

# Edward N Baker

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

293  
papers

15,613  
citations

66  
h-index

116  
g-index

314  
ext. papers

16,717  
ext. citations

5.6  
avg. IF

6.36  
L-index

#	Paper	IF	Citations
293	Inhibition of Indigoidine Synthesis as a High-Throughput Colourimetric Screen for Antibiotics Targeting the Essential Phosphopantetheinyl Transferase PptT. <i>Pharmaceutics</i> , <b>2021</b> , 13,	6.4	2
292	F420-dependent glucose-6-phosphate dehydrogenase: A comprehensive review. <i>Inorganica Chimica Acta</i> , <b>2021</b> , 524, 120417	2.7	0
291	Allosteric regulation of menaquinone (vitamin K) biosynthesis in the human pathogen. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 3759-3770	5.4	9
290	Convergent pathways to biosynthesis of the versatile cofactor F. <i>Current Opinion in Structural Biology</i> , <b>2020</b> , 65, 9-16	8.1	4
289	Engineering of Group A Streptococcus Isopeptide Bonds into Immunoglobulin-Like Protein Domains. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2136, 377-395	1.4	1
288	Group A T Antigens Have a Highly Conserved Structure Concealed under a Heterogeneous Surface That Has Implications for Vaccine Design. <i>Infection and Immunity</i> , <b>2019</b> , 87,	3.7	6
287	A revised biosynthetic pathway for the cofactor F in prokaryotes. <i>Nature Communications</i> , <b>2019</b> , 10, 15587.4	7.4	35
286	The active site of the branched-chain amino acid biosynthesis enzyme dihydroxyacid dehydratase contains a 2Fe-2S cluster. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 13158-13170	5.4	7
285	Regulation of human 4-hydroxy-2-oxoglutarate aldolase by pyruvate and ketoglutarate: implications for primary hyperoxaluria type-3. <i>Biochemical Journal</i> , <b>2019</b> , 476, 3369-3383	3.8	3
284	Anthranilate phosphoribosyltransferase: Binding determinants for 5-phospho-alpha-d-ribosyl-1-pyrophosphate (PRPP) and the implications for inhibitor design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2018</b> , 1866, 264-274	4	4
283	Determining the active site base and order of substrate addition within F420-dependent glucose-6-phosphate using steady-state and pre steady-state kinetics and isotope effects methods. <i>FASEB Journal</i> , <b>2018</b> , 32, 655.30	0.9	
282	Mechanistic insights into F-dependent glucose-6-phosphate dehydrogenase using isotope effects and substrate inhibition studies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2018</b> , 1866, 387-395	4.95	2
281	Engineering a Lys-Asn isopeptide bond into an immunoglobulin-like protein domain enhances its stability. <i>Scientific Reports</i> , <b>2017</b> , 7, 42753	4.9	9
280	Using X-Ray Crystallography to Simplify and Accelerate Biologics Drug Development. <i>Journal of Pharmaceutical Sciences</i> , <b>2017</b> , 106, 477-494	3.9	15
279	Datasets, processing and refinement details for -AnPRT: inhibitor structures with various space groups. <i>Data in Brief</i> , <b>2017</b> , 15, 1019-1029	1.2	1
278	Investigating the Reaction Mechanism of F-Dependent Glucose-6-phosphate Dehydrogenase from Mycobacterium tuberculosis: Kinetic Analysis of the Wild-Type and Mutant Enzymes. <i>Biochemistry</i> , <b>2016</b> , 55, 5566-5577	3.2	12
277	Structural Views along the Mycobacterium tuberculosis MenD Reaction Pathway Illuminate Key Aspects of Thiamin Diphosphate-Dependent Enzyme Mechanisms. <i>Structure</i> , <b>2016</b> , 24, 1167-77	5.2	15

276	PdxH proteins of mycobacteria are typical members of the classical pyridoxine/pyridoxamine 5-phosphate oxidase family. <i>FEBS Letters</i> , <b>2016</b> , 590, 453-60	3.8	4
275	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. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 7256-66	5.4	22
274	Elongation of the Poly- $\gamma$ -glutamate Tail of F420 Requires Both Domains of the F420: $\gamma$ -glutamyl Ligase (FbiB) of Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 6882-94	5.4	19
273	Peptide binding to a bacterial signal peptidase visualized by peptide tethering and carrier-driven crystallization. <i>IUCrJ</i> , <b>2016</b> , 3, 10-9	4.7	10
272	Widening the reach of structural biology. <i>IUCrJ</i> , <b>2016</b> , 3, 84-5	4.7	1
271	Serological Evidence of Immune Priming by Group A Streptococci in Patients with Acute Rheumatic Fever. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1119	5.7	19
270	Synthesis and structural insight into ESX-1 Substrate Protein C, an immunodominant Mycobacterium tuberculosis-secreted antigen. <i>Biopolymers</i> , <b>2016</b> , 106, 267-74	2.2	4
269	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 7930-3	16.4	30
268	Structure of the ectodomain of the electron transporter Rv2874 from Mycobacterium tuberculosis reveals a thioredoxin-like domain combined with a carbohydrate-binding module. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 40-8	5.5	3
267	Mass spectral determination of phosphopantetheinylation specificity for carrier proteins in. <i>FEBS Open Bio</i> , <b>2016</b> , 6, 1220-1226	2.7	2
266	A covalent adduct of MbtN, an acyl-ACP dehydrogenase from Mycobacterium tuberculosis, reveals an unusual acyl-binding pocket. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 862-72		3
265	A functional role of Rv1738 in Mycobacterium tuberculosis persistence suggested by racemic protein crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 4310-5	11.5	34
264	Complex Formation between Two Biosynthetic Enzymes Modifies the Allosteric Regulatory Properties of Both: AN EXAMPLE OF MOLECULAR SYMBIOSIS. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 18187-18198	5.4	21
263	Production of recombinant proteins in Mycobacterium smegmatis for structural and functional studies. <i>Protein Science</i> , <b>2015</b> , 24, 1-10	6.3	23
262	Self-generated covalent cross-links in the cell-surface adhesins of Gram-positive bacteria. <i>Biochemical Society Transactions</i> , <b>2015</b> , 43, 787-94	5.1	17
261	Structure and inhibition of subunit I of the anthranilate synthase complex of Mycobacterium tuberculosis and expression of the active complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 2297-308		15
260	Structures of Mycobacterium tuberculosis Anthranilate Phosphoribosyltransferase Variants Reveal the Conformational Changes That Facilitate Delivery of the Substrate to the Active Site. <i>Biochemistry</i> , <b>2015</b> , 54, 6082-92	3.2	9
259	Expression, purification and crystallization of a membrane-associated, catalytically active type I signal peptidase from Staphylococcus aureus. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 61-5	1.1	3

258	Use of a "silver bullet" to resolve crystal lattice dislocation disorder: a cobalamin complex of $\beta$ -pyrroline-5-carboxylate dehydrogenase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Structural Biology</i> , <b>2015</b> , 189, 153-7	3.4	1
257	Convergent weaponry in a biological arms race. <i>ELife</i> , <b>2015</b> , 4,	8.9	3
256	Biological crystallography: new methods, new challenges. <i>IUCrJ</i> , <b>2015</b> , 2, 155-6	4.7	
255	Structure of the bacterial type II NADH dehydrogenase: a monotopic membrane protein with an essential role in energy generation. <i>Molecular Microbiology</i> , <b>2014</b> , 91, 950-64	4.1	80
254	Crystal structure of PhnF, a GntR-family transcriptional regulator of phosphate transport in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , <b>2014</b> , 196, 3472-81	3.5	12
253	Structural conservation, variability, and immunogenicity of the T6 backbone pilin of serotype M6 <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , <b>2014</b> , 82, 2949-57	3.7	25
252	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> , <b>2014</b> , 70, 1190-201		22
251	Crystal structure of kiwellin, a major cell-wall protein from kiwifruit. <i>Journal of Structural Biology</i> , <b>2014</b> , 187, 276-281	3.4	8
250	Working towards a group A streptococcal vaccine: report of a collaborative Trans-Tasman workshop. <i>Vaccine</i> , <b>2014</b> , 32, 3713-20	4.1	38
249	Repurposing the chemical scaffold of the anti-arthritis drug Lobenzarit to target tryptophan biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>ChemBioChem</i> , <b>2014</b> , 15, 852-64	3.8	14
248	Characterization of the proline-utilization pathway in <i>Mycobacterium tuberculosis</i> through structural and functional studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 968-80		12
247	Structure and activity of <i>Streptococcus pyogenes</i> SipA: a signal peptidase-like protein essential for pilus polymerisation. <i>PLoS ONE</i> , <b>2014</b> , 9, e99135	3.7	10
246	Structural model for covalent adhesion of the <i>Streptococcus pyogenes</i> pilus through a thioester bond. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 177-89	5.4	37
245	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> , <b>2014</b> , 188, 274-8	3.4	11
244	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> , <b>2014</b> , 461, 87-98	3.8	15
243	Preparation of truncated orf virus entry fusion complex proteins by chemical synthesis. <i>Journal of Peptide Science</i> , <b>2014</b> , 20, 398-405	2.1	2
242	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> , <b>2014</b> , 111, 1367-72	11.5	24
241	Use of a novel microtitration protocol to obtain diffraction-quality crystals of 4-hydroxy-2-oxoglutarate aldolase from <i>Bos taurus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1546-9	1.1	1

240	Purification, crystallization and preliminary X-ray crystallographic studies of KstR2 (ketosteroid regulatory protein) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1643-5	1.1	
239	New perspectives in biological crystallography. <i>IUCrJ</i> , <b>2014</b> , 1, 82-3	4.7	2
238	Inhibition studies on <i>Mycobacterium tuberculosis</i> N-acetylglucosamine-1-phosphate uridyltransferase (GlmU). <i>Organic and Biomolecular Chemistry</i> , <b>2013</b> , 11, 8113-26	3.9	21
237	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> , <b>2013</b> , 425, 1582-92	6.5	30
236	Ligand promiscuity within the internal cavity of <i>Epiphyas postvittana</i> Takeout 1 protein. <i>Journal of Structural Biology</i> , <b>2013</b> , 182, 259-63	3.4	10
235	An arm-swapped dimer of the <i>Streptococcus pyogenes</i> pilin specific assembly factor SipA. <i>Journal of Structural Biology</i> , <b>2013</b> , 183, 99-104	3.4	5
234	The substrate capture mechanism of <i>Mycobacterium tuberculosis</i> anthranilate phosphoribosyltransferase provides a mode for inhibition. <i>Biochemistry</i> , <b>2013</b> , 52, 1776-87	3.2	20
233	INTRAMOLECULAR ISOPEPTIDE BONDS: NOVEL POST-TRANSLATIONAL MODIFICATIONS IN BACTERIAL PILI AND CELL-SURFACE ADHESINS <b>2013</b> , 417-427		
232	Structure and function of human xylulokinase, an enzyme with important roles in carbohydrate metabolism. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 1643-52	5.4	16
231	Purification, crystallization and preliminary X-ray studies of MbtN (Rv1346) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2013</b> , 69, 1354-6		1
230	Crystal structures of <i>E. coli</i> native MenH and two active site mutants. <i>PLoS ONE</i> , <b>2013</b> , 8, e61325	3.7	8
229	Structure and assembly of Gram-positive bacterial pili: unique covalent polymers. <i>Current Opinion in Structural Biology</i> , <b>2012</b> , 22, 200-7	8.1	66
228	Structure of phosphoserine aminotransferase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 553-63		10
227	Purification, crystallization and preliminary crystallographic analysis of the adhesion domain of Epf from <i>Streptococcus pyogenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2012</b> , 68, 793-7		2
226	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> , <b>2012</b> , 68, 1259-62		4
225	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> , <b>2012</b> , 10, 9223-36	3.9	16
224	Implications of binding mode and active site flexibility for inhibitor potency against the salicylate synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemistry</i> , <b>2012</b> , 51, 4868-79	3.2	26
223	Removal of the C-terminal regulatory domain of $\beta$ -isopropylmalate synthase disrupts functional substrate binding. <i>Biochemistry</i> , <b>2012</b> , 51, 2289-97	3.2	14

222	A structural perspective on lactoferrin function. <i>Biochemistry and Cell Biology</i> , <b>2012</b> , 90, 320-8	3.6	68
221	Tat-dependent translocation of an F420-binding protein of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e45003	3.7	21
220	Purification, crystallization and preliminary crystallographic analysis of human dihydrodipicolinate synthase-like protein (DHDPSL). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2012</b> , 68, 59-62		6
219	Structural and functional properties of staphylococcal superantigen-like protein 4. <i>Infection and Immunity</i> , <b>2012</b> , 80, 4004-13	3.7	28
218	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> , <b>2012</b> , 287, 38178-89	5.4	17
217	Structural analyses of a purine biosynthetic enzyme from <i>Mycobacterium tuberculosis</i> reveal a novel bound nucleotide. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 40706-16	5.4	7
216	Crystal structure of Spy0129, a <i>Streptococcus pyogenes</i> class B sortase involved in pilus assembly. <i>PLoS ONE</i> , <b>2011</b> , 6, e15969	3.7	40
215	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> , <b>2011</b> , 6, e22095	3.7	30
214	Intramolecular isopeptide bonds: protein crosslinks built for stress?. <i>Trends in Biochemical Sciences</i> , <b>2011</b> , 36, 229-37	10.3	96
213	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , <b>2011</b> , 91, 155-72	2.6	33
212	A non-synonymous nucleotide substitution can account for one evolutionary route to sesquiterpene synthase activity in the TPS-b subgroup. <i>FEBS Letters</i> , <b>2011</b> , 585, 1841-6	3.8	7
211	Cloning, expression, purification, crystallization and preliminary X-ray studies of the C-terminal domain of Rv3262 (FbiB) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2011</b> , 67, 1274-7		2
210	Potent inhibitors of a shikimate pathway enzyme from <i>Mycobacterium tuberculosis</i> : combining mechanism- and modeling-based design. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 16197-207	5.4	30
209	Roles of minor pilin subunits Spy0125 and Spy0130 in the serotype M1 <i>Streptococcus pyogenes</i> strain SF370. <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 4651-9	3.5	44
208	Structural and functional characterization of an RNase HI domain from the bifunctional protein Rv2228c from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , <b>2010</b> , 192, 2878-86	3.5	22
207	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> , <b>2010</b> , 285, 30567-76	5.4	50
206	Crystal structure of the minor pilin FctB reveals determinants of Group A streptococcal pilus anchoring. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 20381-9	5.4	56
205	Inhibition studies of <i>Mycobacterium tuberculosis</i> salicylate synthase (MbtI). <i>ChemMedChem</i> , <b>2010</b> , 5, 1067-79	3.7	41



204	Citations in supplementary material. <i>Journal of Applied Crystallography</i> , <b>2010</b> , 43, 1285-1286	3.8	2
203	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> , <b>2010</b> , 66, 909-17		10
202	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> , <b>2010</b> , 66, 177-9		3
201	Metabolic engineering of cofactor F420 production in <i>Mycobacterium smegmatis</i> . <i>PLoS ONE</i> , <b>2010</b> , 5, e15803	3.7	88
200	The <i>Corynebacterium diphtheriae</i> shaft pilin SpaA is built of tandem Ig-like modules with stabilizing isopeptide and disulfide bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 16967-71	11.5	95
199	The laminin-binding protein Lbp from <i>Streptococcus pyogenes</i> is a zinc receptor. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 5814-23	3.5	49
198	Defining the potassium binding region in an apple terpene synthase. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 8661-9	5.4	34
197	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> , <b>2009</b> , 284, 3496-503	5.4	38
196	Intramolecular isopeptide bonds give thermodynamic and proteolytic stability to the major pilin protein of <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 20729-37	5.4	84
195	The crystal structures of substrate and nucleotide complexes of <i>Enterococcus faecium</i> aminoglycoside-2 $\phi$ phosphotransferase-IIa [APH(2 $\phi$ IIa)] provide insights into substrate selectivity in the APH(2 $\phi$ ) subfamily. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 4133-43	3.5	47
194	Isopeptide bonds in bacterial pili and their characterization by X-ray crystallography and mass spectrometry. <i>Biopolymers</i> , <b>2009</b> , 91, 1126-34	2.2	20
193	Pili in Gram-negative and Gram-positive bacteria - structure, assembly and their role in disease. <i>Cellular and Molecular Life Sciences</i> , <b>2009</b> , 66, 613-35	10.3	352
192	Structure and function of GlmU from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 275-83		46
191	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> , <b>2009</b> , 65, 802-4		3
190	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> , <b>2009</b> , 48, 699-708	3.2	21
189	Crystal structure and metal binding properties of the lipoprotein MtsA, responsible for iron transport in <i>Streptococcus pyogenes</i> . <i>Biochemistry</i> , <b>2009</b> , 48, 6184-90	3.2	43
188	A structural framework for understanding the multifunctional character of lactoferrin. <i>Biochimie</i> , <b>2009</b> , 91, 3-10	4.6	195
187	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> , <b>2009</b> , 389, 722-33	6.5	10

186	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> , <b>2009</b> , 1-9	0.1	
185	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> , <b>2008</b> , 383, 822-36	6.5	19
184	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> , <b>2008</b> , 57, 81-7	2	39
183	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> , <b>2008</b> , 283, 17531-41	5.4	66
182	Mapping of the ATP-binding domain of human fructosamine 3-kinase-related protein by affinity labelling with 5G[p-(fluorosulfonyl)benzoyl]adenosine. <i>Biochemical Journal</i> , <b>2008</b> , 416, 281-8	3.8	10
181	Metal-containing proteins, macrocycles, and coordination complexes in therapeutic applications and disease. <i>Metal-Based Drugs</i> , <b>2008</b> , 2008, 286363		1
180	Structures of <i>Mycobacterium tuberculosis</i> folylpolyglutamate synthase complexed with ADP and AMPPCP. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , D64, 745-53		12
179	Purification, crystallization and preliminary crystallographic analysis of <i>Streptococcus pyogenes</i> laminin-binding protein Lbp. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2008</b> , 64, 141-3		4
178	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> , <b>2008</b> , 64, 746-9		3
177	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> , <b>2008</b> , 72, 510-8	4.2	41
176	Histidine phosphorylation in biological systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2008</b> , 1784, 100-5	4	60
175	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> , <b>2008</b> , 43, 1276-96	6.8	18
174	Synthesis and structure-activity relationships of soluble 8-substituted 4-(2-chlorophenyl)-9-hydroxypyrrrolo[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> , <b>2008</b> , 18, 929-33	2.9	24
173	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> , <b>2007</b> , 46, 1851-9	3.2	45
172	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> , <b>2007</b> , 63, 408-14		8
171	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> , <b>2007</b> , 66, 1342-55 <sup>4.1</sup>		74
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41	X-ray structural analysis of bovine lactoferrin at 2.5 Å resolution. <i>Advances in Experimental Medicine and Biology</i> , <b>1994</b> , 357, 235-8	3.6	12
40	Cloning and expression of the C-terminal lobe of human lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , <b>1994</b> , 357, 259-63	3.6	5
39	Crystallographic studies on metal and anion substituted human lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , <b>1994</b> , 357, 265-9	3.6	4
38	Synergism and substitution in the lactoferrins. <i>Advances in Experimental Medicine and Biology</i> , <b>1994</b> , 357, 33-44	3.6	5
37	Crystallization of the C-terminal domain of rabbit serum hemopexin. <i>Journal of Molecular Biology</i> , <b>1993</b> , 229, 251-2	6.5	9
36	Structure of the recombinant N-terminal lobe of human lactoferrin at 2.0 Å resolution. <i>Journal of Molecular Biology</i> , <b>1993</b> , 232, 1084-100	6.5	75
35	Domain closure in lactoferrin. Two hinges produce a see-saw motion between alternative close-packed interfaces. <i>Journal of Molecular Biology</i> , <b>1993</b> , 234, 357-72	6.5	146
34	Anion binding by human lactoferrin: results from crystallographic and physicochemical studies. <i>Biochemistry</i> , <b>1992</b> , 31, 4451-8	3.2	57
33	Metal substitution in transferrins: the crystal structure of human copper-lactoferrin at 2.1-Å resolution. <i>Biochemistry</i> , <b>1992</b> , 31, 4527-33	3.2	72
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31	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> , <b>1992</b> , 228, 973-4	6.5	11
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29	Synthetic, spectroscopic and X-ray crystallographic studies on phenylcyanamidocopper(II) complexes. <i>Journal of the Chemical Society Dalton Transactions</i> , <b>1991</b> , 1243		21
28	Structure, function and flexibility of human lactoferrin. <i>International Journal of Biological Macromolecules</i> , <b>1991</b> , 13, 122-9	7.9	69
27	Preliminary crystallographic studies of copper(II)- and oxalate-substituted human lactoferrin. <i>Journal of Molecular Biology</i> , <b>1991</b> , 219, 155-9	6.5	20
26	Apolactoferrin structure demonstrates ligand-induced conformational change in transferrins. <i>Nature</i> , <b>1990</b> , 344, 784-7	50.4	358
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20	Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , <b>1989</b> , 209, 711-34	6.5	511
19	The interaction of 1-methylimidazole-2(3H)-thione with copper(II) salts. <i>Journal of the Chemical Society Dalton Transactions</i> , <b>1989</b> , 39		16
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16	Spectrochemical studies on the blue copper protein azurin from <i>Alcaligenes denitrificans</i> . <i>Biochemistry</i> , <b>1987</b> , 26, 71-82	3.2	84
15	Blue copper proteins. The copper site in azurin from <i>Alcaligenes denitrificans</i> . <i>Journal of the American Chemical Society</i> , <b>1986</b> , 108, 2784-2785	16.4	130
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