

Andrzej Joachimiak

List of Publications by Year in descending order

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172
papers

11,448
citations

46918

47
h-index

32761

100
g-index

186
all docs

186
docs citations

186
times ranked

15033
citing authors

#	ARTICLE	IF	CITATIONS
1	The crystal structure of the bacterial chaperonIn GroEL at 2.8 Å... Nature, 1994, 371, 578-586.	13.7	1,363
2	A Virulence Locus of Pseudomonas aeruginosa Encodes a Protein Secretion Apparatus. Science, 2006, 312, 1526-1530.	6.0	984
3	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
4	Structure of a bacterial quorum-sensing transcription factor complexed with pheromone and DNA. Nature, 2002, 417, 971-974.	13.7	407
5	The three-dimensional structure of trp repressor. Nature, 1985, 317, 782-786.	13.7	386
6	Structural plasticity of SARS-CoV-2 3CL Mpro active site cavity revealed by room temperature X-ray crystallography. Nature Communications, 2020, 11, 3202.	5.8	334
7	Structure of papain-like protease from SARS-CoV-2 and its complexes with non-covalent inhibitors. Nature Communications, 2021, 12, 743.	5.8	297
8	Crystal structure of Nsp15 endoribonuclease <sc>NendoU</sc> from <sc>SARSâ€CoV</sc>â€2. Protein Science, 2020, 29, 1596-1605.	3.1	294
9	Crystal structure of the TSP-1 type 1 repeats. Journal of Cell Biology, 2002, 159, 373-382.	2.3	249
10	A Family of LIC Vectors for High-Throughput Cloning and Purification of Proteins. Methods in Molecular Biology, 2009, 498, 105-115.	0.4	244
11	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. Science, 2021, 373, 931-936.	6.0	173
12	Characteristics and Crystal Structure of Bacterial Inosine-5â€-monophosphate Dehydrogenaseâ€â€j. Biochemistry, 1999, 38, 4691-4700.	1.2	169
13	An expression vector tailored for large-scale, high-throughput purification of recombinant proteins. Protein Expression and Purification, 2006, 47, 446-454.	0.6	161
14	NFÎB selectivity of estrogen receptor ligands revealed by comparative crystallographic analyses. Nature Chemical Biology, 2008, 4, 241-247.	3.9	149
15	The Structural Biology Center 19ID undulator beamline: facility specifications and protein crystallographic results. Journal of Synchrotron Radiation, 2006, 13, 30-45.	1.0	143
16	Flexibility of the DNA-binding domains of trp repressor. Proteins: Structure, Function and Bioinformatics, 1988, 3, 18-31.	1.5	142
17	High-throughput protein purification and quality assessment for crystallization. Methods, 2011, 55, 12-28.	1.9	138
18	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

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19	High-throughput crystallography for structural genomics. Current Opinion in Structural Biology, 2009, 19, 573-584.	2.6	114
20	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. Biomacromolecules, 2016, 17, 2027-2039.	2.6	114
21	NDM-1, the ultimate promiscuous enzyme: substrate recognition and catalytic mechanism. FASEB Journal, 2013, 27, 1917-1927.	0.2	108
22	The 60 kDa Heat Shock Proteins in the Hyperthermophilic Archaeon Sulfolobus shibatae. Journal of Molecular Biology, 1995, 253, 712-725.	2.0	105
23	Automation of protein purification for structural genomics. Journal of Structural and Functional Genomics, 2004, 5, 111-118.	1.2	102
24	Taking MAD to the extreme: ultrafast protein structure determination. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1168-1173.	2.5	101
25	Profiling B cell immunodominance after SARS-CoV-2 infection reveals antibody evolution to non-neutralizing viral targets. Immunity, 2021, 54, 1290-1303.e7.	6.6	101
26	A small-molecule allosteric inhibitor of Mycobacterium tuberculosis tryptophan synthase. Nature Chemical Biology, 2017, 13, 943-950.	3.9	100
27	A conformational switch controls cell wall remodelling enzymes required for bacterial cell division. Molecular Microbiology, 2012, 85, 768-781.	1.2	98
28	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. IUCr, 2020, 7, 814-824.	1.0	92
29	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
30	Tipiracil binds to uridine site and inhibits Nsp15 endoribonuclease NendoU from SARS-CoV-2. Communications Biology, 2021, 4, 193.	2.0	85
31	Structure of Apo- and Monometalated Forms of NDM-1: A Highly Potent Carbapenem-Hydrolyzing Metallo- β -Lactamase. PLoS ONE, 2011, 6, e24621.	1.1	84
32	SARS-CoV-2 Infection Severity Is Linked to Superior Humoral Immunity against the Spike. MBio, 2021, 12, .	1.8	81
33	The Structures of the Thrombospondin-1 N-Terminal Domain and Its Complex with a Synthetic Pentameric Heparin. Structure, 2006, 14, 33-42.	1.6	80
34	Characterization of a <i>Bacillus subtilis</i> transporter for petrobactin, an anthrax stealth siderophore. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21854-21859.	3.3	80
35	Towards Fully Automated Structure-based Function Prediction in Structural Genomics: A Case Study. Journal of Molecular Biology, 2007, 367, 1511-1522.	2.0	79
36	The structure of the <i>yrdC</i> gene product from <i>Escherichia coli</i> reveals a new fold and suggests a role in RNA binding. Protein Science, 2000, 9, 2557-2566.	3.1	74

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37	Three conformations of an archaeal chaperonin, TF55 from <i>Sulfolobus shibatae</i> . <i>Journal of Molecular Biology</i> , 2000, 296, 813-819.	2.0	74
38	Optimization of Benzoxazole-Based Inhibitors of <i>Cryptosporidium parvum</i> Inosine 5'-Monophosphate Dehydrogenase. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 4028-4043.	2.9	71
39	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	1.6	70
40	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. <i>Scientific Reports</i> , 2017, 7, 44103.	1.6	67
41	Crystal Structure of <i>Thermotoga maritima</i> 0065, a Member of the IclR Transcriptional Factor Family. <i>Journal of Biological Chemistry</i> , 2002, 277, 19183-19190.	1.6	63
42	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. <i>Structure</i> , 2008, 16, 5-11.	1.6	58
43	Structure of cyclin G-associated kinase (GAK) trapped in different conformations using nanobodies. <i>Biochemical Journal</i> , 2014, 459, 59-69.	1.7	56
44	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. <i>Environmental Science & Technology</i> , 2018, 52, 12388-12401.	4.6	56
45	New LIC vectors for production of proteins from genes containing rare codons. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 135-144.	1.2	55
46	Structural and evolutionary relationships of α -AT-less type I polyketide synthase ketosynthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12693-12698.	3.3	55
47	Structure and Recognition of Sheared Tandem G-A Base Pairs Associated with Human Centromere DNA Sequence at Atomic Resolution. <i>Biochemistry</i> , 1999, 38, 16452-16460.	1.2	54
48	Toroidal Structure and DNA Cleavage by the CRISPR-Associated [4Fe-4S] Cluster Containing Cas4 Nuclease SSO0001 from <i>Sulfolobus solfataricus</i> . <i>Journal of the American Chemical Society</i> , 2013, 135, 17476-17487.	6.6	52
49	Structural basis for suppression of hypernegative DNA supercoiling by <i>E. coli</i> topoisomerase I. <i>Nucleic Acids Research</i> , 2015, 43, 11031-11046.	6.5	52
50	Structural Basis for Catalysis by the Mono- and Dimetalated Forms of the dapE-Encoded N-succinyl-L,Diaminopimelic Acid Desuccinylase. <i>Journal of Molecular Biology</i> , 2010, 397, 617-626.	2.0	51
51	Structure of the ent-Copalyl Diphosphate Synthase PtmT2 from <i>Streptomyces platensis</i> CB00739, a Bacterial Type II Diterpene Synthase. <i>Journal of the American Chemical Society</i> , 2016, 138, 10905-10915.	6.6	50
52	Room-temperature X-ray crystallography reveals the oxidation and reactivity of cysteine residues in SARS-CoV-2 3CL M ^{pro} : insights into enzyme mechanism and drug design. <i>IUCr</i> , 2020, 7, 1028-1035.	1.0	49
53	A family of metal-dependent phosphatases implicated in metabolite damage-control. <i>Nature Chemical Biology</i> , 2016, 12, 621-627.	3.9	48
54	Structural Insights into Substrate Selectivity and Activity of Bacterial Polyphosphate Kinases. <i>ACS Catalysis</i> , 2018, 8, 10746-10760.	5.5	48

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55	Conformational Cycle of the Archaeosome, a TCP1-like Chaperonin from <i>Sulfolobus shibatae</i> . <i>Journal of Biological Chemistry</i> , 1995, 270, 28818-28823.	1.6	47
56	Roles of Intramolecular and Intermolecular Interactions in Functional Regulation of the Hsp70 J-protein Co-Chaperone Sis1. <i>Journal of Molecular Biology</i> , 2015, 427, 1632-1643.	2.0	46
57	Molecular Mechanism of Inhibition of Acid Ceramidase by Carmofur. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 987-992.	2.9	46
58	2â€²-O methylation of RNA cap in SARS-CoV-2 captured by serial crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	46
59	Mitochondrial Hsp90 is a ligand-activated molecular chaperone coupling ATP binding to dimer closure through a coiled-coil intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2952-2957.	3.3	42
60	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. <i>Biophysical Journal</i> , 2021, 120, 3152-3165.	0.2	39
61	Cleavable C-terminal His-tag vectors for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 31-39.	1.2	38
62	A thiolâ€¢disulfide oxidoreductase of the <i>Corynebacterium diphtheriae</i> is essential for viability, pilus assembly, toxin production and virulence. <i>Molecular Microbiology</i> , 2015, 98, 1037-1050.	1.2	37
63	Interaction of antidiabetic Î±â€¢glucosidase inhibitors and gut bacteria Î±â€¢glucosidase. <i>Protein Science</i> , 2018, 27, 1498-1508.	3.1	37
64	Insights from the Structure of <i>Mycobacterium tuberculosis</i> Topoisomerase I with a Novel Protein Fold. <i>Journal of Molecular Biology</i> , 2016, 428, 182-193.	2.0	36
65	Predicting protein crystallization propensity from protein sequence. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 71-80.	1.2	35
66	Structural and Functional Analysis of Human HtrA3 Protease and Its Subdomains. <i>PLoS ONE</i> , 2015, 10, e0131142.	1.1	35
67	<i>Mycobacterium tuberculosis</i> IMPDH in Complexes with Substrates, Products and Antitubercular Compounds. <i>PLoS ONE</i> , 2015, 10, e0138976.	1.1	35
68	Structures of open (R) and close (T) states of prephenate dehydratase (PDT)â€¢Implication of allosteric regulation by l-phenylalanine. <i>Journal of Structural Biology</i> , 2008, 162, 94-107.	1.3	34
69	Crystal structure of secretory protein Hcp3 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 21-26.	1.2	34
70	Heparin-induced cis- and trans-Dimerization Modes of the Thrombospondin-1 N-terminal Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 3932-3941.	1.6	33
71	The crystal structure of BlmI as a model for nonribosomal peptide synthetase peptidyl carrier proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1210-1218.	1.5	33
72	Expanding Benzoxazole-Based Inosine 5â€²-Monophosphate Dehydrogenase (IMPDH) Inhibitor Structureâ€¢Activity As Potential Antituberculosis Agents. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4739-4756.	2.9	33

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73	Crystal structure of <i>Bacillus anthracis</i> virulence regulator <i>AtxA</i> and effects of phosphorylated histidines on multimerization and activity. <i>Molecular Microbiology</i> , 2015, 95, 426-441.	1.2	32
74	<i>Bacillus anthracis</i> Inosine 5'-Monophosphate Dehydrogenase in Action: The First Bacterial Series of Structures of Phosphate Ion-, Substrate-, and Product-Bound Complexes. <i>Biochemistry</i> , 2012, 51, 6148-6163.	1.2	31
75	A Novel Cofactor-binding Mode in Bacterial IMP Dehydrogenases Explains Inhibitor Selectivity. <i>Journal of Biological Chemistry</i> , 2015, 290, 5893-5911.	1.6	31
76	A microbial sensor for organophosphate hydrolysis exploiting an engineered specificity switch in a transcription factor. <i>Nucleic Acids Research</i> , 2016, 44, 8490-8500.	6.5	31
77	Covering complete proteomes with X-ray structures: a current snapshot. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2781-2793.	2.5	30
78	The CDI toxin of <i>Yersinia kristensenii</i> is a novel bacterial member of the RNase A superfamily. <i>Nucleic Acids Research</i> , 2017, 45, 5013-5025.	6.5	30
79	The CRISPR-associated Cas4 protein Pcal_0546 from <i>Pyrobaculum calidifontis</i> contains a [2Fe-2S] cluster: crystal structure and nuclease activity. <i>Nucleic Acids Research</i> , 2014, 42, 11144-11155.	6.5	29
80	Structure of <i>Calcarisporiella thermophila</i> Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. <i>Structure</i> , 2019, 27, 449-463.e7.	1.6	29
81	A Disulfide Bond-forming Machine Is Linked to the Sortase-mediated Pilus Assembly Pathway in the Gram-positive Bacterium <i>Actinomyces oris</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 21393-21405.	1.6	28
82	Crystal Structure of <i>Bacillus anthracis</i> Transpeptidase Enzyme CapD. <i>Journal of Biological Chemistry</i> , 2009, 284, 24406-24414.	1.6	27
83	Biochemical and Structural Analysis of an Eis Family Aminoglycoside Acetyltransferase from <i>Bacillus anthracis</i> . <i>Biochemistry</i> , 2015, 54, 3197-3206.	1.2	27
84	In vitro reconstitution of sortase-catalyzed pilus polymerization reveals structural elements involved in pilin cross-linking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5477-E5486.	3.3	27
85	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
86	A novel transcriptional regulator of L-arabinose utilization in human gut bacteria. <i>Nucleic Acids Research</i> , 2015, 43, gkv1005.	6.5	26
87	Functional plasticity of antibacterial EndoU toxins. <i>Molecular Microbiology</i> , 2018, 109, 509-527.	1.2	25
88	Allosteric inhibitors of <i>Mycobacterium tuberculosis</i> tryptophan synthase. <i>Protein Science</i> , 2020, 29, 779-788.	3.1	25
89	Protein Production for Structural Genomics Using <i>E. coli</i> Expression. <i>Methods in Molecular Biology</i> , 2014, 1140, 89-105.	0.4	25
90	A Novel Polyamine Allosteric Site of SpeG from <i>Vibrio cholerae</i> Is Revealed by Its Dodecameric Structure. <i>Journal of Molecular Biology</i> , 2015, 427, 1316-1334.	2.0	24

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91	A structural insight into the P1 S1 binding mode of diaminoethylphosphonic and phosphinic acids, selective inhibitors of alanine aminopeptidases. <i>European Journal of Medicinal Chemistry</i> , 2016, 117, 187-196.	2.6	24
92	Differential Signatures of Bacterial and Mammalian IMP Dehydrogenase Enzymes. <i>Current Medicinal Chemistry</i> , 1999, 6, 537-543.	1.2	24
93	<i>Streptococcus pneumoniae</i> YlxR at 1.35 Å shows a putative new fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1747-1751.	2.5	23
94	Characterization of Transport Proteins for Aromatic Compounds Derived from Lignin: Benzoate Derivative Binding Proteins. <i>Journal of Molecular Biology</i> , 2012, 423, 555-575.	2.0	23
95	Structure of a novel antibacterial toxin that exploits elongation factor Tu to cleave specific transfer RNAs. <i>Nucleic Acids Research</i> , 2017, 45, 10306-10320.	6.5	23
96	Investigating mycobacterial topoisomerase I mechanism from the analysis of metal and DNA substrate interactions at the active site. <i>Nucleic Acids Research</i> , 2018, 46, 7296-7308.	6.5	23
97	Characterization and Crystal Structure of a Nonheme Diiron Monooxygenase Involved in Platensimycin and Platencin Biosynthesis. <i>Journal of the American Chemical Society</i> , 2019, 141, 12406-12412.	6.6	23
98	Evolution of substrate specificity in a retained enzyme driven by gene loss. <i>ELife</i> , 2017, 6, .	2.8	23
99	Target Selection and Determination of Function in Structural Genomics. <i>IUBMB Life</i> , 2003, 55, 249-255.	1.5	22
100	New aminopeptidase from a microbial dark matter archaeon. <i>FASEB Journal</i> , 2015, 29, 4071-4079.	0.2	22
101	Convergent Evolution of the Barnase/EndoU/Colicin/RelE (BECR) Fold in Antibacterial tRNase Toxins. <i>Structure</i> , 2019, 27, 1660-1674.e5.	1.6	22
102	How Aromatic Compounds Block DNA Binding of HcaR Catabolite Regulator. <i>Journal of Biological Chemistry</i> , 2016, 291, 13243-13256.	1.6	21
103	Resistance to Eneidine Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , 2018, 25, 1075-1085.e4.	2.5	21
104	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. <i>Nature Chemical Biology</i> , 2018, 14, 730-737.	3.9	21
105	Cell-to-cell interaction requires optimal positioning of a pilus tip adhesin modulated by gram-positive transpeptidase enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18041-18049.	3.3	21
106	Structural and biochemical analysis of the metallo-β-lactamase L1 from emerging pathogen <i>Stenotrophomonas maltophilia</i> revealed the subtle but distinct di-metal scaffold for catalytic activity. <i>Protein Science</i> , 2020, 29, 723-743.	3.1	20
107	The dapE-encoded N-succinyl-L, l-diaminopimelic acid desuccinylase from <i>Haemophilus influenzae</i> contains two active-site histidine residues. <i>Journal of Biological Inorganic Chemistry</i> , 2009, 14, 1-10.	1.1	19
108	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 6-20.	1.5	19

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109	[7] Crystallization of protein-DNA complexes. <i>Methods in Enzymology</i> , 1991, 208, 82-99.	0.4	18
110	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Eneidyne Antitumor Antibiotic C-1027 in <i>Streptomyces globisporus</i> . <i>Biochemistry</i> , 2016, 55, 5142-5154.	1.2	18
111	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. <i>Current Research in Structural Biology</i> , 2020, 2, 14-24.	1.1	18
112	Inhibition of the <i>dapE</i> -Encoded <i>N</i> -Succinyl-L-diaminopimelic Acid Desuccinylase from <i>Neisseria meningitidis</i> by Captopril. <i>Biochemistry</i> , 2015, 54, 4834-4844.	1.2	17
113	The Dimerization Domain in DapE Enzymes Is required for Catalysis. <i>PLoS ONE</i> , 2014, 9, e93593.	1.1	17
114	Therapeutic genetic variation revealed in diverse Hsp104 homologs. <i>ELife</i> , 2020, 9, .	2.8	17
115	Structural Evidence of a Major Conformational Change Triggered by Substrate Binding in DapE Enzymes: Impact on the Catalytic Mechanism. <i>Biochemistry</i> , 2018, 57, 574-584.	1.2	16
116	Functional Profiling and Crystal Structures of Isothiocyanate Hydrolases Found in Gut-Associated and Plant-Pathogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
117	Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein. <i>MAbs</i> , 2021, 13, 1905978.	2.6	16
118	Purification of chaperonins from thermophilic bacteria and archaea. <i>Journal of Chromatography A</i> , 1997, 773, 131-138.	1.8	14
119	The Mannitol Operon Repressor MtlR Belongs to a New Class of Transcription Regulators in Bacteria. <i>Journal of Biological Chemistry</i> , 2009, 284, 36670-36679.	1.6	14
120	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , 2014, 9, e101787.	1.1	13
121	Conservation of the structure and function of bacterial tryptophan synthases. <i>IUCr</i> , 2019, 6, 649-664.	1.0	13
122	Substrate-Induced Allosteric Change in the Quaternary Structure of the Spermidine N-Acetyltransferase SpeG. <i>Journal of Molecular Biology</i> , 2015, 427, 3538-3553.	2.0	12
123	EsxB, a secreted protein from <i>Bacillus anthracis</i> forms two distinct helical bundles. <i>Protein Science</i> , 2015, 24, 1389-1400.	3.1	12
124	Loop-to-helix transition in the structure of multidrug regulator AcrR at the entrance of the drug-binding cavity. <i>Journal of Structural Biology</i> , 2016, 194, 18-28.	1.3	12
125	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	1.5	12
126	The crystal structures of the $\hat{1}\pm$ -subunit of the $\hat{1}\pm 2\hat{1}^2$ tetrameric Glycyl-tRNA synthetase. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 233-239.	1.2	11

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127	Sensor Domain of Histidine Kinase KinB of Pseudomonas. <i>Journal of Biological Chemistry</i> , 2014, 289, 12232-12244.	1.6	11
128	Structure of <i>Cryptosporidium</i> IMP dehydrogenase bound to an inhibitor with <i>in vivo</i> antiparasitic activity. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 531-538.	0.4	11
129	Target highlights from the first post-PSI CASP experiment (CASP12, May–August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
130	Structural genomics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021, 296, 100747.	1.6	11
131	Structural characterization of AtmS13, a putative sugar aminotransferase involved in indolocarbazole AT2433 aminopentose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1547-1554.	1.5	10
132	Crystal Structure of Thioesterase SgcE10 Supporting Common Polyene Intermediates in 9- and 10-Membered Eneidyne Core Biosynthesis. <i>ACS Omega</i> , 2017, 2, 5159-5169.	1.6	10
133	Structural Insights into the Free-Standing Condensation Enzyme SgcC5 Catalyzing Ester-Bond Formation in the Biosynthesis of the Eneidyne Antitumor Antibiotic C-1027. <i>Biochemistry</i> , 2018, 57, 3278-3288.	1.2	10
134	Conserved residue His-257 of <i>Vibrio cholerae</i> flavin transferase ApbE plays a critical role in substrate binding and catalysis. <i>Journal of Biological Chemistry</i> , 2019, 294, 13800-13810.	1.6	10
135	Improved integration of single-cell transcriptome and surface protein expression by LinQ-View. <i>Cell Reports Methods</i> , 2021, 1, 100056.	1.4	10
136	Enhanced crystal packing due to solvent reorganization through reductive methylation of lysine residues in oxidoreductase from <i>Streptococcus pneumoniae</i> . <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 101-111.	1.2	9
137	Crystal Structures of the F and pSLT Plasmid TraJ N-Terminal Regions Reveal Similar Homodimeric PAS Folds with Functional Interchangeability. <i>Biochemistry</i> , 2014, 53, 5810-5819.	1.2	9
138	Crystal Structure of the Zorbamycin-Binding Protein ZbmA, the Primary Self-Resistance Element in <i>Streptomyces flavoviridis</i> ATCC21892. <i>Biochemistry</i> , 2015, 54, 6842-6851.	1.2	9
139	Insights into PG-binding, conformational change, and dimerization of the OmpA C-terminal domains from <i>Salmonella enterica</i> serovar Typhimurium and <i>Borrelia burgdorferi</i> . <i>Protein Science</i> , 2017, 26, 1738-1748.	3.1	8
140	Structural Basis of a Thiol-Disulfide Oxidoreductase in the Hedgehog-Forming Actinobacterium <i>Corynebacterium matruchotii</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	8
141	Bisphosphonic acids and related compounds as inhibitors of nucleotide- and polyphosphate-processing enzymes: A PPK1 and PPK2 case study. <i>Chemical Biology and Drug Design</i> , 2019, 93, 1197-1206.	1.5	8
142	Crystal structure of the hypothetical protein TA1238 from <i>Thermoplasma acidophilum</i> : a new type of helical super-bundle. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 231-240.	1.2	7
143	Structural analysis of free and liganded forms of the Fab fragment of a high-affinity anti-cocaine antibody, h2E2. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 697-706.	0.4	7
144	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. <i>Current Protein and Peptide Science</i> , 2017, 19, 200-210.	0.7	7

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