

Ivan Rayment

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	X-ray Structures of the Myosin Motor Domain of Dictyostelium discoideum Complexed with MgADP.cntdot.BeFx and MgADP.cntdot.AIF4-. Biochemistry, 1995, 34, 8960-8972.	2.5	675
2	Mutations in either the essential or regulatory light chains of myosin are associated with a rare myopathy in human heart and skeletal muscle. Nature Genetics, 1996, 13, 63-69.	21.4	559
3	X-ray Structure of the Magnesium(II)Â·ADPÂ·Vanadate Complex of the <i>Dictyostelium discoideum</i> Myosin Motor Domain to 1.9 Å... Resolution[,]. Biochemistry, 1996, 35, 5404-5417.	2.5	537
4	Structure of southern bean mosaic virus at 2.8 Å... resolution. Nature, 1980, 286, 33-39.	27.8	437
5	Structure and Function of Enzymes of the Leloir Pathway for Galactose Metabolism. Journal of Biological Chemistry, 2003, 278, 43885-43888.	3.4	417
6	Three-Dimensional Structure of the Tn5 Synaptic Complex Transposition Intermediate. Science, 2000, 289, 77-85.	12.6	410
7	Structure, mechanism and regulation of pyruvate carboxylase. Biochemical Journal, 2008, 413, 369-387.	3.7	365
8	The Enolase Superfamily:Â A General Strategy for Enzyme-Catalyzed Abstraction of the Î±-Protons of Carboxylic Acidsâ€. Biochemistry, 1996, 35, 16489-16501.	2.5	331
9	Structure of Carbamoyl Phosphate Synthetase:â€% A Journey of 96 Å... from Substrate to Product[,]. Biochemistry, 1997, 36, 6305-6316.	2.5	322
10	Three-dimensional atomic model of F-actin decorated with Dictyostelium myosin S1. Nature, 1993, 364, 171-174.	27.8	311
11	Molecular structure of an apolipoprotein determined at 2.5-ANG. resolution. Biochemistry, 1991, 30, 603-608.	2.5	266
12	The structural basis of blebbistatin inhibition and specificity for myosin II. Nature Structural and Molecular Biology, 2005, 12, 378-379.	8.2	265
13	Conservation within the myosin motor domain: implications for structure and function. Structure, 1996, 4, 969-987.	3.3	224
14	Structure of Rabbit Muscle Pyruvate Kinase Complexed with Mn ²⁺ , K ⁺ , and Pyruvate. Biochemistry, 1994, 33, 6301-6309.	2.5	222
15	Crystallization and structure determination of 2.5-ANG. resolution of the oxidized iron-sulfur [2Fe-2S] ferredoxin isolated from Anabaena 7120. Biochemistry, 1991, 30, 4126-4131.	2.5	197
16	Three-Dimensional Structure of the Biotin Carboxylase Subunit of Acetyl-CoA Carboxylase. Biochemistry, 1994, 33, 10249-10256.	2.5	197
17	X-ray Structures of the MgADP, MgATPÎ³S, and MgAMPPNP Complexes of theDictyostelium discoideumMyosin Motor Domainâ€,â€j. Biochemistry, 1997, 36, 11619-11628.	2.5	194
18	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. Archives of Biochemistry and Biophysics, 2005, 433, 59-70.	3.0	194

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19	Three-Dimensional Structure of Escherichia coli Asparagine Synthetase B: A Short Journey from Substrate to Product. <i>Biochemistry</i> , 1999, 38, 16146-16157.	2.5	191
20	Actin-targeting natural products: structures, properties and mechanisms of action. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 2119-2134.	5.4	188
21	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, 4349-4358.	2.5	150
22	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> , 1992, 227, 840-851.	4.2	149
23	Trisoxazole macrolide toxins mimic the binding of actin-capping proteins to actin. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1058-1063.	8.2	147
24	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> , 1993, 32, 9851-9858.	2.5	132
25	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.	2.5	128
26	The 1.5-Å... Resolution Crystal Structure of Bacterial Luciferase in Low Salt Conditions. <i>Journal of Biological Chemistry</i> , 1996, 271, 21956-21968.	3.4	122
27	X-ray Structures of the Apo and MgATP-bound States of Dictyostelium discoideum Myosin Motor Domain. <i>Journal of Biological Chemistry</i> , 2000, 275, 38494-38499.	3.4	122
28	Construction and use of new cloning vectors for the rapid isolation of recombinant proteins from Escherichia coli. <i>Plasmid</i> , 2008, 59, 231-237.	1.4	122
29	Domain Architecture of Pyruvate Carboxylase, a Biotin-Dependent Multifunctional Enzyme. <i>Science</i> , 2007, 317, 1076-1079.	12.6	119
30	Inside polyomavirus at 25-Å... resolution. <i>Nature</i> , 1992, 355, 652-654.	27.8	118
31	The Structural Basis of the Myosin ATPase Activity. <i>Journal of Biological Chemistry</i> , 1996, 271, 15850-15853.	3.4	117
32	[12] Reductive alkylation of lysine residues to alter crystallization properties of proteins. <i>Methods in Enzymology</i> , 1997, 276, 171-179.	1.0	114
33	Chelation of Serine 39 to Mg ²⁺ Latches a Gate at the Active Site of Enolase: Structure of the Bis(Mg ²⁺) Complex of Yeast Enolase and the Intermediate Analog Phosphonoacetohydroxamate at 2.1-Å Resolution. <i>Biochemistry</i> , 1994, 33, 9333-9342.	2.5	110
34	The molecular structure of UDP-galactose 4-epimerase from Escherichia coli determined at 2.5 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 372-381.	2.6	109
35	Three-dimensional structure of bacterial luciferase from Vibrio harveyi at 2.4-Å resolution. <i>Biochemistry</i> , 1995, 34, 6581-6586.	2.5	109
36	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> , 1992, 228, 672-686.	4.2	104

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37	Molecular structure of kanamycin nucleotidyltransferase determined to 3.0-Å resolution. <i>Biochemistry</i> , 1993, 32, 11977-11984.	2.5	100
38	X-ray Structure of the Magnesium(II)-Pyrophosphate Complex of the Truncated Head of Dictyostelium discoideum Myosin to 2.7-Å Resolution. <i>Biochemistry</i> , 1995, 34, 8973-8981.	2.5	99
39	Molecular structure of the oxidized, recombinant, heterocyst [2Fe-2S] (iron-sulfur) ferredoxin from Anabaena 7120 determined to 1.7-Å resolution. <i>Biochemistry</i> , 1993, 32, 6788-6793.	2.5	97
40	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.	2.5	97
41	Molecular structure of cytochrome c2 isolated from Rhodobacter capsulatus determined at 2.5 Å resolution. <i>Journal of Molecular Biology</i> , 1991, 220, 673-685.	4.2	95
42	The three-dimensional structure of a molecular motor. <i>Trends in Biochemical Sciences</i> , 1994, 19, 129-134.	7.5	94
43	Three-Dimensional Structure of Galactose-1-phosphate Uridyltransferase from Escherichia coli at 1.8-Å Resolution. <i>Biochemistry</i> , 1995, 34, 11049-11061.	2.5	94
44	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.	7.1	91
45	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.	7.1	89
46	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 11-23.	1.2	88
47	Structural and Functional Characterization of the TRI101 Trichothecene 3-O-Acetyltransferase from Fusarium sporotrichioides and Fusarium graminearum. <i>Journal of Biological Chemistry</i> , 2008, 283, 1660-1669.	3.4	86
48	The Structure of Nucleotidylated Histidine-166 of Galactose-1-phosphate Uridyltransferase Provides Insight into Phosphoryl Group Transfer. <i>Biochemistry</i> , 1996, 35, 11560-11569.	2.5	85
49	Structural and mechanistic studies of enolase. <i>Current Opinion in Structural Biology</i> , 1996, 6, 736-743.	5.7	83
50	Ligand-Induced Domain Movement in Pyruvate Kinase: Structure of the Enzyme from Rabbit Muscle with Mg ²⁺ , K ⁺ , and Phospholactate at 2.7 Å Resolution. <i>Archives of Biochemistry and Biophysics</i> , 1997, 345, 199-206.	3.0	82
51	Structure/function insights into Tn5 transposition. <i>Current Opinion in Structural Biology</i> , 2004, 14, 50-57.	5.7	80
52	Vik1 Modulates Microtubule-Kar3 Interactions through a Motor Domain that Lacks an Active Site. <i>Cell</i> , 2007, 128, 1161-1172.	28.9	80
53	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.	3.4	76
54	Two-metal active site binding of a Tn5 transposase synaptic complex. <i>Nature Structural Biology</i> , 2002, 9, 278-281.	9.7	75

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55	Packing analysis of crystalline myosin subfragment-1. <i>Journal of Molecular Biology</i> , 1985, 181, 487-501.	4.2	73
56	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
57	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.	2.5	73
58	Structural Basis of Swinholide A Binding to Actin. <i>Chemistry and Biology</i> , 2005, 12, 287-291.	6.0	73
59	Molecular Structure of the Oxidized High-Potential Iron-Sulfur Protein Isolated from <i>Ectothiorhodospira vacuolata</i> . <i>Biochemistry</i> , 1994, 33, 2476-2483.	2.5	72
60	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.	3.4	72
61	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.	2.5	72
62	A Structural Basis for Regulation of Actin Polymerization by Pectenotoxins. <i>Journal of Molecular Biology</i> , 2007, 371, 959-970.	4.2	72
63	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.	2.5	71
64	Structure of bacterial luciferase. <i>Current Opinion in Structural Biology</i> , 1995, 5, 798-809.	5.7	68
65	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.	2.5	67
66	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.	2.5	65
67	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.	2.5	63
68	Structural Characterization of the Active Site of the PduO-Type ATP:Co(I) Corrinoid Adenosyltransferase from <i>Lactobacillus reuteri</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 2596-2605.	3.4	63
69	Two-dimensional magnetization exchange spectroscopy of <i>Anabaena</i> 7120 ferredoxin. Nuclear Overhauser effect and electron self-exchange cross peaks from amino acid residues surrounding the iron-sulfur (2Fe-2S) cluster. <i>Biochemistry</i> , 1991, 30, 7363-7368.	2.5	60
70	The structure of thiodithiazyl chlorodisulphate, S ₃ N ₂ S ₂ O ₆ Cl and its preparation from thiodithiazyl monochloride, S ₃ N ₂ Cl. <i>Inorganic and Nuclear Chemistry Letters</i> , 1974, 10, 647-654.	0.7	57
71	The structure of Southern bean mosaic virus at 22.5 Å... resolution. <i>Virology</i> , 1976, 75, 394-400.	2.4	57
72	Tn5: A Molecular Window on Transposition. <i>Biochemical and Biophysical Research Communications</i> , 1999, 266, 729-734.	2.1	56

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73	Small-Scale Batch Crystallization of Proteins Revisited. <i>Structure</i> , 2002, 10, 147-151.	3.3	55
74	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.	2.5	55
75	Octahedral coordination at the high-affinity metal site in enolase: Crystallographic analysis of the MglI-enzyme complex from yeast at 1.9 Å resolution. <i>Biochemistry</i> , 1995, 34, 4325-4330.	2.5	54
76	Structural and Functional Analysis of Tetracenomylin F2 Cyclase from <i>Streptomyces glaucescens</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 37956-37963.	3.4	54
77	Three-Dimensional Structure of the Muscle Fatty-Acid-Binding Protein Isolated from the Desert Locust <i>Schistocerca gregaria</i> . <i>Biochemistry</i> , 1994, 33, 12378-12385.	2.5	53
78	Structural studies on myosin II: Communication between distant protein domains. <i>BioEssays</i> , 1997, 19, 561-569.	2.5	51
79	X-ray crystal structure and solution fluorescence characterization of Mg ²⁺ -O-(N-methylanthraniloyl) nucleotides bound to the <i>Dictyostelium discoideum</i> myosin motor domain. <i>Journal of Molecular Biology</i> , 1997, 274, 394-407.	4.2	50
80	Molecular Dynamics Analysis of Structural Factors Influencing Back Door Pi Release in Myosin. <i>Biophysical Journal</i> , 2004, 86, 3794-3803.	0.5	50
81	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.	7.1	50
82	Absolute Stereochemistry of Ulapualide A. <i>Organic Letters</i> , 2004, 6, 597-599.	4.6	49
83	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.	2.5	49
84	Crystal Structure of Os04g0206600 from <i>Oryza sativa</i> : A UDP-glucosyltransferase Involved in the Detoxification of Deoxynivalenol. <i>Biochemistry</i> , 2016, 55, 6175-6186.	2.5	49
85	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.	2.5	46
86	Channel gate! Tension, leak and disclosure. <i>Structure</i> , 1999, 7, R99-R103.	3.3	45
87	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.	3.4	44
88	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.	2.5	44
89	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.	7.1	44
90	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.	2.1	44

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91	Crystal Structure of Polymerization-Competent Actin. <i>Journal of Molecular Biology</i> , 2006, 362, 140-150.	4.2	43
92	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.	2.5	42
93	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.	2.5	42
94	Kinetic characterization of reductively methylated myosin subfragment 1. <i>Biochemistry</i> , 1993, 32, 9859-9865.	2.5	41
95	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.	15.6	40
96	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.	3.4	40
97	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.	2.5	39
98	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.	3.1	39
99	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.	3.4	38
100	Cryo-electron tomography of microtubule-kinesin motor complexes. <i>Journal of Structural Biology</i> , 2010, 170, 257-265.	2.8	38
101	The small molecule tool (S)-(-)-blebbistatin: novel insights of relevance to myosin inhibitor design. <i>Organic and Biomolecular Chemistry</i> , 2008, 6, 2076.	2.8	37
102	Kinesin and myosin: molecular motors with similar engines. <i>Structure</i> , 1996, 4, 501-504.	3.3	36
103	The structure of southern bean mosaic virus at 5 Å... resolution. <i>Virology</i> , 1978, 85, 187-197.	2.4	35
104	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.	2.5	35
105	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.	2.5	35
106	Structural and functional characterization of TRI3 trichothecene 15-O-acetyltransferase from <i>Fusarium sporotrichioides</i> . <i>Protein Science</i> , 2009, 18, 747-761.	7.6	34
107	X-ray structure of putative acyl-ACP desaturase DesA2 from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Protein Science</i> , 2009, 14, 1508-1517.	7.6	34
108	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.	2.5	34

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109	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.	2.5	33
110	Structural and Functional Analyses of the Human-Type Corrinoid Adenosyltransferase (PduO) from <i>Lactobacillus reuteri</i> . <i>Biochemistry</i> , 2007, 46, 13829-13836.	2.5	33
111	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.	3.1	33
112	Kinesin-2 KIF3AC and KIF3AB Can Drive Long-Range Transport along Microtubules. <i>Biophysical Journal</i> , 2015, 109, 1472-1482.	0.5	32
113	Galactose-1-phosphate Uridyltransferase from <i>Escherichia coli</i> , a Zinc and Iron Metalloenzyme. <i>Biochemistry</i> , 1995, 34, 5610-5617.	2.5	31
114	The ATP:Corrinoid 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.	3.4	31
115	Evolution of Enzymatic Activity in the Enolase Superfamily: Structural and Mutagenic Studies of the Mechanism of the Reaction Catalyzed by Succinylbenzoate Synthase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2003, 42, 14427-14433.	2.5	31
116	Structural Organization of FtsB, a Transmembrane Protein of the Bacterial Divisome. <i>Biochemistry</i> , 2013, 52, 2574-2585.	2.5	31
117	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.	2.5	30
118	Determinants and Expansion of Specificity in a Trichothecene UDP-Glucosyltransferase from <i>Oryza sativa</i> . <i>Biochemistry</i> , 2017, 56, 6585-6596.	2.5	30
119	Structure of the γ -irradiation-induced homodimer of bacterial luciferase from <i>Vibrio harveyi</i> : X-ray analysis of a kinetic protein folding trap. <i>Protein Science</i> , 1997, 6, 13-23.	7.6	29
120	Structural Insights into the Mechanism of Four-Coordinate Cob(II)alamin Formation in the Active Site of the <i>Salmonella enterica</i> ATP:Corrinoid Adenosyltransferase Enzyme: Critical Role of Residues Phe91 and Trp93. <i>Biochemistry</i> , 2012, 51, 9647-9657.	2.5	29
121	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.	2.5	28
122	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.	2.5	27
123	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.	5.2	27
124	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.	3.4	26
125	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.	2.5	25
126	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

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127	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.	3.4	25
128	Kinesin-2 motors: Kinetics and biophysics. <i>Journal of Biological Chemistry</i> , 2018, 293, 4510-4518.	3.4	25
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