

# Ivan Rayment

## List of Publications by Citations

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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.

185 papers	12,412 citations	61 h-index	106 g-index
197 ext. papers	13,284 ext. citations	6.2 avg, IF	5.98 L-index

#	Paper	IF	Citations
185	X-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP.BeFx and MgADP.ALF4-. <i>Biochemistry</i> , <b>1995</b> , 34, 8960-72	3.2	631
184	X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9 Å resolution. <i>Biochemistry</i> , <b>1996</b> , 35, 5404-17	3.2	504
183	Mutations in either the essential or regulatory light chains of myosin are associated with a rare myopathy in human heart and skeletal muscle. <i>Nature Genetics</i> , <b>1996</b> , 13, 63-9	36.3	502
182	Structure of southern bean mosaic virus at 2.8 Å resolution. <i>Nature</i> , <b>1980</b> , 286, 33-9	50.4	386
181	Structure and function of enzymes of the Leloir pathway for galactose metabolism. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 43885-8	5.4	342
180	Three-dimensional structure of the Tn5 synaptic complex transposition intermediate. <i>Science</i> , <b>2000</b> , 289, 77-85	33.3	329
179	Structure of carbamoyl phosphate synthetase: a journey of 96 Å from substrate to product. <i>Biochemistry</i> , <b>1997</b> , 36, 6305-16	3.2	302
178	The enolase superfamily: a general strategy for enzyme-catalyzed abstraction of the alpha-protons of carboxylic acids. <i>Biochemistry</i> , <b>1996</b> , 35, 16489-501	3.2	301
177	Structure, mechanism and regulation of pyruvate carboxylase. <i>Biochemical Journal</i> , <b>2008</b> , 413, 369-87	3.8	299
176	Three-dimensional atomic model of F-actin decorated with Dictyostelium myosin S1. <i>Nature</i> , <b>1993</b> , 364, 171-4	50.4	292
175	Molecular structure of an apolipoprotein determined at 2.5-Å resolution. <i>Biochemistry</i> , <b>1991</b> , 30, 603-8	3.2	251
174	The structural basis of blebbistatin inhibition and specificity for myosin II. <i>Nature Structural and Molecular Biology</i> , <b>2005</b> , 12, 378-9	17.6	228
173	Structure of rabbit muscle pyruvate kinase complexed with Mn <sup>2+</sup> , K <sup>+</sup> , and pyruvate. <i>Biochemistry</i> , <b>1994</b> , 33, 6301-9	3.2	205
172	Conservation within the myosin motor domain: implications for structure and function. <i>Structure</i> , <b>1996</b> , 4, 969-87	5.2	201
171	X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP complexes of the Dictyostelium discoideum myosin motor domain. <i>Biochemistry</i> , <b>1997</b> , 36, 11619-28	3.2	188
170	Three-dimensional structure of the biotin carboxylase subunit of acetyl-CoA carboxylase. <i>Biochemistry</i> , <b>1994</b> , 33, 10249-56	3.2	185
169	Crystallization and structure determination to 2.5-Å resolution of the oxidized [2Fe-2S] ferredoxin isolated from Anabaena 7120. <i>Biochemistry</i> , <b>1991</b> , 30, 4126-31	3.2	178

168	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. <i>Archives of Biochemistry and Biophysics</i> , <b>2005</b> , 433, 59-70	4.1	174
167	Three-dimensional structure of Escherichia coli asparagine synthetase B: a short journey from substrate to product. <i>Biochemistry</i> , <b>1999</b> , 38, 16146-57	3.2	163
166	Actin-targeting natural products: structures, properties and mechanisms of action. <i>Cellular and Molecular Life Sciences</i> , <b>2006</b> , 63, 2119-34	10.3	160
165	X-ray structure determination of telokin, the C-terminal domain of myosin light chain kinase, at 2.8 Å resolution. <i>Journal of Molecular Biology</i> , <b>1992</b> , 227, 840-51	6.5	143
164	A carboxylate oxygen of the substrate bridges the magnesium ions at the active site of enolase: structure of the yeast enzyme complexed with the equilibrium mixture of 2-phosphoglycerate and phosphoenolpyruvate at 1.8 Å resolution. <i>Biochemistry</i> , <b>1996</b> , 35, 4349-58	3.2	136
163	Trisoxazole macrolide toxins mimic the binding of actin-capping proteins to actin. <i>Nature Structural and Molecular Biology</i> , <b>2003</b> , 10, 1058-63	17.6	134
162	Structure of the bis(Mg <sup>2+</sup> )-ATP-oxalate complex of the rabbit muscle pyruvate kinase at 2.1 Å resolution: ATP binding over a barrel. <i>Biochemistry</i> , <b>1998</b> , 37, 6247-55	3.2	116
161	Structural consequences of reductive methylation of lysine residues in hen egg white lysozyme: an X-ray analysis at 1.8-Å resolution. <i>Biochemistry</i> , <b>1993</b> , 32, 9851-8	3.2	111
160	[12] Reductive alkylation of lysine residues to alter crystallization properties of proteins. <i>Methods in Enzymology</i> , <b>1997</b> , 276, 171-179	1.7	109
159	Construction and use of new cloning vectors for the rapid isolation of recombinant proteins from Escherichia coli. <i>Plasmid</i> , <b>2008</b> , 59, 231-7	3.3	107
158	Domain architecture of pyruvate carboxylase, a biotin-dependent multifunctional enzyme. <i>Science</i> , <b>2007</b> , 317, 1076-9	33.3	106
157	Chelation of serine 39 to Mg <sup>2+</sup> latches a gate at the active site of enolase: structure of the bis(Mg <sup>2+</sup> ) complex of yeast enolase and the intermediate analog phosphonoacetohydroxamate at 2.1-Å resolution. <i>Biochemistry</i> , <b>1994</b> , 33, 9333-42	3.2	106
156	X-ray structures of the apo and MgATP-bound states of Dictyostelium discoideum myosin motor domain. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 38494-9	5.4	105
155	The structural basis of the myosin ATPase activity. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 15850-3	5.4	104
154	Three-dimensional structure of bacterial luciferase from Vibrio harveyi at 2.4 Å resolution. <i>Biochemistry</i> , <b>1995</b> , 34, 6581-6	3.2	102
153	The 1.5-Å resolution crystal structure of bacterial luciferase in low salt conditions. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 21956-68	5.4	99
152	Three-dimensional structure of the high-potential iron-sulfur protein isolated from the purple phototrophic bacterium Rhodocyclus tenuis determined and refined at 1.5 Å resolution. <i>Journal of Molecular Biology</i> , <b>1992</b> , 228, 672-86	6.5	95
151	Inside polyomavirus at 25-Å resolution. <i>Nature</i> , <b>1992</b> , 355, 652-4	50.4	94

150	The molecular structure of UDP-galactose 4-epimerase from <i>Escherichia coli</i> determined at 2.5 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1992</b> , 12, 372-81	4.2	92
149	X-ray crystal structure of the yeast Kar3 motor domain complexed with Mg.ADP to 2.3 Å resolution. <i>Biochemistry</i> , <b>1998</b> , 37, 1769-76	3.2	91
148	Molecular structure of kanamycin nucleotidyltransferase determined to 3.0-Å resolution. <i>Biochemistry</i> , <b>1993</b> , 32, 11977-84	3.2	89
147	Molecular structure of the oxidized, recombinant, heterocyst [2Fe-2S] ferredoxin from <i>Anabaena</i> 7120 determined to 1.7-Å resolution. <i>Biochemistry</i> , <b>1993</b> , 32, 6788-93	3.2	89
146	Molecular structure of cytochrome c2 isolated from <i>Rhodobacter capsulatus</i> determined at 2.5 Å resolution. <i>Journal of Molecular Biology</i> , <b>1991</b> , 220, 673-85	6.5	89
145	X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated head of <i>Dictyostelium discoideum</i> myosin to 2.7 Å resolution. <i>Biochemistry</i> , <b>1995</b> , 34, 8973-81	3.2	88
144	Three-dimensional structure of galactose-1-phosphate uridylyltransferase from <i>Escherichia coli</i> at 1.8 Å resolution. <i>Biochemistry</i> , <b>1995</b> , 34, 11049-61	3.2	86
143	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 11-23		80
142	Structures of microfilament destabilizing toxins bound to actin provide insight into toxin design and activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 14527-32	11.5	80
141	Biomolecular mimicry in the actin cytoskeleton: mechanisms underlying the cytotoxicity of kabiramide C and related macrolides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 13851-6	11.5	78
140	The three-dimensional structure of a molecular motor. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 129-34	10.3	77
139	Structure/function insights into Tn5 transposition. <i>Current Opinion in Structural Biology</i> , <b>2004</b> , 14, 50-7	8.1	76
138	The structure of nucleotidylated histidine-166 of galactose-1-phosphate uridylyltransferase provides insight into phosphoryl group transfer. <i>Biochemistry</i> , <b>1996</b> , 35, 11560-9	3.2	76
137	Ligand-induced domain movement in pyruvate kinase: structure of the enzyme from rabbit muscle with Mg <sup>2+</sup> , K <sup>+</sup> , and L-phospholactate at 2.7 Å resolution. <i>Archives of Biochemistry and Biophysics</i> , <b>1997</b> , 345, 199-206	4.1	74
136	Vik1 modulates microtubule-Kar3 interactions through a motor domain that lacks an active site. <i>Cell</i> , <b>2007</b> , 128, 1161-72	56.2	72
135	Structural and functional characterization of the TRI101 trichothecene 3-O-acetyltransferase from <i>Fusarium sporotrichioides</i> and <i>Fusarium graminearum</i> : kinetic insights to combating <i>Fusarium</i> head blight. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 1660-1669	5.4	71
134	Structural and mechanistic studies of enolase. <i>Current Opinion in Structural Biology</i> , <b>1996</b> , 6, 736-43	8.1	71
133	The structural determination of an insect sterol carrier protein-2 with a ligand-bound C16 fatty acid at 1.35-Å resolution. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 39085-91	5.4	69

132	Two-metal active site binding of a Tn5 transposase synaptic complex. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 278-81		67
131	Evolution of enzymatic activity in the enolase superfamily: structure of o-succinylbenzoate synthase from <i>Escherichia coli</i> in complex with Mg <sup>2+</sup> and o-succinylbenzoate. <i>Biochemistry</i> , <b>2000</b> , 39, 10662-76	3.2	66
130	The structure of carbamoyl phosphate synthetase determined to 2.1 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>1999</b> , 55, 8-24		66
129	The three-dimensional structure of a Tn5 transposase-related protein determined to 2.9-Å resolution. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 11904-13	5.4	65
128	Molecular structure of the oxidized high-potential iron-sulfur protein isolated from <i>Ectothiorhodospira vacuolata</i> . <i>Biochemistry</i> , <b>1994</b> , 33, 2476-83	3.2	64
127	Three-dimensional structure of ATP:corrinoid adenosyltransferase from <i>Salmonella typhimurium</i> in its free state, complexed with MgATP, or complexed with hydroxycobalamin and MgATP. <i>Biochemistry</i> , <b>2001</b> , 40, 361-74	3.2	63
126	Evolution of enzymatic activity in the enolase superfamily: functional studies of the promiscuous o-succinylbenzoate synthase from <i>Amycolatopsis</i> . <i>Biochemistry</i> , <b>2004</b> , 43, 224-9	3.2	61
125	Homologous (beta/alpha) <sub>8</sub> -barrel enzymes that catalyze unrelated reactions: orotidine 5Rmonophosphate decarboxylase and 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , <b>2002</b> , 41, 3861-9	3.2	61
124	Packing analysis of crystalline myosin subfragment-1. Implications for the size and shape of the myosin head. <i>Journal of Molecular Biology</i> , <b>1985</b> , 181, 487-501	6.5	61
123	Structure of the tropomyosin overlap complex from chicken smooth muscle: insight into the diversity of N-terminal recognition. <i>Biochemistry</i> , <b>2010</b> , 49, 4908-20	3.2	58
122	A structural basis for regulation of actin polymerization by pectenotoxins. <i>Journal of Molecular Biology</i> , <b>2007</b> , 371, 959-70	6.5	58
121	Structural basis of swinholide A binding to actin. <i>Chemistry and Biology</i> , <b>2005</b> , 12, 287-91		58
120	Structural analysis of the H166G site-directed mutant of galactose-1-phosphate uridylyltransferase complexed with either UDP-glucose or UDP-galactose: detailed description of the nucleotide sugar binding site. <i>Biochemistry</i> , <b>1997</b> , 36, 1212-22	3.2	57
119	Structure of bacterial luciferase. <i>Current Opinion in Structural Biology</i> , <b>1995</b> , 5, 798-809	8.1	56
118	The structure of southern bean mosaic virus at 22.5 Å resolution. <i>Virology</i> , <b>1976</b> , 75, 394-400	3.6	54
117	Structural characterization of the active site of the PduO-type ATP:Co(I)rrinoid adenosyltransferase from <i>Lactobacillus reuteri</i> . <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 2596-605	5.4	53
116	Three-dimensional structure of the muscle fatty-acid-binding protein isolated from the desert locust <i>Schistocerca gregaria</i> . <i>Biochemistry</i> , <b>1994</b> , 33, 12378-85	3.2	52
115	Small-scale batch crystallization of proteins revisited: an underutilized way to grow large protein crystals. <i>Structure</i> , <b>2002</b> , 10, 147-51	5.2	51

114	The structure of thiodithiazyl chlorodisulphate, S <sub>3</sub> N <sub>2</sub> S <sub>2</sub> O <sub>6</sub> Cl and its preparation from thiodithiazyl monochloride, S <sub>3</sub> N <sub>2</sub> Cl. <i>Inorganic and Nuclear Chemistry Letters</i> , <b>1974</b> , 10, 647-654		51
113	Tn5: A molecular window on transposition. <i>Biochemical and Biophysical Research Communications</i> , <b>1999</b> , 266, 729-34	3.4	49
112	Octahedral coordination at the high-affinity metal site in enolase: crystallographic analysis of the MgII--enzyme complex from yeast at 1.9 Å resolution. <i>Biochemistry</i> , <b>1995</b> , 34, 4325-30	3.2	49
111	X-ray crystal structure and solution fluorescence characterization of Mg <sub>2</sub> ATP-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoideum myosin motor domain. <i>Journal of Molecular Biology</i> , <b>1997</b> , 274, 394-407	6.5	48
110	Structural characterization of a human-type corrinoid adenosyltransferase confirms that coenzyme B <sub>12</sub> is synthesized through a four-coordinate intermediate. <i>Biochemistry</i> , <b>2008</b> , 47, 5755-66	3.2	48
109	Molecular dynamics analysis of structural factors influencing back door pi release in myosin. <i>Biophysical Journal</i> , <b>2004</b> , 86, 3794-803	2.9	48
108	Two-dimensional magnetization exchange spectroscopy of Anabaena 7120 ferredoxin. Nuclear Overhauser effect and electron self-exchange cross peaks from amino acid residues surrounding the 2Fe-2S <sup>+</sup> cluster. <i>Biochemistry</i> , <b>1991</b> , 30, 7363-8	3.2	48
107	Structural studies on myosin II: communication between distant protein domains. <i>BioEssays</i> , <b>1997</b> , 19, 561-9	4.1	45
106	Absolute stereochemistry of ulapualide A. <i>Organic Letters</i> , <b>2004</b> , 6, 597-9	6.2	45
105	Evolution of enzymatic activity in the enolase superfamily: structural studies of the promiscuous o-succinylbenzoate synthase from Amycolatopsis. <i>Biochemistry</i> , <b>2004</b> , 43, 5716-27	3.2	43
104	Evolution of enzymatic activities in the enolase superfamily: crystallographic and mutagenesis studies of the reaction catalyzed by D-glucarate dehydratase from Escherichia coli. <i>Biochemistry</i> , <b>2000</b> , 39, 4590-602	3.2	43
103	Structural and functional analysis of tetracenomycin F <sub>2</sub> cyclase from Streptomyces glaucescens. A type II polyketide cyclase. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 37956-63	5.4	42
102	Actin-binding cleft closure in myosin II probed by site-directed spin labeling and pulsed EPR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 12867-72	11.5	41
101	Evolution of enzymatic activities in the orotidine 5Rmonophosphate decarboxylase suprafamily: enhancing the promiscuous D-arabino-hex-3-ulose 6-phosphate synthase reaction catalyzed by 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , <b>2005</b> , 44, 1807-15	3.2	41
100	Channel gate! Tension, leak and disclosure. <i>Structure</i> , <b>1999</b> , 7, R99-103	5.2	41
99	X-ray structures of the Dictyostelium discoideum myosin motor domain with six non-nucleotide analogs. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 398-408	5.4	40
98	Kinetic characterization of reductively methylated myosin subfragment 1. <i>Biochemistry</i> , <b>1993</b> , 32, 9859-65	3.2	39
97	Cryo-electron tomography of microtubule-kinesin motor complexes. <i>Journal of Structural Biology</i> , <b>2010</b> , 170, 257-65	3.4	38



96	Crystal structure of polymerization-competent actin. <i>Journal of Molecular Biology</i> , <b>2006</b> , 362, 140-50	6.5	38
95	Understanding the importance of protein structure to nature's routes for divergent evolution in TIM barrel enzymes. <i>Accounts of Chemical Research</i> , <b>2004</b> , 37, 149-58	24.3	37
94	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase from <i>Salmonella typhimurium</i> determined to 2.3 Å resolution. <i>Biochemistry</i> , <b>1998</b> , 37, 7686-95	3.2	36
93	Skip residues modulate the structural properties of the myosin rod and guide thick filament assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E3806-15	11.5	34
92	Evolution of enzymatic activities in the enolase superfamily: crystal structure of (D)-glucarate dehydratase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , <b>1998</b> , 37, 14358-68	3.2	34
91	The three-dimensional structures of nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) from <i>Salmonella typhimurium</i> complexed with 5,6-dimethylbenzimidazole and its reaction products determined to 1.9 Å resolution. <i>Biochemistry</i> , <b>2000</b> , 39, 14105-15	3.2	34
90	Structural investigation of the biosynthesis of alternative lower ligands for cobamides by nicotinate mononucleotide: 5,6-dimethylbenzimidazole phosphoribosyltransferase from <i>Salmonella enterica</i> . <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 37612-20	5.4	33
89	Evolution of enzymatic activities in the enolase superfamily: crystal structures of the L-Ala-D/L-Glu epimerases from <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>Biochemistry</i> , <b>2001</b> , 40, 15716-24	3.2	33
88	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. <i>Molecular Biology of the Cell</i> , <b>2017</b> , 28, 3298-3314	3.5	32
87	Crystal Structure of Os79 (Os04g0206600) from <i>Oryza sativa</i> : A UDP-glucosyltransferase Involved in the Detoxification of Deoxynivalenol. <i>Biochemistry</i> , <b>2016</b> , 55, 6175-6186	3.2	32
86	X-ray structure of putative acyl-ACP desaturase DesA2 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Protein Science</i> , <b>2005</b> , 14, 1508-17	6.3	30
85	Residue Phe112 of the human-type corrinoid adenosyltransferase (PduO) enzyme of <i>Lactobacillus reuteri</i> is critical to the formation of the four-coordinate Co(II) corrinoid substrate and to the activity of the enzyme. <i>Biochemistry</i> , <b>2009</b> , 48, 3138-45	3.2	30
84	Kinesin and myosin: molecular motors with similar engines. <i>Structure</i> , <b>1996</b> , 4, 501-4	5.2	30
83	Bioprospecting for trichothecene 3-O-acetyltransferases in the fungal genus <i>Fusarium</i> yields functional enzymes with different abilities to modify the mycotoxin deoxynivalenol. <i>Applied and Environmental Microbiology</i> , <b>2011</b> , 77, 1162-70	4.8	29
82	The small molecule tool (S)-(-)-blebbistatin: novel insights of relevance to myosin inhibitor design. <i>Organic and Biomolecular Chemistry</i> , <b>2008</b> , 6, 2076-84	3.9	29
81	Structural and functional analyses of the human-type corrinoid adenosyltransferase (PduO) from <i>Lactobacillus reuteri</i> . <i>Biochemistry</i> , <b>2007</b> , 46, 13829-36	3.2	29
80	Galactose-1-phosphate uridylyltransferase from <i>Escherichia coli</i> , a zinc and iron metalloenzyme. <i>Biochemistry</i> , <b>1995</b> , 34, 5610-7	3.2	29
79	Biochemical Characterization of a Recombinant UDP-glucosyltransferase from Rice and Enzymatic Production of Deoxynivalenol-3-O-β-D-glucoside. <i>Toxins</i> , <b>2015</b> , 7, 2685-700	4.9	28

78	The ATP:Co(I)rrinoid adenosyltransferase (CobA) enzyme of <i>Salmonella enterica</i> requires the 2ROH group of ATP for function and yields inorganic triphosphate as its reaction byproduct. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 33127-31	5.4	28
77	Structural and functional characterization of TRI3 trichothecene 15-O-acetyltransferase from <i>Fusarium sporotrichioides</i> . <i>Protein Science</i> , <b>2009</b> , 18, 747-61	6.3	27
76	Structure-guided expansion of the substrate range of methylmalonyl coenzyme A synthetase (MatB) of <i>Rhodopseudomonas palustris</i> . <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 6619-29	4.8	27
75	Evolution of enzymatic activities in the orotidine 5Rmonophosphate decarboxylase suprafamily: structural basis for catalytic promiscuity in wild-type and designed mutants of 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , <b>2005</b> , 44, 1816-23	3.2	27
74	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase (CobU) complexed with GMP: evidence for a substrate-induced transferase active site. <i>Biochemistry</i> , <b>1999</b> , 38, 12995-3005	3.2	27
73	Structural insights into the mechanism of four-coordinate Cob(II)alamin formation in the active site of the <i>Salmonella enterica</i> ATP:Co(I)rrinoid adenosyltransferase enzyme: critical role of residues Phe91 and Trp93. <i>Biochemistry</i> , <b>2012</b> , 51, 9647-57	3.2	25
72	Kar3Vik1, a member of the kinesin-14 superfamily, shows a novel kinesin microtubule binding pattern. <i>Journal of Cell Biology</i> , <b>2012</b> , 197, 957-70	7.3	25
71	Evolution of enzymatic activities in the enolase superfamily: structure of a substrate-liganded complex of the L-Ala-D/L-Glu epimerase from <i>Bacillus subtilis</i> . <i>Biochemistry</i> , <b>2004</b> , 43, 10370-8	3.2	25
70	Evolution of enzymatic activity in the enolase superfamily: structural and mutagenic studies of the mechanism of the reaction catalyzed by o-succinylbenzoate synthase from <i>Escherichia coli</i> . <i>Biochemistry</i> , <b>2003</b> , 42, 14427-33	3.2	25
69	Evolution of enzymatic activities in the enolase superfamily: identification of the general acid catalyst in the active site of D-glucarate dehydratase from <i>Escherichia coli</i> . <i>Biochemistry</i> , <b>2001</b> , 40, 10054-62	3.2	25
68	Structure of the beta 2 homodimer of bacterial luciferase from <i>Vibrio harveyi</i> : X-ray analysis of a kinetic protein folding trap. <i>Protein Science</i> , <b>1997</b> , 6, 13-23	6.3	24
67	Analysis of the adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase (CobU) enzyme of <i>Salmonella typhimurium</i> LT2. Identification of residue His-46 as the site of guanylylation. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 27576-86	5.4	24
66	Structural organization of FtsB, a transmembrane protein of the bacterial divisome. <i>Biochemistry</i> , <b>2013</b> , 52, 2574-85	3.2	23
65	Pentaerythritol propoxylate: a new crystallization agent and cryoprotectant induces crystal growth of 2-methylcitrate dehydratase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 306-9		23
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