

# Hui-Ting Chou

## List of Publications by Year in descending order

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18  
papers

1,403  
citations

623188

14  
h-index

887659

17  
g-index

19  
all docs

19  
docs citations

19  
times ranked

2658  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structures of the human GATOR1-Rag-Ragulator complex reveal a spatial-constraint regulated GAP mechanism. <i>Molecular Cell</i> , 2022, 82, 1836-1849.e5.	4.5	19
2	Cryo-EM structures of the Human GATOR1-Rag-Ragulator Complex Reveal a Spatial-Constraint Regulated GAP Mechanism. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
3	Structural insight into the <i>Staphylococcus aureus</i> ATP-driven exporter of virulent peptide toxins. <i>Science Advances</i> , 2020, 6, .	4.7	9
4	The structural basis of Rubisco phase separation in the pyrenoid. <i>Nature Plants</i> , 2020, 6, 1480-1490.	4.7	68
5	The Molecular Architecture of Native BBSome Obtained by an Integrated Structural Approach. <i>Structure</i> , 2019, 27, 1384-1394.e4.	1.6	51
6	Cryo-EM Structure of the Human FLCN-FNIP2-Rag-Ragulator Complex. <i>Cell</i> , 2019, 179, 1319-1329.e8.	13.5	98
7	Rac1 GTPase activates the WAVE regulatory complex through two distinct binding sites. <i>ELife</i> , 2017, 6, .	2.8	129
8	Molecular architecture of the complete COG tethering complex. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 758-760.	3.6	47
9	CATCHR, HOPS and CORVET tethering complexes share a similar architecture. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 761-763.	3.6	84
10	The EM structure of the TRAPPIII complex leads to the identification of a requirement for COPII vesicles on the macroautophagy pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19432-19437.	3.3	135
11	Ypt1 recruits the Atg1 kinase to the preautophagosomal structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9800-9805.	3.3	112
12	Membrane activity of a C-reactive protein. <i>FEBS Letters</i> , 2009, 583, 1001-1005.	1.3	6
13	Crystal Structures of Limulus SAP-Like Pentraxin Reveal Two Molecular Aggregations. <i>Journal of Molecular Biology</i> , 2009, 386, 1240-1254.	2.0	17
14	The fold of $\beta$ -synuclein fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8637-8642.	3.3	499
15	Structural and Kinetic Studies of Induced Fit in Xylulose Kinase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2007, 365, 783-798.	2.0	37
16	The Structure of the Prokaryotic Cyclic Nucleotide-Modulated Potassium Channel MloK1 at 16 Å Resolution. <i>Structure</i> , 2007, 15, 1053-1064.	1.6	51
17	Structure of the Subunit Binding Domain and Dynamics of the Di-domain Region from the Core of Human Branched Chain $\beta$ -Ketoacid Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 28345-28353.	1.6	12
18	Solution Structure and Dynamics of the Lipoic Acid-bearing Domain of Human Mitochondrial Branched-chain $\beta$ -Keto Acid Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2002, 277, 15865-15873.	1.6	27