

# Barry C Finzel

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

639  
citations

566801

15  
h-index

580395

25  
g-index

32  
all docs

32  
docs citations

32  
times ranked

971  
citing authors

#	ARTICLE	IF	CITATIONS
1	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. <i>ACS Pharmacology and Translational Science</i> , 2022, 5, 20-40.	2.5	9
2	Structural Characterization of the Human Cytosolic Malate Dehydrogenase I. <i>ACS Omega</i> , 2022, 7, 207-214.	1.6	3
3	Characterization of caspase-2 inhibitors based on specific sites of caspase-2-mediated proteolysis. <i>Archiv Der Pharmazie</i> , 2022, 355, .	2.1	2
4	Inhibition of HINT1 Modulates Spinal Nociception and NMDA Evoked Behavior in Mice. <i>ACS Chemical Neuroscience</i> , 2019, 10, 4385-4393.	1.7	10
5	Structure and Functional Characterization of Human Histidine Triad Nucleotide-Binding Protein 1 Mutations Associated with Inherited Axonal Neuropathy with Neuromyotonia. <i>Journal of Molecular Biology</i> , 2018, 430, 2709-2721.	2.0	9
6	Rational Optimization of Mechanism-Based Inhibitors through Determination of the Microscopic Rate Constants of Inactivation. <i>Journal of the American Chemical Society</i> , 2017, 139, 7132-7135.	6.6	8
7	Structure-Based Optimization of Pyridoxal 5-Pyridoxal-5-phosphate-Dependent Transaminase Enzyme (BioA) Inhibitors that Target Biotin Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Medicinal Chemistry</i> , 2017, 60, 5507-5520.	2.9	31
8	A Crystal Structure Based Guide to the Design of Human Histidine Triad Nucleotide Binding Protein 1 (hHint1) Activated ProTides. <i>Molecular Pharmaceutics</i> , 2017, 14, 3987-3997.	2.3	20
9	Inhibition by divalent metal ions of human histidine triad nucleotide binding protein1 (hHint1), a regulator of opioid analgesia and neuropathic pain. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 760-766.	1.0	7
10	Caught before Released: Structural Mapping of the Reaction Trajectory for the Sofosbuvir Activating Enzyme, Human Histidine Triad Nucleotide Binding Protein 1 (hHint1). <i>Biochemistry</i> , 2017, 56, 3559-3570.	1.2	22
11	Design, Synthesis, and Characterization of Sulfamide and Sulfamate Nucleotidomimetic Inhibitors of hHint1. <i>ACS Medicinal Chemistry Letters</i> , 2016, 7, 780-784.	1.3	11
12	Ligand-Induced expansion of the S1 site in the anthrax toxin lethal factor. <i>FEBS Letters</i> , 2015, 589, 3836-3841.	1.3	4
13	Target-Based Identification of Whole-Cell Active Inhibitors of Biotin Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Chemistry and Biology</i> , 2015, 22, 76-86.	6.2	42
14	Fragment-Based Exploration of Binding Site Flexibility in <i>Mycobacterium tuberculosis</i> BioA. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 5208-5217.	2.9	29
15	Probing the S2 Subsite of the Anthrax Toxin Lethal Factor Using Novel N-Alkylated Hydroxamates. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 8723-8733.	2.9	6
16	Targeting <i>Mycobacterium tuberculosis</i> Biotin Protein Ligase (MtBPL) with Nucleoside-Based Bisubstrate Adenylation Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 7349-7369.	2.9	39
17	High-resolution crystal structures of alternate forms of the human CD44 hyaluronan-binding domain reveal a site for protein interaction. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1155-1161.	0.4	19
18	Inhibition of <i>Mycobacterium tuberculosis</i> Transaminase BioA by Aryl Hydrazines and Hydrazides. <i>ChemBioChem</i> , 2014, 15, 575-586.	1.3	44

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19	Anthrax toxin lethal factor domain 3 is highly mobile and responsive to ligand binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2813-2822.	2.5	16
20	Searching for Likeness in a Database of Macromolecular Complexes. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2634-2647.	2.5	1
21	The structure of the TOG-like domain of <i>Drosophila melanogaster</i> Mast/Orbit. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 723-729.	0.7	13
22	Structural characterization of human histidine triad nucleotide-binding protein 2, a member of the histidine triad superfamily. <i>FEBS Journal</i> , 2013, 280, 3389-3398.	2.2	23
23	Rapid efficient macromolecular substructure searching in a cloud. , 2012, , .		1
24	Use of differential scanning fluorimetry to optimize the purification and crystallization of PLP-dependent enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 596-600.	0.7	22
25	Conserved Core Substructures in the Overlay of Protein-Ligand Complexes. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 1931-1941.	2.5	13
26	Mechanism-based Inactivation by Aromatization of the Transaminase BioA Involved in Biotin Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of the American Chemical Society</i> , 2011, 133, 18194-18201.	6.6	34
27	Bisubstrate Adenylation Inhibitors of Biotin Protein Ligase from <i>Mycobacterium tuberculosis</i> . <i>Chemistry and Biology</i> , 2011, 18, 1432-1441.	6.2	83
28	Identification of Novel Non-Hydroxamate Anthrax Toxin Lethal Factor Inhibitors by Topomeric Searching, Docking and Scoring, and in Vitro Screening. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2726-2734.	2.5	26
29	Inhibitors of HCV NS5B polymerase. Part 1: Evaluation of the southern region of (Z)-2-(benzoylamino)-3-(5-phenyl-2-furyl)acrylic acid. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2005, 15, 2481-2486.	1.0	77
30	[12] LORE: Exploiting database of known structures. <i>Methods in Enzymology</i> , 1997, 277, 230-242.	0.4	14