Ashwini Patil

List of Publications by Year
in descending order

31 papers	**1,390** citations	471509 **17** h-index	477307 **29** g-index
33 all docs	**33** docs citations	**33** times ranked	**1904** citing authors

#	Article	IF	Citations
1	B cell–intrinsic TBK1 is essential for germinal center formation during infection and vaccination in mice. Journal of Experimental Medicine, 2022, 219, .	8.5	8
2	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e9294.	2.0	12
3	Protein–Protein Interaction Databases. , 2019, , 849-855.		2
4	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. BMC Bioinformatics, 2019, 19, 378.	2.6	13
5	OPAL+: Length–Specific MoRF Prediction in Intrinsically Disordered Protein Sequences. Proteomics, 2019, 19, e1800058.	2.2	30
6	Generation of tumor antigen-specific murine CD8+ T cells with enhanced anti-tumor activity via highly efficient CRISPR/Cas9 genome editing. International Immunology, 2018, 30, 141-154.	4.0	9
7	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. Bioinformatics, 2018, 34, 1850-1858.	4.1	53
8	MoRFPred-plus: Computational Identification of MoRFs in Protein Sequences using Physicochemical Properties and HMM profiles. Journal of Theoretical Biology, 2018, 437, 9-16.	1.7	43
9	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. Bioinformatics, 2018, 34, 3764-3765.	4.1	0
10	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. Cell, 2017, 171, 398-413.e21.	28.9	69
11	Predicting MoRFs in protein sequences using HMM profiles. BMC Bioinformatics, 2016, 17, 504.	2.6	24
12	HitPredict version 4: comprehensive reliability scoring of physical protein–protein interactions from more than 100 species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav117.	3.0	92
13	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. FEBS Letters, 2015, 589, 2590-2602.	2.8	66
14	Discovery of Intermediary Genes between Pathways Using Sparse Regression. PLoS ONE, 2015, 10, e0137222.	2.5	1
15	Innate Immunity Interactome Dynamics. Gene Regulation and Systems Biology, 2014, 8, GRSB.S12850.	2.3	1
16	TimeXNet: Identifying active gene sub-networks using time-course gene expression profiles. BMC Systems Biology, 2014, 8, S2.	3.0	12
17	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890.	2.5	19
18	Linking Transcriptional Changes over Time in Stimulated Dendritic Cells to Identify Gene Networks Activated during the Innate Immune Response. PLoS Computational Biology, 2013, 9, e1003323.	3.2	24

#	Article	IF	Citations
19	Sequence- and Species-Dependence of Proteasomal Processivity. ACS Chemical Biology, 2012, 7, 1444-1453.	3.4	50
20	Chemical composition is maintained in poorly conserved intrinsically disordered regions and suggests a means for their classification. Molecular BioSystems, 2012, 8, 3262.	2.9	48
21	Functional annotation of intrinsically disordered domains by their amino acid content using IDD Navigator. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 164-75.	0.7	3
22	Assessing the utility of gene co-expression stability in combination with correlation in the analysis of protein-protein interaction networks. BMC Genomics, 2011, 12, S19.	2.8	9
23	HitPredict: a database of quality assessed protein–protein interactions in nine species. Nucleic Acids Research, 2011, 39, D744-D749.	14.5	111
24	Intrinsically disordered domains deviate significantly from random sequences in mammalian proteins. BMC Bioinformatics, 2010, 11, S7.	2.6	9
25	Domain distribution and intrinsic disorder in hubs in the human protein–protein interaction network. Protein Science, 2010, 19, 1461-1468.	7.6	62
26	Hub Promiscuity in Protein-Protein Interaction Networks. International Journal of Molecular Sciences, 2010, 11, 1930-1943.	4.1	148
27	The role of charged surface residues in the binding ability of small hubs in protein-protein interaction networks. Biophysics (Nagoya-shi, Japan), 2007, 3, 27-35.	0.4	10
28	Disordered domains and high surface charge confer hubs with the ability to interact with multiple proteins in interaction networks. FEBS Letters, 2006, 580, 2041-2045.	2.8	262
29	Use of transcriptional synergy to augment sensitivity of a splicing reporter assay. Rna, 2006, 12, 925-930.	3.5	18
30	Filtering high-throughput protein-protein interaction data using a combination of genomic features. BMC Bioinformatics, 2005, 6, 100.	2.6	138
31	HINT: a database of annotated protein-protein interactions and their homologs. Biophysics (Nagoya-shi, Japan), 2005, 1, 21-24.	0.4	35