

Dali server: conservation mapping in 3D

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Citation Report

#	ARTICLE	IF	CITATIONS
13	Botulinum neurotoxin serotype D attacks neurons via two carbohydrate-binding sites in a ganglioside-dependent manner. <i>Biochemical Journal</i> , 2010, 431, 207-216.	1.7	71
14	Molecular characterization of Î²1,4-galactosyltransferase 7 genetic mutations linked to the progeroid form of Ehlers-Danlos syndrome (EDS). <i>FEBS Letters</i> , 2010, 584, 3962-3968.	1.3	23
15	Addendum to "A structural classification of substrate-binding proteins" [FEBS Lett. 584 (2010) 2606-2617]. <i>FEBS Letters</i> , 2010, 584, 4373-4373.	1.3	3
16	<i>Helicobacter pylori</i> proinflammatory protein up-regulates NF-Î²B as a cell-translocating Ser/Thr kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21418-21423.	3.3	49
17	SCOP family fingerprints: An information theoretic approach to structural classification of protein domains. , 2011, , .		0
18	EspR, a key regulator of <i>Mycobacterium tuberculosis</i> virulence, adopts a unique dimeric structure among helix-turn-helix proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13450-13455.	3.3	33
19	Why not consider a spherical protein? Implications of backbone hydrogen bonding for protein structure and function. <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 17044.	1.3	16
20	Toxoflavin Lyase Requires a Novel 1-His-2-Carboxylate Facial Triad. <i>Biochemistry</i> , 2011, 50, 1091-1100.	1.2	13
21	The Crystal Structure of <i>Escherichia coli</i> Group 4 Capsule Protein GfcC Reveals a Domain Organization Resembling That of Wza. <i>Biochemistry</i> , 2011, 50, 5465-5476.	1.2	31
22	Biochemical and Mutational Studies of the <i>Bacillus cereus</i> CECT 5050T Formamidase Support the Existence of a C-E-E-K Tetrad in Several Members of the Nitrilase Superfamily. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5761-5769.	1.4	16
23	Conformational Flexibility in the Allosteric Regulation of Human UDP-Î±-d-Glucose 6-Dehydrogenase. <i>Biochemistry</i> , 2011, 50, 9651-9663.	1.2	20
24	Solution Structure of 4-Phosphopantetheine - GmACP3 from <i>Geobacter metallireducens</i> : A Specialized Acyl Carrier Protein with Atypical Structural Features and a Putative Role in Lipopolysaccharide Biosynthesis. <i>Biochemistry</i> , 2011, 50, 1442-1453.	1.2	7
25	High-Resolution Crystal Structure of MltE, an Outer Membrane-Anchored Endolytic Peptidoglycan Lytic Transglycosylase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2011, 50, 2384-2386.	1.2	39
26	Double-stranded DNA viruses: 20 families and only five different architectural principles for virion assembly. <i>Current Opinion in Virology</i> , 2011, 1, 118-124.	2.6	77
27	The Chp1-Tas3 core is a multifunctional platform critical for gene silencing by RITS. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1351-1357.	3.6	38
28	Classification of Proteins: Available Structural Space for Molecular Modeling. <i>Methods in Molecular Biology</i> , 2011, 857, 1-31.	0.4	7
29	Structural Basis for a Kolbe-Type Decarboxylation Catalyzed by a Glycyl Radical Enzyme. <i>Journal of the American Chemical Society</i> , 2011, 133, 14666-14674.	6.6	56
30	Thermodynamic Characterization of the Binding Interaction between the Histone Demethylase LSD1/KDM1 and CoREST. <i>Biochemistry</i> , 2011, 50, 546-557.	1.2	20

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31	Insights into noncanonical E1 enzyme activation from the structure of autophagic E1 Atg7 with Atg8. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1323-1330.	3.6	89
32	Glutathione Transferases of <i>Phanerochaete chrysosporium</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 9162-9173.	1.6	38
33	Structural and Kinetic Analysis of the Unnatural Fusion Protein 4-Coumaroyl-CoA Ligase::Stilbene Synthase. <i>Journal of the American Chemical Society</i> , 2011, 133, 20684-20687.	6.6	37
34	Simultaneous Binding of Two Peptidyl Ligands by a Src Homology 2 Domain. <i>Biochemistry</i> , 2011, 50, 7637-7646.	1.2	29
35	Inaugural structure from the DUF3349 superfamily of proteins, <i>Mycobacterium tuberculosis</i> Rv0543c. <i>Archives of Biochemistry and Biophysics</i> , 2011, 506, 150-156.	1.4	6
36	Structural and Functional Analysis of a Plant Resistance Protein TIR Domain Reveals Interfaces for Self-Association, Signaling, and Autoregulation. <i>Cell Host and Microbe</i> , 2011, 9, 200-211.	5.1	301
37	Structural Analysis of <i>Pseudomonas syringae</i> AvrPtoB Bound to Host BAK1 Reveals Two Similar Kinase-Interacting Domains in a Type III Effector. <i>Cell Host and Microbe</i> , 2011, 10, 616-626.	5.1	117
38	<i>Marasmius oreades</i> agglutinin (MOA) is a chimerolectin with proteolytic activity. <i>Biochemical and Biophysical Research Communications</i> , 2011, 408, 405-410.	1.0	18
39	Crystal structure of PHYHD1A, a 2OG oxygenase related to phytanoyl-CoA hydroxylase. <i>Biochemical and Biophysical Research Communications</i> , 2011, 408, 553-558.	1.0	20
40	Crystal structure of <i>Pseudomonas aeruginosa</i> PA2196, a putative TetR family transcriptional repressor. <i>Biochemical and Biophysical Research Communications</i> , 2011, 410, 52-56.	1.0	5
41	Solution structure of a defense peptide from wheat with a 10-cysteine motif. <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 14-18.	1.0	36
42	Solution structure of a short-chain insecticidal toxin LalT1 from the venom of scorpion <i>Liocheles australasiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 411, 738-744.	1.0	13
43	Crystal structure of a key enzyme in the agarolytic pathway, β -neoagarobiose hydrolase from <i>Saccharophagus degradans</i> 2â€“40. <i>Biochemical and Biophysical Research Communications</i> , 2011, 412, 238-244.	1.0	76
44	Crystal structure of <i>Salmonella typhimurium</i> 2-methylcitrate synthase: Insights on domain movement and substrate specificity. <i>Journal of Structural Biology</i> , 2011, 174, 58-68.	1.3	9
45	NMR structure of the human Mediator MED25 ACID domain. <i>Journal of Structural Biology</i> , 2011, 174, 245-251.	1.3	35
46	Crystal structure of Sa240: A ribose pyranase homolog with partial active site from <i>Staphylococcus aureus</i> . <i>Journal of Structural Biology</i> , 2011, 174, 413-419.	1.3	0
47	Crystal structures of <i>Pseudomonas aeruginosa</i> guanidinobutyrase and guanidinopropionase, members of the ureohydrolase superfamily. <i>Journal of Structural Biology</i> , 2011, 175, 329-338.	1.3	15
48	Crystal structures of YwqE from <i>Bacillus subtilis</i> and CpsB from <i>Streptococcus pneumoniae</i> , unique metal-dependent tyrosine phosphatases. <i>Journal of Structural Biology</i> , 2011, 175, 442-450.	1.3	21

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49	The unusual extended C-terminal helix of the peroxisomal $\hat{\Gamma}^2$ -hydrolase Lpx1 is involved in dimer contacts but dispensable for dimerization. <i>Journal of Structural Biology</i> , 2011, 175, 362-371.	1.3	19
50	A Novel Structure of an Antikinase and its Inhibitor. <i>Journal of Molecular Biology</i> , 2011, 405, 214-226.	2.0	21
51	Solution NMR Structure of Apo-Calmodulin in Complex with the IQ Motif of Human Cardiac Sodium Channel NaV1.5. <i>Journal of Molecular Biology</i> , 2011, 406, 106-119.	2.0	105
52	Crystal Structures of Enoyl-ACP Reductases I (FabI) and III (FabL) from <i>B. subtilis</i> . <i>Journal of Molecular Biology</i> , 2011, 406, 403-415.	2.0	38
53	Augmenting $\hat{\Gamma}^2$ -Augmentation: Structural Basis of How BamB Binds BamA and May Support Folding of Outer Membrane Proteins. <i>Journal of Molecular Biology</i> , 2011, 406, 659-666.	2.0	77
54	A Model for Group B Streptococcus Pilus Type 1: The Structure of a 35-kDa C-Terminal Fragment of the Major Pilin GBS80. <i>Journal of Molecular Biology</i> , 2011, 407, 731-743.	2.0	35
55	Chlorite Dismutases, DyPs, and EfeB: 3 Microbial Heme Enzyme Families Comprise the CDE Structural Superfamily. <i>Journal of Molecular Biology</i> , 2011, 408, 379-398.	2.0	77
56	The Extra-Membranous Domains of the Competence Protein HofQ Show DNA Binding, Flexibility and a Shared Fold with Type I KH Domains. <i>Journal of Molecular Biology</i> , 2011, 409, 642-653.	2.0	20
57	Structural Insights into the Novel Diadenosine 5â€™ ₂ ,5â€™-P ₁ ,P ₄ -Tetraphosphate Phosphorylase from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Molecular Biology</i> , 2011, 410, 93-104.	2.0	7
58	Structure of the BamC Two-Domain Protein Obtained by Rosetta with a Limited NMR Data Set. <i>Journal of Molecular Biology</i> , 2011, 411, 83-95.	2.0	47
59	Crystal Structure of the Cytoplasmic N-Terminal Domain of Subunit I, a Homolog of Subunit a, of V-ATPase. <i>Journal of Molecular Biology</i> , 2011, 412, 14-21.	2.0	49
60	Structure and Substrate Recognition of the <i>Staphylococcus aureus</i> Protein Tyrosine Phosphatase PtpA. <i>Journal of Molecular Biology</i> , 2011, 413, 24-31.	2.0	22
61	A New Structural Form in the SAM/Metal-Dependent Oâ€™Methyltransferase Family: MycE from the Mycinamicin Biosynthetic Pathway. <i>Journal of Molecular Biology</i> , 2011, 413, 438-450.	2.0	24
62	Crystal Structure of the Passenger Domain of the <i>Escherichia coli</i> Autotransporter EspP. <i>Journal of Molecular Biology</i> , 2011, 413, 985-1000.	2.0	49
63	The Structure of <i>Arabidopsis thaliana</i> OST1 Provides Insights into the Kinase Regulation Mechanism in Response to Osmotic Stress. <i>Journal of Molecular Biology</i> , 2011, 414, 135-144.	2.0	40
64	Structure of the <i>Escherichia coli</i> Phosphonate Binding Protein PhnD and Rationally Optimized Phosphonate Biosensors. <i>Journal of Molecular Biology</i> , 2011, 414, 356-369.	2.0	60
65	Bacterial toxin-antitoxin systems. <i>Mobile Genetic Elements</i> , 2011, 1, 283-306.	1.8	74
66	L,L-Diaminopimelate Aminotransferase from <i>Chlamydomonas reinhardtii</i> : A Target for Algaecide Development. <i>PLoS ONE</i> , 2011, 6, e20439.	1.1	24

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67	Crystal Structures of Histone and p53 Methyltransferase SmyD2 Reveal a Conformational Flexibility of the Autoinhibitory C-Terminal Domain. <i>PLoS ONE</i> , 2011, 6, e21640.	1.1	38
68	Solution Structure of Tensin2 SH2 Domain and Its Phosphotyrosine-Independent Interaction with DLC-1. <i>PLoS ONE</i> , 2011, 6, e21965.	1.1	14
69	Structure of the Full-Length Major Pilin from <i>Streptococcus pneumoniae</i> : Implications for Isopeptide Bond Formation in Gram-Positive Bacterial Pili. <i>PLoS ONE</i> , 2011, 6, e22095.	1.1	33
70	An Inserted $\hat{\text{I}}^{\pm}/\hat{\text{I}}^{\pm 2}$ Subdomain Shapes the Catalytic Pocket of <i>Lactobacillus johnsonii</i> Cinnamoyl Esterase. <i>PLoS ONE</i> , 2011, 6, e23269.	1.1	46
71	Structure and Behavior of Human $\hat{\text{I}}^{\pm}$ -Thrombin upon Ligand Recognition: Thermodynamic and Molecular Dynamics Studies. <i>PLoS ONE</i> , 2011, 6, e24735.	1.1	8
72	A Fungal P450 (CYP5136A3) Capable of Oxidizing Polycyclic Aromatic Hydrocarbons and Endocrine Disrupting Alkylphenols: Role of Trp129 and Leu324. <i>PLoS ONE</i> , 2011, 6, e28286.	1.1	40
73	A Novel N-Acetylglutamate Synthase Architecture Revealed by the Crystal Structure of the Bifunctional Enzyme from <i>Maricaulis maris</i> . <i>PLoS ONE</i> , 2011, 6, e28825.	1.1	14
74	Crystal structure of Ssu72, an essential eukaryotic phosphatase specific for the C-terminal domain of RNA polymerase II, in complex with a transition state analogue. <i>Biochemical Journal</i> , 2011, 434, 435-444.	1.7	35
75	C68 from the <i>Sulfolobus islandicus</i> plasmid $\hat{\text{v}}^{\text{pSSVx}}$ is a novel member of the AbrB-like transcription factor family. <i>Biochemical Journal</i> , 2011, 435, 157-166.	1.7	24
76	Two autonomous structural modules in the fimbrial shaft adhesin FimA mediate <i>Actinomyces</i> interactions with streptococci and host cells during oral biofilm development. <i>Molecular Microbiology</i> , 2011, 81, 1205-1220.	1.2	57
77	Atypical DNA recognition mechanism used by the EspR virulence regulator of <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2011, 82, 251-264.	1.2	22
78	<i>Corynebacterium glutamicum</i> survives arsenic stress with arsenate reductases coupled to two distinct redox mechanisms. <i>Molecular Microbiology</i> , 2011, 82, 998-1014.	1.2	40
79	Separate inputs modulate phosphorylation-dependent and -independent type VI secretion activation. <i>Molecular Microbiology</i> , 2011, 82, 1277-1290.	1.2	96
80	Crystal structures of the apo form of $\hat{\text{I}}^{\pm}$ -fructofuranosidase from <i>Bifidobacterium longum</i> and its complex with fructose. <i>FEBS Journal</i> , 2011, 278, 1728-1744.	2.2	56
81	Crystal structure of basic 7S globulin, a xyloglucan-specific endo- $\hat{\text{I}}^{\pm}$ -1,4- $\hat{\text{I}}^{\pm}$ -glucanase inhibitor protein-like protein from soybean lacking inhibitory activity against endo- $\hat{\text{I}}^{\pm}$ -glucanase. <i>FEBS Journal</i> , 2011, 278, 1944-1954.	2.2	47
82	Crystal structures of open and closed forms of $\hat{\text{I}}^{\pm}$ -serine deaminase from <i>Salmonella typhimurium</i> – implications on substrate specificity and catalysis. <i>FEBS Journal</i> , 2011, 278, 2879-2891.	2.2	12
83	The N-terminal region of the bacterial DNA polymerase PolC features a pair of domains, both distantly related to domain $\hat{\text{I}}^{\pm}$ of the DNA polymerase III $\hat{\text{I}}^{\pm}$, subunit. <i>FEBS Journal</i> , 2011, 278, 3109-3118.	2.2	4
84	Mdm38 is a $\hat{\text{I}}^{\pm}$ -Like Receptor and Associates with the Protein Synthesis Machinery at the Inner Mitochondrial Membrane. <i>Traffic</i> , 2011, 12, 1457-1466.	1.3	30

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85	The DNA-binding domain of the Chd1 chromatin-remodelling enzyme contains SANT and SLIDE domains. <i>EMBO Journal</i> , 2011, 30, 2596-2609.	3.5	104
86	Determinants of laminin polymerization revealed by the structure of the $\alpha 5$ chain amino-terminal region. <i>EMBO Reports</i> , 2011, 12, 276-282.	2.0	60
87	Structure and mechanism of the uracil transporter UraA. <i>Nature</i> , 2011, 472, 243-246.	13.7	186
88	Structural Insight into the Mycobacterium tuberculosis Rv0020c Protein and Its Interaction with the PknB Kinase. <i>Structure</i> , 2011, 19, 1525-1534.	1.6	39
89	Protein function prediction: towards integration of similarity metrics. <i>Current Opinion in Structural Biology</i> , 2011, 21, 180-188.	2.6	42
90	Atomic resolution structure of EhpR: phenazine resistance in <i>Enterobacter agglomerans</i> Eh1087 follows principles of bleomycin/mitomycin C resistance in other bacteria. <i>BMC Structural Biology</i> , 2011, 11, 33.	2.3	4
91	Structural basis for a new tetracycline resistance mechanism relying on the TetX monooxygenase. <i>FEBS Letters</i> , 2011, 585, 1061-1066.	1.3	87
92	Hell's Gate globin I: An acid and thermostable bacterial hemoglobin resembling mammalian neuroglobin. <i>FEBS Letters</i> , 2011, 585, 3250-3258.	1.3	29
93	Zn-binding AZUL domain of human ubiquitin protein ligase Ube3A. <i>Journal of Biomolecular NMR</i> , 2011, 51, 185-190.	1.6	23
94	Structural Insights on Two Hypothetical Secretion Chaperones from <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Protein Journal</i> , 2011, 30, 324-333.	0.7	7
95	Solution NMR structure of Dsy0195 homodimer from <i>Desulfotobacterium hafniense</i> : first structure representative of the YabP domain family of proteins involved in spore coat assembly. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 175-179.	1.2	3
96	Cloning, expression, and physicochemical characterization of a new diheme cytochrome c from <i>Shewanella baltica</i> OS155. <i>Journal of Biological Inorganic Chemistry</i> , 2011, 16, 461-471.	1.1	17
97	Cloning, functional expression, biochemical characterization, and structural analysis of a haloalkane dehalogenase from <i>Plesiocystis pacifica</i> SIR-1. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1049-1060.	1.7	36
98	Crystal structures of <i>Burkholderia cenocepacia</i> dihydropteroate synthase in the apo-form and complexed with the product 7,8-dihydropteroate. <i>BMC Structural Biology</i> , 2011, 11, 21.	2.3	31
99	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. <i>Biology Direct</i> , 2011, 6, 38.	1.9	379
100	Structure of 2-oxo-3-deoxygalactonate kinase from <i>Klebsiella pneumoniae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 678-689.	2.5	4
101	Human Suv3 protein reveals unique features among SF2 helicases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 988-996.	2.5	13
102	Structural analysis of a putative family 32 carbohydrate-binding module from the <i>Streptococcus pneumoniae</i> enzyme EndoD. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 429-433.	0.7	7

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103	Structure of <i>Francisella tularensis</i> peptidyl-tRNA hydrolase. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 446-449.	0.7	20
104	Solution structure of an arsenate reductase-related protein, YffB, from <i>Brucella melitensis</i> , the etiological agent responsible for brucellosis. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1129-1136.	0.7	5
105	Solution-state NMR structure and biophysical characterization of zinc-substituted rubredoxin B (Rv3250c) from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1148-1153.	0.7	9
106	Structures of native and Fe-substituted SOD2 from <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1173-1178.	0.7	12
107	Structure of PA4019, a putative aromatic acid decarboxylase from <i>Pseudomonas aeruginosa</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1184-1188.	0.7	23
108	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
109	The 1.7 Å resolution structure of At2g44920, a pentapeptide-repeat protein in the thylakoid lumen of <i>Arabidopsis thaliana</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1480-1484.	0.7	9
110	Mapping the distribution of packing topologies within protein interiors shows predominant preference for specific packing motifs. BMC Bioinformatics, 2011, 12, 195.	1.2	26
111	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. BMC Evolutionary Biology, 2011, 11, 334.	3.2	9
112	Comparative analysis of two complete <i>Corynebacterium ulcerans</i> genomes and detection of candidate virulence factors. BMC Genomics, 2011, 12, 383.	1.2	85
113	Structure of the C-terminal heme-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
114	Crystal structure of HP0721, a novel secreted protein from <i>Helicobacter pylori</i> . Proteins: Structure, Function and Bioinformatics, 2011, 79, 1678-1681.	1.5	6
115	Crystal structure of a phenol-coupling P450 monooxygenase involved in teicoplanin biosynthesis. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1728-1738.	1.5	24
116	Solution structure of the protein lipocalin 12 from rat epididymis. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2316-2320.	1.5	3
117	Crystal structure of the catalytic domain of cholesterol-1- α -glucosyltransferase from <i>Helicobacter pylori</i> . Proteins: Structure, Function and Bioinformatics, 2011, 79, 2321-2326.	1.5	13
118	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
119	Structural analysis of CPF_2247, a novel β -amylase from <i>Clostridium perfringens</i> . Proteins: Structure, Function and Bioinformatics, 2011, 79, 2771-2777.	1.5	22
120	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	1.5	19

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121	Solution structure of the human HSPC280 protein. <i>Protein Science</i> , 2011, 20, 216-223.	3.1	7
122	Fic domain-catalyzed adenylation: Insight provided by the structural analysis of the type IV secretion system effector BepA. <i>Protein Science</i> , 2011, 20, 492-499.	3.1	50
123	Crystal structure of the bifunctional tRNA modification enzyme MnmC from <i>Escherichia coli</i> . <i>Protein Science</i> , 2011, 20, 1105-1113.	3.1	8
124	Intermolecular versus intramolecular interactions of the vinculin binding site 33 of talin. <i>Protein Science</i> , 2011, 20, 1471-1476.	3.1	9
126	Crystal structure of the read-through domain from bacteriophage Q β A1 protein. <i>Protein Science</i> , 2011, 20, 1707-1712.	3.1	24
127	A similarity matrix-based hybrid algorithm for the contact map overlaps problem. <i>Computers in Biology and Medicine</i> , 2011, 41, 247-252.	3.9	8
128	Structural Characterization of Three Novel Hydroxamate-Based Zinc Chelating Inhibitors of the <i>Clostridium botulinum</i> Serotype A Neurotoxin Light Chain Metalloprotease Reveals a Compact Binding Site Resulting from 60/70 Loop Flexibility. <i>Biochemistry</i> , 2011, 50, 4019-4028.	1.2	28
129	Use of secondary structure element information in drug design: polypharmacology and conserved motifs in protein-ligand binding and protein-protein interfaces. <i>Future Medicinal Chemistry</i> , 2011, 3, 699-708.	1.1	18
130	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. <i>Journal of Bacteriology</i> , 2011, 193, 6039-6056.	1.0	358
131	Protein Structures-based Neighborhood Analysis vs Preferential Interactions Between the Special Pairs of Amino acids?. <i>Journal of Biomolecular Structure and Dynamics</i> , 2011, 28, 629-632.	2.0	3
132	Asymmetric DNA recognition by the OcrAI endonuclease, an isoschizomer of BamHI. <i>Nucleic Acids Research</i> , 2011, 39, 712-719.	6.5	132
133	Structural insights into catalytic and substrate binding mechanisms of the strategic EndA nuclease from <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2011, 39, 2943-2953.	6.5	29
134	Crystal Structures of Bacterial Peptidoglycan Amidase AmpD and an Unprecedented Activation Mechanism. <i>Journal of Biological Chemistry</i> , 2011, 286, 31714-31722.	1.6	49
135	Structure of the Three N-Terminal Immunoglobulin Domains of the Highly Immunogenic Outer Capsid Protein from a T4-Like Bacteriophage. <i>Journal of Virology</i> , 2011, 85, 8141-8148.	1.5	64
136	Nuclear but Not Cytosolic Phosphoinositide 3-Kinase Beta Has an Essential Function in Cell Survival. <i>Molecular and Cellular Biology</i> , 2011, 31, 2122-2133.	1.1	72
137	The E3 Ubiquitin Ligase- and Protein Phosphatase 2A (PP2A)-binding Domains of the Alpha4 Protein Are Both Required for Alpha4 to Inhibit PP2A Degradation. <i>Journal of Biological Chemistry</i> , 2011, 286, 17665-17671.	1.6	40
138	<i>Hyaloperonospora arabidopsidis</i> ATR1 effector is a repeat protein with distributed recognition surfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13323-13328.	3.3	111
139	Characterization and crystal structure of the type IIG restriction endonuclease RM.BpuSI. <i>Nucleic Acids Research</i> , 2011, 39, 8223-8236.	6.5	31

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140	How the Virus Outsmarts the Host: Function and Structure of Cytomegalovirus MHC-I-Like Molecules in the Evasion of Natural Killer Cell Surveillance. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-12.	3.0	33
141	DNA intercalation without flipping in the specific Thalâ€“DNA complex. <i>Nucleic Acids Research</i> , 2011, 39, 744-754.	6.5	35
142	Prp8, the pivotal protein of the spliceosomal catalytic center, evolved from a retroelement-encoded reverse transcriptase. <i>Rna</i> , 2011, 17, 799-808.	1.6	78
143	Structure of the Periplasmic Stress Response Protein CpxP. <i>Journal of Bacteriology</i> , 2011, 193, 2149-2157.	1.0	41
144	KefF, the Regulatory Subunit of the Potassium Efflux System KefC, Shows Quinone Oxidoreductase Activity. <i>Journal of Bacteriology</i> , 2011, 193, 4925-4932.	1.0	16
145	Structural basis for histone H3 Lys 27 demethylation by UTX/KDM6A. <i>Genes and Development</i> , 2011, 25, 2266-2277.	2.7	124
146	A highly conserved protein of unknown function in <i>Sinorhizobium meliloti</i> affects sRNA regulation similar to Hfq. <i>Nucleic Acids Research</i> , 2011, 39, 4691-4708.	6.5	67
147	Structure and Function of the N-terminal Nucleolin Binding Domain of Nuclear Valosin-containing Protein-like 2 (NVL2) Harboring a Nucleolar Localization Signal. <i>Journal of Biological Chemistry</i> , 2011, 286, 21732-21741.	1.6	19
148	Orphan Macrodomein Protein (Human C6orf130) Is an O-Acyl-ADP-ribose Deacylase. <i>Journal of Biological Chemistry</i> , 2011, 286, 35955-35965.	1.6	65
149	On a benderâ€“BARs, ESCRTs, COPs, and finally getting your coat. <i>Journal of Cell Biology</i> , 2011, 193, 963-972.	2.3	88
150	Structure and function of the interacting domains of Spire and Fmn-family formins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11884-11889.	3.3	83
151	Solution Structure of Tandem SH2 Domains from Spt6 Protein and Their Binding to the Phosphorylated RNA Polymerase II C-terminal Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 29218-29226.	1.6	36
152	Structural models of TREK channels and their gating mechanism. <i>Channels</i> , 2011, 5, 23-33.	1.5	15
153	The Crystal Structure of a Self-Activating G Protein Î± Subunit Reveals Its Distinct Mechanism of Signal Initiation. <i>Science Signaling</i> , 2011, 4, ra8.	1.6	115
154	Structure of <i>Streptomyces</i> Maltosyltransferase GlgE, a Homologue of a Genetically Validated Anti-tuberculosis Target*. <i>Journal of Biological Chemistry</i> , 2011, 286, 38298-38310.	1.6	49
155	Fold and Function of the InlB B-repeat. <i>Journal of Biological Chemistry</i> , 2011, 286, 15496-15506.	1.6	38
156	Unique scorpion toxin with a putative ancestral fold provides insight into evolution of the inhibitor cystine knot motif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10478-10483.	3.3	96
157	The Structure of Sucrose Synthase-1 from <i>Arabidopsis thaliana</i> and Its Functional Implications. <i>Journal of Biological Chemistry</i> , 2011, 286, 36108-36118.	1.6	79

#	ARTICLE	IF	CITATIONS
158	Crystal Structure of the Outer Membrane Protein RcsF, a New Substrate for the Periplasmic Protein-disulfide Isomerase DsbC. <i>Journal of Biological Chemistry</i> , 2011, 286, 16734-16742.	1.6	61
159	Structures of Phytophthora RXLR Effector Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 35834-35842.	1.6	178
160	The Crystal Structure and Mechanism of an Unusual Oxidoreductase, GilR, Involved in Gilvocarcin V Biosynthesis. <i>Journal of Biological Chemistry</i> , 2011, 286, 23533-23543.	1.6	21
161	Structural Basis of Outer Membrane Protein Biogenesis in Bacteria. <i>Journal of Biological Chemistry</i> , 2011, 286, 27792-27803.	1.6	80
162	The Rickettsia Surface Cell Antigen 4 Applies Mimicry to Bind to and Activate Vinculin. <i>Journal of Biological Chemistry</i> , 2011, 286, 35096-35103.	1.6	44
163	Structural and Biochemical Characterization of the Salicylyl-acyltransferase SsfX3 from a Tetracycline Biosynthetic Pathway. <i>Journal of Biological Chemistry</i> , 2011, 286, 41539-41551.	1.6	14
164	Processing the Interspecies Quorum-sensing Signal Autoinducer-2 (AI-2). <i>Journal of Biological Chemistry</i> , 2011, 286, 18331-18343.	1.6	55
165	Fructose 1-Phosphate Is the Preferred Effector of the Metabolic Regulator Cra of <i>Pseudomonas putida</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 9351-9359.	1.6	23
166	Structural Determinants of Discrimination of NAD ⁺ from NADH in Yeast Mitochondrial NADH Kinase Pos5. <i>Journal of Biological Chemistry</i> , 2011, 286, 29984-29992.	1.6	16
167	Sneak peak at galactocerebrosidase, Krabbe disease's lysosomal hydrolase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15017-15018.	3.3	4
168	The Virulence Factor PEB4 (Cj0596) and the Periplasmic Protein Cj1289 Are Two Structurally Related SurA-like Chaperones in the Human Pathogen <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 21254-21265.	1.6	33
169	Conservation of the C-type lectin fold for massive sequence variation in a <i>Treponema</i> diversity-generating retroelement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14649-14653.	3.3	39
170	Biochemical Studies and Ligand-bound Structures of Biphenyl Dehydrogenase from <i>Pandoraea pnomenusa</i> Strain B-356 Reveal a Basis for Broad Specificity of the Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 37011-37022.	1.6	29
171	Remote control of regioselectivity in acyl-acyl carrier protein-desaturases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16594-16599.	3.3	59
172	Molecular Basis of 1,6-Anhydro Bond Cleavage and Phosphoryl Transfer by <i>Pseudomonas aeruginosa</i> 1,6-Anhydro-N-acetylmuramic Acid Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 12283-12291.	1.6	24
173	Atomic Resolution X-ray Structure of the Substrate Recognition Domain of Higher Plant Ribulose-bisphosphate Carboxylase/Oxygenase (Rubisco) Activase. <i>Journal of Biological Chemistry</i> , 2011, 286, 35683-35688.	1.6	33
174	Structure of the protein core of the glypican Dally-like and localization of a region important for hedgehog signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13112-13117.	3.3	67
175	Crystal Structure of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Csn2 Protein Revealed Ca ²⁺ -dependent Double-stranded DNA Binding Activity*. <i>Journal of Biological Chemistry</i> , 2011, 286, 30759-30768.	1.6	49

#	ARTICLE	IF	CITATIONS
176	Recognition of the F&H motif by the Lowe syndrome protein OCRL. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 789-795.	3.6	37
177	Structure-Based Modification of a <i>Clostridium difficile</i> -Targeting Endolysin Affects Activity and Host Range. <i>Journal of Bacteriology</i> , 2011, 193, 5477-5486.	1.0	92
178	A Structural Model for Binding of the Serine-Rich Repeat Adhesin GspB to Host Carbohydrate Receptors. <i>PLoS Pathogens</i> , 2011, 7, e1002112.	2.1	75
179	Structural and Functional Studies on the Interaction of GspC and GspD in the Type II Secretion System. <i>PLoS Pathogens</i> , 2011, 7, e1002228.	2.1	83
180	Towards a Structural Comprehension of Bacterial Type VI Secretion Systems: Characterization of the TssJ-TssM Complex of an <i>Escherichia coli</i> Pathovar. <i>PLoS Pathogens</i> , 2011, 7, e1002386.	2.1	132
181	PDBpaint, a visualization webservice to tag protein structures with sequence annotations. <i>Bioinformatics</i> , 2011, 27, 2605-2606.	1.8	3
182	Distinct Single Amino Acid Replacements in the Control of Virulence Regulator Protein Differentially Impact Streptococcal Pathogenesis. <i>PLoS Pathogens</i> , 2011, 7, e1002311.	2.1	42
183	Solution NMR Structure of Hypothetical Protein CV_2116 Encoded by a Viral Prophage Element in <i>Chromobacterium violaceum</i> . <i>International Journal of Molecular Sciences</i> , 2012, 13, 7354-7364.	1.8	1
184	Structural Analysis of Hypothetical Proteins from <i>Helicobacter pylori</i> : An Approach to Estimate Functions of Unknown or Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7109-7137.	1.8	17
185	Crystal structure of the enzyme CapF of <i>Staphylococcus aureus</i> reveals a unique architecture composed of two functional domains. <i>Biochemical Journal</i> , 2012, 443, 671-680.	1.7	12
186	The Ebola Virus Interferon Antagonist VP24 Directly Binds STAT1 and Has a Novel, Pyramidal Fold. <i>PLoS Pathogens</i> , 2012, 8, e1002550.	2.1	128
187	X-ray structure of the fourth type of archaeal tRNA splicing endonuclease: insights into the evolution of a novel three-unit composition and a unique loop involved in broad substrate specificity. <i>Nucleic Acids Research</i> , 2012, 40, 10554-10566.	6.5	25
188	The Interdomain Linker of AAV-2 Rep68 Is an Integral Part of Its Oligomerization Domain: Role of a Conserved SF3 Helicase Residue in Oligomerization. <i>PLoS Pathogens</i> , 2012, 8, e1002764.	2.1	22
189	Molecular docking and ex vivo pharmacological evaluation of constituents of the leaves of <i>Cleistanthus collinus</i> (Roxb.) (Euphorbiaceae). <i>Indian Journal of Pharmacology</i> , 2012, 44, 197.	0.4	15
190	Structure and Functional Analysis of the RNA- and Viral Phosphoprotein-Binding Domain of Respiratory Syncytial Virus M2-1 Protein. <i>PLoS Pathogens</i> , 2012, 8, e1002734.	2.1	70
191	Structural conservation of an ancient tRNA sensor in eukaryotic glutamyl-tRNA synthetase. <i>Nucleic Acids Research</i> , 2012, 40, 3723-3731.	6.5	14
192	Structure of the <i>Plasmodium</i> 6-cysteine s48/45 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6692-6697.	3.3	69
193	Structural Basis for Paxillin Binding and Focal Adhesion Targeting of β -Parvin. <i>Journal of Biological Chemistry</i> , 2012, 287, 32566-32577.	1.6	33

#	ARTICLE	IF	CITATIONS
194	Mutational and Structural Analysis of I - N -Carbamoylase Reveals New Insights into a Peptidase M20/M25/M40 Family Member. <i>Journal of Bacteriology</i> , 2012, 194, 5759-5768.	1.0	23
195	MIPModDB: a central resource for the superfamily of major intrinsic proteins. <i>Nucleic Acids Research</i> , 2012, 40, D362-D369.	6.5	33
196	SPRITE and ASSAM: web servers for side chain 3D-motif searching in protein structures. <i>Nucleic Acids Research</i> , 2012, 40, W380-W386.	6.5	45
197	Crystal Structure of the VgrG1 Actin Cross-linking Domain of the <i>Vibrio cholerae</i> Type VI Secretion System. <i>Journal of Biological Chemistry</i> , 2012, 287, 38190-38199.	1.6	60
198	Structural Insight into the Ion-Exchange Mechanism of the Sodium/Calcium Exchanger. <i>Science</i> , 2012, 335, 686-690.	6.0	228
199	Structural study of MCP1P1 N-terminal conserved domain reveals a PIN-like RNase. <i>Nucleic Acids Research</i> , 2012, 40, 6957-6965.	6.5	73
200	Structural and mechanistic insight into N-glycan processing by endo- β -mannosidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 781-786.	3.3	74
201	Dynamic, Ligand-dependent Conformational Change Triggers Reaction of Ribose-1,5-bisphosphate Isomerase from <i>Thermococcus kodakarensis</i> KOD1. <i>Journal of Biological Chemistry</i> , 2012, 287, 20784-20796.	1.6	22
202	Interaction of MxiG with the cytosolic complex of the type III secretion system controls <i>Shigella</i> virulence. <i>FASEB Journal</i> , 2012, 26, 1717-1726.	0.2	20
203	Crystal Structure of <i>Escherichia coli</i> Diaminopropionate Ammonia-lyase Reveals Mechanism of Enzyme Activation and Catalysis. <i>Journal of Biological Chemistry</i> , 2012, 287, 20369-20381.	1.6	15
204	Solution Structure of IseA, an Inhibitor Protein of dl-Endopeptidases from <i>Bacillus subtilis</i> , Reveals a Novel Fold with a Characteristic Inhibitory Loop. <i>Journal of Biological Chemistry</i> , 2012, 287, 44736-44748.	1.6	13
205	Structural bioinformatics of the human spliceosomal proteome. <i>Nucleic Acids Research</i> , 2012, 40, 7046-7065.	6.5	40
206	Characterization of a <i>Phanerochaete chrysosporium</i> Glutathione Transferase Reveals a Novel Structural and Functional Class with Ligandin Properties. <i>Journal of Biological Chemistry</i> , 2012, 287, 39001-39011.	1.6	33
207	The C-Terminal Domain of the Virulence Factor MgtC Is a Divergent ACT Domain. <i>Journal of Bacteriology</i> , 2012, 194, 6255-6263.	1.0	8
208	Crystal structure of the DNA-bound VapBC2 antitoxin/toxin pair from <i>Rickettsia felis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 3245-3258.	6.5	51
209	Structure of the Cytoplasmic Region of PelD, a Degenerate Diguanylate Cyclase Receptor That Regulates Exopolysaccharide Production in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 23582-23593.	1.6	101
210	Recent Advances in Thymidine Kinase 2 (TK2) Inhibitors and New Perspectives for Potential Applications. <i>Current Pharmaceutical Design</i> , 2012, 18, 2981-2994.	0.9	15
211	Combinatorial readout of unmodified H3R2 and acetylated H3K14 by the tandem PHD finger of MOZ reveals a regulatory mechanism for HOXA9 transcription. <i>Genes and Development</i> , 2012, 26, 1376-1391.	2.7	99

#	ARTICLE	IF	CITATIONS
212	Divergence of multimodular polyketide synthases revealed by a didomain structure. <i>Nature Chemical Biology</i> , 2012, 8, 615-621.	3.9	66
213	Identification of Novel Positive-Strand RNA Viruses by Metagenomic Analysis of Archaea-Dominated Yellowstone Hot Springs. <i>Journal of Virology</i> , 2012, 86, 5562-5573.	1.5	107
214	Structural basis of fibrillar collagen trimerization and related genetic disorders. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1031-1036.	3.6	79
215	Crystal structure of LpxK, the 4â€²-kinase of lipid A biosynthesis and atypical P-loop kinase functioning at the membrane interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12956-12961.	3.3	17
216	Structural and Biochemical Characterization of Human Mitochondrial Branched-chain Î±-Ketoacid Dehydrogenase Phosphatase. <i>Journal of Biological Chemistry</i> , 2012, 287, 9178-9192.	1.6	19
217	The First Structure of Polarity Suppression Protein, Psu from Enterobacteria Phage P4, Reveals a Novel Fold and a Knotted Dimer. <i>Journal of Biological Chemistry</i> , 2012, 287, 44667-44675.	1.6	19
218	Crimeanâ€”Congo hemorrhagic fever virus nucleoprotein reveals endonuclease activity in bunyaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5046-5051.	3.3	97
219	Structure of RPE65 isomerase in a lipidic matrix reveals roles for phospholipids and iron in catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2747-56.	3.3	58
220	Insights into Duffy Binding-like Domains through the Crystal Structure and Function of the Merozoite Surface Protein MSPDBL2 from <i>Plasmodium falciparum</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 32922-32939.	1.6	34
221	The Zinc Regulated Antivirulence Pathway of <i>Salmonella</i> Is a Multiprotein Immunoglobulin Adhesion System. <i>Journal of Biological Chemistry</i> , 2012, 287, 32324-32337.	1.6	11
222	Structure of Factor H-binding Protein B (FhbB) of the Periopathogen, <i>Treponema denticola</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 12715-12722.	1.6	40
223	Structure of C-terminal Tandem BRCT Repeats of Rtt107 Protein Reveals Critical Role in Interaction with Phosphorylated Histone H2A during DNA Damage Repair. <i>Journal of Biological Chemistry</i> , 2012, 287, 9137-9146.	1.6	46
224	Structure and Conservation of the Periplasmic Targeting Factor Tic22 Protein from Plants and Cyanobacteria. <i>Journal of Biological Chemistry</i> , 2012, 287, 24164-24173.	1.6	33
225	Structural Basis for Outer Membrane Sugar Uptake in Pseudomonads. <i>Journal of Biological Chemistry</i> , 2012, 287, 41044-41052.	1.6	39
226	Crystal Structure of the Acyltransferase Domain of the Iterative Polyketide Synthase in Eneidyne Biosynthesis. <i>Journal of Biological Chemistry</i> , 2012, 287, 23203-23215.	1.6	38
227	The Extracellular Protein Factor Epf from <i>Streptococcus pyogenes</i> Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. <i>Journal of Biological Chemistry</i> , 2012, 287, 38178-38189.	1.6	18
228	Biochemical and Structural Studies of Uncharacterized Protein PA0743 from <i>Pseudomonas aeruginosa</i> Revealed NAD ⁺ -dependent L-Serine Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2012, 287, 1874-1883.	1.6	23
229	Structure of Sputnik, a virophage, at 3.5-Å... resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18431-18436.	3.3	73

#	ARTICLE	IF	CITATIONS
230	Structural and mechanistic analysis of the membrane-embedded glycosyltransferase WaaA required for lipopolysaccharide synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6253-6258.	3.3	45
231	The p53 cofactor Strap exhibits an unexpected TPR motif and oligonucleotide-binding (OB) fold structure. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3778-3783.	3.3	17
232	PocketAnnotate: towards site-based function annotation. Nucleic Acids Research, 2012, 40, W400-W408.	6.5	18
233	Structures of the PelD Cyclic Diguanylate Effector Involved in Pellicle Formation in <i>Pseudomonas aeruginosa</i> PAO1. Journal of Biological Chemistry, 2012, 287, 30191-30204.	1.6	37
234	Mitochondrial ribonuclease P structure provides insight into the evolution of catalytic strategies for precursor-tRNA 5' processing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16149-16154.	3.3	110
235	Structure and Interactions of the Cytoplasmic Domain of the <i>Yersinia</i> Type III Secretion Protein YscD. Journal of Bacteriology, 2012, 194, 5949-5958.	1.0	18
236	Yeast Irc6p is a novel type of conserved clathrin coat accessory factor related to small G proteins. Molecular Biology of the Cell, 2012, 23, 4416-4429.	0.9	9
237	Divergence and Convergence in Enzyme Evolution. Journal of Biological Chemistry, 2012, 287, 21-28.	1.6	140
238	Crystal structure of RlmM, the 2'-O-ribose methyltransferase for C2498 of <i>Escherichia coli</i> 23S rRNA. Nucleic Acids Research, 2012, 40, 10507-10520.	6.5	13
239	Structure of androcam supports specialized interactions with myosin VI. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13290-13295.	3.3	4
240	CSA: comprehensive comparison of pairwise protein structure alignments. Nucleic Acids Research, 2012, 40, W303-W309.	6.5	17
241	Structure of the phage TP901-1 1.8 MDa baseplate suggests an alternative host adhesion mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8954-8958.	3.3	121
242	Structure and assembly of a paramyxovirus matrix protein. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13996-14000.	3.3	126
243	<i>Paramecium bursaria</i> Chlorella Virus 1 Encodes a Polyamine Acetyltransferase. Journal of Biological Chemistry, 2012, 287, 9547-9551.	1.6	12
244	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
245	Structural Insights into the <i>Pseudomonas aeruginosa</i> Type VI Virulence Effector Tse1 Bacteriolysis and Self-protection Mechanisms. Journal of Biological Chemistry, 2012, 287, 26911-26920.	1.6	43
246	Structural Characterization of a Conserved, Calcium-Dependent Periplasmic Protease from <i>Legionella pneumophila</i> . Journal of Bacteriology, 2012, 194, 4415-4425.	1.0	48
247	High-level secretion of recombinant monomeric murine and human single-chain Fv antibodies from <i>Drosophila</i> S2 cells. Protein Engineering, Design and Selection, 2012, 25, 59-66.	1.0	31

#	ARTICLE	IF	CITATIONS
248	Structural Determinants of the Î²-Selectivity of a Bacterial Aminotransferase. <i>Journal of Biological Chemistry</i> , 2012, 287, 28495-28502.	1.6	30
249	The N-terminus of the human RecQL4 helicase is a homeodomain-like DNA interaction motif. <i>Nucleic Acids Research</i> , 2012, 40, 8309-8324.	6.5	35
250	A CC-SAM, for Coiled Coilâ€™Sterile Î± Motif, Domain Targets the Scaffold KSR-1 to Specific Sites in the Plasma Membrane. <i>Science Signaling</i> , 2012, 5, ra94.	1.6	26
251	RWD domain: a recurring module in kinetochore architecture shown by a Ctf19â€™Mcm21 complex structure. <i>EMBO Reports</i> , 2012, 13, 216-222.	2.0	62
252	Bacterial Cell Division Regulation by Ser/Thr Kinases: A Structural Perspective. <i>Current Protein and Peptide Science</i> , 2012, 13, 756-766.	0.7	52
253	Functional Characterization of Two M42 Aminopeptidases Erroneously Annotated as Cellulases. <i>PLoS ONE</i> , 2012, 7, e50639.	1.1	13
254	Study of Cnidarian-Algal Symbiosis in the â€™Omicâ€™Age. <i>Biological Bulletin</i> , 2012, 223, 44-65.	0.7	82
255	Insect Genomics. , 2012, , 1-29.		0
256	Crystallographic analysis of the conserved C-terminal domain of transcription factor Cdc73 from <i>Saccharomyces cerevisiae</i> reveals a GTPase-like fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 953-959.	2.5	13
257	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1140-1151.	2.5	14
258	Various cross-reactivity of the grass pollen group 4 allergens: crystallographic study of the Bermuda grass isoallergen Cyn d 4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1303-1310.	2.5	7
259	Crystallization, dehydration and experimental phasing of WbdD, a bifunctional kinase and methyltransferase from <i>Escherichia coli</i> O9a. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1371-1379.	2.5	5
260	Structure of the starch-debranching enzyme barley limit dextrinase reveals homology of the N-terminal domain to CBM21. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1008-1012.	0.7	22
261	Crystal structure of the glycosyltransferase SnogD from the biosynthetic pathway of nogalamycin in <i>Streptomyces f nogalater</i> . <i>FEBS Journal</i> , 2012, 279, 3251-3263.	2.2	17
262	Structure of WbdD: a bifunctional kinase and methyltransferase that regulates the chain length of the O antigen in <i>Escherichia coli</i> O9a. <i>Molecular Microbiology</i> , 2012, 86, 730-742.	1.2	29
263	Determinants of substrate specificity and biochemical properties of the snâ€™glycerolâ€™phosphate ATP binding cassette transporter (UgpBâ€™AEC ₂) of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2012, 86, 908-920.	1.2	30
264	Structural insight into the type-II mitochondrial NADH dehydrogenases. <i>Nature</i> , 2012, 491, 478-482.	13.7	105
265	Structural and Functional Characterization of Bc28.1, Major Erythrocyte-binding Protein from <i>Babesia canis</i> Merozoite Surface. <i>Journal of Biological Chemistry</i> , 2012, 287, 9495-9508.	1.6	14

#	ARTICLE	IF	CITATIONS
266	Structural basis for the activity of a cytoplasmic RNA terminal uridylyl transferase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 782-787.	3.6	47
267	Structure of human POFUT2: insights into thrombospondin type 1 repeat fold and α -fucosylation. <i>EMBO Journal</i> , 2012, 31, 3183-3197.	3.5	59
268	The First Structure of a Lantibiotic Immunity Protein, Spal from <i>Bacillus subtilis</i> , Reveals a Novel Fold. <i>Journal of Biological Chemistry</i> , 2012, 287, 35286-35298.	1.6	20
269	Crystal Structure and RNA Binding Properties of the RNA Recognition Motif (RRM) and AlkB Domains in Human AlkB Homolog 8 (ABH8), an Enzyme Catalyzing tRNA Hypermodification. <i>Journal of Biological Chemistry</i> , 2012, 287, 2130-2143.	1.6	66
270	Crystal Structure of <i>Brucella abortus</i> Deoxyxylulose-5-phosphate Reductoisomerase-like (DRL) Enzyme Involved in Isoprenoid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2012, 287, 15803-15809.	1.6	9
271	Structural basis of mouse cytomegalovirus m152/gp40 interaction with RAE1 β reveals a paradigm for MHC/MHC interaction in immune evasion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3578-87.	3.3	30
272	Structural basis for Arf6-MKLP1 complex formation on the Flemming body responsible for cytokinesis. <i>EMBO Journal</i> , 2012, 31, 2590-2603.	3.5	55
273	Structural Basis of Functional Group Activation by Sulfotransferases in Complex Metabolic Pathways. <i>ACS Chemical Biology</i> , 2012, 7, 1994-2003.	1.6	34
274	A Structural Basis for the Assembly and Functions of a Viral Polymer that Inactivates Multiple Tumor Suppressors. <i>Cell</i> , 2012, 151, 304-319.	13.5	73
275	Atomic resolution structure of human β -tubulin acetyltransferase bound to acetyl-CoA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19649-19654.	3.3	42
276	Architecture of the Nuclease Module of the Yeast Ccr4-Not Complex: the Not1-Caf1-Ccr4 Interaction. <i>Molecular Cell</i> , 2012, 48, 207-218.	4.5	131
277	The crystal structure of the Rv0301-Rv0300 VapBC toxin-antitoxin complex from <i>M. tuberculosis</i> reveals a Mg ²⁺ ion in the active site and a putative RNA-binding site. <i>Protein Science</i> , 2012, 21, 1754-1767.	3.1	54
278	Crystal structure of NirD, the small subunit of the nitrite reductase NirbD from <i>Mycobacterium tuberculosis</i> at 2.0 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2799-2803.	1.5	9
279	Crystal structure of the <i>Campylobacter jejuni</i> Cj0090 protein reveals a novel variant of the immunoglobulin fold among bacterial lipoproteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2804-2809.	1.5	2
280	NMR structure note: repetitive domain of aciniform spidroin 1 from <i>Nephila antipodiana</i> . <i>Journal of Biomolecular NMR</i> , 2012, 54, 415-420.	1.6	22
281	Solution NMR structure of Alr2454 from <i>Nostoc</i> sp. PCC 7120, the first structural representative of Pfam domain family PF11267. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 171-176.	1.2	3
282	Solution NMR and X-ray crystal structures of <i>Pseudomonas syringae</i> Pspto_3016 from protein domain family PF04237 (DUF419) adopt a double wing-DNA binding motif. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 155-162.	1.2	9
283	Structure of the GcpE (IspG)-MEcPP complex from <i>Thermus thermophilus</i> . <i>FEBS Letters</i> , 2012, 586, 3452-3457.	1.3	19

#	ARTICLE	IF	CITATIONS
284	Low-resolution structure of <i>Drosophila</i> translin. FEBS Open Bio, 2012, 2, 37-46.	1.0	6
285	Crystal structure and location of gp131 in the bacteriophage phiKZ virion. Virology, 2012, 434, 257-264.	1.1	14
286	Crystal structure of folliculin reveals a hidDenn function in genetically inherited renal cancer. Open Biology, 2012, 2, 120071.	1.5	97
287	Structural insights into the biogenesis and biofilm formation by the <i>Escherichia coli</i> common pilus. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3950-3955.	3.3	55
288	Structural basis of inhibition of <i>Mycobacterium tuberculosis</i> DprE1 by benzothiazinone inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11354-11359.	3.3	194
289	Solution NMR Structure of Yeast Succinate Dehydrogenase Flavinylation Factor Sdh5 Reveals a Putative Sdh1 Binding Site. Biochemistry, 2012, 51, 8475-8477.	1.2	29
290	Crystal structures of STING protein reveal basis for recognition of cyclic di-GMP. Nature Structural and Molecular Biology, 2012, 19, 725-727.	3.6	184
291	Predicting Ligand Binding Residues and Functional Sites Using Multipositional Correlations with Graph Theoretic Clustering and Kernel CCA. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 992-1001.	1.9	11
292	Helical Repeat Structure of Apoptosis Inhibitor 5 Reveals Protein-Protein Interaction Modules. Journal of Biological Chemistry, 2012, 287, 10727-10737.	1.6	33
293	Structural and Functional Characterization of the Kindlin-1 Pleckstrin Homology Domain. Journal of Biological Chemistry, 2012, 287, 43246-43261.	1.6	27
294	Structural studies of <i>Enterococcus faecalis</i> methionine aminopeptidase and design of microbe specific 2,2'-bipyridine based inhibitors. MedChemComm, 2012, 3, 1406.	3.5	18
295	Mechanism and Diversity of the Erythromycin Esterase Family of Enzymes. Biochemistry, 2012, 51, 1740-1751.	1.2	83
296	Structural Studies of the Spinosyn Rhamnosyltransferase, SpnG. Biochemistry, 2012, 51, 1213-1222.	1.2	22
297	Kinetic Stability of the Streptavidin-Biotin Interaction Enhanced in the Gas Phase. Journal of the American Chemical Society, 2012, 134, 16586-16596.	6.6	22
298	Substrate Specificity, Substrate Channeling, and Allostery in BphJ: An Acylating Aldehyde Dehydrogenase Associated with the Pyruvate Aldolase BphI. Biochemistry, 2012, 51, 4558-4567.	1.2	13
299	Structural and Functional Analysis of the NLRP4 Pyrin Domain. Biochemistry, 2012, 51, 7330-7341.	1.2	42
300	Structure and Catalytic Mechanism of <i>N</i> ⁵ , <i>N</i> ¹⁰ -Methenyl-tetrahydromethanopterin Cyclohydrolase. Biochemistry, 2012, 51, 8435-8443.	1.2	12
301	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

#	ARTICLE	IF	CITATIONS
302	Conserved Signal Peptide Recognition Systems across the Prokaryotic Domains. <i>Biochemistry</i> , 2012, 51, 1678-1686.	1.2	25
303	Mapping the Active Site Helix-to-Strand Conversion of CxxxxC Peroxiredoxin Q Enzymes. <i>Biochemistry</i> , 2012, 51, 7638-7650.	1.2	29
304	The Structure of the BfrBâ€“Bfd Complex Reveals Proteinâ€“Protein Interactions Enabling Iron Release from Bacterioferritin. <i>Journal of the American Chemical Society</i> , 2012, 134, 13470-13481.	6.6	71
305	Further Evidence for the Likely Completeness of the Library of Solved Single Domain Protein Structures. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6654-6664.	1.2	31
306	Solution Structure of Decorin-Binding Protein A from <i>Borrelia burgdorferi</i> . <i>Biochemistry</i> , 2012, 51, 8353-8362.	1.2	19
307	Crystal Structure and Functional Analysis of JMJD5 Indicate an Alternate Specificity and Function. <i>Molecular and Cellular Biology</i> , 2012, 32, 4044-4052.	1.1	59
308	Nuclear Magnetic Resonance Structure and Dynamics of the Response Regulator Sma0114 from <i>Sinorhizobium meliloti</i> . <i>Biochemistry</i> , 2012, 51, 6932-6941.	1.2	13
309	Structural Insight into Recognition of Methylated Histone Tails by Retinoblastoma-binding Protein 1. <i>Journal of Biological Chemistry</i> , 2012, 287, 8531-8540.	1.6	31
310	Structural Basis for Sequence-Specific Recognition of DNA by TAL Effectors. <i>Science</i> , 2012, 335, 720-723.	6.0	528
311	Crystal Structure of Human ADP-ribose Transferase ARTD15/PARP16 Reveals a Novel Putative Regulatory Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 24077-24081.	1.6	23
312	A Helical Conotoxin from <i>Conus imperialis</i> Has a Novel Cysteine Framework and Defines a New Superfamily. <i>Journal of Biological Chemistry</i> , 2012, 287, 14973-14983.	1.6	34
313	The structural basis for the sensing and binding of cyclic di-GMP by STING. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 728-730.	3.6	178
314	Quality assessment of protein model-structures based on structural and functional similarities. <i>BMC Bioinformatics</i> , 2012, 13, 242.	1.2	11
315	Identification of a Ubiquitin-Binding Structure in the S-Locus F-Box Protein Controlling S-RNase-Based Self-Incompatibility. <i>Journal of Genetics and Genomics</i> , 2012, 39, 93-102.	1.7	12
316	Structural Analysis of Chi1 Chitinase from Yen-Tc: The Multisubunit Insecticidal ABC Toxin Complex of <i>Yersinia entomophaga</i> . <i>Journal of Molecular Biology</i> , 2012, 415, 359-371.	2.0	61
317	The Structure and Enzymatic Properties of a Novel RNase II Family Enzyme from <i>Deinococcus radiodurans</i> . <i>Journal of Molecular Biology</i> , 2012, 415, 547-559.	2.0	6
318	Characterization of the Chitinolytic Machinery of <i>Enterococcus faecalis</i> V583 and High-Resolution Structure of Its Oxidative CBM33 Enzyme. <i>Journal of Molecular Biology</i> , 2012, 416, 239-254.	2.0	128
319	Glutathione Biosynthesis in Bacteria by Bifunctional GshF Is Driven by a Modular Structure Featuring a Novel Hybrid ATP-Grasp Fold. <i>Journal of Molecular Biology</i> , 2012, 416, 486-494.	2.0	23

#	ARTICLE	IF	CITATIONS
320	Structural, Bioinformatic, and In Vivo Analyses of Two <i>Treponema pallidum</i> Lipoproteins Reveal a Unique TRAP Transporter. <i>Journal of Molecular Biology</i> , 2012, 416, 678-696.	2.0	30
321	The Structures of Coiled-Coil Domains from Type III Secretion System Translocators Reveal Homology to Pore-Forming Toxins. <i>Journal of Molecular Biology</i> , 2012, 417, 395-405.	2.0	63
322	Antifreeze Protein from Freeze-Tolerant Grass Has a Beta-Roll Fold with an Irregularly Structured Ice-Binding Site. <i>Journal of Molecular Biology</i> , 2012, 416, 713-724.	2.0	120
323	Crystal Structure of Bifunctional Aldos-2-Ulose Dehydratase/Isomerase from <i>Phanerochaete chrysosporium</i> with the Reaction Intermediate Ascopyrone M. <i>Journal of Molecular Biology</i> , 2012, 417, 279-293.	2.0	5
324	The Structure of Subunit E of the <i>Pyrococcus horikoshii</i> OT3 A-ATP Synthase Gives Insight into the Elasticity of the Peripheral Stalk. <i>Journal of Molecular Biology</i> , 2012, 420, 155-163.	2.0	14
325	Structure of the Sensor Domain of <i>Mycobacterium tuberculosis</i> PknH Receptor Kinase Reveals a Conserved Binding Cleft. <i>Journal of Molecular Biology</i> , 2012, 422, 488-494.	2.0	18
326	Structural Basis for Telomerase RNA Recognition and RNP Assembly by the Holoenzyme La Family Protein p65. <i>Molecular Cell</i> , 2012, 47, 16-26.	4.5	94
327	Crystal structure of <i>Apis mellifera</i> OBP14, a C-minus odorant-binding protein, and its complexes with odorant molecules. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 41-50.	1.2	135
328	The Dendritic Cell Receptor Clec9A Binds Damaged Cells via Exposed Actin Filaments. <i>Immunity</i> , 2012, 36, 646-657.	6.6	272
329	Crystal structure of a mono- and diacylglycerol lipase from <i>Malassezia globosa</i> reveals a novel lid conformation and insights into the substrate specificity. <i>Journal of Structural Biology</i> , 2012, 178, 363-369.	1.3	59
330	The crystal structure of the CRISPR-associated protein Csn2 from <i>Streptococcus agalactiae</i> . <i>Journal of Structural Biology</i> , 2012, 178, 350-362.	1.3	24
331	The structure of monoacylglycerol lipase from <i>Bacillus</i> sp. H257 reveals unexpected conservation of the cap architecture between bacterial and human enzymes. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2012, 1821, 1012-1021.	1.2	40
332	Mapping the <i>Anopheles gambiae</i> Odorant Binding Protein 1 (AgamOBP1) using modeling techniques, site directed mutagenesis, circular dichroism and ligand binding assays. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 947-953.	1.1	13
333	The structure of putative N-acetyl glutamate kinase from <i>Thermus thermophilus</i> reveals an intermediate active site conformation of the enzyme. <i>Biochemical and Biophysical Research Communications</i> , 2012, 420, 692-697.	1.0	12
334	CENP-T-W-S-X Forms a Unique Centromeric Chromatin Structure with a Histone-like Fold. <i>Cell</i> , 2012, 148, 487-501.	13.5	229
335	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. <i>Cell</i> , 2012, 149, 1607-1621.	13.5	478
336	Structure of a Peptidoglycan Amidase Effector Targeted to Gram-Negative Bacteria by the Type VI Secretion System. <i>Cell Reports</i> , 2012, 1, 656-664.	2.9	90
337	Structure and function of the transketolase from <i>Mycobacterium tuberculosis</i> and comparison with the human enzyme. <i>Open Biology</i> , 2012, 2, 110026.	1.5	35

#	ARTICLE	IF	CITATIONS
338	Structure of a Proteasome Pba1-Pba2 Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 37371-37382.	1.6	53
339	Mechanism of Foreign DNA Selection in a Bacterial Adaptive Immune System. <i>Molecular Cell</i> , 2012, 46, 606-615.	4.5	229
340	Quorum sensing: How bacteria can coordinate activity and synchronize their response to external signals?. <i>Protein Science</i> , 2012, 21, 1403-1417.	3.1	164
341	Structural basis for an inositol pyrophosphate kinase surmounting phosphate crowding. <i>Nature Chemical Biology</i> , 2012, 8, 111-116.	3.9	123
342	Structure of <i>RdxA</i> , an oxygen-insensitive nitroreductase essential for metronidazole activation in <i>Helicobacter pylori</i> . <i>FEBS Journal</i> , 2012, 279, 4306-4317.	2.2	41
343	Crystal structure of enterotoxigenic <i>Escherichia coli</i> colonization factor <i>CS6</i> reveals a novel type of functional assembly. <i>Molecular Microbiology</i> , 2012, 86, 1100-1115.	1.2	28
344	Characterization of Member of DUF1888 Protein Family, Self-cleaving and Self-assembling Endopeptidase. <i>Journal of Biological Chemistry</i> , 2012, 287, 19452-19461.	1.6	5
345	A ketosynthase homolog uses malonyl units to form esters in cervimycin biosynthesis. <i>Nature Chemical Biology</i> , 2012, 8, 154-161.	3.9	69
346	IFN- γ Induction on Carbohydrate Binding Module of Fungal Immunomodulatory Protein in Human Peripheral Mononuclear Cells. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 4914-4922.	2.4	19
347	MCP-1-induced protein-1, an immune regulator. <i>Protein and Cell</i> , 2012, 3, 903-910.	4.8	26
348	The Structure of Human DNase I Bound to Magnesium and Phosphate Ions Points to a Catalytic Mechanism Common to Members of the DNase I-like Superfamily. <i>Biochemistry</i> , 2012, 51, 10250-10258.	1.2	43
349	The structural biochemistry of Zucchini implicates it as a nuclease in piRNA biogenesis. <i>Nature</i> , 2012, 491, 279-283.	13.7	276
350	Endo- β -D-1,4-mannanase from <i>Chrysonilia sitophila</i> displays a novel loop arrangement for substrate selectivity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1468-1478.	2.5	19
351	Structures of the ribosome-inactivating protein from barley seeds reveal a unique activation mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1488-1500.	2.5	8
352	Structure of <i>Escherichia coli</i> RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the <i>rut</i> operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1294-1299.	0.7	15
353	Structure of the Rho-specific guanine nucleotide-exchange factor Xpln. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1455-1459.	0.7	3
354	<i>Alternaria alternata</i> allergen Alt a 1: A unique β -barrel protein dimer found exclusively in fungi. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 241-247.e9.	1.5	99
355	Solution structure and biophysical properties of MqsA, a Zn-containing antitoxin from <i>Escherichia coli</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 1401-1408.	1.1	7

#	ARTICLE	IF	CITATIONS
356	Self-Complementarity within Proteins: Bridging the Gap between Binding and Folding. <i>Biophysical Journal</i> , 2012, 102, 2605-2614.	0.2	32
357	Structures of Lysenin Reveal a Shared Evolutionary Origin for Pore-Forming Proteins And Its Mode of Sphingomyelin Recognition. <i>Structure</i> , 2012, 20, 1498-1507.	1.6	90
358	DNA Minor Groove Sensing and Widening by the CCAAT-Binding Complex. <i>Structure</i> , 2012, 20, 1757-1768.	1.6	53
359	Structure of the Essential MTERF4:NSUN4 Protein Complex Reveals How an MTERF Protein Collaborates to Facilitate rRNA Modification. <i>Structure</i> , 2012, 20, 1940-1947.	1.6	65
360	Structure and Dynamics of the Second CARD of Human RIG-I Provide Mechanistic Insights into Regulation of RIG-I Activation. <i>Structure</i> , 2012, 20, 2048-2061.	1.6	41
361	Ego3 Functions as a Homodimer to Mediate the Interaction between Gtr1-Ctr2 and Ego1 in the EGO Complex to Activate TORC1. <i>Structure</i> , 2012, 20, 2151-2160.	1.6	56
362	In silico identification of novel hevein-like peptide precursors. <i>Peptides</i> , 2012, 38, 127-136.	1.2	48
363	Crystal Structure of Cucumisin, a Subtilisin-Like Endoprotease from <i>Cucumis melo</i> L.. <i>Journal of Molecular Biology</i> , 2012, 423, 386-396.	2.0	31
364	The Structural Domains of <i>Pseudomonas aeruginosa</i> Phosphorylcholine Phosphatase Cooperate in Substrate Hydrolysis: 3D Structure and Enzymatic Mechanism. <i>Journal of Molecular Biology</i> , 2012, 423, 503-514.	2.0	6
365	Structural Basis of Substrate Specificity and Selectivity of Murine Cytosolic 5â€²-Nucleotidase III. <i>Journal of Molecular Biology</i> , 2012, 423, 540-554.	2.0	6
366	Structure and Catalytic Mechanism of Nicotinate (Vitamin B ₃) Degradative Enzyme Maleamate Amidohydrolase from <i>Bordetella bronchiseptica</i> RB50. <i>Biochemistry</i> , 2012, 51, 545-554.	1.2	15
367	Pseudouridine Monophosphate Glycosidase: A New Glycosidase Mechanism. <i>Biochemistry</i> , 2012, 51, 9245-9255.	1.2	28
368	Up, Down, and Around: Identifying Recurrent Interactions Within and Between Super-secondary Structures in Î²-Propellers. <i>Methods in Molecular Biology</i> , 2012, 932, 35-50.	0.4	2
369	Postcards from the Edge. <i>Advances in Virus Research</i> , 2012, 82, 33-62.	0.9	40
370	Homology modeling and functional sites prediction of azoreductase enzyme from the cyanobacterium <i>Nostoc</i> sp. PCC7120. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2012, 4, 310-318.	2.2	2
371	Enhancement of Initial Equivalency for Protein Structure Alignment Based on Encoded Local Structures. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2012, 16, 1185-1192.	3.6	1
372	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. <i>Molecular BioSystems</i> , 2012, 8, 1661.	2.9	63
373	An ankyrin-repeat ubiquitin-binding domain determines TRABID's specificity for atypical ubiquitin chains. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 62-71.	3.6	122

#	ARTICLE	IF	CITATIONS
374	A rapid 3D protein Structural Classification using Pseudo 2D HMMs. , 2012, , .		0
375	1.8 Structure Validation and Analysis. , 2012, , 116-135.		3
376	Structural Characterization of a Novel Chlamydia pneumoniae Type III Secretion-Associated Protein, Cpn0803. PLoS ONE, 2012, 7, e30220.	1.1	12
377	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
378	Structural Insights into the Effector " Immunity System Tse1/Tsi1 from Pseudomonas aeruginosa. PLoS ONE, 2012, 7, e40453.	1.1	46
379	Crystal Structure of the Sema-PSI Extracellular Domain of Human RON Receptor Tyrosine Kinase. PLoS ONE, 2012, 7, e41912.	1.1	33
380	Crystal Structure of Aura Virus Capsid Protease and Its Complex with Dioxane: New Insights into Capsid-Glycoprotein Molecular Contacts. PLoS ONE, 2012, 7, e51288.	1.1	26
381	Structure of the catalytic domain of the <i>Clostridium thermocellum</i> cellulase CelT. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 310-320.	2.5	14
382	Structure of a pectin methyltransferase from <i>Yersinia enterocolitica</i> . Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 129-133.	0.7	21
383	Solution structure of gp17 from the <i>Siphoviridae</i> bacteriophage SPP1: Insights into its role in virion assembly. Proteins: Structure, Function and Bioinformatics, 2012, 80, 319-326.	1.5	15
384	Solution NMR structure of BT_0084, a conjugative transposon lipoprotein from <i>Bacteroides thetaiotamicron</i> . Proteins: Structure, Function and Bioinformatics, 2012, 80, 667-670.	1.5	2
385	Solution NMR structure of Asl3597 from Nostoc sp. PCC7120, the first structure from protein domain family PF12095, reveals a novel fold. Proteins: Structure, Function and Bioinformatics, 2012, 80, 671-675.	1.5	1
386	Formyl-coenzyme A (CoA):oxalate CoA-transferase from the acidophile <i>Acetobacter acetii</i> has a distinctive electrostatic surface and inherent acid stability. Protein Science, 2012, 21, 686-696.	3.1	18
387	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
388	Crystal structure of the TLDC domain of oxidation resistance protein 2 from zebrafish. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1694-1698.	1.5	31
389	Fold of the conserved DTC domain in deltex proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1495-1499.	1.5	17
390	A new size-independent score for pairwise protein structure alignment and its application to structure classification and nucleic acid binding prediction. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2080-2088.	1.5	69
391	A multi-faceted analysis of RutD reveals a novel family of $\hat{1}\pm/\hat{1}^2$ hydrolases. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2359-2368.	1.5	7

#	ARTICLE	IF	CITATIONS
392	Overcoming sequence misalignments with weighted structural superposition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2523-2535.	1.5	5
393	Identification, structural, and biochemical characterization of a group of large Csn2 proteins involved in CRISPR-mediated bacterial immunity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2573-2582.	1.5	29
394	Crystal Structure of the Superfamily 1 Helicase from Tomato Mosaic Virus. <i>Journal of Virology</i> , 2012, 86, 7565-7576.	1.5	54
395	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. <i>Immunity</i> , 2012, 36, 1073-1086.	6.6	282
396	Deorphanization of Malonyl CoA:ACP Transacylase Drug Target in <i>Plasmodium falciparum</i> (PfFabD) Using Bacterial Antagonists: A "Piggyback" Approach for Antimalarial Drug Discovery. <i>Molecular Informatics</i> , 2012, 31, 281-299.	1.4	8
397	Impairment of prostate cancer cell growth by a selective and reversible lysine-specific demethylase 1 inhibitor. <i>International Journal of Cancer</i> , 2012, 131, 2704-2709.	2.3	118
398	The structure of a GH10 xylanase from <i>Fusarium oxysporum</i> reveals the presence of an extended loop on top of the catalytic cleft. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 735-742.	2.5	12
399	Redox-dependent complex formation by an ATP-dependent activator of the corrinoid/iron-sulfur protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5235-5240.	3.3	40
400	Crystal structure of the ubiquitin-like domain of human TBK1. <i>Protein and Cell</i> , 2012, 3, 383-391.	4.8	26
401	NMR structure note: human esophageal cancer-related gene 2. <i>Journal of Biomolecular NMR</i> , 2012, 53, 65-70.	1.6	5
402	Crystal structure of a putative isochorismatase hydrolase from <i>Oleispira antarctica</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 27-36.	1.2	22
403	Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 15-26.	1.2	7
404	Conservation of structure and mechanism within the transaldolase enzyme family. <i>FEBS Journal</i> , 2012, 279, 766-778.	2.2	14
405	Crystal structure of cce_0566 from <i>Cyanothece 51142</i> , a protein associated with nitrogen fixation in the DUF269 family. <i>FEBS Letters</i> , 2012, 586, 350-355.	1.3	1
406	Crystal structure of <i>Pyrococcus furiosus</i> PF2050, a member of the DUF2666 protein family. <i>FEBS Letters</i> , 2012, 586, 1384-1388.	1.3	0
407	Solution structure of CyanoP from <i>Synechocystis</i> sp. PCC 6803: New insights on the structural basis for functional specialization amongst PsbP family proteins. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2012, 1817, 1331-1338.	0.5	19
408	The use of evolutionary patterns in protein annotation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 316-325.	2.6	28
409	Structural Insight into the Bacterial Mucinase StcE Essential to Adhesion and Immune Evasion during Enterohemorrhagic <i>E. Coli</i> Infection. <i>Structure</i> , 2012, 20, 707-717.	1.6	67

#	ARTICLE	IF	CITATIONS
410	A Protein Export Pathway Involving Escherichia coli Porins. <i>Structure</i> , 2012, 20, 1154-1166.	1.6	42
411	Inositol 5-phosphatases: insights from the Lowe syndrome protein OCRL. <i>Trends in Biochemical Sciences</i> , 2012, 37, 134-143.	3.7	104
412	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 637-648.	2.5	22
413	Three-dimensional structure of a schistosome serpin revealing an unusual configuration of the helical subdomain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 686-694.	2.5	6
414	Crystallization and preliminary X-ray crystallographic analysis of the Bag2 amino-terminal domain from <i>Mus musculus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 647-651.	0.7	6
415	Structure of a short-chain dehydrogenase/reductase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 632-637.	0.7	3
416	Structure of <i>Leishmania major</i> cysteine synthase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 738-743.	0.7	19
417	Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. <i>Biology Direct</i> , 2013, 8, 13.	1.9	45
418	Crystal structures and biochemical studies of human lysophosphatidic acid phosphatase type 6. <i>Protein and Cell</i> , 2013, 4, 548-561.	4.8	9
419	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from <i>Salmonella Typhimurium</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 1-10.	1.2	4
420	Structure-function analysis reveals a novel mechanism for regulation of histone demethylase LSD2/AOF1/KDM1b. <i>Cell Research</i> , 2013, 23, 225-241.	5.7	61
421	Structural and functional characterization of a plant S-nitrosoglutathione reductase from <i>Solanum lycopersicum</i> . <i>Biochimie</i> , 2013, 95, 889-902.	1.3	76
422	The structure of the D3 domain of <i>Plasmodium falciparum</i> myosin tail interacting protein MTIP in complex with a nanobody. <i>Molecular and Biochemical Parasitology</i> , 2013, 190, 87-91.	0.5	13
423	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26. <i>Nature</i> , 2013, 500, 227-231.	13.7	582
424	Structure and Reaction Mechanism of Pyrrolysine Synthase (PylD). <i>Angewandte Chemie - International Edition</i> , 2013, 52, 7033-7037.	7.2	11
425	Pathogens Use Structural Mimicry of Native Host Ligands as a Mechanism for Host Receptor Engagement. <i>Cell Host and Microbe</i> , 2013, 14, 63-73.	5.1	54
426	Expression and efficient secretion of a functional chitinase from <i>Chromobacterium violaceum</i> in <i>Escherichia coli</i> . <i>BMC Biotechnology</i> , 2013, 13, 46.	1.7	30
427	Structural basis for hypermodification of the wobble uridine in tRNA by bifunctional enzyme MnmC. <i>BMC Structural Biology</i> , 2013, 13, 5.	2.3	13

#	ARTICLE	IF	CITATIONS
428	Crystal structure of Junin virus nucleoprotein. <i>Journal of General Virology</i> , 2013, 94, 2175-2183.	1.3	21
429	A Novel Multifunctional α -Amylase from the Thermophilic Fungus <i>Malbranchea cinnamomea</i> : Biochemical Characterization and Three-Dimensional Structure. <i>Applied Biochemistry and Biotechnology</i> , 2013, 170, 420-435.	1.4	31
430	New molecular interaction of IIA ^{Ntr} and HPr from <i>Burkholderia pseudomallei</i> identified by X-ray crystallography and docking studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1499-1508.	1.5	2
431	Expression, purification and molecular modeling of the Nla protease of <i>Cardamom mosaic virus</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 602-611.	2.0	4
432	Structural and Functional Analysis of Angucycline C-6 Ketoreductase LanV Involved in Landomycin Biosynthesis. <i>Biochemistry</i> , 2013, 52, 5304-5314.	1.2	15
433	Conformational Analysis of StrH, the Surface-Attached exo- β -D-N-Acetylglucosaminidase from <i>Streptococcus pneumoniae</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 334-349.	2.0	14
434	Biochemical and structural characterization of a novel bacterial manganese-dependent hydroxynitrile lyase. <i>FEBS Journal</i> , 2013, 280, 5815-5828.	2.2	38
435	Structural and mechanistic studies of theorf12 gene product from the clavulanic acid biosynthesis pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1567-1579.	2.5	8
436	The Structural Motifs for Substrate Binding and Dimerization of the β Subunit of Collagen Prolyl 4-Hydroxylase. <i>Structure</i> , 2013, 21, 2107-2118.	1.6	29
437	An Iml3-Chl4 Heterodimer Links the Core Centromere to Factors Required for Accurate Chromosome Segregation. <i>Cell Reports</i> , 2013, 5, 29-36.	2.9	56
438	Identification, characterization, and crystal structure of an aldo-keto reductase (AKR2E4) from the silkworm <i>Bombyx mori</i> . <i>Archives of Biochemistry and Biophysics</i> , 2013, 538, 156-163.	1.4	16
439	The Structure of the Neisserial Lipooligosaccharide Phosphoethanolamine Transferase A (LptA) Required for Resistance to Polymyxin. <i>Journal of Molecular Biology</i> , 2013, 425, 3389-3402.	2.0	101
440	Structure of the Fibrillin-1 N-Terminal Domains Suggests that Heparan Sulfate Regulates the Early Stages of Microfibril Assembly. <i>Structure</i> , 2013, 21, 1743-1756.	1.6	42
441	Guardians of the actin monomer. <i>European Journal of Cell Biology</i> , 2013, 92, 316-332.	1.6	62
442	Molecular Structure of the <i>Brucella abortus</i> Metalloprotein RicA, a Rab2-Binding Virulence Effector. <i>Biochemistry</i> , 2013, 52, 9020-9028.	1.2	14
443	Crystal Structures of Copper-depleted and Copper-bound Fungal Pro-tyrosinase. <i>Journal of Biological Chemistry</i> , 2013, 288, 22128-22140.	1.6	72
444	Structure of the Mycosin-1 Protease from the Mycobacterial ESX-1 Protein Type VII Secretion System. <i>Journal of Biological Chemistry</i> , 2013, 288, 17782-17790.	1.6	48
445	Understanding specificity of the mycosin proteases in ESX/type VII secretion by structural and functional analysis. <i>Journal of Structural Biology</i> , 2013, 184, 115-128.	1.3	33

#	ARTICLE	IF	CITATIONS
446	Structure-Function Analysis of Arabidopsis thaliana Histidine Kinase AHK5 Bound to Its Cognate Phosphotransfer Protein AHP1. <i>Molecular Plant</i> , 2013, 6, 959-970.	3.9	38
447	The X-ray crystal structure of PA1374 from <i>Pseudomonas aeruginosa</i> , a putative oxidative-stress sensing transcriptional regulator. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 376-381.	1.0	8
448	The Exomer Cargo Adaptor Features a Flexible Hinge Domain. <i>Structure</i> , 2013, 21, 486-492.	1.6	8
449	Binding of the N-Terminal Domain of the Lactococcal Bacteriophage TP901-1 CI Repressor to Its Target DNA: A Crystallography, Small Angle Scattering, and Nuclear Magnetic Resonance Study. <i>Biochemistry</i> , 2013, 52, 6892-6904.	1.2	12
450	CARMIL leading edge localization depends on a non-canonical PH domain and dimerization. <i>Nature Communications</i> , 2013, 4, 2523.	5.8	30
451	Toroidal Structure and DNA Cleavage by the CRISPR-Associated [4Fe-4S] Cluster Containing Cas4 Nuclease SSO0001 from <i>Sulfolobus solfataricus</i> . <i>Journal of the American Chemical Society</i> , 2013, 135, 17476-17487.	6.6	52
452	Structural basis of preferential binding of fucose-containing saccharide by the <i>Caenorhabditis elegans</i> galectin LEC-6. <i>Glycobiology</i> , 2013, 23, 797-805.	1.3	11
453	Crystal Structure of TET2-DNA Complex: Insight into TET-Mediated 5mC Oxidation. <i>Cell</i> , 2013, 155, 1545-1555.	13.5	344
454	Structural analysis for glycolipid recognition by the C-type lectins Mincle and MCL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17438-17443.	3.3	142
455	Cystovirus Maturation at Atomic Resolution. <i>Structure</i> , 2013, 21, 1266-1268.	1.6	3
456	DNA Recognition of 5-Carboxylcytosine by a Zfp57 Mutant at an Atomic Resolution of 0.97 Å... <i>Biochemistry</i> , 2013, 52, 9310-9317.	1.2	19
457	Crystal Structure and Computational Characterization of the Lytic Polysaccharide Monooxygenase GH61D from the Basidiomycota Fungus <i>Phanerochaete chrysosporium</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 12828-12839.	1.6	158
458	Biochemical and Structural Studies of Conserved Maf Proteins Revealed Nucleotide Pyrophosphatases with a Preference for Modified Nucleotides. <i>Chemistry and Biology</i> , 2013, 20, 1386-1398.	6.2	15
459	Neuroglobins, Pivotal Proteins Associated with Emerging Neural Systems and Precursors of Metazoan Globin Diversity. <i>Journal of Biological Chemistry</i> , 2013, 288, 6957-6967.	1.6	31
460	Rubella virus capsid protein structure and its role in virus assembly and infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20105-20110.	3.3	34
461	A PiIT N-terminus domain protein SSO1118 from hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> P2. <i>Journal of Biomolecular NMR</i> , 2013, 57, 363-368.	1.6	2
462	A Thermoacidophile-Specific Protein Family, DUF3211, Functions as a Fatty Acid Carrier with Novel Binding Mode. <i>Journal of Bacteriology</i> , 2013, 195, 4005-4012.	1.0	3
463	Mining Tertiary Structural Motifs for Assessment of Designability. <i>Methods in Enzymology</i> , 2013, 523, 21-40.	0.4	16

#	ARTICLE	IF	CITATIONS
464	Structure of a Pestivirus Envelope Glycoprotein E2 Clarifies Its Role in Cell Entry. <i>Cell Reports</i> , 2013, 3, 30-35.	2.9	124
465	Production of bulk chemicals via novel metabolic pathways in microorganisms. <i>Biotechnology Advances</i> , 2013, 31, 925-935.	6.0	62
466	Structural basis for arabinosyloligosaccharide capture by the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> ... <i>BMC Microbiology</i> , 2013, 90, 1100-1112.	1.2	58
467	Structural and functional studies on urease from pigeon pea (<i>Cajanus cajan</i>). <i>International Journal of Biological Macromolecules</i> , 2013, 58, 301-309.	3.6	59
468	Structure and function of <i>Escherichia coli</i> RimK, an ATP-grasp fold, γ -glutamyl ligase enzyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1847-1854.	1.5	28
469	Crystal structure of the Psb28 accessory factor of <i>Thermosynechococcus elongatus</i> photosystem II at 2.3 Å. <i>Photosynthesis Research</i> , 2013, 117, 375-383.	1.6	10
470	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013, 14, 265.	1.2	3
471	BioSuper: A web tool for the superimposition of biomolecules and assemblies with rotational symmetry. <i>BMC Structural Biology</i> , 2013, 13, 32.	2.3	8
472	Solution structure of a putative FKBP-type peptidyl-propyl cis-trans isomerase from <i>Giardia lamblia</i> . <i>Journal of Biomolecular NMR</i> , 2013, 57, 369-374.	1.6	1
473	Comparative modeling and docking studies of β -galactosidase from <i>Aspergillus niger</i> . <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 297-302.	1.2	2
474	Structure analysis and characterization of the cytochrome c-554 from thermophilic green sulfur photosynthetic bacterium <i>Chlorobaculum tepidum</i> . <i>Photosynthesis Research</i> , 2013, 118, 249-258.	1.6	4
475	Structural analysis of HmtT and HmtN involved in the tailoring steps of himastatin biosynthesis. <i>FEBS Letters</i> , 2013, 587, 1675-1680.	1.3	26
476	The crystal structure of human protein β 1M reveals a chromophore-binding site and two putative protein-protein interfaces. <i>Biochemical and Biophysical Research Communications</i> , 2013, 439, 346-350.	1.0	3
477	Structure of the Mtb CarD/RNAP β -Lobes Complex Reveals the Molecular Basis of Interaction and Presents a Distinct DNA-Binding Domain for Mtb CarD. <i>Structure</i> , 2013, 21, 1859-1869.	1.6	33
478	Structural biology study of human TNF receptor associated factor 4 TRAF domain. <i>Protein and Cell</i> , 2013, 4, 687-694.	4.8	17
479	Crystal structure of the N-terminal domains of the surface cell antigen 4 of <i>Rickettsia</i> . <i>Protein Science</i> , 2013, 22, 1425-1431.	3.1	5
480	Molecular architecture of <i>Streptococcus pneumoniae</i> surface thioredoxin fold lipoproteins crucial for extracellular oxidative stress resistance and maintenance of virulence. <i>EMBO Molecular Medicine</i> , 2013, 5, 1852-1870.	3.3	99
481	The Structural Basis of ZMPSTE24-Dependent Laminopathies. <i>Science</i> , 2013, 339, 1604-1607.	6.0	89

#	ARTICLE	IF	CITATIONS
482	Structural and Mechanistic Characterization of <i>l</i> -Histidinol Phosphate Phosphatase from the Polymerase and Histidinol Phosphatase Family of Proteins. <i>Biochemistry</i> , 2013, 52, 1101-1112.	1.2	31
483	Structural and Functional Studies of <i>Burkholderia cenocepacia</i> <i>d</i> -Glycero- β -manno-heptose 7-Phosphate Kinase (HldA) and Characterization of Inhibitors with Antibiotic Adjuvant and Antivirulence Properties. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 1405-1417.	2.9	14
484	The Myosin Chaperone UNC-45 Is Organized in Tandem Modules to Support Myofilament Formation in <i>C.Âelegans</i> . <i>Cell</i> , 2013, 152, 183-195.	13.5	94
485	Solution Structure of <i>Escherichia coli</i> FeoA and Its Potential Role in Bacterial Ferrous Iron Transport. <i>Journal of Bacteriology</i> , 2013, 195, 46-55.	1.0	50
486	Structural and Mechanistic Studies of HpxO, a Novel Flavin Adenine Dinucleotide-Dependent Urate Oxidase from <i>Klebsiella pneumoniae</i> . <i>Biochemistry</i> , 2013, 52, 477-487.	1.2	27
487	Functional and evolutionary insight from the crystal structure of rubella virus protein E1. <i>Nature</i> , 2013, 493, 552-556.	13.7	91
488	Crystal Structure of the Cowpox Virus-Encoded NKG2D Ligand OMCP. <i>Journal of Virology</i> , 2013, 87, 840-850.	1.5	22
489	Toward a "Structural BLAST" Using structural relationships to infer function. <i>Protein Science</i> , 2013, 22, 359-366.	3.1	23
490	CYP63A2, a Catalytically Versatile Fungal P450 Monooxygenase Capable of Oxidizing Higher-Molecular-Weight Polycyclic Aromatic Hydrocarbons, Alkylphenols, and Alkanes. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2692-2702.	1.4	93
491	A novel mechanism of ligand binding and release in the odorant binding protein 20 from the malaria mosquito <i>Anopheles gambiae</i> . <i>Protein Science</i> , 2013, 22, 11-21.	3.1	30
492	Structure and function of the SPRY/B30.2 domain proteins involved in innate immunity. <i>Protein Science</i> , 2013, 22, 1-10.	3.1	109
493	Crystal structure of decaprenylphosphorylâ€• <i>D</i> -ribose 2'-epimerase from <i>Mycobacterium smegmatis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 538-543.	1.5	12
494	Competition of Cell Adhesion and Immune Recognition: Insights into the Interaction between CRTAM and Nectin-like 2. <i>Structure</i> , 2013, 21, 1430-1439.	1.6	11
495	Catalytic Mechanism of Stereospecific Formation of cis-Configured Prenylated Pyrroloindoline Diketopiperazines by Indole Prenyltransferases. <i>Chemistry and Biology</i> , 2013, 20, 1492-1501.	6.2	43
496	Structure of Stem Cell Growth Factor R-spondin 1 in Complex with the Ectodomain of Its Receptor LGR5. <i>Cell Reports</i> , 2013, 3, 1885-1892.	2.9	80
497	A continuous fluorescence assay for the characterization of Nudix hydrolases. <i>Analytical Biochemistry</i> , 2013, 437, 178-184.	1.1	4
498	Structure of a Ca ²⁺ /CaM:Kv7.4 (KCNQ4) B-Helix Complex Provides Insight into M Current Modulation. <i>Journal of Molecular Biology</i> , 2013, 425, 378-394.	2.0	42
499	Crystal Structure of the Cmr2â€•Cmr3 Subcomplex in the CRISPRâ€•Cas RNA Silencing Effector Complex. <i>Journal of Molecular Biology</i> , 2013, 425, 3811-3823.	2.0	38

#	ARTICLE	IF	CITATIONS
500	Atypical features of a Ure2p glutathione transferase from <i>Phanerochaete chrysosporium</i> . FEBS Letters, 2013, 587, 2125-2130.	1.3	22
501	Subunit Folds and Maturation Pathway of a dsRNA Virus Capsid. Structure, 2013, 21, 1374-1383.	1.6	46
502	The Crystal Structure of the Luminal 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
503	Structural, Functional, and Inhibition Studies of a Gcn5-related N-Acetyltransferase (GNAT) Superfamily Protein PA4794. Journal of Biological Chemistry, 2013, 288, 30223-30235.	1.6	37
504	Crystal structure of GTPase-activating domain from human MgcRacGAP. Biochemical and Biophysical Research Communications, 2013, 435, 367-372.	1.0	6
505	Stuck in the middle: structural insights into the role of the gH/gL heterodimer in herpesvirus entry. Current Opinion in Virology, 2013, 3, 13-19.	2.6	50
506	Crystal structure of a compact α -amylase from <i>Geobacillus thermoleovorans</i> . Enzyme and Microbial Technology, 2013, 53, 46-54.	1.6	33
507	Crystal structure of the N-terminal domain of a glycoside hydrolase family 131 protein from <i>Coprinopsis cinerea</i> . FEBS Letters, 2013, 587, 2193-2198.	1.3	6
508	A new family of proteins related to the HEAT-like repeat DNA glycosylases with affinity for branched DNA structures. Journal of Structural Biology, 2013, 183, 66-75.	1.3	8
509	NMR structure and MD simulations of the AAA protease intermembrane space domain indicates peripheral membrane localization within the hexaoligomer. FEBS Letters, 2013, 587, 3522-3528.	1.3	18
510	Structural insights into the functional role of the Hcn sub-domain of the receptor-binding domain of the botulinum neurotoxin mosaic serotype C/D. Biochimie, 2013, 95, 1379-1385.	1.3	8
511	NMR Structure of Calmodulin Complexed to an N-Terminally Acetylated α -Synuclein Peptide. Biophysical Journal, 2013, 104, 52a.	0.2	7
512	Crystal structure of phospholipase A1 from <i>Streptomyces albidoflavus</i> NA297. Journal of Structural Biology, 2013, 182, 192-196.	1.3	26
513	Structural Basis of mRNA Recognition and Cleavage by Toxin MazF and Its Regulation by Antitoxin MazE in <i>Bacillus subtilis</i> . Molecular Cell, 2013, 52, 447-458.	4.5	77
514	Structure Analysis of Archaeal AMP Phosphorylase Reveals Two Unique Modes of Dimerization. Journal of Molecular Biology, 2013, 425, 2709-2721.	2.0	9
515	Nonspecific Recognition Is Achieved in Pot1pC through the Use of Multiple Binding Modes. Structure, 2013, 21, 121-132.	1.6	29
516	Thermal dissociation of streptavidin homotetramer in the gas phase: Subunit loss versus backbone fragmentation. International Journal of Mass Spectrometry, 2013, 345-347, 97-103.	0.7	4
517	The structure of the deacetylase domain of <i>Escherichia coli</i> PgaB, an enzyme required for biofilm formation: a circularly permuted member of the carbohydrate esterase 4 family. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 44-51.	2.5	15

#	ARTICLE	IF	CITATIONS
518	The structure of a novel glucuronoyl esterase from <i>Myceliophthora thermophila</i> gives new insights into its role as a potential biocatalyst. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 63-73.	2.5	38
519	The AEROPATH project targeting <i>Pseudomonas aeruginosa</i> : crystallographic studies for assessment of potential targets in early-stage drug discovery. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 25-34.	0.7	30
520	Insights into FlaI Functions in Archaeal Motor Assembly and Motility from Structures, Conformations, and Genetics. <i>Molecular Cell</i> , 2013, 49, 1069-1082.	4.5	94
521	Contribution of the two domains of <i>E. coli</i> 5'-nucleotidase to substrate specificity and catalysis. <i>FEBS Letters</i> , 2013, 587, 460-466.	1.3	13
522	Stereochemical Determinants of C-terminal Specificity in PDZ Peptide-binding Domains. <i>Journal of Biological Chemistry</i> , 2013, 288, 5114-5126.	1.6	32
523	Peptide Ligands for Pro-survival Protein Bfl-1 from Computationally Guided Library Screening. <i>ACS Chemical Biology</i> , 2013, 8, 778-788.	1.6	34
524	DNA-binding domains of plant-specific transcription factors: structure, function, and evolution. <i>Trends in Plant Science</i> , 2013, 18, 267-276.	4.3	229
525	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. <i>Structure</i> , 2013, 21, 560-571.	1.6	53
526	Structure of a low-melting-temperature anti-cholera toxin: llama VHH domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 90-93.	0.7	6
527	Crystal structure of the human IgG4 CH3 dimer reveals the role of Arg409 in the mechanism of Fab-arm exchange. <i>Molecular Immunology</i> , 2013, 54, 1-7.	1.0	39
528	Structural Analysis of the DAP5 MIF4G Domain and Its Interaction with eIF4A. <i>Structure</i> , 2013, 21, 517-527.	1.6	33
529	Anions Mediate Ligand Binding in <i>Adineta vaga</i> Glutamate Receptor Ion Channels. <i>Structure</i> , 2013, 21, 414-425.	1.6	14
530	Structure of Ldt _{Mt2} , an L _D -D-transpeptidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 432-441.	2.5	36
531	Structural basis for the inhibition of <i>Mycobacterium tuberculosis</i> L _D -D-transpeptidase by meropenem, a drug effective against extensively drug-resistant strains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 420-431.	2.5	68
532	Design of Chimeric Proteins by Combination of Subdomain-Sized Fragments. <i>Methods in Enzymology</i> , 2013, 523, 389-405.	0.4	8
533	Structure of the C-terminal half of human XPB helicase and the impact of the disease-causing mutation XP11BE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 237-246.	2.5	23
534	Crystal structure and catalytic mechanism of chloromuconolactone dehalogenase ClcF from <i>Rhodococcus opacus</i> 1CP. <i>Molecular Microbiology</i> , 2013, 88, 254-267.	1.2	6
535	Structure of <i>Vibrio cholerae</i> ribosome hibernation promoting factor. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 228-236.	0.7	20

#	ARTICLE	IF	CITATIONS
536	Structure of the NLRP1 caspase recruitment domain suggests potential mechanisms for its association with procaspase-1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1266-1270.	1.5	58
537	Structure of a periplasmic domain of the EpsAB fusion protein of the <i>Vibrio vulnificus</i> type II secretion system. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 142-149.	2.5	10
538	Two Fe-S clusters catalyze sulfur insertion by radical-SAM methylthiotransferases. <i>Nature Chemical Biology</i> , 2013, 9, 333-338.	3.9	113
539	Interactions of the β -subunits of heterotrimeric G-proteins with GPCRs, effectors and RGS proteins: A critical review and analysis of interacting surfaces, conformational shifts, structural diversity and electrostatic potentials. <i>Journal of Structural Biology</i> , 2013, 182, 209-218.	1.3	63
540	Staufen1 dimerizes through a conserved motif and a degenerate dsRNA-binding domain to promote mRNA decay. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 515-524.	3.6	51
541	Structural and Functional Characterization of ScsC, a Periplasmic Thioredoxin-Like Protein from <i>Salmonella enterica</i> Serovar Typhimurium. <i>Antioxidants and Redox Signaling</i> , 2013, 19, 1494-1506.	2.5	26
542	Crystal structures of <i>Plasmodium falciparum</i> cytosolic tryptophanyl-tRNA synthetase and its potential as a target for structure-guided drug design. <i>Molecular and Biochemical Parasitology</i> , 2013, 189, 26-32.	0.5	27
543	Characterization of an Aldolase-Dehydrogenase Complex from the Cholesterol Degradation Pathway of <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , 2013, 52, 3502-3511.	1.2	33
544	Structural basis for protein trans-splicing by a bacterial intein-like domain protein ligation without nucleophilic side chains. <i>FEBS Journal</i> , 2013, 280, 3256-3269.	2.2	14
545	Structural Studies of Wnts and Identification of an LRP6 Binding Site. <i>Structure</i> , 2013, 21, 1235-1242.	1.6	73
546	Structure of the Human Telomeric Stn1-Ten1 Capping Complex. <i>PLoS ONE</i> , 2013, 8, e66756.	1.1	71
547	The Missing Linker: A Dimerization Motif Located within Polyketide Synthase Modules. <i>ACS Chemical Biology</i> , 2013, 8, 1263-1270.	1.6	37
548	Reversal of the Substrate Specificity of CMP-N-Glycosidase to dCMP. <i>Biochemistry</i> , 2013, 52, 4037-4047.	1.2	18
549	Functional and structural studies of a novel cold-adapted esterase from an Arctic intertidal metagenomic library. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 3965-3978.	1.7	77
550	Rif1 and Rif2 Shape Telomere Function and Architecture through Multivalent Rap1 Interactions. <i>Cell</i> , 2013, 153, 1340-1353.	13.5	92
551	Solution Nuclear Magnetic Resonance Structure of the GATase Subunit and Structural Basis of the Interaction between GATase and ATPase Subunits in a two-subunit-type GMPS from <i>Methanocaldococcus jannaschii</i> . <i>Biochemistry</i> , 2013, 52, 4308-4323.	1.2	8
552	<i>Brucella</i> Immunogenic BP26 Forms a Channel-like Structure. <i>Journal of Molecular Biology</i> , 2013, 425, 1119-1126.	2.0	13
553	Polymerase IV occupancy at RNA-directed DNA methylation sites requires SHH1. <i>Nature</i> , 2013, 498, 385-389.	13.7	310

#	ARTICLE	IF	CITATIONS
554	Structural mimicry in transcription regulation of human RNA polymerase II by the DNA helicase RECQL5. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 892-899.	3.6	27
555	Crystal and Solution Studies of the α -Plus-C α -Odorant-binding Protein 48 from <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 33427-33438.	1.6	42
556	Synthesis of β -Glucan in Mycobacteria Involves a Hetero-octameric Complex of Trehalose Synthase TreS and Maltokinase Pep2. <i>ACS Chemical Biology</i> , 2013, 8, 2245-2255.	1.6	27
557	Defining the interaction of perforin with calcium and the phospholipid membrane. <i>Biochemical Journal</i> , 2013, 456, 323-335.	1.7	16
558	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013, 14, 327.	1.2	74
559	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
560	The Coil-to-Helix Transition in IivN Regulates the Allosteric Control of <i>Escherichia coli</i> Acetohydroxyacid Synthase I. <i>Biochemistry</i> , 2013, 52, 70-83.	1.2	11
561	Structure of the Flavoprotein Tryptophan 2-Monooxygenase, a Key Enzyme in the Formation of Galls in Plants. <i>Biochemistry</i> , 2013, 52, 2620-2626.	1.2	26
562	Mycobacterium tuberculosis RNA Polymerase-binding Protein A (RbpA) and Its Interactions with Sigma Factors. <i>Journal of Biological Chemistry</i> , 2013, 288, 14438-14450.	1.6	44
563	Structure of isochorismate synthase Dhbc from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 956-961.	0.7	2
564	Structural and Biochemical Characterization of the Bilin Lyase CpcS from <i>Thermosynechococcus elongatus</i> . <i>Biochemistry</i> , 2013, 52, 8663-8676.	1.2	29
565	Functional Insights from the Crystal Structure of the N-Terminal Domain of the Prototypical Toll Receptor. <i>Structure</i> , 2013, 21, 143-153.	1.6	13
566	The DNA-binding domain of BenM reveals the structural basis for the recognition of a T-N ₁₁ -A sequence motif by LysR-type transcriptional regulators. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1995-2007.	2.5	52
567	Specificity of Processing β -Glucosidase I Is Guided by the Substrate Conformation. <i>Journal of Biological Chemistry</i> , 2013, 288, 13563-13574.	1.6	65
568	Identification and characterization of two new types of bacterial l-serine dehydratases and assessment of the function of the ACT domain. <i>Archives of Biochemistry and Biophysics</i> , 2013, 540, 62-69.	1.4	10
569	Identification, Structure, and Function of a Novel Type VI Secretion Peptidoglycan Glycoside Hydrolase Effector-Immunity Pair. <i>Journal of Biological Chemistry</i> , 2013, 288, 26616-26624.	1.6	110
570	Recognition of Bisecting N-Acetylglucosamine. <i>Journal of Biological Chemistry</i> , 2013, 288, 33598-33610.	1.6	46
571	The Structure of Allophanate Hydrolase from <i>Granulibacter bethesdensis</i> Provides Insights into Substrate Specificity in the Amidase Signature Family. <i>Biochemistry</i> , 2013, 52, 690-700.	1.2	15

#	ARTICLE	IF	CITATIONS
572	Structure of a Clostridium botulinum C143S Thiaminase I/Thiamin Complex Reveals Active Site Architecture. <i>Biochemistry</i> , 2013, 52, 7830-7839.	1.2	10
573	Crystal Structure of 3-Hydroxybenzoate 6-Hydroxylase Uncovers Lipid-assisted Flavoprotein Strategy for Regioselective Aromatic Hydroxylation. <i>Journal of Biological Chemistry</i> , 2013, 288, 26235-26245.	1.6	42
574	Structure and RNA-binding properties of the Not1-Not2-Not5 module of the yeast Ccr4-Not complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1281-1288.	3.6	64
575	Structure of a Dinuclear Iron Cluster-Containing $\hat{2}$ -Hydroxylase Active in Antibiotic Biosynthesis. <i>Biochemistry</i> , 2013, 52, 6662-6671.	1.2	38
576	NMR Structure of Calmodulin Complexed to an N-Terminally Acetylated $\hat{1}$ -Synuclein Peptide. <i>Biochemistry</i> , 2013, 52, 3436-3445.	1.2	24
577	Structural characterizations of the chloroplast translocon protein <i>scp</i> > <i>scp</i> >Tic110</i></i>. <i>Plant Journal</i> , 2013, 75, 847-857.	2.8	29
578	Crystal Structure of Arabidopsis thaliana Dawdle Forkhead-Associated Domain Reveals a Conserved Phospho-Threonine Recognition Cleft for Dicer-Like 1 Binding. <i>Molecular Plant</i> , 2013, 6, 1290-1300.	3.9	34
579	Evidence for an ABC-Type Riboflavin Transporter System in Pathogenic Spirochetes. <i>MBio</i> , 2013, 4, e00615-12.	1.8	38
580	Dissecting the Machinery That Introduces Disulfide Bonds in Pseudomonas aeruginosa. <i>MBio</i> , 2013, 4, e00912-13.	1.8	45
581	Crystal structure of glycoprotein C from Rift Valley fever virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1696-1701.	3.3	115
582	Structural and Functional Studies of gpX of Escherichia coli Phage P2 Reveal a Widespread Role for LysM Domains in the Baseplates of Contractile-Tailed Phages. <i>Journal of Bacteriology</i> , 2013, 195, 5461-5468.	1.0	18
583	Mining the bacterial unknown proteome: identification and characterization of a novel family of highly conserved protective antigens in <i>Staphylococcus aureus</i> . <i>Biochemical Journal</i> , 2013, 455, 273-284.	1.7	26
584	<i>In Silico</i> Determination and Validation of Baumannii Acinetobactin Utilization A Structure and Ligand Binding Site. <i>BioMed Research International</i> , 2013, 2013, 1-14.	0.9	27
585	Structural insights into the inhibition of type VI effector Tae3 by its immunity protein Tai3. <i>Biochemical Journal</i> , 2013, 454, 59-68.	1.7	26
586	Structure of Plasmodium falciparum TRAP (thrombospondin-related anonymous protein) A domain highlights distinct features in apicomplexan von Willebrand factor A homologues. <i>Biochemical Journal</i> , 2013, 450, 469-476.	1.7	22
587	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9054-9059.	3.3	59
588	The Methyltransferase NSD3 Has Chromatin-binding Motifs, PHD5-C5HCH, That Are Distinct from Other NSD (Nuclear Receptor SET Domain) Family Members in Their Histone H3 Recognition. <i>Journal of Biological Chemistry</i> , 2013, 288, 4692-4703.	1.6	56
589	Structures of <i>trans</i> -2-enoyl-CoA reductases from Clostridium acetobutylicum and Treponema denticola: insights into the substrate specificity and the catalytic mechanism. <i>Biochemical Journal</i> , 2013, 449, 79-89.	1.7	9

#	ARTICLE	IF	CITATIONS
590	Assembly of the Type II Secretion System such as Found in <i>Vibrio cholerae</i> Depends on the Novel Pilotin AspS. <i>PLoS Pathogens</i> , 2013, 9, e1003117.	2.1	59
591	Viral Proteins Originated De Novo by Overprinting Can Be Identified by Codon Usage: Application to the "Gene Nursery" of Deltaretroviruses. <i>PLoS Computational Biology</i> , 2013, 9, e1003162.	1.5	61
592	Crystal structure of the TRIM25 B30.2 (PRYSPRY) domain: a key component of antiviral signalling. <i>Biochemical Journal</i> , 2013, 456, 231-240.	1.7	42
593	Crystal structures of Cg1458 reveal a catalytic lid domain and a common catalytic mechanism for the FAH family. <i>Biochemical Journal</i> , 2013, 449, 51-60.	1.7	21
594	Mechanistic Insights Revealed by the Crystal Structure of a Histidine Kinase with Signal Transducer and Sensor Domains. <i>PLoS Biology</i> , 2013, 11, e1001493.	2.6	137
595	Structure of Human Cytomegalovirus UL141 Binding to TRAIL-R2 Reveals Novel, Non-canonical Death Receptor Interactions. <i>PLoS Pathogens</i> , 2013, 9, e1003224.	2.1	36
596	The <i>Escherichia coli</i> Phosphotyrosine Proteome Relates to Core Pathways and Virulence. <i>PLoS Pathogens</i> , 2013, 9, e1003403.	2.1	65
597	Dimerization of Sir3 via its C-terminal winged helix domain is essential for yeast heterochromatin formation. <i>EMBO Journal</i> , 2013, 32, 437-449.	3.5	29
598	Crystal structure of the capsular polysaccharide synthesizing protein CapE of <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2013, 33, .	1.1	16
599	The Velvet Family of Fungal Regulators Contains a DNA-Binding Domain Structurally Similar to NF- κ B. <i>PLoS Biology</i> , 2013, 11, e1001750.	2.6	121
600	A Compact Viral Processing Proteinase/Ubiquitin Hydrolase from the OTU Family. <i>PLoS Pathogens</i> , 2013, 9, e1003560.	2.1	28
601	A Horizontal Alignment Tool for Numerical Trend Discovery in Sequence Data: Application to Protein Hydropathy. <i>PLoS Computational Biology</i> , 2013, 9, e1003247.	1.5	1
602	Structural Basis for Rab1 De-AMPylation by the <i>Legionella pneumophila</i> Effector SidD. <i>PLoS Pathogens</i> , 2013, 9, e1003382.	2.1	28
603	Fungicides Inhibition Analysis by Molecular Docking and Sensitivity Testing of <i>Penicillium italicum</i> . <i>Applied Mechanics and Materials</i> , 0, 380-384, 4170-4174.	0.2	1
604	The structure of latherin, a surfactant allergen protein from horse sweat and saliva. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20130453.	1.5	42
605	Structure of the <i>Arabidopsis</i> Glucan Phosphatase LIKE SEX FOUR2 Reveals a Unique Mechanism for Starch Dephosphorylation. <i>Plant Cell</i> , 2013, 25, 2302-2314.	3.1	35
606	Elucidating the evolutionary conserved DNA-binding specificities of WRKY transcription factors by molecular dynamics and in vitro binding assays. <i>Nucleic Acids Research</i> , 2013, 41, 9764-9778.	6.5	161
607	Crystal structure of the Golgi casein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10574-10579.	3.3	66

#	ARTICLE	IF	CITATIONS
608	Nucleocapsid protein structures from orthobunyaviruses reveal insight into ribonucleoprotein architecture and RNA polymerization. <i>Nucleic Acids Research</i> , 2013, 41, 5912-5926.	6.5	69
609	A Novel Family of Soluble Minimal Scaffolds Provides Structural Insight into the Catalytic Domains of Integral Membrane Metallopeptidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 21279-21294.	1.6	35
610	QsIA disrupts LasR dimerization in antiactivation of bacterial quorum sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20765-20770.	3.3	44
611	A TPR domain-containing N-terminal module of MPS1 is required for its kinetochore localization by Aurora B. <i>Journal of Cell Biology</i> , 2013, 201, 217-231.	2.3	119
612	Dipeptidyl Peptidase IV Is a Human and Murine Neutrophil Chemorepellent. <i>Journal of Immunology</i> , 2013, 190, 6468-6477.	0.4	44
613	Structural Basis for Biofilm Formation via the <i>Vibrio cholerae</i> Matrix Protein RbmA. <i>Journal of Bacteriology</i> , 2013, 195, 3277-3286.	1.0	84
614	Structural and genetic analyses reveal the protein SepF as a new membrane anchor for the Z ring. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4601-10.	3.3	116
615	<i>Rickettsia</i> Sca2 has evolved formin-like activity through a different molecular mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2677-86.	3.3	43
616	Structural and biochemical studies of SLIP1-SLBP identify DBP5 and eIF3g as SLIP1-binding proteins. <i>Nucleic Acids Research</i> , 2013, 41, 7960-7971.	6.5	30
617	In Silico Resurrection of the Major Vault Protein Suggests It Is Ancestral in Modern Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 1567-1583.	1.1	13
618	RNA polymerase III-specific general transcription factor III C contains a heterodimer resembling TFIIF Rap30/Rap74. <i>Nucleic Acids Research</i> , 2013, 41, 9183-9196.	6.5	23
619	Crystal structure analysis of a fatty acid double-bond hydratase from <i>Lactobacillus acidophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 648-657.	2.5	46
620	Amino Acid Sequence of the Ligand-Binding Domain of the Aryl Hydrocarbon Receptor 1 Predicts Sensitivity of Wild Birds to Effects of Dioxin-Like Compounds. <i>Toxicological Sciences</i> , 2013, 131, 139-152.	1.4	101
621	Structural and functional characterization of HP0377, a thioredoxin-fold protein from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 735-746.	2.5	8
622	The structure of a glycoside hydrolase family 81 endo- β -1,3-glucanase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2027-2038.	2.5	15
623	<i>myo</i> -Inositol and <i>d</i> -Ribose Ligand Discrimination in an ABC Periplasmic Binding Protein. <i>Journal of Bacteriology</i> , 2013, 195, 2379-2388.	1.0	14
624	Structural Investigation of a Novel N-Acetyl Glucosamine Binding Chi-Lectin Which Reveals Evolutionary Relationship with Class III Chitinases. <i>PLoS ONE</i> , 2013, 8, e63779.	1.1	19
625	Mutational analysis of the ribosome assembly GTPase RbgA provides insight into ribosome interaction and ribosome-stimulated GTPase activation. <i>Nucleic Acids Research</i> , 2013, 41, 3217-3227.	6.5	24

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626	(4 <i>R</i>)- and (4 <i>S</i>)-Fluoroproline in the Conserved <i>cis</i> -Prolyl Peptide Bond of the Thioredoxin Fold: Tertiary Structure Context Dictates Ring Puckering. <i>ChemBioChem</i> , 2013, 14, 1053-1057.	1.3	26
627	X-Ray crystallographic evidence for the presence of the cysteine tryptophylquinone cofactor in L-lysine μ -oxidase from <i>Marinomonas mediterranea</i> . <i>Journal of Biochemistry</i> , 2013, 154, 233-236.	0.9	32
628	Structures of apo- and ssDNA-bound YdbC from <i>Lactococcus lactis</i> uncover the function of protein domain family DUF2128 and expand the single-stranded DNA-binding domain proteome. <i>Nucleic Acids Research</i> , 2013, 41, 2756-2768.	6.5	10
629	Crystal structure of Cex1p reveals the mechanism of tRNA trafficking between nucleus and cytoplasm. <i>Nucleic Acids Research</i> , 2013, 41, 3901-3914.	6.5	13
630	The Fanconi anemia associated protein FAAP24 uses two substrate specific binding surfaces for DNA recognition. <i>Nucleic Acids Research</i> , 2013, 41, 6739-6749.	6.5	4
631	Crystal structure of glycoprotein E2 from bovine viral diarrhea virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6805-6810.	3.3	108
632	Structural and functional analysis of the yeast <i>N</i> -acetyltransferase Mpr1 involved in oxidative stress tolerance via proline metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11821-11826.	3.3	22
633	Atomic structure of the 75 MDa extremophile <i>Sulfolobus</i> turreted icosahedral virus determined by CryoEM and X-ray crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5504-5509.	3.3	77
634	Structural Asymmetry and Disulfide Bridges among Subunits Modulate the Activity of Human Malonyl-CoA Decarboxylase*. <i>Journal of Biological Chemistry</i> , 2013, 288, 11907-11919.	1.6	10
635	An Uncharacterized Member of the Ribokinase Family in <i>Thermococcus kodakarensis</i> Exhibits myo-Inositol Kinase Activity. <i>Journal of Biological Chemistry</i> , 2013, 288, 20856-20867.	1.6	9
636	Structural Basis for Complement Evasion by Lyme Disease Pathogen <i>Borrelia burgdorferi</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 18685-18695.	1.6	50
637	Structural Basis for a Cofactor-dependent Oxidation Protection and Catalysis of Cyanobacterial Succinic Semialdehyde Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2013, 288, 15760-15770.	1.6	17
638	Dimeric Sfh3 has structural changes in its binding pocket that are associated with a dimer \leftrightarrow monomer state transformation induced by substrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 313-323.	2.5	12
639	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 774-784.	2.5	13
640	Structural analysis of coniferyl alcohol 9-O-methyltransferase from <i>Linum nodiflorum</i> reveals a novel active-site environment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 888-900.	2.5	8
641	Structure of the <i>Triatoma virus</i> capsid. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1026-1037.	2.5	36
642	The structure of full-length human CTNBL1 reveals a distinct member of the armadillo-repeat protein family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1598-1608.	2.5	12
643	Structural and functional analyses of a bacterial homologue of hormone-sensitive lipase from a metagenomic library. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1726-1737.	2.5	33

#	ARTICLE	IF	CITATIONS
644	The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1789-1797.	2.5	6
645	Structure of the periplasmic copper-binding protein CueP from <i>Salmonella enterica</i> serovar Typhimurium. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1867-1875.	2.5	13
646	Complex structure of type VI peptidoglycan muramidase effector and a cognate immunity protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1889-1900.	2.5	18
647	Structure of the JmjC-domain-containing protein JMJD5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1911-1920.	2.5	21
648	High-resolution structure of a papaya plant-defence barwin-like protein solved by in-house sulfur-SAD phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2017-2026.	2.5	16
649	Structural insight into <i>L</i> -ribulose 3-epimerase from <i>Mesorhizobium loti</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2330-2339.	2.5	30
650	Crystallographic identification of an unexpected protein complex in silkworm haemolymph. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2353-2364.	2.5	13
651	The TLR signalling adaptor TRIF/TICAM-1 has an N-terminal helical domain with structural similarity to IFIT proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2420-2430.	2.5	13
652	Structural characterization of the ribonuclease H-like type ASKHA superfamily kinase MK0840 from <i>Methanopyrus kandleri</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2440-2450.	2.5	4
653	Protein design by fusion: implications for protein structure prediction and evolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2451-2460.	2.5	3
654	Structural basis of SUFU-Gli interaction in human Hedgehog signalling regulation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2563-2579.	2.5	54
655	Crystal structure of endo-1,4- β -glucanase from <i>Eisenia fetida</i> . <i>Journal of Synchrotron Radiation</i> , 2013, 20, 884-889.	1.0	21
656	Structure of the hypothetical DUF1811-family protein GK0453 from <i>Geobacillus kaustophilus</i> HTA426. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 342-345.	0.7	0
657	Three-dimensional structure of RBcel1, a metagenome-derived psychrotolerant family GH5 endoglucanase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 828-833.	0.7	9
658	Structure of the caspase-recruitment domain from a zebrafish guanylate-binding protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 855-860.	0.7	14
659	Structure of CT584 from <i>Chlamydia trachomatis</i> refined to 3.05 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1196-1201.	0.7	8
660	The Unique Structure of <i>Haemophilus influenzae</i> Protein E Reveals Multiple Binding Sites for Host Factors. <i>Infection and Immunity</i> , 2013, 81, 801-814.	1.0	46
661	ZnuD, a Potential Candidate for a Simple and Universal <i>Neisseria meningitidis</i> Vaccine. <i>Infection and Immunity</i> , 2013, 81, 1915-1927.	1.0	24

#	ARTICLE	IF	CITATIONS
662	Identification and characterization of a hitherto unknown nucleotide-binding domain and an intricate interdomain regulation in HflX-a ribosome binding GTPase. <i>Nucleic Acids Research</i> , 2013, 41, 9557-9569.	6.5	11
663	Structural and functional insights into the molecular mechanism of rRNA m6A methyltransferase RlmJ. <i>Nucleic Acids Research</i> , 2013, 41, 9537-9548.	6.5	21
664	Ultratight crystal packing of a 10â€¦kDa protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 464-470.	2.5	9
665	Protein HP1028 from the human pathogen <i>Helicobacter pylori</i> belongs to the lipocalin family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1387-1394.	2.5	3
666	A functional and structural study of the major metalloprotease secreted by the pathogenic fungus <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1946-1957.	2.5	22
667	Analysis of periplasmic sensor domains from <i>Anaeromyxobacter dehalogenans</i> 2<sc>CP</sc>â€¦: Structure of one sensor domain from a histidine kinase and another from a chemotaxis protein. <i>MicrobiologyOpen</i> , 2013, 2, 766-777.	1.2	7
668	Crystal Structure and Site-directed Mutagenesis of 3-Ketosteroid 1-Dehydrogenase from <i>Rhodococcus erythropolis</i> SQ1 Explain Its Catalytic Mechanism. <i>Journal of Biological Chemistry</i> , 2013, 288, 35559-35568.	1.6	48
669	Structure and function of Parkin E3 ubiquitin ligase reveals aspects of RING and HECT ligases. <i>Nature Communications</i> , 2013, 4, 1982.	5.8	276
670	A broad specificity nucleoside kinase from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 568-582.	1.5	10
671	Crystal structure and biochemical analyses reveal that the <sc>A</sc>rabidopsis triphosphate tunnel metalloenzyme <sc>A</sc>t<sc>TTM</sc>3 is a tripolyphosphatase involved in root development. <i>Plant Journal</i> , 2013, 76, 615-626.	2.8	33
672	Structure and secretion of <sc>CofJ</sc>, a putative colonization factor of enterotoxigenic <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2013, 90, 898-918.	1.2	18
673	Structure and activity of the NAD(P) ⁺ -dependent succinate semialdehyde dehydrogenase Ynel from <i>Salmonella typhimurium</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1031-1041.	1.5	16
674	Structureâ€¦function analysis of the <sc>LytM</sc> domain of <sc>EnvC</sc>, an activator of cell wall remodelling at the <i>Escherichia coli</i> division site. <i>Molecular Microbiology</i> , 2013, 89, 690-701.	1.2	58
675	Crystal structure of the invertebrate bifunctional purine biosynthesis enzyme PAICS at 2.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1473-1478.	1.5	6
676	Structure, biochemical characterization and analysis of the pleomorphism of carboxylesterase Cest-2923 from <i>Lactobacillus Plantarum</i> WCFS1. <i>FEBS Journal</i> , 2013, 280, 6658-6671.	2.2	32
677	Structure of a translocation signal domain mediating conjugative transfer by type <sc>IV</sc> secretion systems. <i>Molecular Microbiology</i> , 2013, 89, 324-333.	1.2	40
678	Structural and functional aspects of <sc>PR</sc>â€¦10 proteins. <i>FEBS Journal</i> , 2013, 280, 1169-1199.	2.2	191
679	Role of <sc>C</sc>a ²⁺ in folding the tandem 12â€¦sandwich extender domains of a bacterial iceâ€¦binding adhesin. <i>FEBS Journal</i> , 2013, 280, 5919-5932.	2.2	20

#	ARTICLE	IF	CITATIONS
680	Crystal structure of the Î±-aminotransferase from <i>Paracoccus denitrificans</i> and its phylogenetic relationship with other class III aminoâ€•transferases that have biotechnological potential. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 774-787.	1.5	39
681	Structure and Function of the Peanut Panallergen Ara h 8. <i>Journal of Biological Chemistry</i> , 2013, 288, 36890-36901.	1.6	55
682	The Arabidopsis B3 Domain Protein VERNALIZATION1 (VRN1) Is Involved in Processes Essential for Development, with Structural and Mutational Studies Revealing Its DNA-binding Surface. <i>Journal of Biological Chemistry</i> , 2013, 288, 3198-3207.	1.6	32
683	Solution structure of the recombinant target recognition domain of zoocin A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 722-727.	1.5	7
684	Structural and Biochemical Analyses of Glycoside Hydrolase Families 5 and 26 Î²-(1,4)-Mannanases from <i>Podospora anserina</i> Reveal Differences upon Manno-oligosaccharide Catalysis. <i>Journal of Biological Chemistry</i> , 2013, 288, 14624-14635.	1.6	80
685	ubil, a New Gene in <i>Escherichia coli</i> Coenzyme Q Biosynthesis, Is Involved in Aerobic C5-hydroxylation. <i>Journal of Biological Chemistry</i> , 2013, 288, 20085-20092.	1.6	45
686	Deubiquitinase function of arterivirus papain-like protease 2 suppresses the innate immune response in infected host cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E838-47.	3.3	108
687	Structure of the <i>Chlamydia trachomatis</i> Immunodominant Antigen Pgp3. <i>Journal of Biological Chemistry</i> , 2013, 288, 22068-22079.	1.6	41
688	Structure and Function of Allophanate Hydrolase. <i>Journal of Biological Chemistry</i> , 2013, 288, 21422-21432.	1.6	26
689	Molecular Basis for the Recognition of Long-chain Substrates by Plant Î±-Glucosidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 19296-19303.	1.6	83
690	Fusion of Dioxygenase and Lignin-binding Domains in a Novel Secreted Enzyme from Cellulolytic <i>Streptomyces</i> sp. SirexAA-E. <i>Journal of Biological Chemistry</i> , 2013, 288, 18574-18587.	1.6	40
691	Identification and Structural Characterization of a <i>Legionella</i> Phosphoinositide Phosphatase*. <i>Journal of Biological Chemistry</i> , 2013, 288, 24518-24527.	1.6	69
692	Crystal Structure and Mode of Helicase Binding of the C-Terminal Domain of Primase from <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2826-2838.	1.0	25
693	The 2.5 Å... Structure of the <i>Enterococcus</i> Conjugation Protein TraM resembles VirB8 Type IV Secretion Proteins. <i>Journal of Biological Chemistry</i> , 2013, 288, 2018-2028.	1.6	50
694	Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12301-12306.	3.3	68
695	Full-length GÎ± phospholipase C-Î²3 structure reveals interfaces of the C-terminal coiled-coil domain. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 355-362.	3.6	84
696	Structural basis for cytosolic double-stranded RNA surveillance by human oligoadenylate synthetase 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1652-1657.	3.3	142
697	Biochemical Properties and Crystal Structure of a Î²-Phenylalanine Aminotransferase from <i>Variovorax paradoxus</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 185-195.	1.4	29

#	ARTICLE	IF	CITATIONS
698	Catalytic site identification—a web server to identify catalytic site structural matches throughout PDB. <i>Nucleic Acids Research</i> , 2013, 41, W256-W265.	6.5	28
699	Crystal structure of a prokaryotic (6-4) photolyase with an Fe-S cluster and a 6,7-dimethyl-8-ribityllumazine antenna chromophore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7217-7222.	3.3	89
700	Structure of the Absent in Melanoma 2 (AIM2) Pyrin Domain Provides Insights into the Mechanisms of AIM2 Autoinhibition and Inflammasome Assembly. <i>Journal of Biological Chemistry</i> , 2013, 288, 13225-13235.	1.6	138
701	The Structure of the NTPase That Powers DNA Packaging into Sulfolobus Turreted Icosahedral Virus 2. <i>Journal of Virology</i> , 2013, 87, 8388-8398.	1.5	19
702	<i>Porphyromonas gingivalis</i> Virulence Factor Gingipain RgpB Shows a Unique Zymogenic Mechanism for Cysteine Peptidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 14287-14296.	1.6	33
703	Bunyamwera virus possesses a distinct nucleocapsid protein to facilitate genome encapsidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9048-9053.	3.3	52
704	Assembly and mechanism of a group II ECF transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2534-2539.	3.3	51
705	Structure of the archaeal Cascade subunit Csa5. <i>RNA Biology</i> , 2013, 10, 762-769.	1.5	24
706	Functional Diversification of Cerato-Platanins in <i>Moniliophthora perniciosa</i> as Seen by Differential Expression and Protein Function Specialization. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1281-1293.	1.4	58
707	UDP-galactopyranose mutase as a possible drug target for the human filarial parasite, <i>Brugia malayi</i> : an in silico evaluation. <i>International Journal of Medical Engineering and Informatics</i> , 2013, 5, 372.	0.2	3
708	Aberrant 3' oligoadenylation of spliceosomal U6 small nuclear RNA in poikiloderma with neutropenia. <i>Blood</i> , 2013, 121, 1028-1038.	0.6	65
709	The lysine gingipain adhesin domains from <i>Porphyromonas gingivalis</i> interact with erythrocytes and albumin: Structures correlate to function. <i>European Journal of Microbiology and Immunology</i> , 2013, 3, 152-162.	1.5	8
710	Tracking in atomic detail the functional specializations in viral RecA helicases that occur during evolution. <i>Nucleic Acids Research</i> , 2013, 41, 9396-9410.	6.5	23
711	Crystal structure of SsfS6, the putative C-glycosyltransferase involved in SF2575 biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1277-1282.	1.5	24
713	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 526-575.	1.0	13
714	Structural Prediction of [GADV]-Proteins Using Threading and Ab initio Modeling for Investigations of the Origin of Life. <i>Journal of Computer Aided Chemistry</i> , 2013, 14, 23-35.	0.3	1
715	Structural and Functional Insight into ADF/Cofilin from <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2013, 8, e53639.	1.1	8
716	Crystallographic Observation of pH-Induced Conformational Changes in the Amyloid transitella Pheromone-Binding Protein AtrPBP1. <i>PLoS ONE</i> , 2013, 8, e53840.	1.1	43

#	ARTICLE	IF	CITATIONS
717	Combining Functional and Structural Genomics to Sample the Essential Burkholderia Structome. PLoS ONE, 2013, 8, e53851.	1.1	113
718	The <i>Deinococcus radiodurans</i> 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
719	The <i>E. coli</i> Effector Protein NleF Is a Caspase Inhibitor. PLoS ONE, 2013, 8, e58937.	1.1	83
720	Horizontal Transfer of a Subtilisin Gene from Plants into an Ancestor of the Plant Pathogenic Fungal Genus <i>Colletotrichum</i> . PLoS ONE, 2013, 8, e59078.	1.1	28
721	An Archaeal Homolog of Proteasome Assembly Factor Functions as a Proteasome Activator. PLoS ONE, 2013, 8, e60294.	1.1	19
722	Crystal Structures of a Plant Trypsin Inhibitor from <i>Enterolobium contortisiliquum</i> (EcTI) and of Its Complex with Bovine Trypsin. PLoS ONE, 2013, 8, e62252.	1.1	30
723	Structural Insights into the UbiD Protein Family from the Crystal Structure of PA0254 from <i>Pseudomonas aeruginosa</i> . PLoS ONE, 2013, 8, e63161.	1.1	33
724	Engineering of Family-5 Glycoside Hydrolase (Cel5A) from an Uncultured Bacterium for Efficient Hydrolysis of Cellulosic Substrates. PLoS ONE, 2013, 8, e65727.	1.1	20
725	Structural Insights into the Effector $\alpha\epsilon$ Immunity System Tae4/Tai4 from <i>Salmonella typhimurium</i> . PLoS ONE, 2013, 8, e67362.	1.1	26
726	Structural Basis of the Novel <i>S. pneumoniae</i> Virulence Factor, GHIP, a Glycosyl Hydrolase 25 Participating in Host-Cell Invasion. PLoS ONE, 2013, 8, e68647.	1.1	13
727	Structural and Functional Characterisation of TesA - A Novel Lysophospholipase A from <i>Pseudomonas aeruginosa</i> . PLoS ONE, 2013, 8, e69125.	1.1	51
728	Structure Determination and Biochemical Characterization of a Putative HNH Endonuclease from <i>Geobacter metallireducens</i> GS-15. PLoS ONE, 2013, 8, e72114.	1.1	12
729	Mutational and Structural Analyses of <i>Caldanaerobius polysaccharolyticus</i> Man5B Reveal Novel Active Site Residues for Family 5 Glycoside Hydrolases. PLoS ONE, 2013, 8, e80448.	1.1	9
730	Crystal Structures of the Human G3BP1 NTF2-Like Domain Visualize FxFC Nup Repeat Specificity. PLoS ONE, 2013, 8, e80947.	1.1	43
731	Structures of Wnt-Antagonist ZNRF3 and Its Complex with R-Spondin 1 and Implications for Signaling. PLoS ONE, 2013, 8, e83110.	1.1	58
732	Effective Moment Feature Vectors for Protein Domain Structures. PLoS ONE, 2013, 8, e83788.	1.1	4
733	Exoproteome and Secretome Derived Broad Spectrum Novel Drug and Vaccine Candidates in <i>Vibrio cholerae</i> Targeted by Piper betel Derived Compounds. PLoS ONE, 2013, 8, e52773.	1.1	95
734	Bacterial Cell Division Regulation by Ser/Thr Kinases: A Structural Perspective. Current Protein and Peptide Science, 2013, 13, 756-766.	0.7	0

#	ARTICLE	IF	CITATIONS
735	The Receptor for Advanced Glycation End-Products (RAGE) Is Only Present in Mammals, and Belongs to a Family of Cell Adhesion Molecules (CAMs). PLoS ONE, 2014, 9, e86903.	1.1	115
736	Interaction of a Partially Disordered Antisigma Factor with Its Partner, the Signaling Domain of the TonB-Dependent Transporter HasR. PLoS ONE, 2014, 9, e89502.	1.1	13
737	Shedding Some Light over the Floral Metabolism by Arum Lily (<i>Zantedeschia aethiopica</i>) Spathe De Novo Transcriptome Assembly. PLoS ONE, 2014, 9, e90487.	1.1	16
738	Esterase LpEst1 from <i>Lactobacillus plantarum</i> : A Novel and Atypical Member of the $\hat{I}\pm\hat{I}^2$ Hydrolase Superfamily of Enzymes. PLoS ONE, 2014, 9, e92257.	1.1	23
739	Crystal Structure of ORF210 from <i>E. coli</i> O157:H1 Phage CBA120 (TSP1), a Putative Tailspike Protein. PLoS ONE, 2014, 9, e93156.	1.1	18
740	Structural and Biochemical Analysis of a Unique Phosphatase from <i>Bdellovibrio bacteriovorus</i> Reveals Its Structural and Functional Relationship with the Protein Tyrosine Phosphatase Class of Phytase. PLoS ONE, 2014, 9, e94403.	1.1	14
741	Structure of CbpA J-Domain Bound to the Regulatory Protein CbpM Explains Its Specificity and Suggests Evolutionary Link between CbpM and Transcriptional Regulators. PLoS ONE, 2014, 9, e100441.	1.1	8
742	Structural and Functional Characterization of DUF1471 Domains of <i>Salmonella</i> Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	1.1	13
743	The Structure of the TFIIH p34 Subunit Reveals a Von Willebrand Factor A Like Fold. PLoS ONE, 2014, 9, e102389.	1.1	10
744	BdcA, a Protein Important for <i>Escherichia coli</i> Biofilm Dispersal, Is a Short-Chain Dehydrogenase/Reductase that Binds Specifically to NADPH. PLoS ONE, 2014, 9, e105751.	1.1	18
745	The Eps1p Protein Disulfide Isomerase Conserves Classic Thioredoxin Superfamily Amino Acid Motifs but Not Their Functional Geometries. PLoS ONE, 2014, 9, e113431.	1.1	5
746	Structure Based Annotation of <i>Helicobacter pylori</i> Strain 26695 Proteome. PLoS ONE, 2014, 9, e115020.	1.1	3
747	Activation-triggered subunit exchange between CaMKII holoenzymes facilitates the spread of kinase activity. ELife, 2014, 3, e01610.	2.8	87
748	Structural and biochemical characterization of MdaB from cariogenic <i>Streptococcus mutans</i> reveals an NADPH-specific quinone oxidoreductase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 912-921.	2.5	9
749	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. Frontiers in Genetics, 2014, 5, 102.	1.1	164
750	A Ras-like domain in the light intermediate chain bridges the dynein motor to a cargo-binding region. ELife, 2014, 3, e03351.	2.8	84
751	Analysis of Spatial and Temporal Protein Expression in the Cerebral Cortex after Ischemia-Reperfusion		

#	ARTICLE	IF	CITATIONS
753	Structure and Catalytic Mechanism of a Glycoside Hydrolase Family-127 β -L-Arabinofuranosidase (HypBA1). <i>Journal of Bioprocessing & Biotechniques</i> , 2014, 04, .	0.2	1
754	Crystal structure of PfRh5, an essential <i>P. falciparum</i> ligand for invasion of human erythrocytes. <i>ELife</i> , 2014, 3, .	2.8	53
755	Structural Systems Biology: Modeling Interactions and Networks for Systems Studies. , 2014, , 9-19.		0
756	The Crystal Structure of Siroheme Decarboxylase in Complex with Iron-Uroporphyrin III Reveals Two Essential Histidine Residues. <i>Journal of Molecular Biology</i> , 2014, 426, 3272-3286.	2.0	15
757	The highly conserved domain of unknown function 1792 has a distinct glycosyltransferase fold. <i>Nature Communications</i> , 2014, 5, 4339.	5.8	61
758	Structural insights into yeast histone chaperone Hif1: a scaffold protein recruiting protein complexes to core histones. <i>Biochemical Journal</i> , 2014, 462, 465-473.	1.7	14
759	E2-Ub conjugates regulate the kinase activity of Shigella effector OspG during pathogenesis. <i>EMBO Journal</i> , 2014, 33, n/a-n/a.	3.5	53
760	Structural and enzymatic insights into Lambda glutathione transferases from <i>Populus trichocarpa</i> , monomeric enzymes constituting an early divergent class specific to terrestrial plants. <i>Biochemical Journal</i> , 2014, 462, 39-52.	1.7	46
761	Mitochondrial COQ9 is a lipid-binding protein that associates with COQ7 to enable coenzyme Q biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4697-705.	3.3	113
762	Structural and Biochemical Characterization of Chlamydia trachomatis Hypothetical Protein CT263 Supports That Menaquinone Synthesis Occurs through the Futasine Pathway. <i>Journal of Biological Chemistry</i> , 2014, 289, 32214-32229.	1.6	23
763	Structural Basis for Different Phosphoinositide Specificities of the PX Domains of Sorting Nexins Regulating G-protein Signaling. <i>Journal of Biological Chemistry</i> , 2014, 289, 28554-28568.	1.6	43
764	In silico work flow for scaffold hopping in Leishmania. <i>BMC Research Notes</i> , 2014, 7, 802.	0.6	9
765	Mechanisms of Toxin Inhibition and Transcriptional Repression by Escherichia coli DinJ-YafQ. <i>Journal of Biological Chemistry</i> , 2014, 289, 20559-20569.	1.6	42
766	Structural Insights into the Lipoprotein Outer Membrane Regulator of Penicillin-binding Protein 1B. <i>Journal of Biological Chemistry</i> , 2014, 289, 19245-19253.	1.6	17
767	Suppressor Mutations Suggest a Surface on PAT-4 (Integrin-linked Kinase) That Interacts with UNC-112 (Kindlin). <i>Journal of Biological Chemistry</i> , 2014, 289, 14252-14262.	1.6	14
768	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	1.6	28
769	Structural and Functional Insights into the Human Björjeson-Forsman-Lehmann Syndrome-associated Protein PHF6. <i>Journal of Biological Chemistry</i> , 2014, 289, 10069-10083.	1.6	59
770	SbnG, a Citrate Synthase in Staphylococcus aureus. <i>Journal of Biological Chemistry</i> , 2014, 289, 33797-33807.	1.6	18

#	ARTICLE	IF	CITATIONS
771	Structure and Mechanism of Cysteine Peptidase Gingipain K (Kgp), a Major Virulence Factor of <i>Porphyromonas gingivalis</i> in Periodontitis. <i>Journal of Biological Chemistry</i> , 2014, 289, 32291-32302.	1.6	74
772	Structural basis for the broad specificity of a new family of amino-acid racemases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 79-90.	2.5	61
773	FLRT Structure: Balancing Repulsion and Cell Adhesion in Cortical and Vascular Development. <i>Neuron</i> , 2014, 84, 370-385.	3.8	117
774	Structural Basis for Bacterial Quorum Sensing-mediated Oxalogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 11465-11475.	1.6	9
775	A Novel Unsaturated β -Glucuronidase Involved in Ulvan Degradation Unveils the Versatility of Stereochemistry Requirements in Family GH105. <i>Journal of Biological Chemistry</i> , 2014, 289, 6199-6211.	1.6	46
776	Evidence for an evolutionary relationship between the large adaptor nucleoporin Nup192 and karyopherins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2530-2535.	3.3	44
777	Holocyclotoxin-1, a cystine knot toxin from <i>Ixodes holocyclus</i> . <i>Toxicon</i> , 2014, 90, 308-317.	0.8	23
778	Cancer-relevant Splicing Factor CAPER β Engages the Essential Splicing Factor SF3b155 in a Specific Ternary Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 17325-17337.	1.6	49
779	Roquin binding to target mRNAs involves a winged helix-turn-helix motif. <i>Nature Communications</i> , 2014, 5, 5701.	5.8	41
780	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21242-21251.	1.6	9
781	Structure-based investigation into the functional roles of the extended loop and substrate-recognition sites in an endo- β -1,4-d-mannanase from the Antarctic springtail, <i>Cryptopygus antarcticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3217-3223.	1.5	17
782	Lsm2 and Lsm3 bridge the interaction of the Lsm1-7 complex with Pat1 for decapping activation. <i>Cell Research</i> , 2014, 24, 233-246.	5.7	43
783	Structural and functional studies of Bud23 Δ Trm112 reveal 18S rRNA N ⁷ -G1575 methylation occurs on late 40S precursor ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5518-26.	3.3	81
784	Structural and functional characterization of the MERIT40 to understand its role in DNA repair. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 2017-2032.	2.0	6
785	A structure-specific nucleic acid-binding domain conserved among DNA repair proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7618-7623.	3.3	34
786	Molecular insights into the membrane-associated phosphatidylinositol 4-kinase $\text{III}\beta$. <i>Nature Communications</i> , 2014, 5, 3552.	5.8	52
787	Crystal structure of juvenile hormone epoxide hydrolase from the silkworm <i>Bombyx mori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3224-3229.	1.5	18
788	A computational model for non-conserved mature miRNAs from the rice genome. <i>SAR and QSAR in Environmental Research</i> , 2014, 25, 205-220.	1.0	3

#	ARTICLE	IF	CITATIONS
789	ComEA Is Essential for the Transfer of External DNA into the Periplasm in Naturally Transformable <i>Vibrio cholerae</i> Cells. <i>PLoS Genetics</i> , 2014, 10, e1004066.	1.5	107
790	Structural Insight into Host Recognition by Aggregative Adherence Fimbriae of Enteroaggregative <i>Escherichia coli</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004404.	2.1	38
791	Crystal Structure of Calcium Binding Protein-5 from <i>Entamoeba histolytica</i> and Its Involvement in Initiation of Phagocytosis of Human Erythrocytes. <i>PLoS Pathogens</i> , 2014, 10, e1004532.	2.1	22
792	Structure of the Trehalose-6-phosphate Phosphatase from <i>Brugia malayi</i> Reveals Key Design Principles for Anthelmintic Drugs. <i>PLoS Pathogens</i> , 2014, 10, e1004245.	2.1	30
793	Outer-membrane lipoprotein LpoB spans the periplasm to stimulate the peptidoglycan synthase PBP1B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8197-8202.	3.3	95
794	Assessing Proteinase K Resistance of Fish Prion Proteins in a Scrapie-Infected Mouse Neuroblastoma Cell Line. <i>Viruses</i> , 2014, 6, 4398-4421.	1.5	5
795	Dimerization of VirD2 Binding Protein Is Essential for <i>Agrobacterium</i> Induced Tumor Formation in Plants. <i>PLoS Pathogens</i> , 2014, 10, e1003948.	2.1	11
796	Structures of the Inducer-Binding Domain of Pentachlorophenol-Degrading Gene Regulator PcpR from <i>Sphingobium chlorophenolicum</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 20736-20752.	1.8	17
797	Structural Insights into <i>Bacillus thuringiensis</i> Cry, Cyt and Parasporin Toxins. <i>Toxins</i> , 2014, 6, 2732-2770.	1.5	144
798	Crystal Structure of <i>Deinococcus radiodurans</i> RecQ Helicase Catalytic Core Domain: The Interdomain Flexibility. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	6
799	The Mtr4 ratchet helix and arch domain both function to promote RNA unwinding. <i>Nucleic Acids Research</i> , 2014, 42, 13861-13872.	6.5	31
800	Lectin-Like Bacteriocins from <i>Pseudomonas</i> spp. Utilise D-Rhamnose Containing Lipopolysaccharide as a Cellular Receptor. <i>PLoS Pathogens</i> , 2014, 10, e1003898.	2.1	56
801	The TRIM-NHL Protein LIN-41 Controls the Onset of Developmental Plasticity in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2014, 10, e1004533.	1.5	62
802	Viral OTU Deubiquitinases: A Structural and Functional Comparison. <i>PLoS Pathogens</i> , 2014, 10, e1003894.	2.1	33
803	Structural and Biochemical Characterization Reveals LysGH15 as an Unprecedented "EF-Hand-Like" Calcium-Binding Phage Lysin. <i>PLoS Pathogens</i> , 2014, 10, e1004109.	2.1	85
804	Heterodimerization of p45 ^{p75} Modulates p75 Signaling: Structural Basis and Mechanism of Action. <i>PLoS Biology</i> , 2014, 12, e1001918.	2.6	21
805	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	2.1	85
806	Structures of bacterial kynurenine formamidase reveal a crowded binuclear zinc catalytic site primed to generate a potent nucleophile. <i>Biochemical Journal</i> , 2014, 462, 581-589.	1.7	9

#	ARTICLE	IF	CITATIONS
807	Aminoacetone oxidase from <i>Streptococcus oligofermentans</i> belongs to a new three-domain family of bacterial flavoproteins. <i>Biochemical Journal</i> , 2014, 464, 387-399.	1.7	13
808	A novel cytosolic NADH:quinone oxidoreductase from <i>Methanothermobacter marburgensis</i> . <i>Bioscience Reports</i> , 2014, 34, e00167.	1.1	4
809	Crystal structure of the R-protein of the multisubunit ATP-dependent restriction endonuclease NgoAVII. <i>Nucleic Acids Research</i> , 2014, 42, 14022-14030.	6.5	8
810	Crystal structure of PhnZ in complex with substrate reveals a di-iron oxygenase mechanism for catabolism of organophosphonates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5171-5176.	3.3	43
811	Crystal structure of <i>Streptococcus pyogenes</i> EndoS, an immunomodulatory endoglycosidase specific for human IgG antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6714-6719.	3.3	56
812	Unique subunit packing in mycobacterial nanoRNase leads to alternate substrate recognitions in DHH phosphodiesterases. <i>Nucleic Acids Research</i> , 2014, 42, 7894-7910.	6.5	25
813	AmiA is a penicillin target enzyme with dual activity in the intracellular pathogen <i>Chlamydia pneumoniae</i> . <i>Nature Communications</i> , 2014, 5, 4201.	5.8	27
814	Structure and function of a spectrin-like regulator of bacterial cytokinesis. <i>Nature Communications</i> , 2014, 5, 5421.	5.8	41
815	Structural Insights into the Catalytic Mechanism of <i>Synechocystis</i> Magnesium Protoporphyrin IX O-Methyltransferase (ChIM). <i>Journal of Biological Chemistry</i> , 2014, 289, 25690-25698.	1.6	20
816	TDP-43 N terminus encodes a novel ubiquitin-like fold and its unfolded form in equilibrium that can be shifted by binding to ssDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18619-18624.	3.3	128
817	Structural and Biochemical Analysis of the <i>Hordeum vulgare</i> L. HvGR-RBP1 Protein, a Glycine-Rich RNA-Binding Protein Involved in the Regulation of Barley Plant Development and Stress Response. <i>Biochemistry</i> , 2014, 53, 7945-7960.	1.2	11
818	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. <i>Cell</i> , 2014, 159, 1511-1523.	13.5	546
819	Crystal structure of BinB: A receptor binding component of the binary toxin from <i>Lysinibacillus sphaericus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2703-2712.	1.5	41
820	Affinity transfer to the archaeal extremophilic Sac7d protein by insertion of a CDR. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 431-438.	1.0	16
821	Structure of 5-hydroxymethylcytosine-specific restriction enzyme, AbaSI, in complex with DNA. <i>Nucleic Acids Research</i> , 2014, 42, 7947-7959.	6.5	27
822	The Atomic Resolution Structure of Human AlkB Homolog 7 (ALKBH7), a Key Protein for Programmed Necrosis and Fat Metabolism. <i>Journal of Biological Chemistry</i> , 2014, 289, 27924-27936.	1.6	36
823	Structure of the <i>V. cholerae</i> Na ⁺ -pumping NADH:quinone oxidoreductase. <i>Nature</i> , 2014, 516, 62-67.	13.7	107
824	Crystal structure of DszC from <i>Rhodococcus</i> sp. XP at 1.79 Å.... <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1708-1720.	1.5	27

#	ARTICLE	IF	CITATIONS
825	Structure-guided analysis of catalytic specificity of the abundantly secreted chitosanase SACTE_5457 from <i>Streptomyces</i> sp. Sirex. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1245-1257.	1.5	33
826	Crystal structure of the novel di-nucleotide cyclase from <i>Vibrio cholerae</i> (DncV) responsible for synthesizing a hybrid cyclic GMP-AMP. Cell Research, 2014, 24, 1270-1273.	5.7	14
827	Crystal structure of the N-terminal methyltransferase-like domain of anamorsin. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1066-1071.	1.5	12
828	The number and location of EF hand motifs dictates the calcium dependence of polycystin-2 function. FASEB Journal, 2014, 28, 2332-2346.	0.2	20
829	Structure and DNA-Binding Traits of the Transition State Regulator AbrB. Structure, 2014, 22, 1650-1656.	1.6	13
830	A Distinct MaoC-like Enoyl-CoA Hydratase Architecture Mediates Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i> . ACS Chemical Biology, 2014, 9, 2632-2645.	1.6	47
831	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
832	Structure of the effector-binding domain of deoxyribonucleoside regulator DeoR from <i>Bacillus subtilis</i> . FEBS Journal, 2014, 281, 4280-4292.	2.2	9
833	Insights into the Bioactivity of Mensacarcin and Epoxide Formation by MsnO8. ChemBioChem, 2014, 15, 749-756.	1.3	16
834	A Basic Protein Comparative Three-Dimensional Modeling Methodological Workflow Theory and Practice. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1052-1065.	1.9	5
835	Structure of the pneumococcal <i>DacB</i> and pathophysiological effects of disabled cell wall hydrolases <i>DacA</i> and <i>DacB</i> . Molecular Microbiology, 2014, 93, 1183-1206.	1.2	37
836	Structures of lipoyl synthase reveal a compact active site for controlling sequential sulfur insertion reactions. Biochemical Journal, 2014, 464, 123-133.	1.7	66
837	Structure of human peptidylprolyl <i>cis-trans</i> isomerase FKBP22 containing two EF-hand motifs. Protein Science, 2014, 23, 67-75.	3.1	22
838	Three-dimensional NMR Structure of Hen Egg Gallin (Chicken Ovodefensin) Reveals a New Variation of the β^2 -Defensin Fold. Journal of Biological Chemistry, 2014, 289, 7211-7220.	1.6	23
839	Crystal structure of <i>Legionella pneumophila</i> dephospho-CoA kinase reveals a non-canonical conformation of P-loop. Journal of Structural Biology, 2014, 188, 233-239.	1.3	2
840	Crystal structure of the VapBC-15 complex from <i>Mycobacterium tuberculosis</i> reveals a two-metal ion dependent PIN-domain ribonuclease and a variable mode of toxin-antitoxin assembly. Journal of Structural Biology, 2014, 188, 249-258.	1.3	47
841	X-ray structure of a novel endolysin encoded by episomal phage <i>phiSM101</i> of <i>Clostridium perfringens</i> . Molecular Microbiology, 2014, 92, 326-337.	1.2	42
842	A complex gene locus enables xyloglucan utilization in the model saprophyte <i>Vibrio japonicus</i> . Molecular Microbiology, 2014, 94, 418-433.	1.2	63

#	ARTICLE	IF	CITATIONS
843	The structural basis of the Tle4-Tli4 complex reveals the self-protection mechanism of H2-T6SS in <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3233-3243.	2.5	28
844	Murine norovirus protein NS1/2 aspartate to glutamate mutation, sufficient for persistence, reorients side chain of surface exposed tryptophan within a novel structured domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1200-1209.	1.5	19
845	Novel mutations in CYP51B from <i>Penicillium digitatum</i> involved in prochloraz resistance. <i>Journal of Microbiology</i> , 2014, 52, 762-770.	1.3	40
846	Structure of vaccinia virus A46, an inhibitor of TLR4 signaling pathway, shows the conformation of VIPER motif. <i>Protein Science</i> , 2014, 23, 906-914.	3.1	13
847	The Structure of the Catalytic Domain of a Plant Cellulose Synthase and Its Assembly into Dimers. <i>Plant Cell</i> , 2014, 26, 2996-3009.	3.1	61
848	Structural and functional analysis show that the <i>Escherichia coli</i> uncharacterized protein YjcS is likely an alkylsulfatase. <i>Protein Science</i> , 2014, 23, 1442-1450.	3.1	8
849	Structural analysis of human soluble adenylyl cyclase and crystal structures of its nucleotide complexes—implications for cyclase catalysis and evolution. <i>FEBS Journal</i> , 2014, 281, 4151-4164.	2.2	24
850	Protein universe containing a PUA RNA-binding domain. <i>FEBS Journal</i> , 2014, 281, 74-87.	2.2	18
851	RsaM: a transcriptional regulator of <i>Burkholderia</i> spp. with novel fold. <i>FEBS Journal</i> , 2014, 281, 4293-4306.	2.2	14
852	The <i>Legionella pneumophila kai</i> operon is implicated in stress response and confers fitness in competitive environments. <i>Environmental Microbiology</i> , 2014, 16, 359-381.	1.8	26
853	Crystal structures and kinetic properties of enoyl-acyl carrier protein reductase I from <i>Candidatus Liberibacter asiaticus</i> . <i>Protein Science</i> , 2014, 23, 366-377.	3.1	5
854	Structure of the hypothetical protein Ton 1535 from <i>Thermococcus onnurineus</i> NA1 reveals unique structural properties by a left-handed helical turn in normal α -solenoid protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1072-1078.	1.5	1
855	Molecular Basis for DPY-30 Association to COMPASS-like and NURF Complexes. <i>Structure</i> , 2014, 22, 1821-1830.	1.6	40
856	Crystal structure of phospholipase PA2 β , a protease-activated receptor agonist from the <i>Trimeresurus stejnegeri</i> snake venom. <i>FEBS Letters</i> , 2014, 588, 4604-4612.	1.3	6
857	An Ancient Autoproteolytic Domain Found in GAIN, ZU5 and Nucleoporin98. <i>Journal of Molecular Biology</i> , 2014, 426, 3935-3945.	2.0	11
858	Expression from engineered <i>Escherichia coli</i> chromosome and crystallographic study of archaeal N ₁ , N ₂ -diacetylchitobiose deacetylase. <i>FEBS Journal</i> , 2014, 281, 2584-2596.	2.2	22
859	Crystal structure of the secreted protein HP1454 from the human pathogen <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2868-2873.	1.5	2
860	X-ray structure of a novel <i>l</i> -ribose isomerase acting on a non-natural sugar <i>l</i> -ribose as its ideal substrate. <i>FEBS Journal</i> , 2014, 281, 3150-3164.	2.2	14

#	ARTICLE	IF	CITATIONS
861	Sequence, biophysical, and structural analyses of the PstS lipoprotein (BB0215) from <i>Borrelia burgdorferi</i> reveal a likely binding component of an ABC-type phosphate transporter. <i>Protein Science</i> , 2014, 23, 200-212.	3.1	21
862	Structural and functional characterization of BaiA, an enzyme involved in secondary bile acid synthesis in human gut microbe. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 216-229.	1.5	34
863	Structure of the meningococcal vaccine antigen NadA and epitope mapping of a bactericidal antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17128-17133.	3.3	60
864	Identification of Low-Molecular-Weight Compounds Inhibiting Growth of Corynebacteria: Potential Lead Compounds for Antibiotics. <i>ChemMedChem</i> , 2014, 9, 282-285.	1.6	3
865	Molecular dynamics simulations show how the FMRP Ile304Asn mutation destabilizes the KH2 domain structure and affects its function. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 337-350.	2.0	21
866	Structural and functional analysis of the fibronectin-binding protein FNE from <i>Streptococcus equi</i> spp. <i>FEBS Journal</i> , 2014, 281, 5513-5531.	2.2	17
867	Structure of the <i>Mycobacterium tuberculosis</i> type VII secretion system chaperone EspG ₅ in complex with PE ₂₅ –PPE ₄₁ dimer. <i>Molecular Microbiology</i> , 2014, 94, 367-382.	1.2	83
868	Structure solution with ARCIMBOLDO using fragments derived from distant homology models. <i>FEBS Journal</i> , 2014, 281, 4029-4045.	2.2	41
869	Structural characterization of MepB from <i>Staphylococcus aureus</i> reveals homology to endonucleases. <i>Protein Science</i> , 2014, 23, 594-602.	3.1	6
870	The double PHD finger domain of MOZ/MYST3 induces \pm -helical structure of the histone H3 tail to facilitate acetylation and methylation sampling and modification. <i>Nucleic Acids Research</i> , 2014, 42, 822-835.	6.5	72
871	Structural and functional analysis of MiD51, a dynamin receptor required for mitochondrial fission. <i>Journal of Cell Biology</i> , 2014, 204, 477-486.	2.3	91
872	Protein Hit1, a novel box C/D snoRNP assembly factor, controls cellular concentration of the scaffolding protein Rsa1 by direct interaction. <i>Nucleic Acids Research</i> , 2014, 42, 10731-10747.	6.5	37
873	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2014, 7, 109.	6.2	69
874	Mannan specific family 35 carbohydrate-binding module (CtCBM35) of <i>Clostridium thermocellum</i> : structure analysis and ligand binding. <i>Biologia (Poland)</i> , 2014, 69, 1271-1282.	0.8	1
875	Crystal Structure of the <i>Bacillus subtilis</i> Phosphodiesterase PhoD Reveals an Iron and Calcium-containing Active Site. <i>Journal of Biological Chemistry</i> , 2014, 289, 30889-30899.	1.6	96
876	Crystal Structure of the Herpesvirus Inner Tegument Protein UL37 Supports Its Essential Role in Control of Viral Trafficking. <i>Journal of Virology</i> , 2014, 88, 5462-5473.	1.5	37
877	Structural basis of lariat RNA recognition by the intron debranching enzyme Dbr1. <i>Nucleic Acids Research</i> , 2014, 42, 10845-10855.	6.5	42
878	The RIG-I ATPase core has evolved a functional requirement for allosteric stabilization by the Pincer domain. <i>Nucleic Acids Research</i> , 2014, 42, 11601-11611.	6.5	23

#	ARTICLE	IF	CITATIONS
879	MMDB and VAST+: tracking structural similarities between macromolecular complexes. <i>Nucleic Acids Research</i> , 2014, 42, D297-D303.	6.5	278
880	Crystal structure of the essential transcription antiterminator M2-1 protein of human respiratory syncytial virus and implications of its phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1580-1585.	3.3	58
881	Structural Determinants Allowing Transferase Activity in SENSITIVE TO FREEZING 2, Classified as a Family I Glycosyl Hydrolase. <i>Journal of Biological Chemistry</i> , 2014, 289, 26089-26106.	1.6	23
882	Crystal structure of tRNA m1G9 methyltransferase Trm10: insight into the catalytic mechanism and recognition of tRNA substrate. <i>Nucleic Acids Research</i> , 2014, 42, 509-525.	6.5	46
883	A novel Î ² -xylosidase structure from <i>Geobacillus thermoglucosidasius</i> : the first crystal structure of a glycoside hydrolase family GH52 enzyme reveals unpredicted similarity to other glycoside hydrolase folds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1366-1374.	2.5	17
884	Identifying functionally important cis-peptide containing segments in proteins and their utility in molecular function annotation. <i>FEBS Journal</i> , 2014, 281, 5602-5621.	2.2	5
885	Entrapment of DNA in an intersubunit tunnel system of a single-stranded DNA-binding protein. <i>Nucleic Acids Research</i> , 2014, 42, 6698-6708.	6.5	15
886	Structural basis for the regulatory function of a complex zinc-binding domain in a replicative arterivirus helicase resembling a nonsense-mediated mRNA decay helicase. <i>Nucleic Acids Research</i> , 2014, 42, 3464-3477.	6.5	47
887	Structure of tyrosine aminotransferase from <i>Leishmania infantum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 583-587.	0.4	18
888	Structural insights into the dimerization of the response regulator ComE from <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 5302-5313.	6.5	54
889	Structural basis for Klf4 recognition of methylated DNA. <i>Nucleic Acids Research</i> , 2014, 42, 4859-4867.	6.5	81
890	Genome-Wide Search for Eliminating Domains Reveals Novel Function for BLES03-Like Proteins. <i>Genome Biology and Evolution</i> , 2014, 6, 2017-2033.	1.1	2
891	The family-wide structure and function of human dual-specificity protein phosphatases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 421-435.	2.5	34
892	Structures of trehalose synthase from <i>Deinococcus radiodurans</i> reveal that a closed conformation is involved in catalysis of the intramolecular isomerization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3144-3154.	2.5	14
893	Structure of a short-chain dehydrogenase/reductase (SDR) within a genomic island from a clinical strain of <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1318-1323.	0.4	5
894	Crystal structures of IspF from <i>Plasmodium falciparum</i> and <i>Burkholderia cenocepacia</i> : comparisons inform antimicrobial drug target assessment. <i>BMC Structural Biology</i> , 2014, 14, 1.	2.3	34
895	Structural basis for regulation of rhizobial nodulation and symbiosis gene expression by the regulatory protein NodR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6509-6514.	3.3	23
896	Crystal Structures of the Toll/Interleukin-1 Receptor (TIR) Domains from the <i>Brucella</i> Protein TcpB and Host Adaptor TIRAP Reveal Mechanisms of Molecular Mimicry. <i>Journal of Biological Chemistry</i> , 2014, 289, 669-679.	1.6	66

#	ARTICLE	IF	CITATIONS
897	Structure of the TbBILBO1 Protein N-terminal Domain from <i>Trypanosoma brucei</i> Reveals an Essential Requirement for a Conserved Surface Patch. <i>Journal of Biological Chemistry</i> , 2014, 289, 3724-3735.	1.6	15
898	Structural Determinants for Binding of Sorting Nexin 17 (SNX17) to the Cytoplasmic Adaptor Protein Krev Interaction Trapped 1 (KRIT1). <i>Journal of Biological Chemistry</i> , 2014, 289, 25362-25373.	1.6	23
899	Structural Analysis of Glucuronoxylan-specific Xyn30D and Its Attached CBM35 Domain Gives Insights into the Role of Modularity in Specificity*. <i>Journal of Biological Chemistry</i> , 2014, 289, 31088-31101.	1.6	32
900	Structure solution of DNA-binding proteins and complexes with <i>ARCIMBOLDO</i> libraries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1743-1757.	2.5	19
901	The structure of the cysteine protease and lectin-like domains of Cwp84, a surface layer-associated protein from <i>Clostridium difficile</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1983-1993.	2.5	15
902	Structural basis for the substrate selectivity of PvuRtsII, a 5-hydroxymethylcytosine DNA restriction endonuclease. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2477-2486.	2.5	13
903	Structural basis for the recognition of muramyltripeptide by <i>Helicobacter pylori</i> Csd4, a <i>D</i> -carboxypeptidase controlling the helical cell shape. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2800-2812.	2.5	20
904	Structure of the carboxy-terminal domain of <i>Mycobacterium tuberculosis</i> CarD protein: an essential rRNA transcriptional regulator. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 160-165.	0.4	2
905	1.55 Å resolution X-ray crystal structure of Rv3902c from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 414-417.	0.4	1
906	1.15 Å resolution structure of the proteasome-assembly chaperone Nas2 PDZ domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 418-423.	0.4	7
907	Structure of 4-pyridoxolactonase from <i>Mesorhizobium loti</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 424-432.	0.4	0
908	Structure of D-tagatose 3-epimerase-like protein from <i>Methanocaldococcus jannaschii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 890-895.	0.4	3
909	Structure of a DsbF homologue from <i>Corynebacterium diphtheriae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1167-1172.	0.4	3
910	Longin and GAF Domains: Structural Evolution and Adaptation to the Subcellular Trafficking Machinery. <i>Traffic</i> , 2014, 15, 104-121.	1.3	40
911	Structures of a Bifunctional Cell Wall Hydrolase CwlT Containing a Novel Bacterial Lysozyme and an NlpC/P60 dl-Endopeptidase. <i>Journal of Molecular Biology</i> , 2014, 426, 169-184.	2.0	25
912	Multiple Functional Roles of the Accessory I-Domain of Bacteriophage P22 Coat Protein Revealed by NMR Structure and CryoEM Modeling. <i>Structure</i> , 2014, 22, 830-841.	1.6	40
913	Identification of the Active Sites in the Methyltransferases of a Transcribing dsRNA Virus. <i>Journal of Molecular Biology</i> , 2014, 426, 2167-2174.	2.0	15
914	Structural Determinants of Unique Properties of Human IgG4-Fc. <i>Journal of Molecular Biology</i> , 2014, 426, 630-644.	2.0	96

#	ARTICLE	IF	CITATIONS
915	Genomic organization, sequence characterization and expression analysis of <i>Tenebrio molitor</i> apolipoprotein-III in response to an intracellular pathogen, <i>Listeria monocytogenes</i> . <i>Gene</i> , 2014, 534, 204-217.	1.0	17
916	Mechanistic Implications for the Chorismatase FkbO Based on the Crystal Structure. <i>Journal of Molecular Biology</i> , 2014, 426, 105-115.	2.0	15
917	Characterization and crystal structure of a first fungal glyoxylate reductase from <i>Paecilomyces thermophila</i> . <i>Enzyme and Microbial Technology</i> , 2014, 60, 72-79.	1.6	2
918	Biochemical fossils of the ancient transition from geoenergetics to bioenergetics in prokaryotic one carbon compound metabolism. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 964-981.	0.5	78
919	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 103-118.	1.5	3
920	Influence of N- and/or C-terminal regions on activity, expression, characteristics and structure of lipase from <i>Geobacillus</i> sp. 95. <i>Extremophiles</i> , 2014, 18, 131-145.	0.9	18
921	SRP RNA Remodeling by SRP68 Explains Its Role in Protein Translocation. <i>Science</i> , 2014, 344, 101-104.	6.0	37
922	<i>Legionella pneumophila</i> Subversion of Host Vesicular Transport by SidC Effector Proteins. <i>Traffic</i> , 2014, 15, 488-499.	1.3	56
923	Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2014, 156, 935-949.	13.5	1,690
924	Structure of bacteriophage SPN1 S endolysin reveals an unusual two-module fold for the peptidoglycan lytic and binding activity. <i>Molecular Microbiology</i> , 2014, 92, 316-325.	1.2	23
925	Cyclolization of D-Lysergic Acid Alkaloid Peptides. <i>Chemistry and Biology</i> , 2014, 21, 146-155.	6.2	45
926	Molecular basis for AUXIN RESPONSE FACTOR protein interaction and the control of auxin response repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5427-5432.	3.3	249
927	<i>Sulfolobus solfataricus</i> thiol redox puzzle: characterization of an atypical protein disulfide oxidoreductase. <i>Extremophiles</i> , 2014, 18, 219-228.	0.9	13
928	Algorithms, Applications, and Challenges of Protein Structure Alignment. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 94, 121-175.	1.0	40
929	Structure of the core ectodomain of the hepatitis C virus envelope glycoprotein 2. <i>Nature</i> , 2014, 509, 381-384.	13.7	259
930	Structure of the Yeast Mitochondrial Large Ribosomal Subunit. <i>Science</i> , 2014, 343, 1485-1489.	6.0	521
931	Enhancing thermostability and the structural characterization of <i>Microbacterium saccharophilum</i> K-1 β -fructofuranosidase. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6667-6677.	1.7	18
932	Molecular Dynamics Simulations and Structure-Guided Mutagenesis Provide Insight into the Architecture of the Catalytic Core of the Ectoine Hydroxylase. <i>Journal of Molecular Biology</i> , 2014, 426, 586-600.	2.0	43

#	ARTICLE	IF	CITATIONS
933	CdiA from <i>Enterobacter cloacae</i> Delivers a Toxic Ribosomal RNase into Target Bacteria. <i>Structure</i> , 2014, 22, 707-718.	1.6	60
934	Structure of crenactin, an archaeal actin homologue active at 90Å°C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 492-500.	2.5	23
935	Crystal structure of <i>Mycobacterium tuberculosis</i> CarD, an essential RNA polymerase binding protein, reveals a quasidomain-swapped dimeric structural architecture. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 879-884.	1.5	21
936	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. <i>Science</i> , 2014, 344, 299-303.	6.0	300
937	RipD (Rv1566c) from <i>Mycobacterium tuberculosis</i> : adaptation of an NlpC/p60 domain to a non-catalytic peptidoglycan-binding function. <i>Biochemical Journal</i> , 2014, 457, 33-41.	1.7	21
938	Molecular modeling, simulation and virtual screening of ribosomal phosphoprotein P1 from <i>Plasmodium falciparum</i> . <i>Journal of Theoretical Biology</i> , 2014, 343, 113-119.	0.8	4
939	The major cockroach allergen Bla g 4 binds tyramine and octopamine. <i>Molecular Immunology</i> , 2014, 60, 86-94.	1.0	22
940	Structural Basis for Proteasome Formation Controlled by an Assembly Chaperone Nas2. <i>Structure</i> , 2014, 22, 731-743.	1.6	23
941	Structural basis of Flavivirus NS1 assembly and antibody recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4285-4290.	3.3	121
942	<i>Rhodobacter capsulatus</i> ... DprA is essential for RecA-mediated gene transfer agent (RcGTA) recipient capability regulated by quorum-sensing and the CtrA response regulator. <i>Molecular Microbiology</i> , 2014, 92, 1260-1278.	1.2	52
943	Crystal structure of the catalytic domain of PigE: A transaminase involved in the biosynthesis of 2-methyl-3-n-amylyl-pyrrole (MAP) from <i>Serratia</i> sp. FS14. <i>Biochemical and Biophysical Research Communications</i> , 2014, 447, 178-183.	1.0	12
944	Structural insights into the T6SS effector protein Tse3 and the Tse3-Tsi3 complex from <i>Pseudomonas aeruginosa</i> reveal a calcium-dependent membrane-binding mechanism. <i>Molecular Microbiology</i> , 2014, 92, 1092-1112.	1.2	29
945	The unique regulation of iron-sulfur cluster biogenesis in a Gram-positive bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2251-60.	3.3	37
946	Insights into the Architecture of the eIF2B1/2/3 Regulatory Subcomplex. <i>Biochemistry</i> , 2014, 53, 3432-3445.	1.2	32
947	Mechanism of Bacterial Interference with TLR4 Signaling by <i>Brucella</i> Toll/Interleukin-1 Receptor Domain-containing Protein TcpB. <i>Journal of Biological Chemistry</i> , 2014, 289, 654-668.	1.6	73
948	Structural and functional studies on a thermostable polyethylene terephthalate degrading hydrolase from <i>Thermobifida fusca</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7815-7823.	1.7	191
949	Structural Insights into Ubiquinone Biosynthesis in Membranes. <i>Science</i> , 2014, 343, 878-881.	6.0	122
950	Mechanism of Tc toxin action revealed in molecular detail. <i>Nature</i> , 2014, 508, 61-65.	13.7	149

#	ARTICLE	IF	CITATIONS
951	<i>Chlamydia trachomatis</i> CT771 (<i>nudH</i>) Is an Asymmetric Ap ₄ A Hydrolase. <i>Biochemistry</i> , 2014, 53, 214-224.	1.2	1
952	Structural basis for recognition of synaptic vesicle protein 2C by botulinum neurotoxin A. <i>Nature</i> , 2014, 505, 108-111.	13.7	103
953	Structural and functional characterization of a novel $\hat{\pm}/^2$ hydrolase from cariogenic pathogen <i>Streptococcus mutans</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 695-700.	1.5	2
954	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. <i>Cell</i> , 2014, 156, 577-589.	13.5	348
955	Structure of Est3 reveals a bimodal surface with differential roles in telomere replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 214-218.	3.3	36
956	Structural basis for processive DNA synthesis by yeast DNA polymerase ϵ . <i>Nature Structural and Molecular Biology</i> , 2014, 21, 49-55.	3.6	155
957	Genetic and structural characterization of PvSERA4: potential implication as therapeutic target for <i>Plasmodium vivax</i> malaria. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 580-590.	2.0	7
958	Unraveling the multispecificity and catalytic promiscuity of taxadiene monooxygenase. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 110, 154-164.	1.8	18
959	Cytochrome P450 OxyB _{tei} Catalyzes the First Phenolic Coupling Step in Teicoplanin Biosynthesis. <i>ChemBioChem</i> , 2014, 15, 2719-2728.	1.3	49
960	Structural characterization of the virulence factor nuclease A from <i>Streptococcus agalactiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2937-2949.	2.5	7
961	Solution NMR Structures of <i>Pyrenophora tritici-repentis</i> ToxB and Its Inactive Homolog Reveal Potential Determinants of Toxin Activity. <i>Journal of Biological Chemistry</i> , 2014, 289, 25946-25956.	1.6	37
962	Normal Mode Dynamics Comparison of Proteins. <i>Israel Journal of Chemistry</i> , 2014, 54, 1118-1125.	1.0	4
963	An intramolecular lock facilitates folding and stabilizes the tertiary structure of <i>Streptococcus mutans</i> adhesin P1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15746-15751.	3.3	28
964	Functional and structural studies of pullulanase from <i>Anoxybacillus</i> sp. LM18-11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1685-1693.	1.5	55
965	Crystal structure of a <i>Chlamydomonas reinhardtii</i> flagellar RabGAP TBC-domain at 1.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2282-2287.	1.5	4
966	Structure of mouse muskelin discoidin domain and biochemical characterization of its self-association. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2863-2874.	2.5	7
967	Crystal structure of the WOPR-DNA complex and implications for Wor1 function in white-opaque switching of <i>Candida albicans</i> . <i>Cell Research</i> , 2014, 24, 1108-1120.	5.7	15
968	Multiple enzymatic activities of ParB/Srx superfamily mediate sexual conflict among conjugative plasmids. <i>Nature Communications</i> , 2014, 5, 5322.	5.8	28

#	ARTICLE	IF	CITATIONS
969	Interfacial residues of SpcS chaperone affects binding of effector toxin ExoT in <i>Pseudomonas aeruginosa</i> : novel insights from structural and computational studies. FEBS Journal, 2014, 281, 1267-1280.	2.2	2
970	Smoothing 3D Protein Structure Motifs Through Graph Mining and Amino Acid Similarities. Journal of Computational Biology, 2014, 21, 162-172.	0.8	16
971	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. Nature Communications, 2014, 5, 4874.	5.8	72
972	Understanding molecular recognition of promiscuity of thermophilic methionine adenosyltransferase s<sc>MAT</sc> from <i>Sulfolobus solfataricus</i> . FEBS Journal, 2014, 281, 4224-4239.	2.2	36
973	Cog5â€“Cog7 crystal structure reveals interactions essential for the function of a multisubunit tethering complex. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15762-15767.	3.3	19
974	Crystal structure of HlyU, the hemolysin gene transcription activator, from <i>Vibrio cholerae</i> N16961 and functional implications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2346-2354.	1.1	15
975	Structural studies suggest a peptidoglycan hydrolase function for the <i>Mycobacterium tuberculosis</i> Tat-secreted protein Rv2525c. Journal of Structural Biology, 2014, 188, 156-164.	1.3	9
976	Crystal structure of human BS69 Bromo-ZnF-PWWP reveals its role in H3K36me3 nucleosome binding. Cell Research, 2014, 24, 890-893.	5.7	29
977	The Structure of the Cytomegalovirus-Encoded m04 Glycoprotein, a Prototypical Member of the m02 Family of Immuno-evasins. Journal of Biological Chemistry, 2014, 289, 23753-23763.	1.6	15
978	Structural basis of PcsB-mediated cell separation in <i>Streptococcus pneumoniae</i> . Nature Communications, 2014, 5, 3842.	5.8	82
979	Negatively Charged Lipid Membranes Promote a Disorder-Order Transition in the <i>Yersinia</i> YscU Protein. Biophysical Journal, 2014, 107, 1950-1961.	0.2	12
980	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
981	Structure-Based Multiscale Approach for Identification of Interaction Partners of PDZ Domains. Journal of Chemical Information and Modeling, 2014, 54, 1143-1156.	2.5	8
982	Synthesis, bioevaluation and docking study of 5-substitutedphenyl-1,3,4-thiadiazole-based hydroxamic acids as histone deacetylase inhibitors and antitumor agents. Journal of Enzyme Inhibition and Medicinal Chemistry, 2014, 29, 611-618.	2.5	31
983	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
984	Comparative study of two <sc>GH</sc>19 chitinaseâ€“like proteins from <i>Hevea brasiliensis</i> , one exhibiting a novel carbohydrateâ€“binding domain. FEBS Journal, 2014, 281, 4535-4554.	2.2	27
985	Structure and Mechanism of Soybean ATP Sulfurylase and the Committed Step in Plant Sulfur Assimilation. Journal of Biological Chemistry, 2014, 289, 10919-10929.	1.6	39
986	Structural Insights into the Organization of the Cavin Membrane Coat Complex. Developmental Cell, 2014, 31, 405-419.	3.1	79

#	ARTICLE	IF	CITATIONS
987	Evaluating the Significance of Protein Functional Similarity Based on Gene Ontology. <i>Journal of Computational Biology</i> , 2014, 21, 809-822.	0.8	3
988	Latent and active <i>abPPO4</i> mushroom tyrosinase cocrystallized with hexatungstotellurate(VI) in a single crystal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2301-2315.	2.5	109
989	Crystal structures of IFT70/52 and IFT52/46 provide insight into intraflagellar transport B core complex assembly. <i>Journal of Cell Biology</i> , 2014, 207, 269-282.	2.3	115
990	Structural analyses of Ca ²⁺ /CaM interaction with NaV channel C-termini reveal mechanisms of calcium-dependent regulation. <i>Nature Communications</i> , 2014, 5, 4896.	5.8	86
991	Insights into the structure and function of fungal Î²-mannosidases from glycoside hydrolase familyÂ2 based on multiple crystal structures of the <i>TrichodermaÂharzianum</i> enzyme. <i>FEBS Journal</i> , 2014, 281, 4165-4178.	2.2	22
992	Structure of <i>Rhodococcus equi</i> virulence-associated protein B (VapB) reveals an eight-stranded antiparallel Î²-barrel consisting of two Greek-key motifs. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 866-871.	0.4	17
993	The Structure and Specificity of the Type III Secretion System Effector NleC Suggest a DNA Mimicry Mechanism of Substrate Recognition. <i>Biochemistry</i> , 2014, 53, 5131-5139.	1.2	28
994	The crystal structure of archaeal serine hydroxymethyltransferase reveals idiosyncratic features likely required to withstand high temperatures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3437-3449.	1.5	13
995	Crystal structure of the leucine-rich repeat domain of the NOD-like receptor NLRP1: Implications for binding of muramyl dipeptide. <i>FEBS Letters</i> , 2014, 588, 3327-3332.	1.3	37
996	Unusual Structural Features Revealed by the Solution NMR Structure of the NLRC5 Caspase Recruitment Domain. <i>Biochemistry</i> , 2014, 53, 3106-3117.	1.2	28
997	Biochemical and Structural Analysis of RraA Proteins To Decipher Their Relationships with 4-Hydroxy-4-methyl-2-oxoglutarate/4-Carboxy-4-hydroxy-2-oxoadipate Aldolases. <i>Biochemistry</i> , 2014, 53, 542-553.	1.2	6
998	Structural basis for organohalide respiration. <i>Science</i> , 2014, 346, 455-458.	6.0	220
999	Structure-Guided Functional Characterization of Eneidyne Self-Sacrifice Resistance Proteins, CalU16 and CalU19. <i>ACS Chemical Biology</i> , 2014, 9, 2347-2358.	1.6	24
1000	Crystal Structure of PhnF, a GntR-Family Transcriptional Regulator of Phosphate Transport in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , 2014, 196, 3472-3481.	1.0	17
1001	Radical SAM enzyme QueE defines a new minimal core fold and metal-dependent mechanism. <i>Nature Chemical Biology</i> , 2014, 10, 106-112.	3.9	71
1002	Crystal Structure of <i>Escherichia coli</i> SsuE: Defining a General Catalytic Cycle for FMN Reductases of the Flavodoxin-like Superfamily. <i>Biochemistry</i> , 2014, 53, 3509-3519.	1.2	27
1003	The crystal structure of zebrafish IL-22 reveals an evolutionary, conserved structure highly similar to that of human IL-22. <i>Genes and Immunity</i> , 2014, 15, 293-302.	2.2	24
1004	Crystal structure of the papain-like protease of MERS coronavirus reveals unusual, potentially druggable active-site features. <i>Antiviral Research</i> , 2014, 109, 72-82.	1.9	74

#	ARTICLE	IF	CITATIONS
1005	Elongated Structure of the Outer-Membrane Activator of Peptidoglycan Synthesis LpoA: Implications for PBP1A Stimulation. <i>Structure</i> , 2014, 22, 1047-1054.	1.6	53
1006	Comparative Structural Analysis of the Putative Mono-ADP-Ribosyltransferases of the ARTD/PARP Family. <i>Current Topics in Microbiology and Immunology</i> , 2014, 384, 153-166.	0.7	12
1007	Adenylate kinase from <i>Streptococcus pneumoniae</i> is essential for growth through its catalytic activity. <i>FEBS Open Bio</i> , 2014, 4, 672-682.	1.0	14
1008	The Structure of Mouse Cytomegalovirus m04 Protein Obtained from Sparse NMR Data Reveals a Conserved Fold of the m02-m06 Viral Immune Modulator Family. <i>Structure</i> , 2014, 22, 1263-1273.	1.6	23
1009	Structural insights into the substrate-binding mechanism for a novel chitosanase. <i>Biochemical Journal</i> , 2014, 461, 335-345.	1.7	46
1010	Crystal structure of the nucleotide-binding domain of mortalin, the mitochondrial Hsp70 chaperone. <i>Protein Science</i> , 2014, 23, 833-842.	3.1	40
1011	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 26-42.	1.5	53
1012	Structural basis for the recognition "evasion arms race between <i>Tomato mosaic virus</i> and the resistance gene <i>Tm-1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3486-95.	3.3	38
1013	Structure of a Sedoheptulose 7-Phosphate Cyclase: ValA from <i>Streptomyces hygrosopicus</i> . <i>Biochemistry</i> , 2014, 53, 4250-4260.	1.2	14
1014	Identification of Genes Essential for the Biogenesis of Quinohemoprotein Amine Dehydrogenase. <i>Biochemistry</i> , 2014, 53, 895-907.	1.2	14
1015	Crystal structures of two tetrameric Zn^{2+} -carbonic anhydrases from the filamentous ascomycete <i>Sordaria macrospora</i> . <i>FEBS Journal</i> , 2014, 281, 1759-1772.	2.2	40
1016	Structural Characterization of the C3 Domain of Cardiac Myosin Binding Protein C and Its Hypertrophic Cardiomyopathy-Related R502W Mutant. <i>Biochemistry</i> , 2014, 53, 5332-5342.	1.2	20
1017	Structure of <i>Thermoplasma volcanium</i> Ard1 belongs to N-acetyltransferase family member suggesting multiple ligand binding modes with acetyl coenzyme A and coenzyme A. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1790-1797.	1.1	14
1018	SMYD Proteins: Key Regulators in Skeletal and Cardiac Muscle Development and Function. <i>Anatomical Record</i> , 2014, 297, 1650-1662.	0.8	78
1019	Structure and Substrate Specificity of a Eukaryotic Fucosidase from <i>Fusarium graminearum</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 25624-25638.	1.6	33
1020	Crystal structure of a nematode-infecting virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12781-12786.	3.3	28
1021	Discovery of a new ATP-binding motif involved in peptidic azoline biosynthesis. <i>Nature Chemical Biology</i> , 2014, 10, 823-829.	3.9	77
1022	The <i>Legionella</i> effector SidC defines a unique family of ubiquitin ligases important for bacterial phagosomal remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10538-10543.	3.3	98

#	ARTICLE	IF	CITATIONS
1023	Crystal structure of the lytic CHAPK domain of the endolysin LysK from <i>Staphylococcus aureus</i> bacteriophage K. <i>Virology Journal</i> , 2014, 11, 133.	1.4	47
1024	Structure of the large ribosomal subunit from human mitochondria. <i>Science</i> , 2014, 346, 718-722.	6.0	260
1025	A structural and functional investigation of a novel protein from <i>Mycobacterium smegmatis</i> implicated in mycobacterial macrophage survivability. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2264-2276.	2.5	3
1026	Xylan utilization in human gut commensal bacteria is orchestrated by unique modular organization of polysaccharide-degrading enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3708-17.	3.3	137
1027	Structure of the Small <i>Dictyostelium discoideum</i> Myosin Light Chain MlcB Provides Insights into MyoB IQ Motif Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 17030-17042.	1.6	3
1028	Turning points in the evolution of peroxidase-catalase superfamily: molecular phylogeny of hybrid heme peroxidases. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 4681-4696.	2.4	70
1029	The reduction rates of DEPC-modified mutant <i>Thermus thermophilus</i> Rieske proteins differ when there is a negative charge proximal to the cluster. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 1121-1135.	1.1	4
1030	Structure-Function Analysis of <i>Staphylococcus aureus</i> Amidase Reveals the Determinants of Peptidoglycan Recognition and Cleavage. <i>Journal of Biological Chemistry</i> , 2014, 289, 11083-11094.	1.6	37
1031	De novo inference of protein function from coarse-grained dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2443-2454.	1.5	8
1032	Crystal structure of PfbA, a surface adhesin of <i>Streptococcus pneumoniae</i> , provides hints into its interaction with fibronectin. <i>International Journal of Biological Macromolecules</i> , 2014, 64, 168-173.	3.6	25
1033	The Three-dimensional Structure of the Extracellular Adhesion Domain of the Sialic Acid-binding Adhesin SabA from <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6332-6340.	1.6	54
1034	Structure of the pseudokinase domain of BIR2, a regulator of BAK1-mediated immune signaling in <i>Arabidopsis</i> . <i>Journal of Structural Biology</i> , 2014, 186, 112-121.	1.3	53
1035	A slow-forming isopeptide bond in the structure of the major pilin SpaD from <i>Corynebacterium diphtheriae</i> has implications for pilus assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1190-1201.	2.5	27
1036	Gene structure, cDNA characterization and RNAi-based functional analysis of a myeloid differentiation factor 88 homolog in <i>Tenebrio molitor</i> larvae exposed to <i>Staphylococcus aureus</i> infection. <i>Developmental and Comparative Immunology</i> , 2014, 46, 208-221.	1.0	25
1037	Crystal structure of JHP933 from <i>Helicobacter pylori</i> J99 shows two-domain architecture with a DUF1814 family nucleotidyltransferase domain and a helical bundle domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2275-2281.	1.5	3
1038	Crystal Structure of Mox-1, a Unique Plasmid-Mediated Class C β -Lactamase with Hydrolytic Activity towards Moxalactam. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 3914-3920.	1.4	7
1039	A distinct sodium channel voltage-sensor locus determines insect selectivity of the spider toxin Dc1a. <i>Nature Communications</i> , 2014, 5, 4350.	5.8	63
1040	In silico structural characterization and molecular docking studies of first glucuronoxylan-xylanohydrolase (Xyn30A) from family 30 glycosyl hydrolase (GH30) from <i>Clostridium thermocellum</i> . <i>Molecular Biology</i> , 2014, 48, 278-286.	0.4	6

#	ARTICLE	IF	CITATIONS
1041	Structure of <i>Clostridium difficile</i> PilJ Exhibits Unprecedented Divergence from Known Type IV Pilins. <i>Journal of Biological Chemistry</i> , 2014, 289, 4334-4345.	1.6	39
1042	Structural and bioinformatic characterization of an <i>Acinetobacter baumannii</i> type II carrier protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1718-1725.	2.5	18
1043	Doc Toxin Is a Kinase That Inactivates Elongation Factor Tu. <i>Journal of Biological Chemistry</i> , 2014, 289, 7788-7798.	1.6	72
1044	Modification and periplasmic translocation of the biofilm exopolysaccharide poly- β -1,6- N-acetyl- α -D-glucosamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11013-11018.	3.3	48
1045	Structure and Cell Wall Cleavage by Modular Lytic Transglycosylase MltC of <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2014, 9, 2058-2066.	1.6	41
1046	Solution Structure and Molecular Determinants of Hemoglobin Binding of the First NEAT Domain of LsdB in <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2014, 53, 3922-3933.	1.2	40
1047	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	1.6	6
1048	Identification of a Unique Fe-S Cluster Binding Site in a Glycyl-Radical Type Microcompartment Shell Protein. <i>Journal of Molecular Biology</i> , 2014, 426, 3287-3304.	2.0	23
1049	The C-terminal domain of the transcriptional regulator BldD from <i>Streptomyces coelicolor</i> A3(2) constitutes a novel fold of winged-helix domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1093-1098.	1.5	8
1050	Crystal structure of the antimicrobial peptidase lysostaphin from <i>Staphylococcus simulans</i> . <i>FEBS Journal</i> , 2014, 281, 4112-4122.	2.2	79
1051	Is the bovine lysosomal phospholipase B-like protein an amidase?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 300-311.	1.5	14
1052	Structural and mutational analysis of a monomeric and dimeric form of a single domain antibody with implications for protein misfolding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3101-3116.	1.5	14
1053	Crystal structure of PhoU from <i>Pseudomonas aeruginosa</i> , a negative regulator of the Pho regulon. <i>Journal of Structural Biology</i> , 2014, 188, 22-29.	1.3	11
1054	Structure of the double-stranded DNA-binding type IV secretion protein TraN from <i>Enterococcus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2376-2389.	2.5	11
1055	The Solution Structure, Binding Properties, and Dynamics of the Bacterial Siderophore-binding Protein FepB. <i>Journal of Biological Chemistry</i> , 2014, 289, 29219-29234.	1.6	29
1056	The Structure of a Conserved Piezo Channel Domain Reveals a Topologically Distinct β^2 Sandwich Fold. <i>Structure</i> , 2014, 22, 1520-1527.	1.6	41
1057	Binding of OTULIN to the PUB Domain of HOIP Controls NF- κ B Signaling. <i>Molecular Cell</i> , 2014, 54, 349-361.	4.5	155
1058	Structural basis for recognition of the type VI spike protein VgrG3 by a cognate immunity protein. <i>FEBS Letters</i> , 2014, 588, 1891-1898.	1.3	6

#	ARTICLE	IF	CITATIONS
1059	The NreA Protein Functions as a Nitrate Receptor in the Staphylococcal Nitrate Regulation System. <i>Journal of Molecular Biology</i> , 2014, 426, 1539-1553.	2.0	40
1060	Crystal Structure of the Carbapenem Intrinsic Resistance Protein CarG. <i>Journal of Molecular Biology</i> , 2014, 426, 1958-1970.	2.0	6
1061	NMR structural studies of the first catalytic half-domain of ubiquitin activating enzyme. <i>Journal of Structural Biology</i> , 2014, 185, 69-78.	1.3	2
1062	Structural and biochemical study of <i>Bacillus subtilis</i> HmoB in complex with heme. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 286-291.	1.0	11
1063	Investigations of Ramachandran disallowed conformations in protein domain families. <i>International Journal of Biological Macromolecules</i> , 2014, 63, 119-125.	3.6	14
1064	Structural Basis of SOSS1 Complex Assembly and Recognition of ssDNA. <i>Cell Reports</i> , 2014, 6, 982-991.	2.9	42
1065	Structural insights into conserved <i>Escherichia coli</i> arabinose metabolic enzymes reveal the substrate binding site of a thermophilic <i>Thermotoga maritima</i> arabinose isomerase. <i>FEBS Letters</i> , 2014, 588, 1064-1070.	1.3	7
1066	Solution NMR Structure of the DNA-binding Domain from Scml2 (Sex Comb on Midleg-like 2). <i>Journal of Biological Chemistry</i> , 2014, 289, 15739-15749.	1.6	8
1067	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , 2014, 24, 344-358.	5.7	86
1068	The structure of the Pan2-Pan3 core complex reveals cross-talk between deadenylase and pseudokinase. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 591-598.	3.6	45
1069	The <i>Streptococcus pneumoniae</i> denticola AtcR LysR domain-containing response regulator interacts with three architecturally distinct promoter elements: implications for understanding the molecular signaling mechanisms that drive the progression of periodontal disease. <i>Molecular Oral Microbiology</i> , 2014, 29, 219-232.	1.3	10
1070	Crystallographic characterization of the (R)-selective amine transaminase from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1086-1093.	2.5	36
1071	The first structure of a bacterial diterpene cyclase: CotB2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1528-1537.	2.5	48
1072	Ribosomal oxygenases are structurally conserved from prokaryotes to humans. <i>Nature</i> , 2014, 510, 422-426.	13.7	87
1073	Structural characterization of a β^2 -hydroxyacid dehydrogenase from <i>Geobacter sulfurreducens</i> and <i>Geobacter metallireducens</i> with succinic semialdehyde reductase activity. <i>Biochimie</i> , 2014, 104, 61-69.	1.3	14
1074	Crystal structure of a member of a novel family of dioxygenases (PF10014) reveals a conserved cupin fold and active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 164-170.	1.5	15
1075	Structure-based engineering and comparison of novel split inteins for protein ligation. <i>Molecular BioSystems</i> , 2014, 10, 1023-1034.	2.9	48
1076	Sensor Domain of Histidine Kinase KinB of <i>Pseudomonas</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 12232-12244.	1.6	11

#	ARTICLE	IF	CITATIONS
1077	High resolution crystal structure of <i>Clostridium propionicum</i> β -alanine-CoA:ammonia lyase, a new member of the "hot dog fold" protein superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2041-2053.	1.5	6
1078	Structure of the <i>Proteus vulgaris</i> HigB-(HigA) ₂ -HigB Toxin-Antitoxin Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 1060-1070.	1.6	78
1079	Glycan Specificity of the <i>Vibrio vulnificus</i> Hemolysin Lectin Outlines Evolutionary History of Membrane Targeting by a Toxin Family. <i>Journal of Molecular Biology</i> , 2014, 426, 2800-2812.	2.0	31
1080	Structure of the LdcB LD-Carboxypeptidase Reveals the Molecular Basis of Peptidoglycan Recognition. <i>Structure</i> , 2014, 22, 949-960.	1.6	31
1081	Structure determination of archaea-specific ribosomal protein L46a reveals a novel protein fold. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 67-72.	1.0	1
1082	Reciprocal allosteric regulation of p38 β and PTPN3 involves a PDZ domain-mediated complex formation. <i>Science Signaling</i> , 2014, 7, ra98.	1.6	25
1083	Solution structure of the major factor VIII binding region on von Willebrand factor. <i>Blood</i> , 2014, 123, 4143-4151.	0.6	41
1084	Structural insight into glucose dehydrogenase from the thermoacidophilic archaeon <i>Thermoplasma volcanium</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1271-1280.	2.5	3
1085	Crystal Structure and Mutational Analysis of Isomaltose-dextranase, a Member of Glycoside Hydrolase Family 27. <i>Journal of Biological Chemistry</i> , 2015, 290, 26339-26349.	1.6	21
1086	Dealing with oxygen using bare hands. <i>FEBS Journal</i> , 2015, 282, 3259-3261.	2.2	0
1087	Handicap-Recover Evolution Leads to a Chemically Versatile, Nucleophile-Permissive Protease. <i>ChemBioChem</i> , 2015, 16, 1866-1869.	1.3	9
1088	Crystal structure of a COG4313 outer membrane channel. <i>Scientific Reports</i> , 2015, 5, 11927.	1.6	19
1089	Substrate recognition and catalysis by LytB, a pneumococcal peptidoglycan hydrolase involved in virulence. <i>Scientific Reports</i> , 2015, 5, 16198.	1.6	30
1090	Structural and computational analysis of peptide recognition mechanism of class-C type penicillin binding protein, alkaline D-peptidase from <i>Bacillus cereus</i> DF4-B. <i>Scientific Reports</i> , 2015, 5, 13836.	1.6	15
1091	Structural Features of a Bacteroidetes-Affiliated Cellulase Linked with a Polysaccharide Utilization Locus. <i>Scientific Reports</i> , 2015, 5, 11666.	1.6	24
1092	Crystal structure analysis of c4763, a uropathogenic <i>Escherichia coli</i> -specific protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1042-1047.	0.4	1
1093	Structure of AadA from <i>Salmonella enterica</i> : a monomeric aminoglycoside (3'-acetyl)(9) adenylyltransferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2267-2277.	2.5	16
1094	Structure of DnmZ, a nitrososynthase in the <i>Streptomyces peucetius</i> anthracycline biosynthetic pathway. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1205-1214.	0.4	5

#	ARTICLE	IF	CITATIONS
1095	Homotypic dimerization of a maltose kinase for molecular scaffolding. <i>Scientific Reports</i> , 2014, 4, 6418.	1.6	7
1096	A unique GCN5-related glucosamine N-acetyltransferase region exist in the fungal multi-domain glycoside hydrolase family 3 Î²-N-acetylglucosaminidase. <i>Scientific Reports</i> , 2015, 5, 18292.	1.6	10
1097	Structure and function of the N-terminal domain of the human mitochondrial calcium uniporter. <i>EMBO Reports</i> , 2015, 16, 1318-1333.	2.0	81
1098	Biochemical and structural characterization of a novel ubiquitin-conjugating enzyme E2 from <i>Agrocybe aegeria</i> reveals Ube2w family-specific properties. <i>Scientific Reports</i> , 2015, 5, 16056.	1.6	5
1099	Impact of Insulin Degrading Enzyme and Neprilysin in Alzheimer's Disease Biology: Characterization of Putative Cognates for Therapeutic Applications. <i>Journal of Alzheimer's Disease</i> , 2015, 48, 891-917.	1.2	64
1100	Structural basis for Sfm1 functioning as a protein arginine methyltransferase. <i>Cell Discovery</i> , 2015, 1, 15037.	3.1	21
1101	Structure and mechanism of an antibiotics-synthesizing 3-hydroxykynurenine C-methyltransferase. <i>Scientific Reports</i> , 2015, 5, 10100.	1.6	15
1102	Structural analysis of fungus-derived FAD glucose dehydrogenase. <i>Scientific Reports</i> , 2015, 5, 13498.	1.6	89
1103	Open and Lys-His Hexacoordinated Closed Structures of a Globin with Swapped Proximal and Distal Sites. <i>Scientific Reports</i> , 2015, 5, 11407.	1.6	5
1104	E2 superfamily of ubiquitin-conjugating enzymes: constitutively active or activated through phosphorylation in the catalytic cleft. <i>Scientific Reports</i> , 2015, 5, 14849.	1.6	43
1105	Structure of the substrate-binding Î² domain of the Protein disulfide isomerase-like protein of the testis. <i>Scientific Reports</i> , 2015, 4, 4464.	1.6	3
1106	S46 Peptidases are the First Exopeptidases to be Members of Clan PA. <i>Scientific Reports</i> , 2014, 4, 4977.	1.6	21
1107	Identification of an Ideal-like Fingerprint for a Protein Fold using Overlapped Conserved Residues based Approach. <i>Scientific Reports</i> , 2015, 4, 5643.	1.6	6
1108	Structural basis of membrane budding by the nuclear egress complex of herpesviruses. <i>EMBO Journal</i> , 2015, 34, 2921-2936.	3.5	107
1109	Structural and mutational analyses of dipeptidyl peptidase 11 from <i>Porphyromonas gingivalis</i> reveal the molecular basis for strict substrate specificity. <i>Scientific Reports</i> , 2015, 5, 11151.	1.6	13
1110	Crystal Structures of a Hyperthermophilic Archaeal Homoserine Dehydrogenase Suggest a Novel Cofactor Binding Mode for Oxidoreductases. <i>Scientific Reports</i> , 2015, 5, 11674.	1.6	14
1111	Crystal structure of CobK reveals strand-swapping between Rossmann-fold domains and molecular basis of the reduced precorrin product trap. <i>Scientific Reports</i> , 2015, 5, 16943.	1.6	7
1112	Crystal structure of <i>Staphylococcus aureus</i> peptidyl-tRNA hydrolase at a 2.25 Å... resolution. <i>Acta Biochimica Et Biophysica Sinica</i> , 2015, 47, gmv114.	0.9	9

#	ARTICLE	IF	CITATIONS
1113	Molecular basis for the substrate specificity and catalytic mechanism of thymine-7-hydroxylase in fungi. <i>Nucleic Acids Research</i> , 2015, 43, gkv979.	6.5	9
1114	Fast evolutionary rates associated with functional loss in class I glucose transporters of <i>Schistosoma mansoni</i> . <i>BMC Genomics</i> , 2015, 16, 980.	1.2	6
1115	Structure of lpg0406, a carboxymuconolactone decarboxylase family protein possibly involved in antioxidative response from <i>Legionella pneumophila</i> . <i>Protein Science</i> , 2015, 24, 2070-2075.	3.1	12
1116	Structure of the terminal PCP domain of the non-ribosomal peptide synthetase in teicoplanin biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 711-721.	1.5	24
1117	Crystal structure of the <i>Legionella pneumophila</i> lem10 effector reveals a new member of the HD protein superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2319-2325.	1.5	4
1118	A new dehydratase conferring innate resistance to thiacetazone and intra-moebal survival of <i>Mycobacterium smegmatis</i> . <i>Molecular Microbiology</i> , 2015, 96, 1085-1102.	1.2	19
1119	PDB-Explorer: a web-based interactive map of the protein data bank in shape space. <i>BMC Bioinformatics</i> , 2015, 16, 339.	1.2	31
1120	The crystal structure of JNK from <i>Drosophila melanogaster</i> reveals an evolutionarily conserved topology with that of mammalian JNK proteins. <i>BMC Structural Biology</i> , 2015, 15, 17.	2.3	10
1121	Three-dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. <i>BMC Structural Biology</i> , 2015, 15, 20.	2.3	4
1122	Crystal structure of the fibre head domain of bovine adenovirus 4, a ruminant adenovirus. <i>Virology Journal</i> , 2015, 12, 81.	1.4	6
1123	Structural views of quinone oxidoreductase from <i>Mycobacterium tuberculosis</i> reveal large conformational changes induced by the co-factor. <i>FEBS Journal</i> , 2015, 282, 2697-2707.	2.2	8
1124	Structure of amylase-binding protein A of <i>Streptococcus gordonii</i> : A potential receptor for human salivary α -amylase enzyme. <i>Protein Science</i> , 2015, 24, 1013-1018.	3.1	8
1125	Manual classification strategies in the ECOD database. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1238-1251.	1.5	64
1126	Crystal Structure of Hemagglutinin from Type B <i>Clostridium Botulinum</i> . <i>Nihon Kessho Gakkaishi</i> , 2015, 57, 233-238.	0.0	0
1127	Crystal structure of the C-terminal 2 ⁵ ,5 ² -phosphodiesterase domain of group a rotavirus protein VP3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 997-1002.	1.5	14
1128	Structure of Ctk3, a subunit of the RNA polymerase II CTD kinase complex, reveals a noncanonical CTD-interacting domain fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1849-1858.	1.5	4
1129	PspF-binding domain PspA ₁₄₄ and the PspA-F complex: New insights into the coiled-coil dependent regulation of AAA+ proteins. <i>Molecular Microbiology</i> , 2015, 98, 743-759.	1.2	33
1130	A thiol-disulfide oxidoreductase of the Gram-positive pathogen <i>Corynebacterium diphtheriae</i> is essential for viability, pilus assembly, toxin production and virulence. <i>Molecular Microbiology</i> , 2015, 98, 1037-1050.	1.2	37

#	ARTICLE	IF	CITATIONS
1131	Identification, modeling, and characterization studies of <i>Tetrahymena thermophila</i> myosin <scp>FERM</scp> domains suggests a conserved core fold but functional differences. Cytoskeleton, 2015, 72, 585-596.	1.0	1
1132	Crystal structure of the fungal nitroreductase Frm2 from <i>Saccharomyces cerevisiae</i> . Protein Science, 2015, 24, 1158-1163.	3.1	4
1133	Hypothetical protein <scp>CT</scp>398 (<scp>C</scp>ds<scp>Z</scp>) interacts with β -54 (R<scp>po<scp>N</scp>) holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . Protein Science, 2015, 24, 1617-1632.	3.1	23
1134	Structure alignment of membrane proteins: Accuracy of available tools and a consensus strategy. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1720-1732.	1.5	12
1135	Crystal structures of apo-DszC and FMN-bound DszC from <i>Rhodococcus erythropolis</i> . FEBS Journal, 2015, 282, 3126-3135.	2.2	32
1136	A Novel Peptide-Binding Motifs Inference Approach to Understand Deoxynivalenol Molecular Toxicity. Toxins, 2015, 7, 1989-2005.	1.5	32
1137	Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. Viruses, 2015, 7, 5388-5409.	1.5	16
1138	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
1139	Structural basis of death domain signaling in the p75 neurotrophin receptor. ELife, 2015, 4, e11692.	2.8	69
1140	Domain organization of DNase from <i>Thioalkalivibrio</i> sp. provides insights into retention of activity in high salt environments. Frontiers in Microbiology, 2015, 6, 661.	1.5	3
1141	Model-driven discovery of synergistic inhibitors against <i>E. coli</i> and <i>S. enterica</i> serovar Typhimurium targeting a novel synthetic lethal pair, <i>aldA</i> and <i>prpC</i> . Frontiers in Microbiology, 2015, 6, 958.	1.5	8
1142	The Structure of a Novel Thermophilic Esterase from the Planctomycetes Species, <i>Thermogutta terrifontis</i> Reveals an Open Active Site Due to a Minimal α -Cap TM Domain. Frontiers in Microbiology, 2015, 6, 1294.	1.5	20
1143	Positively-Charged Semi-Tunnel Is a Structural and Surface Characteristic of Polyphosphate-Binding Proteins: An In-Silico Study. PLoS ONE, 2015, 10, e0123713.	1.1	9
1144	Structure and Assembly of Group B Streptococcus Pilus 2b Backbone Protein. PLoS ONE, 2015, 10, e0125875.	1.1	15
1145	Optimization of Translation Profiles Enhances Protein Expression and Solubility. PLoS ONE, 2015, 10, e0127039.	1.1	31
1146	Structure Analysis Uncovers a Highly Diverse but Structurally Conserved Effector Family in Phytopathogenic Fungi. PLoS Pathogens, 2015, 11, e1005228.	2.1	188
1147	Structural and Biochemical Characterization of the <i>Francisella tularensis</i> Pathogenicity Regulator, Macrophage Locus Protein A (MglA). PLoS ONE, 2015, 10, e0128225.	1.1	9
1148	Structural and Functional Analysis of Human HtrA3 Protease and Its Subdomains. PLoS ONE, 2015, 10, e0131142.	1.1	35

#	ARTICLE	IF	CITATIONS
1149	Structure of the Glycosyltransferase Ktr4p from <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0136239.	1.1	7
1150	Extrapolation of Inter Domain Communications and Substrate Binding Cavity of Camel HSP70 1A: A Molecular Modeling and Dynamics Simulation Study. <i>PLoS ONE</i> , 2015, 10, e0136630.	1.1	16
1151	Biochemical and Structural Insights into the Mechanism of DNA Recognition by <i>Arabidopsis ETHYLENE INSENSITIVE3</i> . <i>PLoS ONE</i> , 2015, 10, e0137439.	1.1	24
1152	Structure and Sialyllactose Binding of the Carboxy-Terminal Head Domain of the Fibre from a <i>Siadenovirus</i> , Turkey <i>Adenovirus 3</i> . <i>PLoS ONE</i> , 2015, 10, e0139339.	1.1	25
1153	Activity Augmentation of <i>Amphioxus</i> Peptidoglycan Recognition Protein BbtPGRP3 via Fusion with a Chitin Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0140953.	1.1	3
1154	Structural Insight of a Trimodular Halophilic Cellulase with a Family 46 Carbohydrate-Binding Module. <i>PLoS ONE</i> , 2015, 10, e0142107.	1.1	6
1155	Structural and Functional Investigation of Flavin Binding Center of the NqrC Subunit of Sodium-Translocating NADH:Quinone Oxidoreductase from <i>Vibrio harveyi</i> . <i>PLoS ONE</i> , 2015, 10, e0118548.	1.1	21
1156	TRIP13 is a protein-remodeling AAA+ ATPase that catalyzes MAD2 conformation switching. <i>ELife</i> , 2015, 4, .	2.8	137
1157	PGR: A Novel Graph Repository of Protein 3D-Structures. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2015, 06, .	0.5	1
1158	Crystal structure of Hop2â€Mnd1 and mechanistic insights into its role in meiotic recombination. <i>Nucleic Acids Research</i> , 2015, 43, 3841-3856.	6.5	42
1159	Trimeric Structure of (+)-Pinoresinol-forming Dirigent Protein at 1.95 Å... Resolution with Three Isolated Active Sites. <i>Journal of Biological Chemistry</i> , 2015, 290, 1308-1318.	1.6	56
1160	Complex Structure and Biochemical Characterization of the <i>Staphylococcus aureus</i> Cyclic Diadenylate Monophosphate (c-di-AMP)-binding Protein PstA, the Founding Member of a New Signal Transduction Protein Family. <i>Journal of Biological Chemistry</i> , 2015, 290, 2888-2901.	1.6	47
1161	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. <i>Journal of Biological Chemistry</i> , 2015, 290, 13191-13201.	1.6	33
1162	The amino-terminal structure of human fragile X mental retardation protein obtained using precipitant-immobilized imprinted polymers. <i>Nature Communications</i> , 2015, 6, 6634.	5.8	40
1163	A sand fly salivary protein vaccine shows efficacy against vector-transmitted cutaneous leishmaniasis in nonhuman primates. <i>Science Translational Medicine</i> , 2015, 7, 290ra90.	5.8	121
1164	Crystal structure of the catalytic domain of a GH16 Î²-agarase from a deep-sea bacterium, <i>Microbulbifer thermotolerans</i> JAMB-A94. <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 625-632.	0.6	25
1165	Structural and functional analysis of the Rpf2-Rrs1 complex in ribosome biogenesis. <i>Nucleic Acids Research</i> , 2015, 43, 4746-4757.	6.5	42
1166	FlaF Is a Î²-Sandwich Protein that Anchors the Archaeum in the Archaeal Cell Envelope by Binding the S-Layer Protein. <i>Structure</i> , 2015, 23, 863-872.	1.6	60

#	ARTICLE	IF	CITATIONS
1167	Structure and Mechanism of the Siderophore-Interacting Protein from the Fuscachelin Gene Cluster of <i>Thermobifida fusca</i> . <i>Biochemistry</i> , 2015, 54, 3989-4000.	1.2	23
1168	Structure of a bacterial toxin-activating acyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3058-66.	3.3	33
1169	Solution structure of the NDH-1 complex subunit CupS from <i>Thermosynechococcus elongatus</i> . <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1212-1219.	0.5	7
1170	Variable Substrate Preference among Phospholipase D Toxins from Sicariid Spiders. <i>Journal of Biological Chemistry</i> , 2015, 290, 10994-11007.	1.6	34
1171	Structure of Csd3 from <i>Helicobacter pylori</i> , a cell shape-determining metallopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 675-686.	2.5	21
1172	Structure and sequence analyses of <i>Bacteroides</i> proteins BVU_4064 and BF1687 reveal presence of two novel predominantly-beta domains, predicted to be involved in lipid and cell surface interactions. <i>BMC Bioinformatics</i> , 2015, 16, 7.	1.2	8
1173	Crystal Structure of the Rad3/XPD Regulatory Domain of Ssl1/p44. <i>Journal of Biological Chemistry</i> , 2015, 290, 8321-8330.	1.6	12
1174	Crystal Structure of the Human Primase. <i>Journal of Biological Chemistry</i> , 2015, 290, 5635-5646.	1.6	65
1175	NMR Structure of <i>Francisella tularensis</i> Virulence Determinant Reveals Structural Homology to Bet v1 Allergen Proteins. <i>Structure</i> , 2015, 23, 1116-1122.	1.6	11
1176	Dimeric c-di-GMP Is Required for Post-translational Regulation of Alginate Production in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 12451-12462.	1.6	75
1177	Structural analysis of the β -glucosidase HaG provides new insights into substrate specificity and catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1382-1391.	2.5	63
1178	Full-length structure of the major autolysin LytA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1373-1381.	2.5	22
1179	Weaponization of a Hormone: Convergent Recruitment of Hyperglycemic Hormone into the Venom of Arthropod Predators. <i>Structure</i> , 2015, 23, 1283-1292.	1.6	66
1180	The structure of Rpf2 explains its role in ribosome biogenesis. <i>Nucleic Acids Research</i> , 2015, 43, 7083-7095.	6.5	50
1181	Structural Analysis of <i>Streptococcus pyogenes</i> NADH Oxidase: Conformational Dynamics Involved in Formation of the C(4a)-Peroxyflavin Intermediate. <i>Biochemistry</i> , 2015, 54, 6815-6829.	1.2	16
1182	Conformational toggling controls target site choice for the heteromeric transposase element Tn7. <i>Nucleic Acids Research</i> , 2015, 43, 10734-10745.	6.5	18
1183	Structural Studies of Geosmin Synthase, a Bifunctional Sesquiterpene Synthase with β Domain Architecture That Catalyzes a Unique Cyclization-Fragmentation Reaction Sequence. <i>Biochemistry</i> , 2015, 54, 7142-7155.	1.2	36
1184	Molecular basis for specific viral RNA recognition and 2'-O-ribose methylation by the dengue virus nonstructural protein 5 (NS5). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14834-14839.	3.3	89

#	ARTICLE	IF	CITATIONS
1185	Dimerization Mediated by a Divergent Forkhead-associated Domain Is Essential for the DNA Damage and Spindle Functions of Fission Yeast Mdb1. <i>Journal of Biological Chemistry</i> , 2015, 290, 21054-21066.	1.6	9
1186	The Cell Shape-determining Csd6 Protein from <i>Helicobacter pylori</i> Constitutes a New Family of L,d-Carboxypeptidase. <i>Journal of Biological Chemistry</i> , 2015, 290, 25103-25117.	1.6	34
1187	Structure and regulatory role of the C-terminal winged helix domain of the archaeal minichromosome maintenance complex. <i>Nucleic Acids Research</i> , 2015, 43, 2958-2967.	6.5	23
1188	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. <i>Nucleic Acids Research</i> , 2015, 43, 4602-4613.	6.5	23
1189	mRNA maturation in giant viruses: variation on a theme. <i>Nucleic Acids Research</i> , 2015, 43, 3776-3788.	6.5	17
1190	Structural and sequencing analysis of local target DNA recognition by MLV integrase. <i>Nucleic Acids Research</i> , 2015, 43, 5647-5663.	6.5	26
1191	The La-related protein 1-specific domain repurposes HEAT-like repeats to directly bind a 5â€²TOP sequence. <i>Nucleic Acids Research</i> , 2015, 43, 8077-8088.	6.5	55
1192	Functional significance of protein assemblies predicted by the crystal structure of the restriction endonuclease BsaWI. <i>Nucleic Acids Research</i> , 2015, 43, 8100-8110.	6.5	8
1193	Molecular basis of ribosome recognition and mRNA hydrolysis by the <i>E. coli</i> YafQ toxin. <i>Nucleic Acids Research</i> , 2015, 43, 8002-8012.	6.5	31
1194	Structure of the 34â€¦kDa F-actin-bundling protein ABP34 from <i>Dictyostelium discoideum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1835-1849.	2.5	5
1195	Crystal structure and characterization of a novel L-serine ammonia-lyase from <i>Rhizomucor miehei</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 431-437.	1.0	6
1196	Stonefish toxin defines an ancient branch of the perforin-like superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15360-15365.	3.3	69
1197	Structure of Human B12 Trafficking Protein CblD Reveals Molecular Mimicry and Identifies a New Subfamily of Nitro-FMN Reductases. <i>Journal of Biological Chemistry</i> , 2015, 290, 29155-29166.	1.6	25
1198	Octameric structure of <i>Staphylococcus aureus</i> enolase in complex with phosphoenolpyruvate. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2457-2470.	2.5	27
1199	Structural basis of substrate recognition by a bacterial deubiquitinase important for dynamics of phagosome ubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15090-15095.	3.3	88
1200	Structural analysis of haemoglobin binding by HpuA from the Neisseriaceae family. <i>Nature Communications</i> , 2015, 6, 10172.	5.8	42
1201	Identification of novel cytochrome P450 homologs using overlapped conserved residues based approach. <i>Biotechnology and Bioprocess Engineering</i> , 2015, 20, 431-438.	1.4	4
1202	Lst4, the yeast Frip1/2 orthologue, is a DENN-family protein. <i>Open Biology</i> , 2015, 5, 150174.	1.5	27

#	ARTICLE	IF	CITATIONS
1203	Designing New Kinase Inhibitor Derivatives as Therapeutics Against Common Complex Diseases: Structural Basis of Microtubule Affinity-Regulating Kinase 4 (MARK4) Inhibition. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 700-711.	1.0	50
1204	The crystal and solution structure of YdiE from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 919-924.	0.4	1
1205	Sph3 Is a Glycoside Hydrolase Required for the Biosynthesis of Galactosaminogalactan in <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 27438-27450.	1.6	77
1206	Crystal structure analysis of a bacterial aryl acylamidase belonging to the amidase signature enzyme family. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 268-274.	1.0	23
1207	Adaptive Assembly: Maximizing the Potential of a Given Functional Peptide with a Tailor-Made Protein Scaffold. <i>Chemistry and Biology</i> , 2015, 22, 1165-1173.	6.2	4
1208	Actin, actin-related proteins and profilin in diatoms: A comparative genomic analysis. <i>Marine Genomics</i> , 2015, 23, 133-142.	0.4	12
1209	Structure-function relationships in Gan42B, an intracellular GH42 β -galactosidase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2433-2448.	2.5	19
1210	Crystal Structure of a Eukaryotic GEN1 Resolving Enzyme Bound to DNA. <i>Cell Reports</i> , 2015, 13, 2565-2575.	2.9	37
1211	Automated protein motif generation in the structure-based protein function prediction tool ProMOL. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 101-111.	1.2	8
1212	Structural basis for antagonizing a host restriction factor by C7 family of poxvirus host-range proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14858-14863.	3.3	21
1213	Conservation and Covariance in Small Bacterial Phosphoglycosyltransferases Identify the Functional Catalytic Core. <i>Biochemistry</i> , 2015, 54, 7326-7334.	1.2	30
1214	Centromeric binding and activity of Protein Phosphatase 4. <i>Nature Communications</i> , 2015, 6, 5894.	5.8	37
1215	Tri-peptide reference structures for the calculation of relative solvent accessible surface area in protein amino acid residues. <i>Computational Biology and Chemistry</i> , 2015, 54, 33-43.	1.1	7
1216	Modeling the interactions between MC2R and ACTH models from human. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 770-788.	2.0	2
1217	Crystal structure of the <i>Locusta migratoria</i> odorant binding protein. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 737-742.	1.0	41
1218	The Unusual Fold of Herpes Simplex Virus 1 UL21, a Multifunctional Tegument Protein. <i>Journal of Virology</i> , 2015, 89, 2979-2984.	1.5	18
1219	Structure of <i>Salmonella</i> FlhE, Conserved Member of a Flagellar Type III Secretion Operon. <i>Journal of Molecular Biology</i> , 2015, 427, 1254-1262.	2.0	17
1220	<i>Chlamydia trachomatis</i> protein <i>CT009</i> is a structural and functional homolog to the key morphogenesis component <i>RodZ</i> and interacts with division septal plane localized <i>MreB</i> . <i>Molecular Microbiology</i> , 2015, 95, 365-382.	1.2	26

#	ARTICLE	IF	CITATIONS
1221	A structural and functional perspective of DyP-type peroxidase family. Archives of Biochemistry and Biophysics, 2015, 574, 49-55.	1.4	106
1222	Structural and Evolutionary Analyses Show Unique Stabilization Strategies in the Type IV Pili of Clostridium difficile. Structure, 2015, 23, 385-396.	1.6	45
1223	Biochemical and structural study of <i>Arabidopsis</i> hexokinase 1. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 367-375.	2.5	35
1224	Identification, Characterization, and Structure Analysis of the Cyclic di-AMP-binding PII-like Signal Transduction Protein DarA. Journal of Biological Chemistry, 2015, 290, 3069-3080.	1.6	69
1225	Structural dissection of Hippo signaling. Acta Biochimica Et Biophysica Sinica, 2015, 47, 29-38.	0.9	14
1226	Crystal structure of YwpF from <i>S. taphylococcus aureus</i> reveals its architecture comprised of a β -barrel core domain resembling type VI secretion system proteins and a two-helix pair. Proteins: Structure, Function and Bioinformatics, 2015, 83, 781-788.	1.5	0
1227	X-domain of peptide synthetases recruits oxygenases crucial for glycopeptide biosynthesis. Nature, 2015, 521, 105-109.	13.7	158
1228	Molecular insights into the binding of coenzyme F ₄₂₀ to the conserved protein Rv1155 from <i>Mycobacterium tuberculosis</i> . Protein Science, 2015, 24, 729-740.	3.1	16
1229	Horizontal transfer of carbohydrate metabolism genes into ectomycorrhizal <i>Amanita</i> . New Phytologist, 2015, 205, 1552-1564.	3.5	17
1230	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
1231	<i>Entamoeba histolytica</i> RacC Selectively Engages p21-Activated Kinase Effectors. Biochemistry, 2015, 54, 404-412.	1.2	8
1232	Flexibility in the N-terminal actin-binding domain: Clues from <i>in silico</i> mutations and molecular dynamics. Proteins: Structure, Function and Bioinformatics, 2015, 83, 696-710.	1.5	7
1233	Structural and Functional Characterization of a Ketosteroid Transcriptional Regulator of <i>Mycobacterium tuberculosis</i> . Journal of Biological Chemistry, 2015, 290, 872-882.	1.6	29
1234	Coagulation factor XII protease domain crystal structure. Journal of Thrombosis and Haemostasis, 2015, 13, 580-591.	1.9	48
1235	Comparison of <i>Saccharomyces cerevisiae</i> F-BAR Domain Structures Reveals a Conserved Inositol Phosphate Binding Site. Structure, 2015, 23, 352-363.	1.6	40
1236	Crystal Structure of the Csm3-Csm4 Subcomplex in the Type III-A CRISPR-Cas Interference Complex. Journal of Molecular Biology, 2015, 427, 259-273.	2.0	19
1237	The insecticidal spider toxin SFI ₁ is a knottin peptide that blocks the pore of insect voltage-gated sodium channels via a large β -hairpin loop. FEBS Journal, 2015, 282, 904-920.	2.2	34
1238	Solution structure of a bacterial immunoglobulin-like domain of the outer membrane protein (LigB) from <i>Leptospira</i> . Proteins: Structure, Function and Bioinformatics, 2015, 83, 195-200.	1.5	8

#	ARTICLE	IF	CITATIONS
1239	Crystal Structure of LGR4-Rspo1 Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 2455-2465.	1.6	22
1240	Amino acid coevolution reveals three-dimensional structure and functional domains of insect odorant receptors. <i>Nature Communications</i> , 2015, 6, 6077.	5.8	113
1241	Structural and Functional Analysis of Various Globulin Proteins from Soy Seed. <i>Critical Reviews in Food Science and Nutrition</i> , 2015, 55, 1491-1502.	5.4	61
1242	X-ray crystallographic and EPR spectroscopic analysis of HydG, a maturase in [FeFe]-hydrogenase H-cluster assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1362-1367.	3.3	97
1243	Structural and Molecular Basis for Resistance to Aminoglycoside Antibiotics by the Adenylyltransferase ANT(2- ϵ^3)-Ia. <i>MBio</i> , 2015, 6, .	1.8	49
1244	Structure of the GcpE-HMBPP complex from <i>Thermus thermophilus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 458, 246-250.	1.0	6
1245	Structural basis for acceptorâ€‘substrate recognition of UDPâ€‘glucose: anthocyanidin 3- α -O-glucosyltransferase from <i>Clitoria ternatea</i> . <i>Protein Science</i> , 2015, 24, 395-407.	3.1	69
1246	Structure-based functional annotation of hypothetical proteins from <i>Candida dubliniensis</i> : a quest for potential drug targets. <i>3 Biotech</i> , 2015, 5, 561-576.	1.1	27
1247	Bacterial killing via a type IV secretion system. <i>Nature Communications</i> , 2015, 6, 6453.	5.8	197
1248	Annotation of proteins of unknown function: initial enzyme results. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 43-54.	1.2	16
1249	Structural and functional characterization of a cell cycle associated HDAC1/2 complex reveals the structural basis for complex assembly and nucleosome targeting. <i>Nucleic Acids Research</i> , 2015, 43, 2033-2044.	6.5	51
1250	Structural Basis for the Disruption of the Cerebral Cavernous Malformations 2 (CCM2) Interaction with Krev Interaction Trapped 1 (KRIT1) by Disease-associated Mutations. <i>Journal of Biological Chemistry</i> , 2015, 290, 2842-2853.	1.6	37
1251	Helical Shape of <i>Helicobacter pylori</i> Requires an Atypical Glutamine as a Zinc Ligand in the Carboxypeptidase Csd4. <i>Journal of Biological Chemistry</i> , 2015, 290, 3622-3638.	1.6	17
1252	Structure and proposed mechanism of α -glycerophosphate oxidase from <i>Mycoplasma pneumoniae</i> . <i>FEBS Journal</i> , 2015, 282, 3030-3042.	2.2	22
1253	Structural basis for misfolding in myocilin-associated glaucoma. <i>Human Molecular Genetics</i> , 2015, 24, 2111-2124.	1.4	72
1254	The structure of SpnF, a standalone enzyme that catalyzes [4 + 2] cycloaddition. <i>Nature Chemical Biology</i> , 2015, 11, 256-258.	3.9	101
1255	Structural Basis for the Activation and Inhibition of the UCH37 Deubiquitylase. <i>Molecular Cell</i> , 2015, 57, 901-911.	4.5	96
1256	The twisted relation between Pnu and SWEET transporters. <i>Trends in Biochemical Sciences</i> , 2015, 40, 183-188.	3.7	16

#	ARTICLE	IF	CITATIONS
1257	Structural characterization of the late competence protein ComFB from <i>Bacillus subtilis</i> . <i>Bioscience Reports</i> , 2015, 35, .	1.1	10
1258	Structure of <i>Chlamydomonas reinhardtii</i> THB1, a group 1 truncated hemoglobin with a rare histidine-lysine heme ligation. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 718-725.	0.4	15
1259	Cloning, expression analysis, and RNA interference study of a HORMA domain containing autophagy-related gene 13 (ATG13) from the coleopteran beetle, <i>Tenebrio molitor</i> . <i>Frontiers in Physiology</i> , 2015, 6, 180.	1.3	12
1260	Rgg protein structure-function and inhibition by cyclic peptide compounds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5177-5182.	3.3	57
1261	The RAS-Binding Domain of Human BRAF Protein Serine/Threonine Kinase Exhibits Allosteric Conformational Changes upon Binding HRAS. <i>Structure</i> , 2015, 23, 1382-1393.	1.6	31
1262	Electrostatic Architecture of the Infectious Salmon Anemia Virus (ISAV) Core Fusion Protein Illustrates a Carboxyl-Carboxylate pH Sensor. <i>Journal of Biological Chemistry</i> , 2015, 290, 18495-18504.	1.6	11
1263	ATP-dependent Conformational Changes Trigger Substrate Capture and Release by an ECF-type Biotin Transporter. <i>Journal of Biological Chemistry</i> , 2015, 290, 16929-16942.	1.6	24
1264	Crystal structure of GnsA from <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 462, 1-7.	1.0	5
1265	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, 7300.	5.8	18
1266	Structural and functional studies of the <i>Mycobacterium tuberculosis</i> VapBC30 toxin-antitoxin system: implications for the design of novel antimicrobial peptides. <i>Nucleic Acids Research</i> , 2015, 43, 7624-7637.	6.5	68
1267	Crystal Structure and Product Analysis of an Archaeal myo-Inositol Kinase Reveal Substrate Recognition Mode and 3-OH Phosphorylation. <i>Biochemistry</i> , 2015, 54, 3494-3503.	1.2	7
1268	Structural Basis for the Interconversion of Maltodextrins by MalQ, the Amylomaltase of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 21352-21364.	1.6	35
1269	Deciphering the Molecular Basis of Functional Divergence in AMPylating Enzymes by Molecular Dynamics Simulations and Structure Guided Phylogeny. <i>Biochemistry</i> , 2015, 54, 5209-5224.	1.2	8
1270	Structural insight into the thermostable NADP ⁺ -dependent meso-diaminopimelate dehydrogenase from <i>Ureibacillus thermosphaericus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1136-1146.	2.5	12
1271	Towards New Drug Targets? Function Prediction of Putative Proteins of <i>Neisseria meningitidis</i> MC58 and Their Virulence Characterization. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 416-434.	1.0	18
1272	Recognition of microbial glycans by human intelectin-1. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 603-610.	3.6	133
1273	Converting Transaldolase into Aldolase through Swapping of the Multifunctional Acid-Base Catalyst: Common and Divergent Catalytic Principles in F6P Aldolase and Transaldolase. <i>Biochemistry</i> , 2015, 54, 4475-4486.	1.2	18
1274	Structural and Biochemical Characterization of AidC, a Quorum-Quenching Lactonase with Atypical Selectivity. <i>Biochemistry</i> , 2015, 54, 4342-4353.	1.2	19

#	ARTICLE	IF	CITATIONS
1275	Structure and mechanism of a bacterial host-protein citrullinating virulence factor, <i>Porphyromonas gingivalis</i> peptidylarginine deiminase. <i>Scientific Reports</i> , 2015, 5, 11969.	1.6	72
1276	A noncanonical PWI domain in the N-terminal helicase-associated region of the spliceosomal Br2 protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 762-771.	2.5	29
1277	Non-canonical Bromodomain within DNA-PKcs Promotes DNA Damage Response and Radioresistance through Recognizing an IR-Induced Acetyl-Lysine on H2AX. <i>Chemistry and Biology</i> , 2015, 22, 849-861.	6.2	15
1278	The solution structure of the MANEC-type domain from hepatocyte growth factor activator inhibitor-1 reveals an unexpected PAN/apple domain-type fold. <i>Biochemical Journal</i> , 2015, 466, 299-309.	1.7	15
1279	Structural and biochemical analyses of the <i>Streptococcus pneumoniae</i> L ₁ and D ₁ -carboxypeptidase DacB. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 283-292.	2.5	2
1280	VP22 core domain from Herpes simplex virus 1 reveals a surprising structural conservation in both the Alpha- and Gammaherpesvirinae subfamilies. <i>Journal of General Virology</i> , 2015, 96, 1436-1445.	1.3	26
1281	An intermolecular binding mechanism involving multiple LysM domains mediates carbohydrate recognition by an endopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 592-605.	2.5	34
1282	Structural insights into the substrate specificity of two esterases from the thermophilic <i>Rhizomucor miehei</i> . <i>Journal of Lipid Research</i> , 2015, 56, 1616-1624.	2.0	29
1283	Structural basis and functional analysis of the SARS coronavirus nsp14-nsp10 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9436-9441.	3.3	431
1284	Structural and biochemical insights into nucleotide-rhamnose synthase/epimerase-reductase from <i>Arabidopsis thaliana</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1476-1486.	1.1	12
1285	Structure and Biophysical Characterization of the S-Adenosylmethionine-dependent O-Methyltransferase PaMTH1, a Putative Enzyme Accumulating during Senescence of <i>Podospora anserina</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 16415-16430.	1.6	20
1286	Structural Insights into the Distinct Binding Mode of Cyclic Di-AMP with <i>Sa</i> CpaA_RCK. <i>Biochemistry</i> , 2015, 54, 4936-4951.	1.2	48
1287	The N-terminal domain of MuB protein has striking structural similarity to DNA-binding domains and mediates MuB filament-filament interactions. <i>Journal of Structural Biology</i> , 2015, 191, 100-111.	1.3	4
1288	Elusive Structural, Functional, and Immunological Features of Act d 5, the Green Kiwifruit Kiwellin. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 6567-6576.	2.4	25
1289	Crystal structure of UbiX, an aromatic acid decarboxylase from the psychrophilic bacterium <i>Colwellia psychrerythraea</i> that undergoes FMN-induced conformational changes. <i>Scientific Reports</i> , 2015, 5, 8196.	1.6	13
1290	Structure of a herpesvirus nuclear egress complex subunit reveals an interaction groove that is essential for viral replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9010-9015.	3.3	52
1291	Functional characterization of two SOS-regulated genes involved in mitomycin C resistance in <i>Caulobacter crescentus</i> . <i>DNA Repair</i> , 2015, 33, 78-89.	1.3	10
1292	A Disulfide Bond-forming Machine Is Linked to the Sortase-mediated Pilus Assembly Pathway in the Gram-positive Bacterium <i>Actinomyces oris</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 21393-21405.	1.6	28

#	ARTICLE	IF	CITATIONS
1293	A prevalent peptide-binding domain guides ribosomal natural product biosynthesis. <i>Nature Chemical Biology</i> , 2015, 11, 564-570.	3.9	288
1294	Structural basis for the activation of the <i>C. elegans</i> noncanonical cytoplasmic poly(A)-polymerase GLD-2 by GLD-3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8614-8619.	3.3	23
1295	A Compact Structure of Cytochrome <i>c</i> Trapped in a Lysine-Ligated State: Loop Refolding and Functional Implications of a Conformational Switch. <i>Journal of the American Chemical Society</i> , 2015, 137, 8435-8449.	6.6	62
1296	The structure of the folded domain from the signature multifunctional protein ICP27 from herpes simplex virus-1 reveals an intertwined dimer. <i>Scientific Reports</i> , 2015, 5, 11234.	1.6	23
1297	Outer-membrane translocation of bulky small molecules by passive diffusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2991-9.	3.3	70
1298	Tools for macromolecular model building and refinement into electron cryo-microscopy reconstructions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 136-153.	2.5	537
1299	The Thalidomide-Binding Domain of Cereblon Defines the CULT Domain Family and Is a New Member of the Î²-Tent Fold. <i>PLoS Computational Biology</i> , 2015, 11, e1004023.	1.5	34
1300	Structural and functional characterization of TesB from <i>Yersinia pestis</i> reveals a unique octameric arrangement of hotdog domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 986-995.	2.5	8
1301	High-resolution crystal structure of a polyextreme GH43 glycosidase from <i>Halothermothrix orenii</i> with Î±-L-arabinofuranosidase activity. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 338-345.	0.4	8
1302	A protein fold switch joins the circadian oscillator to clock output in cyanobacteria. <i>Science</i> , 2015, 349, 324-328.	6.0	157
1303	Structural Studies of Potassium Transport Protein KtrA Regulator of Conductance of K ⁺ (RCK) C Domain in Complex with Cyclic Diadenosine Monophosphate (c-di-AMP). <i>Journal of Biological Chemistry</i> , 2015, 290, 16393-16402.	1.6	74
1304	Crystal structures reveal transient PERK luminal domain tetramerization in endoplasmic reticulum stress signaling. <i>EMBO Journal</i> , 2015, 34, 1589-1600.	3.5	69
1305	The family 6 Carbohydrate Binding Module (CtCBM6) of glucuronoxylanase (CtXynGH30) of <i>Clostridium thermocellum</i> binds decorated and undecorated xylans through cleft A. <i>Archives of Biochemistry and Biophysics</i> , 2015, 575, 8-21.	1.4	10
1306	Crystal structure of Î²-galactosidase from <i>Bacillus circulans</i> ATCC 31382 (BgaD) and the construction of the thermophilic mutants. <i>FEBS Journal</i> , 2015, 282, 2540-2552.	2.2	44
1307	Structural and Enzymatic Analysis of TarM Glycosyltransferase from <i>Staphylococcus aureus</i> Reveals an Oligomeric Protein Specific for the Glycosylation of Wall Teichoic Acid. <i>Journal of Biological Chemistry</i> , 2015, 290, 9874-9885.	1.6	22
1308	Small-Molecule Transport by CarO, an Abundant Eight-Stranded Î²-Barrel Outer Membrane Protein from <i>Acinetobacter baumannii</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2329-2339.	2.0	54
1309	Solution structure of the RNA-binding cold-shock domain of the <i>Chlamydomonas reinhardtii</i> NAB1 protein and insights into RNA recognition. <i>Biochemical Journal</i> , 2015, 469, 97-106.	1.7	4
1310	A structural model for FOXRED1, an FAD-dependent oxidoreductase necessary for NADH: Ubiquinone oxidoreductase (complex I) assembly. <i>Mitochondrion</i> , 2015, 22, 9-16.	1.6	9

#	ARTICLE	IF	CITATIONS
1311	Thiosulfate Dehydrogenase (TsdA) from <i>Allochromatium vinosum</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 9222-9238.	1.6	46
1312	Crystal Structure and Activity of the Endoribonuclease Domain of the piRNA Pathway Factor Maelstrom. <i>Cell Reports</i> , 2015, 11, 366-375.	2.9	36
1313	Biochemical functional predictions for protein structures of unknown or uncertain function. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 182-191.	1.9	77
1314	Protein-pyridinol thioester precursor for biosynthesis of the organometallic acyl-iron ligand in [Fe]-hydrogenase cofactor. <i>Nature Communications</i> , 2015, 6, 6895.	5.8	26
1315	NMR structure determination of the protein NP_344798.1 as the first representative of Pfam PF06042. <i>Journal of Biomolecular NMR</i> , 2015, 61, 83-87.	1.6	4
1316	Utilization of paramagnetic relaxation enhancements for high-resolution NMR structure determination of a soluble loop-rich protein with sparse NOE distance restraints. <i>Journal of Biomolecular NMR</i> , 2015, 61, 55-64.	1.6	16
1317	Crystal structure of the MazG-related nucleoside triphosphate pyrophosphohydrolase from <i>Thermotoga maritima</i> MSB8. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 81-89.	1.2	1
1318	Structure and Mechanism of Ferulic Acid Decarboxylase (FDC1) from <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 4216-4223.	1.4	30
1319	Crystal structure of extracellular domain of human lectin-like transcript 1 (LLT1), the ligand for natural killer receptor NKG2A . <i>European Journal of Immunology</i> , 2015, 45, 1605-1613.	1.6	16
1320	KDM1 class flavin-dependent protein lysine demethylases. <i>Biopolymers</i> , 2015, 104, 213-246.	1.2	53
1321	High-resolution structure of a type IV pilin from the metal-reducing bacterium <i>Shewanella oneidensis</i> . <i>BMC Structural Biology</i> , 2015, 15, 4.	2.3	15
1322	Structural Basis of Latrophilin-FLRT Interaction. <i>Structure</i> , 2015, 23, 774-781.	1.6	67
1323	Structural Basis for Substrate-specific Acetylation of N^{ϵ} -acetyltransferase Ard1 from <i>Sulfolobus solfataricus</i> . <i>Scientific Reports</i> , 2015, 5, 8673.	1.6	22
1324	Synergic interplay of the La motif, RRM1 and the interdomain linker of LARP6 in the recognition of collagen mRNA expands the RNA binding repertoire of the La module. <i>Nucleic Acids Research</i> , 2015, 43, 645-660.	6.5	68
1325	Structural and functional analysis of betaine aldehyde dehydrogenase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1159-1175.	2.5	16
1326	Crystal Structure of the N-Acetylmuramic Acid 1-Phosphate (MurNAc-1-P) Uridyltransferase MurU, a Minimal Sugar Nucleotidyltransferase and Potential Drug Target Enzyme in Gram-negative Pathogens. <i>Journal of Biological Chemistry</i> , 2015, 290, 10804-10813.	1.6	14
1327	Characterization of the fusion core in zebrafish endogenous retroviral envelope protein. <i>Biochemical and Biophysical Research Communications</i> , 2015, 460, 633-638.	1.0	6
1328	Identification and regulation of the catalytic promiscuity of β -lactamase from <i>Microbacterium hydrocarbonoxydans</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7559-7568.	1.7	9

#	ARTICLE	IF	CITATIONS
1329	Crystal structure of the effector protein HopA1 from <i>Pseudomonas syringae</i> . <i>Journal of Structural Biology</i> , 2015, 189, 276-280.	1.3	11
1330	The structure of PccH from <i>Geobacter sulfurreducens</i> – a novel low reduction potential monoheme cytochrome essential for accepting electrons from an electrode. <i>FEBS Journal</i> , 2015, 282, 2215-2231.	2.2	26
1331	Structural and functional analysis of two universal stress proteins YdaA and YnaF from <i>Salmonella typhimurium</i> : possible roles in microbial stress tolerance. <i>Journal of Structural Biology</i> , 2015, 189, 238-250.	1.3	13
1332	A unique homodimeric NAD ⁺ -linked isocitrate dehydrogenase from the smallest autotrophic eukaryote <i>Ostreococcus tauri</i> . <i>FASEB Journal</i> , 2015, 29, 2462-2472.	0.2	14
1333	Crystal structure of Cry51Aa1: A potential novel insecticidal aerolysin-type β -pore-forming toxin from <i>Bacillus thuringiensis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 462, 184-189.	1.0	32
1334	Insight into the Ebola virus nucleocapsid assembly mechanism: crystal structure of Ebola virus nucleoprotein core domain at 1.8 Å resolution. <i>Protein and Cell</i> , 2015, 6, 351-362.	4.8	61
1335	A Disulfide Stabilized β -Sandwich Defines the Structure of a New Cysteine Framework M-Superfamily Conotoxin. <i>ACS Chemical Biology</i> , 2015, 10, 1847-1860.	1.6	6
1336	Structural and Functional Plasticity of Antibiotic Resistance Nucleotidyltransferases Revealed by Molecular Characterization of Lincosamide Nucleotidyltransferases Lnu(A) and Lnu(D). <i>Journal of Molecular Biology</i> , 2015, 427, 2229-2243.	2.0	7
1337	Structural and functional analysis reveals that human OASL binds dsRNA to enhance RIG-I signaling. <i>Nucleic Acids Research</i> , 2015, 43, 5236-5248.	6.5	57
1338	The structure of the human mitochondrial ribosome. <i>Science</i> , 2015, 348, 95-98.	6.0	432
1339	The structure of <i>S. lividans</i> acetoacetyl-CoA synthetase shows a novel interaction between the C-terminal extension and the N-terminal domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 575-581.	1.5	6
1340	Structure of the GH76 α -mannanase homolog, BT2949, from the gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 408-415.	2.5	8
1341	The Tomato Defensin TPP3 Binds Phosphatidylinositol (4,5)-Bisphosphate via a Conserved Dimeric Cationic Grip Conformation To Mediate Cell Lysis. <i>Molecular and Cellular Biology</i> , 2015, 35, 1964-1978.	1.1	84
1342	Structural insights into the efficient CO ₂ -reducing activity of an NAD-dependent formate dehydrogenase from <i>Thiobacillus</i> sp. KNK65MA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 313-323.	2.5	23
1343	Structure and reaction mechanism of a novel enone reductase. <i>FEBS Journal</i> , 2015, 282, 1526-1537.	2.2	8
1344	Crystal structures of the human adiponectin receptors. <i>Nature</i> , 2015, 520, 312-316.	13.7	176
1345	Structure of <i>Arabidopsis thaliana</i> Rubisco activase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 800-808.	2.5	33
1346	Computational tools for epitope vaccine design and evaluation. <i>Current Opinion in Virology</i> , 2015, 11, 103-112.	2.6	60

#	ARTICLE	IF	CITATIONS
1347	Carbohydrate-binding module tribes. <i>Biopolymers</i> , 2015, 103, 203-214.	1.2	24
1348	Substrate Specificity and Plasticity of FERM-Containing Protein Tyrosine Phosphatases. <i>Structure</i> , 2015, 23, 653-664.	1.6	20
1349	Structural and adhesive properties of the long polar fimbriae protein LpfD from adherent-invasive <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1615-1626.	2.5	8
1350	Structure of the Legionella Effector, lpg1496, Suggests a Role in Nucleotide Metabolism. <i>Journal of Biological Chemistry</i> , 2015, 290, 24727-24737.	1.6	11
1351	Molecular basis for the inhibition of β -hydroxyacyl-ACP dehydratase HadAB complex from <i>Mycobacterium tuberculosis</i> by flavonoid inhibitors. <i>Protein and Cell</i> , 2015, 6, 504-517.	4.8	28
1352	Crystal Structure of PnpCD, a Two-subunit Hydroquinone 1,2-Dioxygenase, Reveals a Novel Structural Class of Fe ²⁺ -dependent Dioxygenases. <i>Journal of Biological Chemistry</i> , 2015, 290, 24547-24560.	1.6	12
1353	Creaserin uses a TOG domain array to regulate microtubules in the primary cilium. <i>Molecular Biology of the Cell</i> , 2015, 26, 4248-4264.	0.9	52
1354	The REC domain mediated dimerization is critical for FleQ from <i>Pseudomonas aeruginosa</i> to function as a c-di-GMP receptor and flagella gene regulator. <i>Journal of Structural Biology</i> , 2015, 192, 1-13.	1.3	41
1355	A Structural Snapshot of Type II Pilus Formation in <i>Streptococcus pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 22581-22592.	1.6	17
1356	Structure of the Ergothioneine Biosynthesis Amidohydrolase EgtC. <i>ChemBioChem</i> , 2015, 16, 1490-1496.	1.3	32
1357	Biochemical Studies of Mycobacterial Fatty Acid Methyltransferase: A Catalyst for the Enzymatic Production of Biodiesel. <i>Chemistry and Biology</i> , 2015, 22, 1480-1490.	6.2	17
1358	Structural and Functional Studies of the <i>Pseudomonas aeruginosa</i> Minor Pilin, PilE. <i>Journal of Biological Chemistry</i> , 2015, 290, 26856-26865.	1.6	23
1359	The Solution Structure of the Lantibiotic Immunity Protein Nisl and Its Interactions with Nisin. <i>Journal of Biological Chemistry</i> , 2015, 290, 28869-28886.	1.6	34
1360	Crystal structures of CRISPR-associated Csx3 reveal a manganese-dependent deadenylation exoribonuclease. <i>RNA Biology</i> , 2015, 12, 749-760.	1.5	24
1361	From residue coevolution to protein conformational ensembles and functional dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13567-13572.	3.3	116
1362	Structural analysis of the KRIT1 ankyrin repeat and FERM domains reveals a conformationally stable ARD-FERM interface. <i>Journal of Structural Biology</i> , 2015, 192, 449-456.	1.3	12
1363	X-ray Structural and Functional Studies of the Three Tandemly Linked Domains of Non-structural Protein 3 (nsp3) from Murine Hepatitis Virus Reveal Conserved Functions. <i>Journal of Biological Chemistry</i> , 2015, 290, 25293-25306.	1.6	34
1364	Can template-based protein models guide the design of sequence fitness for enhanced thermal stability of single domain antibodies?. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 395-402.	1.0	7

#	ARTICLE	IF	CITATIONS
1365	The Substrate-free and -bound Crystal Structures of the Duplicated Taurocyamine Kinase from the Human Parasite <i>Schistosoma mansoni</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 12951-12963.	1.6	9
1366	Self-cleavage of the <i>Pseudomonas aeruginosa</i> Cell-surface Signaling Anti-sigma Factor FoxR Occurs through an N-O Acyl Rearrangement. <i>Journal of Biological Chemistry</i> , 2015, 290, 12237-12246.	1.6	24
1367	Functional and Structural Characterization of the Antiphagocytic Properties of a Novel Transglutaminase from <i>Streptococcus suis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 19081-19092.	1.6	22
1368	A comparative molecular dynamics study of thermophilic and mesophilic β -fructosidase enzymes. <i>Journal of Molecular Modeling</i> , 2015, 21, 228.	0.8	75
1369	An Interbacterial NAD(P) ⁺ Glycohydrolase Toxin Requires Elongation Factor Tu for Delivery to Target Cells. <i>Cell</i> , 2015, 163, 607-619.	13.5	203
1370	Laminin β 4 domain structure resembles adhesion modules in ephrin receptor and other transmembrane glycoproteins. <i>FEBS Journal</i> , 2015, 282, 2746-2757.	2.2	12
1371	STAC ⁺ A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339.	2.0	17
1372	The structure of Erb1-Ytm1 complex reveals the functional importance of a high-affinity binding between two β -propellers during the assembly of large ribosomal subunits in eukaryotes. <i>Nucleic Acids Research</i> , 2015, 43, 11017-11030.	6.5	18
1373	Structural and Antimicrobial Features of Peptides Related to Myticin C, a Special Defense Molecule from the Mediterranean Mussel <i>Mytilus galloprovincialis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 9251-9259.	2.4	28
1374	The first crystal structure of a glycoside hydrolase family 17 β -1,3-glucanosyltransferase displays a unique catalytic cleft. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1714-1724.	2.5	13
1375	Structural basis of mapping the spontaneous mutations with 5-fluorouracil in uracil phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 577-582.	1.0	7
1376	Solution structure of leptospiral LigA4 Big domain. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 288-292.	1.0	5
1377	SANSparallel: interactive homology search against Uniprot. <i>Nucleic Acids Research</i> , 2015, 43, W24-W29.	6.5	38
1378	Structural and Functional Adaptation of Vancomycin Resistance VanT Serine Racemases. <i>MBio</i> , 2015, 6, e00806.	1.8	18
1379	Structural and functional studies of a metallo- β -lactamase unveil a new type of structurally encoded nickel-containing heterodinuclear site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2054-2065.	2.5	3
1380	Structure-function analysis identifies highly sensitive strigolactone receptors in <i>Striga</i> . <i>Science</i> , 2015, 350, 203-207.	6.0	227
1381	Structural and Functional Characterization of the Hazelnut Allergen Cor a 8. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 9150-9158.	2.4	33
1382	Recapitulating the Structural Evolution of Redox Regulation in Adenosine 5'-Phosphosulfate Kinase from Cyanobacteria to Plants. <i>Journal of Biological Chemistry</i> , 2015, 290, 24705-24714.	1.6	15

#	ARTICLE	IF	CITATIONS
1383	Structure of the novel monomeric glyoxalase I from <i>Zea mays</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2009-2020.	2.5	21
1384	Two-step Ligand Binding in a (12±)8 Barrel Enzyme. Journal of Biological Chemistry, 2015, 290, 24657-24668.	1.6	16
1385	Structural and functional studies of a <i>Fusarium oxysporum</i> cutinase with polyethylene terephthalate modification potential. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 2308-2317.	1.1	68
1386	Structures of two bacterial resistance factors mediating tRNA-dependent aminoacylation of phosphatidylglycerol with lysine or alanine. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10691-10696.	3.3	36
1387	Structural basis of Lewis ^b antigen binding by the <i>Helicobacter pylori</i> adhesin BabA. Science Advances, 2015, 1, e1500315.	4.7	58
1388	The Structure and Interactions of Periplasmic Domains of Crucial MmpL Membrane Proteins from <i>Mycobacterium tuberculosis</i> . Chemistry and Biology, 2015, 22, 1098-1107.	6.2	42
1389	Structural and Functional Characterization of a Lytic Polysaccharide Monooxygenase with Broad Substrate Specificity. Journal of Biological Chemistry, 2015, 290, 22955-22969.	1.6	157
1390	Structural and functional analysis of a low-temperature-active alkaline esterase from South China Sea marine sediment microbial metagenomic library. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 1449-1461.	1.4	20
1391	Unraveling the degradation of artificial amide bonds in nylon oligomer hydrolase: from induced-fit to acylation processes. Physical Chemistry Chemical Physics, 2015, 17, 4492-4504.	1.3	12
1392	Mechanistic Insight into Trimethylamine <i>N</i> -Oxide Recognition by the Marine Bacterium <i>Ruegeria pomeroyi</i> DSS-3. Journal of Bacteriology, 2015, 197, 3378-3387.	1.0	21
1393	Structural Characterization of Bardet-Biedl Syndrome 9 Protein (BBS9). Journal of Biological Chemistry, 2015, 290, 19569-19583.	1.6	19
1394	YehZYXW of <i>Escherichia coli</i> Is a Low-Affinity, Non-Osmoregulatory Betaine-Specific ABC Transporter. Biochemistry, 2015, 54, 5735-5747.	1.2	25
1395	Structure of BipA in GTP form bound to the ratcheted ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10944-10949.	3.3	37
1396	Circadian Rhythms in Cyanobacteria. Microbiology and Molecular Biology Reviews, 2015, 79, 373-385.	2.9	222
1397	Noncanonical sortase-mediated assembly of pilus type 2b in group B <i>Streptococcus</i> . FASEB Journal, 2015, 29, 4629-4640.	0.2	10
1398	PslG, a self-produced glycosyl hydrolase, triggers biofilm disassembly by disrupting exopolysaccharide matrix. Cell Research, 2015, 25, 1352-1367.	5.7	123
1399	Structural Basis of Neurohormone Perception by the Receptor Tyrosine Kinase Torso. Molecular Cell, 2015, 60, 941-952.	4.5	15
1400	Structure of Spo0M, a sporulation-control protein from <i>Bacillus subtilis</i> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1488-1497.	0.4	3

#	ARTICLE	IF	CITATIONS
1401	Crystal structure analysis of ornithine transcarbamylase from <i>Thermus thermophilus</i> HB8 provides insights on the plasticity of the active site. <i>Biochemical and Biophysical Research Communications</i> , 2015, 465, 174-179.	1.0	3
1402	The Structure of <i>Escherichia coli</i> TcdA (Also Known As CsdL) Reveals a Novel Topology and Provides Insight into the tRNA Binding Surface Required for N6-Threonylcarbamoyladenine Dehydratase Activity. <i>Journal of Molecular Biology</i> , 2015, 427, 3074-3085.	2.0	7
1403	Structural characterization and modeling of the <i>Borrelia burgdorferi</i> hybrid histidine kinase Hk1 periplasmic sensor: A system for sensing small molecules associated with tick feeding. <i>Journal of Structural Biology</i> , 2015, 192, 48-58.	1.3	24
1404	The SWI/SNF Subunit INI1 Contains an N-Terminal Winged Helix DNA Binding Domain that Is a Target for Mutations in Schwannomatosis. <i>Structure</i> , 2015, 23, 1344-1349.	1.6	33
1405	A deep phylogeny of viral and cellular right-hand polymerases. <i>Infection, Genetics and Evolution</i> , 2015, 36, 275-286.	1.0	10
1406	Identification and Characterization of a Methionine S-Methyltransferase in the Calicheamicin Biosynthetic Cluster of <i>Micromonospora echinospora</i> . <i>ChemBioChem</i> , 2015, 16, 100-109.	1.3	21
1407	Structure-Based Design of a B Cell Antigen from <i>B. pseudomallei</i> . <i>ACS Chemical Biology</i> , 2015, 10, 803-812.	1.6	12
1408	Human FMRP contains an integral tandem Agenet (Tudor) and KH motif in the amino terminal domain. <i>Human Molecular Genetics</i> , 2015, 24, 1733-1740.	1.4	92
1409	Bacterial and algal orthologs of prostaglandin H2 synthase: novel insights into the evolution of an integral membrane protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 83-94.	1.4	4
1410	Structure-Function Analysis of Vaccinia Virus H7 Protein Reveals a Novel Phosphoinositide Binding Fold Essential for Poxvirus Replication. <i>Journal of Virology</i> , 2015, 89, 2209-2219.	1.5	23
1411	Target-Specific Native/Decoy Pose Classifier Improves the Accuracy of Ligand Ranking in the CSAR 2013 Benchmark. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 63-71.	2.5	14
1412	Structure of an APC3-APC16 Complex: Insights into Assembly of the Anaphase-Promoting Complex/Cyclosome. <i>Journal of Molecular Biology</i> , 2015, 427, 1748-1764.	2.0	35
1413	Crystal structure of <i>Bacillus anthracis</i> virulence regulator <i>AtxA</i> and effects of phosphorylated histidines on multimerization and activity. <i>Molecular Microbiology</i> , 2015, 95, 426-441.	1.2	32
1414	Structural and biochemical characterization of a carbohydrate acetyltransferase from <i>Sinorhizobium meliloti</i> 1021. <i>FEBS Letters</i> , 2015, 589, 117-122.	1.3	18
1415	Structural Basis of the Proteolytic and Chaperone Activity of <i>Chlamydia trachomatis</i> CT441. <i>Journal of Bacteriology</i> , 2015, 197, 211-218.	1.0	9
1416	Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. <i>Autophagy</i> , 2015, 11, 75-87.	4.3	59
1417	In-silico characterization of Formin Binding Protein 4 Family of proteins. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 43-64.	2.2	4
1418	Structure of a mammalian ryanodine receptor. <i>Nature</i> , 2015, 517, 44-49.	13.7	350

#	ARTICLE	IF	CITATIONS
1419	Structure of an integral membrane sterol reductase from <i>Methylomicrobium alcaliphilum</i> . <i>Nature</i> , 2015, 517, 104-107.	13.7	48
1420	Insights into the potential function and membrane organization of the TP0435 (^Tp17) lipoprotein from <i>T. reponema pallidum</i> derived from structural and biophysical analyses. <i>Protein Science</i> , 2015, 24, 11-19.	3.1	15
1421	Structure-based functional annotation of putative conserved proteins having lyase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 317-336.	1.1	15
1422	Full genome sequences and molecular characterization of tick-borne encephalitis virus strains isolated from human patients. <i>Ticks and Tick-borne Diseases</i> , 2015, 6, 38-46.	1.1	30
1423	6. Bacterial dye-decolorizing peroxidases. , 2016, , 107-130.		0
1424	Crystal Structure of Hypothetical Fructose-Specific EIIB from <i>Escherichia coli</i> . <i>Molecules and Cells</i> , 2016, 39, 495-500.	1.0	2
1425	Biochemical and structural characterisation of the second oxidative crosslinking step during the biosynthesis of the glycopeptide antibiotic A47934. <i>Beilstein Journal of Organic Chemistry</i> , 2016, 12, 2849-2864.	1.3	14
1426	Structural Investigation and In-silico Characterization of Plasmepsins from <i>Plasmodium falciparum</i> . <i>Journal of Proteomics and Bioinformatics</i> , 2016, 9, .	0.4	3
1427	Function annotation of peptides generated from the non-coding regions of <i>D. melanogaster</i> genome. <i>Bioinformatics</i> , 2016, 12, 202-208.	0.2	4
1428	Ribosome-RelA structures reveal the mechanism of stringent response activation. <i>ELife</i> , 2016, 5, .	2.8	143
1429	Structural characterization of the thermostable <i>Bradyrhizobium japonicum</i> D-sorbitol dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 846-852.	0.4	7
1430	Bacterial dye-decolorizing peroxidases: Biochemical properties and biotechnological opportunities. <i>ChemistrySelect</i> , 2016, 1, .	0.7	15
1431	Characteristics of Sucrose Transport through the Sucrose-Specific Porin ScrY Studied by Molecular Dynamics Simulations. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 9.	2.0	12
1432	Venoms of Heteropteran Insects: A Treasure Trove of Diverse Pharmacological Toolkits. <i>Toxins</i> , 2016, 8, 43.	1.5	62
1433	Identification of <i>Plasmodium falciparum</i> Translation Initiation eIF2 ^γ Subunit: Direct Interaction with Protein Phosphatase Type 1. <i>Frontiers in Microbiology</i> , 2016, 7, 777.	1.5	18
1434	Homology-Based Modeling of Universal Stress Protein from <i>Listeria innocua</i> Up-Regulated under Acid Stress Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 1998.	1.5	21
1435	Crystal Structure of the Substrate-Binding Domain from <i>Listeria monocytogenes</i> Bile-Resistance Determinant BilE. <i>Crystals</i> , 2016, 6, 162.	1.0	7
1436	Crystal structure and DNA binding activity of a PadR family transcription regulator from hypervirulent <i>Clostridium difficile</i> R20291. <i>BMC Microbiology</i> , 2016, 16, 231.	1.3	13

#	ARTICLE	IF	CITATIONS
1437	GPO.4 from bacteriophage T7: in silico characterisation of its structure and interaction with E. coli FtsZ. BMC Research Notes, 2016, 9, 343.	0.6	3
1438	Structure and Function of the Su(H)-Hairless Repressor Complex, the Major Antagonist of Notch Signaling in <i>Drosophila melanogaster</i> . PLoS Biology, 2016, 14, e1002509.	2.6	53
1439	Coenzyme Q Biosynthesis: Evidence for a Substrate Access Channel in the FAD-Dependent Monooxygenase Coq6. PLoS Computational Biology, 2016, 12, e1004690.	1.5	10
1440	Functional and Structural Analysis of a β -Glucosidase Involved in β -1,2-Glucan Metabolism in <i>Listeria innocua</i> . PLoS ONE, 2016, 11, e0148870.	1.1	36
1441	Structural and Biochemical Insights into the Peptidoglycan Hydrolase Domain of FlgJ from <i>Salmonella typhimurium</i> . PLoS ONE, 2016, 11, e0149204.	1.1	20
1442	Crystal Structure of Alcohol Oxidase from <i>Pichia pastoris</i> . PLoS ONE, 2016, 11, e0149846.	1.1	39
1443	Structure of the Response Regulator NsrR from <i>Streptococcus agalactiae</i> , Which Is Involved in Lantibiotic Resistance. PLoS ONE, 2016, 11, e0149903.	1.1	22
1444	Crystal Structure of the FERM-SH2 Module of Human Jak2. PLoS ONE, 2016, 11, e0156218.	1.1	28
1445	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. PLoS ONE, 2016, 11, e0157070.	1.1	8
1446	Crystal Structures of the Global Regulator DasR from <i>Streptomyces coelicolor</i> : Implications for the Allosteric Regulation of GntR/HutC Repressors. PLoS ONE, 2016, 11, e0157691.	1.1	21
1447	The Human Mixed Lineage Leukemia 5 (MLL5), a Sequentially and Structurally Divergent SET Domain-Containing Protein with No Intrinsic Catalytic Activity. PLoS ONE, 2016, 11, e0165139.	1.1	31
1448	The Structure of <i>Treponema pallidum</i> Tp0624 Reveals a Modular Assembly of Divergently Functionalized and Previously Uncharacterized Domains. PLoS ONE, 2016, 11, e0166274.	1.1	10
1449	Structural and Biochemical Characterization of <i>Chlamydia trachomatis</i> DsbA Reveals a Cysteine-Rich and Weakly Oxidising Oxidoreductase. PLoS ONE, 2016, 11, e0168485.	1.1	10
1450	Initiation of RNA Polymerization and Polymerase Encapsidation by a Small dsRNA Virus. PLoS Pathogens, 2016, 12, e1005523.	2.1	42
1451	Crystal Structure of Human Herpesvirus 6B Tegument Protein UI4. PLoS Pathogens, 2016, 12, e1005594.	2.1	12
1452	The Structure of <i>Treponema pallidum</i> Tp0751 (Pallilysin) Reveals a Non-canonical Lipocalin Fold That Mediates Adhesion to Extracellular Matrix Components and Interactions with Host Cells. PLoS Pathogens, 2016, 12, e1005919.	2.1	29
1453	Crystal Structure of Glycoprotein C from a Hantavirus in the Post-fusion Conformation. PLoS Pathogens, 2016, 12, e1005948.	2.1	51
1454	Crystal Structure Analysis and the Identification of Distinctive Functional Regions of the Protein Elicitor Mohrip2. Frontiers in Plant Science, 2016, 7, 1103.	1.7	6

#	ARTICLE	IF	CITATIONS
1456	The crystal structure of the ligand-binding region of serine-glutamate repeat containing protein A (SgrA) of <i>Enterococcus faecium</i> reveals a new protein fold: functional characterization and insights into its adhesion function. <i>FEBS Journal</i> , 2016, 283, 3039-3055.	2.2	3
1457	Structural and biochemical characterization of EDTA monooxygenase and its physical interaction with a partner flavin reductase. <i>Molecular Microbiology</i> , 2016, 100, 989-1003.	1.2	16
1458	Structural characterization of peptidyl-tRNA hydrolase from <i>Mycobacterium smegmatis</i> by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1304-1314.	1.1	9
1459	Crystal structure of Cry6Aa: A novel nematocidal ClyA-type β -pore-forming toxin from <i>Bacillus thuringiensis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 307-313.	1.0	15
1460	Protein purification and crystallization artifacts: The tale usually not told. <i>Protein Science</i> , 2016, 25, 720-733.	3.1	46
1461	Structural and functional features of the NAD(P) dependent Gfo/Idh/MocA protein family oxidoreductases. <i>Protein Science</i> , 2016, 25, 778-786.	3.1	34
1462	Computational modeling of Repeat1 region of INI1/hSNF5: An evolutionary link with ubiquitin. <i>Protein Science</i> , 2016, 25, 1593-1604.	3.1	1
1463	Computational characterization of TTHA0379: A potential glycerophosphocholine binding protein of Ugp ATP-binding cassette transporter. <i>Gene</i> , 2016, 592, 260-268.	1.0	10
1465	Connecting common genetic polymorphisms to protein function: A modular project sequence for lecture or lab. <i>Biochemistry and Molecular Biology Education</i> , 2016, 44, 526-536.	0.5	1
1466	The nucleotide-dependent interaction of FlaH and FlaI is essential for assembly and function of the archaeum motor. <i>Molecular Microbiology</i> , 2016, 99, 674-685.	1.2	47
1467	NMR reveals structural rearrangements associated to substrate insertion in nucleotide-adding enzymes. <i>Protein Science</i> , 2016, 25, 917-925.	3.1	1
1468	The crystal structure of maleylacetate reductase from <i>Rhizobium</i> sp. strain MTP-10005 provides insights into the reaction mechanism of enzymes in its original family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1029-1042.	1.5	4
1469	Crystal structure of a thiolase from <i>Escherichia coli</i> at 1.8 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 534-544.	0.4	8
1470	Solution structure of the calmodulin-like C-terminal domain of <i>Entamoeba</i> β -actinin2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 461-466.	1.5	2
1471	Structural Insights into an Oxalate-producing Serine Hydrolase with an Unusual Oxyanion Hole and Additional Lyase Activity. <i>Journal of Biological Chemistry</i> , 2016, 291, 15185-15195.	1.6	8
1472	Inspired by Nature: NADPH -Dependent Imine Reductases (IREDs) as Catalysts for the Preparation of Chiral Amines. <i>Chemistry - A European Journal</i> , 2016, 22, 1900-1907.	1.7	116
1473	Molecular and Structural Characterization of a Novel <i>Escherichia coli</i> Interleukin Receptor Mimic Protein. <i>MBio</i> , 2016, 7, e02046.	1.8	17
1474	X-ray structure of linalool dehydratase/isomerase from <i>Castellaniella defragrans</i> reveals enzymatic alkene synthesis. <i>FEBS Letters</i> , 2016, 590, 1375-1383.	1.3	21

#	ARTICLE	IF	CITATIONS
1475	The extended structure of the periplasmic region of CdsD, a structural protein of the type III secretion system of <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2016, 25, 987-998.	3.1	2
1476	Crystal structure of the flagellar accessory protein FlaH of <i>Methanocaldococcus jannaschii</i> suggests a regulatory role in archaeal flagellum assembly. <i>Protein Science</i> , 2016, 25, 1147-1155.	3.1	18
1477	Structural and biochemical insights into Δ^2 -hydroxysteroid dehydrogenase stereoselectivity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 859-865.	1.5	22
1478	Potential DNA binding and nuclease functions of ComEC domains characterized <i>in silico</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1431-1442.	1.5	31
1479	Characterization of the structure and catalytic activity of <i>Legionella pneumophila</i> VipF. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1422-1430.	1.5	5
1480	Structural, Functional, and Immunological Characterization of Profilin Panallergens Amb a 8, Art v 4, and Bet v 2. <i>Journal of Biological Chemistry</i> , 2016, 291, 15447-15459.	1.6	32
1481	Toxin structures as evolutionary tools: Using conserved 3D folds to study the evolution of rapidly evolving peptides. <i>BioEssays</i> , 2016, 38, 539-548.	1.2	76
1482	Structure of OxyA _{TEI} : completing our picture of the glycopeptide antibiotic producing Cytochrome P450 cascade. <i>FEBS Letters</i> , 2016, 590, 571-581.	1.3	17
1483	Structural basis for olivetolic acid formation by a polyketide cyclase from <i>Cannabis sativa</i> . <i>FEBS Journal</i> , 2016, 283, 1088-1106.	2.2	33
1484	<i>Leishmania donovani</i> -specific U ₁ -related modifier 1: an early endosome-associated ubiquitin-like conjugation in <i>Leishmania donovani</i> . <i>Molecular Microbiology</i> , 2016, 99, 597-610.	1.2	12
1485	A structural comparison of <i>Listeria monocytogenes</i> protein chaperones PrsA1 and PrsA2 reveals molecular features required for virulence. <i>Molecular Microbiology</i> , 2016, 101, 42-61.	1.2	13
1486	Structure of RagB, a major immunodominant outer-membrane surface receptor antigen of <i>Porphyromonas gingivalis</i> . <i>Molecular Oral Microbiology</i> , 2016, 31, 472-485.	1.3	15
1487	Structure of the ectodomain of the electron transporter Rv2874 from <i>Mycobacterium tuberculosis</i> reveals a thioredoxin-like domain combined with a carbohydrate-binding module. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 40-48.	1.1	4
1488	Pre-40S ribosome biogenesis factor Tsr1 is an inactive structural mimic of translational GTPases. <i>Nature Communications</i> , 2016, 7, 11789.	5.8	40
1489	Biochemical and Structural Analysis of a Novel Esterase from <i>Caulobacter crescentus</i> related to Penicillin-Binding Protein (PBP). <i>Scientific Reports</i> , 2016, 6, 37978.	1.6	16
1490	Atomic structure of the innexin-6 gap junction channel determined by cryo-EM. <i>Nature Communications</i> , 2016, 7, 13681.	5.8	104
1491	Discovery and structural characterisation of new fold type IV-transaminases exemplify the diversity of this enzyme fold. <i>Scientific Reports</i> , 2016, 6, 38183.	1.6	36
1492	The crystal structure of human dopamine β -hydroxylase at 2.9 Å... resolution. <i>Science Advances</i> , 2016, 2, e1500980.	4.7	80

#	ARTICLE	IF	CITATIONS
1493	The crystal structure of the endoglucanase Cel10, a family 8 glycosyl hydrolase from <i>Klebsiella pneumoniae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 870-876.	0.4	8
1494	Key diffusion mechanisms involved in regulating bidirectional water permeation across E. coli outer membrane lectin. Scientific Reports, 2016, 6, 28157.	1.6	7
1495	Rifampin phosphotransferase is an unusual antibiotic resistance kinase. Nature Communications, 2016, 7, 11343.	5.8	36
1496	Structural basis for copper/silver binding by the <i>Synechocystis</i> metallochaperone CopM. Acta Crystallographica Section D: Structural Biology, 2016, 72, 997-1005.	1.1	6
1497	DNA binding to SMC ATPases "trapped for release. EMBO Journal, 2016, 35, 703-705.	3.5	5
1498	Crystal structure of the substrate-recognition domain of the <i>Shigella</i> E3 ligase IpaH9.8. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 269-275.	0.4	12
1499	Dcsbis (PA2771) from <i>Pseudomonas aeruginosa</i> is a highly active diguanylate cyclase with unique activity regulation. Scientific Reports, 2016, 6, 29499.	1.6	31
1500	Crystal structures and inhibition of <i>Trypanosoma brucei</i> hypoxanthine "guanine phosphoribosyltransferase. Scientific Reports, 2016, 6, 35894.	1.6	15
1501	Protein rethreading: A novel approach to protein design. Scientific Reports, 2016, 6, 26847.	1.6	5
1502	Classification of the treble clef zinc finger: noteworthy lessons for structure and function evolution. Scientific Reports, 2016, 6, 32070.	1.6	17
1503	New insights into the mechanism of substrates trafficking in Glyoxylate/Hydroxypyruvate reductases. Scientific Reports, 2016, 6, 20629.	1.6	19
1504	Structural insight into the arginine-binding specificity of CASTOR1 in amino acid-dependent mTORC1 signaling. Cell Discovery, 2016, 2, 16035.	3.1	28
1505	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
1506	Engineering a minimal G protein to facilitate crystallisation of G protein-coupled receptors in their active conformation. Protein Engineering, Design and Selection, 2016, 29, 583-594.	1.0	103
1507	Crystal Structure of Major Envelope Protein VP24 from White Spot Syndrome Virus. Scientific Reports, 2016, 6, 32309.	1.6	11
1508	The PilZ domain of MrkH represents a novel DNA binding motif. Protein and Cell, 2016, 7, 766-772.	4.8	16
1509	High resolution crystal structure of the catalytic domain of MCR-1. Scientific Reports, 2016, 6, 39540.	1.6	65
1510	Crystal structure of MytiLec, a galactose-binding lectin from the mussel <i>Mytilus galloprovincialis</i> with cytotoxicity against certain cancer cell types. Scientific Reports, 2016, 6, 28344.	1.6	39

#	ARTICLE	IF	CITATIONS
1511	Crystal structure of Anoxybacillus α -amylase provides insights into maltose binding of a new glycosyl hydrolase subclass. <i>Scientific Reports</i> , 2016, 6, 23126.	1.6	31
1512	The Crystal Structure of Peroxiredoxin Asp f3 Provides Mechanistic Insight into Oxidative Stress Resistance and Virulence of <i>Aspergillus fumigatus</i> . <i>Scientific Reports</i> , 2016, 6, 33396.	1.6	44
1513	Structural implications of Ca ²⁺ -dependent actin-bundling function of human EFhd2/Swiprosin-1. <i>Scientific Reports</i> , 2016, 6, 39095.	1.6	27
1514	The replication initiator of the cholera pathogen's second chromosome shows structural similarity to plasmid initiators. <i>Nucleic Acids Research</i> , 2017, 45, gkw1288.	6.5	20
1515	Modular Architecture and Unique Teichoic Acid Recognition Features of Choline-Binding Protein L (Cbpl) Contributing to Pneumococcal Pathogenesis. <i>Scientific Reports</i> , 2016, 6, 38094.	1.6	32
1516	Uncovering ancient transcription systems with a novel evolutionary indicator. <i>Scientific Reports</i> , 2016, 6, 27922.	1.6	5
1517	Generation of efficient fingerprint for GFP-like fold and computational identification of potential GFP-like homologs. <i>Biotechnology and Bioprocess Engineering</i> , 2016, 21, 712-719.	1.4	2
1518	MET-activating Residues in the B-repeat of the <i>Listeria monocytogenes</i> Invasion Protein InlB. <i>Journal of Biological Chemistry</i> , 2016, 291, 25567-25577.	1.6	8
1519	Crystal structure of the human Tip41 orthologue, TIPRL, reveals a novel fold and a binding site for the PP2Ac C-terminus. <i>Scientific Reports</i> , 2016, 6, 30813.	1.6	14
1520	Structure of <i>Saccharomyces cerevisiae</i> Rtr1 reveals an active site for an atypical phosphatase. <i>Science Signaling</i> , 2016, 9, ra24.	1.6	17
1521	Crystal structure of the vicilin from <i>Solanum melongena</i> reveals existence of different anionic ligands in structurally similar pockets. <i>Scientific Reports</i> , 2016, 6, 23600.	1.6	19
1522	Phasing and structure of bestrophin-1: a case study in the use of heavy-atom cluster compounds with multi-subunit transmembrane proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 319-325.	1.1	3
1523	Structural basis for the regulation of enzymatic activity of Regnase-1 by domain-domain interactions. <i>Scientific Reports</i> , 2016, 6, 22324.	1.6	38
1524	Functional architecture of the Reb1-Ter complex of <i>Schizosaccharomyces pombe</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2267-76.	3.3	30
1525	Structural and Kinetic Characterization of the 4-Carboxy-2-hydroxymuconate Hydratase from the Gallate and Protocatechuate 4,5-Cleavage Pathways of <i>Pseudomonas putida</i> KT2440. <i>Journal of Biological Chemistry</i> , 2016, 291, 7669-7686.	1.6	16
1526	Some of the most interesting CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	1.5	16
1527	The cyanobacterial cytochrome b6f subunit PetP adopts an SH3 fold in solution. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 705-714.	0.5	7
1528	Common Structural Core of Three-Dozen Residues Reveals Intersuperfamily Relationships. <i>Molecular Biology and Evolution</i> , 2016, 33, 1697-1710.	3.5	12

#	ARTICLE	IF	CITATIONS
1529	Distinct mechanisms contribute to immunity in the lantibiotic <i>Micromonospora</i> producer strain ATCC PTA-5024. <i>Environmental Microbiology</i> , 2016, 18, 118-132.	1.8	24
1530	Structure-Function Relationships in L-Amino Acid Deaminase, a Flavoprotein Belonging to a Novel Class of Biotechnologically Relevant Enzymes. <i>Journal of Biological Chemistry</i> , 2016, 291, 10457-10475.	1.6	46
1531	Structural Analysis of β -Fructofuranosidase from <i>Xanthophyllomyces dendrorhous</i> Reveals Unique Features and the Crucial Role of N-Glycosylation in Oligomerization and Activity. <i>Journal of Biological Chemistry</i> , 2016, 291, 6843-6857.	1.6	50
1532	Structural and kinetic studies on RosA, the enzyme catalysing the methylation of 8-demethyl-8-amino-riboflavin to the antibiotic roseoflavin. <i>FEBS Journal</i> , 2016, 283, 1531-1549.	2.2	13
1533	A Potential Structural Switch for Regulating DNA-Binding by TEAD Transcription Factors. <i>Journal of Molecular Biology</i> , 2016, 428, 2557-2568.	2.0	11
1534	Crystal structure of histone-like protein from <i>Streptococcus mutans</i> refined to 1.9 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 257-262.	0.4	4
1535	Structural and Biochemical Characterization of 6-Hydroxynicotinic Acid 3-Monooxygenase, A Novel Decarboxylative Hydroxylase Involved in Aerobic Nicotinate Degradation. <i>Biochemistry</i> , 2016, 55, 3432-3446.	1.2	21
1536	The Crystal Structure of <i>Burkholderia cenocepacia</i> DfsA Provides Insights into Substrate Recognition and Quorum Sensing Fatty Acid Biosynthesis. <i>Biochemistry</i> , 2016, 55, 3241-3250.	1.2	8
1537	An extended loop in CE7 carbohydrate esterase family is dispensable for oligomerization but required for activity and thermostability. <i>Journal of Structural Biology</i> , 2016, 194, 434-445.	1.3	12
1538	Structure of faustovirus, a large dsDNA virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6206-6211.	3.3	84
1539	Biochemical and Structural Characterization of a Five-domain GH115 β -Glucuronidase from the Marine Bacterium <i>Saccharophagus degradans</i> 2-40T. <i>Journal of Biological Chemistry</i> , 2016, 291, 14120-14133.	1.6	18
1540	Phosphorylation of spore coat proteins by a family of atypical protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3482-91.	3.3	56
1541	Impact of Binding Site Comparisons on Medicinal Chemistry and Rational Molecular Design. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4121-4151.	2.9	104
1542	Crystal structure of the human β 1 receptor. <i>Nature</i> , 2016, 532, 527-530.	13.7	384
1543	Role of bacteriophage T4 baseplate in regulating assembly and infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2654-2659.	3.3	63
1544	Crystal structure and functional analysis of isocitrate lyases from <i>Magnaporthe oryzae</i> and <i>Fusarium graminearum</i> . <i>Journal of Structural Biology</i> , 2016, 194, 395-403.	1.3	13
1545	Structural basis of DNA topoisomerase II β (Top2 β) inhibition: a computational analysis of interactions between Top2 β and its inhibitors. <i>Medicinal Chemistry Research</i> , 2016, 25, 1250-1259.	1.1	8
1546	Computational approaches for classification and prediction of P-type ATPase substrate specificity in <i>Arabidopsis</i> . <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 163-174.	1.4	15

#	ARTICLE	IF	CITATIONS
1547	Novel Structure and Unexpected RNA-Binding Ability of the C-Terminal Domain of Herpes Simplex Virus 1 Tegument Protein UL21. <i>Journal of Virology</i> , 2016, 90, 5759-5769.	1.5	13
1548	High Resolution Structures of Periplasmic Glucose-binding Protein of <i>Pseudomonas putida</i> CSV86 Reveal Structural Basis of Its Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2016, 291, 7844-7857.	1.6	19
1549	<i>Burkholderia glumae</i> ToxA Is a Dual-Specificity Methyltransferase That Catalyzes the Last Two Steps of Toxoflavin Biosynthesis. <i>Biochemistry</i> , 2016, 55, 2748-2759.	1.2	13
1550	<i>Fasciola hepatica</i> calcium-binding protein FhCaBP2: structure of the dynein light chain-like domain. <i>Parasitology Research</i> , 2016, 115, 2879-2886.	0.6	7
1551	Structure and Mutational Analyses of <i>Escherichia coli</i> ZapD Reveal Charged Residues Involved in FtsZ Filament Bundling. <i>Journal of Bacteriology</i> , 2016, 198, 1683-1693.	1.0	12
1552	A comparative analysis of the "other roles" of transcriptional factors from pathogenic organisms. <i>Gene</i> , 2016, 586, 274-280.	1.0	1
1553	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. <i>Biomacromolecules</i> , 2016, 17, 2027-2039.	2.6	114
1554	Structural Analysis of the Phenol-Responsive Sensory Domain of the Transcription Activator PoxR. <i>Structure</i> , 2016, 24, 624-630.	1.6	15
1555	Structural Basis for the Functional Coupling of the Alternative Splicing Factors Smu1 and RED. <i>Structure</i> , 2016, 24, 762-773.	1.6	25
1556	The <i>Klebsiella pneumoniae</i> O12 ATP-binding Cassette (ABC) Transporter Recognizes the Terminal Residue of Its O-antigen Polysaccharide Substrate. <i>Journal of Biological Chemistry</i> , 2016, 291, 9748-9761.	1.6	26
1557	Crystal Structure of a Two-domain Fragment of Hepatocyte Growth Factor Activator Inhibitor-1. <i>Journal of Biological Chemistry</i> , 2016, 291, 14340-14355.	1.6	16
1558	Structural insights into the regulatory mechanism of the <i>Pseudomonas aeruginosa</i> YfiBNR system. <i>Protein and Cell</i> , 2016, 7, 403-416.	4.8	18
1559	Crystal structures of a group II intron maturase reveal a missing link in spliceosome evolution. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 558-565.	3.6	79
1560	Protein Structure Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 31-53.	0.4	3
1561	Design of structurally distinct proteins using strategies inspired by evolution. <i>Science</i> , 2016, 352, 687-690.	6.0	132
1562	Reversible S-nitrosylation in an engineered azurin. <i>Nature Chemistry</i> , 2016, 8, 670-677.	6.6	41
1563	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552
1564	Sister Chromatid Cohesion Establishment Factor ESCO1 Operates by Substrate-Assisted Catalysis. <i>Structure</i> , 2016, 24, 789-796.	1.6	14

#	ARTICLE	IF	CITATIONS
1565	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
1566	Stereoselectivity and Structural Characterization of an Imine Reductase (IRED) from <i>Amycolatopsis orientalis</i> . ACS Catalysis, 2016, 6, 3880-3889.	5.5	96
1567	Structural and Functional Investigation of the Ag ⁺ /Cu ⁺ Binding Domains of the Periplasmic Adaptor Protein SilB from <i>Cupriavidus metallidurans</i> CH34. Biochemistry, 2016, 55, 2883-2897.	1.2	6
1568	Structures of type IV pilins from <i>Thermus thermophilus</i> demonstrate similarities with type II secretion system pseudopilins. Journal of Structural Biology, 2016, 196, 375-384.	1.3	12
1569	Structural and Functional Studies of Pavine N-Methyltransferase from <i>Thalictrum flavum</i> Reveal Novel Insights into Substrate Recognition and Catalytic Mechanism. Journal of Biological Chemistry, 2016, 291, 23403-23415.	1.6	34
1570	A hypervariable genomic island identified in clinical and environmental <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolates from Germany. International Journal of Medical Microbiology, 2016, 306, 495-503.	1.5	12
1571	Structural and Kinetic Properties of the Aldehyde Dehydrogenase NahF, a Broad Substrate Specificity Enzyme for Aldehyde Oxidation. Biochemistry, 2016, 55, 5453-5463.	1.2	12
1572	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
1573	Tying up the Ends: Plasticity in the Recognition of Single-Stranded DNA at Telomeres. Biochemistry, 2016, 55, 5326-5340.	1.2	21
1574	NMR structure and conformational dynamics of AtPDFL2.1, a defensin-like peptide from <i>Arabidopsis thaliana</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1739-1747.	1.1	12
1575	Structural evidence of intramolecular propeptide inhibition of the aspzincin metalloendopeptidase AsaP1. FEBS Letters, 2016, 590, 3280-3294.	1.3	3
1576	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
1577	Structural and dynamic insights into the C-terminal extension of cysteine proteinase B from <i>Leishmania amazonensis</i> . Journal of Molecular Graphics and Modelling, 2016, 70, 30-39.	1.3	2
1578	Structure-Guided Redesign of CYP153A _{M.aq} for the Improved Terminal Hydroxylation of Fatty Acids. ChemCatChem, 2016, 8, 3234-3239.	1.8	18
1579	Biochemical and structural characterization of polyphosphate kinase 2 from the intracellular pathogen <i>Francisella tularensis</i> . Bioscience Reports, 2016, 36, e00294.	1.1	19
1580	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
1581	Structural and functional insight into the N-terminal domain of the clathrin adaptor Ent5 from <i>Saccharomyces cerevisiae</i> . Biochemical and Biophysical Research Communications, 2016, 477, 786-793.	1.0	1
1582	Structural Basis for the Interaction between the IUS-SPRY Domain of RanBPM and DDX-4 in Germ Cell Development. Journal of Molecular Biology, 2016, 428, 4330-4344.	2.0	13

#	ARTICLE	IF	CITATIONS
1583	High-resolution crystal structure of the PDZ1 domain of human protein tyrosine phosphatase PTP-Bas. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1205-1210.	1.0	3
1584	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from <i>Burkholderia pseudomallei</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 19387-19400.	1.6	28
1585	Structural characterization reveals a novel bilobed architecture for the ectodomains of insect stage expressed <i>Trypanosoma brucei</i> PSSA α 2 and <i>Trypanosoma congolense</i> ISA. <i>Protein Science</i> , 2016, 25, 2297-2302.	3.1	1
1586	Crystal structure of pentapeptide-independent chemotaxis receptor methyltransferase (CheR) reveals idiosyncratic structural determinants for receptor recognition. <i>Journal of Structural Biology</i> , 2016, 196, 364-374.	1.3	8
1587	Structural and Functional Characterization of a Ruminal β -Glycosidase Defines a Novel Subfamily of Glycoside Hydrolase Family 3 with Permuted Domain Topology. <i>Journal of Biological Chemistry</i> , 2016, 291, 24200-24214.	1.6	21
1588	Structural and functional characterisation of the cyanobacterial PetC3 Rieske protein family. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1879-1891.	0.5	9
1589	Crystal structure of the CupB6 adhesive tip from the chaperone-usher family of pili from <i>Pseudomonas aeruginosa</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1500-1505.	1.1	5
1590	In silico identification and computational analysis of the nucleotide binding site in the C-terminal domain of Hsp90. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 70, 253-274.	1.3	11
1591	Structural Features of the Box C/D snoRNP Pre-assembly Process Are Conserved through Species. <i>Structure</i> , 2016, 24, 1693-1706.	1.6	15
1592	Structure-guided enzymology of the lipid A acyltransferase LpxM reveals a dual activity mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6064-E6071.	3.3	33
1593	The Chromatin Remodelling Protein CHD1 Contains a Previously Unrecognised C-Terminal Helical Domain. <i>Journal of Molecular Biology</i> , 2016, 428, 4298-4314.	2.0	14
1594	The combination of sequence-specific and nonspecific DNA-binding modes of transcription factor SATB1. <i>Biochemical Journal</i> , 2016, 473, 3321-3339.	1.7	9
1595	The Conserved Tetratricopeptide Repeat-Containing C-Terminal Domain of <i>Pseudomonas aeruginosa</i> FimV Is Required for Its Cyclic AMP-Dependent and -Independent Functions. <i>Journal of Bacteriology</i> , 2016, 198, 2263-2274.	1.0	23
1596	Engineering of <i>Candida glabrata</i> Ketoreductase 1 for Asymmetric Reduction of β -Halo Ketones. <i>ACS Catalysis</i> , 2016, 6, 6135-6140.	5.5	54
1597	Contributions of a unique β -clamp to substrate recognition illuminates the molecular basis of exolysis in ferulic acid esterases. <i>Biochemical Journal</i> , 2016, 473, 839-849.	1.7	20
1598	In-silico studies on DegP protein of <i>Plasmodium falciparum</i> in search of anti-malarials. <i>Journal of Molecular Modeling</i> , 2016, 22, 201.	0.8	5
1599	Crystal structure and catalytic mechanism of pyridoxal kinase from <i>Pseudomonas aeruginosa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 300-306.	1.0	7
1600	Structural identification of the lipopolysaccharide-binding capability of a cupin-family protein from <i>Helicobacter pylori</i> . <i>FEBS Letters</i> , 2016, 590, 2997-3004.	1.3	4

#	ARTICLE	IF	CITATIONS
1601	Solution Binding and Structural Analyses Reveal Potential Multidrug Resistance Functions for SAV2435 and CTR107 and Other GyrI-like Proteins. <i>Biochemistry</i> , 2016, 55, 4850-4863.	1.2	11
1602	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Eneidyne Antitumor Antibiotic C-1027 in <i>Streptomyces globisporus</i> . <i>Biochemistry</i> , 2016, 55, 5142-5154.	1.2	18
1603	Two distinct mechanisms of transcriptional regulation by the redox sensor YodB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5202-11.	3.3	19
1604	Structure features of GH10 xylanase from <i>Caldicellulosiruptor bescii</i> : implication for its thermophilic adaption and substrate binding preference. <i>Acta Biochimica Et Biophysica Sinica</i> , 2016, 48, 948-957.	0.9	25
1605	<i>Mycobacterium tuberculosis</i> LppM Displays an Original Structure and Domain Composition Linked to a Dual Localization. <i>Structure</i> , 2016, 24, 1788-1794.	1.6	4
1606	Archaeal flagellin combines a bacterial type IV pilin domain with an Ig-like domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10352-10357.	3.3	49
1607	Structural insight into dephosphorylation by trehalose 6-phosphate phosphatase (OtsB2) from <i>Mycobacterium tuberculosis</i> . <i>FASEB Journal</i> , 2016, 30, 3989-3996.	0.2	19
1608	Unraveling the essential role of CysK in CDI toxin activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9792-9797.	3.3	37
1609	Renew or die: The molecular mechanisms of peptidoglycan recycling and antibiotic resistance in Gram-negative pathogens. <i>Drug Resistance Updates</i> , 2016, 28, 91-104.	6.5	24
1610	Structure of a pathogen effector reveals the enzymatic mechanism of a novel acetyltransferase family. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 847-852.	3.6	39
1611	Crystal structure and analysis of HdaB: The enteroaggregative <i>Escherichia coli</i> AAF/IV pilus tip protein. <i>Protein Science</i> , 2016, 25, 1898-1905.	3.1	1
1612	Crystal structure of an Fe-S cluster-containing fumarate hydratase enzyme from <i>Leishmania major</i> reveals a unique protein fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9804-9809.	3.3	22
1613	Structure of the Lasso Peptide Isopeptidase Identifies a Topology for Processing Threaded Substrates. <i>Journal of the American Chemical Society</i> , 2016, 138, 16452-16458.	6.6	29
1614	Structural and functional probing of PorZ, an essential bacterial surface component of the type-IX secretion system of human oral-microbiomic <i>Porphyromonas gingivalis</i> . <i>Scientific Reports</i> , 2016, 6, 37708.	1.6	58
1615	Structural Analysis of the Catalytic Mechanism and Substrate Specificity of Anabaena Alkaline Invertase InvA Reveals a Novel Glucosidase. <i>Journal of Biological Chemistry</i> , 2016, 291, 25667-25677.	1.6	24
1616	Ringhalexin from <i>Hemachatus haemachatus</i> : A novel inhibitor of extrinsic tenase complex. <i>Scientific Reports</i> , 2016, 6, 25935.	1.6	21
1617	Crystal structures of two nitroreductases from hypervirulent <i>Clostridium difficile</i> and functionally related interactions with the antibiotic metronidazole. <i>Nitric Oxide - Biology and Chemistry</i> , 2016, 60, 32-39.	1.2	11
1618	Structural studies of a cold-adapted dimeric Î²-D-galactosidase from <i>Paracoccus</i> sp. 32d. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1049-1061.	1.1	17

#	ARTICLE	IF	CITATIONS
1619	Biosynthesis of Violacein, Structure and Function of L-Tryptophan Oxidase VioA from <i>Chromobacterium violaceum</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 20068-20084.	1.6	45
1620	Structure of <i>Arabidopsis thaliana</i> FUT1 Reveals a Variant of the GT-B Class Fold and Provides Insight into Xyloglucan Fucosylation. <i>Plant Cell</i> , 2016, 28, 2352-2364.	3.1	33
1621	An ATP Binding Cassette Transporter Mediates the Uptake of α -(1,6)-Linked Dietary Oligosaccharides in <i>Bifidobacterium</i> and Correlates with Competitive Growth on These Substrates. <i>Journal of Biological Chemistry</i> , 2016, 291, 20220-20231.	1.6	54
1622	Structural insights from a novel invertebrate triosephosphate isomerase from <i>Litopenaeus vannamei</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1696-1706.	1.1	18
1623	Structural Basis for Regulation of GPR56/ADGRG1 by Its Alternatively Spliced Extracellular Domains. <i>Neuron</i> , 2016, 91, 1292-1304.	3.8	92
1624	Structural and biophysical analysis of nuclease protein antibiotics. <i>Biochemical Journal</i> , 2016, 473, 2799-2812.	1.7	12
1625	Structure and Function of the PriC DNA Replication Restart Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 18384-18396.	1.6	17
1626	Structural and mechanistic insights into human splicing factor SF3b complex derived using an integrated approach guided by the cryo-EM density maps. <i>RNA Biology</i> , 2016, 13, 1025-1040.	1.5	5
1627	Facilitating the Evolution of Esterase Activity from a Promiscuous Enzyme (Mhg) with Catalytic Functions of Amide Hydrolysis and Carboxylic Acid Perhydrolysis by Engineering the Substrate Entrance Tunnel. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6748-6756.	1.4	16
1628	Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 899-905.	3.6	366
1629	The Molecular Basis for Ubiquitin and Ubiquitin-like Specificities in Bacterial Effector Proteases. <i>Molecular Cell</i> , 2016, 63, 261-276.	4.5	119
1630	Structural analysis of Notch-regulating Rumi reveals basis for pathogenic mutations. <i>Nature Chemical Biology</i> , 2016, 12, 735-740.	3.9	27
1631	Sensing and signaling of oxidative stress in chloroplasts by inactivation of the SAL1 phosphoadenosine phosphatase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4567-76.	3.3	147
1632	Crystal structure of a membrane-bound L-amino acid deaminase from <i>Proteus vulgaris</i> . <i>Journal of Structural Biology</i> , 2016, 195, 306-315.	1.3	30
1633	More than just recruitment: the X-domain influences catalysis of the first phenolic coupling reaction in A47934 biosynthesis by Cytochrome P450 StaH. <i>Molecular BioSystems</i> , 2016, 12, 2992-3004.	2.9	22
1634	Structural Studies on the Extracellular Domain of Sensor Histidine Kinase YycG from <i>Staphylococcus aureus</i> and Its Functional Implications. <i>Journal of Molecular Biology</i> , 2016, 428, 3074-3089.	2.0	19
1635	Structural Analysis of an Avr4 Effector Ortholog Offers Insight into Chitin Binding and Recognition by the Cf-4 Receptor. <i>Plant Cell</i> , 2016, 28, 1945-1965.	3.1	37
1636	Structural analysis of <i>Pseudomonas aeruginosa</i> H3a6SS immunity proteins. <i>FEBS Letters</i> , 2016, 590, 2787-2796.	1.3	9

#	ARTICLE	IF	CITATIONS
1637	Crystal structure of a putative oligopeptide-binding periplasmic protein from a hyperthermophile. <i>Extremophiles</i> , 2016, 20, 723-731.	0.9	11
1638	Crystal structure of SgcJ, an NTF2-like superfamily protein involved in biosynthesis of the nine-membered enediyne antitumor antibiotic C-1027. <i>Journal of Antibiotics</i> , 2016, 69, 731-740.	1.0	10
1639	Role of the PFXFATG[G/Y] Motif in the Activation of SdrG, a Response Regulator Involved in the Alphaproteobacterial General Stress Response. <i>Structure</i> , 2016, 24, 1237-1247.	1.6	14
1640	Ancient recombination events and the origins of hepatitis E virus. <i>BMC Evolutionary Biology</i> , 2016, 16, 210.	3.2	31
1641	Structural Basis for Phosphorylase Activity of a Class III Transaminase Homologue. <i>ChemBioChem</i> , 2016, 17, 2308-2311.	1.3	4
1642	Dissecting the structural basis of MEIG1 interaction with PACRG. <i>Scientific Reports</i> , 2016, 6, 18278.	1.6	13
1643	Crystal structure of a crustacean hyperglycemic hormone (<sc>CHH</sc>) precursor suggests structural variety in the C-terminal regions of <sc>CHH</sc> superfamily members. <i>FEBS Journal</i> , 2016, 283, 4325-4339.	2.2	14
1644	Probing the Structure of the Escherichia coli Periplasmic Proteins HdeA and YmgD by Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2016, 120, 11845-11855.	1.2	4
1645	Unique coenzyme binding mode of hyperthermophilic archaeal sn-glycerol-1-phosphate dehydrogenase from <i>Pyrobaculum calidifontis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1786-1796.	1.5	1
1646	Crystal structure of raptor adenovirus 1 fibre head and role of the beta-hairpin in siadenovirus fibre head domains. <i>Virology Journal</i> , 2016, 13, 106.	1.4	6
1647	Structural insights of ZIP4 extracellular domain critical for optimal zinc transport. <i>Nature Communications</i> , 2016, 7, 11979.	5.8	65
1648	Structure and catalytic mechanism of monodehydroascorbate reductase, MDHAR, from <i>Oryza sativa L. japonica</i> . <i>Scientific Reports</i> , 2016, 6, 33903.	1.6	39
1649	Comprehensive Analysis of a Novel Ketoreductase for Pentangular Polyphenol Biosynthesis. <i>ACS Chemical Biology</i> , 2016, 11, 3421-3430.	1.6	10
1650	THPP target assignment reveals EchA6 as an essential fatty acid shuttle in mycobacteria. <i>Nature Microbiology</i> , 2016, 1, 15006.	5.9	57
1651	Structural basis of unique ligand specificity of KAI2-like protein from parasitic weed <i>Striga hermonthica</i> . <i>Scientific Reports</i> , 2016, 6, 31386.	1.6	47
1652	Structural basis for ligand recognition by a Cache chemosensory domain that mediates carboxylate sensing in <i>Pseudomonas syringae</i> . <i>Scientific Reports</i> , 2016, 6, 35198.	1.6	28
1653	New Helical Binding Domain Mediates a Glycosyltransferase Activity of a Bifunctional Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 22106-22117.	1.6	19
1654	Determining crystal structures through crowdsourcing and coursework. <i>Nature Communications</i> , 2016, 7, 12549.	5.8	47

#	ARTICLE	IF	CITATIONS
1655	Structure–function analysis of the extracellular domain of the pneumococcal cell division site positioning protein MapZ. <i>Nature Communications</i> , 2016, 7, 12071.	5.8	23
1656	Shared active site architecture between archaeal PolD and multi-subunit RNA polymerases revealed by X-ray crystallography. <i>Nature Communications</i> , 2016, 7, 12227.	5.8	40
1657	Structural insights into the interaction and disease mechanism of neurodegenerative disease-associated optineurin and TBK1 proteins. <i>Nature Communications</i> , 2016, 7, 12708.	5.8	87
1658	A sodium channel inhibitor ISTX-I with a novel structure provides a new hint at the evolutionary link between two toxin folds. <i>Scientific Reports</i> , 2016, 6, 29691.	1.6	6
1659	Bacterial Actins and Their Interactors. <i>Current Topics in Microbiology and Immunology</i> , 2016, 399, 221-242.	0.7	2
1660	Crystal structure of glycogen debranching enzyme and insights into its catalysis and disease-causing mutations. <i>Nature Communications</i> , 2016, 7, 11229.	5.8	37
1661	An Atypical Î±/Î²-Hydrolase Fold Revealed in the Crystal Structure of Pimeloyl-Acyl Carrier Protein Methyl Esterase BioG from <i>Haemophilus influenzae</i> . <i>Biochemistry</i> , 2016, 55, 6705-6717.	1.2	19
1662	The solution structure of an anti-CRISPR protein. <i>Nature Communications</i> , 2016, 7, 13134.	5.8	48
1663	Structural basis of haem-iron acquisition by fungal pathogens. <i>Nature Microbiology</i> , 2016, 1, 16156.	5.9	59
1664	Electron Accepting Units of the Diheme Cytochrome c TsdA, a Bifunctional Thiosulfate Dehydrogenase/Tetrathionate Reductase. <i>Journal of Biological Chemistry</i> , 2016, 291, 24804-24818.	1.6	35
1665	Structure of the sirtuin–linked macrodomain SAV0325 from <i>Staphylococcus aureus</i> . <i>Protein Science</i> , 2016, 25, 1682-1691.	3.1	10
1666	Structural basis for dual specificity of yeast N-terminal amidase in the N-end rule pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12438-12443.	3.3	22
1667	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. <i>Nature Communications</i> , 2016, 7, 13047.	5.8	35
1668	Crystal structures of the UDP-diacylglucosamine pyrophosphohydrolase LpxH from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 32822.	1.6	18
1669	Crystal Structure of the Human Astrovirus Capsid Protein. <i>Journal of Virology</i> , 2016, 90, 9008-9017.	1.5	33
1670	Design of Heteronuclear Metalloenzymes. <i>Methods in Enzymology</i> , 2016, 580, 501-537.	0.4	5
1671	Structural basis of lantibiotic recognition by the nisin resistance protein from <i>Streptococcus agalactiae</i> . <i>Scientific Reports</i> , 2016, 6, 18679.	1.6	42
1672	Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism. <i>Scientific Reports</i> , 2016, 6, 23473.	1.6	25

#	ARTICLE	IF	CITATIONS
1673	Methanobactin transport machinery. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13027-13032.	3.3	43
1674	Crystal structure and SUMO binding of Slx1-Slx4 complex. Scientific Reports, 2016, 6, 19331.	1.6	4
1675	Structure of the fimbrial protein Mfa4 from Porphyromonas gingivalis in its precursor form: implications for a donor-strand complementation mechanism. Scientific Reports, 2016, 6, 22945.	1.6	21
1676	Structural and biochemical characterisation of Archaeoglobus fulgidus esterase reveals a bound CoA molecule in the vicinity of the active site. Scientific Reports, 2016, 6, 25542.	1.6	8
1677	MtrA of the sodium ion pumping methyltransferase binds cobalamin in a unique mode. Scientific Reports, 2016, 6, 28226.	1.6	14
1678	New insights about pilus formation in gut-adapted Lactobacillus rhamnosus GG from the crystal structure of the SpaA backbone-pilin subunit. Scientific Reports, 2016, 6, 28664.	1.6	21
1679	Sequence evidence for common ancestry of eukaryotic endomembrane coatomers. Scientific Reports, 2016, 6, 22311.	1.6	9
1680	Mechanism and rate constants of the Cdc42 GTPase binding with intrinsically disordered effectors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 674-685.	1.5	17
1681	Crystal structure of a [NiFe] hydrogenase maturation protease HybD from Thermococcus kodakarensis KOD1. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1321-1327.	1.5	13
1682	Structural and Functional Investigations of the Effector Protein LpiR1 from Legionella pneumophila. Journal of Biological Chemistry, 2016, 291, 15767-15777.	1.6	3
1683	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. Journal of Biological Chemistry, 2016, 291, 14430-14446.	1.6	16
1685	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. EMBO Reports, 2016, 17, 235-248.	2.0	53
1686	Identification of MltG as a potential terminase for peptidoglycan polymerization in bacteria. Molecular Microbiology, 2016, 99, 700-718.	1.2	99
1687	Structure of the Bacterial Cytoskeleton Protein Bactofilin by NMR Chemical Shifts and Sequence Variation. Biophysical Journal, 2016, 110, 2342-2348.	0.2	15
1688	Structural Basis of the Recruitment of Ubiquitin-specific Protease USP15 by Spliceosome Recycling Factor SART3. Journal of Biological Chemistry, 2016, 291, 17283-17292.	1.6	24
1689	Crystal structure of the TK2203 protein from Thermococcus kodakarensis, a putative extradiol dioxygenase. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 427-433.	0.4	3
1690	Pore-forming activity and structural autoinhibition of the gasdermin family. Nature, 2016, 535, 111-116.	13.7	1,812
1691	Structural basis for recruiting and shuttling of the spliceosomal deubiquitinase USP4 by SART3. Nucleic Acids Research, 2016, 44, 5424-5437.	6.5	32

#	ARTICLE	IF	CITATIONS
1692	Dali server update. <i>Nucleic Acids Research</i> , 2016, 44, W351-W355.	6.5	872
1693	Structural Basis for the Specific Recognition of RhoA by the Dual GTPase-activating Protein ARAP3. <i>Journal of Biological Chemistry</i> , 2016, 291, 16709-16719.	1.6	12
1694	Structural Comparison and Simulation of Pneumococcal Peptidoglycan Hydrolase LytB. <i>Methods in Molecular Biology</i> , 2016, 1440, 271-283.	0.4	0
1695	VgrG C terminus confers the type VI effector transport specificity and is required for binding with PAAR and adaptor effector complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3931-40.	3.3	180
1696	Identification of a Conserved RNA-dependent RNA Polymerase (RdRp)-RNA Interface Required for Flaviviral Replication. <i>Journal of Biological Chemistry</i> , 2016, 291, 17437-17449.	1.6	33
1697	Crystal Structure of Human Leukocyte Cell-derived Chemotaxin 2 (LECT2) Reveals a Mechanistic Basis of Functional Evolution in a Mammalian Protein with an M23 Metalloendopeptidase Fold. <i>Journal of Biological Chemistry</i> , 2016, 291, 17133-17142.	1.6	17
1698	1.2 Å resolution crystal structure of the periplasmic aminotransferase PvdN from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 403-408.	0.4	10
1699	Structures of trehalose-6-phosphate phosphatase from pathogenic fungi reveal the mechanisms of substrate recognition and catalysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7148-7153.	3.3	44
1700	MINDY-1 Is a Member of an Evolutionarily Conserved and Structurally Distinct New Family of Deubiquitinating Enzymes. <i>Molecular Cell</i> , 2016, 63, 146-155.	4.5	297
1701	Structure of human Niemann-Pick C1 protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8212-8217.	3.3	137
1702	Structural basis for DNA recognition by the transcription regulator MetR. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 417-426.	0.4	6
1703	Structure-based Epitope Mapping of Mycobacterium tuberculosis Secretary Antigen MTC28. <i>Journal of Biological Chemistry</i> , 2016, 291, 13943-13954.	1.6	8
1704	Crystal structure and dynamics of Spt16N-domain of FACT complex from <i>Cicer arietinum</i> . <i>International Journal of Biological Macromolecules</i> , 2016, 88, 36-43.	3.6	8
1705	Putative thioredoxin Trx1 from <i>Thermosiphon africanus</i> strain TCF52B: expression, purification and structural determination using S-SAD. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 443-447.	0.4	1
1706	Crystal structure of methylesterase family member 16 (MES16) from <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 226-231.	1.0	9
1707	A Salmonella Toxin Promotes Persister Formation through Acetylation of tRNA. <i>Molecular Cell</i> , 2016, 63, 86-96.	4.5	218
1708	The Tubulation Activity of a Fission Yeast F-BAR Protein Is Dispensable for Its Function in Cytokinesis. <i>Cell Reports</i> , 2016, 14, 534-546.	2.9	27
1709	Nuclear Magnetic Resonance Structure of a Major Lens Protein, Human ¹³ C-Crystallin: Role of the Dipole Moment in Protein Solubility. <i>Biochemistry</i> , 2016, 55, 3136-3149.	1.2	10

#	ARTICLE	IF	CITATIONS
1710	Structural homology guided alignment of cysteine rich proteins. SpringerPlus, 2016, 5, 27.	1.2	19
1712	Virion Structure of Inflavirus Slow Bee Paralysis Virus at 2.6-Angstrom Resolution. Journal of Virology, 2016, 90, 7444-7455.	1.5	25
1713	LmABC3, an atypical mitochondrial ABC transporter essential for Leishmania major virulence, acts in heme and cytosolic iron/sulfur clusters biogenesis. Parasites and Vectors, 2016, 9, 7.	1.0	22
1714	The Defensins Consist of Two Independent, Convergent Protein Superfamilies. Molecular Biology and Evolution, 2016, 33, 2345-2356.	3.5	123
1715	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. Protein Science, 2016, 25, 1545-1550.	3.1	9
1716	Structure and functional characterization of a bile acid 7 α dehydratase <i>BaiE</i> in secondary bile acid synthesis. Proteins: Structure, Function and Bioinformatics, 2016, 84, 316-331.	1.5	35
1717	Structural basis for cellulose binding by the type A carbohydrate-binding module 64 of <i>Spirochaeta thermophila</i> . Proteins: Structure, Function and Bioinformatics, 2016, 84, 855-858.	1.5	16
1718	Suppression of a deletion mutation in the gene encoding essential PBP2b reveals a new lytic transglycosylase involved in peripheral peptidoglycan synthesis in <i>Streptococcus pneumoniae</i> D39. Molecular Microbiology, 2016, 100, 1039-1065.	1.2	77
1719	Structural and Functional Analysis of Cell Wall-anchored Polypeptide Adhesin BspA in Streptococcus agalactiae. Journal of Biological Chemistry, 2016, 291, 15985-16000.	1.6	36
1720	Structural and functional analyses of the archaeal tRNA ^{m²G/m²G} methyltransferase aTrm11 provide mechanistic insights into site specificity of a tRNA methyltransferase that contains common RNA-binding modules. Nucleic Acids Research, 2016, 44, 6377-6390.	6.5	20
1721	Structural Insights into Outer Membrane Permeability of Acinetobacter baumannii. Structure, 2016, 24, 221-231.	1.6	49
1722	Structural basis and function of XRN2 binding by XTB domains. Nature Structural and Molecular Biology, 2016, 23, 164-171.	3.6	17
1723	Leishmania donovani Encodes a Functional Selenocysteinyl-tRNA Synthase. Journal of Biological Chemistry, 2016, 291, 1203-1220.	1.6	12
1724	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
1725	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
1726	Structure and Function of Fusicoccadiene Synthase, a Hexameric Bifunctional Diterpene Synthase. ACS Chemical Biology, 2016, 11, 889-899.	1.6	59
1727	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
1728	Structural and Functional Characterization of the Paal Thioesterase from Streptococcus pneumoniae Reveals a Dual Specificity for Phenylacetyl-CoA and Medium-chain Fatty Acyl-CoAs and a Novel CoA-induced Fit Mechanism. Journal of Biological Chemistry, 2016, 291, 1866-1876.	1.6	6

#	ARTICLE	IF	CITATIONS
1729	Structural analysis and insertion study reveal the ideal sites for surface displaying foreign peptides on a betanodavirus-like particle. <i>Veterinary Research</i> , 2016, 47, 16.	1.1	27
1730	Structural and functional insights into the fly microRNA biogenesis factor Loquacious. <i>Rna</i> , 2016, 22, 383-396.	1.6	11
1731	Structural basis for the endoribonuclease activity of the type III-A CRISPR-associated protein Csm6. <i>Rna</i> , 2016, 22, 318-329.	1.6	128
1732	A β -solenoid model of the Pmel17 repeat domain: insights to the formation of functional amyloid fibrils. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 153-164.	1.3	17
1733	Local structure based method for prediction of the biochemical function of proteins: Applications to glycoside hydrolases. <i>Methods</i> , 2016, 93, 51-63.	1.9	9
1734	Computational modeling of TC0583 as a putative component of the <i>Chlamydia muridarum</i> V-type ATP synthase complex and assessment of its protective capabilities as a vaccine antigen. <i>Microbes and Infection</i> , 2016, 18, 245-253.	1.0	6
1735	Genome-Wide Mapping of the Binding Sites and Structural Analysis of Kaposi's Sarcoma-Associated Herpesvirus Viral Interferon Regulatory Factor 2 Reveal that It Is a DNA-Binding Transcription Factor. <i>Journal of Virology</i> , 2016, 90, 1158-1168.	1.5	10
1736	Crystal Structure of the Core Region of Hantavirus Nucleocapsid Protein Reveals the Mechanism for Ribonucleoprotein Complex Formation. <i>Journal of Virology</i> , 2016, 90, 1048-1061.	1.5	35
1737	Enzymatic and Structural Characterization of the Major Endopeptidase in the Venus Flytrap Digestion Fluid. <i>Journal of Biological Chemistry</i> , 2016, 291, 2271-2287.	1.6	16
1738	Characterization of a Kunitz-type serine protease inhibitor from <i>Solanum tuberosum</i> having lectin activity. <i>International Journal of Biological Macromolecules</i> , 2016, 83, 259-269.	3.6	18
1739	Structures of replication initiation proteins from staphylococcal antibiotic resistance plasmids reveal protein asymmetry and flexibility are necessary for replication. <i>Nucleic Acids Research</i> , 2016, 44, 2417-2428.	6.5	22
1740	Structural basis of the lack of endo-glucanase inhibitory activity of <i>Lupinus albus</i> β -conglutin. <i>Plant Physiology and Biochemistry</i> , 2016, 99, 79-85.	2.8	14
1741	Characterization of Intersubunit Communication in the Virginiamycin <i>trans</i> -Acyl Transferase Polyketide Synthase. <i>Journal of the American Chemical Society</i> , 2016, 138, 4155-4167.	6.6	42
1742	Structural, Mechanistic, and Antigenic Characterization of the Human Astrovirus Capsid. <i>Journal of Virology</i> , 2016, 90, 2254-2263.	1.5	30
1743	Structure and functional analysis of the siderophore periplasmic binding protein from the fuscachelin gene cluster of <i>Thermobifida fusca</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 118-128.	1.5	2
1744	A Multivalent Marine Lectin from <i>Crenomytilus grayanus</i> Possesses Anti-cancer Activity through Recognizing Globotriose Gb3. <i>Journal of the American Chemical Society</i> , 2016, 138, 4787-4795.	6.6	51
1745	Biochemical characterization and structural analysis of a new cold-active and salt-tolerant esterase from the marine bacterium <i>Thalassospira</i> sp.. <i>Extremophiles</i> , 2016, 20, 323-336.	0.9	49
1746	Structural characterization of the virulence factor Sda1 nuclease from <i>Streptococcus pyogenes</i> . <i>Nucleic Acids Research</i> , 2016, 44, 3946-3957.	6.5	19

#	ARTICLE	IF	CITATIONS
1747	Solution structure of Q388A3 PDZ domain from <i>Trypanosoma brucei</i> . <i>Journal of Structural Biology</i> , 2016, 194, 214-217.	1.3	0
1748	PGL germ granule assembly protein is a base-specific, single-stranded RNase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1279-1284.	3.3	21
1749	WrpA Is an Atypical Flavodoxin Family Protein under Regulatory Control of the <i>Brucella abortus</i> General Stress Response System. <i>Journal of Bacteriology</i> , 2016, 198, 1281-1293.	1.0	14
1750	Structural and functional insights into tRNA binding and adenosine N1-methylation by an archaeal Trm10 homologue. <i>Nucleic Acids Research</i> , 2016, 44, 940-953.	6.5	27
1751	Characterization of <i>Enterococcus faecium</i> bacteriophage IME-EFm5 and its endolysin LysEFm5. <i>Virology</i> , 2016, 492, 11-20.	1.1	45
1752	Cryo-electron microscopy structure of a coronavirus spike glycoprotein trimer. <i>Nature</i> , 2016, 531, 114-117.	13.7	453
1753	Identification and Functional Characterization of a Fructooligosaccharides-Forming Enzyme from <i>Aspergillus aculeatus</i> . <i>Applied Biochemistry and Biotechnology</i> , 2016, 179, 497-513.	1.4	12
1754	Alba from <i>Thermoplasma volcanium</i> belongs to Î±-NAT's: An insight into the structural aspects of Tv Alba and its acetylation by Tv Ard1. <i>Archives of Biochemistry and Biophysics</i> , 2016, 590, 90-100.	1.4	3
1755	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i> -Aminosalicylic Acid Resistance. <i>Biochemistry</i> , 2016, 55, 1107-1119.	1.2	22
1756	Structure modeling and functional analysis of recombinant dextranucrase from <i>Weissella confusa</i> Cab3 expressed in <i>Lactococcus lactis</i> . <i>Preparative Biochemistry and Biotechnology</i> , 2016, 46, 822-832.	1.0	5
1757	Crystal Structure Analysis of Wild Type and Fast Hydrolyzing Mutant of EhRabX3, a Tandem Ras Superfamily GTPase from <i>Entamoeba histolytica</i> . <i>Journal of Molecular Biology</i> , 2016, 428, 41-51.	2.0	13
1758	Expression, crystallization and structure elucidation of Î³-terpinene synthase from <i>Thymus vulgaris</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 16-23.	0.4	19
1759	Crystal structure of the homocysteine methyltransferase MmuM from <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 2016, 473, 277-284.	1.7	9
1760	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016, 11, 1362-1371.	1.6	15
1761	Structural Basis for Iron-Mediated Sulfur Transfer in Archaeal and Yeast Thiazole Synthases. <i>Biochemistry</i> , 2016, 55, 1826-1838.	1.2	24
1762	Insight into Structure-Function Relationships and Inhibition of the Fatty Acyl-AMP Ligase (FadD32) Orthologs from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 7973-7989.	1.6	22
1763	Structure of the Hantavirus Nucleoprotein Provides Insights into the Mechanism of RNA Encapsidation. <i>Cell Reports</i> , 2016, 14, 2092-2099.	2.9	28
1764	Structural Basis for the Inhibition of Voltage-gated Sodium Channels by Conotoxin Î¼OÎ±-CVIII. <i>Journal of Biological Chemistry</i> , 2016, 291, 7205-7220.	1.6	4

#	ARTICLE	IF	CITATIONS
1765	Crystal structure of equine serum albumin in complex with cetirizine reveals a novel drug binding site. <i>Molecular Immunology</i> , 2016, 71, 143-151.	1.0	19
1766	Characterization of a Putative Receptor Binding Surface on Skint-1, a Critical Determinant of Dendritic Epidermal T Cell Selection. <i>Journal of Biological Chemistry</i> , 2016, 291, 9310-9321.	1.6	20
1767	The Vaccinia Virus H3 Envelope Protein, a Major Target of Neutralizing Antibodies, Exhibits a Glycosyltransferase Fold and Binds UDP-Glucose. <i>Journal of Virology</i> , 2016, 90, 5020-5030.	1.5	33
1768	Macro Domain from Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Is an Efficient ADP-ribose Binding Module. <i>Journal of Biological Chemistry</i> , 2016, 291, 4894-4902.	1.6	52
1769	Structure of Human DROSHA. <i>Cell</i> , 2016, 164, 81-90.	13.5	187
1770	Current updates on computer aided protein modeling and designing. <i>International Journal of Biological Macromolecules</i> , 2016, 85, 48-62.	3.6	123
1771	Crystal Structure of the Measles Virus Nucleoprotein Core in Complex with an N-Terminal Region of Phosphoprotein. <i>Journal of Virology</i> , 2016, 90, 2849-2857.	1.5	69
1772	Bacterial ferrous iron transport: the Feo system. <i>FEMS Microbiology Reviews</i> , 2016, 40, 273-298.	3.9	301
1773	Experimental evidence and molecular modeling of the interaction between hRSV-NS1 and quercetin. <i>International Journal of Biological Macromolecules</i> , 2016, 85, 40-47.	3.6	11
1774	A Naturally Occurring Peptide with an Elementary Single Disulfide-Directed $\hat{\text{I}}^2$ -Hairpin Fold. <i>Structure</i> , 2016, 24, 293-299.	1.6	16
1775	Nuclear Magnetic Resonance Structure of a Novel Globular Domain in RBM10 Containing OCRE, the Octamer Repeat Sequence Motif. <i>Structure</i> , 2016, 24, 158-164.	1.6	18
1776	A Comprehensive Study of Molecular Evolution at the Self-Incompatibility Locus of Rosaceae. <i>Journal of Molecular Evolution</i> , 2016, 82, 128-145.	0.8	19
1777	Mechanism of Archaeal MCM Helicase Recruitment to DNA Replication Origins. <i>Molecular Cell</i> , 2016, 61, 287-296.	4.5	36
1778	Structural analysis of a penicillin V acylase from <i>Pectobacterium atrosepticum</i> confirms the importance of two Trp residues for activity and specificity. <i>Journal of Structural Biology</i> , 2016, 193, 85-94.	1.3	9
1779	The structure of Resuscitation promoting factor B from <i>M. tuberculosis</i> reveals unexpected ubiquitin-like domains. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 445-451.	1.1	22
1780	Structural basis of collagen recognition by human osteoclast-associated receptor and design of osteoclastogenesis inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1038-1043.	3.3	25
1781	Structural and Biochemical Insight into the Mechanism of Rv2837c from <i>Mycobacterium tuberculosis</i> as a c-di-NMP Phosphodiesterase. <i>Journal of Biological Chemistry</i> , 2016, 291, 3668-3681.	1.6	67
1782	Crystal structure of cleaved vaspin (serpinA12). <i>Biological Chemistry</i> , 2016, 397, 111-123.	1.2	7

#	ARTICLE	IF	CITATIONS
1783	Structure-Function Analysis of a Mixed-linkage β -Glucanase/Xyloglucanase from the Key Ruminal Bacteroidetes <i>Prevotella bryantii</i> B14. <i>Journal of Biological Chemistry</i> , 2016, 291, 1175-1197.	1.6	38
1784	Evaluation of the Conformational Stability of Recombinant Desulfurizing Enzymes from a Newly Isolated <i>Rhodococcus</i> sp.. <i>Molecular Biotechnology</i> , 2016, 58, 1-11.	1.3	5
1785	Functional analysis and crystallographic structure of clotrimazole bound OleP, a cytochrome P450 epoxidase from <i>Streptomyces antibioticus</i> involved in oleandomycin biosynthesis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 465-475.	1.1	19
1786	Rapid and enhanced remote homology detection by cascading hidden Markov model searches in sequence space. <i>Bioinformatics</i> , 2016, 32, 338-344.	1.8	5
1787	Molecular modeling, in silico screening and molecular dynamics of PfPRL-PTP of <i>P. falciparum</i> for identification of potential anti-malarials. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1330-1344.	2.0	2
1788	In silico approach to ascertain the calcium dependent role of <i>Plasmodium falciparum</i> SERA5. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 17-25.	2.0	2
1789	Steered molecular dynamics study reveals insights into the function of the repetitive B region of collagen- and fibrinogen-binding MSCRAMMs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 535-550.	2.0	4
1790	Domain Organization and Evolution of the Highly Divergent 5' Coding Region of Genomes of Arteriviruses, Including the Novel Possum Nidovirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	22
1791	Solution of the structure of a calmodulin-peptide complex in a novel configuration from a variably twinned data set. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 22-31.	1.1	6
1792	The tale of SSB. <i>Progress in Biophysics and Molecular Biology</i> , 2017, 127, 111-118.	1.4	66
1793	Insights into the Mechanistic Basis of Plasmid-Mediated Colistin Resistance from Crystal Structures of the Catalytic Domain of MCR-1. <i>Scientific Reports</i> , 2017, 7, 39392.	1.6	107
1794	The flavinyl transferase ApbE of <i>Pseudomonas stutzeri</i> matures the NosR protein required for nitrous oxide reduction. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 95-102.	0.5	39
1795	Structural and biochemical characterization of FabK from <i>Thermotoga maritima</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 968-974.	1.0	3
1796	Structural basis of the substrate recognition of hydrazidase isolated from <i>Microbacterium</i> sp. strain HM58-2, which catalyzes acylhydrazide compounds as its sole carbon source. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 1007-1012.	1.0	3
1797	In silico characterization of TTHA0596: A potential Zn ²⁺ binding protein of ATP-binding cassette transporter. <i>Gene Reports</i> , 2017, 6, 132-141.	0.4	2
1798	Structural and functional insights into asymmetric enzymatic dehydration of alkenols. <i>Nature Chemical Biology</i> , 2017, 13, 275-281.	3.9	30
1799	X-ray crystal structure of the N-terminal region of Moloney murine leukemia virus integrase and its implications for viral DNA recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 647-656.	1.5	9
1800	<i>Arabidopsis</i> HAP2/GCS1 is a gamete fusion protein homologous to somatic and viral fusogens. <i>Journal of Cell Biology</i> , 2017, 216, 571-581.	2.3	93

#	ARTICLE	IF	CITATIONS
1801	A Complete Structural Inventory of the Mycobacterial Microcompartment Shell Proteins Constrains Models of Global Architecture and Transport. <i>Journal of Biological Chemistry</i> , 2017, 292, 1197-1210.	1.6	41
1802	The structure of the yeast mitochondrial ribosome. <i>Science</i> , 2017, 355, 528-531.	6.0	161
1803	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017, 541, 407-411.	13.7	188
1804	Two Distant Catalytic Sites Are Responsible for C2c2 RNase Activities. <i>Cell</i> , 2017, 168, 121-134.e12.	13.5	248
1805	Crystal Structure of StnA for the Biosynthesis of Antitumor Drug Streptonigrin Reveals a Unique Substrate Binding Mode. <i>Scientific Reports</i> , 2017, 7, 40254.	1.6	5
1806	STK40 Is a Pseudokinase that Binds the E3 Ubiquitin Ligase COP1. <i>Structure</i> , 2017, 25, 287-294.	1.6	37
1807	Functional and structural studies on the <i>Neisseria gonorrhoeae</i> GmhA, the first enzyme in the glycerol-mannose heptose biosynthesis pathways, demonstrate a critical role in lipooligosaccharide synthesis and gonococcal viability. <i>MicrobiologyOpen</i> , 2017, 6, e00432.	1.2	20
1808	Structural diversity of lytic polysaccharide monooxygenases. <i>Current Opinion in Structural Biology</i> , 2017, 44, 67-76.	2.6	162
1809	Structure of the acetophenone carboxylase core complex: prototype of a new class of ATP-dependent carboxylases/hydrolases. <i>Scientific Reports</i> , 2017, 7, 39674.	1.6	23
1810	Mechanisms of <i>Yersinia</i> YopO kinase substrate specificity. <i>Scientific Reports</i> , 2017, 7, 39998.	1.6	10
1811	Human m ⁶ A writers: Two subunits, 2 roles. <i>RNA Biology</i> , 2017, 14, 300-304.	1.5	76
1812	Cellotriose-hydrolyzing activity conferred by truncating the carbohydrate-binding modules of Cel5 from <i>Hahella chejuensis</i> . <i>Bioprocess and Biosystems Engineering</i> , 2017, 40, 241-249.	1.7	5
1813	Computational tools for enzyme improvement: why everyone can “ and should “ use them. <i>Current Opinion in Chemical Biology</i> , 2017, 37, 89-96.	2.8	79
1814	The cytotoxic <i>Staphylococcus aureus</i> PSM ₃ reveals a cross- β amyloid-like fibril. <i>Science</i> , 2017, 355, 831-833.	6.0	249
1815	Structure of the <i>Escherichia coli</i> ProQ RNA-binding protein. <i>Rna</i> , 2017, 23, 696-711.	1.6	50
1816	Structural role of a conserved active site <i>cis</i> proline in the <i>Thermotoga maritima</i> acetyl esterase from the carbohydrate esterase family 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 694-708.	1.5	9
1817	Analysis of plant UDP-arabinopyranose mutase (UAM): Role of divalent metals and structure prediction. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 510-519.	1.1	5
1818	Protein Structure Classification and Loop Modeling Using Multiple Ramachandran Distributions. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 243-254.	1.9	17

#	ARTICLE	IF	CITATIONS
1819	TM0416, a Hyperthermophilic Promiscuous Nonphosphorylated Sugar Isomerase, Catalyzes Various C 5 and C 6 Epimerization Reactions. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	23
1820	Crystal structure of dibenzothiophene sulfone monooxygenase BdsA from <i>Bacillus subtilis</i> . <i>WU&S2B. Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1171-1177.	1.5	17
1821	Structure of deformed wing virus, a major honey bee pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3210-3215.	3.3	43
1822	Bound Substrate in the Structure of Cyanobacterial Branching Enzyme Supports a New Mechanistic Model. <i>Journal of Biological Chemistry</i> , 2017, 292, 5465-5475.	1.6	48
1823	Crystal structure of MBP-PigG fusion protein and the essential function of PigG in the prodigiosin biosynthetic pathway in <i>Serratia marcescens</i> FS14. <i>International Journal of Biological Macromolecules</i> , 2017, 99, 394-400.	3.6	7
1824	Mycobacteria Encode Active and Inactive Classes of TesB Fatty-Acyl CoA Thioesterases Revealed through Structural and Functional Analysis. <i>Biochemistry</i> , 2017, 56, 1460-1472.	1.2	3
1825	Crystal Structure of the Maturation Protein from Bacteriophage Q β . <i>Journal of Molecular Biology</i> , 2017, 429, 688-696.	2.0	24
1826	Structural basis of the specificity of USP18 toward ISG15. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 270-278.	3.6	85
1827	Genetic and Structural Characterization of a Thermo-Tolerant, Cold-Active, and Acidic Endo- β -1,4-glucanase from Antarctic Springtail, <i>Cryptopygus antarcticus</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 1630-1640.	2.4	24
1828	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	13.7	569
1829	Crystallographic structure of recombinant <i>Lactococcus lactis</i> prolidase to support proposed structure-function relationships. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 473-480.	1.1	8
1830	Novel Molecular Insights into the Catalytic Mechanism of Marine Bacterial Alginate Lyase AlyGC from Polysaccharide Lyase Family 6. <i>Journal of Biological Chemistry</i> , 2017, 292, 4457-4468.	1.6	101
1831	Multiple origins of viral capsid proteins from cellular ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2401-E2410.	3.3	211
1832	The mechanism behind the selection of two different cleavage sites in NAG-NAM polymers. <i>IUCrj</i> , 2017, 4, 185-198.	1.0	12
1833	Structural Insights into the Broad Substrate Specificity of a Novel Endoglycoceramidase I Belonging to a New Subfamily of GH5 Glycosidases. <i>Journal of Biological Chemistry</i> , 2017, 292, 4789-4800.	1.6	17
1834	Nmd3 is a structural mimic of ϵ EF5A, and activates the cpGTPase Lsg1 during 60S ribosome biogenesis. <i>EMBO Journal</i> , 2017, 36, 854-868.	3.5	67
1835	A novel signal transduction protein: Combination of solute binding and tandem PAS-like sensor domains in one polypeptide chain. <i>Protein Science</i> , 2017, 26, 857-869.	3.1	1
1836	Structural and dynamic characterization of a freestanding acyl carrier protein involved in the biosynthesis of cyclic lipopeptide antibiotics. <i>Protein Science</i> , 2017, 26, 946-959.	3.1	4

#	ARTICLE	IF	CITATIONS
1837	Computational tools for exploring sequence databases as a resource for antimicrobial peptides. <i>Biotechnology Advances</i> , 2017, 35, 337-349.	6.0	111
1838	A Transition Metal-Binding, Trimeric Zn^{2+} -Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanosaeta thermophila</i> . <i>Biochemistry</i> , 2017, 56, 1299-1310.	1.2	7
1839	Structural Analysis of Mycobacterium tuberculosis Homologues of the Eukaryotic Proteasome Assembly Chaperone 2 (PAC2). <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	3
1840	High affinity anchoring of the decoration protein pb10 onto the bacteriophage T5 capsid. <i>Scientific Reports</i> , 2017, 7, 41662.	1.6	21
1841	Target Elucidation by Cocrystal Structures of NADH-Ubiquinone Oxidoreductase of <i>Plasmodium falciparum</i> (<i>Pf</i> NDH2) with Small Molecule To Eliminate Drug-Resistant Malaria. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 1994-2005.	2.9	51
1842	Structural insights into POT1-TPP1 interaction and POT1 C-terminal mutations in human cancer. <i>Nature Communications</i> , 2017, 8, 14929.	5.8	71
1843	Crystal structures of the Arabidopsis thaliana organellar RNA editing factors MORF1 and MORF9. <i>Nucleic Acids Research</i> , 2017, 45, 4915-4928.	6.5	32
1844	Crystal structure of a bicupin protein HutD involved in histidine utilization in <i>Pseudomonas</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1580-1588.	1.5	2
1845	Structural Analysis Reveals Features of Ribosome Assembly Factor Nsa1/WDR74 Important for Localization and Interaction with Rix7/NVL2. <i>Structure</i> , 2017, 25, 762-772.e4.	1.6	20
1846	Dimerization of Tie2 mediated by its membrane-proximal FNIII domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4382-4387.	3.3	29
1847	Crystal structure and redox properties of a novel cyanobacterial heme protein with a His/Cys heme axial ligation and a Per-Arnt-Sim (PAS)-like domain. <i>Journal of Biological Chemistry</i> , 2017, 292, 9599-9612.	1.6	14
1848	A unique structural domain in <i>Methanococcoides burtonii</i> ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) acts as a small subunit mimic. <i>Journal of Biological Chemistry</i> , 2017, 292, 6838-6850.	1.6	17
1849	<i>Malassezia globosa</i> Mg MDL2 lipase: Crystal structure and rational modification of substrate specificity. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 259-265.	1.0	13
1850	Structure-function analysis of the DNA-binding domain of a transmembrane transcriptional activator. <i>Scientific Reports</i> , 2017, 7, 1051.	1.6	46
1852	2-Alkylquinolone alkaloid biosynthesis in the medicinal plant <i>Evodia rutaecarpa</i> involves collaboration of two novel type III polyketide synthases. <i>Journal of Biological Chemistry</i> , 2017, 292, 9117-9135.	1.6	14
1853	Crystal structure of <i>Pseudomonas aeruginosa</i> N-acetyltransferase PA4534. <i>Biochemical and Biophysical Research Communications</i> , 2017, 487, 236-240.	1.0	2
1854	Structural analysis of the interaction between spiroisoxazoline SMART-420 and the Mycobacterium tuberculosis repressor EthR2. <i>Biochemical and Biophysical Research Communications</i> , 2017, 487, 403-408.	1.0	9
1855	Crystal structures reveal N-terminal Domain of Arabidopsis thaliana ClpD to be highly divergent from that of ClpC1. <i>Scientific Reports</i> , 2017, 7, 44366.	1.6	5

#	ARTICLE	IF	CITATIONS
1856	Structural Study on the Reaction Mechanism of a Free Serine Kinase Involved in Cysteine Biosynthesis. ACS Chemical Biology, 2017, 12, 1514-1523.	1.6	7
1857	Substrate Profiling and High Resolution Co-complex Crystal Structure of a Secreted C11 Protease Conserved across Commensal Bacteria. ACS Chemical Biology, 2017, 12, 1556-1565.	1.6	27
1858	A survey on faculty perspectives on the transition to a biochemistry course-based undergraduate research experience laboratory. Biochemistry and Molecular Biology Education, 2017, 45, 426-436.	0.5	21
1859	Full shut-off of Escherichia coli RNA-polymerase by T7 phage requires a small phage-encoded DNA-binding protein. Nucleic Acids Research, 2017, 45, 7697-7707.	6.5	21
1860	Archaeal Actin-Family Filament Systems. Sub-Cellular Biochemistry, 2017, 84, 379-392.	1.0	9
1861	Quorum Sensing Gene Regulation by LuxR/HapR Master Regulators in Vibrios. Journal of Bacteriology, 2017, 199, .	1.0	111
1862	Structure of the human aminopeptidase XPNPEP3 and comparison of its in vitro activity with lcp55 orthologs: Insights into diverse cellular processes. Journal of Biological Chemistry, 2017, 292, 10035-10047.	1.6	23
1863	The crystal structure of mammalian inositol 1,3,4,5,6-pentakisphosphate 2-kinase reveals a new zinc-binding site and key features for protein function. Journal of Biological Chemistry, 2017, 292, 10534-10548.	1.6	8
1864	Structure of NADP ⁺ -bound Δ^2 -hydroxysteroid dehydrogenase reveals two cofactor-binding modes. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 246-252.	0.4	9
1865	A Generative Angular Model of Protein Structure Evolution. Molecular Biology and Evolution, 2017, 34, 2085-2100.	3.5	13
1866	Insights into links between autophagy and the ubiquitin system from the structure of LC3B bound to the LIR motif from the E3 ligase NEDD4. Protein Science, 2017, 26, 1674-1680.	3.1	18
1867	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
1868	Evolution, structure and membrane association of NDUF6, an assembly factor for NADH:ubiquinone oxidoreductase (Complex I). Mitochondrion, 2017, 35, 13-22.	1.6	12
1869	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
1870	The CDI toxin of Yersinia kristensenii is a novel bacterial member of the RNase A superfamily. Nucleic Acids Research, 2017, 45, 5013-5025.	6.5	30
1871	Rattusin structure reveals a novel defensin scaffold formed by intermolecular disulfide exchanges. Scientific Reports, 2017, 7, 45282.	1.6	15
1872	The Canonical Poly (A) Polymerase PAP1 Polyadenylates Non-Coding RNAs and Is Essential for snoRNA Biogenesis in Trypanosoma brucei. Journal of Molecular Biology, 2017, 429, 3301-3318.	2.0	14
1873	The structure and function of an RNA polymerase interaction domain in the PcrA/UvrD helicase. Nucleic Acids Research, 2017, 45, 3875-3887.	6.5	31

#	ARTICLE	IF	CITATIONS
1874	Uracil DNA glycosylase (UDG) activities in <i>Bradyrhizobium diazoefficiens</i> : characterization of a new class of UDG with broad substrate specificity. <i>Nucleic Acids Research</i> , 2017, 45, 5863-5876.	6.5	12
1876	Computational Design of Ligand Binding Proteins. <i>Methods in Molecular Biology</i> , 2017, 1529, 363-373.	0.4	6
1877	Crystal structure analysis of a hypothetical protein (MJ0366) from <i>Methanocaldococcus jannaschii</i> revealed a novel topological arrangement of the knot fold. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 264-269.	1.0	13
1878	Open and compressed conformations of <i>Francisella tularensis</i> ClpP. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 188-194.	1.5	7
1879	<i>Streptococcus pyogenes</i> quinolinate "salvage pathway" structural and functional studies of quinolinate phosphoribosyl transferase and NH ₃ -dependent NAD ⁺ synthetase. <i>FEBS Journal</i> , 2017, 284, 2425-2441.	2.2	6
1880	Structural Characterization of a Eukaryotic Cyanase from <i>Tetranychus urticae</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 5453-5462.	2.4	11
1881	Crystal structure of BrIR with c-di-GMP. <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 260-264.	1.0	8
1882	Structural insights into the function of ZRANB3 in replication stress response. <i>Nature Communications</i> , 2017, 8, 15847.	5.8	41
1883	Cryptic indole hydroxylation by a non-canonical terpenoid cyclase parallels bacterial xenobiotic detoxification. <i>Nature Communications</i> , 2017, 8, 15804.	5.8	24
1884	Haemolytic actinoporins interact with carbohydrates using their lipid-binding module. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160216.	1.8	9
1885	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 13271-13283.	1.6	26
1886	SARS-unique fold in the <i>Rousettus</i> bat coronavirus HKU9. <i>Protein Science</i> , 2017, 26, 1726-1737.	3.1	6
1887	Boxes of Model Building and Visualization. <i>Methods in Molecular Biology</i> , 2017, 1607, 491-548.	0.4	1
1888	Structure of the Human Lipid Exporter ABCA1. <i>Cell</i> , 2017, 169, 1228-1239.e10.	13.5	214
1889	Catalytic Dyad in the SGNH Hydrolase Superfamily: In-depth Insight into Structural Parameters Tuning the Catalytic Process of Extracellular Lipase from <i>Streptomyces rimosus</i> . <i>ACS Chemical Biology</i> , 2017, 12, 1928-1936.	1.6	27
1890	Crystal structures of U6 snRNA-specific terminal uridylyltransferase. <i>Nature Communications</i> , 2017, 8, 15788.	5.8	32
1891	Discovery and characterization of family 39 glycoside hydrolases from rumen anaerobic fungi with polyspecific activity on rare arabinosyl substrates. <i>Journal of Biological Chemistry</i> , 2017, 292, 12606-12620.	1.6	32
1892	Functional details of the <i>Mycobacterium tuberculosis</i> VapBC26 toxin-antitoxin system based on a structural study: insights into unique binding and antibiotic peptides. <i>Nucleic Acids Research</i> , 2017, 45, 8564-8580.	6.5	44

#	ARTICLE	IF	CITATIONS
1893	Crystal structure of lipoate-bound lipoate ligase 1, LipL1, from <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1777-1783.	1.5	4
1894	Crystal structure of the sensor domain of BaeS from <i>Serratia marcescens</i> FS14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1784-1790.	1.5	3
1895	Structure of a soluble epoxide hydrolase identified in <i>Trichoderma reesei</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1039-1045.	1.1	10
1896	Splicing modulators act at the branch point adenosine binding pocket defined by the PHF5A-SF3b complex. <i>Nature Communications</i> , 2017, 8, 15522.	5.8	113
1897	Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in <i>Enterococcus faecalis</i> . <i>Journal of Molecular Biology</i> , 2017, 429, 2324-2336.	2.0	15
1898	The first crystal structure of a family 129 glycoside hydrolase from a probiotic bacterium reveals critical residues and metal cofactors. <i>Journal of Biological Chemistry</i> , 2017, 292, 12126-12138.	1.6	20
1899	Bacterial RadA is a DnaB-type helicase interacting with RecA to promote bidirectional D-loop extension. <i>Nature Communications</i> , 2017, 8, 15638.	5.8	101
1900	Molecular motions and free-energy landscape of serine proteinase K in relation to its cold-adaptation: a comparative molecular dynamics simulation study and the underlying mechanisms. <i>RSC Advances</i> , 2017, 7, 28580-28590.	1.7	31
1901	The Crystal Structure of a Bacterial l-Arabinonate Dehydratase Contains a [2Fe-2S] Cluster. <i>ACS Chemical Biology</i> , 2017, 12, 1919-1927.	1.6	25
1902	Cryo-EM of bacterial pili and archaeal flagellar filaments. <i>Current Opinion in Structural Biology</i> , 2017, 46, 31-37.	2.6	26
1903	Structural studies of viperin, an antiviral radical SAM enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6806-6811.	3.3	69
1904	<i>Shigella</i> depends on SepA to destabilize the intestinal epithelial integrity via cofilin activation. <i>Gut Microbes</i> , 2017, 8, 544-560.	4.3	46
1905	A structural sketch of RcdA, a transcription factor controlling the master regulator of biofilm formation. <i>FEBS Letters</i> , 2017, 591, 2019-2031.	1.3	7
1906	Selective depletion of uropathogenic <i>E. coli</i> from the gut by a FimH antagonist. <i>Nature</i> , 2017, 546, 528-532.	13.7	231
1907	Structure of the <i>Y. pseudotuberculosis</i> adhesin InvasinE. <i>Protein Science</i> , 2017, 26, 1182-1195.	3.1	10
1908	The conserved protein Seb1 drives transcription termination by binding RNA polymerase II and nascent RNA. <i>Nature Communications</i> , 2017, 8, 14861.	5.8	48
1909	Structure of aryl O-demethylase offers molecular insight into a catalytic tyrosine-dependent mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3205-E3214.	3.3	24
1910	Crystal structures of $\hat{1}^2$ -carboxysome shell protein CcmP: ligand binding correlates with the closed or open central pore. <i>Journal of Experimental Botany</i> , 2017, 68, 3857-3867.	2.4	40

#	ARTICLE	IF	CITATIONS
1911	Structural analysis of SgvP involved in carbon-sulfur bond formation during griseoviridin biosynthesis. <i>FEBS Letters</i> , 2017, 591, 1295-1304.	1.3	7
1912	Architectures of Lipid Transport Systems for the Bacterial Outer Membrane. <i>Cell</i> , 2017, 169, 273-285.e17.	13.5	194
1913	Insights into Substrate Modification by Dehydratases from Type I Polyketide Synthases. <i>Journal of Molecular Biology</i> , 2017, 429, 1554-1569.	2.0	24
1914	Structure of the infectious salmon anemia virus receptor complex illustrates a unique binding strategy for attachment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2929-E2936.	3.3	18
1915	A B12-dependent radical SAM enzyme involved in oxetanocin A biosynthesis. <i>Nature</i> , 2017, 544, 322-326.	13.7	91
1916	Interactions of the periplasmic binding protein CeuE with Fe(III) n-LICAM4 siderophore analogues of varied linker length. <i>Scientific Reports</i> , 2017, 7, 45941.	1.6	16
1917	Structure of the WipA protein reveals a novel tyrosine protein phosphatase effector from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 9240-9251.	1.6	12
1918	Human apo-SRP72 and SRP68/72 complex structures reveal the molecular basis of protein translocation. <i>Journal of Molecular Cell Biology</i> , 2017, 9, 220-230.	1.5	15
1919	Structure Determination of <i>Mycobacterium tuberculosis</i> Serine Protease Hip1 (Rv2224c). <i>Biochemistry</i> , 2017, 56, 2304-2314.	1.2	10
1920	Structure of the Cyanuric Acid Hydrolase TrzD Reveals Product Exit Channel. <i>Scientific Reports</i> , 2017, 7, 45277.	1.6	5
1921	Structural basis of molecular recognition of helical histone H3 tail by PHD finger domains. <i>Biochemical Journal</i> , 2017, 474, 1633-1651.	1.7	31
1922	Structural insights into the architecture of the <i>Shigella flexneri</i> virulence factor IcsA/MirG and motifs involved in polar distribution and secretion. <i>Journal of Structural Biology</i> , 2017, 198, 19-27.	1.3	21
1923	The Rrp4 exosome complex recruits and channels substrate RNA by a unique mechanism. <i>Nature Chemical Biology</i> , 2017, 13, 522-528.	3.9	18
1924	A structural appraisal of sterol carrier protein 2. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 565-577.	1.1	21
1925	Stilbene epoxidation and detoxification in a <i>Photobacterium luminescens</i> -nematode symbiosis. <i>Journal of Biological Chemistry</i> , 2017, 292, 6680-6694.	1.6	20
1926	Structural insights into the β -lactamase activity and substrate enantioselectivity of an isochorismatase-like hydrolase from <i>Microbacterium hydrocarbonoxydans</i> . <i>Scientific Reports</i> , 2017, 7, 44542.	1.6	9
1927	Two alternative binding mechanisms connect the protein translocation Sec71-Sec72 complex with heat shock proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 8007-8018.	1.6	43
1928	Antibiotic Capture by Bacterial Lipocalins Uncovers an Extracellular Mechanism of Intrinsic Antibiotic Resistance. <i>MBio</i> , 2017, 8, .	1.8	31

#	ARTICLE	IF	CITATIONS
1929	New Ulvan-Degrading Polysaccharide Lyase Family: Structure and Catalytic Mechanism Suggests Convergent Evolution of Active Site Architecture. <i>ACS Chemical Biology</i> , 2017, 12, 1269-1280.	1.6	60
1930	MxaJ structure reveals a periplasmic binding protein-like architecture with unique secondary structural elements. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1379-1386.	1.5	12
1931	The structure and function of <i>Mycobacterium tuberculosis</i> MazF-mt6 toxin provide insights into conserved features of MazF endonucleases. <i>Journal of Biological Chemistry</i> , 2017, 292, 7718-7726.	1.6	19
1932	Unraveling Energy and Dynamics Determinants to Interpret Protein Functional Plasticity: The Limonene-1,2-epoxide-hydrolase Case Study. <i>Journal of Chemical Information and Modeling</i> , 2017, 57, 717-725.	2.5	5
1933	Discovery and characterization of an F420-dependent glucose-6-phosphate dehydrogenase (Rh-FGD1) from <i>Rhodococcus jostii</i> RHA1. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2831-2842.	1.7	28
1934	Crystal structure of the inactive state of the receiver domain of SpoOA from <i>Paenisporosarcina</i> sp. TG-14, a psychrophilic bacterium isolated from an Antarctic glacier. <i>Journal of Microbiology</i> , 2017, 55, 464-474.	1.3	3
1935	Inhibition of the MurA enzyme in <i>Fusobacterium nucleatum</i> by potential inhibitors identified through computational and in vitro approaches. <i>Molecular BioSystems</i> , 2017, 13, 939-954.	2.9	25
1936	Structural and functional study of ChuY from <i>Escherichia coli</i> strain CFT073. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 1176-1182.	1.0	9
1937	Structural basis of cucumisin protease activity regulation by its propeptide. <i>Journal of Biochemistry</i> , 2017, 161, 45-53.	0.9	11
1938	Conserved ABC Transport System Regulated by the General Stress Response Pathways of Alpha- and Gammaproteobacteria. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	14
1939	Rice Cellulose SynthaseA8 Plant-Conserved Region Is a Coiled-Coil at the Catalytic Core Entrance. <i>Plant Physiology</i> , 2017, 173, 482-494.	2.3	27
1940	Crystal structure of human chondroadherin: solving a difficult molecular-replacement problem using <i>de novo</i> models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 53-63.	1.1	9
1941	A Two-component NADPH Oxidase (NOX)-like System in Bacteria Is Involved in the Electron Transfer Chain to the Methionine Sulfoxide Reductase MsrP. <i>Journal of Biological Chemistry</i> , 2017, 292, 2485-2494.	1.6	35
1942	Structure-Guided Reprogramming of a Hydroxylase To Halogenate Its Small Molecule Substrate. <i>Biochemistry</i> , 2017, 56, 441-444.	1.2	58
1943	Cleavage of DFNA5 by caspase-3 during apoptosis mediates progression to secondary necrotic/pyroptotic cell death. <i>Nature Communications</i> , 2017, 8, 14128.	5.8	953
1944	Proteome Bioinformatics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	5
1945	Catalytic Mechanism of a Novel Glycoside Hydrolase Family 16 α -Elongating β -1,2-Transglycosylase. <i>Journal of Biological Chemistry</i> , 2017, 292, 1666-1678.	1.6	16
1946	C2c1-sgRNA Complex Structure Reveals RNA-Guided DNA Cleavage Mechanism. <i>Molecular Cell</i> , 2017, 65, 310-322.	4.5	136

#	ARTICLE	IF	CITATIONS
1947	Expansion of divergent SEA domains in cell surface proteins and nucleoporin 54. <i>Protein Science</i> , 2017, 26, 617-630.	3.1	26
1948	Bioinformatics Tools and Resources for Analyzing Protein Structures. <i>Methods in Molecular Biology</i> , 2017, 1549, 209-220.	0.4	21
1949	N ^ε -Fatty acylation of Rho GTPases by a MARTX toxin effector. <i>Science</i> , 2017, 358, 528-531.	6.0	42
1950	Crystal structures of OrfX2 and P47 from a Botulinum neurotoxin OrfX-type gene cluster. <i>FEBS Letters</i> , 2017, 591, 3781-3792.	1.3	14
1951	Structure of PINK1 in complex with its substrate ubiquitin. <i>Nature</i> , 2017, 552, 51-56.	13.7	114
1952	Insights into the Structure of Dimeric RNA Helicase CsdA and Indispensable Role of Its C-Terminal Regions. <i>Structure</i> , 2017, 25, 1795-1808.e5.	1.6	23
1953	Structure of a Reptilian Adenovirus Reveals a Phage Tailspike Fold Stabilizing a Vertebrate Virus Capsid. <i>Structure</i> , 2017, 25, 1562-1573.e5.	1.6	19
1954	Structural analyses of the MazEF4 toxin-antitoxin pair in <i>Mycobacterium tuberculosis</i> provide evidence for a unique extracellular death factor. <i>Journal of Biological Chemistry</i> , 2017, 292, 18832-18847.	1.6	25
1955	Structural basis for the functional role of the Shu complex in homologous recombination. <i>Nucleic Acids Research</i> , 2017, 45, 13068-13079.	6.5	21
1956	Crystal structure and functional characterization of <i>scp</i> SF216 from <i>Shigella flexneri</i> . <i>FEBS Letters</i> , 2017, 591, 3692-3703.	1.3	1
1958	The Compressed Vocabulary of the Proteins of Archaea. , 2017, , 147-174.		7
1959	Crystal structure of <i>Mycobacterium tuberculosis</i> VapC20 toxin and its interactions with cognate antitoxin, VapB20, suggest a model for toxin-antitoxin assembly. <i>FEBS Journal</i> , 2017, 284, 4066-4082.	2.2	23
1960	Protein Function Prediction. <i>Methods in Molecular Biology</i> , 2017, 1654, 55-75.	0.4	28
1961	Structural and Functional Implications of Human Transforming Growth Factor β ² -Induced Protein, TGFBIp, in Corneal Dystrophies. <i>Structure</i> , 2017, 25, 1740-1750.e2.	1.6	24
1962	Crystal structure of the <i>Legionella pneumophila</i> Lpg2936 in complex with the cofactor S-adenosyl-L-methionine reveals novel insights into the mechanism of RsmE family methyltransferases. <i>Protein Science</i> , 2017, 26, 2381-2391.	3.1	9
1963	Structural origins of hemostasis and adaptive immunity. <i>Research and Practice in Thrombosis and Haemostasis</i> , 2017, 1, 286-290.	1.0	1
1964	Molecular Mechanism by which Prominent Human Gut Bacteroidetes Utilize Mixed-Linkage Beta-Glucans, Major Health-Promoting Cereal Polysaccharides. <i>Cell Reports</i> , 2017, 21, 417-430.	2.9	119
1965	Structural basis for maintenance of bacterial outer membrane lipid asymmetry. <i>Nature Microbiology</i> , 2017, 2, 1616-1623.	5.9	118

#	ARTICLE	IF	CITATIONS
1966	Crystal structure of the flexible tandem repeat domain of bacterial cellulose synthesis subunit C. <i>Scientific Reports</i> , 2017, 7, 13018.	1.6	28
1967	Crystal structures of a ZIP zinc transporter reveal a binuclear metal center in the transport pathway. <i>Science Advances</i> , 2017, 3, e1700344.	4.7	149
1968	Structural analyses of the bacterial primosomal protein DnaB reveal that it is a tetramer and forms a complex with a primosomal re-initiation protein. <i>Journal of Biological Chemistry</i> , 2017, 292, 15744-15757.	1.6	8
1969	Structure and Functional Analysis of ClbQ, an Unusual Intermediate-Releasing Thioesterase from the Colibactin Biosynthetic Pathway. <i>ACS Chemical Biology</i> , 2017, 12, 2598-2608.	1.6	32
1970	Dynamic Control of X Chromosome Conformation and Repression by a Histone H4K20 Demethylase. <i>Cell</i> , 2017, 171, 85-102.e23.	13.5	64
1971	Crystal structure of a lipase from <i>Streptomyces</i> sp. strain W007 – implications for thermostability and regioselectivity. <i>FEBS Journal</i> , 2017, 284, 3506-3519.	2.2	44
1972	Structure-function analysis of the <i>Fusarium oxysporum</i> Avr2 effector allows uncoupling of its immune-suppressing activity from recognition. <i>New Phytologist</i> , 2017, 216, 897-914.	3.5	72
1973	Crystal structure of inositol 1,3,4,5,6-pentakisphosphate 2-kinase from <i>Cryptococcus neoformans</i> . <i>Journal of Structural Biology</i> , 2017, 200, 118-123.	1.3	1
1974	Temperature-Sensitive Substrate and Product Binding Underlie Temperature-Compensated Phosphorylation in the Clock. <i>Molecular Cell</i> , 2017, 67, 783-798.e20.	4.5	79
1975	Structural and Functional Analyses of Periplasmic 5-Methylthioadenosine-S-Adenosylhomocysteine Nucleosidase from <i>Aeromonas hydrophila</i> . <i>Biochemistry</i> , 2017, 56, 5347-5355.	1.2	5
1976	Active site geometry of a novel aminopropyltransferase for biosynthesis of hyperthermophile-specific branched-chain polyamine. <i>FEBS Journal</i> , 2017, 284, 3684-3701.	2.2	10
1977	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of <i>Drosophila</i> . <i>Current Biology</i> , 2017, 27, 2869-2877.e6.	1.8	37
1978	Usb1 controls U6 snRNP assembly through evolutionarily divergent cyclic phosphodiesterase activities. <i>Nature Communications</i> , 2017, 8, 497.	5.8	20
1979	The C-terminal residue of phage Vp16 PDF, the smallest peptide deformylase, acts as an offset element locking the active conformation. <i>Scientific Reports</i> , 2017, 7, 11041.	1.6	6
1980	Structural analyses of the <i>Haemophilus influenzae</i> peptidoglycan synthase activator LpoA suggest multiple conformations in solution. <i>Journal of Biological Chemistry</i> , 2017, 292, 17626-17642.	1.6	13
1981	Structural and thermodynamic characterization of metal binding in Vps29 from <i>Entamoeba histolytica</i> : implication in retromer function. <i>Molecular Microbiology</i> , 2017, 106, 562-581.	1.2	8
1982	Distinct Mechanism for the Formation of the Ribonucleoprotein Complex of Tomato Spotted Wilt Virus. <i>Journal of Virology</i> , 2017, 91, .	1.5	21
1983	Potyvirus virion structure shows conserved protein fold and RNA binding site in ssRNA viruses. <i>Science Advances</i> , 2017, 3, eaao2182.	4.7	84

#	ARTICLE	IF	CITATIONS
1984	p190RhoGAP proteins contain pseudoGTPase domains. <i>Nature Communications</i> , 2017, 8, 506.	5.8	21
1985	Bifunctional quorum-quenching and antibiotic-acylase MacQ forms a 170-kDa capsule-shaped molecule containing spacer polypeptides. <i>Scientific Reports</i> , 2017, 7, 8946.	1.6	16
1986	The <i>Legionella</i> effector WipB is a translocated Ser/Thr phosphatase that targets the host lysosomal nutrient sensing machinery. <i>Scientific Reports</i> , 2017, 7, 9450.	1.6	8
1987	Structural and functional insights into the lipopolysaccharide ABC transporter LptB2FG. <i>Nature Communications</i> , 2017, 8, 222.	5.8	64
1989	A family of archaea-like carboxylesterases preferentially expressed in the symbiotic phase of the mycorrhizal fungus <i>Tuber melanosporum</i> . <i>Scientific Reports</i> , 2017, 7, 7628.	1.6	7
1990	Structural analysis of Wss1 protein from <i>saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2017, 7, 8270.	1.6	10
1991	Total Biosynthesis of the Pyrrolo[4,2]benzodiazepine Scaffold Tomaymycin on an In Vitro Reconstituted NRPS System. <i>Cell Chemical Biology</i> , 2017, 24, 1216-1227.e8.	2.5	19
1992	Polycomb-like proteins link the PRC2 complex to CpG islands. <i>Nature</i> , 2017, 549, 287-291.	13.7	238
1993	The lysosomal potassium channel TMEM175 adopts a novel tetrameric architecture. <i>Nature</i> , 2017, 547, 472-475.	13.7	57
1994	Crystal structure of a β -fructofuranosidase with high transfructosylation activity from <i>Aspergillus kawachii</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1786-1795.	0.6	26
1995	A rare polyglycine type II-like helix motif in naturally occurring proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2017-2023.	1.5	17
1996	Crystal structure of cis-dihydrodiol naphthalene dehydrogenase (NahB) from <i>Pseudomonas</i> sp. MC1: Insights into the early binding process of the substrate. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 403-408.	1.0	5
1997	The structure of <i>Plasmodium falciparum</i> 3D7_0606800 reveals a bilobed architecture that supports re-annotation as a Venus Flytrap protein. <i>Protein Science</i> , 2017, 26, 1878-1885.	3.1	2
1998	Architecture of the type IV coupling protein complex of <i>Legionella pneumophila</i> . <i>Nature Microbiology</i> , 2017, 2, 17114.	5.9	60
1999	Structural Insight into the Activation of PknI Kinase from <i>M. tuberculosis</i> via Dimerization of the Extracellular Sensor Domain. <i>Structure</i> , 2017, 25, 1286-1294.e4.	1.6	5
2000	Crystal structure of an orthomyxovirus matrix protein reveals mechanisms for self-polymerization and membrane association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8550-8555.	3.3	20
2001	Structural and In Vivo Studies on Trehalose-6-Phosphate Synthase from Pathogenic Fungi Provide Insights into Its Catalytic Mechanism, Biological Necessity, and Potential for Novel Antifungal Drug Design. <i>MBio</i> , 2017, 8, .	1.8	26
2002	Crystal structure of Sec10, a subunit of the exocyst complex. <i>Scientific Reports</i> , 2017, 7, 40909.	1.6	14

#	ARTICLE	IF	CITATIONS
2003	Molecular basis for the unusual ring reconstruction in fungal meroterpenoid biogenesis. <i>Nature Chemical Biology</i> , 2017, 13, 1066-1073.	3.9	33
2004	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 743-751.	3.6	140
2005	Structural basis of Notch O-glycosylation and O-xxylosylation by mammalian protein O-glycosyltransferase 1 (POGLUT1). <i>Nature Communications</i> , 2017, 8, 185.	5.8	39
2006	Structural insights into a 20.8-kDa tegumental-allergen-like (TAL) protein from <i>Clonorchis sinensis</i> . <i>Scientific Reports</i> , 2017, 7, 1764.	1.6	9
2007	Crystal structure of the DNA-binding domain of Myelin-gene Regulatory Factor. <i>Scientific Reports</i> , 2017, 7, 3696.	1.6	12
2008	The crystal structure of human Rogdi provides insight into the causes of Kohlschutter-TÃ¶nz Syndrome. <i>Scientific Reports</i> , 2017, 7, 3972.	1.6	9
2009	Crystal structure of <i>Pelagibacterium halotolerans</i> PE8: New insight into its substrate-binding pattern. <i>Scientific Reports</i> , 2017, 7, 4422.	1.6	4
2010	X-ray crystallographic structure of a bacterial polysialyltransferase provides insight into the biosynthesis of capsular polysialic acid. <i>Scientific Reports</i> , 2017, 7, 5842.	1.6	13
2011	Computational design of a symmetrical Î²-trefoil lectin with cancer cell binding activity. <i>Scientific Reports</i> , 2017, 7, 5943.	1.6	35
2012	The interleukin-like epithelial-mesenchymal transition inducer ILEI exhibits a non-interleukin-like fold and is active as a domain-swapped dimer. <i>Journal of Biological Chemistry</i> , 2017, 292, 15501-15511.	1.6	15
2013	Structural and SAXS analysis of Tle5-Tli5 complex reveals a novel inhibition mechanism of H2-T6SS in <i>Pseudomonas aeruginosa</i> . <i>Protein Science</i> , 2017, 26, 2083-2091.	3.1	6
2014	Atomic structure of a toxic, oligomeric segment of SOD1 linked to amyotrophic lateral sclerosis (ALS). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8770-8775.	3.3	104
2015	Molecular structure of FoxE, the putative iron oxidase of <i>Rhodobacter ferrooxidans</i> SW2. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 847-853.	0.5	10
2016	Structural basis of the substrate specificity and instability in solution of a glycosidase from <i>Lactobacillus plantarum</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1227-1236.	1.1	6
2017	Structural basis of autoinhibition and activation of the DNA-targeting ADP-ribosyltransferase pierisin-1. <i>Journal of Biological Chemistry</i> , 2017, 292, 15445-15455.	1.6	11
2018	Breaking the mirror: L-Amino acid deaminase, a novel stereoselective biocatalyst. <i>Biotechnology Advances</i> , 2017, 35, 657-668.	6.0	65
2019	Crystal structure of lpg1832, a VirK family protein from <i>Legionella pneumophila</i> , reveals a novel fold for bacterial VirK proteins. <i>FEBS Letters</i> , 2017, 591, 2929-2935.	1.3	4
2020	2-Deoxyribosyltransferase from <i>Leishmania mexicana</i> , an efficient biocatalyst for one-pot, one-step synthesis of nucleosides from poorly soluble purine bases. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7187-7200.	1.7	20

#	ARTICLE	IF	CITATIONS
2021	Structural Basis of Catalysis in the Bacterial Monoterpene Synthases Linalool Synthase and 1,8-Cineole Synthase. <i>ACS Catalysis</i> , 2017, 7, 6268-6282.	5.5	47
2022	Cytotoxic protein from the mushroom <i>Coprinus comatus</i> possesses a unique mode for glycan binding and specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8980-8985.	3.3	21
2023	Methanogenic heterodisulfide reductase (HdrABC-MvhAGD) uses two noncubane [4Fe-4S] clusters for reduction. <i>Science</i> , 2017, 357, 699-703.	6.0	162
2024	Pac13 is a Small, Monomeric Dehydratase that Mediates the Formation of the 3'-Deoxy Nucleoside of Pacidamycins. <i>Angewandte Chemie</i> , 2017, 129, 12666-12671.	1.6	5
2025	Structure of the C-terminal domain of TRADD reveals a novel fold in the death domain superfamily. <i>Scientific Reports</i> , 2017, 7, 7073.	1.6	10
2026	Investigation of intrinsic dynamics of enzymes involved in metabolic pathways using coarse-grained normal mode analysis. <i>Cogent Biology</i> , 2017, 3, 1291877.	1.7	4
2027	Pac13 is a Small, Monomeric Dehydratase that Mediates the Formation of the 3'-Deoxy Nucleoside of Pacidamycins. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 12492-12497.	7.2	16
2028	Molecular mechanism for the subversion of the retromer coat by the <i>Legionella</i> effector RidL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11151-E11160.	3.3	42
2029	Disabling a Type I-E CRISPR-Cas Nuclease with a Bacteriophage-Encoded Anti-CRISPR Protein. <i>MBio</i> , 2017, 8, .	1.8	63
2030	Mitochondrial Ca ²⁺ transport in the endothelium: regulation by ions, redox signalling and mechanical forces. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170672.	1.5	25
2031	Structures of the calcium-activated, non-selective cation channel TRPM4. <i>Nature</i> , 2017, 552, 205-209.	13.7	158
2032	Structural basis of cholesterol binding by a novel clade of dendritic cell modulators from ticks. <i>Scientific Reports</i> , 2017, 7, 16057.	1.6	14
2033	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces <i>Pseudomonas</i> virulence. <i>Scientific Reports</i> , 2017, 7, 16302.	1.6	88
2034	Molecular basis of AKAP79 regulation by calmodulin. <i>Nature Communications</i> , 2017, 8, 1681.	5.8	41
2035	Sterol Oxidation Mediates Stress-Responsive Vms1 Translocation to Mitochondria. <i>Molecular Cell</i> , 2017, 68, 673-685.e6.	4.5	33
2036	Structural insights into <i>Legionella</i> RidL-Vps29 retromer subunit interaction reveal displacement of the regulator TBC1D5. <i>Nature Communications</i> , 2017, 8, 1543.	5.8	47
2037	Structural and functional analyses of the mammalian TIN2-TPP1-TRF2 telomeric complex. <i>Cell Research</i> , 2017, 27, 1485-1502.	5.7	76
2038	Structural Basis for DNA Recognition of a Single-stranded DNA-binding Protein from Enterobacter Phage Enc34. <i>Scientific Reports</i> , 2017, 7, 15529.	1.6	15

#	ARTICLE	IF	CITATIONS
2039	The molecular structure of the glycoside hydrolase domain of Cwp19 from <i>Clostridium difficile</i> . FEBS Journal, 2017, 284, 4343-4357.	2.2	13
2040	A pipeline for proteome-scale identification and studies on hormone sensitive lipases in <i>Mycobacterium tuberculosis</i> . Computational Biology and Chemistry, 2017, 71, 201-206.	1.1	0
2041	Structural basis for tRNA-dependent cysteine biosynthesis. Nature Communications, 2017, 8, 1521.	5.8	6
2042	Mechanistic Insights into Dimethylsuloniopropionate Lyase DddY, a New Member of the Cupin Superfamily. Journal of Molecular Biology, 2017, 429, 3850-3862.	2.0	22
2043	High-resolution structure of a Kazal-type serine protease inhibitor from the dengue vector <i>Aedes aegypti</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 469-475.	0.4	4
2044	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. Scientific Reports, 2017, 7, 14890.	1.6	21
2045	Modular endolysin of Burkholderia AP3 phage has the largest lysozyme-like catalytic subunit discovered to date and no catalytic aspartate residue. Scientific Reports, 2017, 7, 14501.	1.6	28
2046	KIXBASE: A comprehensive web resource for identification and exploration of KIX domains. Scientific Reports, 2017, 7, 14924.	1.6	5
2047	Structural characterization of FlgE2 protein from <i>Helicobacter pylori</i> hook. FEBS Journal, 2017, 284, 4328-4342.	2.2	6
2048	Cdt1 stabilizes an open MCM ring for helicase loading. Nature Communications, 2017, 8, 15720.	5.8	69
2049	Crystal structure of human WBSR16, an RCC1-like protein in mitochondria. Protein Science, 2017, 26, 1870-1877.	3.1	5
2050	Biochemical Characterization and Structural Basis of Reactivity and Regioselectivity Differences between <i>Burkholderia thailandensis</i> and <i>Burkholderia glumae</i> 1,6-Didesmethyltoxoflavin N-Methyltransferase. Biochemistry, 2017, 56, 3934-3944.	1.2	4
2051	Structural and Biophysical Characterization of the <i>Mycobacterium tuberculosis</i> Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the <i>Streptomyces coelicolor</i> Protein KbpA. Biochemistry, 2017, 56, 4015-4027.	1.2	4
2052	A structure-derived snap-trap mechanism of a multispecific serpin from the dysbiotic human oral microbiome. Journal of Biological Chemistry, 2017, 292, 10883-10898.	1.6	17
2053	Biochemical and Structural Analyses of Two Cryptic Esterases in <i>Bacteroides intestinalis</i> and their Synergistic Activities with Cognate Xylanases. Journal of Molecular Biology, 2017, 429, 2509-2527.	2.0	25
2054	The structural and functional characterization of human RecQ4 reveals insights into its helicase mechanism. Nature Communications, 2017, 8, 15907.	5.8	41
2055	NMR structure of the <i>Bacillus cereus</i> hemolysin II C-terminal domain reveals a novel fold. Scientific Reports, 2017, 7, 3277.	1.6	10
2056	Structural and biochemical studies of sulphotransferase 18 from <i>Arabidopsis thaliana</i> explain its substrate specificity and reaction mechanism. Scientific Reports, 2017, 7, 4160.	1.6	18

#	ARTICLE	IF	CITATIONS
2057	Crystal structure and DNA-binding property of the ATPase domain of bacterial mismatch repair endonuclease MutL from <i>Aquifex aeolicus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1178-1187.	1.1	12
2058	Comparative visualization of protein secondary structures. <i>BMC Bioinformatics</i> , 2017, 18, 23.	1.2	11
2059	Molecular cloning, expression, and characterization of four novel thermo-alkaliphilic enzymes retrieved from a metagenomic library. <i>Biotechnology for Biofuels</i> , 2017, 10, 142.	6.2	10
2060	Crystal structure of the novel amino-acid racemase isoleucine 2-epimerase from <i>Lactobacillus buchneri</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 428-437.	1.1	12
2061	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 55-64.	1.1	13
2062	Structure and dynamics study of translation initiation factor 1 from <i>Staphylococcus aureus</i> suggests its RNA binding mode. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 65-75.	1.1	3
2063	Structural Insights into L-Tryptophan Dehydrogenase from a Photoautotrophic Cyanobacterium, <i>Nostoc punctiforme</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	5
2064	Structure of the Open Reading Frame 49 Protein Encoded by Kaposi's Sarcoma-Associated Herpesvirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	3
2065	Structurally diverse dehydroshikimate dehydratase variants participate in microbial quinate catabolism. <i>Molecular Microbiology</i> , 2017, 103, 39-54.	1.2	13
2066	Aromatic claw: A new fold with high aromatic content that evades structural prediction. <i>Protein Science</i> , 2017, 26, 208-217.	3.1	0
2067	Solution structure of the Cys74 to Ala74 mutant of the recombinant catalytic domain of Zoocin A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 177-181.	1.5	9
2068	Structure and Function of a C-C Bond Cleaving Oxygenase in Atypical Angucycline Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 142-152.	1.6	17
2069	Structural Biology of the Arterivirus nsp11 Endoribonucleases. <i>Journal of Virology</i> , 2017, 91, .	1.5	30
2070	Crystal structure of <i>Pseudomonas aeruginosa</i> RsaL bound to promoter DNA reaffirms its role as a global regulator involved in quorum-sensing. <i>Nucleic Acids Research</i> , 2017, 45, 699-710.	6.5	34
2071	Structural and Biochemical Characterization of <i>Acinetobacter</i> spp. Aminoglycoside Acetyltransferases Highlights Functional and Evolutionary Variation among Antibiotic Resistance Enzymes. <i>ACS Infectious Diseases</i> , 2017, 3, 132-143.	1.8	17
2072	Electrostatic potentials of the S-box proteins contribute to the pollen S-specificity in self-incompatibility in <i>Petunia hybrida</i> . <i>Plant Journal</i> , 2017, 89, 45-57.	2.8	28
2073	Structure of the Catalytic Domain of L-Arabinofuranosidase from <i>Coprinopsis cinerea</i> , CcAbf62A, Provides Insights into Structure-Function Relationships in Glycoside Hydrolase Family 62. <i>Applied Biochemistry and Biotechnology</i> , 2017, 181, 511-525.	1.4	14
2074	A molecular dynamics strategy for CS ₂ peptides disulfide-assisted model refinement. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2736-2744.	2.0	1

#	ARTICLE	IF	CITATIONS
2075	Discovery of nanomolar ligands with novel scaffolds for the histamine H4 receptor by virtual screening. <i>European Journal of Medicinal Chemistry</i> , 2017, 125, 565-572.	2.6	10
2076	Distinct roles of Pcf11 zinc-binding domains in pre-mRNA 3' end processing. <i>Nucleic Acids Research</i> , 2017, 45, 10115-10131.	6.5	11
2077	The crystal structure of the <i>Yersinia pestis</i> iron chaperone YiuA reveals a basic triad binding motif for the chelated metal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 921-939.	1.1	5
2078	Crystal structure of Rv1220c, a SAM-dependent O-methyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 315-320.	0.4	2
2079	Alternative substrate-bound conformation of bacterial solute-binding protein involved in the import of mammalian host glycosaminoglycans. <i>Scientific Reports</i> , 2017, 7, 17005.	1.6	7
2080	Structure of the <i>Bacillus anthracis</i> dTDP-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose reductase (RfbD). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 644-650.	0.4	6
2081	Structure of a Wbl protein and implications for NO sensing by <i>M. tuberculosis</i> . <i>Nature Communications</i> , 2017, 8, 2280.	5.8	38
2082	A hydrophobic anchor mechanism defines a deacetylase family that suppresses host response against YopJ effectors. <i>Nature Communications</i> , 2017, 8, 2201.	5.8	22
2083	Deciphering how Cpl-7 cell wall-binding repeats recognize the bacterial peptidoglycan. <i>Scientific Reports</i> , 2017, 7, 16494.	1.6	23
2084	Crystal structure of the <i>Thermoplasma acidophilum</i> protein Ta1207. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 328-335.	0.4	0
2085	Crystal structure of the PEG-bound SH3 domain of myosin IB from <i>Entamoeba histolytica</i> reveals its mode of ligand recognition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 672-682.	1.1	6
2086	Dynamic Control of Chromosome Topology and Gene Expression by a Chromatin Modification. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 279-291.	2.0	10
2087	Geometric 3D protein structures superimposition. , 2017, , .		0
2088	Structural and functional characterization of the <i>Helicobacter pylori</i> cytidine 5''-monophosphate-pseudaminic acid synthase PseF: molecular insight into substrate recognition and catalysis mechanism. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2017, Volume 10, 79-88.	1.6	3
2089	Structural Characterization of Maize SIRK1 Kinase Domain Reveals an Unusual Architecture of the Activation Segment. <i>Frontiers in Plant Science</i> , 2017, 8, 852.	1.7	10
2090	Methods for Structural and Functional Analyses of Intramembrane Prenyltransferases in the UbiA Superfamily. <i>Methods in Enzymology</i> , 2017, 584, 309-347.	0.4	7
2091	Structural Features of Apicomplexan Pore-Forming Proteins and Their Roles in Parasite Cell Traversal and Egress. <i>Toxins</i> , 2017, 9, 265.	1.5	15
2092	Pharmacophore-Based Virtual Screening of Novel Inhibitors and Docking Analysis for CYP51A from <i>Penicillium italicum</i> . <i>Marine Drugs</i> , 2017, 15, 107.	2.2	6

#	ARTICLE	IF	CITATIONS
2093	Crystal Structure of the Carboxy-Terminal Region of the Bacteriophage T4 Proximal Long Tail Fiber Protein Gp34. <i>Viruses</i> , 2017, 9, 168.	1.5	24
2094	Structural insights into RapZ-mediated regulation of bacterial amino-sugar metabolism. <i>Nucleic Acids Research</i> , 2017, 45, 10845-10860.	6.5	30
2095	Crystal structure of the N-terminal domain of VqsR from <i>Pseudomonas aeruginosa</i> at 2.1 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 431-436.	0.4	1
2096	Regulation and Function of Cdt1; A Key Factor in Cell Proliferation and Genome Stability. <i>Genes</i> , 2017, 8, 2.	1.0	94
2097	Molecular and Structural Characterization of the Tegumental 20.6-kDa Protein in <i>Clonorchis sinensis</i> as a Potential Druggable Target. <i>International Journal of Molecular Sciences</i> , 2017, 18, 557.	1.8	13
2098	Structural basis of host recognition and biofilm formation by <i>Salmonella</i> Srf pili. <i>ELife</i> , 2017, 6, .	2.8	20
2099	Structure of the malaria vaccine candidate antigen CyRPA and its complex with a parasite invasion inhibitory antibody. <i>ELife</i> , 2017, 6, .	2.8	50
2100	<i>Staphylococcus aureus</i> Esx Factors Control Human Dendritic Cell Functions Conditioning Th1/Th17 Response. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 330.	1.8	21
2101	Identification of Capsid/Coat Related Protein Folds and Their Utility for Virus Classification. <i>Frontiers in Microbiology</i> , 2017, 8, 380.	1.5	21
2102	New Insights into the Regulation of Cell-Surface Signaling Activity Acquired from a Mutagenesis Screen of the <i>Pseudomonas putida</i> IutY Sigma/Anti-Sigma Factor. <i>Frontiers in Microbiology</i> , 2017, 8, 747.	1.5	11
2103	Decoding the centromeric nucleosome through CENP-N. <i>ELife</i> , 2017, 6, .	2.8	101
2104	Structure of Fam20A reveals a pseudokinase featuring a unique disulfide pattern and inverted ATP-binding. <i>ELife</i> , 2017, 6, .	2.8	29
2105	Crystal structure of the type IV secretion system component CagX from <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 167-173.	0.4	8
2106	UbaLAI is a monomeric Type IIE restriction enzyme. <i>Nucleic Acids Research</i> , 2017, 45, 9583-9594.	6.5	6
2107	Crystal Structure of an Invasivity-Associated Domain of SdrE in <i>S. aureus</i> . <i>PLoS ONE</i> , 2017, 12, e0168814.	1.1	6
2108	Crystal Structure and Functional Characterization of an Esterase (EaEST) from <i>Exiguobacterium antarcticum</i> . <i>PLoS ONE</i> , 2017, 12, e0169540.	1.1	24
2109	Structural insights into the regulation of <i>Bacillus subtilis</i> SigW activity by anti-sigma RsiW. <i>PLoS ONE</i> , 2017, 12, e0174284.	1.1	19
2110	Solution NMR structure of the TRIM21 B-box2 and identification of residues involved in its interaction with the RING domain. <i>PLoS ONE</i> , 2017, 12, e0181551.	1.1	9

#	ARTICLE	IF	CITATIONS
2111	Crystal structure of mimivirus uracil-DNA glycosylase. PLoS ONE, 2017, 12, e0182382.	1.1	6
2112	Structure of the Neisseria Adhesin Complex Protein (ACP) and its role as a novel lysozyme inhibitor. PLoS Pathogens, 2017, 13, e1006448.	2.1	23
2113	A mobile loop near the active site acts as a switch between the dual activities of a viral protease/deubiquitinase. PLoS Pathogens, 2017, 13, e1006714.	2.1	18
2114	Acquisition of functions on the outer capsid surface during evolution of double-stranded RNA fungal viruses. PLoS Pathogens, 2017, 13, e1006755.	2.1	26
2115	Structural insights into reptarenavirus cap-snatching machinery. PLoS Pathogens, 2017, 13, e1006400.	2.1	32
2116	Cellular origin of the viral capsid-like bacterial microcompartments. Biology Direct, 2017, 12, 25.	1.9	17
2117	Structure of the Bacillus anthracis dTDP-L-rhamnose-biosynthetic enzyme glucose-1-phosphate thymidyltransferase (RfbA). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 621-628.	0.4	2
2118	Structure of the Bacillus anthracis dTDP-L-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose 3,5-epimerase (RfbC). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 664-671.	0.4	6
2119	Structure of an innexin gap junction channel and cryo-EM sample preparation. Microscopy (Oxford), 2017, 12, 10.1093/microms/dkx000	8.7	12
2120	DNA recognition by the SmaI restriction endonuclease involves unusual distortion of an 8 base pair A:T-rich target. Nucleic Acids Research, 2017, 45, 1516-1528.	6.5	4
2123	Investigation of structure and function of mitochondrial alcohol dehydrogenase isozyme III from Komagataella phaffii GS115. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1199-1208.	1.1	3
2124	Structural basis for the glycosyltransferase activity of the Salmonella effector SseK3. Journal of Biological Chemistry, 2018, 293, 5064-5078.	1.6	48
2125	Identification and characterization of acetyltransferase type toxin antitoxin locus in Klebsiella pneumoniae. Molecular Microbiology, 2018, 108, 336-349.	1.2	31
2126	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
2127	Secretome Analysis Identifies Potential Pathogenicity/Virulence Factors of Tilletia indica, a Quarantined Fungal Pathogen Inciting Karnal Bunt Disease in Wheat. Proteomics, 2018, 18, e1700473.	1.3	15
2128	Bunyavirales ribonucleoproteins: the viral replication and transcription machinery. Critical Reviews in Microbiology, 2018, 44, 522-540.	2.7	57
2129	Crystal structure of an anti-CRISPR protein, AcrIIA1. Nucleic Acids Research, 2018, 46, 485-492.	6.5	34
2130	An ancient family of lytic polysaccharide monooxygenases with roles in arthropod development and biomass digestion. Nature Communications, 2018, 9, 756.	5.8	192

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2131	Einblicke in die duale Aktivität einer bifunktionalen Dehydratase-Cyclase-Domäne. <i>Angewandte Chemie</i> , 2018, 130, 349-353.	1.6	4
2132	An in silico structural and physicochemical characterization of TonB-dependent copper receptor in <i>A. baumannii</i> . <i>Microbial Pathogenesis</i> , 2018, 118, 18-31.	1.3	12
2133	Treatment of <i>Clostridium difficile</i> Infection with a Small-Molecule Inhibitor of Toxin UDP-Glucose Hydrolysis Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	11
2134	Grouper iridovirus GIV66 is a Bcl-2 protein that inhibits apoptosis by exclusively sequestering Bim. <i>Journal of Biological Chemistry</i> , 2018, 293, 5464-5477.	1.6	27
2135	Structural Basis for DNA Recognition by the Two-Component Response Regulator RcsB. <i>MBio</i> , 2018, 9, .	1.8	15
2136	SbnI is a free serine kinase that generates -phospho-l-serine for staphyloferrin B biosynthesis in. <i>Journal of Biological Chemistry</i> , 2018, 293, 6147-6160.	1.6	12
2137	Crystal structure of a substrate-binding protein from <i>Rhodothermus marinus</i> reveals a single β -sheet domain. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 368-373.	1.0	8
2138	β -Tubulin has a conserved intrinsic property of self-polymerization into double stranded filaments and fibrillar networks. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 734-748.	1.9	19
2139	Snapshots of C-S Cleavage in Egt2 Reveals Substrate Specificity and Reaction Mechanism. <i>Cell Chemical Biology</i> , 2018, 25, 519-529.e4.	2.5	29
2140	Transcriptional profiling, molecular cloning, and functional analysis of C1 inhibitor, the main regulator of the complement system in black rockfish, <i>Sebastes schlegelii</i> . <i>Fish and Shellfish Immunology</i> , 2018, 75, 263-273.	1.6	8
2141	Structural basis for the role of serine-rich repeat proteins from <i>Lactobacillus reuteri</i> in gut microbe-host interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2706-E2715.	3.3	35
2142	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'. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 41-51.	1.1	5
2143	Human <i>N</i> -acetylglucosaminyltransferase II substrate recognition uses a modular architecture that includes a convergent exosite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4637-4642.	3.3	37
2144	Structural and functional studies of Spr1654: an essential aminotransferase in teichoic acid biosynthesis in <i>Streptococcus pneumoniae</i> . <i>Open Biology</i> , 2018, 8, 170248.	1.5	2
2145	Computational screening of potential non-immunoglobulin scaffolds using overlapped conserved residues (OCR)-based fingerprints. <i>Korean Journal of Chemical Engineering</i> , 2018, 35, 717-724.	1.2	2
2146	Crystal structure of the trimeric N-terminal domain of ciliate <i>Euplotes octocarinatus</i> centrin binding with calcium ions. <i>Protein Science</i> , 2018, 27, 1102-1108.	3.1	2
2147	Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. <i>Nature Communications</i> , 2018, 9, 1549.	5.8	35
2148	Structural basis for the regulatory interaction of the methylglyoxal synthase MgsA with the carbon flux regulator Crh in. <i>Journal of Biological Chemistry</i> , 2018, 293, 5781-5792.	1.6	5

#	ARTICLE	IF	CITATIONS
2149	Disulfide isomerase activity of the dynamic, trimeric ScsC protein is primed by the tandem immunoglobulin-fold domain of ScsB. <i>Journal of Biological Chemistry</i> , 2018, 293, 5793-5805.	1.6	19
2150	Towards the structural characterization of the human methyltransferase. <i>Current Opinion in Structural Biology</i> , 2018, 53, 12-21.	2.6	7
2151	Structural basis of DNA target recognition by the B3 domain of Arabidopsis epigenome reader VAL1. <i>Nucleic Acids Research</i> , 2018, 46, 4316-4324.	6.5	27
2152	The inhibitory potential of Brousochalcone A for the human cytochrome P450 2J2 isoform and its anti-cancer effects via FOXO3 activation. <i>Phytomedicine</i> , 2018, 42, 199-206.	2.3	19
2153	Structural basis for the preference of the <i>Arabidopsis thaliana</i> phosphatase RLP2 for tyrosine-phosphorylated substrates. <i>Science Signaling</i> , 2018, 11, .	1.6	4
2154	Probing the opportunities for designing anthelmintic leads by sub-structural topology-based QSAR modelling. <i>Molecular Diversity</i> , 2018, 22, 669-683.	2.1	3
2155	Conserved structural features anchor biofilm-associated RTX adhesins to the outer membrane of bacteria. <i>FEBS Journal</i> , 2018, 285, 1812-1826.	2.2	18
2156	Crystal Structures of Cystathionine Î ² -Synthase from <i>Saccharomyces cerevisiae</i> : One Enzymatic Step at a Time. <i>Biochemistry</i> , 2018, 57, 3134-3145.	1.2	25
2157	Substrate Recognition by a Colistin Resistance Enzyme from <i>Moraxella catarrhalis</i> . <i>ACS Chemical Biology</i> , 2018, 13, 1322-1332.	1.6	15
2158	Molecular basis of GID4-mediated recognition of degrons for the Pro/N-end rule pathway. <i>Nature Chemical Biology</i> , 2018, 14, 466-473.	3.9	80
2159	Molecular control of gene expression by Brucella BaaR, an lclR-type transcriptional repressor. <i>Journal of Biological Chemistry</i> , 2018, 293, 7437-7456.	1.6	5
2161	A <i>Toxoplasma gondii</i> locus required for the direct manipulation of host mitochondria has maintained multiple ancestral functions. <i>Molecular Microbiology</i> , 2018, 108, 519-535.	1.2	20
2162	On the Trails of the Proteasome Fold: Structural and Functional Analysis of the Ancestral Î ² -Subunit Protein Anbu. <i>Journal of Molecular Biology</i> , 2018, 430, 628-640.	2.0	4
2163	Legionella DotM structure reveals a role in effector recruiting to the Type 4B secretion system. <i>Nature Communications</i> , 2018, 9, 507.	5.8	35
2164	Structural and functional characterization of shaft, anchor, and tip proteins of the Mfa1 fimbria from the periodontal pathogen Porphyromonas gingivalis. <i>Scientific Reports</i> , 2018, 8, 1793.	1.6	25
2165	Structural Basis of a Thiol-Disulfide Oxidoreductase in the Hedgehog-Forming Actinobacterium <i>Corynebacterium matruchotii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	8
2166	Structural Characterization and Directed Evolution of a Novel Acetyl Xylan Esterase Reveals Thermostability Determinants of the Carbohydrate Esterase 7 Family. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	18
2167	The Structure of the Biofilm-controlling Response Regulator BfmR from <i>Acinetobacter baumannii</i> Reveals Details of Its DNA-binding Mechanism. <i>Journal of Molecular Biology</i> , 2018, 430, 806-821.	2.0	47

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2168	Cep120 promotes microtubule formation through a unique tubulin binding C2 domain. <i>Journal of Structural Biology</i> , 2018, 203, 62-70.	1.3	10
2169	Structural basis of protein arginine rhamnosylation by glycosyltransferase EarP. <i>Nature Chemical Biology</i> , 2018, 14, 368-374.	3.9	22
2170	Structural studies of <i>Acidianus</i> tailed spindle virus reveal a structural paradigm used in the assembly of spindle-shaped viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2120-2125.	3.3	29
2171	Structure and Enzymatic Properties of an Unusual Cysteine Tryptophylquinone-Dependent Glycine Oxidase from <i>Pseudoalteromonas luteoviolacea</i> . <i>Biochemistry</i> , 2018, 57, 1155-1165.	1.2	18
2172	Novel structural features drive DNA binding properties of Cmr, a CRP family protein in TB complex mycobacteria. <i>Nucleic Acids Research</i> , 2018, 46, 403-420.	6.5	7
2173	Large scale ab initio modeling of structurally uncharacterized antimicrobial peptides reveals known and novel folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 548-565.	1.5	13
2174	A presumed homologue of the regulatory subunits of eIF2B functions as ribose-1,5-bisphosphate isomerase in <i>Pyrococcus horikoshii</i> OT3. <i>Scientific Reports</i> , 2018, 8, 1891.	1.6	5
2175	Crystal structure of the FliF-FliG complex from <i>Helicobacter pylori</i> yields insight into the assembly of the motor MS-C ring in the bacterial flagellum. <i>Journal of Biological Chemistry</i> , 2018, 293, 2066-2078.	1.6	31
2176	Stu2 uses a 15-nm parallel coiled coil for kinetochore localization and concomitant regulation of the mitotic spindle. <i>Molecular Biology of the Cell</i> , 2018, 29, 285-294.	0.9	5
2177	Use of Domain-Swapping to Identify Candidate Amino Acids Involved in Differential Interactions between Two Allelic Variants of Type-1 S-Locus F-Box Protein and S3-RNase in <i>Petunia inflata</i> . <i>Plant and Cell Physiology</i> , 2018, 59, 234-247.	1.5	14
2178	Structures of β^2 -klotho reveal a "zip code"-like mechanism for endocrine FGF signalling. <i>Nature</i> , 2018, 553, 501-505.	13.7	160
2179	Structural basis for chitin acquisition by marine <i>Vibrio</i> species. <i>Nature Communications</i> , 2018, 9, 220.	5.8	37
2180	Environmental <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> have a higher probability to act as a recipient in conjugation than clinical strains. <i>Plasmid</i> , 2018, 95, 28-35.	0.4	7
2181	Snapshots of catalysis: Structure of covalently bound substrate trapped in <i>Mycobacterium tuberculosis</i> thiazole synthase (ThiG). <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 214-219.	1.0	2
2182	Crystal structure of ADP-dependent glucokinase from <i>Methanocaldococcus jannaschii</i> in complex with 5-iodotubercidin reveals phosphoryl transfer mechanism. <i>Protein Science</i> , 2018, 27, 790-797.	3.1	7
2183	A PH-like domain of the Rab12 guanine nucleotide exchange factor DENND3 binds actin and is required for autophagy. <i>Journal of Biological Chemistry</i> , 2018, 293, 4566-4574.	1.6	27
2184	Evolution of Eukaryal and Archaeal Pseudouridine Synthase Pus10. <i>Journal of Molecular Evolution</i> , 2018, 86, 77-89.	0.8	18
2185	Novel Families of Archaeo-Eukaryotic Primases Associated with Mobile Genetic Elements of Bacteria and Archaea. <i>Journal of Molecular Biology</i> , 2018, 430, 737-750.	2.0	31

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2186	Structural basis of the phosphorylation-independent recognition of cyclin D1 by the SCF ^{FBXO31} ubiquitin ligase. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 319-324.	3.3	39
2187	Structural characterization of SpoIIIAB sporulation-essential protein in Bacillus subtilis. Journal of Structural Biology, 2018, 202, 105-112.	1.3	11
2188	Structural mechanisms of centromeric nucleosome recognition by the kinetochore protein CENP-N. Science, 2018, 359, 339-343.	6.0	98
2189	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
2190	Structural analysis of mtEXO mitochondrial RNA degradosome reveals tight coupling of nuclease and helicase components. Nature Communications, 2018, 9, 97.	5.8	23
2191	Ketonization of Proline Residues in the Peptide Chains of Actinomycins by a 4-oxoproline Synthase. ChemBioChem, 2018, 19, 706-715.	1.3	10
2192	Structural ensemble-based docking simulation and biophysical studies discovered new inhibitors of Hsp90 N-terminal domain. Scientific Reports, 2018, 8, 368.	1.6	11
2193	Structure and activity of ChiX: a peptidoglycan hydrolase required for chitinase secretion by <i>Serratia marcescens</i> . Biochemical Journal, 2018, 475, 415-428.	1.7	15
2194	Structure and function of cytoplasmic serine hydroxymethyltransferase from Pichia pastoris. Biochemical and Biophysical Research Communications, 2018, 496, 753-757.	1.0	4
2195	Employing a biochemical protecting group for a sustainable indigo dyeing strategy. Nature Chemical Biology, 2018, 14, 256-261.	3.9	143
2196	Crystal Structure of NisI in a Lipid-Free Form, the Nisin Immunity Protein, from Lactococcus lactis. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	11
2197	A putative RNA binding protein from <i>Plasmodium vivax</i> apicoplast. FEBS Open Bio, 2018, 8, 177-188.	1.0	3
2198	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
2199	Structure of the yeast oligosaccharyltransferase complex gives insight into eukaryotic N-glycosylation. Science, 2018, 359, 545-550.	6.0	157
2200	<i>Bacteroides thetaiotaomicron</i> generates diverse α -mannosidase activities through subtle evolution of a distal substrate-binding motif. Acta Crystallographica Section D: Structural Biology, 2018, 74, 394-404.	1.1	8
2201	The structure of the N-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
2202	Structural basis of the bacteriophage ϕ TP901-1 ϕ Cl repressor dimerization and interaction with ϕ DNA. FEBS Letters, 2018, 592, 1738-1750.	1.3	5
2203	Structure and properties of AB21, a novel <i>Agaricus bisporus</i> protein with structural relation to bacterial pore-forming toxins. Proteins: Structure, Function and Bioinformatics, 2018, 86, 897-911.	1.5	3

#	ARTICLE	IF	CITATIONS
2204	Crystal Structure of Classical Swine Fever Virus NS5B Reveals a Novel N-Terminal Domain. <i>Journal of Virology</i> , 2018, 92, .	1.5	19
2205	Structural and biochemical characterization of the protease domain of the mosaic botulinum neurotoxin type HA. <i>Pathogens and Disease</i> , 2018, 76, .	0.8	12
2206	The aldehyde dehydrogenase AldA contributes to the hypochlorite defense and is redox-controlled by protein S-bacillithiolation in <i>Staphylococcus aureus</i> . <i>Redox Biology</i> , 2018, 15, 557-568.	3.9	38
2207	Crystal Structure of Ripk4 Reveals Dimerization-Dependent Kinase Activity. <i>Structure</i> , 2018, 26, 767-777.e5.	1.6	16
2208	Structures of Angptl3 and Angptl4, modulators of triglyceride levels and coronary artery disease. <i>Scientific Reports</i> , 2018, 8, 6752.	1.6	38
2209	Type II Secretion-Dependent Aminopeptidase LapA and Acyltransferase PlaC Are Redundant for Nutrient Acquisition during <i>Legionella pneumophila</i> Intracellular Infection of Amoebas. <i>MBio</i> , 2018, 9, .	1.8	27
2210	Crystal structure of undecaprenyl-pyrophosphate phosphatase and its role in peptidoglycan biosynthesis. <i>Nature Communications</i> , 2018, 9, 1078.	5.8	47
2211	Structural changes of TasA in biofilm formation of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3237-3242.	3.3	97
2212	Solution structure of an archaeal DUF61 family protein SSO0941 encoded by a gene in the operon of box C/D RNA protein complexes. <i>Journal of Structural Biology</i> , 2018, 203, 179-184.	1.3	0
2213	Discovery and Characterization of ZUFSP/ZUP1, a Distinct Deubiquitinase Class Important for Genome Stability. <i>Molecular Cell</i> , 2018, 70, 150-164.e6.	4.5	142
2214	Structure of the peptidoglycan polymerase RodA resolved by evolutionary coupling analysis. <i>Nature</i> , 2018, 556, 118-121.	13.7	110
2215	Using Chou's general PseAAC to analyze the evolutionary relationship of receptor associated proteins (RAP) with various folding patterns of protein domains. <i>Journal of Theoretical Biology</i> , 2018, 445, 62-74.	0.8	65
2216	Structural and Functional Insights into <i>Bacillus subtilis</i> Sigma Factor Inhibitor, CsfB. <i>Structure</i> , 2018, 26, 640-648.e5.	1.6	12
2217	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in <i>Mycobacterium smegmatis</i> . <i>Biochemical Journal</i> , 2018, 475, 1295-1308.	1.7	13
2218	Structure of Schlafen13 reveals a new class of tRNA/rRNA-targeting RNase engaged in translational control. <i>Nature Communications</i> , 2018, 9, 1165.	5.8	87
2219	The BRD3 ET domain recognizes a short peptide motif through a mechanism that is conserved across chromatin remodelers and transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2018, 293, 7160-7175.	1.6	39
2220	Peptide ion channel toxins from the bootlace worm, the longest animal on Earth. <i>Scientific Reports</i> , 2018, 8, 4596.	1.6	22
2221	The structure of hydrogenase-2 from <i>Escherichia coli</i> : implications for H ₂ -driven proton pumping. <i>Biochemical Journal</i> , 2018, 475, 1353-1370.	1.7	46

#	ARTICLE	IF	CITATIONS
2222	Crystal structures of an archaeal chitinase ChiD and its ligand complexes. <i>Glycobiology</i> , 2018, 28, 418-426.	1.3	3
2223	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. <i>Cell</i> , 2018, 173, 208-220.e20.	13.5	51
2224	Crystal structure and functional analysis of large-terpene synthases belonging to a newly found subclass. <i>Chemical Science</i> , 2018, 9, 3754-3758.	3.7	25
2225	Structural and biochemical characterization of a GH3 Î ² -glucosidase from the probiotic bacteria <i>Bifidobacterium adolescentis</i> . <i>Biochimie</i> , 2018, 148, 107-115.	1.3	38
2226	Structural basis of the Cope rearrangement and cyclization in hapalindole biogenesis. <i>Nature Chemical Biology</i> , 2018, 14, 345-351.	3.9	34
2227	Substrate recognition and mechanism revealed by ligand-bound polyphosphate kinase 2 structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3350-3355.	3.3	52
2228	Structural insight into an evolutionarily ancient programmed cell death regulator – the crystal structure of marine sponge BHP2 bound to LB-Bak-2. <i>Cell Death and Disease</i> , 2018, 8, e2543-e2543.	2.7	23
2229	Building the atomic model of a boreal lake virus of unknown fold in a 3.9-Å cryo-EM map. <i>Journal of Structural Biology</i> , 2018, 202, 94-99.	1.3	3
2230	Insights into the Dual Activity of a Bifunctional Dehydratase-Cyclase Domain. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 343-347.	7.2	22
2231	<i>Rhodococcus erythropolis</i> Oleate Hydratase: a New Member in the Oleate Hydratase Family Tree – Biochemical and Structural Studies. <i>ChemCatChem</i> , 2018, 10, 407-414.	1.8	29
2232	Crystal structure of glycerol 3-phosphate mannose-6-phosphate adenylyltransferase from <i>Burkholderia pseudomallei</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 124-131.	1.5	6
2233	Evolution of catalytic microenvironment governs substrate and product diversity in trichodiene synthase and other terpene fold enzymes. <i>Biochimie</i> , 2018, 144, 9-20.	1.3	5
2234	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
2235	DrFrnE Represents a Hitherto Unknown Class of Eubacterial Cytoplasmic Disulfide Oxido-Reductases. <i>Antioxidants and Redox Signaling</i> , 2018, 28, 296-310.	2.5	6
2236	Ankyrin repeats as a dimerization module. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1002-1007.	1.0	3
2237	Rapid and reliable protein structure determination via chemical shift threading. <i>Journal of Biomolecular NMR</i> , 2018, 70, 33-51.	1.6	4
2238	Fructooligosaccharides production by <i>Schedonorus arundinaceus</i> sucrose:sucrose 1-fructosyltransferase constitutively expressed to high levels in <i>Pichia pastoris</i> . <i>Journal of Biotechnology</i> , 2018, 266, 59-71.	1.9	19
2239	Crystal structure of native N-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. <i>FEBS Journal</i> , 2018, 285, 580-598.	2.2	12

#	ARTICLE	IF	CITATIONS
2240	Crystal structure of the Legionella effector Lem22. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 263-267.	1.5	3
2241	Identification and Experimental Characterization of an Extremophilic Brine Pool Alcohol Dehydrogenase from Single Amplified Genomes. <i>ACS Chemical Biology</i> , 2018, 13, 161-170.	1.6	19
2242	Spatial attributes of the four-helix bundle group of bacteriocins – The high-resolution structure of BacSp222 in solution. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 2715-2724.	3.6	17
2243	Structural and biophysical characterization of Rv3716c, a hypothetical protein from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 982-987.	1.0	2
2244	Serine/Threonine Protein Kinases from Bacteria, Archaea and Eukarya Share a Common Evolutionary Origin Deeply Rooted in the Tree of Life. <i>Journal of Molecular Biology</i> , 2018, 430, 27-32.	2.0	78
2245	Loop of Streptomyces Feruloyl Esterase Plays an Important Role in the Enzyme's Catalyzing the Release of Ferulic Acid from Biomass. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	20
2246	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensor domain protein. <i>Protein Science</i> , 2018, 27, 568-572.	3.1	1
2247	Nsp3 of coronaviruses: Structures and functions of a large multi-domain protein. <i>Antiviral Research</i> , 2018, 149, 58-74.	1.9	542
2248	Crystal structure of the Melampsora lini effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. <i>Molecular Plant Pathology</i> , 2018, 19, 1196-1209.	2.0	24
2249	Design of metalloproteins and novel protein folds using variational autoencoders. <i>Scientific Reports</i> , 2018, 8, 16189.	1.6	82
2250	The conserved mosaic prophage protein paratox inhibits the natural competence regulator ComR in Streptococcus. <i>Scientific Reports</i> , 2018, 8, 16535.	1.6	10
2251	Mechanistic insights into the interactions of NAP1 with the SKICH domains of NDP52 and TAX1BP1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11651-E11660.	3.3	41
2252	Adaptation of a Bacterial Multidrug Resistance System Revealed by the Structure and Function of AlbA. <i>Journal of the American Chemical Society</i> , 2018, 140, 16641-16649.	6.6	14
2253	Structural insights into the function of type VI secretion system TssA subunits. <i>Nature Communications</i> , 2018, 9, 4765.	5.8	41
2254	Ginsentides: Cysteine and Glycine-rich Peptides from the Ginseng Family with Unusual Disulfide Connectivity. <i>Scientific Reports</i> , 2018, 8, 16201.	1.6	26
2255	Structural dissection of sterol glycosyltransferase UGT51 from <i>Saccharomyces cerevisiae</i> for substrate specificity. <i>Journal of Structural Biology</i> , 2018, 204, 371-379.	1.3	19
2256	The N-Terminal GTPase Domain of p190RhoGAP Proteins Is a PseudoGTPase. <i>Structure</i> , 2018, 26, 1451-1461.e4.	1.6	10
2257	Crystal structure of native Î±-D-glucosyl-L-rhamnosidase from <i>Aspergillus terreus</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1078-1084.	1.1	17

#	ARTICLE	IF	CITATIONS
2258	Dynamics based clustering of globin family members. PLoS ONE, 2018, 13, e0208465.	1.1	5
2259	Structure-Guided Mechanisms Behind the Metabolism of 2,4,6-Trinitrotoluene by Glutathione Transferases U25 and U24 That Lead to Alternate Product Distribution. Frontiers in Plant Science, 2018, 9, 1846.	1.7	10
2260	The Structure of the Bifunctional Everninomicin Biosynthetic Enzyme EvdMO1 Suggests Independent Activity of the Fused Methyltransferase-Oxidase Domains. Biochemistry, 2018, 57, 6827-6837.	1.2	7
2261	Periplasmic protein EipA determines envelope stress resistance and virulence in <i>Brucella abortus</i> . Molecular Microbiology, 2019, 111, 637-661.	1.2	21
2262	Crystal Structure of Human Nocturnin Catalytic Domain. Scientific Reports, 2018, 8, 16294.	1.6	13
2263	A novel chlorination-induced ribonuclease YabJ from <i>Staphylococcus aureus</i> . Bioscience Reports, 2018, 38, .	1.1	12
2264	Design and implementation of structural bioinformatics projects for biological sciences undergraduate students. Biochemistry and Molecular Biology Education, 2018, 46, 547-554.	0.5	3
2265	Proteins across scales through graph partitioning: application to the major peanut allergen Ara h 1. Journal of Complex Networks, 2018, 6, 679-692.	1.1	0
2266	Structural characterization of 1-deoxy-D-xylulose 5-phosphate Reductoisomerase from <i>Vibrio vulnificus</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1209-1215.	1.1	1
2267	Biochemical and Structural Characterization of TesA, a Major Thioesterase Required for Outer-Envelope Lipid Biosynthesis in <i>Mycobacterium tuberculosis</i> . Journal of Molecular Biology, 2018, 430, 5120-5136.	2.0	22
2268	How bacterial xenogeneic silencer rok distinguishes foreign from self DNA in its resident genome. Nucleic Acids Research, 2018, 46, 10514-10529.	6.5	23
2269	A structural perspective on the PP-loop ATP pyrophosphatase family. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 607-622.	2.3	14
2270	Interface interactions between β -crystallin domain and IgA-like domain render Ca^{2+} binding site inoperative in abundant perithecial protein of <i>Neurospora crassa</i> . Molecular Microbiology, 2018, 110, 955-972.	1.2	3
2271	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. Cell, 2018, 175, 809-821.e19.	13.5	149
2272	A unique intra-molecular fidelity-modulating mechanism identified in a viral RNA-dependent RNA polymerase. Nucleic Acids Research, 2018, 46, 10840-10854.	6.5	16
2273	Salmonella Phage S16 Tail Fiber Adhesin Features a Rare Polyglycine Rich Domain for Host Recognition. Structure, 2018, 26, 1573-1582.e4.	1.6	69
2274	Structural characterization of the sporulation protein GerM from <i>Bacillus subtilis</i> . Journal of Structural Biology, 2018, 204, 481-490.	1.3	8
2275	Towards a comprehensive understanding of the structural dynamics of a bacterial diterpene synthase during catalysis. Nature Communications, 2018, 9, 3971.	5.8	57

#	ARTICLE	IF	CITATIONS
2276	Structural basis for specific calcium binding by the polycystic-kidney-disease domain of <i>Vibrio anguillarum</i> protease Epp. <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 471-477.	1.0	0
2277	Insights into a dual function amide oxidase/macrocyclase from lankacidin biosynthesis. <i>Nature Communications</i> , 2018, 9, 3998.	5.8	17
2278	The bacterial Ras/Rap1 site-specific endopeptidase RRSP cleaves Ras through an atypical mechanism to disrupt Ras-ERK signaling. <i>Science Signaling</i> , 2018, 11, .	1.6	39
2279	Conformational changes on substrate binding revealed by structures of <i>Methylobacterium extorquens</i> malate dehydrogenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 610-616.	0.4	8
2280	A structural investigation of NRZ mediated apoptosis regulation in zebrafish. <i>Cell Death and Disease</i> , 2018, 9, 967.	2.7	8
2281	Crystal structure of the periplasmic domain of TssL, a key membrane component of Type VI secretion system. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 1474-1479.	3.6	3
2282	Molecular Basis for Membrane Recruitment by the PX and C2 Domains of Class II Phosphoinositide 3-Kinase-C2 β . <i>Structure</i> , 2018, 26, 1612-1625.e4.	1.6	25
2283	Characteristics of the essential pathogenicity factor Rv1828, a MerR family transcription regulator from <i>Mycobacterium tuberculosis</i> . <i>FEBS Journal</i> , 2018, 285, 4424-4444.	2.2	6
2284	Structural and kinetic characterization of (S)-1-amino-2-propanol kinase from the aminoacetone utilization microcompartment of <i>Mycobacterium smegmatis</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 19909-19918.	1.6	14
2285	Transcription apparatus of the yeast virus-like elements: Architecture, function, and evolutionary origin. <i>PLoS Pathogens</i> , 2018, 14, e1007377.	2.1	13
2286	Structural and biochemical analysis of a NOT1 MIF4G-like domain of the CCR4-NOT complex. <i>Journal of Structural Biology</i> , 2018, 204, 388-395.	1.3	14
2287	Structural Analysis of Phosphoserine Aminotransferase (Isoform 1) From <i>Arabidopsis thaliana</i> the Enzyme Involved in the Phosphorylated Pathway of Serine Biosynthesis. <i>Frontiers in Plant Science</i> , 2018, 9, 876.	1.7	21
2288	Classifying Protein Specific Residue Structures Based on Graph Mining. <i>IEEE Access</i> , 2018, 6, 55828-55837.	2.6	3
2289	Structure of the Recombinant <i>Neisseria gonorrhoeae</i> Adhesin Complex Protein (rNg-ACP) and Generation of Murine Antibodies with Bactericidal Activity against Gonococci. <i>MSphere</i> , 2018, 3, .	1.3	17
2290	Structural basis for multiple gene regulation by human DUX4. <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 1161-1167.	1.0	7
2291	Structural, functional and biological insights into the role of <i>Mycobacterium tuberculosis</i> VapBC11 toxin-antitoxin system: targeting a tRNase to tackle mycobacterial adaptation. <i>Nucleic Acids Research</i> , 2018, 46, 11639-11655.	6.5	37
2292	A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition. <i>Molecular Cell</i> , 2018, 72, 700-714.e8.	4.5	25
2293	<i>Mycoplasma genitalium</i> adhesin P110 binds sialic-acid human receptors. <i>Nature Communications</i> , 2018, 9, 4471.	5.8	29

#	ARTICLE	IF	CITATIONS
2294	Structural insights into the architecture and membrane interactions of the conserved COMMD proteins. <i>ELife</i> , 2018, 7, .	2.8	28
2295	Ulvan lyase from <i>Formosa agariphila</i> and its applicability in depolymerisation of ulvan extracted from three different <i>Ulva</i> species. <i>Algal Research</i> , 2018, 36, 106-114.	2.4	21
2296	<i>Arabidopsis</i> AGDP1 links H3K9me2 to DNA methylation in heterochromatin. <i>Nature Communications</i> , 2018, 9, 4547.	5.8	66
2297	Crystal structure of an Lrs14-like archaeal biofilm regulator from <i>Sulfolobus acidocaldarius</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1105-1114.	1.1	4
2298	Archaic and alternative chaperones preserve pilin folding energy by providing incomplete structural information. <i>Journal of Biological Chemistry</i> , 2018, 293, 17070-17080.	1.6	5
2299	Molecular characterisation of Apolipoprotein III gene in <i>Samia cynthia ricini</i> and its roles in response to bacterial infection. <i>Journal of Invertebrate Pathology</i> , 2018, 159, 61-70.	1.5	12
2300	Structural and mechanistic insights into the function of the unconventional class XIV myosin MyoA from <i>Toxoplasma gondii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10548-E10555.	3.3	27
2301	The cyclic nucleotide-binding homology domain of the integral membrane protein CNNM mediates dimerization and is required for Mg ²⁺ efflux activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 19998-20007.	1.6	34
2302	Crystal structure of TcpK in complex with oriT DNA of the antibiotic resistance plasmid pCW3. <i>Nature Communications</i> , 2018, 9, 3732.	5.8	18
2303	Structural insights into antigen recognition of an anti- β -(1,6)- β -(1,3)-D-glucan antibody. <i>Scientific Reports</i> , 2018, 8, 13652.	1.6	7
2304	Dynamical comparison between myoglobin and hemoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1176-1183.	1.5	7
2305	Structure of the mechanosensitive OSCA channels. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 850-858.	3.6	133
2306	A fundamental catalytic difference between zinc and manganese dependent enzymes revealed in a bacterial isatin hydrolase. <i>Scientific Reports</i> , 2018, 8, 13104.	1.6	10
2307	The remote arginine promoting the dehydrogenation of glucose in glucose oxidase via a proton-coupled double-electron transfer mechanism. <i>Journal of Catalysis</i> , 2018, 367, 150-158.	3.1	6
2308	The Thaumarchaeon <i>N. gargensis</i> carries functional bioABD genes and has a promiscuous <i>E. coli</i> β -glucuronidase EstN1. <i>Scientific Reports</i> , 2018, 8, 13823.	1.6	11
2309	A partial reconstitution implicates DltD in catalyzing lipoteichoic acid d-alanylation. <i>Journal of Biological Chemistry</i> , 2018, 293, 17985-17996.	1.6	42
2310	Crystal structure of the <i>Acinetobacter baumannii</i> outer membrane protein Omp33. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 852-860.	1.1	8
2311	Application of alignment-free bioinformatics methods to identify an oomycete protein with structural and functional similarity to the bacterial AvrE effector protein. <i>PLoS ONE</i> , 2018, 13, e0195559.	1.1	16

#	ARTICLE	IF	CITATIONS
2312	Optimization of clinical uricase production by <i>Bacillus cereus</i> under submerged fermentation, its purification and structure characterization. <i>Process Biochemistry</i> , 2018, 75, 49-58.	1.8	8
2313	Structural features of a bacterial cyclic α -maltosyl-(1 \rightarrow 6)-maltose (CMM) hydrolase critical for CMM recognition and hydrolysis. <i>Journal of Biological Chemistry</i> , 2018, 293, 16874-16888.	1.6	7
2314	The crystal structure of an essential high-temperature requirement protein HtrA1 (Rv1223) from <i>Mycobacterium tuberculosis</i> reveals its unique features. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 906-921.	1.1	3
2315	Insights into the role of electrostatics in temperature adaptation: a comparative study of psychrophilic, mesophilic, and thermophilic subtilisin-like serine proteases. <i>RSC Advances</i> , 2018, 8, 29698-29713.	1.7	20
2316	The enzymes of microbial nicotine metabolism. <i>Beilstein Journal of Organic Chemistry</i> , 2018, 14, 2295-2307.	1.3	18
2317	Three metronidazole-resistant <i>Prevotella bivia</i> strains harbour a mobile element, encoding a novel <i>nim</i> gene, <i>nimK</i> , and an efflux small MDR transporter. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2687-2690.	1.3	22
2318	Unique N-terminal extension domain of human asparaginyl-tRNA synthetase elicits CCR3-mediated chemokine activity. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 835-845.	3.6	12
2319	Structural Analysis of the Arabidopsis AL2-PAL and PRC1 Complex Provides Mechanistic Insight into Active-to-Repressive Chromatin State Switch. <i>Journal of Molecular Biology</i> , 2018, 430, 4245-4259.	2.0	11
2320	Substrate-assisted enzymatic formation of lysinoalanine in duramycin. <i>Nature Chemical Biology</i> , 2018, 14, 928-933.	3.9	25
2321	Architecture of the native major royal jelly protein 1 oligomer. <i>Nature Communications</i> , 2018, 9, 3373.	5.8	47
2322	Structure of the <i>Cladosporium fulvum</i> Avr4 effector in complex with (GlcNAc) ₆ reveals the ligand-binding mechanism and uncouples its intrinsic function from recognition by the Cf-4 resistance protein. <i>PLoS Pathogens</i> , 2018, 14, e1007263.	2.1	37
2323	Modeling, dynamics and phosphoinositide binding of the pleckstrin homology domain of two novel PLCs: $\hat{1}$ -1 and $\hat{1}$ -2. <i>Journal of Molecular Graphics and Modelling</i> , 2018, 85, 130-144.	1.3	1
2324	The Characterization of Different Flavodoxin Reductase-Flavodoxin (FNR-Fld) Interactions Reveals an Efficient FNR-Fld Redox Pair and Identifies a Novel FNR Subclass. <i>Biochemistry</i> , 2018, 57, 5427-5436.	1.2	9
2325	GH43 endo-arabinanase from <i>Bacillus licheniformis</i> : Structure, activity and unexpected synergistic effect on cellulose enzymatic hydrolysis. <i>International Journal of Biological Macromolecules</i> , 2018, 117, 7-16.	3.6	10
2326	Structural characterizations of human periostin dimerization and cysteinylation. <i>FEBS Letters</i> , 2018, 592, 1789-1803.	1.3	16
2327	X-ray crystal structures of the type IVb secretion system DotB ATPases. <i>Protein Science</i> , 2018, 27, 1464-1475.	3.1	15
2328	Membrane association of monotopic phosphoglycosyl transferase underpins function. <i>Nature Chemical Biology</i> , 2018, 14, 538-541.	3.9	39
2329	A Hyperthermophilic Phage Decoration Protein Suggests Common Evolutionary Origin with Herpesvirus Triplex Proteins and an Anti-CRISPR Protein. <i>Structure</i> , 2018, 26, 936-947.e3.	1.6	20

#	ARTICLE	IF	CITATIONS
2330	In Silico Analysis of Natural Resistance-Associated Macrophage Protein (NRAMP) Family of Transporters in Rice. <i>Protein Journal</i> , 2018, 37, 237-247.	0.7	44
2331	The crystal structure of P450-TT heme-domain provides the first structural insights into the versatile class VII P450s. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 846-850.	1.0	13
2332	The trimeric solution structure and fucose-binding mechanism of the core fucosylation-specific lectin PhoSL. <i>Scientific Reports</i> , 2018, 8, 7740.	1.6	14
2333	mTM-align: a server for fast protein structure database search and multiple protein structure alignment. <i>Nucleic Acids Research</i> , 2018, 46, W380-W386.	6.5	70
2334	Integrated proteomics, genomics, metabolomics approaches reveal oxalic acid as pathogenicity factor in <i>Tilletia indica</i> inciting Karnal bunt disease of wheat. <i>Scientific Reports</i> , 2018, 8, 7826.	1.6	21
2335	Structural and Biochemical Studies of a Biocatalyst for the Enzymatic Production of Wax Esters. <i>ACS Catalysis</i> , 2018, 8, 6334-6344.	5.5	15
2336	Structural basis for the recognition of complex-type N-glycans by Endoglycosidase S. <i>Nature Communications</i> , 2018, 9, 1874.	5.8	38
2337	Structure and Kinetics of the S-(+)-1-Amino-2-propanol Dehydrogenase from the RMM Microcompartment of <i>Mycobacterium smegmatis</i> . <i>Biochemistry</i> , 2018, 57, 3780-3789.	1.2	16
2338	PgaB orthologues contain a glycoside hydrolase domain that cleaves deacetylated poly- β -(1,6)-N-acetylglucosamine and can disrupt bacterial biofilms. <i>PLoS Pathogens</i> , 2018, 14, e1006998.	2.1	59
2339	Flagella-mediated secretion of a novel <i>Vibrio cholerae</i> cytotoxin affecting both vertebrate and invertebrate hosts. <i>Communications Biology</i> , 2018, 1, 59.	2.0	43
2340	Structural and functional analysis of Dickkopf 4 (Dkk4): New insights into Dkk evolution and regulation of Wnt signaling by Dkk and Kremen proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 12149-12166.	1.6	26
2341	Differences in substrate specificity of <i>V. cholerae</i> FabH enzymes suggest new approaches for the development of novel antibiotics and biofuels. <i>FEBS Journal</i> , 2018, 285, 2900-2921.	2.2	3
2342	Structural basis of L-glucose oxidation by scyllo-inositol dehydrogenase: Implications for a novel enzyme subfamily classification. <i>PLoS ONE</i> , 2018, 13, e0198010.	1.1	10
2343	Structural basis of product inhibition by arabinose and xylose of the thermostable GH43 β -1,4-xylosidase from <i>Geobacillus thermoleovorans</i> IT-08. <i>PLoS ONE</i> , 2018, 13, e0196358.	1.1	25
2344	Crystal structure of the flavin reductase of <i>Acinetobacter baumannii</i> p-hydroxyphenylacetate 3-hydroxylase (HPAH) and identification of amino acid residues underlying its regulation by aromatic ligands. <i>Archives of Biochemistry and Biophysics</i> , 2018, 653, 24-38.	1.4	6
2345	Recognition of Complex Core-Fucosylated N-Glycans by a Mini Lectin. <i>Angewandte Chemie</i> , 2018, 130, 10335-10338.	1.6	2
2346	BrlR from <i>Pseudomonas aeruginosa</i> is a receptor for both cyclic di-GMP and pyocyanin. <i>Nature Communications</i> , 2018, 9, 2563.	5.8	33
2347	Recognition of Complex Core-Fucosylated N-Glycans by a Mini Lectin. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 10178-10181.	7.2	15

#	ARTICLE	IF	CITATIONS
2348	Identification of a novel tRNA wobble uridine modifying activity in the biosynthesis of 5-methoxyuridine. <i>Nucleic Acids Research</i> , 2018, 46, 9160-9169.	6.5	13
2349	The universally conserved GTPase HflX is an RNA helicase that restores heat-damaged <i>Escherichia coli</i> ribosomes. <i>Journal of Cell Biology</i> , 2018, 217, 2519-2529.	2.3	29
2350	Functional plasticity of antibacterial EndoU toxins. <i>Molecular Microbiology</i> , 2018, 109, 509-527.	1.2	25
2351	Structural basis for the substrate recognition of peptidoglycan pentapeptides by <i>Enterococcus faecalis</i> VanYB. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 335-344.	3.6	5
2352	Description of a Non-Canonical Mn(II)-Oxidation Site in Peroxidases. <i>ACS Catalysis</i> , 2018, 8, 8386-8395.	5.5	21
2353	Molecular Basis for the Final Oxidative Rearrangement Steps in Chartreusin Biosynthesis. <i>Journal of the American Chemical Society</i> , 2018, 140, 10909-10914.	6.6	26
2354	Evolutionary convergence in the biosyntheses of the imidazole moieties of histidine and purines. <i>PLoS ONE</i> , 2018, 13, e0196349.	1.1	35
2355	Structural characterization of the hypothetical protein Lpg2622, a new member of the C1 family peptidases from <i>Legionella pneumophila</i> . <i>FEBS Letters</i> , 2018, 592, 2798-2810.	1.3	4
2356	Chloroplastic Serine Hydroxymethyltransferase From <i>Medicago truncatula</i> : A Structural Characterization. <i>Frontiers in Plant Science</i> , 2018, 9, 584.	1.7	18
2357	Structural Basis of Substrate Recognition and Covalent Inhibition of Cdu1 from <i>Chlamydia trachomatis</i> . <i>ChemMedChem</i> , 2018, 13, 2014-2023.	1.6	8
2358	Crystal structure of the <i>Streptococcus agalactiae</i> CAMP factor provides insights into its membrane-permeabilizing activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 11867-11877.	1.6	14
2359	Functional insights into the <i>Streptococcus pneumoniae</i> HicBA toxin-antitoxin system based on a structural study. <i>Nucleic Acids Research</i> , 2018, 46, 6371-6386.	6.5	32
2360	Widespread anti-CRISPR proteins in virulent bacteriophages inhibit a range of Cas9 proteins. <i>Nature Communications</i> , 2018, 9, 2919.	5.8	147
2361	Solution structure of a ubiquitin-like protein from <i>Trypanosoma brucei</i> . <i>Protein Science</i> , 2018, 27, 1831-1836.	3.1	0
2362	The Loss of Expression of a Single Type 3 Effector (CT622) Strongly Reduces <i>Chlamydia trachomatis</i> Infectivity and Growth. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 145.	1.8	21
2363	Structural and Biochemical Characterization of BdsA from <i>Bacillus subtilis</i> WU-S2B, a Key Enzyme in the 4S-Desulfurization Pathway. <i>Frontiers in Microbiology</i> , 2018, 9, 231.	1.5	16
2364	Open Conformation of the <i>Escherichia coli</i> Periplasmic Murein Tripeptide Binding Protein, MppA, at High Resolution. <i>Biology</i> , 2018, 7, 30.	1.3	2
2365	2-Deoxyribosyltransferase from <i>Bacillus psychrosaccharolyticus</i> : A Mesophilic-Like Biocatalyst for the Synthesis of Modified Nucleosides from a Psychrotolerant Bacterium. <i>Catalysts</i> , 2018, 8, 8.	1.6	18

#	ARTICLE	IF	CITATIONS
2366	A Toxin-Antitoxin System VapBC15 from <i>Synechocystis</i> sp. PCC 6803 Shows Distinct Regulatory Features. <i>Genes</i> , 2018, 9, 173.	1.0	5
2367	A conserved human DJ1-subfamily motif (DJSM) is critical for anti-oxidative and deglycase activities of <i>Plasmodium falciparum</i> DJ1. <i>Molecular and Biochemical Parasitology</i> , 2018, 222, 70-80.	0.5	9
2368	<i>Legionella pneumophila</i> effector Lem4 is a membrane-associated protein tyrosine phosphatase. <i>Journal of Biological Chemistry</i> , 2018, 293, 13044-13058.	1.6	14
2369	Bent conformation of a backbone pilin N-terminal domain supports a three-stage pilus assembly mechanism. <i>Communications Biology</i> , 2018, 1, 94.	2.0	9
2370	In vitro genomic and proteomic evidence of a type IV pili-like structure in the fish pathogen <i>Piscirickettsia salmonis</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	9
2371	A positive-charged patch and stabilized hydrophobic core are essential for avirulence function of AvrPib in the rice blast fungus. <i>Plant Journal</i> , 2018, 96, 133-146.	2.8	49
2372	<i>Pseudomonas aeruginosa</i> pyoverdine maturation enzyme PvdP has a noncanonical domain architecture and affords insight into a new subclass of tyrosinases. <i>Journal of Biological Chemistry</i> , 2018, 293, 14926-14936.	1.6	14
2373	Functional Profiling and Crystal Structures of Isothiocyanate Hydrolases Found in Gut-Associated and Plant-Pathogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
2374	Identification of a pyrophosphate-dependent kinase and its donor selectivity determinants. <i>Nature Communications</i> , 2018, 9, 1765.	5.8	17
2375	Structure and mechanism of the two-component α -helical pore-forming toxin YaxAB. <i>Nature Communications</i> , 2018, 9, 1806.	5.8	46
2376	Structural insight into the role of VAL1 B3 domain for targeting to FLC locus in <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 415-422.	1.0	11
2377	Investigating Cytochrome P450 specificity during glycopeptide antibiotic biosynthesis through a homologue hybridization approach. <i>Journal of Inorganic Biochemistry</i> , 2018, 185, 43-51.	1.5	8
2378	Structure, computational and biochemical analysis of PcCel45A endoglucanase from <i>Phanerochaete chrysosporium</i> and catalytic mechanisms of GH45 subfamily C members. <i>Scientific Reports</i> , 2018, 8, 3678.	1.6	14
2379	Higher order scaffoldin assembly in <i>Ruminococcus flavefaciens</i> cellulosome is coordinated by a discrete cohesin-dockerin interaction. <i>Scientific Reports</i> , 2018, 8, 6987.	1.6	6
2380	A bipartite periplasmic receptor-diguanylate cyclase pair (XAC2383-XAC2382) in the bacterium <i>Xanthomonas citri</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 10767-10781.	1.6	2
2381	Lessons from my undergraduate research students. <i>Journal of Biological Chemistry</i> , 2018, 293, 10447-10452.	1.6	24
2382	Cloning and characterization of a chitinase from <i>Thermobifida fusca</i> reveals Tfu_0580 as a thermostable and acidic endochitinase. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 19, e00274.	2.1	17
2383	PrgB promotes aggregation, biofilm formation, and conjugation through DNA binding and compaction. <i>Molecular Microbiology</i> , 2018, 109, 291-305.	1.2	31

#	ARTICLE	IF	CITATIONS
2384	Structures of glycolate oxidase from <i>Nicotiana benthamiana</i> reveal a conserved pH sensor affecting the binding of FMN. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 3050-3056.	1.0	6
2385	Proteobacterial Origin of Protein Arginine Methylation and Regulation of Complex I Assembly by MidA. <i>Cell Reports</i> , 2018, 24, 1996-2004.	2.9	10
2386	The tuberous sclerosis complex subunit TBC1D7 is stabilized by Akt phosphorylation-mediated 14-3-3 binding. <i>Journal of Biological Chemistry</i> , 2018, 293, 16142-16159.	1.6	11
2387	Structural insights into inhibitor binding to a fungal ortholog of aspartate semialdehyde dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 2848-2854.	1.0	9
2388	Structural insight into molecular mechanism of cytokinin activating protein from <i>Pseudomonas aeruginosa</i> PAO1. <i>Environmental Microbiology</i> , 2018, 20, 3214-3223.	1.8	11
2389	The 3-D structure of VNG0258H/RosR – A haloarchaeal DNA-binding protein in its ionic shell. <i>Journal of Structural Biology</i> , 2018, 204, 191-198.	1.3	7
2390	Identification, Characterization, and X-ray Crystallographic Analysis of a Novel Type of Lectin AJLec from the Sea Anemone <i>Anthopleura japonica</i> . <i>Scientific Reports</i> , 2018, 8, 11516.	1.6	8
2391	Biochemical and Structural Insights into an Fe(II)-Ketoglutarate/O ₂ -Dependent Dioxygenase, Kdo 3-Hydroxylase (KdoO). <i>Journal of Molecular Biology</i> , 2018, 430, 4036-4048.	2.0	1
2392	Structure of paused transcription complex Pol II-DSIF-NELF. <i>Nature</i> , 2018, 560, 601-606.	13.7	262
2393	Structural and biochemical characterization of a multidomain alginate lyase reveals a novel role of CBM32 in CAZymes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1862-1869.	1.1	55
2394	The archaeal ATPase PINA interacts with the helicase Hjm via its carboxyl terminal KH domain remodeling and processing replication fork and Holliday junction. <i>Nucleic Acids Research</i> , 2018, 46, 6627-6641.	6.5	19
2395	Structure and analysis of nucleoside diphosphate kinase from <i>Borrelia burgdorferi</i> prepared in a transition-state complex with ADP and vanadate moieties. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 373-384.	0.4	1
2396	The Intracellular Loop of the Na ⁺ /Ca ²⁺ Exchanger Contains an Awareness Ribbon-Shaped Two-Helix Bundle Domain. <i>Biochemistry</i> , 2018, 57, 5096-5104.	1.2	9
2397	The crystal structure of the <i>Helicobacter pylori</i> LlalI.R1 N-terminal domain provides a model for site-specific DNA binding. <i>Journal of Biological Chemistry</i> , 2018, 293, 11758-11771.	1.6	6
2398	High-resolution crystal structures reveal a mixture of conformers of the Gly61-Asp62 peptide bond in an oxidized flavodoxin from <i>Bacillus cereus</i> . <i>Protein Science</i> , 2018, 27, 1439-1449.	3.1	6
2399	Vms1p is a release factor for the ribosome-associated quality control complex. <i>Nature Communications</i> , 2018, 9, 2197.	5.8	80
2400	Biosynthesis of the nickel-pincer nucleotide cofactor of lactate racemase requires a CTP-dependent cyclometallase. <i>Journal of Biological Chemistry</i> , 2018, 293, 12303-12317.	1.6	31
2401	Crystal structure of WA352 provides insight into cytoplasmic male sterility in rice. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 898-904.	1.0	8

#	ARTICLE	IF	CITATIONS
2402	A Rich Man, Poor Man Story of <i>S</i> -Adenosylmethionine and Cobalamin Revisited. Annual Review of Biochemistry, 2018, 87, 555-584.	5.0	52
2403	Structure of a lipid-bound viral membrane assembly protein reveals a modality for enclosing the lipid bilayer. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7028-7032.	3.3	9
2404	A pseudo-receiver domain in Atg32 is required for mitophagy. Autophagy, 2018, 14, 1620-1628.	4.3	21
2405	Crystal structure of the central and the C-terminal RNase domains of colicin D implicated its translocation pathway through inner membrane of target cell. Journal of Biochemistry, 2018, 164, 329-339.	0.9	6
2406	Crystal structure of <i>Arabidopsis thaliana</i> RabA1a. Journal of Integrative Plant Biology, 2019, 61, 93-109.	4.1	1
2407	Homologous Protein Detection. , 2019, , 697-705.		2
2408	Protein Functional Annotation. , 2019, , 8-14.		0
2409	Computational Tools for Structural Analysis of Proteins. , 2019, , 539-549.		0
2410	Genome Analysis – Identification of Genes Involved in Host-Pathogen Protein-Protein Interaction Networks. , 2019, , 410-424.		0
2411	A quantitative map of protein sequence space for the cis-defensin superfamily. Bioinformatics, 2019, 35, 743-752.	1.8	27
2412	The crystal structure of the phytopathogenic bacterial sensor PcrK reveals different cytokinin recognition mechanism from the plant sensor AHK4. Journal of Structural Biology, 2019, 208, 69-76.	1.3	6
2413	Crystal structures of AztD provide mechanistic insights into direct zinc transfer between proteins. Communications Biology, 2019, 2, 308.	2.0	7
2414	Structural characterization of Class 2 OLD family nucleases supports a two-metal catalysis mechanism for cleavage. Nucleic Acids Research, 2019, 47, 9448-9463.	6.5	36
2415	Cell-to-cell interaction requires optimal positioning of a pilus tip adhesin modulated by gram-positive transpeptidase enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18041-18049.	3.3	21
2416	Ega3 from the fungal pathogen <i>Aspergillus fumigatus</i> is an endo- β -1,4-galactosaminidase that disrupts microbial biofilms. Journal of Biological Chemistry, 2019, 294, 13833-13849.	1.6	35
2417	Structural insights into the binding mechanism of <i>Plasmodium falciparum</i> exported Hsp40-Hsp70 chaperone pair. Computational Biology and Chemistry, 2019, 83, 107099.	1.1	10
2418	Membrane protein-regulated networks across human cancers. Nature Communications, 2019, 10, 3131.	5.8	67
2419	The structure of <i>Acinetobacter</i> -secreted protease CpaA complexed with its chaperone CpaB reveals a novel mode of a T2SS chaperone-substrate interaction. Journal of Biological Chemistry, 2019, 294, 13344-13354.	1.6	13

#	ARTICLE	IF	CITATIONS
2420	An Asymmetric Reductase That Intercepts Acyclic Imino Acids Produced <i>in Situ</i> by a Partner Oxidase. <i>Journal of the American Chemical Society</i> , 2019, 141, 12258-12267.	6.6	5
2421	Crystal structures of <i>Trypanosoma brucei</i> hypoxanthine-guanine-xanthine phosphoribosyltransferase in complex with IMP, GMP and XMP. <i>FEBS Journal</i> , 2019, 286, 4721-4736.	2.2	9
2422	Structural characterization of life-extending <i>Caenorhabditis elegans</i> Lipid Binding Protein 8. <i>Scientific Reports</i> , 2019, 9, 9966.	1.6	8
2423	Solution NMR structure and ligand identification of human Gas7 SH3 domain reveal a typical SH3 fold but a non-canonical ligand-binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 1190-1195.	1.0	0
2424	Structural characterization of <i>Treponema pallidum</i> Tp0225 reveals an unexpected leucine-rich repeat architecture. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 489-495.	0.4	5
2425	Crystal Structure of the Japanese Encephalitis Virus Capsid Protein. <i>Viruses</i> , 2019, 11, 623.	1.5	32
2426	Structural basis for stereoselective dehydration and hydrogen-bonding catalysis by the SAM-dependent pericyclase LepI. <i>Nature Chemistry</i> , 2019, 11, 812-820.	6.6	42
2427	Substrate Affinity and Specificity of the ScSth1p Bromodomain Are Fine-Tuned for Versatile Histone Recognition. <i>Structure</i> , 2019, 27, 1460-1468.e3.	1.6	2
2428	Structures of TOG1 and TOG2 from the human microtubule dynamics regulator CLASP1. <i>PLoS ONE</i> , 2019, 14, e0219823.	1.1	15
2429	An Unprecedented Cyclization Mechanism in the Biosynthesis of Carbazole Alkaloids in <i>Streptomyces</i> . <i>Angewandte Chemie - International Edition</i> , 2019, 58, 13349-13353.	7.2	17
2430	The N-Terminal Domain of NPHP1 Folds into a Monomeric Left-Handed Antiparallel Three-Stranded Coiled Coil with Anti-apoptotic Function. <i>ACS Chemical Biology</i> , 2019, 14, 1845-1854.	1.6	4
2431	An Unprecedented Cyclization Mechanism in the Biosynthesis of Carbazole Alkaloids in <i>Streptomyces</i> . <i>Angewandte Chemie</i> , 2019, 131, 13483-13487.	1.6	2
2432	<i>Burkholderia pseudomallei</i> d-Alanine-d-Alanine ligase; detailed characterisation and assessment of a potential antibiotic drug target. <i>FEBS Journal</i> , 2019, 286, 4509-4524.	2.2	4
2433	Impact of hepatitis B virus genotype F on <i>in vitro</i> diagnosis: detection efficiency of HBsAg from Amerindian subgenotypes F1b and F4. <i>Archives of Virology</i> , 2019, 164, 2297-2307.	0.9	5
2434	Crystal Structure of the Ergothioneine Sulfoxide Synthase from <i>Candidatus Chloracidobacterium thermophilum</i> and Structure-Guided Engineering To Modulate Its Substrate Selectivity. <i>ACS Catalysis</i> , 2019, 9, 6955-6961.	5.5	18
2435	<i>Vibrio cholerae</i> YaeO is a Structural Homologue of RNA Chaperone Hfq that Inhibits Rho-dependent Transcription Termination by Dissociating its Hexameric State. <i>Journal of Molecular Biology</i> , 2019, 431, 4749-4766.	2.0	8
2436	Convergent Evolution of the Barnase/EndoU/Colicin/RelE (BECR) Fold in Antibacterial tRNase Toxins. <i>Structure</i> , 2019, 27, 1660-1674.e5.	1.6	22
2437	The 1.9 Å... crystal structure of the extracellular matrix protein Bap1 from <i>Vibrio cholerae</i> provides insights into bacterial biofilm adhesion. <i>Journal of Biological Chemistry</i> , 2019, 294, 14499-14511.	1.6	13

#	ARTICLE	IF	CITATIONS
2438	The Molecular Mechanism of Cellular Attachment for an Archaeal Virus. <i>Structure</i> , 2019, 27, 1634-1646.e3.	1.6	21
2439	Combining Transient Expression and Cryo-EM to Obtain High-Resolution Structures of Luteovirid Particles. <i>Structure</i> , 2019, 27, 1761-1770.e3.	1.6	23
2440	Reprogramming Bacteriophage Host Range through Structure-Guided Design of Chimeric Receptor Binding Proteins. <i>Cell Reports</i> , 2019, 29, 1336-1350.e4.	2.9	135
2441	Streptococcal phosphotransferase system imports unsaturated hyaluronan disaccharide derived from host extracellular matrices. <i>PLoS ONE</i> , 2019, 14, e0224753.	1.1	10
2442	Atomic Structure of the Francisella T6SS Central Spike Reveals a Unique α -Helical Lid and a Putative Cargo. <i>Structure</i> , 2019, 27, 1811-1819.e6.	1.6	6
2443	How BamA recruits OMP substrates via poly-POTRAs domain. <i>FASEB Journal</i> , 2019, 33, 14690-14702.	0.2	3
2444	A Potent Anti-SpuE Antibody Allosterically Inhibits Type III Secretion System and Attenuates Virulence of <i>Pseudomonas Aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 4882-4896.	2.0	9
2445	Polarisome scaffold Spa2-mediated macromolecular condensation of Aip5 for actin polymerization. <i>Nature Communications</i> , 2019, 10, 5078.	5.8	34
2446	Structure and regulation of ZCCHC4 in m6A-methylation of 28S rRNA. <i>Nature Communications</i> , 2019, 10, 5042.	5.8	72
2447	Deciphering the Structural Basis of High Thermostability of Dehalogenase from Psychrophilic Bacterium <i>Marinobacter</i> sp. ELB17. <i>Microorganisms</i> , 2019, 7, 498.	1.6	18
2448	C-terminal Redox Domain of Arabidopsis APR1 is a Non-Canonical Thioredoxin Domain with Glutaredoxin Function. <i>Antioxidants</i> , 2019, 8, 461.	2.2	4
2449	Crystal structure of the Siderophore-interacting protein SIP from <i>Aeromonas hydrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 23-28.	1.0	2
2450	A Novel Way of Comparing Protein 3D Structure Using Graph Partitioning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1361-1368.	1.9	1
2451	Structural and biochemical characterization of iminodiacetate oxidase from <i>Chelativorans</i> sp. BNC1. <i>Molecular Microbiology</i> , 2019, 112, 1863-1874.	1.2	1
2452	Structural and Biochemical Characterization of the YaxAB Pore-forming Toxin from <i>Yersinia Enterocolitica</i> . <i>Springer Theses</i> , 2019, , .	0.0	0
2453	Comparison of <i>Candida Albicans</i> Fatty Acid Amide Hydrolase Structure with Homologous Amidase Signature Family Enzymes. <i>Crystals</i> , 2019, 9, 472.	1.0	2
2454	Interaction of the Ankyrin H Core Effector of <i>Legionella</i> with the Host LARP7 Component of the 7SK snRNP Complex. <i>MBio</i> , 2019, 10, .	1.8	27
2455	Structural and functional insight into the <i>Mycobacterium tuberculosis</i> protein PrpR reveals a novel type of transcription factor. <i>Nucleic Acids Research</i> , 2019, 47, 9934-9949.	6.5	18

#	ARTICLE	IF	CITATIONS
2456	Structural and functional characterization of a novel cold-active S-formylglutathione hydrolase (SfSFGH) homolog from <i>Shewanella frigidimarina</i> , a psychrophilic bacterium. <i>Microbial Cell Factories</i> , 2019, 18, 140.	1.9	11
2457	Measuring similarity between gene interaction profiles. <i>BMC Bioinformatics</i> , 2019, 20, 435.	1.2	3
2458	Structural and functional evidence that lipoprotein LpqN supports cell envelope biogenesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 15711-15723.	1.6	14
2459	Structural and functional analyses of the lipase CinB from <i>Enterobacter asburiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 519, 274-279.	1.0	4
2460	A Bacterial Effector Mimics a Host HSP90 Client to Undermine Immunity. <i>Cell</i> , 2019, 179, 205-218.e21.	13.5	53
2461	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <i>Nature Communications</i> , 2019, 10, 4288.	5.8	65
2462	Structural insight into human N6amt1 Trm112 complex functioning as a protein methyltransferase. <i>Cell Discovery</i> , 2019, 5, 51.	3.1	26
2463	RUPEE: A fast and accurate purely geometric protein structure search. <i>PLoS ONE</i> , 2019, 14, e0213712.	1.1	37
2464	Molecular features of lipoprotein CD0873: A potential vaccine against the human pathogen <i>Clostridioides difficile</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 15850-15861.	1.6	34
2465	An alternative plant-like cyanobacterial ferredoxin with unprecedented structural and functional properties. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 148084.	0.5	13
2466	Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. <i>Science</i> , 2019, 366, 100-104.	6.0	90
2467	Crystal structure and ligand identification of odorant binding protein 4 in the natural predator <i>Chrysopa pallens</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 141, 1004-1012.	3.6	10
2468	Structure of tRNA methyltransferase complex of Trm7 and Trm734 reveals a novel binding interface for tRNA recognition. <i>Nucleic Acids Research</i> , 2019, 47, 10942-10955.	6.5	18
2469	The structure of a highly-conserved picocyanobacterial protein reveals a Tudor domain with an RNA-binding function. <i>Journal of Biological Chemistry</i> , 2019, 294, 14333-14344.	1.6	3
2470	Structural characterization of a putative diguanylate cyclase conserved in hyperthermophiles. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 114-119.	1.0	0
2471	Structural basis for chain release from the enacyloxin polyketide synthase. <i>Nature Chemistry</i> , 2019, 11, 913-923.	6.6	39
2472	Structural Basis for the Selective Inhibition of Cdc2-Like Kinases by CX-4945. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	20
2473	Testosterone meets albumin – the molecular mechanism of sex hormone transport by serum albumins. <i>Chemical Science</i> , 2019, 10, 1607-1618.	3.7	38

#	ARTICLE	IF	CITATIONS
2474	NMR structure of a non-conjugatable, ADP-ribosylation associated, ubiquitin-like domain from <i>Tetrahymena thermophila</i> polyubiquitin locus. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 749-759.	1.1	1
2475	Catalytic mechanism for the conversion of salicylate into catechol by the flavin-dependent monooxygenase salicylate hydroxylase. <i>International Journal of Biological Macromolecules</i> , 2019, 129, 588-600.	3.6	26
2476	Structure of the DP1â€“DP2 PolD complex bound with DNA and its implications for the evolutionary history of DNA and RNA polymerases. <i>PLoS Biology</i> , 2019, 17, e3000122.	2.6	30
2477	Toxin Î¶ Reduces the ATP and Modulates the Uridine Diphosphate-N-acetylglucosamine Pool. <i>Toxins</i> , 2019, 11, 29.	1.5	6
2478	Near-atomic structure of a giant virus. <i>Nature Communications</i> , 2019, 10, 388.	5.8	61
2479	Structural Basis of Karrikin and Non-natural Strigolactone Perception in <i>Physcomitrella patens</i> . <i>Cell Reports</i> , 2019, 26, 855-865.e5.	2.9	61
2480	Illuminating the catalytic core of ectoine synthase through structural and biochemical analysis. <i>Scientific Reports</i> , 2019, 9, 364.	1.6	30
2481	Complementary Proteomics, Genomics approaches identifies potential pathogenicity/virulence factors in <i>Tilletia indica</i> induced under the influence of host factor. <i>Scientific Reports</i> , 2019, 9, 553.	1.6	16
2482	Designating ligand specificities to metal uptake ABC transporters in <i>Thermus thermophilus</i> HB8. <i>Metallomics</i> , 2019, 11, 597-612.	1.0	15
2483	Combinatorial recognition of clustered RNA elements by the multidomain RNA-binding protein IMP3. <i>Nature Communications</i> , 2019, 10, 2266.	5.8	53
2484	Crystallographic structure and molecular dynamics simulations of the major endoglucanase from <i>Xanthomonas campestris</i> pv. <i>campestris</i> shed light on its oligosaccharide products release pattern. <i>International Journal of Biological Macromolecules</i> , 2019, 136, 493-502.	3.6	5
2485	The heme-sensitive regulator SbnI has a bifunctional role in staphyloferrin B production by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 11622-11636.	1.6	11
2486	The pneumococcal Î¶X activator, ComW, is a DNA-binding protein critical for natural transformation. <i>Journal of Biological Chemistry</i> , 2019, 294, 11101-11118.	1.6	8
2487	The cholesterol transfer protein GRAMD1A regulates autophagosome biogenesis. <i>Nature Chemical Biology</i> , 2019, 15, 710-720.	3.9	59
2488	One-step immobilization-purification of enzymes by carbohydrate-binding module family 56 tag fusion. <i>Food Chemistry</i> , 2019, 299, 125037.	4.2	28
2489	Structural basis for recognition and ring-cleavage of the <i>Pseudomonas</i> quinolone signal (PQS) by Aqdc, a mycobacterial dioxygenase of the Î±/Î²-hydrolase fold family. <i>Journal of Structural Biology</i> , 2019, 207, 287-294.	1.3	11
2490	Structural basis for the homotypic fusion of chlamydial inclusions by the SNARE-like protein IncA. <i>Nature Communications</i> , 2019, 10, 2747.	5.8	16
2491	Inhibition of CRISPR-Cas9 ribonucleoprotein complex assembly by anti-CRISPR AcrIIIC2. <i>Nature Communications</i> , 2019, 10, 2806.	5.8	50

#	ARTICLE	IF	CITATIONS
2492	A unified structural model of the mammalian translocator protein (TSPO). <i>Journal of Biomolecular NMR</i> , 2019, 73, 347-364.	1.6	12
2493	Structures of 2-Hydroxyisobutyric Acid-CoA Ligase Reveal Determinants of Substrate Specificity and Describe a Multi-Conformational Catalytic Cycle. <i>Journal of Molecular Biology</i> , 2019, 431, 2747-2761.	2.0	12
2494	Structural features of cold-adapted dimeric GH2 β -D-galactosidase from <i>Arthrobacter</i> sp. 32cB. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 776-786.	1.1	18
2495	Structural comparison strengthens the higher-order classification of proteases related to chymotrypsin. <i>PLoS ONE</i> , 2019, 14, e0216659.	1.1	16
2496	Structural insights into the modulatory role of the accessory protein WYL1 in the Type VI-D CRISPR-Cas system. <i>Nucleic Acids Research</i> , 2019, 47, 5420-5428.	6.5	26
2497	Distinctive ligand-binding specificities of tandem PA14 biomass-sensory elements from <i>Clostridium thermocellum</i> and <i>Clostridium clariflavum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 917-930.	1.5	8
2498	SARAF Luminal Domain Structure Reveals a Novel Domain-Swapped β -Sandwich Fold Important for SOCE Modulation. <i>Journal of Molecular Biology</i> , 2019, 431, 2869-2883.	2.0	12
2499	Structure and Properties of a Natural Competence-Associated Pilin Suggest a Unique Pilus Tip-Associated DNA Receptor. <i>MBio</i> , 2019, 10, .	1.8	23
2500	Structural and immunological characterization of a new nucleotidyltransferase-like antigen from <i>Paracoccidioides brasiliensis</i> . <i>Molecular Immunology</i> , 2019, 112, 151-162.	1.0	5
2501	Structural and functional studies on <i>Salmonella</i> β -pyridoxal kinase: the first structural evidence for the formation of Schiff base with the substrate. <i>FEBS Journal</i> , 2019, 286, 3684-3700.	2.2	8
2502	Crystal structure of CntK, the cofactor-independent histidine racemase in staphylopine-mediated metal acquisition of <i>Staphylococcus aureus</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 135, 725-733.	3.6	11
2503	Bacterial Tetrabromopyrrole Debrominase Shares a Reductive Dehalogenation Strategy with Human Thyroid Deiodinase. <i>Biochemistry</i> , 2019, 58, 5329-5338.	1.2	13
2504	Alternative β /anti- β factors represent a unique form of bacterial β /anti- β complex. <i>Nucleic Acids Research</i> , 2019, 47, 5988-5997.	6.5	19
2505	Bacterial pseudokinase catalyzes protein polyglutamylation to inhibit the SidE-family ubiquitin ligases. <i>Science</i> , 2019, 364, 787-792.	6.0	111
2506	Structural basis for catalysis and substrate specificity of a 3C-like cysteine protease from a mosquito mesonivirus. <i>Virology</i> , 2019, 533, 21-33.	1.1	10
2507	Molecular Basis of Arthritogenic Alphavirus Receptor MXRA8 Binding to Chikungunya Virus Envelope Protein. <i>Cell</i> , 2019, 177, 1714-1724.e12.	13.5	75
2508	An extensively glycosylated archaeal pilus survives extreme conditions. <i>Nature Microbiology</i> , 2019, 4, 1401-1410.	5.9	46
2509	Widely applicable background depletion step enables transaminase evolution through solid-phase screening. <i>Chemical Science</i> , 2019, 10, 5952-5958.	3.7	18

#	ARTICLE	IF	CITATIONS
2510	Mycobacterial transcript cleavage factor Gre, exhibits chaperone-like activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 757-764.	1.1	10
2511	Solution Structure of the Carboxy-Terminal Tandem Repeat Domain of Eukaryotic Elongation Factor 2 Kinase and Its Role in Substrate Recognition. <i>Journal of Molecular Biology</i> , 2019, 431, 2700-2717.	2.0	8
2512	Surface glycan-binding proteins are essential for cereal beta-glucan utilization by the human gut symbiont <i>Bacteroides ovatus</i> . <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4319-4340.	2.4	35
2513	Crystal structure of the cold-adapted haloalkane dehalogenase DpcA from <i>Psychrobacter cryohalolentis</i> K5. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 324-331.	0.4	5
2514	Structure and allosteric coupling of type α antitoxin CopASO. <i>Biochemical and Biophysical Research Communications</i> , 2019, 514, 1122-1127.	1.0	5
2515	Crystal structure of phyllogen, a phylloidy-inducing effector protein of phytoplasma. <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 952-957.	1.0	24
2516	Twenty-Five Years of Structural Parvovirology. <i>Viruses</i> , 2019, 11, 362.	1.5	122
2517	Crystal Structure of GenD2, an NAD-Dependent Oxidoreductase Involved in the Biosynthesis of Gentamicin. <i>ACS Chemical Biology</i> , 2019, 14, 925-933.	1.6	10
2518	Structural insights into RNA recognition by the Chikungunya virus nsP2 helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9558-9567.	3.3	50
2519	Enzymatic Pyran Formation Involved in Xiamenmycin Biosynthesis. <i>ACS Catalysis</i> , 2019, 9, 5391-5399.	5.5	20
2520	Structural Insights into Bacteriophage GIL01 gp7 Inhibition of Host LexA Repressor. <i>Structure</i> , 2019, 27, 1094-1102.e4.	1.6	17
2521	NMR structure of CmPI-II, a non-classical Kazal protease inhibitor: Understanding its conformational dynamics and subtilisin A inhibition. <i>Journal of Structural Biology</i> , 2019, 206, 280-294.	1.3	10
2522	The structure of (E)-biformene synthase provides insights into the biosynthesis of bacterial bicyclic labdane-related diterpenoids. <i>Journal of Structural Biology</i> , 2019, 207, 29-39.	1.3	7
2523	Molecular structure of a 5,10-methylenetetrahydrofolate dehydrogenase from the silkworm <i>Bombyx mori</i> . <i>FEBS Open Bio</i> , 2019, 9, 618-628.	1.0	4
2524	A 192-heme electron transfer network in the hydrazine dehydrogenase complex. <i>Science Advances</i> , 2019, 5, eaav4310.	4.7	47
2525	Structural insight into YcbB-mediated beta-lactam resistance in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 1849.	5.8	29
2526	Structural analysis of a plant fatty acid amide hydrolase provides insights into the evolutionary diversity of bioactive acylethanolamides. <i>Journal of Biological Chemistry</i> , 2019, 294, 7419-7432.	1.6	13
2527	Understanding the binding interaction in therapeutic prevention of inflammation by controlling Hsp90 through curcumin and epigallocatechin. <i>Journal of Proteins and Proteomics</i> , 2019, 10, 121-129.	1.0	1

#	ARTICLE	IF	CITATIONS
2528	Crystal structure of bacterial cyclopropane-fatty-acyl-phospholipid synthase with phospholipid. <i>Journal of Biochemistry</i> , 2019, 166, 139-147.	0.9	16
2529	Developing and Implementing a Free Online Protein Structure and Function Exploration Project To Teach Undergraduate Students Macromolecular Structureâ€“Function Relationships. <i>Journal of Chemical Education</i> , 2019, 96, 729-733.	1.1	5
2530	Structural basis of transcriptional regulation by the HigA antitoxin. <i>Molecular Microbiology</i> , 2019, 111, 1449-1462.	1.2	19
2531	Structural Diversity of Ultralong CDRH3s in Seven Bovine Antibody Heavy Chains. <i>Frontiers in Immunology</i> , 2019, 10, 558.	2.2	32
2532	Structural characterization of the Imm52 family protein TsiT in <i>Pseudomonas aeruginosa</i> . <i>Protein Science</i> , 2019, 28, 971-975.	3.1	2
2533	Essentials of Bioinformatics, Volume I. , 2019, , .		8
2534	Crystal structure and activity-based labeling reveal the mechanisms for linkage-specific substrate recognition by deubiquitinase USP9X. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7288-7297.	3.3	39
2535	Structural characterization of the third scavenger receptor cysteineâ€“rich domain of murine neurotrypsin. <i>Protein Science</i> , 2019, 28, 746-755.	3.1	9
2536	Crystal structure of chloramphenicol-metabolizing enzyme EstDL136 from a metagenome. <i>PLoS ONE</i> , 2019, 14, e0210298.	1.1	9
2537	The fungal ribonuclease-like effector protein CSEP0064/BEC1054 represses plant immunity and interferes with degradation of host ribosomal RNA. <i>PLoS Pathogens</i> , 2019, 15, e1007620.	2.1	105
2538	Structureâ€“guided identification of antimicrobial peptides in the spathe transcriptome of the nonâ€“model plant, arum lily (<i>Zantedeschia aethiopica</i>). <i>Chemical Biology and Drug Design</i> , 2019, 93, 1265-1275.	1.5	7
2539	The Co-chaperone Cns1 and the Recruiter Protein Hgh1 Link Hsp90 to Translation Elongation via Chaperoning Elongation Factor 2. <i>Molecular Cell</i> , 2019, 74, 73-87.e8.	4.5	22
2540	Crystal structure of the TreS:Pep2 complex, initiating Î±-glucan synthesis in the GlgE pathway of mycobacteria. <i>Journal of Biological Chemistry</i> , 2019, 294, 7348-7359.	1.6	8
2541	Structural differences between the ectodomains of murine and human CD98hc. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 693-698.	1.5	8
2542	Structural and Functional Insights into Host Death Domains Inactivation by the Bacterial Arginine GlcNAcyltransferase Effector. <i>Molecular Cell</i> , 2019, 74, 922-935.e6.	4.5	43
2543	Increased versatility despite reduced molecular complexity: evolution, structure and function of metazoan splicing factor PRPF39. <i>Nucleic Acids Research</i> , 2019, 47, 5867-5879.	6.5	7
2544	Structural analysis of <i>Phytophthora</i> suppressor of RNA silencing 2 (PSR2) reveals a conserved modular fold contributing to virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8054-8059.	3.3	46
2545	Highâ€“resolution archaeal structure reveals a conserved metalâ€“binding site. <i>EMBO Reports</i> , 2019, 20, .	2.0	27

#	ARTICLE	IF	CITATIONS
2546	Identification of a α -helical molten globule intermediate and structural characterization of α -cardiotoxin, an all α -sheet protein isolated from the venom of <i>Ophiophagus hannah</i> (king cobra). Protein Science, 2019, 28, 952-963.	3.1	7
2547	Biological 3D Structural Databases. , 2019, , 47-73.		2
2548	<i>Brucella</i> Periplasmic Protein EipB Is a Molecular Determinant of Cell Envelope Integrity and Virulence. Journal of Bacteriology, 2019, 201, .	1.0	12
2549	Crystal structure of a transcription factor, GerE (PaGerE), from spore-forming bacterium <i>Paenispodosarcina</i> sp. TG-14. Biochemical and Biophysical Research Communications, 2019, 513, 374-379.	1.0	0
2550	Identification, characterization, and structural analyses of a fungal endo- β -1,2-glucanase reveal a new glycoside hydrolase family. Journal of Biological Chemistry, 2019, 294, 7942-7965.	1.6	18
2551	Crystal Structure of a Putative Modulator of Gyrase (TIdE) from <i>Thermococcus kodakarensis</i> . Crystals, 2019, 9, 107.	1.0	2
2552	Structural changes of antitoxin HigA from <i>Shigella flexneri</i> by binding of its cognate toxin HigB. International Journal of Biological Macromolecules, 2019, 130, 99-108.	3.6	9
2553	Solution structure of a unicellular microalgae-derived translationally controlled tumor protein revealed both conserved features and structural diversity. Archives of Biochemistry and Biophysics, 2019, 665, 23-29.	1.4	2
2554	Structure-function characterization of an insecticidal protein GNIPIAa, a member of an MACPF and β -tripod families. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2897-2906.	3.3	19
2555	Structural insights into chaperone addiction of toxin-antitoxin systems. Nature Communications, 2019, 10, 782.	5.8	15
2556	The C-terminal domain of HpDprA is a DNA-binding winged helix domain that does not bind double-stranded DNA. FEBS Journal, 2019, 286, 1941-1958.	2.2	1
2557	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
2558	Structural insights into the unique polylactate-degrading mechanism of <i>Thermobifida alba</i> cutinase. FEBS Journal, 2019, 286, 2087-2098.	2.2	42
2559	Identification and characterization of ABC transporters for carbohydrate uptake in <i>Thermus thermophilus</i> HB8. Gene, 2019, 696, 135-148.	1.0	15
2560	Molecular Basis for the Potent Inhibition of the Emerging Carbapenemase VCC-1 by Avibactam. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	4
2561	R pyocin tail fiber structure reveals a receptor-binding domain with a lectin fold. PLoS ONE, 2019, 14, e0211432.	1.1	21
2562	Crystal structure and calcium-induced conformational changes of diacylglycerol kinase β EF-hand domains. Protein Science, 2019, 28, 694-706.	3.1	14
2563	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. Communications Biology, 2019, 2, 56.	2.0	75

#	ARTICLE	IF	CITATIONS
2564	Characterization of Differential Dynamics, Specificity, and Allostery of Lipoxygenase Family Members. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 2496-2508.	2.5	34
2565	Crystal Structure of Urate Oxidase from <i>Bacillus Subtilis</i> 168. <i>Crystallography Reports</i> , 2019, 64, 1126-1133.	0.1	2
2566	<i>Trichoderma reesei</i> Dehydrogenase, a Pyrroloquinoline Quinone-Dependent Member of Auxiliary Activity Family 12 of the Carbohydrate-Active Enzymes Database: Functional and Structural Characterization. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	13
2567	Crystal Structures of Putative Flavin Dependent Monooxygenase from <i>Alicyclobacillus Acidocaldarius</i> . <i>Crystals</i> , 2019, 9, 548.	1.0	1
2568	Crystal structure of the glycoside hydrolase PssZ from <i>Listeria monocytogenes</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 501-506.	0.4	5
2569	Ca^{2+} -Crystallination Endows a Novel Bacterial Glycoside Hydrolase 64 with Ca^{2+} -Dependent Activity Modulation. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	3
2570	Crystal structures of p120RasGAP N-terminal SH2 domain in its apo form and in complex with a p190RhoGAP phosphotyrosine peptide. <i>PLoS ONE</i> , 2019, 14, e0226113.	1.1	13
2571	Dynamical comparison between Drosha and Dicer reveals functional motion similarities and dissimilarities. <i>PLoS ONE</i> , 2019, 14, e0226147.	1.1	5
2572	Structural genomics applied to the rust fungus <i>Melampsora larici-populina</i> reveals two candidate effector proteins adopting cystine knot and NTF2-like protein folds. <i>Scientific Reports</i> , 2019, 9, 18084.	1.6	19
2573	Enzymatic synthesis of l-fucose from l-fuculose using a fucose isomerase from <i>Raoultella</i> sp. and the biochemical and structural analyses of the enzyme. <i>Biotechnology for Biofuels</i> , 2019, 12, 282.	6.2	13
2574	Structure and role for active site lid of lactate monooxygenase from <i>Mycobacterium smegmatis</i> . <i>Protein Science</i> , 2019, 28, 135-149.	3.1	16
2575	Aminoglycoside antibiotic resistance conferred by Hpa2 of MDR <i>Acinetobacter baumannii</i> : an unusual adaptation of a common histone acetyltransferase. <i>Biochemical Journal</i> , 2019, 476, 795-808.	1.7	3
2576	An in-silico Approach for Enhancing the Lipid Productivity in Microalgae by Manipulating the Fatty Acid Biosynthesis. <i>Advances in Intelligent Systems and Computing</i> , 2019, , 877-889.	0.5	3
2577	A novel cysteine carbamoyl-switch is responsible for the inhibition of formamidase, a nitrilase superfamily member. <i>Archives of Biochemistry and Biophysics</i> , 2019, 662, 151-159.	1.4	3
2578	Phage AcrIIA2 DNA Mimicry: Structural Basis of the CRISPR and Anti-CRISPR Arms Race. <i>Molecular Cell</i> , 2019, 73, 611-620.e3.	4.5	74
2579	Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1-O-methyltransferase specific for 3-O-methylated mannosides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 835-844.	3.3	7
2580	Molecular Architecture of the Inositol Phosphatase Siw14. <i>Biochemistry</i> , 2019, 58, 534-545.	1.2	7
2581	Amine Transaminase from <i>Exophiala Xenobiotica</i> —Crystal Structure and Engineering of a Fold IV Transaminase that Naturally Converts Biaryl Ketones. <i>ACS Catalysis</i> , 2019, 9, 1140-1148.	5.5	34

#	ARTICLE	IF	CITATIONS
2582	The structure of <i>Legionella</i> effector protein LpnE provides insights into its interaction with Oculocerebrorenal syndrome of Lowe (OCRL) protein. <i>FEBS Journal</i> , 2019, 286, 710-725.	2.2	9
2583	Structural analysis reveals a molecular calipers mechanism for a LATERAL ORGAN BOUNDARIES DOMAIN transcription factor protein from wheat. <i>Journal of Biological Chemistry</i> , 2019, 294, 142-156.	1.6	21
2584	Cap-specific terminal N ⁶ -methylation of RNA by an RNA polymerase II-associated methyltransferase. <i>Science</i> , 2019, 363, .	6.0	262
2585	Structural Insights into the Dual-Substrate Recognition and Catalytic Mechanisms of a Bifunctional Acetyl Ester Xyloside Hydrolase from <i>Caldicellulosiruptor lactoaceticus</i> . <i>ACS Catalysis</i> , 2019, 9, 1739-1747.	5.5	6
2586	A kiwellin disarms the metabolic activity of a secreted fungal virulence factor. <i>Nature</i> , 2019, 565, 650-653.	13.7	48
2587	Crystal Structure and Substrate Specificity of the 8-oxo-dGTP Hydrolase NUDT1 from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2019, 58, 887-899.	1.2	7
2588	The small RbcS-like domains of the $\hat{1}^2$ -carboxysome structural protein CcmM bind RubisCO at a site distinct from that binding the RbcS subunit. <i>Journal of Biological Chemistry</i> , 2019, 294, 2593-5195.	1.6	44
2589	Subunit Asa3 ensures the attachment of the peripheral stalk to the membrane sector of the dimeric ATP synthase of <i>Polytomella</i> sp.. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 341-347.	1.0	3
2590	Structural mapping of hot spots within human CASPR2 discoidin domain for autoantibody recognition. <i>Journal of Autoimmunity</i> , 2019, 96, 168-177.	3.0	3
2591	Solution NMR structure of CHU_1110 from <i>Cytophaga hutchinsonii</i> , an AHSA1 protein potentially involved in metal ion stress response. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 91-95.	1.5	1
2592	The RES domain toxins of RES toxin antitoxin modules induce cell stasis by degrading NAD ⁺ . <i>Molecular Microbiology</i> , 2019, 111, 221-236.	1.2	46
2593	The Inner Nuclear Membrane Protein Bqt4 in Fission Yeast Contains a DNA-Binding Domain Essential for Telomere Association with the Nuclear Envelope. <i>Structure</i> , 2019, 27, 335-343.e3.	1.6	8
2594	Structural Basis for CD96 Immune Receptor Recognition of Nectin-like Protein-5, CD155. <i>Structure</i> , 2019, 27, 219-228.e3.	1.6	41
2595	Structural and biochemical evaluation of <i>Ceratitis capitata</i> odorant-binding protein 22 affinity for odorants involved in intersex communication. <i>Insect Molecular Biology</i> , 2019, 28, 431-443.	1.0	23
2596	Structural and functional characterization of an intradiol ring-cleavage dioxygenase from the polyphagous spider mite herbivore <i>Tetranychus urticae</i> Koch. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 107, 19-30.	1.2	6
2597	Structural insights into the catalytic mechanism of 5-methylthioribose 1-phosphate isomerase. <i>Journal of Structural Biology</i> , 2019, 205, 67-77.	1.3	3
2598	Assessment of Structure Quality (RNA and Protein). , 2019, , 586-605.		0
2599	Structural and functional insights into the modulation of the activity of a flax cytokinin oxidase by flax rust effector AvrL567. <i>Molecular Plant Pathology</i> , 2019, 20, 211-222.	2.0	15

#	ARTICLE	IF	CITATIONS
2600	Molecular characterization of the hydroxylase HmtN at 1.3Å... resolution. <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 1033-1038.	1.0	1
2601	Insight into a Transcriptional Adaptor Zinc Finger Encoded by a Putative Protein in the White Spot Syndrome Virus Genome. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 145-151.	2.2	3
2602	Computational insights into the interaction of small molecule inhibitors with HRI kinase domain. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1715-1723.	2.0	4
2603	Properties and structure of a low-potential, penta-heme cytochrome c552 from a thermophilic purple sulfur photosynthetic bacterium <i>Thermochromatium tepidum</i> . <i>Photosynthesis Research</i> , 2019, 139, 281-293.	1.6	4
2604	Candidate CSPG4 mutations and induced pluripotent stem cell modeling implicate oligodendrocyte progenitor cell dysfunction in familial schizophrenia. <i>Molecular Psychiatry</i> , 2019, 24, 757-771.	4.1	51
2605	Lebetin Peptides, A New Class of Potent Platelet Aggregation Inhibitors: Chemical Synthesis, Biological Activity and NMR Spectroscopic Study. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 21-31.	0.9	3
2606	<i>In vitro</i> DNA binding activity and molecular docking reveals pierisin-5 as an anti-proliferative agent against gastric cancer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 3474-3488.	2.0	3
2607	DALI and the persistence of protein shape. <i>Protein Science</i> , 2020, 29, 128-140.	3.1	537
2608	Evolutionary significance and functional characterization of streptomycin adenylyltransferase from <i>Serratia marcescens</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4418-4431.	2.0	12
2609	The tripartite architecture of the eukaryotic integral membrane protein zinc metalloprotease Ste24. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 604-615.	1.5	5
2610	Structural and dynamic studies provide insights into specificity and allosteric regulation of ribonuclease as, a key enzyme in mycobacterial virulence. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2455-2467.	2.0	1
2611	Protein functional annotation of simultaneously improved stability, accuracy and false discovery rate achieved by a sequence-based deep learning. <i>Briefings in Bioinformatics</i> , 2020, 21, 1437-1447.	3.2	105
2612	Crystal structure of the complex of the interaction domains of <i>Escherichia coli</i> DnaB helicase and DnaC helicase loader: structural basis implying a distortion-accumulation mechanism for the DnaB ring opening caused by DnaC binding. <i>Journal of Biochemistry</i> , 2020, 167, 1-14.	0.9	13
2613	On the structure and function of <i>Escherichia coli</i> YjhC: An oxidoreductase involved in bacterial sialic acid metabolism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 654-668.	1.5	13
2614	Roles of the N-terminal domain and remote substrate binding subsites in activity of the debranching barley limit dextrinase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140294.	1.1	6
2615	Unique active site formation in a novel galactose 1-phosphate uridylyltransferase from the hyperthermophilic archaeon <i>Pyrobaculum aerophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 669-678.	1.5	0
2616	Crystal structure of a hypothetical T2SS effector Lpg0189 from <i>Legionella pneumophila</i> reveals a novel protein fold. <i>Biochemical and Biophysical Research Communications</i> , 2020, 521, 799-805.	1.0	2
2617	Structures of MERS1, the 5' processing enzyme of mitochondrial mRNAs in <i>Trypanosoma brucei</i> . <i>Rna</i> , 2020, 26, 69-82.	1.6	3

#	ARTICLE	IF	CITATIONS
2618	Structural and thermodynamic correlation illuminates the selective transport mechanism of disaccharide β -glycosides through ABC transporter. <i>FEBS Journal</i> , 2020, 287, 1576-1597.	2.2	12
2619	Structure and Mechanism of a Cyclic Trinucleotide-Activated Bacterial Endonuclease Mediating Bacteriophage Immunity. <i>Molecular Cell</i> , 2020, 77, 723-733.e6.	4.5	148
2620	Structural insights into phosphopantetheinyl hydrolase PptH from <i>Mycobacterium tuberculosis</i> . <i>Protein Science</i> , 2020, 29, 744-757.	3.1	6
2621	Weaponisation $\hat{\infty}$ on the fly $\hat{\infty}$ ™: Convergent recruitment of knottin and defensin peptide scaffolds into the venom of predatory assassin flies. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 118, 103310.	1.2	10
2622	The cryo-EM Structure of <i>Thermotoga maritima</i> $\hat{1}^2$ -Galactosidase: Quaternary Structure Guides Protein Engineering. <i>ACS Chemical Biology</i> , 2020, 15, 179-188.	1.6	14
2623	Structure and kinetic properties of human $\hat{1}^2$ -aspartate oxidase, the enzyme $\hat{1}^2$ -controlling $\hat{1}^2$ -aspartate levels in brain. <i>FASEB Journal</i> , 2020, 34, 1182-1197.	0.2	19
2624	The crystal structure of the mycobacterial trehalose monomycolate transport factor A, TtfA, reveals an atypical fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 809-815.	1.5	8
2625	Structural basis of indisulam-mediated RBM39 recruitment to DCAF15 E3 ligase complex. <i>Nature Chemical Biology</i> , 2020, 16, 15-23.	3.9	150
2626	Characterization of novel lectins from <i>Burkholderia pseudomallei</i> and <i>Chromobacterium violaceum</i> with seven-bladed $\hat{1}^2$ -propeller fold. <i>International Journal of Biological Macromolecules</i> , 2020, 152, 1113-1124.	3.6	5
2627	Structural and Functional Analyses of Human ChaC2 in Glutathione Metabolism. <i>Biomolecules</i> , 2020, 10, 31.	1.8	12
2628	Crystal structures clarify cofactor binding of plant tyrosine decarboxylase. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 500-505.	1.0	7
2629	Functional and Structural Analysis of Predicted Proteins Obtained from <i>Homo sapiens</i> $\hat{1}^2$ Minisatellite 33.15-Tagged Transcript pAKT-45 Variants. <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	1
2630	Characterization and functional insights into the <i>Entamoeba histolytica</i> pyridoxal kinase, an enzyme essential for its survival. <i>Journal of Structural Biology</i> , 2020, 212, 107645.	1.3	5
2631	Structural and molecular basis for the substrate positioning mechanism of a new PL7 subfamily alginate lyase from the arctic. <i>Journal of Biological Chemistry</i> , 2020, 295, 16380-16392.	1.6	35
2632	Characterization of dye-decolorizing peroxidase from <i>Bacillus subtilis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2020, 693, 108590.	1.4	61
2633	Structural and functional study of SaAcP, an acylphosphatase from <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 173-178.	1.0	2
2634	Functional and structural characterization of an $\hat{1}^2$ - $\hat{1}^2$ -arabinofuranosidase from <i>Thermothielavioides terrestris</i> and its exquisite domain-swapped $\hat{1}^2$ -propeller fold crystal packing. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140533.	1.1	5
2635	Neuropilin-1 is a host factor for SARS-CoV-2 infection. <i>Science</i> , 2020, 370, 861-865.	6.0	1,015

#	ARTICLE	IF	CITATIONS
2636	Structural analysis of CACHE domain of the McpA chemoreceptor from <i>Leptospira interrogans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 1323-1329.	1.0	2
2637	Structural Basis for Activation of the Heterodimeric GABAB Receptor. <i>Journal of Molecular Biology</i> , 2020, 432, 5966-5984.	2.0	33
2638	Cryoelectron-Microscopic Structure of the pKpQIL Conjugative Pili from Carbapenem-Resistant <i>Klebsiella pneumoniae</i> . <i>Structure</i> , 2020, 28, 1321-1328.e2.	1.6	26
2639	Conformational Trapping of a \hat{I}^2 -Glucosides-Binding Protein Unveils the Selective Two-Step Ligand-Binding Mechanism of ABC Importers. <i>Journal of Molecular Biology</i> , 2020, 432, 5711-5734.	2.0	8
2640	Structural basis of mammalian mucin processing by the human gut O-glycopeptidase OgpA from <i>Akkermansia muciniphila</i> . <i>Nature Communications</i> , 2020, 11, 4844.	5.8	57
2641	Structural Basis for Enzymatic Off-Loading of Hybrid Polyketides by Dieckmann Condensation. <i>ACS Chemical Biology</i> , 2020, 15, 2783-2791.	1.6	11
2642	Immunodominant proteins P1 and P40/P90 from human pathogen <i>Mycoplasma pneumoniae</i> . <i>Nature Communications</i> , 2020, 11, 5188.	5.8	22
2643	Crystal structure of the indole-3-acetic acid-catabolizing enzyme DAO1 from <i>Arabidopsis thaliana</i> . <i>Journal of Structural Biology</i> , 2020, 212, 107632.	1.3	4
2644	Crystal structure of tomato spotted wilt virus G _N reveals a dimer complex formation and evolutionary link to animal-infecting viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26237-26244.	3.3	12
2645	Crystallization and X-ray analysis of <i>Borrelia burgdorferi</i> \hat{I}^2 -barrel assembly machinery A. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 235-240.	0.4	0
2646	The N-terminal domain of <i>Staphylothermus marinus</i> McrB shares structural homology with PUA-like RNA binding proteins. <i>Journal of Structural Biology</i> , 2020, 211, 107572.	1.3	4
2647	Functional characterization of an aldose reductase (bmALD1) obtained from the silkworm <i>Bombyx mori</i> . <i>Insect Molecular Biology</i> , 2020, 29, 490-497.	1.0	4
2648	Structures of hyperstable ancestral haloalkane dehalogenases show restricted conformational dynamics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1497-1508.	1.9	10
2649	The structures of two archaeal type IV pili illuminate evolutionary relationships. <i>Nature Communications</i> , 2020, 11, 3424.	5.8	24
2650	Ticks Resist Skin Commensals with Immune Factor of Bacterial Origin. <i>Cell</i> , 2020, 183, 1562-1571.e12.	13.5	31
2651	Biophysical and Biochemical Characterization of TP0037, a α -Lactate Dehydrogenase, Supports an Acetogenic Energy Conservation Pathway in <i>Treponema pallidum</i> . <i>MBio</i> , 2020, 11, .	1.8	4
2652	Structural asymmetry governs the assembly and GTPase activity of McrBC restriction complexes. <i>Nature Communications</i> , 2020, 11, 5907.	5.8	7
2653	Ancestral L-amino acid oxidases for deracemization and stereoinversion of amino acids. <i>Communications Chemistry</i> , 2020, 3, .	2.0	21

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2654	Structure of odorant binding proteins and chemosensory proteins determined by X-ray crystallography. <i>Methods in Enzymology</i> , 2020, 642, 151-167.	0.4	2
2655	Tightening the Crosslinking Distance Restraints for Better Resolution of Protein Structure and Dynamics. <i>Structure</i> , 2020, 28, 1160-1167.e3.	1.6	15
2656	Discovery of the cryptic function of terpene cyclases as aromatic prenyltransferases. <i>Nature Communications</i> , 2020, 11, 3958.	5.8	22
2657	Structural and Functional Studies of a <i>Klebsiella</i> Phage Capsule Depolymerase Tailspike: Mechanistic Insights into Capsular Degradation. <i>Structure</i> , 2020, 28, 613-624.e4.	1.6	41
2658	Structural signatures in EPR3 define a unique class of plant carbohydrate receptors. <i>Nature Communications</i> , 2020, 11, 3797.	5.8	31
2659	Primary structures and conformations of stonefish toxin-like toxins from three species of rabbitfish, <i>Siganus puellus</i> , <i>Siganus unimaculatus</i> , and <i>Siganus virgatus</i> . <i>Fisheries Science</i> , 2020, 86, 889-901.	0.7	3
2660	Biophysical analysis of <i>Pseudomonas</i> -phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. <i>Nucleic Acids Research</i> , 2020, 48, 11721-11736.	6.5	14
2661	Alternative conformation of the C-domain of the P140 protein from <i>Mycoplasma genitalium</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 508-516.	0.4	2
2662	Keeping It Together: Structures, Functions, and Applications of Viral Decoration Proteins. <i>Viruses</i> , 2020, 12, 1163.	1.5	15
2663	Structure of the TFIIIC subcomplex \bar{I}_A provides insights into RNA polymerase III pre-initiation complex formation. <i>Nature Communications</i> , 2020, 11, 4905.	5.8	16
2664	New Pathways of Mutational Change in SARS-CoV-2 Proteomes Involve Regions of Intrinsic Disorder Important for Virus Replication and Release. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432096514.	0.6	39
2665	Structural insights into <i>Pseudomonas aeruginosa</i> Type six secretion system exported effector 8. <i>Journal of Structural Biology</i> , 2020, 212, 107651.	1.3	3
2666	Structure of Epstein-Barr virus tegument protein complex BBRF2-BSRF1 reveals its potential role in viral envelopment. <i>Nature Communications</i> , 2020, 11, 5405.	5.8	11
2667	Network-based protein structural classification. <i>Royal Society Open Science</i> , 2020, 7, 191461.	1.1	9
2668	Hexachlorobenzene Monooxygenase Substrate Selectivity and Catalysis: Structural and Biochemical Insights. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	1.4	7
2669	Responses to the COVID-19 Pandemic by the Biochemistry Authentic Scientific Inquiry Lab (BASIL) CURE Consortium: Reflections and a Case Study on the Switch to Remote Learning. <i>Journal of Chemical Education</i> , 2020, 97, 3455-3462.	1.1	14
2670	Structure and Function of the T4 Spackle Protein Gp61.3. <i>Viruses</i> , 2020, 12, 1070.	1.5	4
2671	Cryo-electron Microscopy Structure, Assembly, and Mechanics Show Morphogenesis and Evolution of Human Picobirnavirus. <i>Journal of Virology</i> , 2020, 94, .	1.5	11

#	ARTICLE	IF	CITATIONS
2672	Biochemical Characterization and Crystal Structure of a Novel NAD ⁺ -Dependent Isocitrate Dehydrogenase from <i>Phaeodactylum tricornutum</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5915.	1.8	5
2673	Structural insights of the enzymes from the chitin utilization locus of <i>Flavobacterium johnsoniae</i> . <i>Scientific Reports</i> , 2020, 10, 13775.	1.6	9
2674	Structural and mechanistic basis of capsule O-acetylation in <i>Neisseria meningitidis</i> serogroup A. <i>Nature Communications</i> , 2020, 11, 4723.	5.8	11
2675	Evidence that immunization with TP0751, a bipartite <i>Treponema pallidum</i> lipoprotein with an intrinsically disordered region and lipocalin fold, fails to protect in the rabbit model of experimental syphilis. <i>PLoS Pathogens</i> , 2020, 16, e1008871.	2.1	16
2676	The Structure of the Cysteine-Rich Domain of <i>Plasmodium falciparum</i> P113 Identifies the Location of the RH5 Binding Site. <i>MBio</i> , 2020, 11, .	1.8	7
2677	Decoding the intricate network of molecular interactions of a hyperstable engineered biocatalyst. <i>Chemical Science</i> , 2020, 11, 11162-11178.	3.7	13
2678	Structural and mechanistic insights into the CRISPR inhibition of AcrIF7. <i>Nucleic Acids Research</i> , 2020, 48, 9959-9968.	6.5	13
2679	Divergent architecture of the heterotrimeric NatC complex explains N-terminal acetylation of cognate substrates. <i>Nature Communications</i> , 2020, 11, 5506.	5.8	23
2680	A structurally unique <i>Fusobacterium nucleatum</i> tannase provides detoxicant activity against gallotannins and pathogen resistance. <i>Microbial Biotechnology</i> , 2020, , .	2.0	3
2681	Structural Diversity and Highly Specific Host-Pathogen Transcriptional Regulation of Defensin Genes Is Revealed in Tomato. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9380.	1.8	7
2682	Molecular Basis of Iterative C-H Oxidation by TamI, a Multifunctional P450 Monooxygenase from the Tirandamycin Biosynthetic Pathway. <i>ACS Catalysis</i> , 2020, 10, 13445-13454.	5.5	20
2683	The Structures of SctK and SctD from <i>Pseudomonas aeruginosa</i> Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform. <i>Journal of Molecular Biology</i> , 2020, 432, 166693.	2.0	14
2684	Heterochiral coupling in non-ribosomal peptide macrolactamization. <i>Nature Catalysis</i> , 2020, 3, 507-515.	16.1	18
2685	Evolution of Sequence-Diverse Disordered Regions in a Protein Family: Order within the Chaos. <i>Molecular Biology and Evolution</i> , 2020, 37, 2155-2172.	3.5	20
2686	Structure and functional analysis of the <i>Legionella pneumophila</i> chitinase ChiA reveals a novel mechanism of metal-dependent mucin degradation. <i>PLoS Pathogens</i> , 2020, 16, e1008342.	2.1	29
2687	Structural insights into the putative bacterial acetylcholinesterase ChoE and its substrate inhibition mechanism. <i>Journal of Biological Chemistry</i> , 2020, 295, 8708-8724.	1.6	7
2688	Structural basis for Ca ²⁺ -dependent activation of a plant metacaspase. <i>Nature Communications</i> , 2020, 11, 2249.	5.8	38
2689	Delineation of the molecular determinants of the unique allosteric binding site of the orphan nuclear receptor ROR β . <i>Journal of Biological Chemistry</i> , 2020, 295, 9183-9191.	1.6	5

#	ARTICLE	IF	CITATIONS
2690	The model cyanobacteria <i>Anabaena</i> sp. PCC 7120 possess an intact but partially degenerated gene cluster encoding gas vesicles. <i>BMC Microbiology</i> , 2020, 20, 110.	1.3	8
2691	Structural insight into tanapoxvirus-mediated inhibition of apoptosis. <i>FEBS Journal</i> , 2020, 287, 3733-3750.	2.2	11
2692	Crystal Structure and Active Site Engineering of a Halophilic $\hat{\text{I}}^3$ -Carbonic Anhydrase. <i>Frontiers in Microbiology</i> , 2020, 11, 742.	1.5	16
2693	Structural analysis of the meiosis-related protein MS5 reveals non-canonical papain enhancement by cystatin-like folds. <i>FEBS Letters</i> , 2020, 594, 2462-2471.	1.3	0
2694	Structure, Dynamics and Cellular Insight Into Novel Substrates of the <i>Legionella pneumophila</i> Type II Secretion System. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 112.	1.6	11
2695	Structure and mechanism of DNA delivery of a gene transfer agent. <i>Nature Communications</i> , 2020, 11, 3034.	5.8	71
2696	Structural basis for divergent C-H hydroxylation selectivity in two Rieske oxygenases. <i>Nature Communications</i> , 2020, 11, 2991.	5.8	34
2697	Insights into the Inhibition of <i>Aeromonas hydrophila</i> α -Alanine- α -Alanine Ligase by Integration of Kinetics and Structural Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7509-7519.	2.4	2
2698	The GTPase-activating protein p120RasGAP has an evolutionarily conserved α FLVR-unique-SH2 domain. <i>Journal of Biological Chemistry</i> , 2020, 295, 10511-10521.	1.6	8
2699	Selective interactions between mimivirus uracil-DNA glycosylase and inhibitory proteins determined by a single amino acid. <i>Journal of Structural Biology</i> , 2020, 211, 107552.	1.3	3
2700	Crystal structures of Uso1 membrane tether reveal an alternative conformation in the globular head domain. <i>Scientific Reports</i> , 2020, 10, 9544.	1.6	7
2701	Crystal structure of the YoeBSa1-YefMSa1 complex from <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 264-269.	1.0	1
2702	Structural Basis of Ca ²⁺ -Dependent Self-Processing Activity of Repeat-in-Toxin Proteins. <i>MBio</i> , 2020, 11, .	1.8	5
2703	Intrinsic disorder is essential for Cas9 inhibition of anti-CRISPR AcrIIA5. <i>Nucleic Acids Research</i> , 2020, 48, 7584-7594.	6.5	12
2704	Crystal Structure of Flagellar Export Chaperone FliS in Complex With Flagellin and HP1076 of <i>Helicobacter pylori</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 787.	1.5	6
2705	The Structural Basis of T4 Phage Lysis Control: DNA as the Signal for Lysis Inhibition. <i>Journal of Molecular Biology</i> , 2020, 432, 4623-4636.	2.0	16
2706	Sjögren syndrome/scleroderma autoantigen 1 is a direct Tankyrase binding partner in cancer cells. <i>Communications Biology</i> , 2020, 3, 123.	2.0	5
2707	Structural and functional insights into a novel two-component endolysin encoded by a single gene in <i>Enterococcus faecalis</i> phage. <i>PLoS Pathogens</i> , 2020, 16, e1008394.	2.1	24

#	ARTICLE	IF	CITATIONS
2708	Structural and evolutionary analyses of the Plasmodium falciparum chloroquine resistance transporter. <i>Scientific Reports</i> , 2020, 10, 4842.	1.6	17
2709	Regio- and Stereoselective Steroid Hydroxylation at C7 by Cytochrome P450 Monooxygenase Mutants. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 12499-12505.	7.2	83
2710	Structural analysis of a shrimp thymidylate synthase reveals species-specific interactions with dUMP and raltitrexed. <i>Journal of Oceanology and Limnology</i> , 2020, 38, 1891-1899.	0.6	1
2711	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. <i>Science Signaling</i> , 2020, 13, .	1.6	12
2712	Atomic structure of the <i>Campylobacter jejuni</i> flagellar filament reveals how μ Proteobacteria escaped Toll-like receptor 5 surveillance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16985-16991.	3.3	30
2713	Structure-guided protein engineering increases enzymatic activities of the SCNH family esterases. <i>Biotechnology for Biofuels</i> , 2020, 13, 107.	6.2	9
2714	PelX is a UDP-N-acetylglucosamine C4-epimerase involved in Pel polysaccharide-dependent biofilm formation. <i>Journal of Biological Chemistry</i> , 2020, 295, 11949-11962.	1.6	10
2715	<i>Aedes aegypti</i> Odorant Binding Protein 22 selectively binds fatty acids through a conformational change in its C-terminal tail. <i>Scientific Reports</i> , 2020, 10, 3300.	1.6	21
2716	Structural basis for monolignol oxidation by a maize laccase. <i>Nature Plants</i> , 2020, 6, 231-237.	4.7	35
2717	Structural analyses of the Group A flavin-dependent monooxygenase PieE reveal a sliding FAD cofactor conformation bridging OUT and IN conformations. <i>Journal of Biological Chemistry</i> , 2020, 295, 4709-4722.	1.6	9
2718	The full-length structure of <i>Thermus scotoductus</i> OLD defines the ATP hydrolysis properties and catalytic mechanism of Class 1 OLD family nucleases. <i>Nucleic Acids Research</i> , 2020, 48, 2762-2776.	6.5	17
2719	Substrate Promiscuity of a Paralytic Shellfish Toxin Amidinotransferase. <i>ACS Chemical Biology</i> , 2020, 15, 626-631.	1.6	16
2720	Structural basis for disulphide-CoA inhibition of a butyryl-CoA hexameric thioesterase. <i>Journal of Structural Biology</i> , 2020, 210, 107477.	1.3	1
2721	The <i>Helicobacter pylori</i> HspR-Modulator CbpA Is a Multifunctional Heat-Shock Protein. <i>Microorganisms</i> , 2020, 8, 251.	1.6	3
2722	The structure of the <i>Legionella</i> response regulator LqsR reveals amino acids critical for phosphorylation and dimerization. <i>Molecular Microbiology</i> , 2020, 113, 1070-1084.	1.2	13
2723	Alternative Hydrophobic Core in Proteins—The Effect of Specific Synergy. <i>Symmetry</i> , 2020, 12, 273.	1.1	6
2724	The structure of the <i>Thermococcus gammatolerans</i> McrB N-terminal domain reveals a new mode of substrate recognition and specificity among McrB homologs. <i>Journal of Biological Chemistry</i> , 2020, 295, 743-756.	1.6	13
2725	The First Structure of an Active Mammalian dCTPase and its Complexes With Substrate Analogs and Products. <i>Journal of Molecular Biology</i> , 2020, 432, 1126-1142.	2.0	2

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2726	A Synthetic Human Antibody Antagonizes IL-18R β Signaling Through an Allosteric Mechanism. <i>Journal of Molecular Biology</i> , 2020, 432, 1169-1182.	2.0	5
2727	Peptidoglycan reshaping by a noncanonical peptidase for helical cell shape in <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2020, 11, 458.	5.8	14
2728	The bacterial deubiquitinase Ceg23 regulates the association of Lys-63 ω -linked polyubiquitin molecules on the Legionella phagosome. <i>Journal of Biological Chemistry</i> , 2020, 295, 1646-1657.	1.6	33
2729	Structures of β -glycosidase LXYL-P1-2 reveals the product binding state of GH3 family and a specific pocket for Taxol recognition. <i>Communications Biology</i> , 2020, 3, 22.	2.0	7
2730	Crystal structure of proteolyzed VapBC and DNA ω -bound VapBC from <i>Salmonella enterica</i> Typhimurium LT2 and VapC as a putative Ca ²⁺ -dependent ribonuclease. <i>FASEB Journal</i> , 2020, 34, 3051-3068.	0.2	3
2731	FAM46B is a prokaryotic-like cytoplasmic poly(A) polymerase essential in human embryonic stem cells. <i>Nucleic Acids Research</i> , 2020, 48, 2733-2748.	6.5	13
2732	Structural analysis of the CARB β -lactamase from <i>Vibrio parahaemolyticus</i> facilitates application of the β -lactam/ β -lactamase inhibitor therapy. <i>Biochimie</i> , 2020, 171-172, 213-222.	1.3	4
2733	Mechanistic insights into m6A modification of U6 snRNA by human METTL16. <i>Nucleic Acids Research</i> , 2020, 48, 5157-5168.	6.5	70
2734	Discovery of potential multi-target-directed ligands by targeting host-specific SARS-CoV-2 structurally conserved main protease. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1-16.	2.0	259
2735	Structure and Function of the Cytochrome P450 Monooxygenase Cinnamate 4-hydroxylase from <i>Sorghum bicolor</i> . <i>Plant Physiology</i> , 2020, 183, 957-973.	2.3	36
2736	The crystal structure of a <i>Fusarium oxysporum</i> feruloyl esterase that belongs to the tannase family. <i>FEBS Letters</i> , 2020, 594, 1738-1749.	1.3	15
2737	Crystal structure of the MÄnglÄ virus VP30 C-terminal domain. <i>Biochemical and Biophysical Research Communications</i> , 2020, 525, 392-397.	1.0	2
2738	Regio ω -and Stereoselective Steroid Hydroxylation at C7 by Cytochrome ω ...P450 Monooxygenase Mutants. <i>Angewandte Chemie</i> , 2020, 132, 12599-12605.	1.6	19
2739	Structural basis of elongation factor 2 switching. <i>Current Research in Structural Biology</i> , 2020, 2, 25-34.	1.1	3
2740	Crystal structures of human NSDHL and development of its novel inhibitor with the potential to suppress EGFR activity. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 207-225.	2.4	9
2741	The co ω -existence of cold activity and thermal stability in an Antarctic GH42 β -galactosidase relies on its hexameric quaternary arrangement. <i>FEBS Journal</i> , 2021, 288, 546-565.	2.2	31
2742	Homology modeling, structural insights and <i>in-silico</i> screening for selective inhibitors of mycobacterial CysE. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 1547-1560.	2.0	2
2743	Structure ω -based design of peptides that trigger <i>Streptococcus pneumoniae</i> cell death. <i>FEBS Journal</i> , 2021, 288, 1546-1564.	2.2	13

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2744	The structural basis for signal promiscuity in a bacterial chemoreceptor. <i>FEBS Journal</i> , 2021, 288, 2294-2310.	2.2	9
2745	Bacterial triacylglycerol lipase is a potential cholesterol esterase: Identification of a key determinant for sterol-binding specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 578-586.	3.6	8
2746	Structural insight into the novel iron coordination and domain interactions of transferrin from a model insect, <i>Manduca sexta</i> . <i>Protein Science</i> , 2021, 30, 408-422.	3.1	9
2747	Anti-CRISPR AcrIE2 Binds the Type I-E CRISPR-Cas Complex But Does Not Block DNA Binding. <i>Journal of Molecular Biology</i> , 2021, 433, 166759.	2.0	11
2748	Hydroxynitrile lyase from the cyanogenic millipede, <i>Chamberlinius hualienensis</i> —A new entry to the carrier protein family Lipocalines. <i>FEBS Journal</i> , 2021, 288, 1679-1695.	2.2	8
2749	Expression and in vitro anticancer activity of Lp16-PSP, a member of the YjgF/YER057c/UK114 protein family from the mushroom <i>Lentinula edodes</i> C91-3. <i>Archives of Microbiology</i> , 2021, 203, 1047-1060.	1.0	3
2750	Structural analysis of the N-acetyltransferase Eis1 from <i>Mycobacterium abscessus</i> reveals the molecular determinants of its incapacity to modify aminoglycosides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 94-106.	1.5	2
2751	ADP-ribose and analogues bound to the deMAYlating macrodomain from the bat coronavirus HKU4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
2752	Wzb of <i>Vibrio vulnificus</i> represents a new group of low-molecular-weight protein tyrosine phosphatases with a unique insertion in the W-loop. <i>Journal of Biological Chemistry</i> , 2021, 296, 100280.	1.6	3
2753	Structural basis for recognition of bacterial cell wall teichoic acid by pseudo-symmetric SH3b-like repeats of a viral peptidoglycan hydrolase. <i>Chemical Science</i> , 2021, 12, 576-589.	3.7	11
2754	Structural Characterization of Act c 10.0101 and Pun g 1.0101 Allergens from the Non-Specific Lipid Transfer Protein Family. <i>Molecules</i> , 2021, 26, 256.	1.7	4
2755	Chemical Synthesis and NMR Solution Structure of Conotoxin GXIA from <i>Conus geographus</i> . <i>Marine Drugs</i> , 2021, 19, 60.	2.2	3
2756	Nuclear Egress of Herpesviruses. <i>Current Issues in Molecular Biology</i> , 2021, 41, 125-170.	1.0	68
2758	The HelQ human DNA repair helicase utilizes a PWI-like domain for DNA loading through interaction with RPA, triggering DNA unwinding by the HelQ helicase core. <i>NAR Cancer</i> , 2021, 3, zcaa043.	1.6	11
2759	Crystal structure of bacterial cytotoxic necrotizing factor CNF _Y reveals molecular building blocks for intoxication. <i>EMBO Journal</i> , 2021, 40, e105202.	3.5	14
2760	<i>Porphyromonas gingivalis</i> fimbrial protein Mfa5 contains a von Willebrand factor domain and an intramolecular isopeptide. <i>Communications Biology</i> , 2021, 4, 106.	2.0	10
2761	Cryoelectron-microscopy structure of the enteropathogenic <i>Escherichia coli</i> type III secretion system EspA filament. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
2762	A pentameric protein ring with novel architecture is required for herpesviral packaging. <i>ELife</i> , 2021, 10, .	2.8	9

#	ARTICLE	IF	CITATIONS
2763	Structural and biochemical analyses of the tetrameric cell binding domain of Lys170 from enterococcal phage F170/08. <i>European Biophysics Journal</i> , 2021, 50, 721-729.	1.2	6
2765	Structural Insights into the <i>Trans</i> -Acting Enoyl Reductase in the Biosynthesis of Long-Chain Polyunsaturated Fatty Acids in <i>Shewanella piezotolerans</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 2316-2324.	2.4	5
2766	Discovery of exolytic heparinases and their catalytic mechanism and potential application. <i>Nature Communications</i> , 2021, 12, 1263.	5.8	8
2767	Functional and structural characterization of a flavoprotein monooxygenase essential for biogenesis of tryptophylquinone cofactor. <i>Nature Communications</i> , 2021, 12, 933.	5.8	2
2769	Bioinformatic Analysis of Structure and Function of LIM Domains of Human Zyxin Family Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2647.	1.8	12
2771	A human monoclonal antibody blocks malaria transmission and defines a highly conserved neutralizing epitope on gametes. <i>Nature Communications</i> , 2021, 12, 1750.	5.8	39
2772	Structural analysis of viral ExoN domains reveals polyphyletic hijacking events. <i>PLoS ONE</i> , 2021, 16, e0246981.	1.1	6
2774	In-silico structural analysis of <i>Pseudomonas syringae</i> effector HopZ3 reveals ligand binding activity and virulence function. <i>Journal of Plant Research</i> , 2021, 134, 599-611.	1.2	0
2775	Structural basis for IFN antagonism by human respiratory syncytial virus nonstructural protein 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2020587118.	3.3	12
2776	Crystal Structure of a Phospholipase D from the Plant-Associated Bacteria <i>Serratia plymuthica</i> Strain AS9 Reveals a Unique Arrangement of Catalytic Pocket. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3219.	1.8	8
2777	Crystal structure of timothy grass allergen Phl p 12.0101 reveals an unusual profilin dimer. <i>Acta Biochimica Polonica</i> , 2021, 68, 15-22.	0.3	3
2778	Insight into Shared Properties and Differential Dynamics and Specificity of Secretory Phospholipase A ₂ Family Members. <i>Journal of Physical Chemistry B</i> , 2021, 125, 3353-3363.	1.2	5
2779	Structural and thermodynamic insights into the novel dinucleotide-binding protein of ABC transporter unveils its moonlighting function. <i>FEBS Journal</i> , 2021, 288, 4614-4636.	2.2	3
2780	Structural and functional analysis of the <i>Klebsiella pneumoniae</i> MazEF toxin-antitoxin system. <i>IUCr</i> , 2021, 8, 362-371.	1.0	4
2781	Structural and functional studies of SAV1707 from <i>Staphylococcus aureus</i> elucidate its distinct metal-dependent activity and a crucial residue for catalysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 587-598.	1.1	0
2782	Heme controls the structural rearrangement of its sensor protein mediating the hemolytic bacterial survival. <i>Communications Biology</i> , 2021, 4, 467.	2.0	8
2783	Crystal structures of UDP-N-acetylmuramic acid-L-alanine ligase (MurC) from <i>Mycobacterium bovis</i> with and without UDP-N-acetylglucosamine. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 618-627.	1.1	3
2784	Structure, Immunoreactivity, and In Silico Epitope Determination of SmSPI S. mansonii Serpin for Immunodiagnostic Application. <i>Vaccines</i> , 2021, 9, 322.	2.1	4

#	ARTICLE	IF	CITATIONS
2785	Structures of a non-ribosomal peptide synthetase condensation domain suggest the basis of substrate selectivity. <i>Nature Communications</i> , 2021, 12, 2511.	5.8	53
2786	Sensor Domain of Histidine Kinase VxA of <i>Vibrio cholerae</i> : Hairpin-Swapped Dimer and Its Conformational Change. <i>Journal of Bacteriology</i> , 2021, 203, .	1.0	4
2787	Phosphoregulation, nucleotide binding and ion access control in potassium-chloride cotransporters. <i>EMBO Journal</i> , 2021, 40, e107294.	3.5	19
2788	eCOMPASS: evaluative comparison of multiple protein alignments by statistical score. <i>Bioinformatics</i> , 2021, 37, 3456-3463.	1.8	0
2789	Re-emerging Aspartic Protease Targets: Examining <i>Cryptococcus neoformans</i> Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6706-6719.	2.9	14
2790	Crystal and solution structures reveal oligomerization of individual capsid homology domains of <i>Drosophila</i> Arc. <i>PLoS ONE</i> , 2021, 16, e0251459.	1.1	7
2791	Crystal structure of the DNA-binding domain of <i>Bacillus subtilis</i> CsrR. <i>Biochemical and Biophysical Research Communications</i> , 2021, 555, 26-31.	1.0	2
2792	PIN and CCCH Zn-finger domains coordinate RNA targeting in ZC3H12 family endoribonucleases. <i>Nucleic Acids Research</i> , 2021, 49, 5369-5381.	6.5	9
2793	Structural and functional characterization of a plant alpha-actinin. <i>FEBS Open Bio</i> , 2021, 11, 2198-2210.	1.0	1
2796	The crystal structure of SnTox3 from the necrotrophic fungus <i>Parastagonospora nodorum</i> reveals a unique effector fold and provides insight into Snn3 recognition and prodomain protease processing of fungal effectors. <i>New Phytologist</i> , 2021, 231, 2282-2296.	3.5	24
2799	Mn ²⁺ coordinates Cap-O-RNA to align substrates for efficient 2'-O-methyl transfer by SARS-CoV-2 nsp16. <i>Science Signaling</i> , 2021, 14, .	1.6	17
2800	The structural basis of fatty acid elongation by the ELOVL elongases. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 512-520.	3.6	52
2803	Rational Design for Broadened Substrate Specificity and Enhanced Activity of a Novel Acetyl Xylan Esterase from <i>Bacteroides thetaiotaomicron</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 6665-6675.	2.4	2
2805	Structure of the mini-RNA-guided endonuclease CRISPR-Cas12j3. <i>Nature Communications</i> , 2021, 12, 4476.	5.8	23
2806	Structural Basis for Isomerization Reactions in Fungal Tetrahydroxanthone Biosynthesis and Diversification. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 19458-19465.	7.2	10
2807	Structural basis of LAIR1 targeting by polymorphic Plasmodium RIFINs. <i>Nature Communications</i> , 2021, 12, 4226.	5.8	1
2808	Structural Basis for Isomerization Reactions in Fungal Tetrahydroxanthone Biosynthesis and Diversification. <i>Angewandte Chemie</i> , 2021, 133, 19607-19614.	1.6	3
2809	Molecular insights into the endoperoxide formation by Fe(II)/K ⁺ -dependent oxygenase Nvfl. <i>Nature Communications</i> , 2021, 12, 4417.	5.8	31

#	ARTICLE	IF	CITATIONS
2810	Structural basis of the stereoselective formation of the spirooxindole ring in the biosynthesis of citrinadins. <i>Nature Communications</i> , 2021, 12, 4158.	5.8	17
2811	Structural Dynamics and Perspectives of Vitamin B6 Biosynthesis Enzymes in Plasmodium: Advances and Open Questions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 688380.	1.8	0
2812	Structural Investigation of Orf Virus Bcl-2 Homolog ORFV125 Interactions with BH3-Motifs from BH3-Only Proteins Puma and Hrk. <i>Viruses</i> , 2021, 13, 1374.	1.5	4
2813	Anchoring the T6SS to the cell wall: Crystal structure of the peptidoglycan binding domain of the TagL accessory protein. <i>PLoS ONE</i> , 2021, 16, e0254232.	1.1	7
2814	Cryo-EM structure of the periplasmic tunnel of T7 DNA-ejectosome at 2.7Å... resolution. <i>Molecular Cell</i> , 2021, 81, 3145-3159.e7.	4.5	17
2815	TMEM120A is a coenzyme A-binding membrane protein with structural similarities to ELOVL fatty acid elongase. <i>ELife</i> , 2021, 10, .	2.8	20
2816	Analysis of the mechanosensor channel functionality of TACAN. <i>ELife</i> , 2021, 10, .	2.8	24
2818	Structure and Function of N-Terminal Zinc Finger Domain of SARS-CoV-2 NSP2. <i>Virologica Sinica</i> , 2021, 36, 1104-1112.	1.2	25
2819	Structural and biochemical advances on the recruitment of the autophagy-initiating ULK and TBK1 complexes by autophagy receptor NDP52. <i>Science Advances</i> , 2021, 7, .	4.7	20
2820	Identification and characterization of metal uptake ABC transporters in <i>Mycobacterium tuberculosis</i> unveil their ligand specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 324-337.	3.6	4
2821	Secreted pectin monooxygenases drive plant infection by pathogenic oomycetes. <i>Science</i> , 2021, 373, 774-779.	6.0	106
2822	Cryo-EM structures of human TMEM120A and TMEM120B. <i>Cell Discovery</i> , 2021, 7, 77.	3.1	16
2824	A reverse catalytic triad Asp containing loop shaping a wide substrate binding pocket of a feruloyl esterase from <i>Lactobacillus plantarum</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 184, 92-100.	3.6	9
2825	Structural and mechanistic basis for protein glutamylation by the kinase fold. <i>Molecular Cell</i> , 2021, 81, 4527-4539.e8.	4.5	18
2826	Insights into the structure and RNA-binding specificity of <i>Caenorhabditis elegans</i> Dicer-related helicase 3 (DRH-3). <i>Nucleic Acids Research</i> , 2021, 49, 9978-9991.	6.5	4
2827	Biochemical and Structural Characterisation of a Novel D-Lyxose Isomerase From the Hyperthermophilic Archaeon <i>Thermofilum</i> sp.. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 711487.	2.0	3
2829	The middle lipin domain adopts a membrane-binding dimeric protein fold. <i>Nature Communications</i> , 2021, 12, 4718.	5.8	11
2830	Expanding the Substrate Specificity of Macro Domains toward 3â€³-Isomer of O-Acetyl-ADP-ribose. <i>ACS Catalysis</i> , 2021, 11, 11075-11090.	5.5	0

#	ARTICLE	IF	CITATIONS
2831	Single-Component and Two-Component <i>p</i> -Nitrophenol Monooxygenases: Structural Basis for Their Catalytic Difference. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0117121.	1.4	3
2832	The cryo-EM structure of the bd oxidase from <i>M. tuberculosis</i> reveals a unique structural framework and enables rational drug design to combat TB. <i>Nature Communications</i> , 2021, 12, 5236.	5.8	29
2833	A Novel Lipase from <i>Lasiodiplodia theobromae</i> Efficiently Hydrolyses C8-C10 Methyl Esters for the Preparation of Medium-Chain Triglycerides™ Precursors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10339.	1.8	2
2834	Catalytic mechanism of ancestral L-lysine oxidase assigned by sequence data mining. <i>Journal of Biological Chemistry</i> , 2021, 297, 101043.	1.6	10
2836	Structural changes in bacteriophage T7 upon receptor-induced genome ejection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
2837	Structural and biochemical insights into CRISPR RNA processing by the Cas5c ribonuclease SMU1763 from <i>Streptococcus mutans</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101251.	1.6	2
2838	Crystal structures of NAD ⁺ -linked isocitrate dehydrogenase from the green alga <i>Ostreococcus tauri</i> and its evolutionary relationship with eukaryotic NAD ⁺ -linked homologs. <i>Archives of Biochemistry and Biophysics</i> , 2021, 708, 108898.	1.4	2
2839	Therapeutic targeting of PIM KINASE signaling in cancer therapy: Structural and clinical prospects. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129995.	1.1	16
2840	Crystal structure of a chitinase (RmChiA) from the thermophilic fungus <i>Rhizomucor miehei</i> with a real active site tunnel. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140709.	1.1	7
2841	The core Cas1 protein of CRISPR-Cas I-B in <i>Leptospira</i> shows metal-tunable nuclease activity. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100059.	1.4	1
2842	<i>Pantoea stewartii</i> WceF is a glycan biofilm-modifying enzyme with a bacteriophage tailspike-like fold. <i>Journal of Biological Chemistry</i> , 2021, 296, 100286.	1.6	5
2843	A single residue can modulate nanocage assembly in salt dependent ferritin. <i>Nanoscale</i> , 2021, 13, 11932-11942.	2.8	11
2844	Crystal structures of the sheeppox virus encoded inhibitor of apoptosis SPPV14 bound to the proapoptotic BH3 peptides Hrk and Bax. <i>FEBS Letters</i> , 2020, 594, 2016-2026.	1.3	9
2846	The prospects of quantum computing in computational molecular biology. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2021, 11, e1481.	6.2	108
2847	The Structure of HCV. , 2016, , 31-64.		1
2848	Structural and Functional Characterization of <i>Arabidopsis thaliana</i> WW Domain Containing Protein F4JC80. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2015, , 25-39.	0.2	3
2849	The structure of the <i>Thermococcus gammatolerans</i> McrB N-terminal domain reveals a new mode of substrate recognition and specificity among McrB homologs. <i>Journal of Biological Chemistry</i> , 2020, 295, 743-756.	1.6	7
2850	Structures of <i>Bacillus licheniformis</i> <i>scpA</i> -asparaginase from <i>Bacillus licheniformis</i> Reveal an Essential Residue for its Substrate Stereoselectivity. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 223-231.	2.4	14

#	ARTICLE	IF	CITATIONS
2851	The structure of SeviL, a GM1b/asialo-GM1 binding R-type lectin from the mussel <i>Mytilisepta virgata</i> . <i>Scientific Reports</i> , 2020, 10, 22102.	1.6	4
2852	Structural and biochemical characterization of the catalytic domains of GdpP reveals a unified hydrolysis mechanism for the DHH/DHHA1 phosphodiesterase. <i>Biochemical Journal</i> , 2018, 475, 191-205.	1.7	35
2853	Mechanistic insights into Lhr helicase function in DNA repair. <i>Biochemical Journal</i> , 2020, 477, 2935-2947.	1.7	7
2854	The structural basis of Bcl-2 mediated cell death regulation in hydra. <i>Biochemical Journal</i> , 2020, 477, 3287-3297.	1.7	6
2855	Characterization of the macrocyclase involved in the biosynthesis of RiPP cyclic peptides in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6551-6556.	3.3	49
2856	Crystal structure of human cytoplasmic tRNAHis-specific 5â€²-monomethylphosphate capping enzyme. <i>Nucleic Acids Research</i> , 2020, 48, 1572-1582.	6.5	5
2857	Structure and N-acetylglucosamine binding of the distal domain of mouse adenovirus 2 fibre. <i>Journal of General Virology</i> , 2018, 99, 1494-1508.	1.3	8
2870	Revisiting the <i>Haloarcula marismortui</i> 50S ribosomal subunit model. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 997-1004.	2.5	40
2871	Structural and enzymatic characterization of a host-specificity determinant from <i>Salmonella</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 384-391.	2.5	12
2872	The type IV secretion protein TraK from the <i>Enterococcus</i> conjugative plasmid pIP501 exhibits a novel fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1124-1135.	2.5	9
2873	<i>TEMPY</i> : a Python library for assessment of three-dimensional electron microscopy density fits. <i>Journal of Applied Crystallography</i> , 2015, 48, 1314-1323.	1.9	75
2874	Structure of succinyl-CoA:3-ketoacid CoA transferase from <i>Drosophila melanogaster</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1089-1093.	0.7	3
2875	Structural insights into Wcbl, a novel polysaccharide-biosynthesis enzyme. <i>IUCr</i> , 2014, 1, 28-38.	1.0	5
2876	Structural insights into stressosome assembly. <i>IUCr</i> , 2019, 6, 938-947.	1.0	11
2877	Induced DNA bending by unique dimerization of HigA antitoxin. <i>IUCr</i> , 2020, 7, 748-760.	1.0	6
2878	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. <i>IUCr</i> , 2020, 7, 814-824.	1.0	92
2879	Structure of the human MLH1 N-terminus: implications for predisposition to Lynch syndrome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 981-985.	0.4	21
2880	Structure of the SPRY domain of the human RNA helicase DDX1, a putative interaction platform within a DEAD-box protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1176-1188.	0.4	14

#	ARTICLE	IF	CITATIONS
2881	Crystal structure of a family 6 cellobiohydrolase from the basidiomycete <i>Phanerochaete chrysosporium</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 398-403.	0.4	8
2882	Crystal structure of the MSMEG_4306 gene product from <i>Mycobacterium smegmatis</i> . Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 166-173.	0.4	1
2883	X-ray structure of <i>Arthrobacter globiformis</i> M30 ketose 3-epimerase for the production of <i>D</i> -allulose from <i>D</i> -fructose. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 669-676.	0.4	18
2884	Structure of the <i>Mycobacterium smegmatis</i> α -maltose-1-phosphate synthase GlgM. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 175-181.	0.4	7
2885	1.8 Å resolution crystal structure of the carbapenem intrinsic resistance protein CarF. Acta Crystallographica Section D: Structural Biology, 2017, 73, 549-556.	1.1	1
2886	X-ray structure of the direct electron transfer-type FAD glucose dehydrogenase catalytic subunit complexed with a hitchhiker protein. Acta Crystallographica Section D: Structural Biology, 2019, 75, 841-851.	1.1	18
2887	A practical overview of molecular replacement: <i>Clostridioides difficile</i> PtlA1, a difficult case study. Acta Crystallographica Section D: Structural Biology, 2020, 76, 261-271.	1.1	3
2888	Crystal Structure of EHEC Intimin: Insights into the Complementarity between EPEC and EHEC. PLoS ONE, 2010, 5, e15285.	1.1	19
2889	Crystal Structure of UBA2 _{ufd} -Ubc9: Insights into E1-E2 Interactions in Sumo Pathways. PLoS ONE, 2010, 5, e15805.	1.1	42
2890	Crystal Structure of a Novel Esterase Rv0045c from <i>Mycobacterium tuberculosis</i> . PLoS ONE, 2011, 6, e20506.	1.1	20
2891	The Vein Patterning 1 (VEP1) Gene Family Laterally Spread through an Ecological Network. PLoS ONE, 2011, 6, e22279.	1.1	16
2892	The Crystal Structure of the Human Co-Chaperone P58IPK. PLoS ONE, 2011, 6, e22337.	1.1	20
2893	X-Ray Structure Reveals a New Class and Provides Insight into Evolution of Alkaline Phosphatases. PLoS ONE, 2011, 6, e22767.	1.1	26
2894	Structure of Apo- and Monometalated Forms of NDM-1: A Highly Potent Carbapenem-Hydrolyzing Metallo- β -Lactamase. PLoS ONE, 2011, 6, e24621.	1.1	84
2895	The N-terminus of FILIA Forms an Atypical KH Domain with a Unique Extension Involved in Interaction with RNA. PLoS ONE, 2012, 7, e30209.	1.1	14
2896	Membrane Topology and Predicted RNA-Binding Function of the α -Early Responsive to Dehydration (ERD4) Plant Protein. PLoS ONE, 2012, 7, e32658.	1.1	35
2897	Crystal Structure of Diedel, a Marker of the Immune Response of <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e33416.	1.1	17
2898	Do Natural Proteins Differ from Random Sequences Polypeptides? Natural vs. Random Proteins Classification Using an Evolutionary Neural Network. PLoS ONE, 2012, 7, e36634.	1.1	25

#	ARTICLE	IF	CITATIONS
2899	On the Structure and Function of the Phytoene Desaturase CRTI from <i>Pantoea ananatis</i> , a Membrane-Peripheral and FAD-Dependent Oxidase/Isomerase. PLoS ONE, 2012, 7, e39550.	1.1	87
2900	Molecular Dynamics of a Thermostable Multicopper Oxidase from <i>Thermus thermophilus</i> HB27: Structural Differences between the Apo and Holo Forms. PLoS ONE, 2012, 7, e40700.	1.1	29
2901	N-Terminal Domain of Nuclear IL-1 β Shows Structural Similarity to the C-Terminal Domain of Snf1 and Binds to the HAT/Core Module of the SAGA Complex. PLoS ONE, 2012, 7, e41801.	1.1	23
2902	Characterization of <i>Danio rerio</i> Mn ²⁺ -Dependent ADP-Ribose/CDP-Alcohol Diphosphatase, the Structural Prototype of the ADPRibase-Mn-Like Protein Family. PLoS ONE, 2012, 7, e42249.	1.1	6
2903	Solution Structural Analysis of the Single-Domain Parvulin TbPin1. PLoS ONE, 2012, 7, e43017.	1.1	7
2904	Mechanistic Insights into Validoxyamine A 7'-Phosphate Synthesis by VldE Using the Structure of the Entire Product Complex. PLoS ONE, 2012, 7, e44934.	1.1	17
2905	Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the Acidianus Two-Tailed Virus. PLoS ONE, 2012, 7, e45847.	1.1	7
2906	Solution Structure, Copper Binding and Backbone Dynamics of Recombinant Ber e 1 α —The Major Allergen from Brazil Nut. PLoS ONE, 2012, 7, e46435.	1.1	34
2907	The Metagenome-Derived Enzymes LipS and LipT Increase the Diversity of Known Lipases. PLoS ONE, 2012, 7, e47665.	1.1	72
2908	Solution Structure of a Phytocystatin from <i>Ananas comosus</i> and Its Molecular Interaction with Papain. PLoS ONE, 2012, 7, e47865.	1.1	17
2909	Crystal Structures of Two Transcriptional Regulators from <i>Bacillus cereus</i> Define the Conserved Structural Features of a PadR Subfamily. PLoS ONE, 2012, 7, e48015.	1.1	42
2910	Exploring ORFan Domains in Giant Viruses: Structure of Mimivirus Sulfhydryl Oxidase R596. PLoS ONE, 2012, 7, e50649.	1.1	14
2911	Structural Insights into Cellulolytic and Chitinolytic Enzymes Revealing Crucial Residues of Insect β -N-acetyl-D-hexosaminidase. PLoS ONE, 2012, 7, e52225.	1.1	16
2912	The Carboxy-Terminal β -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
2913	Crystal Structure of <i>Crataeva tapia</i> Bark Protein (CrataBL) and Its Effect in Human Prostate Cancer Cell Lines. PLoS ONE, 2013, 8, e64426.	1.1	19
2914	Crystal Structures of the Sec1/Munc18 (SM) Protein Vps33, Alone and Bound to the Homotypic Fusion and Vacuolar Protein Sorting (HOPS) Subunit Vps16*. PLoS ONE, 2013, 8, e67409.	1.1	51
2915	Three-Dimensional Structure of Human NLRP10/PYNOD Pyrin Domain Reveals a Homotypic Interaction Site Distinct from Its Mouse Homologue. PLoS ONE, 2013, 8, e67843.	1.1	26
2916	Structural Phylogenomics Retrodicts the Origin of the Genetic Code and Uncovers the Evolutionary Impact of Protein Flexibility. PLoS ONE, 2013, 8, e72225.	1.1	61

#	ARTICLE	IF	CITATIONS
2917	Crystal Structure and Substrate Specificity of D-Galactose-6-Phosphate Isomerase Complexed with Substrates. PLoS ONE, 2013, 8, e72902.	1.1	6
2918	Isolation of an Orally Active Insecticidal Toxin from the Venom of an Australian Tarantula. PLoS ONE, 2013, 8, e73136.	1.1	55
2919	Î²-Propeller Blades as Ancestral Peptides in Protein Evolution. PLoS ONE, 2013, 8, e77074.	1.1	77
2920	Transcriptional and Proteolytic Regulation of the Toxin-Antitoxin Locus vapBC10 (ssr2962/slr1767) on the Chromosome of Synechocystis sp. PCC 6803. PLoS ONE, 2013, 8, e80716.	1.1	13
2921	New Insights into Histidine Triad Proteins: Solution Structure of a Streptococcus pneumoniae PhtD Domain and Zinc Transfer to AdcAll. PLoS ONE, 2013, 8, e81168.	1.1	48
2922	Structure of the Catalytic Domain of EZH2 Reveals Conformational Plasticity in Cofactor and Substrate Binding Sites and Explains Oncogenic Mutations. PLoS ONE, 2013, 8, e83737.	1.1	108
2923	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PiO2Bp S-SAD Crystal Structure. PLoS ONE, 2014, 9, e94981.	1.1	4
2924	Structural Basis for the Immunomodulatory Function of Cysteine Protease Inhibitor from Human Roundworm Ascaris lumbricoides. PLoS ONE, 2014, 9, e96069.	1.1	15
2925	Evolution of Tertiary Structure of Viral RNA Dependent Polymerases. PLoS ONE, 2014, 9, e96070.	1.1	57
2926	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
2927	Cyanuric Acid Hydrolase from Azorhizobium caulinodans ORS 571: Crystal Structure and Insights into a New Class of Ser-Lys Dyad Proteins. PLoS ONE, 2014, 9, e99349.	1.1	11
2928	Structural and Biochemical Characterization of Human PR70 in Isolation and in Complex with the Scaffolding Subunit of Protein Phosphatase 2A. PLoS ONE, 2014, 9, e101846.	1.1	14
2929	A Polyketide Synthase Acyltransferase Domain Structure Suggests a Recognition Mechanism for Its Hydroxymalonyl-Acyl Carrier Protein Substrate. PLoS ONE, 2014, 9, e110965.	1.1	23
2930	Crystal Structure of Human Protein N-Terminal Glutamine Amidohydrolase, an Initial Component of the N-End Rule Pathway. PLoS ONE, 2014, 9, e111142.	1.1	9
2931	Crystal Structure of the Fibre Head Domain of the Adenovirus Snake Adenovirus 1. PLoS ONE, 2014, 9, e114373.	1.1	16
2932	Lpg0393 of Legionella pneumophila Is a Guanine-Nucleotide Exchange Factor for Rab5, Rab21 and Rab22. PLoS ONE, 2015, 10, e0118683.	1.1	16
2933	Structural and Enzymatic Characterization of the Choline Kinase LicA from Streptococcus pneumoniae. PLoS ONE, 2015, 10, e0120467.	1.1	11
2934	The Carboxy-Terminal Domain of Erb1 Is a Seven-Bladed Å-Propeller that Binds RNA. PLoS ONE, 2015, 10, e0123463.	1.1	10

#	ARTICLE	IF	CITATIONS
2935	A Kazal-Type Serine Protease Inhibitor from the Defense Gland Secretion of the Subterranean Termite <i>Coptotermes formosanus</i> Shiraki. <i>PLoS ONE</i> , 2015, 10, e0125376.	1.1	9
2936	The Crystal Structure of <i>Thermotoga maritima</i> Class III Ribonucleotide Reductase Lacks a Radical Cysteine Pre-Positioned in the Active Site. <i>PLoS ONE</i> , 2015, 10, e0128199.	1.1	10
2937	Structure-Based Phylogenetic Analysis of the Lipocalin Superfamily. <i>PLoS ONE</i> , 2015, 10, e0135507.	1.1	36
2938	Characterization of <i>Cercospora nicotianae</i> Hypothetical Proteins in Cercosporin Resistance. <i>PLoS ONE</i> , 2015, 10, e0140676.	1.1	8
2939	The <i>Chlamydia trachomatis</i> Protease CPAF Contains a Cryptic PDZ-Like Domain with Similarity to Human Cell Polarity and Tight Junction PDZ-Containing Proteins. <i>PLoS ONE</i> , 2016, 11, e0147233.	1.1	2
2940	Biochemistry and Crystal Structure of Ectoine Synthase: A Metal-Containing Member of the Cupin Superfamily. <i>PLoS ONE</i> , 2016, 11, e0151285.	1.1	30
2941	Structural Analysis and Insights into the Oligomeric State of an Arginine-Dependent Transcriptional Regulator from <i>Bacillus halodurans</i> . <i>PLoS ONE</i> , 2016, 11, e0155396.	1.1	3
2942	Investigation into the Mode of Phosphate Activation in the 4-Hydroxy-4-Methyl-2-Oxoglutarate/4-Carboxy-4-Hydroxy-2-Oxoadipate Aldolase from <i>Pseudomonas putida</i> F1. <i>PLoS ONE</i> , 2016, 11, e0164556.	1.1	3
2943	Exploring Mouse Protein Function via Multiple Approaches. <i>PLoS ONE</i> , 2016, 11, e0166580.	1.1	22
2944	Structure determination of a major facilitator peptide transporter: Inward facing PepTSt from <i>Streptococcus thermophilus</i> crystallized in space group P3121. <i>PLoS ONE</i> , 2017, 12, e0173126.	1.1	35
2945	Structural basis for the substrate selectivity of <i>Helicobacter pylori</i> NucT nuclease activity. <i>PLoS ONE</i> , 2017, 12, e0189049.	1.1	7
2946	Crystal structure of a UDP-GlcNAc epimerase for surface polysaccharide biosynthesis in <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2018, 13, e0191610.	1.1	1
2947	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats. <i>PLoS ONE</i> , 2020, 15, e0242677.	1.1	18
2948	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. <i>PLoS Pathogens</i> , 2017, 13, e1006394.	2.1	53
2949	Structural basis of Zn(II) induced metal detoxification and antibiotic resistance by histidine kinase CzcS in <i>Pseudomonas aeruginosa</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006533.	2.1	29
2950	Structural analysis of <i>P. falciparum</i> KAHRP and PfEMP1 complexes with host erythrocyte spectrin suggests a model for cytoadherent knob protrusions. <i>PLoS Pathogens</i> , 2017, 13, e1006552.	2.1	26
2951	Crystal Structure and Comparative Sequence Analysis of GmhA from <i>Colwellia psychrerythraea</i> Strain 34H Provides Insight into Functional Similarity with DiaA. <i>Molecules and Cells</i> , 2015, 38, 1086-1095.	1.0	9
2952	Structural and Biochemical Studies Reveal a Putative FtsZ Recognition Site on the Z-ring Stabilizer ZapD. <i>Molecules and Cells</i> , 2016, 39, 814-820.	1.0	7

#	ARTICLE	IF	CITATIONS
2953	Homology Modeling: an Overview of Fundamentals and Tools. International Review on Modelling and Simulations, 2017, 10, 129.	0.2	11
2954	Target Based Drug Design - A Reality in Virtual Sphere. Current Medicinal Chemistry, 2015, 22, 1603-1630.	1.2	29
2955	5-Aryl-1,3,4-Thiadiazole-Based Hydroxamic Acids as Histone Deacetylase Inhibitors and Antitumor Agents: Synthesis, Bioevaluation and Docking Study. Medicinal Chemistry, 2015, 11, 296-304.	0.7	6
2956	Heating Affects Structure, Enterocyte Adsorption and Signalling, As Well as Immunogenicity of the Peanut Allergen Ara h 2. The Open Allergy Journal, 2011, 4, 24-34.	0.5	31
2958	Helicase of Type 2 Porcine Reproductive and Respiratory Syndrome Virus Strain HV Reveals a Unique Structure. Viruses, 2020, 12, 215.	1.5	18
2959	Functional assignment to maize group 1 LEA protein EMB564 within the cell nucleus using computational analysis. Bioinformation, 2013, 9, 276-280.	0.2	7
2960	Computational protein structure modeling and analysis of UV-B stress protein in Synechocystis PCC 6803. Bioinformation, 2013, 9, 639-644.	0.2	2
2961	Scaffold nucleoporins Nup188 and Nup192 share structural and functional properties with nuclear transport receptors. ELife, 2013, 2, e00745.	2.8	70
2962	The pseudo GTPase CENP-M drives human kinetochore assembly. ELife, 2014, 3, e02978.	2.8	107
2963	The near-atomic cryoEM structure of a flexible filamentous plant virus shows homology of its coat protein with nucleoproteins of animal viruses. ELife, 2015, 4, e11795.	2.8	61
2964	Human Holliday junction resolvase GEN1 uses a chromodomain for efficient DNA recognition and cleavage. ELife, 2015, 4, .	2.8	27
2965	Architecture and RNA binding of the human negative elongation factor. ELife, 2016, 5, .	2.8	54
2966	Drosophila Nanos acts as a molecular clamp that modulates the RNA-binding and repression activities of Pumilio. ELife, 2016, 5, .	2.8	66
2967	Malaria parasite CelTOS targets the inner leaflet of cell membranes for pore-dependent disruption. ELife, 2016, 5, .	2.8	54
2968	Structural basis for inhibition of erythrocyte invasion by antibodies to Plasmodium falciparum protein CyRPA. ELife, 2017, 6, .	2.8	47
2969	Structure of protein O-mannose kinase reveals a unique active site architecture. ELife, 2016, 5, .	2.8	33
2970	RISC-interacting clearing 3'5' exoribonucleases (RICEs) degrade uridylylated cleavage fragments to maintain functional RISC in Arabidopsis thaliana. ELife, 2017, 6, .	2.8	48
2971	A widespread family of serine/threonine protein phosphatases shares a common regulatory switch with proteasomal proteases. ELife, 2017, 6, .	2.8	28

#	ARTICLE	IF	CITATIONS
2972	Structural basis for interdomain communication in SHIP2 providing high phosphatase activity. <i>ELife</i> , 2017, 6, .	2.8	32
2973	Rift Valley fever phlebovirus NSs protein core domain structure suggests molecular basis for nuclear filaments. <i>ELife</i> , 2017, 6, .	2.8	20
2974	Structural basis of ribosomal peptide macrocyclization in plants. <i>ELife</i> , 2018, 7, .	2.8	52
2975	Mechanisms of opening and closing of the bacterial replicative helicase. <i>ELife</i> , 2018, 7, .	2.8	16
2976	Structural insights into SETD3-mediated histidine methylation on β -actin. <i>ELife</i> , 2019, 8, .	2.8	42
2977	The phage L capsid decoration protein has a novel OB-fold and an unusual capsid binding strategy. <i>ELife</i> , 2019, 8, .	2.8	11
2978	Structural and functional characterization of an otopetrin family proton channel. <i>ELife</i> , 2019, 8, .	2.8	20
2979	Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, .	2.8	41
2980	Structural insights into sodium transport by the oxaloacetate decarboxylase sodium pump. <i>ELife</i> , 2020, 9, .	2.8	13
2981	A putative origin of the insect chemosensory receptor superfamily in the last common eukaryotic ancestor. <i>ELife</i> , 2020, 9, .	2.8	16
2982	Characterisation of <i>Schizosaccharomyces pombe</i> β -actinin. <i>PeerJ</i> , 2016, 4, e1858.	0.9	7
2983	Biochemical and structural characterization of a novel arginine kinase from the spider <i>Polybetes pythagoricus</i> . <i>PeerJ</i> , 2017, 5, e3787.	0.9	11
2984	Crystal structure of human Acinus RNA recognition motif domain. <i>PeerJ</i> , 2018, 6, e5163.	0.9	3
2985	Crystal structure and functional analysis of human C1ORF123. <i>PeerJ</i> , 2018, 6, e5377.	0.9	7
2986	Inverting the Stereoselectivity of an NADH-Dependent Imine-Reductase Variant. <i>ChemCatChem</i> , 2021, 13, 5210-5215.	1.8	8
2987	When the Frequencies of Sensitization and Elicitation of Allergic Reaction Do Not Correlate—The Case of Apple Gibberellin-Regulated Protein Tested in an Italian Population. <i>Frontiers in Allergy</i> , 2021, 2, 745825.	1.2	7
2989	Predicting drug targets by homology modelling of <i>Pseudomonas aeruginosa</i> proteins of unknown function. <i>PLoS ONE</i> , 2021, 16, e0258385.	1.1	0
2992	A Collaborative Web Application for Supporting Researchers in the Task of Generating Protein Datasets. <i>Studies in Computational Intelligence</i> , 2011, , 13-26.	0.7	1

#	ARTICLE	IF	CITATIONS
2993	P3S: Protein Structure Similarity Search. Lecture Notes in Computer Science, 2013, , 228-237.	1.0	0
2994	Protein Closed Loop Prediction from Contact Probabilities. Lecture Notes in Computer Science, 2013, , 199-210.	1.0	0
2995	Molecular Modelling and Structure analysis of S-ribosyl homocysteinase from <i>Aeromonas hydrophila</i> . Biosciences, Biotechnology Research Asia, 2014, 11, 363-368.	0.2	0
2996	Isolation of suppressors of the temperature-sensitive growth caused by a nonsense mutation in gene 1 of <i>Bacillus subtilis</i> phage λ 29 using hydroxylamine. Journal of General and Applied Microbiology, 2015, 61, 88-92.	0.4	0
2997	Structural Protein Function Prediction - A Comprehensive Review. International Journal of Modern Education and Computer Science, 2015, 7, 49-57.	2.4	0
2998	Crystal structure of the flavoenzyme PA4991 from <i>Pseudomonas aeruginosa</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 105-111.	0.4	0
3002	Identification of a Highly Conserved Hypothetical Protein TON_0340 as a Probable Manganese-Dependent Phosphatase. PLoS ONE, 2016, 11, e0167549.	1.1	1
3004	Modeling O ₂ -dependent Heme Enzymes: A Quick Guide for Non-experts. 2-Oxoglutarate-Dependent Oxygenases, 2018, , 222-248.	0.8	0
3028	The Molecular Mechanism of Cellular Attachment for an Archaeal Virus. SSRN Electronic Journal, 0, , .	0.4	0
3054	Homology Modeling of Distant Lipocalin Homologs Using a Structure-based Fingerprint as a Constraint for Sequence Alignment. KSBB Journal, 2020, 35, 157-161.	0.1	0
3058	Structural basis for anti-CRISPR repression mediated by bacterial operon proteins Aca1 and Aca2. Journal of Biological Chemistry, 2021, 297, 101357.	1.6	7
3059	Modulating Glycoside Hydrolase Activity between Hydrolysis and Transfer Reactions Using an Evolutionary Approach. Molecules, 2021, 26, 6586.	1.7	5
3060	Structure and assembly pattern of a freshwater short-tailed cyanophage Pam1. Structure, 2022, 30, 240-251.e4.	1.6	9
3062	Characterization of Enzymes Catalyzing the Formation of the Nonproteinogenic Amino Acid ϵ -Dap in Capreomycin Biosynthesis. Biochemistry, 2021, 60, 77-84.	1.2	11
3063	Suppressor Mutations in Type II Secretion Mutants of <i>Vibrio cholerae</i> : Inactivation of the VesC Protease. MSphere, 2020, 5, .	1.3	2
3064	<i>Bombyx mori</i> -derived aldo-keto reductase AKR2E8 detoxifies aldehydes present in mulberry leaves. Chemico-Biological Interactions, 2022, 351, 109717.	1.7	2
3067	The structure of MP-4 from <i>Mucuna pruriens</i> at 2.22 Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 47-57.	0.4	2
3072	A structural study of TatD from <i>Staphylococcus aureus</i> elucidates a putative DNA-binding mode of a Mg ²⁺ -dependent nuclease. IUCr, 2020, 7, 509-521.	1.0	6

#	ARTICLE	IF	CITATIONS
3073	Assembly of infectious Kaposi's sarcoma-associated herpesvirus progeny requires formation of a pORF19 pentamer. <i>PLoS Biology</i> , 2021, 19, e3001423.	2.6	8
3074	Citrullination Was Introduced into Animals by Horizontal Gene Transfer from Cyanobacteria. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
3075	Structural Basis of Human Parainfluenza Virus 3 Unassembled Nucleoprotein in Complex with Its Viral Chaperone. <i>Journal of Virology</i> , 2022, 96, JVI0164821.	1.5	6
3081	Structural Basis for Recognition of L-lysine, L-ornithine, and L-2,4-diamino Butyric Acid by Lysine Cyclodeaminase. <i>Molecules and Cells</i> , 2018, 41, 331-341.	1.0	2
3082	Crystal Structure of Histidine Triad Nucleotide-Binding Protein from the Pathogenic Fungus. <i>Molecules and Cells</i> , 2019, 42, 56-66.	1.0	1
3083	Bibenzyl synthesis in <i>Cannabis sativa</i> L. <i>Plant Journal</i> , 2021, , .	2.8	6
3084	Structural and Functional Characterization of <i>Legionella pneumophila</i> Effector MavL. <i>Biomolecules</i> , 2021, 11, 1802.	1.8	5
3087	Structural and thermodynamic insights into a novel Mg ²⁺ citrate-binding protein from the ABC transporter superfamily. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1516-1534.	1.1	1
3088	A tripartite cytolytic toxin formed by <i>Vibrio cholerae</i> proteins with flagellum-facilitated secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
3089	Structure of the class C orphan GPCR GPR158 in complex with RGS7-G β 25. <i>Nature Communications</i> , 2021, 12, 6805.	5.8	19
3090	Articulating the exuberant intricacies of bacterial exopolysaccharides to purge environmental pollutants. <i>Heliyon</i> , 2021, 7, e08446.	1.4	13
3092	<i>Legionella</i> effector LegA15/AnkH contains an unrecognized cysteine protease-like domain and displays structural similarity to LegA3/AnkD, but differs in host cell localization. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1535-1542.	1.1	1
3093	De novo macrocyclic peptides for inhibiting, stabilizing, and probing the function of the retromer endosomal trafficking complex. <i>Science Advances</i> , 2021, 7, eabg4007.	4.7	11
3094	Novel Algorithm for Improved Protein Classification Using Graph Similarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 3135-3143.	1.9	1
3095	Role of PemI in the <i>Staphylococcus aureus</i> PemK toxin antitoxin complex: PemI controls PemK by acting as a PemK loop mimic. <i>Nucleic Acids Research</i> , 2022, 50, 2319-2333.	6.5	1
3096	Implications of Membrane Binding by the Fe-S Cluster-Containing N-Terminal Domain in the <i>Drosophila</i> Mitochondrial Replicative DNA Helicase. <i>Frontiers in Genetics</i> , 2021, 12, 790521.	1.1	2
3097	Structural Basis for the Friedel-Crafts Alkylation in Cylindrocyclophane Biosynthesis. <i>ACS Catalysis</i> , 2022, 12, 2108-2117.	5.5	7
3098	Bioinformatic Expansion of Borosins Uncovers Trans-Acting Peptide Backbone <i>N</i> -Methyltransferases in Bacteria. <i>Biochemistry</i> , 2022, 61, 183-194.	1.2	11

#	ARTICLE	IF	CITATIONS
3099	Biochemical and Structural Analysis of a Glucose-Tolerant Î ² -Glucosidase from the Hemicellulose-Degrading Thermoanaerobacterium saccharolyticum. <i>Molecules</i> , 2022, 27, 290.	1.7	13
3100	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, , .	6.5	5
3101	Oxidative desulfurization pathway for complete catabolism of sulfoquinovose by bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	18
3102	The structure and function of modular <i>Escherichia coli</i> O157:H7 bacteriophage FTBEc1 endolysin, LysT84: defining a new endolysin catalytic subfamily. <i>Biochemical Journal</i> , 2022, 479, 207-223.	1.7	5
3103	Structural insights into dihydroxylation of terephthalate, a product of polyethylene terephthalate degradation. <i>Journal of Bacteriology</i> , 2022, , JB0054321.	1.0	7
3104	Identification of a diarylpentanoid-producing polyketide synthase revealing an unusual biosynthetic pathway of 2-(2-phenylethyl)chromones in agarwood. <i>Nature Communications</i> , 2022, 13, 348.	5.8	29
3105	Structural and functional analyses of the Porphyromonas gingivalis type IX secretion system PorN protein. <i>Journal of Biological Chemistry</i> , 2022, 298, 101618.	1.6	3
3106	ARF GTPases activate Salmonella effector SopF to ADP-ribosylate host V-ATPase and inhibit endomembrane damage-induced autophagy. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 67-77.	3.6	29
3107	Structures and function of a tailoring oxidase in complex with a nonribosomal peptide synthetase module. <i>Nature Communications</i> , 2022, 13, 548.	5.8	16
3108	Crystal structures of a new class of pyrimidine/purine nucleoside phosphorylase revealed a Cupin fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1233-1241.	1.5	1
3109	Structural and functional characterization of Î ² -cyanoalanine synthase from Tetranychus urticae. <i>Insect Biochemistry and Molecular Biology</i> , 2022, 142, 103722.	1.2	2
3110	Structural and functional characterization of an auxiliary domain-containing PET hydrolase from Burkholderiales bacterium. <i>Journal of Hazardous Materials</i> , 2022, 429, 128267.	6.5	17
3111	Digital Technology und Artificial Intelligence Facing COVID-19. <i>Advances in Intelligent Systems and Computing</i> , 2022, , 1229-1240.	0.5	2
3112	New Inhibitors of Laccase and Tyrosinase by Examination of Cross-Inhibition between Copper-Containing Enzymes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13661.	1.8	3
3113	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the <i>Pseudomonas</i>-Phage PaP3. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
3114	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2022, , .	6.5	7
3115	Structure of human glycosylphosphatidylinositol transamidase. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 203-209.	3.6	11
3116	Structure of plant RNA-DEPENDENT RNA POLYMERASE 2, an enzyme involved in small interfering RNA production. <i>Plant Cell</i> , 2022, 34, 2140-2149.	3.1	8

#	ARTICLE	IF	CITATIONS
3117	Structure and mechanism for iterative amide <i>N</i> -methylation in the biosynthesis of channel-forming peptide cytotoxins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116578119.	3.3	4
3118	Structural Insight into KsBcl-2 Mediated Apoptosis Inhibition by Kaposi Sarcoma Associated Herpes Virus. <i>Viruses</i> , 2022, 14, 738.	1.5	2
3119	Structural and mechanistic basis for redox sensing by the cyanobacterial transcription regulator RexT. <i>Communications Biology</i> , 2022, 5, 275.	2.0	5
3120	Structural and functional identification of the uncharacterized metallo- β -lactamase superfamily protein TW9814 as a phosphodiesterase with unique metal coordination. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 532-541.	1.1	0
3121	Structural and molecular rationale for the diversification of resistance mediated by the Antibiotic_NAT family. <i>Communications Biology</i> , 2022, 5, 263.	2.0	3
3122	Expression, purification and crystallization of a novel metagenome-derived salicylaldehyde dehydrogenase from Alpine soil. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 161-169.	0.4	0
3124	Structural basis of the strict specificity of a bacterial GH31 α -1,3-glucosidase for nigerooligosaccharides. <i>Journal of Biological Chemistry</i> , 2022, 298, 101827.	1.6	10
3125	Structural Basis for the Prenylation Reaction of Carbazole-Containing Natural Products Catalyzed by Squalene Synthase-Like Enzymes. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	4
3126	Flagellin outer domain dimerization modulates motility in pathogenic and soil bacteria from viscous environments. <i>Nature Communications</i> , 2022, 13, 1422.	5.8	10
3127	Structural Basis for the Prenylation Reaction of Carbazole-Containing Natural Products Catalyzed by Squalene Synthase-Like Enzymes. <i>Angewandte Chemie</i> , 0, , .	1.6	0
3128	Crystal structure and metal binding properties of the periplasmic iron component EfeM from <i>Pseudomonas syringae</i> EfeUOB/M iron-transport system. <i>BioMetals</i> , 2022, 35, 573-589.	1.8	3
3129	Mining folded proteomes in the era of accurate structure prediction. <i>PLoS Computational Biology</i> , 2022, 18, e1009930.	1.5	9
3131	Structure of the type V-C CRISPR-Cas effector enzyme. <i>Molecular Cell</i> , 2022, 82, 1865-1877.e4.	4.5	12
3132	Unique properties of a <i>Dictyostelium discoideum</i> carbohydrate-binding module expand our understanding of CBM-ligand interactions. <i>Journal of Biological Chemistry</i> , 2022, 298, 101891.	1.6	5
3133	Structure-guided mutagenesis of a mucin-selective metalloprotease from <i>Akkermansia muciniphila</i> alters substrate preferences. <i>Journal of Biological Chemistry</i> , 2022, 298, 101917.	1.6	11
3134	Cryo-EM Structure of a Kinetically Trapped Dodecameric Portal Protein from the <i>Pseudomonas</i> -phage PaP3. <i>Journal of Molecular Biology</i> , 2022, 434, 167537.	2.0	6
3135	AlphaFold-Predicted Structures of KCTD Proteins Unravel Previously Undetected Relationships among the Members of the Family. <i>Biomolecules</i> , 2021, 11, 1862.	1.8	13
3136	Structural and Biochemical Investigation of Class I Ribonucleotide Reductase from the Hyperthermophile <i>Aquifex aeolicus</i> . <i>Biochemistry</i> , 2022, 61, 92-106.	1.2	6

#	ARTICLE	IF	CITATIONS
3140	Calmodulin Binding Activates <i>Chromobacterium</i> CopC Effector to ADP-Riboxanate Host Apoptotic Caspases. <i>MBio</i> , 2022, 13, e0069022.	1.8	12
3142	Holliday junction resolution by <i>At</i> -HIGLE: an SLX1 lineage endonuclease from <i>Arabidopsis thaliana</i> with a novel in-built regulatory mechanism. <i>Nucleic Acids Research</i> , 2022, , .	6.5	4
3144	ComFC mediates transport and handling of single-stranded DNA during natural transformation. <i>Nature Communications</i> , 2022, 13, 1961.	5.8	5
3169	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in Rymv Spread. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3171	Molecular basis of antibiotic self-resistance in a bee larvae pathogen. <i>Nature Communications</i> , 2022, 13, 2349.	5.8	4
3172	Structural, mechanistic, and physiological insights into phospholipase A-mediated membrane phospholipid degradation in <i>Pseudomonas aeruginosa</i> . <i>ELife</i> , 2022, 11, .	2.8	13
3173	Role of an orphan substrate-binding protein MhuP in transient heme transfer in <i>Mycobacterium tuberculosis</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 211, 342-356.	3.6	3
3174	Molecular insights into biogenesis of glycosylphosphatidylinositol anchor proteins. <i>Nature Communications</i> , 2022, 13, 2617.	5.8	9
3175	A bioactive phlebovirus-like envelope protein in a hookworm endogenous virus. <i>Science Advances</i> , 2022, 8, eabj6894.	4.7	6
3176	Structures of oxysterol sensor EB12/GPR183, a key regulator of the immune response. <i>Structure</i> , 2022, 30, 1016-1024.e5.	1.6	15
3177	nTreeClus: A tree-based sequence encoder for clustering categorical series. <i>Neurocomputing</i> , 2022, 494, 224-241.	3.5	6
3178	[Review] Structural Features of Cyclic Î±-Maltosyl-(1â€™6)-maltose (CMM) Hydrolase from <i>Arthrobacter</i> Bacteria Critical for CMM Recognition and Hydrolysis. <i>Bulletin of Applied Glycoscience</i> , 2019, 9, 103-112.	0.0	0
3179	Cooperative regulation of PBI1 and MAPKs controls WRKY45 transcription factor in rice immunity. <i>Nature Communications</i> , 2022, 13, 2397.	5.8	20
3183	The structural and functional investigation of the VapBC43 complex from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2022, 616, 19-25.	1.0	2
3184	Bioinformatics in Drug Design and Delivery. , 2022, , 641-664.		2
3185	The Self-Activation Mechanism of Type Iie Restriction Endonuclease Sau3ai. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3186	Insights into the biosynthesis of septacidin I-heptosamine moiety unveils a VOC family sugar epimerase. <i>Acta Pharmaceutica Sinica B</i> , 2023, 13, 765-774.	5.7	3
3187	Quaternary structure independent folding of voltage-gated ion channel pore domain subunits. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 537-548.	3.6	5

#	ARTICLE	IF	CITATIONS
3190	Archaeal bundling pili of <i>Pyrobaculum calidifontis</i> reveal similarities between archaeal and bacterial biofilms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
3191	Nudix hydrolase 18 catalyzes the hydrolysis of active triphosphate metabolites of the antivirals remdesivir, ribavirin, and molnupiravir. <i>Journal of Biological Chemistry</i> , 2022, 298, 102169.	1.6	3
3192	Terminase Subunits from the Pseudomonas-Phage E217. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
3193	An essential role for tungsten in the ecology and evolution of a previously uncultivated lineage of anaerobic, thermophilic Archaea. <i>Nature Communications</i> , 2022, 13, .	5.8	16
3194	Evolution and activation mechanism of the flavivirus class II membrane-fusion machinery. <i>Nature Communications</i> , 2022, 13, .	5.8	17
3195	Structural Characterization of <i>Per Os</i> Infectivity Factor 5 (PIF5) Reveals the Essential Role of Intramolecular Interactions in Baculoviral Oral Infectivity. <i>Journal of Virology</i> , 2022, 96, .	1.5	3
3197	A weak allele of <i>OsNRAMP5</i> confers moderate cadmium uptake while avoiding manganese deficiency in rice. <i>Journal of Experimental Botany</i> , 2022, 73, 6475-6489.	2.4	9
3199	Structural Insights into the NAD(P)H:Quinone Oxidoreductase from <i>Phytophthora capsici</i> . <i>ACS Omega</i> , 2022, 7, 25705-25714.	1.6	4
3200	Crystal structure of the phage-encoded N-acetyltransferase in complex with acetyl-CoA, revealing a novel dimeric arrangement. <i>Journal of Microbiology</i> , 2022, 60, 746-755.	1.3	1
3201	Structural insights into Pot1-ssDNA, Pot1-Tpz1 and Tpz1-Ccq1 Interactions within fission yeast shelterin complex. <i>PLoS Genetics</i> , 2022, 18, e1010308.	1.5	3
3203	Mechanisms and inhibition of Porcupine-mediated Wnt acylation. <i>Nature</i> , 2022, 607, 816-822.	13.7	31
3204	Crystal structure and molecular characterization of NADP ⁺ -farnesol dehydrogenase from cotton bollworm, <i>Helicoverpa armigera</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2022, 147, 103812.	1.2	8
3205	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in RYMV Spread. <i>Journal of Molecular Biology</i> , 2022, 434, 167715.	2.0	6
3206	Molecular mechanism of toxin neutralization in the HipBST toxin-antitoxin system of <i>Legionella pneumophila</i> . <i>Nature Communications</i> , 2022, 13, .	5.8	8
3209	The <i>Haemophilus influenzae</i> HipBA toxin-antitoxin system adopts an unusual three-component regulatory mechanism. <i>IUCr</i> , 2022, 9, 625-631.	1.0	2
3210	Biochemical Evolution of a Potent Target of Mosquito Larvicide, 3-Hydroxykynurenine Transaminase. <i>Molecules</i> , 2022, 27, 4929.	1.7	1
3211	The crystal structure of Cry78Aa from <i>Bacillus thuringiensis</i> provides insights into its insecticidal activity. <i>Communications Biology</i> , 2022, 5, .	2.0	6
3212	Comparative genomic analysis of five freshwater cyanophages and reference-guided metagenomic data mining. <i>Microbiome</i> , 2022, 10, .	4.9	8

#	ARTICLE	IF	CITATIONS
3213	Crystal structure analysis and molecular dynamics simulations of arginase from <i>Thermus thermophilus</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 6811-6821.	2.0	1
3215	SH3 domain regulation of RhoGAP activity: Crosstalk between p120RasGAP and DLC1 RhoGAP. <i>Nature Communications</i> , 2022, 13, .	5.8	8
3216	Structural basis for the dual catalytic activity of the <i>Legionella pneumophila</i> ovarian tumor (OTU) domain deubiquitinase LotA. <i>Journal of Biological Chemistry</i> , 2022, 298, 102414.	1.6	6
3217	Terminase Subunits from the <i>Pseudomonas</i> -Phage E217. <i>Journal of Molecular Biology</i> , 2022, 434, 167799.	2.0	7
3218	The Antibacterial Type VII Secretion System of <i>Bacillus subtilis</i> : Structure and Interactions of the Pseudokinase YukC/EssB. <i>MBio</i> , 2022, 13, .	1.8	16
3219	Structural analysis of VirD4 a type IV ATPase encoded by transmissible plasmids of <i>Salmonella enterica</i> isolated from poultry products. <i>Frontiers in Artificial Intelligence</i> , 0, 5, .	2.0	0
3220	Regioselectivity in inhibition of peptide deformylase from <i>Haemophilus influenzae</i> by 4- vs 5-azaindole hydroxamic acid derivatives: Biochemical, structural and antimicrobial studies. <i>Bioorganic Chemistry</i> , 2022, 128, 106095.	2.0	0
3221	The Structure of <i>Saccharomyces cerevisiae</i> Arginyltransferase 1 (ATE1). <i>Journal of Molecular Biology</i> , 2022, 434, 167816.	2.0	4
3222	Regulation of Different Protonated States of Two Intimate Histidine Residues on Reductive Half-Reaction of Glucose Oxidase. <i>Physical Chemistry Chemical Physics</i> , 0, , .	1.3	1
3223	Structure of the hypothetical protein TTHA1873 from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 338-346.	0.4	1
3224	Structure of the Repurposed Fungal Terpene Cyclase FlvF Implicated in the C-N Bond-Forming Reaction of Flavunoidine Biosynthesis. <i>Biochemistry</i> , 2022, 61, 2014-2024.	1.2	2
3225	Structure of lactate oxidase from <i>Enterococcus hirae</i> revealed new aspects of active site loop function: Product-inhibition mechanism and oxygen gatekeeper. <i>Protein Science</i> , 2022, 31, .	3.1	2
3226	A dedicated C-6 β -hydroxyacyltransferase required for biosynthesis of the glycolipid anchor for Vi antigen capsule in typhoidal <i>Salmonella</i> . <i>Journal of Biological Chemistry</i> , 2022, , 102520.	1.6	0
3227	The SPARC complex defines RNAPII promoters in <i>Trypanosoma brucei</i> . <i>ELife</i> , 0, 11, .	2.8	7
3229	Structure and mechanism for streptococcal fatty acid kinase (Fak) system dedicated to host fatty acid scavenging. <i>Science Advances</i> , 2022, 8, .	4.7	7
3231	Identification of antiparasitic drug targets using a multi-omics workflow in the acanthocephalan model. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
3233	Substrate-induced dimerization of elaiophylin glycosyltransferase reveals a novel self-activating form of glycosyltransferase for symmetric glycosylation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1235-1248.	1.1	0
3235	Crystal structure of a <i>Burkholderia</i> peptidase and modification of the substrate-binding site for enhanced hydrolytic activity toward gluten-derived pro-immunogenic peptides. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2258-2269.	3.6	3

#	ARTICLE	IF	CITATIONS
3236	Crystal structure of <i>Campylobacter jejuni</i> lipoprotein Cj1090c. <i>Proteins: Structure, Function and Bioinformatics</i> , 2023, 91, 293-299.	1.5	4
3237	Poleovirus N-terminal readthrough domain structures reveal molecular strategies for mitigating virus transmission by aphids. <i>Nature Communications</i> , 2022, 13, .	5.8	2
3238	A toxin-deformation dependent inhibition mechanism in the T7SS toxin-antitoxin system of Gram-positive bacteria. <i>Nature Communications</i> , 2022, 13, .	5.8	4
3239	Crystal Structures of Epstein-Barr Virus Bcl-2 Homolog BHRF1 Bound to Bid and Puma BH3 Motif Peptides. <i>Viruses</i> , 2022, 14, 2222.	1.5	1
3240	Identification and molecular modeling of novel endogenous activator proteins of Sirt-1: an <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-16.	2.0	1
3241	The Single-Component Flavin Reductase/Flavin-Dependent Halogenase AetF is a Versatile Catalyst for Selective Bromination and Iodination of Arenes and Olefins. <i>Angewandte Chemie</i> , 0, , .	1.6	0
3242	The Single-Component Flavin Reductase/Flavin-Dependent Halogenase AetF is a Versatile Catalyst for Selective Bromination and Iodination of Arenes and Olefins**. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	13
3243	Crystal Structure and Biochemical Analysis of a Cytochrome P450 CYP101D5 from <i>Sphingomonas echinoides</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13317.	1.8	1
3244	Comparative proteomic analysis identifies potential pathogenicity/virulence factors in <i>Fusarium oxysporum</i> f.sp. <i>ricini</i> inciting vascular wilt disease in castor. <i>Physiological and Molecular Plant Pathology</i> , 2022, 122, 101925.	1.3	1
3245	Endowing homodimeric carbamoyltransferase GdmN with iterative functions through structural characterization and mechanistic studies. <i>Nature Communications</i> , 2022, 13, .	5.8	1
3246	Integrative modeling reveals the molecular architecture of the intraflagellar transport A (IFT-A) complex. <i>ELife</i> , 0, 11, .	2.8	20
3247	Structural Homology-Based Drug Repurposing Approach for Targeting NSP12 SARS-CoV-2. <i>Molecules</i> , 2022, 27, 7732.	1.7	11
3248	Structural features, temperature adaptation and industrial applications of microbial lipases from psychrophilic, mesophilic and thermophilic origins. <i>International Journal of Biological Macromolecules</i> , 2023, 225, 822-839.	3.6	13
3249	Structure and function of the NS5 methyltransferase domain from Usutu virus. <i>Antiviral Research</i> , 2022, 208, 105460.	1.9	0
3250	Reaction Mechanism of Ancestral <i>Lys</i> β -Oxidase from <i>Caulobacter</i> Species Studied by Biochemical, Structural, and Computational Analysis. <i>ACS Omega</i> , 2022, 7, 44407-44419.	1.6	2
3251	A unique network of attack, defence and competence on the outer membrane of the periodontitis pathogen <i>Tannerella forsythia</i> . <i>Chemical Science</i> , 2023, 14, 869-888.	3.7	1
3252	Crystal structure of prodigiosin binding protein PgbP, a GNAT family protein, in <i>Serratia marcescens</i> FS14. <i>Biochemical and Biophysical Research Communications</i> , 2023, 640, 73-79.	1.0	0
3253	Structural and biochemical characterization of <i>Leptospira interrogans</i> Lsa45 reveals a penicillin-binding protein with esterase activity. <i>Process Biochemistry</i> , 2023, 125, 141-153.	1.8	1

#	ARTICLE	IF	CITATIONS
3254	Crystal structure analysis of pyrrolidone carboxyl peptidase from <i>Thermus thermophilus</i> . <i>Biophysical Chemistry</i> , 2023, 293, 106946.	1.5	1
3255	Boosting the Full Potential of PyMOL with Structural Biology Plugins. <i>Biomolecules</i> , 2022, 12, 1764.	1.8	21
3257	Antiviral signalling by a cyclic nucleotide activated CRISPR protease. <i>Nature</i> , 2023, 614, 168-174.	13.7	12
3260	Structural transitions during the cooperative assembly of baculovirus single-stranded DNA-binding protein on ssDNA. <i>Nucleic Acids Research</i> , 0, , .	6.5	1
3261	<scp>COLLAPSE</scp>: A representation learning framework for identification and characterization of protein structural sites. <i>Protein Science</i> , 2023, 32, .	3.1	4
3262	Structural and functional mapping of ars gene cluster in <i>Deinococcus indicus</i> DR1. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 519-534.	1.9	4
3263	High-resolution cryo-EM structure of the <i>Shigella</i> virus Sf6 genome delivery tail machine. <i>Science Advances</i> , 2022, 8, .	4.7	10
3264	The structure of the human LACTB filament reveals the mechanisms of assembly and membrane binding. <i>PLoS Biology</i> , 2022, 20, e3001899.	2.6	4
3265	Towards Effective Consensus Scoring in Structure-Based Virtual Screening. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 0, , .	2.2	2
3266	Cell-surface protein YwfG of <i>Lactococcus lactis</i> binds to α -1,2-linked mannose. <i>PLoS ONE</i> , 2023, 18, e0273955.	1.1	0
3267	Switching Prenyl Donor Specificities in Squalene Synthase-Like Aromatic Prenyltransferases from Bacterial Carbazole Alkaloid Biosynthesis. <i>ACS Chemical Biology</i> , 2023, 18, 123-133.	1.6	4
3268	The compact Cas β (Cas12l) β -bracelet TM provides a unique structural platform for DNA manipulation. <i>Cell Research</i> , 2023, 33, 229-244.	5.7	15
3269	Structural insights into catalytical capability for CPT11 hydrolysis and substrate specificity of a novel marine microbial carboxylesterase, E93. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
3270	Evolutionary analysis of p38 stress-activated kinases in unicellular relatives of animals suggests an ancestral function in osmotic stress. <i>Open Biology</i> , 2023, 13, .	1.5	2
3271	A sorghum ascorbate peroxidase with four binding sites has activity against ascorbate and phenylpropanoids. <i>Plant Physiology</i> , 2023, 192, 102-118.	2.3	7
3273	Comparative analysis of Cf-4 and Cf-19 in tomato (<i>Solanum lycopersicum</i>) β A bioinformatics study. , 2017, 87, .		0
3274	A structure-function analysis of chlorophyllase reveals a mechanism for activity regulation dependent on disulfide bonds. <i>Journal of Biological Chemistry</i> , 2023, 299, 102958.	1.6	3
3275	Staphylococcal Periscope proteins Aap, SasG, and Pls project noncanonical legume-like lectin adhesin domains from the bacterial surface. <i>Journal of Biological Chemistry</i> , 2023, 299, 102936.	1.6	3

#	ARTICLE	IF	CITATIONS
3276	The Î•PA3 phage nucleus is enclosed by a self-assembling 2D crystalline lattice. <i>Nature Communications</i> , 2023, 14, .	5.8	10
3277	<i>Staphylococcus aureus</i> Prophage-Encoded Protein Causes Abortive Infection and Provides Population Immunity against Kayviruses. <i>MBio</i> , 2023, 14, .	1.8	2
3278	Structural basis for the toxic activity of MafB2 from maf genomic island 2 (MGI-2) in <i>N. meningitidis</i> B16B6. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
3279	Computational and Functional Analysis of Structural Features in the ZAKÎ± Kinase. <i>Cells</i> , 2023, 12, 969.	1.8	2
3280	Two different alanine dehydrogenases from <i>Geobacillus kaustophilus</i> : Their biochemical characteristics and differential expression in vegetative cells and spores. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2023, 1871, 140904.	1.1	1
3281	Structural and Biochemical Analyses of the Butanol Dehydrogenase from <i>Fusobacterium nucleatum</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 2994.	1.8	0
3282	Crystal structure of a polyglycine hydrolase determined using a <i>RoseTTAFold</i> model. <i>Acta Crystallographica Section D: Structural Biology</i> , 2023, 79, 168-176.	1.1	3
3283	Atomic crystal structure and sugar specificity of a Î²-trefoil lectin domain from the ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 233, 123507.	3.6	1
3284	Archaeal DNA-import apparatus is homologous to bacterial conjugation machinery. <i>Nature Communications</i> , 2023, 14, .	5.8	9
3285	Insight into the Structural Basis for Dual Nucleic Acidâ€™ Recognition by the Scaffold Attachment Factor B2 Protein. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3286.	1.8	0
3286	Structures of MPND Reveal the Molecular Recognition of Nucleosomes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3368.	1.8	2
3287	Structural and biochemical basis of <i>Arabidopsis</i> FERONIA receptor kinase-mediated early signaling initiation. <i>Plant Communications</i> , 2023, 4, 100559.	3.6	5
3288	A cryptic oxidoreductase safeguards oxidative protein folding in <i>Corynebacterium diphtheriae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	1
3292	TcpA from the <i>Clostridium perfringens</i> plasmid pCW3 is more closely related to the DNA translocase FtsK than to coupling proteins. <i>Structure</i> , 2023, 31, 455-463.e4.	1.6	0
3293	Capsid structure of a fungal dsRNA megabirnavirus reveals its previously unidentified surface architecture. <i>PLoS Pathogens</i> , 2023, 19, e1011162.	2.1	3
3294	Lâ€serine biosynthesis in the human central nervous system: Structure and function of phosphoserine aminotransferase. <i>Protein Science</i> , 2023, 32, .	3.1	6
3295	Crystal structure and identification of amino acid residues for catalysis and binding of GH3 AnBX Î²-xylosidase from <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 2335-2349.	1.7	0
3300	Proteomic analysis defines the interactome of telomerase in the protozoan parasite, <i>Trypanosoma brucei</i> . <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2

#	ARTICLE	IF	CITATIONS
3302	Structural analysis and molecular dynamics simulation studies of HIV-1 antisense protein predict its potential role in HIV replication and pathogenesis. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
3303	AA16 Oxidoreductases Boost Cellulose-Active AA9 Lytic Polysaccharide Monooxygenases from <i>Myceliophthora thermophila</i> . <i>ACS Catalysis</i> , 2023, 13, 4454-4467.	5.5	11
3304	A set of closely related methyltransferases for site-specific tailoring of anthraquinone pigments. <i>Structure</i> , 2023, , .	1.6	1
3305	First and second sphere interactions accelerate non-native <i>N</i> -alkylation catalysis by the thermostable, methanol-tolerant B ₁₂ -dependent enzyme MtaC. <i>Chemical Communications</i> , 2023, 59, 4798-4801.	2.2	3
3306	The <i>Trypanosoma brucei</i> MISP family of invariant proteins is co-expressed with BARP as triple helical bundle structures on the surface of salivary gland forms, but is dispensable for parasite development within the tsetse vector. <i>PLoS Pathogens</i> , 2023, 19, e1011269.	2.1	2
3307	HED, a Human-Engineered Domain, Confers a Unique Fc-Binding Activity to Produce a New Class of Humanized Antibody-like Molecules. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6477.	1.8	0
3308	Crystal Structure and Functional Characterization of an S-Formylglutathione Hydrolase (BuSFGH) from Burkholderiaceae sp.. <i>Crystals</i> , 2023, 13, 621.	1.0	0
3309	A <i>Mycobacterium tuberculosis</i> Effector Targets Mitochondrion, Controls Energy Metabolism, and Limits Cytochrome <i>c</i> Exit. <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	6
3310	Dirigent protein subfamily function and structure in terrestrial plant phenol metabolism. <i>Methods in Enzymology</i> , 2023, , 101-150.	0.4	6
3311	Mirusviruses link herpesviruses to giant viruses. <i>Nature</i> , 2023, 616, 783-789.	13.7	28
3324	New Approach of 3D Protein Structure Superimposition: Case Study of SARS-COV-2 and SARS-COV. <i>Lecture Notes in Networks and Systems</i> , 2023, , 805-815.	0.5	2
3396	Structural Analyses of Bacterial Effectors by X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2024, , 485-502.	0.4	0
3427	How Does Bioinformatics Play a Role in Fungal Drug Discovery?. , 2024, , 725-742.		0
3428	New Smart Optimal Transition Molecules Structure Approach from Discrete to Continuous Based on Three-Dimensional Analysis Method. <i>Lecture Notes in Networks and Systems</i> , 2024, , 307-317.	0.5	0