

Roberto A Steiner

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

10,259
citations

279798

23
h-index

276875

41
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46
all docs

46
docs citations

46
times ranked

17845
citing authors

#	ARTICLE	IF	CITATIONS
1	Joint neutron/X-ray crystal structure of a mechanistically relevant complex of perdeuterated urate oxidase and simulations provide insight into the hydration step of catalysis. <i>IUCr</i> , 2021, 8, 46-59.	2.2	6
2	Molecular mechanism for kinesin-1 direct membrane recognition. <i>Science Advances</i> , 2021, 7, .	10.3	5
3	Fragment-linking peptide design yields a high-affinity ligand for microtubule-based transport. <i>Cell Chemical Biology</i> , 2021, 28, 1347-1355.e5.	5.2	7
4	β 4/ β 9 Integrins Coordinate Epithelial Cell Migration Through Local Suppression of MAP Kinase Signaling Pathways. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 750771.	3.7	5
5	Coagulation Factor XIII-A Subunit Missense Mutation in the Pathobiology of Autosomal Dominant Multiple Dermatofibromas. <i>Journal of Investigative Dermatology</i> , 2020, 140, 624-635.e7.	0.7	12
6	Structural basis for isoform-specific kinesin-1 recognition of Y-acidic cargo adaptors. <i>ELife</i> , 2018, 7, .	6.0	26
7	Keep it together: restraints in crystallographic refinement of macromolecule–ligand complexes. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 93-102.	2.3	19
8	SKIP controls lysosome positioning using a composite kinesin-1 heavy and light chain binding domain. <i>Journal of Cell Science</i> , 2017, 130, 1637-1651.	2.0	25
9	Binding of Myomesin to Obscurin-Like-1 at the Muscle M-Band Provides a Strategy for Isoform-Specific Mechanical Protection. <i>Structure</i> , 2017, 25, 107-120.	3.3	25
10	Online Raman spectroscopy for structural biology on beamline ID29 of the ESRF. <i>Journal of Structural Biology</i> , 2017, 200, 124-127.	2.8	4
11	A small-molecule activator of kinesin-1 drives remodeling of the microtubule network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13738-13743.	7.1	57
12	The Cannabinoid Receptor Interacting Proteins 1 of zebrafish are not required for morphological development, viability or fertility. <i>Scientific Reports</i> , 2017, 7, 4858.	3.3	14
13	Targeted redox inhibition of protein phosphatase 1 by Nox4 regulates eIF2 α -mediated stress signaling. <i>EMBO Journal</i> , 2016, 35, 319-334.	7.8	91
14	The Dynamic Localization of Cytoplasmic Dynein in Neurons Is Driven by Kinesin-1. <i>Neuron</i> , 2016, 90, 1000-1015.	8.1	95
15	New insight into cofactor-free oxygenation from combined experimental and computational approaches. <i>Current Opinion in Structural Biology</i> , 2016, 41, 109-118.	5.7	31
16	The light chains of kinesin-1 are autoinhibited. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2418-2423.	7.1	50
17	Catalytic Mechanism of Cofactor-Free Dioxygenases and How They Circumvent Spin-Forbidden Oxygenation of Their Substrates. <i>Journal of the American Chemical Society</i> , 2015, 137, 7474-7487.	13.7	70
18	The Crystal Structure of the Human Titin:Obscurin Complex Reveals a Conserved yet Specific Muscle M-Band Zipper Module. <i>Journal of Molecular Biology</i> , 2015, 427, 718-736.	4.2	20

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19	Direct Evidence for a Peroxide Intermediate and a Reactive Enzymeâ€‘Substrateâ€‘Dioxygen Configuration in a Cofactorâ€‘free Oxidase. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13710-13714.	13.8	43
20	Origin of the Proton-transfer Step in the Cofactor-free (1H)-3-Hydroxy-4-oxoquinaldine 2,4-Dioxygenase. <i>Journal of Biological Chemistry</i> , 2014, 289, 8620-8632.	3.4	31
21	Structural Basis for Kinesin-1:Cargo Recognition. <i>Science</i> , 2013, 340, 356-359.	12.6	85
22	Model building, refinement and validation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 325-327.	2.5	1
23	<i>REFMAC</i>5 for the refinement of macromolecular crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 355-367.	2.5	7,247
24	Cofactor-independent oxidases and oxygenases. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 791-804.	3.6	122
25	Structural and functional studies on the extracellular domain of BST2/tetherin in reduced and oxidized conformations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17951-17956.	7.1	92
26	Structural basis for cofactor-independent dioxygenation of <i>N</i>-heteroaromatic compounds at the β -hydrolase fold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 657-662.	7.1	77
27	Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2908-2913.	7.1	60
28	Crystallization and preliminary X-ray analysis of 1H-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase from <i>Arthrobacter nitroguajacolicus</i> R461a: a cofactor-devoid dioxygenase of the β -hydrolase-fold superfamily. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 382-385.	0.7	9
29	Variable role of ions in two drug intercalation complexes of DNA. <i>Journal of Biological Inorganic Chemistry</i> , 2005, 10, 476-482.	2.6	10
30	DNA variability in five crystal structures of d(CGCAATTGCG). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 680-685.	2.5	14
31	<i>REFMAC</i>5 dictionary: organization of prior chemical knowledge and guidelines for its use. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2184-2195.	2.5	1,207
32	Fisher's information in maximum-likelihood macromolecular crystallographic refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2114-2124.	2.5	57
33	Single-Crystal EPR Study at 95GHz of the Type 2 Copper Site of the Inhibitor-Bound Quercetin 2,3-Dioxygenase. <i>Biophysical Journal</i> , 2003, 85, 4047-4054.	0.5	8
34	Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: A Inhibition, Ordering Effect, and Mechanistic Insightsâ€. <i>Biochemistry</i> , 2002, 41, 7955-7962.	2.5	73
35	Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 2. X-ray Absorption Studies of Native Enzyme and Anaerobic Complexes with the Substrates Quercetin and Myricetinâ€. <i>Biochemistry</i> , 2002, 41, 7963-7968.	2.5	37
36	Anaerobic enzyme*substrate structures provide insight into the reaction mechanism of the copper-dependent quercetin 2,3-dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16625-16630.	7.1	170

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37	Crystal Structure of the Copper-Containing Quercetin 2,3-Dioxygenase from <i>Aspergillus japonicus</i> . <i>Structure</i> , 2002, 10, 259-268.	3.3	216
38	EPR characterization of the mononuclear Cu-containing <i>Aspergillus japonicus</i> quercetin 2,3-dioxygenase reveals dramatic changes upon anaerobic binding of substrates. <i>FEBS Journal</i> , 2002, 269, 2971-2979.	0.2	87
39	X-ray structure of bovine pancreatic phospholipase A2 at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 516-526.	2.5	26
40	1,3-dipolar cycloaddition of phenyl azide to norbornene in aqueous solutions. <i>Tetrahedron Letters</i> , 1995, 36, 5389-5392.	1.4	15