

John J Tanner

List of Publications by Year in descending order

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161
papers

4,599
citations

117571

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143943

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164
all docs

164
docs citations

164
times ranked

4694
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence in the prediction of proteinâ€“ligand interactions: recent advances and future directions. Briefings in Bioinformatics, 2022, 23, .	3.2	78
2	Structure-affinity relationships of reversible proline analog inhibitors targeting proline dehydrogenase. Organic and Biomolecular Chemistry, 2022, 20, 895-905.	1.5	6
3	Impact of missense mutations in the ALDH7A1 gene on enzyme structure and catalytic function. Biochimie, 2021, 183, 49-54.	1.3	1
4	Structural analysis of prolines and hydroxyprolines binding to the l-glutamate-âˆ³-semialdehyde dehydrogenase active site of bifunctional proline utilization A. Archives of Biochemistry and Biophysics, 2021, 698, 108727.	1.4	6
5	Biochemical Characterization of the Two-Component Flavin-Dependent Monooxygenase Involved in Valanimycin Biosynthesis. Biochemistry, 2021, 60, 31-40.	1.2	6
6	Structure, biochemistry, and gene expression patterns of the proline biosynthetic enzyme pyrroline-5-carboxylate reductase (PYCR), an emerging cancer therapy target. Amino Acids, 2021, 53, 1817-1834.	1.2	20
7	Disease variants of human Î”1-pyrroline-5-carboxylate reductase 2 (PYCR2). Archives of Biochemistry and Biophysics, 2021, 703, 108852.	1.4	9
8	N-Propargylglycine: a unique suicide inhibitor of proline dehydrogenase with anticancer activity and brain-enhancing mitohormesis properties. Amino Acids, 2021, 53, 1927-1939.	1.2	5
9	Structural basis for the stereospecific inhibition of the dual proline/hydroxyproline catabolic enzyme ALDH4A1 by transâ€“4â€“hydroxyâ€“Lâ€“proline. Protein Science, 2021, 30, 1714-1722.	3.1	4
10	Structural and Biochemical Characterization of the Flavin-Dependent Siderophore-Interacting Protein from <i>Acinetobacter baumannii</i> . ACS Omega, 2021, 6, 18537-18547.	1.6	5
11	Optimisation of Neuraminidase Expression for Use in Drug Discovery by Using HEK293-6E Cells. Viruses, 2021, 13, 1893.	1.5	1
12	Photoinduced Covalent Irreversible Inactivation of Proline Dehydrogenase by S-Heterocycles. ACS Chemical Biology, 2021, 16, 2268-2279.	1.6	2
13	Probing the function of a ligand-modulated dynamic tunnel in bifunctional proline utilization A (PutA). Archives of Biochemistry and Biophysics, 2021, 712, 109025.	1.4	3
14	Evidence for Proline Catabolic Enzymes in the Metabolism of Thiazolidine Carboxylates. Biochemistry, 2021, 60, 3610-3620.	1.2	0
15	Kinetics of human pyrroline-5-carboxylate reductase in l-thiopropine metabolism. Amino Acids, 2021, 53, 1863-1874.	1.2	0
16	Structural and biochemical consequences of pyridoxineâ€“dependent epilepsy mutations that target the aldehyde binding site of aldehyde dehydrogenase ALDH 7A1. FEBS Journal, 2020, 287, 173-189.	2.2	7
17	Structural analysis of pathogenic mutations targeting Glu427 of ALDH7A1, the hot spot residue of pyridoxineâ€“dependent epilepsy. Journal of Inherited Metabolic Disease, 2020, 43, 635-644.	1.7	6
18	DeepCryoPicker: fully automated deep neural network for single protein particle picking in cryo-EM. BMC Bioinformatics, 2020, 21, 509.	1.2	30

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19	Trapping conformational states of a flavin-dependent N-monooxygenase in crystallo reveals protein and flavin dynamics. <i>Journal of Biological Chemistry</i> , 2020, 295, 13239-13249.	1.6	13
20	Inhibition, crystal structures, and in-solution oligomeric structure of aldehyde dehydrogenase 9A1. <i>Archives of Biochemistry and Biophysics</i> , 2020, 691, 108477.	1.4	15
21	In crystallo screening for proline analog inhibitors of the proline cycle enzyme PYCR1. <i>Journal of Biological Chemistry</i> , 2020, 295, 18316-18327.	1.6	22
22	Cautionary Tale of Using Tris(alkyl)phosphine Reducing Agents with NAD ⁺ -Dependent Enzymes. <i>Biochemistry</i> , 2020, 59, 3285-3289.	1.2	7
23	Structural Determinants of Flavin Dynamics in a Class B Monooxygenase. <i>Biochemistry</i> , 2020, 59, 4609-4616.	1.2	8
24	Structure and function of a flavin-dependent S-monooxygenase from garlic (<i>Allium sativum</i>). <i>Journal of Biological Chemistry</i> , 2020, 295, 11042-11055.	1.6	14
25	Covalent Modification of the Flavin in Proline Dehydrogenase by Thiazolidine-2-Carboxylate. <i>ACS Chemical Biology</i> , 2020, 15, 936-944.	1.6	10
26	SAXSDom: Modeling multidomain protein structures using small-angle X-ray scattering data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 775-787.	1.5	9
27	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	1.8	134
28	Impaired folate binding of serine hydroxymethyltransferase 8 from soybean underlies resistance to the soybean cyst nematode. <i>Journal of Biological Chemistry</i> , 2020, 295, 3708-3718.	1.6	13
29	A Super-Clustering Approach for Fully Automated Single Particle Picking in Cryo-EM. <i>Genes</i> , 2019, 10, 666.	1.0	12
30	AutoCryoPicker: an unsupervised learning approach for fully automated single particle picking in Cryo-EM images. <i>BMC Bioinformatics</i> , 2019, 20, 326.	1.2	33
31	Structural and Biochemical Characterization of Aldehyde Dehydrogenase 12, the Last Enzyme of Proline Catabolism in Plants. <i>Journal of Molecular Biology</i> , 2019, 431, 576-592.	2.0	20
32	Crystal Structure of Aldehyde Dehydrogenase 16 Reveals Trans-Hierarchical Structural Similarity and a New Dimer. <i>Journal of Molecular Biology</i> , 2019, 431, 524-541.	2.0	15
33	Structural Biology of Proline Catabolic Enzymes. <i>Antioxidants and Redox Signaling</i> , 2019, 30, 650-673.	2.5	37
34	The Proline Cycle As a Potential Cancer Therapy Target. <i>Biochemistry</i> , 2018, 57, 3433-3444.	1.2	107
35	Determination of protein oligomeric structure from small-angle X-ray scattering. <i>Protein Science</i> , 2018, 27, 814-824.	3.1	40
36	Structural Evidence for Rifampicin Monooxygenase Inactivating Rifampicin by Cleaving Its Ansa-Bridge. <i>Biochemistry</i> , 2018, 57, 2065-2068.	1.2	13

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37	Flavin ^{N5} Covalent Intermediate in a Nonredox Dehalogenation Reaction Catalyzed by an Atypical Flavoenzyme. <i>ChemBioChem</i> , 2018, 19, 53-57.	1.3	7
38	NAD ⁺ promotes assembly of the active tetramer of aldehyde dehydrogenase 7A1. <i>FEBS Letters</i> , 2018, 592, 3229-3238.	1.3	11
39	Structural Basis for the Substrate Inhibition of Proline Utilization A by Proline. <i>Molecules</i> , 2018, 23, 32.	1.7	9
40	Steric Control of the Rate-Limiting Step of UDP-Galactopyranose Mutase. <i>Biochemistry</i> , 2018, 57, 3713-3721.	1.2	3
41	Redox Modulation of Oligomeric State in Proline Utilization A. <i>Biophysical Journal</i> , 2018, 114, 2833-2843.	0.2	2
42	Impact of disease-linked mutations targeting the oligomerization interfaces of aldehyde dehydrogenase 7A1. <i>Chemico-Biological Interactions</i> , 2017, 276, 31-39.	1.7	13
43	Structure and characterization of a class 3B proline utilization A: Ligand-induced dimerization and importance of the C-terminal domain for catalysis. <i>Journal of Biological Chemistry</i> , 2017, 292, 9652-9665.	1.6	21
44	Identification of a Conserved Histidine As Being Critical for the Catalytic Mechanism and Functional Switching of the Multifunctional Proline Utilization A Protein. <i>Biochemistry</i> , 2017, 56, 3078-3088.	1.2	5
45	Covalent Allosteric Inactivation of Protein Tyrosine Phosphatase 1B (PTP1B) by an Inhibitor ⁺ Electrophile Conjugate. <i>Biochemistry</i> , 2017, 56, 2051-2060.	1.2	22
46	Resolving the cofactor-binding site in the proline biosynthetic enzyme human pyrroline-5-carboxylate reductase 1. <i>Journal of Biological Chemistry</i> , 2017, 292, 7233-7243.	1.6	42
47	Importance of the C-Terminus of Aldehyde Dehydrogenase 7A1 for Oligomerization and Catalytic Activity. <i>Biochemistry</i> , 2017, 56, 5910-5919.	1.2	7
48	Structure, function, and mechanism of proline utilization A (PutA). <i>Archives of Biochemistry and Biophysics</i> , 2017, 632, 142-157.	1.4	56
49	Biophysical investigation of type A PutAs reveals a conserved core oligomeric structure. <i>FEBS Journal</i> , 2017, 284, 3029-3049.	2.2	14
50	Discovery of the Membrane Binding Domain in Trifunctional Proline Utilization A. <i>Biochemistry</i> , 2017, 56, 6292-6303.	1.2	7
51	Multiple functionalities of reduced flavin in the non-redox reaction catalyzed by UDP-galactopyranose mutase. <i>Archives of Biochemistry and Biophysics</i> , 2017, 632, 59-65.	1.4	11
52	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. <i>Journal of Applied Crystallography</i> , 2016, 49, 2235-2243.	1.9	4
53	The Structure of the Antibiotic Deactivating, N-hydroxylating Rifampicin Monooxygenase. <i>Journal of Biological Chemistry</i> , 2016, 291, 21553-21562.	1.6	36
54	EF5 Is the High-Affinity Mg ²⁺ Site in ALG-2. <i>Biochemistry</i> , 2016, 55, 5128-5141.	1.2	2

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55	Structures of Proline Utilization A (PutA) Reveal the Fold and Functions of the Aldehyde Dehydrogenase Superfamily Domain of Unknown Function. <i>Journal of Biological Chemistry</i> , 2016, 291, 24065-24075.	1.6	27
56	Engineering a trifunctional proline utilization A chimaera by fusing a DNA-binding domain to a bifunctional PutA. <i>Bioscience Reports</i> , 2016, 36, .	1.1	6
57	<i>In Crystallo</i> Capture of a Covalent Intermediate in the UDP-Galactopyranose Mutase Reaction. <i>Biochemistry</i> , 2016, 55, 833-836.	1.2	21
58	Empirical power laws for the radii of gyration of protein oligomers. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1119-1129.	1.1	24
59	SAXS fingerprints of aldehyde dehydrogenase oligomers. <i>Data in Brief</i> , 2015, 5, 745-751.	0.5	7
60	X-ray crystal structures of native HIV-1 capsid protein reveal conformational variability. <i>Science</i> , 2015, 349, 99-103.	6.0	212
61	Diethylaminobenzaldehyde Is a Covalent, Irreversible Inactivator of ALDH7A1. <i>ACS Chemical Biology</i> , 2015, 10, 693-697.	1.6	36
62	First Evidence for Substrate Channeling between Proline Catabolic Enzymes. <i>Journal of Biological Chemistry</i> , 2015, 290, 2225-2234.	1.6	37
63	Crystal structure and tartrate inhibition of <i>Legionella pneumophila</i> histidine acid phosphatase. <i>Archives of Biochemistry and Biophysics</i> , 2015, 585, 32-38.	1.4	9
64	Inactivation of protein tyrosine phosphatases by dietary isothiocyanates. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 4549-4552.	1.0	15
65	Contribution to catalysis of ornithine binding residues in ornithine N5-monooxygenase. <i>Archives of Biochemistry and Biophysics</i> , 2015, 585, 25-31.	1.4	13
66	Structural Basis of Substrate Recognition by Aldehyde Dehydrogenase 7A1. <i>Biochemistry</i> , 2015, 54, 5513-5522.	1.2	36
67	Evidence for Hysteretic Substrate Channeling in the Proline Dehydrogenase and γ -Pyrroline-5-carboxylate Dehydrogenase Coupled Reaction of Proline Utilization A (PutA). <i>Journal of Biological Chemistry</i> , 2014, 289, 3639-3651.	1.6	28
68	Structures of the PutA peripheral membrane flavoenzyme reveal a dynamic substrate-channeling tunnel and the quinone-binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3389-3394.	3.3	63
69	Contributions of Unique Active Site Residues of Eukaryotic UDP-Galactopyranose Mutases to Substrate Recognition and Active Site Dynamics. <i>Biochemistry</i> , 2014, 53, 7794-7804.	1.2	8
70	Kinetic and Structural Characterization of Tunnel-Perturbing Mutants in <i>Bradyrhizobium japonicum</i> Proline Utilization A. <i>Biochemistry</i> , 2014, 53, 5150-5161.	1.2	19
71	Structure, mechanism, and dynamics of UDP-galactopyranose mutase. <i>Archives of Biochemistry and Biophysics</i> , 2014, 544, 128-141.	1.4	49
72	Evidence That the C-Terminal Domain of a Type B PutA Protein Contributes to Aldehyde Dehydrogenase Activity and Substrate Channeling. <i>Biochemistry</i> , 2014, 53, 5661-5673.	1.2	18

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73	Structural Studies of Yeast γ -Pyrroline-5-carboxylate Dehydrogenase (ALDH4A1): Active Site Flexibility and Oligomeric State. <i>Biochemistry</i> , 2014, 53, 1350-1359.	1.2	30
74	Substrate-dependent dynamics of UDP-galactopyranose mutase: Implications for drug design. <i>Protein Science</i> , 2013, 22, 1490-1501.	3.1	11
75	Solution structures of polycalcin Phl p 7 in three ligation states: Apo, hemic, and fully Ca^{2+} -bound. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 300-315.	1.5	12
76	Structural Determinants of Oligomerization of γ -Pyrroline-5-Carboxylate Dehydrogenase: Identification of a Hexamerization Hot Spot. <i>Journal of Molecular Biology</i> , 2013, 425, 3106-3120.	2.0	24
77	Structural basis of substrate selectivity of γ -pyrroline-5-carboxylate dehydrogenase (ALDH4A1): Semialdehyde chain length. <i>Archives of Biochemistry and Biophysics</i> , 2013, 538, 34-40.	1.4	24
78	Involvement of the β 3- β 3 Loop of the Proline Dehydrogenase Domain in Allosteric Regulation of Membrane Association of Proline Utilization A. <i>Biochemistry</i> , 2013, 52, 4482-4491.	1.2	17
79	Targeting UDP-Galactopyranose Mutases from Eukaryotic Human Pathogens. <i>Current Pharmaceutical Design</i> , 2013, 19, 2561-2573.	0.9	19
80	2 PutA and proline metabolism. , 2012, , 31-56.		1
81	Crystal Structures and Small-angle X-ray Scattering Analysis of UDP-galactopyranose Mutase from the Pathogenic Fungus <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 9041-9051.	1.6	33
82	Identification of the NAD(P)H Binding Site of Eukaryotic UDP-Galactopyranose Mutase. <i>Journal of the American Chemical Society</i> , 2012, 134, 18132-18138.	6.6	25
83	Crystal Structures and Kinetics of Monofunctional Proline Dehydrogenase Provide Insight into Substrate Recognition and Conformational Changes Associated with Flavin Reduction and Product Release. <i>Biochemistry</i> , 2012, 51, 10099-10108.	1.2	31
84	Crystal Structures of <i>Trypanosoma cruzi</i> UDP-Galactopyranose Mutase Implicate Flexibility of the Histidine Loop in Enzyme Activation. <i>Biochemistry</i> , 2012, 51, 4968-4979.	1.2	23
85	The Three-Dimensional Structural Basis of Type II Hyperprolinemia. <i>Journal of Molecular Biology</i> , 2012, 420, 176-189.	2.0	57
86	Conservation of Functionally Important Global Motions in an Enzyme Superfamily across Varying Quaternary Structures. <i>Journal of Molecular Biology</i> , 2012, 423, 831-846.	2.0	13
87	Unique structural features and sequence motifs of proline utilization A (PutA). <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 556.	3.0	27
88	Proline: Mother Nature's cryoprotectant applied to protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1010-1018.	2.5	28
89	The Biological Buffer Bicarbonate/ CO_2 Potentiates H_2O_2 -Mediated Inactivation of Protein Tyrosine Phosphatases. <i>Journal of the American Chemical Society</i> , 2011, 133, 15803-15805.	6.6	57
90	Crystal structure and immunogenicity of the class C acid phosphatase from <i>Pasteurella multocida</i> . <i>Archives of Biochemistry and Biophysics</i> , 2011, 509, 76-81.	1.4	4

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91	Steady-state kinetic mechanism of the proline:ubiquinone oxidoreductase activity of proline utilization A (PutA) from <i>Escherichia coli</i> . <i>Archives of Biochemistry and Biophysics</i> , 2011, 516, 113-120.	1.4	43
92	Quaternary structure, conformational variability and global motions of phosphoglucosamine mutase. <i>FEBS Journal</i> , 2011, 278, 3298-3307.	2.2	10
93	Structural basis of the inhibition of class C acid phosphatases by adenosine 5'-phosphorothioate. <i>FEBS Journal</i> , 2011, 278, 4374-4381.	2.2	2
94	Redox Regulation of Protein Tyrosine Phosphatases: Structural and Chemical Aspects. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 77-97.	2.5	149
95	Expression, purification and crystallization of an atypical class C acid phosphatase from <i>Mycoplasma bovis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1296-1299.	0.7	2
96	Solution structures of chicken parvalbumin 3 in the Ca ²⁺ -free and Ca ²⁺ -bound states. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 752-764.	1.5	7
97	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1215-1229.	1.5	29
98	Small-angle X-ray Scattering Studies of the Oligomeric State and Quaternary Structure of the Trifunctional Proline Utilization A (PutA) Flavoprotein from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 43144-43153.	1.6	17
99	Crystal structure of the bifunctional proline utilization A flavoenzyme from <i>Bradyrhizobium japonicum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2878-2883.	3.3	59
100	The Structure of the Proline Utilization A Proline Dehydrogenase Domain Inactivated by N-Propargylglycine Provides Insight into Conformational Changes Induced by Substrate Binding and Flavin Reduction. <i>Biochemistry</i> , 2010, 49, 560-569.	1.2	36
101	Structure of Avian Thymic Hormone, a High-Affinity Avian β -Parvalbumin, in the Ca ²⁺ -Free and Ca ²⁺ -Bound States. <i>Journal of Molecular Biology</i> , 2010, 397, 991-1002.	2.0	8
102	Recognition of Nucleoside Monophosphate Substrates by <i>Haemophilus influenzae</i> Class C Acid Phosphatase. <i>Journal of Molecular Biology</i> , 2010, 404, 639-649.	2.0	14
103	Characterization of a Unique Class C Acid Phosphatase from <i>Clostridium perfringens</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 3745-3754.	1.4	17
104	Expression, purification and crystallization of class C acid phosphatases from <i>Francisella tularensis</i> and <i>Pasteurella multocida</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 226-231.	0.7	3
105	A structurally conserved water molecule in Rossmann dinucleotide-binding domains. <i>Protein Science</i> , 2009, 11, 2125-2137.	3.1	138
106	A Conserved Active Site Tyrosine Residue of Proline Dehydrogenase Helps Enforce the Preference for Proline over Hydroxyproline as the Substrate. <i>Biochemistry</i> , 2009, 48, 951-959.	1.2	30
107	Functional Role for the Conformationally Mobile Phenylalanine 223 in the Reaction of Methylene-tetrahydrofolate Reductase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2009, 48, 7673-7685.	1.2	19
108	Crystal Structures of the Histidine Acid Phosphatase from <i>Francisella tularensis</i> Provide Insight into Substrate Recognition. <i>Journal of Molecular Biology</i> , 2009, 394, 893-904.	2.0	12

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109	Energetics of OCP1â€œOCP2 complex formation. <i>Biophysical Chemistry</i> , 2008, 134, 64-71.	1.5	18
110	Structural biology of proline catabolism. <i>Amino Acids</i> , 2008, 35, 719-730.	1.2	136
111	Three crystal forms of the bifunctional enzyme proline utilization A (PutA) from <i>Bradyrhizobium japonicum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 949-953.	0.7	8
112	Solution structure of Ca ²⁺ -free rat Î±-parvalbumin. <i>Protein Science</i> , 2008, 17, 431-438.	3.1	25
113	Structural Basis of the Transcriptional Regulation of the Proline Utilization Regulon by Multifunctional PutA. <i>Journal of Molecular Biology</i> , 2008, 381, 174-188.	2.0	62
114	Structural Basis for the Inactivation of <i>Thermus thermophilus</i> Proline Dehydrogenase by <i>N</i> -Propargylglycine. <i>Biochemistry</i> , 2008, 47, 5573-5580.	1.2	25
115	Structure and Kinetics of Monofunctional Proline Dehydrogenase from <i>Thermus thermophilus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 14316-14327.	1.6	88
116	Crystallization of Phi29 Spindle-Shaped Nano-Bar Anti-Receptor with Glycosidase Domain. <i>Journal of Nanoscience and Nanotechnology</i> , 2007, 7, 2616-2622.	0.9	2
117	Impact of DNA Hairpin Folding Energetics on Antibodyâ€œssDNA Association. <i>Journal of Molecular Biology</i> , 2007, 374, 1029-1040.	2.0	14
118	Redox-Induced Changes in Flavin Structure and Roles of Flavin N(5) and the Ribityl 2â€œ-OH Group in Regulating PutAâ€™ Membrane Binding. <i>Biochemistry</i> , 2007, 46, 483-491.	1.2	51
119	Structure of Recombinant <i>Haemophilus influenzae</i> e (P4) Acid Phosphatase Reveals a New Member of the Haloacid Dehalogenase Superfamily. <i>Biochemistry</i> , 2007, 46, 11110-11119.	1.2	14
120	Solution structure of Ca ²⁺ -free rat Î±-parvalbumin (oncomodulin). <i>Protein Science</i> , 2007, 16, 1914-1926.	3.1	33
121	<i>Desulfovibrio desulfuricans</i> G20 Tetraheme Cytochrome Structure at 1.5Å... and Cytochrome Interaction with Metal Complexes. <i>Journal of Molecular Biology</i> , 2006, 358, 1314-1327.	2.0	15
122	Characterization of recombinant <i>Francisella tularensis</i> acid phosphatase A. <i>Protein Expression and Purification</i> , 2006, 45, 132-141.	0.6	27
123	High-resolution structure of human D-glyceraldehyde-3-phosphate dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 290-301.	2.5	108
124	Crystallization of a newly discovered histidine acid phosphatase from <i>Francisella tularensis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 32-35.	0.7	7
125	Crystallization of recombinant <i>Haemophilus influenzae</i> e (P4) acid phosphatase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 464-466.	0.7	7
126	Cloning, purification and crystallization of <i>Bacillus anthracis</i> class C acid phosphatase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 705-708.	0.7	19

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127	Exploring structurally conserved solvent sites in protein families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 404-421.	1.5	34
128	Crystal structures of the DNA-binding domain of <i>Escherichia coli</i> proline utilization A flavoprotein and analysis of the role of Lys9 in DNA recognition. <i>Protein Science</i> , 2006, 15, 2630-2641.	3.1	38
129	Structure of <i>Francisella tularensis</i> AcpA. <i>Journal of Biological Chemistry</i> , 2006, 281, 30289-30298.	1.6	67
130	Crystallization of AcpA, a respiratory burst-inhibiting acid phosphatase from <i>Francisella tularensis</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1752, 107-110.	1.1	11
131	Cloning, purification and crystallization of <i>Thermus thermophilus</i> proline dehydrogenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 737-739.	0.7	6
132	Crystal Structure of the D94S/G98E Variant of Rat α -Parvalbumin. An Explanation for the Reduced Divalent Ion Affinity. <i>Biochemistry</i> , 2005, 44, 10966-10976.	1.2	4
133	Evidence for Structural Plasticity of Heavy Chain Complementarity-determining Region 3 in Antibody-ssDNA Recognition. <i>Journal of Molecular Biology</i> , 2005, 347, 965-978.	2.0	28
134	Identification and Characterization of the DNA-binding Domain of the Multifunctional PutA Flavoenzyme. <i>Journal of Biological Chemistry</i> , 2004, 279, 31171-31176.	1.6	46
135	Structure of an anti-DNA fab complexed with a non-DNA ligand provides insights into cross-reactivity and molecular mimicry. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 269-278.	1.5	15
136	Detection of L-lactate in polyethylene glycol solutions confirms the identity of the active-site ligand in a proline dehydrogenase structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 985-986.	2.5	4
137	Probing a hydrogen bond pair and the FAD redox properties in the proline dehydrogenase domain of <i>Escherichia coli</i> PutA. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1701, 49-59.	1.1	14
138	Crystal Structure of a High-Affinity Variant of Rat α -Parvalbumin. <i>Biochemistry</i> , 2004, 43, 10008-10017.	1.2	16
139	Structures of the <i>Escherichia coli</i> PutA Proline Dehydrogenase Domain in Complex with Competitive Inhibitors. <i>Biochemistry</i> , 2004, 43, 12539-12548.	1.2	74
140	Crystal structure of rat α -parvalbumin at 1.05 Å... resolution. <i>Protein Science</i> , 2004, 13, 1724-1734.	3.1	28
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