

Miroslaw Cygler

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.

176 papers	10,355 citations	48 h-index	98 g-index
181 ext. papers	11,166 ext. citations	6.9 avg, IF	5.6 L-index

#	Paper	IF	Citations
176	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> , 2021 , 434, 167357	6.5	7
175	N-terminal tyrosine of ISCU2 triggers [2Fe-2S] cluster synthesis by ISCU2 dimerization. <i>Nature Communications</i> , 2021 , 12, 6902	17.4	4
174	Legionella effector LegA15/AnkH contains an unrecognized cysteine protease-like domain and displays structural similarity to LegA3/AnkD, but differs in host cell localization. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 1535-1542	5.5	1
173	Structural biology of the invasion arsenal of Gram-negative bacterial pathogens. <i>FEBS Journal</i> , 2021 , ,	5.7	2
172	The KH domain facilitates the substrate specificity and unwinding processivity of DDX43 helicase. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100085	5.4	4
171	An Indispensable Role for the MavE Effector of Legionella pneumophila in Lysosomal Evasion. <i>MBio</i> , 2021 , 12,	7.8	2
170	Structural and functional study of Legionella pneumophila effector RavA. <i>Protein Science</i> , 2021 , 30, 940-955	5.5	2
169	Salmonella effector SopD promotes plasma membrane scission by inhibiting Rab10. <i>Nature Communications</i> , 2021 , 12, 4707	17.4	1
168	The 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	11.5	5
167	Interaction of the Ankyrin H Core Effector of with the Host LARP7 Component of the 7SK snRNP Complex. <i>MBio</i> , 2019 , 10,	7.8	13
166	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	7.6	33
165	The structure of Legionella effector protein LpnE provides insights into its interaction with Oculocerebrorenal syndrome of Lowe (OCRL) protein. <i>FEBS Journal</i> , 2019 , 286, 710-725	5.7	6
164	Structure-function analyses of a PL24 family ulvan lyase reveal key features and suggest its catalytic mechanism. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4026-4036	5.4	18
163	effector Lem4 is a membrane-associated protein tyrosine phosphatase. <i>Journal of Biological Chemistry</i> , 2018 , 293, 13044-13058	5.4	6
162	Regulation of Shigella Effector Kinase OspG through Modulation of Its Dynamic Properties. <i>Journal of Molecular Biology</i> , 2018 , 430, 2096-2112	6.5	5
161	Structural and functional characterization of PL28 family ulvan lyase NLR48 from. <i>Journal of Biological Chemistry</i> , 2018 , 293, 11564-11573	5.4	18
160	Structural Mimicry by a Bacterial F Box Effector Hijacks the Host Ubiquitin-Proteasome System. <i>Structure</i> , 2017 , 25, 376-383	5.2	15

159	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	4.9	34
158	Insights from protein-protein interaction studies on bacterial pathogenesis. <i>Expert Review of Proteomics</i> , 2017 , 14, 779-797	4.2	8
157	Structure and functional dynamics of the mitochondrial Fe/S cluster synthesis complex. <i>Nature Communications</i> , 2017 , 8, 1287	17.4	95
156	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	5.8	10
155	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. <i>PLoS Pathogens</i> , 2017 , 13, e1006394	7.6	32
154	Structural and Functional Investigations of the Effector Protein LpiR1 from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , 2016 , 291, 15767-77	5.4	3
153	Crystal Structure of the <i>Salmonella Typhimurium</i> Effector GtgE. <i>PLoS ONE</i> , 2016 , 11, e0166643	3.7	8
152	Structural insight into effector proteins of Gram-negative bacterial pathogens that modulate the phosphoproteome of their host. <i>Protein Science</i> , 2015 , 24, 604-20	6.3	12
151	<i>Salmonella</i> Disrupts Host Endocytic Trafficking by SopD2-Mediated Inhibition of Rab7. <i>Cell Reports</i> , 2015 , 12, 1508-18	10.6	58
150	Quaternary structure of WzzB and WzzE polysaccharide copolymerases. <i>Protein Science</i> , 2015 , 24, 58-69	6.3	18
149	Structural Organization of Enzymes of the Phenylacetate Catabolic Hybrid Pathway. <i>Biology</i> , 2015 , 4, 424-42	4.9	6
148	Progress in understanding the assembly process of bacterial O-antigen. <i>FEMS Microbiology Reviews</i> , 2014 , 38, 1048-65	15.1	69
147	Coiled-coil helix rotation selects repressing or activating state of transcriptional regulator DhaR. <i>Structure</i> , 2014 , 22, 478-87	5.2	15
146	Structural basis for the inhibition of host protein ubiquitination by <i>Shigella</i> effector kinase OspG. <i>Structure</i> , 2014 , 22, 878-88	5.2	33
145	Structure of CbpA J-domain bound to the regulatory protein Cbpm explains its specificity and suggests evolutionary link between Cbpm and transcriptional regulators. <i>PLoS ONE</i> , 2014 , 9, e100441	3.7	6
144	Uronic polysaccharide degrading enzymes. <i>Current Opinion in Structural Biology</i> , 2014 , 28, 87-95	8.1	35
143	A case study on the treatment of protein SIRAS data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2686-91		2
142	NleH defines a new family of bacterial effector kinases. <i>Structure</i> , 2014 , 22, 250-9	5.2	20

141	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, 436-41		9
140	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, 11824-9	11.5	11
139	Cloning, Baeyer-Villiger biooxidations, and structures of the camphor pathway 2-oxo-(B)-4,5,5-trimethylcyclopentenylacetyl-coenzyme A monooxygenase of <i>Pseudomonas putida</i> ATCC 17453. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 2200-12	4.8	48
138	Structural characterization of closely related O-antigen lipopolysaccharide (LPS) chain length regulators. <i>Journal of Biological Chemistry</i> , 2012 , 287, 15696-705	5.4	21
137	Protein-protein interactions in the oxidation part of the phenylacetate utilization pathway: crystal structure of the PaaF-PaaG hydratase-isomerase complex. <i>Journal of Biological Chemistry</i> , 2012 , 287, 37986-96	5.4	9
136	Characterization of interactions between LPS transport proteins of the Lpt system. <i>Biochemical and Biophysical Research Communications</i> , 2011 , 404, 1093-8	3.4	35
135	Genetic selection designed to stabilize proteins uncovers a chaperone called Spy. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 262-9	17.6	115
134	Structure of hydrogenase maturation protein HypF with reaction intermediates shows two active sites. <i>Structure</i> , 2011 , 19, 1773-83	5.2	38
133	Synthesis, structural, and biological studies on a pseudodisaccharide containing a bicyclic, bridged carba-sugar. <i>Tetrahedron: Asymmetry</i> , 2011 , 22, 1404-1410		
132	Asparagine 405 of heparin lyase II prevents the cleavage of glycosidic linkages proximate to a 3-O-sulfoglucosamine residue. <i>FEBS Letters</i> , 2011 , 585, 2461-6	3.8	16
131	Structural and enzymatic characterization of NanS (YjHS), a 9-O-Acetyl N-acetylneuraminic acid esterase from <i>Escherichia coli</i> O157:H7. <i>Protein Science</i> , 2011 , 20, 1208-19	6.3	27
130	Structural and functional studies of the <i>Escherichia coli</i> phenylacetyl-CoA monooxygenase complex. <i>Journal of Biological Chemistry</i> , 2011 , 286, 10735-43	5.4	35
129	Structure-guided investigation of lipopolysaccharide O-antigen chain length regulators reveals regions critical for modal length control. <i>Journal of Bacteriology</i> , 2011 , 193, 3710-21	3.5	24
128	Structural and mechanistic insight into covalent substrate binding by <i>Escherichia coli</i> dihydroxyacetone kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 1302-7	11.5	32
127	Catalytic mechanism of heparinase II investigated by site-directed mutagenesis and the crystal structure with its substrate. <i>Journal of Biological Chemistry</i> , 2010 , 285, 20051-61	5.4	39
126	Structural basis for Fe-S cluster assembly and tRNA thiolation mediated by IscS protein-protein interactions. <i>PLoS Biology</i> , 2010 , 8, e1000354	9.7	194
125	Structural and mechanistic classification of uronic acid-containing polysaccharide lyases. <i>Glycobiology</i> , 2010 , 20, 1547-73	5.8	165
124	Structural basis of the regulation of the CbpA co-chaperone by its specific modulator CbpM. <i>Journal of Molecular Biology</i> , 2010 , 398, 111-21	6.5	10

123	Structural snapshots of heparin depolymerization by heparin lyase I. <i>Journal of Biological Chemistry</i> , 2009 , 284, 34019-27	5.4	44
122	Structural and functional analysis of Campylobacter jejuni PseG: a udp-sugar hydrolase from the pseudaminic acid biosynthetic pathway. <i>Journal of Biological Chemistry</i> , 2009 , 284, 20989-1000	5.4	15
121	Structure-function analysis of Escherichia coli MnmG (GidA), a highly conserved tRNA-modifying enzyme. <i>Journal of Bacteriology</i> , 2009 , 191, 7614-9	3.5	37
120	Structure of the noncatalytic domains and global fold of the protein disulfide isomerase ERp72. <i>Structure</i> , 2009 , 17, 651-9	5.2	41
119	Sequence-structure relationships in polysaccharide co-polymerase (PCP) proteins. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 78-84	10.3	68
118	Trapping open and closed forms of FitE: a group III periplasmic binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 598-609	4.2	26
117	Structure and function of the glycopeptide N-methyltransferase MtfA, a tool for the biosynthesis of modified glycopeptide antibiotics. <i>Chemistry and Biology</i> , 2009 , 16, 401-10		33
116	Liquid chromatography-mass spectrometry to study chondroitin lyase action pattern. <i>Analytical Biochemistry</i> , 2009 , 385, 57-64	3.1	16
115	Preparation and characterization of bacterial protein complexes for structural analysis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009 , 76, 1-42	5.3	4
114	Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 130-8	17.6	89
113	Molecular dynamics-solvated interaction energy studies of protein-protein interactions: the MP1-p14 scaffolding complex. <i>Journal of Molecular Biology</i> , 2008 , 379, 787-802	6.5	115
112	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, 1183-9	4.8	53
111	Structure of L-xylulose-5-Phosphate 3-epimerase (UlaE) from the anaerobic L-ascorbate utilization pathway of Escherichia coli: identification of a novel phosphate binding motif within a TIM barrel fold. <i>Journal of Bacteriology</i> , 2008 , 190, 8137-44	3.5	13
110	Structure of [NiFe] hydrogenase maturation protein HypE from Escherichia coli and its interaction with HypF. <i>Journal of Bacteriology</i> , 2008 , 190, 1447-58	3.5	40
109	The Contribution of Structural Proteomics to Understanding the Function of Hypothetical Proteins 2008 , 135-151		
108	Quantitative continuous assay for hyaluronan synthase. <i>Analytical Biochemistry</i> , 2007 , 361, 218-25	3.1	12
107	NMR structure of YcgL, a conserved protein from Escherichia coli representing the DUF709 family, with a novel alpha/beta/alpha sandwich fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 66, 1004-7	4.2	2
106	Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from Campylobacter jejuni. <i>Protein Science</i> , 2007 , 16, 990-5	6.3	31

105	Insights into the biology of Escherichia coli through structural proteomics. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 45-55		4
104	Crystal structure of StaL, a glycopeptide antibiotic sulfotransferase from Streptomyces toyocaensis. <i>Journal of Biological Chemistry</i> , 2007 , 282, 13073-86	5.4	16
103	Crystal structure of the bbQ domains of the protein disulfide isomerase ERp57. <i>Structure</i> , 2006 , 14, 1331-9.2	9.2	113
102	An atypical approach identifies TYR234 as the key base catalyst in chondroitin AC lyase. <i>ChemBioChem</i> , 2006 , 7, 631-7	3.8	11
101	Structural snapshots of Escherichia coli histidinol phosphate phosphatase along the reaction pathway. <i>Journal of Biological Chemistry</i> , 2006 , 281, 37930-41	5.4	35
100	Structural and functional characterization of PseC, an aminotransferase involved in the biosynthesis of pseudaminic acid, an essential flagellar modification in Helicobacter pylori. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8907-16	5.4	78
99	Crystal structure of heparinase II from Pedobacter heparinus and its complex with a disaccharide product. <i>Journal of Biological Chemistry</i> , 2006 , 281, 15525-35	5.4	73
98	CS lyases: structure, activity, and applications in analysis and the treatment of diseases. <i>Advances in Pharmacology</i> , 2006 , 53, 187-215	5.7	43
97	The architecture of the multisubunit TRAPP I complex suggests a model for vesicle tethering. <i>Cell</i> , 2006 , 127, 817-30	56.2	149
96	Domain organization and crystal structure of the catalytic domain of E.coli RluF, a pseudouridine synthase that acts on 23S rRNA. <i>Journal of Molecular Biology</i> , 2006 , 359, 998-1009	6.5	11
95	The structure of the exopolyphosphatase (PPX) from Escherichia coli O157:H7 suggests a binding mode for long polyphosphate chains. <i>Journal of Molecular Biology</i> , 2006 , 359, 1249-60	6.5	42
94	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 278-84	4.2	21
93	Biochemical and crystallographic studies reveal a specific interaction between TRAPP subunits Trs33p and Bet3p. <i>Traffic</i> , 2005 , 6, 1183-95	5.7	22
92	Crystal structure of ureidoglycolate hydrolase (AllA) from Escherichia coli O157:H7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 454-9	4.2	9
91	Crystal structure of N-succinylarginine dihydrolase AstB, bound to substrate and product, an enzyme from the arginine catabolic pathway of Escherichia coli. <i>Journal of Biological Chemistry</i> , 2005 , 280, 15800-8	5.4	22
90	Site-directed mutagenesis of the active site region in the quinate/shikimate 5-dehydrogenase YdiB of Escherichia coli. <i>Journal of Biological Chemistry</i> , 2005 , 280, 7162-9	5.4	20
89	Identification of an Escherichia coli 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, 16955-60	11.5	77
88	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, 18326-31	11.5	40

87	Crystallographic trapping of the glutamyl-CoA thioester intermediate of family I CoA transferases. <i>Journal of Biological Chemistry</i> , 2005 , 280, 42919-28	5.4	26
86	Crystal structure of a dodecameric FMN-dependent UbiX-like decarboxylase (Pad1) from <i>Escherichia coli</i> O157: H7. <i>Protein Science</i> , 2004 , 13, 3006-16	6.3	42
85	Structural similarity of YbeD protein from <i>Escherichia coli</i> to allosteric regulatory domains. <i>Journal of Bacteriology</i> , 2004 , 186, 8083-8	3.5	10
84	The structure of the MAPK scaffold, MP1, bound to its partner, p14. A complex with a critical role in endosomal map kinase signaling. <i>Journal of Biological Chemistry</i> , 2004 , 279, 23422-30	5.4	59
83	Crystal structures of <i>Escherichia coli</i> ATP-dependent glucokinase and its complex with glucose. <i>Journal of Bacteriology</i> , 2004 , 186, 6915-27	3.5	67
82	The structure of chondroitin B lyase complexed with glycosaminoglycan oligosaccharides unravels a calcium-dependent catalytic machinery. <i>Journal of Biological Chemistry</i> , 2004 , 279, 32882-96	5.4	76
81	¹ H, ¹³ C and ¹⁵ N resonance assignments of human 5,10-methenyltetrahydrofolate synthetase. <i>Journal of Biomolecular NMR</i> , 2004 , 29, 547-8	3	
80	The structural genomics experimental pipeline: insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 201-10	4.2	27
79	Crystallization and preliminary X-ray analysis of heparinase II from <i>Pedobacter heparinus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1644-6		7
78	Insights into function of PSI domains from structure of the Met receptor PSI domain. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 321, 234-40	3.4	33
77	Crystal structure of the RluD pseudouridine synthase catalytic module, an enzyme that modifies 23S rRNA and is essential for normal cell growth of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2004 , 335, 87-101	6.5	36
76	High-resolution crystal structure of <i>Arthrobacter aureus</i> chondroitin AC lyase: an enzyme-substrate complex defines the catalytic mechanism. <i>Journal of Molecular Biology</i> , 2004 , 337, 367-86	6.5	87
75	Essential roles of zinc ligation and enzyme dimerization for catalysis in the aminoacylase-1/M20 family. <i>Journal of Biological Chemistry</i> , 2003 , 278, 44496-504	5.4	66
74	The solution structure of YbcJ from <i>Escherichia coli</i> reveals a recently discovered alphaL motif involved in RNA binding. <i>Journal of Bacteriology</i> , 2003 , 185, 4204-10	3.5	10
73	Coverage of protein sequence space by current structural genomics targets. <i>Journal of Structural and Functional Genomics</i> , 2003 , 4, 47-55		11
72	Lectin control of protein folding and sorting in the secretory pathway. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 49-57	10.3	155
71	The final player in the coenzyme A biosynthetic pathway. <i>Structure</i> , 2003 , 11, 899-900	5.2	2
70	Molecules of <i>Escherichia coli</i> MobB assemble into densely packed hollow cylinders in a crystal lattice with 75% solvent content. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 2348-52		

69	Crystal structure of a trimeric form of dephosphocoenzyme A kinase from Escherichia coli. <i>Protein Science</i> , 2003 , 12, 327-36	6.3	26
68	Crystal structure of Proteus vulgaris chondroitin sulfate ABC lyase I at 1.9Å resolution. <i>Journal of Molecular Biology</i> , 2003 , 328, 623-34	6.5	86
67	Crystal structure of Escherichia coli PdxA, an enzyme involved in the pyridoxal phosphate biosynthesis pathway. <i>Journal of Biological Chemistry</i> , 2003 , 278, 43682-90	5.4	31
66	Structures of shikimate dehydrogenase AroE and its Paralog YdiB. A common structural framework for different activities. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19463-72	5.4	81
65	Contribution of structural genomics to understanding the biology of Escherichia coli. <i>Journal of Bacteriology</i> , 2003 , 185, 3994-4002	3.5	16
64	The structure of the RlmB 23S rRNA methyltransferase reveals a new methyltransferase fold with a unique knot. <i>Structure</i> , 2002 , 10, 1303-15	5.2	84
63	Crystal structure of D-ribose-5-phosphate isomerase (RpiA) from Escherichia coli. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 737-40	4.2	29
62	Structure of the 16S rRNA pseudouridine synthase RsuA bound to uracil and UMP. <i>Nature Structural Biology</i> , 2002 , 9, 353-8		31
61	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, 1859-64	11.5	45
60	Crystal structure of Escherichia coli glucose-1-phosphate thymidyltransferase (RffH) complexed with dTTP and Mg ²⁺ . <i>Journal of Biological Chemistry</i> , 2002 , 277, 44214-9	5.4	61
59	Design of noncovalent inhibitors of human cathepsin L. From the 96-residue proregion to optimized tripeptides. <i>Journal of Medicinal Chemistry</i> , 2002 , 45, 5321-9	8.3	63
58	Structure of Ca(2+)-loaded human grancalcin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 1843-9		12
57	A structural genomics pilot project based on gene targets selected from Escherichia coli. <i>Journal of Crystal Growth</i> , 2001 , 232, 421-425	1.6	1
56	Structure of apoptosis-linked protein ALG-2: insights into Ca ²⁺ -induced changes in penta-EF-hand proteins. <i>Structure</i> , 2001 , 9, 267-75	5.2	65
55	The crystal structure of Escherichia coli MoeA, a protein from the molybdopterin synthesis pathway. <i>Journal of Molecular Biology</i> , 2001 , 310, 419-31	6.5	45
54	Crystal structure of histidinol phosphate aminotransferase (HisC) from Escherichia coli, and its covalent complex with pyridoxal-5-phosphate and L-histidinol phosphate. <i>Journal of Molecular Biology</i> , 2001 , 311, 761-76	6.5	38
53	The Structure of calnexin, an ER chaperone involved in quality control of protein folding. <i>Molecular Cell</i> , 2001 , 8, 633-44	17.6	323
52	Crystallization and preliminary X-ray analysis of human grancalcin, a novel cytosolic Ca ²⁺ -binding protein present in leukocytes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 772-4		4

51	Crystallization and preliminary X-ray analysis of chondroitin sulfate ABC lyases I and II from <i>Proteus vulgaris</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 904-6		5
50	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, 939-51	6.5	76
49	Crystal structure of human grancalcin, a member of the penta-EF-hand protein family. <i>Journal of Molecular Biology</i> , 2000 , 300, 1271-81	6.5	39
48	Crystal structure of wild-type human procathepsin K. <i>Protein Science</i> , 1999 , 8, 283-90	6.3	50
47	Crystallization and preliminary X-ray analysis of chondroitinase B from <i>Flavobacterium heparinum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 1055-7		6
46	Crystal structure of chondroitin AC lyase, a representative of a family of glycosaminoglycan degrading enzymes. <i>Journal of Molecular Biology</i> , 1999 , 288, 635-47	6.5	86
45	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, 1257-69	6.5	95
44	Creation of a ribonuclease abzyme through site-directed mutagenesis. <i>Nature Biotechnology</i> , 1998 , 16, 1065-7	44.5	19
43	The 3-D structure of a folate-dependent dehydrogenase/cyclohydrolase bifunctional enzyme at 1.5 Å resolution. <i>Structure</i> , 1998 , 6, 173-82	5.2	61
42	Crystallization and preliminary analysis of chondroitinase AC from <i>Flavobacterium heparinum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 279-80		7
41	Lipases and alpha/beta hydrolase fold. <i>Methods in Enzymology</i> , 1997 , 284, 85-107	1.7	191
40	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	2	48
39	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	3.8	87
38	Structure as basis for understanding interfacial properties of lipases. <i>Methods in Enzymology</i> , 1997 , 284, 3-27	1.7	67
37	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, 532-8		162
36	The open conformation of a <i>Pseudomonas</i> lipase. <i>Structure</i> , 1997 , 5, 187-202	5.2	257
35	Crystal structure of two new bifunctional nonsubstrate type thrombin inhibitors complexed with human alpha-thrombin. <i>Protein Science</i> , 1996 , 5, 1174-83	6.3	14
34	Purification and characterization of a <i>Penicillium</i> sp. lipase which discriminates against diglycerides. <i>Lipids</i> , 1996 , 31, 379-84	1.6	28

33	Structure of rat procathepsin B: model for inhibition of cysteine protease activity by the proregion. <i>Structure</i> , 1996 , 4, 405-16	5.2	162
32	Crystallization of the bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase domain of the human trifunctional enzyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 479-80	4.2	6
31	Crystallization of a soluble form of the Kex1p serine carboxypeptidase from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , 1996 , 5, 395-7	6.3	10
30	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, 535-7	6.3	25
29	Crystallization and preliminary x-ray diffraction studies of human procathepsin L. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 398-400	4.2	12
28	Redesigning the active site of <i>Geotrichum candidum</i> lipase. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 835-42	1.9	10
27	<i>Bacillus thuringiensis</i> CryIA(a) insecticidal toxin: crystal structure and channel formation. <i>Journal of Molecular Biology</i> , 1995 , 254, 447-64	6.5	450
26	Two conformational states of <i>Candida rugosa</i> lipase. <i>Protein Science</i> , 1994 , 3, 82-91	6.3	306
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24	Crystallization and preliminary X-ray diffraction studies of the lepidopteran-specific insecticidal crystal protein CryIA(a). <i>Journal of Molecular Biology</i> , 1994 , 243, 530-2	6.5	11
23	A Structural Basis for the Chiral Preferences of Lipases. <i>Journal of the American Chemical Society</i> , 1994 , 116, 3180-3186	16.4	308
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19	Crystal structure of the complex of human alpha-thrombin and nonhydrolyzable bifunctional inhibitors, hirutinin-2 and hirutinin-6. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 17, 252-65	4.2	34
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1	Salmonella effectors SseK1 and SseK3 target death domain proteins in the TNF and TRAIL signaling pathways		1