

Ivan Rayment

List of Publications by Year in descending order

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16437

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197
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10446
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#	ARTICLE	IF	CITATIONS
1	Yeast pericentrin/Spc110 contains multiple domains required for tethering the $\hat{\gamma}$ -tubulin complex to the centrosome. <i>Molecular Biology of the Cell</i> , 2020, 31, 1437-1452.	0.9	2
2	Structural and functional analysis of an ϵ -serine α -phosphate decarboxylase involved in norcobamide biosynthesis. <i>FEBS Letters</i> , 2019, 593, 3040-3053.	1.3	4
3	Structure and function of Spc42 coiled-coils in yeast centrosome assembly and duplication. <i>Molecular Biology of the Cell</i> , 2019, 30, 1505-1522.	0.9	7
4	Kinesin-2 motors: Kinetics and biophysics. <i>Journal of Biological Chemistry</i> , 2018, 293, 4510-4518.	1.6	25
5	A Bayesian Integrative Structure Model of the Yeast Centrosome. <i>Biophysical Journal</i> , 2018, 114, 35a.	0.2	0
6	Homodimeric Kinesin-2 KIF3CC Promotes Microtubule Dynamics. <i>Biophysical Journal</i> , 2017, 113, 1845-1857.	0.2	13
7	Reversible swelling of SBMV is associated with reversible disordering. <i>Journal of Structural Biology</i> , 2017, 200, 314-324.	1.3	0
8	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.	1.3	5
9	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.	0.9	44
10	Determinants and Expansion of Specificity in a Trichothecene UDP-Glucosyltransferase from <i>Oryza sativa</i> . <i>Biochemistry</i> , 2017, 56, 6585-6596.	1.2	30
11	Functional characterization of a soluble NADPH-cytochrome P450 reductase from <i>Fusarium graminearum</i> . <i>Protein Expression and Purification</i> , 2017, 138, 69-75.	0.6	5
12	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.	1.1	10
13	A composite approach towards a complete model of the myosin rod. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 172-189.	1.5	15
14	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.	1.2	49
15	Heterodimerization of Kinesin-2 KIF3AB Modulates Entry into the Processive Run. <i>Journal of Biological Chemistry</i> , 2016, 291, 23248-23256.	1.6	9
16	Family-specific Kinesin Structures Reveal Neck-linker Length Based on Initiation of the Coiled-coil. <i>Journal of Biological Chemistry</i> , 2016, 291, 20372-20386.	1.6	17
17	Fast or Slow, Either Head Can Start the Processive Run of Kinesin-2 KIF3AC. <i>Journal of Biological Chemistry</i> , 2016, 291, 4407-4416.	1.6	13
18	Why are Kinesin-2 KIF3AB and KIF3AC so Processive?. <i>Biophysical Journal</i> , 2015, 108, 21a.	0.2	0

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19	Biochemical Characterization of a Recombinant UDP-glucosyltransferase from Rice and Enzymatic Production of Deoxynivalenol-3-O- β -D-glucoside. <i>Toxins</i> , 2015, 7, 2685-2700.	1.5	40
20	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.	3.3	50
21	Kinesin-2 KIF3AC and KIF3AB Can Drive Long-Range Transport along Microtubules. <i>Biophysical Journal</i> , 2015, 109, 1472-1482.	0.2	32
22	Insights into the Specificity of Lysine Acetyltransferases. <i>Journal of Biological Chemistry</i> , 2014, 289, 36249-36262.	1.6	15
23	Kinesin-2 KIF3AB Exhibits Novel ATPase Characteristics. <i>Journal of Biological Chemistry</i> , 2014, 289, 27836-27848.	1.6	15
24	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, 4351-4352.	3.3	2
25	Dissecting cobamide diversity through structural and functional analyses of the base-activating CobT enzyme of <i>Salmonella enterica</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 464-475.	1.1	16
26	Structure of southern bean mosaic virus at 2.8 Å... resolution. , 2014, , 174-180.		0
27	Diffraction and Scattering by X-Rays and Neutrons. , 2013, , 91-112.		0
28	Molecular Biophysics for the Life Sciences. , 2013, , .		2
29	Common mechanistic themes for the powerstroke of kinesin-14 motors. <i>Journal of Structural Biology</i> , 2013, 184, 335-344.	1.3	6
30	Functional asymmetry in kinesin and dynein dimers. <i>Biology of the Cell</i> , 2013, 105, 1-13.	0.7	16
31	Structural Organization of FtsB, a Transmembrane Protein of the Bacterial Divisome. <i>Biochemistry</i> , 2013, 52, 2574-2585.	1.2	31
32	Kar3Vik1 Uses a Minus-End Directed Powerstroke for Movement along Microtubules. <i>PLoS ONE</i> , 2013, 8, e53792.	1.1	7
33	Structural, Physical, and Chemical Principles. , 2013, , 17-30.		0
34	Kar3Vik1, a member of the Kinesin-14 superfamily, shows a novel kinesin microtubule binding pattern. <i>Journal of Cell Biology</i> , 2012, 197, 957-970.	2.3	27
35	The ATPase Pathway That Drives the Kinesin-14 Kar3Vik1 Powerstroke. <i>Journal of Biological Chemistry</i> , 2012, 287, 36673-36682.	1.6	17
36	Structure-Guided Expansion of the Substrate Range of Methylmalonyl Coenzyme A Synthetase (MatB) of <i>Rhodospseudomonas palustris</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 6619-6629.	1.4	33

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37	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> , 2012, 51, 9647-9657.	1.2	29
38	Structural Insights into the Substrate Specificity of the <i>Rhodospseudomonas palustris</i> Protein Acetyltransferase RpPat. <i>Journal of Biological Chemistry</i> , 2012, 287, 41392-41404.	1.6	12
39	Structural Insights into the Function of the Nicotinate Mononucleotide:phenol/p-cresol Phosphoribosyltransferase (ArsAB) Enzyme from <i>Sporomusa ovata</i> . <i>Biochemistry</i> , 2012, 51, 8571-8582.	1.2	14
40	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, 5301-5313.	1.2	6
41	Kinesin Kar3Cik1 ATPase Pathway for Microtubule Cross-linking. <i>Journal of Biological Chemistry</i> , 2011, 286, 29261-29272.	1.6	18
42	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, 18240-18250.	1.6	25
43	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, 1162-1170.	1.4	39
44	Structure of the Tropomyosin Overlap Complex from Chicken Smooth Muscle: Insight into the Diversity of N-Terminal Recognition. <i>Biochemistry</i> , 2010, 49, 4908-4920.	1.2	67
45	Insights into the Importance of Hydrogen Bonding in the $\hat{\gamma}$ -Phosphate Binding Pocket of Myosin: Structural and Functional Studies of Serine 236. <i>Biochemistry</i> , 2010, 49, 4897-4907.	1.2	15
46	Cryo-electron tomography of microtubule-kinesin motor complexes. <i>Journal of Structural Biology</i> , 2010, 170, 257-265.	1.3	38
47	Structural and functional characterization of TRI3 trichothecene 15-O-acetyltransferase from <i>Fusarium sporotrichioides</i> . <i>Protein Science</i> , 2009, 18, 747-761.	3.1	34
48	X-ray structure of putative acyl-ACP desaturase DesA2 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Protein Science</i> , 2009, 14, 1508-1517.	3.1	34
49	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, 3138-3145.	1.2	34
50	Construction and use of new cloning vectors for the rapid isolation of recombinant proteins from <i>Escherichia coli</i> . <i>Plasmid</i> , 2008, 59, 231-237.	0.4	122
51	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, 12867-12872.	3.3	44
52	Structure, mechanism and regulation of pyruvate carboxylase. <i>Biochemical Journal</i> , 2008, 413, 369-387.	1.7	365
53	The small molecule tool (S)-($\hat{\alpha}$)-blebbistatin: novel insights of relevance to myosin inhibitor design. <i>Organic and Biomolecular Chemistry</i> , 2008, 6, 2076.	1.5	37
54	Structural Characterization of a Human-Type Corrinoid Adenosyltransferase Confirms That Coenzyme B ₁₂ Is Synthesized through a Four-Coordinate Intermediate. <i>Biochemistry</i> , 2008, 47, 5755-5766.	1.2	55

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55	Structural and Functional Characterization of the TRI101 Trichothecene 3-O-Acetyltransferase from <i>Fusarium sporotrichioides</i> and <i>Fusarium graminearum</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 1660-1669.	1.6	86
56	Phosphate coordination and movement of DNA in the Tn5 synaptic complex: role of the (R)YREK motif. <i>Nucleic Acids Research</i> , 2008, 36, 5855-5862.	6.5	20
57	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, 2596-2605.	1.6	63
58	Vik1 Modulates Microtubule-Kar3 Interactions through a Motor Domain that Lacks an Active Site. <i>Cell</i> , 2007, 128, 1161-1172.	13.5	80
59	A Structural Basis for Regulation of Actin Polymerization by Pectenotoxins. <i>Journal of Molecular Biology</i> , 2007, 371, 959-970.	2.0	72
60	Domain Architecture of Pyruvate Carboxylase, a Biotin-Dependent Multifunctional Enzyme. <i>Science</i> , 2007, 317, 1076-1079.	6.0	119
61	Structural and Functional Analyses of the Human-Type Corrinoid Adenosyltransferase (PduO) from <i>Lactobacillus reuteri</i> . <i>Biochemistry</i> , 2007, 46, 13829-13836.	1.2	33
62	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, 1274-1284.	3.1	21
63	Crystal Structure of Polymerization-Competent Actin. <i>Journal of Molecular Biology</i> , 2006, 362, 140-150.	2.0	43
64	Actin-targeting natural products: structures, properties and mechanisms of action. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 2119-2134.	2.4	188
65	Structural Basis of Swinholide A Binding to Actin. <i>Chemistry and Biology</i> , 2005, 12, 287-291.	6.2	73
66	The structural basis of blebbistatin inhibition and specificity for myosin II. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 378-379.	3.6	265
67	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, 14527-14532.	3.3	91
68	Evolution of Enzymatic Activities in the Orotidine 5'-Monophosphate 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, 1807-1815.	1.2	42
69	Evolution of Enzymatic Activities in the Orotidine 5'-Monophosphate 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, 1816-1823.	1.2	30
70	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. <i>Archives of Biochemistry and Biophysics</i> , 2005, 433, 59-70.	1.4	194
71	Structural and Functional Analysis of Tetracenomycin F2 Cyclase from <i>Streptomyces glaucescens</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 37956-37963.	1.6	54
72	Structure/function insights into Tn5 transposition. <i>Current Opinion in Structural Biology</i> , 2004, 14, 50-57.	2.6	80

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73	Crystal structure of gene locus At3g16990 from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 221-222.	1.5	4
74	Structure of D-ribulose 5-phosphate 3-epimerase from <i>Synechocystis</i> 1.6 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1687-1690.	2.5	13
75	Understanding the Importance of Protein Structure to Nature's Routes for Divergent Evolution in TIM Barrel Enzymes. <i>ChemInform</i> , 2004, 35, no.	0.1	0
76	Absolute Stereochemistry of Ulupalide A. <i>Organic Letters</i> , 2004, 6, 597-599.	2.4	49
77	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, 224-229.	1.2	73
78	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, 10370-10378.	1.2	35
79	Evolution of Enzymatic Activities in the Orotidine 5'-Monophosphate 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, 6427-6437.	1.2	24
80	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, 5716-5727.	1.2	49
81	Evolution of Enzymatic Activities in the Orotidine 5'-Monophosphate 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, 6438-6446.	1.2	16
82	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, 149-158.	7.6	40
83	Molecular Dynamics Analysis of Structural Factors Influencing Back Door Pi Release in Myosin. <i>Biophysical Journal</i> , 2004, 86, 3794-3803.	0.2	50
84	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 11-23.	1.2	88
85	Trisoxazole macrolide toxins mimic the binding of actin-capping proteins to actin. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1058-1063.	3.6	147
86	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, 14427-14433.	1.2	31
87	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 5'-Monophosphate Decarboxylase Suprafamily. <i>Biochemistry</i> , 2003, 42, 12133-12142.	1.2	16
88	Structure and Function of Enzymes of the Leloir Pathway for Galactose Metabolism. <i>Journal of Biological Chemistry</i> , 2003, 278, 43885-43888.	1.6	417
89	The Three-dimensional Structure of the Core Domain of Naf Y from <i>Azotobacter vinelandii</i> determined at 1.8 Å Resolution. <i>Journal of Biological Chemistry</i> , 2003, 278, 32150-32156.	1.6	22
90	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> , 2003, 278, 39085-39091.	1.6	76

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91	The Structural Determination of Phosphosulfolactate Synthase from <i>Methanococcus jannaschii</i> at 1.7-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2003, 278, 45858-45863.	1.6	16
92	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, 13851-13856.	3.3	89
93	<i>Protein Structure.</i> , 2003, , 191-218.		2
94	The ATP:Co(I)rrinoid Adenosyltransferase (CobA) Enzyme of <i>Salmonella enterica</i> Requires the 2'-OH Group of ATP for Function and Yields Inorganic Triphosphate as Its Reaction Byproduct. <i>Journal of Biological Chemistry</i> , 2002, 277, 33127-33131.	1.6	31
95	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, 41120-41127.	1.6	21
96	Three-Dimensional Structure of the L-Threonine-O-3-phosphate Decarboxylase (CobD) Enzyme from <i>Salmonella enterica</i> . <i>Biochemistry</i> , 2002, 41, 4798-4808.	1.2	28
97	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, 9079-9089.	1.2	25
98	Homologous (β/α)8-Barrel Enzymes That Catalyze Unrelated Reactions: Orotidine 5'-Monophosphate Decarboxylase and 3-Keto-L-Gulonate 6-Phosphate Decarboxylase. <i>Biochemistry</i> , 2002, 41, 3861-3869.	1.2	65
99	Evidence for "Unseen" Transposase-DNA Contacts. <i>Journal of Molecular Biology</i> , 2002, 322, 971-982.	2.0	20
100	Small-Scale Batch Crystallization of Proteins Revisited. <i>Structure</i> , 2002, 10, 147-151.	1.6	55
101	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, 306-309.	2.5	25
102	Two-metal active site binding of a Tn5 transposase synaptic complex. <i>Nature Structural Biology</i> , 2002, 9, 278-281.	9.7	75
103	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, 15716-15724.	1.2	39
104	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, 361-374.	1.2	72
105	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, 10054-10062.	1.2	27
106	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, 37612-37620.	1.6	38
107	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, 38494-38499.	1.6	122
108	Analysis of the Adenosylcobinamide Kinase/Adenosylcobinamide-phosphate Guanylyltransferase (CobU) Enzyme of <i>Salmonella typhimurium</i> LT2. <i>Journal of Biological Chemistry</i> , 2000, 275, 27576-27586.	1.6	26

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109	X-ray Structures of the Dictyostelium discoideum Myosin Motor Domain with Six Non-nucleotide Analogs. <i>Journal of Biological Chemistry</i> , 2000, 275, 398-408.	1.6	44
110	Three-Dimensional Structure of the Tn5 Synaptic Complex Transposition Intermediate. <i>Science</i> , 2000, 289, 77-85.	6.0	410
111	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, 4590-4602.	1.2	44
112	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, 10662-10676.	1.2	71
113	Three-Dimensional Structure of <i>Escherichia coli</i> Asparagine Synthetase B: A Short Journey from Substrate to Product. <i>Biochemistry</i> , 2000, 39, 7330-7330.	1.2	5
114	The Three-dimensional Structure of a Tn5 Transposase-related Protein Determined to 2.9 Å Resolution. <i>Journal of Biological Chemistry</i> , 1999, 274, 11904-11913.	1.6	72
115	The structure of carbamoyl phosphate synthetase determined to 2.1 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 8-24.	2.5	73
116	Channel gate! Tension, leak and disclosure. <i>Structure</i> , 1999, 7, R99-R103.	1.6	45
117	Three-Dimensional Structure of <i>Escherichia coli</i> Asparagine Synthetase B: A Short Journey from Substrate to Product. <i>Biochemistry</i> , 1999, 38, 16146-16157.	1.2	191
118	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, 16125-16135.	1.2	42
119	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, 12995-13005.	1.2	33
120	Tn5: A Molecular Window on Transposition. <i>Biochemical and Biophysical Research Communications</i> , 1999, 266, 729-734.	1.0	56
121	Evolution of Enzymatic Activities in the Enolase Superfamily: Crystal Structure of (D)-Glucarate Dehydratase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 1998, 37, 14358-14368.	1.2	35
122	X-ray Crystal Structure of the Yeast Kar3 Motor Domain Complexed with Mg-ADP to 2.3 Å Resolution. <i>Biochemistry</i> , 1998, 37, 1769-1776.	1.2	97
123	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, 7686-7695.	1.2	46
124	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, 6247-6255.	1.2	128
125	[12] Reductive alkylation of lysine residues to alter crystallization properties of proteins. <i>Methods in Enzymology</i> , 1997, 276, 171-179.	0.4	114
126	Structure of Carbamoyl Phosphate Synthetase: A Journey of 96 Å from Substrate to Product. <i>Biochemistry</i> , 1997, 36, 6305-6316.	1.2	322

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127	Structural Analysis of the H166G Site-Directed Mutant of Galactose-1-phosphate Uridyltransferase Complexed with either UDP-glucose or UDP-galactose: Detailed Description of the Nucleotide Sugar Binding Site. <i>Biochemistry</i> , 1997, 36, 1212-1222.	1.2	63
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