

Stephen K Burley

List of Publications by Year in descending order

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Version: 2024-02-01

245
papers

29,630
citations

6254

80
h-index

5539

163
g-index

261
all docs

261
docs citations

261
times ranked

30072
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of the SARS-CoV-2 proteome in three dimensions (3D) during the first 6 months of the COVID-19 pandemic. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1054-1080.	2.6	31
2	RCSB Protein Data Bank: Celebrating 50 years of the PDB with new tools for understanding and visualizing biological macromolecules in 3D. <i>Protein Science</i> , 2022, 31, 187-208.	7.6	84
3	PDB-101: Educational resources supporting molecular explorations through biology and medicine. <i>Protein Science</i> , 2022, 31, 129-140.	7.6	43
4	RCSB Protein Data Bank resources for structure-facilitated design of mRNA vaccines for existing and emerging viral pathogens. <i>Structure</i> , 2022, 30, 55-68.e2.	3.3	10
5	Simplified quality assessment for small-molecule ligands in the Protein Data Bank. <i>Structure</i> , 2022, 30, 252-262.e4.	3.3	12
6	RCSB Protein Data Bank: improved annotation, search and visualization of membrane protein structures archived in the PDB. <i>Bioinformatics</i> , 2022, 38, 1452-1454.	4.1	41
7	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
8	mTOR regulates aerobic glycolysis through NEAT1 and nuclear paraspeckle-mediated mechanism in hepatocellular carcinoma. <i>Theranostics</i> , 2022, 12, 3518-3533.	10.0	18
9	Genetic and Structural Analysis of SARS-CoV-2 Spike Protein for Universal Epitope Selection. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	7
10	RCSB Protein Data Bank 1D3D module: displaying positional features on macromolecular assemblies. <i>Bioinformatics</i> , 2022, 38, 3304-3305.	4.1	4
11	Exploring protein symmetry at the RCSB Protein Data Bank. <i>Emerging Topics in Life Sciences</i> , 2022, 6, 231-243.	2.6	7
12	RCSB Protein Data Bank: Architectural Advances Towards Integrated Searching and Efficient Access to Macromolecular Structure Data from the PDB Archive. <i>Journal of Molecular Biology</i> , 2021, 433, 166704.	4.2	106
13	The Protein Data Bank Archive. <i>Methods in Molecular Biology</i> , 2021, 2305, 3-21.	0.9	49
14	Impact of structural biologists and the Protein Data Bank on small-molecule drug discovery and development. <i>Journal of Biological Chemistry</i> , 2021, 296, 100559.	3.4	23
15	Enhanced validation of small-molecule ligands and carbohydrates in the Protein Data Bank. <i>Structure</i> , 2021, 29, 393-400.e1.	3.3	28
16	Modernized uniform representation of carbohydrate molecules in the Protein Data Bank. <i>Glycobiology</i> , 2021, 31, 1204-1218.	2.5	17
17	Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures. <i>Nucleic Acids Research</i> , 2021, 49, W431-W437.	14.5	515
18	Toward improving androgen receptor-targeted therapies in male-dominant hepatocellular carcinoma. <i>Drug Discovery Today</i> , 2021, 26, 1539-1546.	6.4	18

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19	Open-access data: A cornerstone for artificial intelligence approaches to protein structure prediction. <i>Structure</i> , 2021, 29, 515-520.	3.3	22
20	Design and proof of concept for targeted phage-based COVID-19 vaccination strategies with a streamlined cold-free supply chain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
21	mTORC1 Promotes ARID1A Degradation and Oncogenic Chromatin Remodeling in Hepatocellular Carcinoma. <i>Cancer Research</i> , 2021, 81, 5652-5665.	0.9	12
22	RCSB Protein Data Bank 1D tools and services. <i>Bioinformatics</i> , 2021, 36, 5526-5527.	4.1	15
23	RCSB Protein Data Bank: powerful new tools for exploring 3D structures of biological macromolecules for basic and applied research and education in fundamental biology, biomedicine, biotechnology, bioengineering and energy sciences. <i>Nucleic Acids Research</i> , 2021, 49, D437-D451.	14.5	918
24	John D. Westbrook Jr (1957–2021). <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1475-1476.	2.3	1
25	Predicting Proteome-Scale Protein Structure with Artificial Intelligence. <i>New England Journal of Medicine</i> , 2021, 385, 2191-2194.	27.0	17
26	RCSB Protein Data Bank: Enabling biomedical research and drug discovery. <i>Protein Science</i> , 2020, 29, 52-65.	7.6	223
27	RCSB Protein Data Bank tools for 3D structure-guided cancer research: human papillomavirus (HPV) case study. <i>Oncogene</i> , 2020, 39, 6623-6632.	5.9	6
28	Integrative illustration for coronavirus outreach. <i>PLoS Biology</i> , 2020, 18, e3000815.	5.6	18
29	Virtual Boot Camp: COVID-19 evolution and structural biology. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 511-513.	1.2	5
30	Insights from 20 years of the Molecule of the Month. <i>Biochemistry and Molecular Biology Education</i> , 2020, 48, 350-355.	1.2	16
31	Real time structural search of the Protein Data Bank. <i>PLoS Computational Biology</i> , 2020, 16, e1007970.	3.2	42
32	Impact of the Protein Data Bank on antineoplastic approvals. <i>Drug Discovery Today</i> , 2020, 25, 837-850.	6.4	24
33	How to help the free market fight coronavirus. <i>Nature</i> , 2020, 580, 167-167.	27.8	11
34	High-performance macromolecular data delivery and visualization for the web. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1167-1173.	2.3	3
35	BinaryCIF and CIFTools—Lightweight, efficient and extensible macromolecular data management. <i>PLoS Computational Biology</i> , 2020, 16, e1008247.	3.2	15
36	Real-time structural motif searching in proteins using an inverted index strategy. <i>PLoS Computational Biology</i> , 2020, 16, e1008502.	3.2	15

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37	Impact of the Protein Data Bank Across Scientific Disciplines. <i>Data Science Journal</i> , 2020, 19, 25.	1.3	17
38	Real time structural search of the Protein Data Bank. , 2020, 16, e1007970.		0
39	Real time structural search of the Protein Data Bank. , 2020, 16, e1007970.		0
40	Real time structural search of the Protein Data Bank. , 2020, 16, e1007970.		0
41	Real time structural search of the Protein Data Bank. , 2020, 16, e1007970.		0
42	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
43	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
44	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
45	Real-time structural motif searching in proteins using an inverted index strategy. , 2020, 16, e1008502.		0
46	A Novel Acquired Exon 20 EGFR M766Q Mutation in Lung Adenocarcinoma Mediates Osimertinib Resistance but is Sensitive to Neratinib and Pozotinib. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1982-1988.	1.1	27
47	BioJava 5: A community driven open-source bioinformatics library. <i>PLoS Computational Biology</i> , 2019, 15, e1006791.	3.2	44
48	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46
49	How Structural Biologists and the Protein Data Bank Contributed to Recent FDA New Drug Approvals. <i>Structure</i> , 2019, 27, 211-217.	3.3	65
50	D3R Grand Challenge 3: blind prediction of protein-ligand poses and affinity rankings. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 1-18.	2.9	104
51	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671
52	RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. <i>Nucleic Acids Research</i> , 2019, 47, D464-D474.	14.5	918
53	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	17.5	520
54	SOD1 Phosphorylation by mTORC1 Couples Nutrient Sensing and Redox Regulation. <i>Molecular Cell</i> , 2018, 70, 502-515.e8.	9.7	94

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55	RCSB Protein Data Bank: Sustaining a living digital data resource that enables breakthroughs in scientific research and biomedical education. <i>Protein Science</i> , 2018, 27, 316-330.	7.6	219
56	D3R Grand Challenge 2: blind prediction of protein-ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 1-20.	2.9	156
57	Outlier analyses of the Protein Data Bank archive using a probability-density-ranking approach. <i>Scientific Data</i> , 2018, 5, 180293.	5.3	7
58	Integrative/Hybrid Methods Structural Biology: Role of Macromolecular Crystallography. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 11-18.	1.6	4
59	Amino acid modifications for conformationally constraining naturally occurring and engineered peptide backbones: Insights from the Protein Data Bank. <i>Biopolymers</i> , 2018, 109, e23230.	2.4	6
60	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	45
61	Investigation of protein quaternary structure via stoichiometry and symmetry information. <i>PLoS ONE</i> , 2018, 13, e0197176.	2.5	12
62	Comparison of <i>Alicyclobacillus acidocaldarius</i> <i>N</i> -Succinylbenzoate Synthase to Its Promiscuous <i>N</i> -Succinylamino Acid Racemase/ <i>N</i> -Succinylbenzoate Synthase Relatives. <i>Biochemistry</i> , 2018, 57, 3676-3689.	2.5	9
63	Analysis of impact metrics for the Protein Data Bank. <i>Scientific Data</i> , 2018, 5, 180212.	5.3	24
64	RCSB Protein Data Bank: Sustaining A Living Digital Data Resource That Enables Breakthroughs In Scientific Research And Biomedical Education. <i>FASEB Journal</i> , 2018, 32, 674.3.	0.5	0
65	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D271-D281.	14.5	619
66	Multivariate Analyses of Quality Metrics for Crystal Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 458-468.	3.3	28
67	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	3.3	130
68	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. <i>Methods in Molecular Biology</i> , 2017, 1607, 627-641.	0.9	592
69	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017, 25, 1317-1318.	3.3	84
70	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
71	Impact of genetic variation on three dimensional structure and function of proteins. <i>PLoS ONE</i> , 2017, 12, e0171355.	2.5	55
72	<i>DCC</i> : a Swiss army knife for structure factor analysis and validation. <i>Journal of Applied Crystallography</i> , 2016, 49, 1081-1084.	4.5	22

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73	Using the Tools and Resources of the RCSB Protein Data Bank. <i>Current Protocols in Bioinformatics</i> , 2016, 55, 1.9.1-1.9.35.	25.8	8
74	D3R grand challenge 2015: Evaluation of protein-ligand pose and affinity predictions. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 651-668.	2.9	178
75	The archiving and dissemination of biological structure data. <i>Current Opinion in Structural Biology</i> , 2016, 40, 17-22.	5.7	28
76	Integrating genomic information with protein sequence and 3D atomic level structure at the RCSB protein data bank. <i>Bioinformatics</i> , 2016, 32, 3833-3835.	4.1	15
77	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193.	2.3	103
78	RCSB Protein Data Bank: A Resource for Chemical, Biochemical, and Structural Explorations of Large and Small Biomolecules. <i>Journal of Chemical Education</i> , 2016, 93, 569-575.	2.3	66
79	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
80	The RCSB PDB "Molecule of the Month" Inspiring a Molecular View of Biology. <i>PLoS Biology</i> , 2015, 13, e1002140.	5.6	88
81	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. <i>Nucleic Acids Research</i> , 2015, 43, D345-D356.	14.5	461
82	Integrative Structure-Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2911-2926.	3.8	67
83	Response to On prompt update of literature references in the Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2780-2780.	2.5	1
84	Crystal structure of <i>Clostridium acetobutylicum</i> aspartate kinase (CaAk): An important allosteric enzyme for amino acids production. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2014, 3, 73-85.	4.4	12
85	Loss of quaternary structure is associated with rapid sequence divergence in the OSBS family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8535-8540.	7.1	29
86	Divergent Evolution of Ligand Binding in the Succinylbenzoate Synthase Family. <i>Biochemistry</i> , 2013, 52, 7512-7521.	2.5	14
87	A public-private partnership to unlock the untargeted kinome. <i>Nature Chemical Biology</i> , 2013, 9, 3-6.	8.0	141
88	PDB40: The Protein Data Bank celebrates its 40th birthday. <i>Biopolymers</i> , 2013, 99, 165-169.	2.4	7
89	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. <i>Structure</i> , 2013, 21, 560-571.	3.3	53
90	Revealing structural views of biology. <i>Biopolymers</i> , 2013, 99, 817-824.	2.4	4

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91	Structure and Catalytic Mechanism of LigI: Insight into the Amidohydrolase Enzymes of cog3618 and Lignin Degradation. <i>Biochemistry</i> , 2012, 51, 3497-3507.	2.5	32
92	Rapid-access, high-throughput synchrotron crystallography for drug discovery. <i>Trends in Pharmacological Sciences</i> , 2012, 33, 261-267.	8.7	28
93	Cas5d processes pre-crRNA and is a member of a larger family of CRISPR RNA endonucleases. <i>Rna</i> , 2012, 18, 2020-2028.	3.5	80
94	Structural insight into mechanism and diverse substrate selection strategy of <i>ScpL</i> ribulokinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 261-268.	2.6	5
95	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2110-2116.	2.6	7
96	Catalytic Mechanism and Three-Dimensional Structure of Adenine Deaminase. <i>Biochemistry</i> , 2011, 50, 1917-1927.	2.5	42
97	Enzymatic Deamination of the Epigenetic Base <i>N</i> -6-Methyladenine. <i>Journal of the American Chemical Society</i> , 2011, 133, 2080-2083.	13.7	24
98	Pa0148 from <i>Pseudomonas aeruginosa</i> Catalyzes the Deamination of Adenine. <i>Biochemistry</i> , 2011, 50, 6589-6597.	2.5	18
99	Gimme Phospho-Serine Five! Capping Enzyme Guanylyltransferase Recognition of the RNA Polymerase II CTD. <i>Molecular Cell</i> , 2011, 43, 163-165.	9.7	7
100	Structural and Functional Studies of Fatty Acyl Adenylate Ligases from <i>E. coli</i> and <i>L. pneumophila</i> . <i>Journal of Molecular Biology</i> , 2011, 406, 313-324.	4.2	29
101	Protein-RNA and Protein-Protein Recognition by Dual KH1/2 Domains of the Neuronal Splicing Factor Nova-1. <i>Structure</i> , 2011, 19, 930-944.	3.3	59
102	Structural basis for a ribofuranosyl binding protein: Insights into the furanose specific transport. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1352-1357.	2.6	4
103	Structure of the C-terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1672-1677.	2.6	16
104	The catalase activity of diiron adenine deaminase. <i>Protein Science</i> , 2011, 20, 2080-2094.	7.6	14
105	Structural Variation in Bacterial Glyoxalase I Enzymes. <i>Journal of Biological Chemistry</i> , 2011, 286, 38367-38374.	3.4	42
106	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011, 21, 898-907.	5.5	41
107	ModBase, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2011, 39, D465-D474.	14.5	506
108	Structural Underpinnings of Nitrogen Regulation by the Prototypical Nitrogen-Responsive Transcriptional Factor NrpR. <i>Structure</i> , 2010, 18, 1512-1521.	3.3	11

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109	Mass spectrometry guided in situ proteolysis to obtain crystals for X-ray structure determination. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1795-1801.	2.8	13
110	Structural studies on cytosolic domain of magnesium transporter MgtE from <i>Enterococcus faecalis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 487-491.	2.6	8
111	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1992-1998.	2.6	13
112	Structure of a putative BenA-like porin from <i>Pseudomonas fluorescens</i> Pf0-5 at 2.6 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3056-3062.	2.6	17
113	Structural Bases of PAS Domain-regulated Kinase (PASK) Activation in the Absence of Activation Loop Phosphorylation. <i>Journal of Biological Chemistry</i> , 2010, 285, 41034-41043.	3.4	26
114	Discovery and Structure Determination of the Orphan Enzyme Isoxanthopterin Deaminase,. <i>Biochemistry</i> , 2010, 49, 4374-4382.	2.5	18
115	Functional Identification and Structure Determination of Two Novel Prolidases from cog1228 in the Amidohydrolase Superfamily,. <i>Biochemistry</i> , 2010, 49, 6791-6803.	2.5	18
116	The Hunt for 8-Oxoguanine Deaminase. <i>Journal of the American Chemical Society</i> , 2010, 132, 1762-1763.	13.7	34
117	Structures of PHR Domains from <i>Mus musculus</i> Phr1 (Mycbp2) Explain the Loss-of-Function Mutation (Gly1092 → Glu) of the <i>C. elegans</i> Ortholog RPM-1. <i>Journal of Molecular Biology</i> , 2010, 397, 883-892.	4.2	3
118	Type VI secretion apparatus and phage tail-associated protein complexes share a common evolutionary origin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4154-4159.	7.1	576
119	SGX523 is an exquisitely selective, ATP-competitive inhibitor of the MET receptor tyrosine kinase with antitumor activity <i>in vivo</i> . <i>Molecular Cancer Therapeutics</i> , 2009, 8, 3181-3190.	4.1	123
120	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 107-125.	1.2	25
121	Blocking UV-induced eIF2 γ Phosphorylation with Small Molecule Inhibitors of GCN2. <i>Chemical Biology and Drug Design</i> , 2009, 74, 57-67.	3.2	32
122	Functional Annotation of Two New Carboxypeptidases from the Amidohydrolase Superfamily of Enzymes. <i>Biochemistry</i> , 2009, 48, 4567-4576.	2.5	19
123	Crystal structure of a conserved protein of unknown function (MJ1651) from <i>Methanococcus jannaschii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 572-577.	2.6	4
124	X-ray crystal structure of the B component of Hemolysin BL from <i>Bacillus cereus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 534-540.	2.6	73
125	A novel mode of dimerization via formation of a glutamate anhydride crosslink in a protein crystal structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1038-1041.	2.6	1
126	Crystal structure of a putative lysostaphin peptidase from <i>Vibrio cholerae</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 1096-1103.	2.6	14

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127	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	19.0	763
128	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. <i>Structure</i> , 2008, 16, 5-11.	3.3	58
129	High Throughput Protein Production and Crystallization at NYSGXRC. <i>Methods in Molecular Biology</i> , 2008, 426, 561-575.	0.9	33
130	A Common Catalytic Mechanism for Proteins of the HutI Family. <i>Biochemistry</i> , 2008, 47, 5608-5615.	2.5	10
131	SGX393 inhibits the CML mutant Bcr-Abl ^{T315I} and preempts <i>in vitro</i> resistance when combined with nilotinib or dasatinib. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5507-5512.	7.1	84
132	Structure of Human Dual Specificity Protein Phosphatase 23, VHZ, Enzyme-Substrate/Product Complex. <i>Journal of Biological Chemistry</i> , 2008, 283, 8946-8953.	3.4	22
133	UPF201 Archaeal Specific Family Members Reveal Structural Similarity to RNA-Binding Proteins but Low Likelihood for RNA-Binding Function. <i>PLoS ONE</i> , 2008, 3, e3903.	2.5	2
134	Structural Analysis of a Ternary Complex of Allantoate Amidohydrolase from <i>Escherichia coli</i> Reveals its Mechanics. <i>Journal of Molecular Biology</i> , 2007, 368, 450-463.	4.2	28
135	X-ray structures of two proteins belonging to Pfam DUF178 revealed unexpected structural similarity to the DUF191 Pfam family. <i>BMC Structural Biology</i> , 2007, 7, 62.	2.3	5
136	Structural genomics of protein phosphatases. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 121-140.	1.2	148
137	SGX70393 Inhibits Bcr-Abl ^{T315I} In Vitro and In Vivo and Completely Suppresses Resistance When Combined with Nilotinib or Dasatinib.. <i>Blood</i> , 2007, 110, 535-535.	1.4	4
138	Structural basis for activation of the therapeutic L-nucleoside analogs 3TC and troxacitabine by human deoxycytidine kinase. <i>Nucleic Acids Research</i> , 2006, 35, 186-192.	14.5	45
139	Structure determination of an FMN reductase from <i>Pseudomonas aeruginosa</i> PA01 using sulfur anomalous signal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 383-391.	2.5	41
140	Crystal structures of two putative phosphoheptose isomerases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1092-1096.	2.6	14
141	Crystal structure of a putative HTH-type transcriptional regulator yxA _F from <i>Bacillus subtilis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 1087-1091.	2.6	5
142	Crystal structure of phosphatidylglycerophosphatase (PGPase), a putative membrane-bound lipid phosphatase, reveals a novel binuclear metal binding site and two "proton wires". <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 851-862.	2.6	10
143	Crystal structure of glycerophosphodiester phosphodiesterase from <i>Agrobacterium tumefaciens</i> by SAD with a large asymmetric unit. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 514-518.	2.6	13
144	Crystal structure of trehalose-6-phosphate phosphatase-related protein: Biochemical and biological implications. <i>Protein Science</i> , 2006, 15, 1735-1744.	7.6	54

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145	Two Structurally Atypical HEAT Domains in the C-Terminal Portion of Human eIF4G Support Binding to eIF4A and Mnk1. <i>Structure</i> , 2006, 14, 913-923.	3.3	56
146	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	3.3	60
147	Mechanism of action of a flavin-containing monooxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9832-9837.	7.1	152
148	Inhibition of T315I Bcr-Abl and Other Imatinib-Resistant Bcr-Abl Mutants by the Selective Abl Kinase Inhibitor SGX70393.. <i>Blood</i> , 2006, 108, 1373-1373.	1.4	3
149	X-Ray Structure of a Rex-Family Repressor/NADH Complex Insights into the Mechanism of Redox Sensing. <i>Structure</i> , 2005, 13, 43-54.	3.3	78
150	High-throughput Limited Proteolysis/Mass Spectrometry for Protein Domain Elucidation. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 129-134.	1.2	55
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