

Edward N Baker

List of Publications by Year in descending order

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306
papers

17,925
citations

12330

69
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16183

124
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314
all docs

314
docs citations

314
times ranked

14748
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen bonding in globular proteins. <i>Progress in Biophysics and Molecular Biology</i> , 1984, 44, 97-179.	2.9	1,636
2	Structure of human lactoferrin: Crystallographic structure analysis and refinement at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , 1989, 209, 711-734.	4.2	577
3	Structure of Rhombohedral 2 Zinc Insulin Crystals. <i>Nature</i> , 1969, 224, 491-495.	27.8	532
4	Structural Basis of the Tanford Transition of Bovine β -Lactoglobulin. <i>Biochemistry</i> , 1998, 37, 14014-14023.	2.5	461
5	Pili in Gram-negative and Gram-positive bacteria: structure, assembly and their role in disease. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 613-635.	5.4	425
6	Apolactoferrin structure demonstrates ligand-induced conformational change in transferrins. <i>Nature</i> , 1990, 344, 784-787.	27.8	398
7	Structure of azurin from <i>Alcaligenes denitrificans</i> refinement at 1.8 Å resolution and comparison of the two crystallographically independent molecules. <i>Journal of Molecular Biology</i> , 1988, 203, 1071-1095.	4.2	395
8	Three-dimensional structure of diferric bovine lactoferrin at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , 1997, 274, 222-236.	4.2	361
9	Lactoferrin. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 2531-2539.	5.4	320
10	Stabilizing Isopeptide Bonds Revealed in Gram-Positive Bacterial Pilus Structure. <i>Science</i> , 2007, 318, 1625-1628.	12.6	295
11	Thiol proteases. <i>Journal of Molecular Biology</i> , 1985, 182, 317-329.	4.2	291
12	Lactoferrin Is a Potent Regulator of Bone Cell Activity and Increases Bone Formation in Vivo. <i>Endocrinology</i> , 2004, 145, 4366-4374.	2.8	253
13	Two High-Resolution Crystal Structures of the Recombinant N-Lobe of Human Transferrin Reveal a Structural Change Implicated in Iron Release. <i>Biochemistry</i> , 1998, 37, 7919-7928.	2.5	242
14	Crystal structure of the protein disulfide bond isomerase, DsbC, from <i>Escherichia coli</i> . <i>Nature Structural Biology</i> , 2000, 7, 196-199.	9.7	227
15	A structural framework for understanding the multifunctional character of lactoferrin. <i>Biochimie</i> , 2009, 91, 3-10.	2.6	225
16	Crystal structure of hemopexin reveals a novel high-affinity heme site formed between two beta-propeller domains. <i>Nature Structural Biology</i> , 1999, 6, 926-931.	9.7	219
17	Dealing with iron: Common structural principles in proteins that transport iron and heme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3579-3583.	7.1	216
18	Sheep liver cytosolic aldehyde dehydrogenase: the structure reveals the basis for the retinal specificity of class 1 aldehyde dehydrogenases. <i>Structure</i> , 1998, 6, 1541-1551.	3.3	200

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19	New perspectives on the structure and function of transferrins. <i>Journal of Inorganic Biochemistry</i> , 1992, 47, 147-160.	3.5	199
20	Transferrins: insights into structure and function from studies on lactoferrin. <i>Trends in Biochemical Sciences</i> , 1987, 12, 350-353.	7.5	185
21	Ligand-Induced Conformational Change in Transferrins: A Crystal Structure of the Open Form of the N-Terminal Half-Molecule of Human Transferrin. <i>Biochemistry</i> , 1998, 37, 13978-13986.	2.5	183
22	Lactoferrin and Iron: structural and dynamic aspects of binding and release. <i>BioMetals</i> , 2004, 17, 209-216.	4.1	183
23	Structure and Reactivity of Transferrins. <i>Advances in Inorganic Chemistry</i> , 1994, 41, 389-463.	1.0	182
24	Lactoferrin and transferrin: Functional variations on a common structural framework. <i>Biochemistry and Cell Biology</i> , 2002, 80, 27-34.	2.0	165
25	Domain Closure in Lactoferrin. <i>Journal of Molecular Biology</i> , 1993, 234, 357-372.	4.2	160
26	Blue copper proteins. The copper site in azurin from <i>Alcaligenes denitrificans</i> . <i>Journal of the American Chemical Society</i> , 1986, 108, 2784-2785.	13.7	153
27	Structure of azurin from <i>Alcaligenes denitrificans</i> at 2.5 Å resolution. <i>Journal of Molecular Biology</i> , 1983, 165, 501-521.	4.2	147
28	Superantigens – powerful modifiers of the immune system. <i>Trends in Molecular Medicine</i> , 2000, 6, 125-132.	2.6	147
29	Crystal structures of <i>Bacillus caldovelox</i> arginase in complex with substrate and inhibitors reveal new insights into activation, inhibition and catalysis in the arginase superfamily. <i>Structure</i> , 1999, 7, 435-448.	3.3	145
30	Crystal structure of <i>Escherichia coli</i> manganese superoxide dismutase at 2.1 Å resolution. <i>Journal of Biological Inorganic Chemistry</i> , 1998, 3, 161-171.	2.6	131
31	Crystal structure of LeuA from <i>Mycobacterium tuberculosis</i> , a key enzyme in leucine biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8295-8300.	7.1	129
32	Calcium-mediated thermostability in the subtilisin superfamily: the crystal structure of <i>Bacillus Ak.1</i> protease at 1.8 Å resolution. <i>Journal of Molecular Biology</i> , 1999, 294, 1027-1040.	4.2	122
33	Functional implications of structural differences between variants A and B of bovine β^2 -lactoglobulin. <i>Protein Science</i> , 1999, 8, 75-83.	7.6	122
34	12-Bromododecanoic acid binds inside the calyx of bovine β^2 -lactoglobulin. <i>FEBS Letters</i> , 1998, 438, 272-278.	2.8	117
35	Intramolecular isopeptide bonds: protein crosslinks built for stress?. <i>Trends in Biochemical Sciences</i> , 2011, 36, 229-237.	7.5	112
36	Human milk lactoferrin inactivates two putative colonization factors expressed by <i>Haemophilus influenzae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 12641-12646.	7.1	111

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37	Metabolic Engineering of Cofactor F420 Production in <i>Mycobacterium smegmatis</i> . PLoS ONE, 2010, 5, e15803.	2.5	110
38	The <i>Corynebacterium diphtheriae</i> shaft pilin SpaA is built of tandem Ig-like modules with stabilizing isopeptide and disulfide bonds. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16967-16971.	7.1	107
39	Crystal structure of the streptococcal superantigen SPE-C: dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules. Nature Structural Biology, 1997, 4, 635-643.	9.7	104
40	Distant Structural Homology Leads to the Functional Characterization of an Archaeal PIN Domain as an Exonuclease. Journal of Biological Chemistry, 2004, 279, 16471-16478.	3.4	103
41	Structure of the bacterial type II NADH dehydrogenase: a monotopic membrane protein with an essential role in energy generation. Molecular Microbiology, 2014, 91, 950-964.	2.5	103
42	1.8 Å crystal structure of the C-terminal domain of rabbit serum haemopexin. Structure, 1995, 3, 551-559.	3.3	100
43	Aminoglycoside Antibiotic Resistance by Enzymatic Deactivation. Current Drug Targets Infectious Disorders, 2002, 2, 143-160.	2.1	98
44	The Crystal Structure of Aminoglycoside-3-Phosphotransferase-IIa, an Enzyme Responsible for Antibiotic Resistance. Journal of Molecular Biology, 2003, 327, 491-506.	4.2	98
45	Crystal structure of the zymogen form of the group A Streptococcus virulence factor SpeB: An integrin-binding cysteine protease. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2235-2240.	7.1	96
46	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. Tuberculosis, 2003, 83, 223-249.	1.9	95
47	Human milk lactoferrin is a serine protease that cleaves Haemophilus surface proteins at arginine-rich sites. Molecular Microbiology, 2003, 47, 607-617.	2.5	95
48	The characterization of both the coordinated and non-coordinated saccharinate ion. The syntheses and crystal structures of aqua(2-formylpyridine thiosemicarbazonato)(saccharinato-N)copper(II) hemihydrate and 2,2'-bipyridyl-(2-formylpyridine thiosemicarbazonato)copper(II) saccharinate dihydrate. Inorganica Chimica Acta, 1990, 172, 185-190.	2.4	93
49	The Structure of MbtI from <i>Mycobacterium tuberculosis</i> , the First Enzyme in the Biosynthesis of the Siderophore Mycobactin, Reveals It To Be a Salicylate Synthase. Journal of Bacteriology, 2006, 188, 6081-6091.	2.2	93
50	Intramolecular Isopeptide Bonds Give Thermodynamic and Proteolytic Stability to the Major Pilin Protein of <i>Streptococcus pyogenes</i> . Journal of Biological Chemistry, 2009, 284, 20729-20737.	3.4	93
51	A structural perspective on lactoferrin function ¹ This article is part of a Special Issue entitled Lactoferrin and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2012, 90, 320-328.	2.0	93
52	Structure of human diferric lactoferrin refined at 2.2 Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 629-646.	2.5	92
53	Structure and Inhibition of the Human Cell Cycle Checkpoint Kinase, Wee1A Kinase. Structure, 2005, 13, 541-550.	3.3	91
54	Crystal structure of a substrate complex of myo-inositol oxygenase, a di-iron oxygenase with a key role in inositol metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15032-15037.	7.1	91

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55	Spectrochemical studies on the blue copper protein azurin from <i>Alcaligenes denitrificans</i> . <i>Biochemistry</i> , 1987, 26, 71-82.	2.5	90
56	The structure of glucose-fructose oxidoreductase from <i>Zymomonas mobilis</i> : an osmoprotective periplasmic enzyme containing non-dissociable NADP. <i>Structure</i> , 1996, 4, 1413-1428.	3.3	87
57	Human melanotransferrin (p97) has only one functional iron-binding site. <i>FEBS Letters</i> , 1992, 298, 215-218.	2.8	86
58	Metal substitution in transferrins: the crystal structure of human copper-lactoferrin at 2.1-Å resolution. <i>Biochemistry</i> , 1992, 31, 4527-4533.	2.5	85
59	The crystal structure of staphylococcal superantigen-like protein 11 in complex with sialyl Lewis X reveals the mechanism for cell binding and immune inhibition. <i>Molecular Microbiology</i> , 2007, 66, 1342-1355.	2.5	85
60	Structure of the Recombinant N-Terminal Lobe of Human Lactoferrin at 2.0 Å Resolution. <i>Journal of Molecular Biology</i> , 1993, 232, 1084-1100.	4.2	83
61	Crystal Structures of F420-dependent Glucose-6-phosphate Dehydrogenase FGD1 Involved in the Activation of the Anti-tuberculosis Drug Candidate PA-824 Reveal the Basis of Coenzyme and Substrate Binding. <i>Journal of Biological Chemistry</i> , 2008, 283, 17531-17541.	3.4	79
62	The Three-dimensional Structure of a Superantigen-like Protein, SET3, from a Pathogenicity Island of the <i>Staphylococcus aureus</i> Genome. <i>Journal of Biological Chemistry</i> , 2002, 277, 32274-32281.	3.4	77
63	Crystal Structure of AhpE from <i>Mycobacterium tuberculosis</i> , a 1-Cys Peroxiredoxin. <i>Journal of Molecular Biology</i> , 2005, 346, 1035-1046.	4.2	77
64	Structure, function and flexibility of human lactoferrin. <i>International Journal of Biological Macromolecules</i> , 1991, 13, 122-129.	7.5	76
65	Crystal structure of the NADP(H)-dependent ketose reductase from <i>Bemisia argentifolii</i> at 2.3 Å resolution. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 306, 239-250.	4.2	76
66	Outer Sphere Mutations Perturb Metal Reactivity in Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2001, 40, 15-27.	2.5	75
67	The Structure of 3-Deoxy-d-arabino-heptulosonate 7-phosphate Synthase from <i>Mycobacterium tuberculosis</i> Reveals a Common Catalytic Scaffold and Ancestry for Type I and Type II Enzymes. <i>Journal of Molecular Biology</i> , 2005, 354, 927-939.	4.2	74
68	Three-Dimensional Structure of Lactoferrin in Various Functional States. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 1-12.	1.6	74
69	Structural homologies with ATP- and folate-binding enzymes in the crystal structure of folic acid polyglutamate synthetase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 6647-6652.	7.1	73
70	Structure and assembly of Gram-positive bacterial pili: unique covalent polymers. <i>Current Opinion in Structural Biology</i> , 2012, 22, 200-207.	5.7	72
71	Conservation and variation in superantigen structure and activity highlighted by the three-dimensional structures of two new superantigens from <i>Streptococcus pyogenes</i> 1. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 299, 157-168.	4.2	69
72	Histidine phosphorylation in biological systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 100-105.	2.3	68

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73	Anion binding by human lactoferrin: results from crystallographic and physicochemical studies. <i>Biochemistry</i> , 1992, 31, 4451-4458.	2.5	67
74	A flexible and economical medium-throughput strategy for protein production and crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1378-1385.	2.5	67
75	The TB Structural Genomics Consortium: Providing a Structural Foundation for Drug Discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002, 2, 121-141.	2.1	66
76	Crystal Structure of Methylmalonyl-Coenzyme A Epimerase from <i>P. shermanii</i> . <i>Structure</i> , 2001, 9, 637-646.	3.3	64
77	Structure of actinidin: Details of the polypeptide chain conformation and active site from an electron density map at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , 1977, 115, 263-277.	4.2	63
78	Crystal Structure of MshB from <i>Mycobacterium tuberculosis</i> , a Deacetylase Involved in Mycothiol Biosynthesis. <i>Journal of Molecular Biology</i> , 2004, 335, 1131-1141.	4.2	63
79	Synergistic Allostery, a Sophisticated Regulatory Network for the Control of Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 30567-30576.	3.4	63
80	Altered Domain Closure and Iron Binding in Transferrins: The Crystal Structure of the Asp60Ser Mutant of the Amino-terminal Half-molecule of Human Lactoferrin. <i>Journal of Molecular Biology</i> , 1996, 256, 352-363.	4.2	62
81	Crystal Structures of the Staphylococcal Toxin SSL5 in Complex with Sialyl Lewis X Reveal a Conserved Binding Site that Shares Common Features with Viral and Bacterial Sialic Acid Binding Proteins. <i>Journal of Molecular Biology</i> , 2007, 374, 1298-1308.	4.2	62
82	Structure of Human Apolactoferrin at 2.0 Å Resolution. Refinement and Analysis of Ligand-Induced Conformational Change. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1319-1335.	2.5	61
83	Crystal Structure of the Minor Pilin FctB Reveals Determinants of Group A Streptococcal Pilus Anchoring. <i>Journal of Biological Chemistry</i> , 2010, 285, 20381-20389.	3.4	61
84	Distinct Metal Environment in Fe-Substituted Manganese Superoxide Dismutase Provides a Structural Basis of Metal Specificity. <i>Journal of the American Chemical Society</i> , 1998, 120, 9684-9685.	13.7	60
85	Structure of recombinant human lactoferrin expressed in <i>Aspergillus awamori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 403-407.	2.5	60
86	Chelation of nickel(II) by citrate. The crystal structure of a nickel-citrate complex, K ₂ [Ni(C ₆ H ₅ O ₇)(H ₂ O) ₂] ₂ ·4H ₂ O. <i>Inorganica Chimica Acta</i> , 1983, 78, 281-285.	2.4	58
87	High-Resolution Crystal Structure of Plant Carboxylesterase AeCXE1, from <i>Actinidia eriantha</i> , and Its Complex with a High-Affinity Inhibitor Paraoxon,. <i>Biochemistry</i> , 2007, 46, 1851-1859.	2.5	58
88	The Laminin-Binding Protein Lbp from <i>Streptococcus pyogenes</i> Is a Zinc Receptor. <i>Journal of Bacteriology</i> , 2009, 191, 5814-5823.	2.2	56
89	Production of recombinant proteins in <i>Mycobacterium smegmatis</i> for structural and functional studies. <i>Protein Science</i> , 2015, 24, 1-10.	7.6	56
90	Folate-binding triggers the activation of folylpolyglutamate synthetase 1 Edited by I. Wilson. <i>Journal of Molecular Biology</i> , 2001, 310, 1067-1078.	4.2	55

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91	A revised biosynthetic pathway for the cofactor F420 in prokaryotes. <i>Nature Communications</i> , 2019, 10, 1558.	12.8	55
92	Structure and function of GlmU from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 275-283.	2.5	54
93	Crystal Structure and Metal Binding Properties of the Lipoprotein MtsA, Responsible for Iron Transport in <i>Streptococcus pyogenes</i> . <i>Biochemistry</i> , 2009, 48, 6184-6190.	2.5	54
94	Mutagenesis of the Histidine Ligand in Human Lactoferrin: Iron Binding Properties and Crystal Structure of the Histidine-253 → Methionine Mutant. <i>Biochemistry</i> , 1997, 36, 341-346.	2.5	52
95	The Crystal Structures of Substrate and Nucleotide Complexes of <i>Enterococcus faecium</i> Aminoglycoside-2-Phosphotransferase-IIa [APH(2)-IIa] Provide Insights into Substrate Selectivity in the APH(2) Subfamily. <i>Journal of Bacteriology</i> , 2009, 191, 4133-4143.		50
96	Inhibition Studies of <i>Mycobacterium tuberculosis</i> Salicylate Synthase (MbtI). <i>ChemMedChem</i> , 2010, 5, 1067-1079.	3.2	50
97	Anion Binding by Transferrins: Importance of Second-Shell Effects Revealed by the Crystal Structure of Oxalate-Substituted Diferric Lactoferrin. <i>Biochemistry</i> , 1996, 35, 9007-9013.	2.5	49
98	Immunological and Biochemical Characterization of Streptococcal Pyrogenic Exotoxins I and J (SPE-I) and J (SPE-J). <i>Journal of Biological Chemistry</i> , 1987, 262, 10787-10792.	0.8	48
99	Roles of Minor Pilin Subunits Spy0125 and Spy0130 in the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. <i>Journal of Bacteriology</i> , 2010, 192, 4651-4659.	2.2	48
100	Crystal structure of PAE0151 from <i>Pyrobaculum aerophilum</i> , a PIN domain (VapC) protein from a toxin-antitoxin operon. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 510-518.	2.6	45
101	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the CASA/Snakin Protein Superfamily. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 7930-7933.	13.8	45
102	Metal substitution in transferrins: specific binding of cerium(IV) revealed by the crystal structure of cerium-substituted human lactoferrin. <i>Journal of Biological Inorganic Chemistry</i> , 2000, 5, 692-698.	2.6	44
103	A new Gateway® vector and expression protocol for fast and efficient recombinant protein expression in <i>Mycobacterium smegmatis</i> . <i>Protein Expression and Purification</i> , 2008, 57, 81-87.	1.3	44
104	Crystal Structure of Spy0129, a <i>Streptococcus pyogenes</i> Class B Sortase Involved in Pilus Assembly. <i>PLoS ONE</i> , 2011, 6, e15969.	2.5	44
105	Working towards a Group A Streptococcal vaccine: Report of a collaborative Trans-Tasman workshop. <i>Vaccine</i> , 2014, 32, 3713-3720.	3.8	44
106	The three-dimensional structure of PNGase F, a glycosyl asparaginase from <i>Flavobacterium meningosepticum</i> . <i>Structure</i> , 1994, 2, 1049-1059.	3.3	43
107	A functional role of Rv1738 in <i>Mycobacterium tuberculosis</i> persistence suggested by racemic protein crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4310-4315.	7.1	43
108	The Crystal Structure of Rv1347c, a Putative Antibiotic Resistance Protein from <i>Mycobacterium tuberculosis</i> , Reveals a GCN5-related Fold and Suggests an Alternative Function in Siderophore Biosynthesis. <i>Journal of Biological Chemistry</i> , 2005, 280, 13978-13986.	3.4	42

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109	The potential impact of structural genomics on tuberculosis drug discovery. <i>Drug Discovery Today</i> , 2006, 11, 28-34.	6.4	42
110	Removing a Hydrogen Bond in the Dimer Interface of <i>Escherichia coli</i> Manganese Superoxide Dismutase Alters Structure and Reactivity. <i>Biochemistry</i> , 2001, 40, 4622-4632.	2.5	41
111	The Crystal Structure of TrpD, a Metabolic Enzyme Essential for Lung Colonization by <i>Mycobacterium tuberculosis</i> , in Complex with its Substrate Phosphoribosylpyrophosphate. <i>Journal of Molecular Biology</i> , 2006, 355, 784-797.	4.2	41
112	Structural Model for Covalent Adhesion of the <i>Streptococcus pyogenes</i> Pilus through a Thioester Bond. <i>Journal of Biological Chemistry</i> , 2014, 289, 177-189.	3.4	41
113	Structural and functional similarities in the ADP-forming amide bond ligase superfamily: implications for a substrate-induced conformational change in folylpolyglutamate synthetase 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 302, 425-438.	4.2	40
114	Crystal Structures of the Precursor Form of Glucose-Fructose Oxidoreductase from <i>Zymomonas mobilis</i> and Its Complexes with Bound Ligands,. <i>Biochemistry</i> , 2001, 40, 13857-13867.	2.5	40
115	Crystal Structure of <i>Epiphyas postvittana</i> Takeout 1 with Bound Ubiquinone Supports a Role as Ligand Carriers for Takeout Proteins in Insects. <i>Journal of Biological Chemistry</i> , 2009, 284, 3496-3503.	3.4	40
116	Structure of XynB, a highly thermostable \hat{I}^2 -1,4-xylanase from <i>Dictyoglomus thermophilum</i> Rt46B.1, at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1367-1375.	2.5	39
117	Structural and Functional Characterization of an RNase HI Domain from the Bifunctional Protein Rv2228c from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2010, 192, 2878-2886.	2.2	39
118	The TB Structural Genomics Consortium: A decade of progress. <i>Tuberculosis</i> , 2011, 91, 155-172.	1.9	39
119	Mutation of the Iron Ligand His 249 to Glu in the N-Lobe of Human Transferrin Abolishes the Dilysine Trigger-but Does Not Significantly Affect Iron Release. <i>Biochemistry</i> , 2000, 39, 1211-1216.	2.5	38
120	Expression, purification and crystallization of native and selenomethionine labeled <i>Mycobacterium tuberculosis</i> FGD1 (Rv0407) using a <i>Mycobacterium smegmatis</i> expression system. <i>Protein Expression and Purification</i> , 2007, 54, 38-44.	1.3	38
121	Three Sites and You Are Out: Ternary Synergistic Allostery Controls Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 1582-1592.	4.2	38
122	Crystal Structures and Iron Release Properties of Mutants (K206A and K296A) That Abolish the Dilysine Interaction in the N-Lobe of Human Transferrin. <i>Biochemistry</i> , 2001, 40, 1616-1623.	2.5	37
123	Potent Inhibitors of a Shikimate Pathway Enzyme from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 16197-16207.	3.4	37
124	Defining the Potassium Binding Region in an Apple Terpene Synthase. <i>Journal of Biological Chemistry</i> , 2009, 284, 8661-8669.	3.4	36
125	Crystal Structure and Iron-Binding Properties of the R210K Mutant of the N-Lobe of Human Lactoferrin: Implications for Iron Release from Transferrins. <i>Biochemistry</i> , 2000, 39, 6625-6633.	2.5	35
126	Mutation of Arginine 121 in Lactoferrin Destabilizes Iron Binding by Disruption of Anion Binding: Crystal Structures of R121S and R121E Mutants. <i>Biochemistry</i> , 1996, 35, 14473-14479.	2.5	34

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127	Three-Dimensional Structure of Lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , 1998, , 1-14.	1.6	34
128	Structure of the Full-Length Major Pilin from <i>Streptococcus pneumoniae</i> : Implications for Isopeptide Bond Formation in Gram-Positive Bacterial Pili. <i>PLoS ONE</i> , 2011, 6, e22095.	2.5	33
129	Structural and Functional Properties of Staphylococcal Superantigen-Like Protein 4. <i>Infection and Immunity</i> , 2012, 80, 4004-4013.	2.2	33
130	Ligand Variation in the Transferrin Family: The Crystal Structure of the H249Q Mutant of the Human Transferrin N-lobe As a Model for Iron Binding in Insect Transferrins. <i>Biochemistry</i> , 2001, 40, 11670-11675.	2.5	32
131	Structural Conservation, Variability, and Immunogenicity of the T6 Backbone Pilin of Serotype M6 <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , 2014, 82, 2949-2957.	2.2	32
132	The Structure of the Transcriptional Repressor KstR in Complex with CoA Thioester Cholesterol Metabolites Sheds Light on the Regulation of Cholesterol Catabolism in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 7256-7266.	3.4	32
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134	Structure of <i>Escherichia coli</i> UDP-N-acetylmuramoyl:L-alanine ligase (MurC). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1466-1474.	2.5	31
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