Chris Soon Heng Tan

List of Publications by Year
in descending order

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	Genome of Acanthamoeba castellanii highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	9.6	296
2	A Mitotic Phosphorylation Feedback Network Connects Cdk1, Plk1, 53BP1, and Chk2 to Inactivate the G2/M DNA Damage Checkpoint. PLoS Biology, 2010, 8, e1000287.	5.6	201
3	Proteome-wide drug and metabolite interaction mapping by thermal-stability profiling. Nature Methods, 2015, 12, 1055-1057.	19.0	183
4	Comparative Analysis Reveals Conserved Protein Phosphorylation Networks Implicated in Multiple Diseases. Science Signaling, 2009, 2, ra39.	3.6	171
5	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. Science, 2018, 359, 1170-1177.	12.6	161
6	Integrative approach for computationally inferring protein domain interactions. Bioinformatics, 2003, 19, 923-929.	4.1	159
7	InterDom: a database of putative interacting protein domains for validating predicted protein interactions and complexes. Nucleic Acids Research, 2003, 31, 251-254.	14.5	130
8	A regression framework incorporating quantitative and negative interaction data improves quantitative prediction of PDZ domain–peptide interaction from primary sequence. Bioinformatics, 2011, 27, 383-390.	4.1	114
9	Positive Selection of Tyrosine Loss in Metazoan Evolution. Science, 2009, 325, 1686-1688.	12.6	91
10	Recognition of protein/gene names from text using an ensemble of classifiers. BMC Bioinformatics, 2005, 6, S7.	2.6	65
11	Recent progress in mass spectrometry-based strategies for elucidating protein–protein interactions. Cellular and Molecular Life Sciences, 2021, 78, 5325-5339.	5.4	53
12	The RNA-binding protein HuR/ELAVL1 regulates IFN-β mRNA abundance and the type I IFN response. European Journal of Immunology, 2015, 45, 1500-1511.	2.9	49
13	Interaction graph mining for protein complexes using local clique merging. Genome Informatics, 2005, 16, 260-9.	0.4	48
14	ADVICE: Automated Detection and Validation of Interaction by Co-Evolution. Nucleic Acids Research, 2004, 32, W69-W72.	14.5	45
15	Mutational properties of amino acid residues: implications for evolvability of phosphorylatable residues. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2584-2593.	4.0	43
16	Sequence-Specific Recognition of a PxLPxI/L Motif by an Ankyrin Repeat Tumbler Lock. Science Signaling, 2012, 5, ra39.	3.6	42
17	An efficient proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions. PLoS ONE, 2018, 13, e0208273.	2.5	41
18	A correlated motif approach for finding short linear motifs from protein interaction networks. BMC Bioinformatics, 2006, 7, 502.	2.6	40

#	ARTICLE	IF	CITATIONS
19	Roles of â€œjunk phosphorylationâ€•in modulating biomolecular association of phosphorylated proteins?. Cell Cycle, 2010, 9, 1276-1280.	2.6	28
20	Experimental and computational tools useful for (re)construction of dynamic kinaseâ€"substrate networks. Proteomics, 2009, 9, 5233-5242.	2.2	19
21	Improving domain-based protein interaction prediction using biologically-significant negative dataset. International Journal of Data Mining and Bioinformatics, 2006, 1, 138.	0.1	18
22	Sequence, Structure, and Network Evolution of Protein PhosphorylationMeeting information: Keystone Symposium: The Evolution of Protein Phosphorylation, 23 to 27 January 2011, Keystone, CO, USA. Science Signaling, 2011, 4, mr6.	3.6	17
23	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. Analytical Chemistry, 2021, 93, 598-619.	6.5	17
24	Response to Comment on â€œPositive Selection of Tyrosine Loss in Metazoan Evolutionâ€• Science, 2011, 332, 917-917.	12.6	15
25	Phosphorylation sites of higher stoichiometry are more conserved. Nature Methods, 2012, 9, 317-317.	19.0	15
26	DISCOVERING PROTEINâ€"PROTEIN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2004, 01, 711-741.	0.8	11
27	Toosendanin, a late-stage autophagy inhibitor, sensitizes triple-negative breast cancer to irinotecan chemotherapy. Chinese Medicine, 2022, 17, 55.	4.0	10
28	ProSAP: a GUI software tool for statistical analysis and assessment of thermal stability data. Briefings in Bioinformatics, 2022, 23, .	6.5	9
29	PPiClust: EFFICIENT CLUSTERING OF 3D PROTEINâ€"PROTEIN INTERACTION INTERFACES. Journal of Bioinformatics and Computational Biology, 2008, 06, 415-433.	0.8	8
30	On combining multiple microarray studies for improved functional classification by whole-dataset feature selection. Genome Informatics, 2003, 14, 44-53.	0.4	8
31	Databases and Computational Tools for Evolutionary Analysis of Protein Phosphorylation. Methods in Molecular Biology, 2017, 1636, 475-484.	0.9	2
32	Challenges in biological literature mining for online discovery of molecular interaction pathways. International Journal of Computer Applications in Technology, 2006, 27, 259.	0.5	0