

# Ashwini Patil

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,390  
citations

471061

17  
h-index

476904

29  
g-index

33  
all docs

33  
docs citations

33  
times ranked

1904  
citing authors

#	ARTICLE	IF	CITATIONS
1	Disordered domains and high surface charge confer hubs with the ability to interact with multiple proteins in interaction networks. <i>FEBS Letters</i> , 2006, 580, 2041-2045.	1.3	262
2	Hub Promiscuity in Protein-Protein Interaction Networks. <i>International Journal of Molecular Sciences</i> , 2010, 11, 1930-1943.	1.8	148
3	Filtering high-throughput protein-protein interaction data using a combination of genomic features. <i>BMC Bioinformatics</i> , 2005, 6, 100.	1.2	138
4	HitPredict: a database of quality assessed protein-protein interactions in nine species. <i>Nucleic Acids Research</i> , 2011, 39, D744-D749.	6.5	111
5	HitPredict version 4: comprehensive reliability scoring of physical protein-protein interactions from more than 100 species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav117.	1.4	92
6	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017, 171, 398-413.e21.	13.5	69
7	Methods for protein complex prediction and their contributions towards understanding the organisation, function and dynamics of complexes. <i>FEBS Letters</i> , 2015, 589, 2590-2602.	1.3	66
8	Domain distribution and intrinsic disorder in hubs in the human protein-protein interaction network. <i>Protein Science</i> , 2010, 19, 1461-1468.	3.1	62
9	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. <i>Bioinformatics</i> , 2018, 34, 1850-1858.	1.8	53
10	Sequence- and Species-Dependence of Proteasomal Processivity. <i>ACS Chemical Biology</i> , 2012, 7, 1444-1453.	1.6	50
11	Chemical composition is maintained in poorly conserved intrinsically disordered regions and suggests a means for their classification. <i>Molecular BioSystems</i> , 2012, 8, 3262.	2.9	48
12	MoRFPred-plus: Computational Identification of MoRFs in Protein Sequences using Physicochemical Properties and HMM profiles. <i>Journal of Theoretical Biology</i> , 2018, 437, 9-16.	0.8	43
13	HINT: a database of annotated protein-protein interactions and their homologs. <i>Biophysics (Nagoya-shi, Japan)</i> , 2005, 1, 21-24.	0.4	35
14	OPAL+: Length-Specific MoRF Prediction in Intrinsically Disordered Protein Sequences. <i>Proteomics</i> , 2019, 19, e1800058.	1.3	30
15	Linking Transcriptional Changes over Time in Stimulated Dendritic Cells to Identify Gene Networks Activated during the Innate Immune Response. <i>PLoS Computational Biology</i> , 2013, 9, e1003323.	1.5	24
16	Predicting MoRFs in protein sequences using HMM profiles. <i>BMC Bioinformatics</i> , 2016, 17, 504.	1.2	24
17	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. <i>PLoS ONE</i> , 2014, 9, e89890.	1.1	19
18	Use of transcriptional synergy to augment sensitivity of a splicing reporter assay. <i>Rna</i> , 2006, 12, 925-930.	1.6	18

#	ARTICLE	IF	CITATIONS
19	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. BMC Bioinformatics, 2019, 19, 378.	1.2	13
20	TimeXNet: Identifying active gene sub-networks using time-course gene expression profiles. BMC Systems Biology, 2014, 8, S2.	3.0	12
21	Whole genome sequencing analysis identifies recurrent structural alterations in esophageal squamous cell carcinoma. PeerJ, 2020, 8, e9294.	0.9	12
22	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
23	Intrinsically disordered domains deviate significantly from random sequences in mammalian proteins. BMC Bioinformatics, 2010, 11, S7.	1.2	9
24	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.	1.2	9
25	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.	1.8	9
26	B cellâ€™intrinsic TBK1 is essential for germinal center formation during infection and vaccination in mice. Journal of Experimental Medicine, 2022, 219, .	4.2	8
27	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
28	Proteinâ€™Protein Interaction Databases. , 2019, , 849-855.		2
29	Innate Immunity Interactome Dynamics. Gene Regulation and Systems Biology, 2014, 8, GRSB.S12850.	2.3	1
30	Discovery of Intermediary Genes between Pathways Using Sparse Regression. PLoS ONE, 2015, 10, e0137222.	1.1	1
31	TimeXNet Web: identifying cellular response networks from diverse omics time-course data. Bioinformatics, 2018, 34, 3764-3765.	1.8	0