Nurcan Tuncbag

List of Publications by Year
in descending order

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	Quantitative Proteomics Identifies Secreted Diagnostic Biomarkers as well as Tumor-Dependent Prognostic Targets for Clear Cell Renal Cell Carcinoma. Molecular Cancer Research, 2022, 19, 1322-1337.	3.4	10
2	Computational approaches leveraging integrated connections of multi-omic data toward clinical applications. Molecular Omics, 2022, 18, 7-18.	2.8	8
3	Artificial intelligence based methods for hot spot prediction. Current Opinion in Structural Biology, 2022, 72, 209-218.	5.7	16
4	Context dependent isoform specific PI3K inhibition confers drug resistance in hepatocellular carcinoma cells. BMC Cancer, 2022, 22, 320.	2.6	3
5	Functional stratification of cancer drugs through integrated network similarity. Npj Systems Biology and Applications, 2022, 8, 11.	3.0	3
6	Editorial overview: Artificial intelligence (AI) methodologies in structural biology. Current Opinion in Structural Biology, 2022, , 102387.	5.7	3
7	The overexpression of DNA repair genes in invasive ductal and lobular breast carcinomas: Insights on individual variations and precision medicine. PLoS ONE, 2021, 16, e0247837.	2.5	6
8	Impaired inhibitory GABAergic synaptic transmission and transcription studied in single neurons by Patch-seq in Huntington's disease. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
9	Normal Mode Analysis of KRas4B Reveals Partner Specific Dynamics. Journal of Physical Chemistry B, 2021, 125, 5210-5221.	2.6	7
10	Structural analysis of mammalian protein phosphorylation at a proteome level. Structure, 2021, 29, 1219-1229.e3.	3.3	8
11	Epitranscriptomics of Ischemic Heart Disease—The IHD-EPITRAN Study Design and Objectives. International Journal of Molecular Sciences, 2021, 22, 6630.	4.1	10
12	Performance Assessment of the Network Reconstruction Approaches on Various Interactomes. Frontiers in Molecular Biosciences, 2021, 8, 666705.	3.5	5
13	Epithelial Wnt secretion drives the progression of inflammation-induced colon carcinoma in murine model. IScience, 2021, 24, 103369.	4.1	4
14	Ischemic Heart Disease Selectively Modifies the Right Atrial Appendage Transcriptome. Frontiers in Cardiovascular Medicine, 2021, 8, 728198.	2.4	3
15	3D spatial organization and network-guided comparison of mutation profiles in Glioblastoma reveals similarities across patients. PLoS Computational Biology, 2019, 15, e1006789.	3.2	11
16	Systems-level Analysis Reveals Multiple Modulators of Epithelial-mesenchymal Transition and Identifies DNAJB4 and CD81 as Novel Metastasis Inducers in Breast Cancer. Molecular and Cellular Proteomics, 2019, 18, 1756-1771.	3.8	29
17	Abstract 996:In silicomodeling andin vitrovalidation of undefined off-target of drugs in hepatocellular carcinoma. , 2019, , .		0
18	Abstract 996:<i>In silico</i>modeling and<i>in vitro</i>validation of undefined off-target of drugs in hepatocellular carcinoma. , 2019, , .		0

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19	Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. Methods in Molecular Biology, 2018, 1762, 51-69.	0.9	4
20	Comparative phosphoproteomic analysis reveals signaling networks regulating monopolar and bipolar cytokinesis. Scientific Reports, 2018, 8, 2269.	3.3	9
21	A Structural Perspective on the Modulation of Protein-Protein Interactions with Small Molecules. Current Topics in Medicinal Chemistry, 2018, 18, 700-713.	2.1	6
22	Genome-Scale Networks Link Neurodegenerative Disease Genes to Î±-Synuclein through Specific Molecular Pathways. Cell Systems, 2017, 4, 157-170.e14.	6.2	102
23	Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs. MBio, 2017, 8, .	4.1	42
24	Prediction of Protein Interactions by Structural Matching: Prediction of PPI Networks and the Effects of Mutations on PPIs that Combines Sequence and Structural Information. Methods in Molecular Biology, 2017, 1558, 255-270.	0.9	6
25	Predicting Proteinâ€"Protein Interactions from the Molecular to the Proteome Level. Chemical Reviews, 2016, 116, 4884-4909.	47.7	289
26	Network Modeling Identifies Patient-specific Pathways in Glioblastoma. Scientific Reports, 2016, 6, 28668.	3.3	25
27	The potential impact of recent developments in three-dimensional quantitative interaction proteomics on structural biology. Expert Review of Proteomics, 2016, 13, 447-449.	3.0	2
28	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. PLoS Computational Biology, 2016, 12, e1004879.	3.2	123
29	Reconstruction of the temporal signaling network in Salmonella-infected human cells. Frontiers in Microbiology, 2015, 6, 730.	3.5	21
30	The PI3K/AKT/mTOR interactive pathway. Molecular BioSystems, 2015, 11, 1946-1954.	2.9	379
31	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. Journal of Computational Biology, 2013, 20, 124-136.	1.6	108
32	SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. Nucleic Acids Research, 2012, 40, W505-W509.	14.5	58
33	Fast and accurate modeling of proteinâ€"protein interactions by combining templateâ€interfaceâ€based docking with flexible refinement. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1239-1249.	2.6	43
34	Simultaneous Reconstruction of Multiple Signaling Pathways via the Prize-Collecting Steiner Forest Problem. Lecture Notes in Computer Science, 2012, , 287-301.	1.3	7
35	Prediction of Protein-Protein Interactions at Genome Scale. Biophysical Journal, 2011, 100, 386a.	0.5	0
36	Predicting protein-protein interactions on a proteome scale by matching evolutionary and structural similarities at interfaces using PRISM. Nature Protocols, 2011, 6, 1341-1354.	12.0	253

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37	Prediction of protein–protein interactions: unifying evolution and structure at protein interfaces. Physical Biology, 2011, 8, 035006.	1.8	58
38	Analysis and network representation of hotspots in protein interfaces using minimum cut trees. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2283-2294.	2.6	58
39	HotPoint: hot spot prediction server for protein interfaces. Nucleic Acids Research, 2010, 38, W402-W406.	14.5	185
40	Towards inferring time dimensionality in protein–protein interaction networks by integrating structures: the p53 example. Molecular BioSystems, 2009, 5, 1770.	2.9	76
41	Identification of computational hot spots in protein interfaces: combining solvent accessibility and inter-residue potentials improves the accuracy. Bioinformatics, 2009, 25, 1513-1520.	4.1	239
42	Large Scale Prediction of Computational Hot Spots in Protein Interfaces. Biophysical Journal, 2009, 96, 650a-651a.	0.5	0
43	Architectures and Functional Coverage of Protein–Protein Interfaces. Journal of Molecular Biology, 2008, 381, 785-802.	4.2	106
44	A survey of available tools and web servers for analysis of protein-protein interactions and interfaces. Briefings in Bioinformatics, 2008, 10, 217-232.	6.5	140
45	Characterization and Prediction of Protein Interfaces to Infer Protein-Protein Interaction Networks. Current Pharmaceutical Biotechnology, 2008, 9, 67-76.	1.6	28
46	HotSprint: database of computational hot spots in protein interfaces. Nucleic Acids Research, 2007, 36, D662-D666.	14.5	102