

# John J Tanner

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1587683/publications.pdf>

Version: 2024-02-01

161  
papers

4,599  
citations

117453

34  
h-index

143772

57  
g-index

164  
all docs

164  
docs citations

164  
times ranked

4694  
citing authors

#	ARTICLE	IF	CITATIONS
1	Determinants of Enzyme Thermostability Observed in the Molecular Structure of <i>Thermus aquaticus</i> d-Glyceraldehyde-3-phosphate Dehydrogenase at 2.5 Å... Resolution,. <i>Biochemistry</i> , 1996, 35, 2597-2609.	1.2	216
2	X-ray crystal structures of native HIV-1 capsid protein reveal conformational variability. <i>Science</i> , 2015, 349, 99-103.	6.0	212
3	Redox Regulation of Protein Tyrosine Phosphatases: Structural and Chemical Aspects. <i>Antioxidants and Redox Signaling</i> , 2011, 15, 77-97.	2.5	149
4	A structurally conserved water molecule in Rossmann dinucleotide-binding domains. <i>Protein Science</i> , 2009, 11, 2125-2137.	3.1	138
5	Structural biology of proline catabolism. <i>Amino Acids</i> , 2008, 35, 719-730.	1.2	136
6	Bioinformatics Methods for Mass Spectrometry-Based Proteomics Data Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2873.	1.8	134
7	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
8	The Proline Cycle As a Potential Cancer Therapy Target. <i>Biochemistry</i> , 2018, 57, 3433-3444.	1.2	107
9	Flavin Reductase P: Structure of a Dimeric Enzyme That Reduces Flavin,. <i>Biochemistry</i> , 1996, 35, 13531-13539.	1.2	98
10	Structure of the proline dehydrogenase domain of the multifunctional PutA flavoprotein. <i>Nature Structural Biology</i> , 2003, 10, 109-114.	9.7	96
11	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
12	Artificial intelligence in the prediction of protein-ligand interactions: recent advances and future directions. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	78
13	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
14	A comparative study of time dependent quantum mechanical wave packet evolution methods. <i>Journal of Chemical Physics</i> , 1992, 96, 2077-2084.	1.2	73
15	Ab initio study of proton transfer in $[H_3N^+H_2]^{+}$ and $[H_3N^+OH_2]^{+}$ . <i>Chemical Physics Letters</i> , 1990, 175, 282-288.	1.2	70
16	Structure of <i>Francisella tularensis</i> AcpA. <i>Journal of Biological Chemistry</i> , 2006, 281, 30289-30298.	1.6	67
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Crystal structure of the bifunctional proline utilization A flavoenzyme from <i>Bradyrhizobium japonicum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2878-2883.	3.3	59
20	The Biological Buffer Bicarbonate/CO <sub>2</sub> Potentiates H <sub>2</sub> O <sub>2</sub> -Mediated Inactivation of Protein Tyrosine Phosphatases. Journal of the American Chemical Society, 2011, 133, 15803-15805.	6.6	57
21	The Three-Dimensional Structural Basis of Type II Hyperprolinemia. Journal of Molecular Biology, 2012, 420, 176-189.	2.0	57
22	Crystal structure of an antigen-binding fragment bound to single-stranded DNA 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 314, 807-822.	2.0	56
23	Structure, function, and mechanism of proline utilization A (PutA). Archives of Biochemistry and Biophysics, 2017, 632, 142-157.	1.4	56
24	Redox-Induced Changes in Flavin Structure and Roles of Flavin N(5) and the Ribityl 2'-OH Group in Regulating PutA Membrane Binding. Biochemistry, 2007, 46, 483-491.	1.2	51
25	Structure, mechanism, and dynamics of UDP-galactopyranose mutase. Archives of Biochemistry and Biophysics, 2014, 544, 128-141.	1.4	49
26	Identification and Characterization of the DNA-binding Domain of the Multifunctional PutA Flavoenzyme. Journal of Biological Chemistry, 2004, 279, 31171-31176.	1.6	46
27	Unusual folded conformation of nicotinamide adenine dinucleotide bound to flavin reductase P. Protein Science, 1999, 8, 1725-1732.	3.1	45
28	Steady-state kinetic mechanism of the proline:ubiquinone oxidoreductase activity of proline utilization A (PutA) from Escherichia coli. Archives of Biochemistry and Biophysics, 2011, 516, 113-120.	1.4	43
29	Resolving the cofactor-binding site in the proline biosynthetic enzyme human pyrroline-5-carboxylate reductase 1. Journal of Biological Chemistry, 2017, 292, 7233-7243.	1.6	42
30	Determination of protein oligomeric structure from small-angle X-ray scattering. Protein Science, 2018, 27, 814-824.	3.1	40
31	Crystal structures of the DNA-binding domain of Escherichia coli proline utilization A flavoprotein and analysis of the role of Lys9 in DNA recognition. Protein Science, 2006, 15, 2630-2641.	3.1	38
32	First Evidence for Substrate Channeling between Proline Catabolic Enzymes. Journal of Biological Chemistry, 2015, 290, 2225-2234.	1.6	37
33	Structural Biology of Proline Catabolic Enzymes. Antioxidants and Redox Signaling, 2019, 30, 650-673.	2.5	37
34	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. Biochemistry, 2010, 49, 560-569.	1.2	36
35	Diethylaminobenzaldehyde Is a Covalent, Irreversible Inactivator of ALDH7A1. ACS Chemical Biology, 2015, 10, 693-697.	1.6	36
36	Structural Basis of Substrate Recognition by Aldehyde Dehydrogenase 7A1. Biochemistry, 2015, 54, 5513-5522.	1.2	36

#	ARTICLE	IF	CITATIONS
37	The Structure of the Antibiotic Deactivating, N-hydroxylating Rifampicin Monooxygenase. <i>Journal of Biological Chemistry</i> , 2016, 291, 21553-21562.	1.6	36
38	Exploring structurally conserved solvent sites in protein families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 404-421.	1.5	34
39	Solution structure of Ca <sup>2+</sup> -free rat Î²-parvalbumin (oncomodulin). <i>Protein Science</i> , 2007, 16, 1914-1926.	3.1	33
40	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
41	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
42	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
43	MRSAD: using anomalous dispersion from S atoms collected at Cu K $\alpha$ wavelength in molecular-replacement structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1731-1736.	2.5	30
44	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
45	Structural Studies of Yeast P <sup>1</sup> -Pyrroline-5-carboxylate Dehydrogenase (ALDH4A1): Active Site Flexibility and Oligomeric State. <i>Biochemistry</i> , 2014, 53, 1350-1359.	1.2	30
46	DeepCryoPicker: fully automated deep neural network for single protein particle picking in cryo-EM. <i>BMC Bioinformatics</i> , 2020, 21, 509.	1.2	30
47	Molecular Dynamics Simulations of NAD <sup>+</sup> in Solution. <i>Journal of the American Chemical Society</i> , 1999, 121, 8637-8644.	6.6	29
48	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
49	Crystal structure of rat Î±-parvalbumin at 1.05 Å... resolution. <i>Protein Science</i> , 2004, 13, 1724-1734.	3.1	28
50	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
51	Proline: Mother Nature's cryoprotectant applied to protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1010-1018.	2.5	28
52	Evidence for Hysteretic Substrate Channeling in the Proline Dehydrogenase and P <sup>1</sup> -Pyrroline-5-carboxylate Dehydrogenase Coupled Reaction of Proline Utilization A (PutA). <i>Journal of Biological Chemistry</i> , 2014, 289, 3639-3651.	1.6	28
53	Conformations of nicotinamide adenine dinucleotide (NAD <sup>+</sup> ) in various environments. , 2000, 13, 27-34.		27
54	Characterization of recombinant <i>Francisella tularensis</i> acid phosphatase A. <i>Protein Expression and Purification</i> , 2006, 45, 132-141.	0.6	27

#	ARTICLE	IF	CITATIONS
55	Unique structural features and sequence motifs of proline utilization A (PutA). <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 556.	3.0	27
56	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
57	Solution structure of Ca <sup>2+</sup> -free rat Î±-parvalbumin. <i>Protein Science</i> , 2008, 17, 431-438.	3.1	25
58	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
59	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
60	Anti-insulin antibody structure and conformation. II. Molecular dynamics with explicit solvent. <i>Biopolymers</i> , 1992, 32, 23-32.	1.2	24
61	Structural Determinants of Oligomerization of <sup>15</sup> N-Pyrroline-5-Carboxylate Dehydrogenase: Identification of a Hexamerization Hot Spot. <i>Journal of Molecular Biology</i> , 2013, 425, 3106-3120.	2.0	24
62	Structural basis of substrate selectivity of <sup>15</sup> N-pyrroline-5-carboxylate dehydrogenase (ALDH4A1): Semialdehyde chain length. <i>Archives of Biochemistry and Biophysics</i> , 2013, 538, 34-40.	1.4	24
63	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
64	A modified landau-teller model for vibrational relaxation of small molecular ions. <i>Chemical Physics Letters</i> , 1987, 138, 495-502.	1.2	23
65	Floquet analysis of the far-infrared dissociation of a Morse oscillator. <i>Physical Review A</i> , 1989, 40, 4054-4064.	1.0	23
66	A computer-based approach to teaching quantum dynamics. <i>Journal of Chemical Education</i> , 1990, 67, 917.	1.1	23
67	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
68	Covalent Allosteric Inactivation of Protein Tyrosine Phosphatase 1B (PTP1B) by an Inhibitor- <sup>64</sup> Electrophile Conjugate. <i>Biochemistry</i> , 2017, 56, 2051-2060.	1.2	22
69	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
70	<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
71	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
72	Molecular dynamics simulations and rigid body (TLS) analysis of aspartate carbamoyltransferase: Evidence for an uncoupled R state. <i>Protein Science</i> , 1993, 2, 927-935.	3.1	20

#	ARTICLE	IF	CITATIONS
73	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
74	Structure, biochemistry, and gene expression patterns of the proline biosynthetic enzyme pyrroline-5-carboxylate reductase (PYCR), an emerging cancer therapy target. <i>Amino Acids</i> , 2021, 53, 1817-1834.	1.2	20
75	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
76	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
77	Targeting UDP-Galactopyranose Mutases from Eukaryotic Human Pathogens. <i>Current Pharmaceutical Design</i> , 2013, 19, 2561-2573.	0.9	19
78	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
79	Structure of Bacterial Luciferase $\hat{2}$ Homodimer: Implications for Flavin Binding. <i>Biochemistry</i> , 1997, 36, 665-672.	1.2	18
80	Energetics of OCP1-OCP2 complex formation. <i>Biophysical Chemistry</i> , 2008, 134, 64-71.	1.5	18
81	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
82	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
83	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
84	Involvement of the $\hat{2}$ - $\hat{3}$ 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
85	Crystal Structure of a High-Affinity Variant of Rat $\hat{2}$ -Parvalbumin. <i>Biochemistry</i> , 2004, 43, 10008-10017.	1.2	16
86	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
87	<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
88	Inactivation of protein tyrosine phosphatases by dietary isothiocyanates. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 4549-4552.	1.0	15
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	Impact of DNA Hairpin Folding Energetics on Antibody-ssDNA Association. <i>Journal of Molecular Biology</i> , 2007, 374, 1029-1040.	2.0	14
93	Structure of Recombinant <i>Haemophilus Influenzae e</i> (P4) Acid Phosphatase Reveals a New Member of the Haloacid Dehalogenase Superfamily,. <i>Biochemistry</i> , 2007, 46, 11110-11119.	1.2	14
94	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
95	Biophysical investigation of type A PutAs reveals a conserved core oligomeric structure. <i>FEBS Journal</i> , 2017, 284, 3029-3049.	2.2	14
96	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
97	Crystallization and preliminary crystallographic analysis of the proline dehydrogenase domain of the multifunctional PutA flavoprotein from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1925-1927.	2.5	13
98	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
99	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
100	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
101	Structural Evidence for Rifampicin Monooxygenase Inactivating Rifampicin by Cleaving Its Ansa-Bridge. <i>Biochemistry</i> , 2018, 57, 2065-2068.	1.2	13
102	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
103	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
104	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
105	Solution structures of polcalcin Phl p 7 in three ligation states: Apo, heme-Mg <sup>2+</sup> -bound, and fully Ca <sup>2+</sup> -bound. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 300-315.	1.5	12
106	A Super-Clustering Approach for Fully Automated Single Particle Picking in Cryo-EM. <i>Genes</i> , 2019, 10, 666.	1.0	12
107	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
108	Substrate-dependent dynamics of UDP-galactopyranose mutase: Implications for drug design. <i>Protein Science</i> , 2013, 22, 1490-1501.	3.1	11

#	ARTICLE	IF	CITATIONS
109	Multiple functionalities of reduced flavin in the non-redox reaction catalyzed by UDP-galactopyranose mutase. Archives of Biochemistry and Biophysics, 2017, 632, 59-65.	1.4	11
110	NAD <sup>+</sup> promotes assembly of the active tetramer of aldehyde dehydrogenase 7A1. FEBS Letters, 2018, 592, 3229-3238.	1.3	11
111	The role of rotation in the vibrational relaxation of diatomic molecules. Chemical Physics, 1988, 119, 307-324.	0.9	10
112	Quaternary structure, conformational variability and global motions of phosphoglucosamine mutase. FEBS Journal, 2011, 278, 3298-3307.	2.2	10
113	Covalent Modification of the Flavin in Proline Dehydrogenase by Thiazolidine-2-Carboxylate. ACS Chemical Biology, 2020, 15, 936-944.	1.6	10
114	Far IR dissociation of a highly excited Morse oscillator. Chemical Physics Letters, 1988, 149, 503-509.	1.2	9
115	Crystal structure and tartrate inhibition of Legionella pneumophila histidine acid phosphatase. Archives of Biochemistry and Biophysics, 2015, 585, 32-38.	1.4	9
116	Structural Basis for the Substrate Inhibition of Proline Utilization A by Proline. Molecules, 2018, 23, 32.	1.7	9
117	SAXSDom: Modeling multidomain protein structures using small-angle X-ray scattering data. Proteins: Structure, Function and Bioinformatics, 2020, 88, 775-787.	1.5	9
118	Disease variants of human $\beta$ -1-pyrroline-5-carboxylate reductase 2 (PYCR2). Archives of Biochemistry and Biophysics, 2021, 703, 108852.	1.4	9
119	Three crystal forms of the bifunctional enzyme proline utilization A (PutA) from Bradyrhizobium japonicum. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 949-953.	0.7	8
120	Structure of Avian Thymic Hormone, a High-Affinity Avian $\beta$ -2-Parvalbumin, in the Ca <sup>2+</sup> -Free and Ca <sup>2+</sup> -Bound States. Journal of Molecular Biology, 2010, 397, 991-1002.	2.0	8
121	Contributions of Unique Active Site Residues of Eukaryotic UDP-Galactopyranose Mutases to Substrate Recognition and Active Site Dynamics. Biochemistry, 2014, 53, 7794-7804.	1.2	8
122	Structural Determinants of Flavin Dynamics in a Class B Monooxygenase. Biochemistry, 2020, 59, 4609-4616.	1.2	8
123	Crystallization of a newly discovered histidine acid phosphatase from Francisella tularensis. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 32-35.	0.7	7
124	Crystallization of recombinant Haemophilus influenzae (P4) acid phosphatase. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 464-466.	0.7	7
125	Solution structures of chicken parvalbumin 3 in the Ca <sup>2+</sup> -free and Ca <sup>2+</sup> -bound states. Proteins: Structure, Function and Bioinformatics, 2011, 79, 752-764.	1.5	7
126	SAXS fingerprints of aldehyde dehydrogenase oligomers. Data in Brief, 2015, 5, 745-751.	0.5	7



#	ARTICLE	IF	CITATIONS
127	Importance of the C-Terminus of Aldehyde Dehydrogenase 7A1 for Oligomerization and Catalytic Activity. <i>Biochemistry</i> , 2017, 56, 5910-5919.	1.2	7
128	Discovery of the Membrane Binding Domain in Trifunctional Proline Utilization A. <i>Biochemistry</i> , 2017, 56, 6292-6303.	1.2	7
129	Flavin- $\epsilon$ N5 Covalent Intermediate in a Nonredox Dehalogenation Reaction Catalyzed by an Atypical Flavoenzyme. <i>ChemBioChem</i> , 2018, 19, 53-57.	1.3	7
130	Structural and biochemical consequences of pyridoxine-dependent epilepsy mutations that target the aldehyde binding site of aldehyde dehydrogenase ALDH 7A1. <i>FEBS Journal</i> , 2020, 287, 173-189.	2.2	7
131	Cautionary Tale of Using Tris(alkyl)phosphine Reducing Agents with NAD <sup>+</sup> -Dependent Enzymes. <i>Biochemistry</i> , 2020, 59, 3285-3289.	1.2	7
132	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
133	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
134	Structural analysis of pathogenic mutations targeting Glu427 of ALDH7A1, the hot spot residue of pyridoxine-dependent epilepsy. <i>Journal of Inherited Metabolic Disease</i> , 2020, 43, 635-644.	1.7	6
135	Structural analysis of prolines and hydroxyprolines binding to the l-glutamate- $\beta$ -semialdehyde dehydrogenase active site of bifunctional proline utilization A. <i>Archives of Biochemistry and Biophysics</i> , 2021, 698, 108727.	1.4	6
136	Biochemical Characterization of the Two-Component Flavin-Dependent Monooxygenase Involved in Valanimycin Biosynthesis. <i>Biochemistry</i> , 2021, 60, 31-40.	1.2	6
137	Structure-affinity relationships of reversible proline analog inhibitors targeting proline dehydrogenase. <i>Organic and Biomolecular Chemistry</i> , 2022, 20, 895-905.	1.5	6
138	Crystallization and molecular-replacement studies of a recombinant antigen-binding fragment complexed with single-stranded DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1007-1011.	2.5	5
139	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
140	N-Propargylglycine: a unique suicide inhibitor of proline dehydrogenase with anticancer activity and brain-enhancing mitohormesis properties. <i>Amino Acids</i> , 2021, 53, 1927-1939.	1.2	5
141	Structural and Biochemical Characterization of the Flavin-Dependent Siderophore-Interacting Protein from <i>Acinetobacter baumannii</i> . <i>ACS Omega</i> , 2021, 6, 18537-18547.	1.6	5
142	Preliminary crystallographic analysis of glyceraldehyde 3-phosphate dehydrogenase from the extreme thermophile <i>Thermus aquaticus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 744-748.	2.5	4
143	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
144	Crystal Structure of the D94S/G98E Variant of Rat $\alpha$ -Parvalbumin. An Explanation for the Reduced Divalent Ion Affinity. <i>Biochemistry</i> , 2005, 44, 10966-10976.	1.2	4

#	ARTICLE	IF	CITATIONS
145	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
146	Synchrotron-based macromolecular crystallography module for an undergraduate biochemistry laboratory course. <i>Journal of Applied Crystallography</i> , 2016, 49, 2235-2243.	1.9	4
147	Structural basis for the stereospecific inhibition of the dual proline/hydroxyproline catabolic enzyme ALDH4A1 by trans-4-hydroxy-L-proline. <i>Protein Science</i> , 2021, 30, 1714-1722.	3.1	4
148	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
149	Steric Control of the Rate-Limiting Step of UDP-Galactopyranose Mutase. <i>Biochemistry</i> , 2018, 57, 3713-3721.	1.2	3
150	Probing the function of a ligand-modulated dynamic tunnel in bifunctional proline utilization A (PutA). <i>Archives of Biochemistry and Biophysics</i> , 2021, 712, 109025.	1.4	3
151	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
152	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
153	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
154	EF5 Is the High-Affinity Mg <sup>2+</sup> Site in ALG-2. <i>Biochemistry</i> , 2016, 55, 5128-5141.	1.2	2
155	Redox Modulation of Oligomeric State in Proline Utilization A. <i>Biophysical Journal</i> , 2018, 114, 2833-2843.	0.2	2
156	Photoinduced Covalent Irreversible Inactivation of Proline Dehydrogenase by S-Heterocycles. <i>ACS Chemical Biology</i> , 2021, 16, 2268-2279.	1.6	2
157	2 PutA and proline metabolism. , 2012, , 31-56.		1
158	Impact of missense mutations in the ALDH7A1 gene on enzyme structure and catalytic function. <i>Biochimie</i> , 2021, 183, 49-54.	1.3	1
159	Optimisation of Neuraminidase Expression for Use in Drug Discovery by Using HEK293-6E Cells. <i>Viruses</i> , 2021, 13, 1893.	1.5	1
160	Evidence for Proline Catabolic Enzymes in the Metabolism of Thiazolidine Carboxylates. <i>Biochemistry</i> , 2021, 60, 3610-3620.	1.2	0
161	Kinetics of human pyrroline-5-carboxylate reductase in l-thiopline metabolism. <i>Amino Acids</i> , 2021, 53, 1863-1874.	1.2	0