Automated protein model building combined with itera

Nature Structural Biology

6, 458-463

DOI: 10.1038/8263

Citation Report

#	ARTICLE	IF	CITATIONS
2	1.68-Ã… Crystal Structure of Endopolygalacturonase II fromAspergillus niger and Identification of Active Site Residues by Site-directed Mutagenesis. Journal of Biological Chemistry, 1999, 274, 30474-30480.	1.6	203
3	Money for structural genomics. , 1999, 6, 707-708.		1
4	Structure of the Human Adenovirus Serotype 2 Fiber Head Domain at 1.5 Ã… Resolution. Virology, 1999, 262, 333-343.	1.1	87
5	Advances in direct methods for protein crystallography. Current Opinion in Structural Biology, 1999, 9, 643-648.	2.6	279
6	Selenium-based MAD phasing: setting the sites on larger structures. Structure, 1999, 7, R161-R166.	1.6	36
7	Structure ofL-aspartate oxidase: implications for the succinate dehydrogenase/fumarate reductase oxidoreductase family. Structure, 1999, 7, 745-756.	1.6	90
8	Crystal structure of the C-terminal SH2 domain of the p85Î± regulatory subunit of phosphoinositide 3-kinase: an SH2 domain mimicking its own substrate. Journal of Molecular Biology, 1999, 292, 763-770.	2.0	31
9	Maximum-likelihood density modification for x-ray crystallography. , 2000, 4123, 243.		0
10	Crystal structure of YbaK protein fromHaemophilus influenzae (HI1434) at 1.8 ? resolution: Functional implications. , 2000, 40, 86-97.		47
11	Structural basis for the inhibition of porcine pepsin by Ascaris pepsin inhibitor-3. Nature Structural Biology, 2000, 7, 653-657.	9.7	59
12	Structural analysis of the catalytic and binding sites of Clostridium botulinum neurotoxin B. , 2000, 7, 693-699.		415
13	Current state of automated crystallographic data analysis. , 2000, 7, 978-981.		74
14	Structure and assembly of the Alu domain of the mammalian signal recognition particle. Nature, 2000, 408, 167-173.	13.7	182
15	Biological function made crystal clear â€” annotation of hypothetical proteins via structural genomics. Current Opinion in Biotechnology, 2000, 11, 25-30.	3.3	114
16	Recent developments in software for the automation of crystallographic macromolecular structure determination. Current Opinion in Structural Biology, 2000, 10, 564-568.	2.6	16
17	The â€˜fingerprintâ€™ that X-rays can leave on structures. Structure, 2000, 8, 315-328.	1.6	302
18	Structure of cyanase reveals that a novel dimeric and decameric arrangement of subunits is required for formation of the enzyme active site. Structure, 2000, 8, 505-514.	1.6	75
19	Crystal structure of a d-aminopeptidase from Ochrobactrum anthropi, a new member of the â€˜penicillin-recognizing enzymeâ€™ family. Structure, 2000, 8, 971-980.	1.6	41

#	Article	IF	Citations
20	Crystal Structure of the Molybdenum Cofactor Biosynthesis Protein MobA from Escherichia coli at Near-Atomic Resolution. Structure, 2000, 8, 1115-1125.	1.6	40
21	Crystal Structure of Protein Isoaspartyl Methyltransferase. Structure, 2000, 8, 1189-1201.	1.6	54
22	Does NMR Mean â€œNot for Molecular Replacementâ€? Using NMR-Based Search Models to Solve Protein Crystal Structures. Structure, 2000, 8, R213-R220.	1.6	31
23	Dimeric Structure of the Coxsackievirus and Adenovirus Receptor D1 Domain at 1.7 Ã… Resolution. Structure, 2000, 8, 1147-1155.	1.6	142
24	Crystal Structure of the Human Acyl Protein Thioesterase I from a Single X-Ray Data Set to 1.5 Ã…. Structure, 2000, 8, 1137-1146.	1.6	124
25	An integrated approach to structural genomics. Progress in Biophysics and Molecular Biology, 2000, 73, 347-362.	1.4	54
26	A novel two-over-two alpha-helical sandwich fold is characteristic of the truncated hemoglobin family. EMBO Journal, 2000, 19, 2424-2434.	3.5	217
27	Crystal structure of the matrix protein VP40 from Ebola virus. EMBO Journal, 2000, 19, 4228-4236.	3.5	158
28	Crystal structure of FadR, a fatty acid-responsive transcription factor with a novel acyl coenzyme A-binding fold. EMBO Journal, 2000, 19, 5167-5177.	3.5	125
29	The structural basis for the recognition of acetylated histone H4 by the bromodomain of histone acetyltransferase Gcn5p. EMBO Journal, 2000, 19, 6141-6149.	3.5	449
30	Crystal structure of Trbp111: a structure-specific tRNA-binding protein. EMBO Journal, 2000, 19, 6287-6298.	3.5	51
31	Crystal structure of the peptidyl-cysteine decarboxylase EpiD complexed with a pentapeptide substrate. EMBO Journal, 2000, 19, 6299-6310.	3.5	88
32	The structural basis of the catalytic mechanism and regulation of glucose-1-phosphate thymidylyltransferase (RmlA). EMBO Journal, 2000, 19, 6652-6663.	3.5	177
33	Crystal structure of the catalytic domain of human complement C1s: a serine protease with a handle. EMBO Journal, 2000, 19, 1755-1765.	3.5	111
34	The Crystal Structure of the Escherichia coliMobA Protein Provides Insight into Molybdopterin Guanine Dinucleotide Biosynthesis. Journal of Biological Chemistry, 2000, 275, 40211-40217.	1.6	64
35	Crystal structure of the zymogen form of the group A Streptococcus virulence factor SpeB: An integrin-binding cysteine protease. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2235-2240.	3.3	96
36	Heparan/Chondroitin Sulfate Biosynthesis. Journal of Biological Chemistry, 2000, 275, 34580-34585.	1.6	178
37	Structure of a two-domain chitotriosidase from Serratia marcescens at 1.9-A resolution. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5842-5847.	3.3	252

#	Article	IF	Citations
38	The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TcR molecules. Journal of Molecular Biology, 2000, 302, 527-537.	2.0	53
39	Crystal Structure of the DNA Binding Domain of the Replication Initiation Protein E1 from Papillomavirus. Molecular Cell, 2000, 6, 149-158.	4.5	80
40	Structural Basis for Nucleotide Exchange and Competition with tRNA in the Yeast Elongation Factor Complex eEF1A:eEF1BÎ±. Molecular Cell, 2000, 6, 1261-1266.	4.5	179
41	Structure of the Molecular Chaperone Prefoldin. Cell, 2000, 103, 621-632.	13.5	298
42	Structure of TPR Domainâ€"Peptide Complexes. Cell, 2000, 101, 199-210.	13.5	1,126
43	Structural Evidence for Evolution of the beta /alpha Barrel Scaffold by Gene Duplication and Fusion. Science, 2000, 289, 1546-1550.	6.0	310
44	The 1.3 Ã… Crystal Structure ofRhodobacter sphaeroidesDimethyl Sulfoxide Reductase Reveals Two Distinct Molybdenum Coordination Environments. Journal of the American Chemical Society, 2000, 122, 7673-7680.	6.6	156
45	The 2 Ã… crystal structure of leucyl-tRNA synthetase and its complex with a leucyl-adenylate analogue. EMBO Journal, 2000, 19, 2351-2361.	3.5	244
46	The structural basis of acyl coenzyme A-dependent regulation of the transcription factor FadR. EMBO Journal, 2001, 20, 2041-2050.	3.5	146
47	Industrializing Structural Biology. Science, 2001, 293, 519-520.	6.0	39
48	The Crystal Structure of Uncomplexed Actin in the ADP State. Science, 2001, 293, 708-711.	6.0	484
49	Crystal structure of auracyanin, a â€œblueâ€•copper protein from the green thermophilic photosynthetic bacterium Chloroflexus aurantiacus11Edited by R Huber. Journal of Molecular Biology, 2001, 306, 47-67.	2.0	50
50	Crystal structure and site-directed mutagenesis studies of N-carbamoyl-d-amino-acid amidohydrolase from Agrobacterium radiobacter reveals a homotetramer and insight into a catalytic cleft11Edited by R. Huber. Journal of Molecular Biology, 2001, 306, 251-261.	2.0	72
51	A thermophilic mini-chaperonin contains a conserved polypeptide-binding surface: combined crystallographic and NMR studies of the GroEL apical domain with implications for substrate interactions11Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 306, 513-525.	2.0	15
52	Transthyretin stability as a key factor in amyloidogenesis: X-ray analysis at atomic resolution. Journal of Molecular Biology, 2001, 306, 733-744.	2.0	85
53	X-ray structure analysis and crystallographic refinement of lumazine synthase from the hyperthermophile Aquifex aeolicus at 1.6 Ã… resolution: determinants of thermostability revealed from structural comparisons. Journal of Molecular Biology, 2001, 306, 1099-1114.	2.0	179
54	Crystal structure of the catalytic core component of the alkylhydroperoxide reductase AhpF from Escherichia coli. Journal of Molecular Biology, 2001, 307, 1-8.	2.0	20
55	An unexpected extended conformation for the third TPR motif of the peroxin PEX5 from Trypanosoma brucei. Journal of Molecular Biology, 2001, 307, 271-282.	2.0	45

#	ARTICLE	IF	CITATIONS
56	Crystal structure of the transcription elongation/anti-termination factor NusA from Mycobacterium tuberculosis at 1.7 Ã… resolution. Journal of Molecular Biology, 2001, 314, 1087-1095.	2.0	57
57	Crystal structure of a heat and protease-stable part of the bacteriophage T4 short tail fibre. Journal of Molecular Biology, 2001, 314, 1137-1146.	2.0	95
58	Structure and function of a novel purine specific nucleoside hydrolase from Trypanosoma vivax11Edited by R. Huber. Journal of Molecular Biology, 2001, 307, 1363-1379.	2.0	89
59	Crystal structure of the PDZ1 domain of human Na+/H+ exchanger regulatory factor provides insights into the mechanism of carboxyl-terminal leucine recognition by class I PDZ domains. Journal of Molecular Biology, 2001, 308, 963-973.	2.0	87
60	The crystal structure of Bacillus subtili lipase: a minimal Î±/Î² hydrolase fold enzyme. Journal of Molecular Biology, 2001, 309, 215-226.	2.0	242
61	The crystal structure of Î”3-Î”2-enoyl-CoA isomerase. Journal of Molecular Biology, 2001, 309, 845-853.	2.0	50
62	Very high resolution structure of a trematode hemoglobin displaying a TyrB10-TyrE7 heme distal residue pair and high oxygen affinity. Journal of Molecular Biology, 2001, 309, 1153-1164.	2.0	44
63	Binding site differences revealed by crystal structures of Plasmodium falciparum and bovine acyl-CoA binding protein. Journal of Molecular Biology, 2001, 309, 181-192.	2.0	66
64	Crystal structure of human peroxiredoxin 5, a novel type of mammalian peroxiredoxin at 1.5 Ã… resolution. Journal of Molecular Biology, 2001, 311, 751-759.	2.0	247
65	Crystal structure of histidinol phosphate aminotransferase (HisC) from Escherichia coli, and its covalent complex with pyridoxal-5â€²-phosphate and l-histidinol phosphate. Journal of Molecular Biology, 2001, 311, 761-776.	2.0	45
66	Structure of the soluble domain of a membrane-anchored thioredoxin-like protein from Bradyrhizobium japonicum reveals unusual properties11Edited by R. Huber. Journal of Molecular Biology, 2001, 311, 1037-1048.	2.0	38
67	Crystal structures of human gephyrin and plant Cnx1 G domains: comparative analysis and functional implications. Journal of Molecular Biology, 2001, 312, 405-418.	2.0	95
68	Crystal structure of the liganded SCP-2-like domain of human peroxisomal multifunctional enzyme type 2 at 1.75 Ã… resolution 1 1Edited by R. Huber. Journal of Molecular Biology, 2001, 313, 1127-1138.	2.0	70
69	Crystal structure of a protein repair methyltransferase from Pyrococcus furiosus with its l -isoaspartyl peptide substrate 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 313, 1103-1116.	2.0	55
70	The Binding Site of Acetylcholine Receptor as Visualized in the X-Ray Structure of a Complex between Î±-Bungarotoxin and a Mimotope Peptide. Neuron, 2001, 32, 265-275.	3.8	125
71	Crystal Structure and Deletion Analysis Show that the Accessory Subunit of Mammalian DNA Polymerase Î³, PolÎ³B, Functions as a Homodimer. Molecular Cell, 2001, 7, 43-54.	4.5	135
72	Crystal Structure of the Human Nuclear Cap Binding Complex. Molecular Cell, 2001, 8, 383-396.	4.5	126
73	Differential Dimer Activities of the Transcription Factor Oct-1 by DNA-Induced Interface Swapping. Molecular Cell, 2001, 8, 569-580.	4.5	114

#	Article	IF	Citations
74	The Crystal Structure of the PX Domain from p40phox Bound to Phosphatidylinositol 3-Phosphate. Molecular Cell, 2001, 8, 829-839.	4.5	263
75	Crystal Structure of a Y-Family DNA Polymerase in Action. Cell, 2001, 107, 91-102.	13.5	588
76	Crystal Structure of Alkaline Phosphatase from Human Placenta at 1.8 Ã… Resolution. Journal of Biological Chemistry, 2001, 276, 9158-9165.	1.6	234
77	Structural requirements of endopolygalacturonase for the interaction with PGIP (polygalacturonase-inhibiting protein). Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13425-13430.	3.3	131
78	Crystal structure of the phosphatidylinositol 3,4-bisphosphate-binding pleckstrin homology (PH) domain of tandem PH-domain-containing protein 1 (TAPP1): molecular basis of lipid specificity. Biochemical Journal, 2001, 358, 287.	1.7	61
79	Using surface-bound rubidium ions for protein phasing. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1008-1012.	2.5	9
80	Maximum-likelihood density modification using pattern recognition of structural motifs. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1755-1762.	2.5	133
81	Map-likelihood phasing. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1763-1775.	2.5	69
82	Streptococcus pneumoniaYlxR at 1.35â€…Ã… shows a putative new fold. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1747-1751.	2.5	23
83	Structural determinants for ligand binding and catalysis of â€˜triosephosphate isomerase. FEBS Journal, 2001, 268, 5189-5196.	0.2	42
84	Crystal structure of Yeco fromHaemophilus influenzae (HI0319) reveals a methyltransferase fold and a boundS-adenosylhomocysteine. Proteins: Structure, Function and Bioinformatics, 2001, 45, 397-407.	1.5	27
85	Substrate flow in catalases deduced from the crystal structures of active site variants of HPII fromEscherichia coli. Proteins: Structure, Function and Bioinformatics, 2001, 44, 270-281.	1.5	50
86	X-ray crystal structure of MTH938 fromMethanobacterium thermoautotrophicumat 2.2 Ã… resolution reveals a novel tertiary protein fold. Proteins: Structure, Function and Bioinformatics, 2001, 45, 486-488.	1.5	5
87	Transmembrane ?-helices in the gap junction membrane channel: Systematic search of packing models based on the pair potential function. Microscopy Research and Technique, 2001, 52, 344-351.	1.2	10
88	Structure of a Family 15 Carbohydrate-binding Module in Complex with Xylopentaose. Journal of Biological Chemistry, 2001, 276, 49061-49065.	1.6	90
89	Structure of the Fiber Head of Ad3, a Non-CAR-Binding Serotype of Adenovirus. Virology, 2001, 285, 302-312.	1.1	62
90	Structure and mechanism of the RNA triphosphatase component of mammalian mRNA capping enzyme. EMBO Journal, 2001, 20, 2575-2586.	3.5	90
91	The crystal structure of Sulfolobus solfataricus elongation factor 1alpha in complex with GDP reveals novel features in nucleotide binding and exchange. EMBO Journal, 2001, 20, 5305-5311.	3.5	63

#	ARTICLE	IF	CITATIONS
92	X-ray structure of the orphan nuclear receptor RORbeta ligand-binding domain in the active conformation. EMBO Journal, 2001, 20, 5822-5831.	3.5	110
93	Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the IkappaB protein family. EMBO Journal, 2001, 20, 6180-6190.	3.5	68
94	Structure of the EMAPII domain of human aminoacyl-tRNA synthetase complex reveals evolutionary dimer mimicry. EMBO Journal, 2001, 20, 570-578.	3.5	60
95	Crystal structure of isopentenyl diphosphate:dimethylallyl diphosphate isomerase. EMBO Journal, 2001, 20, 1530-1537.	3.5	82
96	High-throughput three-dimensional protein structure determination. Current Opinion in Biotechnology, 2001, 12, 348-354.	3.3	52
97	How the Pseudomonas aeruginosa ExoS toxin downregulates Rac. Nature Structural Biology, 2001, 8, 23-26.	9.7	102
98	Crystal structure of molybdopterin synthase and its evolutionary relationship to ubiquitin activation. Nature Structural Biology, 2001, 8, 42-46.	9.7	124
99	The 2.0 A structure of human ferrochelatase, the terminal enzyme of heme biosynthesis. Nature Structural Biology, 2001, 8, 156-160.	9.7	200
100	Carboxyl proteinase from Pseudomonas defines a novel family of subtilisin-like enzymes. Nature Structural Biology, 2001, 8, 442-446.	9.7	91
101	Structure of the Rho-activating domain of Escherichia coli cytotoxic necrotizing factor 1. Nature Structural Biology, 2001, 8, 584-588.	9.7	95
102	Crystal structures of the catalytic domain of human protein kinase associated with apoptosis and tumor suppression. Nature Structural Biology, 2001, 8, 899-907.	9.7	96
103	Structure of the Yersinia type III secretory system chaperone SycE. , 2001, 8, 974-978.		68
104	Maintenance of an unfolded polypeptide by a cognate chaperone in bacterial type III secretion. Nature, 2001, 414, 77-81.	13.7	272
105	Mechanism of ubiquitin activation revealed by the structure of a bacterial MoeBâ€“MoaD complex. Nature, 2001, 414, 325-329.	13.7	229
106	Entering a New Phase. Structure, 2001, 9, R21-R26.	1.6	41
107	Crystal Structure of Streptococcus mutans Pyrophosphatase. Structure, 2001, 9, 289-297.	1.6	69
108	The Crystal Structure of Escherichia coli MoeA and Its Relationship to the Multifunctional Protein Gephyrin. Structure, 2001, 9, 299-310.	1.6	103
109	Crystal Structures of a Novel Ferric Reductase from the Hyperthermophilic Archaeon Archaeoglobus fulgidus and Its Complex with NADP+. Structure, 2001, 9, 311-319.	1.6	65

#	ARTICLE	IF	CITATIONS
110	The Crystal Structure of E. coli Pantothenate Synthetase Confirms It as a Member of the Cytidylyltransferase Superfamily. Structure, 2001, 9, 439-450.	1.6	70
111	1.3 Ã… Structure of Arylsulfatase from Pseudomonas aeruginosa Establishes the Catalytic Mechanism of Sulfate Ester Cleavage in the Sulfatase Family. Structure, 2001, 9, 483-491.	1.6	177
112	Soft X-rays, High Redundancy, and Proper Scaling. Structure, 2001, 9, 771-777.	1.6	40
113	Structure of Thermotoga maritima Stationary Phase Survival Protein SurE. Structure, 2001, 9, 1095-1106.	1.6	105
114	The Structure of the Feruloyl Esterase Module of Xylanase 10B from Clostridium thermocellum Provides Insights into Substrate Recognition. Structure, 2001, 9, 1183-1190.	1.6	112
115	High-throughput x-ray crystallography for structure-based drug design. Drug Discovery Today, 2001, 6, 113-118.	3.2	34
116	Structure of melanoma inhibitory activity protein, a member of a recently identified family of secreted proteins. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5515-5520.	3.3	53
117	High Resolution Structure of the Phosphohistidine-activated Form of Escherichia coli Cofactor-dependent Phosphoglycerate Mutase. Journal of Biological Chemistry, 2001, 276, 3247-3253.	1.6	63
118	Amylosucrase, a Glucan-synthesizing Enzyme from the Î±-Amylase Family. Journal of Biological Chemistry, 2001, 276, 25273-25278.	1.6	135
119	Crystal Structure of Streptococcus pneumoniae N-Acetylglucosamine-1-phosphate Uridyltransferase Bound to Acetyl-coenzyme A Reveals a Novel Active Site Architecture. Journal of Biological Chemistry, 2001, 276, 11844-11851.	1.6	92
120	A New Lysozyme Fold. Journal of Biological Chemistry, 2001, 276, 31994-31999.	1.6	59
121	Structure of Hjc, a Holliday junction resolvase, from Sulfolobus solfataricus. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5509-5514.	3.3	85
122	Crystal Structure of the Dimeric C-terminal Domain of TonB Reveals a Novel Fold. Journal of Biological Chemistry, 2001, 276, 27535-27540.	1.6	117
123	The Crystallographic Structure of the Mannitol 2-Dehydrogenase NADP+ Binary Complex from Agaricus bisporus. Journal of Biological Chemistry, 2001, 276, 27555-27561.	1.6	57
124	X-ray Crystal Structure of the Trimeric N-terminal Domain of Gephyrin. Journal of Biological Chemistry, 2001, 276, 25294-25301.	1.6	83
125	Structural Basis for Ni2+Transport and Assembly of the Urease Active Site by the Metallochaperone UreE from Bacillus pasteurii. Journal of Biological Chemistry, 2001, 276, 49365-49370.	1.6	74
126	The Crystal Structures of Apo and Complexed Saccharomyces cerevisiae GNA1 Shed Light on the Catalytic Mechanism of an Amino-sugar N-Acetyltransferase. Journal of Biological Chemistry, 2001, 276, 16328-16334.	1.6	74
127	The crystal structure of a heptameric archaeal Sm protein: Implications for the eukaryotic snRNP core. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5532-5537.	3.3	100

#	ARTICLE	IF	CITATIONS
128	Oxyanion Binding Alters Conformation and Quaternary Structure of the C-terminal Domain of the Transcriptional Regulator ModE. Journal of Biological Chemistry, 2001, 276, 20641-20647.	1.6	37
129	Structural and Mutational Analysis of the PhoQ Histidine Kinase Catalytic Domain. Journal of Biological Chemistry, 2001, 276, 41182-41190.	1.6	111
130	Disordered to ordered folding in the regulation of diphtheria toxin repressor activity. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11259-11264.	3.3	42
131	Crystal Structure of Klebsiella aerogenesUreE, a Nickel-binding Metallochaperone for Urease Activation. Journal of Biological Chemistry, 2001, 276, 49359-49364.	1.6	86
132	Crystal Structure of the CheA Histidine Phosphotransfer Domain that Mediates Response Regulator Phosphorylation in Bacterial Chemotaxis. Journal of Biological Chemistry, 2001, 276, 31074-31082.	1.6	75
133	Crystal structure and electron transfer kinetics of CueO, a multicopper oxidase required for copper homeostasis in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2766-2771.	3.3	296
134	NAD Binding Induces Conformational Changes in Rho ADP-ribosylating Clostridium botulinum C3 Exoenzyme. Journal of Biological Chemistry, 2002, 277, 30950-30957.	1.6	60
135	The Crystal Structure of Helicobacter pyloriCysteine-rich Protein B Reveals a Novel Fold for a Penicillin-binding Protein. Journal of Biological Chemistry, 2002, 277, 10187-10193.	1.6	37
136	Crystal Structure of Quinohemoprotein Alcohol Dehydrogenase from Comamonas testosteroni. Journal of Biological Chemistry, 2002, 277, 3727-3732.	1.6	78
137	The Crystal Structure of Mycobacterium tuberculosisAlkylhydroperoxidase AhpD, a Potential Target for Antitubercular Drug Design. Journal of Biological Chemistry, 2002, 277, 20033-20040.	1.6	40
138	Structure of 2C-methyl-D-erythritol 2,4- cyclodiphosphate synthase: An essential enzyme for isoprenoid biosynthesis and target for antimicrobial drug development. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6591-6596.	3.3	82
139	A clogged gutter mechanism for protease inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10316-10321.	3.3	138
140	Consensus-derived structural determinants of the ankyrin repeat motif. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16029-16034.	3.3	320
141	Three-dimensional Structure of Human Î³-Glutamyl Hydrolase. Journal of Biological Chemistry, 2002, 277, 24522-24529.	1.6	28
142	The Crystal Structure of Metal-free Human EF-hand Protein S100A3 at 1.7-Ã… Resolution. Journal of Biological Chemistry, 2002, 277, 33092-33098.	1.6	50
143	X-ray Structure of Two Crystalline Forms of aStreptomycete Ribonuclease with Cytotoxic Activity. Journal of Biological Chemistry, 2002, 277, 47325-47330.	1.6	41
144	Nonlinear partial differential equations and applications: Crystal structure of a human aminoacyl-tRNA synthetase cytokine. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15369-15374.	3.3	88
145	Structural genomics of the Thermotoga maritima proteome implemented in a high-throughput structure determination pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11664-11669.	3.3	397

#	Article	IF	Citations
146	Mechanism of action and NAD+-binding mode revealed by the crystal structure of L-histidinol dehydrogenase. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1859-1864.	3.3	52
147	Crystal Structure of the 47-kDa Lipoprotein of Treponema pallidum Reveals a Novel Penicillin-binding Protein. Journal of Biological Chemistry, 2002, 277, 41857-41864.	1.6	49
148	Structure of Mitogen-activated Protein Kinase-activated Protein (MAPKAP) Kinase 2 Suggests a Bifunctional Switch That Couples Kinase Activation with Nuclear Export. Journal of Biological Chemistry, 2002, 277, 37401-37405.	1.6	108
149	Passive Acquisition of Ligand by the MopII Molbindin fromClostridium pasteurianum. Journal of Biological Chemistry, 2002, 277, 15013-15020.	1.6	20
150	X-ray Structure and Ligand Binding Study of a Moth Chemosensory Protein. Journal of Biological Chemistry, 2002, 277, 32094-32098.	1.6	173
151	Macromolecular phasing with SHELXE. Zeitschrift Fur Kristallographie - Crystalline Materials, 2002, 217, 644-650.	0.4	344
152	The Structure of 3-Methylaspartase from Clostridium tetanomorphum Functions via the Common Enolase Chemical Step. Journal of Biological Chemistry, 2002, 277, 8306-8311.	1.6	31
153	Crystal Structures at Atomic Resolution Reveal the Novel Concept of â€œElectron-harvestingâ€•as a Role for the Small Tetraheme Cytochrome c. Journal of Biological Chemistry, 2002, 277, 35703-35711.	1.6	104
154	HLA-B27 Subtypes Differentially Associated with Disease Exhibit Subtle Structural Alterations. Journal of Biological Chemistry, 2002, 277, 47844-47853.	1.6	83
155	The 1.9-A crystal structure of the noncollagenous (NC1) domain of human placenta collagen IV shows stabilization via a novel type of covalent Met-Lys cross-link. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6607-6612.	3.3	130
156	Identification, Characterization, and Crystal Structure ofBacillus subtilis Nicotinic Acid Mononucleotide Adenylyltransferase. Journal of Biological Chemistry, 2002, 277, 3698-3707.	1.6	52
157	Structure of Arterivirus nsp4. Journal of Biological Chemistry, 2002, 277, 39960-39966.	1.6	71
158	Crystal Structure of the Carbohydrate Recognition Domain of p58/ERGIC-53, a Protein Involved in Glycoprotein Export from the Endoplasmic Reticulum. Journal of Biological Chemistry, 2002, 277, 15979-15984.	1.6	80
159	Unusual Binding Properties of the SH3 Domain of the Yeast Actin-binding Protein Abp1. Journal of Biological Chemistry, 2002, 277, 5290-5298.	1.6	103
160	The Active Principle of Garlic at Atomic Resolution. Journal of Biological Chemistry, 2002, 277, 46402-46407.	1.6	58
161	A pilot study of the long-term effects of acipimox in polycystic ovarian syndrome. Human Reproduction, 2002, 17, 647-653.	0.4	9
162	A New Engine for Cleaving Nucleic Acid. ACS Symposium Series, 2002, , 270-293.	0.5	0
163	Crystal structure of the flavoprotein domain of the extracellular flavocytochrome cellobiose dehydrogenase. Journal of Molecular Biology, 2002, 315, 421-434.	2.0	134

#	Article	IF	Citations
164	Detailed architecture of a DNA translocating machine: the high-resolution structure of the bacteriophage Ï†29 connector particle 1 1Edited by R. Huber. Journal of Molecular Biology, 2002, 315, 663-676.	2.0	205
165	Mechanistic implications for Escherichia coli cofactor-dependent phosphoglycerate mutase based on the high-resolution crystal structure of a vanadate complex. Journal of Molecular Biology, 2002, 316, 1071-1081.	2.0	56
166	Crystal structure of the GABA A â€receptorâ€associated protein, GABARAP. EMBO Reports, 2002, 3, 183-189.	2.0	65
167	Domain-swapped structure of a mutant of cyanovirin-N. Biochemical and Biophysical Research Communications, 2002, 294, 184-190.	1.0	23
168	Crystal structure of plant pectin methylesterase. FEBS Letters, 2002, 514, 243-249.	1.3	127
169	The importance of the conserved Arg191-Asp227 salt bridge of triosephosphate isomerase for folding, stability, and catalysis. FEBS Letters, 2002, 518, 39-42.	1.3	36
170	GluR2 ligand-binding core complexes: importance of the isoxazolol moiety and 5-substituent for the binding mode of AMPA-type agonists. FEBS Letters, 2002, 531, 173-178.	1.3	39
171	Crystal Structure of the Homer 1 Family Conserved Region Reveals the Interaction Between the EVH1 Domain and Own Proline-rich Motif. Journal of Molecular Biology, 2002, 318, 1117-1126.	2.0	30
172	Differential Oligosaccharide Recognition by Evolutionarily-related Î²-1,4 and Î²-1,3 Glucan-binding Modules. Journal of Molecular Biology, 2002, 319, 1143-1156.	2.0	135
173	Archaeal Sm Proteins form Heptameric and Hexameric Complexes: Crystal Structures of the Sm1 and Sm2 Proteins from the Hyperthermophile Archaeoglobus fulgidus. Journal of Molecular Biology, 2002, 320, 129-142.	2.0	70
174	X-ray Structure of a Dihydropyrimidinase from Thermus sp. at 1.3Ã… Resolution. Journal of Molecular Biology, 2002, 320, 143-156.	2.0	87
175	Structure of Porphobilinogen Synthase from Pseudomonas aeruginosa in Complex with 5-Fluorolevulinic Acid Suggests a Double Schiff Base Mechanism. Journal of Molecular Biology, 2002, 320, 237-247.	2.0	54
176	Structural Basis for AMPA Receptor Activation and Ligand Selectivity: Crystal Structures of Five Agonist Complexes with the GluR2 Ligand-binding Core. Journal of Molecular Biology, 2002, 322, 93-109.	2.0	155
177	The RUNX1 Runt Domain at 1.25Ã… Resolution: A Structural Switch and Specifically Bound Chloride Ions Modulate DNA Binding. Journal of Molecular Biology, 2002, 322, 259-272.	2.0	52
178	Crystal Structure of a Prostate Kallikrein Isolated from Stallion Seminal Plasma: A Homologue of Human PSA. Journal of Molecular Biology, 2002, 322, 325-337.	2.0	81
179	Trimeric Crystal Structure of the Glycoside Hydrolase Family 42 Î²-Galactosidase from Thermus thermophilus A4 and the Structure of its Complex with Galactose. Journal of Molecular Biology, 2002, 322, 79-91.	2.0	110
180	Crystal Structure of a Thermostable Lipase from Bacillus stearothermophilus P1. Journal of Molecular Biology, 2002, 323, 859-869.	2.0	121
181	Crystal Structure of the C-Terminal Half of Tropomodulin and Structural Basis of Actin Filament Pointed-End Capping. Biophysical Journal, 2002, 83, 2716-2725.	0.2	79

#	Article	IF	Citations
182	Structure of Bacillus subtilis YXKOâ€”A member of the UPF0031 family and a putative kinase. Journal of Structural Biology, 2002, 139, 161-170.	1.3	19
183	Structure of the Bacterial RNA Polymerase Promoter Specificity Ïƒ Subunit. Molecular Cell, 2002, 9, 527-539.	4.5	446
184	High-Resolution Structure of the Pleckstrin Homology Domain of Protein Kinase B/Akt Bound to Phosphatidylinositol (3,4,5)-Trisphosphate. Current Biology, 2002, 12, 1256-1262.	1.8	273
185	Toward a Structural Understanding of the Dehydratase Mechanism. Structure, 2002, 10, 81-92.	1.6	94
186	Insights into Enzyme Evolution Revealed by the Structure of Methylaspartate Ammonia Lyase. Structure, 2002, 10, 105-113.	1.6	37
187	Crystal Structure of the Functional Unit of Interphotoreceptor Retinoid Binding Protein. Structure, 2002, 10, 43-49.	1.6	42
188	The Crystal Structure of Human Tyrosyl-DNA Phosphodiesterase, Tdp1. Structure, 2002, 10, 237-248.	1.6	151
189	Crystal Structures of S100A6 in the Ca2+-Free and Ca2+-Bound States. Structure, 2002, 10, 557-567.	1.6	115
190	The Structural Basis for Catalysis and Specificity of the Pseudomonas cellulosa Î±-Glucuronidase, GlcA67A. Structure, 2002, 10, 547-556.	1.6	74
191	The Structure of Neurospora crassa 3-Carboxy-cis,cis-Muconate Lactonizing Enzyme, a Î² Propeller Cycloisomerase. Structure, 2002, 10, 483-492.	1.6	24
192	The 109 Residue Nerve Tissue Minihemoglobin from Cerebratulus lacteus Highlights Striking Structural Plasticity of the Î±-Helical Globin Fold. Structure, 2002, 10, 725-735.	1.6	66
193	Structure of the Retinal Determination Protein Dachshund Reveals a DNA Binding Motif. Structure, 2002, 10, 787-795.	1.6	70
194	X-Ray Crystallographic Studies on Butyryl-ACP Reveal Flexibility of the Structure around a Putative Acyl Chain Binding Site. Structure, 2002, 10, 825-835.	1.6	114
195	Molecular Basis of Mitomycin C Resistance in Streptomyces. Structure, 2002, 10, 933-942.	1.6	30
196	The 1.1 Ã… Crystal Structure of Human TGF-Î² Type II Receptor Ligand Binding Domain. Structure, 2002, 10, 913-919.	1.6	54
197	Crystal Structure of Recombinant Human Interleukin-22. Structure, 2002, 10, 1051-1062.	1.6	119
198	Gene Sequence and the 1.8 Ã… Crystal Structure of the Tungsten-Containing Formate Dehydrogenase from Desulfovibrio gigas. Structure, 2002, 10, 1261-1272.	1.6	161
199	Structural and Functional Analysis of the Kid Toxin Protein from E. coli Plasmid R1. Structure, 2002, 10, 1425-1433.	1.6	77

#	Article	IF	Citations
200	Crystal Structure of the Human Supernatant Protein Factor. Structure, 2002, 10, 1533-1540.	1.6	62
201	Structures of the Cancer-Related Aurora-A, FAK, and EphA2 Protein Kinases from Nanovolume Crystallography. Structure, 2002, 10, 1659-1667.	1.6	193
202	New approaches to high-throughput phasing. Current Opinion in Structural Biology, 2002, 12, 674-678.	2.6	46
203	Integrated structural genomics in Europe. Gene Function & Disease, 2002, 3, 18-24.	0.3	0
204	Establishing a structural genomics platform: The Berlin-based Protein Structure Factory. Gene Function & Disease, 2002, 3, 25-32.	0.3	6
205	The genesis of high-throughput structure-based drug discovery using protein crystallography. Current Opinion in Chemical Biology, 2002, 6, 704-710.	2.8	118
206	Native interface of the SAM domain polymer of TEL. BMC Structural Biology, 2002, 2, 5.	2.3	35
207	Autotracing ofEscherichia coliacetate CoA-transferase Î±-subunit structure using 3.4â€…Ã… MAD and 1.9â€…Ã… native data. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2116-2121.	2.5	16
208	Crystal structure of theEscherichia coli shikimate kinase I (AroK) that confers sensitivity to mecillinam. Proteins: Structure, Function and Bioinformatics, 2002, 47, 558-562.	1.5	31
209	Crystal structure of theEscherichia coli SbmC protein that protects cells from the DNA replication inhibitor microcin B17. Proteins: Structure, Function and Bioinformatics, 2002, 47, 403-407.	1.5	24
210	Crystal structure of theEscherichia coli glucose-inhibited division protein B (GidB) reveals a methyltransferase fold. Proteins: Structure, Function and Bioinformatics, 2002, 47, 563-567.	1.5	28
211	X-ray structure ofSaccharomyces cerevisiae homologous mitochondrial matrix factor 1 (Hmf1). Proteins: Structure, Function and Bioinformatics, 2002, 48, 431-436.	1.5	22
212	Crystal structure ofBacillus subtilis ioli shows endonuclase IV fold with altered Zn binding. Proteins: Structure, Function and Bioinformatics, 2002, 48, 423-426.	1.5	17
213	Crystal structure ofEscherichia coli EC1530, a glyoxylate induced protein YgbM. Proteins: Structure, Function and Bioinformatics, 2002, 48, 427-430.	1.5	3
214	Crystal structure of the YciO protein fromEscherichia coli. Proteins: Structure, Function and Bioinformatics, 2002, 49, 139-141.	1.5	20
215	Crystal structure of thy1, a thymidylate synthase complementing protein fromThermotoga maritimaat 2.25 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2002, 49, 142-145.	1.5	50
216	Crystal structure of YbaB from Haemophilus influenzae (HI0442), a protein of unknown function coexpressed with the recombinational DNA repair protein RecR. Proteins: Structure, Function and Bioinformatics, 2002, 50, 375-379.	1.5	30
217	Crystal structure of a zinc-containing glycerol dehydrogenase (TM0423) from Thermotoga maritima at 1.5 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2002, 50, 371-374.	1.5	8

#	Article	IF	Citations
218	Structure of a bacterial quorum-sensing transcription factor complexed with pheromone and DNA. Nature, 2002, 417, 971-974.	13.7	407
219	Insights into DNA recombination from the structure of a RAD51â€“BRCA2 complex. Nature, 2002, 420, 287-293.	13.7	615
220	High-throughput crystallography for lead discovery in drug design. Nature Reviews Drug Discovery, 2002, 1, 45-54.	21.5	490
221	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. Nature Structural Biology, 2002, 9, 27-31.	9.7	124
222	Structural basis for the accessory protein recruitment by the Î³-adaptin ear domain. Nature Structural Biology, 2002, 9, 527-31.	9.7	34
223	Structure of the immunodominant surface antigen from the Toxoplasma gondii SRS superfamily. Nature Structural Biology, 2002, 9, 606-11.	9.7	81
224	DNA binding is required for the apoptogenic action of apoptosis inducing factor. Nature Structural Biology, 2002, 9, 680-684.	9.7	319
225	The active site of the SET domain is constructed on a knot. Nature Structural Biology, 2002, 9, 833-8.	9.7	71
226	Structural basis for oligosaccharide-mediated adhesion of Pseudomonas aeruginosa in the lungs of cystic fibrosis patients. Nature Structural Biology, 2002, 9, 918-921.	9.7	247
227	Molecular modelling in structural biology. Micron, 2002, 33, 365-384.	1.1	63
228	Stereoselectivity of Enoyl-CoA Hydratase Results from Preferential Activation of One of Two Bound Substrate Conformers. Chemistry and Biology, 2002, 9, 1247-1255.	6.2	28
229	Structural genomics: A pipeline for providing structures for the biologist. Protein Science, 2002, 11, 723-738.	3.1	168
230	Structure of a functional IGF2R fragment determined from the anomalous scattering of sulfur. EMBO Journal, 2002, 21, 1054-1062.	3.5	91
231	The complex of Arl2-GTP and PDEdelta: from structure to function. EMBO Journal, 2002, 21, 2095-2106.	3.5	206
232	Structure of apo-phosphatidylinositol transfer protein alpha provides insight into membrane association. EMBO Journal, 2002, 21, 2117-2121.	3.5	80
233	Structural analysis of two enzymes catalysing reverse metabolic reactions implies common ancestry. EMBO Journal, 2002, 21, 3245-3254.	3.5	28
234	Class I tyrosyl-tRNA synthetase has a class II mode of cognate tRNA recognition. EMBO Journal, 2002, 21, 3829-3840.	3.5	175
235	High resolution crystal structure of the human PDK1 catalytic domain defines the regulatory phosphopeptide docking site. EMBO Journal, 2002, 21, 4219-4228.	3.5	176

#	Article	IF	Citations
236	The disulfide bond isomerase DsbC is activated by an immunoglobulin-fold thiol oxidoreductase: crystal structure of the DsbC-DsbDalpha complex. EMBO Journal, 2002, 21, 4774-4784.	3.5	117
237	Binding of the PX domain of p47phox to phosphatidylinositol 3,4-bisphosphate and phosphatidic acid is masked by an intramolecular interaction. EMBO Journal, 2002, 21, 5057-5068.	3.5	296
238	The cross-reactive calcium-binding pollen allergen, Phl p 7, reveals a novel dimer assembly. EMBO Journal, 2002, 21, 5007-5016.	3.5	77
239	Structure of the sporulation-specific transcription factor Ndt80 bound to DNA. EMBO Journal, 2002, 21, 5721-5732.	3.5	60
240	A novel variant of the immunoglobulin fold in surface adhesins of Staphylococcus aureus: crystal structure of the fibrinogen-binding MSCRAMM, clumping factor A. EMBO Journal, 2002, 21, 6660-6672.	3.5	151
241	Structural and functional characterization of the Pseudomonas hydroperoxide resistance protein Ohr. EMBO Journal, 2002, 21, 6649-6659.	3.5	86
242	The structure of ActVA-Orf6, a novel type of monooxygenase involved in actinorhodin biosynthesis. EMBO Journal, 2003, 22, 205-215.	3.5	150
243	Structural basis for SH3 domain-mediated high-affinity binding between Mona/Gads and SLP-76. EMBO Journal, 2003, 22, 2571-2582.	3.5	102
244	Insights into ssDNA recognition by the OB fold from a structural and thermodynamic study of Sulfolobus SSB protein. EMBO Journal, 2003, 22, 2561-2570.	3.5	122
245	Channelling and formation of 'active' formaldehyde in dimethylglycine oxidase. EMBO Journal, 2003, 22, 4038-4048.	3.5	73
246	Crystal structure and snapshots along the reaction pathway of a family 51 Â-L-arabinofuranosidase. EMBO Journal, 2003, 22, 4922-4932.	3.5	127
247	The 1.6ÂÃ... resolution structure of Fe-superoxide dismutase from the thermophilic cyanobacterium Thermosynechococcus elongatus. Journal of Biological Inorganic Chemistry, 2003, 8, 707-714.	1.1	25
248	Crystal Structure of Human Riboflavin Kinase Reveals a Î² Barrel Fold and a Novel Active Site Arch. Structure, 2003, 11, 265-273.	1.6	71
249	The Matrix Protein VP40 from Ebola Virus Octamerizes into Pore-like Structures with Specific RNA Binding Properties. Structure, 2003, 11, 423-433.	1.6	137
250	PDZ Tandem of Human Syntenin. Structure, 2003, 11, 459-468.	1.6	90
251	Origins of Peptide Selectivity and Phosphoinositide Binding Revealed by Structures of Disabled-1 PTB Domain Complexes. Structure, 2003, 11, 569-579.	1.6	117
252	The Three-Dimensional Structure of the Human NK Cell Receptor NKp44, a Triggering Partner in Natural Cytotoxicity. Structure, 2003, 11, 725-734.	1.6	89
253	High-Resolution Structures of RmlC from Streptococcus suis in Complex with Substrate Analogs Locate the Active Site of This Class of Enzyme. Structure, 2003, 11, 715-723.	1.6	37

#	Article	IF	Citations
254	Structural and Thermodynamic Dissection of Specific Mannan Recognition by a Carbohydrate Binding Module, TmCBM27. Structure, 2003, 11, 665-675.	1.6	62
255	Dextranase from Penicillium minioluteum. Structure, 2003, 11, 1111-1121.	1.6	80
256	High-throughput structural genomics and proteomics: where are we now?. Targets, 2003, 2, 201-207.	0.3	3
257	Microfluidics in structural biology: smaller, fasterâ€¦ better. Current Opinion in Structural Biology, 2003, 13, 538-544.	2.6	238
258	Structure and Interactions of NCAM Ig1-2-3 Suggest a Novel Zipper Mechanism for Homophilic Adhesion. Structure, 2003, 11, 1291-1301.	1.6	164
259	The high resolution crystal structure of rat liver AKR7A1: understanding the substrate specificites of the AKR7 family. Chemico-Biological Interactions, 2003, 143-144, 289-297.	1.7	11
260	Architecture of a protein central to iron homeostasis: crystal structure and spectroscopic analysis of the ferric uptake regulator. Molecular Microbiology, 2003, 47, 903-915.	1.2	304
261	Automated main-chain model building by template matching and iterative fragment extension. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 38-44.	2.5	528
262	Improving macromolecular atomic models at moderate resolution by automated iterative model building, statistical density modification and refinement. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1174-1182.	2.5	69
263	Statistical density modification using local pattern matching. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1688-1701.	2.5	24
264	Crystal structure of a hypothetical protein, TM841 of Thermotoga maritima, reveals its function as a fatty acid-binding protein. Proteins: Structure, Function and Bioinformatics, 2003, 50, 526-530.	1.5	39
265	Crystal structure of a hypothetical protein, TT1725, fromThermus thermophilusHB8 at 1.7 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2003, 53, 768-771.	1.5	3
266	Crystal structure of Î³-glutamyl phosphate reductase (TM0293) from Thermotoga maritima at 2.0 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2003, 54, 157-161.	1.5	17
267	Crystal structure of an iron-containing 1,3-propanediol dehydrogenase (TM0920) from Thermotoga maritima at 1.3 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2003, 54, 174-177.	1.5	32
268	Ni-Zn-[Fe4-S4] and Ni-Ni-[Fe4-S4] clusters in closed and open Î± subunits of acetyl-CoA synthase/carbon monoxide dehydrogenase. Nature Structural and Molecular Biology, 2003, 10, 271-279.	3.6	418
269	The DCX-domain tandems of doublecortin and doublecortin-like kinase. Nature Structural and Molecular Biology, 2003, 10, 324-333.	3.6	122
270	Molecular mechanism of membrane recruitment of GGA by ARF in lysosomal protein transport. Nature Structural and Molecular Biology, 2003, 10, 386-393.	3.6	122
271	Structure of human dCK suggests strategies to improve anticancer and antiviral therapy. Nature Structural and Molecular Biology, 2003, 10, 513-519.	3.6	153

#	Article	IF	Citations
272	Xâ€ray structure of human acidâ€Î²â€glucosidase, the defective enzyme in Gaucher disease. EMBO Reports, 2003, 4, 704-709.	2.0	244
273	Crystal structure of the PsbQ protein of photosystem II from higher plants. EMBO Reports, 2003, 4, 900-905.	2.0	78
274	The oligomerization and ligand-binding properties of Sm-like archaeal proteins (SmAPs). Protein Science, 2003, 12, 832-847.	3.1	47
275	Crystal structure of a trimeric form of dephosphocoenzyme A kinase from Escherichia coli. Protein Science, 2003, 12, 327-336.	3.1	31
276	The crystal structure of augmenter of liver regeneration: A mammalian FAD-dependent sulfhydryl oxidase. Protein Science, 2003, 12, 1109-1118.	3.1	99
277	Crystal structures of a pantothenate synthetase fromM. tuberculosisand its complexes with substrates and a reaction intermediate. Protein Science, 2003, 12, 1097-1108.	3.1	83
278	Crystal complexes of a predicted S-adenosylmethionine-dependent methyltransferase reveal a typical AdoMet binding domain and a substrate recognition domain. Protein Science, 2003, 12, 1432-1442.	3.1	39
279	The structure ofPseudomonasP51 Cl-muconate lactonizing enzyme: Co-evolution of structure and dynamics with the dehalogenation function. Protein Science, 2003, 12, 1855-1864.	3.1	12
280	Competitive Antagonism of AMPA Receptors by Ligands of Different Classes:â€‰ Crystal Structure of ATPO Bound to the GluR2 Ligand-Binding Core, in Comparison with DNQX. Journal of Medicinal Chemistry, 2003, 46, 214-221.	2.9	101
281	Three-Dimensional Structure of the Ligand-Binding Core of GluR2 in Complex with the Agonist (S)-ATPA:Â Implications for Receptor Subunit Selectivity. Journal of Medicinal Chemistry, 2003, 46, 872-875.	2.9	59
282	Facilities and Methods for the High-Throughput Crystal Structural Analysis of Human Proteins. Accounts of Chemical Research, 2003, 36, 157-163.	7.6	96
283	The 0.93Ã… Crystal Structure of Sphericase: A Calcium-loaded Serine Protease from Bacillus sphaericus. Journal of Molecular Biology, 2003, 332, 1071-1082.	2.0	39
284	Crystal Structure of Putidaredoxin, the [2Feâ€“2S] Component of the P450cam Monooxygenase System from Pseudomonas putida. Journal of Molecular Biology, 2003, 333, 377-392.	2.0	86
285	Atomic Structure of Mycobacterium tuberculosis CYP121 to 1.06 Ã… Reveals Novel Features of Cytochrome P450. Journal of Biological Chemistry, 2003, 278, 5141-5147.	1.6	126
286	The Crystal Structure of the Globular Head of Complement Protein C1q Provides a Basis for Its Versatile Recognition Properties. Journal of Biological Chemistry, 2003, 278, 46974-46982.	1.6	315
287	Structure of a Drosophila Sigma Class Glutathione S-transferase Reveals a Novel Active Site Topography Suited for Lipid Peroxidation Products. Journal of Molecular Biology, 2003, 326, 151-165.	2.0	109
288	Structure and Function of an Archaeal Homolog of Survival Protein E (SurEÎ±): An Acid Phosphatase with Purine Nucleotide Specificity. Journal of Molecular Biology, 2003, 326, 1559-1575.	2.0	28
289	High-resolution X-ray and NMR Structures of the SMN Tudor Domain: Conformational Variation in the Binding Site for Symmetrically Dimethylated Arginine Residues. Journal of Molecular Biology, 2003, 327, 507-520.	2.0	155

#	ARTICLE	IF	CITATIONS
290	Structure and Ligand Binding of Carbohydrate-binding Module CsCBM6-3 Reveals Similarities with Fucose-specific Lectins and â€œGalactose-bindingâ€• Domains. Journal of Molecular Biology, 2003, 327, 659-669.	2.0	65
291	The Active Conformation of Glutamate Synthase and its Binding to Ferredoxin. Journal of Molecular Biology, 2003, 330, 113-128.	2.0	85
292	Crystal Structures of the ATPase Subunit of the Glucose ABC Transporter from Sulfolobus solfataricus: Nucleotide-free and Nucleotide-bound Conformations. Journal of Molecular Biology, 2003, 330, 343-358.	2.0	145
293	The Molecular Basis of Vitamin E Retention: Structure of Human Î±-Tocopherol Transfer Protein. Journal of Molecular Biology, 2003, 331, 725-734.	2.0	133
294	The Structure of the Receptor-binding Domain of the Bacteriophage T4 Short Tail Fibre Reveals a Knitted Trimeric Metal-binding Fold. Journal of Molecular Biology, 2003, 331, 361-373.	2.0	108
295	Crystal Structure of an ADP-dependent Glucokinase from Pyrococcus furiosus: Implications for a Sugar-induced Conformational Change in ADP-dependent Kinase. Journal of Molecular Biology, 2003, 331, 871-883.	2.0	44
296	Structural Analysis of Lipid Complexes of GM2-Activator Protein. Journal of Molecular Biology, 2003, 331, 951-964.	2.0	85
297	The Structural Basis of Receptor-binding by Escherichia coli Associated with Diarrhea and Septicemia. Journal of Molecular Biology, 2003, 331, 897-905.	2.0	44
298	Crystal Structure of Trimestatin, a Disintegrin Containing a Cell Adhesion Recognition Motif RGD. Journal of Molecular Biology, 2003, 332, 1115-1122.	2.0	88
299	Structural basis of calcium and galactose recognition by the lectin PA-IL ofPseudomonas aeruginosa. FEBS Letters, 2003, 555, 297-301.	1.3	175
300	Crystal Structure of Escherichia coli ÏƒE with the Cytoplasmic Domain of Its Anti-Ïƒ RseA. Molecular Cell, 2003, 11, 1067-1078.	4.5	225
301	PB1 Domain-Mediated Heterodimerization in NADPH Oxidase and Signaling Complexes of Atypical Protein Kinase C with Par6 and p62. Molecular Cell, 2003, 12, 39-50.	4.5	183
302	Structural Basis for Arl1-Dependent Targeting of Homodimeric GRIP Domains to the Golgi Apparatus. Molecular Cell, 2003, 12, 863-874.	4.5	135
303	3â€ƒâ€ƒMolecular structure from X-ray diffraction. Annual Reports on the Progress of Chemistry Section C, 2003, 99, 49-86.	4.4	2
304	A Catalytic Mechanism for d-Tyr-tRNATyrDeacylase Based on the Crystal Structure of Hemophilus influenzae HI0670. Journal of Biological Chemistry, 2003, 278, 13496-13502.	1.6	22
305	Moth chemosensory protein exhibits drastic conformational changes and cooperativity on ligand binding. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5069-5074.	3.3	157
306	The Crystal Structure of the Phosphorylation Domain in PhoP Reveals a Functional Tandem Association Mediated by an Asymmetric Interface. Journal of Bacteriology, 2003, 185, 254-261.	1.0	46
307	Crystal Structure of an Archaeal Class I Aldolase and the Evolution of (Î²Î±)8 Barrel Proteins. Journal of Biological Chemistry, 2003, 278, 47253-47260.	1.6	45

#	ARTICLE	IF	CITATIONS
308	X-ray Structure of the Ca2+-binding Interaction Domain of C1s. Journal of Biological Chemistry, 2003, 278, 32157-32164.	1.6	82
309	The Structure of the Periplasmic Ligand-binding Domain of the Sensor Kinase CitA Reveals the First Extracellular PAS Domain. Journal of Biological Chemistry, 2003, 278, 39189-39196.	1.6	126
310	Structural analysis by X-ray crystallography and calorimetry of a haemagglutinin component (HA1) of the progenitor toxin from Clostridium botulinum. Microbiology (United Kingdom), 2003, 149, 3361-3370.	0.7	69
311	Crystal structure of human Â-tocopherol transfer protein bound to its ligand: Implications for ataxia with vitamin E deficiency. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14713-14718.	3.3	121
312	Structure of a cholesterol-binding protein deficient in Niemann-Pick type C2 disease. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2512-2517.	3.3	288
313	Crystal Structure of Rice Î±-Galactosidase Complexed with D-Galactose. Journal of Biological Chemistry, 2003, 278, 20313-20318.	1.6	102
314	Candida tropicalis Expresses Two Mitochondrial 2-Enoyl Thioester Reductases That Are Able to Form Both Homodimers and Heterodimers. Journal of Biological Chemistry, 2003, 278, 41213-41220.	1.6	28
315	Cytochrome c Nitrite Reductase from Desulfovibrio desulfuricans ATCC 27774. Journal of Biological Chemistry, 2003, 278, 17455-17465.	1.6	98
316	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. Journal of Biological Chemistry, 2003, 278, 50371-50376.	1.6	64
317	The Crystal Structure of the Escherichia coli YfdW Gene Product Reveals a New Fold of Two Interlaced Rings Identifying a Wide Family of CoA Transferases. Journal of Biological Chemistry, 2003, 278, 34582-34586.	1.6	34
318	Structural basis for specific binding of Polycomb chromodomain to histone H3 methylated at Lys 27. Genes and Development, 2003, 17, 1823-1828.	2.7	567
319	The 2-Ã… Crystal Structure of 6-Oxo Camphor Hydrolase. Journal of Biological Chemistry, 2003, 278, 1744-1750.	1.6	25
320	Crystal Structure of Mg2+- and Ca2+-bound Gla Domain of Factor IX Complexed with Binding Protein. Journal of Biological Chemistry, 2003, 278, 24090-24094.	1.6	84
321	Structures of Shikimate Dehydrogenase AroE and Its Paralog YdiB. Journal of Biological Chemistry, 2003, 278, 19463-19472.	1.6	111
322	The Sequence and Crystal Structure of the Î±-Amino Acid Ester Hydrolase from Xanthomonas citri Define a New Family of Î²-Lactam Antibiotic Acylases. Journal of Biological Chemistry, 2003, 278, 23076-23084.	1.6	37
323	Crystal Structure of Aclacinomycin Methylesterase with Bound Product Analogues. Journal of Biological Chemistry, 2003, 278, 39006-39013.	1.6	31
324	The Evolutionarily Conserved Trimeric Structure of CutA1 Proteins Suggests a Role in Signal Transduction. Journal of Biological Chemistry, 2003, 278, 45999-46006.	1.6	52
325	Trypsin Revisited. Journal of Biological Chemistry, 2003, 278, 43357-43362.	1.6	57

#	Article	IF	Citations
326	Crystal Structure of the Human Centromere Protein B (CENP-B) Dimerization Domain at 1.65-Ã… Resolution. Journal of Biological Chemistry, 2003, 278, 51454-51461.	1.6	26
327	Crystal Structure of Enterococcus faecalis SlyA-like Transcriptional Factor. Journal of Biological Chemistry, 2003, 278, 20240-20244.	1.6	65
328	From Clone to Crystal: Maximizing the Amount of Protein Samples for Structure Determination. Advances in Protein Chemistry, 2003, 65, 343-352.	4.4	1
329	Crystal structure of the tyrosine kinase domain of the hepatocyte growth factor receptor c-Met and its complex with the microbial alkaloid K-252a. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12654-12659.	3.3	137
330	High-resolution structure of RNase P protein from Thermotoga maritima. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7497-7502.	3.3	87
331	High Resolution Crystal Structures of Siglec-7. Journal of Biological Chemistry, 2003, 278, 3372-3377.	1.6	109
332	SOLVE and RESOLVE: Automated Structure Solution and Density Modification. Methods in Enzymology, 2003, 374, 22-37.	0.4	450
333	Molecular basis for the discrimination of repressive methyl-lysine marks in histone H3 by Polycomb and HP1 chromodomains. Genes and Development, 2003, 17, 1870-1881.	2.7	861
334	Essential Roles of Zinc Ligation and Enzyme Dimerization for Catalysis in the Aminoacylase-1/M20 Family. Journal of Biological Chemistry, 2003, 278, 44496-44504.	1.6	74
335	Crystal Structure and Functional Analysis of Drosophila Wind, a Protein-disulfide Isomerase-related Protein. Journal of Biological Chemistry, 2003, 278, 44600-44607.	1.6	34
336	The Crystal Structure of a Cockroach Pheromone-binding Protein Suggests a New Ligand Binding and Release Mechanism. Journal of Biological Chemistry, 2003, 278, 30213-30218.	1.6	115
337	The Crystal Structure of 1-D-myo-Inosityl 2-Acetamido-2-deoxy-Î±-D-glucopyranoside Deacetylase (MshB) from Mycobacterium tuberculosis Reveals a Zinc Hydrolase with a Lactate Dehydrogenase Fold. Journal of Biological Chemistry, 2003, 278, 47166-47170.	1.6	71
338	Structural Studies of Molybdopterin Synthase Provide Insights into Its Catalytic Mechanism. Journal of Biological Chemistry, 2003, 278, 14514-14522.	1.6	45
339	The Staphostatin-Staphopain Complex. Journal of Biological Chemistry, 2003, 278, 40959-40966.	1.6	59
340	Crystal Structures of the Liganded and Unliganded Nickel-binding Protein NikA from Escherichia coli. Journal of Biological Chemistry, 2003, 278, 50322-50329.	1.6	77
341	Crystal Structures of Engrailed Homeodomain Mutants. Journal of Biological Chemistry, 2003, 278, 43699-43708.	1.6	39
342	Biosynthesis of isoprenoids: Crystal structure of 4-diphosphocytidyl-2C-methyl-D-erythritol kinase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9173-9178.	3.3	96
343	Crystal structures that suggest late development of genetic code components for differentiating aromatic side chains. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15376-15380.	3.3	86

#	Article	IF	Citations
344	Crystal Structure of a Bacterial Endospore Coat Component. Journal of Biological Chemistry, 2003, 278, 19416-19425.	1.6	322
345	Integrating Structure, Bioinformatics, and Enzymology to Discover Function. Journal of Biological Chemistry, 2003, 278, 26039-26045.	1.6	115
346	Structural Basis for Catalysis and Substrate Specificity of Agrobacterium radiobacter N-Carbamoyl-D-amino Acid Amidohydrolase. Journal of Biological Chemistry, 2003, 278, 26194-26201.	1.6	27
347	A mechanism of covalent substrate binding in the x-ray structure of subunit K of theEscherichia colidihydroxyacetone kinase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8188-8192.	3.3	38
348	Crystal Structure of the Measles Virus Phosphoprotein Domain Responsible for the Induced Folding of the C-terminal Domain of the Nucleoprotein. Journal of Biological Chemistry, 2003, 278, 44567-44573.	1.6	143
349	Structural and EPR Characterization of the Soluble Form of Cytochrome c-550 and of the psbV2 Gene Product from the Cyanobacterium Thermosynechococcus elongatus. Plant and Cell Physiology, 2003, 44, 697-706.	1.5	39
350	Crystal Structure of Fungal Lectin. Journal of Biological Chemistry, 2003, 278, 27059-27067.	1.6	164
351	Structural Analysis of the Domain Interface in DrrB, a Response Regulator of the OmpR/PhoB Subfamily. Journal of Bacteriology, 2003, 185, 4186-4194.	1.0	97
352	ARPâ§¸wARP and Automatic Interpretation of Protein Electron Density Maps. Methods in Enzymology, 2003, 374, 229-244.	0.4	482
353	The Î±-Glucuronidase, GlcA67A, of Cellvibrio japonicus Utilizes the Carboxylate and Methyl Groups of Aldobiouronic Acid as Important Substrate Recognition Determinants. Journal of Biological Chemistry, 2003, 278, 20286-20292.	1.6	32
354	Structural and functional features of theEscherichia colihydroperoxide resistance protein OsmC. Protein Science, 2003, 12, 2838-2843.	3.1	106
355	Automatic Solution of Heavy-Atom Substructures. Methods in Enzymology, 2003, 374, 37-83.	0.4	34
356	Phasing on Rapidly Soaked Ions. Methods in Enzymology, 2003, 374, 120-137.	0.4	18
357	TEXTAL System: Artificial Intelligence Techniques for Automated Protein Model Building. Methods in Enzymology, 2003, 374, 244-270.	0.4	45
358	Applications for Macromolecular Map Interpretation: X-AUTOFIT, X-POWERFIT, X-BUILD, X-LIGAND, and X-SOLVATE. Methods in Enzymology, 2003, 374, 271-300.	0.4	6
359	Protein Structures at Atomic Resolution. Methods in Enzymology, 2003, 368, 288-337.	0.4	17
360	Binding of phosphatidylinositol 3,4,5-trisphosphate to the pleckstrin homology domain of protein kinase B induces a conformational change. Biochemical Journal, 2003, 375, 531-538.	1.7	243
361	Prospects for High-Throughput Structure Determination by X-Ray Crystallography. , 2003, , 55-94.		0

#	ARTICLE	IF	CITATIONS
362	Crystal structure of a Baeyer-Villiger monooxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13157-13162.	3.3	267
363	Crystal structure of archaeal ribonuclease P protein Ph1771p from Pyrococcus horikoshii OT3: An archaeal homolog of eukaryotic ribonuclease P protein Rpp29. Rna, 2004, 10, 1423-1432.	1.6	38
364	The Crystal Structure of Escherichia coli MoaB Suggests a Probable Role in Molybdenum Cofactor Synthesis. Journal of Biological Chemistry, 2004, 279, 42139-42146.	1.6	18
365	Structural Basis for the Binding of Compatible Solutes by ProX from the Hyperthermophilic Archaeon Archaeoglobus fulgidus. Journal of Biological Chemistry, 2004, 279, 48270-48281.	1.6	58
366	The Crystal Structure of the Calystegia sepium Agglutinin Reveals a Novel Quaternary Arrangement of Lectin Subunits with a Î²-Prism Fold. Journal of Biological Chemistry, 2004, 279, 527-533.	1.6	54
367	Sulfur Single-wavelength Anomalous Diffraction Crystal Structure of a Pheromone-Binding Protein from the Honeybee Apis mellifera L. Journal of Biological Chemistry, 2004, 279, 4459-4464.	1.6	98
368	Crystallographic and Mutational Data Show That the Streptococcal Pyrogenic Exotoxin J Can Use a Common Binding Surface for T-cell Receptor Binding and Dimerization. Journal of Biological Chemistry, 2004, 279, 38571-38576.	1.6	18
369	The Structure of the MAPK Scaffold, MP1, Bound to Its Partner, p14. Journal of Biological Chemistry, 2004, 279, 23422-23430.	1.6	62
370	Structure and Assembly of the RNA Binding Domain of Bluetongue Virus Non-structural Protein 2. Journal of Biological Chemistry, 2004, 279, 37613-37621.	1.6	24
371	Crystal Structure of the Quorum-sensing Protein TraM and Its Interaction with the Transcriptional Regulator TraR. Journal of Biological Chemistry, 2004, 279, 24291-24296.	1.6	35
372	A Two-domain Structure of One Subunit Explains Unique Features of Eukaryotic Hydratase 2. Journal of Biological Chemistry, 2004, 279, 24666-24672.	1.6	56
373	Structure of a proteolytically resistant core from the severe acute respiratory syndrome coronavirus S2 fusion protein. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17958-17963.	3.3	109
374	T Cell Cross-Reactivity and Conformational Changes during TCR Engagement. Journal of Experimental Medicine, 2004, 200, 1455-1466.	4.2	159
375	Crystal Structure of Human Pirin. Journal of Biological Chemistry, 2004, 279, 1491-1498.	1.6	88
376	Crystal Structures of the Multispecific 17Î²-Hydroxysteroid Dehydrogenase Type 5: Critical Androgen Regulation in Human Peripheral Tissues. Molecular Endocrinology, 2004, 18, 1798-1807.	3.7	72
377	The Structure of the Organic Hydroperoxide Resistance Protein from Deinococcus radiodurans. Journal of Biological Chemistry, 2004, 279, 25830-25837.	1.6	36
378	Structure of the Catalytic Fragment of Translation Initiation Factor 2B and Identification of a Critically Important Catalytic Residue. Journal of Biological Chemistry, 2004, 279, 10584-10592.	1.6	62
379	Crystal Structure of the Bifunctional Chorismate Synthase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 619-625.	1.6	29

#	Article	IF	Citations
380	The thrH Gene Product of Pseudomonas aeruginosa Is a Dual Activity Enzyme with a Novel Phosphoserine:Homoserine Phosphotransferase Activity. Journal of Biological Chemistry, 2004, 279, 13166-13173.	1.6	20
381	Unique Features of the sodC-encoded Superoxide Dismutase from Mycobacterium tuberculosis, a Fully Functional Copper-containing Enzyme Lacking Zinc in the Active Site. Journal of Biological Chemistry, 2004, 279, 33447-33455.	1.6	81
382	Crystal Structure of Yeast Ypr118w, a Methylthioribose-1-phosphate Isomerase Related to Regulatory eIF2B Subunits. Journal of Biological Chemistry, 2004, 279, 37087-37094.	1.6	30
383	Crystal structure of elongation factor P from Thermus thermophilus HB8. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9595-9600.	3.3	102
384	The crystal structure of filamentous hemagglutinin secretion domain and its implications for the two-partner secretion pathway. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6194-6199.	3.3	146
385	The Crystal Structure of Gankyrin, an Oncoprotein Found in Complexes with Cyclin-dependent Kinase 4, a 19 S Proteasomal ATPase Regulator, and the Tumor Suppressors Rb and p53. Journal of Biological Chemistry, 2004, 279, 1541-1545.	1.6	81
386	Structural Insights into Endosomal Sorting Complex Required for Transport (ESCRT-I) Recognition of Ubiquitinated Proteins. Journal of Biological Chemistry, 2004, 279, 28689-28696.	1.6	120
387	Crystal Structure of a Ternary Complex of DnrK, a Methyltransferase in Daunorubicin Biosynthesis, with Bound Products. Journal of Biological Chemistry, 2004, 279, 41149-41156.	1.6	57
388	Structural Insights into Substrate Specificity and Function of Glucodextranase. Journal of Biological Chemistry, 2004, 279, 10575-10583.	1.6	43
389	Structural Studies on Flavin Reductase PheA2 Reveal Binding of NAD in an Unusual Folded Conformation and Support Novel Mechanism of Action. Journal of Biological Chemistry, 2004, 279, 12860-12867.	1.6	69
390	Substrate-induced Conformational Changes in Human UMP/CMP Kinase. Journal of Biological Chemistry, 2004, 279, 33882-33889.	1.6	42
391	Crystal Structure of a Dodecameric Tetrahedral-shaped Aminopeptidase. Journal of Biological Chemistry, 2004, 279, 51275-51281.	1.6	52
392	The C-terminal Basic Tail of RhoG Assists the Guanine Nucleotide Exchange Factor Trio in Binding to Phospholipids. Journal of Biological Chemistry, 2004, 279, 37895-37907.	1.6	46
393	The Structure and Mechanism of Serine Acetyltransferase from Escherichia coli. Journal of Biological Chemistry, 2004, 279, 40729-40736.	1.6	92
394	Structure of Mouse Golgi Î±-Mannosidase IA Reveals the Molecular Basis for Substrate Specificity among Class 1 (Family 47 Glycosylhydrolase) Î±1,2-Mannosidases. Journal of Biological Chemistry, 2004, 279, 29774-29786.	1.6	48
395	Gram-positive DsbE Proteins Function Differently from Gram-negative DsbE Homologs. Journal of Biological Chemistry, 2004, 279, 3516-3524.	1.6	75
396	Identification of Functional Residues on Caenorhabditis elegans Actin-interacting Protein 1 (UNC-78) for Disassembly of Actin Depolymerizing Factor/Cofilin-bound Actin Filaments. Journal of Biological Chemistry, 2004, 279, 31697-31707.	1.6	70
397	Dual, HLA-B27 Subtype-dependent Conformation of a Self-peptide. Journal of Experimental Medicine, 2004, 199, 271-281.	4.2	144

#	ARTICLE	IF	CITATIONS
398	Crystal structure of a human CD3-Â/Â dimer in complex with a UCHT1 single-chain antibody fragment. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16268-16273.	3.3	132
399	The molecular structure and catalytic mechanism of a novel carboxyl peptidase from Scytalidium lignicolum. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3364-3369.	3.3	96
400	Crystal structure of the S-adenosylmethionine-dependent enzyme MoaA and its implications for molybdenum cofactor deficiency in humans. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12870-12875.	3.3	235
401	Crystal structures of the DsbG disulfide isomerase reveal an unstable disulfide. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8876-8881.	3.3	95
402	Substrate recognition and catalysis by the Holliday junction resolving enzyme Hje. Nucleic Acids Research, 2004, 32, 5442-5451.	6.5	41
403	The Family 11 Carbohydrate-binding Module of Clostridium thermocellum Lic26A-Cel5E Accommodates Î²-1,4- and Î²-1,3â€“1,4-Mixed Linked Glucans at a Single Binding Site. Journal of Biological Chemistry, 2004, 279, 34785-34793.	1.6	95
404	Hexameric Assembly of the Bifunctional Methylerythritol 2,4-Cyclodiphosphate Synthase and Protein-Protein Associations in the Deoxy-xylulose-dependent Pathway of Isoprenoid Precursor Biosynthesis. Journal of Biological Chemistry, 2004, 279, 52753-52761.	1.6	43
405	Crystal structure of the von Willebrand factor A domain of human capillary morphogenesis protein 2: An anthrax toxin receptor. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6367-6372.	3.3	117
406	Structural Basis of 5-Nitroimidazole Antibiotic Resistance. Journal of Biological Chemistry, 2004, 279, 55840-55849.	1.6	71
407	In different organisms, the mode of interaction between two signaling proteins is not necessarily conserved. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11646-11651.	3.3	53
408	Crystal Structure of Species D Adenovirus Fiber Knobs and Their Sialic Acid Binding Sites. Journal of Virology, 2004, 78, 7727-7736.	1.5	156
409	Insights into the Molecular Determinants of Substrate Specificity in Glycoside Hydrolase Family 5 Revealed by the Crystal Structure and Kinetics of Cellvibrio mixtus Mannosidase 5A. Journal of Biological Chemistry, 2004, 279, 25517-25526.	1.6	91
410	Structural Basis for the Inhibitory Role of Tomosyn in Exocytosis. Journal of Biological Chemistry, 2004, 279, 47192-47200.	1.6	100
411	Xâ€ray diffraction structure of a plant glycosyl hydrolase family 32 protein: fructan 1â€exohydrolase IIa of<i>Cichorium intybus</i>. Plant Journal, 2005, 41, 400-411.	2.8	107
412	A new Ralstonia solanacearum high-affinity mannose-binding lectin RS-IIL structurally resembling the Pseudomonas aeruginosa fucose-specific lectin PA-IIL. Molecular Microbiology, 2004, 52, 691-700.	1.2	70
413	Structure and assembly of the pseudopilin PulG. Molecular Microbiology, 2004, 54, 647-664.	1.2	96
414	Regulation of the hetero-octameric ATP phosphoribosyl transferase complex from Thermotoga maritima by a tRNA synthetase-like subunit. Molecular Microbiology, 2004, 55, 675-686.	1.2	28
415	The Yersinia adhesin YadA collagen-binding domain structure is a novel left-handed parallel Î²-roll. EMBO Journal, 2004, 23, 701-711.	3.5	175

#	Article	IF	Citations
416	Structural inhibition of the colicin D tRNase by the tRNA-mimicking immunity protein. EMBO Journal, 2004, 23, 1474-1482.	3.5	85
417	Structure of the polyketide cyclase SnoaL reveals a novel mechanism for enzymatic aldol condensation. EMBO Journal, 2004, 23, 1911-1921.	3.5	119
418	A new Î±-helical extension promotes RNA binding by the dsRBD of Rnt1p RNAse III. EMBO Journal, 2004, 23, 2468-2477.	3.5	56
419	Structural basis for L27 domain-mediated assembly of signaling and cell polarity complexes. EMBO Journal, 2004, 23, 2723-2733.	3.5	38
420	Crystal structure of the nuclear effector of Notch signaling, CSL, bound to DNA. EMBO Journal, 2004, 23, 3441-3451.	3.5	141
421	Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. EMBO Journal, 2004, 23, 3632-3642.	3.5	37
422	Tandem LIM domains provide synergistic binding in the LMO4:Ldb1 complex. EMBO Journal, 2004, 23, 3589-3598.	3.5	84
423	Structure of the conserved domain of ANAC, a member of the NAC family of transcription factors. EMBO Reports, 2004, 5, 297-303.	2.0	388
424	Crystal structure of the PsbP protein of photosystem II from Nicotiana tabacum. EMBO Reports, 2004, 5, 362-367.	2.0	99
425	Crystal structure of human otubain 2. EMBO Reports, 2004, 5, 783-788.	2.0	73
426	Crystal structure of MO25Î± in complex with the C terminus of the pseudo kinase STE20-related adaptor. Nature Structural and Molecular Biology, 2004, 11, 193-200.	3.6	62
427	Structural basis of sugar-recognizing ubiquitin ligase. Nature Structural and Molecular Biology, 2004, 11, 365-370.	3.6	82
428	The structural basis for the interaction between nonsense-mediated mRNA decay factors UPF2 and UPF3. Nature Structural and Molecular Biology, 2004, 11, 330-337.	3.6	168
429	Crystal structure of the C-terminal clock-oscillator domain of the cyanobacterial KaiA protein. Nature Structural and Molecular Biology, 2004, 11, 623-631.	3.6	76
430	Structure of the bacterial flagellar hook and implication for the molecular universal joint mechanism. Nature, 2004, 431, 1062-1068.	13.7	176
431	Structural basis for the assembly of a nuclear export complex. Nature, 2004, 432, 872-877.	13.7	188
432	Architecture of NarGH Reveals a Structural Classification of Mo-bisMGD Enzymes. Structure, 2004, 12, 95-104.	1.6	199
433	Crystal Structures of Weissella viridescens FemX and Its Complex with UDP-MurNAc-Pentapeptide: Insights into FemABX Family Substrates Recognition. Structure, 2004, 12, 257-267.	1.6	71

#	ARTICLE	IF	CITATIONS
434	Crystal Structure of RumA, an Iron-Sulfur Cluster Containing E. coli Ribosomal RNA 5-Methyluridine Methyltransferase. Structure, 2004, 12, 397-407.	1.6	40
435	Crystal Structures of Arginine Deiminase with Covalent Reaction Intermediates. Structure, 2004, 12, 657-667.	1.6	90
436	Structural Insights into the Catalytic Mechanism of Trypanosoma cruzi trans-Sialidase. Structure, 2004, 12, 775-784.	1.6	197
437	The Structure of MSK1 Reveals a Novel Autoinhibitory Conformation for a Dual Kinase Protein. Structure, 2004, 12, 1067-1077.	1.6	42
438	Aspergillus niger Protein EstA Defines a New Class of Fungal Esterases within the Î±/Î² Hydrolase Fold Superfamily of Proteins. Structure, 2004, 12, 677-687.	1.6	29
439	Crystal Structure of Phosphotransacetylase from the Methanogenic Archaeon Methanosarcina thermophila. Structure, 2004, 12, 559-567.	1.6	30
440	Crystal Structure to 1.7 Ã… of the Escherichia coli Pyrimidine Nucleoside Hydrolase YeiK, a Novel Candidate for Cancer Gene Therapy. Structure, 2004, 12, 739-749.	1.6	42
441	The Structure of the N-Terminal Domain of the Product of the Lissencephaly Gene Lis1 and Its Functional Implications. Structure, 2004, 12, 987-998.	1.6	106
442	The First Crystal Structure of the Novel Class of Fructose-1,6-Bisphosphatase Present in Thermophilic Archaea. Structure, 2004, 12, 949-959.	1.6	34
443	Chitobiose Phosphorylase from Vibrio proteolyticus, a Member of Glycosyl Transferase Family 36, Has a Clan GH-L-like (Î±/Î±)6 Barrel Fold. Structure, 2004, 12, 937-947.	1.6	96
444	Crystal Structure of the Kinase Domain of WNK1, a Kinase that Causes a Hereditary Form of Hypertension. Structure, 2004, 12, 1303-1311.	1.6	179
445	Ab Initio Structure Determination and Functional Characterization Of CBM36. Structure, 2004, 12, 1177-1187.	1.6	76
446	Crystal Structure of an Acylpeptide Hydrolase/Esterase from Aeropyrum pernix K1. Structure, 2004, 12, 1481-1488.	1.6	73
447	Crystal Structure of A. fulgidus Rio2 Defines a New Family of Serine Protein Kinases. Structure, 2004, 12, 1585-1594.	1.6	72
448	The Crystal Structure of the Reduced, Zn2+-Bound Form of the B. subtilis Hsp33 Chaperone and Its Implications for the Activation Mechanism. Structure, 2004, 12, 1901-1907.	1.6	77
449	A Novel Structure of DNA Repair Protein RecO from Deinococcus radiodurans. Structure, 2004, 12, 1881-1889.	1.6	60
451	The structure of Ski8p, a protein regulating mRNA degradation: Implications for WD protein structure. Protein Science, 2004, 13, 1557-1565.	3.1	47
452	Crystal structure of the hypothetical protein TA1238 from Thermoplasma acidophilum: a new type of helical super-bundle. Journal of Structural and Functional Genomics, 2004, 5, 231-240.	1.2	7

#	Article	IF	Citations
453	Crystal structure of a tandem cystathionine-Î²-synthase (CBS) domain protein (TM0935) from Thermotoga maritima at 1.87 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2004, 57, 213-217.	1.5	35
454	Crystal structure of E. coli yddE protein reveals a striking homology with diaminopimelate epimerase. Proteins: Structure, Function and Bioinformatics, 2004, 55, 764-767.	1.5	7
455	The 1.59 Ã… resolution crystal structure of TM0096, a flavin mononucleotide binding protein from Thermotoga maritima. Proteins: Structure, Function and Bioinformatics, 2004, 55, 772-774.	1.5	18
456	Crystal structure of a ribose-5-phosphate isomerase RpiB (TM1080) from Thermotoga maritima at 1.90 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2004, 56, 171-175.	1.5	14
457	Novel structure and nucleotide binding properties of HI1480 from Haemophilus influenzae: A protein with no known sequence homologues. Proteins: Structure, Function and Bioinformatics, 2004, 56, 564-571.	1.5	5
458	High affinity fucose binding of Pseudomonas aeruginosa lectin PA-IIL: 1.0 Ã… resolution crystal structure of the complex combined with thermodynamics and computational chemistry approaches. Proteins: Structure, Function and Bioinformatics, 2004, 58, 735-746.	1.5	104
459	Structural genomics of Caenorhabditis elegans: Crystal structure of the tropomodulin C-terminal domain. Proteins: Structure, Function and Bioinformatics, 2004, 56, 384-386.	1.5	14
460	Harvesting the high-hanging fruit: the structure of theYdeNgene product fromBacillus subtilisat 1.8â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1101-1107.	2.5	23
461	SOLVE and RESOLVE: automated structure solution, density modification and model building. Journal of Synchrotron Radiation, 2004, 11, 49-52.	1.0	387
462	Breaking good resolutions with ARP/wARP. Journal of Synchrotron Radiation, 2004, 11, 56-59.	1.0	131
463	3,5-Substituted phenyl galactosides as leads in designing effective cholera toxin antagonists. Bioorganic and Medicinal Chemistry, 2004, 12, 907-920.	1.4	44
464	Nonspanning Bivalent Ligands as Improved Surface Receptor Binding Inhibitors of the Cholera Toxin B Pentamer. Chemistry and Biology, 2004, 11, 1205-1215.	6.2	39
465	Crystal structure of adenine phosphoribosyltransferase from Leishmania tarentolae: potential implications for APRT catalytic mechanism. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1696, 31-39.	1.1	13
466	Crystal Structure of Thermotoga maritima Î±-l-Fucosidase. Journal of Biological Chemistry, 2004, 279, 13119-13128.	1.6	141
467	Designing Sequence to Control Protein Function in an EF-Hand Protein. Journal of the American Chemical Society, 2004, 126, 5990-5998.	6.6	33
468	The use of dummy atoms in X-ray macromolecular crystallography. Crystallography Reviews, 2004, 10, 319-343.	0.4	2
469	Atomic Resolution Structure of the HFBII Hydrophobin, a Self-assembling Amphiphile. Journal of Biological Chemistry, 2004, 279, 534-539.	1.6	205
470	Crystal structure of nickel-containing superoxide dismutase reveals another type of active site. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8569-8574.	3.3	328

#	Article	IF	Citations
471	Structure- and Function-based Characterization of a New Phosphoglycolate Phosphatase from Thermoplasma acidophilum. Journal of Biological Chemistry, 2004, 279, 517-526.	1.6	49
472	The Membrane-Associated Lipoprotein-9 GmpC fromStaphylococcus aureusBinds the Dipeptide GlyMet via Side Chain Interactionsâ€,â€¡. Biochemistry, 2004, 43, 16193-16202.	1.2	28
473	Evolution of Enzymatic Activities in the Orotidine 5â€˜-Monophosphate Decarboxylase Suprafamily:Â Crystallographic Evidence for a Proton Relay System in the Active Site of 3-Keto-l-gulonate 6-Phosphate Decarboxylaseâ€,â€¡. Biochemistry, 2004, 43, 6438-6446.	1.2	16
474	Trapping a 96Â° domain rotation in two distinct conformations by engineered disulfide bridges. Protein Science, 2004, 13, 1811-1822.	3.1	24
475	Crystal Structures of Two Cyanobacterial Response Regulators in Apo- and Phosphorylated Form Reveal a Novel Dimerization Motif of Phytochrome-Associated Response Regulators. Biophysical Journal, 2004, 87, 476-487.	0.2	22
476	Contribution of Single Tryptophan Residues to the Fluorescence and Stability of Ribonuclease Sa. Biophysical Journal, 2004, 87, 4036-4047.	0.2	36
477	Protein crystallography at subatomic resolution. Reports on Progress in Physics, 2004, 67, 1565-1605.	8.1	42
478	Atomic Snapshots of an RNA Packaging Motor Reveal Conformational Changes Linking ATP Hydrolysis to RNA Translocation. Cell, 2004, 118, 743-755.	13.5	151
479	High-throughput X-ray crystallography for drug discovery. Current Opinion in Pharmacology, 2004, 4, 490-496.	1.7	106
480	X-ray structure of tRNA pseudouridine synthase TruD reveals an inserted domain with a novel fold. FEBS Letters, 2004, 565, 59-64.	1.3	29
481	Structures ofBacillus subtilisPdaA, a family 4 carbohydrate esterase, and a complex withN-acetyl-glucosamine. FEBS Letters, 2004, 570, 13-19.	1.3	83
482	Crystal structure of the regulatory subunit of archaeal initiation factor 2B (aIF2B) from hyperthermophilic archaeon Pyrococcus horikoshii OT3: a proposed structure of the regulatory subcomplex of eukaryotic IF2B. Biochemical and Biophysical Research Communications, 2004, 319, 725-732.	1.0	24
483	1.42Ã… crystal structure of mini-IGF-1(2): an analysis of the disulfide isomerization property and receptor binding property of IGF-1 based on the three-dimensional structure. Biochemical and Biophysical Research Communications, 2004, 326, 52-59.	1.0	3
484	Structure of a knockout mutant of influenza virus M1 protein that has altered activities in membrane binding, oligomerisation and binding to NEP (NS2). Virus Research, 2004, 99, 115-119.	1.1	24
485	Crystal structure of the AAA+ Î± domain of E. coli Lon protease at 1.9Ã… resolution. Journal of Structural Biology, 2004, 146, 113-122.	1.3	84
486	Crystal structure of Bacillus subtilis YckF: structural and functional evolution. Journal of Structural Biology, 2004, 148, 98-109.	1.3	9
487	Crystal Structure of the RluD Pseudouridine Synthase Catalytic Module, an Enzyme that Modifies 23S rRNA and is Essential for Normal Cell Growth of Escherichia coli. Journal of Molecular Biology, 2004, 335, 87-101.	2.0	38
488	Crystal Structure of Echicetin from Echis carinatus (Indian Saw-scaled Viper) at 2.4Ã… Resolution. Journal of Molecular Biology, 2004, 335, 167-176.	2.0	24

#	ARTICLE	IF	CITATIONS
489	The First Structure of a Bacterial Class B Acid Phosphatase Reveals Further Structural Heterogeneity Among Phosphatases of the Haloacid Dehalogenase Fold. Journal of Molecular Biology, 2004, 335, 761-773.	2.0	27
490	Crystal Structure of MshB from Mycobacterium tuberculosis , a Deacetylase Involved in Mycothiol Biosynthesis. Journal of Molecular Biology, 2004, 335, 1131-1141.	2.0	63
491	Structure of the NCoA-1/SRC-1 PAS-B Domain Bound to the LXXLL Motif of the STAT6 Transactivation Domain. Journal of Molecular Biology, 2004, 336, 319-329.	2.0	69
492	Structural Studies of the Nudix Hydrolase DR1025 From Deinococcus radiodurans and its Ligand Complexes. Journal of Molecular Biology, 2004, 339, 103-116.	2.0	25
493	Crystal Structure of a Dimeric Oxidized form of Human Peroxiredoxin 5. Journal of Molecular Biology, 2004, 337, 1079-1090.	2.0	77
494	Crystal Structure of IscA, an Iron-sulfur Cluster Assembly Protein from Escherichia coli. Journal of Molecular Biology, 2004, 338, 127-137.	2.0	82
495	Crystal Structure of Î±-Galactosidase from Trichoderma reesei and Its Complex with Galactose: Implications for Catalytic Mechanism. Journal of Molecular Biology, 2004, 339, 413-422.	2.0	69
496	X-ray Crystal Structure of a Non-crystalline Cellulose-specific Carbohydrate-binding Module: CBM28. Journal of Molecular Biology, 2004, 339, 253-258.	2.0	32
497	Crystal Structure of the TetR/CamR Family Repressor Mycobacterium tuberculosis EthR Implicated in Ethionamide Resistance. Journal of Molecular Biology, 2004, 340, 1095-1105.	2.0	99
498	Crystal Structure of the 270 kDa Homotetrameric Lignin-degrading Enzyme Pyranose 2-Oxidase. Journal of Molecular Biology, 2004, 341, 781-796.	2.0	117
499	Crystal Structure of Schistatin, a Disintegrin Homodimer from Saw-scaled Viper (Echis carinatus) at 2.5Å… Resolution. Journal of Molecular Biology, 2004, 341, 829-837.	2.0	50
500	Crystal Structure of Aspartic Proteinase from Irpex lacteus in Complex with Inhibitor Pepstatin. Journal of Molecular Biology, 2004, 341, 1227-1235.	2.0	26
501	Structures of Michaelis and Product Complexes of Plant Cytokinin Dehydrogenase: Implications for Flavoenzyme Catalysis. Journal of Molecular Biology, 2004, 341, 1237-1249.	2.0	73
502	Structural Basis for Catalytic Racemization and Substrate Specificity of an N-Acylamino Acid Racemase Homologue from Deinococcus radiodurans. Journal of Molecular Biology, 2004, 342, 155-169.	2.0	24
503	Crystal Structure of the Molecular Chaperone HscA Substrate Binding Domain Complexed with the IscU Recognition Peptide ELPPVKIHC. Journal of Molecular Biology, 2004, 342, 1265-1278.	2.0	90
504	Crystal Structure of E.coli Alcohol Dehydrogenase YqhD: Evidence of a Covalently Modified NADP Coenzyme. Journal of Molecular Biology, 2004, 342, 489-502.	2.0	92
505	The 1.3Å… Crystal Structure of Human Mitochondrial Î”3-Î”2-Enoyl-CoA Isomerase Shows a Novel Mode of Binding for the Fatty Acyl Group. Journal of Molecular Biology, 2004, 342, 1197-1208.	2.0	42
506	The Crystal Structure of a Complex of Campylobacter jejuni dUTPase with Substrate Analogue Sheds Light on the Mechanism and Suggests the â€œBasic Moduleâ€•for Dimeric d(C/U)TPases. Journal of Molecular Biology, 2004, 342, 1583-1597.	2.0	57

#	ARTICLE	IF	CITATIONS
507	The Structure and Ligand Binding Properties of the B.subtilis YkoF Gene Product, a Member of a Novel Family of Thiamin/HMP-binding Proteins. Journal of Molecular Biology, 2004, 343, 395-406.	2.0	43
508	High Resolution Crystal Structure of a Key Editosome Enzyme from Trypanosoma brucei: RNA Editing Ligase 1. Journal of Molecular Biology, 2004, 343, 601-613.	2.0	83
509	Crystal Structures and Electron Micrographs of Fungal Volvatoxin A2. Journal of Molecular Biology, 2004, 343, 477-491.	2.0	32
510	Crystallographic Structure of the Nuclease Domain of 3â€²hExo, a DEDDh Family Member, Bound to rAMP. Journal of Molecular Biology, 2004, 343, 305-312.	2.0	42
511	The Structures of Inhibitor Complexes of Pyrococcus furiosus Phosphoglucose Isomerase Provide Insights into Substrate Binding and Catalysis. Journal of Molecular Biology, 2004, 343, 649-657.	2.0	19
512	Structure and Function of the C-terminal Domain of the Polymerase Cofactor of Rabies Virus. Journal of Molecular Biology, 2004, 343, 819-831.	2.0	97
513	Crystal Structures of Î²-Galactosidase from Penicillium sp. and its Complex with Galactose. Journal of Molecular Biology, 2004, 343, 1281-1292.	2.0	83
514	Independent Movement, Dimerization and Stability of Tandem Repeats of Chicken Brain Î±-Spectrin. Journal of Molecular Biology, 2004, 344, 495-511.	2.0	97
515	Crystal Structure of Exo-inulinase from Aspergillus awamori: The Enzyme Fold and Structural Determinants of Substrate Recognition. Journal of Molecular Biology, 2004, 344, 471-480.	2.0	141
516	Crystal Structure of the Pyrococcus horikoshii Isopropylmalate Isomerase Small Subunit Provides Insight into the Dual Substrate Specificity of the Enzyme. Journal of Molecular Biology, 2004, 344, 325-333.	2.0	52
517	Alanyl-tRNA Synthetase Crystal Structure and Design for Acceptor-Stem Recognition. Molecular Cell, 2004, 13, 829-841.	4.5	50
518	Crystal Structure of the Flagellar Ïƒ/Anti-Ïƒ Complex Ïƒ28/FlgM Reveals an Intact Ïƒ Factor in an Inactive Conformation. Molecular Cell, 2004, 14, 127-138.	4.5	106
519	Crystal Structure and Functional Analysis of the Eukaryotic Class II Release Factor eRF3 from S. pombe. Molecular Cell, 2004, 14, 233-245.	4.5	112
520	The crystal structure of the Escherichia coli lipocalin Blc suggests a possible role in phospholipid binding. FEBS Letters, 2004, 562, 183-188.	1.3	45
521	High-resolution Crystal Structures of Caldicellulosiruptor Strain Rt8B.4 Carbohydrate-binding Module CBM27-1 and its Complex with Mannohexaose. Journal of Molecular Biology, 2004, 340, 543-554.	2.0	17
523	Crystal structure of the proximal BAH domain of the polybromo protein. Biochemical Journal, 2005, 389, 657-664.	1.7	23
524	High Throughput Protein Crystallography. , 2005, , 61-104.		1
525	Crystal structure of azoreductase AzoR from Escherichia coli. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2005, 81, 225-228.	1.6	4

#	Article	IF	Citations
526	Crystal structure of the short-chain flavin reductase HpaC from Sulfolobus tokodaii strain 7. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2005, 81, 229-232.	1.6	0
527	Crystal structure of glutamine amidotransferase from Pyrococcus horikoshii OT3. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2005, 81, 459-462.	1.6	3
528	Developments on methods of solving crystal structures. Science and Technology of Advanced Materials, 2005, 6, 722-724.	2.8	0
529	Structure and mechanism of ADP-ribose-1''-monophosphatase (Appr-1''-pase), a ubiquitous cellular processing enzyme. Protein Science, 2005, 14, 719-726.	3.1	36
530	Crystal structure ofYersinia enterocoliticatype III secretion chaperone SycT. Protein Science, 2005, 14, 1993-2002.	3.1	30
531	Crystal structures of the tryptophan repressor binding protein WrbA and complexes with flavin mononucleotide. Protein Science, 2005, 14, 3004-3012.	3.1	23
532	The crystal structure of a novel SAM-dependent methyltransferase PH1915 fromPyrococcus horikoshii. Protein Science, 2005, 14, 3121-3128.	3.1	11
533	Insights into voltage-gated calcium channel regulation from the structure of the CaV1.2 IQ domainâ€"Ca2+/calmodulin complex. Nature Structural and Molecular Biology, 2005, 12, 1108-1115.	3.6	221
534	Crystal structure of the polysialic acidâ€"degrading endosialidase of bacteriophage K1F. Nature Structural and Molecular Biology, 2005, 12, 90-96.	3.6	180
535	SUMO modification of the ubiquitin-conjugating enzyme E2-25K. Nature Structural and Molecular Biology, 2005, 12, 264-269.	3.6	175
536	Crystal structure of nicotinic acetylcholine receptor homolog AChBP in complex with an Î±-conotoxin PnIA variant. Nature Structural and Molecular Biology, 2005, 12, 582-588.	3.6	311
537	Structure of palmitoylated BET3: insights into TRAPP complex assembly and membrane localization. EMBO Journal, 2005, 24, 875-884.	3.5	57
538	Structural insights into the first incision reaction during nucleotide excision repair. EMBO Journal, 2005, 24, 885-894.	3.5	84
539	Crystal structure and DNA-binding analysis of RecO from Deinococcus radiodurans. EMBO Journal, 2005, 24, 906-918.	3.5	67
540	Dual-mode recognition of noncanonical tRNAsSer by seryl-tRNA synthetase in mammalian mitochondria. EMBO Journal, 2005, 24, 3369-3379.	3.5	88
541	Crystal structure of the C3botâ€"RalA complex reveals a novel type of action of a bacterial exoenzyme. EMBO Journal, 2005, 24, 3670-3680.	3.5	38
542	Structures of Aplysia AChBP complexes with nicotinic agonists and antagonists reveal distinctive binding interfaces and conformations. EMBO Journal, 2005, 24, 3635-3646.	3.5	602
543	Nup50/Npap60 function in nuclear protein import complex disassembly and importin recycling. EMBO Journal, 2005, 24, 3681-3689.	3.5	134

#	ARTICLE	IF	CITATIONS
544	Structural basis for UTP specificity of RNA editing TUTases fromTrypanosoma brucei. EMBO Journal, 2005, 24, 4007-4017.	3.5	73
545	Structural insight into poly(A) binding and catalytic mechanism of human PARN. EMBO Journal, 2005, 24, 4082-4093.	3.5	102
546	Structure of unliganded HSV gD reveals a mechanism for receptor-mediated activation of virus entry. EMBO Journal, 2005, 24, 4144-4153.	3.5	231
547	Crystal structure of Mil (Mth680): internal duplication and similarity between the Imp4/Brix domain and the anticodonâ€‘binding domain of class IIa aminoacylâ€‘tRNA synthetases. EMBO Reports, 2005, 6, 140-146.	2.0	12
548	Structural basis for substrate binding, cleavage and allostery in the tRNA maturase RNase Z. Nature, 2005, 433, 657-661.	13.7	149
549	The structure of the myosin VI motor reveals the mechanism of directionality reversal. Nature, 2005, 435, 779-785.	13.7	206
550	Crystal structure of a bacterial homologue of Na+/Cl--dependent neurotransmitter transporters. Nature, 2005, 437, 215-223.	13.7	1,564
551	Structures of complement component C3 provide insights into the function and evolution of immunity. Nature, 2005, 437, 505-511.	13.7	496
552	A light-sensing knot revealed by the structure of the chromophore-binding domain of phytochrome. Nature, 2005, 438, 325-331.	13.7	495
553	Exploring the GluR2 ligand-binding core in complex with the bicyclical AMPA analogue (S)-4-AHCP. FEBS Journal, 2005, 272, 1639-1648.	2.2	21
554	Autophosphorylation of Archaeoglobus fulgidus Rio2 and crystal structures of its nucleotide-metal ion complexes. FEBS Journal, 2005, 272, 2800-2810.	2.2	45
555	Structure and activity of the atypical serine kinase Rio1. FEBS Journal, 2005, 272, 3698-3713.	2.2	56
556	Structural Basis for Vertebrate Filamin Dimerization. Structure, 2005, 13, 111-119.	1.6	90
557	Structural Basis for the Regulation of Insulin-like Growth Factors by IGF Binding Proteins. Structure, 2005, 13, 155-167.	1.6	72
558	Crystal Structures of a Tetrahedral Open Pore Ferritin from the Hyperthermophilic Archaeon Archaeoglobus fulgidus. Structure, 2005, 13, 637-648.	1.6	114
559	X-Ray Crystallographic and NMR Studies of the Third KH Domain of hnRNP K in Complex with Single-Stranded Nucleic Acids. Structure, 2005, 13, 1055-1067.	1.6	90
560	Structural Basis of FFAT Motif-Mediated ER Targeting. Structure, 2005, 13, 1035-1045.	1.6	218
561	The Molecular Origins of Specificity in the Assembly of a Multienzyme Complex. Structure, 2005, 13, 1119-1130.	1.6	66

#	ARTICLE	IF	CITATIONS
562	Crystallographic Refinement by Knowledge-Based Exploration of Complex Energy Landscapes. Structure, 2005, 13, 1311-1319.	1.6	44
563	The Monomeric dUTPase from Epstein-Barr Virus Mimics Trimeric dUTPases. Structure, 2005, 13, 1299-1310.	1.6	49
564	Liberating Crystallographers. Structure, 2005, 13, 1236-1237.	1.6	0
565	Release of a Damaged Cofactor from a Coenzyme B12-Dependent Enzyme: X-Ray Structures of Diol Dehydratase-Reactivating Factor. Structure, 2005, 13, 1745-1754.	1.6	31
566	Crystal Structure of the Restriction-Modification System Control Element C.BclI and Mapping of Its Binding Site. Structure, 2005, 13, 1837-1847.	1.6	30
567	Life in the fast lane for protein crystallization and X-ray crystallography. Progress in Biophysics and Molecular Biology, 2005, 88, 359-386.	1.4	77
568	A test of enhancing model accuracy in high-throughput crystallography. Journal of Structural and Functional Genomics, 2005, 6, 1-11.	1.2	45
569	Crystal structure of the hypothetical protein TA1238 from Thermoplasma acidophilum: A new type of helical super-bundle. Journal of Structural and Functional Genomics, 2005, 5, 231-240.	1.2	4
570	Atomic resolution (0.97â€…Å…) structure of the triple mutant (K53,56,121M) of bovine pancreatic phospholipase A2. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 3-7.	0.7	4
571	Structure ofMesorhizobium lotiarylamineN-acetyltransferase 1. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 14-16.	0.7	35
572	Preliminary crystallographic analysis of ADP-glucose pyrophosphorylase fromAgrobacterium tumefaciens. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 266-268.	0.7	4
573	Expression, purification, crystallization and preliminary X-ray analysis of YaeQ (XAC2396) fromXanthomonas axonopodispv.citri. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 493-495.	0.7	4
574	The structure at 2.4â€…Å… resolution of the protein from gene locus At3g21360, a putative FeII/2-oxoglutarate-dependent enzyme fromArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 469-472.	0.7	4
575	Structure of PIN-domain protein PH0500 fromPyrococcus horikoshii. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 463-468.	0.7	20
576	The structure at 1.7â€…Å… resolution of the protein product of the At2g17340 gene fromArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 630-635.	0.7	6
577	Structure at 1.6â€…Å… resolution of the protein from gene locus At3g22680 fromArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 647-650.	0.7	11
578	The structure at 2.5â€…Å… resolution of human basophilic leukemia-expressed protein BLES03. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 812-817.	0.7	2
579	Crystallization and preliminary X-ray crystallographic analysis ofSulfolobus solfataricusthioredoxin reductase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 906-909.	0.7	4

#	ARTICLE	IF	CITATIONS
580	Superoxide reductase from the syphilis spirocheteTreponema pallidum: crystallization and structure determination using soft X-rays. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 967-970.	0.7	5
581	Crystallization and preliminary X-ray crystallographic analysis of theSulfolobus solfataricusnucleotide-exchange factor 1Î². Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1000-1002.	0.7	0
582	Structure of the SARS coronavirus main proteinase as an active C2crystallographic dimer. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 964-966.	0.7	25
583	Three-dimesional structure of GlcNAcÎ±1-4Gal releasing Endo-Î²-Galactosidase from Clostridium perfringens. Proteins: Structure, Function and Bioinformatics, 2005, 59, 141-144.	1.5	12
584	Structure of YciI from Haemophilus influenzae (HI0828) reveals a ferredoxin-like Î±/Î²-fold with a histidine/aspartate centered catalytic site. Proteins: Structure, Function and Bioinformatics, 2005, 59, 648-652.	1.5	14
585	Ligand-induced fit in mycobacterial MabA: The sequence-specific C-terminus locks the conformational change. Proteins: Structure, Function and Bioinformatics, 2005, 60, 392-400.	1.5	19
586	Structural analysis of a set of proteins resulting from a bacterial genomics project. Proteins: Structure, Function and Bioinformatics, 2005, 60, 787-796.	1.5	217
587	The crystal structure of 5-keto-4-deoxyuronate isomerase from Escherichia coli. Proteins: Structure, Function and Bioinformatics, 2005, 61, 680-684.	1.5	9
588	Crystal structure of a conserved hypothetical protein (gi: 13879369) from Mouse at 1.90 Ã… resolution reveals a new fold. Proteins: Structure, Function and Bioinformatics, 2005, 61, 1132-1136.	1.5	9
589	Structure of Human Cyclophilin A in Complex with the Novel Immunosuppressant Sanglifehrin A at 1.6 Ã… Resolution. Journal of Biological Chemistry, 2005, 280, 21965-21971.	1.6	38
590	Structure and Kinetics of a Monomeric Glucosamine 6-Phosphate Deaminase. Journal of Biological Chemistry, 2005, 280, 19649-19655.	1.6	37
591	Structural and Biochemical Analysis Reveal Pirins to Possess Quercetinase Activity. Journal of Biological Chemistry, 2005, 280, 28675-28682.	1.6	77
592	Crystal structure and functional analysis of DEAD-box protein Dhh1p. Rna, 2005, 11, 1258-1270.	1.6	111
593	A New Arrangement of (Î²/Î±)8 Barrels in the Synthase Subunit of PLP Synthase. Journal of Biological Chemistry, 2005, 280, 27914-27923.	1.6	55
594	Structure of a nonheme globin in environmental stress signaling. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17320-17325.	3.3	66
595	Structural and Chemical Requirements for Histidine Phosphorylation by the Chemotaxis Kinase CheA. Journal of Biological Chemistry, 2005, 280, 30581-30585.	1.6	34
596	1.6-Ã… Crystal Structure of EntA-im. Journal of Biological Chemistry, 2005, 280, 19045-19050.	1.6	30
597	Structure and Function of Both Domains of ArnA, a Dual Function Decarboxylase and a Formyltransferase, Involved in 4-Amino-4-deoxy-L-arabinose Biosynthesis. Journal of Biological Chemistry, 2005, 280, 23000-23008.	1.6	57

#	ARTICLE	IF	CITATIONS
598	Crystal Structure of Glucooligosaccharide Oxidase from Acremonium strictum. Journal of Biological Chemistry, 2005, 280, 38831-38838.	1.6	85
599	Structural Evidence for Non-canonical Binding of Ca2+ to a Canonical EF-hand of a Conventional Myosin. Journal of Biological Chemistry, 2005, 280, 41458-41464.	1.6	20
600	Structural and Biochemical Evidence for an Enzymatic Quinone Redox Cycle in Escherichia coli. Journal of Biological Chemistry, 2005, 280, 8358-8363.	1.6	57
601	Tyr702 Is an Important Determinant of Agonist Binding and Domain Closure of the Ligand-Binding Core of GluR2. Molecular Pharmacology, 2005, 67, 703-713.	1.0	50
602	DETERMINING RELEVANT FEATURES TO RECOGNIZE ELECTRON DENSITY PATTERNS IN X-RAY PROTEIN CRYSTALLOGRAPHY. Journal of Bioinformatics and Computational Biology, 2005, 03, 645-676.	0.3	4
603	Engineering a Selectable Marker for Hyperthermophiles. Journal of Biological Chemistry, 2005, 280, 11422-11431.	1.6	78
604	Structure and reactivity of hydroxypropylphosphonic acid epoxidase in fosfomycin biosynthesis by a cation- and flavin-dependent mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14221-14226.	3.3	31
605	Single-stranded DNA mimicry in the p53 transactivation domain interaction with replication protein A. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15412-15417.	3.3	266
606	The Crystal Structure of Guinea Pig 11Î²-Hydroxysteroid Dehydrogenase Type 1 Provides a Model for Enzyme-Lipid Bilayer Interactions. Journal of Biological Chemistry, 2005, 280, 3789-3794.	1.6	44
607	Crystal Structure of Human Vacuolar Protein Sorting Protein 29 Reveals a Phosphodiesterase/Nuclease-like Fold and Two Protein-Protein Interaction Sites. Journal of Biological Chemistry, 2005, 280, 22962-22967.	1.6	56
608	Crystal Structure of the Human Cytosolic Sialidase Neu2. Journal of Biological Chemistry, 2005, 280, 469-475.	1.6	148
609	Molecular Basis of Intramolecular Electron Transfer in Sulfite-oxidizing Enzymes Is Revealed by High Resolution Structure of a Heterodimeric Complex of the Catalytic Molybdopterin Subunit and a c-Type Cytochrome Subunit. Journal of Biological Chemistry, 2005, 280, 24999-25007.	1.6	119
610	Crystal Structure of the Cysteine-rich Secretory Protein Stecrisp Reveals That the Cysteine-rich Domain Has a K+ Channel Inhibitor-like Fold. Journal of Biological Chemistry, 2005, 280, 12405-12412.	1.6	132
611	Web based molecular visualization using procedural shaders in X3D. , 2005, , .		3
612	Crystal Structure and Binding Properties of the Serratia marcescens Chitin-binding Protein CBP21. Journal of Biological Chemistry, 2005, 280, 11313-11319.	1.6	257
613	Structure and metal-dependent mechanism of peptidoglycan deacetylase, a streptococcal virulence factor. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15429-15434.	3.3	196
614	How Family 26 Glycoside Hydrolases Orchestrate Catalysis on Different Polysaccharides. Journal of Biological Chemistry, 2005, 280, 32761-32767.	1.6	60
615	High-resolution structure of the catalytic region of MICAL (molecule interacting with CasL), a multidomain flavoenzyme-signaling molecule. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16836-16841.	3.3	75

#	Article	IF	Citations
616	Structural and Mutational Analysis of the SBDS Protein Family. Journal of Biological Chemistry, 2005, 280, 19221-19229.	1.6	104
617	Aclacinomycin 10-Hydroxylase Is a Novel Substrate-assisted Hydroxylase Requiring S-Adenosyl-l-methionine as Cofactor. Journal of Biological Chemistry, 2005, 280, 3636-3644.	1.6	43
618	Allele-dependent Similarity between Viral and Self-peptide Presentation by HLA-B27 Subtypes. Journal of Biological Chemistry, 2005, 280, 2962-2971.	1.6	76
619	A Molecular Mechanism for Lys49-Phospholipase A2 Activity Based on Ligand-induced Conformational Change. Journal of Biological Chemistry, 2005, 280, 7326-7335.	1.6	66
620	Structure of a group A streptococcal phage-encoded virulence factor reveals a catalytically active triple-stranded Â-helix. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17652-17657.	3.3	67
621	The 1.3 Ã… Crystal Structure of the Flavoprotein YqjM Reveals a Novel Class of Old Yellow Enzymes. Journal of Biological Chemistry, 2005, 280, 27904-27913.	1.6	116
622	Structure of Ptr ToxA: An RGD-Containing Host-Selective Toxin from Pyrenophora tritici-repentis Â. Plant Cell, 2005, 17, 3190-3202.	3.1	119
623	Structure and Mechanism of the Alkyl Hydroperoxidase AhpC, a Key Elementof the Mycobacterium tuberculosis Defense System against OxidativeStress. Journal of Biological Chemistry, 2005, 280, 25735-25742.	1.6	92
624	The crystal structure of yeast copper thionein: The solution of a long-lasting enigma. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 51-56.	3.3	146
625	Crystal Structure of the PTPL1/FAP-1 Human Tyrosine Phosphatase Mutated in Colorectal Cancer. Journal of Biological Chemistry, 2005, 280, 8180-8187.	1.6	34
626	Crystal Structure of Acetylcholine-binding Protein from Bulinus truncatus Reveals the Conserved Structural Scaffold and Sites of Variation in Nicotinic Acetylcholine Receptors. Journal of Biological Chemistry, 2005, 280, 26457-26466.	1.6	171
627	Structure and Reactivity of Human Mitochondrial 2,4-Dienoyl-CoA Reductase. Journal of Biological Chemistry, 2005, 280, 3068-3077.	1.6	52
628	Crystal Structure of Enteric Adenovirus Serotype 41 Short Fiber Head. Journal of Virology, 2005, 79, 14088-14094.	1.5	29
629	Structural determinants of agonist-specific kinetics at the ionotropic glutamate receptor 2. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12053-12058.	3.3	31
630	A Major Histocompatibility ComplexÂ·Peptide-restricted Antibody and T Cell Receptor Molecules Recognize Their Target by Distinct Binding Modes. Journal of Biological Chemistry, 2005, 280, 2972-2980.	1.6	69
631	Structural Basis for Metal Ion Coordination and the Catalytic Mechanism of Sphingomyelinases D. Journal of Biological Chemistry, 2005, 280, 13658-13664.	1.6	90
632	Structure of the Major Cytosolic Glutathione S-Transferase from the Parasitic Nematode Onchocerca volvulus. Journal of Biological Chemistry, 2005, 280, 12630-12636.	1.6	27
633	The Fucose-binding Lectin from Ralstonia solanacearum. Journal of Biological Chemistry, 2005, 280, 27839-27849.	1.6	160

#	ARTICLE	IF	CITATIONS
634	Structural and functional analysis of SET8, a histone H4 Lys-20 methyltransferase. Genes and Development, 2005, 19, 1455-1465.	2.7	202
635	Crystal Structure of the Hydroxyquinol 1,2-Dioxygenase from Nocardioides simplex 3E, a Key Enzyme Involved in Polychlorinated Aromatics Biodegradation. Journal of Biological Chemistry, 2005, 280, 21144-21154.	1.6	49
636	The Active Site of O- Acetylserine Sulfhydrylase Is the Anchor Point for Bienzyme Complex Formation with Serine Acetyltransferase. Journal of Bacteriology, 2005, 187, 3201-3205.	1.0	89
637	Crystal Structure of Human Toll-Like Receptor 3 (TLR3) Ectodomain. Science, 2005, 309, 581-585.	6.0	545
638	Crystal Structure of Botulinum Neurotoxin Type G Light Chain:â€‰ Serotype Divergence in Substrate Recognition,. Biochemistry, 2005, 44, 9574-9580.	1.2	59
639	Structural basis for the interaction between human milk oligosaccharides and the bacterial lectin PA-IIL of Pseudomonas aeruginosa. Biochemical Journal, 2005, 389, 325-332.	1.7	129
640	Structure and Function of GDP-Mannose-3â€˜,5â€˜-Epimerase:â€‰ An Enzyme which Performs Three Chemical Reactions at the Same Active Site. Journal of the American Chemical Society, 2005, 127, 18309-18320.	6.6	86
641	Tracking the Evolution of Porphobilinogen Synthase Metal Dependence in Vitro. Journal of Molecular Biology, 2005, 345, 1059-1070.	2.0	16
642	The Structure of the Oligopeptide-binding Protein, AppA, from Bacillus subtilis in Complex with a Nonapeptide. Journal of Molecular Biology, 2005, 345, 879-892.	2.0	66
643	The High-resolution Structure of LeuB (Rv2995c) from Mycobacterium tuberculosis. Journal of Molecular Biology, 2005, 346, 1-11.	2.0	26
644	Crystal Structure of the Phosphoenolpyruvate-binding Enzyme I-Domain from the Thermoanaerobacter tengcongensis PEP: Sugar Phosphotransferase System (PTS). Journal of Molecular Biology, 2005, 346, 521-532.	2.0	34
645	X-ray Structure of Na-ASP-2, a Pathogenesis-related-1 Protein from the Nematode Parasite, Necator americanus, and a Vaccine Antigen for Human Hookworm Infection. Journal of Molecular Biology, 2005, 346, 801-814.	2.0	139
646	Three-dimensional Structure of a Macromolecular Assembly that Regulates Type III Secretion in Yersinia pestis. Journal of Molecular Biology, 2005, 346, 1147-1161.	2.0	98
647	Thermodynamic and Structural Equivalence of Two HLA-B27 Subtypes Complexed with a Self-peptide. Journal of Molecular Biology, 2005, 346, 1367-1379.	2.0	50
648	Crystal Structure of TET Protease Reveals Complementary Protein Degradation Pathways in Prokaryotes. Journal of Molecular Biology, 2005, 346, 1207-1219.	2.0	62
649	Inclining the Purine Base Binding Plane in Protein Kinase CK2 by Exchanging the Flanking Side-chains Generates a Preference for ATP as a Cosubstrate. Journal of Molecular Biology, 2005, 347, 399-414.	2.0	53
650	The Crystal Structure of Human PAPS Synthetase 1 Reveals Asymmetry in Substrate Binding. Journal of Molecular Biology, 2005, 347, 623-635.	2.0	45
651	High Resolution Crystal Structures of Human Cytosolic Thiolase (CT): A Comparison of the Active Sites of Human CT, Bacterial Thiolase, and Bacterial KAS I. Journal of Molecular Biology, 2005, 347, 189-201.	2.0	62

#	Article	IF	Citations
652	Crystal Structures of Human DcpS in Ligand-free and m7GDP-bound forms Suggest a Dynamic Mechanism for Scavenger mRNA Decapping. Journal of Molecular Biology, 2005, 347, 707-718.	2.0	48
653	Crystal Structure of Maltooligosyltrehalose Trehalohydrolase from Deinococcus radiodurans in Complex with Disaccharides. Journal of Molecular Biology, 2005, 347, 949-963.	2.0	26
654	Regulation by Oligomerization in a Mycobacterial Folate Biosynthetic Enzyme. Journal of Molecular Biology, 2005, 349, 61-72.	2.0	39
655	Structural Studies of Human Placental Alkaline Phosphatase in Complex with Functional Ligands. Journal of Molecular Biology, 2005, 350, 441-451.	2.0	85
656	The Three-Dimensional Structures of Tick Carboxypeptidase Inhibitor in Complex with A/B Carboxypeptidases Reveal a Novel Double-headed Binding Mode. Journal of Molecular Biology, 2005, 350, 489-498.	2.0	57
657	Crystal Structure of the Vibrio cholerae Cytolysin (VCC) Pro-toxin and its Assembly into a Heptameric Transmembrane Pore. Journal of Molecular Biology, 2005, 350, 997-1016.	2.0	122
658	Atomic-resolution Crystal Structure of the Proteolytic Domain of Archaeoglobus fulgidus Lon Reveals the Conformational Variability in the Active Sites of Lon Proteases. Journal of Molecular Biology, 2005, 351, 144-157.	2.0	46
659	Crystal Structure of a Putative Type I Restrictionâ€"Modification S Subunit from Mycoplasma genitalium. Journal of Molecular Biology, 2005, 351, 749-762.	2.0	44
660	Structural Basis for the Function of Clostridium difficile Toxin B. Journal of Molecular Biology, 2005, 351, 973-981.	2.0	144
661	Structure of the Conserved Cytoplasmic C-terminal Domain of Occludin: Identification of the ZO-1 Binding Surface. Journal of Molecular Biology, 2005, 352, 151-164.	2.0	105
662	X-ray Structure of Domain I of the Proton-pumping Membrane Protein Transhydrogenase from Escherichia coli. Journal of Molecular Biology, 2005, 352, 299-312.	2.0	32
663	Structure of the Mycobacterium tuberculosis Flavin Dependent Thymidylate Synthase (MtbThyX) at 2.0Ã... Resolution. Journal of Molecular Biology, 2005, 352, 1091-1104.	2.0	65
664	Crystal Structures of Î"1-Pyrroline-5-carboxylate Reductase from Human Pathogens Neisseria meningitides and Streptococcus pyogenes. Journal of Molecular Biology, 2005, 354, 91-106.	2.0	52
665	Structures for the Potential Drug Target Purine Nucleoside Phosphorylase from Schistosoma mansoni Causal Agent of Schistosomiasis. Journal of Molecular Biology, 2005, 353, 584-599.	2.0	32
666	Crystal Structure of a Bacterial Class 2 Histone Deacetylase Homologue. Journal of Molecular Biology, 2005, 354, 107-120.	2.0	151
667	High-resolution Crystal Structure of AKR11C1 from Bacillus halodurans: An NADPH-dependent 4-Hydroxy-2,3-trans-nonenal Reductase. Journal of Molecular Biology, 2005, 354, 304-316.	2.0	11
668	Specificity Determinants in Inositol Polyphosphate Synthesis: Crystal Structure of Inositol 1,3,4-Trisphosphate 5/6-Kinase. Molecular Cell, 2005, 18, 201-212.	4.5	67
669	Regulation of LuxPQ Receptor Activity by the Quorum-Sensing Signal Autoinducer-2. Molecular Cell, 2005, 18, 507-518.	4.5	193

#	ARTICLE	IF	CITATIONS
670	Crystal Structure of Bacteriophage Î»cII and Its DNA Complex. Molecular Cell, 2005, 19, 259-269.	4.5	39
671	Structural Basis for the Activation of Microtubule Assembly by the EB1 and p150Glued Complex. Molecular Cell, 2005, 19, 449-460.	4.5	121
672	Crystal structure of Trypanosoma cruzi pteridine reductase 2 in complex with a substrate and an inhibitor. Journal of Structural Biology, 2005, 152, 64-75.	1.3	23
673	Structure of a non-camelized human M12-VH domain at 1.5Ã… resolution. Journal of Structural Biology, 2005, 152, 84-89.	1.3	1
674	Crystal structure of a biologically functional form of PriB from Escherichia coli reveals a potential single-stranded DNA-binding site. Biochemical and Biophysical Research Communications, 2005, 326, 766-776.	1.0	28
675	2.0Ã… crystal structure of human ARL5-GDP3â€²P, a novel member of the small GTP-binding proteins. Biochemical and Biophysical Research Communications, 2005, 332, 640-645.	1.0	6
676	Crystal structure of heterotetrameric sarcosine oxidase from Corynebacterium sp. U-96. Biochemical and Biophysical Research Communications, 2005, 333, 359-366.	1.0	15
677	1.88Ã… crystal structure of the C domain of hCyP33: A novel domain of peptidyl-prolyl cisâ€“trans isomerase. Biochemical and Biophysical Research Communications, 2005, 333, 845-849.	1.0	9
678	A Unique RNA Fold in the RumA-RNA-Cofactor Ternary Complex Contributes to Substrate Selectivity and Enzymatic Function. Cell, 2005, 120, 599-611.	13.5	99
679	Crystal structure of the conserved hypothetical protein Rv1155 fromMycobacterium tuberculosis. FEBS Letters, 2005, 579, 215-221.	1.3	25
680	Structure of the house dust mite allergen Der f 2: Implications for function and molecular basis of IgE cross-reactivity. FEBS Letters, 2005, 579, 1208-1212.	1.3	44
681	Crystal structure of the kainate receptor GluR5 ligand-binding core in complex with (S)-glutamate. FEBS Letters, 2005, 579, 1154-1160.	1.3	87
682	1.2 Ã… crystal structure of theS. pneumoniaePhtA histidine triad domain a novel zinc binding fold. FEBS Letters, 2005, 579, 5353-5360.	1.3	43
683	Cloning, expression, characterisation and three-dimensional structure determination ofCaenorhabditis elegansspermidine synthase. FEBS Letters, 2005, 579, 6037-6043.	1.3	25
684	Structure of a halophilic nucleoside diphosphate kinase fromHalobacterium salinarum. FEBS Letters, 2005, 579, 6595-6600.	1.3	34
685	Structure-based chemical modification strategy for enzyme replacement treatment of phenylketonuria. Molecular Genetics and Metabolism, 2005, 86, 134-140.	0.5	57
686	Crystal Structure of a Novel Shikimate Dehydrogenase from Haemophilus influenzae. Journal of Biological Chemistry, 2005, 280, 17101-17108.	1.6	33
687	Structure-Based Design of Novel Chk1 Inhibitors:Â Insights into Hydrogen Bonding and Proteinâ^'Ligand Affinity. Journal of Medicinal Chemistry, 2005, 48, 4332-4345.	2.9	92

#	Article	IF	Citations
688	Crystal structure of wild-type human thrombin in the Na+-free state. Biochemical Journal, 2005, 392, 21-28.	1.7	54
689	Structure-Based Engineering of Internal Cavities in Coiled-Coil Peptides,. Biochemistry, 2005, 44, 9723-9732.	1.2	42
690	Computational Aspects of High-Throughput Crystallographic Macromolecular Structure Determination. Methods of Biochemical Analysis, 2005, 44, 75-87.	0.2	0
691	Structure of Testis ACE Glycosylation Mutants and Evidence for Conserved Domain Movementâ€,â€¡. Biochemistry, 2006, 45, 12654-12663.	1.2	53
692	Structures of Apo- and Holo-Tyrosine Phenol-lyase Reveal a Catalytically Critical Closed Conformation and Suggest a Mechanism for Activation by K+ Ions,. Biochemistry, 2006, 45, 7544-7552.	1.2	28
693	Molecular structure from X-ray diffraction. Annual Reports on the Progress of Chemistry Section C, 2006, 102, 92.	4.4	3
694	A Tandem of SH3-like Domains Participates in RNA Binding in KIN17, a Human Protein Activated in Response to Genotoxics. Journal of Molecular Biology, 2006, 364, 764-776.	2.0	20
695	Crystal structure of 3-hydroxyanthranilic acid 3,4-dioxygenase from Saccharomyces cerevisiae: A special subgroup of the type III extradiol dioxygenases. Protein Science, 2006, 15, 761-773.	3.1	34
696	Kinetic, inhibition and structural studies on 3-oxoacyl-ACP reductase from Plasmodium falciparum, a key enzyme in fatty acid biosynthesis. Biochemical Journal, 2006, 393, 447-457.	1.7	72
697	Dissecting the Determinants of Cyclin-Dependent Kinase 2 and Cyclin-Dependent Kinase 4 Inhibitor Selectivityâ€. Journal of Medicinal Chemistry, 2006, 49, 5470-5477.	2.9	39
698	Substrate and Product Trafficking through the Active Center Gorge of Acetylcholinesterase Analyzed by Crystallography and Equilibrium Binding. Journal of Biological Chemistry, 2006, 281, 29256-29267.	1.6	117
699	Xyloglucan Is Recognized by Carbohydrate-binding Modules That Interact with Î²-Glucan Chains. Journal of Biological Chemistry, 2006, 281, 8815-8828.	1.6	102
700	Crystal Structures of the Short-Chain Flavin Reductase HpaC fromSulfolobus tokodaiiStrain 7 in Its Three States:Â NAD(P)+-Free, NAD+-Bound, and NADP+-Boundâ€,â€¡. Biochemistry, 2006, 45, 5103-5110.	1.2	33
701	Structure of Arabidopsis thaliana At1g77540 Protein, a Minimal Acetyltransferase from the COG2388 Family,. Biochemistry, 2006, 45, 14325-14336.	1.2	13
702	Binding of different monosaccharides by lectin PA-IIL fromPseudomonas aeruginosa: Thermodynamics data correlated with X-ray structures. FEBS Letters, 2006, 580, 982-987.	1.3	94
703	Crystal structure of AmyA lacks acidic surface and provide insights into protein stability at poly-extreme condition. FEBS Letters, 2006, 580, 2646-2652.	1.3	64
704	Respective importance of protein folding and glycosylation in the thermal stability of recombinant feruloyl esterase A. FEBS Letters, 2006, 580, 5815-5821.	1.3	54
705	Yersinia Virulence Depends on Mimicry of Host Rho-Family Nucleotide Dissociation Inhibitors. Cell, 2006, 126, 869-880.	13.5	110

#	ARTICLE	IF	CITATIONS
706	The Crystal Structure of the Exon Junction Complex Reveals How It Maintains a Stable Grip on mRNA. Cell, 2006, 126, 713-725.	13.5	352
707	Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. Biochemical and Biophysical Research Communications, 2006, 342, 323-329.	1.0	63
708	Structure of the POZ domain of human LRF, a master regulator of oncogenesis. Biochemical and Biophysical Research Communications, 2006, 351, 1-6.	1.0	32
709	Structural Evidence for Adaptive Ligand Binding of Glycolipid Transfer Protein. Journal of Molecular Biology, 2006, 355, 224-236.	2.0	49
710	A Structure-based Proposal for the Catalytic Mechanism of the Bacterial Acid Phosphatase AphA belonging to the DDDD Superfamily of Phosphohydrolases. Journal of Molecular Biology, 2006, 355, 708-721.	2.0	29
711	Structural Studies of MFE-1: the 1.9Ã… Crystal Structure of the Dehydrogenase Part of Rat Peroxisomal MFE-1. Journal of Molecular Biology, 2006, 355, 734-746.	2.0	11
712	Crystal Structure of Bacillus anthracis ThiI, a tRNA-modifying Enzyme Containing the Predicted RNA-binding THUMP Domain. Journal of Molecular Biology, 2006, 356, 97-110.	2.0	60
713	The Crystal Structure of TrpD, a Metabolic Enzyme Essential for Lung Colonization by Mycobacterium tuberculosis, in Complex with its Substrate Phosphoribosylpyrophosphate. Journal of Molecular Biology, 2006, 355, 784-797.	2.0	41
714	The Crystal Structure of Human Atg4b, a Processing and De-conjugating Enzyme for Autophagosome-forming Modifiers. Journal of Molecular Biology, 2006, 355, 612-618.	2.0	79
715	Structure of a Putative Lipoate Protein Ligase from Thermoplasma acidophilum and the Mechanism of Target Selection for Post-translational Modification. Journal of Molecular Biology, 2006, 356, 625-637.	2.0	27
716	Crystal Structure of Bordetella pertussis BugD Solute Receptor Unveils the Basis of Ligand Binding in a New Family of Periplasmic Binding Proteins. Journal of Molecular Biology, 2006, 356, 1014-1026.	2.0	42
717	Crystal Structure of Papaya Glutaminyl Cyclase, an Archetype for Plant and Bacterial Glutaminyl Cyclases. Journal of Molecular Biology, 2006, 357, 457-470.	2.0	34
718	Crystal Structure of the Polyketide Cyclase AknH with Bound Substrate and Product Analogue: Implications for Catalytic Mechanism and Product Stereoselectivity. Journal of Molecular Biology, 2006, 357, 210-220.	2.0	70
719	Structure of the Regulatory Subunit of Acetohydroxyacid Synthase Isozyme III from Escherichia coli. Journal of Molecular Biology, 2006, 357, 951-963.	2.0	67
720	Crystal Structure of Protein Ph1481p in Complex with Protein Ph1877p of Archaeal RNase P from Pyrococcus horikoshii OT3: Implication of Dimer Formation of the Holoenzyme. Journal of Molecular Biology, 2006, 357, 583-591.	2.0	60
721	Structure of the Mosquitocidal Toxin from Bacillus sphaericus. Journal of Molecular Biology, 2006, 357, 1226-1236.	2.0	26
722	Three-dimensional Crystal Structure and Enzymic Characterization of Î²-Mannanase Man5A from Blue Mussel Mytilus edulis. Journal of Molecular Biology, 2006, 357, 1500-1510.	2.0	76
723	Î²-Propeller Crystal Structure of Psathyrella velutina Lectin: An Integrin-like Fungal Protein Interacting with Monosaccharides and Calcium. Journal of Molecular Biology, 2006, 357, 1575-1591.	2.0	77

#	Article	IF	Citations
724	Crystal Structure of the Murine Cytomegalovirus MHC-I Homolog m144. Journal of Molecular Biology, 2006, 358, 157-171.	2.0	36
725	1.6Ã… Crystal Structure of the Secreted Chorismate Mutase from Mycobacterium tuberculosis: Novel Fold Topology Revealed. Journal of Molecular Biology, 2006, 357, 1483-1499.	2.0	55
726	Crystal Structure of an Archaeal Actin Homolog. Journal of Molecular Biology, 2006, 358, 145-156.	2.0	49
727	Functional and Structural Characterization of Spl Proteases from Staphylococcus aureus. Journal of Molecular Biology, 2006, 358, 270-279.	2.0	47
728	The X-ray Structure of the N-terminal Domain of PILB from Neisseria meningitidis Reveals a Thioredoxin-fold. Journal of Molecular Biology, 2006, 358, 443-454.	2.0	12
729	Crystal Structure of the Archaeal A1AO ATP Synthase Subunit B from Methanosarcina mazei GÃ¶1: Implications of Nucleotide-binding Differences in the Major A1AO Subunits A and B. Journal of Molecular Biology, 2006, 358, 725-740.	2.0	60
730	Alternate Structural Conformations of Streptococcus pneumoniae Hyaluronan Lyase: Insights into Enzyme Flexibility and Underlying Molecular Mechanism of Action. Journal of Molecular Biology, 2006, 358, 1165-1178.	2.0	21
731	Crystal Structure of Yeast Peroxisomal Multifunctional Enzyme: Structural Basis for Substrate Specificity of (3R)-hydroxyacyl-CoA Dehydrogenase Units. Journal of Molecular Biology, 2006, 358, 1286-1295.	2.0	15
732	Evidence Supporting a cis-enediol-based Mechanism for Pyrococcus furiosus Phosphoglucose Isomerase. Journal of Molecular Biology, 2006, 358, 1353-1366.	2.0	29
733	The Crystal Structure of Cdc42 in Complex with Collybistin II, a Gephyrin-interacting Guanine Nucleotide Exchange Factor. Journal of Molecular Biology, 2006, 359, 35-46.	2.0	63
734	Structural Analysis of N-acetylglucosamine-6-phosphate Deacetylase Apoenzyme from Escherichia coli. Journal of Molecular Biology, 2006, 359, 308-321.	2.0	22
735	Crystal Structure of the C-terminal Domain of S.cerevisiae eIF5. Journal of Molecular Biology, 2006, 359, 1-9.	2.0	40
736	Structureâ€"Stabilityâ€"Activity Relationship in Covalently Cross-linked N-Carbamoyl d-Amino acid Amidohydrolase and N-Acylamino acid Racemase. Journal of Molecular Biology, 2006, 359, 741-753.	2.0	31
737	Structure of the N-terminal Domain of the FOP (FGFR1OP) Protein and Implications for its Dimerization and Centrosomal Localization. Journal of Molecular Biology, 2006, 359, 863-875.	2.0	36
738	Structure of the Human Multidrug Resistance Protein 1 Nucleotide Binding Domain 1 bound to Mg2+/ATP Reveals a Non-productive Catalytic Site. Journal of Molecular Biology, 2006, 359, 940-949.	2.0	76
739	Domain Organization and Crystal Structure of the Catalytic Domain of E.coli RluF, a Pseudouridine Synthase that Acts on 23S rRNA. Journal of Molecular Biology, 2006, 359, 998-1009.	2.0	11
740	The Structure of the Exopolyphosphatase (PPX) from Escherichia coli O157:H7 Suggests a Binding Mode for Long Polyphosphate Chains. Journal of Molecular Biology, 2006, 359, 1249-1260.	2.0	51
741	Controlling Quaternary Structure Assembly: Subunit Interface Engineering and Crystal Structure of Dual Chain Avidin. Journal of Molecular Biology, 2006, 359, 1352-1363.	2.0	15

#	ARTICLE	IF	CITATIONS
742	NADP+ Expels both the Co-factor and a Substrate Analog from the Mycobacterium tuberculosis ThyX Active Site: Opportunities for Anti-bacterial Drug Design. Journal of Molecular Biology, 2006, 360, 1-6.	2.0	20
743	The Crystal Structure of the Carboxy-Terminal Domain of Human Translation Initiation Factor eIF5. Journal of Molecular Biology, 2006, 360, 457-465.	2.0	42
744	Crystal Structure of 3-Chlorocatechol 1,2-dioxygenase Key Enzyme of a New Modified Ortho-pathway from the Gram-positive Rhodococcus opacus 1CP Grown on 2-chlorophenol. Journal of Molecular Biology, 2006, 360, 788-799.	2.0	36
745	Crystal Structure of Nicotinic Acid Mononucleotide Adenylyltransferase from Staphyloccocus aureus: Structural Basis for NaAD Interaction in Functional Dimer. Journal of Molecular Biology, 2006, 360, 814-825.	2.0	25
746	Heterotetrameric Sarcosine Oxidase: Structure of a Diflavin Metalloenzyme at 1.85ÂÃ… Resolution. Journal of Molecular Biology, 2006, 360, 1000-1018.	2.0	29
747	Structural Basis of the Nickel Response in Helicobacter pylori: Crystal Structures of HpNikR in Apo and Nickel-bound States. Journal of Molecular Biology, 2006, 361, 715-730.	2.0	74
748	The Crystal Structure of a Thermophilic Glucose Binding Protein Reveals Adaptations that Interconvert Mono and Di-saccharide Binding Sites. Journal of Molecular Biology, 2006, 362, 259-270.	2.0	36
749	The Crystal Structure of the Bacteriophage PSA Endolysin Reveals a Unique Fold Responsible for Specific Recognition of Listeria Cell Walls. Journal of Molecular Biology, 2006, 364, 678-689.	2.0	103
750	Mechanism of Phosphoryl Transfer Catalyzed by Shikimate Kinase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 364, 411-423.	2.0	63
751	Structure and Action of the Binary C2 Toxin from Clostridium botulinum. Journal of Molecular Biology, 2006, 364, 705-715.	2.0	116
752	The Molecular Basis of Filamin Binding to Integrins and Competition with Talin. Molecular Cell, 2006, 21, 337-347.	4.5	359
753	A Common Structural Motif in the Binding of Virulence Factors to Bacterial Secretion Chaperones. Molecular Cell, 2006, 21, 653-664.	4.5	117
754	Structural Basis for CoREST-Dependent Demethylation of Nucleosomes by the Human LSD1 Histone Demethylase. Molecular Cell, 2006, 23, 377-387.	4.5	306
755	Crystal structure of a highly acidic neurotoxin from scorpion Buthus tamulus at 2.2Çº resolution reveals novel structural features. Journal of Structural Biology, 2006, 155, 52-62.	1.3	9
757	The structure of the GPIbâ€"filamin A complex. Blood, 2006, 107, 1925-1932.	0.6	144
758	The structure of siglec-7 in complex with sialosides: leads for rational structure-based inhibitor design. Biochemical Journal, 2006, 397, 271-278.	1.7	70
759	Structural dissection of the reaction mechanism of cellobiose phosphorylase. Biochemical Journal, 2006, 398, 37-43.	1.7	71
760	TAK1-binding protein 1 is a pseudophosphatase. Biochemical Journal, 2006, 399, 427-434.	1.7	73

#	ARTICLE	IF	CITATIONS
763	Structure determination of an FMN reductase fromPseudomonas aeruginosaPA01 using sulfur anomalous signal. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 383-391.	2.5	41
764	Analysis of protein hydration in ultrahigh-resolution structures of the SRP GTPase Ffh. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1520-1534.	2.5	7
765	The Structural Biology Center 19ID undulator beamline: facility specifications and protein crystallographic results. Journal of Synchrotron Radiation, 2006, 13, 30-45.	1.0	143
766	Expression, purification, crystallization and preliminary X-ray analysis of the human RuvB-like protein RuvBL1. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 61-66.	0.7	4
767	Crystallization and preliminary X-ray analysis of cytochromecnitrite reductase fromThioalkalivibrio nitratireducens. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 215-217.	0.7	8
768	Crystallization and molecular-replacement studies of the monoclonal antibody mAbR310 specific for the (R)-HNE-modified protein. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 562-564.	0.7	0
769	Structure of armadillo ACBP: a new member of the acyl-CoA-binding protein family. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 958-961.	0.7	12
770	The copper-containing amine oxidase fromArthrobacter globiformis: refinement at 1.55 and 2.20â€…Å… resolution in two crystal forms. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1052-1057.	0.7	8
771	The 2.1â€…Å… structure ofAerococcus viridansL-lactate oxidase (LOX). Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1185-1190.	0.7	40
772	The molecular structure of Rv1873, a conserved hypothetical protein fromMycobacterium tuberculosis, at 1.38â€…Å… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1201-1205.	0.7	2
773	Overexpression, purification, crystallization and preliminary X-ray crystallographic studies of a proline-specific aminopeptidase fromAneurinibacillusÂsp. strain AM-1. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1266-1268.	0.7	4
774	Structure of a conserved hypothetical protein SA1388 from S. aureus reveals a capped hexameric toroid with two PII domain lids and a dinuclear metal center. BMC Structural Biology, 2006, 6, 27.	2.3	14
775	Crystal structure of hypothetical protein YfiH from Shigella flexneri at 2 Å… resolution. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1097-1101.	1.5	15
776	1.6 Å… Crystal structure of a PA2721 protein from pseudomonas aeruginosa-A potential drug-resistance protein. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1102-1105.	1.5	2
777	Nontoxic crystal protein from Bacillus thuringiensis demonstrates a remarkable structural similarity to Î²-pore-forming toxins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 243-248.	1.5	24
778	Crystal structures of two putative phosphoheptose isomerases. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1092-1096.	1.5	14
779	Crystal structure of a putative HTH-type transcriptional regulator yxaF from Bacillus subtilis. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1087-1091.	1.5	5
780	Crystal structure of Homo sapiens thialysine N Ïµ â€acetyltransferase (HsSSAT2) in complex with acetyl coenzyme A. Proteins: Structure, Function and Bioinformatics, 2006, 64, 288-293.	1.5	11

#	Article	IF	Citations
781	Crystal structure of phosphatidylglycerophosphatase (PGPase), a putative membrane-bound lipid phosphatase, reveals a novel binuclear metal binding site and two â€œproton wiresâ€. Proteins: Structure, Function and Bioinformatics, 2006, 64, 851-862.	1.5	10
782	Crystal structures of human sulfotransferases SULT1B1 and SULT1C1 complexed with the cofactor product adenosine-3â€²- 5â€²-diphosphate (PAP). Proteins: Structure, Function and Bioinformatics, 2006, 64, 1091-1094.	1.5	26
783	Structure of YidB protein from Shigella flexneri shows a new fold with homeodomain motif. Proteins: Structure, Function and Bioinformatics, 2006, 65, 509-513.	1.5	0
784	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. Proteins: Structure, Function and Bioinformatics, 2006, 64, 874-882.	1.5	15
785	Crystal structure of glycerophosphodiester phosphodiesterase from Agrobacterium tumefaciens by SAD with a large asymmetric unit. Proteins: Structure, Function and Bioinformatics, 2006, 65, 514-518.	1.5	13
786	Kinetic and structural properties of inorganic pyrophosphatase from the pathogenic bacteriumHelicobacter pylori. Proteins: Structure, Function and Bioinformatics, 2006, 65, 670-680.	1.5	9
787	High resolution crystal structures of unliganded and liganded human liver ACBP reveal a new mode of binding for the acyl-CoA ligand. Proteins: Structure, Function and Bioinformatics, 2006, 66, 229-238.	1.5	44
788	Crystal structure of the MYB domain of the RAD transcription factor from Antirrhinum majus. Proteins: Structure, Function and Bioinformatics, 2006, 65, 1041-1045.	1.5	22
789	Crystal structure of TTHA1657 (AT-rich DNA-binding protein; p25) from Thermus thermophilus HB8 at 2.16 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2006, 66, 755-759.	1.5	16
790	Crystal structure of the second PDZ domain of SAP97 in complex with a GluR-A C-terminal peptide. FEBS Journal, 2006, 273, 5219-5229.	2.2	31
791	Structural Analysis of the Interaction Between the SNARE Tlg1 and Vps51. Traffic, 2006, 7, 182-190.	1.3	48
792	Structural and biochemical characterization of a mitochondrial peroxiredoxin from Plasmodium falciparum. Molecular Microbiology, 2006, 61, 948-959.	1.2	48
793	Structural definition of the F-actinâ€“binding THATCH domain from HIP1R. Nature Structural and Molecular Biology, 2006, 13, 121-130.	3.6	75
794	Crystal structure of Staphylococcus aureus tRNA adenosine deaminase TadA in complex with RNA. Nature Structural and Molecular Biology, 2006, 13, 153-159.	3.6	151
795	Crystal structure of the essential N-terminal domain of telomerase reverse transcriptase. Nature Structural and Molecular Biology, 2006, 13, 218-225.	3.6	169
796	A native to amyloidogenic transition regulated by a backbone trigger. Nature Structural and Molecular Biology, 2006, 13, 202-208.	3.6	188
797	Structure and mechanism of a bacterial Î²-glucosaminidase having O-GlcNAcase activity. Nature Structural and Molecular Biology, 2006, 13, 365-371.	3.6	182
798	Structural basis for HIV-1 neutralization by a gp41 fusion intermediateâ€“directed antibody. Nature Structural and Molecular Biology, 2006, 13, 740-747.	3.6	122

#	ARTICLE	IF	CITATIONS
799	Development of the signal in sensory rhodopsin and its transfer to the cognate transducer. Nature, 2006, 440, 115-119.	13.7	169
800	Structural basis for the spectral difference in luciferase bioluminescence. Nature, 2006, 440, 372-376.	13.7	482
801	Structure of a flavonoid glucosyltransferase reveals the basis for plant natural product modification. EMBO Journal, 2006, 25, 1396-1405.	3.5	389
802	Structural insights into the mechanism and inhibition of eukaryotic O-GlcNAc hydrolysis. EMBO Journal, 2006, 25, 1569-1578.	3.5	181
803	Deciphering the structural framework of glycine receptor anchoring by gephyrin. EMBO Journal, 2006, 25, 1385-1395.	3.5	117
804	LppX is a lipoprotein required for the translocation of phthiocerol dimycocerosates to the surface of Mycobacterium tuberculosis. EMBO Journal, 2006, 25, 1436-1444.	3.5	126
805	Structure of complement factor H carboxyl-terminus reveals molecular basis of atypical haemolytic uremic syndrome. EMBO Journal, 2006, 25, 1784-1794.	3.5	149
806	The closed structure of presequence protease PreP forms a unique 10 000 Ã…3 chamber for proteolysis. EMBO Journal, 2006, 25, 1977-1986.	3.5	93
807	Crystal structures of VAP1 reveal ADAMs' MDC domain architecture and its unique C-shaped scaffold. EMBO Journal, 2006, 25, 2388-2396.	3.5	187
808	Structure and E3-ligase activity of the Ringâ€“Ring complex of Polycomb proteins Bmi1 and Ring1b. EMBO Journal, 2006, 25, 2465-2474.	3.5	380
809	On the structure of the stator of the mitochondrial ATP synthase. EMBO Journal, 2006, 25, 2911-2918.	3.5	178
810	Structure and function of Tim14 and Tim16, the J and J-like components of the mitochondrial protein import motor. EMBO Journal, 2006, 25, 4675-4685.	3.5	107
811	X-ray structure of the membrane-bound cytochrome c quinol dehydrogenase NrfH reveals novel haem coordination. EMBO Journal, 2006, 25, 5951-5960.	3.5	150
812	Structure of the origin-binding domain of simian virus 40 large T antigen bound to DNA. EMBO Journal, 2006, 25, 5961-5969.	3.5	37
813	A fluorescence polarization assay for inhibitors of Hsp90. Analytical Biochemistry, 2006, 350, 202-213.	1.1	81
814	Crystallisation and preliminary structure determination of a NADH: quinone oxidoreductase from the extremophile Acidianus ambivalens. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 842-845.	1.1	10
815	Inactivation of the phenylpyruvate tautomerase activity of macrophage migration inhibitory factor by 2-oxo-4-phenyl-3-butynoate. Bioorganic Chemistry, 2006, 34, 183-199.	2.0	8
816	Identification of a buried pocket for potent and selective inhibition of Chk1: Prediction and verification. Bioorganic and Medicinal Chemistry, 2006, 14, 1792-1804.	1.4	47

#	ARTICLE	IF	CITATIONS
817	Crystal structures of the free and sterol-bound forms of Î²-cinnamomin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 110-121.	1.1	24
818	The crystal structure of Arabidopsis thaliana RAC7/ROP9: The first RAS superfamily GTPase from the plant kingdom. Phytochemistry, 2006, 67, 2332-2340.	1.4	31
819	Polymeric hydrophobic membranes as a tool to control polymorphism and proteinâ€“ligand interactions. Journal of Membrane Science, 2006, 283, 123-132.	4.1	22
820	X-ray structure of potato epoxide hydrolase sheds light on substrate specificity in plant enzymes. Protein Science, 2006, 15, 1628-1637.	3.1	62
821	Crystal structure of trehalose-6-phosphate phosphatase-related protein: Biochemical and biological implications. Protein Science, 2006, 15, 1735-1744.	3.1	54
822	Structural studies of human alkaline phosphatase in complex with strontium: Implication for its secondary effect in bones. Protein Science, 2006, 15, 1691-1700.	3.1	28
823	Crystal structure of hypothetical protein TTHB192 fromThermus thermophilusHB8 reveals a new protein family with an RNA recognition motif-like domain. Protein Science, 2006, 15, 1494-1499.	3.1	78
824	Structural characterization of GntR/HutC family signaling domain. Protein Science, 2006, 15, 1506-1511.	3.1	30
825	The crystal structure ofMycobacterium tuberculosisadenylate kinase in complex with two molecules of ADP and Mg2+supports an associative mechanism for phosphoryl transfer. Protein Science, 2006, 15, 1489-1493.	3.1	36
826	Stabilization of a binary protein complex by intein-mediated cyclization. Protein Science, 2006, 15, 2612-2618.	3.1	29
827	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
828	Crystal Structure of the His-Tagged Saccharopine Reductase From Saccharomyces cerevisiae at 1.7-Ã… Resolution. Cell Biochemistry and Biophysics, 2006, 46, 17-26.	0.9	8
829	Structure of a [2Feâ€“2S] ferredoxin from Rhodobacter capsulatus likely involved in Feâ€“S cluster biogenesis and conformational changes observed upon reduction. Journal of Biological Inorganic Chemistry, 2006, 11, 235-246.	1.1	24
830	The first crystal structure of class III superoxide reductase from Treponema pallidum. Journal of Biological Inorganic Chemistry, 2006, 11, 548-558.	1.1	37
831	Formate-reduced E. coli formate dehydrogenase H: the reinterpretation of the crystal structure suggests a new reaction mechanism. Journal of Biological Inorganic Chemistry, 2006, 11, 849-854.	1.1	140
832	Activation and Catalysis of the Di-Heme Cytochrome c Peroxidase from Paracoccus pantotrophus. Structure, 2006, 14, 107-117.	1.6	65
833	The Crystal Structure of Murine Coronin-1: A Regulator of Actin Cytoskeletal Dynamics in Lymphocytes. Structure, 2006, 14, 87-96.	1.6	106
834	Crystal Structure of the Human Retinitis Pigmentosa 2 Protein and Its Interaction with Arl3. Structure, 2006, 14, 367-378.	1.6	79

#	ARTICLE	IF	CITATIONS
835	Structural Basis for Sulfur Relay to RNA Mediated by Heterohexameric TusBCD Complex. Structure, 2006, 14, 357-366.	1.6	44
836	Crystal Structures of U8 snoRNA Decapping Nudix Hydrolase, X29, and Its Metal and Cap Complexes. Structure, 2006, 14, 331-343.	1.6	26
837	Biochemical Characterization and Crystal Structure of Synechocystis Arogenate Dehydrogenase Provide Insights into Catalytic Reaction. Structure, 2006, 14, 767-776.	1.6	31
838	The Crystal Structure of Carnitine Palmitoyltransferase 2 and Implications for Diabetes Treatment. Structure, 2006, 14, 713-723.	1.6	56
839	Structure of Artemin Complexed with Its Receptor GFRÎ±3: Convergent Recognition of Glial Cell Line-Derived Neurotrophic Factors. Structure, 2006, 14, 1083-1092.	1.6	65
840	Domain-Swapped Structure of the Potent Antiviral Protein Griffithsin and Its Mode of Carbohydrate Binding. Structure, 2006, 14, 1127-1135.	1.6	149
841	A Steric Antagonism of Actin Polymerization by a Salmonella Virulence Protein. Structure, 2006, 14, 1219-1229.	1.6	73
842	Crystal Structure of Rab11 in Complex with Rab11 Family Interacting Protein 2. Structure, 2006, 14, 1273-1283.	1.6	82
843	Crystal Structure of Ethylbenzene Dehydrogenase from Aromatoleum aromaticum. Structure, 2006, 14, 1377-1388.	1.6	168
844	The Crystal Structure of the Rare-Cutting Restriction Enzyme SdaI Reveals Unexpected Domain Architecture. Structure, 2006, 14, 1389-1400.	1.6	25
845	Structures of Two Bacterial Prolyl-tRNA Synthetases with and without a cis-Editing Domain. Structure, 2006, 14, 1511-1525.	1.6	65
846	Automated Proteinâ€“Ligand Crystallography for Structure-Based Drug Design. ChemMedChem, 2006, 1, 827-838.	1.6	88
847	Structural insight into gene transcriptional regulation and effector binding by the Lrp/AsnC family. Nucleic Acids Research, 2006, 34, 1439-1449.	6.5	106
848	Molecular insights into the selfâ€assembly mechanism of dystrophia myotonica kinase. FASEB Journal, 2006, 20, 1142-1151.	0.2	24
849	Structures of the Carbohydrate Recognition Domain of Ca2+-independent Cargo Receptors Emp46p and Emp47p. Journal of Biological Chemistry, 2006, 281, 10410-10419.	1.6	29
850	Structural basis for mammalian vitamin B12 transport by transcobalamin. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4386-4391.	3.3	169
851	Crystal Structure of Prephenate Dehydrogenase from Aquifex aeolicus. Journal of Biological Chemistry, 2006, 281, 12919-12928.	1.6	19
852	A Structural and Functional Analysis of Î±-Glucan Recognition by Family 25 and 26 Carbohydrate-binding Modules Reveals a Conserved Mode of Starch Recognition. Journal of Biological Chemistry, 2006, 281, 587-598.	1.6	90

#	ARTICLE	IF	CITATIONS
853	The structure of human ADP-ribosylhydrolase 3 (ARH3) provides insights into the reversibility of protein ADP-ribosylation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15026-15031.	3.3	104
854	Amino-terminal Dimerization, NRDP1-Rhodanese Interaction, and Inhibited Catalytic Domain Conformation of the Ubiquitin-specific Protease 8 (USP8). Journal of Biological Chemistry, 2006, 281, 38061-38070.	1.6	131
855	Vitamin B6 Biosynthesis by the Malaria Parasite Plasmodium falciparum. Journal of Biological Chemistry, 2006, 281, 3633-3641.	1.6	77
856	Structure of Pyrimidine 5â€²-Nucleotidase Type 1. Journal of Biological Chemistry, 2006, 281, 20521-20529.	1.6	25
857	Structural Basis for the Redox Control of Plant Glutamate Cysteine Ligase. Journal of Biological Chemistry, 2006, 281, 27557-27565.	1.6	100
858	New Antiviral Target Revealed by the Hexameric Structure of Mouse Hepatitis Virus Nonstructural Protein nsp15. Journal of Virology, 2006, 80, 7909-7917.	1.5	85
859	Structure of aminopeptidase N from Escherichia coli suggests a compartmentalized, gated active site. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13339-13344.	3.3	104
860	Structure of the Mouse Peptide N-Glycanase-HR23 Complex Suggests Co-evolution of the Endoplasmic Reticulum-associated Degradation and DNA Repair Pathways. Journal of Biological Chemistry, 2006, 281, 13751-13761.	1.6	39
861	Regulation of the Dha Operon of Lactococcus lactis. Journal of Biological Chemistry, 2006, 281, 23129-23137.	1.6	35
862	Structural and Mutational Analysis of Human Ad37 and Canine Adenovirus 2 Fiber Heads in Complex with the D1 Domain of Coxsackie and Adenovirus Receptor. Journal of Biological Chemistry, 2006, 281, 33704-33716.	1.6	81
863	Crystal Structure of Neurotropism-Associated Variable Surface Protein 1 (Vsp1) of Borrelia turicatae. Journal of Bacteriology, 2006, 188, 4522-4530.	1.0	19
864	Crystal Structure of a Viral FLIP. Journal of Biological Chemistry, 2006, 281, 2960-2968.	1.6	79
865	Automated Structure Solution With autoSHARP. , 2007, 364, 215-230.		851
866	The crystal structure of SdsA1, an alkylsulfatase from Pseudomonas aeruginosa, defines a third class of sulfatases. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7631-7636.	3.3	115
867	Severe acute respiratory syndrome coronavirus papain-like protease: Structure of a viral deubiquitinating enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5717-5722.	3.3	356
868	The molecular architecture of the metalloprotease FtsH. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3066-3071.	3.3	152
869	Bispecific Abs against modified protein and DNA with oxidized lipids. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6160-6165.	3.3	29
870	The Crystal Structure of Mismatch-specific Uracil-DNA Glycosylase (MUG) from Deinococcus radiodurans Reveals a Novel Catalytic Residue and Broad Substrate Specificity. Journal of Biological Chemistry, 2006, 281, 569-577.	1.6	19

#	Article	IF	Citations
871	The Structural Basis of Substrate Promiscuity in Glucose Dehydrogenase from the Hyperthermophilic Archaeon Sulfolobus solfataricus. Journal of Biological Chemistry, 2006, 281, 14796-14804.	1.6	51
872	Structural and Mutational Analysis of Substrate Complexation by Anthranilate Phosphoribosyltransferase from Sulfolobus solfataricus. Journal of Biological Chemistry, 2006, 281, 21410-21421.	1.6	23
873	The Structure of an Ancient Conserved Domain Establishes a Structural Basis for Stable Histidine Phosphorylation and Identifies a New Family of Adenosine-specific Kinases. Journal of Biological Chemistry, 2006, 281, 22131-22141.	1.6	10
874	Biochemical and Structural Analysis of Helix pomatia Agglutinin. Journal of Biological Chemistry, 2006, 281, 20171-20180.	1.6	129
875	Blood Group Antigen Recognition by a Streptococcus pneumoniae Virulence Factor. Journal of Biological Chemistry, 2006, 281, 35263-35271.	1.6	55
876	Structural and Functional Studies Suggest a Catalytic Mechanism for the Phosphotransacetylase from Methanosarcina thermophila. Journal of Bacteriology, 2006, 188, 1143-1154.	1.0	37
877	Structural Rearrangements of Sucrose Phosphorylase from Bifidobacterium adolescentis during Sucrose Conversion. Journal of Biological Chemistry, 2006, 281, 35576-35584.	1.6	76
878	Crystal Structure and Desulfurization Mechanism of 2â€²-Hydroxybiphenyl-2-sulfinic Acid Desulfinase. Journal of Biological Chemistry, 2006, 281, 32534-32539.	1.6	44
879	Conformational Dimorphism of Self-peptides and Molecular Mimicry in a Disease-associated HLA-B27 Subtype. Journal of Biological Chemistry, 2006, 281, 2306-2316.	1.6	49
880	Structure-based Functional Annotation. Journal of Biological Chemistry, 2006, 281, 30175-30185.	1.6	22
881	Structural Snapshots of Escherichia coli Histidinol Phosphate Phosphatase along the Reaction Pathway. Journal of Biological Chemistry, 2006, 281, 37930-37941.	1.6	39
882	Insights into the serine protease mechanism from atomic resolution structures of trypsin reaction intermediates. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6835-6840.	3.3	118
883	Structural Mechanics of the pH-dependent Activity of Î²-Carbonic Anhydrase from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2006, 281, 4993-4999.	1.6	134
884	Further Insight into S-Adenosylmethionine-dependent Methyltransferases. Journal of Biological Chemistry, 2006, 281, 4434-4445.	1.6	67
885	Crystal Structure of the FERM Domain of Focal Adhesion Kinase. Journal of Biological Chemistry, 2006, 281, 252-259.	1.6	108
886	Siglec-7 Undergoes a Major Conformational Change When Complexed with the Î±(2,8)-Disialylganglioside GT1b. Journal of Biological Chemistry, 2006, 281, 32774-32783.	1.6	82
887	Crystal Structure of Mammalian Cysteine Dioxygenase. Journal of Biological Chemistry, 2006, 281, 18723-18733.	1.6	148
888	The Crystal Structure of a Human PP2A Phosphatase Activator Reveals a Novel Fold and Highly Conserved Cleft Implicated in Protein-Protein Interactions. Journal of Biological Chemistry, 2006, 281, 22434-22438.	1.6	17

#	ARTICLE	IF	CITATIONS
889	Atomic Level Insight into the Oxidative Half-reaction of Aromatic Amine Dehydrogenase. Journal of Biological Chemistry, 2006, 281, 40264-40272.	1.6	12
890	The Zinc Finger Protein Ynr046w Is Plurifunctional and a Component of the eRF1 Methyltransferase in Yeast. Journal of Biological Chemistry, 2006, 281, 36140-36148.	1.6	54
891	Crystal Structures of Chloroperoxidase with Its Bound Substrates and Complexed with Formate, Acetate, and Nitrate. Journal of Biological Chemistry, 2006, 281, 23990-23998.	1.6	83
892	Structure of FliM provides insight into assembly of the switch complex in the bacterial flagella motor. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11886-11891.	3.3	101
893	Structural Basis of Reduction-dependent Activation of Human Cystatin F. Journal of Biological Chemistry, 2006, 281, 16570-16575.	1.6	39
894	Paratope Determination of the Antithrombotic Antibody 82D6A3 Based on the Crystal Structure of Its Complex with the von Willebrand Factor A3-Domain. Journal of Biological Chemistry, 2006, 281, 2225-2231.	1.6	23
895	Structural basis for ligand promiscuity in cytochrome P450 3A4. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13682-13687.	3.3	690
896	Structure and Activity of Two Metal Ion-dependent Acetylxylan Esterases Involved in Plant Cell Wall Degradation Reveals a Close Similarity to Peptidoglycan Deacetylases. Journal of Biological Chemistry, 2006, 281, 10968-10975.	1.6	99
897	Crystal structure of obelin after Ca2+-triggered bioluminescence suggests neutral coelenteramide as the primary excited state. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2570-2575.	3.3	84
898	The Structure of MbtI from Mycobacterium tuberculosis , the First Enzyme in the Biosynthesis of the Siderophore Mycobactin, Reveals It To Be a Salicylate Synthase. Journal of Bacteriology, 2006, 188, 6081-6091.	1.0	93
899	Crystal Structure of Heparinase II from Pedobacter heparinus and Its Complex with a Disaccharide Product*. Journal of Biological Chemistry, 2006, 281, 15525-15535.	1.6	80
900	Three-dimensional Structure of AzoR from Escherichia coli. Journal of Biological Chemistry, 2006, 281, 20567-20576.	1.6	75
901	Crystal Structure of a Bacterial Type IB DNA Topoisomerase Reveals a Preassembled Active Site in the Absence of DNA. Journal of Biological Chemistry, 2006, 281, 6030-6037.	1.6	24
902	Crystal structures of Â-glutamyltranspeptidase from Escherichia coli, a key enzyme in glutathione metabolism, and its reaction intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6471-6476.	3.3	156
903	Mechanism of action of a flavin-containing monooxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9832-9837.	3.3	152
904	The Crystal Structure of (S)-3-O-Geranylgeranylglyceryl Phosphate Synthase Reveals an Ancient Fold for an Ancient Enzyme. Journal of Biological Chemistry, 2006, 281, 6070-6078.	1.6	47
905	Family 6 Carbohydrate Binding Modules in Î²-Agarases Display Exquisite Selectivity for the Non-reducing Termini of Agarose Chains*. Journal of Biological Chemistry, 2006, 281, 17099-17107.	1.6	71
906	Catalytic Mechanism and Structure of Viral Flavin-dependent Thymidylate Synthase ThyX. Journal of Biological Chemistry, 2006, 281, 24048-24057.	1.6	53

#	Article	IF	Citations
907	Structural and biochemical studies of the C-terminal domain of mouse peptide-N-glycanase identify it as a mannose-binding module. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17214-17219.	3.3	40
908	The Structural Basis of Signal Transduction for the Response Regulator PrrA from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2006, 281, 9659-9666.	1.6	75
909	The Structure of Rauvolfia serpentina Strictosidine Synthase Is a Novel Six-Bladed Î²-Propeller Fold in Plant Proteins. Plant Cell, 2006, 18, 907-920.	3.1	126
910	Structure of the nuclear exosome component Rrp6p reveals an interplay between the active site and the HRDC domain. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11898-11903.	3.3	81
911	Structural determinants of selective Â-conotoxin binding to a nicotinic acetylcholine receptor homolog AChBP. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3615-3620.	3.3	187
912	Crystal Structure of the Human Monocyte-activating Receptor, â€œGroup 2â€•Leukocyte Ig-like Receptor A5 (LILRA5/LIR9/ILT11). Journal of Biological Chemistry, 2006, 281, 19536-19544.	1.6	29
913	DENZO and SCALEPACK. , 2006, , 226-235.		29
914	A Trimetal Site and Substrate Distortion in a Family II Inorganic Pyrophosphatase. Journal of Biological Chemistry, 2007, 282, 1422-1431.	1.6	45
915	Crystal Structure of Cel44A, a Glycoside Hydrolase Family 44 Endoglucanase from Clostridium thermocellum. Journal of Biological Chemistry, 2007, 282, 35703-35711.	1.6	43
916	Structure and quantum chemical characterization of chloroperoxidase compound 0, a common reaction intermediate of diverse heme enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 99-104.	3.3	100
917	Studies on peptide:N-glycanase-p97 interaction suggest that p97 phosphorylation modulates endoplasmic reticulum-associated degradation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8785-8790.	3.3	87
918	Structural elucidation of the m157 mouse cytomegalovirus ligand for Ly49 natural killer cell receptors. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10128-10133.	3.3	76
919	Comparison of Apo- and Heme-bound Crystal Structures of a Truncated Human Heme Oxygenase-2. Journal of Biological Chemistry, 2007, 282, 37624-37631.	1.6	56
920	The Structure of Two N-Methyltransferases from the Caffeine Biosynthetic Pathway. Plant Physiology, 2007, 144, 879-889.	2.3	105
921	Open and Closed Structures of the UDP-glucose Pyrophosphorylase from Leishmania major. Journal of Biological Chemistry, 2007, 282, 13003-13010.	1.6	48
922	A Family 2 Pectate Lyase Displays a Rare Fold and Transition Metal-assisted Î²-Elimination. Journal of Biological Chemistry, 2007, 282, 35328-35336.	1.6	35
923	Crystal Structure of the Interleukin-15Â·Interleukin-15 Receptor Î± Complex. Journal of Biological Chemistry, 2007, 282, 37191-37204.	1.6	89
924	Biochemical and Structural Characterization of the Gem GTPase. Journal of Biological Chemistry, 2007, 282, 1905-1915.	1.6	46

#	Article	IF	Citations
925	Structural Basis of the Catalytic Reaction Mechanism of Novel 1,2-Î±-L-Fucosidase from Bifidobacterium bifidum. Journal of Biological Chemistry, 2007, 282, 18497-18509.	1.6	110
926	Mannose Foraging by Bacteroides thetaiotaomicron. Journal of Biological Chemistry, 2007, 282, 11291-11299.	1.6	67
927	Crystal Structure of Human Inosine Triphosphatase. Journal of Biological Chemistry, 2007, 282, 3182-3187.	1.6	48
928	The C2A-C2B Linker Defines the High Affinity Ca2+ Binding Mode of Rabphilin-3A. Journal of Biological Chemistry, 2007, 282, 5015-5025.	1.6	16
929	Structures of Staphylococcus aureus D-Tagatose-6-phosphate Kinase Implicate Domain Motions in Specificity and Mechanism. Journal of Biological Chemistry, 2007, 282, 19948-19957.	1.6	32
930	Structure of aspartoacylase, the brain enzyme impaired in Canavan disease. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 456-461.	3.3	69
931	The Crystal Structure and Mutational Binding Analysis of the Extracellular Domain of the Platelet-activating Receptor CLEC-2. Journal of Biological Chemistry, 2007, 282, 3165-3172.	1.6	64
932	Domain Swapping within PDZ2 Is Responsible for Dimerization of ZO Proteins. Journal of Biological Chemistry, 2007, 282, 37710-37716.	1.6	48
933	A Novel Subunit Structure of Clostridium botulinum Serotype D Toxin Complex with Three Extended Arms. Journal of Biological Chemistry, 2007, 282, 24777-24783.	1.6	102
934	Klotho-related Protein Is a Novel Cytosolic Neutral Î²-Glycosylceramidase. Journal of Biological Chemistry, 2007, 282, 30889-30900.	1.6	84
935	Structural and Mechanistic Studies on the Inhibition of the Hypoxia-inducible Transcription Factor Hydroxylases by Tricarboxylic Acid Cycle Intermediates. Journal of Biological Chemistry, 2007, 282, 3293-3301.	1.6	194
936	Structure of the monooxygenase component of a two-component flavoprotein monooxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1177-1182.	3.3	98
937	Partial Agonism and Antagonism of the Ionotropic Glutamate Receptor iGLuR5. Journal of Biological Chemistry, 2007, 282, 25726-25736.	1.6	48
938	Functional specialization of domains tandemly duplicated within 16S rRNA methyltransferase RsmC. Nucleic Acids Research, 2007, 35, 4264-4274.	6.5	30
939	Nicotinamide Riboside Kinase Structures Reveal New Pathways to NAD+. PLoS Biology, 2007, 5, e263.	2.6	126
940	Structural basis for recognition of breast and colon cancer epitopes Tn antigen and Forssman disaccharide by Helix pomatia lectin. Glycobiology, 2007, 17, 1077-1083.	1.3	56
941	Structural Analysis of Xanthomonas XopD Provides Insights into Substrate Specificity of Ubiquitin-like Protein Proteases. Journal of Biological Chemistry, 2007, 282, 6773-6782.	1.6	71
942	A Novel Structural Fold in Polysaccharide Lyases. Journal of Biological Chemistry, 2007, 282, 37134-37145.	1.6	29

#	ARTICLE	IF	CITATIONS
943	Crystal Structure of Human Cytosolic 5â€²-Nucleotidase II. Journal of Biological Chemistry, 2007, 282, 17828-17836.	1.6	56
944	Structural and Mutational Studies of Anthocyanin Malonyltransferases Establish the Features of BAHD Enzyme Catalysis. Journal of Biological Chemistry, 2007, 282, 15812-15822.	1.6	94
945	The Structure of a Full-length Response Regulator from Mycobacterium tuberculosis in a Stabilized Three-dimensional Domain-swapped, Activated State. Journal of Biological Chemistry, 2007, 282, 37717-37729.	1.6	37
946	Functional and Structural Aspects of Poplar Cytosolic and Plastidial Type A Methionine Sulfoxide Reductases. Journal of Biological Chemistry, 2007, 282, 3367-3378.	1.6	56
947	Crystallographic protein model-building on the web. Bioinformatics, 2007, 23, 375-377.	1.8	4
948	SIR phasing by combination of SOLVE/RESOLVE and dual-space fragment extension involving OASIS. Chinese Physics B, 2007, 16, 3022-3028.	1.3	3
949	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. Journal of General Virology, 2007, 88, 2228-2236.	1.3	52
950	The Crystal Structure of Bacillus subtilis YycI Reveals a Common Fold for Two Members of an Unusual Class of Sensor Histidine Kinase Regulatory Proteins. Journal of Bacteriology, 2007, 189, 3290-3295.	1.0	25
951	Structural and Functional Characterization of a Novel T Cell Receptor Co-regulatory Protein Complex, CD97-CD55. Journal of Biological Chemistry, 2007, 282, 22023-22032.	1.6	60
952	MitoNEET is a uniquely folded 2Feâ€"2S outer mitochondrial membrane protein stabilized by pioglitazone. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14342-14347.	3.3	242
953	The crystal structure of two macrolide glycosyltransferases provides a blueprint for host cell antibiotic immunity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5336-5341.	3.3	132
954	Structure-Based Drug Design â€" The Use of Protein Structure in Drug Discovery. , 2007, , 597-650.		0
955	The Structure of the Macrophage Signal Regulatory Protein Î± (SIRPÎ±) Inhibitory Receptor Reveals a Binding Face Reminiscent of That Used by T Cell Receptors. Journal of Biological Chemistry, 2007, 282, 14567-14575.	1.6	66
956	Crystal Structure of the Cysteine-rich Domain of Scavenger Receptor MARCO Reveals the Presence of a Basic and an Acidic Cluster That Both Contribute to Ligand Recognition. Journal of Biological Chemistry, 2007, 282, 16654-16666.	1.6	88
957	Structure of the C-terminal head domain of the fowl adenovirus type 1 long fiber. Journal of General Virology, 2007, 88, 2407-2416.	1.3	27
958	Rational Conversion of Substrate and Product Specificity in a Salvia Monoterpene Synthase: Structural Insights into the Evolution of Terpene Synthase Function. Plant Cell, 2007, 19, 1994-2005.	3.1	204
959	The crystal structure of human dipeptidyl peptidase I (cathepsin C) in complex with the inhibitor Gly-Phe-CHN2. Biochemical Journal, 2007, 401, 645-650.	1.7	66
960	Structural Basis for the Function of DCN-1 in Protein Neddylation*. Journal of Biological Chemistry, 2007, 282, 24490-24494.	1.6	38

#	Article	IF	Citations
961	Determination of the Role of the Carboxyl-terminal Leucine-122 in FMN-binding Protein by Mutational and Structural Analysis. Journal of Biochemistry, 2007, 141, 459-468.	0.9	10
962	Crystal Structure of the Tp34 (TP0971) Lipoprotein of Treponema pallidum. Journal of Biological Chemistry, 2007, 282, 5944-5958.	1.6	46
963	Unique Thermodynamic Response of Tipranavir to Human Immunodeficiency Virus Type 1 Protease Drug Resistance Mutations. Journal of Virology, 2007, 81, 5144-5154.	1.5	113
964	Crystallographic Studies of Human MitoNEET. Journal of Biological Chemistry, 2007, 282, 33242-33246.	1.6	87
965	The 1.4-A crystal structure of the S. pombe Pop2p deadenylase subunit unveils the configuration of an active enzyme. Nucleic Acids Research, 2007, 35, 3153-3164.	6.5	49
966	Crystal structure of the incretin-bound extracellular domain of a G protein-coupled receptor. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13942-13947.	3.3	222
967	Crystal Structures of an ATP-dependent Hexokinase with Broad Substrate Specificity from the Hyperthermophilic Archaeon Sulfolobus tokodaii. Journal of Biological Chemistry, 2007, 282, 9923-9931.	1.6	53
968	Structural and Membrane Binding Analysis of the Phox Homology Domain of Bem1p. Journal of Biological Chemistry, 2007, 282, 25737-25747.	1.6	53
969	Crystal Structure of an Unusual Thioredoxin Protein with a Zinc Finger Domain. Journal of Biological Chemistry, 2007, 282, 34945-34951.	1.6	15
970	Structural Basis of Substrate-binding Specificity of Human Arylamine N-Acetyltransferases. Journal of Biological Chemistry, 2007, 282, 30189-30197.	1.6	109
971	The Laminin 511/521â€“binding site on the Lutheran blood group glycoprotein is located at the flexible junction of Ig domains 2 and 3. Blood, 2007, 110, 3398-3406.	0.6	39
972	Structural Insight into KCNQ (Kv7) Channel Assembly and Channelopathy. Neuron, 2007, 53, 663-675.	3.8	151
973	Structural Analysis of the Synaptic Protein Neuroligin and Its Î²-Neurexin Complex: Determinants for Folding and Cell Adhesion. Neuron, 2007, 56, 979-991.	3.8	142
974	High resolution crystal structures of the p120 RasGAP SH3 domain. Biochemical and Biophysical Research Communications, 2007, 353, 463-468.	1.0	13
975	Crystal structure study on human S100A13 at 2.0Ã… resolution. Biochemical and Biophysical Research Communications, 2007, 356, 616-621.	1.0	14
976	Crystal structure of scaffolding protein CheW from thermoanaerobacter tengcongensis. Biochemical and Biophysical Research Communications, 2007, 361, 1027-1032.	1.0	8
977	Crystal structure of Ufc1, the Ufm1-conjugating enzyme. Biochemical and Biophysical Research Communications, 2007, 362, 1079-1084.	1.0	38
978	RF3 Induces Ribosomal Conformational Changes Responsible for Dissociation of Class I Release Factors. Cell, 2007, 129, 929-941.	13.5	128

#	Article	IF	Citations
979	p31comet Blocks Mad2 Activation through Structural Mimicry. Cell, 2007, 131, 744-755.	13.5	172
980	Crystal Structure ofHomo sapiensKynureninaseâ€,â€¡. Biochemistry, 2007, 46, 2735-2744.	1.2	41
981	Crystal structure of chagasin, the endogenous cysteine-protease inhibitor from Trypanosoma cruzi. Journal of Structural Biology, 2007, 157, 416-423.	1.3	31
982	The crystal structure of DR2241 from Deinococcus radiodurans at 1.9 Ã… resolution reveals a multi-domain protein with structural similarity to chelatases but also with two additional novel domains. Journal of Structural Biology, 2007, 159, 92-102.	1.3	7
983	Crystal structure of a transcriptional regulator TM1030 from Thermotoga maritima solved by an unusual MAD experiment. Journal of Structural Biology, 2007, 159, 424-432.	1.3	9
984	The Structure and Computational Analysis of Mycobacterium tuberculosis Protein CitE Suggest a Novel Enzymatic Function. Journal of Molecular Biology, 2007, 365, 275-283.	2.0	37
985	Distinct Effector-binding Sites Enable Synergistic Transcriptional Activation by BenM, a LysR-type Regulator. Journal of Molecular Biology, 2007, 367, 616-629.	2.0	89
986	The Structural Basis of Î±-Glucan Recognition by a Family 41 Carbohydrate-binding Module from Thermotoga maritima. Journal of Molecular Biology, 2007, 365, 555-560.	2.0	44
987	Crystal Structure and Functional Characterization of a D-Stereospecific Amino Acid Amidase from Ochrobactrum anthropi SV3, a New Member of the Penicillin-recognizing Proteins. Journal of Molecular Biology, 2007, 368, 79-91.	2.0	29
988	Crystal Structure of Bacillus cereus HlyIIR, a Transcriptional Regulator of the Gene for Pore-forming Toxin Hemolysin II. Journal of Molecular Biology, 2007, 365, 825-834.	2.0	18
989	Crystal Structures of Human IPP Isomerase: New Insights into the Catalytic Mechanism. Journal of Molecular Biology, 2007, 366, 1437-1446.	2.0	19
990	The Crystal Structure of the Dps2 from Deinococcus radiodurans Reveals an Unusual Pore Profile with a Non-specific Metal Binding Site. Journal of Molecular Biology, 2007, 371, 787-799.	2.0	44
991	Two Structures of Alliinase from Alliium sativum L.: Apo Form and Ternary Complex with Aminoacrylate Reaction Intermediate Covalently Bound to the PLP Cofactor. Journal of Molecular Biology, 2007, 366, 611-625.	2.0	55
992	Crystal Structure of Human Cyclin K, a Positive Regulator of Cyclin-dependent Kinase 9. Journal of Molecular Biology, 2007, 366, 563-573.	2.0	27
993	Structure and Dynamics of UDPâ€“Glucose Pyrophosphorylase from Arabidopsis thaliana with Bound UDPâ€“Glucose and UTP. Journal of Molecular Biology, 2007, 366, 830-841.	2.0	43
994	Cryptochrome 3 from Arabidopsis thaliana: Structural and Functional Analysis of its Complex with a Folate Light Antenna. Journal of Molecular Biology, 2007, 366, 954-964.	2.0	74
995	The Structure of a Bacterial l-Amino Acid Oxidase from Rhodococcus opacus Gives New Evidence for the Hydride Mechanism for Dehydrogenation. Journal of Molecular Biology, 2007, 367, 234-248.	2.0	71
996	Structure and Action of a CC Bond Cleaving Î±/Î²-Hydrolase Involved in Nicotine Degration. Journal of Molecular Biology, 2007, 367, 409-418.	2.0	25

#	ARTICLE	IF	CITATIONS
997	Identification and Characterization of a Novel Periplasmic Polygalacturonic Acid Binding Protein from Yersinia enterolitica. Journal of Molecular Biology, 2007, 367, 1023-1033.	2.0	52
998	Structure and Interactions of the First Three RNA Recognition Motifs of Splicing Factor Prp24. Journal of Molecular Biology, 2007, 367, 1447-1458.	2.0	36
999	Crystal Structures of the Substrate Free-enzyme, and Reaction Intermediate of the HAD Superfamily Member, Haloacid Dehalogenase DehIVa from Burkholderia cepacia MBA4. Journal of Molecular Biology, 2007, 368, 706-717.	2.0	49
1000	Apo and Calcium-bound Crystal Structures of Alpha-11 Giardin, an Unusual Annexin from Giardia lamblia. Journal of Molecular Biology, 2007, 368, 493-508.	2.0	16
1001	Chloroplasts Assemble the Major Subunit FaeG of Escherichia coli F4 (K88) Fimbriae to Strand-swapped Dimers. Journal of Molecular Biology, 2007, 368, 791-799.	2.0	27
1002	The Solution and Crystal Structures of a Module Pair from the Staphylococcus aureus-Binding Site of Human Fibronectinâ€"A Tale with a Twist. Journal of Molecular Biology, 2007, 368, 833-844.	2.0	34
1003	Structural Basis for the Carbohydrate Recognition of the Sclerotium rolfsii Lectin. Journal of Molecular Biology, 2007, 368, 1145-1161.	2.0	40
1004	A Tick Protein with a Modified Kunitz Fold Inhibits Human Tryptase. Journal of Molecular Biology, 2007, 368, 1172-1186.	2.0	57
1005	Molecular Implications of Evolutionary Differences in CHD Double Chromodomains. Journal of Molecular Biology, 2007, 369, 334-342.	2.0	51
1006	Specific Recognition of Saturated and 4,5-Unsaturated Hexuronate Sugars by a Periplasmic Binding Protein Involved in Pectin Catabolism. Journal of Molecular Biology, 2007, 369, 759-770.	2.0	27
1007	Structural Characterization of B and non-B Subtypes of HIV-Protease: Insights into the Natural Susceptibility to Drug Resistance Development. Journal of Molecular Biology, 2007, 369, 1029-1040.	2.0	38
1008	The Structure of the Regulatory Domain of the Adenylyl Cyclase Rv1264 from Mycobacterium tuberculosis with Bound Oleic Acid. Journal of Molecular Biology, 2007, 369, 1282-1295.	2.0	13
1009	Crystal Structures of a Poplar Thioredoxin Peroxidase that Exhibits the Structure of Glutathione Peroxidases: Insights into Redox-driven Conformational Changes. Journal of Molecular Biology, 2007, 370, 512-529.	2.0	93
1010	Crystal Structure of the 16 Heme Cytochrome from Desulfovibrio gigas: A Glycosylated Protein in a Sulphate-reducing Bacterium. Journal of Molecular Biology, 2007, 370, 659-673.	2.0	23
1011	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
1012	Structures of Ligand-free and Inhibitor Complexes of Dihydroorotase from Escherichia coli: Implications for Loop Movement in Inhibitor Design. Journal of Molecular Biology, 2007, 370, 812-825.	2.0	35
1013	Structure and Dynamics of LC8 Complexes with KXTQT-Motif Peptides: Swallow and Dynein Intermediate Chain Compete for a Common Site. Journal of Molecular Biology, 2007, 371, 457-468.	2.0	75
1014	Crystal Structure of Bovine Lipoyltransferase in Complex with Lipoyl-AMP. Journal of Molecular Biology, 2007, 371, 222-234.	2.0	28

#	ARTICLE	IF	CITATIONS
1015	Crystal Structure of ll-Diaminopimelate Aminotransferase from Arabidopsis thaliana: A Recently Discovered Enzyme in the Biosynthesis of l-Lysine by Plants and Chlamydia. Journal of Molecular Biology, 2007, 371, 685-702.	2.0	42
1016	Blood Group Antigen Recognition by Escherichia coli Heat-labile Enterotoxin. Journal of Molecular Biology, 2007, 371, 754-764.	2.0	61
1017	The Crystal Structure of the Cytosolic Exopolyphosphatase from Saccharomyces cerevisiae Reveals the Basis for Substrate Specificity. Journal of Molecular Biology, 2007, 371, 1007-1021.	2.0	36
1018	Crystal Structure and Biochemical Properties of the d-Arabinose Dehydrogenase from Sulfolobus solfataricus. Journal of Molecular Biology, 2007, 371, 1249-1260.	2.0	16
1019	Structure and Action of the N-oxygenase AurF from Streptomyces thioluteus. Journal of Molecular Biology, 2007, 373, 65-74.	2.0	52
1020	Structural Basis for Polyproline Recognition by the FE65 WW Domain. Journal of Molecular Biology, 2007, 372, 970-980.	2.0	43
1021	Crystal Structure of the Transcriptional Regulator CmeR from Campylobacter jejuni. Journal of Molecular Biology, 2007, 372, 583-593.	2.0	50
1022	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
1023	Crystal Structures of Human ADAMTS-1 Reveal a Conserved Catalytic Domain and a Disintegrin-like Domain with a Fold Homologous to Cysteine-Rich Domains. Journal of Molecular Biology, 2007, 373, 891-902.	2.0	86
1024	Structureâ€“based Mechanism of Ligand Binding for Periplasmic Solute-binding Protein of the Bug Family. Journal of Molecular Biology, 2007, 373, 954-964.	2.0	21
1025	Biochemical and Structural Characterization of the Paralogous Benzoate CoA Ligases from Burkholderia xenovorans LB400: Defining the Entry Point into the Novel Benzoate Oxidation (box) Pathway. Journal of Molecular Biology, 2007, 373, 965-977.	2.0	43
1026	Structural and Biochemical Basis for Polyamine Binding to the Tp0655 Lipoprotein of Treponema pallidum: Putative Role for Tp0655 (TpPotD) as a Polyamine Receptor. Journal of Molecular Biology, 2007, 373, 681-694.	2.0	37
1027	A Beta-Sheet Interaction Interface Directs the Tetramerisation of the Miz-1 POZ Domain. Journal of Molecular Biology, 2007, 373, 820-826.	2.0	33
1028	Bis-methionyl Coordination in the Crystal Structure of the Heme-binding Domain of the Streptococcal Cell Surface Protein Shp. Journal of Molecular Biology, 2007, 374, 374-383.	2.0	49
1029	Crystal Structure of the Transcriptional Regulator AcrR from Escherichia coli. Journal of Molecular Biology, 2007, 374, 591-603.	2.0	79
1030	Understanding Nicotinamide Dinucleotide Cofactor and Substrate Specificity in Class I Flavoprotein Disulfide Oxidoreductases: Crystallographic Analysis of a Glutathione Amide Reductase. Journal of Molecular Biology, 2007, 374, 883-889.	2.0	9
1031	Structural and Binding Studies of the Three-metal Center in Two Mycobacterial PPM Ser/Thr Protein Phosphatases. Journal of Molecular Biology, 2007, 374, 890-898.	2.0	66
1032	Crystal Structures of the Luciferase and Green Fluorescent Protein from Renilla reniformis. Journal of Molecular Biology, 2007, 374, 1017-1028.	2.0	130

#	Article	IF	Citations
1033	Molecular Basis of the Antimutagenic Activity of the House-Cleaning Inosine Triphosphate Pyrophosphatase RdgB from Escherichia coli. Journal of Molecular Biology, 2007, 374, 1091-1103.	2.0	26
1034	Crystal structure of a family I.3 lipase from <i>Pseudomonas</i> sp. MIS38 in a closed conformation. FEBS Letters, 2007, 581, 5060-5064.	1.3	71
1035	Crystal structure of calf spleen purine nucleoside phosphorylase complexed to a novel purine analogue. FEBS Letters, 2007, 581, 5082-5086.	1.3	10
1036	Crystal structure of a bacterial albumin-binding domain at 1.4 Ã… resolution. FEBS Letters, 2007, 581, 3178-3182.	1.3	13
1037	Methyltransferase That Modifies Guanine 966 of the 16 S rRNA. Journal of Biological Chemistry, 2007, 282, 5880-5887.	1.6	82
1038	Second SH3 Domain of Ponsin Solved from Powder Diffraction. Journal of the American Chemical Society, 2007, 129, 11865-11871.	6.6	42
1039	Crystal structure of AFV3-109, a highly conserved protein from crenarchaeal viruses. Virology Journal, 2007, 4, 12.	1.4	31
1040	Crystallography and Lectin Structure Database. , 2007, , 15-50.		0
1041	Staphylococcal Complement Inhibitor: Structure and Active Sites. Journal of Immunology, 2007, 179, 2989-2998.	0.4	74
1042	DNA binding mechanism revealed by high resolution crystal structure of Arabidopsis thaliana WRKY1 protein. Nucleic Acids Research, 2007, 35, 1145-1154.	6.5	131
1043	A Calcium-gated Lid and a Large Î²-Roll Sandwich Are Revealed by the Crystal Structure of Extracellular Lipase from Serratia marcescens. Journal of Biological Chemistry, 2007, 282, 31477-31483.	1.6	88
1044	Database Approaches and Data Representation in Structural Bioinformatics. , 2007, , .		1
1045	A Complete Structural Description of the Catalytic Cycle of Yeast Pyrophosphataseâ€,â€¡. Biochemistry, 2007, 46, 1228-1239.	1.2	45
1046	The Crystal Structures of the Calcium-Bound con-G and con-T[K7Î³] Dimeric Peptides Demonstrate a Metal-Dependent Helix-Forming Motif. Journal of the American Chemical Society, 2007, 129, 1586-1593.	6.6	27
1047	Crystal Structure of the Bowman-Birk Inhibitor from Vigna unguiculata Seeds in Complex with Î²-Trypsin at 1.55 Ã… Resolution and Its Structural Properties in Association with Proteinases. Biophysical Journal, 2007, 92, 1638-1650.	0.2	44
1048	Structural Ramification for Acetyl-Lysine Recognition by the Bromodomain of Human BRG1 Protein, a Central ATPase of the SWI/SNF Remodeling Complex. ChemBioChem, 2007, 8, 1308-1316.	1.3	56
1049	Role of Asn2 and Glu7 residues in the oxidative folding and on the conformation of theN-terminal loop of apamin. Biopolymers, 2007, 86, 447-462.	1.2	11
1050	Xâ€ray Structures and Thermodynamics of the Interaction of PAâ€IL from <i>Pseudomonas aeruginosa</i> with Disaccharide Derivatives. ChemMedChem, 2007, 2, 1328-1338.	1.6	61

#	Article	IF	Citations
1051	Structural Proof of a Dimeric Positive Modulator Bridging Two Identical AMPA Receptor-Binding Sites. Chemistry and Biology, 2007, 14, 1294-1303.	6.2	63
1052	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
1053	Structure-assisted discovery of an aminothiazole derivative as a lead molecule for inhibition of bacterial fatty-acid synthesis. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1208-1216.	2.5	24
1054	Structure of rat acidic fibroblast growth factor at 1.4â€…Å… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 65-68.	0.7	3
1055	Structure of 5-formyltetrahydrofolate cyclo-ligase fromBacillus anthracis(BA4489). Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 168-172.	0.7	11
1056	Structure of the buffalo secretory signalling glycoprotein at 2.8â€…Å… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 258-265.	0.7	5
1057	Oligomerization of BenM, a LysR-type transcriptional regulator: structural basis for the aggregation of proteins in this family. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 361-368.	0.7	34
1058	Structure of the ThDP-dependent enzyme benzaldehyde lyase refined to 1.65â€…Å… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 546-548.	0.7	9
1059	Crystallization and X-ray diffraction analysis of a novel immune-type receptor fromIctalurus punctatusand phasing by selenium anomalous dispersion methods. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 1035-1037.	0.7	3
1060	Engineering of PA-IIL lectin from Pseudomonas aeruginosa â€“ Unravelling the role of the specificity loop for sugar preference. BMC Structural Biology, 2007, 7, 36.	2.3	40
1061	X-ray structures of two proteins belonging to Pfam DUF178 revealed unexpected structural similarity to the DUF191 Pfam family. BMC Structural Biology, 2007, 7, 62.	2.3	5
1062	Structure and characterization of a novel chicken biotin-binding protein A (BBP-A). BMC Structural Biology, 2007, 7, 8.	2.3	16
1063	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium Moorella thermoacetica. Proteins: Structure, Function and Bioinformatics, 2007, 67, 167-176.	1.5	28
1064	High resolution structure of streptavidin in complex with a novel high affinity peptide tag mimicking the biotin binding motif. Proteins: Structure, Function and Bioinformatics, 2007, 67, 1147-1153.	1.5	8
1065	Structural basis of allele variation of human thiopurine-S-methyltransferase. Proteins: Structure, Function and Bioinformatics, 2007, 67, 198-208.	1.5	38
1066	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
1067	Crystal structure of NMA1982 from <i>Neisseria meningitidis</i> at 1.5 Å… resolution provides a structural scaffold for nonclassical, eukaryoticâ€like phosphatases. Proteins: Structure, Function and Bioinformatics, 2007, 69, 415-421.	1.5	11
1068	Crystal structure and putative function of small Toprim domainâ€containing protein from <i>Bacillus stearothermophilus</i>. Proteins: Structure, Function and Bioinformatics, 2008, 70, 311-319.	1.5	23

#	ARTICLE	IF	CITATIONS
1069	The crystal structure of the effectorâ€binding domain of the trehalose repressor TreR from <i>Bacillus subtilis</i> 168 reveals a unique quarternary assembly. Proteins: Structure, Function and Bioinformatics, 2007, 69, 679-682.	1.5	12
1070	Crystal structures of two novel dyeâ€decolorizing peroxidases reveal a Î²â€barrel fold with a conserved hemeâ€binding motif. Proteins: Structure, Function and Bioinformatics, 2007, 69, 223-233.	1.5	81
1071	Structure of <i>Xanthomonas axonopodis</i> pv. citri YaeQ reveals a new compact protein fold built around a variation of the PDâ€(D/E)XK nuclease motif. Proteins: Structure, Function and Bioinformatics, 2007, 69, 644-651.	1.5	4
1072	The crystal structure of <i>Trypanosoma cruzi</i> arginine kinase. Proteins: Structure, Function and Bioinformatics, 2007, 69, 209-212.	1.5	28
1073	Xâ€ray structure of imidazolonepropionase from <i>Agrobacterium tumefaciens</i> at 1.87 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2007, 69, 652-658.	1.5	2
1074	The 1.3 Ã… crystal structure of a novel endoâ€Î²â€1,3â€glucanase of glycoside hydrolase family 16 from alkaliphilic <i>Nocardiopsis</i> sp. strain F96. Proteins: Structure, Function and Bioinformatics, 2007, 69, 683-690.	1.5	55
1075	Crystal structure of MtnX phosphatase from <i>Bacillus subtilis</i> at 2.0 Ã… resolution provides a structural basis for bipartite phosphomonoester hydrolysis of 2â€hydroxyâ€3â€ketoâ€5â€methylthiopentenylâ€1â€phosphate. Proteins: Structure, Function and Bioinformatics, 2007, 69, 433-439.	1.5	6
1076	The structure of flavinâ€dependent tryptophan 7â€halogenase RebH. Proteins: Structure, Function and Bioinformatics, 2008, 70, 289-293.	1.5	89
1077	Crystal structure of <i>Arabidopsis thaliana</i> cytokinin dehydrogenase. Proteins: Structure, Function and Bioinformatics, 2008, 70, 303-306.	1.5	20
1078	Crystal structure of <i>Homo sapiens</i> protein LOC79017. Proteins: Structure, Function and Bioinformatics, 2008, 70, 588-591.	1.5	0
1079	Bacterial glycosidases for the production of universal red blood cells. Nature Biotechnology, 2007, 25, 454-464.	9.4	259
1080	Prediction and assignment of function for a divergent N-succinyl amino acid racemase. Nature Chemical Biology, 2007, 3, 486-491.	3.9	98
1081	Structure of the C-terminal half of UvrC reveals an RNase H endonuclease domain with an Argonaute-like catalytic triad. EMBO Journal, 2007, 26, 613-622.	3.5	55
1082	Structural conservation of RecF and Rad50: implications for DNA recognition and RecF function. EMBO Journal, 2007, 26, 867-877.	3.5	54
1083	Structural basis for ARF1-mediated recruitment of ARHGAP21 to Golgi membranes. EMBO Journal, 2007, 26, 1953-1962.	3.5	86
1084	Structural basis for enzymatic excision of N1-methyladenine and N3-methylcytosine from DNA. EMBO Journal, 2007, 26, 2206-2217.	3.5	37
1085	Structural basis of the 3â€²-end recognition of a leading strand in stalled replication forks by PriA. EMBO Journal, 2007, 26, 2584-2593.	3.5	55
1086	Atomic resolution insight into host cell recognition by Toxoplasma gondii. EMBO Journal, 2007, 26, 2808-2820.	3.5	98

#	ARTICLE	IF	CITATIONS
1087	Noncovalent interaction between Ubc9 and SUMO promotes SUMO chain formation. EMBO Journal, 2007, 26, 2797-2807.	3.5	177
1088	Molecular basis of the activity of the phytopathogen pectin methylesterase. EMBO Journal, 2007, 26, 3879-3887.	3.5	99
1089	Structural insights into the recognition of substrates and activators by the OSR1 kinase. EMBO Reports, 2007, 8, 839-845.	2.0	89
1091	Identification and structural basis of binding to host lung glycogen by streptococcal virulence factors. Nature Structural and Molecular Biology, 2007, 14, 76-84.	3.6	72
1092	Factor B structure provides insights into activation of the central protease of the complement system. Nature Structural and Molecular Biology, 2007, 14, 224-228.	3.6	97
1093	Structural basis for autoinhibition of Notch. Nature Structural and Molecular Biology, 2007, 14, 295-300.	3.6	317
1094	The multifunctional human p100 protein 'hooks' methylated ligands. Nature Structural and Molecular Biology, 2007, 14, 779-784.	3.6	72
1095	Structural basis for synthesis of inflammatory mediators by human leukotriene C4 synthase. Nature, 2007, 448, 613-616.	13.7	166
1096	Structural basis of Dscam isoform specificity. Nature, 2007, 449, 487-491.	13.7	146
1097	Structure of acid-sensing ion channel 1 at 1.9â€‰Ã… resolution and low pH. Nature, 2007, 449, 316-323.	13.7	979
1098	High-resolution structure prediction and the crystallographic phase problem. Nature, 2007, 450, 259-264.	13.7	296
1099	Intrinsic motions along an enzymatic reaction trajectory. Nature, 2007, 450, 838-844.	13.7	814
1100	An atypical receiver domain controls the dynamic polar localization of the Myxococcus xanthus social motility protein FrzS. Molecular Microbiology, 2007, 65, 319-332.	1.2	32
1101	Structural similarity between the DnaAâ€binding proteins HobA (HP1230) from <i>Helicobacter pylori</i> and DiaA from <i>Escherichia coli</i>. Molecular Microbiology, 2007, 65, 995-1005.	1.2	42
1102	The structure of human collapsin response mediator protein 2, a regulator of axonal growth. Journal of Neurochemistry, 2007, 101, 906-917.	2.1	63
1103	Crystal structure and solution characterization of the activation domain of human methionine synthase. FEBS Journal, 2007, 274, 738-750.	2.2	16
1104	The crystal structure of phenylpyruvate decarboxylase from Azospirillum brasilense at 1.5â€ƒÃ… resolution. FEBS Journal, 2007, 274, 2363-2375.	2.2	35
1105	The crystal structure of the ring-hydroxylating dioxygenase from Sphingomonas CHY-1. FEBS Journal, 2007, 274, 2470-2481.	2.2	46

#	ARTICLE	IF	CITATIONS
1106	Nucleotide binding to human UMPâ€CMP kinase using fluorescent derivativesâ€ƒâˆ’â€ƒa screening based on affinity for the UMPâ€CMP binding site. FEBS Journal, 2007, 274, 3704-3714.	2.2	12
1107	Crystal structures of a familyâ€ƒ19 chitinase from <i>Brassica juncea</i> show flexibility of binding cleft loops. FEBS Journal, 2007, 274, 3695-3703.	2.2	33
1108	High resolution structure and catalysis of <i>O</i>â€acetylserine sulfhydrylase isozymeâ€ƒB from <i>Escherichia coli</i>. FEBS Journal, 2007, 274, 5382-5389.	2.2	18
1109	Compensating Enthalpic and Entropic Changes Hinder Binding Affinity Optimization. Chemical Biology and Drug Design, 2007, 69, 413-422.	1.5	163
1110	Structures of Lung Cancer-Derived EGFR Mutants and Inhibitor Complexes: Mechanism of Activation and Insights into Differential Inhibitor Sensitivity. Cancer Cell, 2007, 11, 217-227.	7.7	933
1111	The Crucial Step in Ether Phospholipid Biosynthesis: Structural Basis of a Noncanonical Reaction Associated with a Peroxisomal Disorder. Structure, 2007, 15, 683-692.	1.6	44
1112	Crystal Structure of the DNA Repair Enzyme Ultraviolet Damage Endonuclease. Structure, 2007, 15, 1316-1324.	1.6	22
1113	Insights into the Catalytic Mechanism of PPM Ser/Thr Phosphatases from the Atomic Resolution Structures of a Mycobacterial Enzyme. Structure, 2007, 15, 863-872.	1.6	46
1114	X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. Quarterly Reviews of Biophysics, 2007, 40, 191-285.	2.4	1,026
1115	Exploring subdomain cooperativity in T4 lysozyme I: Structural and energetic studies of a circular permutant and protein fragment. Protein Science, 2007, 16, 842-851.	3.1	35
1116	Mutation of interfaces in domain-swapped human betaB2-crystallin. Protein Science, 2007, 16, 615-625.	3.1	56
1117	High-resolution structures of formate dehydrogenase fromCandida boidinii. Protein Science, 2007, 16, 1146-1156.	3.1	99
1118	Structural and biochemical characterization of a novel Mn2+-dependent phosphodiesterase encoded by theyfcEgene. Protein Science, 2007, 16, 1338-1348.	3.1	24
1119	Structure of the fungal Î²-glucan-binding immune receptor dectin-1: Implications for function. Protein Science, 2007, 16, 1042-1052.	3.1	168
1120	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Ã… resolution. Protein Science, 2007, 16, 2294-2300.	3.1	30
1121	Crystal structure of activin receptor type IIB kinase domain from human at 2.0 Ã… resolution. Protein Science, 2007, 16, 2272-2277.	3.1	30
1122	Atomicâ€resolution crystal structure of the antiviral lectin scytovirin. Protein Science, 2007, 16, 2756-2760.	3.1	32
1123	Crystal structure of an <i>apo</i> form of <i>Shigella flexneri</i> ArsH protein with an NADPHâ€dependent FMN reductase activity. Protein Science, 2007, 16, 2483-2490.	3.1	37

#	ARTICLE	IF	CITATIONS
1124	RNABC: forward kinematics to reduce all-atom steric clashes in RNA backbone. Journal of Mathematical Biology, 2007, 56, 253-278.	0.8	24
1125	Structural and transcriptional analyses of a purine nucleotide-binding protein from Pyrococcus furiosus: a component of a novel, membrane-bound multiprotein complex unique to this hyperthermophilic archaeon. Journal of Structural and Functional Genomics, 2007, 8, 1-10.	1.2	0
1126	Structure of SO2946 orphan from Shewanella oneidensis shows â€œjelly-rollâ€•fold with carbohydrate-binding module. Journal of Structural and Functional Genomics, 2008, 9, 1-6.	1.2	0
1127	High-throughput crystallization-to-structure pipeline at RIKEN SPring-8 Center. Journal of Structural and Functional Genomics, 2008, 9, 21-28.	1.2	25
1128	Structure and metal binding properties of ZnuA, a periplasmic zinc transporter from Escherichia coli. Journal of Biological Inorganic Chemistry, 2008, 13, 271-288.	1.1	116
1129	The crystal structure of the catalytic domain of a eukaryotic guanylate cyclase. BMC Structural Biology, 2008, 8, 42.	2.3	97
1130	<i>MrBUMP</i>: an automated pipeline for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 119-124.	2.5	148
1131	<i>ARP</i>/<i>wARP</i>and molecular replacement: the next generation. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 49-60.	2.5	142
1132	<i>BALBES</i>: a molecular-replacement pipeline. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 125-132.	2.5	663
1133	Iterative model building, structure refinement and density modification with the<i>PHENIX AutoBuild</i>wizard. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 61-69.	2.5	1,319
1134	Surprises and pitfalls arising from (pseudo)symmetry. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 99-107.	2.5	81
1135	Protein crystallography with a micrometre-sized synchrotron-radiation beam. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 158-166.	2.5	77
1136	A knowledge-driven approach for crystallographic protein model completion. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 416-424.	2.5	23
1137	Structure of acostatin, a dimeric disintegrin from Southern copperhead (<i>Agkistrodon contortrix) Tj ETQq1 1 0.784314 rgBT /Overloc 2008, 64, 466-470.	2.5	20
1138	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 515-524.	2.5	165
1139	Structure of the C-terminal domain of the arginine repressor protein fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 950-956.	2.5	8
1140	Structure of the thioredoxin-like domain of yeast glutaredoxin 3. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 927-932.	2.5	16
1141	Nucleotide-binding flexibility in ultrahigh-resolution structures of the SRP GTPase Ffh. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1043-1053.	2.5	3

#	ARTICLE	IF	CITATIONS
1142	Preliminary X-ray characterization of a novel type of anchoring cohesin from the cellulosome of<i>Ruminococcus flavefaciens</i>. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 77-80.	0.7	5
1143	Structure of calcium-bound human S100A13 at pH 7.5 at 1.8â€…Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 70-76.	0.7	14
1144	Dimerization effect of sucrose octasulfate on rat FGF1. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 448-452.	0.7	7
1145	Structure ofDeinococcus radioduranstunicamycin-resistance protein (TmrD), a phosphotransferase. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 479-486.	0.7	7
1146	Complexes of the copper-containing amine oxidase from<i>Arthrobacter globiformis</i>with the inhibitors benzylhydrazine and tranylcypromine. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 577-583.	0.7	13
1147	Crystallization and preliminary crystallographic analysis of mannosyl-3-phosphoglycerate synthase fromRubrobacter xylanophilus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 760-763.	0.7	9
1148	Coenzyme- and His-tag-induced crystallization of octopine dehydrogenase. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 836-839.	0.7	12
1149	Crystallization and preliminary crystallographic studies of putative threonyl-tRNA synthetases fromAeropyrum pernixandSulfolobus tokodaii. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 903-910.	0.7	3
1150	1.9â€…Ã… structure of the signal receiver domain of the putative response regulator NarL from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1096-1100.	0.7	24
1151	Crystal structure solution of a ParBâ€like nuclease at atomic resolution. Proteins: Structure, Function and Bioinformatics, 2008, 70, 263-267.	1.5	7
1152	First crystallographic models of human TBC domains in the context of a familyâ€wide structural analysis. Proteins: Structure, Function and Bioinformatics, 2008, 71, 497-502.	1.5	9
1153	Crystal structure of the proline iminopeptidaseâ€related protein TTHA1809 from <i>Thermus thermophilus</i> HB8. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1646-1649.	1.5	3
1154	Crystal structure of an ADPâ€ribosylated protein with a cytidine deaminaseâ€like fold, but unknown function (TM1506), from <i>Thermotoga maritima</i> at 2.70 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1546-1552.	1.5	6
1155	Crystal structure of native <i>O</i>â€acetylâ€serine sulfhydrylase from <i>Entamoeba histolytica</i> and its complex with cysteine: Structural evidence for cysteine binding and lack of interactions with serine acetyl transferase. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1222-1232.	1.5	35
1156	RhoB can adopt a Mg²⁺ free conformation prior to GEF binding. Proteins: Structure, Function and Bioinformatics, 2008, 72, 498-505.	1.5	7
1157	Crystal structure of uncharacterized protein TTHA1756 from <i>Thermus thermophilus</i> HB8: Structural variety in UPF0150 family proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 2097-2101.	1.5	3
1158	Crystal structures of MW1337R and lin2004: Representatives of a novel protein family that adopt a fourâ€helical bundle fold. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1589-1596.	1.5	3
1159	Crystal structure of YagE, a putative DHDPSâ€like protein from <i>Escherichia coli K12</i>. Proteins: Structure, Function and Bioinformatics, 2008, 71, 2102-2108.	1.5	5

#	ARTICLE	IF	CITATIONS
1160	Crystal structure of a novel nonâ€Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by Sâ€SAD using a Cr Xâ€ray source. Proteins: Structure, Function and Bioinformatics, 2008, 71, 2109-2113.	1.5	8
1161	Crystal structure of Tflp: A ferredoxinâ€like metalloâ€Î²â€lactamase superfamily protein from <i>Thermoanaerobacter tengcongensis</i>. Proteins: Structure, Function and Bioinformatics, 2008, 72, 531-536.	1.5	6
1162	Crystal structure of human phosphomavelonate kinase at 1.8 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2008, 73, 254-258.	1.5	16
1163	The crystal structure of human cleavage and polyadenylation specific factorâ€5 reveals a dimeric Nudix protein with a conserved catalytic site. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1047-1052.	1.5	10
1164	Structure of the OSR1 kinase, a hypertension drug target. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1082-1087.	1.5	39
1165	Rational Modification of Ligandâ€Binding Preference of Avidin by Circular Permutation and Mutagenesis. ChemBioChem, 2008, 9, 1124-1135.	1.3	24
1166	Crystal Structure and Mechanism of a DNA (6â€4) Photolyase. Angewandte Chemie - International Edition, 2008, 47, 10076-10080.	7.2	174
1167	Structureâ€Based Insight into the Asymmetric Bioreduction of the Cï£¾C Double Bond of Î±,Î²â€Unsaturated Nitroalkenes by Pentaerythritol Tetranitrate Reductase. Advanced Synthesis and Catalysis, 2008, 350, 2789-2803.	2.1	84
1169	X-ray crystal structure of Mycobacterium tuberculosis haloalkane dehalogenase Rv2579. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 351-362.	1.1	28
1170	Crystal structure of Mycobacterium tuberculosis Rv0760c at 1.50ÂÃ… resolution, a structural homolog of Î”5-3-ketosteroid isomerase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1625-1632.	1.1	9
1171	Biochemical and Structural Insights of the Early Glycosylation Steps in Calicheamicin Biosynthesis. Chemistry and Biology, 2008, 15, 842-853.	6.2	51
1172	Design of an engineered Nâ€terminal HIVâ€1 gp41 trimer with enhanced stability and potency. Protein Science, 2008, 17, 633-643.	3.1	24
1173	N15 Cro and Î» Cro: Orthologous DNAâ€binding domains with completely different but equally effective homodimer interfaces. Protein Science, 2008, 17, 803-812.	3.1	17
1174	Conformational gating of dimannose binding to the antiviral protein cyanovirin revealed from the crystal structure at 1.35 Ã… resolution. Protein Science, 2008, 17, 939-944.	3.1	25
1175	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.4	492
1176	High Affinity Interaction between a Bivalve C-type Lectin and a Biantennary Complex-type N-Glycan Revealed by Crystallography and Microcalorimetry. Journal of Biological Chemistry, 2008, 283, 30112-30120.	1.6	35
1177	Structure of Vps26B and Mapping of its Interaction with the Retromer Protein Complex. Traffic, 2008, 9, 366-379.	1.3	104
1178	The crystal structure of human WD40 repeatâ€containing peptidylprolyl isomerase (PPWD1). FEBS Journal, 2008, 275, 2283-2295.	2.2	21

#	ARTICLE	IF	CITATIONS
1179	The sulfur atoms of the substrate CoA and the catalytic cysteine are required for a productive mode of substrate binding in bacterial biosynthetic thiolase, a thioesterâ€dependent enzyme. FEBS Journal, 2008, 275, 6136-6148.	2.2	18
1180	Implementing the LIM code: the structural basis for cell type-specific assembly of LIM-homeodomain complexes. EMBO Journal, 2008, 27, 2018-2029.	3.5	68
1181	Structure and metal exchange in the cadmium carbonic anhydrase of marine diatoms. Nature, 2008, 452, 56-61.	13.7	487
1182	Crystal structure of the polymerase PACâ€“PB1N complex from an avian influenza H5N1 virus. Nature, 2008, 454, 1123-1126.	13.7	248
1183	Structural insights into amino acid binding and gene control by a lysine riboswitch. Nature, 2008, 455, 1263-1267.	13.7	230
1184	Structural basis for gibberellin recognition by its receptor GID1. Nature, 2008, 456, 520-523.	13.7	306
1185	Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. Nature Structural and Molecular Biology, 2008, 15, 130-138.	3.6	103
1186	Structural insights into the dual activity of RNase J. Nature Structural and Molecular Biology, 2008, 15, 206-212.	3.6	167
1187	The structural basis for cap binding by influenza virus polymerase subunit PB2. Nature Structural and Molecular Biology, 2008, 15, 500-506.	3.6	436
1188	Crystal structure of the aquaglyceroporin PfAQP from the malarial parasite Plasmodium falciparum. Nature Structural and Molecular Biology, 2008, 15, 619-625.	3.6	143
1189	Molecular mechanism of energy conservation in polysulfide respiration. Nature Structural and Molecular Biology, 2008, 15, 730-737.	3.6	147
1190	Structure of the Shigella T3SS effector IpaH defines a new class of E3 ubiquitin ligases. Nature Structural and Molecular Biology, 2008, 15, 1293-1301.	3.6	141
1191	Structural insights into RNA recognition by the alternative-splicing regulator muscleblind-like MBNL1. Nature Structural and Molecular Biology, 2008, 15, 1343-1351.	3.6	141
1192	Automated macromolecular model building for X-ray crystallography using ARP/wARP version 7. Nature Protocols, 2008, 3, 1171-1179.	5.5	1,516
1193	Structure of the MDM2/MDMX RING domain heterodimer reveals dimerization is required for their ubiquitylation in trans. Cell Death and Differentiation, 2008, 15, 841-848.	5.0	256
1194	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haemâ€reactivity. EMBO Reports, 2008, 9, 157-163.	2.0	43
1195	Crystal structures of the effectorâ€binding domain of repressor Central glycolytic gene Regulator from <i>Bacillus subtilis</i> reveal ligandâ€induced structural changes upon binding of several glycolytic intermediates. Molecular Microbiology, 2008, 69, 895-910.	1.2	28
1196	Structure of the C-terminal head domain of the fowl adenovirus type 1 short fibre. Virology, 2008, 378, 169-176.	1.1	28

#	ARTICLE	IF	CITATIONS
1197	Inhibition of the glucosyltransferase activity of clostridial Rho/Rasâ€glucosylating toxins by castanospermine. FEBS Letters, 2008, 582, 2277-2282.	1.3	22
1198	Completing the family portrait of the antiâ€apoptotic Bclâ€2 proteins: Crystal structure of human Bflâ€1 in complex with Bim. FEBS Letters, 2008, 582, 3590-3594.	1.3	64
1199	Bifunctional NMN Adenylyltransferase/ADP-Ribose Pyrophosphatase: Structure and Function in Bacterial NAD Metabolism. Structure, 2008, 16, 196-209.	1.6	30
1200	Autoregulation by the Juxtamembrane Region of the Human Ephrin Receptor Tyrosine Kinase A3 (EphA3). Structure, 2008, 16, 873-884.	1.6	63
1201	The tRNA-Induced Conformational Activation of Human Mitochondrial Phenylalanyl-tRNA Synthetase. Structure, 2008, 16, 1095-1104.	1.6	53
1202	Sortase-Mediated Pilus Fiber Biogenesis in Streptococcus pneumoniae. Structure, 2008, 16, 1838-1848.	1.6	77
1203	Structural Characterization of Myotoxic Ecarpholin S From Echis carinatus Venom. Biophysical Journal, 2008, 95, 3366-3380.	0.2	45
1204	Determination of Protein Structuresâ€"A Series of Fortunate Events. Biophysical Journal, 2008, 95, 1-9.	0.2	128
1205	The structure of â€œdefective in induced resistanceâ€•protein of <i>Arabidopsis thaliana</i>, DIR1, reveals a new type of lipid transfer protein. Protein Science, 2008, 17, 1522-1530.	3.1	90
1206	Structural basis for the NADâ€hydrolysis mechanism and the ARTTâ€loop plasticity of C3 exoenzymes. Protein Science, 2008, 17, 878-886.	3.1	24
1207	Crystal structure of the MarR family regulatory protein, ST1710, from Sulfolobus tokodaii strain 7. Journal of Structural Biology, 2008, 161, 9-17.	1.3	29
1208	XtalView, protein structure solution and protein graphics, a short history. Journal of Structural Biology, 2008, 163, 208-213.	1.3	16
1209	Structural Analysis of the Human Galectin-9 N-terminal Carbohydrate Recognition Domain Reveals Unexpected Properties that Differ from the Mouse Orthologue. Journal of Molecular Biology, 2008, 375, 119-135.	2.0	80
1210	Three-dimensional Structure of a Putative Non-cellulosomal Cohesin Module from a Clostridium perfringens Family 84 Glycoside Hydrolase. Journal of Molecular Biology, 2008, 375, 20-28.	2.0	16
1211	Structures of Mutants of Cellulase Cel48F of Clostridium cellulolyticum in Complex with Long Hemithiocellooligosaccharides Give Rise to a New View of the Substrate Pathway during Processive Action. Journal of Molecular Biology, 2008, 375, 499-510.	2.0	53
1212	Crystal Structures and Mutational Analysis of the Arginine-, Lysine-, Histidine-binding Protein ArtJ from Geobacillus stearothermophilus. Implications for Interactions of ArtJ with its Cognate ATP-binding Cassette Transporter, Art(MP)2. Journal of Molecular Biology, 2008, 375, 448-459.	2.0	36
1213	High-resolution Structural Analysis of Mammalian Profilin 2a Complex Formation with Two Physiological Ligands: The Formin Homology 1 Domain of mDia1 and the Proline-rich Domain of VASP. Journal of Molecular Biology, 2008, 375, 270-290.	2.0	60
1214	Biochemical and Structural Characterization of a Novel Family of Cystathionine Î²-Synthase Domain Proteins Fused to a Zn Ribbon-Like Domain. Journal of Molecular Biology, 2008, 375, 301-315.	2.0	44

#	ARTICLE	IF	CITATIONS
1215	A Rationally Designed Monomeric Variant of Anthranilate Phosphoribosyltransferase from Sulfolobus solfataricus is as Active as the Dimeric Wild-type Enzyme but Less Thermostable. Journal of Molecular Biology, 2008, 376, 506-516.	2.0	22
1216	Mechanism of dTTP Inhibition of the Bifunctional dCTP Deaminase:dUTPase Encoded by Mycobacterium tuberculosis. Journal of Molecular Biology, 2008, 376, 554-569.	2.0	32
1217	Active-Site Mobility Revealed by the Crystal Structure of Arylmalonate Decarboxylase from Bordetella bronchiseptica. Journal of Molecular Biology, 2008, 377, 386-394.	2.0	17
1218	A Ligand-Induced Switch in the Periplasmic Domain of Sensor Histidine Kinase CitA. Journal of Molecular Biology, 2008, 377, 512-523.	2.0	110
1219	Structure of the Extracellular Glutathione S-Transferase OvGST1 from the Human Pathogenic Parasite Onchocerca volvulus. Journal of Molecular Biology, 2008, 377, 501-511.	2.0	20
1220	Crystal Structure of Thermus thermophilus tRNA m1A58 Methyltransferase and Biophysical Characterization of Its Interaction with tRNA. Journal of Molecular Biology, 2008, 377, 535-550.	2.0	49
1221	The Crystal Structure of DehI Reveals a New Î±-Haloacid Dehalogenase Fold and Active-Site Mechanism. Journal of Molecular Biology, 2008, 378, 284-294.	2.0	48
1222	Structural Insight into the Mechanism of Substrate Specificity and Catalytic Activity of an HD-Domain Phosphohydrolase: The 5â€²-Deoxyribonucleotidase YfbR from Escherichia coli. Journal of Molecular Biology, 2008, 378, 215-226.	2.0	62
1223	Structure of a Widely Conserved Type IV Pilus Biogenesis Factor that Affects the Stability of Secretin Multimers. Journal of Molecular Biology, 2008, 378, 1031-1039.	2.0	45
1224	Ring-Opening Mechanism Revealed by Crystal Structures of NagB and Its ES Intermediate Complex. Journal of Molecular Biology, 2008, 379, 73-81.	2.0	12
1225	Enzymatic Activity of the Staphylococcus aureus SplB Serine Protease is Induced by Substrates Containing the Sequence Trp-Glu-Leu-Gln. Journal of Molecular Biology, 2008, 379, 343-356.	2.0	43
1226	Crystal Structure of the MACPF Domain of Human Complement Protein C8Î± in Complex with the C8Î³ Subunit. Journal of Molecular Biology, 2008, 379, 331-342.	2.0	70
1227	Structural Insight into Substrate Binding and Catalysis of a Novel 2-Keto-3-deoxy-d-arabinonate Dehydratase Illustrates Common Mechanistic Features of the FAH Superfamily. Journal of Molecular Biology, 2008, 379, 357-371.	2.0	34
1228	From Structure to Function: Insights into the Catalytic Substrate Specificity and Thermostability Displayed by Bacillus subtilis Mannanase BCman. Journal of Molecular Biology, 2008, 379, 535-544.	2.0	53
1229	Thioredoxin A Active-Site Mutants Form Mixed Disulfide Dimers That Resemble Enzymeâ€"Substrate Reaction Intermediates. Journal of Molecular Biology, 2008, 379, 520-534.	2.0	20
1230	Structural and Biochemical Characterization of a Novel Aldehyde Dehydrogenase Encoded by the Benzoate Oxidation Pathway in Burkholderia xenovorans LB400. Journal of Molecular Biology, 2008, 379, 597-608.	2.0	22
1231	DsbL and DsbI Form a Specific Dithiol Oxidase System for Periplasmic Arylsulfate Sulfotransferase in Uropathogenic Escherichia coli. Journal of Molecular Biology, 2008, 380, 667-680.	2.0	71
1232	Salicylate 1,2-Dioxygenase from Pseudaminobacter salicylatoxidans: Crystal Structure of a Peculiar Ring-cleaving Dioxygenase. Journal of Molecular Biology, 2008, 380, 856-868.	2.0	39

#	ARTICLE	IF	CITATIONS
1233	Structural Insights into the Substrate Specificity and Function of Escherichia coli K12 YgjK, a Glucosidase Belonging to the Glycoside Hydrolase Family 63. Journal of Molecular Biology, 2008, 381, 116-128.	2.0	42
1234	Quinol Oxidation by c-Type Cytochromes: Structural Characterization of the Menaquinol Binding Site of NrfHA. Journal of Molecular Biology, 2008, 381, 341-350.	2.0	43
1235	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
1236	Crystal Structure of a Glutamate/Aspartate Binding Protein Complexed with a Glutamate Molecule: Structural Basis of Ligand Specificity at Atomic Resolution. Journal of Molecular Biology, 2008, 382, 99-111.	2.0	26
1237	Crystal Structure of Glucose-6-Phosphate Isomerase from Thermus thermophilus HB8 Showing a Snapshot of Active Dimeric State. Journal of Molecular Biology, 2008, 382, 747-762.	2.0	11
1238	Crystal Structure of the Ig1 Domain of the Neural Cell Adhesion Molecule NCAM2 Displays Domain Swapping. Journal of Molecular Biology, 2008, 382, 1113-1120.	2.0	7
1239	C4-Dicarboxylates Sensing Mechanism Revealed by the Crystal Structures of DctB Sensor Domain. Journal of Molecular Biology, 2008, 383, 49-61.	2.0	75
1240	Crystal Structure of Escherichia coli Rnk, a New RNA Polymerase-Interacting Protein. Journal of Molecular Biology, 2008, 383, 367-379.	2.0	33
1241	Structural and Molecular Characterization of the Prefoldin Î² Subunit from Thermococcus Strain KS-1. Journal of Molecular Biology, 2008, 383, 465-474.	2.0	24
1242	Structure of Staphylococcus aureus EsxA Suggests a Contribution to Virulence by Action as a Transport Chaperone and/or Adaptor Protein. Journal of Molecular Biology, 2008, 383, 603-614.	2.0	70
1243	X-ray Crystal Structure of a TRPM Assembly Domain Reveals an Antiparallel Four-stranded Coiled-coil. Journal of Molecular Biology, 2008, 383, 854-870.	2.0	110
1244	A New Member of the Alkaline Phosphatase Superfamily with a Formylglycine Nucleophile: Structural and Kinetic Characterisation of a Phosphonate Monoester Hydrolase/Phosphodiesterase from Rhizobium leguminosarum. Journal of Molecular Biology, 2008, 384, 120-136.	2.0	65
1245	Crystal Structure of the NanB Sialidase from Streptococcus pneumoniae. Journal of Molecular Biology, 2008, 384, 436-449.	2.0	74
1246	Structural Insights into the Catalytic Mechanism of the Bacterial Class B Phosphatase AphA Belonging to the DDDD Superfamily of Phosphohydrolases. Journal of Molecular Biology, 2008, 384, 478-488.	2.0	5
1247	The Structure of Monoamine Oxidase from Aspergillus niger Provides a Molecular Context for Improvements in Activity Obtained by Directed Evolution. Journal of Molecular Biology, 2008, 384, 1218-1231.	2.0	76
1248	Crystal Structure of the Arginine Repressor Protein in Complex with the DNA Operator from Mycobacterium tuberculosis. Journal of Molecular Biology, 2008, 384, 1330-1340.	2.0	17
1249	Mechanism of Substrate Recognition and PLP-induced Conformational Changes in LL-Diaminopimelate Aminotransferase from Arabidopsis thaliana. Journal of Molecular Biology, 2008, 384, 1314-1329.	2.0	20
1250	Ubc9 Sumoylation Regulates SUMO Target Discrimination. Molecular Cell, 2008, 31, 371-382.	4.5	191

#	ARTICLE	IF	CITATIONS
1251	Paired Receptor Specificity Explained by Structures of Signal Regulatory Proteins Alone and Complexed with CD47. Molecular Cell, 2008, 31, 266-277.	4.5	171
1252	Structure and Substrate Recruitment of the Human Spindle Checkpoint Kinase Bub1. Molecular Cell, 2008, 32, 394-405.	4.5	91
1253	A Bony Fish Immunological Receptor of the NITR Multigene Family Mediates Allogeneic Recognition. Immunity, 2008, 29, 228-237.	6.6	42
1254	Structure of the two-subsite Î²-d-xylosidase from Selenomonas ruminantium in complex with 1,3-bis[tris(hydroxymethyl)methylamino]propane. Archives of Biochemistry and Biophysics, 2008, 474, 157-166.	1.4	47
1255	Structure of the ROC domain from the Parkinson's disease-associated leucine-rich repeat kinase 2 reveals a dimeric GTPase. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1499-1504.	3.3	218
1256	Crystal structure studies on sulfur oxygenase reductase from Acidianus tengchongensis. Biochemical and Biophysical Research Communications, 2008, 369, 919-923.	1.0	25
1257	Crystal structure of ST2348, a CBS domain protein, from hyperthermophilic archaeon Sulfolobus tokodaii. Biochemical and Biophysical Research Communications, 2008, 375, 124-128.	1.0	11
1258	Structural Mechanism of Demethylation and Inactivation of Protein Phosphatase 2A. Cell, 2008, 133, 154-163.	13.5	177
1259	Structure of the DNA Repair Helicase XPD. Cell, 2008, 133, 801-812.	13.5	490
1260	Structural Analysis of ADP-Glucose Pyrophosphorylase from the Bacterium <i>Agrobacterium tumefaciens</i>[,]. Biochemistry, 2008, 47, 4439-4451.	1.2	39
1261	Crystal Structure of the L Protein of <i>Rhodobacter sphaeroides</i> Light-Independent Protochlorophyllide Reductase with MgADP Bound: A Homologue of the Nitrogenase Fe Protein. Biochemistry, 2008, 47, 13004-13015.	1.2	66
1262	Structure and Catalytic Mechanism of Eukaryotic Selenocysteine Synthase. Journal of Biological Chemistry, 2008, 283, 5849-5865.	1.6	49
1263	Structural Analysis of B-Box 2 from MuRF1: Identification of a Novel Self-Association Pattern in a RING-like Fold. Biochemistry, 2008, 47, 10722-10730.	1.2	36
1264	Structure of the Stress Response Protein DR1199 from <i>Deinococcus radiodurans</i>: A Member of the DJ-1 Superfamily. Biochemistry, 2008, 47, 11581-11589.	1.2	17
1265	Crystal Structure and Enantiomer Selection by <scp>d</scp>-Alanyl Carrier Protein Ligase DltA from <i>Bacillus cereus</i>. Biochemistry, 2008, 47, 11473-11480.	1.2	61
1266	Functional and Structural Characterization of Four Glutaminases from Escherichia coli and Bacillus subtilis. Biochemistry, 2008, 47, 5724-5735.	1.2	101
1267	Structures of the Ligand-Binding Core of iGluR2 in Complex with the Agonists (<i>R</i>)- and (<i>S</i>)-2-Amino-3-(4-hydroxy-1,2,5-thiadiazol-3-yl)propionic Acid Explain Their Unusual Equipotency. Journal of Medicinal Chemistry, 2008, 51, 1459-1463.	2.9	9
1268	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

#	Article	IF	Citations
1269	Structural Analyses of the Ankyrin Repeat Domain of TRPV6 and Related TRPV Ion Channels[,]. Biochemistry, 2008, 47, 2476-2484.	1.2	105
1270	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. Journal of Biological Chemistry, 2008, 283, 20361-20371.	1.6	177
1271	2.3 Ã… X-ray Structure of the Heme-Bound GAF Domain of Sensory Histidine Kinase DosT of <i>Mycobacterium tuberculosis</i>. Biochemistry, 2008, 47, 12523-12531.	1.2	71
1272	Structural Complexes of Human Adenine Phosphoribosyltransferase Reveal Novel Features of the APRT Catalytic Mechanism. Journal of Biomolecular Structure and Dynamics, 2008, 25, 589-597.	2.0	15
1273	The Crystal Structure of the Platelet Activator Aggretin Reveals a Novel (Î±Î²)₂Dimeric Structure. Biochemistry, 2008, 47, 7831-7837.	1.2	39
1274	Structural basis for specific lipid recognition by CERT responsible for nonvesicular trafficking of ceramide. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 488-493.	3.3	202
1275	Revealing the moonlighting role of NADP in the structure of a flavin-containing monooxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6572-6577.	3.3	134
1276	Staphylococcus aureus DsbA Does Not Have a Destabilizing Disulfide. Journal of Biological Chemistry, 2008, 283, 4261-4271.	1.6	56
1277	Mycobacterium tuberculosis CYP130. Journal of Biological Chemistry, 2008, 283, 5069-5080.	1.6	83
1278	Divergent Modes of Glycan Recognition by a New Family of Carbohydrate-binding Modules. Journal of Biological Chemistry, 2008, 283, 12604-12613.	1.6	39
1279	The Structure of Clostridium perfringens NanI Sialidase and Its Catalytic Intermediates. Journal of Biological Chemistry, 2008, 283, 9080-9088.	1.6	102
1280	Structural Basis of Proteolytic Activation of l-Phenylalanine Oxidase from Pseudomonas sp. P-501. Journal of Biological Chemistry, 2008, 283, 16584-16590.	1.6	26
1281	Crystal Structure of a UDP-glucose-specific Glycosyltransferase from a Mycobacterium Species. Journal of Biological Chemistry, 2008, 283, 27881-27890.	1.6	23
1282	Structural Basis of the Migfilin-Filamin Interaction and Competition with Integrin Î² Tails. Journal of Biological Chemistry, 2008, 283, 35154-35163.	1.6	97
1283	The First Structure of Dipeptidyl-peptidase III Provides Insight into the Catalytic Mechanism and Mode of Substrate Binding. Journal of Biological Chemistry, 2008, 283, 22316-22324.	1.6	63
1284	Structural Basis for a Distinct Catalytic Mechanism in Trypanosoma brucei Tryparedoxin Peroxidase. Journal of Biological Chemistry, 2008, 283, 30401-30411.	1.6	29
1285	PilF Is an Outer Membrane Lipoprotein Required for Multimerization and Localization of the<i>Pseudomonas aeruginosa</i>Type IV Pilus Secretin. Journal of Bacteriology, 2008, 190, 6961-6969.	1.0	97
1286	The Crystal Structure of Coxsackievirus B3 RNA-Dependent RNA Polymerase in Complex with Its Protein Primer VPg Confirms the Existence of a Second VPg Binding Site on <i>Picornaviridae</i> Polymerases. Journal of Virology, 2008, 82, 9577-9590.	1.5	87

#	Article	IF	Citations
1287	Three-dimensional structure/function analysis of SCP-2-like2 reveals differences among SCP-2 family members. Journal of Lipid Research, 2008, 49, 644-653.	2.0	32
1288	Host Determinant Residue Lysine 627 Lies on the Surface of a Discrete, Folded Domain of Influenza Virus Polymerase PB2 Subunit. PLoS Pathogens, 2008, 4, e1000136.	2.1	165
1289	Structure of the Receptor-Binding Protein of Bacteriophage Det7: a Podoviral Tail Spike in a Myovirus. Journal of Virology, 2008, 82, 2265-2273.	1.5	98
1290	A ternary complex of hydroxycinnamoyl-CoA hydrataseâ€"lyase (HCHL) with acetyl-CoA and vanillin gives insights into substrate specificity and mechanism. Biochemical Journal, 2008, 414, 281-289.	1.7	38
1291	Crystal Structure of the Ligand-bound Glucagon-like Peptide-1 Receptor Extracellular Domain. Journal of Biological Chemistry, 2008, 283, 11340-11347.	1.6	253
1292	Expansion of Substrate Specificity and Catalytic Mechanism of Azoreductase by X-ray Crystallography and Site-directed Mutagenesis. Journal of Biological Chemistry, 2008, 283, 13889-13896.	1.6	58
1293	SAD phasing by OASIS at different resolutions down to 0.30 nm and below. Chinese Physics B, 2008, 17, 1-9.	0.7	12
1294	Cholix Toxin, a Novel ADP-ribosylating Factor from Vibrio cholerae. Journal of Biological Chemistry, 2008, 283, 10671-10678.	1.6	126
1295	Structure of <scp>l</scp> -Xylulose-5-Phosphate 3-Epimerase (UlaE) from the Anaerobic <scp>l</scp> -Ascorbate Utilization Pathway of <i>Escherichia coli</i> : Identification of a Novel Phosphate Binding Motif within a TIM Barrel Fold. Journal of Bacteriology, 2008, 190, 8137-8144.	1.0	15
1296	Alteration of citrine structure by hydrostatic pressure explains the accompanying spectral shift. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13362-13366.	3.3	73
1297	An Oxidized Tryptophan Facilitates Copper Binding in Methylococcus capsulatus-secreted Protein MopE. Journal of Biological Chemistry, 2008, 283, 13897-13904.	1.6	45
1298	Recognition and repair of UV lesions in loop structures of duplex DNA by DASH-type cryptochrome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 21023-21027.	3.3	147
1299	Crystal Structure of Human Kynurenine Aminotransferase II, a Drug Target for the Treatment of Schizophrenia. Journal of Biological Chemistry, 2008, 283, 3559-3566.	1.6	50
1300	Crystal Structure of the Thermus thermophilus 16 S rRNA Methyltransferase RsmC in Complex with Cofactor and Substrate Guanosine. Journal of Biological Chemistry, 2008, 283, 26548-26556.	1.6	19
1301	The Crystal Structure of the Human Toll-like Receptor 10 Cytoplasmic Domain Reveals a Putative Signaling Dimer. Journal of Biological Chemistry, 2008, 283, 11861-11865.	1.6	171
1302	Crystal Structure of Human Plasma Platelet-activating Factor Acetylhydrolase. Journal of Biological Chemistry, 2008, 283, 31617-31624.	1.6	77
1303	Crystal Structure of a Functional Dimer of the PhoQ Sensor Domain. Journal of Biological Chemistry, 2008, 283, 13762-13770.	1.6	83
1304	Structural and Thermodynamic Analyses of Solute-binding Protein from Bifidobacterium longum Specific for Core 1 Disaccharide and Lacto-N-biose I. Journal of Biological Chemistry, 2008, 283, 13165-13173.	1.6	111

#	ARTICLE	IF	CITATIONS
1305	An Atypical Catalytic Mechanism Involving Three Cysteines of Thioredoxin. Journal of Biological Chemistry, 2008, 283, 23062-23072.	1.6	43
1306	Structural basis of <i>Clostridium perfringens</i> toxin complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12194-12199.	3.3	33
1307	The crystal structure of Pyrococcus abyssi tRNA (uracil-54, C5)-methyltransferase provides insights into its tRNA specificity. Nucleic Acids Research, 2008, 36, 4929-4940.	6.5	14
1308	Crystal structure of the cell wall anchor domain of MotB, a stator component of the bacterial flagellar motor: Implications for peptidoglycan recognition. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10348-10353.	3.3	139
1309	<i>In vitro</i> reconstitution and crystal structure of <i>p</i> -aminobenzoate <i>N</i> -oxygenase (AurF) involved in aureothin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6858-6863.	3.3	141
1310	Structure of coronavirus hemagglutinin-esterase offers insight into corona and influenza virus evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9065-9069.	3.3	221
1311	Structural Basis for Substrate Recognition and Hydrolysis by Mouse Carnosinase CN2. Journal of Biological Chemistry, 2008, 283, 27289-27299.	1.6	48
1312	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
1313	Crystal Structure of Botulinum Neurotoxin Type A in Complex with the Cell Surface Co-Receptor GT1bâ€"Insight into the Toxinâ€"Neuron Interaction. PLoS Pathogens, 2008, 4, e1000129.	2.1	150
1314	Structural Basis for the Regulation Mechanism of the Tyrosine Kinase CapB from Staphylococcus aureus. PLoS Biology, 2008, 6, e143.	2.6	89
1315	Molecular basis of thrombin recognition by protein C inhibitor revealed by the 1.6-â„« structure of the heparin-bridged complex. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4661-4666.	3.3	59
1316	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2â€"Like Fold but Have Evolved to Inhibit NF-Î°B rather than Apoptosis. PLoS Pathogens, 2008, 4, e1000128.	2.1	136
1317	Structure and Function of A41, a Vaccinia Virus Chemokine Binding Protein. PLoS Pathogens, 2008, 4, e5.	2.1	66
1318	Crystal structure and kinetic study of dihydrodipicolinate synthase from <i>Mycobacterium tuberculosis</i>. Biochemical Journal, 2008, 411, 351-360.	1.7	74
1319	Structure of Human Dual Specificity Protein Phosphatase 23, VHZ, Enzyme-Substrate/Product Complex. Journal of Biological Chemistry, 2008, 283, 8946-8953.	1.6	22
1320	Structural Basis for Substrate Fatty Acyl Chain Specificity. Journal of Biological Chemistry, 2008, 283, 9435-9443.	1.6	97
1321	Central base pair flipping and discrimination by PspGI. Nucleic Acids Research, 2008, 36, 6109-6117.	6.5	32
1322	Insights into the Catalytic Mechanism of Tyrosine Phenol-lyase from X-ray Structures of Quinonoid Intermediates. Journal of Biological Chemistry, 2008, 283, 29206-29214.	1.6	31

#	Article	IF	Citations
1323	Crystal Structures of C4-Dicarboxylate Ligand Complexes with Sensor Domains of Histidine Kinases DcuS and DctB. Journal of Biological Chemistry, 2008, 283, 30256-30265.	1.6	95
1324	RhaU of <i>Rhizobium leguminosarum</i> Is a Rhamnose Mutarotase. Journal of Bacteriology, 2008, 190, 2903-2910.	1.0	20
1325	Structural and mechanistic insight into the basis of mucopolysaccharidosis IIIB. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6560-6565.	3.3	79
1326	Ruffling of Metalloporphyrins Bound to IsdG and IsdI, Two Heme-degrading Enzymes in Staphylococcus aureus. Journal of Biological Chemistry, 2008, 283, 30957-30963.	1.6	97
1327	New Frontiers in X-ray Crystallography. , 2008, , 601-622.		2
1328	Î²2 integrin phosphorylation on Thr758 acts as a molecular switch to regulate 14-3-3 and filamin binding. Blood, 2008, 112, 1853-1862.	0.6	148
1329	Structural and kinetic differences between human and <i>Aspergillus fumigatus</i> <scp>D</scp>-glucosamine-6-phosphate <i>N</i>-acetyltransferase. Biochemical Journal, 2008, 415, 217-223.	1.7	26
1330	Structural Basis and Catalytic Mechanism for the Dual Functional Endo-Î²-N-Acetylglucosaminidase A. PLoS ONE, 2009, 4, e4658.	1.1	52
1331	Type VI secretion apparatus and phage tail-associated protein complexes share a common evolutionary origin. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4154-4159.	3.3	576
1332	<i>Trypanosoma brucei</i>ATG8: Structural insights into autophagic-like mechanisms in protozoa. Autophagy, 2009, 5, 1085-1091.	4.3	36
1333	<i>Streptococcus mutans</i> SMU.623c Codes for a Functional, Metal-Dependent Polysaccharide Deacetylase That Modulates Interactions with Salivary Agglutinin. Journal of Bacteriology, 2009, 191, 394-402.	1.0	22
1334	Structural Basis for Phototoxicity of the Genetically Encoded Photosensitizer KillerRed. Journal of Biological Chemistry, 2009, 284, 32028-32039.	1.6	123
1335	Crystal Structures of Human SIRT3 Displaying Substrate-induced Conformational Changes. Journal of Biological Chemistry, 2009, 284, 24394-24405.	1.6	177
1336	Crystal structure of isoflurane bound to integrin LFAâ€1 supports a unified mechanism of volatile anesthetic action in the immune and central nervous systems. FASEB Journal, 2009, 23, 2735-2740.	0.2	42
1337	Crystal Structure of Glycoside Hydrolase Family 55 Î²-1,3-Glucanase from the Basidiomycete Phanerochaete chrysosporium. Journal of Biological Chemistry, 2009, 284, 10100-10109.	1.6	48
1338	Bothnia dystrophy is caused by domino-like rearrangements in cellular retinaldehyde-binding protein mutant R234W. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18545-18550.	3.3	58
1339	Multifunctionality and mechanism of ligand binding in a mosquito antiinflammatory protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3728-3733.	3.3	123
1340	Crystal Structures of the Organomercurial Lyase MerB in Its Free and Mercury-bound Forms. Journal of Biological Chemistry, 2009, 284, 938-944.	1.6	49

#	Article	IF	Citations
1341	Molecular Mechanisms of Yeast Cell Wall Glucan Remodeling. Journal of Biological Chemistry, 2009, 284, 8461-8469.	1.6	67
1342	Structure, Binding, and Activity of Syd, a SecY-interacting Protein. Journal of Biological Chemistry, 2009, 284, 7897-7902.	1.6	32
1343	Fatty Acid- and Retinoid-binding Proteins Have Distinct Binding Pockets for the Two Types of Cargo. Journal of Biological Chemistry, 2009, 284, 35818-35826.	1.6	31
1344	Crystal Structure of Family 14 Polysaccharide Lyase with pH-dependent Modes of Action. Journal of Biological Chemistry, 2009, 284, 35572-35579.	1.6	57
1345	Structural and Biophysical Characterization of BoxC from Burkholderia xenovorans LB400. Journal of Biological Chemistry, 2009, 284, 16377-16385.	1.6	12
1346	Mechanism for the Hydrolysis of a Sulfur-Sulfur Bond Based on the Crystal Structure of the Thiosulfohydrolase SoxB. Journal of Biological Chemistry, 2009, 284, 21707-21718.	1.6	37
1347	Mechanistic Insights into the Hydrolysis and Synthesis of Ceramide by Neutral Ceramidase. Journal of Biological Chemistry, 2009, 284, 9566-9577.	1.6	30
1348	Electrostatic Interactions of Hsp-organizing Protein Tetratricopeptide Domains with Hsp70 and Hsp90. Journal of Biological Chemistry, 2009, 284, 25364-25374.	1.6	46
1349	Streptococcus pneumoniae Endohexosaminidase D, Structural and Mechanistic Insight into Substrate-assisted Catalysis in Family 85 Glycoside Hydrolases. Journal of Biological Chemistry, 2009, 284, 11676-11689.	1.6	85
1350	Nimotuzumab, an Antitumor Antibody that Targets the Epidermal Growth Factor Receptor, Blocks Ligand Binding while Permitting the Active Receptor Conformation. Cancer Research, 2009, 69, 5851-5859.	0.4	164
1351	Crystal Structural and Functional Analysis of the Putative Dipeptidase from Pyrococcus horikoshii OT3. Journal of Biophysics, 2009, 2009, 1-12.	0.8	17
1352	Structure and Proposed Activity of a Member of the VapBC Family of Toxin-Antitoxin Systems. Journal of Biological Chemistry, 2009, 284, 276-283.	1.6	118
1353	Functional and structural characterization of the integrase from the prototype foamy virus. Nucleic Acids Research, 2009, 37, 243-255.	6.5	130
1354	Crystal Structure of a Class XIB Phospholipase A2 (PLA2). Journal of Biological Chemistry, 2009, 284, 19371-19379.	1.6	18
1355	Crystal Structure and Catalytic Mechanism of 4-Methylmuconolactone Methylisomerase. Journal of Biological Chemistry, 2009, 284, 32709-32716.	1.6	5
1356	Structures of the Arm-type Binding Domains of HPI and HAI7 Integrases. Journal of Biological Chemistry, 2009, 284, 31664-31671.	1.6	3
1357	Evf, a Virulence Factor Produced by the Drosophila Pathogen Erwinia carotovora, Is an S-Palmitoylated Protein with a New Fold That Binds to Lipid Vesicles. Journal of Biological Chemistry, 2009, 284, 3552-3562.	1.6	27
1358	Functional importance of Crenarchaea-specific extra-loop revealed by an X-ray structure of a heterotetrameric crenarchaeal splicing endonuclease. Nucleic Acids Research, 2009, 37, 4787-4798.	6.5	23

#	Article	IF	Citations
1359	Structural Bioinformatics: From the Sequence to Structure and Function. Current Bioinformatics, 2009, 4, 54-87.	0.7	11
1360	Crystal Structure of Iodotyrosine Deiodinase, a Novel Flavoprotein Responsible for Iodide Salvage in Thyroid Glands. Journal of Biological Chemistry, 2009, 284, 19659-19667.	1.6	73
1361	Dimerization of Hepatitis E Virus Capsid Protein E2s Domain Is Essential for Virusâ€“Host Interaction. PLoS Pathogens, 2009, 5, e1000537.	2.1	123
1362	Structure-Function Relationship of the Chloroplastic Glutaredoxin S12 with an Atypical WCSYS Active Site. Journal of Biological Chemistry, 2009, 284, 9299-9310.	1.6	80
1363	Crystal Structure of a Mucus-binding Protein Repeat Reveals an Unexpected Functional Immunoglobulin Binding Activity. Journal of Biological Chemistry, 2009, 284, 32444-32453.	1.6	70
1364	Zinc-Independent Folate Biosynthesis: Genetic, Biochemical, and Structural Investigations Reveal New Metal Dependence for GTP Cyclohydrolase IB. Journal of Bacteriology, 2009, 191, 6936-6949.	1.0	61
1365	Acidianus filamentous virus 1 coat proteins display a helical fold spanning the filamentous archaeal viruses lineage. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21155-21160.	3.3	41
1366	Incompatibility with Formin Cdc12p Prevents Human Profilin from Substituting for Fission Yeast Profilin. Journal of Biological Chemistry, 2009, 284, 2088-2097.	1.6	45
1367	Crystal Structures of Two Coronavirus ADP-Ribose-1â€³-Monophosphatases and Their Complexes with ADP-Ribose: a Systematic Structural Analysis of the Viral ADRP Domain. Journal of Virology, 2009, 83, 1083-1092.	1.5	52
1368	Crystal structure of the Î²Î²Î±-Me type II restriction endonuclease Hpy99I with target DNA. Nucleic Acids Research, 2009, 37, 3799-3810.	6.5	49
1369	Crystallographic and Mutational Analyses of Substrate Recognition of Endo-Î±-N-acetylgalactosaminidase from Bifidobacterium longum. Journal of Biochemistry, 2009, 146, 389-398.	0.9	48
1370	The 1.5-Ã… Structure of XplA-heme, an Unusual Cytochrome P450 Heme Domain That Catalyzes Reductive Biotransformation of Royal Demolition Explosive. Journal of Biological Chemistry, 2009, 284, 28467-28475.	1.6	32
1371	ST1710â€“DNA complex crystal structure reveals the DNA binding mechanism of the MarR family of regulators. Nucleic Acids Research, 2009, 37, 4723-4735.	6.5	50
1372	Differential Recognition and Hydrolysis of Host Carbohydrate Antigens by Streptococcus pneumoniae Family 98 Glycoside Hydrolases. Journal of Biological Chemistry, 2009, 284, 26161-26173.	1.6	41
1373	The Structure of the Dizinc Subclass B2 Metallo-Î²-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
1374	Structural Characterization of the Bradyzoite Surface Antigen (BSR4) from Toxoplasma gondii, a Unique Addition to the Surface Antigen Glycoprotein 1-related Superfamily. Journal of Biological Chemistry, 2009, 284, 9192-9198.	1.6	31
1375	Crystal Structures of Cytochrome P450 105P1 from <i>Streptomyces avermitilis</i> : Conformational Flexibility and Histidine Ligation State. Journal of Bacteriology, 2009, 191, 1211-1219.	1.0	53
1376	Group B<i>Streptococcus</i>Pullulanase Crystal Structures in the Context of a Novel Strategy for Vaccine Development. Journal of Bacteriology, 2009, 191, 3544-3552.	1.0	30

#	ARTICLE	IF	CITATIONS
1377	Allosteric Coupling between the Lid and Interdomain Linker in DnaK Revealed by Inhibitor Binding Studies. Journal of Bacteriology, 2009, 191, 1456-1462.	1.0	54
1378	Structural and Functional Analysis of SmeT, the Repressor of the Stenotrophomonas maltophilia Multidrug Efflux Pump SmeDEF. Journal of Biological Chemistry, 2009, 284, 14428-14438.	1.6	43
1379	ROP2 from Toxoplasma gondii: A Virulence Factor with a Protein-Kinase Fold and No Enzymatic Activity. Structure, 2009, 17, 139-146.	1.6	76
1380	The Structure of the MAP2K MEK6 Reveals an Autoinhibitory Dimer. Structure, 2009, 17, 96-104.	1.6	31
1381	Insights into the Architecture of the Replicative Helicase from the Structure of an Archaeal MCM Homolog. Structure, 2009, 17, 211-222.	1.6	51
1382	â€œConditional Restraintsâ€: Restraining the Free Atoms in ARP/wARP. Structure, 2009, 17, 183-189.	1.6	20
1383	Structural Analysis of Ligand Stimulation of the Histidine Kinase NarX. Structure, 2009, 17, 190-201.	1.6	114
1384	Recognition of AT-Rich DNA Binding Sites by the MogR Repressor. Structure, 2009, 17, 769-777.	1.6	33
1385	Crystal Structures of Two Archaeal 8-Oxoguanine DNA Glycosylases Provide Structural Insight into Guanine/8-Oxoguanine Distinction. Structure, 2009, 17, 703-712.	1.6	20
1386	Structural Analysis of Sensor Domains from the TMAO-Responsive Histidine Kinase Receptor TorS. Structure, 2009, 17, 1195-1204.	1.6	49
1387	Structure of PAS-Linked Histidine Kinase and the Response Regulator Complex. Structure, 2009, 17, 1333-1344.	1.6	93
1388	Structures of the tumor necrosis factor Î± inducing protein TipÎ±: A novel virulence factor from <i>Helicobacter pylori</i>. FEBS Letters, 2009, 583, 1581-1585.	1.3	19
1389	Biochemical and structural characterization of a short-chain dehydrogenase/reductase of Thermus thermophilus HB8. Chemico-Biological Interactions, 2009, 178, 117-126.	1.7	18
1390	Crystal structure of bovine 3â€hydroxyanthranilate 3,4â€dioxygenase. Biopolymers, 2009, 91, 1189-1195.	1.2	20
1391	The crystal structure of auracyanin A at 1.85ÂÅ resolution: the structures and functions of auracyanins A and B, two almost identical â€œblueâ€•copper proteins, in the photosynthetic bacterium Chloroflexus aurantiacus. Journal of Biological Inorganic Chemistry, 2009, 14, 329-345.	1.1	21
1392	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
1393	The structural basis for the difference in absorbance spectra for the FMO antenna protein from various green sulfur bacteria. Photosynthesis Research, 2009, 100, 79-87.	1.6	273
1394	Biomicrofluidics: Recent trends and future challenges. Sadhana - Academy Proceedings in Engineering Sciences, 2009, 34, 573-590.	0.8	19

#	Article	IF	Citations
1395	Use of iterative OASIS with low resolution SAD laboratory X-ray source (Cr KÎ±) data sets. Indian Journal of Physics, 2009, 83, 1671-1679.	0.9	1
1396	Crystal structures of g-type lysozyme from Atlantic cod shed new light on substrate binding and the catalytic mechanism. Cellular and Molecular Life Sciences, 2009, 66, 2585-2598.	2.4	48
1397	Protein Kinase CK2 in Health and Disease. Cellular and Molecular Life Sciences, 2009, 66, 1800-1816.	2.4	90
1398	Xâ€ray structure of ILL2, an auxinâ€conjugate amidohydrolase from <i>Arabidopsis thaliana</i>. Proteins: Structure, Function and Bioinformatics, 2009, 74, 61-71.	1.5	42
1399	The crystal structure of the protein YhaK from <i>Escherichia coli</i> reveals a new subclass of redox sensitive enterobacterial bicupins. Proteins: Structure, Function and Bioinformatics, 2009, 74, 18-31.	1.5	20
1400	Crystal structure of phosphoglucose isomerase from <i>Trypanosoma brucei</i> complexed with glucoseâ€6â€phosphate at 1.6 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2009, 74, 72-80.	1.5	16
1401	The structure of the PP2A regulatory subunit B56Î³: The remaining piece of the PP2A jigsaw puzzle. Proteins: Structure, Function and Bioinformatics, 2009, 74, 212-221.	1.5	18
1402	The crystal structures of the psychrophilic subtilisin S41 and the mesophilic subtilisin Sph reveal the same calciumâ€loaded state. Proteins: Structure, Function and Bioinformatics, 2009, 74, 489-496.	1.5	29
1403	Crystal structure of the hexamer of human heat shock factor binding protein 1. Proteins: Structure, Function and Bioinformatics, 2009, 75, 1-11.	1.5	24
1404	An intact SAMâ€dependent methyltransferase fold is encoded by the human endothelinâ€converting enzymeâ€2 gene. Proteins: Structure, Function and Bioinformatics, 2009, 74, 789-793.	1.5	8
1405	Characterization of a diagnostic Fab fragment binding trimeric Lewis X. Proteins: Structure, Function and Bioinformatics, 2009, 76, 439-447.	1.5	10
1406	Xâ€ray structure of <i>Danio rerio</i> secretagogin: A hexaâ€EFâ€hand calcium sensor. Proteins: Structure, Function and Bioinformatics, 2009, 76, 477-483.	1.5	22
1407	Structure of a pullulanase from <i>Bacillus acidopullulyticus</i>. Proteins: Structure, Function and Bioinformatics, 2009, 76, 516-519.	1.5	90
1408	Cohesin diversity revealed by the crystal structure of the anchoring cohesin from <i>Ruminococcus flavefaciens</i>. Proteins: Structure, Function and Bioinformatics, 2009, 77, 699-709.	1.5	16
1409	Crystal structure of a histidine kinase sensor domain with similarity to periplasmic binding proteins. Proteins: Structure, Function and Bioinformatics, 2009, 77, 235-241.	1.5	24
1410	Crystal structure of human diphosphoinositol phosphatase 1. Proteins: Structure, Function and Bioinformatics, 2009, 77, 242-246.	1.5	25
1411	Structural basis of typhoid: <i>Salmonella typhi</i> type IVb pilin (PilS) and cystic fibrosis transmembrane conductance regulator interaction. Proteins: Structure, Function and Bioinformatics, 2009, 77, 253-261.	1.5	284
1412	Crystal structure of a putative methylmalonylâ€coenzyme a epimerase from <i>Thermoanaerobacter tengcongensis</i> at 2.0 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2009, 77, 994-999.	1.5	6

#	Article	IF	Citations
1413	Crystal structure of the manganese transport regulatory protein from <i>Escherichia coli</i>. Proteins: Structure, Function and Bioinformatics, 2009, 77, 741-746.	1.5	10
1414	Crystal structure of TTHA0807, a CcpA regulator, from <i>Thermus thermophilus</i> HB8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 747-751.	1.5	0
1415	Structure of the ribosome associating GTPase HflX. Proteins: Structure, Function and Bioinformatics, 2010, 78, 705-713.	1.5	19
1416	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
1417	Crystal structure of PRYâ€SPRY domain of human TRIM72. Proteins: Structure, Function and Bioinformatics, 2010, 78, 790-795.	1.5	37
1418	The thermoâ€and acidoâ€stable ORFâ€99 from the archaeal virus AFV1. Protein Science, 2009, 18, 1316-1320.	3.1	13
1419	Structural and functional characterization of a putative polysaccharide deacetylase of the human parasite <i>Encephalitozoon cuniculi</i>. Protein Science, 2009, 18, 1197-1209.	3.1	27
1420	Mutations of key hydrophobic surface residues of 11Î²â€hydroxysteroid dehydrogenase type 1 increase solubility and monodispersity in a bacterial expression system. Protein Science, 2009, 18, 1552-1563.	3.1	10
1421	The crystal structure of the AF2331 protein from <i>Archaeoglobus fulgidus</i> DSM 4304 forms an unusual interdigitated dimer with a new type of Î± + Î² fold. Protein Science, 2009, 18, 2410-2419.	3.1	11
1422	Involvement of a carboxylated lysine in UV damage endonuclease. Protein Science, 2009, 18, 549-558.	3.1	4
1423	Crystal structure of AFV1â€102, a protein from the acidianus filamentous virus 1. Protein Science, 2009, 18, 845-849.	3.1	7
1424	Selenomethionine incorporation in proteins expressed in <i>Lactococcus lactis</i>. Protein Science, 2009, 18, 1121-1127.	3.1	39
1425	Prospects forde novophasing withde novoprotein models. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 169-175.	2.5	32
1426	Structures of the multicomponent Rieske non-heme iron toluene 2,3-dioxygenase enzyme system. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 24-33.	2.5	52
1427	Re-refinement from deposited X-ray data can deliver improved models for most PDB entries. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 176-185.	2.5	71
1428	Analysis of errors in the structure determination of MsbA. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 193-199.	2.5	9
1429	Decision-making in structure solution using Bayesian estimates of map quality: the<i>PHENIX AutoSol</i>wizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601.	2.5	804
1430	Structure of the C-terminal domain of nsp4 from feline coronavirus. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 839-846.	2.5	23

#	ARTICLE	IF	CITATIONS
1431	A multivariate likelihood SIRAS function for phasing and model refinement. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1051-1061.	2.5	8
1432	On the combination of molecular replacement and single-wavelength anomalous diffraction phasing for automated structure determination. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1089-1097.	2.5	158
1433	Modeling discrete heterogeneity in X-ray diffraction data by fitting multi-conformers. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1107-1117.	2.5	104
1434	The first structure of a cold-adapted superoxide dismutase (SOD): biochemical and structural characterization of iron SOD fromAliivibrio salmonicida. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 84-92.	0.7	27
1435	Crystallization and preliminary X-ray analysis of a cohesin-like module from AF2375 of the archaeon<i>Archaeoglobus fulgidus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 275-278.	0.7	1
1436	Structure of<i>Debaryomyces castellii</i>CBS 2923 phytase. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 321-326.	0.7	22
1437	Structure of the human Nac1 POZ domain. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 445-449.	0.7	17
1438	Crystallization and preliminary crystallographic studies of putative RNA 3â€²-terminal phosphate cyclase from the crenarchaeonSulfolobus tokodaii. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 565-570.	0.7	1
1439	Crystallization and preliminary X-ray crystallographic analysis of two dimeric hyperthermostable thioredoxins isolated fromSulfolobus solfataricus. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 604-607.	0.7	2
1440	Structure of EstA esterase from psychrotrophic<i>Pseudoalteromonas</i>sp. 643A covalently inhibited by monoethylphosphonate. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 862-865.	0.7	17
1441	Structures of two truncated phage-tail hyaluronate lyases fromStreptococcus pyogenesserotype M1. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 963-966.	0.7	11
1442	Crystallization and X-ray structure of cold-shock protein E from<i>Salmonella typhimurium</i>. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1240-1245.	0.7	14
1443	Structure of the adenylation domain of NAD⁺-dependent DNA ligase from<i>Staphylococcus aureus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1078-1082.	0.7	9
1444	Structure of an N-terminally truncated Nudix hydrolase DR2204 fromDeinococcus radiodurans. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1083-1087.	0.7	3
1445	Structures of BIR domains from human NAIP and cIAP2. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1091-1096.	0.7	18
1446	Structure of hypothetical Mo-cofactor biosynthesis protein B (ST2315) fromSulfolobus tokodaii. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1200-1203.	0.7	2
1447	The structure of an archaeal ribose-5-phosphate isomerase from<i>Methanocaldococcus jannaschii</i>(MJ1603). Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1214-1217.	0.7	5
1448	Structure of a putative Î²-phosphoglucomutase (TM1254) fromThermotoga maritima. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1218-1221.	0.7	2

#	ARTICLE	IF	CITATIONS
1449	Development of a shutterless continuous rotation method using an X-ray CMOS detector for protein crystallography. Journal of Applied Crystallography, 2009, 42, 1165-1175.	1.9	19
1450	Structural and functional characteristics of xenavidin, the first frog avidin from Xenopus tropicalis. BMC Structural Biology, 2009, 9, 63.	2.3	25
1451	The structure of the leukemia drug imatinib bound to human quinone reductase 2 (NQO2). BMC Structural Biology, 2009, 9, 7.	2.3	83
1452	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from Streptococcus pyogenes. BMC Structural Biology, 2009, 9, 75.	2.3	6
1453	New insights into intraâ€•and intermolecular interactions of immunoglobulins: crystal structure of mouse IgG2bâ€Fc at 2Â·1â€Å… resolution. Immunology, 2009, 126, 378-385.	2.0	25
1454	Structure and nonâ€essential function of glycerol kinase in <i>Plasmodium falciparum</i> blood stages. Molecular Microbiology, 2009, 71, 533-545.	1.2	27
1455	Genomeâ€wide regulon and crystal structure of BlaI (Rv1846c) from <i>Mycobacterium tuberculosis</i>. Molecular Microbiology, 2009, 71, 1102-1116.	1.2	61
1456	Characterization of staphyloferrin A biosynthetic and transport mutants in <i>Staphylococcus aureus</i>. Molecular Microbiology, 2009, 72, 947-963.	1.2	120
1457	The longâ€chain fatty acid sensor, PsrA, modulates the expression of <i>rpoS</i> and the type III secretion <i>exsCEBA</i> operon in <i>Pseudomonas aeruginosa</i>. Molecular Microbiology, 2009, 73, 120-136.	1.2	44
1458	Insights into complement convertase formation based on the structure of the factor B-cobra venom factor complex. EMBO Journal, 2009, 28, 2469-2478.	3.5	61
1459	Structural determinants for interaction of partial agonists with acetylcholine binding protein and neuronal Î±7 nicotinic acetylcholine receptor. EMBO Journal, 2009, 28, 3040-3051.	3.5	153
1460	The structural basis for peptide selection by the transport receptor OppA. EMBO Journal, 2009, 28, 1332-1340.	3.5	82
1461	Structure and allosteric effects of low-molecular-weight activators on the protein kinase PDK1. Nature Chemical Biology, 2009, 5, 758-764.	3.9	134
1462	The Vibrio cholerae quorum-sensing autoinducer CAI-1: analysis of the biosynthetic enzyme CqsA. Nature Chemical Biology, 2009, 5, 891-895.	3.9	98
1463	Crystallographic ab initio protein structure solution below atomic resolution. Nature Methods, 2009, 6, 651-653.	9.0	167
1464	Truncation of the disordered loop located within the C-terminal domain of the transcriptional regulator HlyIIR remodels its structure. Molecular Biology, 2009, 43, 114-122.	0.4	1
1465	Structures of endonuclease V with DNA reveal initiation of deaminated adenine repair. Nature Structural and Molecular Biology, 2009, 16, 138-143.	3.6	83
1466	Structural insights into hedgehog ligand sequestration by the human hedgehog-interacting protein HHIP. Nature Structural and Molecular Biology, 2009, 16, 698-703.	3.6	123

#	Article	IF	Citations
1467	Structure of a trypanosomatid mitochondrial cytochromeâ€ƒ<i>c</i> with heme attached via only one thioether bond and implications for the substrate recognition requirements of heme lyase. FEBS Journal, 2009, 276, 2822-2832.	2.2	31
1468	Crystal structure of textilininâ€1, a Kunitzâ€type serine protease inhibitor from the venom of the Australian common brown snake (<i>Pseudonajaâ€ƒtextilis</i>). FEBS Journal, 2009, 276, 3163-3175.	2.2	46
1469	The crystal structure of human Î±â€aminoâ€Î²â€carboxymuconateâ€Îµâ€semialdehyde decarboxylase in complex with 1,3â€dihydroxyacetonephosphate suggests a regulatory link between NAD synthesis and glycolysis. FEBS Journal, 2009, 276, 6615-6623.	2.2	24
1470	Crystal structure of the shutoff and exonuclease protein from the oncogenic Kaposiâ€™s sarcomaâ€associated herpesvirus. FEBS Journal, 2009, 276, 6636-6645.	2.2	34
1471	Use of novel selenomethionine-resistant yeast to produce selenomethionyl protein suitable for structural analysis. FEMS Yeast Research, 2009, 9, 439-445.	1.1	8
1472	Structure and Function of the Glycopeptide N-methyltransferase MtfA, a Tool for the Biosynthesis of Modified Glycopeptide Antibiotics. Chemistry and Biology, 2009, 16, 401-410.	6.2	37
1473	The 1.4ÂÅ… crystal structure of the large and cold-active Vibrio sp. alkaline phosphatase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 297-308.	1.1	48
1474	Crystal structures of T. vivax nucleoside hydrolase in complex with new potent and specific inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 953-960.	1.1	22
1475	Structure and stability of a thioredoxin reductase from Sulfolobus solfataricus: A thermostable protein with two functions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 554-562.	1.1	13
1476	MAMMOTH (Matching molecular models obtained from theory): An automated method for model comparison. Protein Science, 2009, 11, 2606-2621.	3.1	416
1477	Crystal structure of the protease-resistant core domain of Yersinia pestis virulence factor YopR. Protein Science, 2009, 14, 1679-1683.	3.1	5
1478	Crystal structure of the collagen triple helix model [(Pro-Pro-Gly)10]3. Protein Science, 2009, 11, 262-270.	3.1	245
1479	Structural analysis of a glycoside hydrolase family 43 arabinoxylan arabinofuranohydrolase in complex with xylotetraose reveals a different binding mechanism compared with other members of the same family. Biochemical Journal, 2009, 418, 39-47.	1.7	72
1480	Molecular Basis of Arabinobio-hydrolase Activity in Phytopathogenic Fungi. Journal of Biological Chemistry, 2009, 284, 12285-12296.	1.6	42
1481	X-ray Crystal Analysis of a TASP: Structural Insights of a Cavitein Dimer. Journal of the American Chemical Society, 2009, 131, 7421-7429.	6.6	24
1482	Structural Basis for DNA Recognition by the Human PAX3 Homeodomain[,]. Biochemistry, 2009, 48, 1148-1155.	1.2	38
1483	Structure of the Ternary Complex of Phosphomevalonate Kinase: The Enzyme and Its Family. Biochemistry, 2009, 48, 6461-6468.	1.2	22
1484	Analysis of the Structural and Functional Diversity of Plant Cell Wall Specific Family 6 Carbohydrate Binding Modules. Biochemistry, 2009, 48, 10395-10404.	1.2	36

#	ARTICLE	IF	CITATIONS
1485	Accurate Solution Structures of Proteins from X-ray Data and a Minimal Set of NMR Data: Calmodulinâˆ’Peptide Complexes As Examples. Journal of the American Chemical Society, 2009, 131, 5134-5144.	6.6	101
1486	Functional Annotation and Three-Dimensional Structure of Dr0930 from <i>Deinococcus radiodurans</i>, a Close Relative of Phosphotriesterase in the Amidohydrolase Superfamily. Biochemistry, 2009, 48, 2237-2247.	1.2	82
1487	The Distal Pocket Histidine Residue in Horse Heart Myoglobin Directs the <i>O</i>-Binding Mode of Nitrite to the Heme Iron. Journal of the American Chemical Society, 2009, 131, 18119-18128.	6.6	88
1488	Structural and Biochemical Characterization of <i>Xylella fastidiosa</i> DsbA Family Members: New Insights into the Enzymeâˆ’Substrate Interaction. Biochemistry, 2009, 48, 3508-3518.	1.2	16
1489	Myosin VI Undergoes Cargo-Mediated Dimerization. Cell, 2009, 138, 537-548.	13.5	123
1490	Crystal structure of the glycosidase family 73 peptidoglycan hydrolase FlgJ. Biochemical and Biophysical Research Communications, 2009, 381, 16-21.	1.0	33
1491	Openâ€“closed conformational change revealed by the crystal structures of 3-keto-l-gulonate 6-phosphate decarboxylase from Streptococcus mutans. Biochemical and Biophysical Research Communications, 2009, 381, 429-433.	1.0	1
1492	Crystal structure of hydrogenase maturating endopeptidase HycI from Escherichia coli. Biochemical and Biophysical Research Communications, 2009, 389, 310-314.	1.0	21
1493	Structural insights into the inhibited states of the Mer receptor tyrosine kinase. Journal of Structural Biology, 2009, 165, 88-96.	1.3	47
1494	The three-dimensional structure of the cytoplasmic domains of EpsF from the type 2 secretion system of Vibrio cholerae. Journal of Structural Biology, 2009, 166, 303-315.	1.3	49
1495	The crystal structure of the secreted aspartic protease 1 from Candida parapsilosis in complex with pepstatin A. Journal of Structural Biology, 2009, 167, 145-152.	1.3	19
1496	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
1497	The Structural Basis of Substrate Recognition in an exo-Î²-d-Glucosaminidase Involved in Chitosan Hydrolysis. Journal of Molecular Biology, 2009, 385, 131-139.	2.0	35
1498	Structure and Action of the Myxobacterial Chondrochloren Halogenase CndH: A New Variant of FAD-dependent Halogenases. Journal of Molecular Biology, 2009, 385, 520-530.	2.0	60
1499	Crystal Structure and Biochemical Properties of a Novel Thermostable Esterase Containing an Immunoglobulin-Like Domain. Journal of Molecular Biology, 2009, 385, 949-962.	2.0	36
1500	Crystal Structure of the HA3 Subcomponent of Clostridium botulinum Type C Progenitor Toxin. Journal of Molecular Biology, 2009, 385, 1193-1206.	2.0	37
1501	Crystal Structure of the Parasporin-2 Bacillus thuringiensis Toxin That Recognizes Cancer Cells. Journal of Molecular Biology, 2009, 386, 121-133.	2.0	80
1502	HisE11 and HisF8 Provide Bis-histidyl Heme Hexa-coordination in the Globin Domain of Geobacter sulfurreducens Globin-coupled Sensor. Journal of Molecular Biology, 2009, 386, 246-260.	2.0	47

#	ARTICLE	IF	CITATIONS
1503	Domain Organization in Clostridium botulinum Neurotoxin Type E Is Unique: Its Implication in Faster Translocation. Journal of Molecular Biology, 2009, 386, 233-245.	2.0	161
1504	Crystal Structure of the IrrE Protein, a Central Regulator of DNA Damage Repair in Deinococcaceae. Journal of Molecular Biology, 2009, 386, 704-716.	2.0	70
1505	Structural Studies on the Pseudomonas aeruginosa Sialidase-Like Enzyme PA2794 Suggest Substrate and Mechanistic Variations. Journal of Molecular Biology, 2009, 386, 828-840.	2.0	18
1506	Structural Characterization of Clostridium acetobutylicum 8-Oxoguanine DNA Glycosylase in Its Apo Form and in Complex with 8-Oxodeoxyguanosine. Journal of Molecular Biology, 2009, 387, 669-679.	2.0	14
1507	Structure and Ligand Binding of the Extended Tudor Domain of D. melanogaster Tudor-SN. Journal of Molecular Biology, 2009, 387, 921-934.	2.0	56
1508	Blood Group Antigen Recognition by a Solute-Binding Protein from a Serotype 3 Strain of Streptococcus pneumoniae. Journal of Molecular Biology, 2009, 388, 299-309.	2.0	22
1509	The X-ray Crystal Structure of an Arthrobacter protophormiae Endo-Î²-N-Acetylglucosaminidase Reveals a (Î²/Î±)8 Catalytic Domain, Two Ancillary Domains and Active Site Residues Key for Transglycosylation Activity. Journal of Molecular Biology, 2009, 389, 1-9.	2.0	36
1510	Structural Snapshots for the Conformation-dependent Catalysis by Human Medium-chain Acyl-coenzyme A Synthetase ACSM2A. Journal of Molecular Biology, 2009, 388, 997-1008.	2.0	93
1511	An Ion-channel Modulator from the Saliva of the Brown Ear Tick has a Highly Modified Kunitz/BPTI Structure. Journal of Molecular Biology, 2009, 389, 734-747.	2.0	42
1512	Structural and Functional Characterisation of a Conserved Archaeal RadA Paralog with Antirecombinase Activity. Journal of Molecular Biology, 2009, 389, 661-673.	2.0	45
1513	Structural and Functional Analysis of the Globular Head Domain of p115 Provides Insight into Membrane Tethering. Journal of Molecular Biology, 2009, 391, 26-41.	2.0	34
1514	N-Acetylglucosamine Recognition by a Family 32 Carbohydrate-Binding Module from Clostridium perfringens NagH. Journal of Molecular Biology, 2009, 390, 208-220.	2.0	35
1515	Crystal Structures of the Human and Fungal Cytosolic Leucyl-tRNA Synthetase Editing Domains: A Structural Basis for the Rational Design of Antifungal Benzoxaboroles. Journal of Molecular Biology, 2009, 390, 196-207.	2.0	89
1516	Structure and Calcium-Binding Activity of LipL32, the Major Surface Antigen of Pathogenic Leptospira sp.. Journal of Molecular Biology, 2009, 390, 722-736.	2.0	41
1517	Crystal Structure of the C-Terminal Domain of Human DPY-30-Like Protein: A Component of the Histone Methyltransferase Complex. Journal of Molecular Biology, 2009, 390, 530-537.	2.0	33
1518	Structural Basis for Resistance of the Genotype 2b Hepatitis C Virus NS5B Polymerase to Site A Non-Nucleoside Inhibitors. Journal of Molecular Biology, 2009, 390, 1048-1059.	2.0	16
1519	Distinct Structural Features of Cyclothiazide Are Responsible for Effects on Peak Current Amplitude and Desensitization Kinetics at iGluR2. Journal of Molecular Biology, 2009, 391, 906-917.	2.0	29
1520	Characterization of Two Novel Aldoâ€"Keto Reductases from Arabidopsis: Expression Patterns, Broad Substrate Specificity, and an Open Active-Site Structure Suggest a Role in Toxicant Metabolism Following Stress. Journal of Molecular Biology, 2009, 392, 465-480.	2.0	123

#	ARTICLE	IF	CITATIONS
1521	Crystal Structure of a Periplasmic Substrate-Binding Protein in Complex with Calcium Lactate. Journal of Molecular Biology, 2009, 392, 559-565.	2.0	20
1522	Biochemical and Structural Study of the Homologues of the Thiolâ€“Disulfide Oxidoreductase DsbA in Neisseria meningitidis. Journal of Molecular Biology, 2009, 392, 952-966.	2.0	45
1523	PILZ Protein Structure and Interactions with PILB and the FIMX EAL Domain: Implications for Control of Type IV Pilus Biogenesis. Journal of Molecular Biology, 2009, 393, 848-866.	2.0	100
1524	Crystal Structure of the Frizzled-Like Cysteine-Rich Domain of the Receptor Tyrosine Kinase MuSK. Journal of Molecular Biology, 2009, 393, 1-9.	2.0	63
1525	Crystal Structure of the Hexameric Catabolic Ornithine Transcarbamylase from Lactobacillus hilgardii: Structural Insights into the Oligomeric Assembly and Metal Binding. Journal of Molecular Biology, 2009, 393, 425-434.	2.0	17
1526	A C-Terminal Phosphatase Module Conserved in Vertebrate CMP-Sialic Acid Synthetases Provides a Tetramerization Interface for the Physiologically Active Enzyme. Journal of Molecular Biology, 2009, 393, 83-97.	2.0	13
1527	Serendipitous Fatty Acid Binding Reveals the Structural Determinants for Ligand Recognition in Apolipoprotein M. Journal of Molecular Biology, 2009, 393, 920-936.	2.0	62
1528	Methionine Sulfoxide Reductase B Displays a High Level of Flexibility. Journal of Molecular Biology, 2009, 394, 83-93.	2.0	40
1529	Two Complementary Enzymes for Threonylation of tRNA in Crenarchaeota: Crystal Structure of Aeropyrum pernix Threonyl-tRNA Synthetase Lacking a cis-Editing Domain. Journal of Molecular Biology, 2009, 394, 286-296.	2.0	12
1530	PilM/N/O/P Proteins Form an Inner Membrane Complex That Affects the Stability of the Pseudomonas aeruginosa Type IV Pilus Secretin. Journal of Molecular Biology, 2009, 394, 128-142.	2.0	137
1531	Periplasmic Domains of Pseudomonas aeruginosa PilN and PilO Form a Stable Heterodimeric Complex. Journal of Molecular Biology, 2009, 394, 143-159.	2.0	72
1532	Autoinhibition of UNC5b Revealed by the Cytoplasmic Domain Structure of the Receptor. Molecular Cell, 2009, 33, 692-703.	4.5	82
1533	Structure and Activity of the N-Terminal Substrate Recognition Domains in Proteasomal ATPases. Molecular Cell, 2009, 34, 580-590.	4.5	116
1534	Crystal structure of an anti-ganglioside antibody, and modelling of the functional mimicry of its NeuGc-GM3 antigen by an anti-idiotypic antibody. Molecular Immunology, 2009, 46, 3466-3475.	1.0	24
1535	Unprecedented Binding Cooperativity between Cu^I and Cu^{II} in the Copper Resistance Protein CopK from <i>Cupriavidus metallidurans</i> CH34: Implications from Structural Studies by NMR Spectroscopy and X-Ray Crystallography. Journal of the American Chemical Society, 2009, 131, 3549-3564.	6.6	38
1536	Crystal structure of a major secreted protein of Mycobacterium tuberculosis-MPT63 at 1.5-Ã… resolution. Protein Science, 2009, 11, 2887-2893.	3.1	37
1537	Staphostatins resemble lipocalins, not cystatins in fold. Protein Science, 2009, 12, 2252-2256.	3.1	25
1538	Crystal structure of truncated human Î²B1-crystallin. Protein Science, 2009, 12, 2606-2612.	3.1	92

#	ARTICLE	IF	CITATIONS
1539	The Novel Structure of a Pyridoxal 5â€²-Phosphate-Dependent Fold-Type I Racemase, Î±-Amino-Îµ-caprolactam Racemase from Achromobacter obae,. Biochemistry, 2009, 48, 941-950.	1.2	30
1540	Functional Annotation of Two New Carboxypeptidases from the Amidohydrolase Superfamily of Enzymes. Biochemistry, 2009, 48, 4567-4576.	1.2	19
1541	Lessons from Structural Genomics. Annual Review of Biophysics, 2009, 38, 371-383.	4.5	115
1542	X-ray Crystal Structure Of A Trpm Assembly Domain Reveals An Antiparallel Four-stranded Coiled-coil. Biophysical Journal, 2009, 96, 392a.	0.2	23
1543	Structural basis for ligand and substrate recognition by torovirus hemagglutinin esterases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15897-15902.	3.3	46
1544	The Glutamate Receptor GluR5 Agonist (<i>S</i>)-2-Amino-3-(3-hydroxy-7,8-dihydro-6<i>H</i>-cyclohepta[<i>d</i>]isoxazol-4-yl)propionic Acid and the 8-Methyl Analogue: Synthesis, Molecular Pharmacology, and Biostructural Characterizationâ€PDB ID: 2WKY.,. Journal of Medicinal Chemistry, 2009, 52, 4911-4922.	2.9	21
1545	The impact of Structural Proteomics on Biotechnology. Biotechnology and Genetic Engineering Reviews, 2009, 26, 353-370.	2.4	4
1546	Structural Analysis of a Multifunctional, Tandemly Repeated Inositol Polyphosphatase. Journal of Molecular Biology, 2009, 392, 75-86.	2.0	15
1547	Crystal Structure of the Acid-Induced Arginine Decarboxylase from <i>Escherichia coli</i>: Reversible Decamer Assembly Controls Enzyme Activity. Biochemistry, 2009, 48, 3915-3927.	1.2	48
1548	Molecular structure from X-ray diffraction. Annual Reports on the Progress of Chemistry Section C, 2010, 106, 192.	4.4	3
1549	Mercaptophosphonate Compounds as Broad-Spectrum Inhibitors of the Metallo-Î²-lactamases. Journal of Medicinal Chemistry, 2010, 53, 4862-4876.	2.9	128
1550	Crystal structure of a novel non-Pfam protein PF2046 solved using low resolution B-factor sharpening and multi-crystal averaging methods. Protein and Cell, 2010, 1, 453-458.	4.8	13
1551	Structures of the N- and C-terminal domains of MHV-A59 nucleocapsid protein corroborate a conserved RNA-protein binding mechanism in coronavirus. Protein and Cell, 2010, 1, 688-697.	4.8	40
1552	The Crystal Structure of Hexamer RraA from Pseudomonas Aeruginosa Reveals Six Conserved Proteinâ€"Protein Interaction Sites. Protein Journal, 2010, 29, 583-590.	0.7	7
1553	To automate or not to automate: this is the question. Journal of Structural and Functional Genomics, 2010, 11, 211-221.	1.2	23
1554	Structural Basis of Host Cell Recognition by the Pilus Adhesin from Streptococcus pneumoniae. Structure, 2010, 18, 106-115.	1.6	120
1555	Conserved Î²-Hairpin Recognition by the GYF Domains of Smy2 and GIGYF2 in mRNA Surveillance and Vesicular Transport Complexes. Structure, 2010, 18, 944-954.	1.6	34
1556	Structure and Cellular Roles of the RMI Core Complex from the Bloom Syndrome Dissolvasome. Structure, 2010, 18, 1149-1158.	1.6	33

#	Article	IF	Citations
1557	Structural Underpinnings of Nitrogen Regulation by the Prototypical Nitrogen-Responsive Transcriptional Factor NrpR. Structure, 2010, 18, 1512-1521.	1.6	11
1558	Allosteric Activation Mechanism of the Mycobacterium tuberculosis Receptor Ser/Thr Protein Kinase, PknB. Structure, 2010, 18, 1667-1677.	1.6	50
1559	Structure of a polyisoprenoid binding domain from <i>Saccharophagus degradans</i> implicated in plant cell wall breakdown. FEBS Letters, 2010, 584, 1577-1584.	1.3	20
1560	Biocatalysis with Thermostable Enzymes: Structure and Properties of a Thermophilic â€˜eneâ€™â€Reductase related to Old Yellow Enzyme. ChemBioChem, 2010, 11, 197-207.	1.3	110
1561	Focused Directed Evolution of Pentaerythritol Tetranitrate Reductase by Using Automated Anaerobic Kinetic Screening of Siteâ€Saturated Libraries. ChemBioChem, 2010, 11, 2433-2447.	1.3	47
1562	Isoprenoid-chained lipid Î²-XylOC16+4â€"A novel molecule for in meso membrane protein crystallization. Journal of Crystal Growth, 2010, 312, 3326-3330.	0.7	34
1563	Family 42 carbohydrate-binding modules display multiple arabinoxylan-binding interfaces presenting different ligand affinities. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 2054-2062.	1.1	9
1564	Rational Design of Inhibitors and Activity-Based Probes Targeting Clostridium difficile Virulence Factor TcdB. Chemistry and Biology, 2010, 17, 1201-1211.	6.2	58
1565	Semi-automated protein crystal mounting device for the sulfur single-wavelength anomalous diffraction method. Journal of Applied Crystallography, 2010, 43, 341-346.	1.9	17
1566	Update on the tutorial for learning and teaching macromolecular crystallography. Journal of Applied Crystallography, 2010, 43, 1230-1237.	1.9	6
1567	Experimental phasing with <i>SHELXC</i>/<i>D</i>/<i>E</i>: combining chain tracing with density modification. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 479-485.	2.5	1,041
1568	Structure of a family 3bâ€² carbohydrate-binding module from the Cel9V glycoside hydrolase from<i>Clostridium thermocellum</i>: structural diversity and implications for carbohydrate binding. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 33-43.	2.5	18
1569	The magic triangle goes MAD: experimental phasing with a bromine derivative. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 374-380.	2.5	25
1570	Rapid chain tracing of polypeptide backbones in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 285-294.	2.5	6
1571	Rapid model building of Î²-sheets in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 276-284.	2.5	4
1572	Rapid model building of Î±-helices in electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 268-275.	2.5	25
1573	High-resolution X-ray crystal structure of bovine H-protein at 0.88â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 698-708.	2.5	9
1574	Multivariate phase combination improves automated crystallographic model building. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 783-788.	2.5	20

#	ARTICLE	IF	CITATIONS
1575	Performance of phased rotation, conformation and translation function: accurate protein model building with tripeptidic and tetrapeptidic fragments. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1012-1023.	2.5	3
1576	Crystallization of small proteins assisted by green fluorescent protein. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1059-1066.	2.5	31
1577	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1174-1181.	0.7	8
1578	Structure of YqgQ protein from<i>Bacillus subtilis</i>, a conserved hypothetical protein. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 8-11.	0.7	7
1579	Structure of uracil-DNAN-glycosylase (UNG) fromVibrio cholerae: mapping temperature adaptation through structural and mutational analysis. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 130-136.	0.7	9
1580	A triclinic crystal form of<i>Escherichia coli</i>4-diphosphocytidyl-2<i>C</i>-methyl-<scp>D</scp>-erythritol kinase and reassessment of the quaternary structure. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 237-241.	0.7	11
1581	Apo and ligand-bound structures of ModA from the archaeon<i>Methanosarcina acetivorans</i>. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 242-250.	0.7	12
1582	Crystallographic study of wild-type carbonic anhydrase Î±CA1 fromChlamydomonas reinhardtii. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1082-1085.	0.7	2
1583	Crystallization and calcium/sulfur SAD phasing of the human EF-hand protein S100A2. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1032-1036.	0.7	6
1584	Globin-like proteins in Caenorhabditis elegans: in vivo localization, ligand binding and structural properties. BMC Biochemistry, 2010, 11, 17.	4.4	21
1585	Structure of the dimerization domain of DiGeorge Critical Region 8. Protein Science, 2010, 19, 1354-1365.	3.1	49
1586	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
1587	Structure of the micronemal protein 2 A/I domain from <i>Toxoplasma gondii</i>. Protein Science, 2010, 19, 1985-1990.	3.1	15
1588	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
1589	Structural and functional characterization of a promiscuous feruloyl esterase (Est1E) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1457-1469.	1.5	62
1590	Structural basis for regulation of polyâ€SUMO chain by a SUMOâ€like domain of Nip45. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1491-1502.	1.5	28
1591	<i>p</i>â€Coumaric acid decarboxylase from <i>Lactobacillus plantarum</i>: Structural insights into the active site and decarboxylation catalytic mechanism. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1662-1676.	1.5	52
1592	Structural investigation of transcriptional regulator HlyIIR: Influence of a disordered region on protein fold and dimerization. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1870-1877.	1.5	2

#	Article	IF	Citations
1593	Crystal structure of an eIF4Gâ€like protein from <i>Danio rerio</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1803-1806.	1.5	2
1594	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1992-1998.	1.5	13
1595	Crystal structure of a truncated urease accessory protein UreF from <i>Helicobacter pylori</i>. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2839-2848.	1.5	37
1596	Direct methods beyond smallâ€molecule crystallography. Physica Status Solidi (A) Applications and Materials Science, 2010, 207, 2621-2638.	0.8	1
1597	How Much Binding Affinity Can be Gained by Filling a Cavity?. Chemical Biology and Drug Design, 2010, 75, 143-151.	1.5	47
1598	Crystal structure of a glycoside hydrolase family 6 enzyme, CcCel6C, a cellulase constitutively produced by <i>Coprinopsisâ€ƒcinerea</i>. FEBS Journal, 2010, 277, 1532-1542.	2.2	28
1599	<i>Staphylococcusâ€ƒaureus</i> elongation factor G â€" structure and analysis of a target for fusidic acid. FEBS Journal, 2010, 277, 3789-3803.	2.2	47
1600	Structural studies on the fullâ€length LysRâ€<i>type</i> regulator TsaR from <i>Comamonas testosteroni</i> Tâ€2 reveal a novel open conformation of the tetrameric LTTR fold. Molecular Microbiology, 2010, 75, 1199-1214.	1.2	72
1601	Structure determination and analysis of a haemolytic gingipain adhesin domain from <i>Porphyromonas gingivalis</i>. Molecular Microbiology, 2010, 76, 861-873.	1.2	30
1602	The molecular basis of glycogen breakdown and transport in <i>Streptococcus pneumoniae</i>. Molecular Microbiology, 2010, 77, 183-199.	1.2	57
1603	SurR regulates hydrogen production in Pyrococcus furiosus by a sulfur-dependent redox switch. Molecular Microbiology, 2010, 77, 1111-1122.	1.2	40
1604	Structure of the Dom34â€"Hbs1 complex and implications for no-go decay. Nature Structural and Molecular Biology, 2010, 17, 1233-1240.	3.6	98
1605	Prp43p contains a processive helicase structural architecture with a specific regulatory domain. EMBO Journal, 2010, 29, 2194-2204.	3.5	124
1606	Crystal structure of the yeast Sac1: implications for its phosphoinositide phosphatase function. EMBO Journal, 2010, 29, 1489-1498.	3.5	107
1607	Coupled chaperone action in folding and assembly of hexadecameric Rubisco. Nature, 2010, 463, 197-202.	13.7	165
1608	Stepwise [FeFe]-hydrogenase H-cluster assembly revealed in the structure of HydAÎ"EFG. Nature, 2010, 465, 248-251.	13.7	295
1609	Structural basis of semaphorinâ€"plexin signalling. Nature, 2010, 467, 1118-1122.	13.7	211
1610	Homologue structure of the SLAC1 anion channel for closing stomata in leaves. Nature, 2010, 467, 1074-1080.	13.7	118

#	Article	IF	Citations
1611	Crystal Structure of the Neutralizing Llama VHH D7 and Its Mode of HIV-1 gp120 Interaction. PLoS ONE, 2010, 5, e10482.	1.1	33
1612	ORF157 from the Archaeal Virus<i>Acidianus</i>Filamentous Virus 1 Defines a New Class of Nuclease. Journal of Virology, 2010, 84, 5025-5031.	1.5	14
1613	Channeling and conformational changes in the heterotetrameric sarcosine oxidase from Corynebacterium sp. U-96. Journal of Biochemistry, 2010, 148, 491-505.	0.9	15
1614	Structure and Protein-Protein Interaction Studies on <i>Chlamydia trachomatis</i> Protein CT670 (YscO Homolog). Journal of Bacteriology, 2010, 192, 2746-2756.	1.0	34
1615	Bardet-Biedl Syndrome-associated Small GTPase ARL6 (BBS3) Functions at or near the Ciliary Gate and Modulates Wnt Signaling. Journal of Biological Chemistry, 2010, 285, 16218-16230.	1.6	100
1616	Crystal structure of a 117 kDa glucansucrase fragment provides insight into evolution and product specificity of GH70 enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21406-21411.	3.3	140
1617	Structure Function Studies of Vaccinia Virus Host Range Protein K1 Reveal a Novel Functional Surface for Ankyrin Repeat Proteins. Journal of Virology, 2010, 84, 3331-3338.	1.5	30
1618	OASIS4.0â€"a new version of the program OASIS for phasing protein diffraction data. Chinese Physics B, 2010, 19, 086103.	0.7	7
1619	Papain-Like Protease 1 from Transmissible Gastroenteritis Virus: Crystal Structure and Enzymatic Activity toward Viral and Cellular Substrates. Journal of Virology, 2010, 84, 10063-10073.	1.5	49
1620	Large-scale Domain Dynamics and Adenosylcobalamin Reorientation Orchestrate Radical Catalysis in Ornithine 4,5-Aminomutase. Journal of Biological Chemistry, 2010, 285, 13942-13950.	1.6	48
1621	Crystal Structure of the Narrow-Spectrum OXA-46 Class D Î²-Lactamase: Relationship between Active-Site Lysine Carbamylation and Inhibition by Polycarboxylates. Antimicrobial Agents and Chemotherapy, 2010, 54, 2167-2174.	1.4	31
1622	Versatile Loops in Mycocypins Inhibit Three Protease Families. Journal of Biological Chemistry, 2010, 285, 308-316.	1.6	55
1623	The Structure of Mammalian Serine Racemase. Journal of Biological Chemistry, 2010, 285, 12873-12881.	1.6	76
1624	Structure and DNA binding activity of the mouse condensin hinge domain highlight common and diverse features of SMC proteins. Nucleic Acids Research, 2010, 38, 3454-3465.	6.5	82
1625	Neuroplastinâ€55 binds to and signals through the fibroblast growth factor receptor. FASEB Journal, 2010, 24, 1139-1150.	0.2	48
1626	New expression of bimodal phase distributions in direct-method phasing of protein single-wavelength anomalous diffraction data. Chinese Physics B, 2010, 19, 086102.	0.7	1
1627	Crystal structure of the P2 C-repressor: a binder of non-palindromic direct DNA repeats. Nucleic Acids Research, 2010, 38, 7778-7790.	6.5	10
1628	Omp85 from the Thermophilic Cyanobacterium Thermosynechococcus elongatus Differs from Proteobacterial Omp85 in Structure and Domain Composition. Journal of Biological Chemistry, 2010, 285, 18003-18015.	1.6	61

#	ARTICLE	IF	CITATIONS
1629	Molecular Characterization of a Class I P450 Electron Transfer System from Novosphingobium aromaticivorans DSM12444. Journal of Biological Chemistry, 2010, 285, 27372-27384.	1.6	74
1630	A novel Î±-N-acetylgalactosaminidase family with an NAD+-dependent catalytic mechanism suitable for enzymatic removal of blood group A antigens. Biocatalysis and Biotransformation, 2010, 28, 22-32.	1.1	3
1631	Structural basis for a reciprocating mechanism of negative cooperativity in dimeric phosphagen kinase activity. FASEB Journal, 2010, 24, 242-252.	0.2	30
1632	Structure and Activity of the Metal-independent Fructose-1,6-bisphosphatase YK23 from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2010, 285, 21049-21059.	1.6	21
1633	Kinetic and Structural Insights into the Mechanism of AMPylation by VopS Fic Domain. Journal of Biological Chemistry, 2010, 285, 20155-20163.	1.6	77
1634	Crystal Structure of Hexokinase KlHxk1 of Kluyveromyces lactis. Journal of Biological Chemistry, 2010, 285, 41019-41033.	1.6	26
1635	Combining SAD/SIR iteration and MR iteration in partial-model extension of proteins. Chinese Physics B, 2010, 19, 096101.	0.7	8
1636	Structural basis of YAP recognition by TEAD4 in the Hippo pathway. Genes and Development, 2010, 24, 290-300.	2.7	202
1637	Structural and Functional Characterization of SporoSAG. Journal of Biological Chemistry, 2010, 285, 12063-12070.	1.6	37
1638	Crystal Structure of Leishmania major Oligopeptidase B Gives Insight into the Enzymatic Properties of a Trypanosomatid Virulence Factor. Journal of Biological Chemistry, 2010, 285, 39249-39259.	1.6	53
1639	Specificity of Staphyloferrin B Recognition by the SirA Receptor from Staphylococcus aureus. Journal of Biological Chemistry, 2010, 285, 34579-34588.	1.6	56
1640	Crystal Structure of Full-length Mycobacterium tuberculosis H37Rv Glycogen Branching Enzyme. Journal of Biological Chemistry, 2010, 285, 20897-20903.	1.6	67
1641	Crystal Structure of the Peptidase Domain of Streptococcus ComA, a Bifunctional ATP-binding Cassette Transporter Involved in the Quorum-sensing Pathway. Journal of Biological Chemistry, 2010, 285, 10777-10785.	1.6	49
1642	Recognition of the Helical Structure of Î²-1,4-Galactan by a New Family of Carbohydrate-binding Modules. Journal of Biological Chemistry, 2010, 285, 35999-36009.	1.6	39
1643	Crystal Structures of Phosphoketolase. Journal of Biological Chemistry, 2010, 285, 34279-34287.	1.6	52
1644	Structural and Biochemical Characterization of the Human Cyclophilin Family of Peptidyl-Prolyl Isomerases. PLoS Biology, 2010, 8, e1000439.	2.6	226
1645	Bunyaviridae RNA Polymerases (L-Protein) Have an N-Terminal, Influenza-Like Endonuclease Domain, Essential for Viral Cap-Dependent Transcription. PLoS Pathogens, 2010, 6, e1001101.	2.1	215
1646	Guiding belief propagation using domain knowledge for protein-structure determination. , 2010, , .		1

#	ARTICLE	IF	CITATIONS
1647	Crystal Structure and Size-Dependent Neutralization Properties of HK20, a Human Monoclonal Antibody Binding to the Highly Conserved Heptad Repeat 1 of gp41. PLoS Pathogens, 2010, 6, e1001195.	2.1	82
1648	Structural and Functional Characterization of a Novel Homodimeric Three-finger Neurotoxin from the Venom of Ophiophagus hannah (King Cobra). Journal of Biological Chemistry, 2010, 285, 8302-8315.	1.6	77
1649	Crystal Structure-Based Selective Targeting of the Pyridoxal 5â€²-Phosphate Dependent Enzyme Kynurenine Aminotransferase II for Cognitive Enhancement. Journal of Medicinal Chemistry, 2010, 53, 5684-5689.	2.9	45
1650	X-Ray Crystallography in Drug Discovery. Methods in Molecular Biology, 2010, 572, 31-56.	0.4	32
1651	Structural studies of BmooMPÎ±-I, a non-hemorrhagic metalloproteinase from Bothrops moojeni venom. Toxicon, 2010, 55, 361-368.	0.8	37
1652	Crystal Structure of a Putative Histidine-containing Phosphotransfer Protein from Oryza sativa. Journal of the Korean Society for Applied Biological Chemistry, 2010, 53, 852-856.	0.9	4
1653	Crystal Structure of Prolyl 4-Hydroxylase from <i>Bacillus anthracis</i>. Biochemistry, 2010, 49, 124-133.	1.2	23
1654	Discovery and Structure Determination of the Orphan Enzyme Isoxanthopterin Deaminase,. Biochemistry, 2010, 49, 4374-4382.	1.2	18
1655	Rational Engineering of Mannosyl Binding in the Distal Glycone Subsites of <i>Cellulomonas fimi</i> Endo-Î²-1,4-mannanase: Mannosyl Binding Promoted at Subsite â˜'2 and Demoted at Subsite â˜'3,. Biochemistry, 2010, 49, 4884-4896.	1.2	34
1656	Biochemical and Structural Properties of Chimeras Constructed by Exchange of Cofactor-Binding Domains in Alcohol Dehydrogenases from Thermophilic and Mesophilic Microorganisms. Biochemistry, 2010, 49, 1943-1953.	1.2	9
1657	Switching Catalysis from Hydrolysis to Perhydrolysis in <i>Pseudomonas fluorescens</i> Esterase[,]. Biochemistry, 2010, 49, 1931-1942.	1.2	54
1658	Structure, Mechanism, and Substrate Profile for Sco3058: The Closest Bacterial Homologue to Human Renal Dipeptidase,. Biochemistry, 2010, 49, 611-622.	1.2	15
1659	Structure of the Dimerization Domain of the Rabies Virus Phosphoprotein. Journal of Virology, 2010, 84, 3707-3710.	1.5	76
1660	Biostructural and Pharmacological Studies of Bicyclic Analogues of the 3-Isoxazolol Glutamate Receptor Agonist Ibotenic Acid. Journal of Medicinal Chemistry, 2010, 53, 8354-8361.	2.9	20
1661	Structural and Biochemical Studies of a Fluoroacetyl-CoA-Specific Thioesterase Reveal a Molecular Basis for Fluorine Selectivity. Biochemistry, 2010, 49, 9269-9279.	1.2	31
1662	Structural Insights into Substrate Specificity and the <i>anti</i> Î²-Elimination Mechanism of Pectate Lyase. Biochemistry, 2010, 49, 539-546.	1.2	46
1663	Mutation of Archaeal Isopentenyl Phosphate Kinase Highlights Mechanism and Guides Phosphorylation of Additional Isoprenoid Monophosphates. ACS Chemical Biology, 2010, 5, 589-601.	1.6	30
1664	Computational Tools in Protein Crystallography. Methods in Molecular Biology, 2010, 673, 129-156.	0.4	6

#	ARTICLE	IF	CITATIONS
1665	Crystal structure and molecular modeling study of N-carbamoylsarcosine amidase Ta0454 from Thermoplasma acidophilum. Journal of Structural Biology, 2010, 169, 304-311.	1.3	13
1666	Catechol 1,2-dioxygenase from the Gram-positive Rhodococcus opacus 1CP: Quantitative structure/activity relationship and the crystal structures of native enzyme and catechols adducts. Journal of Structural Biology, 2010, 170, 548-564.	1.3	46
1667	A transition from strong right-handed to canonical left-handed supercoiling in a conserved coiled-coil segment of trimeric autotransporter adhesins. Journal of Structural Biology, 2010, 170, 236-245.	1.3	41
1668	Crystal Structure of the ATPPase Subunit and Its Substrate-Dependent Association with the GATase Subunit: A Novel Regulatory Mechanism for a Two-Subunit-Type GMP Synthetase from Pyrococcus horikoshii OT3. Journal of Molecular Biology, 2010, 395, 417-429.	2.0	21
1669	Unusual Diheme Conformation of the Heme-Degrading Protein from Mycobacterium tuberculosis. Journal of Molecular Biology, 2010, 395, 595-608.	2.0	89
1670	Crystal Structures of an Oligopeptide-Binding Protein from the Biosynthetic Pathway of the Î²-Lactamase Inhibitor Clavulanic Acid. Journal of Molecular Biology, 2010, 396, 332-344.	2.0	13
1671	Crystal Structure Analysis of Free and Substrate-Bound 6-Hydroxy-l-Nicotine Oxidase from Arthrobacter nicotinovorans. Journal of Molecular Biology, 2010, 396, 785-799.	2.0	33
1672	The Three-Dimensional Structure of [NiFeSe] Hydrogenase from Desulfovibrio vulgaris Hildenborough: A Hydrogenase without a Bridging Ligand in the Active Site in Its Oxidised, â€œas-Isolatedâ€•State. Journal of Molecular Biology, 2010, 396, 893-907.	2.0	110
1673	Crystal Structures of the CERT START Domain with Inhibitors Provide Insights into the Mechanism of Ceramide Transfer. Journal of Molecular Biology, 2010, 396, 245-251.	2.0	69
1674	Insights into Higher-Order Organization of the Cellulosome Revealed by a Dissect-and-Build Approach: Crystal Structure of Interacting Clostridium thermocellum Multimodular Components. Journal of Molecular Biology, 2010, 396, 833-839.	2.0	34
1675	Chloramphenicol Biosynthesis: The Structure of CmlS, a Flavin-Dependent Halogenase Showing a Covalent Flavinâ€“Aspartate Bond. Journal of Molecular Biology, 2010, 397, 316-331.	2.0	103
1676	Structure of Bacteriophage T4 Endonuclease II Mutant E118A, a Tetrameric GIY-YIG Enzyme. Journal of Molecular Biology, 2010, 397, 1003-1016.	2.0	6
1677	Crystal Structure of the Electron Carrier Domain of the Reaction Center Cytochrome cz Subunit from Green Photosynthetic Bacterium Chlorobium tepidum. Journal of Molecular Biology, 2010, 397, 1175-1187.	2.0	15
1678	Structures of PHR Domains from Mus musculus Phr1 (Mycbp2) Explain the Loss-of-Function Mutation (Gly1092 â†’ Glu) of the C. elegans Ortholog RPM-1. Journal of Molecular Biology, 2010, 397, 883-892.	2.0	3
1679	Crystal Structure and Comparative Functional Analyses of a Mycobacterium Aldo-Keto Reductase. Journal of Molecular Biology, 2010, 398, 26-39.	2.0	12
1680	Crystal Structure of the Botulinum Neurotoxin Type G Binding Domain: Insight into Cell Surface Binding. Journal of Molecular Biology, 2010, 397, 1287-1297.	2.0	36
1681	Crystal Structures of Human HMG-CoA Synthase Isoforms Provide Insights into Inherited Ketogenesis Disorders and Inhibitor Design. Journal of Molecular Biology, 2010, 398, 497-506.	2.0	56
1682	Crystal Structure of Yeast FAD Synthetase (Fad1) in Complex with FAD. Journal of Molecular Biology, 2010, 398, 641-646.	2.0	25

#	ARTICLE	IF	CITATIONS
1683	Thermodynamic Characterization of the Interaction between Prefoldin and Group II Chaperonin. Journal of Molecular Biology, 2010, 399, 628-636.	2.0	16
1684	Structural Characterization of the Predominant Family of Histidine Kinase Sensor Domains. Journal of Molecular Biology, 2010, 400, 335-353.	2.0	117
1685	Crystal Structure of the GalNAc/Gal-Specific Agglutinin from the Phytopathogenic Ascomycete Sclerotinia sclerotiorum Reveals Novel Adaptation of a Î²-Trefoil Domain. Journal of Molecular Biology, 2010, 400, 715-723.	2.0	33
1686	The Structure of the FnIII Tandem A77-A78 Points to a Periodically Conserved Architecture in the Myosin-Binding Region of Titin. Journal of Molecular Biology, 2010, 401, 843-853.	2.0	31
1687	Structure-Based Annotation of a Novel Sugar Isomerase from the Pathogenic E. coli O157:H7. Journal of Molecular Biology, 2010, 401, 866-881.	2.0	29
1688	Structure and Properties of a Complex of Î±-Synuclein and a Single-Domain Camelid Antibody. Journal of Molecular Biology, 2010, 402, 326-343.	2.0	164
1689	Structural Insight into the Mechanism of c-di-GMP Hydrolysis by EAL Domain Phosphodiesterases. Journal of Molecular Biology, 2010, 402, 524-538.	2.0	121
1690	Conserved Hydrophobic Clusters on the Surface of the Caf1A Usher C-Terminal Domain Are Important for F1 Antigen Assembly. Journal of Molecular Biology, 2010, 403, 243-259.	2.0	11
1691	Crystal Structure of Î³-Hexachlorocyclohexane Dehydrochlorinase LinA from Sphingobium japonicum UT26. Journal of Molecular Biology, 2010, 403, 260-269.	2.0	38
1692	Structure and Mechanism of the Magnesium-Independent Aromatic Prenyltransferase CloQ from the Clorobiocin Biosynthetic Pathway. Journal of Molecular Biology, 2010, 404, 611-626.	2.0	46
1693	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
1694	Structural characterization of Burkholderia pseudomallei adenylate kinase (Adk): Profound asymmetry in the crystal structure of the â€˜openâ€™ state. Biochemical and Biophysical Research Communications, 2010, 394, 1012-1017.	1.0	3
1695	Crystal structure of TTHA0061, an uncharacterized protein from Thermus thermophilus HB8, reveals a novel fold. Biochemical and Biophysical Research Communications, 2010, 400, 258-264.	1.0	0
1696	Thermodynamics and structure of a salmon cold active goose-type lysozyme. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 156, 254-263.	0.7	7
1697	Pro Isomerization in MLL1 PHD3-Bromo Cassette Connects H3K4me Readout to CyP33 and HDAC-Mediated Repression. Cell, 2010, 141, 1183-1194.	13.5	176
1698	Molecular Basis of the Death-Associated Protein Kinaseâ€“Calcium/Calmodulin Regulator Complex. Science Signaling, 2010, 3, ra6.	1.6	94
1699	Molecular mechanism of elongation factor 1A inhibition by a Legionella pneumophila glycosyltransferase. Biochemical Journal, 2010, 426, 281-292.	1.7	33
1700	Mouse ApoM Displays an Unprecedented Seven-Stranded Lipocalin Fold: Folding Decoy or Alternative Native Fold?. Journal of Molecular Biology, 2010, 404, 363-371.	2.0	8

#	Article	IF	Citations
1701	Induced-fit Mechanism for Prolyl Endopeptidase. Journal of Biological Chemistry, 2010, 285, 21487-21495.	1.6	70
1702	Crystal Structures of Aspergillus japonicus Fructosyltransferase Complex with Donor/Acceptor Substrates Reveal Complete Subsites in the Active Site for Catalysis. Journal of Biological Chemistry, 2010, 285, 23251-23264.	1.6	74
1703	Active site modifications in pentaerythritol tetranitrate reductase can lead to improved product enantiopurity, decreased by-product formation and altered stereochemical outcome in reactions with Î±,Î²-unsaturated nitroolefins. Catalysis Science and Technology, 2011, 1, 948.	2.1	21
1704	Structure and Mechanism of the <i>trans</i>-Acting Acyltransferase from the Disorazole Synthase. Biochemistry, 2011, 50, 6539-6548.	1.2	78
1705	The Crystal Structure of Necrosis- and Ethylene-Inducing Protein 2 from the Causal Agent of Cacaoâ€™s Witchesâ€™ Broom Disease Reveals Key Elements for Its Activity. Biochemistry, 2011, 50, 9901-9910.	1.2	31
1706	Identification of the Binding Modes ofN-Phenylphthalimides Inhibiting Bacterial Thymidylate Synthase through X-Ray Crystallography Screening. Journal of Medicinal Chemistry, 2011, 54, 5454-5467.	2.9	13
1707	Structural Basis for Reductive Radical Formation and Electron Recycling in (<i>R</i>)-2-Hydroxyisocaproyl-CoA Dehydratase. Journal of the American Chemical Society, 2011, 133, 4342-4347.	6.6	51
1708	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A fromEubacterium cellulosolvens. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 491-493.	0.7	2
1709	In situ Geâ€“Ge bond formation under ambient conditions: synthesis, characterization and reactivity of organo-functionalized telluridogermanate complexes. Chemical Communications, 2011, 47, 1881-1883.	2.2	33
1710	Distinctive Attributes of Î²-Lactam Target Proteins in <i>Acinetobacter baumannii</i> Relevant to Development of New Antibiotics. Journal of the American Chemical Society, 2011, 133, 20536-20545.	6.6	85
1712	Glutathione Transferases of Phanerochaete chrysosporium. Journal of Biological Chemistry, 2011, 286, 9162-9173.	1.6	38
1713	Crystallographic Snapshots of Tyrosine Phenol-lyase Show That Substrate Strain Plays a Role in Câ€“C Bond Cleavage. Journal of the American Chemical Society, 2011, 133, 16468-16476.	6.6	43
1714	Selective Kainate Receptor (GluK1) Ligands Structurally Based upon 1<i>H</i>-Cyclopentapyrimidin-2,4(1<i>H</i>,3<i>H</i>)-dione: Synthesis, Molecular Modeling, and Pharmacological and Biostructural Characterization. Journal of Medicinal Chemistry, 2011, 54, 4793-4805.	2.9	21
1715	Diverse substrate recognition mechanism revealed by Thermotoga maritima Cel5A structures in complex with cellotetraose, cellobiose and mannotriose. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1832-1840.	1.1	47
1716	An insight into the interaction mode between CheB and chemoreceptor from two crystal structures of CheB methylesterase catalytic domain. Biochemical and Biophysical Research Communications, 2011, 411, 69-75.	1.0	5
1717	Crystal Structure of the Ubiquitin-associated (UBA) Domain of p62 and Its Interaction with Ubiquitin. Journal of Biological Chemistry, 2011, 286, 31864-31874.	1.6	117
1718	Molecular and Structural Basis of ESCRT-III Recruitment to Membranes during Archaeal Cell Division. Molecular Cell, 2011, 41, 186-196.	4.5	102
1719	Practical applications of structural genomics technologies for mutagen research. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2011, 722, 165-170.	0.9	0

#	ARTICLE	IF	CITATIONS
1720	Structural insight into the low affinity between Thermotoga maritima CheA and CheB compared to their Escherichia coli/Salmonella typhimurium counterparts. International Journal of Biological Macromolecules, 2011, 49, 794-800.	3.6	2
1721	Binding site and interlobe interactions of the ionotropic glutamate receptor GluK3 ligand binding domain revealed by high resolution crystal structure in complex with (S)-glutamate. Journal of Structural Biology, 2011, 176, 307-314.	1.3	26
1722	A Conserved Lysine Residue in the Crenarchaea-Specific Loop is Important for the Crenarchaeal Splicing Endonuclease Activity. Journal of Molecular Biology, 2011, 405, 92-104.	2.0	14
1723	Structural Basis for the Broad Substrate Range of the UDP-Sugar Pyrophosphorylase from Leishmania major. Journal of Molecular Biology, 2011, 405, 461-478.	2.0	36
1724	The Structure of Physarum polycephalum Hemagglutinin I Suggests a Minimal Carbohydrate Recognition Domain of Legume Lectin Fold. Journal of Molecular Biology, 2011, 405, 560-569.	2.0	4
1725	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
1726	Molecular Basis of Bacterial Defense against Host Lysozymes: X-ray Structures of Periplasmic Lysozyme Inhibitors PliI and PliC. Journal of Molecular Biology, 2011, 405, 1233-1245.	2.0	28
1727	The Crystal Structure of l-Sorbose Reductase from Gluconobacter frateurii Complexed with NADPH and l-Sorbose. Journal of Molecular Biology, 2011, 407, 543-555.	2.0	17
1728	Structural Analysis of Protein Folding by the Long-Chain Archaeal Chaperone FKBP26. Journal of Molecular Biology, 2011, 407, 450-464.	2.0	9
1729	Refined Crystal Structures of Human Ca2+/Zn2+-Binding S100A3 Protein Characterized by Two Disulfide Bridges. Journal of Molecular Biology, 2011, 408, 477-490.	2.0	26
1730	Crystal Structure of the Vibrio cholerae Colonization Factor TcpF and Identification of a Functional Immunogenic Site. Journal of Molecular Biology, 2011, 409, 146-158.	2.0	17
1731	Structural Basis for Streptococcus pneumoniae NanA Inhibition by Influenza Antivirals Zanamivir and Oseltamivir Carboxylate. Journal of Molecular Biology, 2011, 409, 496-503.	2.0	50
1732	X-ray-Radiation-Induced Changes in Bacteriorhodopsin Structure. Journal of Molecular Biology, 2011, 409, 813-825.	2.0	39
1733	Structural Analysis of a Putative Aminoglycoside N-Acetyltransferase from Bacillus anthracis. Journal of Molecular Biology, 2011, 410, 411-423.	2.0	17
1734	The Structure of ll-Diaminopimelate Aminotransferase from Chlamydia trachomatis: Implications for Its Broad Substrate Specificity. Journal of Molecular Biology, 2011, 411, 649-660.	2.0	14
1735	Leucettines, a Class of Potent Inhibitors of cdc2-Like Kinases and Dual Specificity, Tyrosine Phosphorylation Regulated Kinases Derived from the Marine Sponge Leucettamine B: Modulation of Alternative Pre-RNA Splicing. Journal of Medicinal Chemistry, 2011, 54, 4172-4186.	2.9	130
1736	Crystal structure of the cell corpse engulfment protein CED-2 in Caenorhabditis elegans. Biochemical and Biophysical Research Communications, 2011, 410, 189-194.	1.0	5
1737	Structural and Functional Profiling of the Human Histone Methyltransferase SMYD3. PLoS ONE, 2011, 6, e22290.	1.1	95

#	ARTICLE	IF	CITATIONS
1738	Crystal Structure of Spy0129, a Streptococcus pyogenes Class B Sortase Involved in Pilus Assembly. PLoS ONE, 2011, 6, e15969.	1.1	44
1739	Crystal Structures of the Transcriptional Repressor RolR Reveals a Novel Recognition Mechanism between Inducer and Regulator. PLoS ONE, 2011, 6, e19529.	1.1	12
1740	Evidence for a Two-Metal-Ion Mechanism in the Cytidyltransferase KdsB, an Enzyme Involved in Lipopolysaccharide Biosynthesis. PLoS ONE, 2011, 6, e23231.	1.1	12
1741	Structural and enzymatic characterization of a glycoside hydrolase family 31 Î±-xylosidase from <i>Cellvibrio japonicus</i> involved in xyloglucan saccharification. Biochemical Journal, 2011, 436, 567-580.	1.7	69
1743	The structure of the <i>Helicobacter pylori</i> ferric uptake regulator Fur reveals three functional metal binding sites. Molecular Microbiology, 2011, 79, 1260-1275.	1.2	109
1744	Crystal structures of DntR inducer binding domains in complex with salicylate offer insights into the activation of LysRâ€type transcriptional regulators. Molecular Microbiology, 2011, 81, 354-367.	1.2	43
1745	Two autonomous structural modules in the fimbrial shaft adhesin FimA mediate <i>Actinomyces</i> interactions with streptococci and host cells during oral biofilm development. Molecular Microbiology, 2011, 81, 1205-1220.	1.2	57
1746	Crystal structures of open and closed forms of <scp>d</scp>â€serine deaminase from <i>Salmonellaâ€ƒtyphimurium â€“</i> implications on substrate specificity and catalysis. FEBS Journal, 2011, 278, 2879-2891.	2.2	12
1747	Mdm38 is a 14â€3â€3â€Like Receptor and Associates with the Protein Synthesis Machinery at the Inner Mitochondrial Membrane. Traffic, 2011, 12, 1457-1466.	1.3	30
1748	Structural Characterization of the Multidomain Regulatory Protein Rv1364c from Mycobacterium tuberculosis. Structure, 2011, 19, 56-69.	1.6	19
1749	Structural Characterization of the Boca/Mesd Maturation Factors for LDL-Receptor-Type Î² Propeller Domains. Structure, 2011, 19, 324-336.	1.6	8
1750	Structural Model and trans-Interaction of the Entire Ectodomain of the Olfactory Cell Adhesion Molecule. Structure, 2011, 19, 203-211.	1.6	26
1751	Structural Basis for ESCRT-III CHMP3 Recruitment of AMSH. Structure, 2011, 19, 1149-1159.	1.6	47
1752	Structure Analysis of the IL-5 Ligand-Receptor Complex Reveals a Wrench-like Architecture for IL-5RÎ±. Structure, 2011, 19, 1864-1875.	1.6	42
1753	Classification of a Haemophilus influenzae ABC Transporter HI1470/71 through Its Cognate Molybdate Periplasmic Binding Protein, MolA. Structure, 2011, 19, 1701-1710.	1.6	29
1754	A structural basis for Staphylococcal complement subversion: X-ray structure of the complement-binding domain of Staphylococcus aureus protein Sbi in complex with ligand C3d. Molecular Immunology, 2011, 48, 452-462.	1.0	32
1755	Novel structure of an N-terminal domain that is crucial for the dimeric assembly and DNA-binding of an archaeal DNA polymerase D large subunit from <i>Pyrococcus horikoshii</i>. FEBS Letters, 2011, 585, 452-458.	1.3	16
1756	Glycine amide shielding on the aromatic surfaces of lysozyme: Implication for suppression of protein aggregation. FEBS Letters, 2011, 585, 555-560.	1.3	15

#	ARTICLE	IF	CITATIONS
1757	Crystal structure of human MTH1 and the 8-oxo-dGMP product complex. FEBS Letters, 2011, 585, 2617-2621.	1.3	70
1758	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
1759	The Significance of G Protein-Coupled Receptor Crystallography for Drug Discovery. Pharmacological Reviews, 2011, 63, 901-937.	7.1	195
1760	The structure and catalytic mechanism of a poly(ADP-ribose) glycohydrolase. Nature, 2011, 477, 616-620.	13.7	295
1761	Structural basis of fumarate hydratase deficiency. Journal of Inherited Metabolic Disease, 2011, 34, 671-676.	1.7	66
1762	Crystal structure and mode of action of a class V chitinase from Nicotiana tabacum. Plant Molecular Biology, 2011, 75, 291-304.	2.0	44
1763	Crystal structure of a putative transcriptional regulator SCO0520 from Streptomyces coelicolor A3(2) reveals an unusual dimer among TetR family proteins. Journal of Structural and Functional Genomics, 2011, 12, 149-157.	1.2	6
1764	Structural characterization of human S100A16, a low-affinity calcium binder. Journal of Biological Inorganic Chemistry, 2011, 16, 243-256.	1.1	18
1765	The structure of the Klf4 DNA-binding domain links to self-renewal and macrophage differentiation. Cellular and Molecular Life Sciences, 2011, 68, 3121-3131.	2.4	69
1766	Distributed structure determination at the JCSG. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 368-375.	2.5	24
1767	<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
1768	Reduction of density-modification bias by Î² correction. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 345-354.	2.5	5
1769	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
1770	Contribution of the 80s loop of HIV-1 protease to the multidrug-resistance mechanism: crystallographic study of MDR769 HIV-1 protease variants. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 524-532.	2.5	28
1771	Structural characterization of the PPIase domain of FKBP51, a cochaperone of human Hsp90. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 549-559.	2.5	57
1772	Accelerating<i>ab initio</i>phasing with<i>de novo</i>models. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 804-812.	2.5	13
1773	The unique structure of carbonic anhydrase Î±CA1 from<i>Chlamydomonas reinhardtii</i>. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 894-901.	2.5	20
1774	Human Suv3 protein reveals unique features among SF2 helicases. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 988-996.	2.5	13

#	Article	IF	Citations
1775	Structural analysis of a putative family 32 carbohydrate-binding module from theStreptococcus pneumoniaeenzyme EndoD. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 429-433.	0.7	7
1776	Expression, crystallization and preliminary X-ray data analysis of NT-Als9-2, a fungal adhesin fromCandida albicans. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 467-470.	0.7	3
1777	High-resolution structure of a new crystal form of BamA POTRA4â€“5 from<i>Escherichia coli</i>. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 734-738.	0.7	30
1778	Crystallization and preliminary X-ray analysis of the RPB5 subunit of human RNA polymerase II. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1391-1393.	0.7	1
1779	Crystallization and preliminary X-ray analysis of peptidyl-tRNA hydrolase from<i>Escherichia coli</i>in complex with the acceptor-TÎ¨C domain of tRNA. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1566-1569.	0.7	9
1780	Structural studies on the enzyme complex isopropylmalate isomerase (LeuCD) from <i>Mycobacterium tuberculosis</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 35-49.	1.5	26
1781	Noncellulosomal cohesin from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 50-60.	1.5	6
1782	Structure of the Câ€terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1672-1677.	1.5	16
1783	Crystal structure of HP0721, a novel secreted protein from <i>Helicobacter pylori</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1678-1681.	1.5	6
1784	Crystal structure of a phenolâ€coupling P450 monooxygenase involved in teicoplanin biosynthesis. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1728-1738.	1.5	24
1785	Structural characterization of the mitomycin 7â€<i>O</i>â€methyltransferase. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2181-2188.	1.5	26
1786	The <i>ygeW</i> encoded protein from <i>Escherichia coli</i> is a knotted ancestral catabolic transcarbamylase. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2327-2334.	1.5	15
1787	Crystal structure of the novel PaiB transcriptional regulator from <i>Geobacillus stearothermophilus</i>. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2578-2582.	1.5	5
1788	Crystal structure of the novel PaiA <i>N</i>â€acetyltransferase from <i>Thermoplasma acidophilum</i> involved in the negative control of sporulation and degradative enzyme production. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2566-2577.	1.5	13
1789	Structures of the first and second doubleâ€stranded RNAâ€binding domains of human TAR RNAâ€binding protein. Protein Science, 2011, 20, 118-130.	3.1	50
1790	Loss of recognition by crossâ€reactive T cells and its relation to a Câ€terminusâ€induced conformational reorientation of an HLAâ€B*2705â€bound peptide. Protein Science, 2011, 20, 278-290.	3.1	5
1791	Structures of domains I and IV from YbbR are representative of a widely distributed protein family. Protein Science, 2011, 20, 396-405.	3.1	16
1792	Apo raver1 structure reveals distinct RRM domain orientations. Protein Science, 2011, 20, 1464-1470.	3.1	3

#	Article	IF	Citations
1793	Chimeric avidin shows stability against harsh chemical conditionsâ€”biochemical analysis and 3D structure. Biotechnology and Bioengineering, 2011, 108, 481-490.	1.7	35
1794	A Siteâ€Saturated Mutagenesis Study of Pentaerythritol Tetranitrate Reductase Reveals that Residues 181 and 184 Influence Ligand Binding, Stereochemistry and Reactivity. ChemBioChem, 2011, 12, 738-749.	1.3	65
1795	Specific CLK Inhibitors from a Novel Chemotype for Regulation of Alternative Splicing. Chemistry and Biology, 2011, 18, 67-76.	6.2	173
1796	X-ray crystallography, mass spectrometry and single crystal microspectrophotometry: A multidisciplinary characterization of catechol 1,2 dioxygenase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 817-823.	1.1	24
1797	High-resolution X-ray analysis reveals binding of arginine to aromatic residues of lysozyme surface: implication of suppression of protein aggregation by arginine. Protein Engineering, Design and Selection, 2011, 24, 269-274.	1.0	75
1798	Crystal Structure of Menin Reveals Binding Site for Mixed Lineage Leukemia (MLL) Protein. Journal of Biological Chemistry, 2011, 286, 31742-31748.	1.6	83
1799	Structural and functional insight into the mechanism of an alkaline exonuclease from Laribacter hongkongensis. Nucleic Acids Research, 2011, 39, 9803-9819.	6.5	13
1800	Structural Basis for the Oxidation of Protein-bound Sulfur by the Sulfur Cycle Molybdohemo-Enzyme Sulfane Dehydrogenase SoxCD. Journal of Biological Chemistry, 2011, 286, 8349-8360.	1.6	39
1801	Structural Basis for Antiviral Inhibition of the Main Protease, 3C, from Human Enterovirus 93. Journal of Virology, 2011, 85, 10764-10773.	1.5	20
1802	Crystal Structures of Human TBC1D1 and TBC1D4 (AS160) RabGTPase-activating Protein (RabGAP) Domains Reveal Critical Elements for GLUT4 Translocation. Journal of Biological Chemistry, 2011, 286, 18130-18138.	1.6	22
1803	Crystal structures of the endoplasmic reticulum aminopeptidase-1 (ERAP1) reveal the molecular basis for N-terminal peptide trimming. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7745-7750.	3.3	216
1804	Crystal Structures of Bacterial Peptidoglycan Amidase AmpD and an Unprecedented Activation Mechanism. Journal of Biological Chemistry, 2011, 286, 31714-31722.	1.6	49
1805	Structural Variation in Bacterial Glyoxalase I Enzymes. Journal of Biological Chemistry, 2011, 286, 38367-38374.	1.6	42
1806	Structural Characterization and Epitope Mapping of the Glutamic Acid/Alanine-rich Protein from Trypanosoma congolense. Journal of Biological Chemistry, 2011, 286, 20658-20665.	1.6	11
1807	Evolution in a family of chelatases facilitated by the introduction of active site asymmetry and protein oligomerization. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 97-102.	3.3	43
1808	Crystal Structure of HugZ, a Novel Heme Oxygenase from Helicobacter pylori. Journal of Biological Chemistry, 2011, 286, 1537-1544.	1.6	52
1809	Characterization of the Deoxynucleotide Triphosphate Triphosphohydrolase (dNTPase) Activity of the EF1143 Protein from Enterococcus faecalis and Crystal Structure of the Activator-Substrate Complex. Journal of Biological Chemistry, 2011, 286, 33158-33166.	1.6	31
1810	Î±-Galactosidase/Sucrose Kinase (AgaSK), a Novel Bifunctional Enzyme from the Human Microbiome Coupling Galactosidase and Kinase Activities. Journal of Biological Chemistry, 2011, 286, 40814-40823.	1.6	32

#	ARTICLE	IF	CITATIONS
1811	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
1812	Structures of Human Golgi-resident Glutaminyl Cyclase and Its Complexes with Inhibitors Reveal a Large Loop Movement upon Inhibitor Binding. Journal of Biological Chemistry, 2011, 286, 12439-12449.	1.6	50
1813	Structural and Evolutionary Basis for the Dual Substrate Selectivity of Human KDM4 Histone Demethylase Family. Journal of Biological Chemistry, 2011, 286, 41616-41625.	1.6	143
1814	Structure of Collagen Receptor Integrin Î±1I Domain Carrying the Activating Mutation E317A. Journal of Biological Chemistry, 2011, 286, 43343-43351.	1.6	20
1815	Crystal Structure of a Zinc-dependent d-Serine Dehydratase from Chicken Kidney. Journal of Biological Chemistry, 2011, 286, 27548-27558.	1.6	26
1816	Cyclic AMP Analog Blocks Kinase Activation by Stabilizing Inactive Conformation: Conformational Selection Highlights a New Concept in Allosteric Inhibitor Design. Molecular and Cellular Proteomics, 2011, 10, M110.004390.	2.5	62
1817	Structure-Function Analyses of a Caffeic Acid <i>O</i>-Methyltransferase from Perennial Ryegrass Reveal the Molecular Basis for Substrate Preference Â. Plant Cell, 2011, 22, 4114-4127.	3.1	84
1818	Structural Basis of Response Regulator Inhibition by a Bacterial Anti-Activator Protein. PLoS Biology, 2011, 9, e1001226.	2.6	50
1819	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
1820	The Vibrio cholerae Colonization Factor GbpA Possesses a Modular Structure that Governs Binding to Different Host Surfaces. PLoS Pathogens, 2012, 8, e1002373.	2.1	150
1821	Structural Basis of Cytotoxicity Mediated by the Type III Secretion Toxin ExoU from Pseudomonas aeruginosa. PLoS Pathogens, 2012, 8, e1002637.	2.1	65
1822	The substrate/product-binding modes of a novel GH120 Î²-xylosidase (XylC) from <i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485. Biochemical Journal, 2012, 448, 401-407.	1.7	16
1823	Crystal structure of a Î²-prism II lectin from Remusatia vivipara. Glycobiology, 2012, 22, 56-69.	1.3	18
1824	Structural basis for the substrate recognition and catalysis of peptidyl-tRNA hydrolase. Nucleic Acids Research, 2012, 40, 10521-10531.	6.5	27
1825	Cloning, Baeyer-Villiger Biooxidations, and Structures of the Camphor Pathway 2-Oxo-Î" ³ -4,5,5-Trimethylcyclopentenylacetyl-Coenzyme A Monooxygenase of Pseudomonas putida ATCC 17453. Applied and Environmental Microbiology, 2012, 78, 2200-2212.	1.4	51
1826	Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. Molecular Biology of the Cell, 2012, 23, 1457-1466.	0.9	53
1827	Structural Enzymology of Cellvibrio japonicus Agd31B Protein Reveals Î±-Transglucosylase Activity in Glycoside Hydrolase Family 31. Journal of Biological Chemistry, 2012, 287, 43288-43299.	1.6	36
1828	Structural insights into the function of 23S rRNA methyltransferase RlmG (m2G1835) from Escherichia coli. Rna, 2012, 18, 1500-1509.	1.6	1

#	Article	IF	Citations
1829	The Gal3p transducer of the <i>GAL</i> regulon interacts with the Gal80p repressor in its ligand-induced closed conformation. Genes and Development, 2012, 26, 294-303.	2.7	42
1830	Identification of the catalytic residues of sequence-specific and histidine-free ribonuclease colicin E5. Journal of Biochemistry, 2012, 152, 365-372.	0.9	6
1831	Structural Basis of Biological Nitrile Reduction. Journal of Biological Chemistry, 2012, 287, 30560-30570.	1.6	27
1832	The cytoplasmic coiled-coil mediates cooperative gating temperature sensitivity in the voltage-gated H+ channel Hv1. Nature Communications, 2012, 3, 816.	5.8	90
1833	Interactions of calmodulin with death-associated protein kinase peptides: experimental and modeling studies. Journal of Biomolecular Structure and Dynamics, 2012, 30, 45-61.	2.0	14
1834	Structure of the c10 ring of the yeast mitochondrial ATP synthase in the open conformation. Nature Structural and Molecular Biology, 2012, 19, 485-491.	3.6	116
1835	Structural insight into how <i>Pseudomonas aeruginosa</i> peptidoglycanhydrolase Tse1 and its immunity protein Tsi1 function. Biochemical Journal, 2012, 448, 201-211.	1.7	22
1836	Structural Insights into Antibody Sequestering and Neutralizing of Na+ Channel Î±-Type Modulator from Old World Scorpion Venom. Journal of Biological Chemistry, 2012, 287, 14136-14148.	1.6	20
1837	Crystal Structure of Reduced MsAcg, a Putative Nitroreductase from Mycobacterium smegmatis and a Close Homologue of Mycobacterium tuberculosis Acg. Journal of Biological Chemistry, 2012, 287, 44372-44383.	1.6	16
1838	The Role of a Voltage-Dependent Ca²⁺Channel Intracellular Linker: A Structure-Function Analysis. Journal of Neuroscience, 2012, 32, 7602-7613.	1.7	34
1839	IQGAP Proteins Reveal an Atypical Phosphoinositide (aPI) Binding Domain with a Pseudo C2 Domain Fold. Journal of Biological Chemistry, 2012, 287, 22483-22496.	1.6	23
1840	Biochemical and Structural Studies of Uncharacterized Protein PA0743 from Pseudomonas aeruginosa Revealed NAD+-dependent l-Serine Dehydrogenase. Journal of Biological Chemistry, 2012, 287, 1874-1883.	1.6	23
1841	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
1842	Kinetic and Crystallographic Studies of Extended-Spectrum GES-11, GES-12, and GES-14 Î²-Lactamases. Antimicrobial Agents and Chemotherapy, 2012, 56, 5618-5625.	1.4	24
1843	Structures of the PelD Cyclic Diguanylate Effector Involved in Pellicle Formation in Pseudomonas aeruginosa PAO1. Journal of Biological Chemistry, 2012, 287, 30191-30204.	1.6	37
1844	PROBABILISTIC ENSEMBLES FOR IMPROVED INFERENCE IN PROTEIN-STRUCTURE DETERMINATION. Journal of Bioinformatics and Computational Biology, 2012, 10, 1240009.	0.3	2
1845	The crystal structure of an intermediate dimer of aspergilloglutamic peptidase that mimics the enzyme-activation product complex produced upon autoproteolysis. Journal of Biochemistry, 2012, 152, 45-52.	0.9	9
1846	Structural Characterization of Closely Related O-antigen Lipopolysaccharide (LPS) Chain Length Regulators. Journal of Biological Chemistry, 2012, 287, 15696-15705.	1.6	24

#	ARTICLE	IF	CITATIONS
1847	Mechanistic Insights into Regulated Cargo Binding by ACAP1 Protein. Journal of Biological Chemistry, 2012, 287, 28675-28685.	1.6	25
1848	Structural Elucidation of Dextran Degradation Mechanism by Streptococcus mutans Dextranase Belonging to Glycoside Hydrolase Family 66. Journal of Biological Chemistry, 2012, 287, 19916-19926.	1.6	42
1849	Crystal Structures of a CTXÏ† pIII Domain Unbound and in Complex with a Vibrio cholerae TolA Domain Reveal Novel Interaction Interfaces. Journal of Biological Chemistry, 2012, 287, 36258-36272.	1.6	16
1850	Structural Characterization of CFA/III and Longus Type IVb Pili from Enterotoxigenic Escherichia coli. Journal of Bacteriology, 2012, 194, 2725-2735.	1.0	22
1851	The high-resolution crystal structure of periplasmic<i>Haemophilus influenzae</i>NAD nucleotidase reveals a novel enzymatic function of human CD73 related to NAD metabolism. Biochemical Journal, 2012, 441, 131-141.	1.7	83
1852	The multiple Tudor domain-containing protein TDRD1 is a molecular scaffold for mouse Piwi proteins and piRNA biogenesis factors. Rna, 2012, 18, 2056-2072.	1.6	41
1853	Crystallographic and X-ray absorption spectroscopic characterization of <i>Helicobacter pylori</i> UreE bound to Ni2+ and Zn2+ reveals a role for the disordered C-terminal arm in metal trafficking. Biochemical Journal, 2012, 441, 1017-1035.	1.7	52
1854	Investigating Terephthalate Biodegradation: Structural Characterization of a Putative Decarboxylating cis-Dihydrodiol Dehydrogenase. Journal of Molecular Biology, 2012, 423, 284-293.	2.0	7
1855	Structural and biochemical characterization of a trapped coenzyme A adduct of<i>Caenorhabditis elegans</i>glucosamine-6-phosphate<i>N</i>-acetyltransferase 1. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1019-1029.	2.5	14
1856	Experimental phasing using zinc anomalous scattering. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1253-1258.	2.5	24
1857	Structure of a thermophilic cyanobacterialb6f-type Rieske protein. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1400-1408.	2.5	11
1858	Purification, crystallization and preliminary crystallographic analysis of banyan peroxidase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 931-934.	0.7	1
1859	Biosynthesis of the 22nd Genetically Encoded Amino Acid Pyrrolysine: Structure and Reaction Mechanism of PylC at 1.5Ã… Resolution. Journal of Molecular Biology, 2012, 424, 270-282.	2.0	17
1860	The <scp>EAGR</scp> box structure: a motif involved in mycoplasma motility. Molecular Microbiology, 2012, 86, 382-393.	1.2	14
1861	Crystal Structure of <i>Arabidopsis</i> Cyclophilin38 Reveals a Previously Uncharacterized Immunophilin Fold and a Possible Autoinhibitory Mechanism. Plant Cell, 2012, 24, 2666-2674.	3.1	42
1862	7,8-Dichloro-1-oxo-Î²-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
1863	Mechanism of CREB recognition and coactivation by the CREB-regulated transcriptional coactivator CRTC2. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20865-20870.	3.3	74
1864	Comparison of the structural changes in two cellobiohydrolases, CcCel6A and CcCel6C, from <i>Coprinopsisâ€ƒcinerea</i>â€ƒâ€“â€ƒa tweezerâ€·like motion in the structure of CcCel6C. FEBS Journal, 2012, 279, 1871-1882.	2.2	17

#	Article	IF	Citations
1865	Utility of anion and cation combinations for phasing of protein structures. Journal of Structural and Functional Genomics, 2012, 13, 135-143.	1.2	7
1866	Solution NMR and X-ray crystal structures of Pseudomonas syringae Pspto_3016 from protein domain family PF04237 (DUF419) adopt a â€œdouble wingâ€• DNA binding motif. Journal of Structural and Functional Genomics, 2012, 13, 155-162.	1.2	9
1867	Small-Molecule Inhibition of BRDT for Male Contraception. Cell, 2012, 150, 673-684.	13.5	353
1868	Structural characterization of the PliG lysozyme inhibitor family. Journal of Structural Biology, 2012, 180, 235-242.	1.3	12
1869	The generation of a 1-hydroxy-2-naphthoate 1,2-dioxygenase by single point mutations of salicylate 1,2-dioxygenase â€" Rational design of mutants and the crystal structures of the A85H and W104Y variants. Journal of Structural Biology, 2012, 180, 563-571.	1.3	13
1870	Crystal structure of the primary piRNA biogenesis factor Zucchini reveals similarity to the bacterial PLD endonuclease Nuc. Rna, 2012, 18, 2128-2134.	1.6	55
1871	Structural Insights into the Ferroxidase Site of Ferritins from Higher Eukaryotes. Journal of the American Chemical Society, 2012, 134, 6169-6176.	6.6	90
1872	The structural characterization of a prophage-encoded extracellular DNase from Streptococcus pyogenes. Nucleic Acids Research, 2012, 40, 928-938.	6.5	23
1874	New Determinants in the Catalytic Mechanism of Nucleoside Hydrolases from the Structures of Two Isozymes from <i>Sulfolobus solfataricus</i>. Biochemistry, 2012, 51, 4590-4599.	1.2	6
1875	Structural Basis of Trypsin Inhibition and Entomotoxicity of Cospin, Serine Protease Inhibitor Involved in Defense of Coprinopsis cinerea Fruiting Bodies. Journal of Biological Chemistry, 2012, 287, 3898-3907.	1.6	46
1876	Improvement in Quality of Protein Crystals Grown in a High Magnetic Field Gradient. Crystal Growth and Design, 2012, 12, 1141-1150.	1.4	33
1877	Cas5d processes pre-crRNA and is a member of a larger family of CRISPR RNA endonucleases. Rna, 2012, 18, 2020-2028.	1.6	80
1878	The Structure and Enzymatic Properties of a Novel RNase II Family Enzyme from Deinococcus radiodurans. Journal of Molecular Biology, 2012, 415, 547-559.	2.0	6
1879	An Exclusive Î±/Î² Code Directs Allostery in TetRâ€"Peptide Complexes. Journal of Molecular Biology, 2012, 416, 46-56.	2.0	14
1880	Structural Basis of Substrate Binding Specificity Revealed by the Crystal Structures of Polyamine Receptors SpuD and SpuE from Pseudomonas aeruginosa. Journal of Molecular Biology, 2012, 416, 697-712.	2.0	37
1881	Structure of the Ultra-High-Affinity Colicin E2 DNaseâ€"Im2 Complex. Journal of Molecular Biology, 2012, 417, 79-94.	2.0	54
1882	CC2D1A Is a Regulator of ESCRT-III CHMP4B. Journal of Molecular Biology, 2012, 419, 75-88.	2.0	54
1883	Structural and Functional Characterization of Microcin C Resistance Peptidase MccF from Bacillus anthracis. Journal of Molecular Biology, 2012, 420, 366-383.	2.0	22

#	ARTICLE	IF	CITATIONS
1884	Structural Studies on the Oligomeric Transition of a Small Heat Shock Protein, StHsp14.0. Journal of Molecular Biology, 2012, 422, 100-108.	2.0	31
1885	Kainate induces various domain closures in AMPA and kainate receptors. Neurochemistry International, 2012, 61, 536-545.	1.9	17
1886	Crystal and solution structures of methyltransferase RsmH provide basis for methylation of C1402 in 16S rRNA. Journal of Structural Biology, 2012, 179, 29-40.	1.3	31
1887	The structure of monoacylglycerol lipase from Bacillus sp. H257 reveals unexpected conservation of the cap architecture between bacterial and human enzymes. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2012, 1821, 1012-1021.	1.2	40
1888	The structure of putative N-acetyl glutamate kinase from Thermus thermophilus reveals an intermediate active site conformation of the enzyme. Biochemical and Biophysical Research Communications, 2012, 420, 692-697.	1.0	12
1889	Crystal structures of multidrug-resistant HIV-1 protease in complex with two potent anti-malarial compounds. Biochemical and Biophysical Research Communications, 2012, 421, 413-417.	1.0	9
1890	Molecular dynamics, crystallography and mutagenesis studies on the substrate gating mechanism of prolyl oligopeptidase. Biochimie, 2012, 94, 1398-1411.	1.3	47
1891	Structure of the corrinoid:coenzyme M methyltransferase MtaA from<i>Methanosarcina mazei</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1549-1557.	2.5	7
1892	Structure of the catalytic domain of the<i>Salmonella</i>virulence factor SseI. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1613-1621.	2.5	16
1893	Structure of<i>Escherichia coli</i>RutC, a member of the YjgF family and putative aminoacrylate peracid reductase of the<i>rut</i>operon. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1294-1299.	0.7	15
1894	Structure of a periplasmic glucose-binding protein from<i>Thermotoga maritima</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1460-1464.	0.7	5
1895	Alternaria alternata allergen Alt a 1: A unique Î²-barrel protein dimer found exclusively in fungi. Journal of Allergy and Clinical Immunology, 2012, 130, 241-247.e9.	1.5	99
1896	Crystal structure of a lactosucrose-producing enzyme, Arthrobacter sp. K-1 Î²-fructofuranosidase. Enzyme and Microbial Technology, 2012, 51, 359-365.	1.6	33
1897	Ego3 Functions as a Homodimer to Mediate the Interaction between Gtr1-Gtr2 and Ego1 in the EGO Complex to Activate TORC1. Structure, 2012, 20, 2151-2160.	1.6	56
1898	Insights into the Catalytic Mechanism of 16S rRNA Methyltransferase RsmE (m3U1498) from Crystal and Solution Structures. Journal of Molecular Biology, 2012, 423, 576-589.	2.0	13
1899	Histone Recognition by Human Malignant Brain Tumor Domains. Journal of Molecular Biology, 2012, 423, 702-718.	2.0	58
1900	Evolution of the chalcone-isomerase fold from fatty-acid binding to stereospecific catalysis. Nature, 2012, 485, 530-533.	13.7	191
1901	Structural basis for recognition of H3K56-acetylated histone H3â€“H4 by the chaperone Rtt106. Nature, 2012, 483, 104-107.	13.7	99

#	ARTICLE	IF	CITATIONS
1902	Structures of Alkaloid Biosynthetic Glucosidases Decode Substrate Specificity. ACS Chemical Biology, 2012, 7, 226-234.	1.6	23
1903	An ankyrin-repeat ubiquitin-binding domain determines TRABID's specificity for atypical ubiquitin chains. Nature Structural and Molecular Biology, 2012, 19, 62-71.	3.6	122
1904	A gp41 MPER-specific llama VHH requires a hydrophobic CDR3 determinant for neutralization but not for antigen recognition. Retrovirology, 2012, 9, .	0.9	0
1905	Macro-to-Micro Structural Proteomics: Native Source Proteins for High-Throughput Crystallization. PLoS ONE, 2012, 7, e32498.	1.1	36
1906	Structures of Human DPP7 Reveal the Molecular Basis of Specific Inhibition and the Architectural Diversity of Proline-Specific Peptidases. PLoS ONE, 2012, 7, e43019.	1.1	23
1907	Structure and function of CYP108D1 from<i>Novosphingobium aromaticivorans</i>DSM12444: an aromatic hydrocarbon-binding P450 enzyme. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 277-291.	2.5	25
1908	Structure of the catalytic domain of the<i>Clostridium thermocellum</i>cellulase CelT. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 310-320.	2.5	14
1909	Challenges of sulfur SAD phasing as a routine method in macromolecular crystallography. Journal of Synchrotron Radiation, 2012, 19, 19-29.	1.0	15
1910	Resolutionâ€adapted recombination of structural features significantly improves sampling in restraintâ€guided structure calculation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 884-895.	1.5	69
1911	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2110-2116.	1.5	7
1912	A multiâ€faceted analysis of RutD reveals a novel family of Î±/Î² hydrolases. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2359-2368.	1.5	7
1913	Matrix Metalloproteinase-10 (MMP-10) Interaction with Tissue Inhibitors of Metalloproteinases TIMP-1 and TIMP-2. Journal of Biological Chemistry, 2012, 287, 15935-15946.	1.6	88
1914	Crystal Structure of the Heterodimeric CLOCK:BMAL1 Transcriptional Activator Complex. Science, 2012, 337, 189-194.	6.0	270
1915	Structural dynamics of the aminoacylation and proofreading functional cycle of bacterial leucyl-tRNA synthetase. Nature Structural and Molecular Biology, 2012, 19, 677-684.	3.6	131
1916	Bivalent Carbohydrate Binding Is Required for Biological Activity of Clitocybe nebularis Lectin (CNL), the N,Nâ€²-Diacetyllactosediamine (GalNAcÎ²1â€"4GlcNAc, LacdiNAc)-specific Lectin from Basidiomycete C. nebularis. Journal of Biological Chemistry, 2012, 287, 10602-10612.	1.6	51
1917	phenix.mr_rosetta: molecular replacement and model rebuilding with Phenix and Rosetta. Journal of Structural and Functional Genomics, 2012, 13, 81-90.	1.2	131
1918	Crystal structure of a putative isochorismatase hydrolase from Oleispira antarctica. Journal of Structural and Functional Genomics, 2012, 13, 27-36.	1.2	22
1919	Crystal structures of putative phosphoglycerate kinases from B. anthracis and C. jejuni. Journal of Structural and Functional Genomics, 2012, 13, 15-26.	1.2	7

#	ARTICLE	IF	CITATIONS
1920	Structural and functional dissection of aminocoumarin antibiotic biosynthesis: a review. Journal of Structural and Functional Genomics, 2012, 13, 125-133.	1.2	4
1921	The crystal structure of AphB, a virulence gene activator from <i>Vibrio cholerae</i>, reveals residues that influence its response to oxygen and pH. Molecular Microbiology, 2012, 83, 457-470.	1.2	56
1922	Small-Molecule Inhibitors of the c-Fes Protein-Tyrosine Kinase. Chemistry and Biology, 2012, 19, 529-540.	6.2	32
1923	Crystal structures of the Tudor domains of human PHF20 reveal novel structural variations on the Royal Family of proteins. FEBS Letters, 2012, 586, 859-865.	1.3	22
1924	Crystal structure of periplasmic catecholateâ€•siderophore binding protein VctP from <i>Vibrio cholerae</i> at 1.7 Å… resolution. FEBS Letters, 2012, 586, 1240-1244.	1.3	23
1925	Benzodiazepines and benzotriazepines as protein interaction inhibitors targeting bromodomains of the BET family. Bioorganic and Medicinal Chemistry, 2012, 20, 1878-1886.	1.4	112
1926	A nonâ€•coldâ€•inducible cold shock protein homolog mainly contributes to translational control under optimal growth conditions. FEBS Journal, 2012, 279, 1014-1029.	2.2	12
1927	Structural characterization of <i>Helicobacterâ€ƒpylori</i> dethiobiotin synthetase reveals differences between family members. FEBS Journal, 2012, 279, 1093-1105.	2.2	15
1928	The Mycobacterium tuberculosis Very-Long-Chain Fatty Acyl-CoA Synthetase: Structural Basis for Housing Lipid Substrates Longer than the Enzyme. Structure, 2012, 20, 1062-1070.	1.6	31
1929	Application of constrained real-space refinement of flexible molecular fragments to automatic model building of RNA structures. Journal of Applied Crystallography, 2012, 45, 309-315.	1.9	4
1930	Structureâ€"function studies of an unusual 3-methyladenine DNA glycosylase II (AlkA) from<i>Deinococcus radiodurans</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 703-712.	2.5	15
1931	Structure of a post-translationally processed heterodimeric double-headed Kunitz-type serine protease inhibitor from potato. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 794-799.	2.5	22
1932	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 861-870.	2.5	37
1933	Crystallization and crystallographic analysis of the ligand-binding domain of thePseudomonas putidachemoreceptor McpS in complex with malate and succinate. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 428-431.	0.7	2
1934	In praise of impurity: 30S ribosomal S15 protein-assisted crystallization of turnip yellow mosaic virus proteinase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 486-490.	0.7	5
1935	Expression, purification, crystallization and preliminary crystallographic studies of<i>Rhagium inquisitor</i>antifreeze protein. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 547-550.	0.7	9
1936	Structure of a short-chain dehydrogenase/reductase from<i>Bacillus anthracis</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 632-637.	0.7	3
1937	Structure of the RBD-PRDI fragment of the antiterminator protein GlcT. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 751-756.	0.7	4

#	Article	IF	Citations
1938	Crystal Structure Analysis of a Recombinant Predicted Acetamidase/Formamidase from the Thermophile Thermoanaerobacter tengcongensis. Protein Journal, 2012, 31, 166-174.	0.7	6
1939	Crystal structure of a putative aspartic proteinase domain of the <i>Mycobacterium tuberculosis</i> cell surface antigen PE_PGRS16. FEBS Open Bio, 2013, 3, 256-262.	1.0	7
1940	Biocatalytic Asymmetric Alkene Reduction: Crystal Structure and Characterization of a Double Bond Reductase from <i>Nicotiana tabacum</i>. ACS Catalysis, 2013, 3, 370-379.	5.5	59
1941	Molecular Basis of Sphingosine Kinase 1 Substrate Recognition and Catalysis. Structure, 2013, 21, 798-809.	1.6	157
1943	Structural biology computing: Lessons for the biomedical research sciences. Biopolymers, 2013, 99, 809-816.	1.2	6
1944	Structural and Functional Analysis of Angucycline C-6 Ketoreductase LanV Involved in Landomycin Biosynthesis. Biochemistry, 2013, 52, 5304-5314.	1.2	15
1945	The crystal structure and biochemical properties of DHBPS from Streptococcus pneumoniae, a potential anti-infective target for Gram-positive bacteria. Protein Expression and Purification, 2013, 91, 161-168.	0.6	4
1946	Gating of the designed trimeric/tetrameric voltageâ€gated H⁺ channel. Journal of Physiology, 2013, 591, 627-640.	1.3	30
1947	Deamination of 6-Aminodeoxyfutalosine in Menaquinone Biosynthesis by Distantly Related Enzymes. Biochemistry, 2013, 52, 6525-6536.	1.2	12
1948	Transient Protein States in Designing Inhibitors of the MDM2-p53 Interaction. Structure, 2013, 21, 2143-2151.	1.6	57
1949	Molecular Basis for the Regulation of the H3K4 Methyltransferase Activity of PRDM9. Cell Reports, 2013, 5, 13-20.	2.9	100
1950	Biochemical and Structural Studies of Conserved Maf Proteins Revealed Nucleotide Pyrophosphatases with a Preference for Modified Nucleotides. Chemistry and Biology, 2013, 20, 1386-1398.	6.2	15
1951	Crystal structure of peroxisomal targeting signal-2 bound to its receptor complex Pex7pâ€“Pex21p. Nature Structural and Molecular Biology, 2013, 20, 987-993.	3.6	56
1952	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
1953	GES-18, a New Carbapenem-Hydrolyzing GES-Type Î²-Lactamase from Pseudomonas aeruginosa That Contains Ile80 and Ser170 Residues. Antimicrobial Agents and Chemotherapy, 2013, 57, 396-401.	1.4	36
1954	Characterization of Staphylococcus aureus EssB, an integral membrane component of the TypeÂVII secretion system: atomic resolution crystal structure of the cytoplasmic segment. Biochemical Journal, 2013, 449, 469-477.	1.7	25
1955	Crystallization and preliminary X-ray diffraction studies of the (<i>R</i>)-selective amine transaminase from<i>Aspergillus fumigatus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1415-1417.	0.7	9
1956	Nonequivalence Observed for the 16-Meric Structure of a Small Heat Shock Protein, SpHsp16.0, from Schizosaccharomyces pombe. Structure, 2013, 21, 220-228.	1.6	56

#	ARTICLE	IF	CITATIONS
1957	Structure analysis of the global metabolic regulator Crc from <i>Pseudomonas aeruginosa</i>. IUBMB Life, 2013, 65, 50-57.	1.5	5
1958	High resolution crystal structure of Sco5413, a widespread actinomycete MarR family transcriptional regulator of unknown function. Proteins: Structure, Function and Bioinformatics, 2013, 81, 176-182.	1.5	7
1959	Crystal Structure of Prp5p Reveals Interdomain Interactions that Impact Spliceosome Assembly. Cell Reports, 2013, 5, 1269-1278.	2.9	23
1960	The crystal structure of an activated Thermotoga maritima CheY with N-terminal region of FliM. International Journal of Biological Macromolecules, 2013, 54, 76-83.	3.6	17
1961	Identification of catalytically important amino acid residues for enzymatic reduction of glyoxylate in plants. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2663-2671.	1.1	11
1962	Isomorphic deactivation of a Pseudomonas aeruginosa oxidoreductase: The crystal structure of Ag(I) metallated azurin at 1.7Ã…. Journal of Inorganic Biochemistry, 2013, 128, 11-16.	1.5	10
1963	Crystal Structures of the Free and Ligand-Bound FK1â€“FK2 Domain Segment of FKBP52 Reveal a Flexible Inter-Domain Hinge. Journal of Molecular Biology, 2013, 425, 4134-4144.	2.0	41
1964	Crystal structure of the Nâ€terminal domain of a glycoside hydrolase family 131 protein from <i>Coprinopsis cinerea</i>. FEBS Letters, 2013, 587, 2193-2198.	1.3	6
1965	Molecular Architecture of the Ankyrin SOCS Box Family of Cul5-Dependent E3 Ubiquitin Ligases. Journal of Molecular Biology, 2013, 425, 3166-3177.	2.0	31
1966	Structure-guided studies of the SHP-1/JAK1 interaction provide new insights into phosphatase catalytic domain substrate recognition. Journal of Structural Biology, 2013, 181, 243-251.	1.3	13
1967	Substrate binding to a GH131 Î²-glucanase catalytic domain from Podospora anserina. Biochemical and Biophysical Research Communications, 2013, 438, 193-197.	1.0	5
1968	Evolution of diffraction methods for solving crystal structures. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 51-59.	0.3	23
1969	Structure of Gentlyase, the neutral metalloprotease ofPaenibacillus polymyxa. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 24-31.	2.5	11
1970	High-resolution structures of AidH complexes provide insights into a novel catalytic mechanism for<i>N</i>-acyl homoserine lactonase. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 82-91.	2.5	26
1971	The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. Structure, 2013, 21, 595-603.	1.6	19
1972	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. Annual Review of Biophysics, 2013, 42, 265-287.	4.5	88
1973	Structure of the C-terminal half of human XPB helicase and the impact of the disease-causing mutation XP11BE. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 237-246.	2.5	23
1974	Glutamine Rotamers in BLUF Photoreceptors: A Mechanistic Reappraisal. Journal of Physical Chemistry B, 2013, 117, 2888-2897.	1.2	42

#	Article	IF	Citations
1975	Comparative Proteomics Identifies the Cell-Associated Lethality of M.Âtuberculosis RelBE-like Toxin-Antitoxin Complexes. Structure, 2013, 21, 627-637.	1.6	27
1976	An arm-swapped dimer of the Streptococcus pyogenes pilin specific assembly factor SipA. Journal of Structural Biology, 2013, 183, 99-104.	1.3	6
1977	The use ofVLD(vive la difference) in the molecular-replacement approach: a pipeline. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1038-1044.	2.5	8
1978	Bacteriophage P23-77 Capsid Protein Structures Reveal the Archetype of an Ancient Branch from a Major Virus Lineage. Structure, 2013, 21, 718-726.	1.6	38
1979	Crystal structures of glycoside hydrolase family 3 Î²-glucosidase 1 from <i>Aspergillus aculeatus</i>. Biochemical Journal, 2013, 452, 211-221.	1.7	77
1980	The loops facing the active site of prolyl oligopeptidase are crucial components in substrate gating and specificity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 98-111.	1.1	29
1981	Functional Annotation and Three-Dimensional Structure of an Incorrectly Annotated Dihydroorotase from cog3964 in the Amidohydrolase Superfamily. Biochemistry, 2013, 52, 228-238.	1.2	8
1982	Structure and Mechanism of Acetolactate Decarboxylase. ACS Chemical Biology, 2013, 8, 2339-2344.	1.6	26
1983	Structure of isochorismate synthase DhbC fromBacillus anthracis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 956-961.	0.7	2
1984	Structural and bioinformatic analysis of the kiwifruit allergen Act d 11, a member of the family of ripening-related proteins. Molecular Immunology, 2013, 56, 794-803.	1.0	43
1985	Discovery of Novel Small-Molecule Inhibitors of BRD4 Using Structure-Based Virtual Screening. Journal of Medicinal Chemistry, 2013, 56, 8073-8088.	2.9	116
1986	Structure of the Homodimeric Glycine Decarboxylase P-protein from Synechocystis sp. PCC 6803 Suggests a Mechanism for Redox Regulation. Journal of Biological Chemistry, 2013, 288, 35333-35345.	1.6	38
1987	Conformational Plasticity and Ligand Binding of Bacterial Monoacylglycerol Lipase. Journal of Biological Chemistry, 2013, 288, 31093-31104.	1.6	44
1988	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant Staphylococcus aureus. Journal of Structural and Functional Genomics, 2013, 14, 97-108.	1.2	9
1989	A gp41 MPER-specific Llama VHH Requires a Hydrophobic CDR3 for Neutralization but not for Antigen Recognition. PLoS Pathogens, 2013, 9, e1003202.	2.1	64
1990	Insight into <i>S</i>-adenosylmethionine biosynthesis from the crystal structures of the human methionine adenosyltransferase catalytic and regulatory subunits. Biochemical Journal, 2013, 452, 27-36.	1.7	51
1991	Structural Determinants for Activity and Specificity of the Bacterial Toxin LlpA. PLoS Pathogens, 2013, 9, e1003199.	2.1	33
1992	A Pathogen Type III Effector with a Novel E3 Ubiquitin Ligase Architecture. PLoS Pathogens, 2013, 9, e1003121.	2.1	82

#	ARTICLE	IF	CITATIONS
1993	Biochemical and Structural Studies of the Mycobacterium tuberculosis <i>O</i> ⁶ -Methylguanine Methyltransferase and Mutated Variants. Journal of Bacteriology, 2013, 195, 2728-2736.	1.0	29
1994	Large FK506-Binding Proteins Shape the Pharmacology of Rapamycin. Molecular and Cellular Biology, 2013, 33, 1357-1367.	1.1	106
1995	The Structure of the CS1 Pilus of Enterotoxigenic Escherichia coli Reveals Structural Polymorphism. Journal of Bacteriology, 2013, 195, 1360-1370.	1.0	18
1996	Long-range Electrostatic Complementarity Governs Substrate Recognition by Human Chymotrypsin C, a Key Regulator of Digestive Enzyme Activation. Journal of Biological Chemistry, 2013, 288, 9848-9859.	1.6	32
1997	Crystal structure analysis of a fatty acid double-bond hydratase from<i>Lactobacillus acidophilus</i>. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 648-657.	2.5	46
1998	Crystal Structure and Site-Directed Mutagenesis Analyses of Haloalkane Dehalogenase LinB from Sphingobium sp. Strain MI1205. Journal of Bacteriology, 2013, 195, 2642-2651.	1.0	20
1999	Advancing Methods for Biomolecular Crystallography. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , .	0.5	3
2000	Crystal Structures of a Glycoside Hydrolase Family 20 Lacto-N-biosidase from Bifidobacterium bifidum. Journal of Biological Chemistry, 2013, 288, 11795-11806.	1.6	53
2001	Model morphing and sequence assignment after molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2244-2250.	2.5	37
2002	High-resolution structure of a papaya plant-defence barwin-like protein solved by in-house sulfur-SAD phasing. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2017-2026.	2.5	16
2003	UV damage endonuclease employs a novel dual-dinucleotide flipping mechanism to recognize different DNA lesions. Nucleic Acids Research, 2013, 41, 1363-1371.	6.5	23
2004	Recent progress in robot-based systems for crystallography and their contribution to drug discovery. Expert Opinion on Drug Discovery, 2013, 8, 835-847.	2.5	19
2005	Structure/Function Analysis of a Type III Polyketide Synthase in the Brown Alga <i>Ectocarpus siliculosus</i> Reveals a Biochemical Pathway in Phlorotannin Monomer Biosynthesis. Plant Cell, 2013, 25, 3089-3103.	3.1	76
2006	Structure and secretion of <scp>CofJ</scp>, a putative colonization factor of enterotoxigenic <i><scp>E</scp>scherichia coli</i>. Molecular Microbiology, 2013, 90, 898-918.	1.2	18
2007	Crystal structure of the CN-hydrolase SA0302 from the pathogenic bacteriumStaphylococcus aureusbelonging to the Nit and NitFhit Branch of the nitrilase superfamily. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1057-1065.	2.0	3
2008	Crystal structure of the protein from <i>Arabidopsis thaliana</i> gene At5g06450, a putative DnaQâ€like exonuclease domainâ€containing protein with homohexameric assembly. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1669-1675.	1.5	5
2009	Structure of an early nativeâ€like intermediate of Î²2â€microglobulin amyloidogenesis. Protein Science, 2013, 22, 1349-1357.	3.1	14
2010	1.37 Ã… Crystal structure of pathogenic factor pectate lyase from Acidovorax citrulli. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1485-1490.	1.5	3

#	Article	IF	Citations
2011	Structural and functional insight into the universal stress protein family. Evolutionary Applications, 2013, 6, 434-449.	1.5	94
2012	Structural Changes during Cysteine Desulfurase CsdA and Sulfur Acceptor CsdE Interactions Provide Insight into the trans-Persulfuration. Journal of Biological Chemistry, 2013, 288, 27172-27180.	1.6	40
2013	The Structure of a Streptomyces avermitilis Î±-l-Rhamnosidase Reveals a Novel Carbohydrate-binding Module CBM67 within the Six-domain Arrangement. Journal of Biological Chemistry, 2013, 288, 12376-12385.	1.6	67
2014	Crystal Structure and Mode of Helicase Binding of the C-Terminal Domain of Primase from Helicobacter pylori. Journal of Bacteriology, 2013, 195, 2826-2838.	1.0	25
2015	Crystal structure of microsomal prostaglandin E ₂ synthase provides insight into diversity in the MAPEG superfamily. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3806-3811.	3.3	90
2016	Structureâ€Based Optimization of the Terminal Tripeptide in Glycopeptide Dendrimer Inhibitors of <i>Pseudomonas aeruginosa</i> Biofilms Targeting LecA. Chemistry - A European Journal, 2013, 19, 17054-17063.	1.7	36
2017	Yeast Mnn9 is both a priming glycosyltransferase and an allosteric activator of mannan biosynthesis. Open Biology, 2013, 3, 130022.	1.5	24
2018	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
2019	Crystal Structure of an Uncommon Cellulosome-Related Protein Module from Ruminococcus flavefaciens That Resembles Papain-Like Cysteine Peptidases. PLoS ONE, 2013, 8, e56138.	1.1	19
2020	Zebavidin - An Avidin-Like Protein from Zebrafish. PLoS ONE, 2013, 8, e77207.	1.1	18
2021	Molecular Characterization of Monoclonal Antibodies that Inhibit Acetylcholinesterase by Targeting the Peripheral Site and Backdoor Region. PLoS ONE, 2013, 8, e77226.	1.1	10
2022	Crystal Structures of Trypanosoma brucei Oligopeptidase B Broaden the Paradigm of Catalytic Regulation in Prolyl Oligopeptidase Family Enzymes. PLoS ONE, 2013, 8, e79349.	1.1	31
2023	Deletion of C7L and K1L Genes Leads to Significantly Decreased Virulence of Recombinant Vaccinia Virus TianTan. PLoS ONE, 2013, 8, e68115.	1.1	12
2024	CorA Is a Copper Repressible Surface-Associated Copper(I)-Binding Protein Produced in Methylomicrobium album BG8. PLoS ONE, 2014, 9, e87750.	1.1	18
2025	Structural Basis for Reversible Phosphorolysis and Hydrolysis Reactions of 2-O-Î±-Glucosylglycerol Phosphorylase. Journal of Biological Chemistry, 2014, 289, 18067-18075.	1.6	14
2026	Structural characterization of the putative ABC-type 2 transporter from Thermotoga maritima MSB8. Journal of Structural and Functional Genomics, 2014, 15, 215-222.	1.2	1
2027	Structural Elucidation of the Cyclization Mechanism of Î±-1,6-Glucan by Bacillus circulans T-3040 Cycloisomaltooligosaccharide Glucanotransferase. Journal of Biological Chemistry, 2014, 289, 12040-12051.	1.6	34
2028	Structural Insights into the Catalytic Mechanism of Synechocystis Magnesium Protoporphyrin IX O-Methyltransferase (ChlM). Journal of Biological Chemistry, 2014, 289, 25690-25698.	1.6	20

#	ARTICLE	IF	CITATIONS
2029	Crystal structure of a feruloyl esterase belonging to the tannase family: A disulfide bond near a catalytic triad. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2857-2867.	1.5	68
2030	Structural and Biochemical Basis for Ubiquitin Ligase Recruitment by Arrestin-related Domain-containing Protein-3 (ARRDC3). Journal of Biological Chemistry, 2014, 289, 4743-4752.	1.6	65
2031	Crystal structure of a putative quorum sensingâ€•regulated protein (PA3611) from the Pseudomonasâ€•specific DUF4146 family. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1086-1092.	1.5	7
2032	Thalidomide mimics uridine binding to an aromatic cage in cereblon. Journal of Structural Biology, 2014, 188, 225-232.	1.3	54
2033	Two Amino Acid Residues Confer Different Binding Affinities of Abelson Family Kinase Src Homology 2 Domains for Phosphorylated Cortactin. Journal of Biological Chemistry, 2014, 289, 19704-19713.	1.6	12
2034	Molecular insights into the interaction of the ribosomal stalk protein with elongation factor 1Î±. Nucleic Acids Research, 2014, 42, 14042-14052.	6.5	35
2035	Conformational flexibility in the catalytic triad revealed by the high-resolution crystal structure of <i>Streptomyces erythraeus</i> trypsin in an unliganded state. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 833-840.	2.5	6
2036	Niemannâ€"Pick type C2 protein mediating chemical communication in the worker ant. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3847-3852.	3.3	90
2037	Anomalous diffraction in crystallographic phase evaluation. Quarterly Reviews of Biophysics, 2014, 47, 49-93.	2.4	92
2038	The<i>PDB_REDO</i>server for macromolecular structure model optimization. IUCrJ, 2014, 1, 213-220.	1.0	709
2039	Engineering specificity in a dynamic protein complex with a single conserved mutation. FEBS Journal, 2014, 281, 4892-4905.	2.2	3
2040	Structure determination of human Fas apoptosis inhibitory molecule and identification of the critical residues linking the interdomain interaction to the anti-apoptotic activity. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1812-1822.	2.5	7
2041	Insights into the relationship between the haem-binding pocket and the redox potential of<i>c</i>₆cytochromes: four atomic resolution structures of<i>c</i>₆and<i>c</i>₆-like proteins from<i>Synechococcus</i>sp. PCC 7002. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2823-2832.	2.5	5
2042	Development and binding characteristics of phosphonate inhibitors of SplA protease from <i>Staphylococcus aureus</i>. Protein Science, 2014, 23, 179-189.	3.1	11
2043	Crystal structure of l-sorbose dehydrogenase, a pyrroloquinoline quinone-dependent enzyme with homodimeric assembly, from Ketogulonicigenium vulgare. Biotechnology Letters, 2014, 36, 1001-1008.	1.1	17
2044	Crystal Structure and Characterization of the Glycoside Hydrolase Family 62 Î±-l-Arabinofuranosidase from Streptomyces coelicolor. Journal of Biological Chemistry, 2014, 289, 7962-7972.	1.6	42
2045	Dual kinase-bromodomain inhibitors for rationally designed polypharmacology. Nature Chemical Biology, 2014, 10, 305-312.	3.9	296
2046	The major cockroach allergen Bla g 4 binds tyramine and octopamine. Molecular Immunology, 2014, 60, 86-94.	1.0	22

#	ARTICLE	IF	CITATIONS
2047	Structural Genomics. Methods in Molecular Biology, 2014, , .	0.4	6
2048	A discrete genetic locus confers xyloglucan metabolism in select human gut Bacteroidetes. Nature, 2014, 506, 498-502.	13.7	400
2049	[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
2050	Structural insights into recognition of acetylated histone ligands by the BRPF1 bromodomain. FEBS Letters, 2014, 588, 3844-3854.	1.3	29
2051	Simultaneous use of solution NMR and X-ray data in<i>REFMAC</i>5 for joint refinement/detection of structural differences. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 958-967.	2.5	45
2052	Fine-structural variance of family 3 carbohydrate-binding modules as extracellular biomass-sensing components of<i>Clostridium thermocellum</i>anti-Ïƒ^Ifactors. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 522-534.	2.5	26
2053	Identification of a new androgen receptor (AR) coâ€regulator BUD31 and related peptides to suppress wildâ€type and mutated ARâ€mediated prostate cancer growth via peptide screening and Xâ€ray structure analysis. Molecular Oncology, 2014, 8, 1575-1587.	2.1	51
2054	Structural Studies of Cinnamoyl-CoA Reductase and Cinnamyl-Alcohol Dehydrogenase, Key Enzymes of Monolignol Biosynthesis Â. Plant Cell, 2014, 26, 3709-3727.	3.1	85
2055	Structural Characterization and Function Determination of a Nonspecific Carboxylate Esterase from the Amidohydrolase Superfamily with a Promiscuous Ability To Hydrolyze Methylphosphonate Esters. Biochemistry, 2014, 53, 3476-3485.	1.2	5
2056	Versatile<i>C</i>₃-symmetric scaffolds and their use for covalent stabilization of the foldon trimer. Organic and Biomolecular Chemistry, 2014, 12, 2606-2614.	1.5	14
2057	DNA Recognition by a Ïƒ54 Transcriptional Activator from Aquifex aeolicus. Journal of Molecular Biology, 2014, 426, 3553-3568.	2.0	13
2058	Structural Insights into Enzymatic Degradation of Oxidized Polyvinyl Alcohol. ChemBioChem, 2014, 15, 1882-1886.	1.3	18
2059	A complex iron-calcium cofactor catalyzing phosphotransfer chemistry. Science, 2014, 345, 1170-1173.	6.0	80
2060	Structural Conservation, Variability, and Immunogenicity of the T6 Backbone Pilin of Serotype M6 Streptococcus pyogenes. Infection and Immunity, 2014, 82, 2949-2957.	1.0	32
2061	E pluribus unum, no more: from one crystal, many conformations. Current Opinion in Structural Biology, 2014, 28, 56-62.	2.6	53
2062	Structural and mechanistic insights into an extracytoplasmic copper trafficking pathway in <i>Streptomyces lividans</i>. Biochemical Journal, 2014, 459, 525-538.	1.7	23
2063	Allostery and Conformational Dynamics in cAMP-binding Acyltransferases. Journal of Biological Chemistry, 2014, 289, 16588-16600.	1.6	15
2064	Double troubleâ€”Buffer selection and <scp>H</scp>isâ€tag presence may be responsible for nonreproducibility of biomedical experiments. Protein Science, 2014, 23, 1359-1368.	3.1	83

#	ARTICLE	IF	CITATIONS
2065	Xylan utilization in human gut commensal bacteria is orchestrated by unique modular organization of polysaccharide-degrading enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3708-17.	3.3	137
2066	Phosphates in the Z-DNA dodecamer are flexible, but their P-SAD signal is sufficient for structure solution. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1790-1800.	2.5	30
2067	Structure of the nisin leader peptidase NisP revealing a C-terminal autocleavage activity. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1499-1505.	2.5	26
2068	Protein phasing at non-atomic resolution by combining Patterson and<i>VLD</i>techniques. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1994-2006.	2.5	9
2069	Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. Nature Communications, 2014, 5, 4764.	5.8	86
2070	Mercury metallation of the copper protein azurin and structural insight into possible heavy metal reactivity. Journal of Inorganic Biochemistry, 2014, 141, 152-160.	1.5	2
2071	Discovery of a Novel <scp>l</scp>-Lyxonate Degradation Pathway in <i>Pseudomonas aeruginosa</i> PAO1. Biochemistry, 2014, 53, 3357-3366.	1.2	29
2072	Structure and protective efficacy of the <i>Staphylococcus aureus</i> autocleaving protease EpiP. FASEB Journal, 2014, 28, 1780-1793.	0.2	17
2073	Mutational and crystallographic analysis of <scp>l</scp>â€amino acid oxidase/monooxygenase from <i>Pseudomonas</i> sp. AIU 813: Interconversion between oxidase and monooxygenase activities. FEBS Open Bio, 2014, 4, 220-228.	1.0	18
2074	Crystal structure of a â€œlooplessâ€• GH19 chitinase in complex with chitin tetrasaccharide spanning the catalytic center. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 793-802.	1.1	31
2075	Synthesis of L-2,3-Diaminopropionic Acid, a Siderophore and Antibiotic Precursor. Chemistry and Biology, 2014, 21, 379-388.	6.2	60
2076	C-terminal motif within Sec7 domain regulates guanine nucleotide exchange activity via tuning protein conformation. Biochemical and Biophysical Research Communications, 2014, 446, 380-386.	1.0	1
2077	Structural and functional analyses of a glutaminyl cyclase from <i>Ixodes scapularis</i> reveal metal-independent catalysis and inhibitor binding. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 789-801.	2.5	10
2078	Functional and molecular features of the calmodulin-interacting protein IQCG required for haematopoiesis in zebrafish. Nature Communications, 2014, 5, 3811.	5.8	18
2079	The dynamic complex of cytochrome c6 and cytochrome f studied with paramagnetic NMR spectroscopy. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1305-1315.	0.5	23
2080	Superoxide reductase from<i>Giardia intestinalis</i>: structural characterization of the first SOR from a eukaryotic organism shows an iron centre that is highly sensitive to photoreduction. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2236-2247.	2.5	6
2081	Diversity in the structures and ligand-binding sites of nematode fatty acid and retinol-binding proteins revealed by Na-FAR-1 from <i>Necator americanus</i>. Biochemical Journal, 2015, 471, 403-414.	1.7	27
2082	Conotoxin Î±D-GeXXA utilizes a novel strategy to antagonize nicotinic acetylcholine receptors. Scientific Reports, 2015, 5, 14261.	1.6	31

#	ARTICLE	IF	CITATIONS
2083	Fully automatic characterization and data collection from crystals of biological macromolecules. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1757-1767.	2.5	102
2084	Increased Conformational Flexibility of HLAâ€“B*27 Subtypes Associated With Ankylosing Spondylitis. Arthritis and Rheumatology, 2016, 68, 1172-1182.	2.9	36
2085	Structural and biochemical characterization of novel bacterial Î±-galactosidases belonging to glycoside hydrolase family 31. Biochemical Journal, 2015, 469, 145-158.	1.7	26
2086	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. Nucleic Acids Research, 2015, 43, 3358-3372.	6.5	43
2087	Structural analysis of haemoglobin binding by HpuA from the Neisseriaceae family. Nature Communications, 2015, 6, 10172.	5.8	42
2088	Data Analysis: Keeping Pace with Extraordinary Change. Synchrotron Radiation News, 2015, 28, 31-36.	0.2	1
2089	The Olfactomedin Domain from Gliomedin Is a Î²-Propeller with Unique Structural Properties. Journal of Biological Chemistry, 2015, 290, 3612-3621.	1.6	19
2090	Vaccinia Virus Protein A49 Is an Unexpected Member of the B-cell Lymphoma (Bcl)-2 Protein Family. Journal of Biological Chemistry, 2015, 290, 5991-6002.	1.6	49
2091	Crystal structure determination and refinement<i>via</i><i>SIR2014</i>. Journal of Applied Crystallography, 2015, 48, 306-309.	1.9	729
2092	<i>N</i>-Myristoyltransferase Is a Cell Wall Target in <i>Aspergillus fumigatus</i>. ACS Chemical Biology, 2015, 10, 1425-1434.	1.6	38
2093	Helical Shape of Helicobacter pylori Requires an Atypical Glutamine as a Zinc Ligand in the Carboxypeptidase Csd4. Journal of Biological Chemistry, 2015, 290, 3622-3638.	1.6	17
2094	CLASP2 Has Two Distinct TOG Domains That Contribute Differently to Microtubule Dynamics. Journal of Molecular Biology, 2015, 427, 2379-2395.	2.0	31
2095	High resolution structures of Plasmodium falciparum GST complexes provide novel insights into the dimerâ€“tetramer transition and a novel ligand-binding site. Journal of Structural Biology, 2015, 191, 365-375.	1.3	8
2096	Crystal structure, biochemical and cellular activities demonstrate separate functions of MTH1 and MTH2. Nature Communications, 2015, 6, 7871.	5.8	96
2097	Structural and functional characterization of two unusual endonuclease III enzymes from Deinococcus radiodurans. Journal of Structural Biology, 2015, 191, 87-99.	1.3	20
2098	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2015, 290, 18678-18698.	1.6	70
2099	Structures of three polycystic kidney disease-like domains from<i>Clostridium histolyticum</i>collagenases ColG and ColH. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 565-577.	2.5	19
2100	Elusive Structural, Functional, and Immunological Features of Act d 5, the Green Kiwifruit Kiwellin. Journal of Agricultural and Food Chemistry, 2015, 63, 6567-6576.	2.4	25

#	ARTICLE	IF	CITATIONS
2101	3-Sulfinopropionyl-coenzyme A (3SP-CoA) desulfinase from<i>Advenella mimigardefordensis</i>DPN7^T: crystal structure and function of a desulfinase with an acyl-CoA dehydrogenase fold. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1360-1372.	2.5	6
2102	Standalone cohesin as a molecular shuttle in cellulosome assembly. FEBS Letters, 2015, 589, 1569-1576.	1.3	14
2103	Crystal structure and substrate-binding mode of GH63 mannosylglycerate hydrolase from Thermus thermophilus HB8. Journal of Structural Biology, 2015, 190, 21-30.	1.3	8
2104	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
2105	Large-Scale Conformational Dynamics Control H5N1 Influenza Polymerase PB2 Binding to Importin Î±. Journal of the American Chemical Society, 2015, 137, 15122-15134.	6.6	49
2106	On the accuracy of unit-cell parameters in protein crystallography. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2217-2226.	2.5	6
2107	Crystal structure of the bacteriophage P2 integrase catalytic domain. FEBS Letters, 2015, 589, 3556-3563.	1.3	3
2108	STACâ€"A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. Journal of Molecular Biology, 2015, 427, 3327-3339.	2.0	17
2109	Structural and Functional Characterization of the Hazelnut Allergen Cor a 8. Journal of Agricultural and Food Chemistry, 2015, 63, 9150-9158.	2.4	33
2110	Advances in molecular-replacement procedures: theREVANpipeline. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1856-1863.	2.5	8
2111	Psoriasis pathogenesis â€" Pso p27 constitutes a compact structure forming large aggregates. Biochemistry and Biophysics Reports, 2015, 2, 132-136.	0.7	4
2112	The Diamond Light Source and the challenges ahead for structural biology: some informal remarks. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2015, 373, 20130156.	1.6	3
2113	Protein crystallography from the perspective of technology developments. Crystallography Reviews, 2015, 21, 122-153.	0.4	33
2114	The side chain of a glycosylated asparagine residue is important for the stability of isopullulanase. Journal of Biochemistry, 2015, 157, 225-234.	0.9	8
2115	Serological, genomic and structural analyses of the major mite allergen Der p 23. Clinical and Experimental Allergy, 2016, 46, 365-376.	1.4	69
2116	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
2117	Structure of the Essential <i>Mtb</i> FadD32 Enzyme: A Promising Drug Target for Treating Tuberculosis. ACS Infectious Diseases, 2016, 2, 579-591.	1.8	37
2118	Identification and characterization of a bacterial hyaluronidase and its production in recombinant form. FEBS Letters, 2016, 590, 2180-2189.	1.3	15

#	Article	IF	Citations
2119	High resolution crystal structure of the catalytic domain of MCR-1. Scientific Reports, 2016, 6, 39540.	1.6	65
2120	Structural basis for haem piracy from host haemopexin by Haemophilus influenzae. Nature Communications, 2016, 7, 11590.	5.8	59
2121	Crystal structure of glutamate-1-semialdehyde-2,1-aminomutase from<i>Arabidopsis thaliana</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 448-456.	0.4	8
2122	Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352.	13.7	231
2123	Structure of Thermobifida fusca DyP-type peroxidase and activity towards Kraft lignin and lignin model compounds. Archives of Biochemistry and Biophysics, 2016, 594, 54-60.	1.4	97
2124	Tracking solvent and protein movement during CO ₂ release in carbonic anhydrase II crystals. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5257-5262.	3.3	30
2125	Data Mining of Macromolecular Structures. Methods in Molecular Biology, 2016, 1415, 107-138.	0.4	12
2126	Biochemical and structural characterization of polyphosphate kinase 2 from the intracellular pathogen <i>Francisella tularensis</i>. Bioscience Reports, 2016, 36, e00294.	1.1	19
2127	Development of Selective CBP/P300 Benzoxazepine Bromodomain Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 8889-8912.	2.9	49
2128	Crystal structure of the enzyme-product complex reveals sugar ring distortion during catalysis by family 63 inverting Î±-glycosidase. Journal of Structural Biology, 2016, 196, 479-486.	1.3	6
2129	Structural and functional characterisation of the cyanobacterial PetC3 Rieske protein family. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 1879-1891.	0.5	9
2130	Crystal Structure of a Complex of the Intracellular Domain of Interferon Î» Receptor 1 (IFNLR1) and the FERM/SH2 Domains of Human JAK1. Journal of Molecular Biology, 2016, 428, 4651-4668.	2.0	37
2131	S-Nitrosylation Induces Structural and Dynamical Changes in a Rhodanese Family Protein. Journal of Molecular Biology, 2016, 428, 3737-3751.	2.0	12
2132	Targeted Disruption of the Interaction between WD-40 Repeat Protein 5 (WDR5) and Mixed Lineage Leukemia (MLL)/SET1 Family Proteins Specifically Inhibits MLL1 and SETd1A Methyltransferase Complexes. Journal of Biological Chemistry, 2016, 291, 22357-22372.	1.6	56
2133	Structural Insights into the M-Channel Proximal C-Terminus/Calmodulin Complex. Biochemistry, 2016, 55, 5353-5365.	1.2	26
2134	Discovery of Novel Oral Protein Synthesis Inhibitors of Mycobacterium tuberculosis That Target Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 6271-6280.	1.4	88
2135	NUDT15 Hydrolyzes 6-Thio-DeoxyGTP to Mediate the Anticancer Efficacy of 6-Thioguanine. Cancer Research, 2016, 76, 5501-5511.	0.4	96
2136	Structural basis for multi-specific peptide recognition by the anti-IDH1/2 monoclonal antibody, MsMab-1. Biochemical and Biophysical Research Communications, 2016, 478, 1274-1279.	1.0	4

#	ARTICLE	IF	CITATIONS
2137	Structural insights into Gemin5-guided selection of pre-snRNAs for snRNP assembly. Genes and Development, 2016, 30, 2376-2390.	2.7	60
2138	How Dextran Sulfate Affects C1-inhibitor Activity: A Model for Polysaccharide Potentiation. Structure, 2016, 24, 2182-2189.	1.6	15
2139	Structural basis for the recognition of guide RNA and target DNA heteroduplex by Argonaute. Nature Communications, 2016, 7, 11846.	5.8	104
2140	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
2141	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 346-358.	1.1	31
2142	Structural basis for the membrane association of ankyrinG via palmitoylation. Scientific Reports, 2016, 6, 23981.	1.6	18
2143	Crystal structures of chitin binding domains of chitinase from <i>ThermococcusÂkodakarensis</i><scp>KOD</scp>1. FEBS Letters, 2016, 590, 298-304.	1.3	22
2144	In vitro heme biotransformation by the HupZ enzyme from Group A streptococcus. BioMetals, 2016, 29, 593-609.	1.8	27
2145	Effect of impurities and post-experimental purification in SAD phasing with serial femtosecond crystallography data. Acta Crystallographica Section D: Structural Biology, 2016, 72, 789-794.	1.1	2
2146	Fully automatic macromolecular crystallography: the impact of MASSIF-1 on the optimum acquisition and quality of data. Crystallography Reviews, 2016, 22, 233-249.	0.4	37
2147	Dissecting the Structural Elements for the Activation of Î²-Ketoacyl-(Acyl Carrier Protein) Reductase from Vibrio cholerae. Journal of Bacteriology, 2016, 198, 463-476.	1.0	14
2148	Initiation of T cell signaling by CD45 segregation at 'close contacts'. Nature Immunology, 2016, 17, 574-582.	7.0	253
2149	Crystal structure of a lipoxygenase from Cyanothece sp. may reveal novel features for substrate acquisition. Journal of Lipid Research, 2016, 57, 276-287.	2.0	30
2150	Structural Basis for Toughness and Flexibility in the C-terminal Passenger Domain of an Acinetobacter Trimeric Autotransporter Adhesin. Journal of Biological Chemistry, 2016, 291, 3705-3724.	1.6	41
2151	Structure-based mutational studies of <i>O</i>-acetylserine sulfhydrylase reveal the reason for the loss of cysteine synthase complex formation in <i>Brucella abortus</i>. Biochemical Journal, 2017, 474, 1221-1239.	1.7	14
2152	Structural basis of the interaction between the putative adhesion-involved and iron-regulated FrpD and FrpC proteins of Neisseria meningitidis. Scientific Reports, 2017, 7, 40408.	1.6	10
2153	Myroilysin Is a New Bacterial Member of the M12A Family of Metzincin Metallopeptidases and Is Activated by a Cysteine Switch Mechanism. Journal of Biological Chemistry, 2017, 292, 5195-5206.	1.6	11
2154	Crystal structure of the N-terminal anticodon-binding domain of the nondiscriminating aspartyl-tRNA synthetase from<i>Helicobacter pylori</i>. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 62-69.	0.4	1

#	ARTICLE	IF	CITATIONS
2155	The Architecture of the Anbu Complex Reflects an Evolutionary Intermediate at the Origin of the Proteasome System. Structure, 2017, 25, 834-845.e5.	1.6	11
2156	Distinct homotypic B-cell receptor interactions shape the outcome of chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 15746.	5.8	93
2157	Discovery of Î±-l-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. Journal of Biological Chemistry, 2017, 292, 21092-21101.	1.6	8
2158	Xâ€ray crystal structure of <i>EscherichiaÂ coli</i> HspQ, a protein involved in the retardation of replication initiation. FEBS Letters, 2017, 591, 3805-3816.	1.3	4
2159	Crystal structure of Porphyromonas gingivalis dipeptidyl peptidase 4 and structure-activity relationships based on inhibitor profiling. European Journal of Medicinal Chemistry, 2017, 139, 482-491.	2.6	16
2160	Crystal Structure and Substrate Specificity Modification of Acetyl Xylan Esterase from Aspergillus luchuensis. Applied and Environmental Microbiology, 2017, 83, .	1.4	25
2161	Refining glass structure in two dimensions. Physical Review B, 2017, 96, .	1.1	3
2162	Inhibition of D-Ala:D-Ala ligase through a phosphorylated form of the antibiotic D-cycloserine. Nature Communications, 2017, 8, 1939.	5.8	59
2163	Synergy among phase-refinement techniques in macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 877-888.	1.1	6
2164	Structure of an unconventional SH3 domain from the postsynaptic density protein Shank3 at ultrahigh resolution. Biochemical and Biophysical Research Communications, 2017, 490, 806-812.	1.0	16
2165	Structural and Biophysical Characterization of the Mycobacterium tuberculosis Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the Streptomyces coelicolor Protein KbpA. Biochemistry, 2017, 56, 4015-4027.	1.2	4
2166	Insight into the 3D structure and substrate specificity of previously uncharacterized GNAT superfamily acetyltransferases from pathogenic bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 55-64.	1.1	13
2167	Polder maps: improving OMIT maps by excluding bulk solvent. Acta Crystallographica Section D: Structural Biology, 2017, 73, 148-157.	1.1	500
2168	Solving proteins at non-atomic resolution by direct methods: update. Journal of Applied Crystallography, 2017, 50, 1048-1055.	1.9	6
2169	Chroman-4-One Derivatives Targeting Pteridine Reductase 1 and Showing Anti-Parasitic Activity. Molecules, 2017, 22, 426.	1.7	39
2170	Structural characterization of core-bradavidin in complex with biotin. PLoS ONE, 2017, 12, e0176086.	1.1	2
2171	Crystal structure of the putative cytoplasmic protein STM0279 (Hcp2) from <i>Salmonella typhimurium</i>. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 463-468.	0.4	5
2172	Crystal structure of yeast nitronate monooxygenase from Cyberlindnera saturnus. Proteins: Structure, Function and Bioinformatics, 2018, 86, 599-605.	1.5	8

#	ARTICLE	IF	CITATIONS
2173	Targeted NUDT5 inhibitors block hormone signaling in breast cancer cells. Nature Communications, 2018, 9, 250.	5.8	56
2174	Human NUDT22 Is a UDP-Glucose/Galactose Hydrolase Exhibiting a Unique Structural Fold. Structure, 2018, 26, 295-303.e6.	1.6	11
2175	Discrete Self-Similarity in Interfacial Hydrodynamics and the Formation of Iterated Structures. Physical Review Letters, 2018, 120, 034505.	2.9	17
2176	Crystal structure of UDP- N -acetylglucosamine-enolpyruvate reductase (MurB) from Mycobacterium tuberculosis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 397-406.	1.1	27
2177	RING tetramerization is required for nuclear body biogenesis and PML sumoylation. Nature Communications, 2018, 9, 1277.	5.8	64
2178	Crystal structure of native Î²â€<i>N</i>â€acetylhexosaminidase isolated from <i>AspergillusÂoryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. FEBS Journal, 2018, 285, 580-598.	2.2	12
2179	Characterization of the [NiFeSe] hydrogenase from Desulfovibrio vulgaris Hildenborough. Methods in Enzymology, 2018, 613, 169-201.	0.4	12
2180	Crystal structure of heme A synthase from <i>Bacillus subtilis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11953-11957.	3.3	14
2181	Identification of a novel zinc-binding protein, C1orf123, as an interactor with a heavy metal-associated domain. PLoS ONE, 2018, 13, e0204355.	1.1	12
2182	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
2183	Structural analyses of 4-phosphate adaptor protein 2 yield mechanistic insights into sphingolipid recognition by the glycolipid transfer protein family. Journal of Biological Chemistry, 2018, 293, 16709-16723.	1.6	9
2184	Structural insights into the interaction of helicase and primase in Mycobacterium tuberculosis. Biochemical Journal, 2018, 475, 3493-3509.	1.7	5
2185	Crystallographically correct but confusing presentation of structural models deposited in the Protein Data Bank. Acta Crystallographica Section D: Structural Biology, 2018, 74, 939-945.	1.1	2
2186	BET bromodomain ligands: Probing the WPF shelf to improve BRD4 bromodomain affinity and metabolic stability. Bioorganic and Medicinal Chemistry, 2018, 26, 2937-2957.	1.4	19
2187	Comparison of <i>Alicyclobacillus acidocaldarius</i> <i>o</i>-Succinylbenzoate Synthase to Its Promiscuous <i>N</i>-Succinylamino Acid Racemase/<i>o</i>-Succinylbenzoate Synthase Relatives. Biochemistry, 2018, 57, 3676-3689.	1.2	9
2188	Active-site solvent replenishment observed during human carbonic anhydrase II catalysis. IUCrJ, 2018, 5, 93-102.	1.0	15
2189	Automatic recognition of ligands in electron density by machine learning. Bioinformatics, 2019, 35, 452-461.	1.8	22
2190	Super Potent Bispecific Llama VHH Antibodies Neutralize HIV via a Combination of gp41 and gp120 Epitopes. Antibodies, 2019, 8, 38.	1.2	25

#	ARTICLE	IF	CITATIONS
2191	B1 oligomerization regulates PML nuclear body biogenesis and leukemogenesis. Nature Communications, 2019, 10, 3789.	5.8	30
2192	The crystal structure of the phosphotriesterase from M.Âtuberculosis, another member of phosphotriesterase-like lactonase family. Biochemical and Biophysical Research Communications, 2019, 510, 224-229.	1.0	4
2193	A Simple Nondestructive, Cost-Effective Method for Differentiation of Protein Crystals from Salt Crystals by Using a Natural Dye. Crystal Growth and Design, 2019, 19, 3612-3615.	1.4	4
2194	Distinctive ligandâ€binding specificities of tandem PA14 biomassâ€sensory elements from <i>Clostridium thermocellum</i> and <i>Clostridium clariflavum</i>. Proteins: Structure, Function and Bioinformatics, 2019, 87, 917-930.	1.5	8
2195	Features and structure of a cold active N-acetylneuraminate lyase. PLoS ONE, 2019, 14, e0217713.	1.1	5
2196	Crystal structure of phosphoribulokinase from<i>Synechococcus</i>sp. strain PCC 6301. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 278-289.	0.4	15
2197	Mechanisms of redundancy and specificity of the Aspergillus fumigatus Crh transglycosylases. Nature Communications, 2019, 10, 1669.	5.8	18
2198	A revised biosynthetic pathway for the cofactor F420 in prokaryotes. Nature Communications, 2019, 10, 1558.	5.8	55
2199	An NAD+ Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. Molecular Cell, 2019, 73, 1282-1291.e8.	4.5	58
2200	Structural knowledge or X-ray damage? A case study on xylose isomerase illustrating both. Journal of Synchrotron Radiation, 2019, 26, 931-944.	1.0	12
2201	Crystal Structure of the Catalytic and Cytochrome <i>b</i> Domains in a Eukaryotic Pyrroloquinoline Quinone-Dependent Dehydrogenase. Applied and Environmental Microbiology, 2019, 85, .	1.4	17
2202	Comparison of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1119-1128.	1.1	11
2203	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. Molecular Cell, 2019, 73, 621-638.e17.	4.5	135
2204	Unique mechanism of target recognition by PfoI restriction endonuclease of the CCGG-family. Nucleic Acids Research, 2019, 47, 997-1010.	6.5	3
2205	Highâ€resolution crystal structure of peptidylâ€tRNA hydrolase from <i>Thermus thermophilus</i>. Proteins: Structure, Function and Bioinformatics, 2019, 87, 226-235.	1.5	2
2206	The structure of <i>PlasmodiumÂfalciparum</i> hydroxymethyldihydropterin pyrophosphokinaseâ€dihydropteroate synthase reveals the basis of sulfa resistance. FEBS Journal, 2020, 287, 3273-3297.	2.2	24
2207	Structure of odorant binding proteins and chemosensory proteins determined by X-ray crystallography. Methods in Enzymology, 2020, 642, 151-167.	0.4	2
2208	Acetylation of Surface Carbohydrates in Bacterial Pathogens Requires Coordinated Action of a Two-Domain Membrane-Bound Acyltransferase. MBio, 2020, 11, .	1.8	22

#	Article	IF	Citations
2209	Structural analysis and reaction mechanism of the disproportionating enzyme (Dâ€enzyme) from potato. Protein Science, 2020, 29, 2085-2100.	3.1	9
2210	Structural insights into ADP-ribosylation of ubiquitin by Deltex family E3 ubiquitin ligases. Science Advances, 2020, 6, .	4.7	51
2211	Structural insights of the enzymes from the chitin utilization locus of Flavobacterium johnsoniae. Scientific Reports, 2020, 10, 13775.	1.6	9
2212	Unique active-site and subsite features in the arabinogalactan-degrading GH43 exo-Î²-1,3-galactanase from Phanerochaete chrysosporium. Journal of Biological Chemistry, 2020, 295, 18539-18552.	1.6	3
2213	Structureâ€"function study of AKR4C14, an aldo-keto reductase from Thai jasmine rice (<i>Oryza) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 76, 472-483.	1.1	4
2214	Ionotropic Glutamate Receptor GluA2 in Complex with Bicyclic Pyrimidinedione-Based Compounds: When Small Compound Modifications Have Distinct Effects on Binding Interactions. ACS Chemical Neuroscience, 2020, 11, 1791-1800.	1.7	8
2215	Structureâ€"function analysis of silkworm sucrose hydrolase uncovers the mechanism of substrate specificity in GH13 subfamily 17 exo-Î±-glucosidases. Journal of Biological Chemistry, 2020, 295, 8784-8797.	1.6	7
2216	A mechanism-inspired UDP-<i>N</i>-acetylglucosamine pyrophosphorylase inhibitor. RSC Chemical Biology, 2020, 1, 13-25.	2.0	20
2217	Regioselectivity of hyoscyamine 6Î²-hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. Dalton Transactions, 2020, 49, 4454-4469.	1.6	15
2218	Conformational Plasticity of HLA-B27 Molecules Correlates Inversely With Efficiency of Negative T Cell Selection. Frontiers in Immunology, 2020, 11, 179.	2.2	6
2219	Crystal structure of O-Acetylserine sulfhydralase (OASS) isoform 3 from Entamoeba histolytica: Pharmacophore-based virtual screening and validation of novel inhibitors. European Journal of Medicinal Chemistry, 2020, 192, 112157.	2.6	9
2221	The thrombospondin module 1 domain of the matricellular protein CCN3 shows an atypical disulfide pattern and incomplete CWR layers. Acta Crystallographica Section D: Structural Biology, 2020, 76, 124-134.	1.1	5
2222	A polysaccharide utilization locus from the gut bacterium Dysgonomonas mossii encodes functionally distinct carbohydrate esterases. Journal of Biological Chemistry, 2021, 296, 100500.	1.6	21
2223	Structure analysis suggests Ess1 isomerizes the carboxy-terminal domain of RNA polymerase II via a bivalent anchoring mechanism. Communications Biology, 2021, 4, 398.	2.0	7
2225	Archaeal Connectase is a specific and efficient protein ligase related to proteasome Î² subunits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7
2226	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. Nature Communications, 2021, 12, 1988.	5.8	16
2227	Simplified heavy-atom derivatization of protein structures via co-crystallization with the MAD tetragon tetrabromoterephthalic acid. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 156-162.	0.4	2
2228	A Unique Carboxylic-Acid Hydrogen-Bond Network (CAHBN) Confers Glutaminyl Cyclase Activity on M28 Family Enzymes. Journal of Molecular Biology, 2021, 433, 166960.	2.0	1

#	Article	IF	Citations
2229	Structural insights into the Switching Off of the Interaction between the Archaeal Ribosomal Stalk and aEF1A by Nucleotide Exchange Factor aEF1B. Journal of Molecular Biology, 2021, 433, 167046.	2.0	1
2230	The PilB-PilZ-FimX regulatory complex of the Type IV pilus from Xanthomonas citri. PLoS Pathogens, 2021, 17, e1009808.	2.1	6
2231	Crystal structures of the EVE-HNH endonuclease VcaM4I in the presence and absence of DNA. Nucleic Acids Research, 2021, 49, 1708-1723.	6.5	4
2233	Density Modification In Main. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 111-122.	0.1	2
2234	Low Resolution Refinement of Atomic Models Against Crystallographic Data. Methods in Molecular Biology, 2017, 1607, 565-593.	0.4	10
2235	Structural Genomics of Minimal Organisms: Pipeline and Results. Methods in Molecular Biology, 2008, 426, 475-496.	0.4	3
2236	High Throughput Crystallography at SGC Toronto: an Overview. Methods in Molecular Biology, 2008, 426, 515-521.	0.4	5
2237	The Quality and Validation of Structures from Structural Genomics. Methods in Molecular Biology, 2014, 1091, 297-314.	0.4	23
2238	Ligand Electron Density Shape Recognition Using 3D Zernike Descriptors. Lecture Notes in Computer Science, 2009, , 125-136.	1.0	3
2239	Model-Building and Reduction of Model Bias in Electron Density Maps. NATO Science for Peace and Security Series A: Chemistry and Biology, 2013, , 193-203.	0.5	1
2240	The SAM domain of polyhomeotic forms a helical polymer. Nature Structural Biology, 2002, 9, 453-7.	9.7	131
2241	Electron density fitting and structure validation. , 2007, , 191-200.		2
2244	Automating crystallographic structure solution and refinement of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 144-154.	2.5	43
2245	New structural forms of a mycobacterial adenylyl cyclase Rv1625c. IUCrJ, 2014, 1, 338-348.	1.0	6
2246	Peptide binding to a bacterial signal peptidase visualized by peptide tethering and carrier-driven crystallization. IUCrJ, 2016, 3, 10-19.	1.0	15
2247	Structural analysis of a function-associated loop mutant of the substrate-recognition domain of Fbs1 ubiquitin ligase. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 619-626.	0.4	6
2248	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. Acta Crystallographica Section D: Structural Biology, 2016, 72, 966-975.	1.1	35
2249	Long-wavelength <i>Mesh&Collect</i> native SAD phasing from microcrystals. Acta Crystallographica Section D: Structural Biology, 2019, 75, 192-199.	1.1	8

#	ARTICLE	IF	CITATIONS
2250	Combining random microseed matrix screening and the magic triangle for the efficient structure solution of a potential lysin from bacteriophage P68. Acta Crystallographica Section D: Structural Biology, 2019, 75, 670-681.	1.1	3
2251	Density modification of cryo-EM maps. Acta Crystallographica Section D: Structural Biology, 2020, 76, 912-925.	1.1	28
2252	Structure of a bacterial glycoside hydrolase familyÂ63 enzyme in complex with its glycosynthase product, and insights into the substrate specificity. FEBS Journal, 2013, 280, 4560-4571.	2.2	7
2253	Thiolation-enhanced substrate recognition by D-alanyl carrier protein ligase DltA from Bacillus cereus. F1000Research, 2014, 3, 106.	0.8	8
2254	The Active Site of a Carbohydrate Esterase Displays Divergent Catalytic and Noncatalytic Binding Functions. PLoS Biology, 2009, 7, e1000071.	2.6	56
2255	UPF201 Archaeal Specific Family Members Reveal Structural Similarity to RNA-Binding Proteins but Low Likelihood for RNA-Binding Function. PLoS ONE, 2008, 3, e3903.	1.1	2
2256	Insights into the Function of the CRM1 Cofactor RanBP3 from the Structure of Its Ran-Binding Domain. PLoS ONE, 2011, 6, e17011.	1.1	18
2257	Structure of HsdS Subunit from Thermoanaerobacter tengcongensis Sheds Lights on Mechanism of Dynamic Opening and Closing of Type I Methyltransferase. PLoS ONE, 2011, 6, e17346.	1.1	19
2258	Crystal Structure Analysis Reveals Functional Flexibility in the Selenocysteine-Specific tRNA from Mouse. PLoS ONE, 2011, 6, e20032.	1.1	17
2259	Crystal Structure of Diedel, a Marker of the Immune Response of Drosophila melanogaster. PLoS ONE, 2012, 7, e33416.	1.1	17
2260	Structure of Bradavidin â€“ C-Terminal Residues Act as Intrinsic Ligands. PLoS ONE, 2012, 7, e35962.	1.1	8
2261	Crystal Structure of ChrRâ€”A Quinone Reductase with the Capacity to Reduce Chromate. PLoS ONE, 2012, 7, e36017.	1.1	60
2262	Comparative Structural and Functional Analysis of Orthomyxovirus Polymerase Cap-Snatching Domains. PLoS ONE, 2014, 9, e84973.	1.1	18
2263	A Novel Chimeric Avidin with Increased Thermal Stability Using DNA Shuffling. PLoS ONE, 2014, 9, e92058.	1.1	11
2264	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from Mycobacterium tuberculosis. PLoS ONE, 2014, 9, e116249.	1.1	6
2265	Archaeal Mo-Containing Glyceraldehyde Oxidoreductase Isozymes Exhibit Diverse Substrate Specificities through Unique Subunit Assemblies. PLoS ONE, 2016, 11, e0147333.	1.1	8
2266	Effect of BET Missense Mutations on Bromodomain Function, Inhibitor Binding and Stability. PLoS ONE, 2016, 11, e0159180.	1.1	17
2267	Comparative Structural and Functional Analysis of Bunyavirus and Arenavirus Cap-Snatching Endonucleases. PLoS Pathogens, 2016, 12, e1005636.	2.1	84

#	ARTICLE	IF	CITATIONS
2268	SHP Family Protein Tyrosine Phosphatases Adopt Canonical Active-Site Conformations in the Apo and Phosphate-Bound States. Protein and Peptide Letters, 2013, 20, 1039-1048.	0.4	7
2269	Î±/Î² coiled coils. ELife, 2016, 5, .	2.8	27
2270	Reassembly and co-crystallization of a family 9 processive endoglucanase from its component parts: structural and functional significance of the intermodular linker. PeerJ, 2015, 3, e1126.	0.9	29
2272	The Berlin â€œProtein Structure Factoryâ€•Initiative: A Technology-Oriented Approach to Structural Genomics. , 2001, , 101-121.		1
2273	Protein Crystallography. , 2001, , .		2
2274	X-ray Crystallography of a Novel Thermostable .BETA.-Galactosidase from Thermus thermophilus A4, and Its Complex Structure with Galactose.. Journal of Applied Glycoscience (1999), 2002, 49, 175-180.	0.3	2
2275	Structural Genomics in Europe and beyond - Shifting Scientific Directions at EMBL Hamburg. Acta Physica Polonica A, 2002, 101, 635-646.	0.2	0
2276	MolekÃ¼lmodelle und ModellmolekÃ¼le: Strukturanalyse groÃŸer biologischer MolekÃ¼le fÃ¼r die Medizin. , 2003, , 340-359.		0
2277	High-Throughput X-Ray Techniques and Drug Discovery. , 2003, , 43-58.		0
2278	Some Applications of Dummy Point Scatterers for Phasing in Macromolecular X-Ray Crystallography. Lecture Notes in Computer Science, 2005, , 35-45.	1.0	0
2279	Accelerating Protein Structure Recovery Using Graphics Processing Units. Lecture Notes in Computer Science, 2005, , 451-459.	1.0	0
2281	Use of Longer Wavelength X-ray in Protein Crystallography. Seibutsu Butsuri, 2007, 47, 174-178.	0.0	0
2282	Structure Determination of the Motor Domain of Yeast Kinesin Kar3 by X-Ray Crystallography. Methods in Molecular Biology, 2007, 392, 199-211.	0.4	0
2283	Structural genomics of mycobacterium tuberculosis: a search for function and new drug targets. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 135-144.	0.1	0
2284	Bacterial Structural Genomics Initiative: Overview of Methods and Technologies Applied to the Process of Structure Determination. Methods in Molecular Biology, 2008, 426, 537-559.	0.4	0
2285	Macromolecular Crystallographic Computing. Advances in Bioinformatics and Biomedical Engineering Book Series, 2010, , 1-36.	0.2	0
2286	Enhancing Lab Source Anomalous Scattering Using Cr KÎ± Radiation for Its Potential Application in Determining Macromolecular Structures. Crystal Structure Theory and Applications, 2012, 01, 84-91.	0.3	0
2287	Ce-SAD Phasing of Glucose Isomerase and Thermolysin Using Cu &lt;i&gt;KÎ±&lt;/i&gt; Radiation. Crystal Structure Theory and Applications, 2013, 02, 93-99.	0.3	0

#	Article	IF	Citations
2288	Protein Crystallography at Subatomic Resolution. , 2013, , 95-124.		0
2289	Techniques in Biophysics. , 2017, , 205-243.		0
2290	Studies on Crystallization of Peptidyl-prolyl cis-trans Isomerase and AreB from Aspergillus flavus. Journal of Bacteriology & Mycology Open Access, 2017, 5, .	0.2	0
2294	Prediction of models for ordered solvent in macromolecular structures by a classifier based upon resolution-independent projections of local feature data. Acta Crystallographica Section D: Structural Biology, 2019, 75, 696-717.	1.1	0
2297	Pairwise running of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2020, 76, 814-823.	1.1	2
2300	MolekÃ¼lmodelle und ModellmolekÃ¼le: Strukturanalyse groÃŸer biologischer MolekÃ¼le fÃ¼r die Medizin. , 2008, , 275-294.		0
2302	The crystal structure of benzophenone synthase from<i>Garcinia mangostana</i>L. pericarps reveals the basis for substrate specificity and catalysis. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 597-603.	0.4	5
2308	The young person's guide to the PDB. Postepy Biochemii, 2016, 62, 242-249.	0.5	2
2309	Predicting the performance of automated crystallographic model-building pipelines. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1591-1601.	1.1	2
2311	The young personÃ¢Â€Â™s guide to the PDB. Postepy Biochemii, 2016, 62, 242-249.	0.5	3
2313	Crystal Structure of the Bifunctional Wax Synthase 1 from <i>Acinetobacter baylyi</i> Suggests a Conformational Change upon Substrate Binding and Formation of Additional Substrate Binding Sites. ACS Catalysis, 2022, 12, 9753-9765.	5.5	3
2314	Improved AlphaFold modeling with implicit experimental information. Nature Methods, 2022, 19, 1376-1382.	9.0	62
2316	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
2317	Accelerating crystal structure determination with iterative <i>AlphaFold</i> prediction. Acta Crystallographica Section D: Structural Biology, 2023, 79, 234-244.	1.1	17
2318	<i>Buccaneer</i> model building with neural network fragment selection. Acta Crystallographica Section D: Structural Biology, 2023, 79, 326-338.	1.1	0
2320	Best Practices of Using AI-Based Models in Crystallography and Their Impact in Structural Biology. Journal of Chemical Information and Modeling, 2023, 63, 3637-3646.	2.5	3