

Mirosław Cygler

List of Publications by Year in descending order

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180
papers

12,075
citations

38660

50
h-index

28224

105
g-index

181
all docs

181
docs citations

181
times ranked

11652
citing authors

#	ARTICLE	IF	CITATIONS
1	The α/β hydrolase fold. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 197-211.	1.0	1,887
2	Ser-His-Glu triad forms the catalytic site of the lipase from <i>Geotrichum candidum</i> . <i>Nature</i> , 1991, 351, 761-764.	13.7	552
3	<i>Bacillus thuringiensis</i> CryIA(a) Insecticidal Toxin: Crystal Structure and Channel Formation. <i>Journal of Molecular Biology</i> , 1995, 254, 447-464.	2.0	516
4	Relationship between sequence conservation and three-dimensional structure in a large family of esterases, lipases, and related proteins. <i>Protein Science</i> , 1993, 2, 366-382.	3.1	506
5	The Structure of Calnexin, an ER Chaperone Involved in Quality Control of Protein Folding. <i>Molecular Cell</i> , 2001, 8, 633-644.	4.5	363
6	Two conformational states of <i>Candida rugosa</i> lipase. <i>Protein Science</i> , 1994, 3, 82-91.	3.1	346
7	A Structural Basis for the Chiral Preferences of Lipases. <i>Journal of the American Chemical Society</i> , 1994, 116, 3180-3186.	6.6	328
8	The open conformation of a <i>Pseudomonas</i> lipase. <i>Structure</i> , 1997, 5, 187-202.	1.6	275
9	[4] Lipases and hydrolase fold. <i>Methods in Enzymology</i> , 1997, 284, 85-107.	0.4	224
10	Structural Basis for Fe-S Cluster Assembly and tRNA Thiolation Mediated by IscS Protein-Protein Interactions. <i>PLoS Biology</i> , 2010, 8, e1000354.	2.6	224
11	Structural and mechanistic classification of uronic acid-containing polysaccharide lyases. <i>Glycobiology</i> , 2010, 20, 1547-1573.	1.3	207
12	Structure of a calpain Ca ²⁺ -binding domain reveals a novel EF-hand and Ca ²⁺ -induced conformational changes. <i>Nature Structural Biology</i> , 1997, 4, 532-538.	9.7	192
13	Structure of rat procathepsin B: model for inhibition of cysteine protease activity by the proregion. <i>Structure</i> , 1996, 4, 405-416.	1.6	174
14	Lectin control of protein folding and sorting in the secretory pathway. <i>Trends in Biochemical Sciences</i> , 2003, 28, 49-57.	3.7	170
15	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. <i>Cell</i> , 2006, 127, 817-830.	13.5	166
16	1.8 Å Refined Structure of the Lipase from <i>Geotrichum candidum</i> . <i>Journal of Molecular Biology</i> , 1993, 230, 575-591.	2.0	154
17	Structure and functional dynamics of the mitochondrial Fe/S cluster synthesis complex. <i>Nature Communications</i> , 2017, 8, 1287.	5.8	144
18	Genetic selection designed to stabilize proteins uncovers a chaperone called Spy. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 262-269.	3.6	138

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19	Molecular Dynamics Solvated Interaction Energy Studies of Protein-Protein Interactions: The MP14 Scaffolding Complex. <i>Journal of Molecular Biology</i> , 2008, 379, 787-802.	2.0	135
20	Crystal Structure of the β^2 Domains of the Protein Disulfide Isomerase ERp57. <i>Structure</i> , 2006, 14, 1331-1339.	1.6	127
21	Structures of Shikimate Dehydrogenase AroE and Its Paralog YdiB. <i>Journal of Biological Chemistry</i> , 2003, 278, 19463-19472.	1.6	111
22	Restriction of intramolecular movements within the Cry1Aa toxin molecule of <i>Bacillus thuringiensis</i> through disulfide bond engineering. <i>FEBS Letters</i> , 1997, 410, 397-402.	1.3	110
23	Crystal structure of chondroitinase B from <i>Flavobacterium heparinum</i> and its complex with a disaccharide product at 1.7 Å... resolution. <i>Journal of Molecular Biology</i> , 1999, 294, 1257-1269.	2.0	107
24	Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 130-138.	3.6	103
25	Crystal Structure of <i>Proteus vulgaris</i> Chondroitin Sulfate ABC Lyase I at 1.9 Å... Resolution. <i>Journal of Molecular Biology</i> , 2003, 328, 623-634.	2.0	98
26	High-resolution Crystal Structure of <i>Arthrobacter aurescens</i> Chondroitin AC Lyase: An Enzyme-Substrate Complex Defines the Catalytic Mechanism. <i>Journal of Molecular Biology</i> , 2004, 337, 367-386.	2.0	97
27	Crystal structure of chondroitin AC lyase, a representative of a family of glycosaminoglycan degrading enzymes 1 Edited by D. Rees. <i>Journal of Molecular Biology</i> , 1999, 288, 635-647.	2.0	96
28	Progress in understanding the assembly process of bacterial O-antigen. <i>FEMS Microbiology Reviews</i> , 2014, 38, 1048-1065.	3.9	96
29	The Structure of the RlmB 23S rRNA Methyltransferase Reveals a New Methyltransferase Fold with a Unique Knot. <i>Structure</i> , 2002, 10, 1303-1315.	1.6	92
30	The Structure of Chondroitin B Lyase Complexed with Glycosaminoglycan Oligosaccharides Unravels a Calcium-dependent Catalytic Machinery. <i>Journal of Biological Chemistry</i> , 2004, 279, 32882-32896.	1.6	91
31	Structural and Functional Characterization of PseC, an Aminotransferase Involved in the Biosynthesis of Pseudaminic Acid, an Essential Flagellar Modification in <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 8907-8916.	1.6	88
32	Identification of an <i>Escherichia coli</i> O157:H7 heme oxygenase with tandem functional repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16955-16960.	3.3	86
33	<i>Salmonella</i> Disrupts Host Endocytic Trafficking by SopD2-Mediated Inhibition of Rab7. <i>Cell Reports</i> , 2015, 12, 1508-1518.	2.9	83
34	Crystal structure of human procathepsin X: a cysteine protease with the proregion covalently linked to the active site cysteine. <i>Journal of Molecular Biology</i> , 2000, 295, 939-951.	2.0	82
35	[1] Structure as basis for understanding interfacial properties of lipases. <i>Methods in Enzymology</i> , 1997, 284, 3-27.	0.4	81
36	Crystal Structure of Heparinase II from <i>Pedobacter heparinus</i> and Its Complex with a Disaccharide Product*. <i>Journal of Biological Chemistry</i> , 2006, 281, 15525-15535.	1.6	80

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37	Structure of Apoptosis-Linked Protein ALG-2. <i>Structure</i> , 2001, 9, 267-275.	1.6	77
38	Sequence-structure relationships in polysaccharide co-polymerase (PCP) proteins. <i>Trends in Biochemical Sciences</i> , 2009, 34, 78-84.	3.7	76
39	Crystal Structures of <i>Escherichia coli</i> ATP-Dependent Glucokinase and Its Complex with Glucose. <i>Journal of Bacteriology</i> , 2004, 186, 6915-6927.	1.0	75
40	Essential Roles of Zinc Ligation and Enzyme Dimerization for Catalysis in the Aminoacylase-1/M20 Family. <i>Journal of Biological Chemistry</i> , 2003, 278, 44496-44504.	1.6	74
41	The 3-D structure of a folate-dependent dehydrogenase/cyclohydrolase bifunctional enzyme at 1.5 Å resolution. <i>Structure</i> , 1998, 6, 173-182.	1.6	68
42	Design of Noncovalent Inhibitors of Human Cathepsin L. From the 96-Residue Proregion to Optimized Tripeptides. <i>Journal of Medicinal Chemistry</i> , 2002, 45, 5321-5329.	2.9	68
43	Crystal Structure of <i>Escherichia coli</i> Glucose-1-Phosphate Thymidyltransferase (RffH) Complexed with dTTP and Mg ²⁺ . <i>Journal of Biological Chemistry</i> , 2002, 277, 44214-44219.	1.6	67
44	Preparation, Characterization and Crystallization of an Antibody Fab Fragment that Recognizes RNA. <i>Journal of Molecular Biology</i> , 1994, 243, 283-297.	2.0	62
45	The Structure of the MAPK Scaffold, MP1, Bound to Its Partner, p14. <i>Journal of Biological Chemistry</i> , 2004, 279, 23422-23430.	1.6	62
46	New Ulvan-Degrading Polysaccharide Lyase Family: Structure and Catalytic Mechanism Suggests Convergent Evolution of Active Site Architecture. <i>ACS Chemical Biology</i> , 2017, 12, 1269-1280.	1.6	60
47	Crystal structure of wild-type human procathepsin K. <i>Protein Science</i> , 1999, 8, 283-290.	3.1	58
48	Structural Snapshots of Heparin Depolymerization by Heparin Lyase I. <i>Journal of Biological Chemistry</i> , 2009, 284, 34019-34027.	1.6	58
49	Improvement of the Thermostability and Activity of a Pectate Lyase by Single Amino Acid Substitutions, Using a Strategy Based on Melting-Temperature-Guided Sequence Alignment. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1183-1189.	1.4	57
50	Salmonella Effectors SseK1 and SseK3 Target Death Domain Proteins in the TNF and TRAIL Signaling Pathways*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1138-1156.	2.5	55
51	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. <i>PLoS Pathogens</i> , 2017, 13, e1006394.	2.1	53
52	Conformational features of acyclonucleosides: structure of acyclovir, an antiherpes agent. <i>Canadian Journal of Chemistry</i> , 1984, 62, 2646-2652.	0.6	52
53	Mechanism of action and NAD ⁺ -binding mode revealed by the crystal structure of L-histidinol dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1859-1864.	3.3	52
54	The Structure of the Exopolyphosphatase (PPX) from <i>Escherichia coli</i> O157:H7 Suggests a Binding Mode for Long Polyphosphate Chains. <i>Journal of Molecular Biology</i> , 2006, 359, 1249-1260.	2.0	51

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55	Cloning, Baeyer-Villiger Biooxidations, and Structures of the Camphor Pathway 2-Oxo- β -4,5,5-Trimethylcyclopentenylacetyl-Coenzyme A Monooxygenase of <i>Pseudomonas putida</i> ATCC 17453. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2200-2212.	1.4	51
56	High-Level Production of Recombinant <i>Geotrichum candidum</i> Lipases in Yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1997, 11, 35-40.	0.6	50
57	CS Lyases: Structure, Activity, and Applications in Analysis and the Treatment of Diseases. <i>Advances in Pharmacology</i> , 2006, 53, 187-215.	1.2	50
58	Crystal structure of human grancalcin, a member of the penta-EF-hand protein family 11 Edited by I. Wilson. <i>Journal of Molecular Biology</i> , 2000, 300, 1271-1281.	2.0	49
59	The crystal structure of <i>Escherichia coli</i> MoeA, a protein from the molybdopterin synthesis pathway. <i>Journal of Molecular Biology</i> , 2001, 310, 419-431.	2.0	49
60	Uronic polysaccharide degrading enzymes. <i>Current Opinion in Structural Biology</i> , 2014, 28, 87-95.	2.6	49
61	Insights into function of PSI domains from structure of the Met receptor PSI domain. <i>Biochemical and Biophysical Research Communications</i> , 2004, 321, 234-240.	1.0	48
62	Crystal structure of a dodecameric FMN-dependent UbiX-like decarboxylase (Pad1) from <i>Escherichia coli</i> O157: H7. <i>Protein Science</i> , 2008, 13, 3006-3016.	3.1	48
63	Advances in Structural Understanding of Lipases. <i>Biotechnology and Genetic Engineering Reviews</i> , 1992, 10, 143-184.	2.4	47
64	The crystal structure of benzenediazonium tetrafluoroborate, $C_6H_5N_2^+BF_4^-$. <i>Canadian Journal of Chemistry</i> , 1982, 60, 2852-2855.	0.6	45
65	Crystal structure of histidinol phosphate aminotransferase (HisC) from <i>Escherichia coli</i> , and its covalent complex with pyridoxal-5-phosphate and l-histidinol phosphate. <i>Journal of Molecular Biology</i> , 2001, 311, 761-776.	2.0	45
66	Structure-Function Analysis of <i>Escherichia coli</i> MnmG (GidA), a Highly Conserved tRNA-Modifying Enzyme. <i>Journal of Bacteriology</i> , 2009, 191, 7614-7619.	1.0	45
67	The crystal structure of CREG, a secreted glycoprotein involved in cellular growth and differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18326-18331.	3.3	44
68	Structure of the Noncatalytic Domains and Global Fold of the Protein Disulfide Isomerase ERp72. <i>Structure</i> , 2009, 17, 651-659.	1.6	44
69	Structure of Hydrogenase Maturation Protein HypF with Reaction Intermediates Shows Two Active Sites. <i>Structure</i> , 2011, 19, 1773-1783.	1.6	44
70	Structure of [NiFe] Hydrogenase Maturation Protein HypE from <i>Escherichia coli</i> and Its Interaction with HypF. <i>Journal of Bacteriology</i> , 2008, 190, 1447-1458.	1.0	43
71	Disulfide Bonds Play a Critical Role in the Structure and Function of the Receptor-binding Domain of the SARS-CoV-2 Spike Antigen. <i>Journal of Molecular Biology</i> , 2022, 434, 167357.	2.0	43
72	Characterization of interactions between LPS transport proteins of the Lpt system. <i>Biochemical and Biophysical Research Communications</i> , 2011, 404, 1093-1098.	1.0	41

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73	Structural and Functional Studies of the Escherichia coli Phenylacetyl-CoA Monooxygenase Complex. Journal of Biological Chemistry, 2011, 286, 10735-10743.	1.6	41
74	Structural Basis for the Inhibition of Host Protein Ubiquitination by Shigella Effector Kinase OspG. Structure, 2014, 22, 878-888.	1.6	40
75	Structural Snapshots of Escherichia coli Histidinol Phosphate Phosphatase along the Reaction Pathway. Journal of Biological Chemistry, 2006, 281, 37930-37941.	1.6	39
76	Catalytic Mechanism of Heparinase II Investigated by Site-directed Mutagenesis and the Crystal Structure with Its Substrate. Journal of Biological Chemistry, 2010, 285, 20051-20061.	1.6	39
77	Structure-function analyses of a PL24 family ulvan lyase reveal key features and suggest its catalytic mechanism. Journal of Biological Chemistry, 2018, 293, 4026-4036.	1.6	39
78	Crystal structure of the complex of human Î±-thrombin and nonhydrolyzable bifunctional inhibitors, hirutininâ€”2 and hirutininâ€”6. Proteins: Structure, Function and Bioinformatics, 1993, 17, 252-265.	1.5	38
79	Crystal Structure of the RluD Pseudouridine Synthase Catalytic Module, an Enzyme that Modifies 23S rRNA and is Essential for Normal Cell Growth of Escherichia coli. Journal of Molecular Biology, 2004, 335, 87-101.	2.0	38
80	Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from Campylobacter jejuni. Protein Science, 2007, 16, 990-995.	3.1	38
81	Crystal Structure of Escherichia coli PdxA, an Enzyme Involved in the Pyridoxal Phosphate Biosynthesis Pathway. Journal of Biological Chemistry, 2003, 278, 43682-43690.	1.6	37
82	Structure and Function of the Glycopeptide N-methyltransferase MtfA, a Tool for the Biosynthesis of Modified Glycopeptide Antibiotics. Chemistry and Biology, 2009, 16, 401-410.	6.2	37
83	Structural and mechanistic insight into covalent substrate binding by Escherichia coli dihydroxyacetone kinase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1302-1307.	3.3	37
84	Conformation of Complementarity Determining Region L1 Loop in Murine IgG Î» Light Chain Extends the Repertoire of Canonical Forms. Journal of Molecular Biology, 1993, 229, 597-601.	2.0	36
85	The structural genomics experimental pipeline: Insights from global target lists. Proteins: Structure, Function and Bioinformatics, 2004, 56, 201-210.	1.5	36
86	Recognition of a carbohydrate antigenic determinant of Salmonella by an antibody. Biochemical Society Transactions, 1993, 21, 437-441.	1.6	34
87	Crystallographic Trapping of the Glutamyl-CoA Thioester Intermediate of Family I CoA Transferases. Journal of Biological Chemistry, 2005, 280, 42919-42928.	1.6	34
88	Structural and enzymatic characterization of NanS (YjhS), a 9â€”Acetyl Nâ€”acetylneuraminic acid esterase from Escherichia coli O157:H7. Protein Science, 2011, 20, 1208-1219.	3.1	33
89	Purification and characterization of a Penicillium sp. lipase which discriminates against diglycerides. Lipids, 1996, 31, 379-384.	0.7	32
90	Crystal structure of D-ribose-5-phosphate isomerase (RpiA) from Escherichia coli. Proteins: Structure, Function and Bioinformatics, 2002, 48, 737-740.	1.5	32

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91	Structure of the 16S rRNA pseudouridine synthase RsuA bound to uracil and UMP. <i>Nature Structural Biology</i> , 2002, 9, 353-8.	9.7	32
92	Ca ²⁺ -Binding domain VI of rat calpain is a homodimer in solution: Hydrodynamic, crystallization and preliminary X-ray diffraction studies. <i>Protein Science</i> , 1996, 5, 535-537.	3.1	31
93	Crystal structure of a trimeric form of dephosphocoenzyme A kinase from <i>Escherichia coli</i> . <i>Protein Science</i> , 2003, 12, 327-336.	3.1	31
94	Structure-Guided Investigation of Lipopolysaccharide O-Antigen Chain Length Regulators Reveals Regions Critical for Modal Length Control. <i>Journal of Bacteriology</i> , 2011, 193, 3710-3721.	1.0	31
95	Trapping open and closed forms of FitA group III periplasmic binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 598-609.	1.5	29
96	NleH Defines a New Family of Bacterial Effector Kinases. <i>Structure</i> , 2014, 22, 250-259.	1.6	28
97	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	1.5	27
98	Site-directed Mutagenesis of the Active Site Region in the Quinate/Shikimate 5-Dehydrogenase YdiB of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 7162-7169.	1.6	27
99	Interaction of the Ankyrin H Core Effector of <i>Legionella</i> with the Host LARP7 Component of the 7SK snRNP Complex. <i>MBio</i> , 2019, 10, .	1.8	27
100	Biochemical and Crystallographic Studies Reveal a Specific Interaction Between TRAPP Subunits Trs33p and Bet3p. <i>Traffic</i> , 2005, 6, 1183-1195.	1.3	26
101	Structural and functional characterization of PL28 family ulvan lyase NLR48 from <i>Nonlabens ulvanivorans</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 11564-11573.	1.6	25
102	Structure and conformation of the antiviral nucleoside 2'-fluoro-5-iodoarabinosylcytosine (FIAC). The gauche effect in nucleosides. <i>Journal of the American Chemical Society</i> , 1982, 104, 7626-7630.	6.6	24
103	Structural Characterization of Closely Related O-antigen Lipopolysaccharide (LPS) Chain Length Regulators. <i>Journal of Biological Chemistry</i> , 2012, 287, 15696-15705.	1.6	24
104	Crystal Structure of N-Succinylarginine Dihydrolase AstB, Bound to Substrate and Product, an Enzyme from the Arginine Catabolic Pathway of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 15800-15808.	1.6	23
105	Creation of a ribonuclease abzyme through site-directed mutagenesis. <i>Nature Biotechnology</i> , 1998, 16, 1065-1067.	9.4	22
106	Crystal Structure of StaL, a Glycopeptide Antibiotic Sulfotransferase from <i>Streptomyces toyocaensis</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 13073-13086.	1.6	22
107	Structural Mimicry by a Bacterial F Box Effector Hijacks the Host Ubiquitin-Proteasome System. <i>Structure</i> , 2017, 25, 376-383.	1.6	22
108	Structural and Functional Analysis of <i>Campylobacter jejuni</i> PseG. <i>Journal of Biological Chemistry</i> , 2009, 284, 20989-21000.	1.6	21

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109	Contribution of Structural Genomics to Understanding the Biology of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2003, 185, 3994-4002.	1.0	20
110	Crystallographic data for complexes of the Cro repressor with DNA. <i>Journal of Molecular Biology</i> , 1983, 168, 903-906.	2.0	19
111	Liquid chromatography-mass spectrometry to study chondroitin lyase action pattern. <i>Analytical Biochemistry</i> , 2009, 385, 57-64.	1.1	19
112	Quaternary structure of <i>WzzB</i> and <i>WzzE</i> polysaccharide copolymerases. <i>Protein Science</i> , 2015, 24, 58-69.	3.1	19
113	Structure and conformation of the potent antiherpes agent 9-(2-hydroxyethoxymethyl)guanine (acycloguanosine). <i>Biochemical and Biophysical Research Communications</i> , 1981, 103, 968-974.	1.0	18
114	Asparagine 405 of heparin lyase II prevents the cleavage of glycosidic linkages proximate to a sulfoglucosamine residue. <i>FEBS Letters</i> , 2011, 585, 2461-2466.	1.3	18
115	Coiled-Coil Helix Rotation Selects Repressing or Activating State of Transcriptional Regulator DhaR. <i>Structure</i> , 2014, 22, 478-487.	1.6	18
116	Structural insight into effector proteins of Gram-negative bacterial pathogens that modulate the phosphoproteome of their host. <i>Protein Science</i> , 2015, 24, 604-620.	3.1	17
117	Crystal structure of two new bifunctional nonsubstrate type thrombin inhibitors complexed with human thrombin. <i>Protein Science</i> , 1996, 5, 1174-1183.	3.1	16
118	Structure of Ca ²⁺ -loaded human grancalcin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1843-1849.	2.5	16
119	Structure of <i>Xylulose-5-Phosphate 3-Epimerase (UlaE)</i> from the Anaerobic <i>Escherichia coli</i> : Identification of a Novel Phosphate Binding Motif within a TIM Barrel Fold. <i>Journal of Bacteriology</i> , 2008, 190, 8137-8144.	1.0	15
120	The KH domain facilitates the substrate specificity and unwinding processivity of DDX43 helicase. <i>Journal of Biological Chemistry</i> , 2021, 296, 100085.	1.6	15
121	N-terminal tyrosine of ISCU2 triggers [2Fe-2S] cluster synthesis by ISCU2 dimerization. <i>Nature Communications</i> , 2021, 12, 6902.	5.8	15
122	Structural Basis of the Regulation of the CbpA Co-chaperone by its Specific Modulator CbpM. <i>Journal of Molecular Biology</i> , 2010, 398, 111-121.	2.0	14
123	Sulfonation of glycopeptide antibiotics by sulfotransferase StaL depends on conformational flexibility of aglycone scaffold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11824-11829.	3.3	14
124	Conformational flexibility of PL12 family heparinases: structure and substrate specificity of heparinase III from <i>Bacteroides thetaiotaomicron</i> (BT4657). <i>Glycobiology</i> , 2017, 27, 176-187.	1.3	14
125	<i>Legionella pneumophila</i> effector Lem4 is a membrane-associated protein tyrosine phosphatase. <i>Journal of Biological Chemistry</i> , 2018, 293, 13044-13058.	1.6	14
126	Crystallization and Preliminary X-ray Diffraction Studies of the Lepidopteran-specific Insecticidal Crystal Protein CryIA(a). <i>Journal of Molecular Biology</i> , 1994, 243, 530-532.	2.0	13

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127	Coverage of protein sequence space by current structural genomics targets. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 47-55.	1.2	13
128	An Atypical Approach Identifies TYR234 as the Key Base Catalyst in Chondroitin AC Lyase. <i>ChemBioChem</i> , 2006, 7, 631-637.	1.3	13
129	Quantitative continuous assay for hyaluronan synthase. <i>Analytical Biochemistry</i> , 2007, 361, 218-225.	1.1	13
130	The Solution Structure of YbcJ from <i>Escherichia coli</i> Reveals a Recently Discovered $\hat{\pm}$ L Motif Involved in RNA Binding. <i>Journal of Bacteriology</i> , 2003, 185, 4204-4210.	1.0	12
131	Structural Similarity of YbeD Protein from <i>Escherichia coli</i> to Allosteric Regulatory Domains. <i>Journal of Bacteriology</i> , 2004, 186, 8083-8088.	1.0	12
132	Protein-Protein Interactions in the $\hat{2}$ -Oxidation Part of the Phenylacetate Utilization Pathway. <i>Journal of Biological Chemistry</i> , 2012, 287, 37986-37996.	1.6	12
133	Crystallization and preliminary x-ray diffraction studies of human procathepsin L. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 398-400.	1.5	12
134	Structure and reactions of 4-(2,4,6-trimethyl)benzylidene-2-phenyloxazolin-5-one. <i>Canadian Journal of Chemistry</i> , 1986, 64, 2064-2067.	0.6	11
135	Redesigning the active site of <i>Geotrichum candidum</i> lipase. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 835-842.	1.0	11
136	Crystal structure of ureidoglycolate hydrolase (AllA) from <i>Escherichia coli</i> O157:H7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 454-459.	1.5	11
137	Domain Organization and Crystal Structure of the Catalytic Domain of <i>E.coli</i> RluF, a Pseudouridine Synthase that Acts on 23S rRNA. <i>Journal of Molecular Biology</i> , 2006, 359, 998-1009.	2.0	11
138	Insights from protein-protein interaction studies on bacterial pathogenesis. <i>Expert Review of Proteomics</i> , 2017, 14, 779-797.	1.3	11
139	Structure and conformation of 8-bromo-9-beta-D-xylofuranosyladenine in the solid state and in solution. <i>Journal of the American Chemical Society</i> , 1982, 104, 3957-3964.	6.6	10
140	Crystallization of a soluble form of the Kexlp serine carboxypeptidase from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , 1996, 5, 395-397.	3.1	10
141	Structural Organization of Enzymes of the Phenylacetate Catabolic Hybrid Pathway. <i>Biology</i> , 2015, 4, 424-442.	1.3	10
142	The <i>Legionella</i> kinase LegK7 exploits the Hippo pathway scaffold protein MOB1A for allostery and substrate phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14433-14443.	3.3	10
143	Structure of the N-terminal domain of the effector protein LegC3 from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 436-441.	2.5	10
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