Andrzej Joachimiak

List of Publications by Citations

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175 papers	8,840 citations	42 h-index	90 g-index
186 ext. papers	10,334 ext. citations	7.6 avg, IF	5.8 L-index

#	Paper	IF	Citations
175	The crystal structure of the bacterial chaperonin GroEL at 2.8 A. *Nature*, **1994**, 371, 578-86	50.4	1250
174	A virulence locus of Pseudomonas aeruginosa encodes a protein secretion apparatus. *Science*, **2006**, 312, 1526-30	33.3	787
173	Protein production and purification. *Nature Methods*, **2008**, 5, 135-46	21.6	655
172	Structure of a bacterial quorum-sensing transcription factor complexed with pheromone and DNA. *Nature*, **2002**, 417, 971-4	50.4	381
171	The three-dimensional structure of trp repressor. *Nature*, **1985**, 317, 782-6	50.4	352
170	Crystal structure of the TSP-1 type 1 repeats: a novel layered fold and its biological implication. *Journal of Cell Biology*, **2002**, 159, 373-82	7.3	214
169	A family of LIC vectors for high-throughput cloning and purification of proteins. *Methods in Molecular Biology*, **2009**, 498, 105-15	1.4	202
168	Crystal structure of Nsp15 endoribonuclease NendoU from SARS-CoV-2. *Protein Science*, **2020**, 29, 1596-1605	6.9	199
167	Structural plasticity of SARS-CoV-2 3CL M active site cavity revealed by room temperature X-ray crystallography. *Nature Communications*, **2020**, 11, 3202	17.4	185
166	Characteristics and crystal structure of bacterial inosine-5Smonophosphate dehydrogenase. *Biochemistry*, **1999**, 38, 4691-700	3.2	157
165	An expression vector tailored for large-scale, high-throughput purification of recombinant proteins. *Protein Expression and Purification*, **2006**, 47, 446-54	2	149
164	Flexibility of the DNA-binding domains of trp repressor. *Proteins: Structure, Function and Bioinformatics*, **1988**, 3, 18-31	4.2	134
163	The Structural Biology Center 19ID undulator beamline: facility specifications and protein crystallographic results. *Journal of Synchrotron Radiation*, **2006**, 13, 30-45	2.4	124
162	NFkappaB selectivity of estrogen receptor ligands revealed by comparative crystallographic analyses. *Nature Chemical Biology*, **2008**, 4, 241-7	11.7	123
161	Structure of papain-like protease from SARS-CoV-2 and its complexes with non-covalent inhibitors. *Nature Communications*, **2021**, 12, 743	17.4	121
160	High-throughput protein purification and quality assessment for crystallization. *Methods*, **2011**, 55, 12-28	4.6	110
159	High-throughput crystallography for structural genomics. *Current Opinion in Structural Biology*, **2009**, 19, 573-84	8.1	100

(2002-2004)

158	Automation of protein purification for structural genomics. *Journal of Structural and Functional Genomics*, **2004**, 5, 111-8		96
157	NDM-1, the ultimate promiscuous enzyme: substrate recognition and catalytic mechanism. *FASEB Journal*, **2013**, 27, 1917-27	0.9	91
156	Taking MAD to the extreme: ultrafast protein structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1168-73		88
155	The 60 kDa heat shock proteins in the hyperthermophilic archaeon Sulfolobus shibatae. *Journal of Molecular Biology*, **1995**, 253, 712-25	6.5	87
154	Structural insight into the mechanism of c-di-GMP hydrolysis by EAL domain phosphodiesterases. *Journal of Molecular Biology*, **2010**, 402, 524-38	6.5	86
153	Towards fully automated structure-based function prediction in structural genomics: a case study. *Journal of Molecular Biology*, **2007**, 367, 1511-22	6.5	76
152	A conformational switch controls cell wall-remodelling enzymes required for bacterial cell division. *Molecular Microbiology*, **2012**, 85, 768-81	4.1	75
151	A small-molecule allosteric inhibitor of Mycobacterium tuberculosis tryptophan synthase. *Nature Chemical Biology*, **2017**, 13, 943-950	11.7	75
150	Structure of apo- and monometalated forms of NDM-1--a highly potent carbapenem-hydrolyzing metallo-□lactamase. *PLoS ONE*, **2011**, 6, e24621	3.7	73
149	New antiviral target revealed by the hexameric structure of mouse hepatitis virus nonstructural protein nsp15. *Journal of Virology*, **2006**, 80, 7909-17	6.6	70
148	The structures of the thrombospondin-1 N-terminal domain and its complex with a synthetic pentameric heparin. *Structure*, **2006**, 14, 33-42	5.2	69
147	Characterization of a Bacillus subtilis transporter for petrobactin, an anthrax stealth siderophore. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 21854-9	11.5	68
146	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. *Biomacromolecules*, **2016**, 17, 2027-39	6.9	68
145	The structure of the yrdC gene product from Escherichia coli reveals a new fold and suggests a role in RNA binding. *Protein Science*, **2000**, 9, 2557-66	6.3	65
144	Optimization of benzoxazole-based inhibitors of Cryptosporidium parvum inosine 5Smonophosphate dehydrogenase. *Journal of Medicinal Chemistry*, **2013**, 56, 4028-43	8.3	64
143	Three conformations of an archaeal chaperonin, TF55 from Sulfolobus shibatae. *Journal of Molecular Biology*, **2000**, 296, 813-9	6.5	64
142	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. *IUCrJ*, **2020**, 7, 814-824	4.7	59
141	Crystal structure of Thermotoga maritima 0065, a member of the IclR transcriptional factor family. *Journal of Biological Chemistry*, **2002**, 277, 19183-90	5.4	58

140	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. *Structure*, **2008**, 16, 5-11	5.2	55
139	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae: BIOCHEMICAL, STRUCTURAL, AND EVOLUTIONARY INSIGHTS. *Journal of Biological Chemistry*, **2015**, 290, 18678-98	5.4	52
138	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. *Science*, **2021**, 373, 931-936	33.3	49
137	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. *Scientific Reports*, **2017**, 7, 44103	4.9	48
136	SARS-CoV-2 Infection Severity Is Linked to Superior Humoral Immunity against the Spike. *MBio*, **2021**, 12,	7.8	46
135	Structural basis for catalysis by the mono- and dimetalated forms of the dapE-encoded N-succinyl-L,L-diaminopimelic acid desuccinylase. *Journal of Molecular Biology*, **2010**, 397, 617-26	6.5	42
134	Structure and recognition of sheared tandem G x A base pairs associated with human centromere DNA sequence at atomic resolution. *Biochemistry*, **1999**, 38, 16452-60	3.2	42
133	Toroidal structure and DNA cleavage by the CRISPR-associated [4Fe-4S] cluster containing Cas4 nuclease SSO0001 from Sulfolobus solfataricus. *Journal of the American Chemical Society*, **2013**, 135, 17476-87	16.4	41
132	Conformational cycle of the archaeosome, a TCP1-like chaperonin from Sulfolobus shibatae. *Journal of Biological Chemistry*, **1995**, 270, 28818-23	5.4	40
131	Structural and evolutionary relationships of "AT-less" type I polyketide synthase ketosynthases. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 12693-8	11.5	38
130	New LIC vectors for production of proteins from genes containing rare codons. *Journal of Structural and Functional Genomics*, **2013**, 14, 135-44		38
129	Structure of cyclin G-associated kinase (GAK) trapped in different conformations using nanobodies. *Biochemical Journal*, **2014**, 459, 59-69	3.8	36
128	Tipiracil binds to uridine site and inhibits Nsp15 endoribonuclease NendoU from SARS-CoV-2. *Communications Biology*, **2021**, 4, 193	6.7	36
127	Structural basis for suppression of hypernegative DNA supercoiling by E. coli topoisomerase I. *Nucleic Acids Research*, **2015**, 43, 11031-46	20.1	35
126	Profiling B cell immunodominance after SARS-CoV-2 infection reveals antibody evolution to non-neutralizing viral targets. *Immunity*, **2021**, 54, 1290-1303.e7	32.3	35
125	Cleavable C-terminal His-tag vectors for structure determination. *Journal of Structural and Functional Genomics*, **2010**, 11, 31-9		33
124	Crystal structure of secretory protein Hcp3 from Pseudomonas aeruginosa. *Journal of Structural and Functional Genomics*, **2011**, 12, 21-6		32
123	Roles of intramolecular and intermolecular interactions in functional regulation of the Hsp70 J-protein co-chaperone Sis1. *Journal of Molecular Biology*, **2015**, 427, 1632-43	6.5	31

122	The crystal structure of BlmI as a model for nonribosomal peptide synthetase peptidyl carrier proteins. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82, 1210-8	4.2	31
121	Structures of open (R) and close (T) states of prephenate dehydratase (PDT)--implication of allosteric regulation by L-phenylalanine. *Journal of Structural Biology*, **2008**, 162, 94-107	3.4	31
120	Molecular Mechanism of Inhibition of Acid Ceramidase by Carmofur. *Journal of Medicinal Chemistry*, **2019**, 62, 987-992	8.3	30
119	Mitochondrial Hsp90 is a ligand-activated molecular chaperone coupling ATP binding to dimer closure through a coiled-coil intermediate. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 2952-7	11.5	29
118	Covering complete proteomes with X-ray structures: a current snapshot. *Acta Crystallographica Section D: Biological Crystallography*, **2014**, 70, 2781-93		29
117	Predicting protein crystallization propensity from protein sequence. *Journal of Structural and Functional Genomics*, **2010**, 11, 71-80		29
116	Structure of the ent-Copalyl Diphosphate Synthase PtmT2 from Streptomyces platensis CB00739, a Bacterial Type II Diterpene Synthase. *Journal of the American Chemical Society*, **2016**, 138, 10905-15	16.4	29
115	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. *Environmental Science & Technology*, **2018**, 52, 12388-12401	10.3	28
114	Structural and Functional Analysis of Human HtrA3 Protease and Its Subdomains. *PLoS ONE*, **2015**, 10, e0131142	3.7	27
113	Heparin-induced cis- and trans-dimerization modes of the thrombospondin-1 N-terminal domain. *Journal of Biological Chemistry*, **2008**, 283, 3932-41	5.4	27
112	Room-temperature X-ray crystallography reveals the oxidation and reactivity of cysteine residues in SARS-CoV-2 3CL M: insights into enzyme mechanism and drug design. *IUCrJ*, **2020**, 7,	4.7	27
111	Mycobacterium tuberculosis IMPDH in Complexes with Substrates, Products and Antitubercular Compounds. *PLoS ONE*, **2015**, 10, e0138976	3.7	27
110	The crystal structure of nsp10-nsp16 heterodimer from SARS-CoV-2 in complex with S-adenosylmethionine **2020**,		27
109	A family of metal-dependent phosphatases implicated in metabolite damage-control. *Nature Chemical Biology*, **2016**, 12, 621-7	11.7	26
108	Expanding Benzoxazole-Based Inosine 5SMonophosphate Dehydrogenase (IMPDH) Inhibitor Structure-Activity As Potential Antituberculosis Agents. *Journal of Medicinal Chemistry*, **2018**, 61, 4739-4756	8.3	26
107	A thiol-disulfide oxidoreductase of the Gram-positive pathogen Corynebacterium diphtheriae is essential for viability, pilus assembly, toxin production and virulence. *Molecular Microbiology*, **2015**, 98, 1037-50	4.1	26
106	A novel cofactor-binding mode in bacterial IMP dehydrogenases explains inhibitor selectivity. *Journal of Biological Chemistry*, **2015**, 290, 5893-911	5.4	25
105	A Disulfide Bond-forming Machine Is Linked to the Sortase-mediated Pilus Assembly Pathway in the Gram-positive Bacterium Actinomyces oris. *Journal of Biological Chemistry*, **2015**, 290, 21393-405	5.4	25

104	Crystal structure of Bacillus anthracis virulence regulator AtxA and effects of phosphorylated histidines on multimerization and activity. *Molecular Microbiology*, **2015**, 95, 426-41	4.1	25
103	The CRISPR-associated Cas4 protein Pcal_0546 from Pyrobaculum calidifontis contains a [2Fe-2S] cluster: crystal structure and nuclease activity. *Nucleic Acids Research*, **2014**, 42, 11144-55	20.1	25
102	Bacillus anthracis inosine 5Smonophosphate dehydrogenase in action: the first bacterial series of structures of phosphate ion-, substrate-, and product-bound complexes. *Biochemistry*, **2012**, 51, 6148-63	3.2	24
101	Insights from the Structure of Mycobacterium tuberculosis Topoisomerase I with a Novel Protein Fold. *Journal of Molecular Biology*, **2016**, 428, 182-193	6.5	23
100	Structural Insights into Substrate Selectivity and Activity of Bacterial Polyphosphate Kinases. *ACS Catalysis*, **2018**, 8, 10746-10760	13.1	23
99	Characterization of transport proteins for aromatic compounds derived from lignin: benzoate derivative binding proteins. *Journal of Molecular Biology*, **2012**, 423, 555-75	6.5	22
98	Crystal structure of Bacillus anthracis transpeptidase enzyme CapD. *Journal of Biological Chemistry*, **2009**, 284, 24406-14	5.4	22
97	Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. *Structure*, **2019**, 27, 449-463.e7	5.2	22
96	Biochemical and structural analysis of an Eis family aminoglycoside acetyltransferase from bacillus anthracis. *Biochemistry*, **2015**, 54, 3197-206	3.2	21
95	A microbial sensor for organophosphate hydrolysis exploiting an engineered specificity switch in a transcription factor. *Nucleic Acids Research*, **2016**, 44, 8490-500	20.1	21
94	The CDI toxin of Yersinia kristensenii is a novel bacterial member of the RNase A superfamily. *Nucleic Acids Research*, **2017**, 45, 5013-5025	20.1	20
93	A structural insight into the P1S1 binding mode of diaminoethylphosphonic and phosphinic acids, selective inhibitors of alanine aminopeptidases. *European Journal of Medicinal Chemistry*, **2016**, 117, 187-96	6.8	20
92	Functional plasticity of antibacterial EndoU toxins. *Molecular Microbiology*, **2018**, 109, 509-527	4.1	20
91	A novel polyamine allosteric site of SpeG from Vibrio cholerae is revealed by its dodecameric structure. *Journal of Molecular Biology*, **2015**, 427, 1316-1334	6.5	19
90	Evolution of substrate specificity in a retained enzyme driven by gene loss. *ELife*, **2017**, 6,	8.9	19
89	Protein production for structural genomics using E. coli expression. *Methods in Molecular Biology*, **2014**, 1140, 89-105	1.4	19
88	Differential Signatures of Bacterial and Mammalian IMP Dehydrogenase Enzymest. *Current Medicinal Chemistry*, **1999**, 6, 537-543	4.3	19
87	Target selection and determination of function in structural genomics. *IUBMB Life*, **2003**, 55, 249-55	4.7	18

86	Crystallization of protein-DNA complexes. *Methods in Enzymology*, **1991**, 208, 82-99	1.7	18
85	Interaction of antidiabetic glucosidase inhibitors and gut bacteria glucosidase. *Protein Science*, **2018**, 27, 1498-1508	6.3	18
84	A novel transcriptional regulator of L-arabinose utilization in human gut bacteria. *Nucleic Acids Research*, **2015**, 43, 10546-59	20.1	17
83	Investigating mycobacterial topoisomerase I mechanism from the analysis of metal and DNA substrate interactions at the active site. *Nucleic Acids Research*, **2018**, 46, 7296-7308	20.1	16
82	Streptococcus pneumonia YlxR at 1.35 A shows a putative new fold. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1747-51		16
81	Crystal Structures of SgcE6 and SgcC, the Two-Component Monooxygenase That Catalyzes Hydroxylation of a Carrier Protein-Tethered Substrate during the Biosynthesis of the Enediyne Antitumor Antibiotic C-1027 in Streptomyces globisporus. *Biochemistry*, **2016**, 55, 5142-54	3.2	15
80	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. *Nature Chemical Biology*, **2018**, 14, 730-737	11.7	15
79	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 6-20	4.2	15
78	Structure of a novel antibacterial toxin that exploits elongation factor Tu to cleave specific transfer RNAs. *Nucleic Acids Research*, **2017**, 45, 10306-10320	20.1	14
77	Resistance to Enediyne Antitumor Antibiotics by Sequestration. *Cell Chemical Biology*, **2018**, 25, 1075-1085.e4	8.2	14
76	Characterization and Crystal Structure of a Nonheme Diiron Monooxygenase Involved in Platensimycin and Platencin Biosynthesis. *Journal of the American Chemical Society*, **2019**, 141, 12406-12412	16.4	14
75	The dapE-encoded N-succinyl-L,L-diaminopimelic acid desuccinylase from Haemophilus influenzae contains two active-site histidine residues. *Journal of Biological Inorganic Chemistry*, **2009**, 14, 1-10	3.7	14
74	How Aromatic Compounds Block DNA Binding of HcaR Catabolite Regulator. *Journal of Biological Chemistry*, **2016**, 291, 13243-56	5.4	14
73	Cell-to-cell interaction requires optimal positioning of a pilus tip adhesin modulated by gram-positive transpeptidase enzymes. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 18041-18049	11.5	13
72	Convergent Evolution of the Barnase/EndoU/Colicin/RelE (BECR) Fold in Antibacterial tRNase Toxins. *Structure*, **2019**, 27, 1660-1674.e5	5.2	13
71	2SO methylation of RNA cap in SARS-CoV-2 captured by serial crystallography. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	13
70	Inhibition of the dapE-Encoded N-Succinyl-L,L-diaminopimelic Acid Desuccinylase from Neisseria meningitidis by L-Captopril. *Biochemistry*, **2015**, 54, 4834-44	3.2	12
69	Allosteric inhibitors of Mycobacterium tuberculosis tryptophan synthase. *Protein Science*, **2020**, 29, 779-788	6.3	12

68	The mannitol operon repressor MtlR belongs to a new class of transcription regulators in bacteria. *Journal of Biological Chemistry*, **2009**, 284, 36670-36679	5.4	12
67	Structure of Cryptosporidium IMP dehydrogenase bound to an inhibitor with in vivo antiparasitic activity. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 531-8	1.1	11
66	Structural and biochemical analysis of the metallo-βlactamase L1 from emerging pathogen Stenotrophomonas maltophilia revealed the subtle but distinct di-metal scaffold for catalytic activity. *Protein Science*, **2020**, 29, 723-743	6.3	11
65	In vitro reconstitution of sortase-catalyzed pilus polymerization reveals structural elements involved in pilin cross-linking. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E5477-E5486	11.5	11
64	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. *Biophysical Journal*, **2021**, 120, 3152-3165	2.9	11
63	New aminopeptidase from "microbial dark matter" archaeon. *FASEB Journal*, **2015**, 29, 4071-9	0.9	10
62	Loop-to-helix transition in the structure of multidrug regulator AcrR at the entrance of the drug-binding cavity. *Journal of Structural Biology*, **2016**, 194, 18-28	3.4	10
61	The dimerization domain in DapE enzymes is required for catalysis. *PLoS ONE*, **2014**, 9, e93593	3.7	10
60	Target highlights in CASP13: Experimental target structures through the eyes of their authors. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1037-1057	4.2	9
59	Structural Insights into the Free-Standing Condensation Enzyme SgcC5 Catalyzing Ester-Bond Formation in the Biosynthesis of the Enediyne Antitumor Antibiotic C-1027. *Biochemistry*, **2018**, 57, 3278-3288	3.2	9
58	Functional Profiling and Crystal Structures of Isothiocyanate Hydrolases Found in Gut-Associated and Plant-Pathogenic Bacteria. *Applied and Environmental Microbiology*, **2018**, 84,	4.8	9
57	Substrate-Induced Allosteric Change in the Quaternary Structure of the Spermidine N-Acetyltransferase SpeG. *Journal of Molecular Biology*, **2015**, 427, 3538-3553	6.5	9
56	Structural characterization of AtmS13, a putative sugar aminotransferase involved in indolocarbazole AT2433 aminopentose biosynthesis. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1547-54	4.2	9
55	Crystal Structure of the Zorbamycin-Binding Protein ZbmA, the Primary Self-Resistance Element in Streptomyces flavoviridis ATCC21892. *Biochemistry*, **2015**, 54, 6842-51	3.2	8
54	Structural and functional characterization of DUF1471 domains of Salmonella proteins SrfN, YdgH/SssB, and YahO. *PLoS ONE*, **2014**, 9, e101787	3.7	8
53	Enhanced crystal packing due to solvent reorganization through reductive methylation of lysine residues in oxidoreductase from Streptococcus pneumoniae. *Journal of Structural and Functional Genomics*, **2010**, 11, 101-11		8
52	Purification of chaperonins from thermophilic bacteria and archaea. *Journal of Chromatography A*, **1997**, 773, 131-138	4.5	8
51	Tipiracil binds to uridine site and inhibits Nsp15 endoribonuclease NendoU from SARS-CoV-2		8

50	Structural Evidence of a Major Conformational Change Triggered by Substrate Binding in DapE Enzymes: Impact on the Catalytic Mechanism. *Biochemistry*, **2018**, 57, 574-584	3.2	7
49	EsxB, a secreted protein from Bacillus anthracis forms two distinct helical bundles. *Protein Science*, **2015**, 24, 1389-400	6.3	7
48	The crystal structures of the □subunit of the □(2)□(2) tetrameric Glycyl-tRNA synthetase. *Journal of Structural and Functional Genomics*, **2012**, 13, 233-9		7
47	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		7
46	SARS-CoV-2 infection severity is linked to superior humoral immunity against the spike **2020**,		7
45	Target highlights in CASP14: Analysis of models by structure providers. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1647-1672	4.2	7
44	Insights into PG-binding, conformational change, and dimerization of the OmpA C-terminal domains from Salmonella enterica serovar Typhimurium and Borrelia burgdorferi. *Protein Science*, **2017**, 26, 1738-1748	6.3	6
43	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. *Current Research in Structural Biology*, **2020**, 2, 14-24	2.8	6
42	Structural Basis of a Thiol-Disulfide Oxidoreductase in the Hedgehog-Forming Actinobacterium Corynebacterium matruchotii. *Journal of Bacteriology*, **2018**, 200,	3.5	6
41	Sensor domain of histidine kinase KinB of Pseudomonas: a helix-swapped dimer. *Journal of Biological Chemistry*, **2014**, 289, 12232-44	5.4	6
40	Conservation of the structure and function of bacterial tryptophan synthases. *IUCrJ*, **2019**, 6, 649-664	4.7	6
39	Survey of Predictors of Propensity for Protein Production and Crystallization with Application to Predict Resolution of Crystal Structures. *Current Protein and Peptide Science*, **2018**, 19, 200-210	2.8	6
38	Therapeutic genetic variation revealed in diverse Hsp104 homologs. *ELife*, **2020**, 9,	8.9	6
37	Co-occurrence of analogous enzymes determines evolution of a novel (□)8-isomerase sub-family after non-conserved mutations in flexible loop. *Biochemical Journal*, **2016**, 473, 1141-52	3.8	6
36	Bisphosphonic acids and related compounds as inhibitors of nucleotide- and polyphosphate-processing enzymes: A PPK1 and PPK2 case study. *Chemical Biology and Drug Design* , **2019**, 93, 1197-1206	2.9	6
35	Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein. *MAbs*, **2021**, 13, 1905978	6.6	6
34	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 27-50	4.2	5
33	Conserved residue His-257 of flavin transferase ApbE plays a critical role in substrate binding and catalysis. *Journal of Biological Chemistry*, **2019**, 294, 13800-13810	5.4	5

32	Crystal structures of the F and pSLT plasmid TraJ N-terminal regions reveal similar homodimeric PAS folds with functional interchangeability. *Biochemistry*, **2014**, 53, 5810-9	3.2	5
31	Crystal Structure of Thioesterase SgcE10 Supporting Common Polyene Intermediates in 9- and 10-Membered Enediyne Core Biosynthesis. *ACS Omega*, **2017**, 2, 5159-5169	3.9	5
30	Structural analysis of free and liganded forms of the Fab fragment of a high-affinity anti-cocaine antibody, h2E2. *Acta Crystallographica Section F, Structural Biology Communications*, **2019**, 75, 697-706	1.1	5
29	Structural dynamics of a methionine □lyase for calicheamicin biosynthesis: Rotation of the conserved tyrosine stacking with pyridoxal phosphate. *Structural Dynamics*, **2016**, 3, 034702	3.2	4
28	Potent and Selective Covalent Inhibitors of the Papain-like Protease from SARS-CoV-2 **2021**,		4
27	Catalytically impaired TrpA subunit of tryptophan synthase from Chlamydia trachomatis is an allosteric regulator of TrpB. *Protein Science*, **2021**, 30, 1904-1918	6.3	4
26	X-ray crystal structures of the pheromone-binding domains of two quorum-hindered transcription factors, YenR of Yersinia enterocolitica and CepR2 of Burkholderia cenocepacia. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 1831-1844	4.2	3
25	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. *Methods in Enzymology*, **2021**, 661, 407-431	1.7	3
24	Structural genomics and the Protein Data Bank. *Journal of Biological Chemistry*, **2021**, 296, 100747	5.4	3
23	Structural Characterization of CalS8, a TDP-□D-Glucose Dehydrogenase Involved in Calicheamicin Aminodideoxypentose Biosynthesis. *Journal of Biological Chemistry*, **2015**, 290, 26249-58	5.4	2
22	Structure of a cupin protein Plu4264 from Photorhabdus luminescens subsp. laumondii TTO1 at 1.35 □resolution. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 383-8	4.2	2
21	Purification of chaperonins. *Biomedical Applications*, **1999**, 722, 153-77		2
20	3D domain swapping in the TIM barrel of the □subunit of Streptococcus pneumoniae tryptophan synthase. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 166-175	5.5	2
19	Structural Plasticity of the SARS-CoV-2 3CL Mpro Active Site Cavity Revealed by Room Temperature X-ray Crystallography		2
18	A Genomic Island of Vibrio cholerae Encodes a Three-Component Cytotoxin with Monomer and Protomer Forms Structurally Similar to Alpha-Pore-Forming Toxins.. *Journal of Bacteriology*, **2022**, e0055521	3.5	2
17	A novel signal transduction protein: Combination of solute binding and tandem PAS-like sensor domains in one polypeptide chain. *Protein Science*, **2017**, 26, 857-869	6.3	1
16	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. *Methods in Enzymology*, **2021**, 661, 407-431	1.7	1
15	Three-dimensional Domain Swapping in the □Subunit of Tryptophan Synthase. *FASEB Journal*, **2015**, 29, LB215	0.9	1

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14	Structural Insight into Allosteric Inhibition of Mycobacterium tuberculosis Tryptophan Synthase. *FASEB Journal*, **2017**, 31, 765.12	0.9	1
13	Mycobacterium tuberculosis Phe-tRNA synthetase: structural insights into tRNA recognition and aminoacylation. *Nucleic Acids Research*, **2021**, 49, 5351-5368	20.1	1
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