Roberto A Steiner

List of Publications by Year in descending order

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40 papers

10,259 citations

279798 23 h-index 276875 41 g-index

46 all docs

46 docs citations

46 times ranked

17845 citing authors

#	Article	IF	CITATIONS
1	$\langle i \rangle$ REFMAC $\langle i \rangle$ 5 for the refinement of macromolecular crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 355-367.	2.5	7,247
2	<i>REFMAC</i> 5 dictionary: organization of prior chemical knowledge and guidelines for its use. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2184-2195.	2.5	1,207
3	Crystal Structure of the Copper-Containing Quercetin 2,3-Dioxygenase from Aspergillus japonicus. Structure, 2002, 10, 259-268.	3.3	216
4	Anaerobic enzyme*substrate structures provide insight into the reaction mechanism of the copper-dependent quercetin 2,3-dioxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16625-16630.	7.1	170
5	Cofactor-independent oxidases and oxygenases. Applied Microbiology and Biotechnology, 2010, 86, 791-804.	3.6	122
6	The Dynamic Localization of Cytoplasmic Dynein in Neurons Is Driven by Kinesin-1. Neuron, 2016, 90, 1000-1015.	8.1	95
7	Structural and functional studies on the extracellular domain of BST2/tetherin in reduced and oxidized conformations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17951-17956.	7.1	92
8	Targeted redox inhibition of protein phosphatase 1 by Nox4 regulates <scp>elF</scp> 2αâ€mediated stress signaling. EMBO Journal, 2016, 35, 319-334.	7.8	91
9	EPR characterization of the mononuclear Cu-containing Aspergillus japonicus quercetin 2,3-dioxygenase reveals dramatic changes upon anaerobic binding of substrates. FEBS Journal, 2002, 269, 2971-2979.	0.2	87
10	Structural Basis for Kinesin-1:Cargo Recognition. Science, 2013, 340, 356-359.		o-
10	Structural basis for Killesiir I. Cargo Recognition. Science, 2013, 340, 330-337.	12.6	85
11	Structural basis for cofactor-independent dioxygenation of <i>N</i> -heteroaromatic compounds at the α/β-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662.	7.1	77
	Structural basis for cofactor-independent dioxygenation of $\langle i \rangle N \langle i \rangle$ -heteroaromatic compounds at the $\hat{l} \pm \hat{l}^2$ -hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America,		
11	Structural basis for cofactor-independent dioxygenation of <i>N</i> -heteroaromatic compounds at the α/β-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662. Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography:Â Inhibition, Ordering Effect, and Mechanistic	7.1	77
11 12	Structural basis for cofactor-independent dioxygenation of ⟨i>N⟨li⟩ -heteroaromatic compounds at the α/β-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662. Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: Inhibition, Ordering Effect, and Mechanistic Insightsâ€. Biochemistry, 2002, 41, 7955-7962. Catalytic Mechanism of Cofactor-Free Dioxygenases and How They Circumvent Spin-Forbidden	7.1	77
11 12 13	Structural basis for cofactor-independent dioxygenation of ⟨i>N⟨li⟩ -heteroaromatic compounds at the α/β-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662. Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: Inhibition, Ordering Effect, and Mechanistic Insightsâ€. Biochemistry, 2002, 41, 7955-7962. Catalytic Mechanism of Cofactor-Free Dioxygenases and How They Circumvent Spin-Forbidden Oxygenation of Their Substrates. Journal of the American Chemical Society, 2015, 137, 7474-7487. Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex.	7.1 2.5 13.7	77 73 70
11 12 13	Structural basis for cofactor-independent dioxygenation of <i>N</i> -heteroaromatic compounds at the î±ſ²-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662. Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: Inhibition, Ordering Effect, and Mechanistic Insightsâ€. Biochemistry, 2002, 41, 7955-7962. Catalytic Mechanism of Cofactor-Free Dioxygenases and How They Circumvent Spin-Forbidden Oxygenation of Their Substrates. Journal of the American Chemical Society, 2015, 137, 7474-7487. Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2908-2913. Fisher's information in maximum-likelihood macromolecular crystallographic refinement. Acta	7.1 2.5 13.7 7.1	77 73 70 60
11 12 13 14	Structural basis for cofactor-independent dioxygenation of ⟨i>N⟨ i⟩ -heteroaromatic compounds at the α l²-hydrolase fold. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 657-662. Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: Inhibition, Ordering Effect, and Mechanistic Insightsâ€. Biochemistry, 2002, 41, 7955-7962. Catalytic Mechanism of Cofactor-Free Dioxygenases and How They Circumvent Spin-Forbidden Oxygenation of Their Substrates. Journal of the American Chemical Society, 2015, 137, 7474-7487. Structural insight into M-band assembly and mechanics from the titin-obscurin-like-1 complex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2908-2913. Fisher's information in maximum-likelihood macromolecular crystallographic refinement. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2114-2124. A small-molecule activator of kinesin-1 drives remodeling of the microtubule network. Proceedings of	7.1 2.5 13.7 7.1 2.5	77 73 70 60 57

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19	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€. Biochemistry, 2002, 41, 7963-7968.	2.5	37
20	Origin of the Proton-transfer Step in the Cofactor-free (1H)-3-Hydroxy-4-oxoquinaldine 2,4-Dioxygenase. Journal of Biological Chemistry, 2014, 289, 8620-8632.	3.4	31
21	New insight into cofactor-free oxygenation from combined experimental and computational approaches. Current Opinion in Structural Biology, 2016, 41, 109-118.	5.7	31
22	X-ray structure of bovine pancreatic phospholipase A2at atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 516-526.	2.5	26
23	Structural basis for isoform-specific kinesin-1 recognition of Y-acidic cargo adaptors. ELife, 2018, 7, .	6.0	26
24	SKIP controls lysosome positioning using a composite kinesin-1 heavy and light chain binding domain. Journal of Cell Science, 2017, 130, 1637-1651.	2.0	25
25	Binding of Myomesin to Obscurin-Like-1 at the Muscle M-Band Provides a Strategy for Isoform-Specific Mechanical Protection. Structure, 2017, 25, 107-120.	3.3	25
26	The Crystal Structure of the Human Titin:Obscurin Complex Reveals a Conserved yet Specific Muscle M-Band Zipper Module. Journal of Molecular Biology, 2015, 427, 718-736.	4.2	20
27	Keep it together: restraints in crystallographic refinement of macromolecule–ligand complexes. Acta Crystallographica Section D: Structural Biology, 2017, 73, 93-102.	2.3	19
28	1,3-dipolar cycloaddition of phenyl azide to norbornene in aqueous solutions. Tetrahedron Letters, 1995, 36, 5389-5392.	1.4	15
29	DNA variability in five crystal structures of d(CGCAATTGCG). Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 680-685.	2.5	14
30	The Cannabinoid Receptor Interacting Proteins 1 of zebrafish are not required for morphological development, viability or fertility. Scientific Reports, 2017, 7, 4858.	3.3	14
31	Coagulation Factor XIII-A Subunit Missense Mutation in the Pathobiology of Autosomal Dominant Multiple Dermatofibromas. Journal of Investigative Dermatology, 2020, 140, 624-635.e7.	0.7	12
32	Variable role of ions in two drug intercalation complexes of DNA. Journal of Biological Inorganic Chemistry, 2005, 10, 476-482.	2.6	10
33	Crystallization and preliminary X-ray analysis of 1H-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase from Arthrobacter nitroguajacolicus $\mathbb{A}^{1}/461$ a: a cofactor-devoid dioxygenase of the \mathbb{I}^{2} -hydrolase-fold superfamily. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 382-385.	0.7	9
34	Single-Crystal EPR Study at 95GHz of the Type 2 Copper Site of the Inhibitor-Bound Quercetin 2,3-Dioxygenase. Biophysical Journal, 2003, 85, 4047-4054.	0.5	8
35	Fragment-linking peptide design yields a high-affinity ligand for microtubule-based transport. Cell Chemical Biology, 2021, 28, 1347-1355.e5.	5.2	7
36	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. IUCrJ, 2021, 8, 46-59.	2.2	6

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37	Molecular mechanism for kinesin-1 direct membrane recognition. Science Advances, 2021, 7, .	10.3	5
38	$\hat{l}\pm 4/\hat{l}\pm 9$ Integrins Coordinate Epithelial Cell Migration Through Local Suppression of MAP Kinase Signaling Pathways. Frontiers in Cell and Developmental Biology, 2021, 9, 750771.	3.7	5
39	Online Raman spectroscopy for structural biology on beamline ID29 of the ESRF. Journal of Structural Biology, 2017, 200, 124-127.	2.8	4
40	Model building, refinement and validation. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 325-327.	2.5	1