Biological Chemistry, 2021, 296, 100110.	1.6	15
5376	Structural basis for multifunctional roles of human Ints3 C-terminal domain. Journal of Biological Chemistry, 2021, 296, 100112.	1.6	12
5377	Reprogramming the Specificity of a Protein Interface by Computational and Data-Driven Design. Structure, 2021, 29, 292-304.e3.	1.6	2
5378	Structure of the radial spoke head and insights into its role in mechanoregulation of ciliary beating. Nature Structural and Molecular Biology, 2021, 28, 20-28.	3.6	39
5379	Cryo-EM structure of CtBP2 confirms tetrameric architecture. Structure, 2021, 29, 310-319.e5.	1.6	15
5380	Structural basis for antigen recognition by methylated lysineâ€“specific antibodies. Journal of Biological Chemistry, 2021, 296, 100176.	1.6	6

#	Article	IF	Citations
5381	Conformational dynamics of SARS-CoV-2 trimeric spike glycoprotein in complex with receptor ACE2 revealed by cryo-EM. Science Advances, 2021, 7, .	4.7	320
5382	Capping pores of alphavirus nsP1 gate membranous viral replication factories. Nature, 2021, 589, 615-619.	13.7	67
5383	Structure of a GRK5-Calmodulin Complex Reveals Molecular Mechanism of GRK Activation and Substrate Targeting. Molecular Cell, 2021, 81, 323-339.e11.	4.5	13
5384	Novel Î²â€Glucocerebrosidase Activators That Bind to a New Pocket at a Dimer Interface and Induce Dimerization. Angewandte Chemie, 2021, 133, 5496-5502.	1.6	4
5385	Effect of N-linked glycosylation at position 162 of hemagglutinin in influenza A virus A(H1N1)pdm09. Meta Gene, 2021, 27, 100828.	0.3	2
5386	Structural Basis of CYRI-B Direct Competition with Scar/WAVE Complex for Rac1. Structure, 2021, 29, 226-237.e4.	1.6	15
5387	Structure of an affinity-matured inhibitory recombinant fab against urokinase plasminogen activator reveals basis of potency and specificity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140562.	1.1	1
5388	Purification, characterization, and crystal structure of <scp>YhdA</scp>â€type azoreductase from <i>Bacillus velezensis</i>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 483-492.	1.5	6
5389	<i>R</i>â€hydroxynitrile lyase from the cyanogenic millipede, <i>Chamberlinius hualienensis</i>â€"A new entry to the carrier protein family Lipocalines. FEBS Journal, 2021, 288, 1679-1695.	2.2	8
5390	Nucleoside selectivity of <i>Aspergillus fumigatus</i> nucleosideâ€diphosphate kinase. FEBS Journal, 2021, 288, 2398-2417.	2.2	6
5391	Quaternary variations in the structural assembly ofNâ€acetylglucosamineâ€6â€phosphate deacetylase fromPasteurella multocida. Proteins: Structure, Function and Bioinformatics, 2021, 89, 81-93.	1.5	5
5392	Multiple structural states of Ca2+-regulated PET hydrolase, Cut190, and its correlation with activity and stability. Journal of Biochemistry, 2021, 169, 207-213.	0.9	12
5393	Structural and spectroscopic characterization of a HdrAâ€like subunit from <i>HyphomicrobiumÂdenitrificans</i>. FEBS Journal, 2021, 288, 1664-1678.	2.2	11
5394	Inhibition of Maize Caffeate 3-O-Methyltransferase by Nitecapone as a Possible Approach to Reduce Lignocellulosic Biomass Recalcitrance. Plant Molecular Biology Reporter, 2021, 39, 179-191.	1.0	5
5395	Revealing secrets of the enigmatic omega subunit of bacterial RNA polymerase. Molecular Microbiology, 2021, 115, 1-11.	1.2	16
5396	Predicting interfacial hot-spot residues that stabilize protein-protein interfaces in oligomeric membrane-toxin pores through hydrogen bonds and salt bridges. Journal of Biomolecular Structure and Dynamics, 2021, 39, 20-34.	2.0	6
5397	Improved epitope resolution of the prefusion trimer-specific antibody AM14 bound to the RSV F glycoprotein. MAbs, 2021, 13, 1955812.	2.6	6
5398	ADP-ribose and analogues bound to the deMARylating macrodomain from the bat coronavirus HKU4. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7

#	ARTICLE	IF	CITATIONS
5399	Development of a structural epitope mimic: an idiotypic approach to HCV vaccine design. Npj Vaccines, 2021, 6, 7.	2.9	10
5400	A novel catalytic heme cofactor in SfmD with a single thioether bond and a <i>bis</i>-His ligand set revealed by a <i>de novo</i> crystal structural and spectroscopic study. Chemical Science, 2021, 12, 3984-3998.	3.7	7
5401	Prediction, Analysis, Visualization, and Storage of Proteinâ€"Protein Interactions Using Computational Approaches. , 2021, , 265-346.		1
5402	Crystal structure of the MyRF ICA domain with its upstream Î²-helical stalk reveals the molecular mechanisms underlying its trimerization and self-cleavage. International Journal of Biological Sciences, 2021, 17, 2931-2943.	2.6	4
5403	Wzb of Vibrio vulnificus represents a new group of low-molecular-weight protein tyrosine phosphatases with a unique insertion in the W-loop. Journal of Biological Chemistry, 2021, 296, 100280.	1.6	3
5404	Designing a multi-epitope vaccine against the Lassa virus through reverse vaccinology, subtractive proteomics, and immunoinformatics approaches. Informatics in Medicine Unlocked, 2021, 25, 100683.	1.9	6
5406	Dynamic association of human Ebp1 with the ribosome. Rna, 2021, 27, 411-419.	1.6	9
5407	Co-evolutionary landscape at the interface and non-interface regions of protein-protein interaction complexes. Computational and Structural Biotechnology Journal, 2021, 19, 3779-3795.	1.9	3
5408	Peptidoglycan binding by a pocket on the accessory NTF2-domain of Pgp2 directs helical cell shape of Campylobacter jejuni. Journal of Biological Chemistry, 2021, 296, 100528.	1.6	5
5409	SARS-CoV-2 3D database: understanding the coronavirus proteome and evaluating possible drug targets. Briefings in Bioinformatics, 2021, 22, 769-780.	3.2	31
5411	Facile Fabrication of Proteinâ€"Macrocycle Frameworks. Journal of the American Chemical Society, 2021, 143, 1896-1907.	6.6	39
5412	The complex structure of GRL0617 and SARS-CoV-2 PLpro reveals a hot spot for antiviral drug discovery. Nature Communications, 2021, 12, 488.	5.8	196
5413	C-phycocyanin as a highly attractive model system in protein crystallography: unique crystallization properties and packing-diversity screening. Acta Crystallographica Section D: Structural Biology, 2021, 77, 224-236.	1.1	5
5414	Crystal structure of CD38 in complex with daratumumab, a first-in-class anti-CD38 antibody drug for treating multiple myeloma. Biochemical and Biophysical Research Communications, 2021, 536, 26-31.	1.0	17
5416	Structural Characterization of Act c 10.0101 and Pun g 1.0101â€"Allergens from the Non-Specific Lipid Transfer Protein Family. Molecules, 2021, 26, 256.	1.7	4
5417	A fragment-based protein interface design algorithm for symmetric assemblies. Protein Engineering, Design and Selection, 2021, 34, .	1.0	11
5418	Computational Methods for the Elucidation of Protein Structure and Interactions. Methods in Molecular Biology, 2021, 2305, 23-52.	0.4	1
5419	A GalNAc/Gal-specific lectin modulates immune responses <i>via</i> toll-like receptor 4 independently of carbohydrate-binding ability. Chemical Communications, 2021, 57, 6209-6212.	2.2	1

#	Article	IF	Citations
5420	Unique structural solution from a VH3-30 antibody targeting the hemagglutinin stem of influenza A viruses. Nature Communications, 2021, 12, 559.	5.8	11
5421	Potent SARS-CoV-2 binding and neutralization through maturation of iconic SARS-CoV-1 antibodies. MAbs, 2021, 13, 1922134.	2.6	22
5422	A sweet protein monellin as a non-antibody scaffold for synthetic binding proteins. Journal of Biochemistry, 2021, 169, 585-599.	0.9	6
5423	Rewards of divergence in sequences, 3-D structures and dynamics of yeast and human spliceosome SF3b complexes. Current Research in Structural Biology, 2021, 3, 133-145.	1.1	4
5424	Solution NMR and racemic crystallography provide insights into a novel structural class of cyclic plant peptides. RSC Chemical Biology, 2021, 2, 1682-1691.	2.0	1
5425	Large-scale movement of eIF3 domains during translation initiation modulate start codon selection. Nucleic Acids Research, 2021, 49, 11491-11511.	6.5	14
5426	Structural insights into photoactivation of plant Cryptochrome-2. Communications Biology, 2021, 4, 28.	2.0	33
5427	A computationally designed Î²-amino acid-containing miniprotein. Chemical Communications, 2021, 57, 6015-6018.	2.2	5
5428	Structural Bioinformatics to Unveil Weaknesses of Coronavirus Spike Glycoprotein Stability. Methods in Pharmacology and Toxicology, 2021, , 203.	0.1	0
5429	Integrated analysis of Shank1 PDZ interactions with C-terminal and internal binding motifs. Current Research in Structural Biology, 2021, 3, 41-50.	1.1	4
5430	Structural characterization of a GNAT family acetyltransferase from Elizabethkingia anophelis bound to acetyl-CoA reveals a new dimeric interface. Scientific Reports, 2021, 11, 1274.	1.6	9
5431	SWOTein: a structure-based approach to predict stability Strengths and Weaknesses of prOTEINs. Bioinformatics, 2021, 37, 1963-1971.	1.8	13
5432	Multiple variants of the fungal effector AVR-Pik bind the HMA domain of the rice protein OsHIPP19, providing a foundation to engineer plant defense. Journal of Biological Chemistry, 2021, 296, 100371.	1.6	57
5433	Classification and prediction of proteinâ€“protein interaction interface using machine learning algorithm. Scientific Reports, 2021, 11, 1761.	1.6	50
5434	A polysaccharide utilization locus from the gut bacterium Dysgonomonas mossii encodes functionally distinct carbohydrate esterases. Journal of Biological Chemistry, 2021, 296, 100500.	1.6	21
5435	PIM-induced phosphorylation of Notch3 promotes breast cancer tumorigenicity in a CSL-independent fashion. Journal of Biological Chemistry, 2021, 296, 100593.	1.6	9
5436	Crystal structure and mutational analysis of the human TRIM7 B30.2 domain provide insights into the molecular basis of its binding to glycogenin-1. Journal of Biological Chemistry, 2021, 296, 100772.	1.6	5
5437	Deep Learning for Proteinâ€“Protein Interaction Site Prediction. Methods in Molecular Biology, 2021, 2361, 263-288.	0.4	10

#	ARTICLE	IF	CITATIONS
5438	Structural and Biochemical Characterization of EFhd1/Swiprosin-2, an Actin-Binding Protein in Mitochondria. Frontiers in Cell and Developmental Biology, 2020, 8, 628222.	1.8	7
5441	On the estimation of the molecular inaccessible volume and the molecular accessible surface of a ligand in proteinâ€“ligand systems. Molecular Systems Design and Engineering, 2021, 6, 946-963.	1.7	4
5442	Inositol pyrophosphates promote the interaction of SPX domains with the coiled-coil motif of PHR transcription factors to regulate plant phosphate homeostasis. Nature Communications, 2021, 12, 384.	5.8	105
5443	Using yeast two-hybrid system and molecular dynamics simulation to detect venom protein-protein interactions. Current Research in Toxicology, 2021, 2, 93-98.	1.3	4
5444	Advances in integrative structural biology: Towards understanding protein complexes in their cellular context. Computational and Structural Biotechnology Journal, 2021, 19, 214-225.	1.9	23
5445	A two-site flexible clamp mechanism for RET-GDNF-GFRÎ±1 assembly reveals both conformational adaptation and strict geometric spacing. Structure, 2021, 29, 694-708.e7.	1.6	6
5446	Crystal structure and DNA cleavage mechanism of the restriction DNA glycosylase R.CcoLI from Campylobacter coli. Scientific Reports, 2021, 11, 859.	1.6	1
5447	Structural and Biochemical Characterization of a Cold-Active PMGL3 Esterase with Unusual Oligomeric Structure. Biomolecules, 2021, 11, 57.	1.8	6
5448	Structural basis of Naa20 activity towards a canonical NatB substrate. Communications Biology, 2021, 4, 2.	2.0	6
5450	Structural characterization of Myxococcus xanthus MglC, a component of the polarity control system, and its interactions with its paralog MglB. Journal of Biological Chemistry, 2021, 296, 100308.	1.6	7
5451	Crystal structure of bacterial cytotoxic necrotizing factor CNF_Y reveals molecular building blocks for intoxication. EMBO Journal, 2021, 40, e105202.	3.5	14
5452	Molecular basis for the adaptive evolution of environment-sensing by H-NS proteins. ELife, 2021, 10, .	2.8	9
5453	How Far Are We from the Rapid Prediction of Drug Resistance Arising Due to Kinase Mutations?. ACS Omega, 2021, 6, 1254-1265.	1.6	4
5454	Mechanistic insights into the effect of phosphorylation on Ras conformational dynamics and its interactions with cell signaling proteins. Computational and Structural Biotechnology Journal, 2021, 19, 1184-1199.	1.9	51
5455	Cryo-EM structure of Helicobacter pylori urease with an inhibitor in the active site at 2.0â€‰Ã… resolution. Nature Communications, 2021, 12, 230.	5.8	39
5456	Structural analysis of cross Î±-helical nanotubes provides insight into the designability of filamentous peptide nanomaterials. Nature Communications, 2021, 12, 407.	5.8	35
5457	A therapeutic neutralizing antibody targeting receptor binding domain of SARS-CoV-2 spike protein. Nature Communications, 2021, 12, 288.	5.8	224
5458	Structure and mechanism of the proton-driven motor that powers type 9 secretion and gliding motility. Nature Microbiology, 2021, 6, 221-233.	5.9	47

#	Article	IF	Citations
5459	Structural basis for transcription complex disruption by the Mfd translocase. ELife, 2021, 10, .	2.8	36
5460	Crystal structure of human interleukin-2 in complex with TCB2, a new antibody-drug candidate with antitumor activity. OncoImmunology, 2021, 10, 1899671.	2.1	3
5461	Homotypic CARD-CARD interaction is critical for the activation of NLRP1 inflammasome. Cell Death and Disease, 2021, 12, 57.	2.7	10
5462	Multivalent Display of SARS-CoV-2 Spike (RBD Domain) of COVID-19 to Nanomaterial, Protein Ferritin Nanocages. Biomolecules, 2021, 11, 297.	1.8	20
5464	Crystal structure of acetoacetyl-CoA reductase from<i>Rickettsia felis</i>. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 54-60.	0.4	1
5465	Three-dimensional structure of human cyclooxygenase (hCOX)-1. Scientific Reports, 2021, 11, 4312.	1.6	29
5467	Exploiting Allosteric Properties of RAF and MEK Inhibitors to Target Therapy-Resistant Tumors Driven by Oncogenic BRAF Signaling. Cancer Discovery, 2021, 11, 1716-1735.	7.7	30
5469	Crystal structures of adenylylated and unadenylylated P_{II}protein GlnK from<i>Corynebacterium glutamicum</i>. Acta Crystallographica Section D: Structural Biology, 2021, 77, 325-335.	1.1	4
5470	Crystal structure of the human PRPKâ€"TPRKB complex. Communications Biology, 2021, 4, 167.	2.0	9
5471	Second distinct conformation of the phosphohistidine loop in succinyl-CoA synthetase. Acta Crystallographica Section D: Structural Biology, 2021, 77, 357-368.	1.1	3
5472	Structure and functional properties of the cold-adapted catalase from <i>Acinetobacter</i> sp. Ver3 native to the Atacama plateau in northern Argentina. Acta Crystallographica Section D: Structural Biology, 2021, 77, 369-379.	1.1	4
5474	Protein A does not induce allosteric structural changes in an IgG1 antibody during binding. Journal of Pharmaceutical Sciences, 2021, 110, 2355-2361.	1.6	9
5476	Structural Basis for Toxin Inhibition in the VapXD Toxin-Antitoxin System. Structure, 2021, 29, 139-150.e3.	1.6	12
5477	The allosteric modulation of complement C5 by knob domain peptides. ELife, 2021, 10, .	2.8	21
5478	Interplay between hevin, SPARC, and MDGAs: Modulators of neurexin-neuroligin transsynaptic bridges. Structure, 2021, 29, 664-678.e6.	1.6	16
5482	Structural Insights into the <i>Trans</i>-Acting Enoyl Reductase in the Biosynthesis of Long-Chain Polyunsaturated Fatty Acids in <i>Shewanella piezotolerans</i>. Journal of Agricultural and Food Chemistry, 2021, 69, 2316-2324.	2.4	5
5483	Crystal Structure and Regiospecificity of Catechol <i>O</i>-Methyltransferase from <i>Niastella koreensis</i>. Journal of Agricultural and Food Chemistry, 2021, 69, 2531-2538.	2.4	7
5484	C. elegans germ granules require both assembly and localized regulators for mRNA repression. Nature Communications, 2021, 12, 996.	5.8	26

#	Article	IF	Citations
5485	A scaffold lncRNA shapes the mitosis to meiosis switch. Nature Communications, 2021, 12, 770.	5.8	22
5486	Structural analyses of PCNA from the fungal pathogen <i>Candida albicans</i> identify three regions with speciesâ€specific conformations. FEBS Letters, 2021, 595, 1328-1349.	1.3	5
5489	Crystallographic models of SARS-CoV-2 3CL^{pro}: in-depth assessment of structure quality and validation. IUCrJ, 2021, 8, 238-256.	1.0	21
5490	Granulovirus PK-1 kinase activity relies on a side-to-side dimerization mode centered on the regulatory Î±C helix. Nature Communications, 2021, 12, 1002.	5.8	7
5491	Structural analysis of alternate sigma factor ComX with RpoC, RpoB and its cognate CIN promoter reveals a distinctive promoter melting mechanism. Journal of Biomolecular Structure and Dynamics, 2022, 40, 6272-6285.	2.0	2
5492	Shedding Light on the Inhibitory Mechanisms of SARS-CoV-1/CoV-2 Spike Proteins by ACE2-Designed Peptides. Journal of Chemical Information and Modeling, 2021, 61, 1226-1243.	2.5	24
5493	Insights into Ubiquitin Product Release in Hydrolysis Catalyzed by the Bacterial Deubiquitinase SdeA. Biochemistry, 2021, 60, 584-596.	1.2	4
5494	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. Science, 2021, 371, .	6.0	304
5495	Inhibition of Carbonic Anhydrase Using SLC-149: Support for a Noncatalytic Function of CAIX in Breast Cancer. Journal of Medicinal Chemistry, 2021, 64, 1713-1724.	2.9	14
5496	Interactions of Sea Anemone Toxins with Insect Sodium Channelâ€"Insights from Electrophysiology and Molecular Docking Studies. Molecules, 2021, 26, 1302.	1.7	5
5497	The tetrameric structure of the novel haloalkane dehalogenase DpaA from <i>Paraglaciecola agarilytica</i> NO2. Acta Crystallographica Section D: Structural Biology, 2021, 77, 347-356.	1.1	5
5498	Prokaryotic Argonaute from Archaeoglobus fulgidus interacts with DNA as a homodimer. Scientific Reports, 2021, 11, 4518.	1.6	9
5499	Small-Angle X-ray Scattering Models of APOBEC3B Catalytic Domain in a Complex with a Single-Stranded DNA Inhibitor. Viruses, 2021, 13, 290.	1.5	6
5501	Structural analysis and biochemical properties of laccase enzymes from two <i>Pediococcus</i> species. Microbial Biotechnology, 2021, 14, 1026-1043.	2.0	21
5502	The Majority of Typhoid Toxin-Positive <i>Salmonella</i> Serovars Encode ArtB, an Alternate Binding Subunit. MSphere, 2021, 6, .	1.3	10
5504	Nonstructural protein 7 and 8 complexes of SARSâ€CoVâ€2. Protein Science, 2021, 30, 873-881.	3.1	15
5505	Structural basis of diversity and homodimerization specificity of zinc-finger-associated domains in Drosophila. Nucleic Acids Research, 2021, 49, 2375-2389.	6.5	17
5506	Functional and structural characterization of a flavoprotein monooxygenase essential for biogenesis of tryptophylquinone cofactor. Nature Communications, 2021, 12, 933.	5.8	2

#	Article	IF	Citations
5507	Crystal structure of fungal tannase from <i>Aspergillus niger</i>. Acta Crystallographica Section D: Structural Biology, 2021, 77, 267-277.	1.1	6
5508	Structural basis for IL-12 and IL-23 receptor sharing reveals a gateway for shaping actions on T versus NK cells. Cell, 2021, 184, 983-999.e24.	13.5	78
5509	Characterization of the sorbitol dehydrogenase SmoS from <i>Sinorhizobium meliloti</i> 1021. Acta Crystallographica Section D: Structural Biology, 2021, 77, 380-390.	1.1	2
5510	Structural Characterization of Diazabicyclooctane Î²-Lactam â€œEnhancersâ€•in Complex with Penicillin-Binding Proteins PBP2 and PBP3 of Pseudomonas aeruginosa. MBio, 2021, 12, .	1.8	19
5511	An Eight Amino Acid Segment Controls Oligomerization and Preferred Conformation of the two Non-visual Arrestins. Journal of Molecular Biology, 2021, 433, 166790.	2.0	15
5512	Domain Stability Regulated through the Dimer Interface Controls the Formation Kinetics of a Specific NF-ÎºB Dimer. Biochemistry, 2021, 60, 513-523.	1.2	2
5514	<i>Leishmania major</i> biotin protein ligase forms a unique cross-handshake dimer. Acta Crystallographica Section D: Structural Biology, 2021, 77, 510-521.	1.1	2
5515	Insights into mineralocorticoid receptor homodimerization from a combined molecular modeling and bioinformatics study. Proteins: Structure, Function and Bioinformatics, 2021, 89, 952-965.	1.5	6
5516	Broad Reactivity Single Domain Antibodies against Influenza Virus and Their Applications to Vaccine Potency Testing and Immunotherapy. Biomolecules, 2021, 11, 407.	1.8	6
5517	A human monoclonal antibody blocks malaria transmission and defines a highly conserved neutralizing epitope on gametes. Nature Communications, 2021, 12, 1750.	5.8	39
5520	DPP9 sequesters the CÂterminus of NLRP1 to repress inflammasome activation. Nature, 2021, 592, 778-783.	13.7	114
5521	Crystal structures of influenza nucleoprotein complexed with nucleic acid provide insights into the mechanism of RNA interaction. Nucleic Acids Research, 2021, 49, 4144-4154.	6.5	24
5522	The actomyosin interface contains an evolutionary conserved core and an ancillary interface involved in specificity. Nature Communications, 2021, 12, 1892.	5.8	23
5524	Impact of Structural Observables From Simulations to Predict the Effect of Single-Point Mutations in MHC Class II Peptide Binders. Frontiers in Molecular Biosciences, 2021, 8, 636562.	1.6	3
5525	Maximizing (Electro)catalytic CO₂ Reduction with a Ferredoxin-Based Reduction Potential Gradient. ACS Catalysis, 2021, 11, 4009-4023.	5.5	10
5526	Expanding the recognition interface of the thrombin-binding aptamer HD1 through modification of residues T3 and T12. Molecular Therapy - Nucleic Acids, 2021, 23, 863-871.	2.3	15
5527	From examining the relationship between (corona)viral adhesins and galectins to glyco-perspectives. Biophysical Journal, 2021, 120, 1031-1039.	0.2	5
5528	Crystal structure of the 6-phosphogluconate dehydrogenase from Gluconobacter oxydans reveals tetrameric 6PGDHs as the crucial intermediate in the evolution of structure and cofactor preference in the 6PGDH family. Wellcome Open Research, 0, 6, 48.	0.9	2

#	ARTICLE	IF	CITATIONS
5529	Structural and functional characterisation of a cold-active yet heat-tolerant dehydroquinase from Glaciozyma antarctica PI12. Journal of Biotechnology, 2021, 329, 118-127.	1.9	3
5532	Sortase-assembled pili in <i>Corynebacterium diphtheriae</i> are built using a latch mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7
5533	Oncogenic mutations on Rac1 affect global intrinsic dynamics underlying GTP and PAK1 binding. Biophysical Journal, 2021, 120, 866-876.	0.2	12
5534	Structural determinants underlying the adduct lifetime in the LOV proteins of <i>Pseudomonas putida</i>. FEBS Journal, 2021, 288, 4955-4972.	2.2	9
5535	Biophysical and structural investigation of the regulation of human GTP cyclohydrolase I by its regulatory protein GFRP. Journal of Structural Biology, 2021, 213, 107691.	1.3	1
5536	Unveiling the binding mode of perfluorooctanoic acid to human serum albumin. Protein Science, 2021, 30, 830-841.	3.1	25
5538	Structure of <i>Arabidopsis</i> CESA3 catalytic domain with its substrate UDP-glucose provides insight into the mechanism of cellulose synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	22
5539	Crystal structure of timothy grass allergen Phl p 12.0101 reveals an unusual profilin dimer. Acta Biochimica Polonica, 2021, 68, 15-22.	0.3	3
5540	Canonical versus non-canonical transsynaptic signaling of neuroligin 3 tunes development of sociality in mice. Nature Communications, 2021, 12, 1848.	5.8	19
5541	Crystal structure of the nonclassical cadherin-17 N-terminus and implications for its adhesive binding mechanism. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 85-94.	0.4	3
5542	Structural characterization of the microbial enzyme urocanate reductase mediating imidazole propionate production. Nature Communications, 2021, 12, 1347.	5.8	9
5543	Structural insights into histone chaperone Asf1 and its characterization from Plasmodium falciparum. Biochemical Journal, 2021, 478, 1117-1136.	1.7	1
5544	Jacalin domain-containing protein OsSalT interacts with OsDREB2A and OsNAC1 to impart drought stress tolerance in planta. Environmental and Experimental Botany, 2021, 183, 104362.	2.0	7
5545	The Crystal Structure of Bacillus cereus HblL1. Toxins, 2021, 13, 253.	1.5	9
5548	In Silico Investigation of Potential Applications of Gamma Carbonic Anhydrases as Catalysts of CO2 Biomineralization Processes: A Visit to the Thermophilic Bacteria Persephonella hydrogeniphila, Persephonella marina, Thermosulfidibacter takaii, and Thermus thermophilus. International Journal of Molecular Sciences, 2021, 22, 2861.	1.8	5
5549	Large-scale discovery of protein interactions at residue resolution using co-evolution calculated from genomic sequences. Nature Communications, 2021, 12, 1396.	5.8	68
5551	Crystal structure of P. falciparum Cpn60 bound to ATP reveals an open dynamic conformation before substrate binding. Scientific Reports, 2021, 11, 5930.	1.6	2
5552	Structural and Biochemical Analysis of OrfG: The VirB8-like Component of the Conjugative Type IV Secretion System of ICESt3 From Streptococcus thermophilus. Frontiers in Molecular Biosciences, 2021, 8, 642606.	1.6	3

#	Article	IF	Citations
5553	Evolved increases in hemoglobin-oxygen affinity and the Bohr effect coincided with the aquatic specialization of penguins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
5555	Structural basis for the design of bisubstrate inhibitors of protein kinase CK2 provided by complex structures with the substrate-competitive inhibitor heparin. European Journal of Medicinal Chemistry, 2021, 214, 113223.	2.6	5
5556	Structural and Drug Screening Analysis of the Non-structural Proteins of Severe Acute Respiratory Syndrome Coronavirus 2 Virus Extracted From Indian Coronavirus Disease 2019 Patients. Frontiers in Genetics, 2021, 12, 626642.	1.1	16
5558	Structure of the microbial carboxypeptidase T complexed with the transition state analog N-sulfamoyl-l-lysine. Biophysical Chemistry, 2021, 270, 106535.	1.5	1
5559	Structural basis of the dynamic human CEACAM1 monomer-dimer equilibrium. Communications Biology, 2021, 4, 360.	2.0	6
5560	One Atom Makes All the Difference: Getting a Foot in the Door between SOS1 and KRAS. Journal of Medicinal Chemistry, 2021, 64, 6569-6580.	2.9	31
5561	Targeting a neoantigen derived from a common <i>TP53</i> mutation. Science, 2021, 371, .	6.0	194
5562	Structural and functional analysis of the <i>Klebsiella pneumoniae</i> MazEF toxinâ€"antitoxin system. IUCrJ, 2021, 8, 362-371.	1.0	4
5565	Oligomeric quaternary structure of <i>Escherichia coli</i> and <i>Mycobacterium smegmatis</i> Lhr helicases is nucleated by a novel C-terminal domain composed of five winged-helix modules. Nucleic Acids Research, 2021, 49, 3876-3887.	6.5	4
5566	MCPdb: The bacterial microcompartment database. PLoS ONE, 2021, 16, e0248269.	1.1	11
5567	Structural and functional studies of SAV1707 from <i>Staphylococcus aureus</i> elucidate its distinct metal-dependent activity and a crucial residue for catalysis. Acta Crystallographica Section D: Structural Biology, 2021, 77, 587-598.	1.1	0
5568	Structure of the E. coli agmatinase, SPEB. PLoS ONE, 2021, 16, e0248991.	1.1	4
5569	Structural bioinformatics survey on disease-inducing missense mutations. Journal of Bioinformatics and Computational Biology, 2021, 19, 2150008.	0.3	0
5571	A unique leucine-valine adhesive motif supports structure and function of protein disulfide isomerase P5 via dimerization. Structure, 2021, 29, 1357-1370.e6.	1.6	8
5573	Structure of the complete, membrane-assembled COPII coat reveals a complex interaction network. Nature Communications, 2021, 12, 2034.	5.8	40
5574	Broad and potent neutralizing human antibodies to tick-borne flaviviruses protect mice from disease. Journal of Experimental Medicine, 2021, 218, .	4.2	25
5575	Simultaneous binding of Guidance Cues NET1 and RGM blocks extracellular NEO1 signaling. Cell, 2021, 184, 2103-2120.e31.	13.5	20
5576	Modular basis for potent SARS-CoV-2 neutralization by a prevalent VH1-2-derived antibody class. Cell Reports, 2021, 35, 108950.	2.9	54

#	ARTICLE	IF	CITATIONS
5577	SARM1 is a metabolic sensor activated by an increased NMN/NAD+ ratio to trigger axon degeneration. Neuron, 2021, 109, 1118-1136.e11.	3.8	168
5580	Crystal structure of an inulosucrase from <i>Halalkalicoccus</i><i>jeotgali</i> B3T, a halophilic archaeal strain. FEBS Journal, 2021, 288, 5723-5736.	2.2	8
5582	Crystal Structure of Escherichia coli Agmatinase: Catalytic Mechanism and Residues Relevant for Substrate Specificity. International Journal of Molecular Sciences, 2021, 22, 4769.	1.8	7
5583	Dimer Asymmetry and Light Activation Mechanism in <i>Brucella</i> Blue-Light Sensor Histidine Kinase. MBio, 2021, 12, .	1.8	12
5584	Structural basis of FANCD2 deubiquitination by USP1â^’UAF1. Nature Structural and Molecular Biology, 2021, 28, 356-364.	3.6	21
5585	Specificity of AMPylation of the human chaperone BiP is mediated by TPR motifs of FICD. Nature Communications, 2021, 12, 2426.	5.8	15
5589	Multiple substrate recognition by yeast diadenosine and diphosphoinositol polyphosphate phosphohydrolase through phosphate clamping. Science Advances, 2021, 7, .	4.7	12
5590	Structural basis of chitin utilization by a GH20 Î²-<i>N</i>-acetylglucosaminidase from <i>Vibrio campbellii</i> strain ATCC BAA-1116. Acta Crystallographica Section D: Structural Biology, 2021, 77, 674-689.	1.1	2
5593	Protein Footprinting, Conformational Dynamics, and Core Interface-Adjacent Neutralization â€œHotspotsâ€•in the SARS-CoV-2 Spike Protein Receptor Binding Domain/Human ACE2 Interaction. Journal of the American Society for Mass Spectrometry, 2021, 32, 1593-1600.	1.2	23
5594	The Role of Changing Loop Conformations in Streptavidin Versions Engineered for High-affinity Binding of the Strep-tag II Peptide. Journal of Molecular Biology, 2021, 433, 166893.	2.0	8
5596	The SARSâ€unique domain (SUD) of SARSâ€CoV and SARSâ€CoVâ€2 interacts with human Paip1 to enhance viral RNA translation. EMBO Journal, 2021, 40, e102277.	3.5	26
5598	Human <scp>DND1â€RRM2</scp> forms a nonâ€canonical domain swapped dimer. Protein Science, 2021, 30, 1184-1195.	3.1	5
5599	Solution and Membrane Interaction Dynamics of <i>Mycobacterium tuberculosis</i> Fatty Acyl-CoA Synthetase FadD13. Biochemistry, 2021, 60, 1520-1532.	1.2	1
5601	The â€˜Shape-Shifterâ€™ Peptide from the Disulphide Isomerase PmScsC Shows Context-Dependent Conformational Preferences. Biomolecules, 2021, 11, 642.	1.8	1
5602	Structural basis for substrate specificity of the peroxisomal acylâ€CoA hydrolase MpaHâ€™ involved in mycophenolic acid biosynthesis. FEBS Journal, 2021, 288, 5768-5780.	2.2	4
5603	Crystal structures reveal a novel dimer of the RWD domain of human general control nonderepressible 2. Biochemical and Biophysical Research Communications, 2021, 549, 164-170.	1.0	1
5604	SARS-CoV-2 and other human coronaviruses: Mapping of protease recognition sites, antigenic variation of spike protein and their grouping through molecular phylogenetics. Infection, Genetics and Evolution, 2021, 89, 104729.	1.0	5
5606	A Structural Landscape of Neutralizing Antibodies Against SARS-CoV-2 Receptor Binding Domain. Frontiers in Immunology, 2021, 12, 647934.	2.2	52

#	ARTICLE	IF	CITATIONS
5607	Structural basis for the exolytic activity of polysaccharide lyase family 6 alginate lyase BcAlyPL6 from human gut microbe Bacteroides clarus. Biochemical and Biophysical Research Communications, 2021, 547, 111-117.	1.0	9
5608	Effective rational humanization of a PASylated anti-galectin-3 Fab for the sensitive PET imaging of thyroid cancer in vivo. Scientific Reports, 2021, 11, 7358.	1.6	5
5609	The tissue protective functions of interleukin-22 can be decoupled from pro-inflammatory actions through structure-based design. Immunity, 2021, 54, 660-672.e9.	6.6	36
5610	The Botrytis cinerea Crh1 transglycosylase is a cytoplasmic effector triggering plant cell death and defense response. Nature Communications, 2021, 12, 2166.	5.8	47
5611	Conformational interconversion of MLKL and disengagement from RIPK3 precede cell death by necroptosis. Nature Communications, 2021, 12, 2211.	5.8	56
5612	Membrane Barrels Are Taller, Fatter, Inside-Out Soluble Barrels. Journal of Physical Chemistry B, 2021, 125, 3622-3628.	1.2	13
5614	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. Cell, 2021, 184, 2201-2211.e7.	13.5	442
5615	Structure and dynamics of a mycobacterial typeÂVII secretion system. Nature, 2021, 593, 445-448.	13.7	54
5616	Structural Profiling of Bacterial Effectors Reveals Enrichment of Host-Interacting Domains and Motifs. Frontiers in Molecular Biosciences, 2021, 8, 626600.	1.6	4
5617	Surface-Induced Dissociation of Anionic vs Cationic Native-Like Protein Complexes. Journal of the American Chemical Society, 2021, 143, 7698-7706.	6.6	8
5618	Structural and biochemical analyses of concanavalin A circular permutation by jack bean asparaginyl endopeptidase. Plant Cell, 2021, 33, 2794-2811.	3.1	9
5619	Structural and functional characterization of the N-terminal acetyltransferase Naa50. Structure, 2021, 29, 413-425.e5.	1.6	6
5620	Virion Structure and <i>In Vitro</i> Genome Release Mechanism of Dicistrovirus Kashmir Bee Virus. Journal of Virology, 2021, 95, .	1.5	4
5622	Structural Basis for the Interactions of the Colibactin Resistance Gene Product ClbS with DNA. Biochemistry, 2021, 60, 1619-1625.	1.2	8
5624	Structural and Functional Analyses of the Tridomainâ€Nonribosomal Peptide Synthetase FmoA3 for 4â€Methyloxazoline Ring Formation. Angewandte Chemie, 2021, 133, 14675-14683.	1.6	0
5625	Structure-kinetic relationship reveals the mechanism of selectivity of FAK inhibitors over PYK2. Cell Chemical Biology, 2021, 28, 686-698.e7.	2.5	36
5626	KEAP1 Cancer Mutants: A Large-Scale Molecular Dynamics Study of Protein Stability. International Journal of Molecular Sciences, 2021, 22, 5408.	1.8	7
5628	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. Science, 2021, 373, 818-823.	6.0	309

#	ARTICLE	IF	CITATIONS
5629	Phospholipid translocation captured in a bifunctional membrane protein MprF. Nature Communications, 2021, 12, 2927.	5.8	21
5630	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. Nature Communications, 2021, 12, 2578.	5.8	55
5631	The structure of POMGNT2 provides new insights into the mechanism to determine the functional O â€mannosylation site on Î±â€dystroglycan. Genes To Cells, 2021, 26, 485-494.	0.5	5
5632	Attacking COVID-19 Progression Using Multi-Drug Therapy for Synergetic Target Engagement. Biomolecules, 2021, 11, 787.	1.8	14
5633	Cryo-EM structure of the EspA filament from enteropathogenic Escherichia coli: Revealing the mechanism of effector translocation in the T3SS. Structure, 2021, 29, 479-487.e4.	1.6	7
5635	Structures of a non-ribosomal peptide synthetase condensation domain suggest the basis of substrate selectivity. Nature Communications, 2021, 12, 2511.	5.8	53
5636	A combination of cross-neutralizing antibodies synergizes to prevent SARS-CoV-2 and SARS-CoV pseudovirus infection. Cell Host and Microbe, 2021, 29, 806-818.e6.	5.1	49
5638	ProtCHOIR: a tool for proteome-scale generation of homo-oligomers. Briefings in Bioinformatics, 2021, 22, .	3.2	3
5639	Structure of detergent-activated BAK dimers derived from the inert monomer. Molecular Cell, 2021, 81, 2123-2134.e5.	4.5	26
5641	A comprehensive review of m6A/m6Am RNA methyltransferase structures. Nucleic Acids Research, 2021, 49, 7239-7255.	6.5	190
5642	Structure prediction and function characterization of WC-2 proteins in Blakeslea trispora. International Microbiology, 2021, 24, 427-439.	1.1	3
5643	Cryo-EM structure of mammalian RNA polymerase II in complex with human RPAP2. Communications Biology, 2021, 4, 606.	2.0	11
5644	Crystal structure of a novel homodimeric <scp>l</scp>â€ribulose 3â€epimerase from <i>Methylomonus</i> sp.. FEBS Open Bio, 2021, 11, 1621-1637.	1.0	8
5645	Designing Novel Teduglutide Analogues with Improved Binding Affinity: An In Silico Peptide Engineering Approach. Current Computer-Aided Drug Design, 2021, 17, 225-234.	0.8	2
5646	Structural and mechanistic insights into the bifunctional HISN2 enzyme catalyzing the second and third steps of histidine biosynthesis in plants. Scientific Reports, 2021, 11, 9647.	1.6	5
5647	Molecular mechanism of N-terminal acetylation by the ternary NatC complex. Structure, 2021, 29, 1094-1104.e4.	1.6	7
5648	Structural model of the M7G46 Methyltransferase TrmB in complex with tRNA. RNA Biology, 2021, 18, 2466-2479.	1.5	8
5649	Clustering of Zika Viruses Originating from Different Geographical Regions using Computational Sequence Descriptors. Current Computer-Aided Drug Design, 2021, 17, 314-322.	0.8	4

#	ARTICLE	IF	CITATIONS
5650	Characterization of a novel type of carbonic anhydrase that acts without metal cofactors. BMC Biology, 2021, 19, 105.	1.7	37
5652	Bacterial Evolutionary Precursors of Eukaryotic Copperâ€"Zinc Superoxide Dismutases. Molecular Biology and Evolution, 2021, 38, 3789-3803.	3.5	5
5653	Putative hexameric glycosyltransferase functional unit revealed by the crystal structure of <i>Acinetobacter baumannii</i> MurG. IUCrJ, 2021, 8, 574-583.	1.0	4
5654	Potent SARS-CoV-2 neutralizing antibodies directed against spike N-terminal domain target a single supersite. Cell Host and Microbe, 2021, 29, 819-833.e7.	5.1	444
5655	Polysaccharide utilization loci-driven enzyme discovery reveals BD-FAE: a bifunctional feruloyl and acetyl xylan esterase active on complex natural xylans. Biotechnology for Biofuels, 2021, 14, 127.	6.2	10
5656	Antibody evasion by the P.1 strain of SARS-CoV-2. Cell, 2021, 184, 2939-2954.e9.	13.5	519
5657	RGS5â€"TGFÎ²â€"Smad2/3 axis switches pro- to anti-apoptotic signaling in tumor-residing pericytes, assisting tumor growth. Cell Death and Differentiation, 2021, 28, 3052-3076.	5.0	21
5658	Computational Studies of the Structural Basis of Human RPS19 Mutations Associated With Diamond-Blackfan Anemia. Frontiers in Genetics, 2021, 12, 650897.	1.1	3
5659	Structural Design and Analysis of the RHOA-ARHGEF1 Binding Mode: Challenges and Applications for Protein-Protein Interface Prediction. Frontiers in Molecular Biosciences, 2021, 8, 643728.	1.6	1
5660	Structure and Mechanism of d-Glucosaminate-6-phosphate Ammonia-lyase: A Novel Octameric Assembly for a Pyridoxal 5â€²-Phosphate-Dependent Enzyme, and Unprecedented Stereochemical Inversion in the Elimination Reaction of a d-Amino Acid. Biochemistry, 2021, 60, 1609-1618.	1.2	3
5661	Functional and structural characterization of a two-MAb cocktail for delayed treatment of enterovirus D68 infections. Nature Communications, 2021, 12, 2904.	5.8	19
5663	Phylogenetic and Structural Analysis of NIN-Like Proteins With a Type I/II PB1 Domain That Regulates Oligomerization for Nitrate Response. Frontiers in Plant Science, 2021, 12, 672035.	1.7	7
5664	Cryo-EM structure of type 1 IP3R channel in a lipid bilayer. Communications Biology, 2021, 4, 625.	2.0	64
5665	Crystal structure and molecular dynamics of human <scp>POLDIP2</scp>, a multifaceted adaptor protein in metabolism and genome stability. Protein Science, 2021, 30, 1196-1209.	3.1	6
5666	Destabilization of EpCAM dimer is associated with increased susceptibility towards cleavage by TACE. PeerJ, 2021, 9, e11484.	0.9	3
5667	Crystal structure of enoyl-CoA hydratase from <i>Thermus thermophilus</i> HB8. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 148-155.	0.4	2
5668	Structure and Thermal Stability of wtRop and RM6 Proteins through All-Atom Molecular Dynamics Simulations and Experiments. International Journal of Molecular Sciences, 2021, 22, 5931.	1.8	7
5669	Crystal Structure of the [4Feâ€"4S] Cluster-Containing Adenosine-5â€²-phosphosulfate Reductase from <i>Mycobacterium tuberculosis</i>. ACS Omega, 2021, 6, 13756-13765.	1.6	1

#	Article	IF	Citations
5670	Computational designing of a peptide that potentially blocks the entry of SARS-CoV, SARS-CoV-2 and MERS-CoV. PLoS ONE, 2021, 16, e0251913.	1.1	8
5671	Crystal and solution structures reveal oligomerization of individual capsid homology domains of Drosophila Arc. PLoS ONE, 2021, 16, e0251459.	1.1	7
5673	Structural and Functional Analyses of the Tridomainâ€Nonribosomal Peptide Synthetase FmoA3 for 4â€Methyloxazoline Ring Formation. Angewandte Chemie - International Edition, 2021, 60, 14554-14562.	7.2	21
5674	Metabolic bifunctionality of Rv0812 couples folate and peptidoglycan biosynthesis in <i>Mycobacterium tuberculosis</i>. Journal of Experimental Medicine, 2021, 218, .	4.2	4
5675	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with Î±-actinin. Science Advances, 2021, 7, .	4.7	15
5679	Significantly improving the thermostability of a hyperthermophilic GH10 family xylanase XynAF1 by semi-rational design. Applied Microbiology and Biotechnology, 2021, 105, 4561-4576.	1.7	17
5680	Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. Cell Reports, 2021, 35, 109109.	2.9	21
5681	The structure of an infectious immature flavivirus redefines viral architecture and maturation. Science Advances, 2021, 7, .	4.7	33
5682	Actin binding to galectin-13/placental protein-13 occurs independently of the galectin canonical ligand-binding site. Glycobiology, 2021, 31, 1219-1229.	1.3	5
5683	Noncanonical protein kinase A activation by oligomerization of regulatory subunits as revealed by inherited Carney complex mutations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
5684	Structural insights into the cross-neutralization of SARS-CoV and SARS-CoV-2 by the human monoclonal antibody 47D11. Science Advances, 2021, 7, .	4.7	42
5685	Assessment of proteinâ€“protein interfaces in cryo-EM derived assemblies. Nature Communications, 2021, 12, 3399.	5.8	20
5687	PDBe aggregated API: programmatic access to an integrative knowledge graph of molecular structure data. Bioinformatics, 2021, 37, 3950-3952.	1.8	12
5689	The MLKL kinase-like domain dimerization is an indispensable step of mammalian MLKL activation in necroptosis signaling. Cell Death and Disease, 2021, 12, 638.	2.7	15
5690	Crystal structures of HER3 extracellular domain 4 in complex with the designed ankyrin-repeat protein D5. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 192-201.	0.4	4
5691	The Structure of a Peptide-Loaded Shark MHC Class I Molecule Reveals Features of the Binding between Î²2-Microglobulin and H Chain Conserved in Evolution. Journal of Immunology, 2021, 207, 308-321.	0.4	13
5692	Fixed-target serial femtosecond crystallography using <i>in cellulo</i> grown microcrystals. IUCrJ, 2021, 8, 665-677.	1.0	10
5693	Novel 4-Hydroxybenzyl Adducts in Human Hemoglobin: Structures and Mechanisms of Formation. Chemical Research in Toxicology, 2021, 34, 1769-1781.	1.7	4

#	ARTICLE	IF	CITATIONS
5694	Reviving lost binding sites: Exploring calciumâ€•binding site transitions between human and murine CD23. FEBS Open Bio, 2021, 11, 1827-1840.	1.0	2
5695	Computational Resources for Bioscience Education. Applied Biochemistry and Biotechnology, 2021, 193, 3418-3424.	1.4	0
5696	Unexpected Gating Behaviour of an Engineered Potassium Channel Kir. Frontiers in Molecular Biosciences, 2021, 8, 691901.	1.6	3
5697	The Plastid-Encoded RNA Polymerase-Associated Protein PAP9 Is a Superoxide Dismutase With Unusual Structural Features. Frontiers in Plant Science, 2021, 12, 668897.	1.7	11
5698	Up State of the SARS-COV-2 Spike Homotrimer Favors an Increased Virulence for New Variants. Frontiers in Medical Technology, 2021, 3, 694347.	1.3	22
5699	Quantitative description of a contractile macromolecular machine. Science Advances, 2021, 7, .	4.7	9
5700	Structural and functional analysis of the simultaneous binding of two duplex/quadruplex aptamers to human Î±-thrombin. International Journal of Biological Macromolecules, 2021, 181, 858-867.	3.6	8
5701	Two human antibodies to a meningococcal serogroup B vaccine antigen enhance binding of complement Factor H by stabilizing the Factor H binding site. PLoS Pathogens, 2021, 17, e1009655.	2.1	1
5702	Structures of the human cholecystokinin 1 (CCK1) receptor bound to Gs and Gq mimetic proteins provide insight into mechanisms of G protein selectivity. PLoS Biology, 2021, 19, e3001295.	2.6	41
5703	The crystal structure of yeast regulatory subunit reveals key evolutionary insights into Protein Kinase A oligomerization. Journal of Structural Biology, 2021, 213, 107732.	1.3	1
5704	Structural Evidence of Active Site Adaptability towards Different Sized Substrates of Aromatic Amino Acid Aminotransferase from Psychrobacter Sp. B6. Materials, 2021, 14, 3351.	1.3	3
5707	The Molecular Basis for Escherichia coli O157:H7 Phage FAHEc1 Endolysin Function and Protein Engineering to Increase Thermal Stability. Viruses, 2021, 13, 1101.	1.5	10
5708	Learning from Nature: From a Marine Natural Product to Synthetic Cyclooxygenaseâ€•1 Inhibitors by Automated De Novo Design. Advanced Science, 2021, 8, e2100832.	5.6	17
5709	Snapshots along the catalytic path of KabA, a PLP-dependent aminotransferase required for kanosamine biosynthesis in Bacillus cereus UW85. Journal of Structural Biology, 2021, 213, 107744.	1.3	1
5710	Porous assembly of an antifungal protein mediated by zinc and sulfonato-calix[8]arene. Journal of Structural Biology, 2021, 213, 107711.	1.3	8
5711	Redefining Protein Interfaces within Protein Single Crystals with DNA. Journal of the American Chemical Society, 2021, 143, 8925-8934.	6.6	16
5712	Nse5/6 inhibits the Smc5/6 ATPase and modulates DNA substrate binding. EMBO Journal, 2021, 40, e107807.	3.5	30
5715	Xyloglucan processing machinery in Xanthomonas pathogens and its role in the transcriptional activation of virulence factors. Nature Communications, 2021, 12, 4049.	5.8	26

#	ARTICLE	IF	CITATIONS
5716	Copper binding by a unique family of metalloproteins is dependent on kynurenine formation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
5717	Co-crystallization with diabodies: A case study for the introduction of synthetic symmetry. Structure, 2021, 29, 598-605.e3.	1.6	3
5718	Epitope Classification and RBD Binding Properties of Neutralizing Antibodies Against SARS-CoV-2 Variants of Concern. Frontiers in Immunology, 2021, 12, 691715.	2.2	76
5719	Transamidation Down-Regulates Intestinal Immunity of Recombinant Î±-Gliadin in HLA-DQ8 Transgenic Mice. International Journal of Molecular Sciences, 2021, 22, 7019.	1.8	6
5720	Structural Comparison Between MHC Classes I and II; in Evolution, a Class-II-Like Molecule Probably Came First. Frontiers in Immunology, 2021, 12, 621153.	2.2	17
5721	RAS-inhibiting biologics identify and probe druggable pockets including an SII-Î±3 allosteric site. Nature Communications, 2021, 12, 4045.	5.8	19
5722	Native mass spectrometry analyses of chaperonin complex TRiC/CCT reveal subunit N-terminal processing and re-association patterns. Scientific Reports, 2021, 11, 13084.	1.6	7
5723	Targeting a Cryptic Pocket in a Proteinâ€“Protein Contact by Disulfide-Induced Rupture of a Homodimeric Interface. ACS Chemical Biology, 2021, 16, 1090-1098.	1.6	2
5724	Crystal structure of the C-terminal domain of envelope protein VP37 from white spot syndrome virus reveals sulphate binding sites responsible for heparin binding. Journal of General Virology, 2021, 102, .	1.3	4
5725	Structural insights into dpCoA-RNA decapping by NudC. RNA Biology, 2021, 18, 244-253.	1.5	10
5726	A Norovirus Uses Bile Salts To Escape Antibody Recognition While Enhancing Receptor Binding. Journal of Virology, 2021, 95, e0017621.	1.5	14
5727	Entropic pressure controls the oligomerization of the <i>Vibrio cholerae</i> ParD2 antitoxin. Acta Crystallographica Section D: Structural Biology, 2021, 77, 904-920.	1.1	5
5728	Structural and Biochemical Characterization of a Dye-Decolorizing Peroxidase from Dictyostelium discoideum. International Journal of Molecular Sciences, 2021, 22, 6265.	1.8	11
5729	A systematic bioinformatics approach for large-scale identification and characterization of host-pathogen shared sequences. BMC Genomics, 2021, 22, 700.	1.2	0
5730	Structure of the dihydrolipoamide succinyltransferase (E2) component of the human alpha-ketoglutarate dehydrogenase complex (hKGDHc) revealed by cryo-EM and cross-linking mass spectrometry: Implications for the overall hKGDHc structure. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129889.	1.1	23
5731	NAD(H)-mediated tetramerization controls the activity of <i>Legionella pneumophila</i> phospholipase PlaB. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	3
5732	The zinc-finger protein Red1 orchestrates MTREC submodules and binds the Mtl1 helicase arch domain. Nature Communications, 2021, 12, 3456.	5.8	19
5733	Protein-macrocycle framework engineering: supramolecular copolymerisation with two disparate calixarenes. Supramolecular Chemistry, 2021, 33, 122-128.	1.5	3

#	Article	IF	Citations
5735	Sphingomonas sp. KT-1 PahZ2 Structure Reveals a Role for Conformational Dynamics in Peptide Bond Hydrolysis. Journal of Physical Chemistry B, 2021, 125, 5722-5739.	1.2	1
5736	Inhibitors of bacterial H ₂ S biogenesis targeting antibiotic resistance and tolerance. Science, 2021, 372, 1169-1175.	6.0	112
5737	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. Cell, 2021, 184, 3205-3221.e24.	13.5	73
5739	PDBrenum: A webserver and program providing Protein Data Bank files renumbered according to their UniProt sequences. PLoS ONE, 2021, 16, e0253411.	1.1	21
5740	Conserved features of the <scp>MlaD</scp> domain aid the trafficking of hydrophobic molecules. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1473-1488.	1.5	1
5741	Conformational changes of loops highlight a potential binding site in <i>Rhodococcus equi</i> VapB. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 246-253.	0.4	3
5742	Structural basis of the cooperative activation of type II citrate synthase (HyCS) from Hymenobacter sp. PAMC 26554. International Journal of Biological Macromolecules, 2021, 183, 213-221.	3.6	5
5744	Structural and Biochemical Characterization of the Flavin-Dependent Siderophore-Interacting Protein from <i>Acinetobacter baumannii</i>. ACS Omega, 2021, 6, 18537-18547.	1.6	5
5745	Cryo-EM structure and dynamics of the green-light absorbing proteorhodopsin. Nature Communications, 2021, 12, 4107.	5.8	15
5746	Structural basis of the conformational changes in Microbacterium hydrocarbonoxydans IclR transcription factor homolog due to ligand binding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140644.	1.1	1
5747	Probing the role of the residues in the active site of the transaminase from Thermobaculum terrenum. PLoS ONE, 2021, 16, e0255098.	1.1	1
5748	<i>Trypanosoma cruzi</i> Malic Enzyme Is the Target for Sulfonamide Hits from the GSK Chagas Box. ACS Infectious Diseases, 2021, 7, 2455-2471.	1.8	1
5750	Structural and evolutionary exploration of the IL-3 family and its alpha subunit receptors. Amino Acids, 2021, 53, 1211-1227.	1.2	3
5752	Structural basis for accommodation of emerging B.1.351 and B.1.1.7 variants by two potent SARS-CoV-2 neutralizing antibodies. Structure, 2021, 29, 655-663.e4.	1.6	52
5753	Structure of RNA polymerase II pre-initiation complex at 2.9ÂÃ… defines initial DNA opening. Cell, 2021, 184, 4064-4072.e28.	13.5	42
5754	CIB2 and CIB3 are auxiliary subunits of the mechanotransduction channel of hair cells. Neuron, 2021, 109, 2131-2149.e15.	3.8	35
5757	MycobacteriumÂtuberculosisÂProtein PE6 (Rv0335c), a Novel TLR4 Agonist, Evokes an Inflammatory Response and Modulates the Cell Death Pathways in Macrophages to Enhance Intracellular Survival. Frontiers in Immunology, 2021, 12, 696491.	2.2	40
5758	Screening of in vitro and in silico Î±-amylase, Î±-glucosidase, and lipase inhibitory activity of oxyprenylated natural compounds and semisynthetic derivatives. Phytochemistry, 2021, 187, 112781.	1.4	9

#	Article	IF	Citations
5759	Structural and conformational analysis of SARS CoV 2ÂN-CTD revealing monomeric and dimeric active sites during the RNA-binding and stabilization: Insights towards potential inhibitors for N-CTD. Computers in Biology and Medicine, 2021, 134, 104495.	3.9	14
5760	The structural features of an ancient ribonuclease from Salmo salar reveal an intriguing case of auto-inhibition. International Journal of Biological Macromolecules, 2021, 182, 659-668.	3.6	3
5762	Crystal Structure of a Retroviral Polyprotein: Prototype Foamy Virus Protease-Reverse Transcriptase (PR-RT). Viruses, 2021, 13, 1495.	1.5	4
5763	Mutation-induced dimerization of transforming growth factor-Î²â€“induced protein may drive protein aggregation in granular corneal dystrophy. Journal of Biological Chemistry, 2021, 297, 100858.	1.6	3
5764	Structures of the alkanesulfonate monooxygenase MsuD provide insight into Câ€“S bond cleavage, substrate scope, and an unexpected role for the tetramer. Journal of Biological Chemistry, 2021, 297, 100823.	1.6	5
5765	Identification of a BAZ2A Bromodomain Hit Compound by Fragment Joining. ACS Bio & Med Chem Au, 2021, 1, 5-10.	1.7	3
5766	Evolution of a Ïƒâ€“(c-di-GMP)â€“anti-Ïƒ switch. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
5767	Haven't got a glue: Protein surface variation for the design of molecular glue degraders. Cell Chemical Biology, 2021, 28, 1032-1047.	2.5	78
5768	Structural insights into the functional divergence of WhiB-like proteins in Mycobacterium tuberculosis. Molecular Cell, 2021, 81, 2887-2900.e5.	4.5	13
5770	Crystal Structure Reveals the Full Rasâ€“Raf Interface and Advances Mechanistic Understanding of Raf Activation. Biomolecules, 2021, 11, 996.	1.8	35
5772	Talin rod domainâ€“containing protein 1 (TLNRD1) is a novel actin-bundling protein which promotes filopodia formation. Journal of Cell Biology, 2021, 220, .	2.3	9
5773	The archaeal triphosphate tunnel metalloenzyme SaTTM defines structural determinants for the diverse activities in the CYTH protein family. Journal of Biological Chemistry, 2021, 297, 100820.	1.6	10
5774	An atomic model for the human septin hexamer by cryo-EM. Journal of Molecular Biology, 2021, 433, 167096.	2.0	26
5775	Dipeptidyl peptidase 9 sets a threshold for CARD8 inflammasome formation by sequestering its active C-terminal fragment. Immunity, 2021, 54, 1392-1404.e10.	6.6	47
5777	A synthetic nanobody targeting RBD protects hamsters from SARS-CoV-2 infection. Nature Communications, 2021, 12, 4635.	5.8	72
5778	TSC1 binding to lysosomal PIPs is required for TSC complex translocation and mTORC1 regulation. Molecular Cell, 2021, 81, 2705-2721.e8.	4.5	25
5779	Binding Properties of Photosynthetic Herbicides with the QB Site of the D1 Protein in Plant Photosystem II: A Combined Functional and Molecular Docking Study. Plants, 2021, 10, 1501.	1.6	22
5780	Structural studies of complexes of kallikrein 4 with wild-type and mutated forms of the Kunitz-type inhibitor BbKI. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1084-1098.	1.1	1

#	ARTICLE	IF	CITATIONS
5781	Crystal structure of the TLDc domain of human NCOA7-AS. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 230-237.	0.4	3
5782	The X-ray structure of<scp>L</scp>-threonine dehydrogenase from the common hospital pathogen<i>Clostridium difficile</i>. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 269-274.	0.4	1
5784	Comparative analysis of two paradigm bacteriophytochromes reveals opposite functionalities in two-component signaling. Nature Communications, 2021, 12, 4394.	5.8	22
5785	Structure and regulation of the microtubule plus-end tracking protein Kar9. Structure, 2021, 29, 1266-1278.e4.	1.6	5
5786	Structures of full-length VanR from <i>Streptomyces coelicolor</i> in both the inactive and activated states. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1027-1039.	1.1	10
5787	Modeling and Structure Determination of Homo-Oligomeric Proteins: An Overview of Challenges and Current Approaches. International Journal of Molecular Sciences, 2021, 22, 9081.	1.8	10
5788	The Uncommon Active Site of D-Amino Acid Transaminase from Haliscomenobacter hydrossis: Biochemical and Structural Insights into the New Enzyme. Molecules, 2021, 26, 5053.	1.7	14
5789	Effect of SARS-CoV-2 B.1.1.7 mutations on spike protein structure and function. Nature Structural and Molecular Biology, 2021, 28, 731-739.	3.6	124
5790	Characterization of a triad of genes in cyanophage S-2L sufficient to replace adenine by 2-aminoadenine in bacterial DNA. Nature Communications, 2021, 12, 4710.	5.8	15
5791	Cryo-EM structure of the periplasmic tunnel of T7 DNA-ejectosome at 2.7ÂÅ... resolution. Molecular Cell, 2021, 81, 3145-3159.e7.	4.5	17
5792	SAMase of Bacteriophage T3 Inactivates Escherichia coliâ€™s Methionine <i>S</i> -Adenosyltransferase by Forming Heteropolymers. MBio, 2021, 12, e0124221.	1.8	5
5793	High-resolution structure of the amino acid transporter AdiC reveals insights into the role of water molecules and networks in oligomerization and substrate binding. BMC Biology, 2021, 19, 179.	1.7	10
5795	Allosteric transcription stimulation by RNA polymerase II super elongation complex. Molecular Cell, 2021, 81, 3386-3399.e10.	4.5	17
5796	Assessing the binding properties of <scp>CASP14</scp> targets and models. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1922-1939.	1.5	11
5797	Understanding and Engineering the Stereoselectivity of Humulene Synthase. Angewandte Chemie - International Edition, 2021, 60, 20308-20312.	7.2	15
5798	Rapid selection of HIV envelopes that bind to neutralizing antibody B cell lineage members with functional improbable mutations. Cell Reports, 2021, 36, 109561.	2.9	9
5799	Identification of Ubiquitin Variants That Inhibit the E2 Ubiquitin Conjugating Enzyme, Ube2k. ACS Chemical Biology, 2021, 16, 1745-1756.	1.6	12
5800	Neutralization of the anthrax toxin by antibody-mediated stapling of its membrane-penetrating loop. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1197-1205.	1.1	2

#	ARTICLE	IF	CITATIONS
5801	Directâ€MS analysis of antibodyâ€antigen complexes. Proteomics, 2021, 21, e2000300.	1.3	8
5803	UbiD domain dynamics underpins aromatic decarboxylation. Nature Communications, 2021, 12, 5065.	5.8	14
5805	Potent Human Single-Domain Antibodies Specific for a Novel Prefusion Epitope of Respiratory Syncytial Virus F Glycoprotein. Journal of Virology, 2021, 95, e0048521.	1.5	7
5806	The intervening domain is required for DNA-binding and functional identity of plant MADS transcription factors. Nature Communications, 2021, 12, 4760.	5.8	29
5807	Structural insights into Cullin4-RING ubiquitin ligase remodelling by Vpr from simian immunodeficiency viruses. PLoS Pathogens, 2021, 17, e1009775.	2.1	11
5808	Structural insight into host plasma membrane association and assembly of HIV-1 matrix protein. Scientific Reports, 2021, 11, 15819.	1.6	6
5809	Perturbation of ACE2 Structural Ensembles by SARS-CoV-2 Spike Protein Binding. Journal of Chemical Theory and Computation, 2021, 17, 5896-5906.	2.3	3
5810	The Chemical Synthesis of Knob Domain Antibody Fragments. ACS Chemical Biology, 2021, 16, 1757-1769.	1.6	10
5811	Structure of the Arabidopsis thaliana glutamate receptor-like channel GLR3.4. Molecular Cell, 2021, 81, 3216-3226.e8.	4.5	39
5812	Near-Pan-neutralizing, Plasma Deconvoluted Antibody N49P6 Mimics Host Receptor CD4 in Its Quaternary Interactions with the HIV-1 Envelope Trimer. MBio, 2021, 12, e0127421.	1.8	4
5814	The extracellular region of bovine milk butyrophilin exhibits closer structural similarity to human myelin oligodendrocyte glycoprotein than to immunological BTN family receptors. Biological Chemistry, 2021, 402, 1187-1202.	1.2	4
5815	Unfolding Mechanisms and Conformational Stability of the Dimeric Endophilin N-BAR Domain. ACS Omega, 2021, 6, 20790-20803.	1.6	3
5817	<i>Bdellovibrio bacteriovorus</i> phosphoglucose isomerase structures reveal novel rigidity in the active site of a selected subset of enzymes upon substrate binding. Open Biology, 2021, 11, 210098.	1.5	2
5819	Structural and biochemical characterization of the novel serpin Iripin-5 from <i>Ixodes ricinus</i>. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1183-1196.	1.1	8
5820	Ankyrin repeats in context with human population variation. PLoS Computational Biology, 2021, 17, e1009335.	1.5	5
5821	Crystal Structure of a Sucrose-6-phosphate Hydrolase from <i>Lactobacillus gasseri</i> with Potential Applications in Fructan Production and the Food Industry. Journal of Agricultural and Food Chemistry, 2021, 69, 10223-10234.	2.4	6
5822	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. Nucleic Acids Research, 2021, 49, 10166-10177.	6.5	11
5823	A reverse catalytic triad Asp containing loop shaping a wide substrate binding pocket of a feruloyl esterase from Lactobacillus plantarum. International Journal of Biological Macromolecules, 2021, 184, 92-100.	3.6	9

#	ARTICLE	IF	CITATIONS
5824	Structural basis of staphylococcal Stl inhibition on a eukaryotic dUTPase. International Journal of Biological Macromolecules, 2021, 184, 821-830.	3.6	2
5825	Affinity maturation of SARS-CoV-2 neutralizing antibodies confers potency, breadth, and resilience to viral escape mutations. Immunity, 2021, 54, 1853-1868.e7.	6.6	230
5826	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell, 2021, 184, 4220-4236.e13.	13.5	630
5827	Complex structure of the acyltransferase VinK and the carrier protein VinL with a pantetheine cross-linking probe. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 294-302.	0.4	6
5828	The PilB-PilZ-FimX regulatory complex of the Type IV pilus from Xanthomonas citri. PLoS Pathogens, 2021, 17, e1009808.	2.1	6
5829	The Repressor C Protein, Pf4r, Controls Superinfection of Pseudomonas aeruginosa PAO1 by the Pf4 Filamentous Phage and Regulates Host Gene Expression. Viruses, 2021, 13, 1614.	1.5	11
5831	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. Communications Biology, 2021, 4, 949.	2.0	2
5833	A SARS-CoV-2 antibody broadly neutralizes SARS-related coronaviruses and variants by coordinated recognition of a virus-vulnerable site. Immunity, 2021, 54, 2385-2398.e10.	6.6	46
5834	Insights into the structure and RNA-binding specificity of <i>Caenorhabditis elegans</i> Dicer-related helicase 3 (DRH-3). Nucleic Acids Research, 2021, 49, 9978-9991.	6.5	4
5835	Structural features of Cryptococcus neoformans bifunctional GAR/AIR synthetase may present novel antifungal drug targets. Journal of Biological Chemistry, 2021, 297, 101091.	1.6	2
5836	Biochemical and Structural Characterisation of a Novel D-Lyxose Isomerase From the Hyperthermophilic Archaeon Thermofilum sp.. Frontiers in Bioengineering and Biotechnology, 2021, 9, 711487.	2.0	3
5837	Cryo-EM structure of a microtubule-bound parasite kinesin motor and implications for its mechanism and inhibition. Journal of Biological Chemistry, 2021, 297, 101063.	1.6	13
5838	Structure of a meiosis-specific complex central to BRCA2 localization at recombination sites. Nature Structural and Molecular Biology, 2021, 28, 671-680.	3.6	7
5839	Structural Basis of Inhibition of DCLK1 by Ruxolitinib. International Journal of Molecular Sciences, 2021, 22, 8488.	1.8	6
5840	Structural Basis for a Neutralizing Antibody Response Elicited by a Recombinant Hantaan Virus Gn Immunogen. MBio, 2021, 12, e0253120.	1.8	13
5841	Crystal structure of restriction endonuclease Kpn2I of CCGG-family. Biochimica Et Biophysica Acta - General Subjects, 2021, 1865, 129926.	1.1	0
5842	Crystal structure of the INTS3/INTS6 complex reveals the functional importance of INTS3 dimerization in DSB repair. Cell Discovery, 2021, 7, 66.	3.1	10
5846	Untersuchungen zum VerstÃndnis und zur Kontrolle der StereoselektivitÃt der Humulenâ€Synthase. Angewandte Chemie, 2021, 133, 20470-20475.	1.6	0

#	Article	IF	Citations
5847	Mechanism of DNA Interaction and Translocation by the Replicase of a Circular Rep-Encoding Single-Stranded DNA Virus. MBio, 2021, 12, e0076321.	1.8	12
5848	Structural insights into the function of the catalytically active human Taspase1. Structure, 2021, 29, 873-885.e5.	1.6	4
5849	X-shaped structure of bacterial heterotetrameric tRNA synthetase suggests cryptic prokaryote functions and a rationale for synthetase classifications. Nucleic Acids Research, 2021, 49, 10106-10119.	6.5	12
5850	Structural basis for the initiation of COPII vesicle biogenesis. Structure, 2021, 29, 859-872.e6.	1.6	10
5851	Structures of a deAMPylation complex rationalise the switch between antagonistic catalytic activities of FICD. Nature Communications, 2021, 12, 5004.	5.8	13
5852	Glycogen phosphorylase revisited: extending the resolution of the R- and T-state structures of the free enzyme and in complex with allosteric activators. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 303-311.	0.4	5
5855	DNA Aptamers Block the Receptor Binding Domain at the Spike Protein of SARS-CoV-2. Frontiers in Molecular Biosciences, 2021, 8, 713003.	1.6	11
5856	Structural Dissection of Viral Spike-Protein Binding of SARS-CoV-2 and SARS-CoV-1 to the Human Angiotensin-Converting Enzyme 2 (ACE2) as Cellular Receptor. Biomedicines, 2021, 9, 1038.	1.4	15
5857	Native structure of the RhopH complex, a key determinant of malaria parasite nutrient acquisition. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20
5858	The ongoing evolution of variants of concern and interest of SARS-CoV-2 in Brazil revealed by convergent indels in the amino (N)-terminal domain of the spike protein. Virus Evolution, 2021, 7, veab069.	2.2	31
5860	A potently neutralizing SARS-CoV-2 antibody inhibits variants of concern by utilizing unique binding residues in a highly conserved epitope. Immunity, 2021, 54, 2399-2416.e6.	6.6	79
5861	The endopeptidase of the maize-affecting Marafivirus type member maize rayado fino virus doubles as a deubiquitinase. Journal of Biological Chemistry, 2021, 297, 100957.	1.6	5
5862	SNX27-FERM-SNX1 complex structure rationalizes divergent trafficking pathways by SNX17 and SNX27. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
5863	Structural and Biochemical Basis for Higher-Order Assembly between A20-Binding Inhibitor of NF-Î°B 1 (ABIN1) and M1-Linked Ubiquitins. Journal of Molecular Biology, 2021, 433, 167116.	2.0	2
5864	Molecular recognition of structurally disordered Pro/Ala-rich sequences (PAS) by antibodies involves an Ala residue at the hot spot of the epitope. Journal of Molecular Biology, 2021, 433, 167113.	2.0	8
5865	Focal accumulation of aromaticity at the CDRH3 loop mitigates 4E10 polyreactivity without altering its HIV neutralization profile. IScience, 2021, 24, 102987.	1.9	1
5866	Cryo-EM structure of the cetacean morbillivirus nucleoprotein-RNA complex. Journal of Structural Biology, 2021, 213, 107750.	1.3	12
5869	Peptides Targeting the Interaction Between Erb1 and Ytm1 Ribosome Assembly Factors. Frontiers in Molecular Biosciences, 2021, 8, 718941.	1.6	1

#	ARTICLE	IF	CITATIONS
5870	Conformational control of Cas9 by CRISPR hybrid RNA-DNA guides mitigates off-target activity in TÂcells. Molecular Cell, 2021, 81, 3637-3649.e5.	4.5	27
5871	Solenoid architecture of HUWE1 contributes to ligase activity and substrate recognition. Molecular Cell, 2021, 81, 3468-3480.e7.	4.5	23
5872	In vivo pharmacokinetic enhancement of monomeric Fc and monovalent bispecific designs through structural guidance. Communications Biology, 2021, 4, 1048.	2.0	1
5874	Improved pathogenicity prediction for rare human missense variants. American Journal of Human Genetics, 2021, 108, 1891-1906.	2.6	51
5875	Capsid Structure of <i>Anabaena</i> Cyanophage A-1(L). Journal of Virology, 2021, 95, e0135621.	1.5	4
5876	Effect of Lithium Drug on Binding Affinities of Glycogen Synthase Kinase-3 Î² to Its Network Partners: A New Computational Approach. Journal of Chemical Information and Modeling, 2021, 61, 5280-5292.	2.5	1
5878	Mechanism of dimerization and structural features of human LI-cadherin. Journal of Biological Chemistry, 2021, 297, 101054.	1.6	4
5879	Intermolecular latency regulates the essential C-terminal signal peptidase and sortase of the <i>Porphyromonas gingivalis</i> type-IX secretion system. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	8
5880	Trop2 Forms a Stable Dimer with Significant Structural Differences within the Membrane-Distal Region as Compared to EpCAM. International Journal of Molecular Sciences, 2021, 22, 10640.	1.8	15
5881	Crystal Structure of a Cu,Zn Superoxide Dismutase From the Thermophilic Fungus Chaetomium thermophilum. Protein and Peptide Letters, 2021, 28, 1043-1053.	0.4	1
5882	Broad cross-reactivity across sarbecoviruses exhibited by a subset of COVID-19 donor-derived neutralizing antibodies. Cell Reports, 2021, 36, 109760.	2.9	80
5883	Bispecific antibodies targeting distinct regions of the spike protein potently neutralize SARS-CoV-2 variants of concern. Science Translational Medicine, 2021, 13, eabj5413.	5.8	79
5884	Structural basis for membrane recruitment of ATG16L1 by WIPI2 in autophagy. ELife, 2021, 10, .	2.8	32
5885	The hypervariable region of atlastin-1 is a site for intrinsic and extrinsic regulation. Journal of Cell Biology, 2021, 220, .	2.3	3
5886	A lipoprotein allosterically activates the CwlD amidase during Clostridioides difficile spore formation. PLoS Genetics, 2021, 17, e1009791.	1.5	8
5887	Structural characterization of human peptidyl-arginine deiminase type III by X-ray crystallography. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 334-340.	0.4	2
5888	Molecular basis of dimerization of lytic transglycosylase revealed by the crystal structure of MltA from <i>Acinetobacter baumannii</i>. IUCrJ, 2021, 8, 921-930.	1.0	1
5889	Structural biology of ionotropic glutamate delta receptors and their crosstalk with metabotropic glutamate receptors. Neuropharmacology, 2021, 196, 108683.	2.0	8

#	Article	IF	Citations
5890	Helical reconstruction of Salmonella and Shigella needle filaments attached to type 3 basal bodies. Biochemistry and Biophysics Reports, 2021, 27, 101039.	0.7	2
5891	Structural basis for the dimerization mechanism of human transcription factor E3. Biochemical and Biophysical Research Communications, 2021, 569, 41-46.	1.0	1
5893	Structure, interface stability and hot-spots identification for RBD(SARS-CoV-2):hACE2 complex formation. Molecular Simulation, 2021, 47, 1443-1454.	0.9	3
5895	Genetic diversity of bat coronaviruses and comparative genetic analysis of MERSâ€related coronaviruses in South Korea. Transboundary and Emerging Diseases, 2021, , .	1.3	1
5896	Understanding the molecular interaction of SARS-CoV-2 spike mutants with ACE2 (angiotensin) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	2.0	19
5897	A Crystallographic Snapshot of SARS-CoV-2 Main Protease Maturation Process. Journal of Molecular Biology, 2021, 433, 167118.	2.0	45
5898	Profiling CD8+ TÂcell epitopes of COVID-19 convalescents reveals reduced cellular immune responses to SARS-CoV-2 variants. Cell Reports, 2021, 36, 109708.	2.9	42
5900	A Novel Lipase from Lasiodiplodia theobromae Efficiently Hydrolyses C8-C10 Methyl Esters for the Preparation of Medium-Chain Triglyceridesâ€™ Precursors. International Journal of Molecular Sciences, 2021, 22, 10339.	1.8	2
5901	3D Domain Swapping Dimerization of the Receiver Domain of Cytokinin Receptor CRE1 From Arabidopsis thaliana and Medicago truncatula. Frontiers in Plant Science, 2021, 12, 756341.	1.7	3
5902	Comparison of Spatial Structures and Packaging of Phosphorybosil Pyrophosphate Synthetase 2 from Thermus thermophilus HB27 in Rhombohedral and Tetragonal Crystals. Crystals, 2021, 11, 1128.	1.0	1
5904	Auxiliary interfaces support the evolution of specific toxinâ€“antitoxin pairing. Nature Chemical Biology, 2021, 17, 1296-1304.	3.9	7
5905	Multiple Signals in the Gut Contract the Mouse Norovirus Capsid To Block Antibody Binding While Enhancing Receptor Affinity. Journal of Virology, 2021, 95, e0147121.	1.5	7
5906	N-Thio-Î²-lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of Mycobacterium tuberculosis. Cell Chemical Biology, 2021, 28, 1321-1332.e5.	2.5	8
5908	PDB-wide identification of physiological hetero-oligomeric assemblies based on conserved quaternary structure geometry. Structure, 2021, 29, 1303-1311.e3.	1.6	10
5910	Network theory reveals principles of spliceosome structure and dynamics. Structure, 2022, 30, 190-200.e2.	1.6	5
5912	Structure of the native pyruvate dehydrogenase complex reveals the mechanism of substrate insertion. Nature Communications, 2021, 12, 5277.	5.8	39
5913	Crystal structure of aspartyl dipeptidase from <scp><i>Xenopus laevis</i></scp> revealed ligand binding induced loop ordering and catalytic triad assembly. Proteins: Structure, Function and Bioinformatics, 2022, 90, 299-308.	1.5	0
5915	Structural basis of RNA polymerase inhibition by viral and host factors. Nature Communications, 2021, 12, 5523.	5.8	6

#	Article	IF	Citations
5916	Structural characterization of NrnC identifies unifying features of dinucleases. ELife, 2021, 10, .	2.8	6
5917	Phosphopantetheinyl transferase binding and inhibition by amidino-urea and hydroxypyrimidinethione compounds. Scientific Reports, 2021, 11, 18042.	1.6	2
5918	Association of the malate dehydrogenase-citrate synthase metabolon is modulated by intermediates of the Krebs tricarboxylic acid cycle. Scientific Reports, 2021, 11, 18770.	1.6	8
5920	Structural Insights into the Inhibition of Undecaprenyl Pyrophosphate Synthase from Gram-Positive Bacteria. Journal of Medicinal Chemistry, 2021, 64, 13540-13550.	2.9	2
5921	Optimisation of Neuraminidase Expression for Use in Drug Discovery by Using HEK293-6E Cells. Viruses, 2021, 13, 1893.	1.5	1
5923	Gamma Carbonic Anhydrases from Hydrothermal Vent Bacteria: Cases of Alternating Active Site Due to a Long Loop with Proton Shuttle Residue. Catalysts, 2021, 11, 1177.	1.6	1
5924	Landscape of human antibody recognition of the SARS-CoV-2 receptor binding domain. Cell Reports, 2021, 37, 109822.	2.9	35
5925	Structural and biochemical insights into CRISPR RNA processing by the Cas5c ribonuclease SMU1763 from Streptococcus mutans. Journal of Biological Chemistry, 2021, 297, 101251.	1.6	2
5927	Calmodulin extracts the Ras family protein RalA from lipid bilayers by engagement with two membrane-targeting motifs. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	5
5928	The unique structure of the zebrafish TNF-Î± homotrimer. Developmental and Comparative Immunology, 2021, 122, 104129.	1.0	2
5929	Regulation of human mTOR complexes by DEPTOR. ELife, 2021, 10, .	2.8	15
5930	Structure of a Ty1 restriction factor reveals the molecular basis of transposition copy number control. Nature Communications, 2021, 12, 5590.	5.8	12
5931	Structures of heat shock factor trimers bound to DNA. IScience, 2021, 24, 102951.	1.9	9
5932	Substrate specificity and conformational flexibility properties of the Mycobacterium tuberculosis Î²-oxidation trifunctional enzyme. Journal of Structural Biology, 2021, 213, 107776.	1.3	7
5933	Crystal structure and molecular mechanism of phosphotransbutyrylase from Clostridium acetobutylicum. Journal of Microbiology and Biotechnology, 2021, 31, 1393-1400.	0.9	0
5936	A complete Protocadherin-19 ectodomain model for evaluating epilepsy-causing mutations and potential protein interaction sites. Structure, 2021, 29, 1128-1143.e4.	1.6	4
5937	The 5-Ketofructose Reductase of <i>Gluconobacter</i> sp. Strain CHM43 Is a Novel Class in the Shikimate Dehydrogenase Family. Journal of Bacteriology, 2021, 203, e0055820.	1.0	1
5938	Conformational dynamics linked to domain closure and substrate binding explain the ERAP1 allosteric regulation mechanism. Nature Communications, 2021, 12, 5302.	5.8	22

#	ARTICLE	IF	CITATIONS
5939	Structure and substrate specificity determinants of NfnB, a dinitroaniline herbicideâ€“catabolizing nitroreductase from Sphingopyxis sp. strain HMH. Journal of Biological Chemistry, 2021, 297, 101143.	1.6	6
5940	Structural and functional characterization of ubiquitin variant inhibitors for the JAMM-family deubiquitinases STAMBP and STAMBPL1. Journal of Biological Chemistry, 2021, 297, 101107.	1.6	9
5941	Chemical-recognition-driven selectivity of SnO2-nanowire-based gas sensors. Nano Today, 2021, 40, 101265.	6.2	25
5942	Structure and SAXS studies unveiled a novel inhibition mechanism of the Pseudomonas aeruginosa T6SS TseT-TsiT complex. International Journal of Biological Macromolecules, 2021, 188, 450-459.	3.6	4
5943	Conformational changes in tubulin upon binding cryptophycin-52 reveal its mechanism of action. Journal of Biological Chemistry, 2021, 297, 101138.	1.6	8
5944	Exploring nod factor receptors activation process in chickpea by bridging modelling, docking and molecular dynamics simulations. International Journal of Biological Macromolecules, 2021, 189, 965-979.	3.6	3
5946	Structure-function analysis reveals Trichoderma virens Tsp1 to be a novel fungal effector protein modulating plant defence. International Journal of Biological Macromolecules, 2021, 191, 267-276.	3.6	4
5947	Crystal structure of histone chaperone Vps75 from Candida albicans. Biochemical and Biophysical Research Communications, 2021, 578, 136-141.	1.0	0
5948	BthTX-II from Bothrops jararacussu venom has variants with different oligomeric assemblies: An example of snake venom phospholipases A2 versatility. International Journal of Biological Macromolecules, 2021, 191, 255-266.	3.6	6
5949	Surface Exposed Free Cysteine Suppresses Crystallization of Human Î³D-Crystallin. Journal of Molecular Biology, 2021, 433, 167252.	2.0	3
5950	Child to adulthood clinical description of MDPL syndrome due to a novel variant in POLD1. European Journal of Medical Genetics, 2021, 64, 104333.	0.7	1
5951	Novel quaternary structures of the human prion protein globular domain. Biochimie, 2021, 191, 118-125.	1.3	4
5953	Structureâ€“function studies of the C3/C5 epimerases and C4 reductases of the Campylobacter jejuni capsular heptose modification pathways. Journal of Biological Chemistry, 2021, 296, 100352.	1.6	12
5954	Predicted structural mimicry of spike receptor-binding motifs from highly pathogenic human coronaviruses. Computational and Structural Biotechnology Journal, 2021, 19, 3938-3953.	1.9	25
5955	Functional and structural investigation of N-terminal domain of the SpTad2/3 heterodimeric tRNA deaminase. Computational and Structural Biotechnology Journal, 2021, 19, 3384-3393.	1.9	0
5956	Structure of transmembrane prolyl 4-hydroxylase reveals unique organization of EF and dioxygenase domains. Journal of Biological Chemistry, 2021, 296, 100197.	1.6	7
5957	Molecular basis of IRGB10 oligomerization and membrane association for pathogen membrane disruption. Communications Biology, 2021, 4, 92.	2.0	8
5958	Structural basis of trehalose recognition by the mycobacterial LpqY-SugABC transporter. Journal of Biological Chemistry, 2021, 296, 100307.	1.6	13

#	Article	IF	Citations
5959	Rational selection of building blocks for the assembly of bispecific antibodies. MAbs, 2021, 13, 1870058.	2.6	10
5960	A Novel Design of Multi-epitope Vaccine Against Helicobacter pylori by Immunoinformatics Approach. International Journal of Peptide Research and Therapeutics, 2021, 27, 1027-1042.	0.9	8
5962	Surface hydrophobics mediate functional dimerization of CYP121A1 of Mycobacterium tuberculosis. Scientific Reports, 2021, 11, 394.	1.6	7
5963	Crystal structures of the EVE-HNH endonuclease VcaM4I in the presence and absence of DNA. Nucleic Acids Research, 2021, 49, 1708-1723.	6.5	4
5964	Inhibition of the Complement Alternative Pathway by Chemically Modified DNA Aptamers That Bind with Picomolar Affinity to Factor B. Journal of Immunology, 2021, 206, 861-873.	0.4	10
5965	Rab1-AMPylation by Legionella DrrA is allosterically activated by Rab1. Nature Communications, 2021, 12, 460.	5.8	14
5966	Crystal and solution structure of NDRG1, a membraneâ€binding protein linked to myelination and tumour suppression. FEBS Journal, 2021, 288, 3507-3529.	2.2	10
5967	Structural characterization of a PCPâ€“R didomain from an archaeal nonribosomal peptide synthetase reveals novel interdomain interactions. Journal of Biological Chemistry, 2021, 296, 100432.	1.6	8
5970	GTP Binding to Translation Factor eIF2B Stimulates Its Guanine Nucleotide Exchange Activity. SSRN Electronic Journal, 0, , .	0.4	0
5971	A computational-cum-experimental study provides some clues on the druggable binding site and design of anticancer therapeutics on ETV1 transcription factor oncoprotein. Molecular Systems Design and Engineering, 0, , .	1.7	1
5972	A single residue can modulate nanocage assembly in salt dependent ferritin. Nanoscale, 2021, 13, 11932-11942.	2.8	11
5973	Molecular basis for Ras suppressor-1 binding to PINCH-1 in focal adhesion assembly. Journal of Biological Chemistry, 2021, 296, 100685.	1.6	5
5974	The flexible N-terminus of BchL autoinhibits activity through interaction with its [4Fe-4S] cluster and released upon ATP binding. Journal of Biological Chemistry, 2021, 296, 100107.	1.6	4
5975	B0AT1 Amino Acid Transporter Complexed With SARS-CoV-2 Receptor ACE2 Forms a Heterodimer Functional Unit:<i>In Situ</i>Conformation Using Radiation Inactivation Analysis. Function, 2021, 2, zqab027.	1.1	13
5976	Structural characterization of nonstructural protein 1 from SARS-CoV-2. IScience, 2021, 24, 101903.	1.9	60
5977	Structure of 3-mercaptopropionic acid dioxygenase with a substrate analog reveals bidentate substrate binding at the iron center. Journal of Biological Chemistry, 2021, 296, 100492.	1.6	12
5978	ZapG (YhcB/DUF1043), a novel cell division protein in gamma-proteobacteria linking the Z-ring to septal peptidoglycan synthesis. Journal of Biological Chemistry, 2021, 296, 100700.	1.6	9
5979	Crystal structures of the sheeppox virus encoded inhibitor of apoptosis SPPV14 bound to the proapoptotic BH3 peptides Hrk and Bax. FEBS Letters, 2020, 594, 2016-2026.	1.3	9

#	ARTICLE	IF	CITATIONS
5980	In Silico Analysis of Class III Peroxidases: Hypothetical Structure, Ligand Binding Sites, Posttranslational Modifications, and Interaction with Substrates. Methods in Molecular Biology, 2020, 2139, 325-339.	0.4	4
5981	Dockground Tool for Development and Benchmarking of Protein Docking Procedures. Methods in Molecular Biology, 2020, 2165, 289-300.	0.4	8
5982	Template-Based Modeling of Protein Complexes Using the PPI3D Web Server. Methods in Molecular Biology, 2020, 2165, 139-155.	0.4	6
5983	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.4	21
5984	Protein Structure Annotation Resources. Methods in Molecular Biology, 2015, 1261, 3-20.	0.4	1
5985	Databases, Repositories, and Other Data Resources in Structural Biology. Methods in Molecular Biology, 2017, 1607, 643-665.	0.4	6
5986	Analysis and Prediction of Protein Quaternary Structure. Methods in Molecular Biology, 2010, 609, 349-364.	0.4	22
5987	Evolutionary Trace for Prediction and Redesign of Protein Functional Sites. Methods in Molecular Biology, 2012, 819, 29-42.	0.4	59
5988	Effectors of Rab GTPases: Rab Binding Specificity and Their Role in Coordination of Rab Function and Localization. , 2014, , 39-66.		5
5989	Structural Basis of CK2 Regulation by Autoinhibitory Oligomerization. , 2015, , 35-47.		2
5990	MHC Molecules, T cell Receptors, Natural Killer Cell Receptors, and Viral Immunoevasinsâ€"Key Elements of Adaptive and Innate Immunity. Advances in Experimental Medicine and Biology, 2019, 1172, 21-62.	0.8	28
5991	Structures of Immune Checkpoints: An Overview on the CD28-B7 Family. Advances in Experimental Medicine and Biology, 2019, 1172, 63-78.	0.8	15
5992	Intrinsic thermodynamics of high affinity inhibitor binding to recombinant human carbonic anhydrase IV. European Biophysics Journal, 2018, 47, 271-290.	1.2	14
5993	Integrated In Silico-In Vitro Identification and Optimization of Bone Morphogenic Protein-2 Armpit Epitope as Its Antagonist Binding Site. Protein Journal, 2020, 39, 703-710.	0.7	5
5994	Molecular evolution of an oligomeric biocatalyst functioning in lysine biosynthesis. Biophysical Reviews, 2018, 10, 153-162.	1.5	16
5995	Molecular Insight into Recognition of the CGRPR Complex by Migraine Prevention Therapy Aimovig (Erenumab). Cell Reports, 2020, 30, 1714-1723.e6.	2.9	34
5996	Opposite Surfaces of the Cdc15 F-BAR Domain Create a Membrane Platform That Coordinates Cytoskeletal and Signaling Components for Cytokinesis. Cell Reports, 2020, 33, 108526.	2.9	12
5997	The crystal structure of protein-transporting chaperone BCP1 from Saccharomyces cerevisiae. Journal of Structural Biology, 2020, 212, 107605.	1.3	4

#	Article	IF	Citations
5999	Crystal structures of fukutin-related protein (FKRP), a ribitol-phosphate transferase related to muscular dystrophy. Nature Communications, 2020, 11, 303.	5.8	21
6000	Structure of the prefusion-locking broadly neutralizing antibody RVC20 bound to the rabies virus glycoprotein. Nature Communications, 2020, 11, 596.	5.8	28
6001	Structural insights into selective interaction between type IIa receptor protein tyrosine phosphatases and Liprin-Î±. Nature Communications, 2020, 11, 649.	5.8	12
6002	Mycobacterial HelD is a nucleic acids-clearing factor for RNA polymerase. Nature Communications, 2020, 11, 6419.	5.8	22
6003	Molecular basis for the assembly of RuBisCO assisted by the chaperone Raf1. Nature Plants, 2020, 6, 708-717.	4.7	24
6004	Potent Zika and dengue cross-neutralizing antibodies induced by Zika vaccination in a dengue-experienced donor. Nature Medicine, 2020, 26, 228-235.	15.2	61
6005	The structure of SeviL, a GM1b/asialo-GM1 binding R-type lectin from the mussel Mytilisepta virgata. Scientific Reports, 2020, 10, 22102.	1.6	4
6006	Structures of c-di-GMP/cGAMP degrading phosphodiesterase VcEAL: identification of a novel conformational switch and its implication. Biochemical Journal, 2019, 476, 3333-3353.	1.7	11
6007	Crystal structures of plant inorganic pyrophosphatase, an enzyme with a moonlighting autoproteolytic activity. Biochemical Journal, 2019, 476, 2297-2319.	1.7	10
6008	Interrogation of 3D-swapped structure and functional attributes of quintessential Sortase A from <i>Streptococcus pneumoniae</i>. Biochemical Journal, 2020, 477, 4711-4728.	1.7	2
6009	Biochemical and transcript level differences between the three human phosphofructokinases show optimisation of each isoform for specific metabolic niches. Biochemical Journal, 2020, 477, 4425-4441.	1.7	20
6010	The Trp triad within the V-domain of the receptor for advanced glycation end products modulates folding, stability and ligand binding. Bioscience Reports, 2020, 40, .	1.1	3
6011	Does it take two to tango? RING domain self-association and activity in TRIM E3 ubiquitin ligases. Biochemical Society Transactions, 2020, 48, 2615-2624.	1.6	27
6013	Structures and enzymatic mechanisms of phycobiliprotein lyases CpcE/F and PecE/F. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13170-13175.	3.3	37
6014	Energetic dependencies dictate folding mechanism in a complex protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25641-25648.	3.3	35
6015	A complete rule set for designing symmetry combination materials from protein molecules. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31817-31823.	3.3	29
6016	Insights into bacterial cell division from a structure of EnvC bound to the FtsX periplasmic domain. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28355-28365.	3.3	32
6017	Structure of SARS-CoV-2 ORF8, a rapidly evolving immune evasion protein. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	198

#	ARTICLE	IF	CITATIONS
6018	RIM-binding protein couples synaptic vesicle recruitment to release sites. Journal of Cell Biology, 2020, 219, .	2.3	26
6019	Molecular basis of MKLP2-dependent Aurora B transport from chromatin to the anaphase central spindle. Journal of Cell Biology, 2020, 219, .	2.3	25
6020	pH-dependent conformational changes of a Thogoto virus matrix protein reveal mechanisms of viral assembly and uncoating. Journal of General Virology, 2016, 97, 2149-2156.	1.3	7
6021	Structure and N-acetylglucosamine binding of the distal domain of mouse adenovirus 2 fibre. Journal of General Virology, 2018, 99, 1494-1508.	1.3	8
6090	Structural enzymology of<i>Helicobacter pylori</i>methylthioadenosine nucleosidase in the futalosine pathway. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 177-185.	2.5	13
6091	Structural analysis of Î²-glucosidase mutants derived from a hyperthermophilic tetrameric structure. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 877-888.	2.5	8
6092	Partial rotational lattice orderâ€"disorder in stefin B crystals. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1015-1025.	2.5	11
6093	The quaternary structure of the eukaryotic DNA replication proteins Sld7 and Sld3. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1649-1656.	2.5	34
6094	Structural insights into the interaction of human IgG1 with FcÎ³RI: no direct role of glycans in binding. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2354-2361.	2.5	21
6095	Sent packing: protein engineering generates a new crystal form of<i>Pseudomonas aeruginosa</i>DsbA1 with increased catalytic surface accessibility. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2386-2395.	2.5	5
6096	Structure of succinyl-CoA:3-ketoacid CoA transferase from<i>Drosophila melanogaster</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1089-1093.	0.7	3
6097	Avoidable errors in deposited macromolecular structures: an impediment to efficient data mining. IUCrJ, 2014, 1, 179-193.	1.0	58
6098	The potential of hexatungstotellurate(VI) to induce a significant entropic gain during protein crystallization. IUCrJ, 2017, 4, 734-740.	1.0	30
6099	Small-angle neutron scattering studies on the AMPA receptor GluA2 in the resting, AMPA-bound and GYKI-53655-bound states. IUCrJ, 2018, 5, 780-793.	1.0	9
6100	A cytosine modification mechanism revealed by the structure of a ternary complex of deoxycytidylate hydroxymethylase from bacteriophage T4 with its cofactor and substrate. IUCrJ, 2019, 6, 206-217.	1.0	4
6101	Structure of mammalian plasma fetuin-B and its mechanism of selective metallopeptidase inhibition. IUCrJ, 2019, 6, 317-330.	1.0	28
6102	The structural characterization of a glucosylglycerate hydrolase provides insights into the molecular mechanism of mycobacterial recovery from nitrogen starvation. IUCrJ, 2019, 6, 572-585.	1.0	16
6103	Structures of three ependymin-related proteins suggest their function as a hydrophobic molecule binder. IUCrJ, 2019, 6, 729-739.	1.0	10

#	ARTICLE	IF	CITATIONS
6104	Structural insights into stressosome assembly. IUCrJ, 2019, 6, 938-947.	1.0	11
6105	The DRSâ€“AIMP2â€“EPRS subcomplex acts as a pivot in the multi-tRNA synthetase complex. IUCrJ, 2019, 6, 958-967.	1.0	12
6106	Structure-based mechanism of cysteine-switch latency and of catalysis by pappalysin-family metallopeptidases. IUCrJ, 2020, 7, 18-29.	1.0	9
6107	Structure of the MICU1â€“MICU2 heterodimer provides insights into the gatekeeping threshold shift. IUCrJ, 2020, 7, 355-365.	1.0	23
6108	Induced DNA bending by unique dimerization of HigA antitoxin. IUCrJ, 2020, 7, 748-760.	1.0	6
6109	Crystal structure and interaction studies of human DHTKD1 provide insight into a mitochondrial megacomplex in lysine catabolism. IUCrJ, 2020, 7, 693-706.	1.0	19
6110	Structural insights into the regulation of SigB activity by RsbV and RsbW. IUCrJ, 2020, 7, 737-747.	1.0	11
6111	Structure of the human MLH1 N-terminus: implications for predisposition to Lynch syndrome. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 981-985.	0.4	21
6112	Crystal structure of a phosphoribosyl anthranilate isomerase from the hyperthermophilic archaeon<i>Thermococcus kodakaraensis</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 804-812.	0.4	3
6113	Crystal structures of human Fabs targeting the Bexsero meningococcal vaccine antigen NHBA. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 305-314.	0.4	5
6114	Crystal structure of theMSMEG_4306gene product fromMycobacterium smegmatis. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 166-173.	0.4	1
6115	Crystal structure of an inferred ancestral bacterial pyruvate decarboxylase. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 179-186.	0.4	3
6116	Structure of the tandem PX-PH domains of Bem3 from Saccharomyces cerevisiae. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 315-321.	0.4	5
6117	Structure of the Fc fragment of the NIST reference antibody RM8671. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 524-529.	0.4	13
6118	X-ray structure of <i>Arthrobacter globiformis</i> M30 ketose 3-epimerase for the production of <scp>D</scp>-allulose from <scp>D</scp>-fructose. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 669-676.	0.4	18
6119	Crystal structures and kinetics of<i>N</i>-acetylneuraminate lyase from<i>Fusobacterium nucleatum</i>. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 725-732.	0.4	5
6120	Structural studies of a glycoside hydrolase family 3 Î²-glucosidase from the model fungus<i>Neurospora crassa</i>. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 787-796.	0.4	7
6121	Crystal structure of (<i>S</i>)-3-<i>O</i>-geranylgeranylglyceryl phosphate synthase from<i>Thermoplasma acidophilum</i>in complex with the substrate<i>sn</i>-glycerol 1-phosphate. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 470-479.	0.4	3

#	Article	IF	Citations
6122	High-resolution crystal structures of <i>Escherichia coli</i> FtsZ bound to GDP and GTP. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 94-102.	0.4	22
6123	Structural characterization of three noncanonical NTF2-like superfamily proteins: implications for polyketide biosynthesis. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 372-383.	0.4	11
6124	The structure of the Moco carrier protein from<i>Rippkaea orientalis</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 453-463.	0.4	6
6125	Structure of the substrate-binding domain of <i>Plasmodium falciparum</i> heat-shock protein 70-x. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 495-500.	0.4	8
6126	Empirical power laws for the radii of gyration of protein oligomers. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1119-1129.	1.1	24
6127	1.8â€…Å… resolution crystal structure of the carbapenem intrinsic resistance protein CarF. Acta Crystallographica Section D: Structural Biology, 2017, 73, 549-556.	1.1	1
6128	Binding of hydroxycitrate to human ATP-citrate lyase. Acta Crystallographica Section D: Structural Biology, 2017, 73, 660-671.	1.1	23
6129	Distributed computing for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 143-151.	1.1	54
6130	Ensembles generated from crystal structures of single distant homologues solve challenging molecular-replacement cases in<i>AMPLE</i>. Acta Crystallographica Section D: Structural Biology, 2018, 74, 183-193.	1.1	16
6131	Recent developments in<i>MrBUMP</i>: better search-model preparation, graphical interaction with search models, and solution improvement and assessment. Acta Crystallographica Section D: Structural Biology, 2018, 74, 167-182.	1.1	35
6132	The crystal structure of the<i>N</i>-acetylglucosamine 2-epimerase from<i>Nostoc</i>sp. KVJ10 reveals the true dimer. Acta Crystallographica Section D: Structural Biology, 2019, 75, 90-100.	1.1	6
6133	Crystal structure of the leucine-rich repeat ectodomain of the plant immune receptor kinase SOBIR1. Acta Crystallographica Section D: Structural Biology, 2019, 75, 488-497.	1.1	11
6134	Structures of the transcriptional regulator BgaR, a lactose sensor. Acta Crystallographica Section D: Structural Biology, 2019, 75, 639-646.	1.1	7
6135	Structural comparison of protiated, H/D-exchanged and deuterated human carbonic anhydrase IX. Acta Crystallographica Section D: Structural Biology, 2019, 75, 895-903.	1.1	11
6136	3D domain swapping in the TIM barrel of the Î± subunit of<i>Streptococcus pneumoniae</i>tryptophan synthase. Acta Crystallographica Section D: Structural Biology, 2020, 76, 166-175.	1.1	4
6137	A practical overview of molecular replacement: <i>Clostridioides difficile</i> PilA1, a difficult case study. Acta Crystallographica Section D: Structural Biology, 2020, 76, 261-271.	1.1	3
6138	Structural analysis of the PATZ1 BTB domain homodimer. Acta Crystallographica Section D: Structural Biology, 2020, 76, 581-593.	1.1	5
6139	Structure of apo flavin-dependent halogenase Xcc4156 hints at a reason for cofactor-soaking difficulties. Acta Crystallographica Section D: Structural Biology, 2020, 76, 687-697.	1.1	6

#	Article	IF	Citations
6140	The RING domain of TRIM69 promotes higher-order assembly. Acta Crystallographica Section D: Structural Biology, 2020, 76, 954-961.	1.1	9
6141	Crystal structures of human ENPP1 in apo and bound forms. Acta Crystallographica Section D: Structural Biology, 2020, 76, 889-898.	1.1	24
6142	Marked structural rearrangement of mannose 6-phosphate/IGF2 receptor at different pH environments. Science Advances, 2020, 6, eaaz1466.	4.7	15
6143	HIV vaccine delayed boosting increases Env variable region 2â€"specific antibody effector functions. JCI Insight, 2020, 5, .	2.3	18
6144	Anti-citrullinated protein antibodies cause arthritis by cross-reactivity to joint cartilage. JCI Insight, 2017, 2, .	2.3	51
6145	Stereotyped antibody responses target posttranslationally modified gluten in celiac disease. JCI Insight, 2017, 2, .	2.3	20
6146	Loss of viral fitness and cross-recognition by CD8+ T cells limit HCV escape from a protective HLA-B27â€"restricted human immune response. Journal of Clinical Investigation, 2009, 119, 376-86.	3.9	99
6147	Inhibition of the GAS6/AXL pathway augments the efficacy of chemotherapies. Journal of Clinical Investigation, 2016, 127, 183-198.	3.9	86
6148	Quantitative cross-linking/mass spectrometry reveals subtle protein conformational changes. Wellcome Open Research, 2016, 1, 5.	0.9	30
6150	Structural and Functional Analyses of PAS Domain Interactions of the Clock Proteins Drosophila PERIOD and Mouse PERIOD2. PLoS Biology, 2009, 7, e1000094.	2.6	71
6151	Structural Basis for c-di-GMP-Mediated Inside-Out Signaling Controlling Periplasmic Proteolysis. PLoS Biology, 2011, 9, e1000588.	2.6	159
6152	Aequoreaâ€™s secrets revealed: New fluorescent proteins with unique properties for bioimaging and biosensing. PLoS Biology, 2020, 18, e3000936.	2.6	40
6153	Differences in structure and hibernation mechanism highlight diversification of the microsporidian ribosome. PLoS Biology, 2020, 18, e3000958.	2.6	18
6154	Alternative Protein-Protein Interfaces Are Frequent Exceptions. PLoS Computational Biology, 2012, 8, e1002623.	1.5	26
6155	Structure-Based Statistical Mechanical Model Accounts for the Causality and Energetics of Allosteric Communication. PLoS Computational Biology, 2016, 12, e1004678.	1.5	117
6156	Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. PLoS Computational Biology, 2017, 13, e1005625.	1.5	22
6157	Rhoptry Proteins ROP5 and ROP18 Are Major Murine Virulence Factors in Genetically Divergent South American Strains of Toxoplasma gondii. PLoS Genetics, 2015, 11, e1005434.	1.5	99
6158	Convergent Evolution of Hemoglobin Function in High-Altitude Andean Waterfowl Involves Limited Parallelism at the Molecular Sequence Level. PLoS Genetics, 2015, 11, e1005681.	1.5	103

#	Article	IF	Citations
6159	The Anti-sigma Factor RsiV Is a Bacterial Receptor for Lysozyme: Co-crystal Structure Determination and Demonstration That Binding of Lysozyme to RsiV Is Required for ÏƒV Activation. PLoS Genetics, 2016, 12, e1006287.	1.5	31
6160	A novel circulating tamiami mammarenavirus shows potential for zoonotic spillover. PLoS Neglected Tropical Diseases, 2020, 14, e0009004.	1.3	4
6161	Crystal Structure of the N-Acetylmannosamine Kinase Domain of GNE. PLoS ONE, 2009, 4, e7165.	1.1	28
6162	Transient Dimers of Allergens. PLoS ONE, 2010, 5, e9037.	1.1	60
6163	Structural Insights into the Quinolone Resistance Mechanism of Mycobacterium tuberculosis DNA Gyrase. PLoS ONE, 2010, 5, e12245.	1.1	118
6164	The Crystal Structure of Toxoplasma gondii Pyruvate Kinase 1. PLoS ONE, 2010, 5, e12736.	1.1	18
6165	Additional Serine/Threonine Phosphorylation Reduces Binding Affinity but Preserves Interface Topography of Substrate Proteins to the c-Cbl TKB Domain. PLoS ONE, 2010, 5, e12819.	1.1	19
6166	Structure and Function of the First Full-Length Murein Peptide Ligase (Mpl) Cell Wall Recycling Protein. PLoS ONE, 2011, 6, e17624.	1.1	30
6167	Comparative Structural Analysis of Lipid Binding START Domains. PLoS ONE, 2011, 6, e19521.	1.1	117
6168	Characterization of Protein-Protein Interaction Interfaces from a Single Species. PLoS ONE, 2011, 6, e21053.	1.1	43
6169	The Crystal Structure of the Human Co-Chaperone P58IPK. PLoS ONE, 2011, 6, e22337.	1.1	20
6170	X-Ray Structure Reveals a New Class and Provides Insight into Evolution of Alkaline Phosphatases. PLoS ONE, 2011, 6, e22767.	1.1	26
6171	A Crystal Structure of the Catalytic Core Domain of an Avian Sarcoma and Leukemia Virus Integrase Suggests an Alternate Dimeric Assembly. PLoS ONE, 2011, 6, e23032.	1.1	11
6172	Oligomeric Structure of the MALT1 Tandem Ig-Like Domains. PLoS ONE, 2011, 6, e23220.	1.1	19
6173	In Silico Approach to Inhibition of Signaling Pathways of Toll-Like Receptors 2 and 4 by ST2L. PLoS ONE, 2011, 6, e23989.	1.1	59
6174	Pseudomonas aeruginosa 4-Amino-4-Deoxychorismate Lyase: Spatial Conservation of an Active Site Tyrosine and Classification of Two Types of Enzyme. PLoS ONE, 2011, 6, e24158.	1.1	11
6175	Insights into the Membrane Interactions of the Saposin-Like Proteins Na-SLP-1 and Ac-SLP-1 from Human and Dog Hookworm. PLoS ONE, 2011, 6, e25369.	1.1	14
6176	Bioinformatic Analysis of Pathogenic Missense Mutations of Activin Receptor Like Kinase 1 Ectodomain. PLoS ONE, 2011, 6, e26431.	1.1	14

#	ARTICLE	IF	CITATIONS
6177	A Highly Stable Plastidic-Type Ferredoxin-NADP(H) Reductase in the Pathogenic Bacterium Leptospira interrogans. PLoS ONE, 2011, 6, e26736.	1.1	13
6178	Homology Inference of Protein-Protein Interactions via Conserved Binding Sites. PLoS ONE, 2012, 7, e28896.	1.1	15
6179	Tetrahydrodipicolinate N-Succinyltransferase and Dihydrodipicolinate Synthase from Pseudomonas aeruginosa: Structure Analysis and Gene Deletion. PLoS ONE, 2012, 7, e31133.	1.1	20
6180	Composite Structural Motifs of Binding Sites for Delineating Biological Functions of Proteins. PLoS ONE, 2012, 7, e31437.	1.1	8
6181	New Insight into the Transcarbamylase Family: The Structure of Putrescine Transcarbamylase, a Key Catalyst for Fermentative Utilization of Agmatine. PLoS ONE, 2012, 7, e31528.	1.1	5
6182	Low-Resolution Molecular Models Reveal the Oligomeric State of the PPAR and the Conformational Organization of Its Domains in Solution. PLoS ONE, 2012, 7, e31852.	1.1	23
6183	Crystal Structure of Streptococcus pyogenes Csn2 Reveals Calcium-Dependent Conformational Changes in Its Tertiary and Quaternary Structure. PLoS ONE, 2012, 7, e33401.	1.1	29
6184	A Glutathione Transferase from Agrobacterium tumefaciens Reveals a Novel Class of Bacterial GST Superfamily. PLoS ONE, 2012, 7, e34263.	1.1	26
6185	Non-Agonistic Bivalent Antibodies That Promote c-MET Degradation and Inhibit Tumor Growth and Others Specific for Tumor Related c-MET. PLoS ONE, 2012, 7, e34658.	1.1	28
6186	Extent of Structural Asymmetry in Homodimeric Proteins: Prevalence and Relevance. PLoS ONE, 2012, 7, e36688.	1.1	56
6187	Interaction of Rio1 Kinase with Toyocamycin Reveals a Conformational Switch That Controls Oligomeric State and Catalytic Activity. PLoS ONE, 2012, 7, e37371.	1.1	31
6188	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. PLoS ONE, 2012, 7, e38318.	1.1	32
6189	Ipomoelin, a Jacalin-Related Lectin with a Compact Tetrameric Association and Versatile Carbohydrate Binding Properties Regulated by Its N Terminus. PLoS ONE, 2012, 7, e40618.	1.1	10
6190	The Metagenome-Derived Enzymes LipS and LipT Increase the Diversity of Known Lipases. PLoS ONE, 2012, 7, e47665.	1.1	72
6191	Influence of Structural Symmetry on Protein Dynamics. PLoS ONE, 2012, 7, e50011.	1.1	14
6192	Crystal Structure of an EAL Domain in Complex with Reaction Product 5â€²-pGpG. PLoS ONE, 2012, 7, e52424.	1.1	19
6193	Structural Insight into DFMO Resistant Ornithine Decarboxylase from Entamoeba histolytica: An Inkling to Adaptive Evolution. PLoS ONE, 2013, 8, e53397.	1.1	15
6194	A Novel Trans Conformation of Ligand-Free Calmodulin. PLoS ONE, 2013, 8, e54834.	1.1	14

#	Article	IF	Citations
6195	Dramatic Structural Changes Resulting from the Loss of a Crucial Hydrogen Bond in the Hinge Region Involved in C-Terminal Helix Swapping in SurE: A Survival Protein from Salmonella typhimurium. PLoS ONE, 2013, 8, e55978.	1.1	4
6196	Use of a Molecular Decoy to Segregate Transport from Antigenicity in the FrpB Iron Transporter from Neisseria meningitidis. PLoS ONE, 2013, 8, e56746.	1.1	25
6197	Intersubunit Ionic Interactions Stabilize the Nucleoside Diphosphate Kinase of Mycobacterium tuberculosis. PLoS ONE, 2013, 8, e57867.	1.1	12
6198	Structural Insights into Putative Molybdenum Cofactor Biosynthesis Protein C (MoaC2) from Mycobacterium tuberculosis H37Rv. PLoS ONE, 2013, 8, e58333.	1.1	3
6199	Interaction and Inhibition of Dengue Envelope Glycoprotein with Mammalian Receptor DC-Sign, an In-Silico Approach. PLoS ONE, 2013, 8, e59211.	1.1	17
6200	Crystal Structure of KLHL3 in Complex with Cullin3. PLoS ONE, 2013, 8, e60445.	1.1	63
6201	Structural and Phylogenetic Studies with MjTX-I Reveal a Multi-Oligomeric Toxin â€“ a Novel Feature in Lys49-PLA2s Protein Class. PLoS ONE, 2013, 8, e60610.	1.1	16
6202	Crystal Structures of E. coli Native MenH and Two Active Site Mutants. PLoS ONE, 2013, 8, e61325.	1.1	10
6203	The Carboxy-Terminal Î±N Helix of the Archaeal XerA Tyrosine Recombinase Is a Molecular Switch to Control Site-Specific Recombination. PLoS ONE, 2013, 8, e63010.	1.1	21
6204	N-Terminal Helix-Cap in Î±-Helix 2 Modulates Î²-State Misfolding in Rabbit and Hamster Prion Proteins. PLoS ONE, 2013, 8, e63047.	1.1	17
6205	Structural Basis of the Induced-Fit Mechanism of 1,4-Dihydroxy-2-Naphthoyl Coenzyme A Synthase from the Crotonase Fold Superfamily. PLoS ONE, 2013, 8, e63095.	1.1	5
6206	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. PLoS ONE, 2013, 8, e66273.	1.1	102
6207	Substrate Channel Flexibility in Pseudomonas aeruginosa MurB Accommodates Two Distinct Substrates. PLoS ONE, 2013, 8, e66936.	1.1	5
6208	Structure of the SCAN Domain of Human Paternally Expressed Gene 3 Protein. PLoS ONE, 2013, 8, e69538.	1.1	11
6209	A Comparison of Structural and Evolutionary Attributes of Escherichia coli and Thermus thermophilus Small Ribosomal Subunits: Signatures of Thermal Adaptation. PLoS ONE, 2013, 8, e69898.	1.1	13
6210	Crystal Structure of the N-Acetyltransferase Domain of Human N-Acetyl-L-Glutamate Synthase in Complex with N-Acetyl-L-Glutamate Provides Insights into Its Catalytic and Regulatory Mechanisms. PLoS ONE, 2013, 8, e70369.	1.1	21
6211	The Tip of the Tail Needle Affects the Rate of DNA Delivery by Bacteriophage P22. PLoS ONE, 2013, 8, e70936.	1.1	26
6212	Selection of Specific Protein Binders for Pre-Defined Targets from an Optimized Library of Artificial Helicoidal Repeat Proteins (alphaRep). PLoS ONE, 2013, 8, e71512.	1.1	47

#	Article	IF	Citations
6213	Crystal Structure and Substrate Specificity of D-Galactose-6-Phosphate Isomerase Complexed with Substrates. PLoS ONE, 2013, 8, e72902.	1.1	6
6214	Distinct Ubiquitin Binding Modes Exhibited by SH3 Domains: Molecular Determinants and Functional Implications. PLoS ONE, 2013, 8, e73018.	1.1	17
6215	Cross-Link Guided Molecular Modeling with ROSETTA. PLoS ONE, 2013, 8, e73411.	1.1	144
6216	Matrix Metalloproteinase-10/TIMP-2 Structure and Analyses Define Conserved Core Interactions and Diverse Exosite Interactions in MMP/TIMP Complexes. PLoS ONE, 2013, 8, e75836.	1.1	39
6217	Comparative Analysis of the Tyr-Kinases CapB1 and CapB2 Fused to Their Cognate Modulators CapA1 and CapA2 from Staphylococcus aureus. PLoS ONE, 2013, 8, e75958.	1.1	10
6218	Solution and Crystallographic Structures of the Central Region of the Phosphoprotein from Human Metapneumovirus. PLoS ONE, 2013, 8, e80371.	1.1	34
6219	X-Ray Crystal Structure of the Ancestral 3-Ketosteroid Receptorâ€"Progesteroneâ€"Mifepristone Complex Shows Mifepristone Bound at the Coactivator Binding Interface. PLoS ONE, 2013, 8, e80761.	1.1	11
6220	Structural Propensities of Human Ubiquitination Sites: Accessibility, Centrality and Local Conformation. PLoS ONE, 2013, 8, e83167.	1.1	10
6221	From Knock-Out Phenotype to Three-Dimensional Structure of a Promising Antibiotic Target from Streptococcus pneumoniae. PLoS ONE, 2013, 8, e83419.	1.1	22
6222	Structure and Function of a Novel Cellulase 5 from Sugarcane Soil Metagenome. PLoS ONE, 2013, 8, e83635.	1.1	59
6223	Deriving a Mutation Index of Carcinogenicity Using Protein Structure and Protein Interfaces. PLoS ONE, 2014, 9, e84598.	1.1	22
6224	Structural Basis of Thermal Stability of the Tungsten Cofactor Synthesis Protein MoaB from Pyrococcus furiosus. PLoS ONE, 2014, 9, e86030.	1.1	4
6225	Improving Predictions of Protein-Protein Interfaces by Combining Amino Acid-Specific Classifiers Based on Structural and Physicochemical Descriptors with Their Weighted Neighbor Averages. PLoS ONE, 2014, 9, e87107.	1.1	9
6226	Structural and Functional Characterization of Cargo-Binding Sites on the Î¼4-Subunit of Adaptor Protein Complex 4. PLoS ONE, 2014, 9, e88147.	1.1	30
6227	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PilO2Bp S-SAD Crystal Structure. PLoS ONE, 2014, 9, e94981.	1.1	4
6228	The Structural and Functional Basis of Catalysis Mediated by NAD(P)H:acceptor Oxidoreductase (FerB) of Paracoccus denitrificans. PLoS ONE, 2014, 9, e96262.	1.1	22
6229	A Loose Domain Swapping Organization Confers a Remarkable Stability to the Dimeric Structure of the Arginine Binding Protein from Thermotoga maritima. PLoS ONE, 2014, 9, e96560.	1.1	31
6230	Structural Studies of an Anti-Inflammatory Lectin from Canavalia boliviana Seeds in Complex with Dimannosides. PLoS ONE, 2014, 9, e97015.	1.1	22

#	ARTICLE	IF	CITATIONS
6231	BioAssemblyModeler (BAM): User-Friendly Homology Modeling of Protein Homo- and Heterooligomers. PLoS ONE, 2014, 9, e98309.	1.1	16
6232	Transplanting Supersites of HIV-1 Vulnerability. PLoS ONE, 2014, 9, e99881.	1.1	51
6233	Crystal Structure of the Mineralocorticoid Receptor DNA Binding Domain in Complex with DNA. PLoS ONE, 2014, 9, e107000.	1.1	40
6234	The Structure, Stability and Pheromone Binding of the Male Mouse Protein Sex Pheromone Darcin. PLoS ONE, 2014, 9, e108415.	1.1	24
6235	The Structure of an LIM-Only Protein 4 (LMO4) and Deformed Epidermal Autoregulatory Factor-1 (DEAF1) Complex Reveals a Common Mode of Binding to LMO4. PLoS ONE, 2014, 9, e109108.	1.1	13
6236	Crystal Structures of Influenza A Virus Matrix Protein M1: Variations on a Theme. PLoS ONE, 2014, 9, e109510.	1.1	32
6237	Covariance of Charged Amino Acids at Positions 322 and 440 of HIV-1 Env Contributes to Coreceptor Specificity of Subtype B Viruses, and Can Be Used to Improve the Performance of V3 Sequence-Based Coreceptor Usage Prediction Algorithms. PLoS ONE, 2014, 9, e109771.	1.1	10
6238	Crystal Structure of the Fibre Head Domain of the Atadenovirus Snake Adenovirus 1. PLoS ONE, 2014, 9, e114373.	1.1	16
6239	An Integrative Approach to the Study of Filamentous Oligomeric Assemblies, with Application to RecA. PLoS ONE, 2015, 10, e0116414.	1.1	14
6240	Biophysical Analysis of Anopheles gambiae Leucine-Rich Repeat Proteins APL1A1, APL1B and APL1C and Their Interaction with LRIM1. PLoS ONE, 2015, 10, e0118911.	1.1	16
6241	The Carboxy-Terminal Domain of Erb1 Is a Seven-Bladed ÃŸ-Propeller that Binds RNA. PLoS ONE, 2015, 10, e0123463.	1.1	10
6242	LucY: A Versatile New Fluorescent Reporter Protein. PLoS ONE, 2015, 10, e0124272.	1.1	4
6243	Crystal Structure of Allophycocyanin from Marine Cyanobacterium Phormidium sp. A09DM. PLoS ONE, 2015, 10, e0124580.	1.1	30
6244	Distinctive Structure of the EphA3/Ephrin-A5 Complex Reveals a Dual Mode of Eph Receptor Interaction for Ephrin-A5. PLoS ONE, 2015, 10, e0127081.	1.1	11
6245	Methylatable Signaling Helix Coordinated Inhibitory Receiver Domain in Sensor Kinase Modulates Environmental Stress Response in Bacillus Cereus. PLoS ONE, 2015, 10, e0137952.	1.1	11
6246	The Structure of Plasmodium falciparum Blood-Stage 6-Cys Protein Pf41 Reveals an Unexpected Intra-Domain Insertion Required for Pf12 Coordination. PLoS ONE, 2015, 10, e0139407.	1.1	23
6247	CAB-Align: A Flexible Protein Structure Alignment Method Based on the Residue-Residue Contact Area. PLoS ONE, 2015, 10, e0141440.	1.1	3
6248	Structural and Enzymatic Characterization of a Nucleoside Diphosphate Sugar Hydrolase from Bdellovibrio bacteriovorus. PLoS ONE, 2015, 10, e0141716.	1.1	6

#	Article	IF	Citations
6249	The Functional Unit of Neisseria meningitidis 3-Deoxy-á´…-Arabino-Heptulosonate 7-Phosphate Synthase Is Dimeric. PLoS ONE, 2016, 11, e0145187.	1.1	6
6250	On Natureâ€™s Strategy for Assigning Genetic Code Multiplicity. PLoS ONE, 2016, 11, e0148174.	1.1	18
6251	Structures of Two Melanoma-Associated Antigens Suggest Allosteric Regulation of Effector Binding. PLoS ONE, 2016, 11, e0148762.	1.1	26
6252	Biochemistry and Crystal Structure of Ectoine Synthase: A Metal-Containing Member of the Cupin Superfamily. PLoS ONE, 2016, 11, e0151285.	1.1	30
6253	Crystal Structure of Human Myotubularin-Related Protein 1 Provides Insight into the Structural Basis of Substrate Specificity. PLoS ONE, 2016, 11, e0152611.	1.1	7
6254	Structure-Based Design of Head-Only Fusion Glycoprotein Immunogens for Respiratory Syncytial Virus. PLoS ONE, 2016, 11, e0159709.	1.1	27
6255	Structural and Functional Studies of H. seropedicae RecA Protein â€“ Insights into the Polymerization of RecA Protein as Nucleoprotein Filament. PLoS ONE, 2016, 11, e0159871.	1.1	7
6256	Structural Basis of the Heterodimer Formation between Cell Shape-Determining Proteins Csd1 and Csd2 from Helicobacter pylori. PLoS ONE, 2016, 11, e0164243.	1.1	17
6257	Characterisation of a New Family of Carboxyl Esterases with an OsmC Domain. PLoS ONE, 2016, 11, e0166128.	1.1	16
6258	Biophysical Studies of the Induced Dimerization of Human VEGF Receptor 1 Binding Domain by Divalent Metals Competing with VEGF-A. PLoS ONE, 2016, 11, e0167755.	1.1	10
6259	Crystal Structure and Catalytic Mechanism of CouO, a Versatile C-Methyltransferase from Streptomyces rishiriensis. PLoS ONE, 2017, 12, e0171056.	1.1	16
6260	A three-way approach for protein function classification. PLoS ONE, 2017, 12, e0171702.	1.1	11
6261	Structural and biochemical studies on Vibrio cholerae Hsp31 reveals a novel dimeric form and Glutathione-independent Glyoxalase activity. PLoS ONE, 2017, 12, e0172629.	1.1	2
6262	Symmetry based assembly of a 2 dimensional protein lattice. PLoS ONE, 2017, 12, e0174485.	1.1	5
6263	Characterization and mutational analysis of a nicotinamide mononucleotide deamidase from Agrobacterium tumefaciens showing high thermal stability and catalytic efficiency. PLoS ONE, 2017, 12, e0174759.	1.1	7
6264	Quaternary structure is an essential component that contributes to the sophisticated allosteric regulation mechanism in a key enzyme from Mycobacterium tuberculosis. PLoS ONE, 2017, 12, e0180052.	1.1	18
6265	Systematic studies of the interactions between a model polyphenol compound and microbial Î²-glucosidases. PLoS ONE, 2017, 12, e0181629.	1.1	6
6266	Biophysical characterization of the calmodulin-like domain of Plasmodium falciparum calcium dependent protein kinase 3. PLoS ONE, 2017, 12, e0181721.	1.1	1

#	Article	IF	Citations
6267	Structural and biochemical analysis of atypically low dephosphorylating activity of human dual-specificity phosphatase 28. PLoS ONE, 2017, 12, e0187701.	1.1	3
6268	A mutant of phosphomannomutase1 retains full enzymatic activity, but is not activated by IMP: Possible implications for the disease PMM2-CDG. PLoS ONE, 2017, 12, e0189629.	1.1	12
6269	SAXS studies of X-ray induced disulfide bond damage: Engineering high-resolution insight from a low-resolution technique. PLoS ONE, 2020, 15, e0239702.	1.1	9
6270	Time-lapse sentinel surveillance of SARS-CoV-2 spread in India. PLoS ONE, 2020, 15, e0241172.	1.1	3
6271	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats. PLoS ONE, 2020, 15, e0242677.	1.1	18
6272	Identification of the Clostridial cellulose synthase and characterization of the cognate glycosyl hydrolase, CcsZ. PLoS ONE, 2020, 15, e0242686.	1.1	13
6273	Structural and Functional Analysis of Murine Polyomavirus Capsid Proteins Establish the Determinants of Ligand Recognition and Pathogenicity. PLoS Pathogens, 2015, 11, e1005104.	2.1	22
6274	Molecular Basis of Ligand-Dependent Regulation of NadR, the Transcriptional Repressor of Meningococcal Virulence Factor NadA. PLoS Pathogens, 2016, 12, e1005557.	2.1	24
6275	How Quorum Sensing Connects Sporulation to Necrotrophism in Bacillus thuringiensis. PLoS Pathogens, 2016, 12, e1005779.	2.1	46
6276	The Ebola Virus VP30-NP Interaction Is a Regulator of Viral RNA Synthesis. PLoS Pathogens, 2016, 12, e1005937.	2.1	61
6277	Pheromone Recognition and Selectivity by ComR Proteins among Streptococcus Species. PLoS Pathogens, 2016, 12, e1005979.	2.1	46
6278	Structural Insights into Streptococcal Competence Regulation by the Cell-to-Cell Communication System ComRS. PLoS Pathogens, 2016, 12, e1005980.	2.1	44
6279	Structure and Mechanism of Staphylococcus aureus TarS, the Wall Teichoic Acid Î²-glycosyltransferase Involved in Methicillin Resistance. PLoS Pathogens, 2016, 12, e1006067.	2.1	46
6280	Structural basis of mammalian glycan targeting by Vibrio cholerae cytolysin and biofilm proteins. PLoS Pathogens, 2018, 14, e1006841.	2.1	11
6281	Schistosoma mansoni SmKI-1 serine protease inhibitor binds to elastase and impairs neutrophil function and inflammation. PLoS Pathogens, 2018, 14, e1006870.	2.1	58
6282	Leishmania differentiation requires ubiquitin conjugation mediated by a UBC2-UEV1 E2 complex. PLoS Pathogens, 2020, 16, e1008784.	2.1	15
6283	4CMenB vaccine induces elite cross-protective human antibodies that compete with human factor H for binding to meningococcal fHbp. PLoS Pathogens, 2020, 16, e1008882.	2.1	6
6284	Convergent structural features of respiratory syncytial virus neutralizing antibodies and plasticity of the site V epitope on prefusion F. PLoS Pathogens, 2020, 16, e1008943.	2.1	7

#	ARTICLE	IF	CITATIONS
6285	Crystal Structure and Comparative Sequence Analysis of GmhA from Colwellia psychrerythraea Strain 34H Provides Insight into Functional Similarity with DiaA. Molecules and Cells, 2015, 38, 1086-1095.	1.0	9
6286	Structural and Biochemical Studies Reveal a Putative FtsZ Recognition Site on the Z-ring Stabilizer ZapD. Molecules and Cells, 2016, 39, 814-820.	1.0	7
6287	Structural basis of Focal Adhesion Kinase activation on lipid membranes. EMBO Journal, 2020, 39, e104743.	3.5	47
6288	Structures of <scp> IS <i>C</i> </scp> <i>th4</i> transpososomes reveal the roleÂof asymmetry in copyâ€out/pasteâ€in <scp>DNA</scp> transposition. EMBO Journal, 2021, 40, e105666.	3.5	16
6289	Cryoâ€EM structure of native human uromodulin, a zona pellucida module polymer. EMBO Journal, 2020, 39, e106807.	3.5	31
6290	Structural basis for exploring the allosteric inhibition of human kidney type glutaminase. Oncotarget, 2016, 7, 57943-57954.	0.8	39
6291	Validation of a multi-omics strategy for prioritizing personalized candidate driver genes. Oncotarget, 2016, 7, 38440-38450.	0.8	6
6292	Crystal Structure and Immunogenicity of the DS-Cav1-Stabilized Fusion Glycoprotein From Respiratory Syncytial Virus Subtype B. Pathogens and Immunity, 2019, 4, 294.	1.4	26
6294	Structure of the Cytoplasmic Segment of Histidine Kinase Receptor QseC: A Key Player in Bacterial Virulence. Protein and Peptide Letters, 2010, 17, 1383-1391.	0.4	13
6295	Current Trends in Biotherapeutic Higher Order Structure Characterization by Irreversible Covalent Footprinting Mass Spectrometry. Protein and Peptide Letters, 2019, 26, 35-43.	0.4	5
6296	A Review of Methods Available to Estimate Solvent-Accessible Surface Areas of Soluble Proteins in the Folded and Unfolded States. Current Protein and Peptide Science, 2014, 15, 456-476.	0.7	197
6297	Achieving Functionality Through Modular Build-up: Structure and Size Selection of Serine Oligopeptidases. Current Protein and Peptide Science, 2019, 20, 1089-1101.	0.7	6
6298	Exploring Proteomic Drug Targets, Therapeutic Strategies and Protein - Protein Interactions in Cancer: Mechanistic View. Current Cancer Drug Targets, 2019, 19, 430-448.	0.8	10
6299	Targeting Kinase Interaction Networks: A New Paradigm in PPI Based Design of Kinase Inhibitors. Current Topics in Medicinal Chemistry, 2019, 19, 467-485.	1.0	14
6300	Characterization of Carbonic Anhydrase Isozyme Specific Inhibition by Sulfamated 2-Ethylestra Compounds. Letters in Drug Design and Discovery, 2011, 8, 678-684.	0.4	8
6302	The crystal structure of Staufen1 in complex with a physiological RNA sheds light on substrate selectivity. Life Science Alliance, 2018, 1, e201800187.	1.3	17
6303	Direct binding of Cdt2 to PCNA is important for targeting the CRL4^{Cdt2} E3 ligase activity to Cdt1. Life Science Alliance, 2018, 1, e201800238.	1.3	18
6304	Molecular characterization of CHAD domains as inorganic polyphosphate-binding modules. Life Science Alliance, 2019, 2, e201900385.	1.3	24

#	Article	IF	Citations
6305	Structural and functional characterization of the mitochondrial complex IV assembly factor Coa6. Life Science Alliance, 2019, 2, e201900458.	1.3	15
6306	A key region of molecular specificity orchestrates unique ephrin-B1 utilization by Cedar virus. Life Science Alliance, 2020, 3, e201900578.	1.3	22
6307	Partial Characterization of Two Cathepsin D Family Aspartic Peptidases of Clonorchis sinensis. Korean Journal of Parasitology, 2019, 57, 671-680.	0.5	7
6308	Helicase of Type 2 Porcine Reproductive and Respiratory Syndrome Virus Strain HV Reveals a Unique Structure. Viruses, 2020, 12, 215.	1.5	18
6309	In silico analysis of SARS-CoV-2 spike glycoprotein and insights into antibody binding. Research Ideas and Outcomes, 0, 6, .	1.0	5
6310	Structure of the cystic fibrosis transmembrane conductance regulator in the inward-facing conformation revealed by single particle electron microscopy. AIMS Biophysics, 2015, 2, 131-152.	0.3	4
6311	Unloading RNAs in the cytoplasm: An â€œimportinâ€•task. Nucleus, 2010, 1, 139-143.	0.6	11
6312	ACCEPT-NMR: A New Tool for the Analysis of Crystal Contacts and Their Links to NMR Chemical Shift Perturbations. Journal of Crystallization Process and Technology, 2013, 03, 12-27.	0.6	1
6313	Biochemical and Structural Analysis of Hormone-sensitive Lipase Homolog EstE7: Insight into the Stabilized Dimerization of HSL-Homolog Proteins. Bulletin of the Korean Chemical Society, 2010, 31, 2627-2632.	1.0	4
6314	X-ray Crystallographic Structure of TIR-Domain from the Human TIR-Domain Containing Adaptor Protein/MyD88-Adaptor-Like Protein (TIRAP/MAL). Bulletin of the Korean Chemical Society, 2012, 33, 3091-3094.	1.0	13
6315	Computational Methods for Prediction of Protein-Protein Interaction Sites. , 0, , .		10
6316	An Immuno-informatics driven Epitope study from the molecular interaction of JEV non-structural (NS) proteins with Ribophorin (RPN). Bioinformation, 2014, 10, 496-501.	0.2	4
6317	Molecular Docking of Known Carcinogen 4-(Methyl-nitrosamino)-1-(3-pyridyl)-1-butanone (NNK) with Cyclin Dependent Kinases towards Its Potential Role in Cell Cycle Perturbation. Bioinformation, 2014, 10, 526-532.	0.2	5
6318	Blind prediction of quaternary structures of homo-oligomeric proteins from amino acid sequences based on templates. Journal of Proteome Science and Computational Biology, 2012, 1, 1.	1.0	2
6319	The AFF4 scaffold binds human P-TEFb adjacent to HIV Tat. ELife, 2013, 2, e00327.	2.8	65
6320	Fungal effector Ecp6 outcompetes host immune receptor for chitin binding through intrachain LysM dimerization. ELife, 2013, 2, e00790.	2.8	217
6321	Re-examining how complexin inhibits neurotransmitter release. ELife, 2014, 3, e02391.	2.8	68
6322	Drastic changes in conformational dynamics of the antiterminator M2-1 regulate transcription efficiency in Pneumovirinae. ELife, 2014, 3, e02674.	2.8	39

#	ARTICLE	IF	CITATIONS
6323	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. ELife, 2014, 3, .	2.8	47
6324	A novel N-terminal extension in mitochondrial TRAP1 serves as a thermal regulator of chaperone activity. ELife, 2014, 3, .	2.8	40
6325	Mechanistic insight into the conserved allosteric regulation of periplasmic proteolysis by the signaling molecule cyclic-di-GMP. ELife, 2014, 3, e03650.	2.8	41
6326	Structure and functional properties of Norrin mimic Wnt for signalling with Frizzled4, Lrp5/6, and proteoglycan. ELife, 2015, 4, .	2.8	90
6327	Regulation of the PI3K pathway through a p85Î± monomerâ€"homodimer equilibrium. ELife, 2015, 4, e06866.	2.8	65
6328	The homo-oligomerisation of both Sas-6 and Ana2 is required for efficient centriole assembly in flies. ELife, 2015, 4, e07236.	2.8	49
6329	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. ELife, 2015, 4, .	2.8	19
6330	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. ELife, 2015, 4, .	2.8	109
6331	CarD uses a minor groove wedge mechanism to stabilize the RNA polymerase open promoter complex. ELife, 2015, 4, .	2.8	59
6332	Structural basis of pathogen recognition by an integrated HMA domain in a plant NLR immune receptor. ELife, 2015, 4, .	2.8	246
6333	Structural basis of interprotein electron transfer in bacterial sulfite oxidation. ELife, 2015, 4, e09066.	2.8	19
6334	Bile salt receptor complex activates a pathogenic type III secretion system. ELife, 2016, 5, .	2.8	68
6335	Antiparallel protocadherin homodimers use distinct affinity- and specificity-mediating regions in cadherin repeats 1-4. ELife, 2016, 5, .	2.8	53
6336	A computational interactome and functional annotation for the human proteome. ELife, 2016, 5, .	2.8	58
6337	Molecular basis of sidekick-mediated cell-cell adhesion and specificity. ELife, 2016, 5, .	2.8	36
6338	Malaria parasite CelTOS targets the inner leaflet of cell membranes for pore-dependent disruption. ELife, 2016, 5, .	2.8	54
6339	Î³-Protocadherin structural diversity and functional implications. ELife, 2016, 5, .	2.8	54
6340	Structure of protein O-mannose kinase reveals a unique active site architecture. ELife, 2016, 5, .	2.8	33

#	ARTICLE	IF	CITATIONS
6341	Structure-based analysis of CysZ-mediated cellular uptake of sulfate. ELife, 2018, 7, .	2.8	10
6342	Rift Valley fever phlebovirus NSs protein core domain structure suggests molecular basis for nuclear filaments. ELife, 2017, 6, .	2.8	20
6343	Asymmetric activation mechanism of a homodimeric red light-regulated photoreceptor. ELife, 2018, 7, .	2.8	46
6344	Hexameric and pentameric complexes of the ExbBD energizer in the Ton system. ELife, 2018, 7, .	2.8	45
6345	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. ELife, 2018, 7, .	2.8	45
6346	Structural basis for isoform-specific kinesin-1 recognition of Y-acidic cargo adaptors. ELife, 2018, 7, .	2.8	26
6347	Biosynthesis of histone messenger RNA employs a specific 3' end endonuclease. ELife, 2018, 7, .	2.8	14
6348	Molecular basis of synaptic specificity by immunoglobulin superfamily receptors in Drosophila. ELife, 2019, 8, .	2.8	35
6349	Cryo-EM structure of the mechanically activated ion channel OSCA1.2. ELife, 2018, 7, .	2.8	118
6350	Preacinetobactin not acinetobactin is essential for iron uptake by the BauA transporter of the pathogen Acinetobacter baumannii. ELife, 2018, 7, .	2.8	41
6351	The complete structure of the human TFIIH core complex. ELife, 2019, 8, .	2.8	91
6352	Conformational switches control early maturation of the eukaryotic small ribosomal subunit. ELife, 2019, 8, .	2.8	32
6353	Heparan sulfates are critical regulators of the inhibitory megakaryocyte-platelet receptor G6b-B. ELife, 2019, 8, .	2.8	33
6354	Evolution of (p)ppGpp-HPRT regulation through diversification of an allosteric oligomeric interaction. ELife, 2019, 8, .	2.8	40
6355	Casposase structure and the mechanistic link between DNA transposition and spacer acquisition by CRISPR-Cas. ELife, 2020, 9, .	2.8	16
6356	Structural model for differential cap maturation at growing microtubule ends. ELife, 2020, 9, .	2.8	44
6357	The mechanosensitive ion channel TRAAK is localized to the mammalian node of Ranvier. ELife, 2019, 8, .	2.8	74
6358	An ultralong CDRH2 in HCV neutralizing antibody demonstrates structural plasticity of antibodies against E2 glycoprotein. ELife, 2020, 9, .	2.8	21

#	ARTICLE	IF	CITATIONS
6359	Structure of the human BBSome core complex. ELife, 2020, 9, .	2.8	59
6360	The structures of secretory and dimeric immunoglobulin A. ELife, 2020, 9, .	2.8	37
6361	Atomic structure of a mitochondrial complex I intermediate from vascular plants. ELife, 2020, 9, .	2.8	42
6362	Molecular basis for N-terminal alpha-synuclein acetylation by human NatB. ELife, 2020, 9, .	2.8	25
6363	The architecture of EMC reveals a path for membrane protein insertion. ELife, 2020, 9, .	2.8	81
6364	Molecular rationale for antibody-mediated targeting of the hantavirus fusion glycoprotein. ELife, 2020, 9, .	2.8	19
6365	Large domain movements through the lipid bilayer mediate substrate release and inhibition of glutamate transporters. ELife, 2020, 9, .	2.8	43
6366	Structural ordering of the Plasmodium berghei circumsporozoite protein repeats by inhibitory antibody 3D11. ELife, 2020, 9, .	2.8	15
6367	The cryo-EM structure of the human uromodulin filament core reveals a unique assembly mechanism. ELife, 2020, 9, .	2.8	26
6368	Cryo-EM analysis of PIP2 regulation in mammalian GIRK channels. ELife, 2020, 9, .	2.8	52
6369	Molecular mechanism for direct actin force-sensing by Î±-catenin. ELife, 2020, 9, .	2.8	62
6370	Reassembly and co-crystallization of a family 9 processive endoglucanase from its component parts: structural and functional significance of the intermodular linker. PeerJ, 2015, 3, e1126.	0.9	29
6371	Cellular production of a counterfeit viral protein confers immunity to infection by a related virus. PeerJ, 2018, 6, e5679.	0.9	3
6372	Structural insights into kinetoplastid coronin oligomerization domain and F-actin interaction. Current Research in Structural Biology, 2021, 3, 268-276.	1.1	2
6373	Constant pH molecular dynamics of porcine circovirus 2 capsid protein reveals a mechanism for capsid assembly. Physical Chemistry Chemical Physics, 2021, 23, 24617-24626.	1.3	1
6374	Investigating molecular mechanisms of 2A-stimulated ribosomal pausing and frameshifting in <i>Theilovirus</i>. Nucleic Acids Research, 2021, 49, 11938-11958.	6.5	11
6375	Three-Dimensional Structure of Single-Point Mutant of Esterase PMGL2. Crystallography Reports, 2021, 66, 811-814.	0.1	0
6376	Three-Dimensional Structure of Recombinant Thermophilic Ribokinase from Thermus speÑ•es 2.9 in Complex with Adenosine Diphosphate. Crystallography Reports, 2021, 66, 769-776.	0.1	1

#	Article	IF	Citations
6377	Role of Conformational Changes of Hexameric Bacterial Uridine Phosphorylases in Substrate Binding. Crystallography Reports, 2021, 66, 786-790.	0.1	1
6378	Structural basis for the inhibition of the Bacillus subtilis c-di-AMP cyclase CdaA by the phosphoglucomutase GlmM. Journal of Biological Chemistry, 2021, 297, 101317.	1.6	10
6379	The novel anti-CRISPR AcrIIA22 relieves DNA torsion in target plasmids and impairs SpyCas9 activity. PLoS Biology, 2021, 19, e3001428.	2.6	13
6380	Identification of difructose dianhydride I synthase/hydrolase from an oral bacterium establishes a novel glycoside hydrolase family. Journal of Biological Chemistry, 2021, 297, 101324.	1.6	13
6381	Development of 2-(5,6,7-Trifluoro-1H-Indol-3-yl)-quinoline-5-carboxamide as a Potent, Selective, and Orally Available Inhibitor of Human Androgen Receptor Targeting Its Binding Function-3 for the Treatment of Castration-Resistant Prostate Cancer. Journal of Medicinal Chemistry, 2021, 64, 14968-14982.	2.9	9
6382	Structural insight into DNA recognition by bacterial transcriptional regulators of the SorC/DeoR family. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1411-1424.	1.1	3
6383	Exceptionally potent human monoclonal antibodies are effective for prophylaxis and treatment of tetanus in mice. Journal of Clinical Investigation, 2021, 131, .	3.9	8
6384	Retinal pigment epithelium 65ÂkDa protein (RPE65): An update. Progress in Retinal and Eye Research, 2022, 88, 101013.	7.3	36
6385	Crystal Structure and Functional Characterization of the Bifunctional N-(5â€²-Phosphoribosyl)anthranilate Isomerase-indole-3-glycerol-phosphate Synthase from Corynebacterium glutamicum. Journal of Agricultural and Food Chemistry, 2021, 69, 12485-12493.	2.4	1
6388	Elevated expression of MKRN3 in squamous cell carcinoma of the head and neck and its clinical significance. Cancer Cell International, 2021, 21, 557.	1.8	3
6389	Mutually Exclusive Expression of Closely Related Odorant-Binding Proteins 9A and 9B in the Antenna of the Red Flour Beetle Tribolium castaneum. Biomolecules, 2021, 11, 1502.	1.8	4
6390	Uncovering a conserved vulnerability site in SARSâ€CoVâ€2 by a human antibody. EMBO Molecular Medicine, 2021, 13, e14544.	3.3	17
6391	Structural and Biochemical Studies of Bacillus subtilis MobB. Crystals, 2021, 11, 1262.	1.0	1
6393	Neutralizing antibody 5-7 defines a distinct site of vulnerability in SARS-CoV-2 spike N-terminal domain. Cell Reports, 2021, 37, 109928.	2.9	52
6395	Systematic Evaluation of Fluorination as Modification for Peptideâ€Based Fusion Inhibitors against HIVâ€1 Infection. ChemBioChem, 2021, 22, 3443-3451.	1.3	4
6396	Structure of a human replisome shows the organisation and interactions of a DNA replication machine. EMBO Journal, 2021, 40, e108819.	3.5	60
6397	The structural basis of PTEN regulation by multi-site phosphorylation. Nature Structural and Molecular Biology, 2021, 28, 858-868.	3.6	20
6400	First Crystal Structure of Bacterial Oligopeptidase B in an Intermediate State: The Roles of the Hinge Region Modification and Spermine. Biology, 2021, 10, 1021.	1.3	7

#	Article	IF	Citations
6402	Weaving of bacterial cellulose by the Bcs secretion systems. FEMS Microbiology Reviews, 2022, 46, .	3.9	28
6403	Full Neutralization of Centruroides sculpturatus Scorpion Venom by Combining Two Human Antibody Fragments. Toxins, 2021, 13, 708.	1.5	6
6404	Exosite Binding in Thrombin: A Global Structural/Dynamic Overview of Complexes with Aptamers and Other Ligands. International Journal of Molecular Sciences, 2021, 22, 10803.	1.8	24
6406	Crystal structure of the [2Feâ€"2S] protein I (Shethna protein I) from <i>Azotobacter vinelandii</i>. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 407-411.	0.4	2
6407	An Atypical Autoinflammatory Disease Due to an LRR Domain NLRP3 Mutation Enhancing Binding to NEK7. Journal of Clinical Immunology, 2022, 42, 158-170.	2.0	8
6409	Structural basis for SdgB- and SdgA-mediated glycosylation of staphylococcal adhesive proteins. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1460-1474.	1.1	1
6411	The inner mechanics of rhodopsin guanylyl cyclase during cGMP-formation revealed by real-time FTIR spectroscopy. ELife, 2021, 10, .	2.8	6
6413	The tertiary structure of the human Xkr8â€"Basigin complex that scrambles phospholipids at plasma membranes. Nature Structural and Molecular Biology, 2021, 28, 825-834.	3.6	26
6414	Deciphering the enigma of missing DNA binding domain of LacI family transcription factors. Archives of Biochemistry and Biophysics, 2021, 713, 109060.	1.4	3
6415	Catalytic and structural insights into a stereospecific and thermostable Class II aldolase HpaI from Acinetobacter baumannii. Journal of Biological Chemistry, 2021, 297, 101280.	1.6	6
6416	Biochemical and structural studies of two tetrameric nucleoside 2â€²-deoxyribosyltransferases from psychrophilic and mesophilic bacteria: Insights into cold-adaptation. International Journal of Biological Macromolecules, 2021, 192, 138-150.	3.6	4
6418	Applications of Bioinformatics to Protein Structures: How Protein Structure and Bioinformatics Overlap. Methods in Molecular Biology, 2009, 569, 157-172.	0.4	0
6419	Protein Structure Databases. Methods in Molecular Biology, 2010, 609, 59-82.	0.4	1
6420	The future of HOPE: what can and cannot be predicted about the molecular effects of a disease causing point mutation in a protein?. EMBnet Journal, 2011, 17, 25.	0.2	3
6422	Proteopedia: Exciting Advances in the 3D Encyclopedia of Biomolecular Structure. NATO Science for Peace and Security Series A: Chemistry and Biology, 2012, , 149-161.	0.5	0
6423	IFACE: A BIOINFORMATICS TOOL FOR THE ANALYSIS OF PROTEIN-PROTEIN INTERFACE. International Journal for Computational Biology, 2012, 1, 37.	0.1	0
6424	Alkaline Endopeptidase (Nesterenkonia). , 2013, , 3084-3088.		0
6425	Proteinâ€"Protein Interactions in the Solid State: The Troubles of Crystallizing Proteinâ€"Protein Complexes. , 2013, , 113-134.		1

#	Article	IF	Citations
6426	Carbon-Concentrating Mechanism. SpringerBriefs in Materials, 2014, , 5-38.	0.1	5
6428	Dynamics of Î²B2-Crystallin Motion Based on Principal Component Analysis and Normal Mode Analysis. Computational Biology and Bioinformatics, 2015, 3, 31.	0.3	0
6429	Crystal structure of the flavoenzyme PA4991 fromPseudomonas aeruginosa. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 105-111.	0.4	0
6435	Proteolysis of truncated hemolysin A yields a stable dimerization interface. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 138-145.	0.4	1
6444	Structure of the staphylococcal enterotoxin B vaccine candidate S19 showing eliminated superantigen activity. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 595-600.	0.4	0
6448	Structure of aspartate Î²-semialdehyde dehydrogenase from<i>Francisella tularensis</i>. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 14-22.	0.4	7
6449	Protein Docking and Drug Design. Advances in Bioinformatics and Biomedical Engineering Book Series, 2018, , 207-241.	0.2	0
6452	Mannose in Complex with Colocasia esculenta Tuber Agglutinin. Journal of Glycobiology, 2018, 07, .	0.2	0
6454	Structural and Functional Studies of the RBPJ-SHARP Complex Reveal Conserved Corepressor Binding Site. SSRN Electronic Journal, 0, , .	0.4	0
6500	Crystal structure of the programmed cell death 5 protein from <i>Sulfolobus solfataricus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 73-79.	0.4	0
6505	Crystal Structures of REF6 and Its Complex with DNA Reveal Diverse Recognition Mechanisms. SSRN Electronic Journal, 0, , .	0.4	0
6506	Protein Docking and Drug Design. , 2019, , 889-922.		0
6564	Structural insights into the substrate specificity of SP_0149, the substrate-binding protein of a methionine ABC transporter from <i>Streptococcus pneumoniae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 520-528.	0.4	0
6580	Spectroscopic and molecular modeling investigations on heat induced behaviour of soy proteins. Emirates Journal of Food and Agriculture, 0, , 569.	1.0	5
6606	Crystallographic snapshots of the EF-hand protein MCFD2 complexed with the intracellular lectin ERGIC-53 involved in glycoprotein transport. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 216-221.	0.4	8
6611	Structural basis of the dominant inheritance of hypermethioninemia associated with the Arg264His mutation in the <i>MAT1A</i> gene. Acta Crystallographica Section D: Structural Biology, 2020, 76, 594-607.	1.1	5
6621	Structural basis of self-assembly in the lipid-binding domain of mycobacterial polar growth factor Wag31. IUCrJ, 2020, 7, 767-776.	1.0	7
6622	Extracellular alpha/beta-hydrolase from Paenibacillus species shares structural and functional homology to tobacco salicylic acid binding protein 2. Journal of Structural Biology, 2020, 210, 107496.	1.3	2

#	ARTICLE	IF	CITATIONS
6628	Molecular docking analysis of P2X7 receptor with the beta toxin from Clostridium perfringens. Bioinformation, 2020, 16, 594-601.	0.2	3
6631	The structure of <i>Pf</i>GH50B, an agarase from the marine bacterium <i>Pseudoalteromonas fuliginea</i> PS47. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 422-427.	0.4	1
6632	High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 414-421.	0.4	1
6635	Structural insights into the histidine-containing phosphotransfer protein and receiver domain of sensor histidine kinase suggest a complex model in the two-component regulatory system in<i>Pseudomonas aeruginosa</i>. IUCrJ, 2020, 7, 934-948.	1.0	3
6640	The structure of neurofibromin isoform 2 reveals different functional states. Nature, 2021, 599, 315-319.	13.7	22
6641	Vascular K _{ATP} channel structural dynamics reveal regulatory mechanism by Mg-nucleotides. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
6642	Naturally occurring cancer-associated mutations disrupt oligomerization and activity of protein arginine methyltransferase 1 (PRMT1). Journal of Biological Chemistry, 2021, 297, 101336.	1.6	9
6643	Cryo-EM structure of the needle filament tip complex of the<i>Salmonella</i>type III secretion injectisome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
6644	Non-conventional octameric structure of C-phycocyanin. Communications Biology, 2021, 4, 1238.	2.0	15
6645	Dispatched uses Na+ flux to power release of lipid-modified Hedgehog. Nature, 2021, 599, 320-324.	13.7	16
6646	Neutralizing Antibodies to SARSâ€CoVâ€2 Selected from a Human Antibody Library Constructed Decades Ago. Advanced Science, 2022, 9, e2102181.	5.6	14
6648	Analysis of 272 Genetic Variants in the Upgraded Interactive FXI Web Database Reveals New Insights into FXI Deficiency. TH Open, 2021, 05, e543-e556.	0.7	8
6649	Structural basis for the substrate specificity and catalytic features of pseudouridine kinase from Arabidopsis thaliana. Nucleic Acids Research, 2021, 49, 491-503.	6.5	9
6651	Suppressor Mutations in Type II Secretion Mutants of Vibrio cholerae: Inactivation of the VesC Protease. MSphere, 2020, 5, .	1.3	2
6654	Small molecule interactions with the SARS-CoV-2 main protease: In silico all-atom microsecond MD simulations, PELE Monte Carlo simulations, and determination of in vitro activity inhibition. Journal of Molecular Graphics and Modelling, 2022, 110, 108050.	1.3	5
6660	Structural and Biophysical Principles of Degrader Ternary Complexes. RSC Drug Discovery Series, 2020, , 14-54.	0.2	1
6674	Engineering the Fab fragment of the anti-IgE omalizumab to prevent Fab crystallization and permit IgE-Fc complex crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 116-129.	0.4	5
6675	Structural characterization of human <i>O</i>-phosphoethanolamine phospho-lyase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 160-167.	0.4	1

#	Article	IF	Citations
6680	Structure of a tRNA-specific deaminase with compromised deamination activity. Biochemical Journal, 2020, 477, 1483-1497.	1.7	0
6683	A structural study of TatD from <i>Staphylococcus aureus</i> elucidates a putative DNA-binding mode of a Mg²⁺-dependent nuclease. IUCrJ, 2020, 7, 509-521.	1.0	6
6685	Structural basis of glycan276-dependent recognition by HIV-1 broadly neutralizing antibodies. Cell Reports, 2021, 37, 109922.	2.9	5
6686	The minimal structure for iodotyrosine deiodinase function is defined by an outlier protein from the thermophilic bacterium Thermotoga neapolitana. Journal of Biological Chemistry, 2021, 297, 101385.	1.6	4
6688	Surface-induced Dissociation Mass Spectrometry as a Structural Biology Tool. Chemical Reviews, 2022, 122, 7442-7487.	23.0	31
6689	Computational redesign of a fluorogen activating protein with Rosetta. PLoS Computational Biology, 2021, 17, e1009555.	1.5	0
6690	A site of vulnerability at V3 crown defined by HIV-1 bNAb M4008_N1. Nature Communications, 2021, 12, 6464.	5.8	2
6691	Structural Biology of Nanobodies against the Spike Protein of SARS-CoV-2. Viruses, 2021, 13, 2214.	1.5	16
6692	Assessing the effects of PMM2 variants on protein stability. Molecular Genetics and Metabolism, 2021, 134, 344-352.	0.5	2
6693	An insight into the simulation directed understanding of the mechanism in SARS CoV-2 N-CTD, dimer integrity, and RNA-binding: Identifying potential antiviral inhibitors. Journal of Biomolecular Structure and Dynamics, 2022, 40, 13912-13924.	2.0	4
6695	Structures of the Human SPAK and OSR1 Conserved <i>C</i>â€Terminal (CCT) Domains**. ChemBioChem, 2022, 23, .	1.3	2
6702	Structural analysis of a novel substrate-free form of the aminoglycoside 6â€²-<i>N</i>-acetyltransferase from <i>Enterococcus faecium</i>. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 364-371.	0.4	1
6703	Case Studies: Function Predictions of Structural Genomics Results. , 2009, , 273-291.		0
6704	X-ray crystal structure and specificity of the Toxoplasma gondii ME49 TgAPN2. Biochemical Journal, 2020, 477, 3819-3832.	1.7	2
6705	Comparison of tyrosine kinase domain properties for the neurotrophin receptors TrkA and TrkB. Biochemical Journal, 2020, 477, 4053-4070.	1.7	4
6711	Crystal structure of XCC3289 from <i>Xanthomonas campestris</i>: homology with the N-terminal substrate-binding domain of Lon peptidase. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 488-494.	0.4	0
6712	Development of a structure-analysis pipeline using multiple-solvent crystal structures of barrier-to-autointegration factor. Acta Crystallographica Section D: Structural Biology, 2020, 76, 1001-1014.	1.1	1
6713	Review of multimer proteinâ€"protein interaction complex topology and structure prediction*. Chinese Physics B, 2020, 29, 108707.	0.7	4

#	Article	IF	Citations
6716	Pseudoâ€repeats in doublecortin make distinct mechanistic contributions to microtubule regulation. EMBO Reports, 2020, 21, e51534.	2.0	20
6726	The hypothetical periplasmic protein PA1624 from<i>Pseudomonas aeruginosa</i>folds into a unique two-domain structure. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 609-615.	0.4	1
6727	Structural basis of heparin binding to camel peptidoglycan recognition protein-S. International Journal of Biochemistry and Molecular Biology, 2012, 3, 86-94.	0.1	4
6730	Structural Basis for Recognition of L-lysine, L-ornithine, and L-2,4-diamino Butyric Acid by Lysine Cyclodeaminase. Molecules and Cells, 2018, 41, 331-341.	1.0	2
6731	Crystal Structure of Histidine Triad Nucleotide-Binding Protein from the Pathogenic Fungus. Molecules and Cells, 2019, 42, 56-66.	1.0	1
6732	Analysis of interleukin-20 receptor complexes in trabecular meshwork cells and effects of cytokine signaling in anterior segment perfusion culture. Molecular Vision, 2019, 25, 266-282.	1.1	1
6733	Oligomer Model of PB1 Domain of p62/SQSTM1 Based on Crystal Structure of Homo-Dimer and Calculation of Helical Characteristics. Molecules and Cells, 2019, 42, 729-738.	1.0	2
6734	Structural Basis for How Biologic Medicines Bind their Targets in Psoriasis Therapy. Yale Journal of Biology and Medicine, 2020, 93, 19-27.	0.2	1
6735	Structures and therapeutic potential of anti-RBD human monoclonal antibodies against SARS-CoV-2. Theranostics, 2022, 12, 1-17.	4.6	6
6736	Dimeric architecture of maltodextrin glucosidase (MalZ) provides insights into the substrate recognition and hydrolysis mechanism. Biochemical and Biophysical Research Communications, 2022, 586, 49-54.	1.0	2
6737	Crystal structure of the pheromone Er-13 from the ciliate Euplotes raikovi, with implications for a proteinâ€"protein association model in pheromone/receptor interactions. Journal of Structural Biology, 2022, 214, 107812.	1.3	5
6738	In-silico design of peptides for inhibition of HLA-A*03-KLIETYFSK complex as a new drug design for treatment of multiples sclerosis disease. Journal of Molecular Graphics and Modelling, 2022, 111, 108079.	1.3	1
6739	A Structural Basis for Inhibition of the Complement Initiator Protease C1r by Lyme Disease Spirochetes. Journal of Immunology, 2021, 207, 2856-2867.	0.4	11
6740	Highâ€resolution structure of native toxin A from <i>Clostridioides difficile</i>. EMBO Reports, 2022, 23, e53597.	2.0	8
6742	A structured RNA motif locks Argonaute2:miR-122 onto the 5â€™ end of the HCV genome. Nature Communications, 2021, 12, 6836.	5.8	11
6743	A monoclonal antibody that neutralizes SARS-CoV-2 variants, SARS-CoV, and other sarbecoviruses. Emerging Microbes and Infections, 2022, 11, 147-157.	3.0	25
6744	A single amino acid polymorphism in a conserved effector of the multihost blast fungus pathogen expands host-target binding spectrum. PLoS Pathogens, 2021, 17, e1009957.	2.1	32
6745	Chromosome segregation in Archaea: SegAâ€"Âand SegBâ€"DNA complex structures provide insights into segrosome assembly. Nucleic Acids Research, 2021, , .	6.5	5

#	Article	IF	Citations
6746	A Bacterial Cell-Based Assay To Study SARS-CoV-2 Protein-Protein Interactions. MBio, 2021, , e0293621.	1.8	1
6747	Structure, Function and Regulation of a Second Pyruvate Kinase Isozyme in Pseudomonas aeruginosa. Frontiers in Microbiology, 2021, 12, 790742.	1.5	3
6750	Human RIPK3 maintains MLKL in an inactive conformation prior to cell death by necroptosis. Nature Communications, 2021, 12, 6783.	5.8	47
6751	Mechanisms of CP190 Interaction with Architectural Proteins in Drosophila Melanogaster. International Journal of Molecular Sciences, 2021, 22, 12400.	1.8	11
6752	A Structural Overview of Vascular Endothelial Growth Factors Pharmacological Ligands: From Macromolecules to Designed Peptidomimetics. Molecules, 2021, 26, 6759.	1.7	8
6753	The Crystal Structure of NÎ±-p-tosyl-lysyl Chloromethylketone-Bound Oligopeptidase B from Serratia Proteamaculans Revealed a New Type of Inhibitor Binding. Crystals, 2021, 11, 1438.	1.0	4
6754	Design of a Novel Fabâ€Like Antibody Fragment with Enhanced Stability and Affinity for Clinical use. Small Methods, 2022, 6, 2100966.	4.6	1
6755	Structurally Mapping Antigenic Epitopes of Adeno-associated Virus 9: Development of Antibody Escape Variants. Journal of Virology, 2022, 96, JVI0125121.	1.5	11
6756	Proteinâ€“Protein Docking: Past, Present, and Future. Protein Journal, 2022, 41, 1-26.	0.7	12
6757	Crystal structures of the elusive Rhizobium etli l-asparaginase reveal a peculiar active site. Nature Communications, 2021, 12, 6717.	5.8	5
6758	The X-ray structure of juvenile hormone diol kinase from the silkworm <i>Bombyx mori</i>. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 465-472.	0.4	0
6759	Unique functional insights into the antioxidant response of the cyanobacterial Mn-catalase (KatB). Free Radical Biology and Medicine, 2022, 179, 266-276.	1.3	6
6761	LSSmScarlet, dCyRFP2s, dCyOFP2s and CRISPRed2s, Genetically Encoded Red Fluorescent Proteins with a Large Stokes Shift. International Journal of Molecular Sciences, 2021, 22, 12887.	1.8	9
6762	Scaffolding protein CcmM directs multiprotein phase separation in Î²-carboxysome biogenesis. Nature Structural and Molecular Biology, 2021, 28, 909-922.	3.6	24
6764	Mutation-Induced Long-Range Allosteric Interactions in the Spike Protein Determine the Infectivity of SARS-CoV-2 Emerging Variants. ACS Omega, 2021, 6, 31305-31320.	1.6	8
6767	Radioprotective Role of Vitamins C and E against the Gamma Ray-Induced Damage to the Chemical Structure of Bovine Serum Albumin. Antioxidants, 2021, 10, 1875.	2.2	3
6768	Exploring the mechanism of Yixinyin for myocardial infarction by weighted co-expression network and molecular docking. Scientific Reports, 2021, 11, 22567.	1.6	1
6769	Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. PLoS Computational Biology, 2021, 17, e1009560.	1.5	5

#	ARTICLE	IF	CITATIONS
6770	Structural insights into Ubr1-mediated N-degron polyubiquitination. Nature, 2021, 600, 334-338.	13.7	54
6772	The tetrameric assembly of 2â€aminomuconic 6â€semialdehyde dehydrogenase is a functional requirement of cofactor NAD + binding. Environmental Microbiology, 2021, , .	1.8	1
6773	The human microbiome encodes resistance to the antidiabetic drug acarbose. Nature, 2021, 600, 110-115.	13.7	44
6774	HYPK coordinates degradation of polyneddylated proteins by autophagy. Autophagy, 2022, 18, 1763-1784.	4.3	9
6776	The antibody response to SARS-CoV-2 Beta underscores the antigenic distance to other variants. Cell Host and Microbe, 2022, 30, 53-68.e12.	5.1	52
6778	The Structural Biology of Septins and Their Filaments: An Update. Frontiers in Cell and Developmental Biology, 2021, 9, 765085.	1.8	41
6780	BRANEart: Identify Stability Strength and Weakness Regions in Membrane Proteins. Frontiers in Bioinformatics, 2021, 1, .	1.0	3
6781	Next generation Fc scaffold for multispecific antibodies. IScience, 2021, 24, 103447.	1.9	6
6782	Structure and <i>in silico</i> simulations of a cold-active esterase reveals its prime cold-adaptation mechanism. Open Biology, 2021, 11, 210182.	1.5	10
6783	DeepRank: a deep learning framework for data mining 3D protein-protein interfaces. Nature Communications, 2021, 12, 7068.	5.8	56
6784	GTP binding to translation factor eIF2B stimulates its guanine nucleotide exchange activity. IScience, 2021, 24, 103454.	1.9	6
6785	Catalytic flexibility of rice glycosyltransferase OsUGT91C1 for the production of palatable steviol glycosides. Nature Communications, 2021, 12, 7030.	5.8	24
6786	Discovery of an exosite on the SOCS2-SH2 domain that enhances SH2 binding to phosphorylated ligands. Nature Communications, 2021, 12, 7032.	5.8	8
6788	Cross-linking mass spectrometry reveals structural insights of the glutamine synthetase from Leishmania braziliensis. Memorias Do Instituto Oswaldo Cruz, 2022, 116, e210209.	0.8	0
6789	Thermal Stability and Inhibitory Action of Red Grape Skin Phytochemicals against Enzymes Associated with Metabolic Syndrome. Antioxidants, 2022, 11, 118.	2.2	8
6790	Role of PemI in the <i>Staphylococcus aureus</i> PemIK toxinâ€"antitoxin complex: PemI controls PemK by acting as a PemK loop mimic. Nucleic Acids Research, 2022, 50, 2319-2333.	6.5	1
6791	The Mysterious Multitude: Structural Perspective on the Accessory Subunits of Respiratory Complex I. Frontiers in Molecular Biosciences, 2021, 8, 798353.	1.6	35
6792	Structural basis and mode of action for two broadly neutralizing antibodies against SARS-CoV-2 emerging variants of concern. Cell Reports, 2022, 38, 110210.	2.9	96

#	Article	IF	Citations
6793	Observation of robust energy transfer in the photosynthetic protein allophycocyanin using single-molecule pumpâ€"probe spectroscopy. Nature Chemistry, 2022, 14, 153-159.	6.6	16
6795	Structural Basis of Antibody Conformation and Stability Modulation by Framework Somatic Hypermutation. Frontiers in Immunology, 2021, 12, 811632.	2.2	3
6796	The crystal structure of DynF from the dynemicin-biosynthesis pathway of <i>Micromonospora chersina</i>. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 1-7.	0.4	1
6798	In silico analysis and characterization of medicinal mushroom cystathionine beta-synthase as an angiotensin converting enzyme (ACE) inhibitory protein. Computational Biology and Chemistry, 2022, 96, 107620.	1.1	6
6799	Mechanistic Insights into the Preference for Tandem Binding Sites in DNA Recognition by FOXM1. Journal of Molecular Biology, 2022, 434, 167426.	2.0	3
6800	Structural analysis of cysteine-free Nt.BspD6 nicking endonuclease and its functional features. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140756.	1.1	1
6801	High-valency Anti-CD99 Antibodies Toward the Treatment of T Cell Acute Lymphoblastic Leukemia. Journal of Molecular Biology, 2022, 434, 167402.	2.0	3
6802	Alpha-lipoic acid analogues in the regulation of redox balance in epilepsy: A molecular docking and simulation study. Journal of Molecular Graphics and Modelling, 2022, 112, 108116.	1.3	5
6803	A Tetrameric Assembly of Saposin A: Increasing Structural Diversity in Lipid Transfer Proteins. Contact (Thousand Oaks (Ventura County, Calif)), 2021, 4, 251525642110523.	0.4	1
6804	Hedgehog-Interacting Protein is a multimodal antagonist of Hedgehog signalling. Nature Communications, 2021, 12, 7171.	5.8	16
6805	Structurally-discovered KLF4 variants accelerate and stabilize reprogramming to pluripotency. IScience, 2022, 25, 103525.	1.9	4
6806	The intrinsically disordered TSSC4 protein acts as a helicase inhibitor, placeholder and multi-interaction coordinator during snRNP assembly and recycling. Nucleic Acids Research, 2022, 50, 2938-2958.	6.5	11
6807	Insights on the mutational landscape of the SARS-CoV-2 Omicron variant receptor-binding domain. Cell Reports Medicine, 2022, 3, 100527.	3.3	47
6808	Methods to determine the oligomeric structure of proteins. , 2022, , 49-76.		2
6810	Teneurin4 dimer structures reveal a calciumâ€stabilized compact conformation supporting homomeric transâ€interactions. EMBO Journal, 2022, 41, e107505.	3.5	6
6812	Barcode fusion genetics-protein-fragment complementation assay (BFG-PCA): tools and resources that expand the potential for binary protein interaction discovery. Nucleic Acids Research, 2022, 50, e54-e54.	6.5	4
6813	A bispecific monomeric nanobody induces spike trimer dimers and neutralizes SARS-CoV-2 in vivo. Nature Communications, 2022, 13, 155.	5.8	49
6814	Mechanism of transcription regulation by <i>Acinetobacter baumannii</i> HpaR in the catabolism of <i>p</i>â€hydroxyphenylacetate. FEBS Journal, 2022, 289, 3217-3240.	2.2	2

#	ARTICLE	IF	CITATIONS
6815	QSalignWeb: A Server to Predict and Analyze Protein Quaternary Structure. Frontiers in Molecular Biosciences, 2021, 8, 787510.	1.6	3
6817	A Fc-enhanced NTD-binding non-neutralizing antibody delays virus spread and synergizes with a nAb to protect mice from lethal SARS-CoV-2 infection. Cell Reports, 2022, 38, 110368.	2.9	82
6818	Structural and functional characterization of a monoclonal antibody blocking TIGIT. MAbs, 2022, 14, 2013750.	2.6	6
6819	Structure of the human ATM kinase and mechanism of Nbs1 binding. ELife, 2022, 11, .	2.8	21
6820	Major tail proteins of bacteriophages of the order Caudovirales. Journal of Biological Chemistry, 2022, 298, 101472.	1.6	37
6821	Interfacial Peptides as Affinity Modulating Agents of Protein-Protein Interactions. Biomolecules, 2022, 12, 106.	1.8	3
6823	A small RNA that cooperatively senses two stacked metabolites in one pocket for gene control. Nature Communications, 2022, 13, 199.	5.8	19
6825	Subsite Ligand Recognition and Cooperativity in the TPP Riboswitch: Implications for Fragment-Linking in RNA Ligand Discovery. ACS Chemical Biology, 2022, 17, 438-448.	1.6	18
6827	Crystal structure and initial characterization of a novel archaeal-like Holliday junction-resolving enzyme from <i>Thermus thermophilus</i> phage Tth15-6. Acta Crystallographica Section D: Structural Biology, 2022, 78, 212-227.	1.1	5
6828	MITOL-mediated DRP1 ubiquitylation and degradation promotes mitochondrial hyperfusion in a CMT2A-linked MFN2 mutant. Journal of Cell Science, 2022, 135, .	1.2	10
6829	The Structure and Immune Regulatory Implications of the Ubiquitin-Like Tandem Domain Within an Avian 2â€™-5â€™ Oligoadenylate Synthetase-Like Protein. Frontiers in Immunology, 2021, 12, 794664.	2.2	1
6830	A Model for Allosteric Communication in Drug Transport by the AcrAB-TolC Tripartite Efflux Pump. Antibiotics, 2022, 11, 52.	1.5	6
6831	The Species-Specific 282 Residue in the PB2 Subunit of the Polymerase Regulates RNA Synthesis and Replication of Influenza A Viruses Infecting Bat and Nonbat Hosts. Journal of Virology, 2022, 96, jvi0219021.	1.5	2
6832	Solid-State NMR Dipolar and Chemical Shift Anisotropy Recoupling Techniques for Structural and Dynamical Studies in Biological Systems. Chemical Reviews, 2022, 122, 9880-9942.	23.0	23
6833	CPVT-associated calmodulin variants N53I and A102V dysregulate Ca2+ signalling via different mechanisms. Journal of Cell Science, 2022, 135, .	1.2	7
6834	Structure and function of a family of tick-derived complement inhibitors targeting properdin. Nature Communications, 2022, 13, 317.	5.8	8
6835	Inhibition of Tau seeding by targeting Tau nucleation core within neurons with a single domain antibody fragment. Molecular Therapy, 2022, 30, 1484-1499.	3.7	31
6836	Structural insights into the antifungal drug target guanosine monophosphate synthase from <i>Aspergillus fumigatus</i>. Acta Crystallographica Section D: Structural Biology, 2022, 78, 248-259.	1.1	2

#	Article	IF	Citations
6837	An engineered protein-based submicromolar competitive inhibitor of the Staphylococcus aureus virulence factor aureolysin. Computational and Structural Biotechnology Journal, 2022, 20, 534-544.	1.9	5
6838	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. Cell, 2022, 185, 467-484.e15.	13.5	788
6839	The structure and function of modular <i>Escherichia coli</i> O157:H7 bacteriophage FTBEc1 endolysin, LysT84: defining a new endolysin catalytic subfamily. Biochemical Journal, 2022, 479, 207-223.	1.7	5
6840	Rapid identification of neutralizing antibodies against SARS-CoV-2 variants by mRNA display. Cell Reports, 2022, 38, 110348.	2.9	14
6841	<i>PERCC1</i>, a new member of the<i>Yap/TAZ</i>/<i>FAM181</i>transcriptional co-regulator family. Bioinformatics Advances, 2022, 2, .	0.9	2
6842	Biochemical propensity mapping for structural and functional anatomy of importin Î± IBB domain. Genes To Cells, 2022, 27, 173-191.	0.5	4
6843	Catalytically active holo<i>Homo sapiens</i>adenosine deaminase I adopts a closed conformation. Acta Crystallographica Section D: Structural Biology, 2022, 78, 91-103.	1.1	3
6844	Genotype-specific features reduce the susceptibility of South American yellow fever virus strains to vaccine-induced antibodies. Cell Host and Microbe, 2022, 30, 248-259.e6.	5.1	11
6845	Advanced computational tools for quantitative analysis of proteinâ€"nucleic acid interfaces. , 2022, , 163-180.		0
6846	Analysis of antibodies from HCV elite neutralizers identifies genetic determinants of broad neutralization. Immunity, 2022, 55, 341-354.e7.	6.6	21
6847	Omicron: A Heavily Mutated SARS-CoV-2 Variant Exhibits Stronger Binding to ACE2 and Potently Escapes Approved COVID-19 Therapeutic Antibodies. Frontiers in Immunology, 2021, 12, 830527.	2.2	165
6848	IMPDH1 retinal variants control filament architecture to tune allosteric regulation. Nature Structural and Molecular Biology, 2022, 29, 47-58.	3.6	29
6849	Deconvolution of the MBP-Bri2 Interaction by a Yeast Two Hybrid System and Synergy of the AlphaFold2 and High Ambiguity Driven Protein-Protein Docking. Crystals, 2022, 12, 197.	1.0	4
6850	Antibodies to Cartilage Oligomeric Matrix Protein Are Pathogenic in Mice and May Be Clinically Relevant in Rheumatoid Arthritis. Arthritis and Rheumatology, 2022, 74, 961-971.	2.9	9
6851	Characterization and structural analyses of a novel glycosyltransferase acting on the Î²-1,2-glucosidic linkages. Journal of Biological Chemistry, 2022, 298, 101606.	1.6	5
6853	From complete cross-docking to partners identification and binding sites predictions. PLoS Computational Biology, 2022, 18, e1009825.	1.5	9
6854	Structural basis of cyclic oligoadenylate binding to the transcription factor Csa3 outlines cross talk between type III and type I CRISPR systems. Journal of Biological Chemistry, 2022, 298, 101591.	1.6	2
6855	Structural basis for safe and efficient energy conversion in a respiratory supercomplex. Nature Communications, 2022, 13, 545.	5.8	10

#	ARTICLE	IF	CITATIONS
6856	Effects of Myristate on the Induced Circular Dichroism Spectra of Aripiprazole Bound to Human Serum Albumin: A Structuralâ€“Chemical Investigation. ACS Omega, 2022, 7, 4413-4419.	1.6	4
6857	Structural characterization of the ANTAR antiterminator domain bound to RNA. Nucleic Acids Research, 2022, 50, 2889-2904.	6.5	2
6858	D155Y substitution of SARS-CoV-2 ORF3a weakens binding with Caveolin-1. Computational and Structural Biotechnology Journal, 2022, 20, 766-778.	1.9	8
6859	Structural basis of Plasmodium vivax inhibition by antibodies binding to the circumsporozoite protein repeats. ELife, 2022, 11, .	2.8	5
6860	An infectious SARS-CoV-2 B.1.1.529 Omicron virus escapes neutralization by therapeutic monoclonal antibodies. Nature Medicine, 2022, 28, 490-495.	15.2	577
6861	Members of the vertebrate contactin and amyloid precursor protein families interact through a conserved interface. Journal of Biological Chemistry, 2022, 298, 101541.	1.6	8
6862	Crystal structure of the Toll/interleukinâ€•1 receptor (TIR) domain of ILâ€•1R10 provides structural insights into TIR domain signalling. FEBS Letters, 2022, 596, 886-897.	1.3	5
6863	Development of a potent high-affinity human therapeutic antibody via novel application of recombination signal sequenceâ€“based affinity maturation. Journal of Biological Chemistry, 2022, 298, 101533.	1.6	3
6864	Mechanisms of Cre recombinase synaptic complex assembly and activation illuminated by Cryo-EM. Nucleic Acids Research, 2022, 50, 1753-1769.	6.5	6
6865	Crystal structure of the plant feruloylâ€“coenzyme A monolignol transferase provides insights into the formation of monolignol ferulate conjugates. Biochemical and Biophysical Research Communications, 2022, 594, 8-14.	1.0	4
6866	Crystal structure of the cytokinin-producing enzyme â€œlonely guyâ€•(LOG) from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2022, 598, 113-118.	1.0	1
6867	PplD is a de-N-acetylase of the cell wall linkage unit of streptococcal rhamnopolysaccharides. Nature Communications, 2022, 13, 590.	5.8	7
6869	Identification of molecular basis that underlie enzymatic specificity of AzoRo from Rhodococcus opacus 1CP: A potential NADH:quinone oxidoreductase. Archives of Biochemistry and Biophysics, 2022, 717, 109123.	1.4	5
6870	Protection of the Prodomain Î±1-Helix Correlates with Latency in the Transforming Growth Factor-Î² Family. Journal of Molecular Biology, 2022, 434, 167439.	2.0	2
6871	Structural and functional characterization of Î²-cyanoalanine synthase from Tetranychus urticae. Insect Biochemistry and Molecular Biology, 2022, 142, 103722.	1.2	2
6872	Structural insight into a molecular mechanism of methenyltetrahydrofolate cyclohydrolase from Methylobacterium extorquens AM1. International Journal of Biological Macromolecules, 2022, 202, 234-240.	3.6	1
6873	Tousled-like kinase 2 targets ASF1 histone chaperones through client mimicry. Nature Communications, 2022, 13, 749.	5.8	9
6874	Inhibitory Effects of Bacterial Silk-like Biopolymer on Herpes Simplex Virus Type 1, Adenovirus Type 7 and Hepatitis C Virus Infection. Journal of Functional Biomaterials, 2022, 13, 17.	1.8	1

#	Article	IF	Citations
6875	A human antibody reveals a conserved site on beta-coronavirus spike proteins and confers protection against SARS-CoV-2 infection. Science Translational Medicine, 2022, 14, eabi9215.	5.8	123
6877	Crystal structure and molecular mechanism of an E/F type bilin lyase-isomerase. Structure, 2022, 30, 564-574.e3.	1.6	4
6878	An archaellum filament composed of two alternating subunits. Nature Communications, 2022, 13, 710.	5.8	18
6879	Hot spots-making directed evolution easier. Biotechnology Advances, 2022, 56, 107926.	6.0	35
6880	PSTPIP1-LYP phosphatase interaction: structural basis and implications for autoinflammatory disorders. Cellular and Molecular Life Sciences, 2022, 79, 131.	2.4	6
6881	Structural characterization of the Myxococcus xanthus encapsulin and ferritin-like cargo system gives insight into its iron storage mechanism. Structure, 2022, 30, 551-563.e4.	1.6	16
6883	The first structureâ€“function study of GH151 Î±â€‹<scp>l</scp>â€‘fucosidase uncovers new oligomerization pattern, active site complementation, and selective substrate specificity. FEBS Journal, 2022, 289, 4998-5020.	2.2	3
6884	Cryo-EM structure of the SARS-CoV-2 Omicron spike. Cell Reports, 2022, 38, 110428.	2.9	82
6886	Neutralizing antibodies induced in immunized macaques recognize the CD4-binding site on an occluded-open HIV-1 envelope trimer. Nature Communications, 2022, 13, 732.	5.8	19
6887	Structure of the NLRP3 decamer bound to the cytokine release inhibitor CRID3. Nature, 2022, 604, 184-189.	13.7	109
6889	Unusual substrate specificity in GH family 12: structureâ€“function analysis of glucanases Bgh12A and Xgh12B from Aspergillus cervinus, and Egh12 from Thielavia terrestris. Applied Microbiology and Biotechnology, 2022, 106, 1493-1509.	1.7	4
6890	Crystal structure of a tandem B-box domain from Arabidopsis CONSTANS. Biochemical and Biophysical Research Communications, 2022, 599, 38-42.	1.0	2
6891	Striking antibody evasion manifested by the Omicron variant of SARS-CoV-2. Nature, 0, , .	13.7	72
6892	Conformational changes in Lassa virus L protein associated with promoter binding and RNA synthesis activity. Nature Communications, 2021, 12, 7018.	5.8	26
6893	Conformational dynamics of the Beta and Kappa SARS-CoV-2 spike proteins and their complexes with ACE2 receptor revealed by cryo-EM. Nature Communications, 2021, 12, 7345.	5.8	58
6894	Structural and molecular basis for Cardiovirus 2A protein as a viral gene expression switch. Nature Communications, 2021, 12, 7166.	5.8	18
6895	Striking antibody evasion manifested by the Omicron variant of SARS-CoV-2. Nature, 2022, 602, 676-681.	13.7	1,038
6904	Neurotoxin-mediated potent activation of the axon degeneration regulator SARM1. ELife, 2021, 10, .	2.8	22

#	Article	IF	Citations
6905	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the <i>Pseudomonas</i>-Phage PaP3. SSRN Electronic Journal, 0, , .	0.4	1
6906	Trends of antimalarial marine natural products: progresses, challenges and opportunities. Natural Product Reports, 2022, 39, 969-990.	5.2	14
6907	Deciphering the structure of Arabidopsis thaliana 5-enol-pyruvyl-shikimate-3-phosphate synthase: An essential step toward the discovery of novel inhibitors to supersede glyphosate. Computational and Structural Biotechnology Journal, 2022, 20, 1494-1505.	1.9	2
6909	Computational Design of Single-Peptide Nanocages with Nanoparticle Templating. Molecules, 2022, 27, 1237.	1.7	5
6912	The endoplasmic reticulum proteostasis network profoundly shapes the protein sequence space accessible to HIV envelope. PLoS Biology, 2022, 20, e3001569.	2.6	7
6913	A Peptide Derived from GAPDH Enhances Resistance to DNA Damage in Saccharomyces cerevisiae Cells. Applied and Environmental Microbiology, 2022, 88, aem0219421.	1.4	3
6914	Impact of distant peptide substrate residues on enzymatic activity of SlyD. Cellular and Molecular Life Sciences, 2022, 79, 138.	2.4	1
6915	Cryo-EM structures reveal high-resolution mechanism of a DNA polymerase sliding clamp loader. ELife, 2022, 11, .	2.8	27
6916	SARS-CoV-2 Beta variant infection elicits potent lineage-specific and cross-reactive antibodies. Science, 2022, 375, 782-787.	6.0	60
6917	A recurring packing contact in crystals of InlB pinpoints functional binding sites in the internalin domain and the B repeat. Acta Crystallographica Section D: Structural Biology, 2022, 78, 310-320.	1.1	1
6918	Molecular basis of receptor binding and antibody neutralization of Omicron. Nature, 2022, 604, 546-552.	13.7	135
6920	Identification of novel inhibitors targeting TIRAP interactions with BTK and PKCÎ´ in inflammation through an in silico approach. SAR and QSAR in Environmental Research, 2022, 33, 141-166.	1.0	4
6921	The structure of the <scp><i>Clostridium thermocellum</i> RsgI9</scp> ectodomain provides insight into the mechanism of biomass sensing. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1457-1467.	1.5	3
6923	Visualizing protein breathing motions associated with aromatic ring flipping. Nature, 2022, 602, 695-700.	13.7	26
6924	A mechanism of origin licensing control through autoinhibition of S. cerevisiae ORCÂ·DNAÂ·Cdc6. Nature Communications, 2022, 13, 1059.	5.8	7
6925	Heterodimer of A2A and Oxytocin Receptors Regulating Glutamate Release in Adult Striatal Astrocytes. International Journal of Molecular Sciences, 2022, 23, 2326.	1.8	11
6926	The Structure of the Arabidopsis PEX4-PEX22 Peroxin Complexâ€"Insights Into Ubiquitination at the Peroxisomal Membrane. Frontiers in Cell and Developmental Biology, 2022, 10, 838923.	1.8	5
6927	Structural basis for SARS-CoV-2 Delta variant recognition of ACE2 receptor and broadly neutralizing antibodies. Nature Communications, 2022, 13, 871.	5.8	107

#	ARTICLE	IF	CITATIONS
6928	A new inactive conformation of SARS-CoV-2 main protease. Acta Crystallographica Section D: Structural Biology, 2022, 78, 363-378.	1.1	13
6929	Structure and assembly of the S-layer in C. difficile. Nature Communications, 2022, 13, 970.	5.8	30
6930	Cryo-EM structures of staphylococcal IsdB bound to human hemoglobin reveal the process of heme extraction. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116708119.	3.3	6
6931	The Family Keeps on Growing: Four Novel Fungal OYEs Characterized. International Journal of Molecular Sciences, 2022, 23, 3050.	1.8	4
6932	Conformational plasticity of the HIV-1 gp41 immunodominant region is recognized by multiple non-neutralizing antibodies. Communications Biology, 2022, 5, 291.	2.0	3
6933	EvoRator: Prediction of Residue-level Evolutionary Rates from Protein Structures Using Machine Learning. Journal of Molecular Biology, 2022, 434, 167538.	2.0	4
6934	Double drugging of prolyl-tRNA synthetase provides a new paradigm for anti-infective drug development. PLoS Pathogens, 2022, 18, e1010363.	2.1	12
6935	A multi-factor trafficking site on the spliceosome remodeling enzyme BRR2 recruits C9ORF78 to regulate alternative splicing. Nature Communications, 2022, 13, 1132.	5.8	7
6936	Mouse and human antibodies bind HLA-E-leader peptide complexes and enhance NK cell cytotoxicity. Communications Biology, 2022, 5, 271.	2.0	14
6937	Structural basis of SARM1 activation, substrate recognition, and inhibition by small molecules. Molecular Cell, 2022, 82, 1643-1659.e10.	4.5	66
6938	Ubiquitin and a charged loop regulate the ubiquitin E3 ligase activity of Ark2C. Nature Communications, 2022, 13, 1181.	5.8	8
6939	Machine learning solutions for predicting proteinâ€"protein interactions. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	19
6940	Structural basis of Alzheimer <i>Î²</i>-amyloid peptide recognition by engineered lipocalin proteins with aggregation-blocking activity. Biological Chemistry, 2022, 403, 557-571.	1.2	2
6942	Structural Insight into KsBcl-2 Mediated Apoptosis Inhibition by Kaposi Sarcoma Associated Herpes Virus. Viruses, 2022, 14, 738.	1.5	2
6943	Mechanism of cooperative N-glycan processing by the multi-modular endoglycosidase EndoE. Nature Communications, 2022, 13, 1137.	5.8	10
6944	Structure and activity of the DHNA Coenzyme-A Thioesterase from Staphylococcus aureus providing insights for innovative drug development. Scientific Reports, 2022, 12, 4313.	1.6	1
6945	Structure and conformational dynamics of <i>Clostridioides difficile</i> toxin A. Life Science Alliance, 2022, 5, e202201383.	1.3	8
6946	How clustered protocadherin binding specificity is tuned for neuronal self-/nonself-recognition. ELife, 2022, 11, .	2.8	18

#	ARTICLE	IF	CITATIONS
6947	Investigating the Effects of Amino Acid Variations in Human Menin. Molecules, 2022, 27, 1747.	1.7	8
6950	Structures of a deltacoronavirus spike protein bound to porcine and human receptors. Nature Communications, 2022, 13, 1467.	5.8	24
6952	Structures of synthetic helical filaments and tubes based on peptide and peptido-mimetic polymers. Quarterly Reviews of Biophysics, 2022, 55, 1-103.	2.4	8
6953	Biocatalytically Active and Stable Crossâ€Linked Enzyme Crystals of Halohydrin Dehalogenase HheG by Protein Engineering. ChemCatChem, 2022, 14, .	1.8	9
6954	Structural basis for peptide recognition by archaeal oligopeptide permease A. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1434-1442.	1.5	1
6955	Computational Cosolvent Mapping Analysis Leads to Identify Salicylic Acid Analogs as Weak Inhibitors of ST2 and IL33 Binding. Journal of Physical Chemistry B, 2022, 126, 2394-2406.	1.2	0
6956	Glutathione binding to the plant AtAtm3 transporter and implications for the conformational coupling of ABC transporters. ELife, 2022, 11, .	2.8	8
6957	Structural and molecular rationale for the diversification of resistance mediated by the Antibiotic_NAT family. Communications Biology, 2022, 5, 263.	2.0	3
6959	Structural Characterization of Cytochrome câ€²Î²â€Met from an Ammonia-Oxidizing Bacterium. Biochemistry, 2022, 61, 563-574.	1.2	4
6960	<i>Finis tolueni</i>: a new type of thiolase with an integrated Znâ€finger subunit catalyzes the final step of anaerobic toluene metabolism. FEBS Journal, 2022, 289, 5599-5616.	2.2	3
6962	Crystal structure report of the ImmR transcriptional regulator DNA-binding domain of the Bacillus subtilis ICEBs1 transposon. Scientific Reports, 2022, 12, 5258.	1.6	1
6964	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. Immunity, 2022, 55, 1105-1117.e4.	6.6	44
6965	Nebulized delivery of a broadly neutralizing SARS-CoV-2 RBD-specific nanobody prevents clinical, virological, and pathological disease in a Syrian hamster model of COVID-19. MAbs, 2022, 14, 2047144.	2.6	10
6966	Crystal structure analysis of phycoerythrin from marine cyanobacterium <i>Halomicronema</i>. Journal of Biomolecular Structure and Dynamics, 2023, 41, 3752-3761.	2.0	2
6968	Atomic structure of the predominant GII.4 human norovirus capsid reveals novel stability and plasticity. Nature Communications, 2022, 13, 1241.	5.8	19
6970	C-type lectin-(like) fold â€“ Protein-protein interaction patterns and utilization. Biotechnology Advances, 2022, 58, 107944.	6.0	2
6971	Structure of the poxvirus decapping enzyme D9 reveals its mechanism of cap recognition and catalysis. Structure, 2022, 30, 721-732.e4.	1.6	8
6972	Flagellin outer domain dimerization modulates motility in pathogenic and soil bacteria from viscous environments. Nature Communications, 2022, 13, 1422.	5.8	10

#	ARTICLE	IF	CITATIONS
6973	A structural model of the human plasminogen and <i>Aspergillus fumigatus</i> enolase complex. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1509-1520.	1.5	0
6974	Contrasting Modes of New World Arenavirus Neutralization by Immunization-Elicited Monoclonal Antibodies. MBio, 2022, 13, e0265021.	1.8	7
6977	The mRubyFT Protein, Genetically Encoded Blue-to-Red Fluorescent Timer. International Journal of Molecular Sciences, 2022, 23, 3208.	1.8	5
6978	Driving E3 Ligase Substrate Specificity for Targeted Protein Degradation: Lessons from Nature and the Laboratory. Annual Review of Biochemistry, 2022, 91, 295-319.	5.0	41
6979	Substrate-binding loop interactions with pseudouridine trigger conformational changes that promote catalytic efficiency of pseudouridine kinase PUKI. Journal of Biological Chemistry, 2022, 298, 101869.	1.6	4
6980	Structure of BrxA from <i>Staphylococcus aureus</i>, a bacilliredoxin involved in redox homeostasis in Firmicutes. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 144-149.	0.4	1
6981	Crystal structure of the ternary complex of <i>Leishmania major</i> pteridine reductase 1 with the cofactor NADP⁺/NADPH and the substrate folic acid. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 170-176.	0.4	9
6982	Enzymatic and structural characterization of Î²-fructofuranosidase from the honeybee gut bacterium Frischella perrara. Applied Microbiology and Biotechnology, 2022, 106, 2455-2470.	1.7	4
6984	SARS-CoV-2 Membrane Protein: From Genomic Data to Structural New Insights. International Journal of Molecular Sciences, 2022, 23, 2986.	1.8	15
6986	Differential recognition of canonical NF-Îº B dimers by Importin Î±3. Nature Communications, 2022, 13, 1207.	5.8	23
6988	Mechanism of Borrelia immune evasion by FhbA-related proteins. PLoS Pathogens, 2022, 18, e1010338.	2.1	1
6989	Molecular basis of specificity and deamidation of eIF4A by Burkholderia Lethal Factor 1. Communications Biology, 2022, 5, 272.	2.0	2
6990	Mechanism of proteasome gate modulation by assembly chaperones Pba1 and Pba2. Journal of Biological Chemistry, 2022, 298, 101906.	1.6	2
6992	Structural basis of human IL-18 sequestration by the decoy receptor IL-18 binding protein in inflammation and tumor immunity. Journal of Biological Chemistry, 2022, 298, 101908.	1.6	9
6993	Structural and biochemical characterisation of the Providencia stuartii arginine decarboxylase shows distinct polymerisation and regulation. Communications Biology, 2022, 5, 317.	2.0	1
6994	One for All, All for One: The Peculiar Dynamics of TNF-Receptor-Associated Factor (TRAF2) Subunits. Symmetry, 2022, 14, 720.	1.1	3
6995	The biosynthetic origin of ribofuranose in bacterial polysaccharides. Nature Chemical Biology, 2022, 18, 530-537.	3.9	3
6996	Autopromotion of K-Ras4B Feedback Activation Through an SOS-Mediated Long-Range Allosteric Effect. Frontiers in Molecular Biosciences, 2022, 9, 860962.	1.6	10

#	Article	IF	Citations
6997	CPR-C4 is a highly conserved novel protease from the Candidate Phyla Radiation with remote structural homology to human vasohibins. Journal of Biological Chemistry, 2022, 298, 101919.	1.6	2
6999	Analysis of memory B cells identifies conserved neutralizing epitopes on the N-terminal domain of variant SARS-Cov-2 spike proteins. Immunity, 2022, 55, 998-1012.e8.	6.6	86
7000	Panel of Engineered Ubiquitin Variants Targeting the Family of Human Ubiquitin Interacting Motifs. ACS Chemical Biology, 2022, 17, 941-956.	1.6	5
7001	Structure of a Janus kinase cytokine receptor complex reveals the basis for dimeric activation. Science, 2022, 376, 163-169.	6.0	78
7002	Small Molecule Alkoxy Oriented Selectiveness on Human Carbonic Anhydrase II and IX Inhibition. ChemMedChem, 2022, 17, .	1.6	3
7004	Crystal structure of Arabidopsis thaliana HPPK/DHPS, a bifunctional enzyme and target of the herbicide asulam. Plant Communications, 2022, 3, 100322.	3.6	3
7005	Directed Evolution-Driven Increase of Structural Plasticity Is a Prerequisite for Binding the Complement Lectin Pathway Blocking MASP-Inhibitor Peptides. ACS Chemical Biology, 2022, , .	1.6	1
7006	High-resolution structures of malaria parasite actomyosin and actin filaments. PLoS Pathogens, 2022, 18, e1010408.	2.1	12
7007	Structural characterization of the homotropic cooperative binding of azamulin to human cytochrome P450 3A5. Journal of Biological Chemistry, 2022, 298, 101909.	1.6	5
7008	The structure of <i>Synechococcus elongatus</i> enolase reveals key aspects of phosphoenolpyruvate binding. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 177-184.	0.4	1
7009	Structural studies of a novel auxiliary-domain-containing phenylalanine hydroxylase from <i>Bacillus cereus</i> ATCC 14579. Acta Crystallographica Section D: Structural Biology, 2022, 78, 586-598.	1.1	0
7010	Structural Basis of Human Dimeric Î±-Amino-Î²-Carboxymuconate-Îµ-Semialdehyde Decarboxylase Inhibition With TES-1025. Frontiers in Molecular Biosciences, 2022, 9, 834700.	1.6	3
7011	Rational design of bioactive chimeric construct by exploring archaeal antimicrobial peptides: an in silico approach. , 0, , 1.		0
7012	In silico analysis of the predicted protein-protein interaction of syntaxin-18, a putative receptor of <i>Peregrinus maidis</i> Ashmead (Hemiptera: <i>Delphacidae</i>) with Maize mosaic virus glycoprotein. Journal of Biomolecular Structure and Dynamics, 2023, 41, 3956-3963.	2.0	1
7014	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the Pseudomonas-phage PaP3. Journal of Molecular Biology, 2022, 434, 167537.	2.0	6
7015	Crystal structure of a novel type of ornithine Î´-aminotransferase from the hyperthermophilic archaeon Pyrococcus horikoshii. International Journal of Biological Macromolecules, 2022, 208, 731-740.	3.6	1
7016	Structures of RGL1 RAS-Association Domain in Complex with KRAS and the Oncogenic G12V Mutant. Journal of Molecular Biology, 2022, 434, 167527.	2.0	4
7017	Structural Dynamics of the C-terminal X Domain of Nipah and Hendra Viruses Controls the Attachment to the C-terminal Tail of the Nucleocapsid Protein. Journal of Molecular Biology, 2022, 434, 167551.	2.0	3

#	Article	IF	Citations
7018	Acquired Disorder and Asymmetry in a Domain-Swapped Model for Î³-Crystallin Aggregation. Journal of Molecular Biology, 2022, 434, 167559.	2.0	1
7019	Biochemical and structural basis for Moraxella catarrhalis enoyl-acyl carrier protein reductase (FabI) inhibition by triclosan and estradiol. Biochimie, 2022, 198, 8-22.	1.3	1
7020	Probing terahertz dynamics of multidomain protein in cell-like confinement. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2022, 275, 121173.	2.0	2
7021	Computational Evolution Protocol for Peptide Design. Methods in Molecular Biology, 2022, 2405, 335-359.	0.4	3
7023	Cryo-EM structure of the autoinhibited state of myosin-2. Science Advances, 2021, 7, eabk3273.	4.7	24
7024	Exosome-Mediated eCIRP Release From Macrophages to Induce Inflammation in Sepsis. Frontiers in Pharmacology, 2021, 12, 791648.	1.6	23
7025	Purification, Characterization, and Structural Studies of a Sulfatase from Pedobacter yulinensis. Molecules, 2022, 27, 87.	1.7	1
7028	ParD Antitoxin Hotspot Alters a Disorder-to-Order Transition upon Binding to Its Cognate ParE Toxin, Lessening Its Interaction Affinity and Increasing Its Protease Degradation Kinetics. Biochemistry, 2022, 61, 34-45.	1.2	7
7029	Structural basis of malaria transmission blockade by a monoclonal antibody to gamete fusogen HAP2. ELife, 2021, 10, .	2.8	7
7030	Molecular Basis of Selective Cytokine Signaling Inhibition by Antibodies Targeting a Shared Receptor. Frontiers in Immunology, 2021, 12, 779100.	2.2	9
7031	Structural Insight into the Mechanism of PALB2 Interaction with MRG15. Genes, 2021, 12, 2002.	1.0	6
7032	Structural Characterization of Rat Galectin-5, an N-Tailed Monomeric Proto-Type-like Galectin. Biomolecules, 2021, 11, 1854.	1.8	1
7033	Epitope Mapping with Diethylpyrocarbonate Covalent Labeling-Mass Spectrometry. Analytical Chemistry, 2022, 94, 1052-1059.	3.2	9
7035	A Structural Perspective of Reps from CRESS-DNA Viruses and Their Bacterial Plasmid Homologues. Viruses, 2022, 14, 37.	1.5	11
7036	Perception of structurally distinct effectors by the integrated WRKY domain of a plant immune receptor. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	32
7038	Molecular Basis for the Substrate Promiscuity of Isopentenyl Phosphate Kinase from <i>Candidatus methanomethylophilus alvus</i>. ACS Chemical Biology, 2022, 17, 85-102.	1.6	2
7039	Oxidative stress protein Oxr1 promotes Vâ€ATPase holoenzyme disassembly in catalytic activityâ€independent manner. EMBO Journal, 2022, 41, e109360.	3.5	15
7040	Integrative Study of the Structural and Dynamical Properties of a KirBac3.1 Mutant: Functional Implication of a Highly Conserved Tryptophan in the Transmembrane Domain. International Journal of Molecular Sciences, 2022, 23, 335.	1.8	0

#	ARTICLE	IF	CITATIONS
7041	Molecular insights into substrate recognition and catalysis by phthalate dioxygenase from Comamonas testosteroni. Journal of Biological Chemistry, 2021, 297, 101416.	1.6	17
7042	NLRP3 cages revealed by full-length mouse NLRP3 structure control pathway activation. Cell, 2021, 184, 6299-6312.e22.	13.5	120
7043	Insight on molecular pathogenesis and pharmacochaperoning potential in phosphomannomutase 2 deficiency, provided by novel human <scp>phosphomannomutase 2</scp> structures. Journal of Inherited Metabolic Disease, 2022, 45, 318-333.	1.7	6
7045	Electrostatic Interactions Contribute to the Overall Structural Stability in Small Interfaces of Corona Viral Spike Glycoproteins. Biomedical and Pharmacology Journal, 2022, 15, 433-444.	0.2	0
7046	Structural analysis of the regulation of blue-light receptors by GIGANTEA. Cell Reports, 2022, 39, 110700.	2.9	3
7049	Antibody recognition of complement Factor H reveals a flexible loop involved in Atypical Hemolytic Uremic Syndrome pathogenesis. Journal of Biological Chemistry, 2022, , 101962.	1.6	2
7050	Structural patterns in class 1 major histocompatibility complexâ€restricted nonamer peptide binding to Tâ€cell receptors. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1645-1654.	1.5	5
7051	The Structure of Bilirubin Oxidase from Bacillus pumilus Reveals a Unique Disulfide Bond for Site-Specific Direct Electron Transfer. Biosensors, 2022, 12, 258.	2.3	0
7052	Structural basis for llama nanobody recognition and neutralization of HIV-1 at the CD4-binding site. Structure, 2022, 30, 862-875.e4.	1.6	4
7053	An antibody class with a common CDRH3 motif broadly neutralizes sarbecoviruses. Science Translational Medicine, 2022, 14, eabn6859.	5.8	31
7054	Molecular Organisation of Tick-Borne Encephalitis Virus. Viruses, 2022, 14, 792.	1.5	19
7055	Residual Structure in the Denatured State of the Fast-Folding UBA(1) Domain from the Human DNA Excision Repair Protein HHR23A. Biochemistry, 2022, , .	1.2	3
7056	Isolation, characterization, and structure-based engineering of a neutralizing nanobody against SARS-CoV-2. International Journal of Biological Macromolecules, 2022, 209, 1379-1388.	3.6	3
7058	ComFC mediates transport and handling of single-stranded DNA during natural transformation. Nature Communications, 2022, 13, 1961.	5.8	5
7059	Identification and Tetramer Structure of Hemin-Binding Protein SPD_0310 Linked to Iron Homeostasis and Virulence of Streptococcus pneumoniae. MSystems, 2022, 7, e0022122.	1.7	5
7060	Mechanism of RNA polymerase I selection by transcription factor UAF. Science Advances, 2022, 8, eabn5725.	4.7	9
7063	Active Release of eCIRP via Gasdermin D Channels to Induce Inflammation in Sepsis. Journal of Immunology, 2022, 208, 2184-2195.	0.4	15
7064	Thermostabilizing ketoreductase ChKRED20 by consensus mutagenesis at dimeric interfaces. Enzyme and Microbial Technology, 2022, 158, 110052.	1.6	4

#	Article	IF	Citations
7065	Structural characterization of a cross-protective natural chimera of factor H binding protein from meningococcal serogroup B strain NL096. Computational and Structural Biotechnology Journal, 2022, 20, 2070-2081.	1.9	0
7066	Non-Canonical Allostery in Cyclic Nucleotide Dependent Kinases. Journal of Molecular Biology, 2022, 434, 167584.	2.0	7
7125	Surface Ig variable domain glycosylation affects autoantigen binding and acts as threshold for human autoreactive B cell activation. Science Advances, 2022, 8, eabm1759.	4.7	30
7126	Structural basis for C-type inactivation in a Shaker family voltage-gated K ⁺ channel. Science Advances, 2022, 8, eabm8804.	4.7	26
7127	An ACE2-blocking antibody confers broad neutralization and protection against Omicron and other SARS-CoV-2 variants of concern. Science Immunology, 2022, 7, eabp9312.	5.6	35
7128	Anti-SARS-CoV-2 potential of Cissampelos pareira L. identified by connectivity map-based analysis and in vitro studies. BMC Complementary Medicine and Therapies, 2022, 22, 114.	1.2	4
7132	Canavanine resistance mutation in is a missense mutation in the ubiquitin ligase adaptor gene .. MicroPublication Biology, 2022, 2022, .	0.1	3
7133	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in Rymv Spread. SSRN Electronic Journal, 0, , .	0.4	0
7134	SARS-CoV-2 pan-variant inhibitory peptides deter S1-ACE2 interaction and neutralize delta and omicron pseudoviruses. Computational and Structural Biotechnology Journal, 2022, 20, 2042-2056.	1.9	8
7135	Structural Insight into Molecular Inhibitory Mechanism of InsP ₆ on African Swine Fever Virus mRNA-Decapping Enzyme g5Rp. Journal of Virology, 2022, 96, e0190521.	1.5	3
7136	Molecular basis of antibiotic self-resistance in a bee larvae pathogen. Nature Communications, 2022, 13, 2349.	5.8	4
7137	A Puzzling Protein from Variovorax paradoxus Has a PLP Fold Type IV Transaminase Structure and Binds PLP without Catalytic Lysine. Crystals, 2022, 12, 619.	1.0	0
7138	L-tyrosine-bound ThiH structure reveals Câ€“C bond break differences within radical SAM aromatic amino acid lyases. Nature Communications, 2022, 13, 2284.	5.8	7
7140	Structure of an influenza group 2-neutralizing antibody targeting the hemagglutinin stem supersite. Structure, 2022, , .	1.6	1
7142	Multiple-Allele MHC Class II Epitope Engineering by a Molecular Dynamics-Based Evolution Protocol. Frontiers in Immunology, 2022, 13, 862851.	2.2	7
7143	Structure and role of the linker domain of the iron surface-determinant protein IsdH in heme transportation in Staphylococcus aureus. Journal of Biological Chemistry, 2022, 298, 101995.	1.6	4
7144	Quantum Mechanics/Molecular Mechanics Studies on the Catalytic Mechanism of a Novel Esterase (FmtA) of <i>Staphylococcus aureus</i>. Journal of Chemical Information and Modeling, 2022, 62, 2409-2420.	2.5	23
7145	Structural and functional characterization of <scp>TrmM</scp> in <scp> m ⁶ A </scp> modification of bacterial <scp>tRNA</scp>. Protein Science, 2022, 31, e4319.	3.1	2

#	ARTICLE	IF	CITATIONS
7146	Functional and Structural Diversity of Bacterial Contact-Dependent Growth Inhibition Effectors. Frontiers in Molecular Biosciences, 2022, 9, 866854.	1.6	6
7147	Characterization and Structural Analysis of Emodin-<i>O</i>-Methyltransferase from <i>Aspergillus terreus</i>. Journal of Agricultural and Food Chemistry, 2022, 70, 5728-5737.	2.4	7
7148	The structure of<i>Phocaeicola vulgatus</i>sialic acid acetylesterase. Acta Crystallographica Section D: Structural Biology, 2022, 78, 647-657.	1.1	2
7149	USP14-regulated allostery of the human proteasome by time-resolved cryo-EM. Nature, 2022, 605, 567-574.	13.7	38
7150	Reverse Engineering Analysis of the High-Temperature Reversible Oligomerization and Amyloidogenicity of PSD95-PDZ3. Molecules, 2022, 27, 2813.	1.7	2
7151	Structural insights into choline-<i>O</i>-sulfatase reveal the molecular determinants for ligand binding. Acta Crystallographica Section D: Structural Biology, 2022, 78, 669-682.	1.1	0
7152	Clade-Specific Alterations within the HIV-1 Capsid Protein with Implications for Nuclear Translocation. Biomolecules, 2022, 12, 695.	1.8	3
7154	Optimization of IL-1RA structure to achieve a smaller protein with a higher affinity to its receptor. Scientific Reports, 2022, 12, 7483.	1.6	2
7155	Novel super-neutralizing antibody UT28K is capable of protecting against infection from a wide variety of SARS-CoV-2 variants. MAbs, 2022, 14, 2072455.	2.6	9
7156	Designing a novel E2-IFN-Î³ fusion protein against CSFV by immunoinformatics and structural vaccinology approaches. Applied Microbiology and Biotechnology, 2022, , .	1.7	1
7157	Structural, mechanistic, and physiological insights into phospholipase A-mediated membrane phospholipid degradation in Pseudomonas aeruginosa. ELife, 2022, 11, .	2.8	13
7158	Glycyrrhetinic acid restricts mitochondrial energy metabolism by targeting SHMT2. IScience, 2022, 25, 104349.	1.9	6
7159	New structural insights into the <scp>PI</scp>â€•2 pilus from <i>Streptococcus oralis</i>, an early dental plaque colonizer. FEBS Journal, 2022, 289, 6342-6366.	2.2	5
7160	The mechanism of activation of MEK1 by B-Raf and KSR1. Cellular and Molecular Life Sciences, 2022, 79, 281.	2.4	7
7161	Structural basis of human LRG1 recognition by Magacizumab, a humanized monoclonal antibody with therapeutic potential. Acta Crystallographica Section D: Structural Biology, 2022, 78, 725-734.	1.1	2
7162	Biophysical Insight into the SARS-CoV2 Spikeâ€"ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach. ACS Omega, 2022, 7, 17024-17042.	1.6	9
7163	Structural insights of a highly potent pan-neutralizing SARS-CoV-2 human monoclonal antibody. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120976119.	3.3	27
7164	The ArsH Protein Product of the Paracoccus denitrificans ars Operon Has an Activity of Organoarsenic Reductase and Is Regulated by a Redox-Responsive Repressor. Antioxidants, 2022, 11, 902.	2.2	3

#	ARTICLE	IF	CITATIONS
7165	Kunitz-Type Peptides from Sea Anemones Protect Neuronal Cells against Parkinsonâ€™s Disease Inductors via Inhibition of ROS Production and ATP-Induced P2X7 Receptor Activation. International Journal of Molecular Sciences, 2022, 23, 5115.	1.8	7
7166	Metal-Induced Fluorescence Quenching of Photoconvertible Fluorescent Protein DendFP. Molecules, 2022, 27, 2922.	1.7	8
7167	Phenol-soluble modulins PSMÎ±3 and PSMÎ²2 form nanotubes that are cross-Î± amyloids. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121586119.	3.3	16
7169	Advanced Insights into Catalytic and Structural Features of the Zincâ€Đependent Alcohol Dehydrogenase from <i>Thauera aromatica</i>. ChemBioChem, 2022, 23, .	1.3	2
7170	Structural basis of sodium-dependent bile salt uptake into the liver. Nature, 2022, 606, 1015-1020.	13.7	35
7171	Posttranslational modification of microtubules by the MATCAP detyrosinase. Science, 2022, 376, eabn6020.	6.0	33
7172	The <i>apo</i> â€form of the <i>Vibrio cholerae</i> replicative helicase <scp>DnaB</scp> is a labile and inactive planar trimer of dimers. FEBS Letters, 2022, , .	1.3	2
7173	Mapping paratopes of nanobodies using native mass spectrometry and ultraviolet photodissociation. Chemical Science, 2022, 13, 6610-6618.	3.7	2
7174	Crystal structure of the polyketide cyclase from &lt;italic&gt;Mycobacterium tuberculosis&lt;/italic&gt;. Acta Biochimica Et Biophysica Sinica, 2022, 54, 474-481.	0.9	0
7175	A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases. Nature Communications, 2022, 13, 2700.	5.8	2
7176	Mpe1 senses the binding of pre-mRNA and controls 3â€² end processing by CPF. Molecular Cell, 2022, 82, 2490-2504.e12.	4.5	9
7177	Elucidation of the Conformational Transition of Oligopeptidase B by an Integrative Approach Based on the Combination of X-ray, SAXS, and Essential Dynamics Sampling Simulation. Crystals, 2022, 12, 712.	1.0	2
7178	Structure of the IL-27 quaternary receptor signaling complex. ELife, 2022, 11, .	2.8	18
7179	Structural insights into highly similar spatial organization of zinc-finger associated domains with a very low sequence similarity. Structure, 2022, 30, 1004-1015.e4.	1.6	6
7180	Complex Mutation Pattern of Omicron BA.2: Evading Antibodies without Losing Receptor Interactions. International Journal of Molecular Sciences, 2022, 23, 5534.	1.8	10
7181	Large-Size Subunit Catalases Are Chimeric Proteins: A H2O2 Selecting Domain with Catalase Activity Fused to a Hsp31-Derived Domain Conferring Protein Stability and Chaperone Activity. Antioxidants, 2022, 11, 979.	2.2	4
7182	A truncated anti-CRISPR protein prevents spacer acquisition but not interference. Nature Communications, 2022, 13, 2802.	5.8	8
7183	Cryo-EM structure of acylpeptide hydrolase reveals substrate selection by multimerization and a multi-state serine-protease triad. Chemical Science, 2022, 13, 7132-7142.	3.7	5

#	ARTICLE	IF	CITATIONS
7184	Solid-state nanopore analysis on the conformation change of DNA polymerase I induced by a DNA substrate. Analyst, The, 2022, 147, 3087-3095.	1.7	2
7186	Structural comparisons reveal diverse binding modes between nucleosome assembly proteins and histones. Epigenetics and Chromatin, 2022, 15, .	1.8	8
7187	In silico design and analyses of a multi-epitope vaccine against Crimean-Congo hemorrhagic fever virus through reverse vaccinology and immunoinformatics approaches. Scientific Reports, 2022, 12, .	1.6	18
7188	Ancient plant-like terpene biosynthesis in corals. Nature Chemical Biology, 2022, 18, 664-669.	3.9	40
7189	Linking the thermostability of FIP-nha (Nectria haematococca) to its structural properties. International Journal of Biological Macromolecules, 2022, 213, 555-564.	3.6	2
7190	Crystal structure of thermally stable homodimeric cytochrome <i>c</i>â€²-Î² from <i>Thermus thermophilus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 217-225.	0.4	4
7191	Structure-based interface engineering methodology in designing a thermostable amylose-forming transglucosylase. Journal of Biological Chemistry, 2022, 298, 102074.	1.6	4
7192	High-resolution structures of the SAMHD1 dGTPase homolog from Leeuwenhoekiella blandensis reveal a novel mechanism of allosteric activation by dATP. Journal of Biological Chemistry, 2022, , 102073.	1.6	3
7193	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. Cell, 2022, 185, 2116-2131.e18.	13.5	105
7195	In vitro Evolution of Uracil Glycosylase Towards DnaKJ and GroEL Binding Evolves Different Misfolded States. Journal of Molecular Biology, 2022, 434, 167627.	2.0	0
7196	The structural and functional investigation of the VapBC43 complex from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2022, 616, 19-25.	1.0	2
7197	Proteome-Wide and Protein-Specific Multi-Epitope Vaccine Constructs Against the Rift Valley Fever Virus Outbreak Using Integrated Omics Approaches. Frontiers in Microbiology, 2022, 13, .	1.5	2
7198	Cryo-EM structures of human A2ML1 elucidate the protease-inhibitory mechanism of the A2M family. Nature Communications, 2022, 13, .	5.8	4
7199	Brachypodium Antifreeze Protein Gene Products Inhibit Ice Recrystallisation, Attenuate Ice Nucleation, and Reduce Immune Response. Plants, 2022, 11, 1475.	1.6	3
7201	The Toxoplasma glucan phosphatase TgLaforin utilizes a distinct functional mechanism that can be exploited by therapeutic inhibitors. Journal of Biological Chemistry, 2022, 298, 102089.	1.6	8
7202	Pentameric assembly of the Kv2.1 tetramerization domain. Acta Crystallographica Section D: Structural Biology, 2022, 78, 792-802.	1.1	1
7204	Type II BMP and activin receptors BMPR2 and ACVR2A share a conserved mode of growth factor recognition. Journal of Biological Chemistry, 2022, 298, 102076.	1.6	4
7205	Antigenic structure of the human coronavirus OC43 spike reveals exposed and occluded neutralizing epitopes. Nature Communications, 2022, 13, .	5.8	12

#	ARTICLE	IF	CITATIONS
7206	Competition for dominance within replicating quasispecies during prolonged SARS-CoV-2 infection in an immunocompromised host. Virus Evolution, 2022, 8, .	2.2	21
7209	Evaluation of Current Methods to Detect Cellular Leucine-Rich Repeat Kinase 2 (LRRK2) Kinase Activity. Journal of Parkinson's Disease, 2022, 12, 1423-1447.	1.5	8
7211	Crystal Structure of an Intramolecular Mesaconyl-Coenzyme A Transferase From the 3-Hydroxypropionic Acid Cycle of Roseiflexus castenholzii. Frontiers in Microbiology, 2022, 13, .	1.5	4
7212	Structural Model of the Human BTG2â€"PABPC1 Complex by Combining Mutagenesis, NMR Chemical Shift Perturbation Data and Molecular Docking. Journal of Molecular Biology, 2022, 434, 167662.	2.0	2
7213	Structure of the glucosyltransferase domain of TcdA in complex with RhoA provides insights into substrate recognition. Scientific Reports, 2022, 12, .	1.6	4
7215	Human IgE monoclonal antibody recognition of mite allergen Der p 2 defines structural basis of an epitope for IgE cross-linking and anaphylaxis <i>in vivo</i>. , 2022, 1, .		11
7216	In silico SARS-CoV-2 vaccine development for Omicron strain using reverse vaccinology. Genes and Genomics, 2022, 44, 937-944.	0.5	3
7217	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. Genes, 2022, 13, 1018.	1.0	4
7218	Structural basis of the IL-1 receptor TIR domain-mediated IL-1 signaling. IScience, 2022, , 104508.	1.9	1
7219	Conformational flexibility enables catalysis of phthalate cis-4,5-dihydrodiol dehydrogenase. Archives of Biochemistry and Biophysics, 2022, 727, 109314.	1.4	2
7220	Direct interaction of a chaperone-bound type III secretion substrate with the export gate. Nature Communications, 2022, 13, .	5.8	9
7221	A comprehensive structural analysis of the ATPase domain of human DNA topoisomerase II beta bound to AMPPNP, ADP, and the bisdioxopiperazine, ICRF193. Structure, 2022, 30, 1129-1145.e3.	1.6	6
7222	Structural Characterization of a Neutralizing Nanobody With Broad Activity Against SARS-CoV-2 Variants. Frontiers in Microbiology, 2022, 13, .	1.5	5
7223	Structural insights into the binding of nanobody Rh57 to active RhoA-GTP. Biochemical and Biophysical Research Communications, 2022, 616, 122-128.	1.0	0
7226	<i>In silico</i>study on the effects of disulfide bonds in ORF8 of SARS-CoV-2. Physical Chemistry Chemical Physics, 2022, 24, 16876-16883.	1.3	4
7227	Crystal structure of the BREX phage defence protein BrxA. Current Research in Structural Biology, 2022, 4, 211-219.	1.1	4
7229	High-affinity anti-Arc nanobodies provide tools for structural and functional studies. PLoS ONE, 2022, 17, e0269281.	1.1	5
7230	An M protein coiled coil unfurls and exposes its hydrophobic core to capture LL-37. ELife, 0, 11, .	2.8	7

#	ARTICLE	IF	CITATIONS
7231	Crystal structure of mevalonate 3,5-bisphosphate decarboxylase reveals insight into the evolution of decarboxylases in the mevalonate metabolic pathways. Journal of Biological Chemistry, 2022, 298, 102111.	1.6	3
7232	The First Structure of Human MTHFD2L and Its Implications for the Development of Isoformâ€Selective Inhibitors. ChemMedChem, 2022, 17, .	1.6	6
7233	Structural insights into the lysophospholipid brain uptake mechanism and its inhibition by syncytin-2. Nature Structural and Molecular Biology, 2022, 29, 604-612.	3.6	20
7234	Crystal structures of the molecular class A Î²-lactamase TEM-171 and its complexes with tazobactam. Acta Crystallographica Section D: Structural Biology, 2022, 78, 825-834.	1.1	3
7235	When Alphafold2 predictions go wrong for proteinâ€“protein complexes, is there something to be learnt?. Quarterly Reviews of Biophysics, 2022, 55, .	2.4	10
7237	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. Communications Biology, 2022, 5, .	2.0	12
7238	Potent human broadly SARS-CoV-2â€“neutralizing IgA and IgG antibodies effective against Omicron BA.1 and BA.2. Journal of Experimental Medicine, 2022, 219, .	4.2	34
7239	Studies on the antiviral activity of chebulinic acid against dengue and chikungunya viruses and in silico investigation of its mechanism of inhibition. Scientific Reports, 2022, 12, .	1.6	1
7241	Sequence Divergence in the Arginase Domain of Ornithine Decarboxylase/Arginase in <i>Fusobacteriacea</i> Leads to Loss of Function in Oral Associated Species. Biochemistry, 2022, 61, 1378-1391.	1.2	2
7242	Identification, structure determination and analysis of <i>Mycobacterium smegmatis</i> acyl-carrier protein synthase (AcpS) crystallized serendipitously. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 252-264.	0.4	0
7243	Biochemical and structural insights into an unusual, alkali-metal-independent <i>S</i>-adenosyl-<scp>L</scp>-homocysteine hydrolase from <i>Synechocystis</i> sp. PCC 6803. Acta Crystallographica Section D: Structural Biology, 2022, 78, 865-882.	1.1	1
7244	A single sensor controls large variations in zinc quotas in a marine cyanobacterium. Nature Chemical Biology, 2022, 18, 869-877.	3.9	7
7245	Metal cofactor stabilization by a partner protein is a widespread strategy employed for amidase activation. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
7246	Structural variations between small alarmone hydrolase dimers support different modes of regulation of the stringent response. Journal of Biological Chemistry, 2022, 298, 102142.	1.6	4
7247	Structure-based electron-confurcation mechanism of the Ldh-EtfAB complex. ELife, 0, 11, .	2.8	9
7248	Crystal structure of BtrK, a decarboxylase involved in the (S)-4-amino-2-hydroxybutyrate (AHBA) formation during butirosin biosynthesis. Journal of Molecular Structure, 2022, , 133576.	1.8	0
7249	Penicillin-Binding Protein 1 (PBP1) of Staphylococcus aureus Has Multiple Essential Functions in Cell Division. MBio, 2022, 13, .	1.8	11
7250	Cryo-EM structure of a type IV secretion system. Nature, 2022, 607, 191-196.	13.7	56

#	ARTICLE	IF	CITATIONS
7251	Bioinformatics Approaches to Predict Mutation Effects in the Binding Site of the Proangiogenic Molecule CD93. Frontiers in Bioinformatics, 0, 2, .	1.0	1
7252	Evolution of homoâ€oligomerization of methionine Sâ€adenosyltransferases is replete with structureâ€"function constrains. Protein Science, 2022, 31, .	3.1	2
7254	Primary and secondary functions of HLA-E are determined by stability and conformation of the peptide-bound complexes. Cell Reports, 2022, 39, 110959.	2.9	8
7255	AI-based structure prediction empowers integrative structural analysis of human nuclear pores. Science, 2022, 376, .	6.0	136
7256	In Vitro Neutralisation of Zika Virus by an Engineered Protein Targeting the Viral Envelope Fusion Loop. SSRN Electronic Journal, 0, , .	0.4	1
7257	Terminase Subunits from the Pseudomonas-Phage E217. SSRN Electronic Journal, 0, , .	0.4	1
7259	Identification of 2-(4-N,N-Dimethylaminophenyl)-5-methyl-1-phenethyl-1H-benzimidazole targeting HIV-1 CA capsid protein and inhibiting HIV-1 replication in cellulo. BMC Pharmacology & Toxicology, 2022, 23, .	1.0	0
7260	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. Nature Communications, 2022, 13, .	5.8	14
7261	Evolution and activation mechanism of the flavivirus class II membrane-fusion machinery. Nature Communications, 2022, 13, .	5.8	17
7262	In Silico Designed Multi-Epitope Immunogen â€œTpme-VAC/LGCM-2022â€•May Induce Both Cellular and Humoral Immunity against Treponema pallidum Infection. Vaccines, 2022, 10, 1019.	2.1	3
7264	Protein misfolding and clearance in the pathogenesis of a new infantile onset ataxia caused by mutations in <i>PRDX3</i>. Human Molecular Genetics, 2022, 31, 3897-3913.	1.4	8
7266	LAG3 ectodomain structure reveals functional interfaces for ligand and antibody recognition. Nature Immunology, 2022, 23, 1031-1041.	7.0	15
7267	Recognition of the TDP-43 nuclear localization signal by importin Î±1/Î². Cell Reports, 2022, 39, 111007.	2.9	32
7270	A broad and potent neutralization epitope in SARS-related coronaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	34
7271	Structural Characterization of L-Galactose Dehydrogenase: An Essential Enzyme for Vitamin C Biosynthesis. Plant and Cell Physiology, 2022, 63, 1140-1155.	1.5	6
7272	Biochemical and Structural Characterization of Thermostable GH159 Glycoside Hydrolases Exhibiting Î±-L-Arabinofuranosidase Activity. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
7273	Structure of cytoplasmic ring of nuclear pore complex by integrative cryo-EM and AlphaFold. Science, 2022, 376, .	6.0	89
7275	Hinge disulfides in human IgG2 CD40 antibodies modulate receptor signaling by regulation of conformation and flexibility. Science Immunology, 2022, 7, .	5.6	18

#	Article	IF	Citations
7276	Allosteric Hotspots in the Main Protease of SARS-CoV-2. Journal of Molecular Biology, 2022, 434, 167748.	2.0	10
7277	Structure of the human RAD17â€"RFC clamp loader and 9â€"1â€"1 checkpoint clamp bound to a dsDNAâ€"ssDNA junction. Nucleic Acids Research, 2022, 50, 8279-8289.	6.5	13
7278	Molecular dissection of the glutamine synthetase-GlnR nitrogen regulatory circuitry in Gram-positive bacteria. Nature Communications, 2022, 13, .	5.8	12
7279	A panel of nanobodies recognizing conserved hidden clefts of all SARS-CoV-2 spike variants including Omicron. Communications Biology, 2022, 5, .	2.0	26
7281	The Hidden Intricacies of Aquaporins: Remarkable Details in a Common Structural Scaffold. Small, 2022, 18, .	5.2	8
7283	Vaccine-elicited murine antibody WS6 neutralizes diverse beta-coronaviruses by recognizing a helical stem supersite of vulnerability. Structure, 2022, 30, 1233-1244.e7.	1.6	13
7284	Omicron Binding Mode: Contact Analysis and Dynamics of the Omicron Receptor-Binding Domain in Complex with ACE2. Journal of Chemical Information and Modeling, 2022, 62, 3844-3853.	2.5	11
7285	Organism-specific differences in the binding of ketoprofen to serum albumin. IUCrJ, 2022, 9, 551-561.	1.0	6
7286	Structures of VWF tubules before and after concatemerization reveal a mechanism of disulfide bond exchange. Blood, 2022, 140, 1419-1430.	0.6	10
7287	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. Nature Communications, 2022, 13, .	5.8	17
7288	Mechanistic insights into the rational design of masked antibodies. MAbs, 2022, 14, .	2.6	4
7289	Exploring protein symmetry at the RCSB Protein Data Bank. Emerging Topics in Life Sciences, 2022, 6, 231-243.	1.1	7
7291	A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. Nature Communications, 2022, 13, .	5.8	5
7292	Necroptosis-Mediated eCIRP Release in Sepsis. Journal of Inflammation Research, 0, Volume 15, 4047-4059.	1.6	5
7293	Structural and functional characterization of DdrC, a novel DNA damage-induced nucleoid associated protein involved in DNA compaction. Nucleic Acids Research, 2022, 50, 7680-7696.	6.5	8
7294	The nuclear egress complex of Epstein-Barr virus buds membranes through an oligomerization-driven mechanism. PLoS Pathogens, 2022, 18, e1010623.	2.1	7
7295	Broadly neutralizing antibodies target the coronavirus fusion peptide. Science, 2022, 377, 728-735.	6.0	111
7296	Antibody evasion by SARS-CoV-2 Omicron subvariants BA.2.12.1, BA.4 and BA.5. Nature, 2022, 608, 603-608.	13.7	541

#	Article	IF	Citations
7298	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
7299	Fusion of two unrelated protein domains in a chimera protein and its <scp>3D</scp> prediction: Justification of the xâ€ray reference structures as a prediction benchmark. Proteins: Structure, Function and Bioinformatics, 2022, 90, 2067-2079.	1.5	2
7300	The two-domain elevator-type mechanism of zinc-transporting ZIP proteins. Science Advances, 2022, 8, .	4.7	19
7301	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in RYMV Spread. Journal of Molecular Biology, 2022, 434, 167715.	2.0	6
7302	Structural basis of the bHLH domains of MyoD-E47 heterodimer. Biochemical and Biophysical Research Communications, 2022, 621, 88-93.	1.0	1
7303	In silico analysis of SARS-CoV-2 spike protein N501Y and N501T mutation effects on human ACE2 binding. Journal of Molecular Graphics and Modelling, 2022, 116, 108260.	1.3	4
7304	Measles and Nipah virus assembly: Specific lipid binding drives matrix polymerization. Science Advances, 2022, 8, .	4.7	13
7305	Discovery of a Transferrin Receptor 1-Binding Aptamer and Its Application in Cancer Cell Depletion for Adoptive T-Cell Therapy Manufacturing. Journal of the American Chemical Society, 2022, 144, 13851-13864.	6.6	20
7306	Modeling and computational characterization of a <i>Xanthomonas</i> sp. Hypothetical protein identifies a remote ortholog of <i>Burkholderia</i> lethal factor 1. Journal of Biomolecular Structure and Dynamics, 2023, 41, 6027-6039.	2.0	1
7308	Rep15 interacts with several Rab GTPases and has a distinct fold for a Rab effector. Nature Communications, 2022, 13, .	5.8	1
7309	The crystal structure of CbpD clarifies substrate-specificity motifs in chitin-active lytic polysaccharide monooxygenases. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1064-1078.	1.1	6
7310	Suppressing crucial oncogenes of leukemia initiator cells by major royal jelly protein 2 for mediating apoptosis in myeloid and lymphoid leukemia cells. Food and Function, 2022, 13, 8951-8966.	2.1	4
7311	Structural determinants of DNA recognition by the NO sensor NsrR and related Rrf2-type [FeS]-transcription factors. Communications Biology, 2022, 5, .	2.0	8
7312	De novo determination of mosquitocidal Cry11Aa and Cry11Ba structures from naturally-occurring nanocrystals. Nature Communications, 2022, 13, .	5.8	9
7314	Structural assembly of the nucleic-acid-binding Thp3â€“Csn12â€“Sem1 complex functioning in mRNA splicing. Nucleic Acids Research, 2022, 50, 8882-8897.	6.5	1
7315	Crystal structure of human NADK2 reveals a dimeric organization and active site occlusion by lysine acetylation. Molecular Cell, 2022, , .	4.5	5
7317	Panoramic Perspective on Human Phosphosites. Journal of Proteome Research, 2022, 21, 1894-1915.	1.8	3
7318	Organizing structural principles of the IL-17 ligandâ€“receptor axis. Nature, 2022, 609, 622-629.	13.7	16

#	Article	IF	Citations
7321	Anti-apoptotic Bcl-2 protein in apo and holo conformation anchored to the membrane: comparative molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2023, 41, 6074-6088.	2.0	3
7322	Peptide Centric Vβ Specific Germline Contacts Shape a Specialist T Cell Response. Frontiers in Immunology, 0, 13, .	2.2	0
7323	Structural and mechanistic insights into the cleavage of clustered O-glycan patches-containing glycoproteins by mucinases of the human gut. Nature Communications, 2022, 13, .	5.8	15
7324	Human antibodies to SARS-CoV-2 with a recurring YYDRxG motif retain binding and neutralization to variants of concern including Omicron. Communications Biology, 2022, 5, .	2.0	9
7325	Bivalent BET Bromodomain Inhibitors Confer Increased Potency and Selectivity for BRDT via Protein Conformational Plasticity. Journal of Medicinal Chemistry, 2022, 65, 10441-10458.	2.9	8
7326	The <i>Haemophilus influenzae</i> HipBA toxinâ€“antitoxin system adopts an unusual three-component regulatory mechanism. IUCrJ, 2022, 9, 625-631.	1.0	2
7328	RL-MLZerD: Multimeric protein docking using reinforcement learning. Frontiers in Molecular Biosciences, 0, 9, .	1.6	7
7329	R-loop formation and conformational activation mechanisms of Cas9. Nature, 2022, 609, 191-196.	13.7	43
7330	Crystal structure of ChbG from Klebsiella pneumoniae reveals the molecular basis of diacetylchitobiose deacetylation. Communications Biology, 2022, 5, .	2.0	1
7331	Structural characterisation of a <scp>MAPR</scp>â€related archaeal cytochrome <scp>b_{5M}</scp> protein. FEBS Letters, 2022, 596, 2409-2417.	1.3	1
7332	Insight into the structural basis of the dual inhibitory mode of Lima bean (<scp><i>Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 347 91, 22-31.	1.5	2
7333	The Crystal Structure of the Defense Conferring Rice Protein OsJAC1 Reveals a Carbohydrate Binding Site on the Dirigent-like Domain. Biomolecules, 2022, 12, 1126.	1.8	3
7334	Mammalian derived lipocalin and secretoglobin respiratory allergens strongly bind ligands with potentially immune modulating properties. Frontiers in Allergy, 0, 3, .	1.2	9
7335	Structures of topoisomerase V in complex with DNA reveal unusual DNA-binding mode and novel relaxation mechanism. ELife, 0, 11, .	2.8	2
7337	Crystal structure of <i>Methanococcus jannaschii</i> dihydroorotase. Proteins: Structure, Function and Bioinformatics, 2023, 91, 91-98.	1.5	1
7339	Structural and functional characterisation of a stable, broad-specificity multimeric sialidase from the oral pathogen <i>Tannerella forsythia</i>. Biochemical Journal, 2022, 479, 1785-1806.	1.7	4
7340	Structural characterization of aspartate-semialdehyde dehydrogenase from Pseudomonas aeruginosa and Neisseria gonorrhoeae. Scientific Reports, 2022, 12, .	1.6	5
7341	Architecture and self-assembly of the jumbo bacteriophage nuclear shell. Nature, 2022, 608, 429-435.	13.7	37

#	ARTICLE	IF	CITATIONS
7343	Structure of a fully assembled tumor-specific T cell receptor ligated by pMHC. Cell, 2022, 185, 3201-3213.e19.	13.5	40
7344	Endogenous ligand recognition and structural transition of a human PTH receptor. Molecular Cell, 2022, 82, 3468-3483.e5.	4.5	28
7345	Augmenting apoptosis-mediated anticancer activity of lactoperoxidase and lactoferrin by nanocombination with copper and iron hybrid nanometals. Scientific Reports, 2022, 12, .	1.6	9
7346	SH3 domain regulation of RhoGAP activity: Crosstalk between p120RasGAP and DLC1 RhoGAP. Nature Communications, 2022, 13, .	5.8	8
7347	Molecular Basis for Enzymatic Aziridine Formation via Sulfate Elimination. Journal of the American Chemical Society, 2022, 144, 16164-16170.	6.6	10
7348	Structures of L-BC virus and its open particle provide insight into Totivirus capsid assembly. Communications Biology, 2022, 5, .	2.0	2
7350	Development, structure, and mechanism of synthetic antibodies that target claudin and Clostridium perfringens enterotoxin complexes. Journal of Biological Chemistry, 2022, 298, 102357.	1.6	2
7351	Structural basis of transcriptional regulation by a nascent RNA element, HK022 putRNA. Nature Communications, 2022, 13, .	5.8	6
7353	Structural analysis of Red1 as a conserved scaffold of the RNA-targeting MTREC/PAXT complex. Nature Communications, 2022, 13, .	5.8	11
7354	In-Silico Characterization of von Willebrand Factor Bound to FVIII. Applied Sciences (Switzerland), 2022, 12, 7855.	1.3	1
7355	Evidence of an intracellular interaction between the Escherichia coli enzymes EntC and EntB and identification of a potential electrostatic channeling surface. Biochimie, 2022, 202, 159-165.	1.3	2
7356	Structural Comparison of hMDH2 Complexed with Natural Substrates and Cofactors: The Importance of Phosphate Binding for Active Conformation and Catalysis. Biomolecules, 2022, 12, 1175.	1.8	1
7357	CD8 coreceptor engagement of MR1 enhances antigen responsiveness by human MAIT and other MR1-reactive T cells. Journal of Experimental Medicine, 2022, 219, .	4.2	15
7360	Terminase Subunits from the Pseudomonas-Phage E217. Journal of Molecular Biology, 2022, 434, 167799.	2.0	7
7362	Structural insights into partner selection for MYB and bHLH transcription factor complexes. Nature Plants, 2022, 8, 1108-1117.	4.7	19
7363	Structures of the mannose-6-phosphate pathway enzyme, GlcNAc-1-phosphotransferase. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
7364	Molecular and in vivo studies of a glutamate-class prolyl-endopeptidase for coeliac disease therapy. Nature Communications, 2022, 13, .	5.8	6
7365	A naturally arising broad and potent CD4-binding site antibody with low somatic mutation. Science Advances, 2022, 8, .	4.7	11

#	ARTICLE	IF	CITATIONS
7366	Visualizing molecular interactions that determine assembly of a bullet-shaped vesicular stomatitis virus particle. Nature Communications, 2022, 13, .	5.8	13
7367	Structural insights into the assembly and activation of the <scp>IL</scp>â€27 signaling complex. EMBO Reports, 2022, 23, .	2.0	9
7368	Identification of IOMA-class neutralizing antibodies targeting the CD4-binding site on the HIV-1 envelope glycoprotein. Nature Communications, 2022, 13, .	5.8	5
7369	Differential modulation of collybistin conformational dynamics by the closely related GTPases Cdc42 and TC10. Frontiers in Synaptic Neuroscience, 0, 14, .	1.3	1
7370	Structural and mechanistic analysis of a tripartite ATP-independent periplasmic TRAP transporter. Nature Communications, 2022, 13, .	5.8	16
7371	Crystal structure of the Escherichia coli CusS kinase core. Journal of Structural Biology, 2022, 214, 107883.	1.3	3
7372	Structural and functional studies of legumain-mycocypin complexes revealed a competitive, exosite-regulated mode of interaction. Journal of Biological Chemistry, 2022, , 102502.	1.6	0
7374	The Antibacterial Type VII Secretion System of Bacillus subtilis: Structure and Interactions of the Pseudokinase YukC/EssB. MBio, 2022, 13, .	1.8	16
7376	Molecular dynamics simulations highlight the altered binding landscape at the spike-ACE2 interface between the Delta and Omicron variants compared to the SARS-CoV-2 original strain. Computers in Biology and Medicine, 2022, 149, 106035.	3.9	14
7377	Characterisation of a Seneca Valley virus thermostable mutant. Virology, 2022, 575, 74-82.	1.1	0
7378	Structural basis for the substrate specificity of an S-formylglutathione hydrolase derived from Variovorax sp. PAMC 28711. Biochemical and Biophysical Research Communications, 2022, 629, 159-164.	1.0	1
7379	Unveiling molecular details behind improved activity at neutral to alkaline pH of an engineered DyP-type peroxidase. Computational and Structural Biotechnology Journal, 2022, 20, 3899-3910.	1.9	5
7380	Protein quaternary structures in solution are a mixture of multiple forms. Chemical Science, 2022, 13, 11680-11695.	3.7	14
7381	Proteinâ€“protein interaction prediction with deep learning: A comprehensive review. Computational and Structural Biotechnology Journal, 2022, 20, 5316-5341.	1.9	38
7382	Preclinial Safety and Efficacy of a Therapeutic Antibody That Targets SARS-CoV-2 at the Sotrovimab Face But is Escaped by Omicron. SSRN Electronic Journal, 0, , .	0.4	0
7383	Antibody interfaces revealed through structural mining. Computational and Structural Biotechnology Journal, 2022, 20, 4952-4968.	1.9	3
7384	The Endoplasmic Reticulum Signal Peptidase Complex. , 2022, , .		0
7385	ATP-Binding Cassette Transporters: Snap-on Complexes?. Sub-Cellular Biochemistry, 2022, , 35-82.	1.0	1

#	ARTICLE	IF	CITATIONS
7386	Structures of a phycobilisome in light-harvesting and photoprotected states. Nature, 2022, 609, 835-845.	13.7	65
7387	The BAF A12T mutation disrupts lamin A/C interaction, impairing robust repair of nuclear envelope ruptures in Nestorâ€"Guillermo progeria syndrome cells. Nucleic Acids Research, 2022, 50, 9260-9278.	6.5	16
7388	Î±2Î´-4 and Cachd1 Proteins Are Regulators of Presynaptic Functions. International Journal of Molecular Sciences, 2022, 23, 9885.	1.8	4
7390	Staphylococcus aureus Exfoliative Toxin E, Oligomeric State and Flip of P186: Implications for Its Action Mechanism. International Journal of Molecular Sciences, 2022, 23, 9857.	1.8	3
7391	<i>CCP</i>4 Cloud for structure determination and project management in macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1079-1089.	1.1	21
7392	Structure of the Repurposed Fungal Terpene Cyclase FlvF Implicated in the Câ€"N Bond-Forming Reaction of Flavunoidine Biosynthesis. Biochemistry, 2022, 61, 2014-2024.	1.2	2
7393	Structure of angiogenin dimer bound to double-stranded RNA. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 330-337.	0.4	0
7394	Dual Targeting Factors Are Required for LXG Toxin Export by the Bacterial Type VIIb Secretion System. MBio, 2022, 13, .	1.8	15
7395	Design of immunogens for eliciting antibody responses that may protect against SARS-CoV-2 variants. PLoS Computational Biology, 2022, 18, e1010563.	1.5	4
7397	LSSmScarlet2 and LSSmScarlet3, Chemically Stable Genetically Encoded Red Fluorescent Proteins with a Large Stokesâ€™ Shift. International Journal of Molecular Sciences, 2022, 23, 11051.	1.8	2
7398	A dedicated C-6 Î²-hydroxyacyltransferase required for biosynthesis of the glycolipid anchor for Vi antigen capsule in typhoidal Salmonella.. Journal of Biological Chemistry, 2022, , 102520.	1.6	0
7399	The staphylococcal inhibitory protein SPIN binds to human myeloperoxidase with picomolar affinity but only dampens halide oxidation. Journal of Biological Chemistry, 2022, 298, 102514.	1.6	2
7400	The structure of a polyketide synthase bimodule core. Science Advances, 2022, 8, .	4.7	9
7401	Gain of function studies on predicted host receptors for white spot virus. Fish and Shellfish Immunology, 2022, 131, 196-205.	1.6	2
7402	Molecular basis for thermal stability and affinity in a VHH: Contribution of the framework region and its influence in the conformation of the CDR3. Protein Science, 2022, 31, .	3.1	5
7403	Small-Angle X-ray Scattering (SAXS) Measurements of APOBEC3G Provide Structural Basis for Binding of Single-Stranded DNA and Processivity. Viruses, 2022, 14, 1974.	1.5	1
7404	Affinity-matured DLL4 ligands as broad-spectrum modulators of Notch signaling. Nature Chemical Biology, 2023, 19, 9-17.	3.9	6
7406	Human immunoglobulin repertoire analysis guides design of vaccine priming immunogens targeting HIV V2-apex broadly neutralizing antibody precursors. Immunity, 2022, 55, 2149-2167.e9.	6.6	21

#	ARTICLE	IF	CITATIONS
7407	Mechanism by which T7 bacteriophage protein Gp1.2 inhibits <i>Escherichia coli</i> dGTPase. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	2
7408	High-resolution crystal structure and chemical screening reveal pantothenate kinase as a new target for antifungal development. Structure, 2022, , .	1.6	4
7409	X-ray crystallographic characterization of the SARS-CoV-2 main protease polyprotein cleavage sites essential for viral processing and maturation. Nature Communications, 2022, 13, .	5.8	32
7413	Structural features of chloroplast trigger factor determined at 2.6â€…Ã… resolution. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1259-1272.	1.1	1
7414	Repositioning small molecule drugs as allosteric inhibitors of the BFTâ€3 toxin from enterotoxigenic <i>Bacteroides fragilis</i>. Protein Science, 2022, 31, .	3.1	1
7415	Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3. Nature Communications, 2022, 13, .	5.8	2
7416	Physical Characteristics of von Willebrand Factor Binding with Platelet Glycoprotein IbÉ‘ Mutants at Residue 233 Causing Various Biological Functions. TH Open, 2022, 06, e421-e428.	0.7	0
7417	Y98 Mutation Leads to the Loss of RsfS Anti-Association Activity in Staphylococcus aureus. International Journal of Molecular Sciences, 2022, 23, 10931.	1.8	1
7418	Modeling of the thermal properties of SARS-CoV-2 S-protein. Frontiers in Molecular Biosciences, 0, 9, .	1.6	2
7419	Cryo-electron microscopy and image classification reveal the existence and structure of the coxsackievirus A6 virion. Communications Biology, 2022, 5, .	2.0	3
7420	Multiscale Modeling of Hepatitis B Virus Capsid Assembly and Its Dimorphism. ACS Nano, 2022, 16, 13845-13859.	7.3	18
7421	Hotspots and Mechanisms of Action of the Thermostable Framework of a Microbial Thermolipase. ACS Synthetic Biology, 2022, 11, 3460-3470.	1.9	4
7422	Computational Dissection of the Role of Trp305 in the Regulation of the Death-Associated Protein Kinaseâ€“Calmodulin Interaction. Biomolecules, 2022, 12, 1395.	1.8	4
7424	Bidirectional sequestration between a bacterial hibernation factor and a glutamate metabolizing protein. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
7425	Structural Basis of Substrate Promiscuity and Catalysis by the Reverse Prenyltransferase <i>N</i>-Dimethylallyl-<scp>l</scp>-tryptophan Synthase from <i>Fusarium fujikuroi</i>. Biochemistry, 2022, 61, 2025-2035.	1.2	4
7426	Nanobodies identify an activated state of the TRIB2 pseudokinase. Structure, 2022, , .	1.6	2
7427	Cellular and structural characterisation of VP1 and VP2 knockout mutants of AAV3B serotype and implications for AAV manufacturing. Human Gene Therapy, 0, , .	1.4	1
7428	Efficacy Evaluation of SDF-1Î±-Based Polypeptides in an Acute Myocardial Infarction Model Using Structure-Based Drug Design. ACS Biomaterials Science and Engineering, 2022, 8, 4486-4496.	2.6	1

#	ARTICLE	IF	CITATIONS
7429	Structural analysis of human CEACAM1 oligomerization. Communications Biology, 2022, 5, .	2.0	0
7430	Fip1 is a multivalent interaction scaffold for processing factors in human mRNA 3â€² end biogenesis. ELife, 0, 11, .	2.8	3
7431	Improved mammalian retromer cryo-EM structures reveal a new assembly interface. Journal of Biological Chemistry, 2022, 298, 102523.	1.6	2
7432	Substrate-induced dimerization of elaiophylin glycosyltransferase reveals a novel self-activating form of glycosyltransferase for symmetric glycosylation. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1235-1248.	1.1	0
7433	<i>Fusarium verticillioides</i><scp>NAT1</scp> (<scp>FDB2</scp>) <i>N</i>â€malonyltransferase is structurally, functionally and phylogenetically distinct from its <i>N</i>â€acetyltransferase (<scp>NAT</scp>) homologues. FEBS Journal, 2023, 290, 2412-2436.	2.2	3
7434	Structure determination of an unstable macromolecular complex enabled by nanobodyâ€peptide bridging. Protein Science, 2022, 31, .	3.1	2
7435	Structural insights into crista junction formation by the Mic60-Mic19 complex. Science Advances, 2022, 8, .	4.7	14
7437	Structureâ€based design, synthesis and biological evaluation of a <scp>NAD</scp>⁺ analogue targeting <i>Pseudomonas aeruginosa</i><scp>NAD</scp> kinase. FEBS Journal, 2023, 290, 482-501.	2.2	0
7438	Structural characterization of SARS-CoV-2 dimeric ORF9b reveals potential fold-switching trigger mechanism. Science China Life Sciences, 2023, 66, 152-164.	2.3	2
7439	Non-canonical <i>Staphylococcus aureus</i> pathogenicity island repression. Nucleic Acids Research, 2022, 50, 11109-11127.	6.5	5
7442	Structural model for ligand binding and channel opening of an insect gustatory receptor. Journal of Biological Chemistry, 2022, 298, 102573.	1.6	10
7443	Metal binding and oligomerization properties of FurC (PerR) from <i>Anabaena</i> sp. PCC7120: an additional layer of regulation?. Metallomics, 2022, 14, .	1.0	2
7445	High-resolution structures of a siderophore-producing cyclization domain from Yersinia pestis offer a refined proposal of substrate binding. Journal of Biological Chemistry, 2022, 298, 102454.	1.6	4
7446	SPACA9 is a lumenal protein of human ciliary singlet and doublet microtubules. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	25
7447	Cell-free protein crystallization for nanocrystal structure determination. Scientific Reports, 2022, 12, .	1.6	5
7448	The dimeric form of bacterial <scp>l</scp>â€asparaginase <scp>YpAI</scp> is fully active. FEBS Journal, 2023, 290, 780-795.	2.2	3
7449	Neighboring mutationâ€mediated enhancement of dengue virus infectivity and spread. EMBO Reports, 2022, 23, .	2.0	5
7450	Crystal structure of the Phospholipase A and acyltransferase 4 (PLAAT4) catalytic domain. Journal of Structural Biology, 2022, , 107903.	1.3	0

#	ARTICLE	IF	CITATIONS
7451	Structural insights for neutralization of Omicron variants BA.1, BA.2, BA.4, and BA.5 by a broadly neutralizing SARS-CoV-2 antibody. Science Advances, 2022, 8, .	4.7	25
7452	Crystal structure and biochemical analysis suggest that YjoB ATPase is a putative substrate-specific molecular chaperone. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	0
7453	Combining small angle X-ray scattering (SAXS) with protein structure predictions to characterize conformations in solution. Methods in Enzymology, 2023, , 351-376.	0.4	1
7455	Molecular basis of dual anti-CRISPR and auto-regulatory functions of AcrIF24. Nucleic Acids Research, 2022, 50, 11344-11358.	6.5	6
7456	Three-dimensional structure of a mycobacterial oligoribonuclease reveals a unique C-terminal tail that stabilizes the homodimer. Journal of Biological Chemistry, 2022, , 102595.	1.6	0
7457	Molecular insights into DNA recognition and methylation by non-canonical type I restriction-modification systems. Nature Communications, 2022, 13, .	5.8	2
7458	BRD9 Inhibition by Natural Polyphenols Targets DNA Damage/Repair and Apoptosis in Human Colon Cancer Cells. Nutrients, 2022, 14, 4317.	1.7	5
7460	The protein common assembly database (ProtCAD)â€"a comprehensive structural resource of protein complexes. Nucleic Acids Research, 2023, 51, D466-D478.	6.5	2
7464	Structural insight into Tn3 family transposition mechanism. Nature Communications, 2022, 13, .	5.8	4
7465	Kinetic and Structural Characterization of a Flavin-Dependent Putrescine <i>N</i>-Hydroxylase from <i>Acinetobacter baumannii</i>. Biochemistry, 2022, 61, 2607-2620.	1.2	4
7467	HIV-1 CD4-binding site germline antibodyâ€"Env structures inform vaccine design. Nature Communications, 2022, 13, .	5.8	5
7469	Structural insight into the ligand binding mechanism of aryl hydrocarbon receptor. Nature Communications, 2022, 13, .	5.8	16
7470	Zymogenic latency in an âˆ¼250-million-year-old astacin metallopeptidase. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1347-1357.	1.1	2
7471	Molecular mechanism of Afadin substrate recruitment to the receptor phosphatase PTPRK via its pseudophosphatase domain. ELife, 0, 11, .	2.8	0
7473	Structural basis of colibactin activation by the ClbP peptidase. Nature Chemical Biology, 2023, 19, 151-158.	3.9	12
7474	Structural and functional studies of a snake venom phospholipase A2-like protein complexed to an inhibitor from Tabernaemontana catharinensis. Biochimie, 2023, 206, 105-115.	1.3	4
7476	Molecular analysis of a public cross-neutralizing antibody response to SARS-CoV-2. Cell Reports, 2022, 41, 111650.	2.9	12
7477	Unravelling the regulation pathway of photosynthetic AB-GAPDH. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1399-1411.	1.1	2

#	Article	IF	Citations
7478	A selective and orally bioavailable VHL-recruiting PROTAC achieves SMARCA2 degradation in vivo. Nature Communications, 2022, 13, .	5.8	60
7479	Structural principles of B cell antigen receptor assembly. Nature, 2022, 612, 156-161.	13.7	26
7480	Atomic model of vesicular stomatitis virus and mechanism of assembly. Nature Communications, 2022, 13, .	5.8	8
7482	Neutralizing monoclonal antibodies elicited by mosaic RBD nanoparticles bind conserved sarbecovirus epitopes. Immunity, 2022, 55, 2419-2435.e10.	6.6	23
7483	Structure and functionality of a multimeric human COQ7:COQ9 complex. Molecular Cell, 2022, 82, 4307-4323.e10.	4.5	21
7485	Dimerization of the C-type lectin-like receptor CD93 promotes its binding to Multimerin-2 in endothelial cells. International Journal of Biological Macromolecules, 2023, 224, 453-464.	3.6	3
7487	High-Resolution Crystal Structure of Muscle Phosphoglycerate Mutase Provides Insight into Its Nuclear Import and Role. International Journal of Molecular Sciences, 2022, 23, 13198.	1.8	0
7488	Structural basis for Cas9 off-target activity. Cell, 2022, 185, 4067-4081.e21.	13.5	54
7489	Isoform-specific inhibition of FGFR signaling achieved by a de-novo-designed mini-protein. Cell Reports, 2022, 41, 111545.	2.9	2
7490	Glycoside hydrolase subfamily GH5_57 features a highly redesigned catalytic interface to process complex hetero-Î²-mannans. Acta Crystallographica Section D: Structural Biology, 2022, 78, 1358-1372.	1.1	1
7491	Structural basis for host recognition and superinfection exclusion by bacteriophage T5. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	14
7492	BACTERIAL NADQ (COG4111) IS A NUDIX-LIKE, ATP-RESPONSIVE REGULATOR OF NAD BIOSYNTHESIS. Journal of Structural Biology, 2022, , 107917.	1.3	0
7493	AAA+ protease-adaptor structures reveal altered conformations and ring specialization. Nature Structural and Molecular Biology, 2022, 29, 1068-1079.	3.6	6
7494	Enzymatic C3-Methylation of Indoles Using Methyltransferase PsmDâ"€Crystal Structure, Catalytic Mechanism, and Preparative Applications. ACS Catalysis, 2022, 12, 14130-14139.	5.5	1
7495	Selection of a <scp>PD</scp>â€1 blocking antibody from a novel fully human phage display library. Protein Science, 2022, 31, .	3.1	7
7496	Characterization of the Gateway Decarboxylase for Psilocybin Biosynthesis. ChemBioChem, 2022, 23, .	1.3	3
7498	A comprehensive set of ER protein disulfide isomerase family members supports the biogenesis of proinflammatory interleukin 12 family cytokines. Journal of Biological Chemistry, 2022, 298, 102677.	1.6	2
7499	Cryo-EM Structure of the Type IV Pilus Extension ATPase from Enteropathogenic Escherichia coli. MBio, 2022, 13, .	1.8	2

#	ARTICLE	IF	CITATIONS
7500	Endowing homodimeric carbamoyltransferase GdmN with iterative functions through structural characterization and mechanistic studies. Nature Communications, 2022, 13, .	5.8	1
7501	Nanobodies targeting LexA autocleavage disclose a novel suppression strategy of SOS-response pathway. Structure, 2022, 30, 1479-1493.e9.	1.6	6
7502	Synthesis of new sulphonate derivatives containing adamantane and 4-chlorophenyl moieties as nucleotide pyrophosphatase/phosphodiesterase-1 and -3 inhibitors. Journal of Molecular Structure, 2023, 1274, 134494.	1.8	0
7503	Targeting apoptosis in MCF-7 and Ehrlich ascites carcinoma cells by saponifiable fractions from green and black Vitis vinifera seed oil. Biomedicine and Pharmacotherapy, 2023, 157, 114017.	2.5	6
7504	Structural insights at acidic <scp>pH</scp> of dyeâ€decolorizing peroxidase from <i>Bacillus subtilis</i>. Proteins: Structure, Function and Bioinformatics, 2023, 91, 508-517.	1.5	2
7505	Dynamic acylome reveals metabolite driven modifications in Syntrophomonas wolfei. Frontiers in Microbiology, 0, 13, .	1.5	1
7507	Inhibiting ACK1-mediated phosphorylation of C-terminal Src kinase counteracts prostate cancer immune checkpoint blockade resistance. Nature Communications, 2022, 13, .	5.8	16
7508	Antigenic mapping reveals sites of vulnerability on Î±-HCoV spike protein. Communications Biology, 2022, 5, .	2.0	2
7509	Rare, convergent antibodies targeting the stem helix broadly neutralize diverse betacoronaviruses. Cell Host and Microbe, 2023, 31, 97-111.e12.	5.1	21
7510	Do Go Chasing Waterfalls: Enoyl Reductase (FabI) in Complex with Inhibitors Stabilizes the Tetrameric Structure and Opens Water Channels. Journal of Chemical Information and Modeling, 2022, 62, 5746-5761.	2.5	1
7511	Cryo-EM structures of prefusion SIV envelope trimer. Nature Structural and Molecular Biology, 2022, 29, 1080-1091.	3.6	7
7512	Fragment-based computational design of antibodies targeting structured epitopes. Science Advances, 2022, 8, .	4.7	14
7513	The Nse5/6-like SIMC1-SLF2 complex localizes SMC5/6 to viral replication centers. ELife, 0, 11, .	2.8	10
7514	Co-immunization with hemagglutinin stem immunogens elicits cross-group neutralizing antibodies and broad protection against influenza A viruses. Immunity, 2022, 55, 2405-2418.e7.	6.6	14
7515	Structural insights into broadly neutralizing antibodies elicited by hybrid immunity against SARS-CoV-2. Emerging Microbes and Infections, 2023, 12, .	3.0	3
7516	Exploring Structural Diversity among Adhesion Devices Encoded by Lactococcal P335 Phages with AlphaFold2. Microorganisms, 2022, 10, 2278.	1.6	2
7517	Neutralizing epitopes on Clostridioides difficile toxin A revealed by the structures of two camelid VHH antibodies. Frontiers in Immunology, 0, 13, .	2.2	0
7518	A terminal functionalization strategy reveals unusual binding abilities of anti-thrombin anticoagulant aptamers. Molecular Therapy - Nucleic Acids, 2022, 30, 585-594.	2.3	6

#	Article	IF	Citations
7519	Stability profile of vimentin rod domain. Protein Science, 2022, 31, .	3.1	10
7520	Structural and biochemical basis of interdependent <scp>FANCIâ€FANCD2</scp> ubiquitination. EMBO Journal, 2023, 42, .	3.5	5
7521	Structures of a mobile intron retroelement poised to attack its structured DNA target. Science, 2022, 378, 627-634.	6.0	11
7522	Conformational motions and ligand-binding underlying gating and regulation in IP3R channel. Nature Communications, 2022, 13, .	5.8	19
7524	Designing a multi-epitope vaccine against coxsackievirus B based on immunoinformatics approaches. Frontiers in Immunology, 0, 13, .	2.2	5
7525	Human B Cell Epitope Map of the Lyme Disease Vaccine Antigen, OspA. ACS Infectious Diseases, 2022, 8, 2515-2528.	1.8	8
7526	Structural and mutational studies suggest key residues to determine whether stomatin SPFH domains form dimers or trimers. Biochemistry and Biophysics Reports, 2022, 32, 101384.	0.7	1
7527	Structure and function of the NS5 methyltransferase domain from Usutu virus. Antiviral Research, 2022, 208, 105460.	1.9	0
7528	Structural basis of the myotoxic inhibition of the Bothrops pirajai PrTX-I by the synthetic varespladib. Biochimie, 2023, 207, 1-10.	1.3	5
7529	Cryo-EM structure of ex vivo fibrils associated with extreme AA amyloidosis prevalence in a cat shelter. Nature Communications, 2022, 13, .	5.8	8
7533	Complementary antibody lineages achieve neutralization breadth in an HIV-1 infected elite neutralizer. PLoS Pathogens, 2022, 18, e1010945.	2.1	0
7536	A unique network of attack, defence and competence on the outer membrane of the periodontitis pathogen <i>Tannerella forsythia</i>. Chemical Science, 2023, 14, 869-888.	3.7	1
7537	Molecular basis for antiviral activity of two pediatric neutralizing antibodies targeting SARS-CoV-2 Spike RBD. IScience, 2023, 26, 105783.	1.9	4
7538	In vitro neutralisation of Zika virus by an engineered protein targeting the viral envelope fusion loop. Molecular Systems Design and Engineering, 0, , .	1.7	0
7539	Crystal structure of prodigiosin binding protein PgbP, a GNAT family protein, in Serratia marcescens FS14. Biochemical and Biophysical Research Communications, 2023, 640, 73-79.	1.0	0
7540	The structure of a tautomerase superfamily member linked to the type VI secretion system of <i>Acinetobacter baumannii</i>. Acta Crystallographica Section F, Structural Biology Communications, 2023, 79, 8-16.	0.4	0
7541	The pursuit of new alternative ways to eradicate Helicobacter pylori continues: Detailed characterization of interactions in the adenylosuccinate synthetase active site. International Journal of Biological Macromolecules, 2023, 226, 37-50.	3.6	2
7542	Paramyxoviruses from bats: changes in receptor specificity and their role in host adaptation. Current Opinion in Virology, 2023, 58, 101292.	2.6	4

#	Article	IF	Citations
7543	Structural and biochemical characterization of Leptospira interrogans Lsa45 reveals a penicillin-binding protein with esterase activity. Process Biochemistry, 2023, 125, 141-153.	1.8	1
7544	Structure of human placental steroid sulfatase at 2.0 angstrom resolution: Catalysis, quaternary association, and a secondary ligand site. Journal of Steroid Biochemistry and Molecular Biology, 2023, 227, 106228.	1.2	3
7545	Computer- and NMR-Aided Design of Small-Molecule Inhibitors of the Hub1 Protein. Molecules, 2022, 27, 8282.	1.7	0
7546	Cryo-EM structures of the active NLRP3 inflammasome disc. Nature, 2023, 613, 595-600.	13.7	64
7547	Switching of Receptor Binding Poses between Closely Related Enteroviruses. Viruses, 2022, 14, 2625.	1.5	1
7548	Structural characterization of protective non-neutralizing antibodies targeting Crimean-Congo hemorrhagic fever virus. Nature Communications, 2022, 13, .	5.8	6
7549	CryoEM structure and assembly mechanism of a bacterial virus genome gatekeeper. Nature Communications, 2022, 13, .	5.8	7
7551	Structure-based engineering of minimal Proline dehydrogenase domains for inhibitor discovery. Protein Engineering, Design and Selection, 0, , .	1.0	0
7552	Structural Studies of Bypass of Forespore Protein C from Bacillus Subtilis to Reveal Its Inhibitory Molecular Mechanism for SpoIVB. Catalysts, 2022, 12, 1530.	1.6	0
7554	A conserved glutathione binding site in poliovirus is a target for antivirals and vaccine stabilisation. Communications Biology, 2022, 5, .	2.0	3
7555	Insights into the Structure of the Highly Glycosylated Ffase from Rhodotorula dairenensis Enhance Its Biotechnological Potential. International Journal of Molecular Sciences, 2022, 23, 14981.	1.8	2
7556	Structural basis of tankyrase activation by polymerization. Nature, 2022, 612, 162-169.	13.7	9
7557	Vaccination with the Omicron spike RBD boosts broadly neutralizing antibody levels and confers sustained protection even after acquiring immunity to the original antigen. International Immunology, 2023, 35, 197-207.	1.8	4
7558	High-density binding to Plasmodium falciparum circumsporozoite protein repeats by inhibitory antibody elicited in mouse with human immunoglobulin repertoire. PLoS Pathogens, 2022, 18, e1010999.	2.1	6
7559	A structural model of the profilinâ€“formin pacemaker system for actin filament elongation. Scientific Reports, 2022, 12, .	1.6	3
7561	cNTnC and fYTnC2, Genetically Encoded Green Calcium Indicators Based on Troponin C from Fast Animals. International Journal of Molecular Sciences, 2022, 23, 14614.	1.8	2
7562	Antiviral signalling by a cyclic nucleotide activated CRISPR protease. Nature, 2023, 614, 168-174.	13.7	12
7564	Structural and biochemical characterizations of Thermus thermophilus HB8 transketolase producing a heptulose. Applied Microbiology and Biotechnology, 2023, 107, 233-245.	1.7	0

#	ARTICLE	IF	CITATIONS
7565	Uptake mechanism of iron-phytosiderophore from the soil based on the structure of yellow stripe transporter. Nature Communications, 2022, 13, .	5.8	5
7566	Next-generation retinoid X receptor agonists increase ATRA signaling in organotypic epithelium cultures and have distinct effects on receptor dynamics. Journal of Biological Chemistry, 2022, , 102746.	1.6	1
7568	Structural insights into mechanism and specificity of the plant protein O-fucosyltransferase SPINDLY. Nature Communications, 2022, 13, .	5.8	7
7569	A broad specificity Î²-propeller enzyme from Rhodopseudomonas palustris that hydrolyzes many lactones including Î³-valerolactone. Journal of Biological Chemistry, 2022, , 102782.	1.6	0
7571	Structural basis for a human broadly neutralizing influenza A hemagglutinin stem-specific antibody including H17/18 subtypes. Nature Communications, 2022, 13, .	5.8	4
7573	Discovery of Î±-<scp>l</scp>-Glucosidase Raises the Possibility of Î±-<scp>l</scp>-Glucosides in Nature. ACS Omega, 2022, 7, 47411-47423.	1.6	2
7574	Molecular mechanism of antibody neutralization of coxsackievirus A16. Nature Communications, 2022, 13, .	5.8	2
7575	Xâ€ray structure and mechanism of <scp>ZgHAD</scp>, a <scp>l</scp>â€2â€haloacid dehalogenase from the marine Flavobacterium <i>Zobellia galactanivorans</i>. Protein Science, 2023, 32, .	3.1	2
7576	Mapping the protein binding site of the (pro)renin receptor using in silico 3D structural analysis. Hypertension Research, 2023, 46, 959-971.	1.5	1
7577	Structures of the Inhibitory Receptor Siglec-8 in Complex with a High-Affinity Sialoside Analogue and a Therapeutic Antibody. Jacs Au, 2023, 3, 204-215.	3.6	5
7578	HBD-2 variants and SARS-CoV-2: New insights into inter-individual susceptibility. Frontiers in Immunology, 0, 13, .	2.2	2
7580	Calmodulin variant E140G associated with long QT syndrome impairs CaMKIIÎ´ autophosphorylation and L-type calcium channel inactivation. Journal of Biological Chemistry, 2023, 299, 102777.	1.6	2
7581	Bacterial crystalline cellulose secretion via a supramolecular BcsHD scaffold. Science Advances, 2022, 8, .	4.7	10
7583	Tandem engagement of phosphotyrosines by the dual SH2 domains of p120RasGAP. Structure, 2022, 30, 1603-1614.e5.	1.6	3
7584	High-resolution cryo-EM structure of the <i>Shigella</i> virus Sf6 genome delivery tail machine. Science Advances, 2022, 8, .	4.7	10
7585	The structure of the human LACTB filament reveals the mechanisms of assembly and membrane binding. PLoS Biology, 2022, 20, e3001899.	2.6	4
7586	Structural basis of sequence-specific RNA recognition by the antiviral factor APOBEC3G. Nature Communications, 2022, 13, .	5.8	3
7587	Structure and Dynamics of the Unassembled Nucleoprotein of Rabies Virus in Complex with Its Phosphoprotein Chaperone Module. Viruses, 2022, 14, 2813.	1.5	4

#	ARTICLE	IF	CITATIONS
7588	Characterization of a glycoside hydrolase endolysin from <i>Acinetobacter baumannii</i> phage <scp><i>Ab</i>TZA1</scp> with high antibacterial potency and novel structural features. FEBS Journal, 2023, 290, 2146-2164.	2.2	8
7589	Multivalency ensures persistence of a +TIP body at specialized microtubule ends. Nature Cell Biology, 2023, 25, 56-67.	4.6	16
7590	DNAâ€"TCP complex structures reveal a unique recognition mechanism for TCP transcription factor families. Nucleic Acids Research, 2023, 51, 434-448.	6.5	6
7591	The structure, bindingÂand function of a Notch transcription complex involving RBPJ and the epigenetic reader protein L3MBTL3. Nucleic Acids Research, 0, , .	6.5	1
7592	Structure of the AlgKX modification and secretion complex required for alginate production and biofilm attachment in Pseudomonas aeruginosa. Nature Communications, 2022, 13, .	5.8	11
7593	Diethylpyrocarbonate-Based Covalent Labeling Mass Spectrometry of Protein Interactions in a Membrane Complex System. Journal of the American Society for Mass Spectrometry, 0, , .	1.2	8
7594	From passage to inhibition: Uncovering the structural and physiological inhibitory mechanisms of <scp>MCUb</scp> in mitochondrial calcium regulation. FASEB Journal, 2023, 37, .	0.2	2
7595	Crystal Contact Engineering for Enhanced Cross-Linking Efficiency of HheG Crystals. Catalysts, 2022, 12, 1553.	1.6	1
7598	Extracellular CIRP dysregulates macrophage bacterial phagocytosis in sepsis. , 2023, 20, 80-93.		12
7600	The Crystal Structure of Bacillus thuringiensis Tpp80Aa1 and Its Interaction with Galactose-Containing Glycolipids. Toxins, 2022, 14, 863.	1.5	5
7601	Probing the Role of a Conserved Phenylalanine in the Active Site of Thiocyanate Dehydrogenase. Crystals, 2022, 12, 1787.	1.0	0
7602	Crystal structure of the feruloyl esterase from Lentilactobacillus buchneri reveals a novel homodimeric state. Frontiers in Microbiology, 0, 13, .	1.5	4
7604	Explicit versus implicit consideration of binding partners in proteinâ€"protein complex to elucidate intrinsic dynamics. Biophysical Reviews, 0, , .	1.5	1
7605	Extensive substrate recognition by the streptococcal antibody-degrading enzymes IdeS and EndoS. Nature Communications, 2022, 13, .	5.8	8
7607	The crystal structure of the EspB-EspK virulence factor-chaperone complex suggests an additional type VII secretion mechanism in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2023, 299, 102761.	1.6	5
7608	Antibody Recognition of CD4-Induced Open HIV-1 Env Trimers. Journal of Virology, 2022, 96, .	1.5	4
7611	Hsp70 and Hsp110 Chaperones Promote Early Steps of Proteasome Assembly. Biomolecules, 2023, 13, 11.	1.8	1
7612	Identification, binding, and structural characterization of single domain anti-PD-L1 antibodies inhibitory of immune regulatory proteins PD-1 and CD80. Journal of Biological Chemistry, 2023, 299, 102769.	1.6	4

#	ARTICLE	IF	CITATIONS
7613	Structural Insights into the Dimeric Form of Bacillus subtilis RNase Y Using NMR and AlphaFold. Biomolecules, 2022, 12, 1798.	1.8	3
7614	RanBP9 controls the oligomeric state of CTLH complex assemblies. Journal of Biological Chemistry, 2023, 299, 102869.	1.6	2
7615	A data-driven interpretation of the stability of organic molecular crystals. Chemical Science, 2023, 14, 1272-1285.	3.7	4
7616	Conservation and divergence of the Gâ€interfaces of <i>Drosophila melanogaster</i> septins. Cytoskeleton, 2023, 80, 153-168.	1.0	3
7617	Changes within the central stalk of E. coli F1Fo ATP synthase observed after addition of ATP. Communications Biology, 2023, 6, .	2.0	9
7618	Rhanteriol, a New Rhanterium suaveolens Desf. Lignan with Pharmacological Potential as an Inhibitor of Enzymes Involved in Neurodegeneration and Type 2 Diabetes. Plants, 2023, 12, 301.	1.6	2
7619	Solution Xâ€ray scattering highlights discrepancies in <i>Plasmodium</i><scp>multiâ€aminoacylâ€tRNA</scp> synthetase complexes. Protein Science, 2023, 32, .	3.1	6
7620	Structural Basis of the Inhibition of L-Methionine Î³-Lyase from Fusobacterium nucleatum. International Journal of Molecular Sciences, 2023, 24, 1651.	1.8	3
7621	Emergence of an Auxin Sensing Domain in Plant-Associated Bacteria. MBio, 2023, 14, .	1.8	5
7622	Inâ€silico identification of Tyr232 in <scp>AMPKÎ±2</scp> as a dephosphorylation site for the protein tyrosine phosphatase <scp>PTPâ€PEST</scp>. Proteins: Structure, Function and Bioinformatics, 2023, 91, 831-846.	1.5	2
7623	Molecular Dynamics Simulation as a Tool to Identify Mutual Synergistic Folding Proteins. International Journal of Molecular Sciences, 2023, 24, 1790.	1.8	1
7624	The Bacteriophageâ€"Phage-Inducible Chromosomal Island Arms Race Designs an Interkingdom Inhibitor of dUTPases. Microbiology Spectrum, 2023, 11, .	1.2	1
7626	New Insights into the Role of the Trypanosoma cruzi Aldo-Keto Reductase TcAKR. Pathogens, 2023, 12, 85.	1.2	1
7627	Structural basis of broad-spectrum Î²-lactam resistance in Staphylococcus aureus. Nature, 2023, 613, 375-382.	13.7	11
7628	Analysis of critical proteinâ€"protein interactions of SARS-CoV-2 capping and proofreading molecular machineries towards designing dual target inhibitory peptides. Scientific Reports, 2023, 13, .	1.6	3
7629	Structural and Functional Characterization of the Ureidoacrylate Amidohydrolase RutB from <i>Escherichia coli</i>. Biochemistry, 0, , .	1.2	1
7630	Phosphorylation Regulation Mechanism of Î²2 Integrin for the Binding of Filamin Revealed by Markov State Model. Journal of Chemical Information and Modeling, 2023, 63, 605-618.	2.5	1
7631	Cryo-EM structure of hnRNPDL-2 fibrils, a functional amyloid associated with limb-girdle muscular dystrophyÂD3. Nature Communications, 2023, 14, .	5.8	15

#	Article	IF	Citations
7632	Complexed Crystal Structure of the Dihydroorotase Domain of Human CAD Protein with the Anticancer Drug 5-Fluorouracil. Biomolecules, 2023, 13, 149.	1.8	4
7633	Activity of Cytosolic Ascorbate Peroxidase (APX) from Panicum virgatum against Ascorbate and Phenylpropanoids. International Journal of Molecular Sciences, 2023, 24, 1778.	1.8	3
7634	Activity and Crystal Structure of the Adherent-Invasive Escherichia coli Tle3/Tli3 T6SS Effector/Immunity Complex Determined Using an AlphaFold2 Predicted Model. International Journal of Molecular Sciences, 2023, 24, 1740.	1.8	2
7638	Extracellular Fe(III) reductase structure reveals a modular organization enabling S-layer insertion and electron transfer to insoluble substrates. Structure, 2023, 31, 174-184.e3.	1.6	0
7639	Structure-guided mutagenesis of the capsid protein indicates that a nanovirus requires assembled viral particles for systemic infection. PLoS Pathogens, 2023, 19, e1011086.	2.1	4
7640	Structures of permuted halves of a modern ribose-binding protein. Acta Crystallographica Section D: Structural Biology, 2023, 79, 40-49.	1.1	1
7642	Major royal jelly proteins elicited suppression of SARS-CoV-2 entry and replication with halting lung injury. International Journal of Biological Macromolecules, 2023, 228, 715-731.	3.6	4
7643	Targeted degradation via direct 26S proteasome recruitment. Nature Chemical Biology, 2023, 19, 55-63.	3.9	31
7645	Potent ClpP agonists with anticancer properties bind with improved structural complementarity and alter the mitochondrial N-terminome. Structure, 2023, 31, 185-200.e10.	1.6	8
7646	A sorghum ascorbate peroxidase with four binding sites has activity against ascorbate and phenylpropanoids. Plant Physiology, 2023, 192, 102-118.	2.3	7
7647	5-Formyltetrahydrofolate Promotes Conformational Remodeling in a Methylenetetrahydrofolate Reductase Active Site and Inhibits Its Activity. Journal of Biological Chemistry, 2022, , 102855.	1.6	1
7648	Evolution of Rev7 interactions in eukaryotic TLS DNA polymerase PolÎ¶. Journal of Biological Chemistry, 2023, 299, 102859.	1.6	1
7649	Structure and dynamic association of an assembly platform subcomplex of the bacterial type II secretion system. Structure, 2023, 31, 152-165.e7.	1.6	4
7650	Preparation and Structural Studies of the Silkworm Carotenoid-Binding Protein Complexed with a New Pigment. Crystallography Reports, 2022, 67, 909-917.	0.1	0
7651	Machine learning in computational modelling of membrane protein sequences and structures: From methodologies to applications. Computational and Structural Biotechnology Journal, 2023, 21, 1205-1226.	1.9	3
7652	The allosteric effect of the upper half of SENP1 contributes to its substrate selectivity for SUMO1 over SUMO2. Journal of Biomolecular Structure and Dynamics, 0, , 1-15.	2.0	1
7653	Asymmetric horseshoe-like assembly of peroxisomal yeast oxalyl-CoA synthetase. Biological Chemistry, 2023, 404, 195-207.	1.2	1
7656	PTCHD1 Binds Cholesterol but Not Sonic Hedgehog, Suggesting a Distinct Cellular Function. International Journal of Molecular Sciences, 2023, 24, 2682.	1.8	2

#	ARTICLE	IF	CITATIONS
7657	Design, Production, and Characterization of Catalytically Active Inclusion Bodies. Methods in Molecular Biology, 2023, , 49-74.	0.4	0
7658	Structure and supramolecular organization of the canine distemper virus attachment glycoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
7659	Trimeric Architecture Ensures the Stability and Biological Activity of the Calf Purine Nucleoside Phosphorylase: In Silico and In Vitro Studies of Monomeric and Trimeric Forms of the Enzyme. International Journal of Molecular Sciences, 2023, 24, 2157.	1.8	1
7660	Human neutralizing antibodies to cold linear epitopes and subdomain 1 of the SARS-CoV-2 spike glycoprotein. Science Immunology, 2023, 8, .	5.6	33
7661	Nodavirus RNA replication crown architecture reveals proto-crown precursor and viral protein A conformational switching. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
7662	Mechanisms of Sugar Aminotransferase-like Enzymes to Synthesize Stereoisomers of Non-proteinogenic Amino Acids in Natural Product Biosynthesis. ACS Chemical Biology, 2023, 18, 385-395.	1.6	1
7663	Staphylococcal Periscope proteins Aap, SasG, and Pls project noncanonical legume-like lectin adhesin domains from the bacterial surface. Journal of Biological Chemistry, 2023, 299, 102936.	1.6	3
7664	Self-recycling and partially conservative replication of mycobacterial methylmannose polysaccharides. Communications Biology, 2023, 6, .	2.0	2
7665	Biophysical evaluation of the oligomerization and conformational properties of the N-terminal domain of TDP-43. Archives of Biochemistry and Biophysics, 2023, 737, 109533.	1.4	0
7666	An unusual disulfide-linked dimerization in the fluorescent protein rsCherryRev1.4. Acta Crystallographica Section F, Structural Biology Communications, 2023, 79, 38-44.	0.4	0
7667	Structure of the human CLC-7/Ostm1 complex reveals a novel state. , 2023, 53, 0306.		0
7668	Connection between MHC class II binding and aggregation propensity: The antigenic peptide 10 of Paracoccidioides brasiliensis as a benchmark study. Computational and Structural Biotechnology Journal, 2023, 21, 1746-1758.	1.9	1
7669	Probing the E1o-E2o and E1a-E2o Interactions in Binary Subcomplexes of the Human 2-Oxoglutarate Dehydrogenase and 2-Oxoadipate Dehydrogenase Complexes by Chemical Cross-Linking Mass Spectrometry and Molecular Dynamics Simulation. International Journal of Molecular Sciences, 2023, 24, 4555.	1.8	3
7670	The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in Arabidopsis thaliana. International Journal of Molecular Sciences, 2023, 24, 3580.	1.8	1
7671	Screening and epitope characterization of diagnostic nanobody against total and activated Bacteroides fragilis toxin. Frontiers in Immunology, 0, 14, .	2.2	4
7672	Unique alcohol dehydrogenases involved in algal sugar utilization by marine bacteria. Applied Microbiology and Biotechnology, 2023, 107, 2363-2384.	1.7	1
7673	Structure and regulation of the myotonic dystrophy kinase-related Cdc42-binding kinase. Structure, 2023, 31, 435-446.e4.	1.6	3
7674	Structural insights into the chromodomain of Oxpecker in complex with histone H3 lysine 9 trimethylation reveal a transposon silencing mechanism by heterodimerization. Biochemical and Biophysical Research Communications, 2023, 652, 95-102.	1.0	0

#	ARTICLE	IF	CITATIONS
7675	Toll-Like Receptor 3 Mediates Aortic Stenosis Through a Conserved Mechanism of Calcification. Circulation, 2023, 147, 1518-1533.	1.6	5
7676	Molecular determinants for differential activation of the bile acid receptor from the pathogen Vibrio parahaemolyticus. Journal of Biological Chemistry, 2023, 299, 104591.	1.6	4
7679	Multistep Engineering of a Penicillin G Acylase for Systematic Improvement of Crystallization Efficiency. Crystal Growth and Design, 0, , .	1.4	0
7680	CryoEM Reveals Oligomeric Isomers of a Multienzyme Complex and Assembly Mechanics. Journal of Structural Biology: X, 2023, , 100088.	0.7	1
7681	Characterization of new highly selective pyrazolo[4,3-d]pyrimidine inhibitor of CDK7. Biomedicine and Pharmacotherapy, 2023, 161, 114492.	2.5	4
7682	The Conserved Yeast Protein Knr4 Involved in Cell Wall Integrity Is a Multi-domain Intrinsically Disordered Protein. Journal of Molecular Biology, 2023, 435, 168048.	2.0	0
7683	ERRÎ³-DBD undergoes dimerization and conformational rearrangement upon binding to the downstream site of the DR1 element. Biochemical and Biophysical Research Communications, 2023, 656, 16-22.	1.0	0
7684	Unveiling mutation effects on the structural dynamics of the main protease from SARS-CoV-2 with hybrid simulation methods. Journal of Molecular Graphics and Modelling, 2023, 121, 108443.	1.3	2
7685	Characterization of two distinct neutrophil serine proteaseâ€“binding modes within a Staphylococcus aureus innate immune evasion protein family. Journal of Biological Chemistry, 2023, 299, 102969.	1.6	1
7686	Two different alanine dehydrogenases from Geobacillus kaustophilus: Their biochemical characteristics and differential expression in vegetative cells and spores. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2023, 1871, 140904.	1.1	1
7687	A systematic study on the binding affinity of SARS-CoV-2 spike protein to antibodies. AIMS Microbiology, 2022, 8, 595-611.	1.0	2
7688	Structures of the sulfite detoxifying F420-dependent enzyme from Methanococcales. Nature Chemical Biology, 2023, 19, 695-702.	3.9	7
7689	Crystal Structure of Inhibitor-Bound Bacterial Oligopeptidase B in the Closed State: Similarity and Difference between Protozoan and Bacterial Enzymes. International Journal of Molecular Sciences, 2023, 24, 2286.	1.8	3
7690	Mechanism of regulation of the Helicobacter pylori CagÎ² ATPase by CagZ. Nature Communications, 2023, 14, .	5.8	4
7691	Heterogeneity in winged helixâ€turnâ€helix and substrate DNA interactions: Insights from theory and experiments. Journal of Cellular Biochemistry, 2023, 124, 337-358.	1.2	1
7692	Recognition of the <scp>CCT5 diâ€Glu</scp> degron by <scp>CRL4^{DCAF12}</scp> is dependent on <scp>TRiC</scp> assembly. EMBO Journal, 2023, 42, .	3.5	9
7693	<scp>DNAJB8</scp> facilitates autophagicâ€lysosomal degradation of viral Vif protein and restricts <scp>HIV</scp>â€1 virion infectivity by rescuing <scp>APOBEC3G</scp> expression in host cells. FASEB Journal, 2023, 37, .	0.2	2
7694	Formation and characterization of BMP2/GDF5 and BMP4/GDF5 heterodimers. BMC Biology, 2023, 21, .	1.7	3

#	Article	IF	Citations
7695	Reducing affinity as a strategy to boost immunomodulatory antibody agonism. Nature, 2023, 614, 539-547.	13.7	36
7696	Structure of pyridoxal 5â€²-phosphate-bound <scp>D</scp>-threonine aldolase from <i>Chlamydomonas reinhardtii</i>. Acta Crystallographica Section F, Structural Biology Communications, 2023, 79, 31-37.	0.4	0
7697	The uncharacterized <i>Pseudomonas aeruginosa</i> PA4189 is a novel and efficient aminoacetaldehyde dehydrogenase. Biochemical Journal, 2023, 480, 259-281.	1.7	0
7698	Regulation of alanine racemase activity by carboxylates and the <scp>d</scp>â€type substrate <scp>d</scp>â€alanine. FEBS Journal, 2023, 290, 2954-2967.	2.2	0
7699	<i>Escherichia coli</i> YgiC and YjfC Possess Peptideâ”€Spermidine Ligase Activity. Biochemistry, 2023, 62, 899-911.	1.2	2
7700	The LHâ€"DH module of bacterial replicative helicases is the common binding site for DciA and other helicase loaders. Acta Crystallographica Section D: Structural Biology, 2023, 79, 177-187.	1.1	1
7701	Structural Insight into the Working Mechanism of the FAD Synthetase from the Human Pathogen Streptococcus pneumoniae: A Molecular Docking Simulation Study. International Journal of Molecular Sciences, 2023, 24, 3121.	1.8	1
7702	Quaternary glucocorticoid receptor structure highlights allosteric interdomain communication. Nature Structural and Molecular Biology, 2023, 30, 286-295.	3.6	5
7703	Atomic crystal structure and sugar specificity of a Î²-trefoil lectin domain from the ectomycorrhizal basidiomycete Laccaria bicolor. International Journal of Biological Macromolecules, 2023, 233, 123507.	3.6	1
7704	A high-quality reference genome for the fission yeast <i>Schizosaccharomyces osmophilus</i>. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	13
7705	Blue-to-Red TagFT, mTagFT, mTsFT, and Green-to-FarRed mNeptusFT2 Proteins, Genetically Encoded True and Tandem Fluorescent Timers. International Journal of Molecular Sciences, 2023, 24, 3279.	1.8	1
7706	Structures of MPND Reveal the Molecular Recognition of Nucleosomes. International Journal of Molecular Sciences, 2023, 24, 3368.	1.8	2
7707	The binding mode of orphan glycyl-tRNA synthetase with tRNA supports the synthetase classification and reveals large domain movements. Science Advances, 2023, 9, .	4.7	5
7708	Structural and Functional Analysis of a Highly Active Designed Phosphotriesterase for the Detoxification of Organophosphate Nerve Agents Reveals an Unpredicted Conformation of the Active Site Loop. Biochemistry, 2023, 62, 942-955.	1.2	3
7709	Structures of BIRC6-client complexes provide a mechanism of SMAC-mediated release of caspases. Science, 2023, 379, 1105-1111.	6.0	10
7710	Structure-Based Optimization of Proteaseâ€"Inhibitor Interactions to Enhance Specificity of Human Stefin-A against Falcipain-2 from the <i>Plasmodium falciparum</i> 3D7 Strain. Biochemistry, 2023, 62, 1053-1069.	1.2	0
7712	Structure and dynamics of the essential endogenous mycobacterial polyketide synthase Pks13. Nature Structural and Molecular Biology, 2023, 30, 296-308.	3.6	9
7713	An engineered miRNA PS-OMe miR130 inhibits acute lung injury by targeting eCIRP in sepsis. Molecular Medicine, 2023, 29, .	1.9	3

#	ARTICLE	IF	CITATIONS
7714	Cross-protective antibodies against common endemic respiratory viruses. Nature Communications, 2023, 14, .	5.8	6
7715	Structures of NF-Î°B p52 homodimer-DNA complexes rationalize binding mechanisms and transcription activation. ELife, 0, 12, .	2.8	1
7716	Conformational dynamics control assembly of an extremely long bacteriophage tail tube. Journal of Biological Chemistry, 2023, 299, 103021.	1.6	1
7717	Integration of immunoinformatics and cheminformatics to design and evaluate a multitope vaccine against Klebsiella pneumoniae and Pseudomonas aeruginosa coinfection. Frontiers in Molecular Biosciences, 0, 10, .	1.6	1
7718	A conserved zinc-binding site in <i>Acinetobacter baumannii</i> PBP2 required for elongasome-directed bacterial cell shape. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	3
7719	A Fijivirus Major Viroplasm Protein Shows RNA-Stimulated ATPase Activity by Adopting Pentameric and Hexameric Assemblies of Dimers. MBio, 0, , .	1.8	0
7721	Integrative structural analysis of the type <scp>III</scp> secretion system needle complex from <i>Shigella flexneri</i>. Protein Science, 2023, 32, .	3.1	7
7722	Structural and Biochemical Insights into Post-Translational Arginine-to-Ornithine Peptide Modifications by an Atypical Arginase. ACS Chemical Biology, 2023, 18, 528-536.	1.6	3
7724	Crystal Structure of Mesaconyl-CoA Hydratase from <i>Methylorubrum extorquens</i> CM4. Journal of Microbiology and Biotechnology, 2023, , .	0.9	0
7725	N-Glycoprofiling of SLC35A2-CDG: Patient with a Novel Hemizygous Variant. Biomedicines, 2023, 11, 580.	1.4	1
7726	Structure, substrate binding and activity of a unique AAA+Âprotein: the BrxL phage restriction factor. Nucleic Acids Research, 2023, 51, 3513-3528.	6.5	3
7727	An ensemble of interconverting conformations of the elemental paused transcription complex creates regulatory options. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	5
7728	Engineering the Thermostability of Sucrose Synthase by Reshaping the Subunit Interaction Contributes to Efficient UDP-Glucose Production. Journal of Agricultural and Food Chemistry, 2023, 71, 3832-3841.	2.4	4
7729	Monobody Inhibitor Selective to the Phosphatase Domain of SHP2 and its Use as a Probe for Quantifying SHP2 Allosteric Regulation. Journal of Molecular Biology, 2023, 435, 168010.	2.0	0
7730	Broadly neutralizing anti-S2 antibodies protect against all three human betacoronaviruses that cause deadly disease. Immunity, 2023, 56, 669-686.e7.	6.6	43
7731	Structure of the planar cell polarity cadherins Fat4 and Dachsous1. Nature Communications, 2023, 14, .	5.8	5
7733	Improved Assessment of Globularity of Protein Structures and the Ellipsoid Profile of the Biological Assemblies from the PDB. Biomolecules, 2023, 13, 385.	1.8	1
7734	CDK4/6 inhibitor palbociclib promotes SARS-CoV-2Âcell entry by down-regulating SKP2 dependent ACE2 degradation. Antiviral Research, 2023, 212, 105558.	1.9	4

#	Article	IF	Citations
7735	CvkR is a MerR-type transcriptional repressor of class 2 type V-K CRISPR-associated transposase systems. Nature Communications, 2023, 14, .	5.8	3
7736	Structural insights into ribonucleoprotein dissociation by nucleocapsid protein interacting with non-structural protein 3 in SARS-CoV-2. Communications Biology, 2023, 6, .	2.0	3
7738	Avidity engineering of human heavy-chain-only antibodies mitigates neutralization resistance of SARS-CoV-2 variants. Frontiers in Immunology, 0, 14, .	2.2	2
7739	Development of a human antibody fragment cross-neutralizing scorpion toxins. Molecular Immunology, 2023, 155, 165-174.	1.0	1
7740	Uncovering the Interaction Interface Between Harpin (Hpa1) and Rice Aquaporin (OsPIP1;3) Through Proteinâ€“Protein Docking: An In Silico Approach. Molecular Biotechnology, 0, , .	1.3	3
7742	Ion Mobility Mass Spectrometry (IM-MS) for Structural Biology: Insights Gained by Measuring Mass, Charge, and Collision Cross Section. Chemical Reviews, 2023, 123, 2902-2949.	23.0	35
7743	To the Understanding of Catalysis by D-Amino Acid Transaminases: A Case Study of the Enzyme from Aminobacterium colombiense. Molecules, 2023, 28, 2109.	1.7	2
7744	TcpA from the Clostridium perfringens plasmid pCW3 is more closely related to the DNA translocase FtsK than to coupling proteins. Structure, 2023, 31, 455-463.e4.	1.6	0
7745	Parasite Metalo-aminopeptidases as Targets in Human Infectious Diseases. Current Drug Targets, 2023, 24, 416-461.	1.0	1
7746	Hierarchical graph learning for proteinâ€“protein interaction. Nature Communications, 2023, 14, .	5.8	18
7747	Ubiquitin-like conjugation by bacterial cGAS enhances anti-phage defence. Nature, 2023, 616, 326-331.	13.7	37
7749	The NGF R100W Mutation, Associated with Hereditary Sensory Autonomic Neuropathy Type V, Specifically Affects the Binding Energetic Landscapes of NGF and of Its Precursor proNGF and p75NTR. Biology, 2023, 12, 364.	1.3	0
7751	Heteromerization of Dopamine D2 and Oxytocin Receptor in Adult Striatal Astrocytes. International Journal of Molecular Sciences, 2023, 24, 4677.	1.8	4
7752	Preclinical safety and efficacy of a therapeutic antibody that targets SARS-CoV-2 at the sotrovimab face but is escaped by Omicron. IScience, 2023, 26, 106323.	1.9	0
7753	Structure of the T. brucei kinetoplastid RNA editing substrate-binding complex core component, RESC5. PLoS ONE, 2023, 18, e0282155.	1.1	2
7754	The dynamic nature of netrin-1 and the structural basis for glycosaminoglycan fragment-induced filament formation. Nature Communications, 2023, 14, .	5.8	4
7755	Structure of a HIV-1 IN-Allosteric inhibitor complex at 2.93 Ã… resolution: Routes to inhibitor optimization. PLoS Pathogens, 2023, 19, e1011097.	2.1	3
7756	First pan-specific vNAR against human TGF-Î² as a potential therapeutic application: in silico modeling assessment. Scientific Reports, 2023, 13, .	1.6	6

#	ARTICLE	IF	CITATIONS
7757	A molecular basis for tetramer destabilization and aggregation of transthyretin <scp>Ala97Ser</scp>. Protein Science, 2023, 32, .	3.1	4
7758	Crystal structure and identification of amino acid residues for catalysis and binding of GH3 AnBX Î²-xylosidase from Aspergillus niger. Applied Microbiology and Biotechnology, 2023, 107, 2335-2349.	1.7	0
7759	The crystal structure of a simian Foamy Virus receptor binding domain provides clues about entry into host cells. Nature Communications, 2023, 14, .	5.8	1
7760	Monomer and dimer structures of cytochrome <i> bo ₃ </i> ubiquinol oxidase from <i>Escherichia coli</i>. Protein Science, 2023, 32, .	3.1	1
7761	Designer molecules of the synaptic organizer MDGA1 reveal 3D conformational control of biological function. Journal of Biological Chemistry, 2023, 299, 104586.	1.6	2
7762	Structure of the Wntâ€"Frizzledâ€"LRP6 initiation complex reveals the basis for coreceptor discrimination. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
7763	Function and Structure of <i>Lacticaseibacillus casei </i>GH35 Î²-Galactosidase LBCZ_0230 with High Hydrolytic Activity to Lacto-<i>N</i>-biose I and Galacto-<i>N</i>-biose. Journal of Applied Glycoscience (1999), 2023, 70, 43-52.	0.3	1
7764	A novel mAb broadly neutralizes SARSâ€CoVâ€2 VOCs in vitro and in vivo, including the Omicron variants. Journal of Medical Virology, 2023, 95, .	2.5	1
7765	Design of Synthetic Hydrogel Compositions for Noncovalent Protein Recognition. ACS Applied Materials & Interfaces, 2023, 15, 50586-50597.	4.0	2
7767	Heterocomplex structure of a polyketide synthase component involved in modular backbone halogenation. Structure, 2023, 31, 565-572.e4.	1.6	2
7768	7-Deazaguanines in DNA: functional and structural elucidation of a DNA modification system. Nucleic Acids Research, 2023, 51, 3836-3854.	6.5	2
7769	A splicing variant of <scp>EDS1</scp> from <i>Vitis vinifera</i> forms homodimers but no heterodimers with <scp>PAD4</scp>. Protein Science, 2023, 32, .	3.1	1
7771	The Josephin domain (JD) containing proteins are predicted to bind to the same interactors: Implications for spinocerebellar ataxia type 3 (SCA3) studies using Drosophila melanogaster mutants. Frontiers in Molecular Neuroscience, 0, 16, .	1.4	2
7773	Cryo-EM structures of anti-malarial antibody L9 with circumsporozoite protein reveal trimeric L9 association and complete 27-residue epitope. Structure, 2023, 31, 480-491.e4.	1.6	2
7774	Production of neutralizing antibody fragment variants in the cytoplasm of E. coli for rapid screening: SARS-CoV-2 a case study. Scientific Reports, 2023, 13, .	1.6	1
7775	Structures, activityÂand mechanism of the Type IIS restriction endonuclease PaqCI. Nucleic Acids Research, 2023, 51, 4467-4487.	6.5	3
7776	PrePPI: A Structure Informed Proteome-wide Database of Proteinâ€"Protein Interactions. Journal of Molecular Biology, 2023, 435, 168052.	2.0	12
7777	Structural insights into the assembly of gp130 family cytokine signaling complexes. Science Advances, 2023, 9, .	4.7	14

#	Article	IF	Citations
7778	MERS virus spike protein HTL-epitopes selection and multi-epitope vaccine design using computational biology. Journal of Biomolecular Structure and Dynamics, 2023, 41, 12464-12479.	2.0	3
7780	Identification of a peptide ligand for human ALDH3A1 through peptide phage display: Prediction and characterization of protein interaction sites and inhibition of ALDH3A1 enzymatic activity. Frontiers in Molecular Biosciences, 0, 10, .	1.6	2
7781	Cryo-EM analyses of KIT and oncogenic mutants reveal structural oncogenic plasticity and a target for therapeutic intervention. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	5
7783	From primordial clocks to circadian oscillators. Nature, 2023, 616, 183-189.	13.7	6
7784	Modeling of Protein Complexes. Methods in Molecular Biology, 2023, , 349-371.	0.4	1
7785	Structural insights into the regulation of peptidoglycan DL-endopeptidases by inhibitory protein IseA. Structure, 2023, , .	1.6	0
7787	Structural constraints link differences in neutralization potency of human anti-Eastern equine encephalitis virus monoclonal antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	0
7788	Structural basis of bacteriophage T5 infection trigger and <i>E. coli</i> cell wall perforation. Science Advances, 2023, 9, .	4.7	12
7789	ClpC2 protects mycobacteria against a natural antibiotic targeting ClpC1-dependent protein degradation. Communications Biology, 2023, 6, .	2.0	4
7791	Crystal structures of dimeric and heptameric mtHsp60 reveal the mechanism of chaperonin inactivation. Life Science Alliance, 2023, 6, e202201753.	1.3	0
7792	Mechanism of antibody-specific deglycosylation and immune evasion by Streptococcal IgG-specific endoglycosidases. Nature Communications, 2023, 14, .	5.8	2
7793	Direct Blockade of the Norovirus Histo-Blood Group Antigen Binding Pocket by Nanobodies. Journal of Virology, 0, , .	1.5	0
7794	Structural Characterization of Neisseria gonorrhoeae Bacterial Peroxidaseâ€"Insights into the Catalytic Cycle of Bacterial Peroxidases. International Journal of Molecular Sciences, 2023, 24, 6246.	1.8	3
7797	A DNA damageâ€"induced phosphorylation circuit enhances Mec1 ^{ATR} Ddc2 ^{ATRIP} recruitment to Replication Protein A. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
7798	Itch receptor MRGPRX4 interacts with the receptor activityâ€"modifying proteins. Journal of Biological Chemistry, 2023, 299, 104664.	1.6	1
7800	Rational strategies for enhancing mAb binding to SARS-CoV-2 variants through CDR diversification and antibody-escape prediction. Frontiers in Immunology, 0, 14, .	2.2	1
7804	Pseudouridine-Modifying Enzymes SapB and SapH Control Entry into the Pseudouridimycin Biosynthetic Pathway. ACS Chemical Biology, 2023, 18, 794-802.	1.6	2
7805	Modular adjuvant-free pan-HLA-DR-immunotargeting subunit vaccine against SARS-CoV-2 elicits broad sarbecovirus-neutralizing antibody responses. Cell Reports, 2023, 42, 112391.	2.9	1

#	ARTICLE	IF	CITATIONS
7806	Yeast PIC-mediator structure with RNA polymerase II C-terminal domain. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	6
7807	Crystal Structure and Functional Characterization of an S-Formylglutathione Hydrolase (BuSFGH) from Burkholderiaceae sp.. Crystals, 2023, 13, 621.	1.0	0
7808	Extended DNA threading through a dual-engine motor module of the activating signal co-integrator 1 complex. Nature Communications, 2023, 14, .	5.8	0
7809	Crystal structure of a highly conserved enteroviral 5â€² cloverleaf RNA replication element. Nature Communications, 2023, 14, .	5.8	6
7811	BopN is a Gatekeeper of the <i>Bordetella</i> Type III Secretion System. Microbiology Spectrum, 2023, 11, .	1.2	3
7812	Structural basis of spike RBM-specific human antibodies counteracting broad SARS-CoV-2 variants. Communications Biology, 2023, 6, .	2.0	0
7814	Amyloid fibril formation, structure and domain swapping of <scp>acylâ€coenzyme A</scp> thioesteraseâ€7. FEBS Journal, 2023, 290, 4057-4073.	2.2	2
7815	Structural basis of sensory receptor evolution in octopus. Nature, 2023, 616, 373-377.	13.7	9
7816	Sensory specializations drive octopus and squid behaviour. Nature, 2023, 616, 378-383.	13.7	10
7817	Pangenomic Study of Fusobacterium nucleatum Reveals the Distribution of Pathogenic Genes and Functional Clusters at the Subspecies and Strain Levels. Microbiology Spectrum, 2023, 11, .	1.2	2
7819	Domain swapping of the Câ€terminal helix promotes the dimerization of a novel ribonuclease protein from <i>Mycobacterium tuberculosis</i>. Protein Science, 0, , .	3.1	1
7820	Cross-linking mass spectrometry discovers, evaluates, and corroborates structures and proteinâ€“protein interactions in the human cell. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	9
7824	CryoEM and stability analysis of virus-like particles of potyvirus and ipomovirus infecting a common host. Communications Biology, 2023, 6, .	2.0	4
7825	Soluble domains of cytochrome c-556 and Rieske ironâ€“sulfur protein from Chlorobaculum tepidum: Crystal structures and interaction analysis. Current Research in Structural Biology, 2023, 5, 100101.	1.1	0
7827	The structure of a 12-segmented dsRNA reovirus: New insights into capsid stabilization and organization. PLoS Pathogens, 2023, 19, e1011341.	2.1	2
7830	DNA-binding mechanism and evolution of replication protein A. Nature Communications, 2023, 14, .	5.8	4
7831	TRIM56 coiled-coil domain structure provides insights into its E3 ligase functions. Computational and Structural Biotechnology Journal, 2023, 21, 2801-2808.	1.9	0
7889	Structural Basis of Low-Molecular-Weight Thiol Glycosylation in Lincomycin A Biosynthesis. ACS Chemical Biology, 2023, 18, 1271-1277.	1.6	1

#	Article	IF	Citations
7922	Computational and pharmacogenomic resources. , 2023, , 345-362.		0
8078	Application of Computational Techniques in Antibody Fc-Fused Molecule Design for Therapeutics. Molecular Biotechnology, 0, , .	1.3	0
8246	Structural Analyses of Bacterial Effectors by X-Ray Crystallography. Methods in Molecular Biology, 2024, , 485-502.	0.4	0
8282	A monomeric StayGold fluorescent protein. Nature Biotechnology, 0, , .	9.4	5