

# Sushmita Roy

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

2,798  
citations

394421

19  
h-index

276875

41  
g-index

63  
all docs

63  
docs citations

63  
times ranked

4988  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
2	Comparative Analysis of Gene Regulatory Networks: From Network Reconstruction to Evolution. <i>Annual Review of Cell and Developmental Biology</i> , 2015, 31, 399-428.	9.4	170
3	Deep Sequencing of the <i>Medicago truncatula</i> Root Transcriptome Reveals a Massive and Early Interaction between Nodulation Factor and Ethylene Signals. <i>Plant Physiology</i> , 2015, 169, 233-265.	4.8	164
4	SIRT3 Mediates Multi-Tissue Coupling for Metabolic Fuel Switching. <i>Cell Metabolism</i> , 2015, 21, 637-646.	16.2	154
5	A proteomic atlas of the legume <i>Medicago truncatula</i> and its nitrogen-fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Nature Biotechnology</i> , 2016, 34, 1198-1205.	17.5	133
6	A predictive modeling approach for cell line-specific long-range regulatory interactions. <i>Nucleic Acids Research</i> , 2015, 43, 8694-8712.	14.5	118
7	Predictive regulatory models in <i>Drosophila melanogaster</i> by integrative inference of transcriptional networks. <i>Genome Research</i> , 2012, 22, 1334-1349.	5.5	104
8	Integrated Module and Gene-Specific Regulatory Inference Implicates Upstream Signaling Networks. <i>PLoS Computational Biology</i> , 2013, 9, e1003252.	3.2	78
9	Evolutionary principles of modular gene regulation in yeasts. <i>ELife</i> , 2013, 2, e00603.	6.0	73
10	Network-based approaches for analysis of complex biological systems. <i>Current Opinion in Biotechnology</i> , 2016, 39, 157-166.	6.6	71
11	Arboretum: Reconstruction and analysis of the evolutionary history of condition-specific transcriptional modules. <i>Genome Research</i> , 2013, 23, 1039-1050.	5.5	60
12	Identification of FMR1-regulated molecular networks in human neurodevelopment. <i>Genome Research</i> , 2020, 30, 361-374.	5.5	47
13	In silico prediction of high-resolution Hi-C interaction matrices. <i>Nature Communications</i> , 2019, 10, 5449.	12.8	46
14	A prior-based integrative framework for functional transcriptional regulatory network inference. <i>Nucleic Acids Research</i> , 2017, 45, gkw963.	14.5	41
15	Inference and Evolutionary Analysis of Genome-Scale Regulatory Networks in Large Phylogenies. <i>Cell Systems</i> , 2017, 4, 543-558.e8.	6.2	40
16	Collaborative rewiring of the pluripotency network by chromatin and signalling modulating pathways. <i>Nature Communications</i> , 2015, 6, 6188.	12.8	34
17	A multi-task graph-clustering approach for chromosome conformation capture data sets identifies conserved modules of chromosomal interactions. <i>Genome Biology</i> , 2016, 17, 114.	8.8	30
18	Integrating Transcriptomic and Proteomic Data Using Predictive Regulatory Network Models of Host Response to Pathogens. <i>PLoS Computational Biology</i> , 2016, 12, e1005013.	3.2	24

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19	High-order interactions observed in multi-task intrinsic networks are dominant indicators of aberrant brain function in schizophrenia. <i>NeuroImage</i> , 2014, 102, 35-48.	4.2	22
20	Imputed gene associations identify replicable <i>transacting</i> genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019, 43, 596-608.	1.3	19
21	A Pan-Cancer Modular Regulatory Network Analysis to Identify Common and Cancer-Specific Network Components. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14058.	1.9	18
22	Evolution of regulatory networks associated with traits under selection in cichlids. <i>Genome Biology</i> , 2021, 22, 25.	8.8	17
23	Inference of cell type specific regulatory networks on mammalian lineages. <i>Current Opinion in Systems Biology</i> , 2017, 2, 130-139.	2.6	16
24	GRINCH: simultaneous smoothing and detection of topological units of genome organization from sparse chromatin contact count matrices with matrix factorization. <i>Genome Biology</i> , 2021, 22, 164.	8.8	16
25	Chromatin module inference on cellular trajectories identifies key transition points and poised epigenetic states in diverse developmental processes. <i>Genome Research</i> , 2017, 27, 1250-1262.	5.5	14
26	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. <i>PLoS Genetics</i> , 2021, 17, e1009309.	3.5	14
27	Inferring Regulatory Programs Governing Region Specificity of Neuroepithelial Stem Cells during Early Hindbrain and Spinal Cord Development. <i>Cell Systems</i> , 2019, 9, 167-186.e12.	6.2	13
28	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	19.0	9
29	Evolution of regulatory networks in <i>Candida glabrata</i> : learning to live with the human host. <i>FEMS Yeast Research</i> , 2015, 15, fov087.	2.3	8
30	Multi-task consensus clustering of genome-wide transcriptomes from related biological conditions. <i>Bioinformatics</i> , 2016, 32, 1509-1517.	4.1	6
31	Data integration for inferring context-specific gene regulatory networks. <i>Current Opinion in Systems Biology</i> , 2020, 23, 38-46.	2.6	6
32	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. <i>Nucleic Acids Research</i> , 2021, 49, e3-e3.	14.5	5
33	Evolution of miRNA-Binding Sites and Regulatory Networks in Cichlids. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	4
34	Integrative Approaches for Inference of Genome-Scale Gene Regulatory Networks. <i>Methods in Molecular Biology</i> , 2019, 1883, 161-194.	0.9	3
35	ABC-CWAS: Functional Annotation of Estrogen Receptor-Positive Breast Cancer Genetic Variants. <i>Frontiers in Genetics</i> , 2020, 11, 730.	2.3	3
36	Deciphering the Role of 3D Genome Organization in Breast Cancer Susceptibility. <i>Frontiers in Genetics</i> , 2021, 12, 788318.	2.3	3

#	ARTICLE	IF	CITATIONS
37	Reconstruction and Analysis of the Evolution of Modular Transcriptional Regulatory Programs Using Arboretum. <i>Methods in Molecular Biology</i> , 2016, 1361, 375-389.	0.9	2
38	Functional and comparative genomics reveals conserved noncoding sequences in the nitrogen-fixing clade. <i>New Phytologist</i> , 2022, 234, 634-649.	7.3	2
39	ISMB 2022 proceedings. <i>Bioinformatics</i> , 2022, 38, i8-i9.	4.1	0
40	Enabling Studies of Genome-Scale Regulatory Network Evolution in Large Phylogenies with MRTLE. <i>Methods in Molecular Biology</i> , 2022, 2477, 439-455.	0.9	0