## Optimal description of a protein structure in terms of n motion

Acta Crystallographica Section D: Biological Crystallography 62, 439-450

DOI: 10.1107/s0907444906005270

**Citation Report** 

#	Article	IF	CITATIONS
1	Conformational restriction blocks glutamate receptor desensitization. Nature Structural and Molecular Biology, 2006, 13, 1120-1127.	3.6	106
2	Structure of the human beta-ketoacyl [ACP] synthase from the mitochondrial type II fatty acid synthase. Protein Science, 2006, 16, 261-272.	3.1	56
3	Structure of A197 from Sulfolobus Turreted Icosahedral Virus: a Crenarchaeal Viral Glycosyltransferase Exhibiting the GT-A Fold. Journal of Virology, 2006, 80, 7636-7644.	1.5	47
4	Structural basis for ligand and heparin binding to neuropilin B domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6152-6157.	3.3	201
5	Asp-120 Locates Zn2 for Optimal Metallo-β-lactamase Activity. Journal of Biological Chemistry, 2007, 282, 18276-18285.	1.6	40
6	Escherichia coli MutS Tetramerization Domain Structure Reveals That Stable Dimers but Not Tetramers Are Essential for DNA Mismatch Repair in Vivo. Journal of Biological Chemistry, 2007, 282, 16345-16354.	1.6	55
7	Normal mode refinement of anisotropic thermal parameters for a supramolecular complex at 3.42-A crystallographic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7869-7874.	3.3	56
8	Crystal Structure of the VP4 Protease from Infectious Pancreatic Necrosis Virus Reveals the Acyl-Enzyme Complex for an Intermolecular Self-cleavage Reaction. Journal of Biological Chemistry, 2007, 282, 24928-24937.	1.6	25
9	Structural Insights into Catalysis and Inhibition of O-Acetylserine Sulfhydrylase from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2007, 282, 23473-23481.	1.6	82
10	Heme Coordination by Staphylococcus aureus IsdE. Journal of Biological Chemistry, 2007, 282, 28815-28822.	1.6	86
11	Crystal Structure of the ECH2 Catalytic Domain of CurF from Lyngbya majuscula. Journal of Biological Chemistry, 2007, 282, 35954-35963.	1.6	50
12	Structural Analysis of the Synaptic Protein Neuroligin and Its β-Neurexin Complex: Determinants for Folding and Cell Adhesion. Neuron, 2007, 56, 979-991.	3.8	142
13	Crystal Structure of the TLR4-MD-2 Complex with Bound Endotoxin Antagonist Eritoran. Cell, 2007, 130, 906-917.	13.5	1,499
14	Structure and Dynamics of UDP–Clucose Pyrophosphorylase from Arabidopsis thaliana with Bound UDP–Clucose and UTP. Journal of Molecular Biology, 2007, 366, 830-841.	2.0	43
15	The Structure and Function of a Novel Glycerophosphodiesterase from Enterobacter aerogenes. Journal of Molecular Biology, 2007, 367, 1047-1062.	2.0	66
16	Structures of Perfringolysin O Suggest a Pathway for Activation of Cholesterol-dependent Cytolysins. Journal of Molecular Biology, 2007, 367, 1227-1236.	2.0	87
17	The Structure of a Tandem Pair of Spectrin Repeats of Plectin Reveals a Modular Organization of the Plakin Domain. Journal of Molecular Biology, 2007, 368, 1379-1391.	2.0	52
18	The Crystal Structure of the Human Mov34 MPN Domain Reveals a Metal-free Dimer. Journal of Molecular Biology, 2007, 370, 846-855.	2.0	51

#	Article	IF	CITATIONS
19	Blood Group Antigen Recognition by Escherichia coli Heat-labile Enterotoxin. Journal of Molecular Biology, 2007, 371, 754-764.	2.0	61
20	Crystal Structure of Conserved Domains 1 and 2 of the Human DEAD-box Helicase DDX3X in Complex with the Mononucleotide AMP. Journal of Molecular Biology, 2007, 372, 150-159.	2.0	117
21	Structure of an Amide Bond Forming F420:Î <sup>3</sup> γ-glutamyl Ligase from Archaeoglobus Fulgidus - A Member of a New Family of Non-ribosomal Peptide Synthases. Journal of Molecular Biology, 2007, 372, 456-469.	2.0	31
22	Crystal Structures of Two Aromatic Hydroxylases Involved in the Early Tailoring Steps of Angucycline Biosynthesis. Journal of Molecular Biology, 2007, 372, 633-648.	2.0	59
23	Molecular Cloning, Characterisation and Ligand-bound Structure of an Azoreductase from Pseudomonas aeruginosa. Journal of Molecular Biology, 2007, 373, 1213-1228.	2.0	66
24	Structure of the Janus Protein Human CLIC2. Journal of Molecular Biology, 2007, 374, 719-731.	2.0	64
25	Structure of the Human MutSα DNA Lesion Recognition Complex. Molecular Cell, 2007, 26, 579-592.	4.5	311
26	Nanosecond-Timescale Conformational Dynamics of the Human α7 Nicotinic Acetylcholine Receptor. Biophysical Journal, 2007, 93, 2622-2634.	0.2	70
27	Structure of the C-terminal effector-binding domain of AhrC bound to its corepressor <scp>L</scp> -arginine. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 918-921.	0.7	16
28	A previously unobserved conformation for the human Pex5p receptor suggests roles for intrinsic flexibility and rigid domain motions in ligand binding. BMC Structural Biology, 2007, 7, 24.	2.3	23
29	Crystal structure of aminopeptidase <i>N</i> from human pathogen <i>Neisseria meningitidis</i> . Proteins: Structure, Function and Bioinformatics, 2008, 70, 273-279.	1.5	43
30	The structure of flavinâ€dependent tryptophan 7â€halogenase RebH. Proteins: Structure, Function and Bioinformatics, 2008, 70, 289-293.	1.5	89
31	Nucleotide recognition by the cytoplasmic domain of the human chloride transporter ClC-5. Nature Structural and Molecular Biology, 2007, 14, 60-67.	3.6	136
32	Mechanism of auxin perception by the TIR1 ubiquitin ligase. Nature, 2007, 446, 640-645.	13.7	1,367
33	High resolution structure and catalysis of <i>O</i> â€acetylserine sulfhydrylase isozyme B from <i>Escherichia coli</i> . FEBS Journal, 2007, 274, 5382-5389.	2.2	18
34	Hinge Atlas: relating protein sequence to sites of structural flexibility. BMC Bioinformatics, 2007, 8, 167.	1.2	43
35	A new DNA binding protein highly conserved in diverse crenarchaeal viruses. Virology, 2007, 363, 387-396.	1.1	48
36	A winged-helix protein from sulfolobus turreted icosahedral virus points toward stabilizing disulfide bonds in the intracellular proteins of a hyperthermophilic virus. Virology, 2007, 368, 249-261.	1.1	57

#	Article	IF	CITATIONS
37	Fragile X Mental Retardation Syndrome: Structure of the KH1-KH2 Domains of Fragile X Mental Retardation Protein. Structure, 2007, 15, 1090-1098.	1.6	57
38	Conformational Heterogeneity of KaryopherinÎ <sup>2</sup> 2 Is Segmental. Structure, 2007, 15, 1431-1441.	1.6	37
39	Domain motions of glucosamine-6P synthase: Comparison of the anisotropic displacements in the crystals and the catalytic hinge-bending rotation. Protein Science, 2007, 16, 485-493.	3.1	12
40	Crystal structure of human IPS-1/MAVS/VISA/Cardif caspase activation recruitment domain. BMC Structural Biology, 2008, 8, 11.	2.3	86
41	Dealing with structural variability in molecular replacement and crystallographic refinement through normal-mode analysis. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 40-48.	2.5	20
42	Structural characterization of a human Fc fragment engineered for lack of effector functions. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 700-704.	2.5	150
43	X-ray structure of a soluble Rieske-type ferredoxin fromMus musculus. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 933-940.	2.5	5
44	Structure of a <i>Trypanosoma brucei</i> α/β-hydrolase fold protein with unknown function. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 474-478.	0.7	5
45	There is a baby in the bath water: AcrB contamination is a major problem in membrane-protein crystallization. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 880-885.	0.7	40
46	Rv0802c fromMycobacterium tuberculosis: the first structure of a succinyltransferase with the GNAT fold. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 978-985.	0.7	21
47	HingeMaster: Normal mode hinge prediction approach and integration of complementary predictors. Proteins: Structure, Function and Bioinformatics, 2008, 73, 299-319.	1.5	38
48	Crystal structure of glutathioneâ€dependent phospholipid peroxidase Hyr1 from the yeast <i>Saccharomyces cerevisiae</i> . Proteins: Structure, Function and Bioinformatics, 2008, 73, 1058-1062.	1.5	19
49	Biochemical and Structural Insights of the Early Glycosylation Steps in Calicheamicin Biosynthesis. Chemistry and Biology, 2008, 15, 842-853.	6.2	51
50	Protein crystallography for nonâ€crystallographers, or how to get the best (but not more) from published macromolecular structures. FEBS Journal, 2008, 275, 1-21.	2.2	231
51	Molecular mechanism of ligand recognition by NR3 subtype glutamate receptors. EMBO Journal, 2008, 27, 2158-2170.	3.5	93
52	A structural explanation for the binding of endocytic dileucine motifs by the AP2 complex. Nature, 2008, 456, 976-979.	13.7	280
53	Crystal structure of the ZP-N domain of ZP3 reveals the core fold of animal egg coats. Nature, 2008, 456, 653-657.	13.7	120
54	Structure of the CspK–Gspl–GspJ complex from the enterotoxigenic Escherichia coli type 2 secretion system. Nature Structural and Molecular Biology, 2008, 15, 462-468.	3.6	131

#	Article	IF	CITATIONS
55	Structural and functional studies of ALIX interactions with YPXnL late domains of HIV-1 and EIAV. Nature Structural and Molecular Biology, 2008, 15, 43-49.	3.6	129
56	Cysteine usage in Sulfolobus spindle-shaped virus 1 and extension to hyperthermophilic viruses in general. Virology, 2008, 376, 270-278.	1.1	31
57	Crystal Structure of the CaV2 IQ Domain in Complex with Ca2+/Calmodulin: High-Resolution Mechanistic Implications for Channel Regulation by Ca2+. Structure, 2008, 16, 607-620.	1.6	92
58	Structure of a NEMO/IKK-Associating Domain Reveals Architecture of the Interaction Site. Structure, 2008, 16, 798-808.	1.6	119
59	Sortase-Mediated Pilus Fiber Biogenesis in Streptococcus pneumoniae. Structure, 2008, 16, 1838-1848.	1.6	77
60	Small- and Large-Scale Conformational Changes of Adenylate Kinase: A Molecular Dynamics Study of the Subdomain Motion and Mechanics. Biophysical Journal, 2008, 95, 5901-5912.	0.2	75
61	Functional Proteomic and Structural Insights into Molecular Recognition in the Nitrilase Family Enzymes. Biochemistry, 2008, 47, 13514-13523.	1.2	45
62	Structure of the Minor Pseudopilin EpsH from the Type 2 Secretion System of Vibrio cholerae. Journal of Molecular Biology, 2008, 377, 91-103.	2.0	49
63	Crystal Structures of Mammalian Glutamine Synthetases Illustrate Substrate-Induced Conformational Changes and Provide Opportunities for Drug and Herbicide Design. Journal of Molecular Biology, 2008, 375, 217-228.	2.0	125
64	The Crystal Structure of a Binary Complex of two Pseudopilins: EpsI and EpsJ from the Type 2 Secretion System of Vibrio vulnificus. Journal of Molecular Biology, 2008, 375, 471-486.	2.0	43
65	Crystal Structure of a Bacterial Signal Peptide Peptidase. Journal of Molecular Biology, 2008, 376, 352-366.	2.0	44
66	Structure of the N-Terminal Mlp1-Binding Domain of the Saccharomyces cerevisiae mRNA-Binding Protein, Nab2. Journal of Molecular Biology, 2008, 376, 1048-1059.	2.0	47
67	Insect Juvenile Hormone Binding Protein Shows Ancestral Fold Present in Human Lipid-Binding Proteins. Journal of Molecular Biology, 2008, 377, 870-881.	2.0	53
68	Crystal Structure of the Polyextremophilic α-Amylase AmyB from Halothermothrix orenii: Details of a Productive Enzyme–Substrate Complex and an N Domain with a Role in Binding Raw Starch. Journal of Molecular Biology, 2008, 378, 852-870.	2.0	80
69	Structure and Function of the Arginine Repressor-Operator Complex from Bacillus subtilis. Journal of Molecular Biology, 2008, 379, 284-298.	2.0	29
70	NO sensing in Pseudomonas aeruginosa: Structure of the Transcriptional Regulator DNR. Journal of Molecular Biology, 2008, 378, 1002-1015.	2.0	80
71	Phage Display and Crystallographic Analysis Reveals Potential Substrate/Binding Site Interactions in the Protein Secretion Chaperone CsaA from Agrobacterium tumefaciens. Journal of Molecular Biology, 2008, 379, 457-470.	2.0	4
72	Zinc Binding Catalytic Domain of Human Tankyrase 1. Journal of Molecular Biology, 2008, 379, 136-145.	2.0	56

#	Article	IF	CITATIONS
73	Structural Insights into the Recognition of Peroxisomal Targeting Signal 1 by Trypanosoma brucei Peroxin 5. Journal of Molecular Biology, 2008, 381, 867-880.	2.0	48
74	Structures of Substrate- and Inhibitor-Bound Adenosine Deaminase from a Human Malaria Parasite Show a Dramatic Conformational Change and Shed Light on Drug Selectivity. Journal of Molecular Biology, 2008, 381, 975-988.	2.0	33
75	Structure of an Archaeal Homolog of the Human Protein Complex Rpp21–Rpp29 That Is a Key Core Component for the Assembly of Active Ribonuclease P. Journal of Molecular Biology, 2008, 384, 652-662.	2.0	43
76	Structural Basis of the Nic96 Subcomplex Organization in the Nuclear Pore Channel. Molecular Cell, 2008, 29, 46-55.	4.5	83
77	Cooperative Assembly of TGF-Î <sup>2</sup> Superfamily Signaling Complexes Is Mediated by Two Disparate Mechanisms and Distinct Modes of Receptor Binding. Molecular Cell, 2008, 29, 157-168.	4.5	247
78	Structural characterization of a mutated, ADCC-enhanced human Fc fragment. Molecular Immunology, 2008, 45, 1872-1882.	1.0	81
79	Crystal structure of chimeric antibody C2H7 Fab in complex with a CD20 peptide. Molecular Immunology, 2008, 45, 2861-2868.	1.0	39
80	Complexes of mutants of Escherichia coli aminopeptidase P and the tripeptide substrate ValProLeu. Archives of Biochemistry and Biophysics, 2008, 469, 200-208.	1.4	19
81	Molecular Basis of Kainate Receptor Modulation by Sodium. Neuron, 2008, 58, 720-735.	3.8	85
82	Structural Coupling of SH2-Kinase Domains Links Fes and Abl Substrate Recognition and Kinase Activation. Cell, 2008, 134, 793-803.	13.5	190
83	Preventing serpin aggregation: The molecular mechanism of citrate action upon antitrypsin unfolding. Protein Science, 2008, 17, 2127-2133.	3.1	23
84	Active Site and Loop 4 Movements within Human Glycolate Oxidase:  Implications for Substrate Specificity and Drug Design. Biochemistry, 2008, 47, 2439-2449.	1.2	51
85	Structural Basis for the Inactivation of Thermus thermophilus Proline Dehydrogenase by <i>N-</i> Propargylglycine <sup>,</sup> . Biochemistry, 2008, 47, 5573-5580.	1.2	25
86	Structure and Mechanistic Implications of a Uroporphyrinogen III Synthaseâ^ Product Complex. Biochemistry, 2008, 47, 8648-8655.	1.2	32
87	Function-Biased Choice of Additives for Optimization of Protein Crystallization: The Case of the Putative Thioesterase PA5185 from Pseudomonas aeruginosa PAO1. Crystal Growth and Design, 2008, 8, 4054-4061.	1.4	5
88	Molecular Dynamics Simulations of Biotin Carboxylase. Journal of Physical Chemistry B, 2008, 112, 3149-3156.	1.2	12
89	The Structure of FSTL3·Activin A Complex. Journal of Biological Chemistry, 2008, 283, 32831-32838.	1.6	63
90	Structural basis for distinctive recognition of fibrinogen γC peptide by the platelet integrin αllbβ3. Journal of Cell Biology, 2008, 182, 791-800.	2.3	205

#	Article	IF	CITATIONS
91	Mixture models for protein structure ensembles. Bioinformatics, 2008, 24, 2184-2192.	1.8	8
92	A protein functional leap: how a single mutation reverses the function of the transcription regulator TetR. Nucleic Acids Research, 2008, 36, 4390-4401.	6.5	32
93	Elimination of competing hydrolysis and coupling side reactions of a cyclodextrin glucanotransferase by directed evolution. Biochemical Journal, 2008, 413, 517-525.	1.7	47
94	Crystal Structure of the BARD1 Ankyrin Repeat Domain and Its Functional Consequences. Journal of Biological Chemistry, 2008, 283, 21179-21186.	1.6	35
95	Critical evaluation of simple network models of protein dynamics and their comparison with crystallographic B-factors. Physical Biology, 2008, 5, 026008.	0.8	48
96	Structure of the membrane proximal oxidoreductase domain of human Steap3, the dominant ferrireductase of the erythroid transferrin cycle. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7410-7415.	3.3	83
97	Transitive homology-guided structural studies lead to discovery of Cro proteins with 40% sequence identity but different folds. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2343-2348.	3.3	85
98	Interaction of CheY with the C-Terminal Peptide of CheZ. Journal of Bacteriology, 2008, 190, 1419-1428.	1.0	13
99	Crystal Structure of the GAF-B Domain from Human Phosphodiesterase 10A Complexed with Its Ligand, cAMP. Journal of Biological Chemistry, 2008, 283, 19657-19664.	1.6	52
100	The Crystal Structure of N-Acetyl-L-glutamate Synthase from Neisseria gonorrhoeae Provides Insights into Mechanisms of Catalysis and Regulation. Journal of Biological Chemistry, 2008, 283, 7176-7184.	1.6	33
101	Enzymes with lid-gated active sites must operate by an induced fit mechanism instead of conformational selection. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13829-13834.	3.3	143
102	Structural basis for antagonism of human interleukin 18 by poxvirus interleukin 18-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20711-20715.	3.3	64
103	Structure and Mechanism of the Rebeccamycin Sugar 4′-O-Methyltransferase RebM. Journal of Biological Chemistry, 2008, 283, 22628-22636.	1.6	57
104	Structure and function of SirC from Bacillus megaterium: a metal-binding precorrin-2 dehydrogenase. Biochemical Journal, 2008, 415, 257-263.	1.7	19
105	Domain Swapping and Different Oligomeric States for the Complex Between Calmodulin and the Calmodulin-Binding Domain of Calcineurin A. PLoS ONE, 2009, 4, e5402.	1.1	37
106	Calcium Is Essential for the Major Pseudopilin in the Type 2 Secretion System. Journal of Biological Chemistry, 2009, 284, 25466-25470.	1.6	41
107	Crystal Structure and Function of a DARPin Neutralizing Inhibitor of Lactococcal Phage TP901-1. Journal of Biological Chemistry, 2009, 284, 30718-30726.	1.6	55
108	Structural Determinants of G-protein α Subunit Selectivity by Regulator of G-protein Signaling 2 (RCS2). Journal of Biological Chemistry, 2009, 284, 19402-19411.	1.6	62

#	Article	IF	CITATIONS
109	Physical Interactions between Mcm10, DNA, and DNA Polymerase α. Journal of Biological Chemistry, 2009, 284, 24662-24672.	1.6	55
110	Crystal Structure and Autoactivation Pathway of the Precursor Form of Human Tripeptidyl-peptidase 1, the Enzyme Deficient in Late Infantile Ceroid Lipofuscinosis. Journal of Biological Chemistry, 2009, 284, 3985-3997.	1.6	50
111	Structural Insight into the Activation Mechanism of Human Pancreatic Prophospholipase A2. Journal of Biological Chemistry, 2009, 284, 16659-16666.	1.6	25
112	Multiple Binding Modes between HNF4α and the LXXLL Motifs of PGC-1α Lead to Full Activation. Journal of Biological Chemistry, 2009, 284, 35165-35176.	1.6	29
113	Structural and Kinetic Characterizations of the Polysialic Acid O-Acetyltransferase OatWY from Neisseria meningitidis. Journal of Biological Chemistry, 2009, 284, 24501-24511.	1.6	18
114	Crystal structure of the membrane-bound bifunctional transglycosylase PBP1b from <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8824-8829.	3.3	180
115	Mechanism of Allosteric Inhibition of N-Acetyl-L-glutamate Synthase by L-Arginine. Journal of Biological Chemistry, 2009, 284, 4873-4880.	1.6	27
116	Structure of the 12-Subunit RNA Polymerase II Refined with the Aid of Anomalous Diffraction Data. Journal of Biological Chemistry, 2009, 284, 12933-12939.	1.6	18
117	Toxoplasma gondii Cathepsin L Is the Primary Target of the Invasion-inhibitory Compound Morpholinurea-leucyl-homophenyl-vinyl Sulfone Phenyl. Journal of Biological Chemistry, 2009, 284, 26839-26850.	1.6	60
118	Incompatibility with Formin Cdc12p Prevents Human Profilin from Substituting for Fission Yeast Profilin. Journal of Biological Chemistry, 2009, 284, 2088-2097.	1.6	45
119	The Structure of the Dizinc Subclass B2 Metallo-β-Lactamase CphA Reveals that the Second Inhibitory Zinc Ion Binds in the Histidine Site. Antimicrobial Agents and Chemotherapy, 2009, 53, 4464-4471.	1.4	75
120	Crystal Structure of the N-terminal Domain of Anaphase-promoting Complex Subunit 7. Journal of Biological Chemistry, 2009, 284, 15137-15146.	1.6	20
121	The Structure of the MAP2K MEK6 Reveals an Autoinhibitory Dimer. Structure, 2009, 17, 96-104.	1.6	31
122	Crystal Structure of the N-Terminal Domain of the Secretin GspD from ETEC Determined with the Assistance of a Nanobody. Structure, 2009, 17, 255-265.	1.6	164
123	The Structure of a Bacterial DUF199/WhiA Protein: Domestication of an Invasive Endonuclease. Structure, 2009, 17, 1368-1376.	1.6	33
124	Structural analysis reveals DNA binding properties of Rv2827c, a hypothetical protein from MycobacteriumÂtuberculosis. Journal of Structural and Functional Genomics, 2009, 10, 137-150.	1.2	13
125	Structural characterization of CalO2: A putative orsellinic acid P450 oxidase in the calicheamicin biosynthetic pathway. Proteins: Structure, Function and Bioinformatics, 2009, 74, 50-60.	1.5	27
126	Structural analysis of fish versus mammalian hemoglobins: Effect of the heme pocket environment on autooxidation and hemin loss. Proteins: Structure, Function and Bioinformatics, 2009, 75, 217-230.	1.5	79

#	Article	IF	CITATIONS
127	Crystal structure of human eIF5A1: Insight into functional similarity of human eIF5A1 and eIF5A2. Proteins: Structure, Function and Bioinformatics, 2009, 75, 1040-1045.	1.5	48
128	The crystal structure of the outer membrane lipoprotein YbhC from <i>Escherichia coli</i> sheds new light on the phylogeny of carbohydrate esterase family 8. Proteins: Structure, Function and Bioinformatics, 2009, 76, 1029-1036.	1.5	13
129	The crystal structure of XGâ€34, an evolved xyloglucanâ€specific carbohydrateâ€binding module. Proteins: Structure, Function and Bioinformatics, 2010, 78, 785-789.	1.5	11
130	The thermo―and acidoâ€stable ORFâ€99 from the archaeal virus AFV1. Protein Science, 2009, 18, 1316-1320.	3.1	13
131	Detailed insights from microarray and crystallographic studies into carbohydrate recognition by microneme protein 1 (MIC1) of <i>Toxoplasma gondii</i> . Protein Science, 2009, 18, 1935-1947.	3.1	37
132	<i>StoneHinge</i> : Hinge prediction by network analysis of individual protein structures. Protein Science, 2009, 18, 359-371.	3.1	44
133	Redesign of a protein–peptide interaction: Characterization and applications. Protein Science, 2009, 18, 762-774.	3.1	35
134	Application of normal-mode refinement to X-ray crystal structures at the lower resolution limit. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 633-643.	2.5	12
135	Structure of <i>Hordeum vulgare</i> NADPH-dependent thioredoxin reductase 2. Unwinding the reaction mechanism. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 932-941.	2.5	18
136	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. Journal of Applied Crystallography, 2009, 42, 376-384.	1.9	204
137	Conservation of structure and activity in Plasmodium purine nucleoside phosphorylases. BMC Structural Biology, 2009, 9, 42.	2.3	15
138	Crystal structure and association behaviour of the GluR2 amino-terminal domain. EMBO Journal, 2009, 28, 1812-1823.	3.5	146
139	Crystal structure of A3B3 complex of V-ATPase from Thermus thermophilus. EMBO Journal, 2009, 28, 3771-3779.	3.5	59
140	Encounter and extrusion of an intrahelical lesion by a DNA repair enzyme. Nature, 2009, 462, 762-766.	13.7	129
141	The mRNA export protein DBP5 binds RNA and the cytoplasmic nucleoporin NUP214 in a mutually exclusive manner. Nature Structural and Molecular Biology, 2009, 16, 247-254.	3.6	151
142	The N-terminal domain of GluR6-subtype glutamate receptor ion channels. Nature Structural and Molecular Biology, 2009, 16, 631-638.	3.6	97
143	Improving thermostability and catalytic activity of pyranose 2â€oxidase from <i>Trametes multicolor</i> by rational and semiâ€rational design. FEBS Journal, 2009, 276, 776-792.	2.2	37
144	Structural and mutational analysis of TenA protein (HP1287) from the <i>Helicobacter pylori</i> thiamin salvage pathway – evidence of a different substrate specificity. FEBS Journal, 2009, 276, 6227-6235.	2.2	12

ARTICLE IF CITATIONS # A thermostable triple mutant of pyranose 2â€oxidase from <i>Trametes multicolor</i> with improved 145 1.8 21 properties for biotechnological applications. Biotechnology Journal, 2009, 4, 525-534. Structural and Biochemical Characterization of the Interaction between KPC-2 Î2-Lactamase and 146 1.2 29 Î<sup>2</sup>-Lactamase Inhibitor Protein,. Biochemistry, 2009, 48, 9185-9193. Structural Basis for the Sugar Nucleotide and Acyl-Chain Selectivity of Leptospira interrogans LpxA. 147 1.2 29 Biochemistry, 2009, 48, 6191-6201. Structural and Thermodynamic Analysis of a Conformationally Strained Circular Permutant of 148 Barnase. Biochemistry, 2009, 48, 3497-3507. Ring1B Contains a Ubiquitin-Like Docking Module for Interaction with Cbx Proteins<sup>,</sup>. 149 1.2 37 Biochemistry, 2009, 48, 10542-10548. Characterization and Structure of the Manganese-Responsive Transcriptional Regulator ScaR<sup>,</sup>. Biochemistry, 2009, 48, 10308-10320. 1.2 BlockMaster: Partitioning Protein Kinase Structures Using Normal-Mode Analysis. Journal of Physical 151 1.1 17 Chemistry A, 2009, 113, 7528-7534. Structural and Biochemical Characterization of <i>Xylella fastidiosa</i> DsbA Family Members: New 1.2 16 Insights into the Enzymea<sup>^</sup>Substrate Interaction. Biochemistry, 2009, 48, 3508-3518. Crystal structure of human aquaporin 4 at 1.8 â,, « and its mechanism of conductance. Proceedings of the 153 3.3 297 National Academy of Sciences of the United States of America, 2009, 106, 7437-7442. Resistance mechanism revealed by crystal structures of unliganded nelfinavir-resistant HIV-1 protease non-active site mutants N88D and N88S. Biochemical and Biophysical Research Communications, 2009, 154 1.0 389, 295-300. ACET is a highly potent and specific kainate receptor antagonist: Characterisation and effects on 155 2.0 44 hippocampal mossy fibre function. Neuropharmacology, 2009, 56, 121-130. Nanobody-aided structure determination of the Epsl:EpsJ pseudopilin heterodimer from Vibrio 1.3 vulnificus. Journal of Structural Biology, 2009, 166, 8-15. The three-dimensional structure of the cytoplasmic domains of EpsF from the type 2 secretion system 157 1.3 49 of Vibrio cholerae. Journal of Structural Biology, 2009, 166, 303-315. The dimer formed by the periplasmic domain of EpsL from the Type 2 Secretion System of Vibrio parahaemolyticus. Journal of Structural Biology, 2009, 168, 313-322. 1.3 44 The HupR Receiver Domain Crystal Structure in its Nonphospho and Inhibitory Phospho States. Journal 159 2.0 15 of Molecular Biology, 2009, 385, 51-64. Crystal Structure of a Major Outer Membrane Protein from Thermus thermophilus HB27. Journal of Mólecular Biology, 2009, 385, 1445-1455. Insights into the Conformational Variability and Regulation of Human Nek2 Kinase. Journal of 161 2.0 47 Molecular Biology, 2009, 386, 476-485. Structural Basis for Catalysis of a Tetrameric Class IIa Fructose 1,6-Bisphosphate Aldolase from 38 Mycobacterium tuberculosis. Journal of Molecular Biology, 2009, 386, 1038-1053.

ARTICLE IF CITATIONS Structural Analysis of a Monomeric Form of the Twin-Arginine Leader Peptide Binding Chaperone 163 2.0 31 Escherichia coli DmsD. Journal of Molecular Biology, 2009, 389, 124-133. Active-Site Gating Regulates Substrate Selectivity in a Chymotrypsin-Like Serine Protease. Journal of 164 Molecular Biology, 2009, 389, 559-574. Structure and Calcium-Binding Activity of LipL32, the Major Surface Antigen of Pathogenic Leptospira 165 2.0 41 sp.. Journal of Molecular Biology, 2009, 390, 722-736. Crystal Structure of Dicamba Monooxygenase: A Rieske Nonheme Oxygenase that Catalyzes Oxidative Démethylation. Journal of Molecular Biology, 2009, 392, 498-510. PILZ Protein Structure and Interactions with PILB and the FIMX EAL Domain: Implications for Control 167 2.0 100 of Type IV Pilus Biogenesis. Journal of Molecular Biology, 2009, 393, 848-866. Structure and Function of the Oxidoreductase DsbA1 from Neisseria meningitidis. Journal of Molecular Biology, 2009, 394, 931-943. An Autoinhibitory Tyrosine Motif in the Cell-Cycle-Regulated Nek7 Kinase Is Released through Binding 169 4.5 83 of Nek9. Molecular Cell, 2009, 36, 560-570. PBP Active Site Flexibility as the Key Mechanism for Î<sup>2</sup>-Lactam Resistance in Pneumococci. Journal of 2.0 78 Molecular Biology, 2009, 387, 899-909. Structural Basis of the Inhibition of Class A Î<sup>2</sup>-Lactamases and Penicillin-Binding Proteins by 171 6.6 17 6-Î<sup>2</sup>-Iodopenicillanate. Journal of the American Chemical Society, 2009, 131, 15262-15269. Coarse-Grained Description of Protein Internal Dynamics: An Optimal Strategy for Decomposing 0.2 Proteins in Rigid Subunits. Biophysical Journal, 2009, 96, 4993-5002. Unprecedented Binding Cooperativity between Cu<sup>I</sup> and Cu<sup>II</sup> in the Copper Resistance Protein CopK from <i>Cupriavidus metallidurans</i> CH34: Implications from Structural 173 6.6 38 Studies by NMR Spectroscopy and X-Ray Crystallography. Journal of the American Chemical Society, <u>2009, 131, 3549-3564.</u> Structural and Kinetic Analyses of Macrophage Migration Inhibitory Factor Active Site Interactions. 174 1.2 Biochemistry, 2009, 48, 132-139. Natural micropolymorphism in human leukocyte antigens provides a basis for genetic control of 175 4.2 93 antigen recognition. Journal of Experimental Medicine, 2009, 206, 209-219. Synthesis, Kinase Inhibitory Potencies, and in Vitro Antiproliferative Evaluation of New Pim Kinase Inhibitors. Journal of Medicinal Chemistry, 2009, 52, 6369-6381. Crystal Structure of the Acid-Induced Arginine Decarboxylase from <i>Escherichia coli</i>: Reversible 177 1.2 48 Decamer Assembly Controls Enzyme Activity. Biochemistry, 2009, 48, 3915-3927. The crystal structure of rabbit IgG-Fc. Biochemical Journal, 2009, 417, 77-83. Crystal structure of cytotoxin protein suilysin from Streptococcus suis. Protein and Cell, 2010, 1, 179 4.8 73 96-105. Crystal Structure of the APOBEC3C Catalytic Domain Reveals Potential Oligomerization Interfaces. Structure, 2010, 18, 28-38.

#	Article	IF	CITATIONS
181	The Prp19 WD40 Domain Contains a Conserved Protein Interaction Region Essential for Its Function. Structure, 2010, 18, 584-593.	1.6	33
182	Computational Design of Epitope-Scaffolds Allows Induction of Antibodies Specific for a Poorly Immunogenic HIV Vaccine Epitope. Structure, 2010, 18, 1116-1126.	1.6	203
183	Quantitative Structural Analysis of Importin-β Flexibility: Paradigm for Solenoid Protein Structures. Structure, 2010, 18, 1171-1183.	1.6	89
184	The Structure of the Talin Head Reveals a NovelÂExtended Conformation of the FERM Domain. Structure, 2010, 18, 1289-1299.	1.6	132
185	Structure of the GTPase and GDI domains of FeoB, the ferrous iron transporter of <i>Legionella pneumophila</i> . FEBS Letters, 2010, 584, 733-738.	1.3	25
186	Structure of theMethanothermobacter thermautotrophicusexosome RNase PH ring. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 522-528.	2.5	7
187	Validation of crystallographic models containing TLS or other descriptions of anisotropy. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 889-900.	2.5	52
188	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 979-987.	2.5	12
189	The structure of the first representative of Pfam family PF06475 reveals a new fold with possible involvement in glycolipid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1211-1217.	0.7	10
190	Role of tyrosine 131 in the active site of paAzoR1, an azoreductase with specificity for the inflammatory bowel disease prodrug balsalazide. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 2-7.	0.7	23
191	Structure of <i>Bacillus amyloliquefaciens</i> α-amylase at high resolution: implications for thermal stability. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 121-129.	0.7	48
192	A conserved mechanism of autoinhibition for the AMPK kinase domain: ATP-binding site and catalytic loop refolding as a means of regulation. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 143-151.	0.7	34
193	The 1.4â€Ã resolution structure of <i>Paracoccus pantotrophus</i> pseudoazurin. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 627-635.	0.7	15
194	Structure of uracil-DNA glycosylase fromMycobacterium tuberculosis: insights into interactions with ligands. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 887-892.	0.7	8
195	Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05â€Ã resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1287-1296.	0.7	2
196	Coordination sphere of the third metal site is essential to the activity and metal selectivity of alkaline phosphatases. Protein Science, 2010, 19, 75-84.	3.1	12
197	Cysteineâ€free rop: A fourâ€helix bundle core mutant has wildâ€ŧype stability and structure but dramatically different unfolding kinetics. Protein Science, 2010, 19, 670-679.	3.1	11
198	The crystal structure of the Y140F mutant of ADPâ€ <scp>L</scp> â€ <i>glycero</i> â€ <scp>D</scp> â€ <i>manno</i> â€heptose 6â€epimerase bound to ADPâ€Î²â€ <scp>D</scp> â€mannose suggests a one base mechanism. Protein Science, 2010, 19, 1337-1343.	3.1	11

#	Article	IF	CITATIONS
199	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp22 shares fold similarity with a domain of lactococcal phage p2 RBP. Protein Science, 2010, 19, 1439-1443.	3.1	12
200	The crystal structure of the <i>mycobacterium tuberculosis</i> Rv3019câ€Rv3020c ESX complex reveals a domainâ€swapped heterotetramer. Protein Science, 2010, 19, 1692-1703.	3.1	27
201	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp23.1, a putative chaperone. Protein Science, 2010, 19, 1812-1816.	3.1	11
202	The structure and NO binding properties of the nitrophorinâ€like hemeâ€binding protein from <i>Arabidopsis thaliana</i> gene locus At1g79260.1. Proteins: Structure, Function and Bioinformatics, 2010, 78, 917-931.	1.5	49
203	<i>Helicobacter pylori</i> acidic stress response factor HP1286 is a Ycel homolog with new binding specificity. FEBS Journal, 2010, 277, 1896-1905.	2.2	26
204	Importance of the gating segment in the substrateâ€recognition loop of pyranose 2â€oxidase. FEBS Journal, 2010, 277, 2892-2909.	2.2	34
205	Biological and structural characterization of the Mycobacterium smegmatis nitroreductase NfnB, and its role in benzothiazinone resistance. Molecular Microbiology, 2010, 77, 1172-1185.	1.2	63
206	Structural basis for dsRNA recognition and interferon antagonism by Ebola VP35. Nature Structural and Molecular Biology, 2010, 17, 165-172.	3.6	177
207	Structure of a clade C HIV-1 gp120 bound to CD4 and CD4-induced antibody reveals anti-CD4 polyreactivity. Nature Structural and Molecular Biology, 2010, 17, 608-613.	3.6	92
208	Structural basis for selective activation of ABA receptors. Nature Structural and Molecular Biology, 2010, 17, 1109-1113.	3.6	104
209	Structural insights into a novel histone demethylase PHF8. Cell Research, 2010, 20, 166-173.	5.7	67
210	Structural insights into the exquisite selectivity of neurexin/neuroligin synaptic interactions. EMBO Journal, 2010, 29, 2461-2471.	3.5	38
211	Self-assembly of spider silk proteins is controlled by a pH-sensitive relay. Nature, 2010, 465, 236-238.	13.7	393
212	Coupling of receptor conformation and ligand orientation determine graded activity. Nature Chemical Biology, 2010, 6, 837-843.	3.9	121
213	Structural and Mutational Analysis of Escherichia coli AlkB Provides Insight into Substrate Specificity and DNA Damage Searching. PLoS ONE, 2010, 5, e8680.	1.1	56
214	Mutations Abrogating VP35 Interaction with Double-Stranded RNA Render Ebola Virus Avirulent in Guinea Pigs. Journal of Virology, 2010, 84, 3004-3015.	1.5	135
215	Computational reprogramming of homing endonuclease specificity at multiple adjacent base pairs. Nucleic Acids Research, 2010, 38, 5601-5608.	6.5	90
216	A domain insertion in Escherichia coli GyrB adopts a novel fold that plays a critical role in gyrase function. Nucleic Acids Research, 2010, 38, 7830-7844.	6.5	68

#	Article	IF	CITATIONS
217	Structural and functional studies on the extracellular domain of BST2/tetherin in reduced and oxidized conformations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17951-17956.	3.3	92
218	Structural Homology between the C-Terminal Domain of the PapC Usher and Its Plug. Journal of Bacteriology, 2010, 192, 1824-1831.	1.0	25
219	Structural studies of tri-functional human GART. Nucleic Acids Research, 2010, 38, 7308-7319.	6.5	28
220	Defining the Molecular Basis of BubR1 Kinetochore Interactions and APC/C-CDC20 Inhibition. Journal of Biological Chemistry, 2010, 285, 14764-14776.	1.6	37
221	The Staphylococcus aureus Siderophore Receptor HtsA Undergoes Localized Conformational Changes to Enclose Staphyloferrin A in an Arginine-rich Binding Pocket. Journal of Biological Chemistry, 2010, 285, 11162-11171.	1.6	65
222	The N Domain of Human Angiotensin-l-converting Enzyme. Journal of Biological Chemistry, 2010, 285, 35685-35693.	1.6	76
223	Interactions between Lipids and Human Anti-HIV Antibody 4E10 Can Be Reduced without Ablating Neutralizing Activity. Journal of Virology, 2010, 84, 1076-1088.	1.5	45
224	Mechanism of Concerted Inhibition of α2β2-type Hetero-oligomeric Aspartate Kinase from Corynebacterium glutamicum. Journal of Biological Chemistry, 2010, 285, 27477-27486.	1.6	35
225	Insight into the induction mechanism of the GntR/HutC bacterial transcription regulator YvoA. Nucleic Acids Research, 2010, 38, 2485-2497.	6.5	44
226	Optimal modeling of atomic fluctuations in protein crystal structures for weak crystal contact interactions. Journal of Chemical Physics, 2010, 132, 014111.	1.2	21
227	<i>Ebolavirus</i> VP35 uses a bimodal strategy to bind dsRNA for innate immune suppression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 314-319.	3.3	124
228	New potent dual inhibitors of CK2 and Pim kinases: discovery and structural insights. FASEB Journal, 2010, 24, 3171-3185.	0.2	55
229	Structural Basis of Fatty Acid Substrate Binding to Cyclooxygenase-2. Journal of Biological Chemistry, 2010, 285, 22152-22163.	1.6	132
230	The Effect of Clade-Specific Sequence Polymorphisms on HIV-1 Protease Activity and Inhibitor Resistance Pathways. Journal of Virology, 2010, 84, 9995-10003.	1.5	33
231	The Crystal Structure of D212 from <i>Sulfolobus</i> Spindle-Shaped Virus Ragged Hills Reveals a New Member of the PD-(D/E)XK Nuclease Superfamily. Journal of Virology, 2010, 84, 5890-5897.	1.5	20
232	Specificity of Staphyloferrin B Recognition by the SirA Receptor from Staphylococcus aureus. Journal of Biological Chemistry, 2010, 285, 34579-34588.	1.6	56
233	Structural and Functional Characterization of Three DsbA Paralogues from Salmonella enterica Serovar Typhimurium. Journal of Biological Chemistry, 2010, 285, 18423-18432.	1.6	47
234	Magnesium Coordination Controls the Molecular Switch Function of DNA Mismatch Repair Protein MutS. Journal of Biological Chemistry, 2010, 285, 13131-13141.	1.6	48

#	Article	IF	CITATIONS
235	Structural Characterization of OxyD, a Cytochrome P450 Involved in β-Hydroxytyrosine Formation in Vancomycin Biosynthesis. Journal of Biological Chemistry, 2010, 285, 24562-24574.	1.6	64
236	Insights into Peroxisome Function from the Structure of PEX3 in Complex with a Soluble Fragment of PEX19. Journal of Biological Chemistry, 2010, 285, 25410-25417.	1.6	46
237	Inhibition of Antibiotic-Resistant Staphylococcus aureus by the Broad-Spectrum Dihydrofolate Reductase Inhibitor RAB1. Antimicrobial Agents and Chemotherapy, 2010, 54, 3825-3833.	1.4	38
238	Structural Insights into the Catalytic Mechanism of Bacterial Guanosine-diphospho-d-mannose Pyrophosphorylase and Its Regulation by Divalent Ions. Journal of Biological Chemistry, 2010, 285, 27468-27476.	1.6	33
239	Structure of the HCMV UL16-MICB Complex Elucidates Select Binding of a Viral Immunoevasin to Diverse NKG2D Ligands. PLoS Pathogens, 2010, 6, e1000723.	2.1	52
240	The Subtilisin-Like Protease AprV2 Is Required for Virulence and Uses a Novel Disulphide-Tethered Exosite to Bind Substrates. PLoS Pathogens, 2010, 6, e1001210.	2.1	81
241	Peroxisomal Plant 3-Ketoacyl-CoA Thiolase Structure and Activity Are Regulated by a Sensitive Redox Switch. Journal of Biological Chemistry, 2010, 285, 24078-24088.	1.6	62
242	Structure of a Thyroid Hormone Receptor DNA-Binding Domain Homodimer Bound to an Inverted Palindrome DNA Response Element. Molecular Endocrinology, 2010, 24, 1650-1664.	3.7	29
243	Mechanism of Cohesin Loading onto Chromosomes: A Conformational Dynamics Study. Biophysical Journal, 2010, 99, 1212-1220.	0.2	10
244	Structural Basis of Drug Binding to CYP46A1, an Enzyme That Controls Cholesterol Turnover in the Brain. Journal of Biological Chemistry, 2010, 285, 31783-31795.	1.6	63
245	Structural and Biochemical Characterization of the Cytochrome P450 CypX (CYP134A1) from <i>Bacillus subtilis</i> : A Cyclo- <scp>l</scp> -leucyl- <scp>l</scp> -leucyl Dipeptide Oxidase. Biochemistry, 2010, 49, 7282-7296.	1.2	93
246	Insights into the Reaction of Protein-tyrosine Phosphatase 1B. Journal of Biological Chemistry, 2010, 285, 15874-15883.	1.6	125
247	Crystal Structure of a Complex between the <i>Actinomadura</i> R39 <scp>dd</scp> -Peptidase and a Peptidoglycan-mimetic Boronate Inhibitor: Interpretation of a Transition State Analogue in Terms of Catalytic Mechanism. Biochemistry, 2010, 49, 6411-6419.	1.2	29
248	Structural, NMR Spectroscopic, and Computational Investigation of Hemin Loading in the Hemophore HasAp from <i>Pseudomonas aeruginosa</i> . Journal of the American Chemical Society, 2010, 132, 9857-9872.	6.6	82
249	Holo-Ni(II)HpNikR Is an Asymmetric Tetramer Containing Two Different Nickel-Binding Sites. Journal of the American Chemical Society, 2010, 132, 14447-14456.	6.6	36
250	Structural Analysis of Botulinum Neurotoxin Type G Receptor Binding,. Biochemistry, 2010, 49, 5200-5205.	1.2	32
251	Increasing the Conformational Entropy of the Ω-Loop Lid Domain in Phosphoenolpyruvate Carboxykinase Impairs Catalysis and Decreases Catalytic Fidelity,. Biochemistry, 2010, 49, 5176-5187.	1.2	21
252	Structural Basis for the Interaction of Lactivicins with Serine Î <sup>2</sup> -Lactamases. Journal of Medicinal Chemistry, 2010, 53, 5890-5894.	2.9	17

#	Article	IF	CITATIONS
253	Structure and Biological Importance of the Spn1-Spt6 Interaction, and Its Regulatory Role in Nucleosome Binding. Molecular Cell, 2010, 40, 725-735.	4.5	66
254	Structural and functional comparison of MIF ortholog from Plasmodium yoelii with MIF from its rodent host. Molecular Immunology, 2010, 47, 726-737.	1.0	20
255	Monoclonal antibody MN423 as a stable mold facilitates structure determination of disordered tau protein. Journal of Structural Biology, 2010, 171, 74-81.	1.3	11
256	Structure of the MthK RCK in complex with cadmium. Journal of Structural Biology, 2010, 171, 231-237.	1.3	14
257	Putting an N-terminal end to the Clostridium thermocellum xylanase Xyn10B story: Crystal structure of the CBM22-1–GH10 modules complexed with xylohexaose. Journal of Structural Biology, 2010, 172, 353-362.	1.3	52
258	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. Journal of Molecular Biology, 2010, 396, 1244-1259.	2.0	16
259	Crystal Structures of Trypanosomal Histidyl-tRNA Synthetase Illuminate Differences between Eukaryotic and Prokaryotic Homologs. Journal of Molecular Biology, 2010, 397, 481-494.	2.0	37
260	Structural and Functional Characterization of Reston Ebola Virus VP35 Interferon Inhibitory Domain. Journal of Molecular Biology, 2010, 399, 347-357.	2.0	61
261	A Novel Mechanism for Azoreduction. Journal of Molecular Biology, 2010, 400, 24-37.	2.0	48
262	Structural Basis for Par-4 Recognition by the SPRY Domain- and SOCS Box-Containing Proteins SPSB1, SPSB2, and SPSB4. Journal of Molecular Biology, 2010, 401, 389-402.	2.0	63
263	The Unique Binding Mode of Cellulosomal CBM4 from Clostridium thermocellum Cellobiohydrolase A. Journal of Molecular Biology, 2010, 402, 374-387.	2.0	28
264	H-Bonding and Positive Charge at the N(5)/O(4) Locus Are Critical for Covalent Flavin Attachment in Trametes Pyranose 2-Oxidase. Journal of Molecular Biology, 2010, 402, 578-594.	2.0	33
265	Two Stacked Heme Molecules in the Binding Pocket of the Periplasmic Heme-Binding Protein HmuT from Yersinia pestis. Journal of Molecular Biology, 2010, 404, 220-231.	2.0	63
266	Crystal Structure of an Essential Enzyme in Seed Starch Degradation: Barley Limit Dextrinase in Complex with Cyclodextrins. Journal of Molecular Biology, 2010, 403, 739-750.	2.0	55
267	Crystal Structures of the Glutamate Receptor Ion Channel GluK3 and GluK5 Amino-Terminal Domains. Journal of Molecular Biology, 2010, 404, 680-696.	2.0	41
268	Crystal Structures of NodS N-Methyltransferase from Bradyrhizobium japonicum in Ligand-Free Form and as SAH Complex. Journal of Molecular Biology, 2010, 404, 874-889.	2.0	13
269	Crystal structure of the NADP-dependent mannitol dehydrogenase from Cladosporium herbarum: Implications for oligomerisation and catalysis. Biochimie, 2010, 92, 985-993.	1.3	14
270	Structure of mitochondrial transcription termination factor 3 reveals a novel nucleic acid-binding domain. Biochemical and Biophysical Research Communications, 2010, 397, 386-390.	1.0	43

		CITATION R	EPORT	
#	Article		IF	Citations
271	Structure and control of the actin regulatory WAVE complex. Nature, 2010, 468, 533-53	8.	13.7	424
272	Crystal structure of the aspartyl-tRNA synthetase from Entamoeba histolytica. Molecular Biochemical Parasitology, 2010, 169, 95-100.	and	0.5	14
273	Inhibition of the PLP-dependent enzyme serine palmitoyltransferase by cycloserine: evide novel decarboxylative mechanism of inactivation. Molecular BioSystems, 2010, 6, 1682.	nce for a	2.9	39
274	Flavin-Induced Oligomerization in <i>Escherichia coli</i> Adaptive Response Protein AidB Biochemistry, 2011, 50, 10159-10169.		1.2	9
275	Structure of the USP15 N-Terminal Domains: A Î <sup>2</sup> -Hairpin Mediates Close Association bet and UBL Domains. Biochemistry, 2011, 50, 7995-8004.	ween the DUSP	1.2	25
276	Structure of Estradiol Metal Chelate and Estrogen Receptor Complex: The Basis for Desig Class of Selective Estrogen Receptor Modulators. Journal of Medicinal Chemistry, 2011, 5	ning a New 54, 3575-3580.	2.9	28
277	Reaction of Cresyl Saligenin Phosphate, the Organophosphorus Agent Implicated in Aero Syndrome, with Human Cholinesterases: Mechanistic Studies Employing Kinetics, Mass S and X-ray Structure Analysis. Chemical Research in Toxicology, 2011, 24, 797-808.	toxic pectrometry,	1.7	60
278	The elastic network model reveals a consistent picture on intrinsic functional dynamics o restriction endonucleases. Physical Biology, 2011, 8, 056001.	f type II	0.8	10
279	Structurally Sophisticated Octahedral Metal Complexes as Highly Selective Protein Kinase Journal of the American Chemical Society, 2011, 133, 5976-5986.	e Inhibitors.	6.6	218
280	Structure and kinetic characterization of human sperm-specific glyceraldehyde-3-phosphodehydrogenase, GAPDS. Biochemical Journal, 2011, 435, 401-409.	ate	1.7	29
281	Impact of BRCA1 BRCT Domain Missense Substitutions on Phosphopeptide Recognition. 2011, 50, 4579-4589.	Biochemistry,	1.2	42
282	Fragment Screening of Infectious Disease Targets in a Structural Genomics Environment. Enzymology, 2011, 493, 533-556.	Methods in	0.4	5
283	Dynamics of glucosamine-6-phosphate synthase catalysis. Archives of Biochemistry and E 2011, 505, 1-12.	3iophysics,	1.4	43
284	Structural characterization of CYP165D3, a cytochrome P450 involved in phenolic coupli teicoplanin biosynthesis. Archives of Biochemistry and Biophysics, 2011, 507, 163-173.	ng in	1.4	33
285	Targeting the SH2-Kinase Interface in Bcr-Abl Inhibits Leukemogenesis. Cell, 2011, 147, 3	06-319.	13.5	122
286	Structure of Leishmania major methionyl-tRNA synthetase in complex with intermediate methionyladenylate and pyrophosphate. Biochimie, 2011, 93, 570-582.	products	1.3	50
287	Characterization of monomeric dihydrodipicolinate synthase variant reveals the importar substrate binding in optimizing oligomerization. Biochimica Et Biophysica Acta - Proteins Proteomics, 2011, 1814, 1900-1909.		1.1	14
288	Unexpected Tricovalent Binding Mode of Boronic Acids within the Active Site of a Penicill Protein. Journal of the American Chemical Society, 2011, 133, 10839-10848.	in-Binding	6.6	37

#	Article	IF	CITATIONS
289	Hinge-loop mutation can be used to control 3D domain swapping and amyloidogenesis of human cystatin C. Journal of Structural Biology, 2011, 173, 406-413.	1.3	55
290	The Structure of the CRISPR-Associated Protein Csa3 Provides Insight into the Regulation of the CRISPR/Cas System. Journal of Molecular Biology, 2011, 405, 939-955.	2.0	87
291	Crystal Structures Exploring the Origins of the Broader Specificity of Escherichia coli Heat-Labile Enterotoxin Compared to Cholera Toxin. Journal of Molecular Biology, 2011, 406, 387-402.	2.0	25
292	Structural Studies of ROK Fructokinase YdhR from Bacillus subtilis: Insights into Substrate Binding and Fructose Specificity. Journal of Molecular Biology, 2011, 406, 325-342.	2.0	29
293	Crystal Structure of Arrestin-3 Reveals the Basis of the Difference in Receptor Binding Between Two Non-visual Subtypes. Journal of Molecular Biology, 2011, 406, 467-478.	2.0	185
294	Crystal Structures of the S. cerevisiae Spt6 Core and C-Terminal Tandem SH2 Domain. Journal of Molecular Biology, 2011, 408, 697-713.	2.0	54
295	The Double-Length Tyrosyl-tRNA Synthetase from the Eukaryote Leishmania major Forms an Intrinsically Asymmetric Pseudo-Dimer. Journal of Molecular Biology, 2011, 409, 159-176.	2.0	40
296	Probing the Evolution of Hydroxyisourate Hydrolase into Transthyretin through Active-Site Redesign. Journal of Molecular Biology, 2011, 409, 504-512.	2.0	15
297	Crystal Structure of a Rigid Four-Spectrin-Repeat Fragment of the Human Desmoplakin Plakin Domain. Journal of Molecular Biology, 2011, 409, 800-812.	2.0	47
298	The Structure of BRMS1 Nuclear Export Signal and SNX6 Interacting Region Reveals a Hexamer Formed by Antiparallel Coiled Coils. Journal of Molecular Biology, 2011, 411, 1114-1127.	2.0	13
299	Structural and Functional Characterization of an Agonistic Anti-Human EphA2 Monoclonal Antibody. Journal of Molecular Biology, 2011, 413, 390-405.	2.0	23
300	A New Structural Form in the SAM/Metal-Dependent O‑Methyltransferase Family: MycE from the Mycinamicin Biosynthetic Pathway. Journal of Molecular Biology, 2011, 413, 438-450.	2.0	24
301	Crystal Structure of Cardiac Troponin C Regulatory Domain in Complex with Cadmium and Deoxycholic Acid Reveals Novel Conformation. Journal of Molecular Biology, 2011, 413, 699-711.	2.0	4
302	High-Throughput Genetic Identification of Functionally Important Regions of the Yeast DEAD-Box Protein Mss116p. Journal of Molecular Biology, 2011, 413, 952-972.	2.0	15
303	Structure of the Escherichia coli Phosphonate Binding Protein PhnD and Rationally Optimized Phosphonate Biosensors. Journal of Molecular Biology, 2011, 414, 356-369.	2.0	60
304	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	1.9	764
305	Expression, purification and structural characterization of functionally replete thrombospondin-1 type 1 repeats in a bacterial expression system. Protein Expression and Purification, 2011, 80, 253-259.	0.6	16
306	Binding site and ligand flexibility revealed by high resolution crystal structures of GluK1 competitive antagonists. Neuropharmacology, 2011, 60, 126-134.	2.0	24

	CITATION	Report	
#	Article	IF	CITATIONS
307	Structural Study of the Complex Stereoselectivity of Human Butyrylcholinesterase for the Neurotoxic V-agents. Journal of Biological Chemistry, 2011, 286, 16783-16789.	1.6	41
308	Structural and Functional Characterization of an Archaeal Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-associated Complex for Antiviral Defense (CASCADE). Journal of Biological Chemistry, 2011, 286, 21643-21656.	1.6	183
309	Identification of the Allosteric Regulatory Site of Insulysin. PLoS ONE, 2011, 6, e20864.	1.1	34
310	An Inserted α∫β Subdomain Shapes the Catalytic Pocket of Lactobacillus johnsonii Cinnamoyl Esterase. PLoS ONE, 2011, 6, e23269.	1.1	46
311	A Novel N-Acetylglutamate Synthase Architecture Revealed by the Crystal Structure of the Bifunctional Enzyme from Maricaulis maris. PLoS ONE, 2011, 6, e28825.	1.1	14
312	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. Journal of Biological Chemistry, 2011, 286, 28256-28264.	1.6	19
313	The crystal structure of the cephalosporin deacetylating enzyme acetyl xylan esterase bound to paraoxon explains the low sensitivity of this serine hydrolase to organophosphate inactivation. Biochemical Journal, 2011, 436, 321-330.	1.7	22
314	Functional and structural characterization of a novel mannosylâ€3â€phosphoglycerate synthase from <i>Rubrobacter xylanophilus</i> reveals its dual substrate specificity. Molecular Microbiology, 2011, 79, 76-93.	1.2	18
315	Determination of the structure of the MinD–ATP complex reveals the orientation of MinD on the membrane and the relative location of the binding sites for MinE and MinC. Molecular Microbiology, 2011, 79, 1515-1528.	1.2	95
316	Atypical DNA recognition mechanism used by the EspR virulence regulator of <i>Mycobacterium tuberculosis</i> . Molecular Microbiology, 2011, 82, 251-264.	1.2	22
317	Applying Molecular Dynamics Simulations to Identify Rarely Sampled Ligandâ€bound Conformational States of Undecaprenyl Pyrophosphate Synthase, an Antibacterial Target. Chemical Biology and Drug Design, 2011, 77, 412-420.	1.5	38
318	Allosteric control of ligand-binding affinity using engineered conformation-specific effector proteins. Nature Structural and Molecular Biology, 2011, 18, 437-442.	3.6	62
319	The DNA-binding domain of the Chd1 chromatin-remodelling enzyme contains SANT and SLIDE domains. EMBO Journal, 2011, 30, 2596-2609.	3.5	104
320	Structure of human O-GlcNAc transferase and its complex with a peptide substrate. Nature, 2011, 469, 564-567.	13.7	385
321	Briefly Bound to Activate: Transient Binding of a Second Catalytic Magnesium Activates the Structure and Dynamics of CDK2 Kinase for Catalysis. Structure, 2011, 19, 675-690.	1.6	93
322	Structure of a Three-Domain Sesquiterpene Synthase: A Prospective Target for Advanced Biofuels Production. Structure, 2011, 19, 1876-1884.	1.6	76
323	Crystal structures of three protozoan homologs of tryptophanyl-tRNA synthetase. Molecular and Biochemical Parasitology, 2011, 177, 20-28.	0.5	16
324	The crystal structures of human S100B in the zinc- and calcium-loaded state at three pH values reveal zinc ligand swapping. Biochimica Et Biophysica Acta - Molecular Cell Research, 2011, 1813, 1083-1091.	1.9	43

#	Article	IF	CITATIONS
325	Leveraging structure determination with fragment screening for infectious disease drug targets: MECP synthase from Burkholderia pseudomallei. Journal of Structural and Functional Genomics, 2011, 12, 63-76.	1.2	19
326	Some <i>B</i> <sub>eq</sub> are more equivalent than others. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, 512-516.	0.3	11
327	Structure of the minor pseudopilin XcpW from thePseudomonas aeruginosatype II secretion system. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 124-130.	2.5	18
328	<i>REFMAC</i> 5 for the refinement of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 355-367.	2.5	7,247
329	Structural characterization of CalO1: a putative orsellinic acid methyltransferase in the calicheamicin-biosynthetic pathway. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 197-203.	2.5	16
330	Structure of human dual-specificity phosphatase 27 at 2.38â€Ã resolution. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 471-479.	2.5	17
331	Structure-based design of a disulfide-linked oligomeric form of the simian virus 40 (SV40) large T antigen DNA-binding domain. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 560-567.	2.5	6
332	Streptavidin and its biotin complex at atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 813-821.	2.5	83
333	The active conformation of human glucokinase is not altered by allosteric activators. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 929-935.	2.5	53
334	Structure of the dimeric form of CTP synthase from <i>Sulfolobus solfataricus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 201-208.	0.7	20
335	Structure of a mutant β toxin from <i>Staphylococcus aureus</i> reveals domain swapping and conformational flexibility. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 438-441.	0.7	3
336	Structure of a cyclin-dependent kinase fromGiardia lamblia. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1084-1089.	0.7	1
337	Structure of the RuBisCO chaperone RbcX from the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 851-857.	0.7	9
338	Structure of filamin A immunoglobulin-like repeat 10 from <i>Homo sapiens</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 871-876.	0.7	14
339	X-ray structure of the SH3 domain of the phosphoinositide 3-kinase p85β subunit. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1328-1333.	0.7	2
340	Structure of the catalytic domain of <i>Plasmodium falciparum</i> ARF GTPase-activating protein (ARFGAP). Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1339-1344.	0.7	1
341	Predicting protein ligand binding motions with the conformation explorer. BMC Bioinformatics, 2011, 12, 417.	1.2	8
342	The crystal structure of alanine racemase from Streptococcus pneumoniae, a target for structure-based drug design. BMC Microbiology, 2011, 11, 116.	1.3	30

#	ARTICLE	IF	CITATIONS
343	Crystal structure of the dimeric Oct6 (POU3f1) POU domain bound to palindromic MORE DNA. Proteins: Structure, Function and Bioinformatics, 2011, 79, 674-677.	1.5	21
344	Crystal structure of native <i>Anopheles gambiae</i> serpinâ€2, a negative regulator of melanization in mosquitoes. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1999-2003.	1.5	11
345	Structure of an archaealâ€ŧype phosphoenolpyruvate carboxylase sensitive to inhibition by aspartate. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1820-1829.	1.5	6
346	Intermolecular versus intramolecular interactions of the vinculin binding site 33 of talin. Protein Science, 2011, 20, 1471-1476.	3.1	9
347	Structural and biochemical consequences of NF1 associated nontruncating mutations in the Sec14-PH module of neurofibromin. Human Mutation, 2011, 32, 191-197.	1.1	29
348	Specific CLK Inhibitors from a Novel Chemotype for Regulation of Alternative Splicing. Chemistry and Biology, 2011, 18, 67-76.	6.2	173
349	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. Biochemistry, 2011, 50, 4019-4028.	1.2	28
350	The Crystal Structure of the Leishmania major Deoxyuridine Triphosphate Nucleotidohydrolase in Complex with Nucleotide Analogues, dUMP, and Deoxyuridine. Journal of Biological Chemistry, 2011, 286, 16470-16481.	1.6	37
351	X-ray crystallographic snapshots of reaction intermediates in the G117H mutant of human butyrylcholinesterase, a nerve agent target engineered into a catalytic bioscavenger. Biochemical Journal, 2011, 434, 73-82.	1.7	42
352	Activation of nitrofurazone by azoreductases: multiple activities in one enzyme. Scientific Reports, 2011, 1, 63.	1.6	30
353	Crystal Structure of a Viral Protease Intramolecular Acyl-enzyme Complex. Journal of Biological Chemistry, 2011, 286, 12475-12482.	1.6	15
354	Terminal Alkene Formation by the Thioesterase of Curacin A Biosynthesis. Journal of Biological Chemistry, 2011, 286, 14445-14454.	1.6	67
355	Evidence for an allosteric mechanism of substrate release from membrane-transporter accessory binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1285-92.	3.3	34
356	Structural and Kinetic Analysis of Substrate Binding to the Sialyltransferase Cst-II from Campylobacter jejuni*. Journal of Biological Chemistry, 2011, 286, 35922-35932.	1.6	27
357	Structural insights into cis element recognition of non-polyadenylated RNAs by the Nab3-RRM. Nucleic Acids Research, 2011, 39, 337-346.	6.5	33
358	Crystal Structures Explain Functional Differences in the Two Actin Depolymerization Factors of the Malaria Parasite. Journal of Biological Chemistry, 2011, 286, 28256-28264.	1.6	34
359	Structural Analysis of Histo-Blood Group Antigen Binding Specificity in a Norovirus GII.4 Epidemic Variant: Implications for Epochal Evolution. Journal of Virology, 2011, 85, 8635-8645.	1.5	138
360	Escherichia coli Thioredoxin-like Protein YbbN Contains an Atypical Tetratricopeptide Repeat Motif and Is a Negative Regulator of GroEL. Journal of Biological Chemistry, 2011, 286, 19459-19469.	1.6	15

#	Article	IF	CITATIONS
361	Expanding the Nucleotide and Sugar 1-Phosphate Promiscuity of Nucleotidyltransferase RmlA via Directed Evolution. Journal of Biological Chemistry, 2011, 286, 13235-13243.	1.6	37
362	Daedalus: a robust, turnkey platform for rapid production of decigram quantities of active recombinant proteins in human cell lines using novel lentiviral vectors. Nucleic Acids Research, 2011, 39, e143-e143.	6.5	74
363	Structural basis for nematode elF4E binding an m 2,2,7 G-Cap and its implications for translation initiation. Nucleic Acids Research, 2011, 39, 8820-8832.	6.5	38
364	Recombinant Phenotyping of Cytomegalovirus UL54 Mutations That Emerged during Cell Passages in the Presence of either Ganciclovir or Foscarnet. Antimicrobial Agents and Chemotherapy, 2011, 55, 4019-4027.	1.4	28
365	Identification and Structural Characterization of the ALIX-Binding Late Domains of Simian Immunodeficiency Virus SIV <sub>mac239</sub> and SIV <sub>agmTan-1</sub> . Journal of Virology, 2011, 85, 632-637.	1.5	41
366	The crystal structure of the TetR family transcriptional repressor SimR bound to DNA and the role of a flexible N-terminal extension in minor groove binding. Nucleic Acids Research, 2011, 39, 9433-9447.	6.5	61
367	Mechanism for selectivity-inactivation coupling in KcsA potassium channels. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5272-5277.	3.3	80
368	Geometric Restraint Drives On- and Off-pathway Catalysis by the Escherichia coli Menaquinol:Fumarate Reductase. Journal of Biological Chemistry, 2011, 286, 3047-3056.	1.6	20
369	Asparagine and Aspartate Hydroxylation of the Cytoskeletal Ankyrin Family Is Catalyzed by Factor-inhibiting Hypoxia-inducible Factor. Journal of Biological Chemistry, 2011, 286, 7648-7660.	1.6	63
370	Apo- and Cellopentaose-bound Structures of the Bacterial Cellulose Synthase Subunit BcsZ. Journal of Biological Chemistry, 2011, 286, 17601-17606.	1.6	76
371	Molecular Basis for the Unique Role of the AAA+ Chaperone ClpV in Type VI Protein Secretion. Journal of Biological Chemistry, 2011, 286, 30010-30021.	1.6	95
372	Structural insight into the functional mechanism of Nep1/Emg1 N1-specific pseudouridine methyltransferase in ribosome biogenesis. Nucleic Acids Research, 2011, 39, 2445-2457.	6.5	52
373	Unique Structural and Nucleotide Exchange Features of the Rho1 GTPase of Entamoeba histolytica. Journal of Biological Chemistry, 2011, 286, 39236-39246.	1.6	16
374	Structural and Functional Insights into DR2231 Protein, the MazG-like Nucleoside Triphosphate Pyrophosphohydrolase from Deinococcus radiodurans. Journal of Biological Chemistry, 2011, 286, 30691-30705.	1.6	22
375	Analysis of the Binding Forces Driving the Tight Interactions between β-Lactamase Inhibitory Protein-II (BLIP-II) and Class A β-Lactamases. Journal of Biological Chemistry, 2011, 286, 32723-32735.	1.6	18
376	The Structure of the Plakin Domain of Plectin Reveals a Non-canonical SH3 Domain Interacting with Its Fourth Spectrin Repeat. Journal of Biological Chemistry, 2011, 286, 12429-12438.	1.6	43
377	Crystal Structure of the Heme d1 Biosynthesis Enzyme NirE in Complex with Its Substrate Reveals New Insights into the Catalytic Mechanism of S-Adenosyl-I-methionine-dependent Uroporphyrinogen III Methyltransferases. Journal of Biological Chemistry, 2011, 286, 26754-26767.	1.6	35
378	The Atypical Response Regulator Protein ChxR Has Structural Characteristics and Dimer Interface Interactions That Are Unique within the OmpR/PhoB Subfamily. Journal of Biological Chemistry, 2011, 286. 32606-32616.	1.6	12

#	Article	IF	CITATIONS
379	Unexpected Diversity of Chlorite Dismutases: a Catalytically Efficient Dimeric Enzyme from Nitrobacter winogradskyi. Journal of Bacteriology, 2011, 193, 2408-2417.	1.0	76
380	Crystal structure of a Î <sup>3</sup> δT-cell receptor specific for the human MHC class I homolog MICA. Proceedings of the United States of America, 2011, 108, 2414-2419.	3.3	133
381	Unique active site promotes error-free replication opposite an 8-oxo-guanine lesion by human DNA polymerase iota. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3210-3215.	3.3	57
382	Investigation of the Molecular Origins of Protein-arginine Methyltransferase I (PRMT1) Product Specificity Reveals a Role for Two Conserved Methionine Residues. Journal of Biological Chemistry, 2011, 286, 29118-29126.	1.6	26
383	Structure and Mechanism of the Diiron Benzoyl-Coenzyme A Epoxidase BoxB. Journal of Biological Chemistry, 2011, 286, 29241-29248.	1.6	30
384	Structure of collagenase G reveals a chew-and-digest mechanism of bacterial collagenolysis. Nature Structural and Molecular Biology, 2011, 18, 1109-1114.	3.6	85
385	The Structural Basis of Endocannabinoid Oxygenation by Cyclooxygenase-2. Journal of Biological Chemistry, 2011, 286, 20736-20745.	1.6	42
386	Structural basis for the removal of ubiquitin and interferon-stimulated gene 15 by a viral ovarian tumor domain-containing protease. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2222-2227.	3.3	90
387	Crystal structure of a KSHV–SOX–DNA complex: insights into the molecular mechanisms underlying DNase activity and host shutoff. Nucleic Acids Research, 2011, 39, 5744-5756.	6.5	33
388	Structural and Functional Studies on the Interaction of GspC and GspD in the Type II Secretion System. PLoS Pathogens, 2011, 7, e1002228.	2.1	83
389	Structure and activity of the <i>Pseudomonas aeruginosa</i> hotdog-fold thioesterases PA5202 and PA2801. Biochemical Journal, 2012, 444, 445-455.	1.7	6
390	Crystal structures of the tRNA:m 2 G6 methyltransferase Trm14/TrmN from two domains of life. Nucleic Acids Research, 2012, 40, 5149-5161.	6.5	33
391	The crystal structure of the Sox4 HMG domain–DNA complex suggests a mechanism for positional interdependence in DNA recognition. Biochemical Journal, 2012, 443, 39-47.	1.7	59
392	Structures of Merkel Cell Polyomavirus VP1 Complexes Define a Sialic Acid Binding Site Required for Infection. PLoS Pathogens, 2012, 8, e1002738.	2.1	79
393	A Unique Bivalent Binding and Inhibition Mechanism by the Yatapoxvirus Interleukin 18 Binding Protein. PLoS Pathogens, 2012, 8, e1002876.	2.1	24
394	Tail-anchor targeting by a Get3 tetramer: the structure of an archaeal homologue. EMBO Journal, 2012, 31, 707-719.	3.5	37
395	Structural and Biochemical Characterization of the Vaccinia Virus Envelope Protein D8 and Its Recognition by the Antibody LA5. Journal of Virology, 2012, 86, 8050-8058.	1.5	33
396	Structure and activity of the only human RNase T2. Nucleic Acids Research, 2012, 40, 8733-8742.	6.5	37

#	Article	IF	CITATIONS
397	The dynamic stator stalk of rotary ATPases. Nature Communications, 2012, 3, 687.	5.8	60
398	Iron and bismuth bound human serum transferrin reveals a partially-opened conformation in the N-lobe. Scientific Reports, 2012, 2, 999.	1.6	91
399	The First Structure of Polarity Suppression Protein, Psu from Enterobacteria Phage P4, Reveals a Novel Fold and a Knotted Dimer. Journal of Biological Chemistry, 2012, 287, 44667-44675.	1.6	19
400	Extra-domain B in Oncofetal Fibronectin Structurally Promotes Fibrillar Head-to-tail Dimerization of Extracellular Matrix Protein. Journal of Biological Chemistry, 2012, 287, 17578-17588.	1.6	34
401	Identification and Characterization of the Thermus thermophilus 5-Methylcytidine (m5C) Methyltransferase Modifying 23 S Ribosomal RNA (rRNA) Base C1942. Journal of Biological Chemistry, 2012, 287, 27593-27600.	1.6	7
402	Structural Insight into Activation Mechanism of Toxoplasma gondii Nucleoside Triphosphate Diphosphohydrolases by Disulfide Reduction*. Journal of Biological Chemistry, 2012, 287, 3051-3066.	1.6	21
403	A Unique Sugar-binding Site Mediates the Distinct Anti-influenza Activity of Pig Surfactant Protein D. Journal of Biological Chemistry, 2012, 287, 26666-26677.	1.6	23
404	Investigating Substrate Promiscuity in Cyclooxygenase-2. Journal of Biological Chemistry, 2012, 287, 24619-24630.	1.6	46
405	Structure of the Bone Morphogenetic Protein Receptor ALK2 and Implications for Fibrodysplasia Ossificans Progressiva. Journal of Biological Chemistry, 2012, 287, 36990-36998.	1.6	159
406	Staphylococcal biofilm-forming protein has a contiguous rod-like structure. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1011-8.	3.3	73
407	Structure of the surface layer of the methanogenic archaean <i>Methanosarcina acetivorans</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11812-11817.	3.3	67
408	Human Protein-disulfide Isomerase Is a Redox-regulated Chaperone Activated by Oxidation of Domain a′. Journal of Biological Chemistry, 2012, 287, 1139-1149.	1.6	110
409	Kinetic and Crystallographic Studies of Extended-Spectrum GES-11, GES-12, and GES-14 β-Lactamases. Antimicrobial Agents and Chemotherapy, 2012, 56, 5618-5625.	1.4	24
410	Crystal Structure of the Japanese Encephalitis Virus Envelope Protein. Journal of Virology, 2012, 86, 2337-2346.	1.5	184
411	Crystal structure of a heterodimer of editosome interaction proteins in complex with two copies of a cross-reacting nanobody. Nucleic Acids Research, 2012, 40, 1828-1840.	6.5	35
412	Structure, Function, and Evolution of the Crimean-Congo Hemorrhagic Fever Virus Nucleocapsid Protein. Journal of Virology, 2012, 86, 10914-10923.	1.5	94
413	Novel fragments of clavulanate observed in the structure of the class A Â-lactamase from Bacillus licheniformis BS3. Journal of Antimicrobial Chemotherapy, 2012, 67, 2379-2387.	1.3	4
414	The crystal structure of human UDP-glucose pyrophosphorylase reveals a latch effect that influences enzymatic activity. Biochemical Journal, 2012, 442, 283-291.	1.7	20

#	Article	IF	CITATIONS
415	High-resolution structure of <i>Bombyx mori</i> lipoprotein 7: crystallographic determination of the identity of the protein and its potential role in detoxification. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1140-1151.	2.5	14
416	Structure of the prolyl-tRNA synthetase from the eukaryotic pathogen <i>Giardia lamblia</i> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1194-1200.	2.5	9
417	The structure of <i>Enterococcus faecalis</i> thymidylate synthase provides clues about folate bacterial metabolism. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1232-1241.	2.5	28
418	Structure of human Rack1 protein at a resolution of 2.45â€Ã Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 867-872.	0.7	35
419	Suppression of Electron Transfer to Dioxygen by Charge Transfer and Electron Transfer Complexes in the FAD-dependent Reductase Component of Toluene Dioxygenase. Journal of Biological Chemistry, 2012, 287, 38338-38346.	1.6	17
420	Zinc Potentiates GluK3 Glutamate Receptor Function by Stabilizing the Ligand Binding Domain Dimer Interface. Neuron, 2012, 76, 565-578.	3.8	59
421	Structural basis for the activity of a cytoplasmic RNA terminal uridylyl transferase. Nature Structural and Molecular Biology, 2012, 19, 782-787.	3.6	47
422	Structure-Based Alteration of Substrate Specificity and Catalytic Activity of Sulfite Oxidase from Sulfite Oxidation to Nitrate Reduction. Biochemistry, 2012, 51, 1134-1147.	1.2	14
423	7,8-Dichloro-1-oxo-β-carbolines as a Versatile Scaffold for the Development of Potent and Selective Kinase Inhibitors with Unusual Binding Modes. Journal of Medicinal Chemistry, 2012, 55, 403-413.	2.9	64
424	Structural basis for Arf6-MKLP1 complex formation on the Flemming body responsible for cytokinesis. EMBO Journal, 2012, 31, 2590-2603.	3.5	55
425	Structural Basis of Functional Group Activation by Sulfotransferases in Complex Metabolic Pathways. ACS Chemical Biology, 2012, 7, 1994-2003.	1.6	34
426	Uncoupling Intramolecular Processing and Substrate Hydrolysis in the N-Terminal Nucleophile Hydrolase hASRGL1 by Circular Permutation. ACS Chemical Biology, 2012, 7, 1840-1847.	1.6	18
427	Small-Molecule Inhibition of BRDT for Male Contraception. Cell, 2012, 150, 673-684.	13.5	353
428	Structural characterization and inhibition of the Plasmodium Atg8–Atg3 interaction. Journal of Structural Biology, 2012, 180, 551-562.	1.3	58
429	Ligand Binding Stepwise Disrupts Water Network in Thrombin: Enthalpic and Entropic Changes Reveal Classical Hydrophobic Effect. Journal of Medicinal Chemistry, 2012, 55, 6094-6110.	2.9	86
430	The dynamic disulphide relay of quiescin sulphydryl oxidase. Nature, 2012, 488, 414-418.	13.7	70
431	Evolution of the receptor binding properties of the influenza A(H3N2) hemagglutinin. Proceedings of the United States of America, 2012, 109, 21474-21479.	3.3	250
432	Structural and Functional Characterization of the Kindlin-1 Pleckstrin Homology Domain. Journal of Biological Chemistry, 2012, 287, 43246-43261.	1.6	27

#	Article	IF	CITATIONS
433	Price To Be Paid for Two-Metal Catalysis: Magnesium Ions That Accelerate Chemistry Unavoidably Limit Product Release from a Protein Kinase. Journal of the American Chemical Society, 2012, 134, 15357-15370.	6.6	67
434	The structure of the C-terminal domain of the largest editosome interaction protein and its role in promoting RNA binding by RNA-editing ligase L2. Nucleic Acids Research, 2012, 40, 6966-6977.	6.5	19
435	Activity and Crystal Structure ofArabidopsis thalianaUDP-N-Acetylglucosamine Acyltransferase. Biochemistry, 2012, 51, 4322-4330.	1.2	12
436	<i>Entamoeba histolytica</i> Rho1 Regulates Actin Polymerization through a Divergent, Diaphanous-Related Formin. Biochemistry, 2012, 51, 8791-8801.	1.2	16
437	Structural Insights into the Conformation and Oligomerization of E2â^¼Ubiquitin Conjugates. Biochemistry, 2012, 51, 4175-4187.	1.2	78
438	Impact of Ligand and Protein Desolvation on Ligand Binding to the S1 Pocket of Thrombin. Journal of Molecular Biology, 2012, 418, 350-366.	2.0	43
439	Crystal Structure of Bacillus subtilis Signal Peptide Peptidase A. Journal of Molecular Biology, 2012, 419, 347-358.	2.0	15
440	Structural and Functional Characterization of Microcin C Resistance Peptidase MccF from Bacillus anthracis. Journal of Molecular Biology, 2012, 420, 366-383.	2.0	22
441	Structural Basis for Telomerase RNA Recognition and RNP Assembly by the Holoenzyme La Family Protein p65. Molecular Cell, 2012, 47, 16-26.	4.5	94
442	Structures of the HIN Domain:DNA Complexes Reveal Ligand Binding and Activation Mechanisms of the AIM2 Inflammasome and IFI16 Receptor. Immunity, 2012, 36, 561-571.	6.6	456
443	The sulfate-binding site structure of the human eosinophil cationic protein as revealed by a new crystal form. Journal of Structural Biology, 2012, 179, 1-9.	1.3	10
444	Promoting crystallisation of the Salmonella enteritidis fimbriae 14 pilin SefD using deuterium oxide. Biochemical and Biophysical Research Communications, 2012, 421, 208-213.	1.0	3
445	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. Cell, 2012, 149, 214-231.	13.5	1,368
446	Inter-domain movements in polyketide synthases: a molecular dynamics study. Molecular BioSystems, 2012, 8, 1157.	2.9	8
447	Crystal structures of the JAK2 pseudokinase domain and the pathogenic mutant V617F. Nature Structural and Molecular Biology, 2012, 19, 754-759.	3.6	196
448	<i>AcinetobacterÂbaumannii </i> <scp>F</scp> ol <scp>D</scp> ligand complexes–Âpotent inhibitors of folate metabolism and a reâ€evaluation of the structure of <scp>LY</scp> 374571. FEBS Journal, 2012, 279, 4350-4360.	2.2	14
449	A Basis Set of <i>de Novo</i> Coiled-Coil Peptide Oligomers for Rational Protein Design and Synthetic Biology. ACS Synthetic Biology, 2012, 1, 240-250.	1.9	226
450	Structural insights into the broadened substrate profile of the extended-spectrum β-lactamase OXY-1-1 fromKlebsiella oxytoca. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1460-1467.	2.5	2

#	Article	IF	CITATIONS
451	Structure of extracellular signal-regulated kinase 2 in complex with ATP and ADP. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1434-1439.	0.7	13
452	Structural Basis of the PNRC2-Mediated Link between mRNA Surveillance and Decapping. Structure, 2012, 20, 2025-2037.	1.6	59
453	Structural, Biochemical, and Functional Characterization of the Cyclic Nucleotide Binding Homology Domain from the Mouse EAG1 Potassium Channel. Journal of Molecular Biology, 2012, 423, 34-46.	2.0	52
454	The Structure of DNA-Bound Human Topoisomerase II Alpha: Conformational Mechanisms for Coordinating Inter-Subunit Interactions with DNA Cleavage. Journal of Molecular Biology, 2012, 424, 109-124.	2.0	176
455	Molecular Recognition of Canonical and Deaminated Bases by P. abyssi Family B DNA Polymerase. Journal of Molecular Biology, 2012, 423, 315-336.	2.0	36
456	Structural Basis for ASPP2 Recognition by the Tumor Suppressor p73. Journal of Molecular Biology, 2012, 423, 515-527.	2.0	20
457	A new family of covalent inhibitors block nucleotide binding to the active site of pyruvate kinase. Biochemical Journal, 2012, 448, 67-72.	1.7	21
458	X-ray structures of LeuT in substrate-free outward-open and apo inward-open states. Nature, 2012, 481, 469-474.	13.7	488
459	1.7 Refinement of X-ray Crystal Structures. , 2012, , 105-115.		3
460	Optimal Number of Coarse-Grained Sites in Different Components of Large Biomolecular Complexes. Journal of Physical Chemistry B, 2012, 116, 8363-8374.	1.2	54
461	Crystal Structures of the Tetratricopeptide Repeat Domains of Kinesin Light Chains: Insight into Cargo Recognition Mechanisms. PLoS ONE, 2012, 7, e33943.	1.1	46
462	Assessment of Pseudomonas aeruginosa N5,N10-Methylenetetrahydrofolate Dehydrogenase - Cyclohydrolase as a Potential Antibacterial Drug Target. PLoS ONE, 2012, 7, e35973.	1.1	18
463	Corticosteroid-Binding Globulin: Structure-Function Implications from Species Differences. PLoS ONE, 2012, 7, e52759.	1.1	51
464	Structure of the cytoplasmic domain of <i>Yersinia pestis</i> YscD, an essential component of the type III secretion system. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 201-209.	2.5	14
465	Structure and function of theClostridium thermocellumcellobiohydrolase A X1-module repeat: enhancement through stabilization of the CbhA complex. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 292-299.	2.5	15
466	Improving the diffraction of apoA-IV crystals through extreme dehydration. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 105-110.	0.7	10
467	Structural characterization of human Uch37. Proteins: Structure, Function and Bioinformatics, 2012, 80, 649-654.	1.5	34
468	Structural basis of interleukinâ€5 dimer recognition by its α receptor. Protein Science, 2012, 21, 850-864.	3.1	57

ARTICLE IF CITATIONS Structural analysis of a 3â€deoxyâ€Dâ€arabinoâ€heptulosonate 7â€phosphate synthase with an Nâ€terminal 3.1 31 469 chorismate mutaseâ€like regulatory domain. Protein Science, 2012, 21, 887-895. Structural, kinetic, and thermodynamic studies of specificity designed HIVâ€1 protease. Protein Science, 470 3.1 2012, 21, 1029-1041. 471 Structure of the mitotic checkpoint complex. Nature, 2012, 484, 208-213. 13.7 270 Multimode, Cooperative Mechanism of Action of Allosteric HIV-1 Integrase Inhibitors. Journal of Biological Chemistry, 2012, 287, 16801-16811. Crystal structure of a voltage-gated sodium channel in two potentially inactivated states. Nature, 473 13.7 435 2012, 486, 135-139. Sequence-dependent Structural Variation in DNA Undergoing Intrahelical Inspection by the DNA glycosylase MutM. Journal of Biological Chemistry, 2012, 287, 18044-18054. 474 1.6 Structure and permeation mechanism of a mammalian urea transporter. Proceedings of the National 475 3.3 68 Academy of Sciences of the United States of America, 2012, 109, 11194-11199. Water Makes the Difference: Rearrangement of Water Solvation Layer Triggers Nonâ€additivity of 1.6 64 Functional Group Contributions in Protein–Ligand Binding. ChemMedChem, 2012, 7, 1423-1434. Crystal structures of putative phosphoglycerate kinases from B. anthracis and C. jejuni. Journal of 477 1.2 7 Structural and Functional Genomics, 2012, 13, 15-26. The crystal structure of AphB, a virulence gene activator from <i>Vibrio cholerae</i>, reveals 1.2 residues that influence its response to oxygen and pH. Molecular Microbiology, 2012, 83, 457-470. Small-Molecule Inhibitors of the c-Fes Protein-Tyrosine Kinase. Chemistry and Biology, 2012, 19, 529-540. 479 6.2 32 Defects in DNA degradation revealed in crystal structures of TREX1 exonuclease mutations linked to 480 1.3 autoimmune disease. DNA Repair, 2012, 11, 65-73. Benzodiazepines and benzotriazepines as protein interaction inhibitors targeting bromodomains of 481 1.4 112 the BET family. Bioorganic and Medicinal Chemistry, 2012, 20, 1878-1886. Structural characterization of <i>Helicobacterâ  $\in f$  pylori</i> dethiobiotin synthetase reveals differences between family members. FEBS Journal, 2012, 279, 1093-1105. 2.2 A recurrent Dâ $\in$ strand association interface is observed in  $\hat{l}^2 \hat{a} \in 2$  microglobulin oligomers. FEBS Journal, 483 2.2 18 2012, 279, 1131-1143. The crystal structure of Leishmania major N5,N10-methylenetetrahydrofolate dehydrogenase/cyclohydrolase and assessment of a potential drug target. Molecular and Biochemical 484 Parasitology, 2012, 181, 178-185. Structure of the Yersinia pestis FabV Enoyl-ACP Reductase and Its Interaction with Two 2-Pyridone 485 1.6 18 Inhibitors. Structure, 2012, 20, 89-100. Structural Insight into the Bacterial Mucinase StcE Essential to Adhesion and Immune Evasion during 1.6 Enterohemorrhagic E. Acoli Infection. Structure, 2012, 20, 707-717.

#	Article	IF	CITATIONS
487	Automated Illustration of Molecular Flexibility. IEEE Transactions on Visualization and Computer Graphics, 2012, 18, 132-145.	2.9	21
488	To B or not to B: a question of resolution?. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 468-477.	2.5	62
489	<i>PDB_REDO</i> : constructive validation, more than just looking for errors. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 484-496.	2.5	195
490	Towards automated crystallographic structure refinement with <i>phenix.refine</i> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 352-367.	2.5	4,573
491	The structure of aXanthomonasgeneral stress protein involved in citrus canker reveals its flavin-binding property. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 846-853.	2.5	7
492	Structures of the pleckstrin homology domain of <i>Saccharomyces cerevisiae</i> Avo1 and its human orthologue Sin1, an essential subunit of TOR complex 2. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 386-392.	0.7	24
493	Detection and analysis of unusual features in the structural model and structure-factor data of a birch pollen allergen. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 366-376.	0.7	18
494	Structure of the Legionella effector AnkX reveals the mechanism of phosphocholine transfer by the FIC domain. EMBO Journal, 2013, 32, 1469-1477.	3.5	68
495	<i><scp>M</scp>edicagoÂtruncatula</i> histidineâ€containing phosphotransfer protein. FEBS Journal, 2013, 280, 3709-3720.	2.2	15
496	Molecular basis for N-terminal acetylation by the heterodimeric NatA complex. Nature Structural and Molecular Biology, 2013, 20, 1098-1105.	3.6	137
497	A dodecameric ring-like structure of the NO domain of the type II secretin from enterotoxigenic Escherichia coli. Journal of Structural Biology, 2013, 183, 354-362.	1.3	19
498	Combinatorial Design of an Anticalin Directed against the Extra-Domain B for the Specific Targeting of Oncofetal Fibronectin. Journal of Molecular Biology, 2013, 425, 780-802.	2.0	64
499	An additional substrate binding site in a bacterial phenylalanine hydroxylase. European Biophysics Journal, 2013, 42, 691-708.	1.2	10
500	Structural Rearrangement of Ebola Virus VP40 Begets Multiple Functions in the Virus Life Cycle. Cell, 2013, 154, 763-774.	13.5	201
501	The Yeast Ski Complex: Crystal Structure and RNA Channeling to the Exosome Complex. Cell, 2013, 154, 814-826.	13.5	177
502	Paralog-selective Hsp90 inhibitors define tumor-specific regulation of HER2. Nature Chemical Biology, 2013, 9, 677-684.	3.9	180
503	Flexibility of the Bacterial Chaperone Trigger Factor in Microsecond-Timescale Molecular Dynamics Simulations. Biophysical Journal, 2013, 105, 732-744.	0.2	17
504	Inhibition of <scp>dd</scp> -Peptidases by a Specific Trifluoroketone: Crystal Structure of a Complex with the <i>Actinomadura</i> R39 <scp>dd</scp> -Peptidase. Biochemistry, 2013, 52, 2128-2138.	1.2	8

#	Article	IF	CITATIONS
505	An Iml3-Chl4 Heterodimer Links the Core Centromere to Factors Required for Accurate Chromosome Segregation. Cell Reports, 2013, 5, 29-36.	2.9	56
506	Structural Determinants of RGS-RhoGEF Signaling Critical to Entamoeba histolytica Pathogenesis. Structure, 2013, 21, 65-75.	1.6	7
507	Structural Basis for the Enzymatic Formation of the Key Strawberry Flavor Compound 4-Hydroxy-2,5-dimethyl-3(2H)-furanone. Journal of Biological Chemistry, 2013, 288, 16815-16826.	1.6	25
508	Understanding specificity of the mycosin proteases in ESX/type VII secretion by structural and functional analysis. Journal of Structural Biology, 2013, 184, 115-128.	1.3	33
509	The crystal structure reveals the molecular mechanism of bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (Rv1415) fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1633-1644.	2.5	13
510	New Nucleotide-Competitive Non-Nucleoside Inhibitors of Terminal Deoxynucleotidyl Transferase: Discovery, Characterization, and Crystal Structure in Complex with the Target. Journal of Medicinal Chemistry, 2013, 56, 7431-7441.	2.9	24
511	Cytochrome P450 <sub>sky</sub> Interacts Directly with the Nonribosomal Peptide Synthetase to Generate Three Amino Acid Precursors in Skyllamycin Biosynthesis. ACS Chemical Biology, 2013, 8, 2586-2596.	1.6	76
512	<i>TLS</i> from fundamentals to practice. Crystallography Reviews, 2013, 19, 230-270.	0.4	46
513	The Structural Basis for Phospholamban Inhibition of the Calcium Pump in Sarcoplasmic Reticulum. Journal of Biological Chemistry, 2013, 288, 30181-30191.	1.6	107
514	Conformational Analysis of NMDA Receptor GluN1, GluN2, and GluN3 Ligand-Binding Domains Reveals Subtype-Specific Characteristics. Structure, 2013, 21, 1788-1799.	1.6	86
515	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. Journal of Biological Chemistry, 2013, 288, 34131-34145.	1.6	29
516	Design, synthesis, biological and structural evaluation of functionalized resveratrol analogues as inhibitors of quinone reductase 2. Bioorganic and Medicinal Chemistry, 2013, 21, 6022-6037.	1.4	24
517	HCF-1 Is Cleaved in the Active Site of O-GlcNAc Transferase. Science, 2013, 342, 1235-1239.	6.0	162
518	A Photo-Labile Thioether Linkage to Phycoviolobilin Provides the Foundation for the Blue/Green Photocycles in DXCF-Cyanobacteriochromes. Structure, 2013, 21, 88-97.	1.6	92
519	Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination. FEBS Journal, 2013, 280, 5705-5736.	2.2	95
520	Improved Crystallographic Structures Using Extensive Combinatorial Refinement. Structure, 2013, 21, 1923-1930.	1.6	18
521	GES-18, a New Carbapenem-Hydrolyzing GES-Type β-Lactamase from Pseudomonas aeruginosa That Contains Ile80 and Ser170 Residues. Antimicrobial Agents and Chemotherapy, 2013, 57, 396-401.	1.4	36
522	Insights into mucopolysaccharidosis I from the structure and action of α-L-iduronidase. Nature Chemical Biology, 2013, 9, 739-745.	3.9	48

#	Article	IF	CITATIONS
523	<scp>M</scp> re <scp>B</scp> and <scp>M</scp> ur <scp>G</scp> as scaffolds for the cytoplasmic steps of peptidoglycan biosynthesis. Environmental Microbiology, 2013, 15, 3218-3228.	1.8	54
524	Structural and Functional Characterization of Pseudomonas aeruginosa AlgX. Journal of Biological Chemistry, 2013, 288, 22299-22314.	1.6	48
525	Structural Basis for dsRNA Recognition, Filament Formation, and Antiviral Signal Activation by MDA5. Cell, 2013, 152, 276-289.	13.5	447
526	A Strategy for Modulation of Enzymes in the Ubiquitin System. Science, 2013, 339, 590-595.	6.0	257
527	Crystallographic snapshot of cellulose synthesis and membrane translocation. Nature, 2013, 493, 181-186.	13.7	492
528	Self-Assembly and Conformational Heterogeneity of the AXH Domain ofÂAtaxin-1: An Unusual Example of a Chameleon Fold. Biophysical Journal, 2013, 104, 1304-1313.	0.2	19
529	Crystal Structure of Prp5p Reveals Interdomain Interactions that Impact Spliceosome Assembly. Cell Reports, 2013, 5, 1269-1278.	2.9	23
530	In vivo phosphorylation and in vitro autophosphorylation-inactivation of Kluyveromyces lactis hexokinase KlHxk1. Biochemical and Biophysical Research Communications, 2013, 435, 313-318.	1.0	6
531	In Human Pseudouridine Synthase 1 (hPus1), a C-Terminal Helical Insert Blocks tRNA from Binding in the Same Orientation as in the Pus1 Bacterial Homologue TruA, Consistent with Their Different Target Selectivities. Journal of Molecular Biology, 2013, 425, 3875-3887.	2.0	27
532	Development of RNA Aptamers Targeting Ebola Virus VP35. Biochemistry, 2013, 52, 8406-8419.	1.2	73
533	Structure of <scp>NADP</scp> <sup>+</sup> â€dependent glutamate dehydrogenase from <i>EscherichiaÂcoli</i> –Âreflections on the basis of coenzyme specificity in the family of glutamate dehydrogenases. FEBS Journal, 2013, 280, 4681-4692.	2.2	18
534	Structures of Intermediates along the Catalytic Cycle of Terminal Deoxynucleotidyltransferase: Dynamical Aspects of the Two-Metal Ion Mechanism. Journal of Molecular Biology, 2013, 425, 4334-4352.	2.0	41
535	Conformational plasticity at the IgE-binding site of the B-cell receptor CD23. Molecular Immunology, 2013, 56, 693-697.	1.0	16
536	Crystal structures of <i>Phanerochaete chrysosporium</i> pyranose 2â€oxidase suggest that the Nâ€terminus acts as a propeptide that assists in homotetramer assembly. FEBS Open Bio, 2013, 3, 496-504.	1.0	21
537	Structural evidence for native state stabilization of a conformationally labile amyloidogenic transthyretin variant by fibrillogenesis inhibitors. FEBS Letters, 2013, 587, 2325-2331.	1.3	21
538	BRMS151–98 and BRMS151–84 Are Crystal Oligomeric Coiled Coils with Different Oligomerization States, Which Behave as Disordered Protein Fragments in Solution. Journal of Molecular Biology, 2013, 425, 2147-2163.	2.0	5
539	Active-Site Monovalent Cations Revealed in a 1.55-ÃResolution Hammerhead Ribozyme Structure. Journal of Molecular Biology, 2013, 425, 3790-3798.	2.0	34
540	Redox state-dependent changes in the crystal structure ofÂ[NiFeSe] hydrogenase from Desulfovibrio vulgaris Hildenborough. International Journal of Hydrogen Energy, 2013, 38, 8664-8682.	3.8	34

#	Article	IF	CITATIONS
541	A 2.1-ÃResolution Crystal Structure of Unliganded CRM1 Reveals the Mechanism of Autoinhibition. Journal of Molecular Biology, 2013, 425, 350-364.	2.0	32
542	Crystal Structures of the Catalytic Domain of Human Soluble Guanylate Cyclase. PLoS ONE, 2013, 8, e57644.	1.1	78
543	Structure of the Trypanosoma cruzi protein tyrosine phosphatase TcPTP1, a potential therapeutic target for Chagas' disease. Molecular and Biochemical Parasitology, 2013, 187, 1-8.	0.5	7
544	Structure of a periplasmic domain of the EpsAB fusion protein of the <i>Vibrio vulnificus</i> type II secretion system. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 142-149.	2.5	10
545	Single residues dictate the co-evolution of dual esterases: MCP hydrolases from the $\hat{l}\pm/\hat{l}^2$ hydrolase family. Biochemical Journal, 2013, 454, 157-166.	1.7	34
546	Structural and Functional Characterization of MppR, an Enduracididine Biosynthetic Enzyme from <i>Streptomyces hygroscopicus</i> : Functional Diversity in the Acetoacetate Decarboxylase-like Superfamily. Biochemistry, 2013, 52, 4492-4506.	1.2	31
547	Studies of IscR reveal a unique mechanism for metal-dependent regulation of DNA binding specificity. Nature Structural and Molecular Biology, 2013, 20, 740-747.	3.6	104
548	Metal Binding Properties of <i>Escherichia coli</i> YjiA, a Member of the Metal Homeostasis-Associated COG0523 Family of GTPases. Biochemistry, 2013, 52, 1788-1801.	1.2	43
549	High-resolution structure of an atypical α-phosphoglucomutase related to eukaryotic phosphomannomutases. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2008-2016.	2.5	4
550	The structure of Rv3717 reveals a novel amidase from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2543-2554.	2.5	25
551	The DNA-binding domain of BenM reveals the structural basis for the recognition of a T-N <sub>11</sub> -A sequence motif by LysR-type transcriptional regulators. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1995-2007.	2.5	52
552	Discovery of Novel Small-Molecule Inhibitors of BRD4 Using Structure-Based Virtual Screening. Journal of Medicinal Chemistry, 2013, 56, 8073-8088.	2.9	116
553	Design, construction, and characterization of a secondâ€generation DARPin library with reduced hydrophobicity. Protein Science, 2013, 22, 1239-1257.	3.1	64
554	Progressive Multifocal Leukoencephalopathy-Associated Mutations in the JC Polyomavirus Capsid Disrupt Lactoseries Tetrasaccharide c Binding. MBio, 2013, 4, e00247-13.	1.8	48
555	Structural characterization of the mechanism through which human glutamic acid decarboxylase auto-activates. Bioscience Reports, 2013, 33, 137-44.	1.1	16
556	Autoreactivity and Exceptional CDR Plasticity (but Not Unusual Polyspecificity) Hinder Elicitation of the Anti-HIV Antibody 4E10. PLoS Pathogens, 2013, 9, e1003639.	2.1	44
557	Molecular Mechanism of Fascin Function in Filopodial Formation. Journal of Biological Chemistry, 2013, 288, 274-284.	1.6	112
558	A Unique Spumavirus Gag N-terminal Domain with Functional Properties of Orthoretroviral Matrix and Capsid. PLoS Pathogens, 2013, 9, e1003376.	2.1	29

#	Article	IF	CITATIONS
559	Structure of a dimeric crenarchaeal Cas6 enzyme with an atypical active site for CRISPR RNA processing. Biochemical Journal, 2013, 452, 223-230.	1.7	32
560	Structural and Biochemical Analysis of DNA Helix Invasion by the Bacterial 8-Oxoguanine DNA Glycosylase MutM. Journal of Biological Chemistry, 2013, 288, 10012-10023.	1.6	24
561	Structural and Thermodynamic Basis of Amprenavir/Darunavir and Atazanavir Resistance in HIV-1 Protease with Mutations at Residue 50. Journal of Virology, 2013, 87, 4176-4184.	1.5	26
562	From Soil to Structure, a Novel Dimeric Î <sup>2</sup> -Glucosidase Belonging to Glycoside Hydrolase Family 3 Isolated from Compost Using Metagenomic Analysis. Journal of Biological Chemistry, 2013, 288, 14985-14992.	1.6	42
563	Structural and Functional Characterization of the Mumps Virus Phosphoprotein. Journal of Virology, 2013, 87, 7558-7568.	1.5	52
564	Mycobacterium tuberculosis RsdA provides a conformational rationale for selective regulation of Ï <i>f</i> -factor activity by proteolysis. Nucleic Acids Research, 2013, 41, 3414-3423.	6.5	15
565	Structural Determinants of Ubiquitin Conjugation in Entamoeba histolytica. Journal of Biological Chemistry, 2013, 288, 2290-2302.	1.6	14
566	Study of PcaV from Streptomyces coelicolor yields new insights into ligand-responsive MarR family transcription factors. Nucleic Acids Research, 2013, 41, 3888-3900.	6.5	58
567	Structure of formaldehyde dehydrogenase from <i>Pseudomonas aeruginosa</i> : the binary complex with the cofactor NAD <sup>+</sup> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 967-972.	0.7	11
568	Identification of one of the apurinic/apyrimidinic lyase active sites of topoisomerase V by structural and functional studies. Nucleic Acids Research, 2013, 41, 657-666.	6.5	8
569	Structure of an amidohydrolase, SACOL0085, from methicillin-resistant <i>Staphylococcus aureus</i> COL. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 103-108.	0.7	3
570	Structural and Functional Characterization of K339T Substitution Identified in the PB2 Subunit Cap-binding Pocket of Influenza A Virus. Journal of Biological Chemistry, 2013, 288, 11013-11023.	1.6	35
571	Structural characterization of V57D and V57P mutants of human cystatin C, an amyloidogenic protein. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 577-586.	2.5	8
572	Inhibition of a type III secretion system by the deletion of a short loop in one of its membrane proteins. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 812-820.	2.5	31
573	SCEDS: protein fragments for molecular replacement in <i>Phaser</i> . Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2216-2225.	2.5	16
574	Crystallographic identification of an unexpected protein complex in silkworm haemolymph. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2353-2364.	2.5	13
575	Structural characterization of the ribonuclease H-like type ASKHA superfamily kinase MK0840 fromMethanopyrus kandleri. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2440-2450.	2.5	4
576	Investigation of DNA sequence recognition by a streptomycete MarR family transcriptional regulator through surface plasmon resonance and X-ray crystallography. Nucleic Acids Research, 2013, 41, 7009-7022.	6.5	39

#	Article	IF	CITATIONS
577	A Substrate Access Tunnel in the Cytosolic Domain Is Not an Essential Feature of the Solute Carrier 4 (SLC4) Family of Bicarbonate Transporters. Journal of Biological Chemistry, 2013, 288, 33848-33860.	1.6	32
578	Structure of an early nativeâ€like intermediate of β2â€microglobulin amyloidogenesis. Protein Science, 2013, 22, 1349-1357.	3.1	14
579	Structural Basis of Substrate Specificity and Protease Inhibition in Norwalk Virus. Journal of Virology, 2013, 87, 4281-4292.	1.5	47
580	Base-modified Donor Analogues Reveal Novel Dynamic Features of a Glycosyltransferase. Journal of Biological Chemistry, 2013, 288, 26201-26208.	1.6	17
581	Structural basis for 2′-phosphate incorporation into glycogen by glycogen synthase. Proceedings of the United States of America, 2013, 110, 20976-20981.	3.3	29
582	NrdH-redoxin of Mycobacterium tuberculosis and Corynebacterium glutamicum Dimerizes at High Protein Concentration and Exclusively Receives Electrons from Thioredoxin Reductase. Journal of Biological Chemistry, 2013, 288, 7942-7955.	1.6	14
583	Crystal Structure of IL-17 Receptor B SEFIR Domain. Journal of Immunology, 2013, 190, 2320-2326.	0.4	30
584	Ca2+-dependent Structural Changes in the B-cell Receptor CD23 Increase Its Affinity for Human Immunoglobulin E. Journal of Biological Chemistry, 2013, 288, 21667-21677.	1.6	27
585	MAIT Recognition of a Stimulatory Bacterial Antigen Bound to MR1. Journal of Immunology, 2013, 191, 5268-5277.	0.4	69
586	Fusion of Dioxygenase and Lignin-binding Domains in a Novel Secreted Enzyme from Cellulolytic Streptomyces sp. SirexAA-E. Journal of Biological Chemistry, 2013, 288, 18574-18587.	1.6	40
587	Dimerization of Bacterial Diaminopimelate Epimerase Is Essential for Catalysis. Journal of Biological Chemistry, 2013, 288, 9238-9248.	1.6	41
588	RAGE is a nucleic acid receptor that promotes inflammatory responses to DNA. Journal of Experimental Medicine, 2013, 210, 2447-2463.	4.2	177
589	Antileukemic activity of nuclear export inhibitors that spare normal hematopoietic cells. Leukemia, 2013, 27, 66-74.	3.3	166
590	The A128T Resistance Mutation Reveals Aberrant Protein Multimerization as the Primary Mechanism of Action of Allosteric HIV-1 Integrase Inhibitors. Journal of Biological Chemistry, 2013, 288, 15813-15820.	1.6	85
591	Structural Basis for Activity Regulation and Substrate Preference of Clostridial Collagenases G, H, and T. Journal of Biological Chemistry, 2013, 288, 20184-20194.	1.6	64
592	Structure of the archaeal Cascade subunit Csa5. RNA Biology, 2013, 10, 762-769.	1.5	24
593	The Structure of Glycerol Trinitrate Reductase NerA from <i>Agrobacterium radiobacter</i> Reveals the Molecular Reason for Nitro―and Eneâ€Reductase Activity in OYE Homologues. ChemBioChem, 2013, 14, 836-845.	1.3	10
594	The 1.6 Ã Crystal Structure of Pyranose Dehydrogenase from Agaricus meleagris Rationalizes Substrate Specificity and Reveals a Flavin Intermediate. PLoS ONE, 2013, 8, e53567.	1.1	44

#	Article	IF	CITATIONS
595	Human Rotavirus VP6-Specific Antibodies Mediate Intracellular Neutralization by Binding to a Quaternary Structure in the Transcriptional Pore. PLoS ONE, 2013, 8, e61101.	1.1	51
596	Two Crystal Structures of Bombyx mori Lipoprotein 3 - Structural Characterization of a New 30-kDa Lipoprotein Family Member. PLoS ONE, 2013, 8, e61303.	1.1	6
597	Development of Novel In Vivo Chemical Probes to Address CNS Protein Kinase Involvement in Synaptic Dysfunction. PLoS ONE, 2013, 8, e66226.	1.1	58
598	Structural Insights into the Abscisic Acid Stereospecificity by the ABA Receptors PYR/PYL/RCAR. PLoS ONE, 2013, 8, e67477.	1.1	38
599	Crystal Structure of Penicillin-Binding Protein 3 (PBP3) from Escherichia coli. PLoS ONE, 2014, 9, e98042.	1.1	48
600	Crystal Structure of Bombyx mori Lipoprotein 6: Comparative Structural Analysis of the 30-kDa Lipoprotein Family. PLoS ONE, 2014, 9, e108761.	1.1	11
601	An experimental point of view on hydration/solvation in halophilic proteins. Frontiers in Microbiology, 2014, 5, 66.	1.5	37
602	The structure of cytomegalovirus immune modulator UL141 highlights structural Ig-fold versatility for receptor binding. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 851-862.	2.5	5
603	B-factor Analysis and Conformational Rearrangement of Aldose Reductase. Current Proteomics, 2014, 11, 151-160.	0.1	8
604	E2~Ub conjugates regulate the kinase activity ofShigellaeffector OspG during pathogenesis. EMBO Journal, 2014, 33, n/a-n/a.	3.5	53
605	Structural and Biochemical Characterization of Chlamydia trachomatis Hypothetical Protein CT263 Supports That Menaquinone Synthesis Occurs through the Futalosine Pathway. Journal of Biological Chemistry, 2014, 289, 32214-32229.	1.6	23
606	The structure of Rv2372c identifies an RsmE-like methyltransferase from <i>Mycobacterium tuberculosis</i> . Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 821-832.	2.5	10
607	The antigen 43 structure reveals a molecular Velcro-like mechanism of autotransporter-mediated bacterial clumping. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 457-462.	3.3	116
608	Conformational Itinerary of Pseudomonas aeruginosa 1,6-Anhydro-N-acetylmuramic Acid Kinase during Its Catalytic Cycle. Journal of Biological Chemistry, 2014, 289, 4504-4514.	1.6	7
609	SbnG, a Citrate Synthase in Staphylococcus aureus. Journal of Biological Chemistry, 2014, 289, 33797-33807.	1.6	18
610	Mechanisms of Neutralization of a Human Anti-α-toxin Antibody. Journal of Biological Chemistry, 2014, 289, 29874-29880.	1.6	74
611	Electrostatic transition state stabilization rather than reactant destabilization provides the chemical basis for efficient chorismate mutase catalysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17516-17521.	3.3	31
612	Structures of AzrA and of AzrC complexed with substrate or inhibitor: insight into substrate specificity and catalytic mechanism. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 553-564.	2.5	21

#	Article	IF	CITATIONS
613	Crystal Structure of the Human Fatty Acid Synthase Enoyl-Acyl Carrier Protein-Reductase Domain Complexed with Triclosan Reveals Allosteric Protein-Protein Interface Inhibition. Journal of Biological Chemistry, 2014, 289, 33287-33295.	1.6	21
614	Restricted Diversity of Antigen Binding Residues of Antibodies Revealed by Computational Alanine Scanning of 227 Antibody–Antigen Complexes. Journal of Molecular Biology, 2014, 426, 3729-3743.	2.0	74
615	P. aeruginosa SGNH Hydrolase-Like Proteins AlgJ and AlgX Have Similar Topology but Separate and Distinct Roles in Alginate Acetylation. PLoS Pathogens, 2014, 10, e1004334.	2.1	54
616	A New Class of Multimerization Selective Inhibitors of HIV-1 Integrase. PLoS Pathogens, 2014, 10, e1004171.	2.1	112
617	Ca2+-stabilized adhesin helps an Antarctic bacterium reach out and bind ice. Bioscience Reports, 2014, 34, .	1.1	32
618	Unique subunit packing in mycobacterial nanoRNase leads to alternate substrate recognitions in DHH phosphodiesterases. Nucleic Acids Research, 2014, 42, 7894-7910.	6.5	25
619	Structure of the unique SEFIR domain from human interleukin 17 receptor A reveals a composite ligand-binding site containing a conserved α-helix for Act1 binding and IL-17 signaling. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1476-1483.	2.5	31
620	Structure of 5-hydroxymethylcytosine-specific restriction enzyme, AbaSI, in complex with DNA. Nucleic Acids Research, 2014, 42, 7947-7959.	6.5	27
621	Structureâ€guided analysis of catalytic specificity of the abundantly secreted chitosanase SACTE_5457 from <i>Streptomyces</i> sp. SirexAAâ€E. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1245-1257.	1.5	33
622	Refined structures of mouse Pâ€glycoprotein. Protein Science, 2014, 23, 34-46.	3.1	319
623	The 2/2 hemoglobin from the cyanobacterium <i>Synechococcus</i> sp. PCC 7002 with covalently attached heme: Comparison of Xâ€ray and NMR structures. Proteins: Structure, Function and Bioinformatics, 2014, 82, 528-534.	1.5	18
624	Cleaning Unexpected Fruits from Hardâ€Won Synthetases: Probing Principles of Permissivity in Nonâ€canonical Amino Acid–tRNA Synthetases. ChemBioChem, 2014, 15, 1810-1819.	1.3	35
625	Structure of the monofunctional heme catalase <scp>DR</scp> 1998 from <i><scp>D</scp>einococcusÂradiodurans</i> . FEBS Journal, 2014, 281, 4138-4150.	2.2	16
626	Natural single amino acid polymorphism (F19Y) in human galectinâ€8: detection of structural alterations and increased growthâ€regulatory activity on tumor cells. FEBS Journal, 2014, 281, 1446-1464.	2.2	40
627	The future of crystallography in drug discovery. Expert Opinion on Drug Discovery, 2014, 9, 125-137.	2.5	70
628	Crystallographic study of FABP5 as an intracellular endocannabinoid transporter. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 290-298.	2.5	44
629	Structure of the <scp><i>M</i></scp> <i>ycobacterium tuberculosis</i> type <scp>VII</scp> secretion system chaperone <scp>EspG</scp> <sub>5</sub> in complex with <scp>PE</scp> 25– <scp>PPE</scp> 41 dimer. Molecular Microbiology, 2014, 94, 367-382.	1.2	83
630	BDB: Databank of PDB files with consistent B-factors. Protein Engineering, Design and Selection, 2014, 27, 457-462.	1.0	28

#	Article	IF	CITATIONS
631	Structural Basis for the De-N-acetylation of Poly-β-1,6-N-acetyl-d-glucosamine in Gram-positive Bacteria. Journal of Biological Chemistry, 2014, 289, 35907-35917.	1.6	24
632	Structural basis for the regulatory function of a complex zinc-binding domain in a replicative arterivirus helicase resembling a nonsense-mediated mRNA decay helicase. Nucleic Acids Research, 2014, 42, 3464-3477.	6.5	47
633	The mechanism of pseudouridine synthases from a covalent complex with RNA, and alternate specificity for U2605 versus U2604 between close homologs. Nucleic Acids Research, 2014, 42, 2037-2048.	6.5	19
634	Structure of sugar-bound LacY. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1784-1788.	3.3	111
635	Na <sup>+</sup> /K <sup>+</sup> exchange switches the catalytic apparatus of potassium-dependent plant <scp>L</scp> -asparaginase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1854-1872.	2.5	23
636	Structural and catalytic effects of an invariant purine substitution in the hammerhead ribozyme: implications for the mechanism of acid–base catalysis. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2256-2263.	2.5	6
637	Conformation-independent structural comparison of macromolecules with <i>ProSMART</i> . Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2487-2499.	2.5	161
638	Structure of the OsSERK2 leucine-rich repeat extracellular domain. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 3080-3086.	2.5	16
639	A range of Câ^Š3–Câ^Š4 interdomain angles in IgE Fc accommodate binding to its receptor CD23. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 305-309.	0.4	12
640	High-resolution crystal structures of two crystal forms of human cyclophilin D in complex with PEG 400 molecules. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 717-722.	0.4	5
641	Enhancing ubiquitin crystallization through surface-entropy reduction. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1434-1442.	0.4	4
642	The structure of the cyanobactin domain of unknown function from PatG in the patellamide gene cluster. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1597-1603.	0.4	15
643	Translocation and Rotation of tRNA during Template-Independent RNA Polymerization by tRNA Nucleotidyltransferase. Structure, 2014, 22, 315-325.	1.6	31
644	Thermodynamic and structural analysis of <scp>HIV</scp> protease resistance to darunavir–Âanalysis of heavily mutated patientâ€derived <scp>HIV</scp> â€i proteases. FEBS Journal, 2014, 281, 1834-1847.	2.2	48
645	Dual kinase-bromodomain inhibitors for rationally designed polypharmacology. Nature Chemical Biology, 2014, 10, 305-312.	3.9	296
646	Crystallographic and Glycan Microarray Analysis of Human Polyomavirus 9 VP1 Identifies <i>N</i> -Glycolyl Neuraminic Acid as a Receptor Candidate. Journal of Virology, 2014, 88, 6100-6111.	1.5	36
647	Functional and Structural Characterization of Vibrio cholerae Extracellular Serine Protease B, VesB. Journal of Biological Chemistry, 2014, 289, 8288-8298.	1.6	24
648	Structural Basis of Improved Second-Generation 3-Nitro-tyrosine tRNA Synthetases. Biochemistry, 2014, 53, 1916-1924.	1.2	51

#	Article	IF	CITATIONS
649	Structure of Dihydromethanopterin Reductase, a Cubic Protein Cage for Redox Transfer. Journal of Biological Chemistry, 2014, 289, 8852-8864.	1.6	11
650	<i>Chlamydia trachomatis</i> CT771 ( <i>nudH</i> ) Is an Asymmetric Ap <sub>4</sub> A Hydrolase. Biochemistry, 2014, 53, 214-224.	1.2	1
651	A structural characterization of the isoniazidMycobacterium tuberculosisdrug target, Rv2971, in its unliganded form. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 572-577.	0.4	3
652	Crystal Structure of pb9, the Distal Tail Protein of Bacteriophage T5: a Conserved Structural Motif among All Siphophages. Journal of Virology, 2014, 88, 820-828.	1.5	43
653	[1,2,4]Triazolo[4,3- <i>a</i> ]phthalazines: Inhibitors of Diverse Bromodomains. Journal of Medicinal Chemistry, 2014, 57, 462-476.	2.9	84
654	The multiple antibiotic resistance regulator MarR is a copper sensor in Escherichia coli. Nature Chemical Biology, 2014, 10, 21-28.	3.9	128
655	A bump-and-hole approach to engineer controlled selectivity of BET bromodomain chemical probes. Science, 2014, 346, 638-641.	6.0	128
656	Enzyme–substrate complex structures of CYP154C5 shed light on its mode of highly selective steroid hydroxylation. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2875-2889.	2.5	19
657	Structure-based approaches towards identification of fragments for the low-druggability ATAD2 bromodomain. MedChemComm, 2014, 5, 1843-1848.	3.5	46
658	Crystal structures and functional studies clarify substrate selectivity and catalytic residues for the unique orphan enzyme N-acetyl-D-mannosamine dehydrogenase. Biochemical Journal, 2014, 462, 499-511.	1.7	2
659	Structure of the eukaryotic translation initiation factor eIF4E in complex with 4EGI-1 reveals an allosteric mechanism for dissociating eIF4C. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3187-95.	3.3	72
660	Crystal Structure of the Extended-Spectrum β-Lactamase PER-2 and Insights into the Role of Specific Residues in the Interaction with β-Lactams and β-Lactamase Inhibitors. Antimicrobial Agents and Chemotherapy, 2014, 58, 5994-6002.	1.4	16
661	The crystal structure of archaeal serine hydroxymethyltransferase reveals idiosyncratic features likely required to withstand high temperatures. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3437-3449.	1.5	13
662	Structure and stability of an unusual zinc-binding protein from Bacteroides thetaiotaomicron. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2298-2305.	1.1	1
663	Structure Analysis of the Major Capsid Proteins of Human Polyomaviruses 6 and 7 Reveals an Obstructed Sialic Acid Binding Site. Journal of Virology, 2014, 88, 10831-10839.	1.5	22
664	X-ray structures of GluCl in apo states reveal a gating mechanism of Cys-loop receptors. Nature, 2014, 512, 333-337.	13.7	236
665	Radical SAM enzyme QueE defines a new minimal core fold and metal-dependent mechanism. Nature Chemical Biology, 2014, 10, 106-112.	3.9	71
666	Chasing Protons: How Isothermal Titration Calorimetry, Mutagenesis, and p <i>K</i> <sub>a</sub> Calculations Trace the Locus of Charge in Ligand Binding to a tRNA-Binding Enzyme. Journal of Medicinal Chemistry, 2014, 57, 5554-5565.	2.9	26

#	Article	IF	CITATIONS
667	E pluribus unum, no more: from one crystal, many conformations. Current Opinion in Structural Biology, 2014, 28, 56-62.	2.6	53
668	Effects of Cavities at the Nicotinamide Binding Site of Liver Alcohol Dehydrogenase on Structure, Dynamics and Catalysis. Biochemistry, 2014, 53, 881-894.	1.2	17
669	<sup>19</sup> F Nuclear Magnetic Resonance and Crystallographic Studies of 5-Fluorotryptophan-Labeled Anthrax Protective Antigen and Effects of the Receptor on Stability. Biochemistry, 2014, 53, 690-701.	1.2	13
670	Insights into the Mechanism of Deubiquitination by JAMM Deubiquitinases from Cocrystal Structures of the Enzyme with the Substrate and Product. Biochemistry, 2014, 53, 3199-3217.	1.2	56
671	A unique inhibitor binding site in ERK1/2 is associated with slow binding kinetics. Nature Chemical Biology, 2014, 10, 853-860.	3.9	187
672	Structure and Catalytic Regulatory Function of Ubiquitin Specific Protease 11 N-Terminal and Ubiquitin-like Domains. Biochemistry, 2014, 53, 2966-2978.	1.2	34
673	Structure–Activity Relationship of 3,5-Diaryl-2-aminopyridine ALK2 Inhibitors Reveals Unaltered Binding Affinity for Fibrodysplasia Ossificans Progressiva Causing Mutants. Journal of Medicinal Chemistry, 2014, 57, 7900-7915.	2.9	84
674	Combined inhibition of caspase 3 and caspase 7 by two highly selective DARPins slows down cellular demise. Biochemical Journal, 2014, 461, 279-290.	1.7	12
675	Alanine Scanning Mutagenesis Identifies an Asparagine–Arginine–Lysine Triad Essential to Assembly of the Shell of the Pdu Microcompartment. Journal of Molecular Biology, 2014, 426, 2328-2345.	2.0	66
676	A New Crystal Structure of the Bifunctional Antibiotic Simocyclinone D8 Bound to DNA Gyrase Gives Fresh Insight into the Mechanism of Inhibition. Journal of Molecular Biology, 2014, 426, 2023-2033.	2.0	39
677	Structural Mechanisms Determining Inhibition of the Collagen Receptor DDR1 by Selective and Multi-Targeted Type II Kinase Inhibitors. Journal of Molecular Biology, 2014, 426, 2457-2470.	2.0	77
678	Characterization of two homologous $2\hat{a}\in^2$ -O-methyltransferases showing different specificities for their tRNA substrates. Rna, 2014, 20, 1257-1271.	1.6	69
679	Targeting Mycobacterium tuberculosis nucleoid-associated protein HU with structure-based inhibitors. Nature Communications, 2014, 5, 4124.	5.8	96
680	Crystal structure of the N-terminal domain of EccA1 ATPase from the ESX-1 secretion system of Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2014, 82, 159-163.	1.5	26
681	The structure of a novel electron-transfer ferredoxin from <i>Rhodopseudomonas palustris</i> HaA2 which contains a histidine residue in its iron–sulfur cluster-binding motif. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1453-1464.	2.5	8
682	A unique serpin P1′ glutamate and a conserved β-sheet C arginine are key residues for activity, protease recognition and stability of serpinA12 (vaspin). Biochemical Journal, 2015, 470, 357-367.	1.7	17
683	An enzyme captured in two conformational states: crystal structure of <i>S</i> -adenosyl- <scp>L</scp> -homocysteine hydrolase from <i>Bradyrhizobium elkanii</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2422-2432.	2.5	9
684	Structure of importin-α bound to a non-classical nuclear localization signal of the influenza A virus nucleoprotein. Scientific Reports, 2015, 5, 15055.	1.6	41

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#	Article	IF	CITATIONS
685	Predicting X-ray diffuse scattering from translation–libration–screw structural ensembles. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1657-1667.	2.5	14
686	Combining Crystallography and Hydrogen–Deuterium Exchange to Study Galectin–Ligand Complexes. Chemistry - A European Journal, 2015, 21, 13558-13568.	1.7	16
687	Hypothetical protein <scp>CT</scp> 398 ( <scp>C</scp> ds <scp>Z</scp> ) interacts with σ <sup>54</sup> ( <scp>R</scp> po <scp>N</scp> )â€holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . Protein Science, 2015, 24, 1617-1632.	3.1	23
688	From bacterial to human dihydrouridine synthase: automated structure determination. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1564-1571.	2.5	14
689	Functional Coupling of Duplex Translocation to DNA Cleavage in a Type I Restriction Enzyme. PLoS ONE, 2015, 10, e0128700.	1.1	7
690	Trichodysplasia spinulosa-Associated Polyomavirus Uses a Displaced Binding Site on VP1 to Engage Sialylated Clycolipids. PLoS Pathogens, 2015, 11, e1005112.	2.1	20
691	How pH Modulates the Dimer-Decamer Interconversion of 2-Cys Peroxiredoxins from the Prx1 Subfamily. Journal of Biological Chemistry, 2015, 290, 8582-8590.	1.6	43
692	Complex Structure and Biochemical Characterization of the Staphylococcus aureus Cyclic Diadenylate Monophosphate (c-di-AMP)-binding Protein PstA, the Founding Member of a New Signal Transduction Protein Family. Journal of Biological Chemistry, 2015, 290, 2888-2901.	1.6	47
693	Structure of EspB, a secreted substrate of the ESX-1 secretion system of Mycobacterium tuberculosis. Journal of Structural Biology, 2015, 191, 236-244.	1.3	51
694	Variable Substrate Preference among Phospholipase D Toxins from Sicariid Spiders. Journal of Biological Chemistry, 2015, 290, 10994-11007.	1.6	34
695	Structures of potent anticancer compounds bound to tubulin. Protein Science, 2015, 24, 1164-1172.	3.1	20
696	Modulation of a Pore in the Capsid of JC Polyomavirus Reduces Infectivity and Prevents Exposure of the Minor Capsid Proteins. Journal of Virology, 2015, 89, 3910-3921.	1.5	17
697	Structural impact of complete CpG methylation within target DNA on specific complex formation of the inducible transcription factor Egrâ€1. FEBS Letters, 2015, 589, 1748-1753.	1.3	39
698	Structural basis for antagonizing a host restriction factor by C7 family of poxvirus host-range proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14858-14863.	3.3	21
699	Characterization of Two Distinct Structural Classes of Selective Aldehyde Dehydrogenase 1A1 Inhibitors. Journal of Medicinal Chemistry, 2015, 58, 1964-1975.	2.9	67
700	<i>Entamoeba histolytica</i> RacC Selectively Engages p21-Activated Kinase Effectors. Biochemistry, 2015, 54, 404-412.	1.2	8
701	Bacterial killing via a type IV secretion system. Nature Communications, 2015, 6, 6453.	5.8	197
702	Small Molecules Dorsomorphin and LDN-193189 Inhibit Myostatin/GDF8 Signaling and Promote Functional Myoblast Differentiation. Journal of Biological Chemistry, 2015, 290, 3390-3404.	1.6	46

#	Article	IF	CITATIONS
703	Structural basis for chemokine recognition and activation of a viral G protein–coupled receptor. Science, 2015, 347, 1113-1117.	6.0	261
704	Crystal Structure of Apo and Ligand Bound Vibrio cholerae Ribokinase (Vc-RK): Role of Monovalent Cation Induced Activation and Structural Flexibility in Sugar Phosphorylation. Advances in Experimental Medicine and Biology, 2015, 842, 293-307.	0.8	13
705	Structural prerequisites for G-protein activation by the neurotensin receptor. Nature Communications, 2015, 6, 7895.	5.8	89
706	Crystal structure of the karyopherin Kap121p bound to the extreme C-terminus of the protein phosphatase Cdc14p. Biochemical and Biophysical Research Communications, 2015, 463, 309-314.	1.0	9
707	Domain-Swapping Switch Point in Ste20 Protein Kinase SPAK. Biochemistry, 2015, 54, 5063-5071.	1.2	19
708	Structural Basis for the Interconversion of Maltodextrins by MalQ, the Amylomaltase of Escherichia coli. Journal of Biological Chemistry, 2015, 290, 21352-21364.	1.6	35
709	Structural and Kinetic Insights into the "Ceftazidimase―Behavior of the Extended-Spectrum β-Lactamase CTX-M-96. Biochemistry, 2015, 54, 5072-5082.	1.2	8
710	Structural basis for the catalytic mechanism of homoserine dehydrogenase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1216-1225.	2.5	11
711	X-ray structure of a mammalian stearoyl-CoA desaturase. Nature, 2015, 524, 252-256.	13.7	213
712	The role of monovalent cations in the ATPase reaction of DNA gyrase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 996-1005.	2.5	16
713	Vaccine-elicited antibody that neutralizes H5N1 influenza and variants binds the receptor site and polymorphic sites. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9346-9351.	3.3	26
714	Crystal structures of a polypeptide processing and secretion transporter. Nature, 2015, 523, 425-430.	13.7	102
715	Triazole linker-based trivalent sialic acid inhibitors of adenovirus type 37 infection of human corneal epithelial cells. Organic and Biomolecular Chemistry, 2015, 13, 9194-9205.	1.5	31
716	Biochemical and Structural Basis for Controlling Chemical Modularity in Fungal Polyketide Biosynthesis. Journal of the American Chemical Society, 2015, 137, 9885-9893.	6.6	53
717	Crystallization of interleukin-18 for structure-based inhibitor design. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 710-717.	0.4	1
718	Development of a high-throughput in vitro assay to identify selective inhibitors for human ALDH1A1. Chemico-Biological Interactions, 2015, 234, 29-37.	1.7	66
719	Structural basis for a novel mechanism of <scp>DNA</scp> bridging and alignment in eukaryotic <scp>DSB DNA</scp> repair. EMBO Journal, 2015, 34, 1126-1142.	3.5	21
720	The use of ene adducts to study and engineer enoyl-thioester reductases. Nature Chemical Biology, 2015, 11, 398-400.	3.9	27

#	Article	IF	CITATIONS
721	The Greater Affinity of JC Polyomavirus Capsid for α2,6-Linked Lactoseries Tetrasaccharide c than for Other Sialylated Glycans Is a Major Determinant of Infectivity. Journal of Virology, 2015, 89, 6364-6375.	1.5	52
722	Structural and functional analysis of betaine aldehyde dehydrogenase from <i>Staphylococcus aureus</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1159-1175.	2.5	16
723	Molecular recognition of human ephrinB2 cell surface receptor by an emergent African henipavirus. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2156-65.	3.3	47
724	Crystal Structures Capture Three States in the Catalytic Cycle of a Pyridoxal Phosphate (PLP) Synthase. Journal of Biological Chemistry, 2015, 290, 5226-5239.	1.6	19
725	Structural and Inhibitory Effects of Hinge Loop Mutagenesis in Serpin-2 from the Malaria Vector Anopheles gambiae. Journal of Biological Chemistry, 2015, 290, 2946-2956.	1.6	7
726	9 <i>H</i> -Purine Scaffold Reveals Induced-Fit Pocket Plasticity of the BRD9 Bromodomain. Journal of Medicinal Chemistry, 2015, 58, 2718-2736.	2.9	63
727	10-Iodo-11 <i>H</i> -indolo[3,2- <i>c</i> ]quinoline-6-carboxylic Acids Are Selective Inhibitors of DYRK1A. Journal of Medicinal Chemistry, 2015, 58, 3131-3143.	2.9	87
728	The dimeric crystal structure of the human fertility lipocalin glycodelin reveals a protein scaffold for the presentation of complex glycans. Biochemical Journal, 2015, 466, 95-104.	1.7	20
729	Identifying and quantifying radiation damage atÂtheÂatomic level. Journal of Synchrotron Radiation, 2015, 22, 201-212.	1.0	51
730	Allosteric Coupling via Distant Disorder-to-Order Transitions. Journal of Molecular Biology, 2015, 427, 1695-1704.	2.0	26
731	Structural basis for gene regulation by a B12-dependent photoreceptor. Nature, 2015, 526, 536-541.	13.7	149
732	Crystal structure and biophysical characterization of the nucleoside diphosphate kinase from Leishmania braziliensis. BMC Structural Biology, 2015, 15, 2.	2.3	7
733	Structural basis of the mercury(II)-mediated conformational switching of the dual-function transcriptional regulator MerR. Nucleic Acids Research, 2015, 43, 7612-7623.	6.5	61
734	Structural evidence for asymmetric ligand binding to transthyretin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1582-1592.	2.5	21
735	Thymine DNA glycosylase exhibits negligible affinity for nucleobases that it removes from DNA. Nucleic Acids Research, 2015, 43, 9541-9552.	6.5	28
736	Structural Basis for Substrate Specificity in Adenosylcobalamin-dependent Isobutyryl-CoA Mutase and Related Acyl-CoA Mutases. Journal of Biological Chemistry, 2015, 290, 26882-26898.	1.6	24
737	Structural Insights into the Neutralization Properties of the Fully Human, Anti-interferon Monoclonal Antibody Sifalimumab. Journal of Biological Chemistry, 2015, 290, 14979-14985.	1.6	7
738	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. Structure, 2015, 23, 1754-1768.	1.6	30

	Сітатіо	n Report	
#	Article	IF	CITATIONS
739	Crystal structure of the bacteriophage P2 integrase catalytic domain. FEBS Letters, 2015, 589, 3556-3563.	1.3	3
740	Dynamics of an Active-Site Flap Contributes to Catalysis in a JAMM Family Metallo Deubiquitinase. Biochemistry, 2015, 54, 6038-6051.	1.2	10
741	Characterization of the Pseudomonas aeruginosa Glycoside Hydrolase PslG Reveals That Its Levels Are Critical for Psl Polysaccharide Biosynthesis and Biofilm Formation. Journal of Biological Chemistry, 2015, 290, 28374-28387.	1.6	68
742	Structural Insights into Nonspecific Binding of DNA by TrmBL2, an Archaeal Chromatin Protein. Journal of Molecular Biology, 2015, 427, 3216-3229.	2.0	14
743	Discovery and structure of a new inhibitor scaffold of the autophagy initiating kinase ULK1. Bioorganic and Medicinal Chemistry, 2015, 23, 5483-5488.	1.4	58
744	Entropic Enhancement of Protein-DNA Affinity by Oxygen-to-Sulfur Substitution in DNA Phosphate. Biophysical Journal, 2015, 109, 1026-1037.	0.2	46
745	The Cysteine Dioxygenase Homologue from Pseudomonas aeruginosa Is a 3-Mercaptopropionate Dioxygenase. Journal of Biological Chemistry, 2015, 290, 24424-24437.	1.6	47
746	Sequential substitution of K+ bound to Na+,K+-ATPase visualized by X-ray crystallography. Nature Communications, 2015, 6, 8004.	5.8	27
747	The Protein BpsB Is a Poly-β-1,6-N-acetyl-d-glucosamine Deacetylase Required for Biofilm Formation in Bordetella bronchiseptica. Journal of Biological Chemistry, 2015, 290, 22827-22840.	1.6	31
748	Oxidation of Monolignols by Members of the Berberine Bridge Enzyme Family Suggests a Role in Plant Cell Wall Metabolism. Journal of Biological Chemistry, 2015, 290, 18770-18781.	1.6	83
749	Characterization of 2,4-Diamino-6-oxo-1,6-dihydropyrimidin-5-yl Ureido Based Inhibitors of <i>Trypanosoma brucei</i> FolD and Testing for Antiparasitic Activity. Journal of Medicinal Chemistry, 2015, 58, 7938-7948.	2.9	12
750	Structural mechanism for signal transduction in RXR nuclear receptor heterodimers. Nature Communications, 2015, 6, 8013.	5.8	101
751	Mechanistic Implications of the Unique Structural Features and Dimerization of the Cytoplasmic Domain of the <i>Pseudomonas</i> Sigma Regulator, PupR. Biochemistry, 2015, 54, 5867-5877.	1.2	6
752	Quaternary structure of <i>Dioclea grandiflora</i> lectin assessed by equilibrium sedimentation and crystallographic analysis of recombinant mutants. FEBS Letters, 2015, 589, 2290-2296.	1.3	9
753	Cytochrome P450 125A4, the Third Cholesterol C-26 Hydroxylase from <i>Mycobacterium smegmatis</i> . Biochemistry, 2015, 54, 6909-6916.	1.2	19
754	LRAT-specific domain facilitates vitamin A metabolism by domain swapping in HRASLS3. Nature Chemical Biology, 2015, 11, 26-32.	3.9	49
755	The structure of ibuprofen bound to cyclooxygenase-2. Journal of Structural Biology, 2015, 189, 62-66.	1.3	116
756	Structural and Functional Divergence of the Aldolase Fold in Toxoplasma gondii. Journal of Molecular Biology, 2015, 427, 840-852.	2.0	11

#	Article	IF	CITATIONS
757	Biochemical and structural characterisation of the second oxidative crosslinking step during the biosynthesis of the glycopeptide antibiotic A47934. Beilstein Journal of Organic Chemistry, 2016, 12, 2849-2864.	1.3	14
758	Structure of chromatin remodeler Swi2/Snf2 in the resting state. Nature Structural and Molecular Biology, 2016, 23, 722-729.	3.6	55
759	Structures of Rpn1 T1:Rad23 and hRpn13:hPLIC2 Reveal Distinct Binding Mechanisms between Substrate Receptors and Shuttle Factors of the Proteasome. Structure, 2016, 24, 1257-1270.	1.6	72
760	Molecular Dynamics Simulations and Kinetic Measurements to Estimate and Predict Protein–Ligand Residence Times. Journal of Medicinal Chemistry, 2016, 59, 7167-7176.	2.9	81
761	Crystal structure of Mycobacterium tuberculosis ketolâ€acid reductoisomerase at 1.0 à resolution – a potential target for antiâ€ŧuberculosis drug discovery. FEBS Journal, 2016, 283, 1184-1196.	2.2	33
762	Artificial domain duplication replicates evolutionary history of ketolâ€acid reductoisomerases. Protein Science, 2016, 25, 1241-1248.	3.1	4
763	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. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1029-1042.	1.5	4
764	Identification and characterization of a bacterial hyaluronidase and its production in recombinant form. FEBS Letters, 2016, 590, 2180-2189.	1.3	15
765	Stereospecific Effects of Oxygenâ€ŧoâ€Sulfur Substitution in DNA Phosphate on Ion Pair Dynamics and Protein–DNA Affinity. ChemBioChem, 2016, 17, 1636-1642.	1.3	15
766	Structure and mechanism of NOV1, a resveratrol-cleaving dioxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14324-14329.	3.3	50
767	Fatty Acid Binding to the Allosteric Subunit of Cyclooxygenase-2 Relieves a Tonic Inhibition of the Catalytic Subunit. Journal of Biological Chemistry, 2016, 291, 25641-25655.	1.6	25
768	New insights into the mechanism of substrates trafficking in Glyoxylate/Hydroxypyruvate reductases. Scientific Reports, 2016, 6, 20629.	1.6	19
769	Diverse mechanisms of metaeffector activity in an intracellular bacterial pathogen, <i>Legionella pneumophila</i> . Molecular Systems Biology, 2016, 12, 893.	3.2	108
770	Structure and dynamics of a constitutively active neurotensin receptor. Scientific Reports, 2016, 6, 38564.	1.6	59
771	1.45â€Ã resolution structure of SRPN18 from the malaria vector <i>Anopheles gambiae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 853-862.	0.4	3
772	Super-complexes of adhesion GPCRs and neural guidance receptors. Nature Communications, 2016, 7, 11184.	5.8	84
773	Crystal structures and mutagenesis of PPP-family ser/thr protein phosphatases elucidate the selectivity of cantharidin and novel norcantharidin-based inhibitors of PP5C. Biochemical Pharmacology, 2016, 109, 14-26.	2.0	26
774	Measuring and modeling diffuse scattering in protein X-ray crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4069-4074.	3.3	48

#	Article	IF	CITATIONS
775	Structural and kinetic studies on RosA, the enzyme catalysing the methylation of 8â€demethylâ€8â€aminoâ€ <scp>d</scp> â€riboflavin to the antibiotic roseoflavin. FEBS Journal, 2016, 283, 1531-1549.	2.2	13
776	Crystal structure of histone-like protein fromStreptococcus mutansrefined to 1.9â€Ã resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 257-262.	0.4	4
777	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. Journal of Structural Biology, 2016, 195, 19-30.	1.3	15
778	The Structure of a Sugar Transporter of the Glucose EIIC Superfamily Provides Insight into the Elevator Mechanism of Membrane Transport. Structure, 2016, 24, 956-964.	1.6	37
779	Distinct Structural Pathways Coordinate the Activation of AMPA Receptor-Auxiliary Subunit Complexes. Neuron, 2016, 89, 1264-1276.	3.8	61
780	High Resolution Structures of Periplasmic Glucose-binding Protein of Pseudomonas putida CSV86 Reveal Structural Basis of Its Substrate Specificity. Journal of Biological Chemistry, 2016, 291, 7844-7857.	1.6	19
781	<i>Burkholderia glumae</i> ToxA Is a Dual-Specificity Methyltransferase That Catalyzes the Last Two Steps of Toxoflavin Biosynthesis. Biochemistry, 2016, 55, 2748-2759.	1.2	13
782	Crystal Structure of PKG I:cGMP Complex Reveals a cGMP-Mediated Dimeric Interface that Facilitates cGMP-Induced Activation. Structure, 2016, 24, 710-720.	1.6	39
783	Functional dichotomy in the 16S rRNA (m <sup>1</sup> A1408) methyltransferase family and control of catalytic activity via a novel tryptophan mediated loop reorganization. Nucleic Acids Research, 2016, 44, 342-353.	6.5	8
784	Removal of the Side Chain at the Active-Site Serine by a Glycine Substitution Increases the Stability of a Wide Range of Serine β-Lactamases by Relieving Steric Strain. Biochemistry, 2016, 55, 2479-2490.	1.2	20
785	Allosteric Inhibition of Bcr-Abl Kinase by High Affinity Monobody Inhibitors Directed to the Src Homology 2 (SH2)-Kinase Interface. Journal of Biological Chemistry, 2016, 291, 8836-8847.	1.6	33
786	Selectivity of Pyridone- and Diphenyl Ether-Based Inhibitors for the <i>Yersinia pestis</i> FabV Enoyl-ACP Reductase. Biochemistry, 2016, 55, 2992-3006.	1.2	6
787	A Novel Fic (Filamentation Induced by cAMP) Protein from Clostridium difficile Reveals an Inhibitory Motif-independent Adenylylation/AMPylation Mechanism. Journal of Biological Chemistry, 2016, 291, 13286-13300.	1.6	14
788	Discovery and Optimization of a Selective Ligand for the Switch/Sucrose Nonfermenting-Related Bromodomains of Polybromo Protein-1 by the Use of Virtual Screening and Hydration Analysis. Journal of Medicinal Chemistry, 2016, 59, 8787-8803.	2.9	41
789	The Sampling of Conformational Dynamics in Ambient-Temperature Crystal Structures of Arginine Kinase. Structure, 2016, 24, 1658-1667.	1.6	5
790	Development of Selective CBP/P300 Benzoxazepine Bromodomain Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 8889-8912.	2.9	49
791	Structural basis of damage recognition by thymine DNA glycosylase: Key roles for N-terminal residues. Nucleic Acids Research, 2016, 44, gkw768.	6.5	44
792	Structure of Escherichia coli Flavodiiron Nitric Oxide Reductase. Journal of Molecular Biology, 2016, 428, 4686-4707.	2.0	30

#	Article	IF	CITATIONS
793	Structural Basis for a New Templated Activity by Terminal Deoxynucleotidyl Transferase: Implications for V(D)J Recombination. Structure, 2016, 24, 1452-1463.	1.6	28
794	Solution Binding and Structural Analyses Reveal Potential Multidrug Resistance Functions for SAV2435 and CTR107 and Other Gyrl-like Proteins. Biochemistry, 2016, 55, 4850-4863.	1.2	11
795	Anatomy of the Î <sup>2</sup> -branching enzyme of polyketide biosynthesis and its interaction with an acyl-ACP substrate. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10316-10321.	3.3	29
796	Crystal structure of truncated aspartate transcarbamoylase fromPlasmodium falciparum. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 523-533.	0.4	12
797	Host-Primed Ebola Virus GP Exposes a Hydrophobic NPC1 Receptor-Binding Pocket, Revealing a Target for Broadly Neutralizing Antibodies. MBio, 2016, 7, e02154-15.	1.8	86
798	Molecular Insights into the Mechanism of Calmodulin Inhibition of the EAG1 Potassium Channel. Structure, 2016, 24, 1742-1754.	1.6	11
799	EssC: domain structures inform on the elusive translocation channel in the TypeÂVII secretion system. Biochemical Journal, 2016, 473, 1941-1952.	1.7	48
800	More than just recruitment: the X-domain influences catalysis of the first phenolic coupling reaction in A47934 biosynthesis by Cytochrome P450 StaH. Molecular BioSystems, 2016, 12, 2992-3004.	2.9	22
801	The structure of a <i>Trypanosoma cruzi</i> glucoseâ€6â€phosphate dehydrogenase reveals differences from the mammalian enzyme. FEBS Letters, 2016, 590, 2776-2786.	1.3	19
802	Structure of the Catalytic Domain of the Class I Polyhydroxybutyrate Synthase from Cupriavidus necator. Journal of Biological Chemistry, 2016, 291, 25264-25277.	1.6	69
803	<i>Deinococcus radiodurans </i> <scp>DR</scp> 2231 is a twoâ€metalâ€ion mechanism hydrolase with exclusive activity on d <scp>UTP</scp> . FEBS Journal, 2016, 283, 4274-4290.	2.2	4
804	A/T Run Geometry of B-form DNA Is Independent of Bound Methyl-CpG Binding Domain, Cytosine Methylation and Flanking Sequence. Scientific Reports, 2016, 6, 31210.	1.6	7
805	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. Science Advances, 2016, 2, e1600760.	4.7	90
806	Shared active site architecture between archaeal PolD and multi-subunit RNA polymerases revealed by X-ray crystallography. Nature Communications, 2016, 7, 12227.	5.8	40
807	Conservation in the mechanism of glucuronoxylan hydrolysis revealed by the structure of glucuronoxylan xylanohydrolase ( <i>Ct</i> Xyn30A) from <i>Clostridium thermocellum</i> . Acta Crystallographica Section D: Structural Biology, 2016, 72, 1162-1173.	1.1	9
808	Substrate-selective Inhibition of Cyclooxygeanse-2 by Fenamic Acid Derivatives Is Dependent on Peroxide Tone. Journal of Biological Chemistry, 2016, 291, 15069-15081.	1.6	129
809	Structures of EccB1 and EccD1 from the core complex of the mycobacterial ESX-1 type VII secretion system. BMC Structural Biology, 2016, 16, 5.	2.3	27
810	Involvement of budding yeast Rad5 in translesion DNA synthesis through physical interaction with Rev1. Nucleic Acids Research, 2016, 44, 5231-5245.	6.5	71

#	Article	IF	CITATIONS
811	Deciphering the Substrate Specificity of SbnA, the Enzyme Catalyzing the First Step in Staphyloferrin B Biosynthesis. Biochemistry, 2016, 55, 927-939.	1.2	22
812	Visualizing the tunnel in tryptophan synthase with crystallography: Insights into a selective filter for accommodating indole and rejecting water. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 268-279.	1.1	26
813	Structure of a HOIP/E2~ubiquitin complex reveals RBR E3 ligase mechanism and regulation. Nature, 2016, 529, 546-550.	13.7	141
814	Crystal structure and stability of gyrase–fluoroquinolone cleaved complexes from <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 1706-1713.	3.3	164
815	Utilization of Substrate Intrinsic Binding Energy for Conformational Change and Catalytic Function in Phosphoenolpyruvate Carboxykinase. Biochemistry, 2016, 55, 575-587.	1.2	19
816	Aminoglycoside binding and catalysis specificity of aminoglycoside 2″-phosphotransferase IVa: A thermodynamic, structural and kinetic study. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 802-813.	1.1	8
817	KatB, a cyanobacterial Mn-catalase with unique active site configuration: Implications for enzyme function. Free Radical Biology and Medicine, 2016, 93, 118-129.	1.3	21
818	Structures of an all-α protein running along the DNA major groove. Nucleic Acids Research, 2016, 44, 3936-3945.	6.5	5
819	Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses. Acta Crystallographica Section D: Structural Biology, 2016, 72, 49-58.	1.1	14
820	Transferase Versus Hydrolase: The Role of Conformational Flexibility in Reaction Specificity. Structure, 2017, 25, 295-304.	1.6	23
821	Structures of the Karyopherins Kap121p and Kap60p Bound to the Nuclear Pore-Targeting Domain of the SUMO Protease Ulp1p. Journal of Molecular Biology, 2017, 429, 249-260.	2.0	9
822	Novel Aldo-Keto Reductases for the Biocatalytic Conversion of 3-Hydroxybutanal to 1,3-Butanediol: Structural and Biochemical Studies. Applied and Environmental Microbiology, 2017, 83, .	1.4	24
823	Inhibition of the Aldehyde Dehydrogenase 1/2 Family by Psoralen and Coumarin Derivatives. Journal of Medicinal Chemistry, 2017, 60, 2439-2455.	2.9	35
824	Structure of a Type-1 Secretion System ABC Transporter. Structure, 2017, 25, 522-529.	1.6	63
825	Structural and functional characterization of a ubiquitin variant engineered for tight and specific binding to an alphaâ€helical ubiquitin interacting motif. Protein Science, 2017, 26, 1060-1069.	3.1	20
826	Crystallization of a fungal lytic polysaccharide monooxygenase expressed from glycoengineered <i>Pichia pastoris</i> for X-ray and neutron diffraction. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 70-78.	0.4	14
827	Notch-Jagged complex structure implicates a catch bond in tuning ligand sensitivity. Science, 2017, 355, 1320-1324.	6.0	232
828	Visualization of the Reaction Trajectory and Transition State in a Hydrolytic Reaction Catalyzed by a Metalloenzyme. Chemistry - A European Journal, 2017, 23, 4778-4781.	1.7	27

#	Article	IF	Citations
829	Structural and biochemical analysis of Escherichia coli ObgE, a central regulator of bacterial persistence. Journal of Biological Chemistry, 2017, 292, 5871-5883.	1.6	20
830	Structural insights into the mechanism of the drastic changes in enzymatic activity of the cytochrome P450 vitamin D <sub>3</sub> hydroxylase (CYP107BR1) caused by a mutation distant from the active site. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 266-275.	0.4	12
831	Structural Insight into Ubiquitin-Like Protein Recognition and Oligomeric States of JAMM/MPN+ Proteases. Structure, 2017, 25, 823-833.e6.	1.6	16
832	Mutations of PKA cyclic nucleotide-binding domains reveal novel aspects of cyclic nucleotide selectivity. Biochemical Journal, 2017, 474, 2389-2403.	1.7	21
833	X-ray Scattering Studies of Protein Structural Dynamics. Chemical Reviews, 2017, 117, 7615-7672.	23.0	83
834	Structural Basis for Mitotic Centrosome Assembly in Flies. Cell, 2017, 169, 1078-1089.e13.	13.5	99
835	Structural studies of viperin, an antiviral radical SAM enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6806-6811.	3.3	69
836	Conformational Control of UDP-Galactopyranose Mutase Inhibition. Biochemistry, 2017, 56, 3983-3992.	1.2	2
837	IgE binds asymmetrically to its B cell receptor CD23. Scientific Reports, 2017, 7, 45533.	1.6	25
838	Crystal structure of truncated human coatomer protein complex subunit ζ1 (Copζ1). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 1-8.	0.4	0
839	The Origins of Specificity in the Microcin-Processing Protease TldD/E. Structure, 2017, 25, 1549-1561.e5.	1.6	34
840	Clinical Variants of New Delhi Metallo-β-Lactamase Are Evolving To Overcome Zinc Scarcity. ACS Infectious Diseases, 2017, 3, 927-940.	1.8	49
841	Molecular architecture of the PBP2–MreC core bacterial cell wall synthesis complex. Nature Communications, 2017, 8, 776.	5.8	57
842	Single-domain antibodies pinpoint potential targets within Shigella invasion plasmid antigen D of the needle tip complex for inhibition of type III secretion. Journal of Biological Chemistry, 2017, 292, 16677-16687.	1.6	16
843	Total Biosynthesis of the Pyrrolo[4,2]benzodiazepine Scaffold Tomaymycin on an InÂVitro Reconstituted NRPS System. Cell Chemical Biology, 2017, 24, 1216-1227.e8.	2.5	19
844	Crystal Structure of Cocosin, A Potential Food Allergen from Coconut ( <i>Cocos nucifera</i> ). Journal of Agricultural and Food Chemistry, 2017, 65, 7560-7568.	2.4	10
845	Crystal structure of the UBRâ€box from UBR6/FBXO11 reveals domain swapping mediated by zinc binding. Protein Science, 2017, 26, 2092-2097.	3.1	9
846	Small molecule metalloprotease inhibitor with inÂvitro, exÂvivo and inÂvivo efficacy against botulinum neurotoxin serotype A. Toxicon, 2017, 137, 36-47.	0.8	9

#	Article	IF	CITATIONS
847	Molecular structure of FoxE, the putative iron oxidase of Rhodobacter ferrooxidans SW2. Biochimica Et Biophysica Acta - Bioenergetics, 2017, 1858, 847-853.	0.5	10
848	Crystal structure of the Xpo1p nuclear export complex bound to the Sx <scp>FG</scp> /Px <scp>FG</scp> repeats of the nucleoporin Nup42p. Genes To Cells, 2017, 22, 861-875.	0.5	8
849	Generation of specific inhibitors of SUMO-1– and SUMO-2/3–mediated protein-protein interactions using Affimer (Adhiron) technology. Science Signaling, 2017, 10, .	1.6	44
850	Biochemical Characterization and Structural Basis of Reactivity and Regioselectivity Differences between <i>Burkholderia thailandensis</i> and <i>Burkholderia glumae</i> 1,6-Didesmethyltoxoflavin <i>N</i> -Methyltransferase. Biochemistry, 2017, 56, 3934-3944.	1.2	4
851	The Crystal Structure of a Maxi/Mini-Ferritin Chimera Reveals Guiding Principles for the Assembly of Protein Cages. Biochemistry, 2017, 56, 3894-3899.	1.2	8
852	Convergent immunological solutions to Argentine hemorrhagic fever virus neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7031-7036.	3.3	31
853	Biochemical and Structural Characterization of Selective Allosteric Inhibitors of the <i>Plasmodium falciparum</i> Drug Target, Prolyl-tRNA-synthetase. ACS Infectious Diseases, 2017, 3, 34-44.	1.8	45
854	Structure to function of an α-glucan metabolic pathway that promotes Listeria monocytogenes pathogenesis. Nature Microbiology, 2017, 2, 16202.	5.9	33
855	Stability of isolated antibody-antigen complexes as a predictive tool for selecting toxin neutralizing antibodies. MAbs, 2017, 9, 43-57.	2.6	16
856	Activating mutations in quorum-sensing regulator Rgg2 and its conformational flexibility in the absence of an intermolecular disulfide bond. Journal of Biological Chemistry, 2017, 292, 20544-20557.	1.6	4
857	Activator Protein-1: redox switch controlling structure and DNA-binding. Nucleic Acids Research, 2017, 45, 11425-11436.	6.5	54
858	Structure of the <i>Bacillus anthracis</i> dTDP- <scp>L</scp> -rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose reductase (RfbD). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 644-650.	0.4	6
859	Crystallographic and SAXS studies of <i>S</i> -adenosyl- <scp>L</scp> -homocysteine hydrolase from <i>Bradyrhizobium elkanii</i> . IUCrJ, 2017, 4, 271-282.	1.0	11
860	Soaking suggests "alternative factsâ€: Only co-crystallization discloses major ligand-induced interface rearrangements of a homodimeric tRNA-binding protein indicating a novel mode-of-inhibition. PLoS ONE, 2017, 12, e0175723.	1.1	30
861	Crystal structure and kinetic analysis of the class B3 di-zinc metallo-Î <sup>2</sup> -lactamase LRA-12 from an Alaskan soil metagenome. PLoS ONE, 2017, 12, e0182043.	1.1	12
862	In vitro characterization of the antivirulence target of Gram-positive pathogens, peptidoglycan O-acetyltransferase A (OatA). PLoS Pathogens, 2017, 13, e1006667.	2.1	35
863	Structure of theBacillus anthracisdTDP-L-rhamnose-biosynthetic enzyme glucose-1-phosphate thymidylyltransferase (RfbA). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 621-628.	0.4	2
864	Structure of the <i>Bacillus anthracis</i> dTDP- <scp>L</scp> -rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose 3,5-epimerase (RfbC). Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 664-671.	0.4	6

# 865	ARTICLE Identification of a non-competitive inhibitor of Plasmodium falciparum aspartate transcarbamoylase. Biochemical and Biophysical Research Communications, 2018, 497, 835-842.	IF 1.0	Citations 4
866	SbnI is a free serine kinase that generates -phospho-l-serine for staphyloferrin B biosynthesis in. Journal of Biological Chemistry, 2018, 293, 6147-6160.	1.6	12
867	Using disruptive insertional mutagenesis to identify the <i>in situ</i> structureâ€function landscape of the <i>Shigella</i> translocator protein IpaB. Protein Science, 2018, 27, 1392-1406.	3.1	13
868	Structural insights into the RNA methyltransferase domain of METTL16. Scientific Reports, 2018, 8, 5311.	1.6	80
869	Regulation of Kinase Activity in the Caenorhabditis elegans EGF Receptor, LET-23. Structure, 2018, 26, 270-281.e4.	1.6	5
870	Characterization of the Fast and Promiscuous Macrocyclase from Plant PCY1 Enables the Use of Simple Substrates. ACS Chemical Biology, 2018, 13, 801-811.	1.6	29
871	Imidazole Nitrogens of Two Histidine Residues Participating in N–H···N Hydrogen Bonds in Protein Structures: Structural Bioinformatics Approach Combined with Quantum Chemical Calculations. Journal of Physical Chemistry B, 2018, 122, 1205-1212.	1.2	13
872	Structural, Biochemical, and Evolutionary Characterizations of Glyoxylate/Hydroxypyruvate Reductases Show Their Division into Two Distinct Subfamilies. Biochemistry, 2018, 57, 963-977.	1.2	12
873	Architecture of a channel-forming O-antigen polysaccharide ABC transporter. Nature, 2018, 553, 361-365.	13.7	82
874	Structure-guided design and functional characterization of an artificial red light–regulated guanylate/adenylate cyclase for optogenetic applications. Journal of Biological Chemistry, 2018, 293, 9078-9089.	1.6	45
875	Organometallic and radical intermediates reveal mechanism of diphthamide biosynthesis. Science, 2018, 359, 1247-1250.	6.0	48
876	Structural atlas of dynein motors at atomic resolution. Biophysical Reviews, 2018, 10, 677-686.	1.5	4
877	Structural studies of two thermostable laccases from the white-rot fungus Pycnoporus sanguineus. International Journal of Biological Macromolecules, 2018, 107, 1629-1640.	3.6	38
878	Structural basis for the potent and selective binding of LDN-212854 to the BMP receptor kinase ALK2. Bone, 2018, 109, 251-258.	1.4	32
879	Crystal structure of the Legionella effector Lem22. Proteins: Structure, Function and Bioinformatics, 2018, 86, 263-267.	1.5	3
880	Redox-dependent rearrangements of the NiFeS cluster of carbon monoxide dehydrogenase. ELife, 2018, 7, .	2.8	43
881	Characterization of the [NiFeSe] hydrogenase from Desulfovibrio vulgaris Hildenborough. Methods in Enzymology, 2018, 613, 169-201.	0.4	12
882	Refining the macromolecular model – achieving the best agreement with the data from X-ray diffraction experiment. Crystallography Reviews, 2018, 24, 236-262.	0.4	43

#	Article	IF	CITATIONS
883	The bacterial Ras/Rap1 site-specific endopeptidase RRSP cleaves Ras through an atypical mechanism to disrupt Ras-ERK signaling. Science Signaling, 2018, 11, .	1.6	39
884	Probing the role of Arg97 in Heat shock protein 90 N-terminal domain from the parasite Leishmania braziliensis through site-directed mutagenesis on the human counterpart. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1190-1198.	1.1	6
885	Structural modulation of a periplasmic sugar-binding protein probes into its evolutionary ancestry. Journal of Structural Biology, 2018, 204, 498-506.	1.3	0
886	The Streptococcus pyogenes Shr protein captures human hemoglobin using two structurally unique binding domains. Journal of Biological Chemistry, 2018, 293, 18365-18377.	1.6	8
887	Engineering glycoside hydrolase stability by the introduction of zinc binding. Acta Crystallographica Section D: Structural Biology, 2018, 74, 702-710.	1.1	1
888	Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. Cell, 2018, 175, 1380-1392.e14.	13.5	109
889	The hit-and-return system enables efficient time-resolved serial synchrotron crystallography. Nature Methods, 2018, 15, 901-904.	9.0	67
890	The cyclic nucleotide–binding homology domain of the integral membrane protein CNNM mediates dimerization and is required for Mg2+ efflux activity. Journal of Biological Chemistry, 2018, 293, 19998-20007.	1.6	34
891	Structure-Based Optimization of a Novel Class of Aldehyde Dehydrogenase 1A (ALDH1A) Subfamily-Selective Inhibitors as Potential Adjuncts to Ovarian Cancer Chemotherapy. Journal of Medicinal Chemistry, 2018, 61, 8754-8773.	2.9	49
892	Biochemical Characterization and Structural Modeling of Fused Glucose-6-Phosphate Dehydrogenase-Phosphogluconolactonase from Giardia Iamblia. International Journal of Molecular Sciences, 2018, 19, 2518.	1.8	11
893	A close look onto structural models and primary ligands of metallo-β-lactamases. Drug Resistance Updates, 2018, 40, 1-12.	6.5	47
894	Structure and Analysis of R1 and R2 Pyocin Receptor-Binding Fibers. Viruses, 2018, 10, 427.	1.5	35
895	Interaction of antidiabetic αâ€glucosidase inhibitors and gut bacteria αâ€glucosidase. Protein Science, 2018, 27, 1498-1508.	3.1	37
896	Convergent Use of Heptacoordination for Cation Selectivity by RNA and Protein Metalloregulators. Cell Chemical Biology, 2018, 25, 962-973.e5.	2.5	23
897	Structural and biochemical analysis of the dual-specificity Trm10 enzyme from <i>Thermococcus kodakaraensis</i> prompts reconsideration of its catalytic mechanism. Rna, 2018, 24, 1080-1092.	1.6	16
898	PgaB orthologues contain a glycoside hydrolase domain that cleaves deacetylated poly-β(1,6)-N-acetylglucosamine and can disrupt bacterial biofilms. PLoS Pathogens, 2018, 14, e1006998.	2.1	59
899	Structural basis for recognition of human 7SK long noncoding RNA by the La-related protein Larp7. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6457-E6466.	3.3	51
900	Deciphering the mechanism of potent peptidomimetic inhibitors targeting plasmepsins – biochemical and structural insights. FEBS Journal, 2018, 285, 3077-3096.	2.2	11

#	Article	IF	CITATIONS
901	On the Implication of Water on Fragmentâ€to‣igand Growth in Kinase Binding Thermodynamics. ChemMedChem, 2018, 13, 1988-1996.	1.6	8
902	A Structure-Based Strategy for Engineering Selective Ubiquitin Variant Inhibitors of Skp1-Cul1-F-Box Ubiquitin Ligases. Structure, 2018, 26, 1226-1236.e3.	1.6	27
903	The Loss of Expression of a Single Type 3 Effector (CT622) Strongly Reduces Chlamydia trachomatis Infectivity and Growth. Frontiers in Cellular and Infection Microbiology, 2018, 8, 145.	1.8	21
904	S-Adenosyl-L-Homocysteine Hydrolase Inhibition by a Synthetic Nicotinamide Cofactor Biomimetic. Frontiers in Microbiology, 2018, 9, 505.	1.5	7
905	Insights into the Structures of Superoxide Reductases from the Symbionts <i>Ignicoccus hospitalis</i> and <i>Nanoarchaeum equitans</i> . Biochemistry, 2018, 57, 5271-5281.	1.2	5
906	Hopâ€family <i>Helicobacter</i> outer membrane adhesins form a novel class of TypeÂ5â€like secretion proteins with an interrupted βâ€barrel domain. Molecular Microbiology, 2018, 110, 33-46.	1.2	24
907	A Noncanonical Metal Center Drives the Activity of the <i>Sediminispirochaeta smaragdinae</i> Metallo-β-lactamase SPS-1. Biochemistry, 2018, 57, 5218-5229.	1.2	11
908	From deep TLS validation to ensembles of atomic models built from elemental motions. II. Analysis of TLS refinement results by explicit interpretation. Acta Crystallographica Section D: Structural Biology, 2018, 74, 621-631.	1.1	7
909	Snapshots of an evolved DNA polymerase pre- and post-incorporation of an unnatural nucleotide. Nucleic Acids Research, 2018, 46, 7977-7988.	6.5	18
910	Molecular basis for CesT recognition of type III secretion effectors in enteropathogenic Escherichia coli. PLoS Pathogens, 2018, 14, e1007224.	2.1	16
911	The first dipeptidyl peptidase III from a thermophile: Structural basis for thermal stability and reduced activity. PLoS ONE, 2018, 13, e0192488.	1.1	7
912	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
913	The MTR4 helicase recruits nuclear adaptors of the human RNA exosome using distinct arch-interacting motifs. Nature Communications, 2019, 10, 3393.	5.8	41
914	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. Structure, 2019, 27, 1427-1442.e4.	1.6	12
915	Structural insights into the recognition of nucleoside reverse transcriptase inhibitors by HIVâ€1 reverse transcriptase: First crystal structures with reverse transcriptase and the active triphosphate forms of lamivudine and emtricitabine. Protein Science, 2019, 28, 1664-1675.	3.1	20
916	The archaeal LDH-like malate dehydrogenase from Ignicoccus islandicus displays dual substrate recognition, hidden allostery and a non-canonical tetrameric oligomeric organization. Journal of Structural Biology, 2019, 208, 7-17.	1.3	13
917	Structural insight into metallocofactor maturation in carbon monoxide dehydrogenase. Journal of Biological Chemistry, 2019, 294, 13017-13026.	1.6	15
918	Structural evidence for an in trans base selection mechanism involving Loop1 in polymerase μ at an NHEJ double-strand break junction. Journal of Biological Chemistry, 2019, 294, 10579-10595.	1.6	7

#	Article	IF	CITATIONS
919	Extreme divergence between one-to-one orthologs: the structure of N15 Cro bound to operator DNA and its relationship to the λ Cro complex. Nucleic Acids Research, 2019, 47, 7118-7129.	6.5	6
920	Structure and assembly of pilotin-dependent and -independent secretins of the type II secretion system. PLoS Pathogens, 2019, 15, e1007731.	2.1	22
921	The Crystal Structure of Dph2 in Complex with Elongation Factor 2 Reveals the Structural Basis for the First Step of Diphthamide Biosynthesis. Biochemistry, 2019, 58, 4343-4351.	1.2	7
922	Excision of 5-Carboxylcytosine by Thymine DNA Glycosylase. Journal of the American Chemical Society, 2019, 141, 18851-18861.	6.6	21
923	Deciphering the Structural Basis of High Thermostability of Dehalogenase from Psychrophilic Bacterium Marinobacter sp. ELB17. Microorganisms, 2019, 7, 498.	1.6	18
924	Comparative studies of <i>Aspergillus fumigatus</i> 2-methylcitrate synthase and human citrate synthase. Biological Chemistry, 2019, 400, 1567-1581.	1.2	3
925	Monomeric YoeB toxin retains RNase activity but adopts an obligate dimeric form for thermal stability. Nucleic Acids Research, 2019, 47, 10400-10413.	6.5	15
926	Testosterone meets albumin – the molecular mechanism of sex hormone transport by serum albumins. Chemical Science, 2019, 10, 1607-1618.	3.7	38
927	Molecular mechanism of Aspergillus fumigatus biofilm disruption by fungal and bacterial glycoside hydrolases. Journal of Biological Chemistry, 2019, 294, 10760-10772.	1.6	50
928	First crystal structure of an endo-levanase – the BT1760 from a human gut commensal Bacteroides thetaiotaomicron. Scientific Reports, 2019, 9, 8443.	1.6	18
929	Structural insights into dehydratase substrate selection for the borrelidin and fluvirucin polyketide synthases. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1225-1235.	1.4	7
930	Suicide inactivation of the uracil DNA glycosylase UdgX by covalent complex formation. Nature Chemical Biology, 2019, 15, 615-622.	3.9	22
931	IMP1 KH1 and KH2 domains create a structural platform with unique RNA recognition and re-modelling properties. Nucleic Acids Research, 2019, 47, 4334-4348.	6.5	16
932	Crystal structure and activation mechanism of DR3 death domain. FEBS Journal, 2019, 286, 2593-2610.	2.2	6
933	N-terminal residues are crucial for quaternary structure and active site conformation for the phosphoserine aminotransferase from enteric human parasite E. histolytica. International Journal of Biological Macromolecules, 2019, 132, 1012-1023.	3.6	8
934	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. Protein Science, 2019, 28, 848-856.	3.1	9
935	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. Journal of Molecular Biology, 2019, 431, 1160-1171.	2.0	6
936	Overall Structures of Mycobacterium tuberculosis DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. Structure, 2019, 27, 579-589.e5.	1.6	24

		REPORT	
#	Article	IF	Citations
937	Structure of the IFNÎ <sup>3</sup> receptor complex guides design of biased agonists. Nature, 2019, 567, 56-60.	13.7	85
938	A lipid gating mechanism for the channel-forming O antigen ABC transporter. Nature Communications, 2019, 10, 824.	5.8	44
939	Structural basis for Fullerene geometry in a human endogenous retrovirus capsid. Nature Communications, 2019, 10, 5822.	5.8	20
940	Molecular and structural insights into anÂasymmetric proteolytic complexÂ(ClpP1P2)ÂfromÂMycobacterium smegmatis. Scientific Reports, 2019, 9, 18019.	1.6	16
941	The Cyclic AMP Receptor Protein Regulates Quorum Sensing and Global Gene Expression in Yersinia pestis during Planktonic Growth and Growth in Biofilms. MBio, 2019, 10, .	1.8	24
942	Structural consequences of BMPR2 kinase domain mutations causing pulmonary arterial hypertension. Scientific Reports, 2019, 9, 18351.	1.6	9
943	Structural basis of 7SK RNA 5′-γ-phosphate methylation and retention by MePCE. Nature Chemical Biology, 2019, 15, 132-140.	3.9	38
944	Structural Variability of EspG Chaperones from Mycobacterial ESX-1, ESX-3, and ESX-5 Type VII Secretion Systems. Journal of Molecular Biology, 2019, 431, 289-307.	2.0	21
945	Analysis of a new flavodiiron core structural arrangement in Flv1-ΔFlR protein from Synechocystis sp. PCC6803. Journal of Structural Biology, 2019, 205, 91-102.	1.3	12
946	Structural and ligand binding analyses of the periplasmic sensor domain of RsbU in Chlamydia trachomatis support a role in TCA cycle regulation. Molecular Microbiology, 2020, 113, 68-88.	1.2	11
947	Comprehensive analysis of all evolutionary paths between two divergent PDZ domain specificities. Protein Science, 2020, 29, 433-442.	3.1	17
948	Structural Basis of the Substrate Selectivity of Viperin. Biochemistry, 2020, 59, 652-662.	1.2	28
949	Mg2+-ATP Sensing in CNNM, a Putative Magnesium Transporter. Structure, 2020, 28, 324-335.e4.	1.6	28
950	Design and structure of two new protein cages illustrate successes and ongoing challenges in protein engineering. Protein Science, 2020, 29, 919-929.	3.1	32
951	Structure of galactarate dehydratase, a new fold in an enolase involved in bacterial fitness after antibiotic treatment. Protein Science, 2020, 29, 711-722.	3.1	4
952	High-resolution structures of the SARS-CoV-2 2′- <i>O</i> -methyltransferase reveal strategies for structure-based inhibitor design. Science Signaling, 2020, 13, .	1.6	143
953	Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7–11ÂUncovers the Mannose 6-Phosphate Binding Site of Domain 9. Structure, 2020, 28, 1300-1312.e5.	1.6	8
954	Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. Molecular Pharmacology, 2020, 98, 648-657.	1.0	7

#	Article	IF	CITATIONS
955	Evidence for Pentapeptide-Dependent and Independent CheB Methylesterases. International Journal of Molecular Sciences, 2020, 21, 8459.	1.8	5
956	Structural Basis and Evolution of Glycan Receptor Specificities within the Polyomavirus Family. MBio, 2020, 11, .	1.8	9
957	Structure of <i>S. pombe</i> telomerase protein Pof8 C-terminal domain is an xRRM conserved among LARP7 proteins. RNA Biology, 2021, 18, 1181-1192.	1.5	13
958	Post-Catalytic Complexes with Emtricitabine or Stavudine and HIV-1 Reverse Transcriptase Reveal New Mechanistic Insights for Nucleotide Incorporation and Drug Resistance. Molecules, 2020, 25, 4868.	1.7	3
959	How to Separate Kinase Inhibition from Undesired Monoamine Oxidase A Inhibition—The Development of the DYRK1A Inhibitor AnnH75 from the Alkaloid Harmine. Molecules, 2020, 25, 5962.	1.7	10
960	The Structures of SctK and SctD from Pseudomonas aeruginosa Reveal the Interface of the Type III Secretion System Basal Body and Sorting Platform. Journal of Molecular Biology, 2020, 432, 166693.	2.0	14
961	Structure and functional analysis of theÂLegionella pneumophila chitinase ChiA reveals a novel mechanism of metal-dependent mucin degradation. PLoS Pathogens, 2020, 16, e1008342.	2.1	29
962	Ligandâ€centered assessment of SARSâ€CoVâ€2 drug target models in the Protein Data Bank. FEBS Journal, 2020, 287, 3703-3718.	2.2	35
963	Methionine-Rich Loop of Multicopper Oxidase McoA Follows Open-to-Close Transitions with a Role in Enzyme Catalysis. ACS Catalysis, 2020, 10, 7162-7176.	5.5	15
964	Albumin-Based Transport of Nonsteroidal Anti-Inflammatory Drugs in Mammalian Blood Plasma. Journal of Medicinal Chemistry, 2020, 63, 6847-6862.	2.9	37
965	The Solvent-Exposed Fe–S D-Cluster Contributes to Oxygen-Resistance in <i>Desulfovibrio vulgaris</i> Ni–Fe Carbon Monoxide Dehydrogenase. ACS Catalysis, 2020, 10, 7328-7335.	5.5	18
966	Structural basis of cell-surface signaling by a conserved sigma regulator in Gram-negative bacteria. Journal of Biological Chemistry, 2020, 295, 5795-5806.	1.6	3
967	Diffuse X-ray scattering from correlated motions in a protein crystal. Nature Communications, 2020, 11, 1271.	5.8	37
968	Mutant ACVR1 Arrests Clial Cell Differentiation to Drive Tumorigenesis in Pediatric Cliomas. Cancer Cell, 2020, 37, 308-323.e12.	7.7	56
969	Structural analysis of avibactam-mediated activation of the bla and mec divergons in methicillin-resistant Staphylococcus aureus. Journal of Biological Chemistry, 2020, 295, 10870-10884.	1.6	7
970	A bacterial cytidine deaminase toxin enables CRISPR-free mitochondrial base editing. Nature, 2020, 583, 631-637.	13.7	409
971	Solidâ€State Dynamics and Highâ€Pressure Studies of a Supramolecular Spiral Gear. Chemistry - A European Journal, 2020, 26, 5061-5069.	1.7	9
972	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered δ-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7.	2.9	35

		CITATION R	EPORT	
#	Article		IF	Citations
973	Structure of the processive human Pol δholoenzyme. Nature Communications, 2020,	11, 1109.	5.8	103
974	Synthesis and Biological Validation of a Harmine-Based, Central Nervous System (CNS) Selective, Human β-Cell Regenerative Dual-Specificity Tyrosine Phosphorylation-Regula (DYRK1A) Inhibitor. Journal of Medicinal Chemistry, 2020, 63, 2986-3003.	-Avoidant, Ited Kinase A	2.9	36
975	Comparison of metalâ€bound and unbound structures of aminopeptidase B proteins fi <scp><i>Escherichia coli</i></scp> and <scp><i>Yersinia pestis</i></scp> . Protein Sci 1618-1628.		3.1	3
976	Activation mechanism of plasmepsins, pepsinâ€like aspartic proteases from Plasmodiu unique transâ€activation pathway. FEBS Journal, 2021, 288, 678-698.	m, follows a	2.2	3
977	Reprogramming Substrate and Catalytic Promiscuity of Tryptophan Prenyltransferases Molecular Biology, 2021, 433, 166726.	. Journal of	2.0	12
978	Crystal structures of NUDT15 variants enabled by a potent inhibitor reveal the structur thiopurine sensitivity. Journal of Biological Chemistry, 2021, 296, 100568.	al basis for	1.6	8
979	Myomedin scaffold variants targeted to 10E8 HIV-1 broadly neutralizing antibody mim and elicit HIV-1 virus-neutralizing sera in mice. Virulence, 2021, 12, 1271-1287.	ic gp41 epitope	1.8	2
980	Phage-assisted evolution of botulinum neurotoxin proteases with reprogrammed speci 2021, 371, 803-810.	ficity. Science,	6.0	46
982	Development of 2,5-dihydro-4H-pyrazolo[3,4-d]pyrimidin-4-one inhibitors of aldehyde o (ALDH1A) as potential adjuncts to ovarian cancer chemotherapy. European Journal of 1 Chemistry, 2021, 211, 113060.	Jehydrogenase 1A Medicinal	2.6	7
985	Structural basis for IFN antagonism by human respiratory syncytial virus nonstructural Proceedings of the National Academy of Sciences of the United States of America, 202 e2020587118.	protein 2. 1, 118,	3.3	12
986	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo re in plants. Acta Crystallographica Section D: Structural Biology, 2021, 77, 522-533.	ecognition	1.1	0
987	Gcn5-Related N-Acetyltransferases (GNATs) With a Catalytic Serine Residue Can Play P Frontiers in Molecular Biosciences, 2021, 8, 646046.	ing-Pong Too.	1.6	8
988	A third purine biosynthetic pathway encoded by aminoadenine-based viral DNA genom 372, 516-520.	es. Science, 2021,	6.0	40
989	The ChiS-Family DNA-Binding Domain Contains a Cryptic Helix-Turn-Helix Variant. MBio	, 2021, 12, .	1.8	3
992	Saracatinib is an efficacious clinical candidate for fibrodysplasia ossificans progressiva. 2021, 6, .	JCI Insight,	2.3	29
993	Validation of Recombinant Chicken Liver Bile Acid Binding Protein as a Tool for Cholic A Biomolecules, 2021, 11, 645.	Acid Hosting.	1.8	1
994	Self-association of MreC as a regulatory signal in bacterial cell wall elongation. Nature Communications, 2021, 12, 2987.		5.8	13
995	PIN and CCCH Zn-finger domains coordinate RNA targeting in ZC3H12 family endoribc Nucleic Acids Research, 2021, 49, 5369-5381.	nucleases.	6.5	9

ARTICLE IF CITATIONS # A trimethoprim derivative impedes antibiotic resistance evolution. Nature Communications, 2021, 12, 996 5.8 41 2949 Crystal structure of an archaeal CorB magnesium transporter. Nature Communications, 2021, 12, 4028. 997 5.8 23 MagC is a NplC/P60 $\hat{a}\in \mathbb{N}$  member of the  $\hat{1}\pm\hat{a}\in \hat{2}\hat{a}\in \mathbb{N}$  macroglobulin Mag complex of <i>Pseudomonas aeruginosa</i> 998 2 that interacts with peptidoglycan. FEBS Letters, 2021, 595, 2034-2046. Crystal structure of <i>Escherichia coli</i> class II hybrid cluster protein, HCP, reveals a [4Feâ€4S] 999 2.2 cluster at the Nâ€terminal protrusion. FEBS Journal, 2021, 288, 6752-6768. Mn  $\langle sup \rangle 2 + \langle sup \rangle$  coordinates Cap-O-RNA to align substrates for efficient  $2\hat{a} \in 2^{-} \langle i \rangle O \langle i \rangle$  -methyl transfer 1000 1.6 17 by SARS-CoV-2 nsp16. Science Signaling, 2021, 14, . Correlated Motions in Structural Biology. Biochemistry, 2021, 60, 2331-2340. 1.2 Structures of the <scp>TetR</scp>â€ike transcription regulator <scp>RcdA</scp> alone and in 1002 1.56 complexes with ligands. Proteins: Structure, Function and Bioinformatics, 2022, 90, 33-44. Structure of the unique tetrameric STENOFOLIA homeodomain bound with target promoter DNA. Acta 1003 1.1 Crystallographica Section D: Structural Biology, 2021, 77, 1050-1063. Evolutionary Diversification of Host-Targeted Bartonella Effectors Proteins Derived from a 1004 1.6 5 Conserved FicTA Toxin-Antitoxin Module. Microorganisms, 2021, 9, 1645. Structural Insights into the Mechanism of Base Excision by MBD4. Journal of Molecular Biology, 2021, 433, 167097. Biochemical, structural and dynamical studies reveal strong differences in the thermal-dependent allosteric behavior of two extremophilic lactate dehydrogenases. Journal of Structural Biology, 1006 4 1.3 2021, 213, 107769. Structural characterization of human peptidyl-arginine deiminase type III by X-ray crystallography. 0.4 Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 334-340. Comprehensive Assessment of the Relationship Between Siteâ<sup>2</sup> 2 Specificity and Helix α2 in the Erbin PDZ 1009 2.0 0 Domain. Journal of Molecular Biology, 2021, 433, 167115. Structure of a Ty1 restriction factor reveals the molecular basis of transposition copy number 5.8 control. Nature Communications, 2021, 12, 5590. Structure of the Human Cholesterol Transporter ABCG1. Journal of Molecular Biology, 2021, 433, 1012 2.0 22 167218. Potent DNA gyrase inhibitors bind asymmetrically to their target using symmetrical bifurcated 5.8 30 halogen bonds. Nature Communications, 2021, 12, 150. Mechanistic Basis of OXA-48-like Î<sup>2</sup>-Lactamases' Hydrolysis of Carbapenems. ACS Infectious Diseases, 2021, 1014 1.8 18 7,445-460. Acknowledging Errors: Advanced Molecular Replacement with Phaser. Methods in Molecular Biology, 46 2017, 1607, 421-453.

#	Article	IF	CITATIONS
1016	Databases, Repositories, and Other Data Resources in Structural Biology. Methods in Molecular Biology, 2017, 1607, 643-665.	0.4	6
1017	Crystal structures of plant inorganic pyrophosphatase, an enzyme with a moonlighting autoproteolytic activity. Biochemical Journal, 2019, 476, 2297-2319.	1.7	10
1018	Selectivity filter ion binding affinity determines inactivation in a potassium channel. Proceedings of the United States of America, 2020, 117, 29968-29978.	3.3	29
1024	A challenging interpretation of a hexagonally layered protein structure. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 203-208.	2.5	4
1025	From deep TLS validation to ensembles of atomic models built from elemental motions. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1668-1683.	2.5	14
1026	Estimating temperature-dependent anisotropic hydrogen displacements with the invariom database and a new segmented rigid-body analysis program. Journal of Applied Crystallography, 2015, 48, 1785-1793.	1.9	8
1027	Protein crystals IR laser ablated from aqueous solution at high speed retain their diffractive properties: applications in high-speed serial crystallography. Journal of Applied Crystallography, 2017, 50, 1773-1781.	1.9	10
1028	A jumping crystal predicted with molecular dynamics and analysed with TLS refinement against powder diffraction data. IUCrJ, 2019, 6, 136-144.	1.0	5
1029	Fixed-target serial oscillation crystallography at room temperature. IUCrJ, 2019, 6, 305-316.	1.0	26
1030	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. IUCrJ, 2020, 7, 1048-1058.	1.0	12
1031	1.65â€Ã resolution structure of the AraC-family transcriptional activator ToxT from <i>Vibrio cholerae</i> . Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 726-731.	0.4	13
1032	Structural comparison of <i>p</i> -hydroxybenzoate hydroxylase (PobA) from <i>Pseudomonas putida</i> with PobA from other <i>Pseudomonas</i> spp. and other monooxygenases. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 507-514.	0.4	3
1033	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
1034	Structural Comparison of Human Mammalian Ste20-Like Kinases. PLoS ONE, 2010, 5, e11905.	1.1	46
1035	The "Phantom Effect―of the Rexinoid LG100754: Structural and Functional Insights. PLoS ONE, 2010, 5, e15119.	1.1	64
1036	X-Ray Structure Reveals a New Class and Provides Insight into Evolution of Alkaline Phosphatases. PLoS ONE, 2011, 6, e22767.	1.1	26
1037	Structure of the Bro1 Domain Protein BROX and Functional Analyses of the ALIX Bro1 Domain in HIV-1 Budding. PLoS ONE, 2011, 6, e27466.	1.1	28
1038	Rationalization and Design of the Complementarity Determining Region Sequences in an Antibody-Antigen Recognition Interface. PLoS ONE, 2012, 7, e33340.	1.1	42

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	IAH		REPC	JKT

#	Article	IF	CITATIONS
1039	Rational Design and Characterization of D-Phe-Pro-D-Arg-Derived Direct Thrombin Inhibitors. PLoS ONE, 2012, 7, e34354.	1.1	23
1040	Mechanistic Insights into Validoxylamine A 7'-Phosphate Synthesis by VldE Using the Structure of the Entire Product Complex. PLoS ONE, 2012, 7, e44934.	1.1	17
1041	Crystal Structure of Cryptosporidium parvum Pyruvate Kinase. PLoS ONE, 2012, 7, e46875.	1.1	13
1042	Structure-Based Engineering Increased the Catalytic Turnover Rate of a Novel Phenazine Prenyltransferase. PLoS ONE, 2012, 7, e48427.	1.1	24
1043	Recovery of Red Fluorescent Protein Chromophore Maturation Deficiency through Rational Design. PLoS ONE, 2012, 7, e52463.	1.1	17
1044	Structural Properties of PAS Domains from the KCNH Potassium Channels. PLoS ONE, 2013, 8, e59265.	1.1	47
1045	A New Class of Small Molecule Inhibitor of BMP Signaling. PLoS ONE, 2013, 8, e62721.	1.1	219
1046	Substrate Channel Flexibility in Pseudomonas aeruginosa MurB Accommodates Two Distinct Substrates. PLoS ONE, 2013, 8, e66936.	1.1	5
1047	Tracking Molecular Recognition at the Atomic Level with a New Protein Scaffold Based on the OB-Fold. PLoS ONE, 2014, 9, e86050.	1.1	20
1048	Structural Basis for Binding of Fluorinated Glucose and Galactose to Trametes multicolor Pyranose 2-Oxidase Variants with Improved Galactose Conversion. PLoS ONE, 2014, 9, e86736.	1.1	10
1049	Crystal Structure of DIM-1, an Acquired Subclass B1 Metallo-β-Lactamase from Pseudomonas stutzeri. PLoS ONE, 2015, 10, e0140059.	1.1	3
1050	Structure of a Berberine Bridge Enzyme-Like Enzyme with an Active Site Specific to the Plant Family Brassicaceae. PLoS ONE, 2016, 11, e0156892.	1.1	30
1051	Effect of BET Missense Mutations on Bromodomain Function, Inhibitor Binding and Stability. PLoS ONE, 2016, 11, e0159180.	1.1	17
1052	Structural and Functional Studies of H. seropedicae RecA Protein – Insights into the Polymerization of RecA Protein as Nucleoprotein Filament. PLoS ONE, 2016, 11, e0159871.	1.1	7
1053	Brucella melitensis Methionyl-tRNA-Synthetase (MetRS), a Potential Drug Target for Brucellosis. PLoS ONE, 2016, 11, e0160350.	1.1	21
1054	Crystal structure of dipeptidyl peptidase III from the human gut symbiont Bacteroides thetaiotaomicron. PLoS ONE, 2017, 12, e0187295.	1.1	14
1055	Novel Escape Mutants Suggest an Extensive TRIM5α Binding Site Spanning the Entire Outer Surface of the Murine Leukemia Virus Capsid Protein. PLoS Pathogens, 2011, 7, e1002011.	2.1	49
1056	Structural and Functional Analysis of Murine Polyomavirus Capsid Proteins Establish the Determinants of Ligand Recognition and Pathogenicity. PLoS Pathogens, 2015, 11, e1005104.	2.1	22

#	Article	IF	CITATIONS
1057	Atomic Structure and Biochemical Characterization of an RNA Endonuclease in the N Terminus of Andes Virus L Protein. PLoS Pathogens, 2016, 12, e1005635.	2.1	31
1058	Host-parasite co-metabolic activation of antitrypanosomal aminomethyl-benzoxaboroles. PLoS Pathogens, 2018, 14, e1006850.	2.1	26
1059	Progress in protein crystallography. Protein and Peptide Letters, 2016, 23, 201-210.	0.4	23
1060	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. ELife, 2014, 3, .	2.8	81
1061	Structural evidence for Scc4-dependent localization of cohesin loading. ELife, 2015, 4, e06057.	2.8	69
1062	The Sec7 N-terminal regulatory domains facilitate membrane-proximal activation of the Arf1 GTPase. ELife, 2016, 5, .	2.8	17
1063	Model-based local density sharpening of cryo-EM maps. ELife, 2017, 6, .	2.8	200
1064	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. ELife, 2020, 9, .	2.8	27
1065	Characterisation of <i>Schizosaccharomyces pombe <math>\hat{l}_{\pm}</math></i> -actinin. PeerJ, 2016, 4, e1858.	0.9	7
1066	Computational anti-COVID-19 drug design: progress and challenges. Briefings in Bioinformatics, 2022, 23, .	3.2	8
1067	Loops around the Heme Pocket Have a Critical Role in the Function and Stability of BsDyP from Bacillus subtilis. International Journal of Molecular Sciences, 2021, 22, 10862.	1.8	9
1068	Molecular basis for reduced cleavage activity and drug resistance in D30N HIV-1 protease. Journal of Biomolecular Structure and Dynamics, 2022, 40, 13127-13135.	2.0	3
1070	Chapter 12. The Use of X-ray Crystallography to Study Enzymic H-tunnelling. RSC Biomolecular Sciences, 2009, , 268-290.	0.4	0
1071	Crystal Structure of a Two-Subunit TrkA Octameric Gating Ring Assembly. PLoS ONE, 2015, 10, e0122512.	1.1	2
1089	Structure of a bacterial α-1,2-glucosidase defines mechanisms of hydrolysis and substrate specificity in GH65 family hydrolases. Journal of Biological Chemistry, 2021, 297, 101366.	1.6	7
1095	Crystal structure of the pheromone Er-13 from the ciliate Euplotes raikovi, with implications for a protein–protein association model in pheromone/receptor interactions. Journal of Structural Biology, 2022, 214, 107812.	1.3	5
1096	Optimal structure determination from subâ€optimal diffraction data. Protein Science, 2022, 31, 259-268.	3.1	6
1097	Complete Model of Vinculin Suggests the Mechanism of Activation by Helical Super-Bundle Unfurling. Protein Journal, 2022, 41, 55-70.	0.7	4

#	Article	IF	CITATIONS
1098	Engineering of tissue inhibitor of metalloproteinases TIMP-1 for fine discrimination between closely related stromelysins MMP-3 and MMP-10. Journal of Biological Chemistry, 2022, 298, 101654.	1.6	13
1100	The Pseudomonas aeruginosa homeostasis enzyme AlgL clears the periplasmic space of accumulated alginate during polymer biosynthesis. Journal of Biological Chemistry, 2022, 298, 101560.	1.6	8
1101	Cyclic Tetra-Adenylate (cA4) Recognition by Csa3; Implications for an Integrated Class 1 CRISPR-Cas Immune Response in Saccharolobus solfataricus. Biomolecules, 2021, 11, 1852.	1.8	6
1102	The structure of the <scp><i>Clostridium thermocellum</i> Rsgl9</scp> ectodomain provides insight into the mechanism of biomass sensing. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1457-1467.	1.5	3
1103	Interleukin-2 superkines by computational design. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2117401119.	3.3	12
1105	Crystal structure of ArOYE6 reveals a novel Câ€ŧerminal helical extension and mechanistic insights into the distinct class III OYEs from pathogenic fungi. FEBS Journal, 2022, 289, 5531-5550.	2.2	2
1107	Variation of Antigen 43 self-association modulates bacterial compacting within aggregates and biofilms. Npj Biofilms and Microbiomes, 2022, 8, 20.	2.9	5
1108	Crystal structure of the middle and C-terminal domains of Hsp90α labeled with a coumarin derivative reveals a potential allosteric binding site as a drug target. Acta Crystallographica Section D: Structural Biology, 2022, 78, 571-585.	1.1	10
1109	Visualizing the gas channel of a monofunctional carbon monoxide dehydrogenase. Journal of Inorganic Biochemistry, 2022, 230, 111774.	1.5	11
1110	A New L-Proline Amide Hydrolase with Potential Application within the Amidase Process. Crystals, 2022, 12, 18.	1.0	1
1111	Distal Mutations Shape Substrate-Binding Sites during Evolution of a Metallo-Oxidase into a Laccase. ACS Catalysis, 2022, 12, 5022-5035.	5.5	9
1112	Crystal structure of an RNA/DNA strand exchange junction. PLoS ONE, 2022, 17, e0263547.	1.1	3
1124	Disrupting the HDAC6-ubiquitin interaction impairs infection by influenza and Zika virus and cellular stress pathways. Cell Reports, 2022, 39, 110736.	2.9	19
1125	Structural insights into choline- <i>O</i> -sulfatase reveal the molecular determinants for ligand binding. Acta Crystallographica Section D: Structural Biology, 2022, 78, 669-682.	1.1	0
1128	Architecture of the linker-scaffold in the nuclear pore. Science, 2022, 376, .	6.0	51
1129	Structural variations between small alarmone hydrolase dimers support different modes of regulation of the stringent response. Journal of Biological Chemistry, 2022, 298, 102142.	1.6	4
1130	Disentangling Unusual Catalytic Properties and the Role of the [4Fe-4S] Cluster of Three Endonuclease III from the Extremophile D. radiodurans. Molecules, 2022, 27, 4270.	1.7	2
1131	Organism-specific differences in the binding of ketoprofen to serum albumin. IUCrJ, 2022, 9, 551-561.	1.0	6

#	Article	IF	CITATIONS
1132	Measles and Nipah virus assembly: Specific lipid binding drives matrix polymerization. Science Advances, 2022, 8, .	4.7	13
1133	Mechanistic insight into the RNA-stimulated ATPase activity of tick-borne encephalitis virus helicase. Journal of Biological Chemistry, 2022, 298, 102383.	1.6	2
1134	Unveiling molecular details behind improved activity at neutral to alkaline pH of an engineered DyP-type peroxidase. Computational and Structural Biotechnology Journal, 2022, 20, 3899-3910.	1.9	5
1135	Combined Structural Analysis and Molecular Dynamics Reveal Penicillin-Binding Protein Inhibition Mode with β-Lactones. ACS Chemical Biology, 2022, 17, 3110-3120.	1.6	5
1136	Functional and Structural Characterization of OXA-935, a Novel OXA-10-Family β-Lactamase from Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2022, 66, .	1.4	3
1137	Crystal structure and sugar-binding ability of the C-terminal domain of <i>N</i> -acetylglucosaminyltransferase IV establish a new carbohydrate-binding module family. Glycobiology, 2022, 32, 1153-1163.	1.3	2
1139	Structural basis of the key residue W320 responsible for Hsp90 conformational change. Journal of Biomolecular Structure and Dynamics, 2023, 41, 9745-9755.	2.0	1
1141	Fragment screening using biolayer interferometry reveals ligands targeting the SHP-motif binding site of the AAA+ÂATPase p97. Communications Chemistry, 2022, 5, .	2.0	2
1142	Structure of the AlgKX modification and secretion complex required for alginate production and biofilm attachment in Pseudomonas aeruginosa. Nature Communications, 2022, 13, .	5.8	11
1143	Structural insights into 3Fe–4S ferredoxins diversity in M. tuberculosis highlighted by a first redox complex with P450. Frontiers in Molecular Biosciences, 0, 9, .	1.6	1
1144	Characterizing inhibitors of human AP endonuclease 1. PLoS ONE, 2023, 18, e0280526.	1.1	5
1145	A Structural Systems Biology Approach to High-Risk CG23 Klebsiella pneumoniae. Microbiology Resource Announcements, 2023, 12, .	0.3	1
1146	Staphylococcal Periscope proteins Aap, SasG, and Pls project noncanonical legume-like lectin adhesin domains from the bacterial surface. Journal of Biological Chemistry, 2023, 299, 102936.	1.6	3
1147	Structure of the Ndc80 complex and its interactions at the yeast kinetochore–microtubule interface. Open Biology, 2023, 13, .	1.5	12
1148	Structure of the Wnt–Frizzled–LRP6 initiation complex reveals the basis for coreceptor discrimination. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	7
1149	Diversification in the inositol tris/tetrakisphosphate kinase (ITPK) family: crystal structure and enzymology of the outlier <i>At</i> ITPK4. Biochemical Journal, 2023, 480, 433-453.	1.7	2
1150	Discovery of the Universal tRNA Binding Mode for the TsaD-like Components of the t6A tRNA Modification Pathway. Biophysica, 2023, 3, 288-306.	0.6	0