

Mona Singh

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,191
citations

448610

19
h-index

536525

29
g-index

37
all docs

37
docs citations

37
times ranked

3818
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. | 6.5 | 5 |
| 2 | Improved inference of tandem domain duplications. <i>Bioinformatics</i> , 2021, 37, i133-i141. | 1.8 | 0 |
| 3 | DeMaSk: a deep mutational scanning substitution matrix and its use for variant impact prediction. <i>Bioinformatics</i> , 2021, 36, 5322-5329. | 1.8 | 24 |
| 4 | Comparative genomic analysis reveals varying levels of mammalian adaptation to coronavirus infections. <i>PLoS Computational Biology</i> , 2021, 17, e1009560. | 1.5 | 5 |
| 5 | Sharing DNA-binding information across structurally similar proteins enables accurate specificity determination. <i>Nucleic Acids Research</i> , 2020, 48, e9-e9. | 6.5 | 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. | 2.9 | 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. | 2.9 | 11 |
| 8 | Differential Allele-Specific Expression Uncovers Breast Cancer Genes Dysregulated by Cis Noncoding Mutations. <i>Cell Systems</i> , 2020, 10, 193-203.e4. | 2.9 | 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. | 6.5 | 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. | 1.5 | 31 |
| 11 | Network-Based Coverage of Mutational Profiles Reveals Cancer Genes. <i>Cell Systems</i> , 2017, 5, 221-229.e4. | 2.9 | 40 |
| 12 | Differential analysis between somatic mutation and germline variation profiles reveals cancer-related genes. <i>Genome Medicine</i> , 2017, 9, 79. | 3.6 | 30 |
| 13 | Genome-Wide Detection and Analysis of Multifunctional Genes. <i>PLoS Computational Biology</i> , 2015, 11, e1004467. | 1.5 | 36 |
| 14 | Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. <i>PLoS Computational Biology</i> , 2015, 11, e1004509. | 1.5 | 19 |
| 15 | A systematic survey of the Cys2His2 zinc finger DNA-binding landscape. <i>Nucleic Acids Research</i> , 2015, 43, 1965-1984. | 6.5 | 86 |
| 16 | Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011. | 1.5 | 29 |
| 17 | Interaction-based discovery of functionally important genes in cancers. <i>Nucleic Acids Research</i> , 2014, 42, e18-e18. | 6.5 | 25 |
| 18 | De novo prediction of DNA-binding specificities for Cys2His2 zinc finger proteins. <i>Nucleic Acids Research</i> , 2014, 42, 97-108. | 6.5 | 173 |

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|----|---|-----|-----------|
| 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. | 6.5 | 31 |
| 20 | molBLOCKS: decomposing small molecule sets and uncovering enriched fragments. <i>Bioinformatics</i> , 2014, 30, 2081-2083. | 1.8 | 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. | 1.5 | 36 |
| 23 | Guest Editorial for ACM BCB. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1089-1090. | 1.9 | 1 |
| 24 | Using context to improve protein domain identification. <i>BMC Bioinformatics</i> , 2011, 12, 90. | 1.2 | 44 |
| 25 | An expanded binding model for Cys ₂ His ₂ zinc finger proteinâ€™DNA interfaces. <i>Physical Biology</i> , 2011, 8, 035010. | 0.8 | 29 |
| 26 | SPICi: a fast clustering algorithm for large biological networks. <i>Bioinformatics</i> , 2010, 26, 1105-1111. | 1.8 | 210 |
| 27 | Predicting DNA recognition by Cys2His2 zinc finger proteins. <i>Bioinformatics</i> , 2009, 25, 22-29. | 1.8 | 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. | 1.8 | 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. | 1.8 | 590 |
| 32 | Whole-proteome prediction of protein function via graph-theoretic analysis of interaction maps. <i>Bioinformatics</i> , 2005, 21, i302-i310. | 1.8 | 421 |