

Mirosław Cygler

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9373721/publications.pdf>

Version: 2024-02-01

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	Structural biology of the invasion arsenal of Gram-negative bacterial pathogens. FEBS Journal, 2022, 289, 1385-1427.	2.2	5
2	Disulfide Bonds Play a Critical Role in the Structure and Function of the Receptor-binding Domain of the SARS-CoV-2 Spike Antigen. Journal of Molecular Biology, 2022, 434, 167357.	2.0	43
3	Structural study of <i>Legionella pneumophila</i> effector DotY (Lpg0294), a component of the Dot/Icm type IV secretion system. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 276-280.	0.4	0
4	The KH domain facilitates the substrate specificity and unwinding processivity of DDX43 helicase. Journal of Biological Chemistry, 2021, 296, 100085.	1.6	15
5	An Indispensable Role for the MavE Effector of <i>Legionella pneumophila</i> in Lysosomal Evasion. MBio, 2021, 12, .	1.8	5
6	Structural and functional study of <i>Legionella pneumophila</i> effector RavA. Protein Science, 2021, 30, 940-955.	3.1	6
7	Salmonella effector SopD promotes plasma membrane scission by inhibiting Rab10. Nature Communications, 2021, 12, 4707.	5.8	8
8	Structural and Functional Characterization of <i>Legionella pneumophila</i> Effector MavL. Biomolecules, 2021, 11, 1802.	1.8	5
9	N-terminal tyrosine of ISCU2 triggers [2Fe-2S] cluster synthesis by ISCU2 dimerization. Nature Communications, 2021, 12, 6902.	5.8	15
10	<i>Legionella</i> effector LegA15/AnkH contains an unrecognized cysteine protease-like domain and displays structural similarity to LegA3/AnkD, but differs in host cell localization. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1535-1542.	1.1	1
11	The <i>Legionella</i> kinase LegK7 exploits the Hippo pathway scaffold protein MOB1A for allostery and substrate phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14433-14443.	3.3	10
12	Interaction of the Ankyrin H Core Effector of <i>Legionella</i> with the Host LARP7 Component of the 7SK snRNP Complex. MBio, 2019, 10, .	1.8	27
13	Salmonella Effectors SseK1 and SseK3 Target Death Domain Proteins in the TNF and TRAIL Signaling Pathways*. Molecular and Cellular Proteomics, 2019, 18, 1138-1156.	2.5	55
14	The structure of <i>Legionella</i> effector protein LpnE provides insights into its interaction with Oculocerebrorenal syndrome of Lowe (OCRL) protein. FEBS Journal, 2019, 286, 710-725.	2.2	9
15	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
16	Regulation of Shigella Effector Kinase OspG through Modulation of Its Dynamic Properties. Journal of Molecular Biology, 2018, 430, 2096-2112.	2.0	8
17	Structural and functional characterization of PL28 family ulvan lyase NLR48 from <i>Nonlabens ulvanivorans</i> . Journal of Biological Chemistry, 2018, 293, 11564-11573.	1.6	25
18	<i>Legionella pneumophila</i> effector Lem4 is a membrane-associated protein tyrosine phosphatase. Journal of Biological Chemistry, 2018, 293, 13044-13058.	1.6	14

#	ARTICLE	IF	CITATIONS
19	Structural And Functional Characterization Of Ulvan Degrading Polysaccharide Lyase Enzymes. FASEB Journal, 2018, 32, .	0.2	0
20	Structural Mimicry by a Bacterial F Box Effector Hijacks the Host Ubiquitin-Proteasome System. Structure, 2017, 25, 376-383.	1.6	22
21	New Ulvan-Degrading Polysaccharide Lyase Family: Structure and Catalytic Mechanism Suggests Convergent Evolution of Active Site Architecture. ACS Chemical Biology, 2017, 12, 1269-1280.	1.6	60
22	Insights from protein-protein interaction studies on bacterial pathogenesis. Expert Review of Proteomics, 2017, 14, 779-797.	1.3	11
23	Structure and functional dynamics of the mitochondrial Fe/S cluster synthesis complex. Nature Communications, 2017, 8, 1287.	5.8	144
24	Conformational flexibility of PL12 family heparinases: structure and substrate specificity of heparinase III from <i>Bacteroides thetaiotaomicron</i> (BT4657). Glycobiology, 2017, 27, 176-187.	1.3	14
25	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. PLoS Pathogens, 2017, 13, e1006394.	2.1	53
26	Crystal Structure of the Salmonella Typhimurium Effector GtgE. PLoS ONE, 2016, 11, e0166643.	1.1	9
27	Structural and Functional Investigations of the Effector Protein LpIR1 from Legionella pneumophila. Journal of Biological Chemistry, 2016, 291, 15767-15777.	1.6	3
28	Structural Organization of Enzymes of the Phenylacetate Catabolic Hybrid Pathway. Biology, 2015, 4, 424-442.	1.3	10
29	Structural insight into effector proteins of Gram-negative bacterial pathogens that modulate the phosphoproteome of their host. Protein Science, 2015, 24, 604-620.	3.1	17
30	Salmonella Disrupts Host Endocytic Trafficking by SopD2-Mediated Inhibition of Rab7. Cell Reports, 2015, 12, 1508-1518.	2.9	83
31	Quaternary structure of WzzB and WzzE polysaccharide copolymerases. Protein Science, 2015, 24, 58-69.	3.1	19
32	Structure of CbpA J-Domain Bound to the Regulatory Protein CbpM Explains Its Specificity and Suggests Evolutionary Link between CbpM and Transcriptional Regulators. PLoS ONE, 2014, 9, e100441.	1.1	8
33	Uronic polysaccharide degrading enzymes. Current Opinion in Structural Biology, 2014, 28, 87-95.	2.6	49
34	A case study on the treatment of protein SIRAS data. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2686-2691.	2.5	3
35	NleH Defines a New Family of Bacterial Effector Kinases. Structure, 2014, 22, 250-259.	1.6	28
36	Progress in understanding the assembly process of bacterial O-antigen. FEMS Microbiology Reviews, 2014, 38, 1048-1065.	3.9	96

#	ARTICLE	IF	CITATIONS
37	Coiled-Coil Helix Rotation Selects Repressing or Activating State of Transcriptional Regulator DhaR. <i>Structure</i> , 2014, 22, 478-487.	1.6	18
38	Structural Basis for the Inhibition of Host Protein Ubiquitination by <i>Shigella</i> Effector Kinase OspG. <i>Structure</i> , 2014, 22, 878-888.	1.6	40
39	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
40	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
41	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
42	Protein-Protein Interactions in the β^2 -Oxidation Part of the Phenylacetate Utilization Pathway. <i>Journal of Biological Chemistry</i> , 2012, 287, 37986-37996.	1.6	12
43	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
44	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
45	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
46	Structure of Hydrogenase Maturation Protein HypF with Reaction Intermediates Shows Two Active Sites. <i>Structure</i> , 2011, 19, 1773-1783.	1.6	44
47	Synthesis, structural, and biological studies on a pseudodisaccharide containing a bicyclic, bridged carba-sugar. <i>Tetrahedron: Asymmetry</i> , 2011, 22, 1404-1410.	1.8	0
48	Asparagine 405 of heparin lyase II prevents the cleavage of glycosidic linkages proximate to a β -sulfoglucosamine residue. <i>FEBS Letters</i> , 2011, 585, 2461-2466.	1.3	18
49	Structural and enzymatic characterization of NanS (YjhS), a β -Acetyl β -N-acetylneuraminic acid esterase from <i>Escherichia coli</i> O157:H7. <i>Protein Science</i> , 2011, 20, 1208-1219.	3.1	33
50	Structural and Functional Studies of the <i>Escherichia coli</i> Phenylacetyl-CoA Monooxygenase Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 10735-10743.	1.6	41
51	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
52	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, 1302-1307.	3.3	37
53	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, 20051-20061.	1.6	39
54	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

#	ARTICLE	IF	CITATIONS
55	Structural and mechanistic classification of uronic acid-containing polysaccharide lyases. <i>Glycobiology</i> , 2010, 20, 1547-1573.	1.3	207
56	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
57	Structural Snapshots of Heparin Depolymerization by Heparin Lyase I. <i>Journal of Biological Chemistry</i> , 2009, 284, 34019-34027.	1.6	58
58	Structural and Functional Analysis of <i>Campylobacter jejuni</i> PseG. <i>Journal of Biological Chemistry</i> , 2009, 284, 20989-21000.	1.6	21
59	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
60	Structure of the Noncatalytic Domains and Global Fold of the Protein Disulfide Isomerase ERp72. <i>Structure</i> , 2009, 17, 651-659.	1.6	44
61	Sequence-structure relationships in polysaccharide co-polymerase (PCP) proteins. <i>Trends in Biochemical Sciences</i> , 2009, 34, 78-84.	3.7	76
62	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
63	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, 401-410.	6.2	37
64	Liquid chromatography-mass spectrometry to study chondroitin lyase action pattern. <i>Analytical Biochemistry</i> , 2009, 385, 57-64.	1.1	19
65	Preparation and Characterization of Bacterial Protein Complexes for Structural Analysis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 76, 1-42.	1.0	4
66	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
67	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
68	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
69	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
70	Structure of Xylulose-5-Phosphate 3-Epimerase (UlaE) from the Anaerobic -Ascorbate Utilization Pathway of <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
71	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
72	The Contribution of Structural Proteomics to Understanding the Function of Hypothetical Proteins. , 2008, , 135-151.		0

#	ARTICLE	IF	CITATIONS
73	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
74	Quantitative continuous assay for hyaluronan synthase. <i>Analytical Biochemistry</i> , 2007, 361, 218-225.	1.1	13
75	NMR structure of YcgL, a conserved protein from <i>Escherichia coli</i> representing the DUF709 family, with a novel $\beta\alpha\beta\alpha$ sandwich fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 66, 1004-1007.	1.5	2
76	Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from <i>Campylobacter jejuni</i> . <i>Protein Science</i> , 2007, 16, 990-995.	3.1	38
77	Insights into the biology of <i>Escherichia coli</i> through structural proteomics. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 45-55.	1.2	5
78	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
79	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. <i>Cell</i> , 2006, 127, 817-830.	13.5	166
80	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
81	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
82	Crystal Structure of the β^2 Domains of the Protein Disulfide Isomerase ERp57. <i>Structure</i> , 2006, 14, 1331-1339.	1.6	127
83	An Atypical Approach Identifies TYR234 as the Key Base Catalyst in Chondroitin AC Lyase. <i>ChemBioChem</i> , 2006, 7, 631-637.	1.3	13
84	Structural Snapshots of <i>Escherichia coli</i> Histidinol Phosphate Phosphatase along the Reaction Pathway. <i>Journal of Biological Chemistry</i> , 2006, 281, 37930-37941.	1.6	39
85	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
86	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
87	Biochemical and Crystallographic Studies Reveal a Specific Interaction Between TRAPP Subunits Trs33p and Bet3p. <i>Traffic</i> , 2005, 6, 1183-1195.	1.3	26
88	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
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	Crystallographic Trapping of the Glutamyl-CoA Thioester Intermediate of Family I CoA Transferases. <i>Journal of Biological Chemistry</i> , 2005, 280, 42919-42928.	1.6	34
94	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
95	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
96	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
97	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
98	Defining Substrate Characteristics from 3D Structure. <i>Structure</i> , 2004, 12, 521-522.	1.6	3
99	Letter to the Editor: ¹ H, ¹³ C and ¹⁵ N resonance assignments of human 5,10-methylenetetrahydrofolate synthetase. <i>Journal of Biomolecular NMR</i> , 2004, 29, 547-548.	1.6	0
100	The structural genomics experimental pipeline: Insights from global target lists. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 201-210.	1.5	36
101	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
102	Crystallization and preliminary X-ray analysis of heparinase II from <i>Pedobacter heparinus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1644-1646.	2.5	7
103	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
104	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.	2.0	38
105	High-resolution Crystal Structure of <i>Arthrobacter aurescens</i> Chondroitin AC Lyase: An Enzyme's Substrate Complex Defines the Catalytic Mechanism. <i>Journal of Molecular Biology</i> , 2004, 337, 367-386.	2.0	97
106	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
107	Lectin control of protein folding and sorting in the secretory pathway. <i>Trends in Biochemical Sciences</i> , 2003, 28, 49-57.	3.7	170
108	The Final Player in the Coenzyme A Biosynthetic Pathway. <i>Structure</i> , 2003, 11, 899-900.	1.6	2

#	ARTICLE	IF	CITATIONS
109	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, 2348-2352.	2.5	1
110	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
111	Crystal Structure of <i>Proteus vulgaris</i> Chondroitin Sulfate ABC Lyase I at 1.9Å... Resolution. <i>Journal of Molecular Biology</i> , 2003, 328, 623-634.	2.0	98
112	Crystal Structure of <i>Escherichia coli</i> PdxA, an Enzyme Involved in the Pyridoxal Phosphate Biosynthesis Pathway. <i>Journal of Biological Chemistry</i> , 2003, 278, 43682-43690.	1.6	37
113	Structures of Shikimate Dehydrogenase AroE and Its Paralog YdiB. <i>Journal of Biological Chemistry</i> , 2003, 278, 19463-19472.	1.6	111
114	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
115	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
116	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
117	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
118	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
119	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
120	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
121	Crystal structure of D-ribose-5-phosphate isomerase (RpiA) from <i>Escherichia coli</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 737-740.	1.5	32
122	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
123	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
124	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
125	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
126	Structure of Ca ²⁺ -loaded human grancalcin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1843-1849.	2.5	16

#	ARTICLE	IF	CITATIONS
127	A structural genomics pilot project based on gene targets selected from Escherichia coli. Journal of Crystal Growth, 2001, 232, 421-425.	0.7	1
128	Structure of Apoptosis-Linked Protein ALG-2. Structure, 2001, 9, 267-275.	1.6	77
129	Crystallization and preliminary X-ray analysis of human grancalcin, a novel cytosolic Ca ²⁺ -binding protein present in leukocytes. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 772-774.	2.5	5
130	Crystallization and preliminary X-ray analysis of chondroitin sulfate ABC lyases I and II from Proteus vulgaris. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 904-906.	2.5	9
131	Crystal structure of human procathepsin X: a cysteine protease with the proregion covalently linked to the active site cysteine. Journal of Molecular Biology, 2000, 295, 939-951.	2.0	82
132	Crystal structure of human grancalcin, a member of the penta-EF-hand protein family 11 Edited by I. Wilson. Journal of Molecular Biology, 2000, 300, 1271-1281.	2.0	49
133	Crystallization and preliminary X-ray analysis of chondroitinase B from Flavobacterium heparinum. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1055-1057.	2.5	8
134	Crystal structure of chondroitin AC lyase, a representative of a family of glycosaminoglycan degrading enzymes 1 Edited by D. Rees. Journal of Molecular Biology, 1999, 288, 635-647.	2.0	96
135	Crystal structure of chondroitinase B from Flavobacterium heparinum and its complex with a disaccharide product at 1.7 Å resolution. Journal of Molecular Biology, 1999, 294, 1257-1269.	2.0	107
136	Crystal structure of wild-type human procathepsin K. Protein Science, 1999, 8, 283-290.	3.1	58
137	Creation of a ribonuclease abzyme through site-directed mutagenesis. Nature Biotechnology, 1998, 16, 1065-1067.	9.4	22
138	The 3-D structure of a folate-dependent dehydrogenase/cyclohydrolase bifunctional enzyme at 1.5 Å resolution. Structure, 1998, 6, 173-182.	1.6	68
139	Crystallization and preliminary analysis of chondroitinase AC from Flavobacterium heparinum. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 279-280.	2.5	9
140	[4] Lipases and hydrolase fold. Methods in Enzymology, 1997, 284, 85-107.	0.4	224
141	High-Level Production of Recombinant Geotrichum candidum Lipases in Yeast Pichia pastoris. Protein Expression and Purification, 1997, 11, 35-40.	0.6	50
142	Restriction of intramolecular movements within the Cry1Aa toxin molecule of Bacillus thuringiensis through disulfide bond engineering. FEBS Letters, 1997, 410, 397-402.	1.3	110
143	[1] Structure as basis for understanding interfacial properties of lipases. Methods in Enzymology, 1997, 284, 3-27.	0.4	81
144	Structure of a calpain Ca ²⁺ -binding domain reveals a novel EF-hand and Ca ²⁺ -induced conformational changes. Nature Structural Biology, 1997, 4, 532-538.	9.7	192

#	ARTICLE	IF	CITATIONS
145	The open conformation of a <i>Pseudomonas</i> lipase. <i>Structure</i> , 1997, 5, 187-202.	1.6	275
146	Crystal structure of two new bifunctional nonsubstrate type thrombin inhibitors complexed with human α_2 -thrombin. <i>Protein Science</i> , 1996, 5, 1174-1183.	3.1	16
147	Purification and characterization of a <i>Penicillium</i> sp. lipase which discriminates against diglycerides. <i>Lipids</i> , 1996, 31, 379-384.	0.7	32
148	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
149	Crystallization of the bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase domain of the human trifunctional enzyme. <i>Structure</i> , 1996, 26, 479-480.		6
150	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
151	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
152	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
153	Redesigning the active site of <i>Geotrichum candidum</i> lipase. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 835-842.	1.0	11
154	<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
155	Two conformational states of <i>Candida rugosa</i> lipase. <i>Protein Science</i> , 1994, 3, 82-91.	3.1	346
156	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
157	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
158	A Structural Basis for the Chiral Preferences of Lipases. <i>Journal of the American Chemical Society</i> , 1994, 116, 3180-3186.	6.6	328
159	Crystal structure of the complex of human α_2 -thrombin and nonhydrolyzable bifunctional inhibitors, hirutinin ² and hirutinin ⁶ . <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 252-265.	1.5	38
160	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
161	Snapshots along the pathway. <i>Nature</i> , 1993, 363, 674-675.	13.7	1
162	Conformation of Complementarity Determining Region L1 Loop in Murine IgG λ Light Chain Extends the Repertoire of Canonical Forms. <i>Journal of Molecular Biology</i> , 1993, 229, 597-601.	2.0	36

#	ARTICLE	IF	CITATIONS
163	1Å-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
164	Recognition of a carbohydrate antigenic determinant of <i>Salmonella</i> by an antibody. <i>Biochemical Society Transactions</i> , 1993, 21, 437-441.	1.6	34
165	Advances in Structural Understanding of Lipases. <i>Biotechnology and Genetic Engineering Reviews</i> , 1992, 10, 143-184.	2.4	47
166	The α/β hydrolase fold. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 197-211.	1.0	1,887
167	Multiple crystal forms of lipases from <i>Geotrichum candidum</i> . <i>Journal of Molecular Biology</i> , 1991, 220, 541-543.	2.0	6
168	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
169	Sindbis virus core protein crystals. <i>Journal of Molecular Biology</i> , 1989, 208, 79-82.	2.0	9
170	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
171	Prediction of 3-D Structure of the Cro Protein from Phage 434. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 3, 1055-1066.	2.0	1
172	Computer modeling studies of the structure of a repressor. <i>BioSystems</i> , 1985, 18, 3-14.	0.9	5
173	Conformational features of acyclonucleosides: structure of acyclovir, an antiherpes agent. <i>Canadian Journal of Chemistry</i> , 1984, 62, 2646-2652.	0.6	52
174	Conformation of azaphosphorinane ring. Crystal structures of 2,2,6,6-tetramethyl-4,4-diphenyl-1,4-azaphosphorinanium perchlorate and 2,2,6,6-tetramethyl-4-oxo-4-phenyl-1,4-azaphosphorinane-1-oxyl (stable nitroxyl radical). <i>Canadian Journal of Chemistry</i> , 1983, 61, 427-433.	0.6	4
175	Electrophilic cleavage of cyclopropanes. IV. The reaction of 2-nitrobenzenesulphenyl chloride with tetracyclo[3.2.0.0 ^{2,7} .0 ^{4,6}]heptane in methanol and acetic acid: the crystal structure of exo-3-(2-nitrophenylthio)-exo-5-methoxytricyclo[2.2.1.0 ^{2,6}]heptane, C ₁₄ H ₁₅ NO ₃ S. <i>Canadian Journal of Chemistry</i> , 1983, 61, 1176-1184.	0.6	9
176	Crystallographic data for complexes of the Cro repressor with DNA. <i>Journal of Molecular Biology</i> , 1983, 168, 903-906.	2.0	19
177	The crystal structure of benzenediazonium tetrafluoroborate, C ₆ H ₅ N ₂ ⁺ BF ₄ ⁻ . <i>Canadian Journal of Chemistry</i> , 1982, 60, 2852-2855.	0.6	45
178	Structure and conformation of 8-bromo-9-β-D-xylofuranosyladenine in the solid state and in solution. <i>Journal of the American Chemical Society</i> , 1982, 104, 3957-3964.	6.6	10
179	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
180	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