

Ivan Rayment

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.

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	Yeast pericentrin/Spc110 contains multiple domains required for tethering the γ -tubulin complex to the centrosome. <i>Molecular Biology of the Cell</i> , 2020 , 31, 1437-1452	3.5	1
184	Structure and function of Spc42 coiled-coils in yeast centrosome assembly and duplication. <i>Molecular Biology of the Cell</i> , 2019 , 30, 1505-1522	3.5	6
183	Structural and functional analysis of an L-serine O-phosphate decarboxylase involved in norcobamide biosynthesis. <i>FEBS Letters</i> , 2019 , 593, 3040-3053	3.8	3
182	Kinesin-2 motors: Kinetics and biophysics. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4510-4518	5.4	16
181	Homodimeric Kinesin-2 KIF3CC Promotes Microtubule Dynamics. <i>Biophysical Journal</i> , 2017 , 113, 1845-1857	5.7	11
180	Reversible swelling of SBMV is associated with reversible disordering. <i>Journal of Structural Biology</i> , 2017 , 200, 314-324	3.4	
179	Design considerations in coiled-coil fusion constructs for the structural determination of a problematic region of the human cardiac myosin rod. <i>Journal of Structural Biology</i> , 2017 , 200, 219-228	3.4	4
178	The molecular architecture of the yeast spindle pole body core determined by Bayesian integrative modeling. <i>Molecular Biology of the Cell</i> , 2017 , 28, 3298-3314	3.5	32
177	Determinants and Expansion of Specificity in a Trichothecene UDP-Glucosyltransferase from <i>Oryza sativa</i> . <i>Biochemistry</i> , 2017 , 56, 6585-6596	3.2	14
176	Functional characterization of a soluble NADPH-cytochrome P450 reductase from <i>Fusarium graminearum</i> . <i>Protein Expression and Purification</i> , 2017 , 138, 69-75	2	4
175	The PrpF protein of <i>Shewanella oneidensis</i> MR-1 catalyzes the isomerization of 2-methyl-cis-aconitate during the catabolism of propionate via the AcnD-dependent 2-methylcitric acid cycle. <i>PLoS ONE</i> , 2017 , 12, e0188130	3.7	8
174	Heterodimerization of Kinesin-2 KIF3AB Modulates Entry into the Processive Run. <i>Journal of Biological Chemistry</i> , 2016 , 291, 23248-23256	5.4	7
173	Family-specific Kinesin Structures Reveal Neck-linker Length Based on Initiation of the Coiled-coil. <i>Journal of Biological Chemistry</i> , 2016 , 291, 20372-86	5.4	12
172	Fast or Slow, Either Head Can Start the Processive Run of Kinesin-2 KIF3AC. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4407-16	5.4	10
171	A composite approach towards a complete model of the myosin rod. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 172-189	4.2	8
170	Crystal Structure of Os79 (Os04g0206600) from <i>Oryza sativa</i> : A UDP-glucosyltransferase Involved in the Detoxification of Deoxynivalenol. <i>Biochemistry</i> , 2016 , 55, 6175-6186	3.2	32
169	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> , 2015 , 112, E3806-15	11.5	34

168	Kinesin-2 KIF3AC and KIF3AB Can Drive Long-Range Transport along Microtubules. <i>Biophysical Journal</i> , 2015 , 109, 1472-82	2.9	21
167	Biochemical Characterization of a Recombinant UDP-glucosyltransferase from Rice and Enzymatic Production of Deoxynivalenol-3-O-β-D-glucoside. <i>Toxins</i> , 2015 , 7, 2685-700	4.9	28
166	Structural insights into the assembly of a monomeric class V myosin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4351-2	11.5	2
165	Dissecting cobamide diversity through structural and functional analyses of the base-activating CobT enzyme of Salmonella enterica. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014 , 1840, 464-754	7.4	14
164	Insights into the specificity of lysine acetyltransferases. <i>Journal of Biological Chemistry</i> , 2014 , 289, 36249-62	5.4	12
163	Kinesin-2 KIF3AB exhibits novel ATPase characteristics. <i>Journal of Biological Chemistry</i> , 2014 , 289, 27836-48	5.4	15
162	Diffraction and Scattering by X-Rays and Neutrons 2013 , 91-112		
161	Molecular Biophysics for the Life Sciences 2013 ,		1
160	Common mechanistic themes for the powerstroke of kinesin-14 motors. <i>Journal of Structural Biology</i> , 2013 , 184, 335-44	3.4	5
159	Functional asymmetry in kinesin and dynein dimers. <i>Biology of the Cell</i> , 2013 , 105, 1-13	3.5	12
158	Structural organization of FtsB, a transmembrane protein of the bacterial divisome. <i>Biochemistry</i> , 2013 , 52, 2574-85	3.2	23
157	Kar3Vik1 uses a minus-end directed powerstroke for movement along microtubules. <i>PLoS ONE</i> , 2013 , 8, e53792	3.7	6
156	Structural, Physical, and Chemical Principles 2013 , 17-30		
155	Structural insights into the mechanism of four-coordinate Cob(II)alamin formation in the active site of the Salmonella enterica ATP:Co(I)rrinoid adenosyltransferase enzyme: critical role of residues Phe91 and Trp93. <i>Biochemistry</i> , 2012 , 51, 9647-57	3.2	25
154	Structural insights into the substrate specificity of the Rhodopseudomonas palustris protein acetyltransferase RpPat: identification of a loop critical for recognition by RpPat. <i>Journal of Biological Chemistry</i> , 2012 , 287, 41392-404	5.4	12
153	Structural insights into the function of the nicotinate mononucleotide:phenol/p-cresol phosphoribosyltransferase (ArsAB) enzyme from Sporomusa ovata. <i>Biochemistry</i> , 2012 , 51, 8571-82	3.2	12
152	Kar3Vik1, a member of the kinesin-14 superfamily, shows a novel kinesin microtubule binding pattern. <i>Journal of Cell Biology</i> , 2012 , 197, 957-70	7.3	25
151	The ATPase pathway that drives the kinesin-14 Kar3Vik1 powerstroke. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36673-82	5.4	16

150	Structure-guided expansion of the substrate range of methylmalonyl coenzyme A synthetase (MatB) of <i>Rhodopseudomonas palustris</i> . <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6619-29	4.8	27
149	Structure and mutational analysis of the archaeal GTP:AdoCbi-P guanylyltransferase (CobY) from <i>Methanocaldococcus jannaschii</i> : insights into GTP binding and dimerization. <i>Biochemistry</i> , 2011 , 50, 5301-13	4.3	5
148	Kinesin Kar3Cik1 ATPase pathway for microtubule cross-linking. <i>Journal of Biological Chemistry</i> , 2011 , 286, 29261-29272	5.4	18
147	Structure-function analysis of the C-terminal domain of CNM67, a core component of the <i>Saccharomyces cerevisiae</i> spindle pole body. <i>Journal of Biological Chemistry</i> , 2011 , 286, 18240-50	5.4	21
146	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> , 2011 , 77, 1162-70	4.8	29
145	Structure of the tropomyosin overlap complex from chicken smooth muscle: insight into the diversity of N-terminal recognition. <i>Biochemistry</i> , 2010 , 49, 4908-20	3.2	58
144	Insights into the importance of hydrogen bonding in the gamma-phosphate binding pocket of myosin: structural and functional studies of serine 236. <i>Biochemistry</i> , 2010 , 49, 4897-907	3.2	13
143	Cryo-electron tomography of microtubule-kinesin motor complexes. <i>Journal of Structural Biology</i> , 2010 , 170, 257-65	3.4	38
142	Structural and functional characterization of TRI3 trichothecene 15-O-acetyltransferase from <i>Fusarium sporotrichioides</i> . <i>Protein Science</i> , 2009 , 18, 747-61	6.3	27
141	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> , 2009 , 48, 3138-45	3.2	30
140	Construction and use of new cloning vectors for the rapid isolation of recombinant proteins from <i>Escherichia coli</i> . <i>Plasmid</i> , 2008 , 59, 231-7	3.3	107
139	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> , 2008 , 105, 12867-72	11.5	41
138	Structure, mechanism and regulation of pyruvate carboxylase. <i>Biochemical Journal</i> , 2008 , 413, 369-87	3.8	299
137	The small molecule tool (S)-(-)-blebbistatin: novel insights of relevance to myosin inhibitor design. <i>Organic and Biomolecular Chemistry</i> , 2008 , 6, 2076-84	3.9	29
136	Structural characterization of a human-type corrinoid adenosyltransferase confirms that coenzyme B12 is synthesized through a four-coordinate intermediate. <i>Biochemistry</i> , 2008 , 47, 5755-66	3.2	48
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> , 2008 , 283, 1660-1669	5.4	71
134	Phosphate coordination and movement of DNA in the Tn5 synaptic complex: role of the (R)YREK motif. <i>Nucleic Acids Research</i> , 2008 , 36, 5855-62	20.1	18
133	Structural and functional analyses of the human-type corrinoid adenosyltransferase (PduO) from <i>Lactobacillus reuteri</i> . <i>Biochemistry</i> , 2007 , 46, 13829-36	3.2	29

132	The three-dimensional crystal structure of the PrpF protein of <i>Shewanella oneidensis</i> complexed with trans-aconitate: insights into its biological function. <i>Protein Science</i> , 2007 , 16, 1274-84	6.3	18
131	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> , 2007 , 282, 2596-605	5.4	53
130	Vik1 modulates microtubule-Kar3 interactions through a motor domain that lacks an active site. <i>Cell</i> , 2007 , 128, 1161-72	56.2	72
129	A structural basis for regulation of actin polymerization by pectenotoxins. <i>Journal of Molecular Biology</i> , 2007 , 371, 959-70	6.5	58
128	Domain architecture of pyruvate carboxylase, a biotin-dependent multifunctional enzyme. <i>Science</i> , 2007 , 317, 1076-9	33.3	106
127	Actin-targeting natural products: structures, properties and mechanisms of action. <i>Cellular and Molecular Life Sciences</i> , 2006 , 63, 2119-34	10.3	160
126	Crystal structure of polymerization-competent actin. <i>Journal of Molecular Biology</i> , 2006 , 362, 140-50	6.5	38
125	X-ray structure of putative acyl-ACP desaturase DesA2 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Protein Science</i> , 2005 , 14, 1508-17	6.3	30
124	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> , 2005 , 44, 1807-15	3.2	41
123	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> , 2005 , 44, 1816-23	3.2	27
122	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. <i>Archives of Biochemistry and Biophysics</i> , 2005 , 433, 59-70	4.1	174
121	Structural basis of swinholide A binding to actin. <i>Chemistry and Biology</i> , 2005 , 12, 287-91		58
120	The structural basis of blebbistatin inhibition and specificity for myosin II. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 378-9	17.6	228
119	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> , 2005 , 102, 14527-32	11.5	80
118	Structural and functional analysis of tetracenomycin F2 cyclase from <i>Streptomyces glaucescens</i> . A type II polyketide cyclase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 37956-63	5.4	42
117	Structure/function insights into Tn5 transposition. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 50-7	8.1	76
116	Crystal structure of gene locus At3g16990 from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 221-2	4.2	4
115	Structure of D-ribulose 5-phosphate 3-epimerase from <i>Synechocystis</i> to 1.6 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1687-90		9

114	Absolute stereochemistry of ulapualide A. <i>Organic Letters</i> , 2004 , 6, 597-9	6.2	45
113	Evolution of enzymatic activity in the enolase superfamily: functional studies of the promiscuous o-succinylbenzoate synthase from <i>Amycolatopsis</i> . <i>Biochemistry</i> , 2004 , 43, 224-9	3.2	61
112	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> , 2004 , 43, 10370-8	3.2	25
111	Evolution of enzymatic activities in the orotidine 5Rmonophosphate decarboxylase suprafamily: mechanistic evidence for a proton relay system in the active site of 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , 2004 , 43, 6427-37	3.2	22
110	Evolution of enzymatic activity in the enolase superfamily: structural studies of the promiscuous o-succinylbenzoate synthase from <i>Amycolatopsis</i> . <i>Biochemistry</i> , 2004 , 43, 5716-27	3.2	43
109	Evolution of enzymatic activities in the orotidine 5Rmonophosphate decarboxylase suprafamily: crystallographic evidence for a proton relay system in the active site of 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , 2004 , 43, 6438-46	3.2	15
108	Understanding the importance of protein structure to nature's routes for divergent evolution in TIM barrel enzymes. <i>Accounts of Chemical Research</i> , 2004 , 37, 149-58	24.3	37
107	Molecular dynamics analysis of structural factors influencing back door pi release in myosin. <i>Biophysical Journal</i> , 2004 , 86, 3794-803	2.9	48
106	The structural determination of an insect sterol carrier protein-2 with a ligand-bound C16 fatty acid at 1.35-A resolution. <i>Journal of Biological Chemistry</i> , 2003 , 278, 39085-91	5.4	69
105	The structural determination of phosphosulfolactate synthase from <i>Methanococcus jannaschii</i> at 1.7-A resolution: an enolase that is not an enolase. <i>Journal of Biological Chemistry</i> , 2003 , 278, 45858-63	5.4	13
104	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> , 2003 , 100, 13851-6	11.5	78
103	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , 2003 , 4, 11-23		80
102	Trisoxazole macrolide toxins mimic the binding of actin-capping proteins to actin. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 1058-63	17.6	134
101	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> , 2003 , 42, 14427-33	3.2	25
100	Structural evidence for a 1,2-enediolate intermediate in the reaction catalyzed by 3-keto-L-gulonate 6-phosphate decarboxylase, a member of the orotidine 5Rmonophosphate decarboxylase suprafamily. <i>Biochemistry</i> , 2003 , 42, 12133-42	3.2	13
99	Structure and function of enzymes of the Leloir pathway for galactose metabolism. <i>Journal of Biological Chemistry</i> , 2003 , 278, 43885-8	5.4	342
98	The three-dimensional structure of the core domain of Naf Y from <i>Azotobacter vinelandii</i> determined at 1.8-A resolution. <i>Journal of Biological Chemistry</i> , 2003 , 278, 32150-6	5.4	20
97	Protein Structure 2003 , 191-218		1

96	Small-scale batch crystallization of proteins revisited: an underutilized way to grow large protein crystals. <i>Structure</i> , 2002 , 10, 147-51	5.2	51
95	Pentaerythritol propoxylate: a new crystallization agent and cryoprotectant induces crystal growth of 2-methylcitrate dehydratase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 306-9		23
94	Two-metal active site binding of a Tn5 transposase synaptic complex. <i>Nature Structural Biology</i> , 2002 , 9, 278-81		67
93	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> , 2002 , 277, 33127-31	5.4	28
92	Capture of a labile substrate by expulsion of water molecules from the active site of nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) from <i>Salmonella enterica</i> . <i>Journal of Biological Chemistry</i> , 2002 , 277, 41120-7	5.4	19
91	Three-dimensional structure of the L-threonine-O-3-phosphate decarboxylase (CobD) enzyme from <i>Salmonella enterica</i> . <i>Biochemistry</i> , 2002 , 41, 4798-808	3.2	23
90	Structural studies of the L-threonine-O-3-phosphate decarboxylase (CobD) enzyme from <i>Salmonella enterica</i> : the apo, substrate, and product-aldimine complexes. <i>Biochemistry</i> , 2002 , 41, 9079-89 ^{3,2}		22
89	Homologous (beta/alpha)8-barrel enzymes that catalyze unrelated reactions: orotidine 5Rmonophosphate decarboxylase and 3-keto-L-gulonate 6-phosphate decarboxylase. <i>Biochemistry</i> , 2002 , 41, 3861-9	3.2	61
88	Evidence for "unseen" transposase--DNA contacts. <i>Journal of Molecular Biology</i> , 2002 , 322, 971-82	6.5	19
87	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> , 2001 , 276, 37612-20	5.4	33
86	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> , 2001 , 40, 15716-24	3.2	33
85	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> , 2001 , 40, 361-74	3.2	63
84	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> , 2001 , 40, 10054-62 ^{3,2}	3.2	25
83	X-ray structures of the apo and MgATP-bound states of <i>Dictyostelium discoideum</i> myosin motor domain. <i>Journal of Biological Chemistry</i> , 2000 , 275, 38494-9	5.4	105
82	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> , 2000 , 275, 27576-86	5.4	24
81	X-ray structures of the <i>Dictyostelium discoideum</i> myosin motor domain with six non-nucleotide analogs. <i>Journal of Biological Chemistry</i> , 2000 , 275, 398-408	5.4	40
80	Three-dimensional structure of the Tn5 synaptic complex transposition intermediate. <i>Science</i> , 2000 , 289, 77-85	33.3	329
79	Evolution of enzymatic activities in the enolase superfamily: crystallographic and mutagenesis studies of the reaction catalyzed by D-glucarate dehydratase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2000 , 39, 4590-602	3.2	43

78	Evolution of enzymatic activity in the enolase superfamily: structure of o-succinylbenzoate synthase from <i>Escherichia coli</i> in complex with Mg ²⁺ and o-succinylbenzoate. <i>Biochemistry</i> , 2000 , 39, 10662-76	3.2	66
77	Three-dimensional structure of <i>Escherichia coli</i> asparagine synthetase B: A short journey from substrate to product. <i>Biochemistry</i> , 2000 , 39, 7330	3.2	5
76	The three-dimensional structure of a Tn5 transposase-related protein determined to 2.9-A resolution. <i>Journal of Biological Chemistry</i> , 1999 , 274, 11904-13	5.4	65
75	The structure of carbamoyl phosphate synthetase determined to 2.1 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 8-24		66
74	Channel gate! Tension, leak and disclosure. <i>Structure</i> , 1999 , 7, R99-103	5.2	41
73	Three-dimensional structure of <i>Escherichia coli</i> asparagine synthetase B: a short journey from substrate to product. <i>Biochemistry</i> , 1999 , 38, 16146-57	3.2	163
72	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> , 1999 , 38, 16125-35	3.2	34
71	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase (CobU) complexed with GMP: evidence for a substrate-induced transferase active site. <i>Biochemistry</i> , 1999 , 38, 12995-3005	3.2	27
70	Tn5: A molecular window on transposition. <i>Biochemical and Biophysical Research Communications</i> , 1999 , 266, 729-34	3.4	49
69	Evolution of enzymatic activities in the enolase superfamily: crystal structure of (D)-glucarate dehydratase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 1998 , 37, 14358-68	3.2	34
68	X-ray crystal structure of the yeast Kar3 motor domain complexed with Mg.ADP to 2.3 Å resolution. <i>Biochemistry</i> , 1998 , 37, 1769-76	3.2	91
67	Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase from <i>Salmonella typhimurium</i> determined to 2.3 Å resolution,. <i>Biochemistry</i> , 1998 , 37, 7686-95	3.2	36
66	Structure of the bis(Mg ²⁺)-ATP-oxalate complex of the rabbit muscle pyruvate kinase at 2.1 Å resolution: ATP binding over a barrel. <i>Biochemistry</i> , 1998 , 37, 6247-55	3.2	116
65	[12] Reductive alkylation of lysine residues to alter crystallization properties of proteins. <i>Methods in Enzymology</i> , 1997 , 276, 171-179	1.7	109
64	Structure of carbamoyl phosphate synthetase: a journey of 96 Å from substrate to product. <i>Biochemistry</i> , 1997 , 36, 6305-16	3.2	302
63	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> , 1997 , 36, 1212-22	3.2	57
62	X-ray structures of the MgADP, MgATPγS, and MgAMPPNP complexes of the <i>Dictyostelium discoideum</i> myosin motor domain. <i>Biochemistry</i> , 1997 , 36, 11619-28	3.2	188
61	Ligand-induced domain movement in pyruvate kinase: structure of the enzyme from rabbit muscle with Mg ²⁺ , K ⁺ , and L-phospholactate at 2.7 Å resolution. <i>Archives of Biochemistry and Biophysics</i> , 1997 , 345, 199-206	4.1	74

60	X-ray crystal structure and solution fluorescence characterization of Mg.2R3R-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoideum myosin motor domain. <i>Journal of Molecular Biology</i> , 1997 , 274, 394-407	6.5	48
59	Structure of the beta 2 homodimer of bacterial luciferase from Vibrio harveyi: X-ray analysis of a kinetic protein folding trap. <i>Protein Science</i> , 1997 , 6, 13-23	6.3	24
58	Structural studies on myosin II: communication between distant protein domains. <i>BioEssays</i> , 1997 , 19, 561-9	4.1	45
57	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> , 1996 , 35, 4349-58	3.2	136
56	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> , 1996 , 35, 5404-17	3.2	504
55	The enolase superfamily: a general strategy for enzyme-catalyzed abstraction of the alpha-protons of carboxylic acids. <i>Biochemistry</i> , 1996 , 35, 16489-501	3.2	301
54	The structure of nucleotidylated histidine-166 of galactose-1-phosphate uridylyltransferase provides insight into phosphoryl group transfer. <i>Biochemistry</i> , 1996 , 35, 11560-9	3.2	76
53	Structural and mechanistic studies of enolase. <i>Current Opinion in Structural Biology</i> , 1996 , 6, 736-43	8.1	71
52	The 1.5-Å resolution crystal structure of bacterial luciferase in low salt conditions. <i>Journal of Biological Chemistry</i> , 1996 , 271, 21956-68	5.4	99
51	Kinesin and myosin: molecular motors with similar engines. <i>Structure</i> , 1996 , 4, 501-4	5.2	30
50	Conservation within the myosin motor domain: implications for structure and function. <i>Structure</i> , 1996 , 4, 969-87	5.2	201
49	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> , 1996 , 13, 63-9	36.3	502
48	The structural basis of the myosin ATPase activity. <i>Journal of Biological Chemistry</i> , 1996 , 271, 15850-3	5.4	104
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