

Zhi-Jie Liu

List of Publications by Year in descending order

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155
papers

7,939
citations

57631

44
h-index

58464

82
g-index

164
all docs

164
docs citations

164
times ranked

10290
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights into the activation of chemokine receptor CXCR2. <i>FEBS Journal</i> , 2022, 289, 386-393.	2.2	7
2	MD Simulations Revealing Special Activation Mechanism of Cannabinoid Receptor 1. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 860035.	1.6	4
3	Molecular insights into ligand recognition and G protein coupling of the neuromodulatory orphan receptor GPR139. <i>Cell Research</i> , 2022, 32, 210-213.	5.7	13
4	Structural insights into the activation initiation of full-length mGlu1. <i>Protein and Cell</i> , 2021, 12, 662-667.	4.8	19
5	Cryo-EM analysis of the HCoV-229E spike glycoprotein reveals dynamic prefusion conformational changes. <i>Nature Communications</i> , 2021, 12, 141.	5.8	17
6	Novel Functionalized Cannabinoid Receptor Probes: Development of Exceptionally Potent Agonists. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 3870-3884.	2.9	8
7	Inhibition mechanism of SARS-CoV-2 main protease by ebiselen and its derivatives. <i>Nature Communications</i> , 2021, 12, 3061.	5.8	149
8	Protocol for crystal structure determination of the antagonist-bound human cannabinoid receptor CB2. <i>STAR Protocols</i> , 2021, 2, 100584.	0.5	1
9	Rational Remodeling of Atypical Scaffolds for the Design of Photoswitchable Cannabinoid Receptor Tools. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 13752-13765.	2.9	9
10	A Genetically Encoded F-19 NMR Probe Reveals the Allosteric Modulation Mechanism of Cannabinoid Receptor 1. <i>Journal of the American Chemical Society</i> , 2021, 143, 16320-16325.	6.6	44
11	Carbon-silicon switch led to the discovery of novel synthetic cannabinoids with therapeutic effects in a mouse model of multiple sclerosis. <i>European Journal of Medicinal Chemistry</i> , 2021, 226, 113878.	2.6	2
12	Crystal structure of semisynthetic obelinâ€•v. <i>Protein Science</i> , 2021, , .	3.1	4
13	Organized cannabinoid receptor distribution in neurons revealed by super-resolution fluorescence imaging. <i>Nature Communications</i> , 2020, 11, 5699.	5.8	18
14	Structural and Functional Insights into Cannabinoid Receptors. <i>Trends in Pharmacological Sciences</i> , 2020, 41, 665-677.	4.0	40
15	Structural basis of CXC chemokine receptor 2 activation and signalling. <i>Nature</i> , 2020, 585, 135-140.	13.7	128
16	Structural features of activated GPCR signaling complexes. <i>Current Opinion in Structural Biology</i> , 2020, 63, 82-89.	2.6	50
17	A Novel G Protein-Biased and Subtype-Selective Agonist for a G Protein-Coupled Receptor Discovered from Screening Herbal Extracts. <i>ACS Central Science</i> , 2020, 6, 213-225.	5.3	25
18	Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. <i>Cell</i> , 2020, 180, 655-665.e18.	13.5	212

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19	The structural study of mutation-induced inactivation of human muscarinic receptor M4. <i>IUCr</i> , 2020, 7, 294-305.	1.0	9
20	Disulfide-Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins. <i>Chemistry - A European Journal</i> , 2019, 25, 11635-11640.	1.7	5
21	Probing the CB ₁ Cannabinoid Receptor Binding Pocket with AM6538, a High-Affinity Irreversible Antagonist. <i>Molecular Pharmacology</i> , 2019, 96, 619-628.	1.0	4
22	Functionality-Independent DNA Encoding of Complex Natural Products. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9254-9261.	7.2	54
23	A Chemical Strategy for Amphiphile Replacement in Membrane Protein Research. <i>Langmuir</i> , 2019, 35, 4319-4327.	1.6	6
24	Molecular Mechanism for Ligand Recognition and Subtype Selectivity of β_2 Adrenergic Receptor. <i>Cell Reports</i> , 2019, 29, 2936-2943.e4.	2.9	17
25	Elucidating the active μ -opioid receptor crystal structure with peptide and small-molecule agonists. <i>Science Advances</i> , 2019, 5, eaax9115.	4.7	81
26	Structural Basis of the Diversity of Adrenergic Receptors. <i>Cell Reports</i> , 2019, 29, 2929-2935.e4.	2.9	30
27	Crystal Structure of the Human Cannabinoid Receptor CB2. <i>Cell</i> , 2019, 176, 459-467.e13.	13.5	268
28	Self-capping of nucleoprotein filaments protects the Newcastle disease virus genome. <i>ELife</i> , 2019, 8, .	2.8	18
29	Common activation mechanism of class A GPCRs. <i>ELife</i> , 2019, 8, .	2.8	339
30	High-throughput identification of G protein-coupled receptor modulators through affinity mass spectrometry screening. <i>Chemical Science</i> , 2018, 9, 3192-3199.	3.7	33
31	5-HT _{2C} Receptor Structures Reveal the Structural Basis of GPCR Polypharmacology. <i>Cell</i> , 2018, 172, 719-730.e14.	13.5	185
32	Identification of natural products as novel ligands for the human 5-HT _{2C} receptor. <i>Biophysics Reports</i> , 2018, 4, 50-61.	0.2	23
33	Protein crystal quality oriented disulfide bond engineering. <i>Protein and Cell</i> , 2018, 9, 659-663.	4.8	14
34	Computational design of thermostabilizing point mutations for G protein-coupled receptors. <i>ELife</i> , 2018, 7, .	2.8	60
35	Exploring a new ligand binding site of G protein-coupled receptors. <i>Chemical Science</i> , 2018, 9, 6480-6489.	3.7	37
36	Crystal Structure of ATP-Bound Human ABCF1 Demonstrates a Unique Conformation of ABC Proteins. <i>Structure</i> , 2018, 26, 1259-1265.e3.	1.6	14

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37	Structural and functional analyses of human DDX41 DEAD domain. <i>Protein and Cell</i> , 2017, 8, 72-76.	4.8	20
38	Human GLP-1 receptor transmembrane domain structure in complex with allosteric modulators. <i>Nature</i> , 2017, 546, 312-315.	13.7	192
39	Ligand identification of the adenosine A _{2A} receptor in self-assembled nanodiscs by affinity mass spectrometry. <i>Analytical Methods</i> , 2017, 9, 5851-5858.	1.3	7
40	Crystal structures of agonist-bound human cannabinoid receptor CB1. <i>Nature</i> , 2017, 547, 468-471.	13.7	379
41	Structure and Function of a C-C Bond Cleaving Oxygenase in Atypical Angucycline Biosynthesis. <i>ACS Chemical Biology</i> , 2017, 12, 142-152.	1.6	17
42	The emerging roles of the DDX41 protein in immunity and diseases. <i>Protein and Cell</i> , 2017, 8, 83-89.	4.8	72
43	Biochemical features of the adhesion G protein-coupled receptor CD97 related to its auto-proteolysis and HeLa cell attachment activities. <i>Acta Pharmacologica Sinica</i> , 2017, 38, 56-68.	2.8	6
44	Mitrocomin from the jellyfish <i>Mitrocoma cellularia</i> with deleted C-terminal tyrosine reveals a higher bioluminescence activity compared to wild type photoprotein. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2016, 162, 286-297.	1.7	18
45	Crystal structure of hGEF-H1 PH domain provides insight into incapability in phosphoinositide binding. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 621-627.	1.0	2
46	In vitro expression and analysis of the 826 human G protein-coupled receptors. <i>Protein and Cell</i> , 2016, 7, 325-337.	4.8	53
47	Native phasing of x-ray free-electron laser data for a G protein-coupled receptor. <i>Science Advances</i> , 2016, 2, e1600292.	4.7	97
48	Crystal Structure of the Human Cannabinoid Receptor CB1. <i>Cell</i> , 2016, 167, 750-762.e14.	13.5	468
49	Structural basis for DNA recognition by STAT6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13015-13020.	3.3	46
50	aKMT Catalyzes Extensive Protein Lysine Methylation in the Hyperthermophilic Archaeon <i>Sulfolobus islandicus</i> but is Dispensable for the Growth of the Organism. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2908-2923.	2.5	16
51	All Ca ²⁺ -binding loops of light-sensitive ctenophore photoprotein berovin bind magnesium ions: The spatial structure of Mg ²⁺ -loaded apo-berovin. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2016, 154, 57-66.	1.7	16
52	New insights into the structural basis of DNA recognition by HINa and HINb domains of IFI16. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 51-61.	1.5	48
53	Combination Therapy of LysGH15 and Apigenin as a New Strategy for Treating Pneumonia Caused by <i>Staphylococcus aureus</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 87-94.	1.4	51
54	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, 7300.	5.8	18

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55	Structures of the Ca ²⁺ -regulated photoprotein obelin Y138F mutant before and after bioluminescence support the catalytic function of a water molecule in the reaction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 720-732.	2.5	23
56	Structural and Biochemical Characterization Reveals LysGH15 as an Unprecedented "EF-Hand-Like" Calcium-Binding Phage Lysin. <i>PLoS Pathogens</i> , 2014, 10, e1004109.	2.1	85
57	Crystal structure of the N-terminal methyltransferase-like domain of anamorsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1066-1071.	1.5	12
58	Crystal structures of the F88Y obelin mutant before and after bioluminescence provide molecular insight into spectral tuning among hydromedusan photoproteins. <i>FEBS Journal</i> , 2014, 281, 1432-1445.	2.2	26
59	Structural and functional analyses of human tryptophan 2,3-dioxygenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3210-3216.	1.5	46
60	Crystallization, preliminary X-ray crystallographic and cryo-electron microscopy analysis of a bifunctional enzyme fucokinase/fucose-1-P-guanylyltransferase from <i>Bacteroides fragilis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1206-1210.	0.4	2
61	NLRC3, a Member of the NLR Family of Proteins, Is a Negative Regulator of Innate Immune Signaling Induced by the DNA Sensor STING. <i>Immunity</i> , 2014, 40, 329-341.	6.6	245
62	Role of the HIN Domain in Regulation of Innate Immune Responses. <i>Molecular and Cellular Biology</i> , 2014, 34, 2-15.	1.1	36
63	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630.	4.8	27
64	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , 2014, 24, 344-358.	5.7	86
65	Binding of bacterial secondary messenger molecule c-di-GMP is a STING operation. <i>Protein and Cell</i> , 2013, 4, 117-129.	4.8	18
66	Spatial structure of the novel light-sensitive photoprotein berovin from the ctenophore <i>Beroë abyssicola</i> in the Ca ²⁺ -loaded apoprotein conformation state. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2139-2146.	1.1	25
67	Structural biology study of human TNF receptor associated factor 4 TRAF domain. <i>Protein and Cell</i> , 2013, 4, 687-694.	4.8	17
68	Oxygen Activation of Apo-obelin-Coelenterazine Complex. <i>ChemBioChem</i> , 2013, 14, 739-745.	1.3	31
69	Structural basis for termination of AIM2-mediated signaling by p202. <i>Cell Research</i> , 2013, 23, 855-858.	5.7	38
70	Structure of the Leanyer orthobunyavirus nucleoprotein-RNA complex reveals unique architecture for RNA encapsidation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9054-9059.	3.3	59
71	Structure of Severe Fever with Thrombocytopenia Syndrome Virus Nucleocapsid Protein in Complex with Suramin Reveals Therapeutic Potential. <i>Journal of Virology</i> , 2013, 87, 6829-6839.	1.5	67
72	High-resolution crystal structure of the catalytic domain of human dual-specificity phosphatase 26. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1160-1170.	2.5	10

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73	Studies of Human 2,4-Dienoyl CoA Reductase Shed New Light on Peroxisomal \hat{I}^2 -Oxidation of Unsaturated Fatty Acids. <i>Journal of Biological Chemistry</i> , 2012, 287, 28956-28965.	1.6	17
74	The helicase DDX41 recognizes the bacterial secondary messengers cyclic di-GMP and cyclic di-AMP to activate a type I interferon immune response. <i>Nature Immunology</i> , 2012, 13, 1155-1161.	7.0	363
75	Structural View of a Non Pfam Singleton and Crystal Packing Analysis. <i>PLoS ONE</i> , 2012, 7, e31673.	1.1	2
76	Structural Analysis of the STING Adaptor Protein Reveals a Hydrophobic Dimer Interface and Mode of Cyclic di-GMP Binding. <i>Immunity</i> , 2012, 36, 1073-1086.	6.6	282
77	Structural insights into a human anti-IFN antibody exerting therapeutic potential for systemic lupus erythematosus. <i>Journal of Molecular Medicine</i> , 2012, 90, 837-846.	1.7	25
78	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 521-530.	2.5	24
79	Structural and functional characterization of the C-terminal catalytic domain of SSV1 integrase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 659-670.	2.5	13
80	Conversion of α -D-ribulose 5-phosphate to α -D-xylulose 5-phosphate: new insights from structural and biochemical studies on human RPE. <i>FASEB Journal</i> , 2011, 25, 497-504.	0.2	28
81	Protein-protein complexation in bioluminescence. <i>Protein and Cell</i> , 2011, 2, 957-972.	4.8	20
82	A multi-dataset data-collection strategy produces better diffraction data. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2011, 67, 544-549.	0.3	25
83	Altered architecture of substrate binding region defines the unique specificity of UDP-GalNAc 4-epimerases. <i>Protein Science</i> , 2011, 20, 856-866.	3.1	14
84	Crystal structure of a novel non-Pfam protein PF2046 solved using low resolution B-factor sharpening and multi-crystal averaging methods. <i>Protein and Cell</i> , 2010, 1, 453-458.	4.8	13
85	Sequence fingerprint and structural analysis of the SCOR enzyme A3DFK9 from <i>Clostridium thermocellum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 603-613.	1.5	1
86	Structure-function analysis of human $\text{l-}\alpha$ -prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.2	1
87	NMR-derived Topology of a GFP-photoprotein Energy Transfer Complex*. <i>Journal of Biological Chemistry</i> , 2010, 285, 40891-40900.	1.6	47
88	Structure-function analysis of human $\text{l-}\alpha$ -prostaglandin D synthase bound with fatty acid molecules. <i>FASEB Journal</i> , 2010, 24, 4668-4677.	0.2	40
89	Structural Basis and Catalytic Mechanism for the Dual Functional Endo- \hat{I}^2 -N-Acetylglucosaminidase A. <i>PLoS ONE</i> , 2009, 4, e4658.	1.1	52
90	Structural insight into acute intermittent porphyria. <i>FASEB Journal</i> , 2009, 23, 396-404.	0.2	45

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91	Crystal structure of human esterase D: a potential genetic marker of retinoblastoma. <i>FASEB Journal</i> , 2009, 23, 1441-1446.	0.2	31
92	Structural Basis for the Inhibition of Human 5,10-Methenyltetrahydrofolate Synthetase by N10-Substituted Folate Analogues. <i>Cancer Research</i> , 2009, 69, 7294-7301.	0.4	16
93	Structure based mechanism of the Ca ²⁺ -induced release of coelenterazine from the <i>Renilla</i> binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 583-593.	1.5	19
94	Novel dimerization mode of the human Bcl-2 family protein Bak, a mitochondrial apoptosis regulator. <i>Journal of Structural Biology</i> , 2009, 166, 32-37.	1.3	46
95	Structure of acostatin, a dimeric disintegrin from Southern copperhead (<i>Agkistrodon contortrix</i>) Tj ETQq1 1 0.784314 rgBT /Overl... 2008, 64, 466-470.	2.5	20
96	Purification, crystallization and preliminary crystallographic analysis of the non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 91-93.	0.7	0
97	Crystal structure solution of a ParB-like nuclease at atomic resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 263-267.	1.5	7
98	Crystal structure of a novel non-Pfam protein AF1514 from <i>Archeoglobus fulgidus</i> DSM 4304 solved by SAD using a Cr X-ray source. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2109-2113.	1.5	8
99	Crystal structure of coelenterazine-binding protein from <i>Renilla muelleri</i> at 1.7 Å...: Why it is not a calcium-regulated photoprotein. <i>Photochemical and Photobiological Sciences</i> , 2008, 7, 442.	1.6	31
100	The First Agmatine/Cadaverine Aminopropyl Transferase: Biochemical and Structural Characterization of an Enzyme Involved in Polyamine Biosynthesis in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6057-6067.	1.0	31
101	Crystal structure of an aerobic FMN-dependent azoreductase (AzoA) from <i>Enterococcus faecalis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2007, 463, 68-77.	1.4	66
102	Curved EFC/F-BAR-Domain Dimers Are Joined End to End into a Filament for Membrane Invagination in Endocytosis. <i>Cell</i> , 2007, 129, 761-772.	13.5	366
103	Structure of dNTP-inducible dNTP triphosphohydrolase: insight into broad specificity for dNTPs and triphosphohydrolase-type hydrolysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 230-239.	2.5	27
104	Structure of the human Tim44 C-terminal domain in complex with pentaethylene glycol: ligand-bound form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1225-1234.	2.5	16
105	Crystallization and preliminary crystallographic analysis of molybdenum-cofactor biosynthesis protein C from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 27-29.	0.7	4
106	Structure of the hypothetical protein PF0899 from <i>Pyrococcus furiosus</i> at 1.85 Å... resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 549-552.	0.7	6
107	(NZ)CH...O Contacts assist crystallization of a ParB-like nuclease. <i>BMC Structural Biology</i> , 2007, 7, 46.	2.3	17
108	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium <i>Moorella thermoacetica</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 167-176.	1.5	28

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109	The multifunctional human p100 protein 'hooks' methylated ligands. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 779-784.	3.6	72
110	Structural basis of CoA recognition by the <i>Pyrococcus</i> single-domain CoA-binding proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 7, 119-129.	1.2	3
111	Structural and transcriptional analyses of a purine nucleotide-binding protein from <i>Pyrococcus furiosus</i> : a component of a novel, membrane-bound multiprotein complex unique to this hyperthermophilic archaeon. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 1-10.	1.2	0
112	Crystal Structures of Tyrosyl-tRNA Synthetases from Archaea. <i>Journal of Molecular Biology</i> , 2006, 355, 395-408.	2.0	27
113	Crystal Structures of the Lytic Transglycosylase MltA from <i>N.gonorrhoeae</i> and <i>E.coli</i> : Insights into Interdomain Movements and Substrate Binding. <i>Journal of Molecular Biology</i> , 2006, 359, 122-136.	2.0	25
114	Crystal structure of obelin after Ca ²⁺ -triggered bioluminescence suggests neutral coelenteramide as the primary excited state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2570-2575.	3.3	84
115	All three Ca ²⁺ -binding loops of photoproteins bind calcium ions: The crystal structures of calcium-loaded apo-aequorin and apo-obelin. <i>Protein Science</i> , 2005, 14, 663-675.	3.1	85
116	Life in the fast lane for protein crystallization and X-ray crystallography. <i>Progress in Biophysics and Molecular Biology</i> , 2005, 88, 359-386.	1.4	77
117	Protein Production and Crystallization at SECSG – An Overview. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 233-243.	1.2	14
118	A test of enhancing model accuracy in high-throughput crystallography. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 1-11.	1.2	45
119	Salvaging <i>Pyrococcus furiosus</i> Protein Targets at SECSG. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 121-127.	1.2	2
120	A non-natural dinucleotide containing an isomeric L-related deoxynucleoside: dinucleotide inhibitors of anti-HIV integrase activity. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2005, 61, o518-o520.	0.4	1
121	On increasing protein-crystallization throughput for X-ray diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 123-129.	2.5	17
122	Parameter-space screening: a powerful tool for high-throughput crystal structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 520-527.	2.5	25
123	Away from the edge II: in-house Se-SAS phasing with chromium radiation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 960-966.	2.5	10
124	The high-throughput protein-to-structure pipeline at SECSG. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 679-684.	2.5	22
125	Isolation, crystallization and preliminary X-ray analysis of a methanol-induced corrinoid protein from <i>Moorella thermoacetica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 537-540.	0.7	8
126	Three-dimensional structure of GlcNAc \pm 1-4Gal releasing Endo- β -Galactosidase from <i>Clostridium perfringens</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 141-144.	1.5	12

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127	Mechanism of Class 1 (Glycosylhydrolase Family 47) α -Mannosidases Involved in N-Glycan Processing and Endoplasmic Reticulum Quality Control. <i>Journal of Biological Chemistry</i> , 2005, 280, 16197-16207.	1.6	106
128	Structure of the Conserved Transcriptional Repressor Enhancer of Rudimentary Homolog α - β . <i>Biochemistry</i> , 2005, 44, 5017-5023.	1.2	34
129	Crystal Structure of a Ca ²⁺ -discharged Photoprotein. <i>Journal of Biological Chemistry</i> , 2004, 279, 33647-33652.	1.6	51
130	Structure of Mouse Golgi α -Mannosidase IA Reveals the Molecular Basis for Substrate Specificity among Class 1 (Family 47 Glycosylhydrolase) α -1,2-Mannosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 29774-29786.	1.6	48
131	Structural genomics of <i>Pyrococcus furiosus</i> : X-ray crystallography reveals 3D domain swapping in rubrerythrin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 878-882.	1.5	18
132	Preparation and X-ray crystallographic analysis of the Ca ²⁺ -discharged photoprotein obelin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 512-514.	2.5	7
133	Crystallization and preliminary X-ray analysis of GlcNAc α -1,4Gal-releasing endo- β -galactosidase from <i>Clostridium perfringens</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 537-538.	2.5	2
134	Displacement of iron by zinc at the diiron site of <i>Desulfovibrio vulgaris</i> rubrerythrin: X-ray crystal structure and anomalous scattering analysis. <i>Journal of Inorganic Biochemistry</i> , 2004, 98, 786-796.	1.5	19
135	X-ray Crystal Structure of <i>Desulfovibrio vulgaris</i> Rubrerythrin with Zinc Substituted into the [Fe(SCys) ₄] Site and Alternative Diiron Site Structures α - β . <i>Biochemistry</i> , 2004, 43, 3204-3213.	1.2	14
136	Structure determination of fibrillar in from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 315, 726-732.	1.0	19
137	The Hyperthermophile Protein Sso10a is a Dimer of Winged Helix DNA-binding Domains Linked by an Antiparallel Coiled Coil Rod. <i>Journal of Molecular Biology</i> , 2004, 341, 73-91.	2.0	35
138	Crystallization and preliminary X-ray diffraction analysis of lectin-1 from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1241-1242.	2.5	8
139	Atomic resolution structure of obelin: soaking with calcium enhances electron density of the second oxygen atom substituted at the C2-position of coelenterazine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 311, 433-439.	1.0	56
140	Violet Bioluminescence and Fast Kinetics from W92F Obelin: A Structure-Based Proposals for the Bioluminescence Triggering and the Identification of the Emitting Species α - β . <i>Biochemistry</i> , 2003, 42, 6013-6024.	1.2	57
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