

Wanting Jiao

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,162
citations

471509

17
h-index

434195

31
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48
all docs

48
docs citations

48
times ranked

1738
citing authors

#	ARTICLE	IF	CITATIONS
1	Change in Heat Capacity for Enzyme Catalysis Determines Temperature Dependence of Enzyme Catalyzed Rates. ACS Chemical Biology, 2013, 8, 2388-2393.	3.4	164
2	Structure of the bacterial type II NADH dehydrogenase: a monotopic membrane protein with an essential role in energy generation. Molecular Microbiology, 2014, 91, 950-964.	2.5	103
3	Molecular Mechanism of CCAAT-Enhancer Binding Protein Recruitment by the TRIB1 Pseudokinase. Structure, 2015, 23, 2111-2121.	3.3	93
4	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions. Microbiology Spectrum, 2017, 5, .	3.0	89
5	Free charge photogeneration in a single component high photovoltaic efficiency organic semiconductor. Nature Communications, 2022, 13, .	12.8	66
6	Synergistic Allostery, a Sophisticated Regulatory Network for the Control of Aromatic Amino Acid Biosynthesis in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2010, 285, 30567-30576.	3.4	63
7	The mechanism of catalysis by type-II NADH:quinone oxidoreductases. Scientific Reports, 2017, 7, 40165.	3.3	45
8	Dynamic Cross-Talk among Remote Binding Sites: The Molecular Basis for Unusual Synergistic Allostery. Journal of Molecular Biology, 2012, 415, 716-726.	4.2	39
9	Three Sites and You Are Out: Ternary Synergistic Allostery Controls Aromatic Amino Acid Biosynthesis in Mycobacterium tuberculosis. Journal of Molecular Biology, 2013, 425, 1582-1592.	4.2	38
10	Potent Inhibitors of a Shikimate Pathway Enzyme from Mycobacterium tuberculosis. Journal of Biological Chemistry, 2011, 286, 16197-16207.	3.4	37
11	Structures of Orf Virus Chemokine Binding Protein in Complex with Host Chemokines Reveal Clues to Broad Binding Specificity. Structure, 2015, 23, 1199-1213.	3.3	28
12	Role of Alanine Racemase Mutations in Mycobacterium tuberculosis d-Cycloserine Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	24
13	Multiple Bactericidal Mechanisms of the Zinc Ionophore PBT2. MSphere, 2020, 5, .	2.9	24
14	Acetyl-CoA-mediated activation of Mycobacterium tuberculosis isocitrate lyase 2. Nature Communications, 2019, 10, 4639.	12.8	23
15	Structure of the NDH-2 H ₂ O inhibited complex provides molecular insight into quinone-binding site inhibitors. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, 482-490.	1.0	20
16	Unprecedented Properties of Phenothiazines Unraveled by a NDH-2 Bioelectrochemical Assay Platform. Journal of the American Chemical Society, 2020, 142, 1311-1320.	13.7	18
17	A Broad-Spectrum Chemokine-Binding Protein of Bovine Papular Stomatitis Virus Inhibits Neutrophil and Monocyte Infiltration in Inflammatory and Wound Models of Mouse Skin. PLoS ONE, 2016, 11, e0168007.	2.5	18
18	Quaternary structure is an essential component that contributes to the sophisticated allosteric regulation mechanism in a key enzyme from Mycobacterium tuberculosis. PLoS ONE, 2017, 12, e0180052.	2.5	18

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19	New Tripeptide-Based Macrocyclic Calpain Inhibitors Formed by N-Alkylation of Histidine. Chemistry and Biodiversity, 2012, 9, 2473-2484.	2.1	17
20	Exploring the structure of glutamate racemase from Mycobacterium tuberculosis as a template for anti-mycobacterial drug discovery. Biochemical Journal, 2016, 473, 1267-1280.	3.7	17
21	Long-range exciton diffusion in a non-fullerene acceptor: approaching the incoherent limit. Journal of Materials Chemistry C, 2021, 9, 1419-1428.	5.5	15
22	Extracellular Electron Transfer: Respiratory or Nutrient Homeostasis?. Journal of Bacteriology, 2020, 202, .	2.2	14
23	Synthesis and evaluation of dual site inhibitors of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 5092-5097.	2.2	13
24	A single amino acid substitution uncouples catalysis and allostery in an essential biosynthetic enzyme in Mycobacterium tuberculosis. Journal of Biological Chemistry, 2020, 295, 6252-6262.	3.4	13
25	A dimeric catalytic core relates the short and long forms of ATP-phosphoribosyltransferase. Biochemical Journal, 2018, 475, 247-260.	3.7	12
26	Antitubercular polyhalogenated phenothiazines and phenoselenazine with reduced binding to CNS receptors. European Journal of Medicinal Chemistry, 2020, 201, 112420.	5.5	12
27	Using a Combination of Computational and Experimental Techniques to Understand the Molecular Basis for Protein Allostery. Advances in Protein Chemistry and Structural Biology, 2012, 87, 391-413.	2.3	11
28	Diverse allosteric componentry and mechanisms control entry into aromatic metabolite biosynthesis. Current Opinion in Structural Biology, 2020, 65, 159-167.	5.7	11
29	Tethering fragment-based drug discovery to identify inhibitors of the essential respiratory membrane protein type II NADH dehydrogenase. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 2239-2243.	2.2	10
30	Crystal structure of type II NADH:quinone oxidoreductase from Caldalkalibacillus thermarum with an improved resolution of 2.15 Å. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 541-549.	0.8	10
31	Arg314 Is Essential for Catalysis by N-Acetyl Neuraminic Acid Synthase from Neisseria meningitidis. Biochemistry, 2013, 52, 2609-2619.	2.5	9
32	Synthesis of sulfamide analogues of deoxythymidine monophosphate as potential inhibitors of mycobacterial cell wall biosynthesis. Carbohydrate Research, 2018, 457, 32-40.	2.3	9
33	Structural plasticity and in vivo activity of Cas1 from the type I-F CRISPR-Cas system. Biochemical Journal, 2016, 473, 1063-1072.	3.7	8
34	Chemokine-Binding Proteins Encoded by Parapoxvirus of Red Deer of New Zealand Display Evidence of Gene Duplication and Divergence of Ligand Specificity. Frontiers in Microbiology, 2019, 10, 1421.	3.5	8
35	Synthesis of Novel Glycolipid Mimetics of Heparan Sulfate and Their Application in Colorectal Cancer Treatment in a Mouse Model. Chemistry - an Asian Journal, 2022, 17, .	3.3	8
36	Molecular Modeling Studies of Peptide Inhibitors Highlight the Importance of Conformational Prearrangement for Inhibition of Calpain. Biochemistry, 2010, 49, 5533-5539.	2.5	7

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37	Anti-IL4/IL13 Allergic hormone signaling is influenced by Follistatin 288, but not 14 other transforming growth factor beta superfamily regulators. <i>Molecular Reproduction and Development</i> , 2017, 84, 626-637.	2.0	7
38	Functional characterization of BcrR: a one-component transmembrane signal transduction system for bacitracin resistance. <i>Microbiology (United Kingdom)</i> , 2019, 165, 475-487.	1.8	7
39	Probing the Sophisticated Synergistic Allosteric Regulation of Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> Using α -Amino Acids. <i>PLoS ONE</i> , 2016, 11, e0152723.	2.5	6
40	An Extended β 7 Substrate-Binding Loop Is Essential for Efficient Catalysis by 3-Deoxy- α -manno-Octulosonate 8-Phosphate Synthase. <i>Biochemistry</i> , 2011, 50, 9318-9327.	2.5	5
41	Probing the determinants of phosphorylated sugar-substrate binding for human sialic acid synthase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2257-2264.	2.3	4
42	Oxidative Phosphorylation as a Target Space for Tuberculosis: Success, Caution, and Future Directions. , 0, , 295-316.		4
43	The Synthesis and Anti-tumour Properties of Poly Ethoxy Ethyl Glycinamide (PEEG) Scaffolds with Multiple PD-1 Peptides Attached. <i>ChemMedChem</i> , 2020, 15, 1128-1138.	3.2	4
44	Structure of F ₁ -ATPase from the obligate anaerobe <i>Fusobacterium nucleatum</i> . <i>Open Biology</i> , 2019, 9, 190066.	3.6	3
45	Hinge Twists and Population Shifts Deliver Regulated Catalysis for ATP-PRT in Histidine Biosynthesis. <i>Biophysical Journal</i> , 2019, 116, 1887-1897.	0.5	3
46	Computational investigations of allostery in aromatic amino acid biosynthetic enzymes. <i>Biochemical Society Transactions</i> , 2021, 49, 415-429.	3.4	3
47	Substrate-mediated control of the conformation of an ancillary domain delivers a competent catalytic site for N-acetylneuraminic acid synthase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2054-2066.	2.6	2