

Edward N Baker

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#	Paper	IF	Citations
293	Hydrogen bonding in globular proteins. <i>Progress in Biophysics and Molecular Biology</i> , 1984 , 44, 97-179	4.7	1422
292	Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8 A resolution. <i>Journal of Molecular Biology</i> , 1989 , 209, 711-34	6.5	511
291	Structure of Rhombohedral 2 Zinc Insulin Crystals. <i>Nature</i> , 1969 , 224, 491-495	50.4	435
290	Structural basis of the Tanford transition of bovine beta-lactoglobulin. <i>Biochemistry</i> , 1998 , 37, 14014-23	3.2	432
289	Structure of azurin from <i>Alcaligenes denitrificans</i> refinement at 1.8 A resolution and comparison of the two crystallographically independent molecules. <i>Journal of Molecular Biology</i> , 1988 , 203, 1071-95	6.5	360
288	Apolactoferrin structure demonstrates ligand-induced conformational change in transferrins. <i>Nature</i> , 1990 , 344, 784-7	50.4	358
287	Pili in Gram-negative and Gram-positive bacteria - structure, assembly and their role in disease. <i>Cellular and Molecular Life Sciences</i> , 2009 , 66, 613-35	10.3	352
286	Three-dimensional structure of diferric bovine lactoferrin at 2.8 A resolution. <i>Journal of Molecular Biology</i> , 1997 , 274, 222-36	6.5	312
285	Thiol proteases. Comparative studies based on the high-resolution structures of papain and actinidin, and on amino acid sequence information for cathepsins B and H, and stem bromelain. <i>Journal of Molecular Biology</i> , 1985 , 182, 317-29	6.5	270
284	Stabilizing isopeptide bonds revealed in gram-positive bacterial pilus structure. <i>Science</i> , 2007 , 318, 1625-8	39.3	262
283	Molecular structure, binding properties and dynamics of lactoferrin. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 2531-9	10.3	252
282	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, 7919-28	3.2	224
281	Lactoferrin is a potent regulator of bone cell activity and increases bone formation in vivo. <i>Endocrinology</i> , 2004 , 145, 4366-74	4.8	215
280	Crystal structure of the protein disulfide bond isomerase, DsbC, from <i>Escherichia coli</i> . <i>Nature Structural Biology</i> , 2000 , 7, 196-9		211
279	A structural framework for understanding the multifunctional character of lactoferrin. <i>Biochimie</i> , 2009 , 91, 3-10	4.6	195
278	Crystal structure of hemopexin reveals a novel high-affinity heme site formed between two beta-propeller domains. <i>Nature Structural Biology</i> , 1999 , 6, 926-31		195
277	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, 3579-83	11.5	192

276	Sheep liver cytosolic aldehyde dehydrogenase: the structure reveals the basis for the retinal specificity of class 1 aldehyde dehydrogenases. <i>Structure</i> , 1998 , 6, 1541-51	5.2	181
275	New perspectives on the structure and function of transferrins. <i>Journal of Inorganic Biochemistry</i> , 1992 , 47, 147-60	4.2	170
274	Transferrins: insights into structure and function from studies on lactoferrin. <i>Trends in Biochemical Sciences</i> , 1987 , 12, 350-353	10.3	170
273	Ligand-induced conformational change in transferrins: crystal structure of the open form of the N-terminal half-molecule of human transferrin. <i>Biochemistry</i> , 1998 , 37, 13978-86	3.2	169
272	Domain closure in lactoferrin. Two hinges produce a see-saw motion between alternative close-packed interfaces. <i>Journal of Molecular Biology</i> , 1993 , 234, 357-72	6.5	146
271	Structure and Reactivity of Transferrins. <i>Advances in Inorganic Chemistry</i> , 1994 , 41, 389-463	2.1	146
270	Lactoferrin and iron: structural and dynamic aspects of binding and release. <i>BioMetals</i> , 2004 , 17, 209-16	3.4	135
269	Lactoferrin and transferrin: functional variations on a common structural framework. <i>Biochemistry and Cell Biology</i> , 2002 , 80, 27-34	3.6	135
268	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	16.4	130
267	Structure of azurin from <i>Alcaligenes denitrificans</i> at 2.5 Å resolution. <i>Journal of Molecular Biology</i> , 1983 , 165, 501-21	6.5	128
266	Superantigens - powerful modifiers of the immune system. <i>Trends in Molecular Medicine</i> , 2000 , 6, 125-32		126
265	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	3.7	122
264	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, 435-48	5.2	120
263	Functional implications of structural differences between variants A and B of bovine beta-lactoglobulin. <i>Protein Science</i> , 1999 , 8, 75-83	6.3	110
262	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, 1027-40	6.5	110
261	12-Bromododecanoic acid binds inside the calyx of bovine beta-lactoglobulin. <i>FEBS Letters</i> , 1998 , 438, 272-8	3.8	109
260	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, 8295-300	11.5	109
259	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, 12641-6	11.5	102

258	Intramolecular isopeptide bonds: protein crosslinks built for stress?. <i>Trends in Biochemical Sciences</i> , 2011 , 36, 229-37	10.3	96
257	Distant structural homology leads to the functional characterization of an archaeal PIN domain as an exonuclease. <i>Journal of Biological Chemistry</i> , 2004 , 279, 16471-8	5.4	96
256	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> , 2009 , 106, 16967-71	11.5	95
255	Crystal structure of the streptococcal superantigen SPE-C: dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules. <i>Nature Structural Biology</i> , 1997 , 4, 635-43		95
254	1.8 Å crystal structure of the C-terminal domain of rabbit serum haemopexin. <i>Structure</i> , 1995 , 3, 551-9	5.2	94
253	The crystal structure of aminoglycoside-3-O-phosphotransferase-IIa, an enzyme responsible for antibiotic resistance. <i>Journal of Molecular Biology</i> , 2003 , 327, 491-506	6.5	90
252	Aminoglycoside antibiotic resistance by enzymatic deactivation. <i>Current Drug Targets Infectious Disorders</i> , 2002 , 2, 143-60		90
251	Crystal structure of the zymogen form of the group A <i>Streptococcus</i> virulence factor SpeB: an integrin-binding cysteine protease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 2235-40	11.5	89
250	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. <i>Journal of Bacteriology</i> , 2006 , 188, 6081-9	11.5	88
249	Metabolic engineering of cofactor F420 production in <i>Mycobacterium smegmatis</i> . <i>PLoS ONE</i> , 2010 , 5, e15803	3.7	88
248	The TB structural genomics consortium: a resource for <i>Mycobacterium tuberculosis</i> biology. <i>Tuberculosis</i> , 2003 , 83, 223-49	2.6	86
247	Intramolecular isopeptide bonds give thermodynamic and proteolytic stability to the major pilin protein of <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2009 , 284, 20729-37	5.4	84
246	Human milk lactoferrin is a serine protease that cleaves <i>Haemophilus</i> surface proteins at arginine-rich sites. <i>Molecular Microbiology</i> , 2003 , 47, 607-17	4.1	84
245	Spectrochemical studies on the blue copper protein azurin from <i>Alcaligenes denitrificans</i> . <i>Biochemistry</i> , 1987 , 26, 71-82	3.2	84
244	Structure of the bacterial type II NADH dehydrogenase: a monotopic membrane protein with an essential role in energy generation. <i>Molecular Microbiology</i> , 2014 , 91, 950-64	4.1	80
243	The structure of glucose-fructose oxidoreductase from <i>Zymomonas mobilis</i> : an osmoprotective periplasmic enzyme containing non-dissociable NADP. <i>Structure</i> , 1996 , 4, 1413-28	5.2	80
242	Structure of human diferric lactoferrin refined at 2.2 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995 , 51, 629-46		78
241	Crystal structure of a substrate complex of myo-inositol oxygenase, a di-iron oxygenase with a key role in inositol metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15032-7	11.5	77

240	Structure and inhibition of the human cell cycle checkpoint kinase, Wee1A kinase: an atypical tyrosine kinase with a key role in CDK1 regulation. <i>Structure</i> , 2005 , 13, 541-50	5.2	76
239	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. <i>Inorganica Chimica Acta</i> , 1990 , 172, 185-190	2.7	76
238	Structure of the recombinant N-terminal lobe of human lactoferrin at 2.0 Å resolution. <i>Journal of Molecular Biology</i> , 1993 , 232, 1084-100	6.5	75
237	Human melanotransferrin (p97) has only one functional iron-binding site. <i>FEBS Letters</i> , 1992 , 298, 215-8	3.8	75
236	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, 1342-55	4.1	74
235	Metal substitution in transferrins: the crystal structure of human copper-lactoferrin at 2.1-Å resolution. <i>Biochemistry</i> , 1992 , 31, 4527-33	3.2	72
234	Crystal Structure of AhpE from Mycobacterium tuberculosis, a 1-Cys peroxiredoxin. <i>Journal of Molecular Biology</i> , 2005 , 346, 1035-46	6.5	70
233	Outer sphere mutations perturb metal reactivity in manganese superoxide dismutase. <i>Biochemistry</i> , 2001 , 40, 15-27	3.2	69
232	Structure, function and flexibility of human lactoferrin. <i>International Journal of Biological Macromolecules</i> , 1991 , 13, 122-9	7.9	69
231	A structural perspective on lactoferrin function. <i>Biochemistry and Cell Biology</i> , 2012 , 90, 320-8	3.6	68
230	The structure of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase from Mycobacterium tuberculosis reveals a common catalytic scaffold and ancestry for type I and type II enzymes. <i>Journal of Molecular Biology</i> , 2005 , 354, 927-39	6.5	68
229	Structure and assembly of Gram-positive bacterial pili: unique covalent polymers. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 200-7	8.1	66
228	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, 17531-41	5.4	66
227	A flexible and economical medium-throughput strategy for protein production and crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1378-85		65
226	Crystal structure of the NADP(H)-dependent ketose reductase from Bemisia argentifolii at 2.3 Å resolution. <i>Journal of Molecular Biology</i> , 2001 , 306, 239-50	6.5	65
225	Conservation and variation in superantigen structure and activity highlighted by the three-dimensional structures of two new superantigens from Streptococcus pyogenes. <i>Journal of Molecular Biology</i> , 2000 , 299, 157-68	6.5	64
224	Structural homologies with ATP- and folate-binding enzymes in the crystal structure of folylpolyglutamate synthetase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 6647-52	11.5	64
223	Three-dimensional structure of lactoferrin in various functional states. <i>Advances in Experimental Medicine and Biology</i> , 1994 , 357, 1-12	3.6	61

222	Histidine phosphorylation in biological systems. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008 , 1784, 100-5	4	60
221	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, 32274-81	5.4	60
220	The TB structural genomics consortium: providing a structural foundation for drug discovery. <i>Current Drug Targets Infectious Disorders</i> , 2002 , 2, 121-41		60
219	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, 1298-308	6.5	57
218	Crystal structure of MshB from <i>Mycobacterium tuberculosis</i> , a deacetylase involved in mycothiol biosynthesis. <i>Journal of Molecular Biology</i> , 2004 , 335, 1131-41	6.5	57
217	Anion binding by human lactoferrin: results from crystallographic and physicochemical studies. <i>Biochemistry</i> , 1992 , 31, 4451-8	3.2	57
216	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, 263-77	6.5	57
215	Crystal structure of the minor pilin FctB reveals determinants of Group A streptococcal pilus anchoring. <i>Journal of Biological Chemistry</i> , 2010 , 285, 20381-9	5.4	56
214	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, 1319-35		55
213	Crystal structure of methylmalonyl-coenzyme A epimerase from <i>P. shermanii</i> : a novel enzymatic function on an ancient metal binding scaffold. <i>Structure</i> , 2001 , 9, 637-46	5.2	53
212	Folate-binding triggers the activation of polyglutamate synthetase. <i>Journal of Molecular Biology</i> , 2001 , 310, 1067-78	6.5	53
211	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	16.4	53
210	Structure of recombinant human lactoferrin expressed in <i>Aspergillus awamori</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 403-7		53
209	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, 352-63	6.5	52
208	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, 30567-76	5.4	50
207	The laminin-binding protein Lbp from <i>Streptococcus pyogenes</i> is a zinc receptor. <i>Journal of Bacteriology</i> , 2009 , 191, 5814-23	3.5	49
206	Chelation of nickel(II) by citrate. The crystal structure of a nickel citrate complex, $K_2[Ni(C_6H_5O_7)(H_2O)_2] \cdot 4H_2O$. <i>Inorganica Chimica Acta</i> , 1983 , 78, 281-285	2.7	49
205	The crystal structures of substrate and nucleotide complexes of <i>Enterococcus faecium</i> aminoglycoside-2-phosphotransferase-IIa [APH(2-PTIIa)] provide insights into substrate selectivity in the APH(2-PT) subfamily. <i>Journal of Bacteriology</i> , 2009 , 191, 4133-43	3.5	47

204	Structure and function of GlmU from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 275-83		46
203	Immunological and biochemical characterization of streptococcal pyrogenic exotoxins I and J (SPE-I and SPE-J) from <i>Streptococcus pyogenes</i> . <i>Journal of Immunology</i> , 2001 , 166, 6711-9	5.3	46
202	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, 1851-9	3.2	45
201	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, 4651-9	3.5	44
200	Crystal structure and metal binding properties of the lipoprotein MtsA, responsible for iron transport in <i>Streptococcus pyogenes</i> . <i>Biochemistry</i> , 2009 , 48, 6184-90	3.2	43
199	Inhibition studies of <i>Mycobacterium tuberculosis</i> salicylate synthase (MbtI). <i>ChemMedChem</i> , 2010 , 5, 1067-79	3.7	41
198	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, 510-8	4.2	41
197	Anion binding by transferrins: importance of second-shell effects revealed by the crystal structure of oxalate-substituted diferric lactoferrin. <i>Biochemistry</i> , 1996 , 35, 9007-13	3.2	41
196	Crystal structure of Spy0129, a <i>Streptococcus pyogenes</i> class B sortase involved in pilus assembly. <i>PLoS ONE</i> , 2011 , 6, e15969	3.7	40
195	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, 341-6	3.2	40
194	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, 81-7	2	39
193	Working towards a group A streptococcal vaccine: report of a collaborative Trans-Tasman workshop. <i>Vaccine</i> , 2014 , 32, 3713-20	4.1	38
192	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, 3496-503	5.4	38
191	The potential impact of structural genomics on tuberculosis drug discovery. <i>Drug Discovery Today</i> , 2006 , 11, 28-34	8.8	38
190	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, 13978-86	5.4	38
189	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, 13857-67	3.2	38
188	The three-dimensional structure of PNGase F, a glycosylasparaginase from <i>Flavobacterium meningosepticum</i> . <i>Structure</i> , 1994 , 2, 1049-59	5.2	38
187	Structural model for covalent adhesion of the <i>Streptococcus pyogenes</i> pilus through a thioester bond. <i>Journal of Biological Chemistry</i> , 2014 , 289, 177-89	5.4	37

186	Expression, purification and crystallization of native and selenomethionine labeled Mycobacterium tuberculosis FGD1 (Rv0407) using a Mycobacterium smegmatis expression system. <i>Protein Expression and Purification</i> , 2007 , 54, 38-44	2	37
185	The crystal structure of TrpD, a metabolic enzyme essential for lung colonization by Mycobacterium tuberculosis, in complex with its substrate phosphoribosylpyrophosphate. <i>Journal of Molecular Biology</i> , 2006 , 355, 784-97	6.5	37
184	Structure of XynB, a highly thermostable beta-1,4-xylanase from Dictyoglomus thermophilum Rt46B.1, at 1.8 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 1367-75		37
183	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, 692-8	3.7	37
182	Removing a hydrogen bond in the dimer interface of Escherichia coli manganese superoxide dismutase alters structure and reactivity. <i>Biochemistry</i> , 2001 , 40, 4622-32	3.2	37
181	A revised biosynthetic pathway for the cofactor F in prokaryotes. <i>Nature Communications</i> , 2019 , 10, 1558	7.4	35
180	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> , 2015 , 112, 4310-5	11.5	34
179	Defining the potassium binding region in an apple terpene synthase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 8661-9	5.4	34
178	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, 1211-6	3.2	34
177	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , 2011 , 91, 155-72	2.6	33
176	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, 1616-23	3.2	33
175	Three-Dimensional Structure of Lactoferrin. <i>Advances in Experimental Medicine and Biology</i> , 1998 , 1-14	3.6	33
174	Structural and functional similarities in the ADP-forming amide bond ligase superfamily: implications for a substrate-induced conformational change in folylpolyglutamate synthetase. <i>Journal of Molecular Biology</i> , 2000 , 302, 427-40	6.5	32
173	Three sites and you are out: ternary synergistic allostery controls aromatic amino acid biosynthesis in Mycobacterium tuberculosis. <i>Journal of Molecular Biology</i> , 2013 , 425, 1582-92	6.5	30
172	Structure of the full-length major pilin from Streptococcus pneumoniae: implications for isopeptide bond formation in gram-positive bacterial pili. <i>PLoS ONE</i> , 2011 , 6, e22095	3.7	30
171	Potent inhibitors of a shikimate pathway enzyme from Mycobacterium tuberculosis: combining mechanism- and modeling-based design. <i>Journal of Biological Chemistry</i> , 2011 , 286, 16197-207	5.4	30
170	Radiation Damage and Racemic Protein Crystallography Reveal the Unique Structure of the GASA/Snakin Protein Superfamily. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 7930-3	16.4	30
169	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, 7084-9	2.3	29

168	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, 511-23	6.5	29
167	Structural and functional properties of staphylococcal superantigen-like protein 4. <i>Infection and Immunity</i> , 2012 , 80, 4004-13	3.7	28
166	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, 6625-33	3.2	28
165	Crystal and molecular structure of pentacarbonyl(trimethylphosphine sulphide)chromium(0). <i>Journal of the Chemical Society Dalton Transactions</i> , 1973 , 2205		28
164	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, 4868-79	3.2	26
163	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, 4057-65	3.5	26
162	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, 11670-5	3.2	26
161	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, 14473-9	3.2	26
160	Structural conservation, variability, and immunogenicity of the T6 backbone pilin of serotype M6 <i>Streptococcus pyogenes</i> . <i>Infection and Immunity</i> , 2014 , 82, 2949-57	3.7	25
159	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, 1367-72	11.5	24
158	Synthesis and structure-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. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2008 , 18, 929-33	2.9	24
157	Interaction of benzo-1,3-thiazoline-2-thione and related ligands with copper(II) salts and the single-crystal X-ray structure of μ -[1,2-bis-(diphenylphosphino)ethane]-bis{(benzo-1,3-thiazole-2-thiolato-S)[1,2-bis(diphenylphosphinoethane)]copper(II)}. <i>Journal of the Chemical Society Dalton Transactions</i> , 1999 , 2167-2171		24
156	Production of recombinant proteins in <i>Mycobacterium smegmatis</i> for structural and functional studies. <i>Protein Science</i> , 2015 , 24, 1-10	6.3	23
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