Mona Singh

List of Publications by Year
in descending order

32 papers	2,191 citations	394421 19 h-index	477307 29 g-index
37 all docs	37 docs citations	37 times ranked	3378 citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting functionally important residues from sequence conservation. Bioinformatics, 2007, 23, 1875-1882.	4.1	590
2	Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. Bioinformatics, 2005, 21, i302-i310.	4.1	421
3	SPICi: a fast clustering algorithm for large biological networks. Bioinformatics, 2010, 26, 1105-1111.	4.1	210
4	De novo prediction of DNA-binding specificities for Cys2His2 zinc finger proteins. Nucleic Acids Research, 2014, 42, 97-108.	14.5	173
5	Characterization and prediction of residues determining protein functional specificity. Bioinformatics, 2008, 24, 1473-1480.	4.1	109
6	Predicting DNA recognition by Cys2His2 zinc finger proteins. Bioinformatics, 2009, 25, 22-29.	4.1	109
7	A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. Nucleic Acids Research, 2015, 43, 1965-1984.	14.5	86
8	Using context to improve protein domain identification. BMC Bioinformatics, 2011, 12, 90.	2.6	44
9	Network-Based Coverage of Mutational Profiles Reveals Cancer Genes. Cell Systems, 2017, 5, 221-229.e4.	6.2	40
10	Simple Topological Features Reflect Dynamics and Modularity in Protein Interaction Networks. PLoS Computational Biology, 2013, 9, e1003243.	3.2	36
11	Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Computational Biology, 2015, 11, e1004467.	3.2	36
12	molBLOCKS: decomposing small molecule sets and uncovering enriched fragments. Bioinformatics, 2014, 30, 2081-2083.	4.1	32
13	Deep sequencing of large library selections allows computational discovery of diverse sets of zinc fingers that bind common targets. Nucleic Acids Research, 2014, 42, 1497-1508.	14.5	31
14	Two critical positions in zinc finger domains are heavily mutated in three human cancer types. PLoS Computational Biology, 2018, 14, e1006290.	3.2	31
15	Differential analysis between somatic mutation and germline variation profiles reveals cancer-related genes. Genome Medicine, 2017, 9, 79.	8.2	30
16	An expanded binding model for Cys_2His_2 zinc finger protein–DNA interfaces. Physical Biology, 2011, 8, 035010.	1.8	29
17	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. PLoS Genetics, 2015, 11, e1005011.	3.5	29
18	Interaction-based discovery of functionally important genes in cancers. Nucleic Acids Research, 2014, 42, e18-e18.	14.5	25

#	Article	IF	Citations
19	DeMaSk: a deep mutational scanning substitution matrix and its use for variant impact prediction. Bioinformatics, 2021, 36, 5322-5329.	4.1	24
20	Disentangling function from topology to infer the network properties of disease genes. BMC Systems Biology, 2013, 7, 5.	3.0	20
21	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. PLoS Computational Biology, 2015, 11, e1004509.	3.2	19
22	Systematic domain-based aggregation of protein structures highlights DNA-, RNA- and other ligand-binding positions. Nucleic Acids Research, 2019, 47, 582-593.	14.5	16
23	Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. Cell Systems, 2020, 10, 193-203.e4.	6.2	15
24	uKIN Combines New and Prior Information with Guided Network Propagation to Accurately Identify Disease Genes. Cell Systems, 2020, 10, 470-479.e3.	6.2	11
25	PertInInt: An Integrative, Analytical Approach to Rapidly Uncover Cancer Driver Genes with Perturbed Interactions and Functionalities. Cell Systems, 2020, 11, 63-74.e7.	6.2	8
26	dSPRINT: predicting DNA, RNA, ion, peptide and small molecule interaction sites within protein domains. Nucleic Acids Research, 2021, 49, e78-e78.	14.5	5
27	Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. PLoS Computational Biology, 2021, 17, e1009560.	3.2	5
28	Sharing DNA-binding information across structurally similar proteins enables accurate specificity determination. Nucleic Acids Research, 2020, 48, e9-e9.	14.5	3
29	Protein Function Prediction via Analysis of Interactomes. , 2008, , 231-258.		1
30	Guest Editorial for ACM BCB. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1089-1090.	3.0	1
31	DYNAMICS OF BIOLOGICAL NETWORKS â€" SESSION INTRODUCTION. , 2008, , .		0
32	Improved inference of tandem domain duplications. Bioinformatics, 2021, 37, i133-i141.	4.1	0