Ray Yu-Ruei Wang

List of Publications by Year
in descending order

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	Structure of Hsp90–Hsp70–Hop–GR reveals the Hsp90 client-loading mechanism. Nature, 2022, 601, 460-464.	27.8	90
2	Structure of Hsp90–p23–GR reveals the Hsp90 client-remodelling mechanism. Nature, 2022, 601, 465-469.	27.8	80
3	Macromolecular modeling and design in Rosetta: recent methods and frameworks. Nature Methods, 2020, 17, 665-680.	19.0	513
4	Structural basis of mitochondrial receptor binding and constriction by DRP1. Nature, 2018, 558, 401-405.	27.8	219
5	Structure prediction using sparse simulated NOE restraints with Rosetta in CASP11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 181-188.	2.6	16
6	Improved de novo structure prediction in CASP11 by incorporating coevolution information into Rosetta. Proteins: Structure, Function and Bioinformatics, 2016, 84, 67-75.	2.6	96
7	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. Science, 2016, 352, 1542-1547.	12.6	354
8	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. ELife, 2016, 5, .	6.0	407
9	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	28.9	216
10	De novo protein structure determination from near-atomic-resolution cryo-EM maps. Nature Methods, 2015, 12, 335-338.	19.0	172
11	Unique double-ring structure of the peroxisomal Pex1/Pex6 ATPase complex revealed by cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4017-25.	7.1	72
12	EMRinger: side chain–directed model and map validation for 3D cryo-electron microscopy. Nature Methods, 2015, 12, 943-946.	19.0	799
13	One contact for every twelve residues allows robust and accurate topology–level protein structure modeling. Proteins: Structure, Function and Bioinformatics, 2014, 82, 208-218.	2.6	87
14	High-Resolution Comparative Modeling with RosettaCM. Structure, 2013, 21, 1735-1742.	3.3	1,010