Edward N Baker

List of Publications by Year
in descending order

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306 papers	17,925 citations	12330 69 h-index	16183 124 g-index
314 all docs	314 docs citations	314 times ranked	14748 citing authors

#	Article	IF	Citations
1	Inhibition of Indigoidine Synthesis as a High-Throughput Colourimetric Screen for Antibiotics Targeting the Essential Mycobacterium tuberculosis Phosphopantetheinyl Transferase PptT. Pharmaceutics, 2021, 13, 1066.	4.5	4
2	F420-dependent glucose-6-phosphate dehydrogenase: A comprehensive review. Inorganica Chimica Acta, 2021, 524, 120417.	2.4	3
3	Convergent pathways to biosynthesis of the versatile cofactor F420. Current Opinion in Structural Biology, 2020, 65, 9-16.	5.7	14
4	Allosteric regulation of menaquinone (vitamin K2) biosynthesis in the human pathogen Mycobacterium tuberculosis. Journal of Biological Chemistry, 2020, 295, 3759-3770.	3.4	15
5	Engineering of Group A Streptococcus Isopeptide Bonds into Immunoglobulin-Like Protein Domains. Methods in Molecular Biology, 2020, 2136, 377-395.	0.9	1
6	The active site of the Mycobacterium tuberculosis branched-chain amino acid biosynthesis enzyme dihydroxyacid dehydratase contains a 2Feâ€“2S cluster. Journal of Biological Chemistry, 2019, 294, 13158-13170.	3.4	12
7	Group A <i>Streptococcus</i> T Antigens Have a Highly Conserved Structure Concealed under a Heterogeneous Surface That Has Implications for Vaccine Design. Infection and Immunity, 2019, 87, .	2.2	14
8	A revised biosynthetic pathway for the cofactor F420 in prokaryotes. Nature Communications, 2019, 10, 1558.	12.8	55
9	Regulation of human 4-hydroxy-2-oxoglutarate aldolase by pyruvate and Î±-ketoglutarate: implications for primary hyperoxaluria type-3. Biochemical Journal, 2019, 476, 3369-3383.	3.7	6
10	Anthranilate phosphoribosyltransferase: Binding determinants for 5â€²-phospho-alpha- d -ribosyl-1â€²-pyrophosphate (PRPP) and the implications for inhibitor design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 264-274.	2.3	5
11	Mechanistic insights into F 420 -dependent glucose-6-phosphate dehydrogenase using isotope effects and substrate inhibition studies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 387-395.	2.3	3
12	Determining the active site base and order of substrate addition within F 420 â€dependent glucoseâ€6â€phosphate using steadyâ€state and pre steadyâ€state kinetics and isotope effects methods. FASEB Journal, 2018, 32, 655.30.	0.5	0
13	Engineering a Lys-Asn isopeptide bond into an immunoglobulin-like protein domain enhances its stability. Scientific Reports, 2017, 7, 42753.	3.3	12
14	Using X-Ray Crystallography to Simplify and Accelerate Biologics Drug Development. Journal of Pharmaceutical Sciences, 2017, 106, 477-494.	3.3	24
15	Datasets, processing and refinement details for Mtb -AnPRT: inhibitor structures with various space groups. Data in Brief, 2017, 15, 1019-1029.	1.0	2
16	Serological Evidence of Immune Priming by Group A Streptococci in Patients with Acute Rheumatic Fever. Frontiers in Microbiology, 2016, 7, 1119.	3.5	26
17	Synthesis and structural insight into ESXâ€1 Substrate Protein C, an immunodominant <i>Mycobacterium tuberculosisâ€</i>secreted antigen. Biopolymers, 2016, 106, 267-274.	2.4	4
18	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. Angewandte Chemie - International Edition, 2016, 55, 7930-7933.	13.8	45

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19	Structure of the ectodomain of the electron transporter Rv2874 fromMycobacterium tuberculosisreveals a thioredoxin-like domain combined with a carbohydrate-binding module. Acta Crystallographica Section D: Structural Biology, 2016, 72, 40-48.	2.3	4
20	Mass spectral determination of phosphopantetheinylation specificity for carrier proteins in Mycobacterium tuberculosis. FEBS Open Bio, 2016, 6, 1220-1226.	2.3	2
21	Investigating the Reaction Mechanism of F₄₂₀-Dependent Glucose-6-phosphate Dehydrogenase from <i>Mycobacterium tuberculosis</i>: Kinetic Analysis of the Wild-Type and Mutant Enzymes. Biochemistry, 2016, 55, 5566-5577.	2.5	12
22	Structural Views along the Mycobacterium tuberculosis MenD Reaction Pathway Illuminate Key Aspects of Thiamin Diphosphate-Dependent Enzyme Mechanisms. Structure, 2016, 24, 1167-1177.	3.3	18
23	PdxH proteins of mycobacteria are typical members of the classical pyridoxine/pyridoxamine 5â€²â€phosphate oxidase family. FEBS Letters, 2016, 590, 453-460.	2.8	5
24	The Structure of the Transcriptional Repressor KstR in Complex with CoA Thioester Cholesterol Metabolites Sheds Light on the Regulation of Cholesterol Catabolism in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2016, 291, 7256-7266.	3.4	32
25	Elongation of the Poly-Î³-glutamate Tail of F420 Requires Both Domains of the F420:Î³-Glutamyl Ligase (FbiB) of Mycobacterium tuberculosis. Journal of Biological Chemistry, 2016, 291, 6882-6894.	3.4	24
26	Peptide binding to a bacterial signal peptidase visualized by peptide tethering and carrier-driven crystallization. IUCrJ, 2016, 3, 10-19.	2.2	15
27	Widening the reach of structural biology. IUCrJ, 2016, 3, 84-85.	2.2	1
28	Self-generated covalent cross-links in the cell-surface adhesins of Gram-positive bacteria. Biochemical Society Transactions, 2015, 43, 787-794.	3.4	24
29	Structure and inhibition of subunit I of the anthranilate synthase complex of <i>Mycobacterium tuberculosis</i> and expression of the active complex. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2297-2308.	2.5	17
30	Structures of <i>Mycobacterium tuberculosis</i> Anthranilate Phosphoribosyltransferase Variants Reveal the Conformational Changes That Facilitate Delivery of the Substrate to the Active Site. Biochemistry, 2015, 54, 6082-6092.	2.5	11
31	Expression, purification and crystallization of a membrane-associated, catalytically active type I signal peptidase from<i>Staphylococcus aureus</i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 61-65.	0.8	4
32	Use of a â€œsilver bulletâ€•to resolve crystal lattice dislocation disorder: A cobalamin complex of Î”1-pyrroline-5-carboxylate dehydrogenase from Mycobacterium tuberculosis. Journal of Structural Biology, 2015, 189, 153-157.	2.8	1
33	A covalent adduct of MbtN, an acyl-ACP dehydrogenase from<i>Mycobacterium tuberculosis</i>, reveals an unusual acyl-binding pocket. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 862-872.	2.5	6
34	A functional role of Rv1738 in <i>Mycobacterium tuberculosis</i> persistence suggested by racemic protein crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4310-4315.	7.1	43
35	Complex Formation between Two Biosynthetic Enzymes Modifies the Allosteric Regulatory Properties of Both. Journal of Biological Chemistry, 2015, 290, 18187-18198.	3.4	26
36	Production of recombinant proteins in <i>Mycobacterium smegmatis</i> for structural and functional studies. Protein Science, 2015, 24, 1-10.	7.6	56

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37	Convergent weaponry in a biological arms race. ELife, 2015, 4, .	6.0	3
38	Biological crystallography: new methods, new challenges. IUCrJ, 2015, 2, 155-156.	2.2	0
39	Structure and Activity of Streptococcus pyogenes SipA: A Signal Peptidase-Like Protein Essential for Pilus Polymerisation. PLoS ONE, 2014, 9, e99135.	2.5	14
40	Structural Model for Covalent Adhesion of the Streptococcus pyogenes Pilus through a Thioester Bond. Journal of Biological Chemistry, 2014, 289, 177-189.	3.4	41
41	Crystal structure of the essential Mycobacterium tuberculosis phosphopantetheinyl transferase PptT, solved as a fusion protein with maltose binding protein. Journal of Structural Biology, 2014, 188, 274-278.	2.8	13
42	Alternative substrates reveal catalytic cycle and key binding events in the reaction catalysed by anthranilate phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i>. Biochemical Journal, 2014, 461, 87-98.	3.7	18
43	Preparation of truncated orf virus entry fusion complex proteins by chemical synthesis. Journal of Peptide Science, 2014, 20, 398-405.	1.4	2
44	Autocatalytically generated Thr-Gln ester bond cross-links stabilize the repetitive Ig-domain shaft of a bacterial cell surface adhesin. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1367-1372.	7.1	31
45	Use of a novel microtitration protocol to obtain diffraction-quality crystals of 4-hydroxy-2-oxoglutarate aldolase fromBos taurus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1546-1549.	0.8	1
46	Purification, crystallization and preliminary X-ray crystallographic studies of KstR2 (ketosteroid) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38 Biology Communications, 2014, 70, 1643-1645.	0.8	0
47	Structure of the bacterial type <scp>II NADH</scp> dehydrogenase: a monotopic membrane protein with an essential role in energy generation. Molecular Microbiology, 2014, 91, 950-964.	2.5	103
48	Crystal Structure of PhnF, a GntR-Family Transcriptional Regulator of Phosphate Transport in Mycobacterium smegmatis. Journal of Bacteriology, 2014, 196, 3472-3481.	2.2	17
49	Structural Conservation, Variability, and Immunogenicity of the T6 Backbone Pilin of Serotype M6 Streptococcus pyogenes. Infection and Immunity, 2014, 82, 2949-2957.	2.2	32
50	A slow-forming isopeptide bond in the structure of the major pilin SpaD from<i>Corynebacterium diphtheriae</i>has implications for pilus assembly. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1190-1201.	2.5	27
51	Crystal structure of kiwellin, a major cell-wall protein from kiwifruit. Journal of Structural Biology, 2014, 187, 276-281.	2.8	15
52	Working towards a Group A Streptococcal vaccine: Report of a collaborative Trans-Tasman workshop. Vaccine, 2014, 32, 3713-3720.	3.8	44
53	Repurposing the Chemical Scaffold of the Antiâ€Arthritic Drug Lobenzarit to Target Tryptophan Biosynthesis in <i>Mycobacterium tuberculosis</i>. ChemBioChem, 2014, 15, 852-864.	2.6	15
54	Characterization of the proline-utilization pathway in<i>Mycobacterium tuberculosis</i>through structural and functional studies. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 968-980.	2.5	14

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55	New perspectives in biological crystallography. IUCrJ, 2014, 1, 82-83.	2.2	2
56	Inhibition studies on Mycobacterium tuberculosis N-acetylglucosamine-1-phosphate uridyltransferase (GlmU). Organic and Biomolecular Chemistry, 2013, 11, 8113.	2.8	26
57	Three Sites and You Are Out: Ternary Synergistic Allostery Controls Aromatic Amino Acid Biosynthesis in Mycobacterium tuberculosis. Journal of Molecular Biology, 2013, 425, 1582-1592.	4.2	38
58	Celebrating biological crystallography:Acta Dtwenty years on. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1-1.	2.5	2
59	Ligand promiscuity within the internal cavity of Epiphyas postvittana Takeout 1 protein. Journal of Structural Biology, 2013, 182, 259-263.	2.8	12
60	An arm-swapped dimer of the Streptococcus pyogenes pilin specific assembly factor SipA. Journal of Structural Biology, 2013, 183, 99-104.	2.8	6
61	The Substrate Capture Mechanism of Mycobacterium tuberculosis Anthranilate Phosphoribosyltransferase Provides a Mode for Inhibition. Biochemistry, 2013, 52, 1776-1787.	2.5	23
62	INTRAMOLECULAR ISOPEPTIDE BONDS: NOVEL POST-TRANSLATIONAL MODIFICATIONS IN BACTERIAL PILI AND CELL-SURFACE ADHESINS. , 2013, , 417-427.		0
63	Structure and Function of Human Xylulokinase, an Enzyme with Important Roles in Carbohydrate Metabolism. Journal of Biological Chemistry, 2013, 288, 1643-1652.	3.4	23
64	Expectation bias and information content. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 141-141.	2.5	1
65	Expectation bias and information content. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 83-83.	0.7	3
66	Purification, crystallization and preliminary X-ray studies of MbtN (Rv1346) fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1354-1356.	0.7	1
67	Crystal Structures of E. coli Native MenH and Two Active Site Mutants. PLoS ONE, 2013, 8, e61325.	2.5	10
68	Structural and Functional Properties of Staphylococcal Superantigen-Like Protein 4. Infection and Immunity, 2012, 80, 4004-4013.	2.2	33
69	The Extracellular Protein Factor Epf from Streptococcus pyogenes Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. Journal of Biological Chemistry, 2012, 287, 38178-38189.	3.4	18
70	Use of a repetitive seeding protocol to obtain diffraction-quality crystals of a putative humanD-xylulokinase. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1259-1262.	0.7	4
71	Synthesis and evaluation of M. tuberculosis salicylate synthase (MbtI) inhibitors designed to probe plasticity in the active site. Organic and Biomolecular Chemistry, 2012, 10, 9223.	2.8	20
72	Implications of Binding Mode and Active Site Flexibility for Inhibitor Potency against the Salicylate Synthase from <i>Mycobacterium tuberculosis</i>. Biochemistry, 2012, 51, 4868-4879.	2.5	31

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73	Removal of the C-Terminal Regulatory Domain of Î±-Isopropylmalate Synthase Disrupts Functional Substrate Binding. Biochemistry, 2012, 51, 2289-2297.	2.5	18
74	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.	2.0	93
75	Tatâ€"Dependent Translocation of an F420â€"Binding Protein of Mycobacterium tuberculosis. PLoS ONE, 2012, 7, e45003.	2.5	26
76	Purification, crystallization and preliminary crystallographic analysis of human dihydrodipicolinate synthase-like protein (DHDPSL). Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 59-62.	0.7	8
77	Structure and assembly of Gram-positive bacterial pili: unique covalent polymers. Current Opinion in Structural Biology, 2012, 22, 200-207.	5.7	72
78	Structure of phosphoserine aminotransferase from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 553-563.	2.5	11
79	Small angle scattering â€" moving forward. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 619-619.	2.5	0
80	Purification, crystallization and preliminary crystallographic analysis of the adhesion domain of Epf fromStreptococcus pyogenes. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 793-797.	0.7	2
81	Structural Analyses of a Purine Biosynthetic Enzyme from Mycobacterium tuberculosis Reveal a Novel Bound Nucleotide. Journal of Biological Chemistry, 2011, 286, 40706-40716.	3.4	15
82	Crystal Structure of Spy0129, a Streptococcus pyogenes Class B Sortase Involved in Pilus Assembly. PLoS ONE, 2011, 6, e15969.	2.5	44
83	Structure of the Full-Length Major Pilin from Streptococcus pneumoniae: Implications for Isopeptide Bond Formation in Gram-Positive Bacterial Pili. PLoS ONE, 2011, 6, e22095.	2.5	33
84	Intramolecular isopeptide bonds: protein crosslinks built for stress?. Trends in Biochemical Sciences, 2011, 36, 229-237.	7.5	112
85	The TB Structural Genomics Consortium: A decade of progress. Tuberculosis, 2011, 91, 155-172.	1.9	39
86	A non-synonymous nucleotide substitution can account for one evolutionary route to sesquiterpene synthase activity in the TPS-b subgroup. FEBS Letters, 2011, 585, 1841-1846.	2.8	8
87	Cloning, expression, purification, crystallization and preliminary X-ray studies of the C-terminal domain of Rv3262 (FbiB) fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1274-1277.	0.7	2
88	Potent Inhibitors of a Shikimate Pathway Enzyme from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2011, 286, 16197-16207.	3.4	37
89	Inhibition Studies of <i>Mycobacterium tuberculosis</i> Salicylate Synthase (MbtI). ChemMedChem, 2010, 5, 1067-1079.	3.2	50
90	Citations in supplementary material. Journal of Applied Crystallography, 2010, 43, 1285-1286.	4.5	2

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91	Black sheep among the flock of protein structures. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1-1.	2.5	7
92	In defence of our science â€“ validation now!. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 115-115.	2.5	7
93	Structural and functional analysis of Rv0554 from<i>Mycobacterium tuberculosis</i>: testing a putative role in menaquinone biosynthesis. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 909-917.	2.5	12
94	Citations in supplementary material. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1269-1270.	2.5	2
95	Purification, crystallization and preliminary crystallographic analysis of the minor pilin FctB fromStreptococcus pyogenes. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 177-179.	0.7	3
96	In defence of our science â€“ validation now!. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 112-112.	0.7	4
97	Citations in supplementary material. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1550-1551.	0.7	0
98	Roles of Minor Pilin Subunits Spy0125 and Spy0130 in the Serotype M1 <i>Streptococcus pyogenes</i> Strain SF370. Journal of Bacteriology, 2010, 192, 4651-4659.	2.2	48
99	Structural and Functional Characterization of an RNase HI Domain from the Bifunctional Protein Rv2228c from <i>Mycobacterium tuberculosis</i>. Journal of Bacteriology, 2010, 192, 2878-2886.	2.2	39
100	Synergistic Allostery, a Sophisticated Regulatory Network for the Control of Aromatic Amino Acid Biosynthesis in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2010, 285, 30567-30576.	3.4	63
101	Crystal Structure of the Minor Pilin FctB Reveals Determinants of Group A Streptococcal Pilus Anchoring. Journal of Biological Chemistry, 2010, 285, 20381-20389.	3.4	61
102	Metabolic Engineering of Cofactor F420 Production in Mycobacterium smegmatis. PLoS ONE, 2010, 5, e15803.	2.5	110
103	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
104	The Laminin-Binding Protein Lbp from Streptococcus pyogenes Is a Zinc Receptor. Journal of Bacteriology, 2009, 191, 5814-5823.	2.2	56
105	Defining the Potassium Binding Region in an Apple Terpene Synthase. Journal of Biological Chemistry, 2009, 284, 8661-8669.	3.4	36
106	Crystal Structure of Epiphyas postvittana Takeout 1 with Bound Ubiquinone Supports a Role as Ligand Carriers for Takeout Proteins in Insects. Journal of Biological Chemistry, 2009, 284, 3496-3503.	3.4	40
107	Intramolecular Isopeptide Bonds Give Thermodynamic and Proteolytic Stability to the Major Pilin Protein of Streptococcus pyogenes. Journal of Biological Chemistry, 2009, 284, 20729-20737.	3.4	93
108	The Crystal Structures of Substrate and Nucleotide Complexes of <i>Enterococcus faecium</i> Aminoglycoside-2â€²â€²-Phosphotransferase-IIa [APH(2â€²â€²)-IIa] Provide Insights into Substrate Selectivity in the APH(2â€²â€²) Subfamily. Journal of Bacteriology, 2009, 191, 4133-4143.	2.2	50

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109	Isopeptide bonds in bacterial pili and their characterization by Xâ€ray crystallography and mass spectrometry. Biopolymers, 2009, 91, 1126-1134.	2.4	22
110	Pili in Gram-negative and Gram-positive bacteria â€" structure, assembly and their role in disease. Cellular and Molecular Life Sciences, 2009, 66, 613-635.	5.4	425
111	Structure and function of GlmU from<i>Mycobacterium tuberculosis</i>. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 275-283.	2.5	54
112	Expression, purification, crystallization and preliminary crystallographic analysis of SpaA, a major pilin fromCorynebacterium diphtheriae. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 802-804.	0.7	3
113	Making Sense of a Missense Mutation: Characterization of MutT2, a Nudix Hydrolase from Mycobacterium tuberculosis, and the G58R Mutant Encoded in W-Beijing Strains of M. tuberculosis. Biochemistry, 2009, 48, 699-708.	2.5	23
114	Crystal Structure and Metal Binding Properties of the Lipoprotein MtsA, Responsible for Iron Transport in <i>Streptococcus pyogenes</i>. Biochemistry, 2009, 48, 6184-6190.	2.5	54
115	A structural framework for understanding the multifunctional character of lactoferrin. Biochimie, 2009, 91, 3-10.	2.6	225
116	Structures of Glycinamide Ribonucleotide Transformylase (PurN) from Mycobacterium tuberculosis Reveal a Novel Dimer with Relevance to Drug Discovery. Journal of Molecular Biology, 2009, 389, 722-733.	4.2	15
117	Surface Proteins of Gram-Positive Pathogens: Using Crystallography to Uncover Novel Features in Drug and Vaccine Candidates. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 1-9.	0.5	0
118	The crystal structure of staphylococcal superantigenâ€like protein 11 in complex with sialyl Lewis X reveals the mechanism for cell binding and immune inhibition. Molecular Microbiology, 2008, 67, 473-473.	2.5	0
119	Structures of<i>Mycobacterium tuberculosis</i>folylpolyglutamate synthase complexed with ADP and AMPPCP. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 745-753.	2.5	13
120	Purification, crystallization and preliminary crystallographic analysis of<i>Streptococcus pyogenes</i>laminin-binding protein Lbp. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 141-143.	0.7	4
121	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
122	Cloning, expression, purification and preliminary crystallographic analysis of the RNase HI domain of theMycobacterium tuberculosisprotein Rv2228c as a maltose-binding protein fusion. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 746-749.	0.7	3
123	Crystal structure of PAE0151 from <i>Pyrobaculum aerophilum</i>, a PINâ€domain (VapC) protein from a toxinâ€antitoxin operon. Proteins: Structure, Function and Bioinformatics, 2008, 72, 510-518.	2.6	45
124	Histidine phosphorylation in biological systems. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 100-105.	2.3	68
125	Synthesis and structureâ€"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. European Journal of Medicinal Chemistry, 2008, 43, 1276-1296.	5.5	26
126	Synthesis and structureâ€"activity relationships of soluble 8-substituted 4-(2-chlorophenyl)-9-hydroxypyrrolo[3,4-c]carbazole-1,3(2H,6H)-diones as inhibitors of the Wee1 and Chk1 checkpoint kinases. Bioorganic and Medicinal Chemistry Letters, 2008, 18, 929-933.	2.2	27

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127	The Structure and Unusual Protein Chemistry of Hypoxic Response Protein 1, a Latency Antigen and Highly Expressed Member of the DosR Regulon in Mycobacterium tuberculosis. Journal of Molecular Biology, 2008, 383, 822-836.	4.2	20
128	A new GatewayÂ® vector and expression protocol for fast and efficient recombinant protein expression in Mycobacterium smegmatis. Protein Expression and Purification, 2008, 57, 81-87.	1.3	44
129	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. Journal of Biological Chemistry, 2008, 283, 17531-17541.	3.4	79
130	Mapping of the ATP-binding domain of human fructosamine 3-kinase-related protein by affinity labelling with 5â€²-[<i>p</i>-(fluorosulfonyl)benzoyl]adenosine. Biochemical Journal, 2008, 416, 281-288.	3.7	11
131	Metal-Containing Proteins, Macrocycles, and Coordination Complexes in Therapeutic Applications and Disease. Metal-Based Drugs, 2008, 2008, 1-2.	3.8	3
132	Stabilizing Isopeptide Bonds Revealed in Gram-Positive Bacterial Pilus Structure. Science, 2007, 318, 1625-1628.	12.6	295
133	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. Journal of Virology, 2007, 81, 11075-11083.	3.4	19
134	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>. Biochemical Journal, 2007, 408, 29-38.	3.7	11
135	Expression, purification and crystallization of native and selenomethionine labeled Mycobacterium tuberculosis FGD1 (Rv0407) using a Mycobacterium smegmatis expression system. Protein Expression and Purification, 2007, 54, 38-44.	1.3	38
136	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. Journal of Molecular Biology, 2007, 374, 1298-1308.	4.2	62
137	High-Resolution Crystal Structure of Plant Carboxylesterase AeCXE1, from Actinidia eriantha, and Its Complex with a High-Affinity Inhibitor Paraoxon,. Biochemistry, 2007, 46, 1851-1859.	2.5	58
138	Structures of two mutants that probe the role in iron release of the dilysine pair in the N-lobe of human transferrin. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 408-414.	2.5	9
139	The crystal structure of staphylococcal superantigenâ€•like protein 11 in complex with sialyl Lewis X reveals the mechanism for cell binding and immune inhibition. Molecular Microbiology, 2007, 66, 1342-1355.	2.5	85
140	Structural genomics as an approach towards understanding the biology of tuberculosis. Journal of Structural and Functional Genomics, 2007, 8, 57-65.	1.2	20
141	The Crystal Structure of TrpD, a Metabolic Enzyme Essential for Lung Colonization by Mycobacterium tuberculosis, in Complex with its Substrate Phosphoribosylpyrophosphate. Journal of Molecular Biology, 2006, 355, 784-797.	4.2	41
142	Structure ofEscherichia coliUDP-N-acetylmuramoyl:L-alanine ligase (MurC). Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1466-1474.	2.5	31
143	Purification, crystallization and preliminary crystallographic analysis of mousemyo-inositol oxygenase. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 811-813.	0.7	10
144	The potential impact of structural genomics on tuberculosis drug discovery. Drug Discovery Today, 2006, 11, 28-34.	6.4	42

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145	Structural and Functional Analysis of Rv3214 from Mycobacterium tuberculosis , a Protein with Conflicting Functional Annotations, Leads to Its Characterization as a Phosphatase. Journal of Bacteriology, 2006, 188, 3589-3599.	2.2	23
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