Juan A Hermoso

List of Publications by Year
in descending order

171	6,732	57758	85541
papers	citations	44 h-index	71 g-index

179	179	179	7156
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Taking aim on bacterial pathogens: from phage therapy to enzybiotics. Current Opinion in Microbiology, 2007, 10, 461-472.	5.1	238
2	How allosteric control of Staphylococcus aureus penicillin binding protein 2a enables methicillin resistance and physiological function. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16808-16813.	7.1	235
3	Crystal and Electron Microscopy Structures of Sticholysin II Actinoporin Reveal Insights into the Mechanism of Membrane Pore Formation. Structure, 2003, 11, 1319-1328.	3.3	218
4	Lipase Activation by Nonionic Detergents. Journal of Biological Chemistry, 1996, 271, 18007-18016.	3.4	196
5	Activation of Bacterial Thermoalkalophilic Lipases Is Spurred by Dramatic Structural Rearrangements. Journal of Biological Chemistry, 2009, 284, 4365-4372.	3.4	196
6	Penicillinâ€binding protein 2a of methicillinâ€resistant Staphylococcus aureus. IUBMB Life, 2014, 66, 572-577.	3.4	176
7	Crystal structure of Î²-glucosidase A from Bacillus polymyxa: insights into the catalytic activity in family 1 glycosyl hydrolases. Journal of Molecular Biology, 1998, 275, 491-502.	4.2	166
8	Structural Basis for Selective Recognition of Pneumococcal Cell Wall by Modular Endolysin from Phage Cp-1. Structure, 2003, 11, 1239-1249.	3.3	149
9	Discovery of Antibiotic (E)-3-(3-Carboxyphenyl)-2-(4-cyanostyryl)quinazolin-4(3H)-one. Journal of the American Chemical Society, 2015, 137, 1738-1741.	13.7	116
10	Stabilization of Penicillin G Acylase from Escherichia coli : Site-Directed Mutagenesis of the Protein Surface To Increase Multipoint Covalent Attachment. Applied and Environmental Microbiology, 2004, 70, 1249-1251.	3.1	111
11	The Crystal Structure of Feruloyl Esterase A from Aspergillus niger Suggests Evolutive Functional Convergence in Feruloyl Esterase Family. Journal of Molecular Biology, 2004, 338, 495-506.	4.2	110
12	Structural Analysis of the Laetiporus sulphureus Hemolytic Pore-forming Lectin in Complex with Sugars. Journal of Biological Chemistry, 2005, 280, 17251-17259.	3.4	109
13	Molecular architecture of Streptococcus pneumoniae surface thioredoxinâ€fold lipoproteins crucial for extracellular oxidative stress resistance and maintenance of virulence. EMBO Molecular Medicine, 2013, 5, 1852-1870.	6.9	99
14	Solid-Phase Chemical Amination of a Lipase from Bacillus thermocatenulatus To Improve Its Stabilization via Covalent Immobilization on Highly Activated Glyoxyl-Agarose. Biomacromolecules, 2008, 9, 2553-2561.	5.4	98
15	Neutron crystallographic evidence of lipase-colipase complex activation by a micelle. EMBO Journal, 1997, 16, 5531-5536.	7.8	96
16	Structural Insights into the Lipase/esterase Behavior in the Candida rugosa Lipases Family: Crystal Structure of the Lipase 2 Isoenzyme at 1.97Ã... Resolution. Journal of Molecular Biology, 2003, 332, 1059-1069.	4.2	95
17	Disruption of Allosteric Response as an Unprecedented Mechanism of Resistance to Antibiotics. Journal of the American Chemical Society, 2014, 136, 9814-9817.	13.7	93
18	Pneumococcal surface proteins: when the whole is greater than the sum of its parts. Molecular Oral Microbiology, 2012, 27, 221-245.	2.7	92

#	Article	IF	Citations
19	Insights into pneumococcal pathogenesis from the crystal structure of the modular teichoic acid phosphorylcholine esterase Pce. Nature Structural and Molecular Biology, 2005, 12, 533-538.	8.2	89
20	Structural basis of PcsB-mediated cell separation in Streptococcus pneumoniae. Nature Communications, 2014, 5, 3842.	12.8	82
21	The crystal structure of Canavalia brasiliensis lectin suggests a correlation between its quaternary conformation and its distinct biological properties from Concanavalin A. FEBS Letters, 1997, 405, 114-118.	2.8	79
22	Directed Evolution of Î²-Glucosidase A from Paenibacillus polymyxa to Thermal Resistance. Journal of Biological Chemistry, 2000, 275, 13708-13712.	3.4	76
23	Pneumococcal CbpD is a murein hydrolase that requires a dual cell envelope binding specificity to kill target cells during fratricide. Molecular Microbiology, 2010, 76, 905-917.	2.5	74
24	Mechanism of Coenzyme Recognition and Binding Revealed by Crystal Structure Analysis of Ferredoxinâ€“NADP+ Reductase Complexed with NADP+. Journal of Molecular Biology, 2002, 319, 1133-1142.	4.2	73
25	The crystal structure of tetrameric methionine adenosyltransferase from rat liver reveals the methionine-binding site 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 300, 363-375.	4.2	72
26	Conformational Dynamics in Penicillin-Binding Protein 2a of Methicillin-Resistant Staphylococcus aureus, Allosteric Communication Network and Enablement of Catalysis. Journal of the American Chemical Society, 2017, 139, 2102-2110.	13.7	65
27	Elucidation of the Molecular Recognition of Bacterial Cell Wall by Modular Pneumococcal Phage Endolysin CPL-1. Journal of Biological Chemistry, 2007, 282, 24990-24999.	3.4	61
28	Structural basis for the broad specificity of a new family of amino-acid racemases. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 79-90.	2.5	61
29	The 1.49Ã... Resolution Crystal Structure of PsbQ from Photosystem II of Spinacia oleracea Reveals a PPII Structure in the N-terminal Region. Journal of Molecular Biology, 2005, 350, 1051-1060.	4.2	60
30	Probing the determinants of substrate specificity of a feruloyl esterase, AnFaeA, from Aspergillus niger. FEBS Journal, 2005, 272, 4362-4371.	4.7	59
31	Hydroxo and azolate derivatives of pentafluorophenyl-nickel(II) complexes. Crystal structure of [NBu4]2[{Ni(C6F5)2(.mu.-OH)}2] and [NBu4]2[{Ni(C6F5)2}2(.mu.-OH)(.mu.-pyrazolato)]. Inorganic Chemistry, 1992, 31, 1518-1523.	4.0	57
32	Insights into pneumococcal fratricide from the crystal structures of the modular killing factor LytC. Nature Structural and Molecular Biology, 2010, 17, 576-581.	8.2	57
33	Crystal structure of CbpF, a bifunctional cholineâ€binding protein and autolysis regulator from Streptococcus pneumoniae. EMBO Reports, 2009, 10, 246-251.	4.5	56
34	Synthesis and reactivity of hydroxo-bridged binuclear platinum complexes. Crystal structure of [NBu4]2[{Pt(C6F5)2(Âµ-OH)}2]. Journal of the Chemical Society Dalton Transactions, 1992, , 53-58.	1.1	55
35	Promotion of multipoint covalent immobilization through different regions of genetically modified penicillin G acylase from E. coli. Process Biochemistry, 2010, 45, 390-398.	3.7	55
36	Probing the Determinants of Coenzyme Specificity in Ferredoxin-NADP+ Reductase by Site-directed Mutagenesis. Journal of Biological Chemistry, 2001, 276, 11902-11912.	3.4	54

#	Article	IF	Citations
37	Structural Insights into the Coenzyme Mediated Monomerâ€“Dimer Transition of the Pro-Apoptotic Apoptosis Inducing Factor. Biochemistry, 2014, 53, 4204-4215.	2.5	52
38	C-Terminal Tyrosine of Ferredoxinâ˜NADP+ Reductase in Hydride Transfer Processes with NAD(P)+/H. Biochemistry, 2005, 44, 13477-13490.	2.5	51
39	New Alkaloid Antibiotics That Target the DNA Topoisomerase I of Streptococcus pneumoniae. Journal of Biological Chemistry, 2011, 286, 6402-6413.	3.4	51
40	Crystal Structures of Bacterial Peptidoglycan Amidase AmpD and an Unprecedented Activation Mechanism. Journal of Biological Chemistry, 2011, 286, 31714-31722.	3.4	49
41	Role of Arg100 and Arg264 fromAnabaenaPCC 7119 Ferredoxinâ˜NADP+Reductase for Optimal NADP+Binding and Electron Transferâ€. Biochemistry, 1998, 37, 17680-17691.	2.5	48
42	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against Helicobacter pylori Infection. ACS Chemical Biology, 2009, 4, 928-938.	3.4	48
43	Crystal Structures of Methionine Adenosyltransferase Complexed with Substrates and Products Reveal the Methionine-ATP Recognition and Give Insights into the Catalytic Mechanism. Journal of Molecular Biology, 2003, 331, 407-416.	4.2	47
44	Critical Role of Micelles in Pancreatic Lipase Activation Revealed by Small Angle Neutron Scattering. Journal of Biological Chemistry, 2000, 275, 4220-4224.	3.4	46
45	Chemical Modification of Protein Surfaces To Improve Their Reversible Enzyme Immobilization on Ionic Exchangers. Biomacromolecules, 2006, 7, 3052-3058.	5.4	46
46	Carbohydrate recognition and lysis by bacterial peptidoglycan hydrolases. Current Opinion in Structural Biology, 2017, 44, 87-100.	5.7	45
47	Structure of full-length human phenylalanine hydroxylase in complex with tetrahydrobiopterin. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11229-11234.	7.1	44
48	Influence of the conformational flexibility on the kinetics and dimerisation process of twoCandida rugosalipase isoenzymes. FEBS Letters, 2001, 501, 87-91.	2.8	42
49	Muropeptide Binding and the X-ray Structure of the Effector Domain of the Transcriptional Regulator AmpR of Pseudomonas aeruginosa. Journal of the American Chemical Society, 2017, 139, 1448-1451.	13.7	42
50	Genetic Modification of the Penicillin G Acylase Surface To Improve Its Reversible Immobilization on Ionic Exchangers. Applied and Environmental Microbiology, 2007, 73, 312-319.	3.1	41
51	Cell-Wall Remodeling by the Zinc-Protease AmpDh3 from Pseudomonas aeruginosa. Journal of the American Chemical Society, 2013, 135, 12604-12607.	13.7	41
52	Structure solution with <scp>ARCIMBOLDO</scp> using fragments derived from distant homology models. FEBS Journal, 2014, 281, 4029-4045.	4.7	41
53	Structure and Cell Wall Cleavage by Modular Lytic Transglycosylase MltC of Escherichia coli. ACS Chemical Biology, 2014, 9, 2058-2066.	3.4	41
54	Mixed Ion Exchange Supports as Useful Ion Exchangers for Protein Purification:Â Purification of Penicillin G Acylase fromEscherichia coli. Biomacromolecules, 2007, 8, 703-707.	5.4	40

#	Article	IF	Citations
55	Oligomeric State in the Crystal Structure of Modular FAD Synthetase Provides Insights into Its Sequential Catalysis in Prokaryotes. Journal of Molecular Biology, 2010, 400, 218-230.	4.2	40
56	The Quinazolinone Allosteric Inhibitor of PBP 2a Synergizes with Piperacillin and Tazobactam against Methicillin-Resistant Staphylococcus aureus. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	40
57	Class A PBPs have a distinct and unique role in the construction of the pneumococcal cell wall. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6129-6138.	7.1	40
58	High-Resolution Crystal Structure of MltE, an Outer Membrane-Anchored Endolytic Peptidoglycan Lytic Transglycosylase from Escherichia coli. Biochemistry, 2011, 50, 2384-2386.	2.5	39
59	Synthesis of a heterogeneous artificial metallolipase with chimeric catalytic activity. Chemical Communications, 2015, 51, 9324-9327.	4.1	39
60	Improved Stabilization of Genetically Modified Penicillin G Acylase in the Presence of Organic Cosolvents by Co- Immobilization of the Enzyme with Polyethyleneimine. Advanced Synthesis and Catalysis, 2007, 349, 459-464.	4.3	38
61	Reaction Products and the X-ray Structure of AmpDh2, a Virulence Determinant of Pseudomonas aeruginosa. Journal of the American Chemical Society, 2013, 135, 10318-10321.	13.7	38
62	Role of a Cluster of Hydrophobic Residues Near the FAD Cofactor in Anabaena PCC 7119 Ferredoxin-NADP+Reductase for Optimal Complex Formation and Electron Transfer to Ferredoxin. Journal of Biological Chemistry, 2001, 276, 27498-27510.	3.4	37
63	Flavodoxin: A compromise between efficiency and versatility in the electron transfer from Photosystem I to Ferredoxin-NADP+ reductase. Biochimica Et Biophysica Acta - Bioenergetics, 2009, 1787, 144-154.	1.0	37
64	Pneumococcal phosphoglycerate kinase interacts with plasminogen and its tissue activator. Thrombosis and Haemostasis, 2014, 112, 401-416.	3.4	37
65	Structure of the pneumococcal <scp>l</scp>,<scp>d</scp>â€carboxypeptidase <scp>DacB</scp> and pathophysiological effects of disabled cell wall hydrolases <scp>DacA</scp> and <scp>DacB</scp>. Molecular Microbiology, 2014, 93, 1183-1206.	2.5	37
66	The Ferredoxin-NADP(H) Reductase from Rhodobacter capsulatus:â€‰ Molecular Structure and Catalytic Mechanism,. Biochemistry, 2005, 44, 11730-11740.	2.5	36
67	Nickel-catalyzed Cyclotrimerization of Malononitrile: The Dicyanomethanide-bridged, Anionic NiII Complex[{Ni(C5F5)2(Î¼-NCCHCN)}2]2âŠ–. Angewandte Chemie International Edition in English, 1991, 30, 716-718.	4.4	35
68	Structure of the Large Extracellular Loop of FtsX and Its Interaction with the Essential Peptidoglycan Hydrolase PcsB in Streptococcus pneumoniae. MBio, 2019, 10, .	4.1	35
69	Involvement of the Pyrophosphate and the 2â€²-Phosphate Binding Regions of Ferredoxin-NADP+ Reductase in Coenzyme Specificity. Journal of Biological Chemistry, 2003, 278, 49203-49214.	3.4	34
70	A one-pot, simple methodology for cassette randomisation and recombination for focused directed evolution. Protein Engineering, Design and Selection, 2008, 21, 567-576.	2.1	34
71	Reactivity of the [Ni(C6F5)2(Î¼-OH)2]2â^' ion towards Î²-diketones, 8-hydroxiquinoline and heterocyclic thiones. Crystal structure of [NBu4][Ni(C6F5)2(C5H4NS-2)]. Journal of Organometallic Chemistry, 1992, 435, 193-202.	1.8	33
72	Peptidoglycan Remodeling by the Coordinated Action of Multispecific Enzymes. Microbial Drug Resistance, 2014, 20, 190-198.	2.0	33

#	Article	IF	Citations
73	Crystal structures of Ophiostoma piceae sterol esterase: Structural insights into activation mechanism and product release. Journal of Structural Biology, 2014, 187, 215-222.	2.8	32
74	The Allosteric Site for the Nascent Cell Wall in Penicillin-Binding Protein 2a: An Achillesâ€™ Heel of Methicillin-Resistant Staphylococcus aureus. Current Medicinal Chemistry, 2015, 22, 1678-1686.	2.4	32
75	Modular Architecture and Unique Teichoic Acid Recognition Features of Choline-Binding Protein L (CbpL) Contributing to Pneumococcal Pathogenesis. Scientific Reports, 2016, 6, 38094.	3.3	32
76	Reactions of cationic ruthenium hydrides with 1-alkynes: formation of .sigma.-alkynyl ruthenium complexes and reduction of 1-alkynes to 1-alkenes. Organometallics, 1991, 10, 2371-2376.	2.3	31
77	New methoxo-, hydroxo- and pyrazolate-bridged platinum(II) complexes. Crystal structure of [NBu4]2[{Pt(C6F5)2}2(Âµ-OH)(Âµ-dmpz)](dmpz = 3,5-dimethylpyrazolate). Journal of the Chemical Society Dalton Transactions, 1992, , 1681-1686.	1.1	31
78	Semisynthetic peptideâ€“lipase conjugates for improved biotransformations. Chemical Communications, 2012, 48, 9053.	4.1	31
79	Structural Basis for Selective Recognition of Endogenous and Microbial Polysaccharides by Macrophage Receptor SIGN-R1. Structure, 2014, 22, 1595-1606.	3.3	31
80	Structure and Function of Choline-Binding Proteins. , 2015, , 207-230.		31
81	Exolytic and endolytic turnover of peptidoglycan by lytic transglycosylase Slt of Pseudomonas aeruginosa. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4393-4398.	7.1	31
82	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. Acta Crystallographica Section D: Structural Biology, 2018, 74, 290-304.	2.3	30
83	Promiscuous enantioselective (â^')-Î³-lactamase activity in the Pseudomonas fluorescens esterase I. Organic and Biomolecular Chemistry, 2012, 10, 3388.	2.8	29
84	Allostery, Recognition of Nascent Peptidoglycan, and Cross-linking of the Cell Wall by the Essential Penicillin-Binding Protein 2x of Streptococcus pneumoniae. ACS Chemical Biology, 2018, 13, 694-702.	3.4	29
85	Structural basis of denuded glycan recognition by SPOR domains in bacterial cell division. Nature Communications, 2019, 10, 5567.	12.8	29
86	Enhancement of the Stability of a Prolipase from Rhizopus oryzae toward Aldehydes by Saturation Mutagenesis. Applied and Environmental Microbiology, 2007, 73, 7291-7299.	3.1	28
87	Heteroresistance to Fosfomycin Is Predominant in Streptococcus pneumoniae and Depends on the murA1 Gene. Antimicrobial Agents and Chemotherapy, 2013, 57, 2801-2808.	3.2	28
88	Catalytic Cycle of the N-Acetylglucosaminidase NagZ from Pseudomonas aeruginosa. Journal of the American Chemical Society, 2017, 139, 6795-6798.	13.7	28
89	Comparative study of two <scp>GH</scp>19 chitinaseâ€like proteins from HeveaÂbrasiliensis, one exhibiting a novel carbohydrateâ€binding domain. FEBS Journal, 2014, 281, 4535-4554.	4.7	27
90	Activation by Allostery in Cell-Wall Remodeling by a Modular Membrane-Bound Lytic Transglycosylase from Pseudomonas aeruginosa. Structure, 2016, 24, 1729-1741.	3.3	27

#	Article	IF	Citations
91	Mechanism of the Escherichia coli MltE lytic transglycosylase, the cell-wall-penetrating enzyme for Type VI secretion system assembly. Scientific Reports, 2018, 8, 4110.	3.3	27
92	Structural basis of increased resistance to thermal denaturation induced by single amino acid substitution in the sequence of Î²-glucosidase A fromBacillus polymyxa. , 1998, 33, 567-576.		26
93	Pancreatic Lipase-Related Protein Type 1: A Double Mutation Restores a Significant Lipase Activity. Biochemical and Biophysical Research Communications, 1998, 246, 513-517.	2.1	26
94	Pyrrolopyrimidine vs Imidazole-Phenyl-Thiazole Scaffolds in Nonpeptidic Dimerization Inhibitors of Leishmania infantum Trypanothione Reductase. ACS Infectious Diseases, 2019, 5, 873-891.	3.8	26
95	Structural insights into the synthesis of FMN in prokaryotic organisms. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2526-2542.	2.5	25
96	Pancreatic lipase-related protein type I: a specialized lipase or an inactive enzyme. Protein Engineering, Design and Selection, 1998, 11, 135-142.	2.1	24
97	Structural analysis of interactions for complex formation between Ferredoxin-NADP+ reductase and its protein partners. Proteins: Structure, Function and Bioinformatics, 2005, 59, 592-602.	2.6	24
98	Tuning of the FMN binding and oxido-reduction properties by neighboring side chains in Anabaena flavodoxin. Archives of Biochemistry and Biophysics, 2007, 467, 206-217.	3.0	24
99	Common conformational changes in flavodoxins induced by FMN and anion binding: The structure of Helicobacter pylori apoflavodoxin. Proteins: Structure, Function and Bioinformatics, 2007, 69, 581-594.	2.6	24
100	Renew or die: The molecular mechanisms of peptidoglycan recycling and antibiotic resistance in Gram-negative pathogens. Drug Resistance Updates, 2016, 28, 91-104.	14.4	24
101	Synthesis and structural study of [{Pd(C6H4CH2N(CH3)2)}2(Î¼-Br) (Î¼-X)] complexes (X = hydroxide, amide) Tj ETQq1 1 0.784314	1.8	23
102	Insights into Molecular Plasticity of Choline Binding Proteins (Pneumococcal Surface Proteins) by SAXS. Journal of Molecular Biology, 2007, 365, 411-424.	4.2	23
103	Orthologous and Paralogous AmpD Peptidoglycan Amidases from Gram-Negative Bacteria. Microbial Drug Resistance, 2016, 22, 470-476.	2.0	23
104	Deciphering how Cpl-7 cell wall-binding repeats recognize the bacterial peptidoglycan. Scientific Reports, 2017, 7, 16494.	3.3	23
105	Di- and tri-nuclear nickel(II) complexes with bridging thiolato groups. Crystal structure of [NBu4]2[Ni3(C6F5)4(Âµ-SEt)4]. Journal of the Chemical Society Dalton Transactions, 1994, , 19-23.	1.1	22
106	The lipase/colipase complex is activated by a micelle: neutron crystallographic evidence. Chemistry and Physics of Lipids, 1998, 93, 123-129.	3.2	21
107	An esterase from Thermus thermophilus HB27 with hyper-thermoalkalophilic properties: Purification, characterisation and structural modelling. Journal of Molecular Catalysis B: Enzymatic, 2011, 70, 127-137.	1.8	21
108	Unconventional Antibacterials and Adjuvants. Accounts of Chemical Research, 2021, 54, 917-929.	15.6	20

#	Article	IF	Citations
109	Synthesis and structural study of neutral mononuclear and anionic binuclear 2,4,6-trifluorophenyl derivatives of palladium(II). Crystal structure of [P(CH2Ph)Ph3]2[(C6F3H2)2Pd(Âµ-SCN)(Âµ-NCS)Pd(C6F3H2)2]. Journal of the Chemical Society Dalton Transactions, 1990, , 1621-1626.	1.1	19
110	Structural basis of the catalytic role of Glu301 inAnabaena PCC 7119 ferredoxin-NADP+ reductase revealed by x-ray crystallography. , 2000, 38, 60-69.		18
111	Coenzyme binding and hydride transfer in Rhodobacter capsulatus ferredoxin/flavodoxin NADP(H) oxidoreductase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 199-210.	2.3	18
112	A single amino acid polymorphism in the glycosyltransferase CpsK defines four Streptococcus suis serotypes. Scientific Reports, 2017, 7, 4066.	3.3	18
113	Biochemical and Structural Characterization of a novel thermophilic esterase EstD11 provide catalytic insights for the HSL family. Computational and Structural Biotechnology Journal, 2021, 19, 1214-1232.	4.1	17
114	Ion Pairing between Lipase and Colipase Plays a Critical Role in Catalysis. Journal of Biological Chemistry, 1998, 273, 33604-33609.	3.4	16
115	Turnover of Bacterial Cell Wall by SltB3, a Multidomain Lytic Transglycosylase of Pseudomonas aeruginosa. ACS Chemical Biology, 2016, 11, 1525-1531.	3.4	16
116	Crystallization and preliminary crystallographic analysis of a novel haemolytic lectin from the mushroomLaetiporus sulphureus. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1139-1141.	2.5	15
117	Protein Motifs Involved in Coenzyme Interaction and Enzymatic Efficiency in Anabaena Ferredoxin-NADP⁺ Reductase,. Biochemistry, 2009, 48, 3109-3119.	2.5	15
118	Regioselective resolution of 1,n-diols catalysed by lipases: a rational explanation of the enzymayic selectivity. Journal of Molecular Catalysis B: Enzymatic, 2001, 11, 1013-1024.	1.8	14
119	Activation of Horse PLRP2 by Bile Salts Does Not Require Colipaseâ€. Biochemistry, 2002, 41, 8422-8428.	2.5	13
120	Activation in the family of Candida rugosa isolipases by polyethylene glycol. Journal of Molecular Catalysis B: Enzymatic, 2005, 32, 225-229.	1.8	13
121	Structural and Phylogenetic Analysis of Rhodobacter capsulatus NifF: Uncovering General Features of Nitrogen-fixation (nif)-Flavodoxins. International Journal of Molecular Sciences, 2013, 14, 1152-1163.	4.1	13
122	Disulfide Engineered Lipase to Enhance the Catalytic Activity: A Structure-Based Approach on BTL2. International Journal of Molecular Sciences, 2019, 20, 5245.	4.1	13
123	Structural insights into the binding and catalytic mechanisms of the Listeria monocytogenes bacteriophage glycosyl hydrolase PlyP40. Molecular Microbiology, 2018, 108, 128-142.	2.5	12
124	Crystallization and preliminary X-ray diffraction studies of the pneumococcal teichoic acid phosphorylcholine esterase Pce. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 221-224.	0.7	11
125	Three-dimensional structures of Lipoproteins from Streptococcus pneumoniae and Staphylococcus aureus. International Journal of Medical Microbiology, 2018, 308, 692-704.	3.6	11
126	Catalytic Cycle of Glycoside Hydrolase BglX from Pseudomonas aeruginosa and Its Implications for Biofilm Formation. ACS Chemical Biology, 2020, 15, 189-196.	3.4	11

#	Article	IF	Citations
127	Structural Characterization of the Essential Cell Division Protein FtsE and Its Interaction with FtsX in Streptococcus pneumoniae. MBio, 2020, 11, .	4.1	11
128	Probing the role of glutamic acid 139 ofAnabaenaferredoxin-NADP+reductase in the interaction with substrates. FEBS Journal, 2002, 269, 4938-4947.	0.2	10
129	Pneumococcal phosphorylcholine esterase, Pce, contains a metal binuclear center that is essential for substrate binding and catalysis. Protein Science, 2005, 14, 3013-3024.	7.6	10
130	Crystallization and preliminary X-ray diffraction studies of FAD synthetase fromCorynebacterium ammoniagenes. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1285-1288.	0.7	10
131	Crystal structures of CbpF complexed with atropine and ipratropium reveal clues for the design of novel antimicrobials against Streptococcus pneumoniae. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 129-135.	2.4	10
132	SEQUENCE SLIDER: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. Acta Crystallographica Section D: Structural Biology, 2020, 76, 221-237.	2.3	10
133	Acyclic phenylalkanediols as substrates for the study of enzyme recognition. Regioselective acylation by porcine pancreatic lipase: a structural hypothesis for the enzymatic selectivity. Tetrahedron, 1999, 55, 14961-14974.	1.9	9
134	Structural Basis for Membrane Anchorage of Viral Ï•29 DNA during Replication*. Journal of Biological Chemistry, 2005, 280, 42486-42488.	3.4	9
135	X-ray Structure of Catenated Lytic Transglycosylase SltB1. Biochemistry, 2017, 56, 6317-6320.	2.5	9
136	Structural basis for the kinetics of Candida rugosa Lip1 and Lip3 isoenzymes. Colloids and Surfaces B: Biointerfaces, 2002, 26, 67-74.	5.0	8
137	Structure of the Functional Domain of Ï†29 Replication Organizer. Journal of Biological Chemistry, 2005, 280, 20730-20739.	3.4	8
138	Crystallization and preliminary X-ray diffraction studies of choline-binding protein F fromStreptococcus pneumoniae. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 742-745.	0.7	8
139	Characterization of gadolinium complexes for SAD phasing in macromolecular crystallography: application to CbpF. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 823-831.	2.5	8
140	Crystallization and preliminary X-ray diffraction analysis of the lytic transglycosylase MltE fromEscherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 161-163.	0.7	8
141	Crystallization and preliminary X-ray diffraction analysis of phosphoglycerate kinase fromStreptococcus pneumoniae. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1285-1289.	0.7	8
142	The C-terminal extension of bacterial flavodoxin-reductases: Involvement in the hydride transfer mechanism from the coenzyme. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 33-43.	1.0	8
143	Structural Cues for Understanding eEF1A2 Moonlighting. ChemBioChem, 2021, 22, 374-391.	2.6	8
144	Crystal growth and crystal structure of KTb(CrO4)2. Journal of Solid State Chemistry, 1990, 85, 83-87.	2.9	7

#	Article	IF	Citations
145	Crystallization and preliminary X-ray diffraction studies of the BTL2 lipase from the extremophilic microorganismBacillus thermocatenulatus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1043-1045.	0.7	7
146	Crystallization and preliminary crystallographic analysis of the catalytic module of endolysin from Cp-7, a phage infectingStreptococcus pneumoniae. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 670-673.	0.7	7
147	A complement to the modern crystallographer's toolbox: caged gadolinium complexes with versatile binding modes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1506-1516.	2.5	7
148	Crystallization of a proteolyzed form of the horse pancreatic lipase-related protein 2: structural basis for the specific detergent requirement. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2107-2109.	2.5	6
149	Crystallization and preliminary X-ray diffraction studies of two different crystal forms of the lipase 2 isoform from the yeastCandida rugosa. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 499-501.	2.5	5
150	Crystallization and preliminary X-ray diffraction studies of the transcriptional repressor PaaX, the main regulator of the phenylacetic acid degradation pathway inEscherichia coliW. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1278-1280.	0.7	5
151	Binding of non-canonical peptidoglycan controls Vibrio cholerae broad spectrum racemase activity. Computational and Structural Biotechnology Journal, 2021, 19, 1119-1126.	4.1	5
152	Distortions of molecular geometry in pentafluorophenyl rings bonded to metals. Journal of Chemical Crystallography, 1994, 24, 457-464.	1.1	4
153	Crystallization and preliminary X-ray diffraction studies of the carbohydrate-recognition domain of SIGN-R1, a receptor for microbial polysaccharides and sialylated antibody on splenic marginal zone macrophages. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1264-1266.	0.7	4
154	Structural Bioinformatics in Broad-Spectrum Racemases: A New Path in Antimicrobial Research. Current Organic Chemistry, 2016, 20, 1222-1231.	1.6	4
155	Crystallization and preliminary X-ray diffraction studies of the water-soluble state of the pore-forming toxin sticholysin II from the sea anemoneStichodactyla helianthus. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1229-1231.	2.5	3
156	Crystallization of a flavodoxin involved in nitrogen fixation inRhodobacter capsulatus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 375-377.	0.7	3
157	Crystallization of the pneumococcal autolysin LytC: in-house phasing using novel lanthanide complexes. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 448-451.	0.7	3
158	Escherichia coli LacZ Î²-galactosidase inhibition by monohydroxy acetylated glycopyranosides: Role of the acetyl groups. Journal of Molecular Catalysis B: Enzymatic, 2014, 107, 31-38.	1.8	3
159	A new approach to structure resolution by molecular dynamics: variable force constants strategy. Acta Crystallographica Section B: Structural Science, 1995, 51, 76-80.	1.8	2
160	Crystallization and preliminary X-ray diffraction studies of the complete modular endolysin from Cp-1, a phage infectingStreptococcus pneumoniae. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1487-1489.	2.5	2
161	Crystallization and preliminary X-ray diffraction analysis of ferredoxin-NADP(H) reductase fromRhodobacter capsulatus. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2332-2335.	2.5	2
162	Crystal structure of CbpF, a bifunctional cholineâ€binding protein and autolysis regulator from Streptococcus pneumoniae. EMBO Reports, 2009, 10, 413-413.	4.5	2

#	Article	IF	Citations
163	Getting CAD in Shape: The Atomic Structure of Human Dihydroorotase Domain. Structure, 2014, 22, 179-181.	3.3	2
164	A Structural Dissection of the Active Site of the Lytic Transglycosylase MltE from Escherichia coli. Biochemistry, 2018, 57, 6090-6098.	2.5	2
165	Cold-induced aldimine bond cleavage by Tris inBacillus subtilisalanine racemase. Organic and Biomolecular Chemistry, 2019, 17, 4350-4358.	2.8	2
166	Crystal Structure and Pathophysiological Role of the Pneumococcal Nucleoside-binding Protein PnrA. Journal of Molecular Biology, 2021, 433, 166723.	4.2	2
167	Integrative structural biology of the penicillin-binding protein-1 from Staphylococcus aureus, an essential component of the divisome machinery. Computational and Structural Biotechnology Journal, 2021, 19, 5392-5405.	4.1	2
168	Structural basis of the catalytic role of Glu301 in Anabaena PCC 7119 ferredoxin-NADP+ reductase revealed by x-ray crystallography. Proteins: Structure, Function and Bioinformatics, 2000, 38, 60.	2.6	2
169	First Lanthanide Complex for De Novo Phasing in Native Protein Crystallography at 1 Ã... Radiation. ACS Applied Bio Materials, 2021, 4, 4575-4581.	4.6	1
170	Teaching an old dog new tricks: repurposing Î²-lactams. Trends in Pharmacological Sciences, 2021, 42, 617-619.	8.7	1
171	X-ray and Neutron Diffraction Approaches to the Structural Analysis of Protein-Lipid Interactions. , 2006, , 63-110.		1