Barry C Finzel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1802211/publications.pdf

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30	639	567144	580701
papers	citations	15 h-index	25 g-index

32	32	32	971
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bisubstrate Adenylation Inhibitors of Biotin Protein Ligase from Mycobacterium tuberculosis. Chemistry and Biology, 2011, 18, 1432-1441.	6.2	83
2	Inhibitors of HCV NS5B polymerase. Part 1: Evaluation of the southern region of (2Z)-2-(benzoylamino)-3-(5-phenyl-2-furyl)acrylic acid. Bioorganic and Medicinal Chemistry Letters, 2005, 15, 2481-2486.	1.0	77
3	Inhibition of Mycobacterium tuberculosis Transaminase BioA by Aryl Hydrazines and Hydrazides. ChemBioChem, 2014, 15, 575-586.	1.3	44
4	Target-Based Identification of Whole-Cell Active Inhibitors of Biotin Biosynthesis in Mycobacterium tuberculosis. Chemistry and Biology, 2015, 22, 76-86.	6.2	42
5	Targeting Mycobacterium tuberculosis Biotin Protein Ligase (MtBPL) with Nucleoside-Based Bisubstrate Adenylation Inhibitors. Journal of Medicinal Chemistry, 2015, 58, 7349-7369.	2.9	39
6	Mechanism-based Inactivation by Aromatization of the Transaminase BioA Involved in Biotin Biosynthesis in Mycobaterium tuberculosis. Journal of the American Chemical Society, 2011, 133, 18194-18201.	6.6	34
7	Structure-Based Optimization of Pyridoxal 5â€²-Phosphate-Dependent Transaminase Enzyme (BioA) Inhibitors that Target Biotin Biosynthesis in Mycobacterium tuberculosis. Journal of Medicinal Chemistry, 2017, 60, 5507-5520.	2.9	31
8	Fragment-Based Exploration of Binding Site Flexibility in Mycobacterium tuberculosis BioA. Journal of Medicinal Chemistry, 2015, 58, 5208-5217.	2.9	29
9	Identification of Novel Non-Hydroxamate Anthrax Toxin Lethal Factor Inhibitors by Topomeric Searching, Docking and Scoring, and in Vitro Screening. Journal of Chemical Information and Modeling, 2009, 49, 2726-2734.	2.5	26
10	Structural characterization of human histidine triad nucleotideâ€binding protein 2, a member of the histidine triad superfamily. FEBS Journal, 2013, 280, 3389-3398.	2.2	23
11	Use of differential scanning fluorimetry to optimize the purification and crystallization of PLP-dependent enzymes. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 596-600.	0.7	22
12	Caught before Released: Structural Mapping of the Reaction Trajectory for the Sofosbuvir Activating Enzyme, Human Histidine Triad Nucleotide Binding Protein 1 (hHint1). Biochemistry, 2017, 56, 3559-3570.	1.2	22
13	A Crystal Structure Based Guide to the Design of Human Histidine Triad Nucleotide Binding Protein 1 (hHint1) Activated ProTides. Molecular Pharmaceutics, 2017, 14, 3987-3997.	2.3	20
14	High-resolution crystal structures of alternate forms of the human CD44 hyaluronan-binding domain reveal a site for protein interaction. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1155-1161.	0.4	19
15	Anthrax toxin lethal factor domain 3 is highly mobile and responsive to ligand binding. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2813-2822.	2.5	16
16	[12] LORE: Exploiting database of known structures. Methods in Enzymology, 1997, 277, 230-242.	0.4	14
17	Conserved Core Substructures in the Overlay of Proteinâ€“Ligand Complexes. Journal of Chemical Information and Modeling, 2011, 51, 1931-1941.	2.5	13
18	The structure of the TOG-like domain ofDrosophila melanogasterMast/Orbit. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 723-729.	0.7	13

#	Article	IF	Citations
19	Design, Synthesis, and Characterization of Sulfamide and Sulfamate Nucleotidomimetic Inhibitors of hHint1. ACS Medicinal Chemistry Letters, 2016, 7, 780-784.	1.3	11
20	Inhibition of HINT1 Modulates Spinal Nociception and NMDA Evoked Behavior in Mice. ACS Chemical Neuroscience, 2019, 10, 4385-4393.	1.7	10
21	Structure and Functional Characterization of Human Histidine Triad Nucleotide-Binding Protein 1 Mutations Associated with Inherited Axonal Neuropathy with Neuromyotonia. Journal of Molecular Biology, 2018, 430, 2709-2721.	2.0	9
22	Structure-Based Design and Biological Evaluation of Novel Caspase-2 Inhibitors Based on the Peptide AcVDVAD-CHO and the Caspase-2-Mediated Tau Cleavage Sequence YKPVD314. ACS Pharmacology and Translational Science, 2022, 5, 20-40.	2.5	9
23	Rational Optimization of Mechanism-Based Inhibitors through Determination of the Microscopic Rate Constants of Inactivation. Journal of the American Chemical Society, 2017, 139, 7132-7135.	6.6	8
24	Inhibition by divalent metal ions of human histidine triad nucleotide binding protein1 (hHint1), a regulator of opioid analgesia and neuropathic pain. Biochemical and Biophysical Research Communications, 2017, 491, 760-766.	1.0	7
25	Probing the S2â€² Subsite of the Anthrax Toxin Lethal Factor Using Novel N-Alkylated Hydroxamates. Journal of Medicinal Chemistry, 2015, 58, 8723-8733.	2.9	6
26	Ligandâ€induced expansion of the S1â€² site in the anthrax toxin lethal factor. FEBS Letters, 2015, 589, 3836-3841.	1.3	4
27	Structural Characterization of the Human Cytosolic Malate Dehydrogenase I. ACS Omega, 2022, 7, 207-214.	1.6	3
28	Characterization of caspaseâ€2 inhibitors based on specific sites of caspaseâ€2â€mediated proteolysis. Archiv Der Pharmazie, 2022, 355, .	2.1	2
29	Rapid efficient macromolecular substructure searching in a cloud. , 2012, , .		1
30	Searching for Likeness in a Database of Macromolecular Complexes. Journal of Chemical Information and Modeling, 2013, 53, 2634-2647.	2.5	1