

Mona Singh

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,191
citations

394390
19
h-index

477281
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. Nucleic Acids Research, 2021, 49, e78-e78.	14.5	5
2	Improved inference of tandem domain duplications. Bioinformatics, 2021, 37, i133-i141.	4.1	0
3	DeMaSk: a deep mutational scanning substitution matrix and its use for variant impact prediction. Bioinformatics, 2021, 36, 5322-5329.	4.1	24
4	Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. PLoS Computational Biology, 2021, 17, e1009560.	3.2	5
5	Sharing DNA-binding information across structurally similar proteins enables accurate specificity determination. Nucleic Acids Research, 2020, 48, e9-e9.	14.5	3
6	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
7	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
8	Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. Cell Systems, 2020, 10, 193-203.e4.	6.2	15
9	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
10	Two critical positions in zinc finger domains are heavily mutated in three human cancer types. PLoS Computational Biology, 2018, 14, e1006290.	3.2	31
11	Network-Based Coverage of Mutational Profiles Reveals Cancer Genes. Cell Systems, 2017, 5, 221-229.e4.	6.2	40
12	Differential analysis between somatic mutation and germline variation profiles reveals cancer-related genes. Genome Medicine, 2017, 9, 79.	8.2	30
13	Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Computational Biology, 2015, 11, e1004467.	3.2	36
14	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. PLoS Computational Biology, 2015, 11, e1004509.	3.2	19
15	A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. Nucleic Acids Research, 2015, 43, 1965-1984.	14.5	86
16	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. PLoS Genetics, 2015, 11, e1005011.	3.5	29
17	Interaction-based discovery of functionally important genes in cancers. Nucleic Acids Research, 2014, 42, e18-e18.	14.5	25
18	De novo prediction of DNA-binding specificities for Cys2His2 zinc finger proteins. Nucleic Acids Research, 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. Nucleic Acids Research, 2014, 42, 1497-1508.	14.5	31
20	molBLOCKS: decomposing small molecule sets and uncovering enriched fragments. Bioinformatics, 2014, 30, 2081-2083.	4.1	32
21	Disentangling function from topology to infer the network properties of disease genes. BMC Systems Biology, 2013, 7, 5.	3.0	20
22	Simple Topological Features Reflect Dynamics and Modularity in Protein Interaction Networks. PLoS Computational Biology, 2013, 9, e1003243.	3.2	36
23	Guest Editorial for ACM BCB. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1089-1090.	3.0	1
24	Using context to improve protein domain identification. BMC Bioinformatics, 2011, 12, 90.	2.6	44
25	An expanded binding model for Cys ₂ His ₂ zinc finger proteinâ€DNA interfaces. Physical Biology, 2011, 8, 035010.	1.8	29
26	SPICi: a fast clustering algorithm for large biological networks. Bioinformatics, 2010, 26, 1105-1111.	4.1	210
27	Predicting DNA recognition by Cys2His2 zinc finger proteins. Bioinformatics, 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. Bioinformatics, 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. Bioinformatics, 2007, 23, 1875-1882.	4.1	590
32	Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. Bioinformatics, 2005, 21, i302-i310.	4.1	421