

Andrzej Joachimiak

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Functional and Structural Characterization of Diverse NfsB Chloramphenicol Reductase Enzymes from Human Pathogens.. <i>Microbiology Spectrum</i> , 2022 , e0013922	8.9	1
174	A Genomic Island of <i>Vibrio cholerae</i> Encodes a Three-Component Cytotoxin with Monomer and Protomer Forms Structurally Similar to Alpha-Pore-Forming Toxins.. <i>Journal of Bacteriology</i> , 2022 , e0055321	3.5	2
173	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. <i>Methods in Enzymology</i> , 2021 , 661, 407-431	1.7	1
172	An efficient chemical screening method for structure-based inhibitors to nucleic acid enzymes targeting the DNA repair-replication interface and SARS CoV-2. <i>Methods in Enzymology</i> , 2021 , 661, 407-431	1.7	3
171	Potent and Selective Covalent Inhibitors of the Papain-like Protease from SARS-CoV-2 2021 ,		4
170	Biochemical and structural studies of two tetrameric nucleoside 2Sdeoxyribosyltransferases from psychrophilic and mesophilic bacteria: Insights into cold-adaptation. <i>International Journal of Biological Macromolecules</i> , 2021 , 192, 138-150	7.9	0
169	Mycobacterium tuberculosis Phe-tRNA synthetase: structural insights into tRNA recognition and aminoacylation. <i>Nucleic Acids Research</i> , 2021 , 49, 5351-5368	20.1	1
168	25O 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,	11.5	13
167	Catalytically impaired TrpA subunit of tryptophan synthase from <i>Chlamydia trachomatis</i> is an allosteric regulator of TrpB. <i>Protein Science</i> , 2021 , 30, 1904-1918	6.3	4
166	Profiling B cell immunodominance after SARS-CoV-2 infection reveals antibody evolution to non-neutralizing viral targets. <i>Immunity</i> , 2021 , 54, 1290-1303.e7	32.3	35
165	Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein. <i>MAbs</i> , 2021 , 13, 1905978	6.6	6
164	SARS-CoV-2 Infection Severity Is Linked to Superior Humoral Immunity against the Spike. <i>MBio</i> , 2021 , 12,	7.8	46
163	Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein 2021 ,		1
162	Tipiracil binds to uridine site and inhibits Nsp15 endoribonuclease NendoU from SARS-CoV-2. <i>Communications Biology</i> , 2021 , 4, 193	6.7	36
161	Structure of papain-like protease from SARS-CoV-2 and its complexes with non-covalent inhibitors. <i>Nature Communications</i> , 2021 , 12, 743	17.4	121
160	Masitinib is a broad coronavirus 3CL inhibitor that blocks replication of SARS-CoV-2. <i>Science</i> , 2021 , 373, 931-936	33.3	49
159	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. <i>Biophysical Journal</i> , 2021 , 120, 3152-3165	2.9	11

158	Improved integration of single-cell transcriptome and surface protein expression by LinQ-View.. <i>Cell Reports Methods</i> , 2021 , 1, 100056		1
157	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1647-1672	4.2	7
156	The Enzymatic Activity of Inosine 5SMonophosphate Dehydrogenase May Not Be a Vulnerable Target for Infections. <i>ACS Infectious Diseases</i> , 2021 , 7, 3062-3076	5.5	1
155	Structural and biochemical insights into CRISPR RNA processing by the Cas5c ribonuclease SMU1763 from <i>Streptococcus mutans</i> . <i>Journal of Biological Chemistry</i> , 2021 , 297, 101251	5.4	
154	Structural genomics and the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100747	5.4	3
153	Structural plasticity of SARS-CoV-2 3CL M active site cavity revealed by room temperature X-ray crystallography. <i>Nature Communications</i> , 2020 , 11, 3202	17.4	185
152	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. <i>Current Research in Structural Biology</i> , 2020 , 2, 14-24	2.8	6
151	Allosteric inhibitors of <i>Mycobacterium tuberculosis</i> tryptophan synthase. <i>Protein Science</i> , 2020 , 29, 779-788		12
150	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. <i>IUCrJ</i> , 2020 , 7, 814-824	4.7	59
149	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. <i>IUCrJ</i> , 2020 , 7,	4.7	27
148	3D domain swapping in the TIM barrel of the β subunit of <i>Streptococcus pneumoniae</i> tryptophan synthase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 166-175	5.5	2
147	Therapeutic genetic variation revealed in diverse Hsp104 homologs. <i>ELife</i> , 2020 , 9,	8.9	6
146	The crystal structure of nsp10-nsp16 heterodimer from SARS-CoV-2 in complex with S-adenosylmethionine 2020 ,		27
145	SARS-CoV-2 infection severity is linked to superior humoral immunity against the spike 2020 ,		7
144	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	6.3	11
143	Crystal structure of Nsp15 endoribonuclease NendoU from SARS-CoV-2. <i>Protein Science</i> , 2020 , 29, 1596-1605		199
142	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1037-1057	4.2	9
141	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	11.5	13

140	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	16.4	14
139	Conserved residue His-257 of flavin transferase ApbE plays a critical role in substrate binding and catalysis. <i>Journal of Biological Chemistry</i> , 2019 , 294, 13800-13810	5.4	5
138	Convergent Evolution of the Barnase/EndoU/Colicin/RelE (BECR) Fold in Antibacterial tRNase Toxins. <i>Structure</i> , 2019 , 27, 1660-1674.e5	5.2	13
137	Conservation of the structure and function of bacterial tryptophan synthases. <i>IUCrJ</i> , 2019 , 6, 649-664	4.7	6
136	Oxanosine Monophosphate Is a Covalent Inhibitor of Inosine 5SMonophosphate Dehydrogenase. <i>Chemical Research in Toxicology</i> , 2019 , 32, 456-466	4	
135	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	1.1	5
134	Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. <i>Structure</i> , 2019 , 27, 449-463.e7	5.2	22
133	Molecular Mechanism of Inhibition of Acid Ceramidase by Carmofur. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 987-992	8.3	30
132	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	2.9	6
131	Structural Basis of a Thiol-Disulfide Oxidoreductase in the Hedgehog-Forming Actinobacterium <i>Corynebacterium matruchotii</i> . <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	6
130	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	3.2	7
129	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	3.2	9
128	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 27-50	4.2	5
127	Resistance to Eneidyne Antitumor Antibiotics by Sequestration. <i>Cell Chemical Biology</i> , 2018 , 25, 1075-1085.e4	5.4	14
126	Functional plasticity of antibacterial EndoU toxins. <i>Molecular Microbiology</i> , 2018 , 109, 509-527	4.1	20
125	Expanding Benzoxazole-Based Inosine 5SMonophosphate Dehydrogenase (IMPDH) Inhibitor Structure-Activity As Potential Antituberculosis Agents. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 4739-4756	8.3	26
124	Functional Profiling and Crystal Structures of Isothiocyanate Hydrolases Found in Gut-Associated and Plant-Pathogenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	9
123	Natural separation of the acyl-CoA ligase reaction results in a non-adenylating enzyme. <i>Nature Chemical Biology</i> , 2018 , 14, 730-737	11.7	15

122	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	20.1	16
121	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> , 2018 , 19, 200-210	2.8	6
120	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	10.3	28
119	Structural Insights into Substrate Selectivity and Activity of Bacterial Polyphosphate Kinases. <i>ACS Catalysis</i> , 2018 , 8, 10746-10760	13.1	23
118	Interaction of antidiabetic α -glucosidase inhibitors and gut bacteria α -glucosidase. <i>Protein Science</i> , 2018 , 27, 1498-1508	6.3	18
117	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	11.5	11
116	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. <i>Scientific Reports</i> , 2017 , 7, 44103	4.9	48
115	A novel signal transduction protein: Combination of solute binding and tandem PAS-like sensor domains in one polypeptide chain. <i>Protein Science</i> , 2017 , 26, 857-869	6.3	1
114	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	20.1	20
113	X-ray crystal structures of the pheromone-binding domains of two quorum-hindered transcription factors, YenR of <i>Yersinia enterocolitica</i> and CepR2 of <i>Burkholderia cenocepacia</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 1831-1844	4.2	3
112	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	6.3	6
111	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	20.1	14
110	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	3.9	5
109	A small-molecule allosteric inhibitor of <i>Mycobacterium tuberculosis</i> tryptophan synthase. <i>Nature Chemical Biology</i> , 2017 , 13, 943-950	11.7	75
108	Aromatic claw: A new fold with high aromatic content that evades structural prediction. <i>Protein Science</i> , 2017 , 26, 208-217	6.3	
107	Evolution of substrate specificity in a retained enzyme driven by gene loss. <i>ELife</i> , 2017 , 6,	8.9	19
106	Structural Insight into Allosteric Inhibition of <i>Mycobacterium tuberculosis</i> Tryptophan Synthase. <i>FASEB Journal</i> , 2017 , 31, 765.12	0.9	1
105	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, 5142-54	3.2	15

104	Structural dynamics of a methionine lyase for calicheamicin biosynthesis: Rotation of the conserved tyrosine stacking with pyridoxal phosphate. <i>Structural Dynamics</i> , 2016 , 3, 034702	3.2	4
103	A family of metal-dependent phosphatases implicated in metabolite damage-control. <i>Nature Chemical Biology</i> , 2016 , 12, 621-7	11.7	26
102	A structural insight into the P1S1 binding mode of diaminoethylphosphonic and phosphinic acids, selective inhibitors of alanine aminopeptidases. <i>European Journal of Medicinal Chemistry</i> , 2016 , 117, 187-98	6.8	20
101	Insights from the Structure of Mycobacterium tuberculosis Topoisomerase I with a Novel Protein Fold. <i>Journal of Molecular Biology</i> , 2016 , 428, 182-193	6.5	23
100	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	3.4	10
99	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, 2952-7	11.5	29
98	Fluorescence-based thermal shift data on multidrug regulator AcrR from Salmonella enterica subsp. enterica serovar Typhimurium str. LT2. <i>Data in Brief</i> , 2016 , 7, 537-9	1.2	
97	How Aromatic Compounds Block DNA Binding of HcaR Catabolite Regulator. <i>Journal of Biological Chemistry</i> , 2016 , 291, 13243-56	5.4	14
96	Co-occurrence of analogous enzymes determines evolution of a novel α -isomerase sub-family after non-conserved mutations in flexible loop. <i>Biochemical Journal</i> , 2016 , 473, 1141-52	3.8	6
95	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. <i>Biomacromolecules</i> , 2016 , 17, 2027-39	6.9	68
94	A microbial sensor for organophosphate hydrolysis exploiting an engineered specificity switch in a transcription factor. <i>Nucleic Acids Research</i> , 2016 , 44, 8490-500	20.1	21
93	Structure of the ent-Copalyl Diphosphate Synthase PtmT2 from Streptomyces platensis CB00739, a Bacterial Type II Diterpene Synthase. <i>Journal of the American Chemical Society</i> , 2016 , 138, 10905-15	16.4	29
92	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, 1632-43	6.5	31
91	A novel cofactor-binding mode in bacterial IMP dehydrogenases explains inhibitor selectivity. <i>Journal of Biological Chemistry</i> , 2015 , 290, 5893-911	5.4	25
90	A novel polyamine allosteric site of SpeG from Vibrio cholerae is revealed by its dodecameric structure. <i>Journal of Molecular Biology</i> , 2015 , 427, 1316-1334	6.5	19
89	New aminopeptidase from "microbial dark matter" archaeon. <i>FASEB Journal</i> , 2015 , 29, 4071-9	0.9	10
88	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae: BIOCHEMICAL, STRUCTURAL, AND EVOLUTIONARY INSIGHTS. <i>Journal of Biological Chemistry</i> , 2015 , 290, 18678-98	5.4	52
87	Inhibition of the dapE-Encoded N-Succinyl-L,L-diaminopimelic Acid Desuccinylase from Neisseria meningitidis by L-Captopril. <i>Biochemistry</i> , 2015 , 54, 4834-44	3.2	12

86	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, 21393-405	5.4	25
85	Structure of <i>Cryptosporidium</i> IMP dehydrogenase bound to an inhibitor with in vivo antiparasitic activity. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 531-8	1.1	11
84	Biochemical and structural analysis of an Eis family aminoglycoside acetyltransferase from <i>Bacillus anthracis</i> . <i>Biochemistry</i> , 2015 , 54, 3197-206	3.2	21
83	Structural and evolutionary relationships of "AT-less" type I polyketide synthase ketosynthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 12693-8	11.5	38
82	A novel transcriptional regulator of L-arabinose utilization in human gut bacteria. <i>Nucleic Acids Research</i> , 2015 , 43, 10546-59	20.1	17
81	Crystal structure of <i>Bacillus anthracis</i> virulence regulator AtxA and effects of phosphorylated histidines on multimerization and activity. <i>Molecular Microbiology</i> , 2015 , 95, 426-41	4.1	25
80	Substrate-Induced Allosteric Change in the Quaternary Structure of the Spermidine N-Acetyltransferase SpeG. <i>Journal of Molecular Biology</i> , 2015 , 427, 3538-3553	6.5	9
79	EsxB, a secreted protein from <i>Bacillus anthracis</i> forms two distinct helical bundles. <i>Protein Science</i> , 2015 , 24, 1389-400	6.3	7
78	Structural basis for suppression of hypernegative DNA supercoiling by <i>E. coli</i> topoisomerase I. <i>Nucleic Acids Research</i> , 2015 , 43, 11031-46	20.1	35
77	Structural characterization of AtmS13, a putative sugar aminotransferase involved in indolocarbazole AT2433 aminopentose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 1547-54	4.2	9
76	A thiol-disulfide oxidoreductase of the Gram-positive pathogen <i>Corynebacterium diphtheriae</i> is essential for viability, pilus assembly, toxin production and virulence. <i>Molecular Microbiology</i> , 2015 , 98, 1037-50	4.1	26
75	Structural and Functional Analysis of Human HtrA3 Protease and Its Subdomains. <i>PLoS ONE</i> , 2015 , 10, e0131142	3.7	27
74	Structural Characterization of CalS8, a TDP- β -Glucose Dehydrogenase Involved in Calicheamicin Aminodideoxypentose Biosynthesis. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26249-58	5.4	2
73	Crystal Structure of the Zorbamycin-Binding Protein ZbmA, the Primary Self-Resistance Element in <i>Streptomyces flavoviridis</i> ATCC21892. <i>Biochemistry</i> , 2015 , 54, 6842-51	3.2	8
72	Structure of a cupin protein Plu4264 from <i>Photobacterium luminescens</i> subsp. <i>laumondii</i> TTO1 at 1.35 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 383-8	4.2	2
71	<i>Mycobacterium tuberculosis</i> IMPDH in Complexes with Substrates, Products and Antitubercular Compounds. <i>PLoS ONE</i> , 2015 , 10, e0138976	3.7	27
70	Three-dimensional Domain Swapping in the β Subunit of Tryptophan Synthase. <i>FASEB Journal</i> , 2015 , 29, LB215	0.9	1
69	Structure of cyclin G-associated kinase (GAK) trapped in different conformations using nanobodies. <i>Biochemical Journal</i> , 2014 , 459, 59-69	3.8	36

68	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, 5810-9	3.2	5
67	Sensor domain of histidine kinase KinB of <i>Pseudomonas</i> : a helix-swapped dimer. <i>Journal of Biological Chemistry</i> , 2014 , 289, 12232-44	5.4	6
66	Structural and functional characterization of DUF1471 domains of <i>Salmonella</i> proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , 2014 , 9, e101787	3.7	8
65	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, 11144-55	20.1	25
64	Covering complete proteomes with X-ray structures: a current snapshot. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2781-93		29
63	The crystal structure of Blml as a model for nonribosomal peptide synthetase peptidyl carrier proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 1210-8	4.2	31
62	The dimerization domain in DapE enzymes is required for catalysis. <i>PLoS ONE</i> , 2014 , 9, e93593	3.7	10
61	Protein production for structural genomics using <i>E. coli</i> expression. <i>Methods in Molecular Biology</i> , 2014 , 1140, 89-105	1.4	19
60	New LIC vectors for production of proteins from genes containing rare codons. <i>Journal of Structural and Functional Genomics</i> , 2013 , 14, 135-44		38
59	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, 17476-87	16.4	41
58	NDM-1, the ultimate promiscuous enzyme: substrate recognition and catalytic mechanism. <i>FASEB Journal</i> , 2013 , 27, 1917-27	0.9	91
57	Optimization of benzoxazole-based inhibitors of <i>Cryptosporidium parvum</i> inosine 5Smonophosphate dehydrogenase. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 4028-43	8.3	64
56	A conformational switch controls cell wall-remodelling enzymes required for bacterial cell division. <i>Molecular Microbiology</i> , 2012 , 85, 768-81	4.1	75
55	The crystal structures of the β subunit of the (P)(I)2 tetrameric Glycyl-tRNA synthetase. <i>Journal of Structural and Functional Genomics</i> , 2012 , 13, 233-9		7
54	Characterization of transport proteins for aromatic compounds derived from lignin: benzoate derivative binding proteins. <i>Journal of Molecular Biology</i> , 2012 , 423, 555-75	6.5	22
53	<i>Bacillus anthracis</i> inosine 5Smonophosphate dehydrogenase in action: the first bacterial series of structures of phosphate ion-, substrate-, and product-bound complexes. <i>Biochemistry</i> , 2012 , 51, 6148-63 ³⁻²		24
52	High-throughput protein purification and quality assessment for crystallization. <i>Methods</i> , 2011 , 55, 12-28	1.6	110
51	Crystal structure of secretory protein Hcp3 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Structural and Functional Genomics</i> , 2011 , 12, 21-6		32

50	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 Suppl 10, 6-20	4.2	15
49	Structure of apo- and monometalated forms of NDM-1--a highly potent carbapenem-hydrolyzing metallo-β-lactamase. <i>PLoS ONE</i> , 2011 , 6, e24621	3.7	73
48	Structural basis for catalysis by the mono- and dimetalated forms of the dapE-encoded N-succinyl-L,L-diaminopimelic acid desuccinylase. <i>Journal of Molecular Biology</i> , 2010 , 397, 617-26	6.5	42
47	Structural insight into the mechanism of c-di-GMP hydrolysis by EAL domain phosphodiesterases. <i>Journal of Molecular Biology</i> , 2010 , 402, 524-38	6.5	86
46	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, 101-11		8
45	Predicting protein crystallization propensity from protein sequence. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 71-80		29
44	Cleavable C-terminal His-tag vectors for structure determination. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 31-9		33
43	Metagenomics - the next structural frontier. <i>FASEB Journal</i> , 2010 , 24, lb225	0.9	
42	Characterization of a <i>Bacillus subtilis</i> transporter for petrobactin, an anthrax stealth siderophore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21854-9	11.5	68
41	Crystal structure of <i>Bacillus anthracis</i> transpeptidase enzyme CapD. <i>Journal of Biological Chemistry</i> , 2009 , 284, 24406-14	5.4	22
40	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	5.4	12
39	High-throughput crystallography for structural genomics. <i>Current Opinion in Structural Biology</i> , 2009 , 19, 573-84	8.1	100
38	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	3.7	14
37	A family of LIC vectors for high-throughput cloning and purification of proteins. <i>Methods in Molecular Biology</i> , 2009 , 498, 105-15	1.4	202
36	NFκB selectivity of estrogen receptor ligands revealed by comparative crystallographic analyses. <i>Nature Chemical Biology</i> , 2008 , 4, 241-7	11.7	123
35	Protein production and purification. <i>Nature Methods</i> , 2008 , 5, 135-46	21.6	655
34	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. <i>Structure</i> , 2008 , 16, 5-11	5.2	55
33	Structures of open (R) and close (T) states of prephenate dehydratase (PDT)--implication of allosteric regulation by L-phenylalanine. <i>Journal of Structural Biology</i> , 2008 , 162, 94-107	3.4	31

32	Heparin-induced cis- and trans-dimerization modes of the thrombospondin-1 N-terminal domain. <i>Journal of Biological Chemistry</i> , 2008 , 283, 3932-41	5.4	27
31	High-throughput Technologies for Structural Biology: The Protein Structure Initiative Perspective 2008 , 435-461		
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