

Mona Singh

List of Publications by Year in descending order

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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	dSPRINT: predicting DNA, RNA, ion, peptide and small molecule interaction sites within protein domains. <i>Nucleic Acids Research</i> , 2021, 49, e78-e78.	14.5	5
2	Improved inference of tandem domain duplications. <i>Bioinformatics</i> , 2021, 37, i133-i141.	4.1	0
3	DeMaSk: a deep mutational scanning substitution matrix and its use for variant impact prediction. <i>Bioinformatics</i> , 2021, 36, 5322-5329.	4.1	24
4	Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. <i>PLoS Computational Biology</i> , 2021, 17, e1009560.	3.2	5
5	Sharing DNA-binding information across structurally similar proteins enables accurate specificity determination. <i>Nucleic Acids Research</i> , 2020, 48, e9-e9.	14.5	3
6	PertInInt: An Integrative, Analytical Approach to Rapidly Uncover Cancer Driver Genes with Perturbed Interactions and Functionalities. <i>Cell Systems</i> , 2020, 11, 63-74.e7.	6.2	8
7	uKIN Combines New and Prior Information with Guided Network Propagation to Accurately Identify Disease Genes. <i>Cell Systems</i> , 2020, 10, 470-479.e3.	6.2	11
8	Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. <i>Cell Systems</i> , 2020, 10, 193-203.e4.	6.2	15
9	Systematic domain-based aggregation of protein structures highlights DNA-, RNA- and other ligand-binding positions. <i>Nucleic Acids Research</i> , 2019, 47, 582-593.	14.5	16
10	Two critical positions in zinc finger domains are heavily mutated in three human cancer types. <i>PLoS Computational Biology</i> , 2018, 14, e1006290.	3.2	31
11	Network-Based Coverage of Mutational Profiles Reveals Cancer Genes. <i>Cell Systems</i> , 2017, 5, 221-229.e4.	6.2	40
12	Differential analysis between somatic mutation and germline variation profiles reveals cancer-related genes. <i>Genome Medicine</i> , 2017, 9, 79.	8.2	30
13	Genome-Wide Detection and Analysis of Multifunctional Genes. <i>PLoS Computational Biology</i> , 2015, 11, e1004467.	3.2	36
14	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015, 11, e1004509.	3.2	19
15	A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. <i>Nucleic Acids Research</i> , 2015, 43, 1965-1984.	14.5	86
16	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011.	3.5	29
17	Interaction-based discovery of functionally important genes in cancers. <i>Nucleic Acids Research</i> , 2014, 42, e18-e18.	14.5	25
18	De novo prediction of DNA-binding specificities for Cys2His2 zinc finger proteins. <i>Nucleic Acids Research</i> , 2014, 42, 97-108.	14.5	173

#	ARTICLE	IF	CITATIONS
19	Deep sequencing of large library selections allows computational discovery of diverse sets of zinc fingers that bind common targets. <i>Nucleic Acids Research</i> , 2014, 42, 1497-1508.	14.5	31
20	molBLOCKS: decomposing small molecule sets and uncovering enriched fragments. <i>Bioinformatics</i> , 2014, 30, 2081-2083.	4.1	32
21	Disentangling function from topology to infer the network properties of disease genes. <i>BMC Systems Biology</i> , 2013, 7, 5.	3.0	20
22	Simple Topological Features Reflect Dynamics and Modularity in Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003243.	3.2	36
23	Guest Editorial for ACM BCB. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1089-1090.	3.0	1
24	Using context to improve protein domain identification. <i>BMC Bioinformatics</i> , 2011, 12, 90.	2.6	44
25	An expanded binding model for Cys ₂ His ₂ zinc finger proteinâ€™DNA interfaces. <i>Physical Biology</i> , 2011, 8, 035010.	1.8	29
26	SPICi: a fast clustering algorithm for large biological networks. <i>Bioinformatics</i> , 2010, 26, 1105-1111.	4.1	210
27	Predicting DNA recognition by Cys2His2 zinc finger proteins. <i>Bioinformatics</i> , 2009, 25, 22-29.	4.1	109
28	Protein Function Prediction via Analysis of Interactomes. , 2008, , 231-258.		1
29	Characterization and prediction of residues determining protein functional specificity. <i>Bioinformatics</i> , 2008, 24, 1473-1480.	4.1	109
30	DYNAMICS OF BIOLOGICAL NETWORKS â€™ SESSION INTRODUCTION. , 2008, , .		0
31	Predicting functionally important residues from sequence conservation. <i>Bioinformatics</i> , 2007, 23, 1875-1882.	4.1	590
32	Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. <i>Bioinformatics</i> , 2005, 21, i302-i310.	4.1	421