

Edward N Baker

List of Publications by Year in descending order

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306
papers

17,925
citations

12303

69
h-index

16127

124
g-index

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.	1.4	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.	2.0	577
3	Structure of Rhombohedral 2 Zinc Insulin Crystals. <i>Nature</i> , 1969, 224, 491-495.	13.7	532
4	Structural Basis of the Tanford Transition of Bovine β -Lactoglobulin. <i>Biochemistry</i> , 1998, 37, 14014-14023.	1.2	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.	2.4	425
6	Apolactoferrin structure demonstrates ligand-induced conformational change in transferrins. <i>Nature</i> , 1990, 344, 784-787.	13.7	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.	2.0	395
8	Three-dimensional structure of diferric bovine lactoferrin at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , 1997, 274, 222-236.	2.0	361
9	Lactoferrin. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 2531-2539.	2.4	320
10	Stabilizing Isopeptide Bonds Revealed in Gram-Positive Bacterial Pilus Structure. <i>Science</i> , 2007, 318, 1625-1628.	6.0	295
11	Thiol proteases. <i>Journal of Molecular Biology</i> , 1985, 182, 317-329.	2.0	291
12	Lactoferrin Is a Potent Regulator of Bone Cell Activity and Increases Bone Formation in Vivo. <i>Endocrinology</i> , 2004, 145, 4366-4374.	1.4	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.	1.2	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.	1.3	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.	3.3	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.	1.6	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.	1.5	199
20	Transferrins: insights into structure and function from studies on lactoferrin. <i>Trends in Biochemical Sciences</i> , 1987, 12, 350-353.	3.7	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.	1.2	183
22	Lactoferrin and Iron: structural and dynamic aspects of binding and release. <i>BioMetals</i> , 2004, 17, 209-216.	1.8	183
23	Structure and Reactivity of Transferrins. <i>Advances in Inorganic Chemistry</i> , 1994, 41, 389-463.	0.4	182
24	Lactoferrin and transferrin: Functional variations on a common structural framework. <i>Biochemistry and Cell Biology</i> , 2002, 80, 27-34.	0.9	165
25	Domain Closure in Lactoferrin. <i>Journal of Molecular Biology</i> , 1993, 234, 357-372.	2.0	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.	6.6	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.	2.0	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.	1.6	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.	1.1	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.	3.3	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.	2.0	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.	3.1	122
34	12-Bromododecanoic acid binds inside the calyx of bovine β^2 -lactoglobulin. <i>FEBS Letters</i> , 1998, 438, 272-278.	1.3	117
35	Intramolecular isopeptide bonds: protein crosslinks built for stress?. <i>Trends in Biochemical Sciences</i> , 2011, 36, 229-237.	3.7	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.	3.3	111

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37	Metabolic Engineering of Cofactor F420 Production in <i>Mycobacterium smegmatis</i> . PLoS ONE, 2010, 5, e15803.	1.1	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.	3.3	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.	1.6	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.	1.2	103
42	1.8 Å crystal structure of the C-terminal domain of rabbit serum haemopexin. Structure, 1995, 3, 551-559.	1.6	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.	2.0	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.	3.3	96
46	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. Tuberculosis, 2003, 83, 223-249.	0.8	95
47	Human milk lactoferrin is a serine protease that cleaves Haemophilus surface proteins at arginine-rich sites. Molecular Microbiology, 2003, 47, 607-617.	1.2	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.	1.2	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.	1.0	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.	1.6	93
51	A structural perspective on lactoferrin function¹This 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.	0.9	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.	1.6	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.	3.3	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.	1.2	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.	1.6	87
57	Human melanotransferrin (p97) has only one functional iron-binding site. <i>FEBS Letters</i> , 1992, 298, 215-218.	1.3	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.	1.2	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.	1.2	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.	2.0	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.	1.6	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.	1.6	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.	2.0	77
64	Structure, function and flexibility of human lactoferrin. <i>International Journal of Biological Macromolecules</i> , 1991, 13, 122-129.	3.6	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.	2.0	76
66	Outer Sphere Mutations Perturb Metal Reactivity in Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2001, 40, 15-27.	1.2	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.	2.0	74
68	Three-Dimensional Structure of Lactoferrin in Various Functional States. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 1-12.	0.8	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.	3.3	73
70	Structure and assembly of Gram-positive bacterial pili: unique covalent polymers. <i>Current Opinion in Structural Biology</i> , 2012, 22, 200-207.	2.6	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.	2.0	69
72	Histidine phosphorylation in biological systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 100-105.	1.1	68

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73	Anion binding by human lactoferrin: results from crystallographic and physicochemical studies. <i>Biochemistry</i> , 1992, 31, 4451-4458.	1.2	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.	1.6	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.	2.0	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.	2.0	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.	1.6	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.	2.0	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.	2.0	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.	1.6	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.	6.6	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.	1.2	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.	1.2	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.	1.0	56
89	Production of recombinant proteins in <i>Mycobacterium smegmatis</i> for structural and functional studies. <i>Protein Science</i> , 2015, 24, 1-10.	3.1	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.	2.0	55

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91	A revised biosynthetic pathway for the cofactor F420 in prokaryotes. <i>Nature Communications</i> , 2019, 10, 1558.	5.8	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.	1.2	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.	1.2	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.	1.6	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.	1.2	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, 10700-10706.	0.4	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.	1.0	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.	1.5	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.	7.2	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.	1.1	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.	0.6	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.	1.1	44
105	Working towards a Group A Streptococcal vaccine: Report of a collaborative Trans-Tasman workshop. <i>Vaccine</i> , 2014, 32, 3713-3720.	1.7	44
106	The three-dimensional structure of PNGase F, a glycosyl asparaginase from <i>Flavobacterium meningosepticum</i> . <i>Structure</i> , 1994, 2, 1049-1059.	1.6	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.	3.3	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.	1.6	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.	3.2	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.	1.2	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.	2.0	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.	1.6	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.	2.0	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.	1.2	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.	1.6	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.	1.0	39
118	The TB Structural Genomics Consortium: A decade of progress. <i>Tuberculosis</i> , 2011, 91, 155-172.	0.8	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.	1.2	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.	0.6	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.	2.0	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.	1.2	37
123	Potent Inhibitors of a Shikimate Pathway Enzyme from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 16197-16207.	1.6	37
124	Defining the Potassium Binding Region in an Apple Terpene Synthase. <i>Journal of Biological Chemistry</i> , 2009, 284, 8661-8669.	1.6	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.	1.2	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.	1.2	34

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127	Three-Dimensional Structure of Lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , 1998, , 1-14.	0.8	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.	1.1	33
129	Structural and Functional Properties of Staphylococcal Superantigen-Like Protein 4. <i>Infection and Immunity</i> , 2012, 80, 4004-4013.	1.0	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.	1.2	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.	1.0	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.	1.6	32
133	The Structure of Truncated Recombinant Human Bile Salt-stimulated Lipase Reveals Bile Salt-independent Conformational Flexibility at the Active-site Loop and Provides Insights into Heparin Binding. <i>Journal of Molecular Biology</i> , 2001, 312, 511-523.	2.0	31
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
135	Implications of Binding Mode and Active Site Flexibility for Inhibitor Potency against the Salicylate Synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , 2012, 51, 4868-4879.	1.2	31
136	Autocatalytically generated Thr-Gln ester bond cross-links stabilize the repetitive Ig-domain shaft of a bacterial cell surface adhesin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1367-1372.	3.3	31
137	Crystal and molecular structure of pentacarbonyl(trimethylphosphine sulphide)chromium(0). <i>Journal of the Chemical Society Dalton Transactions</i> , 1973, , 2205.	1.1	30
138	Specific binding of cerium by human lactoferrin stimulates the oxidation of Ce ³⁺ to Ce ⁴⁺ . <i>Journal of the American Chemical Society</i> , 1994, 116, 7889-7890.	6.6	30
139	Structural and Functional Consequences of Binding Site Mutations in Transferrin: Crystal Structures of the Asp63Glu and Arg124Ala Mutants of the N-Lobe of Human Transferrin. <i>Biochemistry</i> , 2003, 42, 7084-7089.	1.2	30
140	Crystal Structure of a Putative Methyltransferase from <i>Mycobacterium tuberculosis</i> : Misannotation of a Genome Clarified by Protein Structural Analysis. <i>Journal of Bacteriology</i> , 2003, 185, 4057-4065.	1.0	29
141	Synthesis and structure-activity relationships of soluble 8-substituted 4-(2-chlorophenyl)-9-hydroxypyrolo[3,4-c]carbazole-1,3(2H,6H)-diones as inhibitors of the Wee1 and Chk1 checkpoint kinases. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008, 18, 929-933.	1.0	27
142	A slow-forming isopeptide bond in the structure of the major pilin SpaD from <i>Corynebacterium diphtheriae</i> has implications for pilus assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1190-1201.	2.5	27
143	Interaction of benzo-1,3-thiazoline-2-thione and related ligands with copper(II) salts and the single-crystal X-ray structure of		

#	ARTICLE	IF	CITATIONS
145	Synthesis and structure-activity relationships of N-6 substituted analogues of 9-hydroxy-4-phenylpyrrolo[3,4-c]carbazole-1,3(2H,6H)-diones as inhibitors of Wee1 and Chk1 checkpoint kinases. <i>European Journal of Medicinal Chemistry</i> , 2008, 43, 1276-1296.	2.6	26
146	Tat-Dependent Translocation of an F420-Binding Protein of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2012, 7, e45003.	1.1	26
147	Inhibition studies on <i>Mycobacterium tuberculosis</i> N-acetylglucosamine-1-phosphate uridylyltransferase (GlmU). <i>Organic and Biomolecular Chemistry</i> , 2013, 11, 8113.	1.5	26
148	Complex Formation between Two Biosynthetic Enzymes Modifies the Allosteric Regulatory Properties of Both. <i>Journal of Biological Chemistry</i> , 2015, 290, 18187-18198.	1.6	26
149	Serological Evidence of Immune Priming by Group A Streptococci in Patients with Acute Rheumatic Fever. <i>Frontiers in Microbiology</i> , 2016, 7, 1119.	1.5	26
150	Preliminary crystallographic studies of copper(II)- and oxalate-substituted human lactoferrin. <i>Journal of Molecular Biology</i> , 1991, 219, 155-159.	2.0	25
151	X-ray Crystallography and Mass Spectroscopy Reveal that the N-lobe of Human Transferrin Expressed in <i>Pichia pastoris</i> Folded Correctly but Is Glycosylated on Serine-32. <i>Biochemistry</i> , 1999, 38, 2535-2541.	1.2	25
152	Oligomerization and ligand binding in a homotetrameric hemoglobin: Two high-resolution crystal structures of hemoglobin Bart's (β^{34}), a marker for β -thalassemia. <i>Protein Science</i> , 2001, 10, 1739-1749.	3.1	25
153	Crystal and molecular structure of tetracarbonyl(3,6-dithiooctane)chromium(0): evidence for π bonding by a thioether ligand. <i>Journal of the Chemical Society Dalton Transactions</i> , 1976, , 1769.	1.1	24
154	Self-generated covalent cross-links in the cell-surface adhesins of Gram-positive bacteria. <i>Biochemical Society Transactions</i> , 2015, 43, 787-794.	1.6	24
155	Elongation of the Poly- β -glutamate Tail of F420 Requires Both Domains of the F420- β -Glutamyl Ligase (FbiB) of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 6882-6894.	1.6	24
156	Using X-Ray Crystallography to Simplify and Accelerate Biologics Drug Development. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 477-494.	1.6	24
157	Synthetic, spectroscopic and X-ray crystallographic studies on phenylcyanamidocopper(I) complexes. <i>Journal of the Chemical Society Dalton Transactions</i> , 1991, , 1243.	1.1	23
158	Structural and Functional Analysis of Rv3214 from <i>Mycobacterium tuberculosis</i> , a Protein with Conflicting Functional Annotations, Leads to Its Characterization as a Phosphatase. <i>Journal of Bacteriology</i> , 2006, 188, 3589-3599.	1.0	23
159	Making Sense of a Missense Mutation: Characterization of MutT2, a Nudix Hydrolase from <i>Mycobacterium tuberculosis</i> , and the G58R Mutant Encoded in W-Beijing Strains of <i>M. tuberculosis</i> . <i>Biochemistry</i> , 2009, 48, 699-708.	1.2	23
160	The Substrate Capture Mechanism of <i>Mycobacterium tuberculosis</i> Anthranilate Phosphoribosyltransferase Provides a Mode for Inhibition. <i>Biochemistry</i> , 2013, 52, 1776-1787.	1.2	23
161	Structure and Function of Human Xylulokinase, an Enzyme with Important Roles in Carbohydrate Metabolism. <i>Journal of Biological Chemistry</i> , 2013, 288, 1643-1652.	1.6	23
162	Single Crystal Polarized Spectroscopy of Manganese Superoxide Dismutase and Electronic Structure of the Active Site Metal Complex. <i>Journal of Physical Chemistry B</i> , 1998, 102, 4668-4677.	1.2	22

#	ARTICLE	IF	CITATIONS
163	â€œDilysine Triggerâ€in Transferrins Probed by Mutagenesis of Lactoferrin:â€ Crystal Structures of the R210G, R210E, and R210L Mutants of Human Lactoferrinâ€. <i>Biochemistry</i> , 2002, 41, 14167-14175.	1.2	22
164	Isopeptide bonds in bacterial pili and their characterization by Xâ€ray crystallography and mass spectrometry. <i>Biopolymers</i> , 2009, 91, 1126-1134.	1.2	22
165	Synthetic, spectroscopic, and X-ray crystallographic studies on phenylcyanamidocopper(II) complexes. The characterization of three different co-ordination modes for phenylcyanamide anions. <i>Journal of the Chemical Society Dalton Transactions</i> , 1990, , 2785.	1.1	21
166	Purification and characterization of Ak.1 protease, a thermostable subtilisin with a disulphide bond in the substrate-binding cleft. <i>Biochemical Journal</i> , 2000, 350, 321-328.	1.7	21
167	Copper co-ordination to thioether ligands: crystal and molecular structures of bis(2,5-dithiahexane)copper(II) bis(tetrafluoroborate) and bis(3,6-dithiaoctane)copper(I) tetrafluoroborates. <i>Journal of the Chemical Society Dalton Transactions</i> , 1977, , 877.	1.1	20
168	Crystal structure of a human embryonic haemoglobin: the carbonmonoxy form of gower II ($\hat{1}\pm 2 \hat{1}\mu 2$) haemoglobin at 2.9 Å resolution $\hat{1} 1$ Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 280, 475-484.	2.0	20
169	Structural genomics as an approach towards understanding the biology of tuberculosis. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 57-65.	1.2	20
170	The Structure and Unusual Protein Chemistry of Hypoxic Response Protein 1, a Latency Antigen and Highly Expressed Member of the DosR Regulon in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2008, 383, 822-836.	2.0	20
171	Synthesis and evaluation of <i>M. tuberculosis</i> salicylate synthase (MbtI) inhibitors designed to probe plasticity in the active site. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 9223.	1.5	20
172	Structure of naphthoate synthase (MenB) from <i>Mycobacterium tuberculosis</i> in both native and product-bound forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1199-1206.	2.5	19
173	The Structure of a Putative Scaffolding Protein of Immature Poxvirus Particles as Determined by Electron Microscopy Suggests Similarity with Capsid Proteins of Large Icosahedral DNA Viruses. <i>Journal of Virology</i> , 2007, 81, 11075-11083.	1.5	19
174	Crystallographic and Mutational Data Show That the Streptococcal Pyrogenic Exotoxin J Can Use a Common Binding Surface for T-cell Receptor Binding and Dimerization. <i>Journal of Biological Chemistry</i> , 2004, 279, 38571-38576.	1.6	18
175	The Extracellular Protein Factor Epf from <i>Streptococcus pyogenes</i> Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. <i>Journal of Biological Chemistry</i> , 2012, 287, 38178-38189.	1.6	18
176	Removal of the C-Terminal Regulatory Domain of $\hat{1}\pm$ -Isopropylmalate Synthase Disrupts Functional Substrate Binding. <i>Biochemistry</i> , 2012, 51, 2289-2297.	1.2	18
177	Alternative substrates reveal catalytic cycle and key binding events in the reaction catalysed by anthranilate phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2014, 461, 87-98.	1.7	18
178	Structural Views along the <i>Mycobacterium tuberculosis</i> MenD Reaction Pathway Illuminate Key Aspects of Thiamin Diphosphate-Dependent Enzyme Mechanisms. <i>Structure</i> , 2016, 24, 1167-1177.	1.6	18
179	The interaction of 1-methylimidazoline-2(3H)-thione with copper(II) salts. <i>Journal of the Chemical Society Dalton Transactions</i> , 1989, , 39.	1.1	17
180	Crystal Structure of PhnF, a GntR-Family Transcriptional Regulator of Phosphate Transport in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , 2014, 196, 3472-3481.	1.0	17

#	ARTICLE	IF	CITATIONS
181	Structure and inhibition of subunit I of the anthranilate synthase complex of <i>Mycobacterium tuberculosis</i> and expression of the active complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2297-2308.	2.5	17
182	Copper co-ordination to thioether ligands. Chemical, spectroscopic, and crystallographic studies on copper(I) complexes of 2-(3,3-dimethyl-2-thiabutyl)pyridine and the 2-(3,3-dimethyl-2-thiabutyl)pyridinium cation. <i>Journal of the Chemical Society Dalton Transactions</i> , 1981, , 1746.	1.1	15
183	Copper promoted reactions of the heterocyclic thioamide, 2-thiazolidinethione. <i>Inorganica Chimica Acta</i> , 1985, 105, L5-L7.	1.2	15
184	Structures of Glycinamide Ribonucleotide Transformylase (PurN) from <i>Mycobacterium tuberculosis</i> Reveal a Novel Dimer with Relevance to Drug Discovery. <i>Journal of Molecular Biology</i> , 2009, 389, 722-733.	2.0	15
185	Structural Analyses of a Purine Biosynthetic Enzyme from <i>Mycobacterium tuberculosis</i> Reveal a Novel Bound Nucleotide. <i>Journal of Biological Chemistry</i> , 2011, 286, 40706-40716.	1.6	15
186	Crystal structure of kiwellin, a major cell-wall protein from kiwifruit. <i>Journal of Structural Biology</i> , 2014, 187, 276-281.	1.3	15
187	Repurposing the Chemical Scaffold of the Anti-Arthritic Drug Lobenzarit to Target Tryptophan Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>ChemBioChem</i> , 2014, 15, 852-864.	1.3	15
188	Allosteric regulation of menaquinone (vitamin K2) biosynthesis in the human pathogen <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 3759-3770.	1.6	15
189	X-Ray Structural Analysis of Bovine Lactoferrin at 2.5 Å... Resolution. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 235-238.	0.8	15
190	Peptide binding to a bacterial signal peptidase visualized by peptide tethering and carrier-driven crystallization. <i>IUCr</i> , 2016, 3, 10-19.	1.0	15
191	Copper(II) promoted desulphurization of N-phenylthiourea. The synthesis and X-ray structure of $[\{Cu(bipy)(pc)_2\}_2]$ (bipy = 2,2'-bipyridine, pc = phenylcyanamide). <i>Polyhedron</i> , 1989, 8, 2219-2221.	1.0	14
192	Crystal Structure of a Truncated Mutant of Glucose-Fructose Oxidoreductase Shows that an N-terminal Arm Controls Tetramer Formation. <i>Journal of Molecular Biology</i> , 2000, 304, 575-584.	2.0	14
193	Structure and Activity of <i>Streptococcus pyogenes</i> SipA: A Signal Peptidase-Like Protein Essential for Pilus Polymerisation. <i>PLoS ONE</i> , 2014, 9, e99135.	1.1	14
194	Characterization of the proline-utilization pathway in <i>Mycobacterium tuberculosis</i> through structural and functional studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 968-980.	2.5	14
195	Group A <i>Streptococcus</i> T Antigens Have a Highly Conserved Structure Concealed under a Heterogeneous Surface That Has Implications for Vaccine Design. <i>Infection and Immunity</i> , 2019, 87, .	1.0	14
196	Convergent pathways to biosynthesis of the versatile cofactor F420. <i>Current Opinion in Structural Biology</i> , 2020, 65, 9-16.	2.6	14
197	Preliminary crystallographic studies of the amino terminal half of human lactoferrin in its iron-saturated and iron-free forms. <i>Journal of Molecular Biology</i> , 1992, 228, 973-974.	2.0	13
198	Structures of <i>Mycobacterium tuberculosis</i> folylpolyglutamate synthase complexed with ADP and AMPPCP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 745-753.	2.5	13

#	ARTICLE	IF	CITATIONS
199	Crystal structure of the essential <i>Mycobacterium tuberculosis</i> phosphopantetheinyl transferase PptT, solved as a fusion protein with maltose binding protein. <i>Journal of Structural Biology</i> , 2014, 188, 274-278.	1.3	13
200	A modeling study of the interaction and electron transfer between cytochrome b 5 and some oxidized haemoglobins. <i>Journal of Biological Inorganic Chemistry</i> , 2002, 7, 23-30.	1.1	12
201	Crystallization and preliminary X-ray crystallographic analysis of MbtI, a protein essential for siderophore biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 121-123.	0.7	12
202	Structural and functional analysis of Rv0554 from <i>Mycobacterium tuberculosis</i> : testing a putative role in menaquinone biosynthesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 909-917.	2.5	12
203	Ligand promiscuity within the internal cavity of <i>Epiphyas postvittana</i> Takeout 1 protein. <i>Journal of Structural Biology</i> , 2013, 182, 259-263.	1.3	12
204	Investigating the Reaction Mechanism of F ₄₂₀ -Dependent Glucose-6-phosphate Dehydrogenase from <i>Mycobacterium tuberculosis</i> : Kinetic Analysis of the Wild-Type and Mutant Enzymes. <i>Biochemistry</i> , 2016, 55, 5566-5577.	1.2	12
205	Engineering a Lys-Asn isopeptide bond into an immunoglobulin-like protein domain enhances its stability. <i>Scientific Reports</i> , 2017, 7, 42753.	1.6	12
206	The active site of the <i>Mycobacterium tuberculosis</i> branched-chain amino acid biosynthesis enzyme dihydroxyacid dehydratase contains a 2Fe ²⁺ S cluster. <i>Journal of Biological Chemistry</i> , 2019, 294, 13158-13170.	1.6	12
207	Crystal and molecular structure of the polymeric complex chloro(2,5-dithiahexane)copper(I). <i>Journal of the Chemical Society Dalton Transactions</i> , 1978, , 416.	1.1	11
208	Crystallization and preliminary X-ray crystallographic analysis of 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 403-406.	0.7	11
209	Three-dimensional structure and ligand binding properties of trichosurin, a metatherian lipocalin from the milk whey of the common brushtail possum <i>Trichosurus vulpecula</i> . <i>Biochemical Journal</i> , 2007, 408, 29-38.	1.7	11
210	Mapping of the ATP-binding domain of human fructosamine 3-kinase-related protein by affinity labelling with 5 ^α -[(fluorosulfonyl)benzoyl]adenosine. <i>Biochemical Journal</i> , 2008, 416, 281-288.	1.7	11
211	Structure of phosphoserine aminotransferase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 553-563.	2.5	11
212	Structures of <i>Mycobacterium tuberculosis</i> Anthranilate Phosphoribosyltransferase Variants Reveal the Conformational Changes That Facilitate Delivery of the Substrate to the Active Site. <i>Biochemistry</i> , 2015, 54, 6082-6092.	1.2	11
213	Crystallization of the C-terminal Domain of Rabbit Serum Hemopexin. <i>Journal of Molecular Biology</i> , 1993, 229, 251-252.	2.0	10
214	LISA: an intranet-based flexible database for protein crystallography project management. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1341-1343.	2.5	10
215	Structure of a domain-opened mutant (R121D) of the human lactoferrin N-lobe refined from a merohedrally twinned crystal form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 955-962.	2.5	10
216	Purification, crystallization and preliminary crystallographic analysis of mouse myo-inositol oxygenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 811-813.	0.7	10

#	ARTICLE	IF	CITATIONS
217	The Structure of an Ancient Conserved Domain Establishes a Structural Basis for Stable Histidine Phosphorylation and Identifies a New Family of Adenosine-specific Kinases. <i>Journal of Biological Chemistry</i> , 2006, 281, 22131-22141.	1.6	10
218	Crystal Structures of <i>E. coli</i> Native MenH and Two Active Site Mutants. <i>PLoS ONE</i> , 2013, 8, e61325.	1.1	10
219	Copper(II)-promoted oxidation of mercaptocarboxylic acids. The characterization of disulphide- and oxalate-containing products. Crystal structures of $[\{Cu(bipy)(2,2\text{-}dtdp)\}_n] \cdot 3nH_2O$ and $[\{Cu(bipy)(3,3\text{-}dtdp)\}_n] \cdot 2nH_2O$ (bipy = 2,2'-bipyridine, dtdp = dithiodipropanoate). <i>Journal of the Chemical Society Dalton Transactions</i> , 1990, , 2089-2094.	1.1	9
220	Purification and characterization of Ak.1 protease, a thermostable subtilisin with a disulphide bond in the substrate-binding cleft. <i>Biochemical Journal</i> , 2000, 350, 321.	1.7	9
221	Expression, crystallization and preliminary characterization of methylmalonyl coenzyme A epimerase from <i>Propionibacterium shermanii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 706-708.	2.5	9
222	Structure of HisF, a histidine biosynthetic protein from <i>Pyrobaculum aerophilum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1518-1525.	2.5	9
223	Crystallization and preliminary X-ray analysis of N-acetyl-1-D-myo-inositol-2-deoxy- β -D-glucopyranoside deacetylase (MshB) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2316-2318.	2.5	9
224	Structures of two mutants that probe the role in iron release of the dilysine pair in the N-lobe of human transferrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 408-414.	2.5	9
225	Synergism and Substitution in the Lactoferrins. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 33-44.	0.8	9
226	Copper co-ordination to thioether ligands. Spectroscopic studies of dimeric copper(II) complexes of 2-(3,3-dimethyl-2-thiabutyl)pyridine and the crystal structure of di- μ -bromo-bis{bromo[2-(3,3-dimethyl-2-thiabutyl)pyridine-NS]copper(II)}. <i>Journal of the Chemical Society Dalton Transactions</i> , 1981, , 2054-2058.	1.1	8
227	A Structural Explanation for the Retinal Specificity of Class 1 ALDH Enzymes. <i>Advances in Experimental Medicine and Biology</i> , 1999, 463, 27-38.	0.8	8
228	A non-synonymous nucleotide substitution can account for one evolutionary route to sesquiterpene synthase activity in the TPS-b subgroup. <i>FEBS Letters</i> , 2011, 585, 1841-1846.	1.3	8
229	Purification, crystallization and preliminary crystallographic analysis of human dihydrodipicolinate synthase-like protein (DHDPSL). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 59-62.	0.7	8
230	Crystallization and Preliminary X-ray Diffraction Studies on Cytosolic (Class 1) Aldehyde Dehydrogenase from Sheep Liver. <i>Journal of Molecular Biology</i> , 1994, 241, 263-264.	2.0	7
231	Iron-ic twists of fate. <i>Nature Structural and Molecular Biology</i> , 1997, 4, 869-871.	3.6	7
232	On the molecular-replacement problem in the presence of merohedral twinning: structure of the N-terminal half-molecule of human lactoferrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 129-138.	2.5	7
233	The Role of β Chains in the Control of the Hemoglobin Oxygen Binding Function: Chimeric Human/Mouse Proteins, Structure, and Function. <i>Biochemistry</i> , 2001, 40, 15669-15675.	1.2	7
234	Subunit dissociation and reassociation leads to preferential crystallization of haemoglobin Bart's (β ³⁴) from solutions of human embryonic haemoglobin Portland (β ²¹³²) at low pH. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 921-924.	2.5	7

#	ARTICLE	IF	CITATIONS
235	Electron transfer between cytochrome b5 and some oxidised haemoglobins: the role of ionic strength. <i>Journal of Inorganic Biochemistry</i> , 2002, 88, 328-334.	1.5	7
236	Crystallization and preliminary X-ray analysis of \hat{L} -isopropylmalate synthase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1167-1169.	2.5	7
237	Black sheep among the flock of protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1-1.	2.5	7
238	In defence of our science – validation now!. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 115-115.	2.5	7
239	Isolation and characterization of a gene encoding a drought-induced cysteine protease in tomato (<i>Lycopersicon esculentum</i>). <i>Genome</i> , 2001, 44, 368-374.	0.9	7
240	Purification and Crystallization of the Endoglycosidase PNGase F, a Peptide:N-glycosidase from <i>Flavobacterium meningosepticum</i> . <i>Journal of Molecular Biology</i> , 1994, 241, 624-626.	2.0	6
241	Crystallization and preliminary diffraction studies of the C-terminal domain of the DipZ homologue from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 243-245.	0.7	6
242	An arm-swapped dimer of the <i>Streptococcus pyogenes</i> pilin specific assembly factor SipA. <i>Journal of Structural Biology</i> , 2013, 183, 99-104.	1.3	6
243	A covalent adduct of MbtN, an acyl-ACP dehydrogenase from <i>Mycobacterium tuberculosis</i> , reveals an unusual acyl-binding pocket. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 862-872.	2.5	6
244	Regulation of human 4-hydroxy-2-oxoglutarate aldolase by pyruvate and \hat{L} -ketoglutarate: implications for primary hyperoxaluria type-3. <i>Biochemical Journal</i> , 2019, 476, 3369-3383.	1.7	6
245	Spectroscopic studies on metal complexes of <i>Aspergillus awamori</i> -derived recombinant human lactoferrin. <i>Inorganica Chimica Acta</i> , 2000, 298, 187-194.	1.2	5
246	PdxH proteins of mycobacteria are typical members of the classical pyridoxine/pyridoxamine 5-phosphate oxidase family. <i>FEBS Letters</i> , 2016, 590, 453-460.	1.3	5
247	Anthranilate phosphoribosyltransferase: Binding determinants for 5-phospho-alpha-d-ribose-1-pyrophosphate (PRPP) and the implications for inhibitor design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 264-274.	1.1	5
248	Cloning and Expression of the C-Terminal Lobe of Human Lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 259-263.	0.8	5
249	Crystallographic Studies on Metal and Anion Substituted Human Lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 265-269.	0.8	5
250	Crystallographic data deposition. <i>Nature</i> , 1996, 379, 202-202.	13.7	4
251	Crystallization and preliminary X-ray analysis of a conserved hypothetical protein PAE2754 from <i>Pyrobaculum aerophilum</i> and of a double Leu ⁺ Met mutant engineered for MAD phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 733-735.	2.5	4
252	Purification, crystallization and preliminary crystallographic analysis of <i>Streptococcus pyogenes</i> laminin-binding protein Lbp. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 141-143.	0.7	4

#	ARTICLE	IF	CITATIONS
253	In defence of our science – validation now!. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 112-112.	0.7	4
254	Use of a repetitive seeding protocol to obtain diffraction-quality crystals of a putative human D-xylulokinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1259-1262.	0.7	4
255	Expression, purification and crystallization of a membrane-associated, catalytically active type I signal peptidase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 61-65.	0.4	4
256	Synthesis and structural insight into ESX-4 Substrate Protein C, an immunodominant <i>Mycobacterium tuberculosis</i> secreted antigen. <i>Biopolymers</i> , 2016, 106, 267-274.	1.2	4
257	Structure of the ectodomain of the electron transporter Rv2874 from <i>Mycobacterium tuberculosis</i> reveals a thioredoxin-like domain combined with a carbohydrate-binding module. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 40-48.	1.1	4
258	Inhibition of Indigoidine Synthesis as a High-Throughput Colourimetric Screen for Antibiotics Targeting the Essential <i>Mycobacterium tuberculosis</i> Phosphopantetheinyl Transferase PptT. <i>Pharmaceutics</i> , 2021, 13, 1066.	2.0	4
259	Deposition and release of macromolecular structural data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 2-3.	2.5	3
260	Crystallization and preliminary X-ray analysis of native and recombinant human bile-salt dependent lipase: strategies for improvement of diffraction quality. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 478-480.	2.5	3
261	Purification, crystallization and preliminary X-ray analysis of <i>Enterococcus faecium</i> aminoglycoside-2-phosphotransferase-Ib [APH(2-phosphotransferase)-Ib]. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 410-413.	0.7	3
262	Cloning, expression, purification and preliminary crystallographic data for Rv3214 (EntD), a predicted cofactor-dependent phosphoglycerate mutase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 753-755.	0.7	3
263	Cloning, expression, purification and preliminary crystallographic analysis of the RNase HI domain of the <i>Mycobacterium tuberculosis</i> protein Rv2228c as a maltose-binding protein fusion. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 746-749.	0.7	3
264	Metal-Containing Proteins, Macrocycles, and Coordination Complexes in Therapeutic Applications and Disease. <i>Metal-Based Drugs</i> , 2008, 2008, 1-2.	3.8	3
265	Expression, purification, crystallization and preliminary crystallographic analysis of SpaA, a major pilin from <i>Corynebacterium diphtheriae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 802-804.	0.7	3
266	Purification, crystallization and preliminary crystallographic analysis of the minor pilin FctB from <i>Streptococcus pyogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 177-179.	0.7	3
267	Expectation bias and information content. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 83-83.	0.7	3
268	Mechanistic insights into F 420 -dependent glucose-6-phosphate dehydrogenase using isotope effects and substrate inhibition studies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 387-395.	1.1	3
269	F420-dependent glucose-6-phosphate dehydrogenase: A comprehensive review. <i>Inorganica Chimica Acta</i> , 2021, 524, 120417.	1.2	3
270	Convergent weaponry in a biological arms race. <i>ELife</i> , 2015, 4, .	2.8	3

#	ARTICLE	IF	CITATIONS
271	From Penicillin to the Ribosome: Revolutions in the Determination and Use of Molecular Structure in Chemistry and Biology. Australian Journal of Chemistry, 2004, 57, 829.	0.5	2
272	Crystallization of a protein using dehydration without a precipitant. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 565-568.	0.7	2
273	Deposition of diffraction images to be discussed at the Open Meeting of the Commission on Biological Macromolecules of the IUCr in Osaka. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 231-232.	0.7	2
274	Citations in supplementary material. Journal of Applied Crystallography, 2010, 43, 1285-1286.	1.9	2
275	Citations in supplementary material. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1269-1270.	2.5	2
276	Cloning, expression, purification, crystallization and preliminary X-ray studies of the C-terminal domain of Rv3262 (FbiB) from Mycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1274-1277.	0.7	2
277	Purification, crystallization and preliminary crystallographic analysis of the adhesion domain of Epf from Streptococcus pyogenes. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 793-797.	0.7	2
278	Celebrating biological crystallography: Acta D twenty years on. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1-1.	2.5	2
279	Preparation of truncated orf virus entry fusion complex proteins by chemical synthesis. Journal of Peptide Science, 2014, 20, 398-405.	0.8	2
280	Mass spectral determination of phosphopantetheinylation specificity for carrier proteins in Mycobacterium tuberculosis. FEBS Open Bio, 2016, 6, 1220-1226.	1.0	2
281	Datasets, processing and refinement details for Mtb -AnPRT: inhibitor structures with various space groups. Data in Brief, 2017, 15, 1019-1029.	0.5	2
282	New perspectives in biological crystallography. IUCrJ, 2014, 1, 82-83.	1.0	2
283	Proteins: accelerating towards the new millennium. Current Opinion in Structural Biology, 1999, 9, 705-706.	2.6	1
284	Purification, crystallization and preliminary X-ray analysis of Escherichia coli UDP-N-acetylmuramoyl:L-alanine ligase (MurC). Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1510-1513.	2.5	1
285	Making the most of two crystals: structural analysis of a conserved hypothetical protein using native gel screening and SAD phasing. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2242-2246.	2.5	1
286	Expectation bias and information content. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 141-141.	2.5	1
287	Purification, crystallization and preliminary X-ray studies of MbtN (Rv1346) from Mycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1354-1356.	0.7	1
288	Use of a novel microtitration protocol to obtain diffraction-quality crystals of 4-hydroxy-2-oxoglutarate aldolase from Bos taurus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1546-1549.	0.4	1

#	ARTICLE	IF	CITATIONS
289	Use of a silver bullet to resolve crystal lattice dislocation disorder: A cobalamin complex of γ -L-pyrroline-5-carboxylate dehydrogenase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , 2015, 189, 153-157.	1.3	1
290	Engineering of Group A Streptococcus Isopeptide Bonds into Immunoglobulin-Like Protein Domains. <i>Methods in Molecular Biology</i> , 2020, 2136, 377-395.	0.4	1
291	Widening the reach of structural biology. <i>IUCr</i> , 2016, 3, 84-85.	1.0	1
292	Letter to the Editor. <i>Journal of Biomolecular Structure and Dynamics</i> , 1996, 13, 583-583.	2.0	0
293	Using Structural Genomics to Understand <i>Mycobacterium Tuberculosis</i> . <i>IUBMB Life</i> , 2004, 56, 113-117.	1.5	0
294	From Penicillin to the Ribosome: Revolutions in the Determination and Use of Molecular Structure in Chemistry and Biology.. <i>ChemInform</i> , 2004, 35, no.	0.1	0
295	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> , 2008, 67, 473-473.	1.2	0
296	Citations in supplementary material. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1550-1551.	0.7	0
297	Small angle scattering $\hat{=}$ moving forward. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 619-619.	2.5	0
298	INTRAMOLECULAR ISOPEPTIDE BONDS: NOVEL POST-TRANSLATIONAL MODIFICATIONS IN BACTERIAL PILI AND CELL-SURFACE ADHESINS. , 2013, , 417-427.		0
299	Purification, crystallization and preliminary X-ray crystallographic studies of KstR2 (ketosteroid) Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>Biology Communications</i> , 2014, 70, 1643-1645.	0.4	0
300	Surface Proteins of Gram-Positive Pathogens: Using Crystallography to Uncover Novel Features in Drug and Vaccine Candidates. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2009, , 1-9.	0.5	0
301	X-Ray Structural Studies of Lactoferrin. , 1987, , 376-376.		0
302	Altered Domain Closure and Iron Binding in Lactoferrin Mutants. , 1997, , 25-38.		0
303	Mutagenesis of Human Lactoferrin and Expression in Baby Hamster Kidney Cells. , 1997, , 97-110.		0
304	Superantigen Architecture: Functional Decoration on a Conserved Scaffold. , 0, , 91-102.		0
305	Biological crystallography: new methods, new challenges. <i>IUCr</i> , 2015, 2, 155-156.	1.0	0
306	Determining the active site base and order of substrate addition within F 420 $\hat{=}$ dependent glucose-6-phosphate using steady-state and pre steady-state kinetics and isotope effects methods. <i>FASEB Journal</i> , 2018, 32, 655-30.	0.2	0