

Alexander B Taylor

List of Publications by Year in descending order

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77
papers

4,919
citations

117625

34
h-index

95266

68
g-index

82
all docs

82
docs citations

82
times ranked

6824
citing authors

#	ARTICLE	IF	CITATIONS
1	Schistosome Sulfotransferases: Mode of Action, Expression and Localization. <i>Pharmaceutics</i> , 2022, 14, 1416.	4.5	3
2	Nucleic acid binding by SAMHD1 contributes to the antiretroviral activity and is enhanced by the GpsN modification. <i>Nature Communications</i> , 2021, 12, 731.	12.8	26
3	A pH Switch Controls Zinc Binding in Tomato Copperâ€Zinc Superoxide Dismutase. <i>Biochemistry</i> , 2021, 60, 1597-1608.	2.5	0
4	Rational approach to drug discovery for human schistosomiasis. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 16, 140-147.	3.4	8
5	An iterative process produces oxamniquine derivatives that kill the major species of schistosomes infecting humans. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008517.	3.0	10
6	Molecular basis for hycanthonone drug action in schistosome parasites. <i>Molecular and Biochemical Parasitology</i> , 2020, 236, 111257.	1.1	10
7	Why does oxamniquine kill <i>Schistosoma mansoni</i> and not <i>S. haematobium</i> and <i>S. japonicum</i> ?. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2020, 13, 8-15.	3.4	15
8	Structure of a Zinc Porphyrin-Substituted Bacterioferritin and Photophysical Properties of Iron Reduction. <i>Biochemistry</i> , 2020, 59, 1618-1629.	2.5	2
9	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. <i>Structure</i> , 2019, 27, 1427-1442.e4.	3.3	12
10	Paratope Duality and Gulying are Among the Atypical Recognition Mechanisms Used by a Trio of Nanobodies to Differentiate Ebolavirus Nucleoproteins. <i>Journal of Molecular Biology</i> , 2019, 431, 4848-4867.	4.2	5
11	Oxamniquine resistance alleles are widespread in Old World <i>Schistosoma mansoni</i> and predate drug deployment. <i>PLoS Pathogens</i> , 2019, 15, e1007881.	4.7	28
12	Disulfide bond of <i>Mycoplasma pneumoniae</i> community-acquired respiratory distress syndrome toxin is essential to maintain the ADP-ribosylating and vacuolating activities. <i>Cellular Microbiology</i> , 2019, 21, e13032.	2.1	7
13	A mutually induced conformational fit underlies Ca ²⁺ -directed interactions between calmodulin and the proximal C terminus of KCNQ4 K ⁺ channels. <i>Journal of Biological Chemistry</i> , 2019, 294, 6094-6112.	3.4	13
14	<i>Mycoplasma pneumoniae</i> Community-Acquired Respiratory Distress Syndrome Toxin Uses a Novel KELED Sequence for Retrograde Transport and Subsequent Cytotoxicity. <i>MBio</i> , 2018, 9, .	4.1	14
15	Design, Synthesis, and Characterization of Novel Small Molecules as Broad Range Antischistosomal Agents. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 967-973.	2.8	17
16	High affinity interactions of Pb ²⁺ with synaptotagmin I. <i>Metallomics</i> , 2018, 10, 1211-1222.	2.4	6
17	An engineered transforming growth factor Î² (TGF-Î²) monomer that functions as a dominant negative to block TGF-Î² signaling. <i>Journal of Biological Chemistry</i> , 2017, 292, 7173-7188.	3.4	34
18	Non-Native Metal Ion Reveals the Role of Electrostatics in Synaptotagmin Iâ€™Membrane Interactions. <i>Biochemistry</i> , 2017, 56, 3283-3295.	2.5	20

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19	Copper-zinc superoxide dismutase is activated through a sulfenic acid intermediate at a copper ion entry site. <i>Journal of Biological Chemistry</i> , 2017, 292, 12025-12040.	3.4	48
20	Structural and enzymatic insights into species-specific resistance to schistosome parasite drug therapy. <i>Journal of Biological Chemistry</i> , 2017, 292, 11154-11164.	3.4	24
21	Structure-Based Design and Synthesis of Potent and Selective Matrix Metalloproteinase 13 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5816-5825.	6.4	35
22	Unveiling a Drift Resistant Cryptotope within Marburgvirus Nucleoprotein Recognized by Llama Single-Domain Antibodies. <i>Frontiers in Immunology</i> , 2017, 8, 1234.	4.8	15
23	Metal dependence and branched RNA cocystal structures of the RNA lariat debranching enzyme Dbr1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14727-14732.	7.1	24
24	Domain Movements upon Activation of Phenylalanine Hydroxylase Characterized by Crystallography and Chromatography-Coupled Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2016, 138, 6506-6516.	13.7	100
25	KDM2B Recruitment of the Polycomb Group Complex, PRC1.1, Requires Cooperation between PCGF1 and BCORL1. <i>Structure</i> , 2016, 24, 1795-1801.	3.3	49
26	The Phylogeny and Active Site Design of Eukaryotic Copper-only Superoxide Dismutases. <i>Journal of Biological Chemistry</i> , 2016, 291, 20911-20923.	3.4	27
27	RING Dimerization Links Higher-Order Assembly of TRIM5 α to Synthesis of K63-Linked Polyubiquitin. <i>Cell Reports</i> , 2015, 12, 788-797.	6.4	72
28	Structure of CARDS toxin, a unique ADP-ribosylating and vacuolating cytotoxin from <i>Mycoplasma pneumoniae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5165-5170.	7.1	61
29	Insights into the Role of the Unusual Disulfide Bond in Copper-Zinc Superoxide Dismutase. <i>Journal of Biological Chemistry</i> , 2015, 290, 2405-2418.	3.4	61
30	Structural and Functional Characterization of the Enantiomers of the Antischistosomal Drug Oxamniquine. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004132.	3.0	20
31	Structural basis of HIV-1 capsid recognition by PF74 and CPSF6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18625-18630.	7.1	215
32	Characterization of Selective Exosite-Binding Inhibitors of Matrix Metalloproteinase 13 That Prevent Articular Cartilage Degradation in Vitro. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 9598-9611.	6.4	29
33	Structural basis of lariat RNA recognition by the intron debranching enzyme Dbr1. <i>Nucleic Acids Research</i> , 2014, 42, 10845-10855.	14.5	42
34	<i>Candida albicans</i> SOD5 represents the prototype of an unprecedented class of Cu-only superoxide dismutases required for pathogen defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5866-5871.	7.1	99
35	Multiple polymer architectures of human polyhomeotic homolog 3 sterile alpha motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2823-2830.	2.6	11
36	Structure of the Polycomb Group Protein PCGF1 in Complex with BCOR Reveals Basis for Binding Selectivity of PCGF Homologs. <i>Structure</i> , 2013, 21, 665-671.	3.3	89

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37	Genetic and Molecular Basis of Drug Resistance and Species-Specific Drug Action in Schistosome Parasites. <i>Science</i> , 2013, 342, 1385-1389.	12.6	137
38	Cd ²⁺ as a Ca ²⁺ Surrogate in Protein-Membrane Interactions: Isostructural but Not Isofunctional. <i>Journal of the American Chemical Society</i> , 2013, 135, 12980-12983.	13.7	12
39	Structure of the Flavoprotein Tryptophan 2-Monooxygenase, a Key Enzyme in the Formation of Galls in Plants. <i>Biochemistry</i> , 2013, 52, 2620-2626.	2.5	26
40	Structure of the Chlamydia trachomatis Immunodominant Antigen Pgp3. <i>Journal of Biological Chemistry</i> , 2013, 288, 22068-22079.	3.4	41
41	Evaluation of competing J domain:Hsp70 complex models in light of existing mutational and NMR data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E734; author reply E735.	7.1	13
42	Structure of the rhesus monkey TRIM5 α PRYSPRY domain, the HIV capsid recognition module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13278-13283.	7.1	83
43	Mechanistic and Structural Analyses of the Role of His67 in the Yeast Polyamine Oxidase Fms1. <i>Biochemistry</i> , 2012, 51, 4888-4897.	2.5	8
44	Mechanistic and Structural Analyses of the Roles of Active Site Residues in Yeast Polyamine Oxidase Fms1: Characterization of the N195A and D94N Enzymes. <i>Biochemistry</i> , 2012, 51, 8690-8697.	2.5	7
45	Histidine ligand variants of a flavo-diiron protein: effects on structure and activities. <i>Journal of Biological Inorganic Chemistry</i> , 2012, 17, 1231-1239.	2.6	32
46	Molecular Recognition of Insulin by a Synthetic Receptor. <i>Journal of the American Chemical Society</i> , 2011, 133, 8810-8813.	13.7	291
47	Structure and function of multiple Ca ²⁺ -binding sites in a K ⁺ channel regulator of K ⁺ conductance (RCK) domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17684-17689.	7.1	35
48	Polycomb Group Targeting through Different Binding Partners of RING1B C-Terminal Domain. <i>Structure</i> , 2010, 18, 966-975.	3.3	81
49	Crystallization of community-acquired respiratory distress syndrome toxin from <i>Mycoplasma pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 294-296.	0.7	4
50	Characterization of a Covalent Polysulfane Bridge in Copper-Zinc Superoxide Dismutase. <i>Biochemistry</i> , 2010, 49, 1191-1198.	2.5	34
51	Identification of a Hypothetical Protein from <i>Podospora anserina</i> as a Nitroalkane Oxidase. <i>Biochemistry</i> , 2010, 49, 5035-5041.	2.5	14
52	Structures of mouse SOD1 and human/mouse SOD1 chimeras. <i>Archives of Biochemistry and Biophysics</i> , 2010, 503, 183-190.	3.0	20
53	Disrupted Zinc-Binding Sites in Structures of Pathogenic SOD1 Variants D124V and H80R. <i>Biochemistry</i> , 2010, 49, 5714-5725.	2.5	50
54	Effects of pH on the Rieske Protein from <i>Thermus thermophilus</i> : A Spectroscopic and Structural Analysis. <i>Biochemistry</i> , 2009, 48, 9848-9857.	2.5	32

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55	Structural and biophysical properties of metal-free pathogenic SOD1 mutants A4V and G93A. <i>Archives of Biochemistry and Biophysics</i> , 2009, 492, 40-47.	3.0	74
56	GAPDH Is Conformationally and Functionally Altered in Association with Oxidative Stress in Mouse Models of Amyotrophic Lateral Sclerosis. <i>Journal of Molecular Biology</i> , 2008, 382, 1195-1210.	4.2	70
57	Cooperative Assembly of TGF- β 2 Superfamily Signaling Complexes Is Mediated by Two Disparate Mechanisms and Distinct Modes of Receptor Binding. <i>Molecular Cell</i> , 2008, 29, 157-168.	9.7	247
58	Structure of the Hsp110:Hsc70 Nucleotide Exchange Machine. <i>Molecular Cell</i> , 2008, 31, 232-243.	9.7	202
59	The crystal structure of Nep1 reveals an extended SPOUT-class methyltransferase fold and a pre-organized SAM-binding site. <i>Nucleic Acids Research</i> , 2008, 36, 1542-1554.	14.5	37
60	Allosteric Motions in Structures of Yeast NAD ⁺ -specific Isocitrate Dehydrogenase. <i>Journal of Biological Chemistry</i> , 2008, 283, 10872-10880.	3.4	44
61	Structures of the G85R Variant of SOD1 in Familial Amyotrophic Lateral Sclerosis. <i>Journal of Biological Chemistry</i> , 2008, 283, 16169-16177.	3.4	85
62	Crystal structure of the yeast nicotinamidase Pnc1p. <i>Archives of Biochemistry and Biophysics</i> , 2007, 461, 66-75.	3.0	27
63	Structural Basis of J Cochaperone Binding and Regulation of Hsp70. <i>Molecular Cell</i> , 2007, 28, 422-433.	9.7	206
64	Shall We Dance? How A Multicopper Oxidase Chooses Its Electron Transfer Partner. <i>Accounts of Chemical Research</i> , 2007, 40, 445-452.	15.6	194
65	Sequence-Specific Recognition and Cooperative Dimerization of N-Terminal Aromatic Peptides in Aqueous Solution by a Synthetic Host. <i>Journal of the American Chemical Society</i> , 2006, 128, 12574-12581.	13.7	304
66	Crystallization and preliminary X-ray crystallographic analysis of yeast NAD ⁺ -specific isocitrate dehydrogenase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 486-488.	0.7	6
67	The copper-iron connection in biology: Structure of the metallo-oxidase Fet3p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15459-15464.	7.1	176
68	Amyloid-like filaments and water-filled nanotubes formed by SOD1 mutant proteins linked to familial ALS. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 461-467.	8.2	311
69	Structure-Function Analysis of the Auxilin J-Domain Reveals an Extended Hsc70 Interaction Interface. <i>Biochemistry</i> , 2003, 42, 5748-5753.	2.5	58
70	Structure of Mycobacterium tuberculosis Methionine Sulfoxide Reductase A in Complex with Protein-Bound Methionine. <i>Journal of Bacteriology</i> , 2003, 185, 4119-4126.	2.2	70
71	An Alternative Mechanism of Bicarbonate-mediated Peroxidation by Copper-Zinc Superoxide Dismutase. <i>Journal of Biological Chemistry</i> , 2003, 278, 21032-21039.	3.4	77
72	Copper chaperones. <i>Advances in Protein Chemistry</i> , 2002, 60, 151-219.	4.4	33

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73	Crystal structure of the human TÎ²R2 ectodomainâ€™TGF-Î²3 complex. Nature Structural Biology, 2002, 9, 203-8.	9.7	130
74	Crystal Structures of Mitochondrial Processing Peptidase Reveal the Mode for Specific Cleavage of Import Signal Sequences. Structure, 2001, 9, 615-625.	3.3	208
75	Mechanism of the Phenylpyruvate Tautomerase Activity of Macrophage Migration Inhibitory Factor:â€™ Properties of the P1G, P1A, Y95F, and N97A Mutants,. Biochemistry, 2000, 39, 9671-9678.	2.5	26
76	Crystal Structure of Macrophage Migration Inhibitory Factor Complexed with (E)-2-Fluoro-p-hydroxycinnamate at 1.8 Å... Resolution:â€™ Implications for Enzymatic Catalysis and Inhibition,. Biochemistry, 1999, 38, 7444-7452.	2.5	83
77	Crystal Structure of 4-Oxalocrotonate Tautomerase Inactivated by 2-Oxo-3-pentynoate at 2.4 Å... Resolution:Â Analysis and Implications for the Mechanism of Inactivation and Catalysisâ€™â€™. Biochemistry, 1998, 37, 14692-14700.	2.5	73