

# Chris Soon Heng Tan

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

2,109  
citations

394421

19  
h-index

434195

31  
g-index

32  
all docs

32  
docs citations

32  
times ranked

3416  
citing authors

#	ARTICLE	IF	CITATIONS
1	ProSAP: a GUI software tool for statistical analysis and assessment of thermal stability data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	9
2	Toosendanin, a late-stage autophagy inhibitor, sensitizes triple-negative breast cancer to irinotecan chemotherapy. <i>Chinese Medicine</i> , 2022, 17, 55.	4.0	10
3	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <i>Analytical Chemistry</i> , 2021, 93, 598-619.	6.5	17
4	Recent progress in mass spectrometry-based strategies for elucidating protein-protein interactions. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 5325-5339.	5.4	53
5	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. <i>Science</i> , 2018, 359, 1170-1177.	12.6	161
6	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. <i>PLoS ONE</i> , 2018, 13, e0208273.	2.5	41
7	Databases and Computational Tools for Evolutionary Analysis of Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2017, 1636, 475-484.	0.9	2
8	The RNA-binding protein HuR/ELAVL1 regulates IFN $\alpha$ 2 mRNA abundance and the type I IFN response. <i>European Journal of Immunology</i> , 2015, 45, 1500-1511.	2.9	49
9	Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. <i>Nature Methods</i> , 2015, 12, 1055-1057.	19.0	183
10	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	9.6	296
11	Mutational properties of amino acid residues: implications for evolvability of phosphorylatable residues. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 2584-2593.	4.0	43
12	Sequence-Specific Recognition of a PxLPxI/L Motif by an Ankyrin Repeat Tumbler Lock. <i>Science Signaling</i> , 2012, 5, ra39.	3.6	42
13	Phosphorylation sites of higher stoichiometry are more conserved. <i>Nature Methods</i> , 2012, 9, 317-317.	19.0	15
14	Response to Comment on "Positive Selection of Tyrosine Loss in Metazoan Evolution". <i>Science</i> , 2011, 332, 917-917.	12.6	15
15	Sequence, Structure, and Network Evolution of Protein Phosphorylation Meeting information: Keystone Symposium: The Evolution of Protein Phosphorylation, 23 to 27 January 2011, Keystone, CO, USA. <i>Science Signaling</i> , 2011, 4, mr6.	3.6	17
16	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domain-peptide interaction from primary sequence. <i>Bioinformatics</i> , 2011, 27, 383-390.	4.1	114
17	A Mitotic Phosphorylation Feedback Network Connects Cdk1, Plk1, 53BP1, and Chk2 to Inactivate the G2/M DNA Damage Checkpoint. <i>PLoS Biology</i> , 2010, 8, e1000287.	5.6	201
18	Roles of "junk phosphorylation" in modulating biomolecular association of phosphorylated proteins?. <i>Cell Cycle</i> , 2010, 9, 1276-1280.	2.6	28

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19	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. <i>Science Signaling</i> , 2009, 2, ra39.	3.6	171
20	Experimental and computational tools useful for (re)construction of dynamic kinase-substrate networks. <i>Proteomics</i> , 2009, 9, 5233-5242.	2.2	19
21	Positive Selection of Tyrosine Loss in Metazoan Evolution. <i>Science</i> , 2009, 325, 1686-1688.	12.6	91
22	PPiClust: EFFICIENT CLUSTERING OF 3D PROTEIN-PROTEIN INTERACTION INTERFACES. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 415-433.	0.8	8
23	Challenges in biological literature mining for online discovery of molecular interaction pathways. <i>International Journal of Computer Applications in Technology</i> , 2006, 27, 259.	0.5	0
24	Improving domain-based protein interaction prediction using biologically-significant negative dataset. <i>International Journal of Data Mining and Bioinformatics</i> , 2006, 1, 138.	0.1	18
25	A correlated motif approach for finding short linear motifs from protein interaction networks. <i>BMC Bioinformatics</i> , 2006, 7, 502.	2.6	40
26	Recognition of protein/gene names from text using an ensemble of classifiers. <i>BMC Bioinformatics</i> , 2005, 6, S7.	2.6	65
27	Interaction graph mining for protein complexes using local clique merging. <i>Genome Informatics</i> , 2005, 16, 260-9.	0.4	48
28	ADVICE: Automated Detection and Validation of Interaction by Co-Evolution. <i>Nucleic Acids Research</i> , 2004, 32, W69-W72.	14.5	45
29	DISCOVERING PROTEIN-PROTEIN INTERACTIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 711-741.	0.8	11
30	InterDom: a database of putative interacting protein domains for validating predicted protein interactions and complexes. <i>Nucleic Acids Research</i> , 2003, 31, 251-254.	14.5	130
31	Integrative approach for computationally inferring protein domain interactions. <i>Bioinformatics</i> , 2003, 19, 923-929.	4.1	159
32	On combining multiple microarray studies for improved functional classification by whole-dataset feature selection. <i>Genome Informatics</i> , 2003, 14, 44-53.	0.4	8