

Nurcan Tuncbag

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

2,607
citations

361413

20
h-index

265206

42
g-index

52
all docs

52
docs citations

52
times ranked

3489
citing authors

#	ARTICLE	IF	CITATIONS
1	The PI3K/AKT/mTOR interactive pathway. <i>Molecular BioSystems</i> , 2015, 11, 1946-1954.	2.9	379
2	Predicting Protein-Protein Interactions from the Molecular to the Proteome Level. <i>Chemical Reviews</i> , 2016, 116, 4884-4909.	47.7	289
3	Predicting protein-protein interactions on a proteome scale by matching evolutionary and structural similarities at interfaces using PRISM. <i>Nature Protocols</i> , 2011, 6, 1341-1354.	12.0	253
4	Identification of computational hot spots in protein interfaces: combining solvent accessibility and inter-residue potentials improves the accuracy. <i>Bioinformatics</i> , 2009, 25, 1513-1520.	4.1	239
5	HotPoint: hot spot prediction server for protein interfaces. <i>Nucleic Acids Research</i> , 2010, 38, W402-W406.	14.5	185
6	A survey of available tools and web servers for analysis of protein-protein interactions and interfaces. <i>Briefings in Bioinformatics</i> , 2008, 10, 217-232.	6.5	140
7	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. <i>PLoS Computational Biology</i> , 2016, 12, e1004879.	3.2	123
8	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Journal of Computational Biology</i> , 2013, 20, 124-136.	1.6	108
9	Architectures and Functional Coverage of Protein-Protein Interfaces. <i>Journal of Molecular Biology</i> , 2008, 381, 785-802.	4.2	106
10	HotSprint: database of computational hot spots in protein interfaces. <i>Nucleic Acids Research</i> , 2007, 36, D662-D666.	14.5	102
11	Genome-Scale Networks Link Neurodegenerative Disease Genes to \pm -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14.	6.2	102
12	Towards inferring time dimensionality in protein-protein interaction networks by integrating structures: the p53 example. <i>Molecular BioSystems</i> , 2009, 5, 1770.	2.9	76
13	Analysis and network representation of hotspots in protein interfaces using minimum cut trees. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2283-2294.	2.6	58
14	Prediction of protein-protein interactions: unifying evolution and structure at protein interfaces. <i>Physical Biology</i> , 2011, 8, 035006.	1.8	58
15	SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. <i>Nucleic Acids Research</i> , 2012, 40, W505-W509.	14.5	58
16	Fast and accurate modeling of protein-protein interactions by combining template-interface-based docking with flexible refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1239-1249.	2.6	43
17	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. <i>MBio</i> , 2017, 8, .	4.1	42
18	Systems-level Analysis Reveals Multiple Modulators of Epithelial-mesenchymal Transition and Identifies DNAJB4 and CD81 as Novel Metastasis Inducers in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1756-1771.	3.8	29

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19	Characterization and Prediction of Protein Interfaces to Infer Protein-Protein Interaction Networks. <i>Current Pharmaceutical Biotechnology</i> , 2008, 9, 67-76.	1.6	28
20	Network Modeling Identifies Patient-specific Pathways in Glioblastoma. <i>Scientific Reports</i> , 2016, 6, 28668.	3.3	25
21	Reconstruction of the temporal signaling network in Salmonella-infected human cells. <i>Frontiers in Microbiology</i> , 2015, 6, 730.	3.5	21
22	Artificial intelligence based methods for hot spot prediction. <i>Current Opinion in Structural Biology</i> , 2022, 72, 209-218.	5.7	16
23	3D spatial organization and network-guided comparison of mutation profiles in Glioblastoma reveals similarities across patients. <i>PLoS Computational Biology</i> , 2019, 15, e1006789.	3.2	11
24	Quantitative Proteomics Identifies Secreted Diagnostic Biomarkers as well as Tumor-Dependent Prognostic Targets for Clear Cell Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2022, 19, 1322-1337.	3.4	10
25	Epitranscriptomics of Ischemic Heart Diseaseâ€”The IHD-EPITRAN Study Design and Objectives. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6630.	4.1	10
26	Comparative phosphoproteomic analysis reveals signaling networks regulating monopolar and bipolar cytokinesis. <i>Scientific Reports</i> , 2018, 8, 2269.	3.3	9
27	Impaired inhibitory GABAergic synaptic transmission and transcription studied in single neurons by Patch-seq in Huntingtonâ€™s disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	9
28	Structural analysis of mammalian protein phosphorylation at a proteome level. <i>Structure</i> , 2021, 29, 1219-1229.e3.	3.3	8
29	Computational approaches leveraging integrated connections of multi-omic data toward clinical applications. <i>Molecular Omics</i> , 2022, 18, 7-18.	2.8	8
30	Normal Mode Analysis of KRas4B Reveals Partner Specific Dynamics. <i>Journal of Physical Chemistry B</i> , 2021, 125, 5210-5221.	2.6	7
31	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. <i>Lecture Notes in Computer Science</i> , 2012, , 287-301.	1.3	7
32	The overexpression of DNA repair genes in invasive ductal and lobular breast carcinomas: Insights on individual variations and precision medicine. <i>PLoS ONE</i> , 2021, 16, e0247837.	2.5	6
33	Prediction of Protein Interactions by Structural Matching: Prediction of PPI Networks and the Effects of Mutations on PPIs that Combines Sequence and Structural Information. <i>Methods in Molecular Biology</i> , 2017, 1558, 255-270.	0.9	6
34	A Structural Perspective on the Modulation of Protein-Protein Interactions with Small Molecules. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 700-713.	2.1	6
35	Performance Assessment of the Network Reconstruction Approaches on Various Interactomes. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 666705.	3.5	5
36	Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. <i>Methods in Molecular Biology</i> , 2018, 1762, 51-69.	0.9	4

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37	Epithelial Wnt secretion drives the progression of inflammation-induced colon carcinoma in murine model. <i>IScience</i> , 2021, 24, 103369.	4.1	4
38	Context dependent isoform specific PI3K inhibition confers drug resistance in hepatocellular carcinoma cells. <i>BMC Cancer</i> , 2022, 22, 320.	2.6	3
39	Ischemic Heart Disease Selectively Modifies the Right Atrial Appendage Transcriptome. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 728198.	2.4	3
40	Functional stratification of cancer drugs through integrated network similarity. <i>Npj Systems Biology and Applications</i> , 2022, 8, 11.	3.0	3
41	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. <i>Current Opinion in Structural Biology</i> , 2022, , 102387.	5.7	3
42	The potential impact of recent developments in three-dimensional quantitative interaction proteomics on structural biology. <i>Expert Review of Proteomics</i> , 2016, 13, 447-449.	3.0	2
43	Large Scale Prediction of Computational Hot Spots in Protein Interfaces. <i>Biophysical Journal</i> , 2009, 96, 650a-651a.	0.5	0
44	Prediction of Protein-Protein Interactions at Genome Scale. <i>Biophysical Journal</i> , 2011, 100, 386a.	0.5	0
45	Abstract 996: In silico modeling and in vitro validation of undefined off-target of drugs in hepatocellular carcinoma. , 2019, , .		0
46	Abstract 996: In silico modeling and in vitro validation of undefined off-target of drugs in hepatocellular carcinoma. , 2019, , .		0