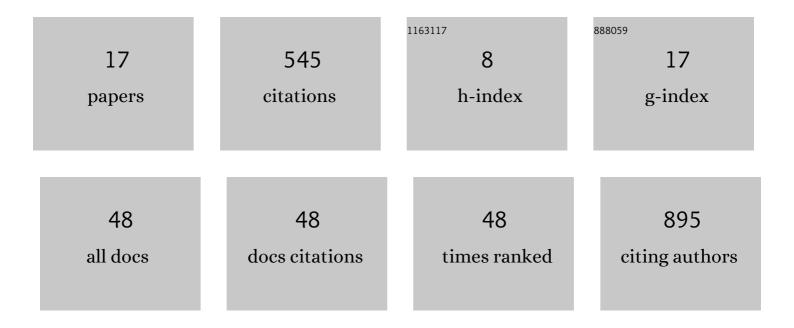
Pritha Ghosh

List of Publications by Year in descending order

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Ρριτην Ομοςη

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements. Nucleic Acids Research, 2020, 48, 12436-12452. | 14.5 | 195 |
| 2 | Genome sequencing of herb Tulsi (Ocimum tenuiflorum) unravels key genes behind its strong medicinal properties. BMC Plant Biology, 2015, 15, 212. | 3.6 | 80 |
| 3 | Computational modeling of RNA 3D structure based on experimental data. Bioscience Reports, 2019, 39, | 2.4 | 42 |
| 4 | Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. Nature Communications, 2018, 9, 1549. | 12.8 | 35 |
| 5 | Bioinformatics Tools and Benchmarks for Computational Docking and 3D Structure Prediction of RNA-Protein Complexes. Genes, 2018, 9, 432. | 2.4 | 30 |
| 6 | The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (Moringa oleifera). Genomics, 2020, 112, 621-628. | 2.9 | 22 |
| 7 | Genome-wide survey of putative RNA-binding proteins encoded in the human proteome. Molecular BioSystems, 2016, 12, 532-540. | 2.9 | 21 |
| 8 | High diversity in Delta variant across countries revealed by genomeâ€wide analysis of SARSâ€CoVâ€⊋ beyond the Spike protein. Molecular Systems Biology, 2022, 18, e10673. | 7.2 | 18 |
| 9 | RStrucFam: a web server to associate structure and cognate RNA for RNA-binding proteins from sequence information. BMC Bioinformatics, 2016, 17, 411. | 2.6 | 9 |
| 10 | A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1979-1986. | 3.5 | 5 |
| 11 | PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. Nucleic Acids Research, 2016, 44, D410-D414. | 14.5 | 4 |
| 12 | A knowledge-driven protocol for prediction of proteins of interest with an emphasis on biosynthetic pathways. MethodsX, 2020, 7, 101053. | 1.6 | 4 |
| 13 | Dataset for the combined transcriptome assembly of M. oleifera and functional annotation. Data in Brief, 2020, 30, 105416. | 1.0 | 4 |
| 14 | Bioinformatics comparisons of RNA-binding proteins of pathogenic and non-pathogenic Escherichia coli strains reveal novel virulence factors. BMC Genomics, 2017, 18, 658. | 2.8 | 3 |
| 15 | Molecular insights into RNA recognition and gene regulation by the TRIM-NHL protein Mei-P26. Life Science Alliance, 2022, 5, e202201418. | 2.8 | 3 |
| 16 | EcRBPome: a comprehensive database of all known E. coli RNA-binding proteins. BMC Genomics, 2019, 20, 403. | 2.8 | 2 |
| 17 | PASS2 version 6: a database of structure-based sequence alignments of protein domain superfamilies in accordance with SCOPe. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 3.0 | 2 |