

Ray Yu-Ruei Wang

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

4,168
citations

687363

13
h-index

1058476

14
g-index

21
all docs

21
docs citations

21
times ranked

7474
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Comparative Modeling with RosettaCM. <i>Structure</i> , 2013, 21, 1735-1742.	3.3	1,010
2	EMRinger: side chain-directed model and map validation for 3D cryo-electron microscopy. <i>Nature Methods</i> , 2015, 12, 943-946.	19.0	799
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
4	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. <i>ELife</i> , 2016, 5, .	6.0	407
5	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. <i>Science</i> , 2016, 352, 1542-1547.	12.6	354
6	Structural basis of mitochondrial receptor binding and constriction by DRP1. <i>Nature</i> , 2018, 558, 401-405.	27.8	219
7	Structure of the Type VI Secretion System Contractile Sheath. <i>Cell</i> , 2015, 160, 952-962.	28.9	216
8	De novo protein structure determination from near-atomic-resolution cryo-EM maps. <i>Nature Methods</i> , 2015, 12, 335-338.	19.0	172
9	Improved de novo structure prediction in <sc>CASP</sc>11 by incorporating coevolution information into Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 67-75.	2.6	96
10	Structure of Hsp90-Hsp70-Hop-GR reveals the Hsp90 client-loading mechanism. <i>Nature</i> , 2022, 601, 460-464.	27.8	90
11	One contact for every twelve residues allows robust and accurate topology-level protein structure modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 208-218.	2.6	87
12	Structure of Hsp90-p23-GR reveals the Hsp90 client-remodelling mechanism. <i>Nature</i> , 2022, 601, 465-469.	27.8	80
13	Unique double-ring structure of the peroxisomal Pex1/Pex6 ATPase complex revealed by cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4017-25.	7.1	72
14	Structure prediction using sparse simulated <sc>NOE</sc> restraints with Rosetta in <sc>CASP</sc>11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 181-188.	2.6	16