

# Sridhar Hannenhalli

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

17,409  
citations

126907

33  
h-index

64796

79  
g-index

87  
all docs

87  
docs citations

87  
times ranked

20673  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cross-species identification of PIP5K1-, splicing- and ubiquitin-related pathways as potential targets for RB1-deficient cells. <i>PLoS Genetics</i> , 2021, 17, e1009354.	3.5	5
2	A transcription-centric model of SNP-age interaction. <i>PLoS Genetics</i> , 2021, 17, e1009427.	3.5	7
3	Predicting tissue-specific gene expression from whole blood transcriptome. <i>Science Advances</i> , 2021, 7, .	10.3	50
4	A Transcriptionally Distinct Subpopulation of Healthy Acinar Cells Exhibit Features of Pancreatic Progenitors and PDAC. <i>Cancer Research</i> , 2021, 81, 3958-3970.	0.9	9
5	Prioritizing and characterizing functionally relevant genes across human tissues. <i>PLoS Computational Biology</i> , 2021, 17, e1009194.	3.2	4
6	Ligand dependent gene regulation by transient ER $\alpha$ clustered enhancers. <i>PLoS Genetics</i> , 2020, 16, e1008516.	3.5	20
7	Beyond Synthetic Lethality: Charting the Landscape of Pairwise Gene Expression States Associated with Survival in Cancer. <i>Cell Reports</i> , 2019, 28, 938-948.e6.	6.4	29
8	Migration rather than proliferation transcriptomic signatures are strongly associated with breast cancer patient survival. <i>Scientific Reports</i> , 2019, 9, 10989.	3.3	28
9	Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. <i>Nature Communications</i> , 2019, 10, 2760.	12.8	22
10	Allele-specific enhancers mediate associations between LCAT and ABCA1 polymorphisms and HDL metabolism. <i>PLoS ONE</i> , 2019, 14, e0215911.	2.5	3
11	ChIPulate: A comprehensive ChIP-seq simulation pipeline. <i>PLoS Computational Biology</i> , 2019, 15, e1006921.	3.2	9
12	Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. <i>Molecular Systems Biology</i> , 2019, 15, e8323.	7.2	25
13	Single-Cell Profiling Defines Transcriptomic Signatures Specific to Tumor-Reactive versus Virus-Responsive CD4+ T Cells. <i>Cell Reports</i> , 2019, 29, 3019-3032.e6.	6.4	50
14	Putative functional genes in idiopathic dilated cardiomyopathy. <i>Scientific Reports</i> , 2018, 8, 66.	3.3	7
15	Orphan CpG islands as alternative promoters. <i>Transcription</i> , 2018, 9, 171-176.	3.1	11
16	Analysis and correction of compositional bias in sparse sequencing count data. <i>BMC Genomics</i> , 2018, 19, 799.	2.8	85
17	Harnessing synthetic lethality to predict the response to cancer treatment. <i>Nature Communications</i> , 2018, 9, 2546.	12.8	97
18	Comprehensive map of age-associated splicing changes across human tissues and their contributions to age-associated diseases. <i>Scientific Reports</i> , 2018, 8, 10929.	3.3	46

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19	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. <i>Cell</i> , 2018, 174, 1559-1570.e22.	28.9	183
20	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. <i>Genome Research</i> , 2017, 27, 553-566.	5.5	32
21	New Role for Interleukin-13 Receptor $\alpha 1$ in Myocardial Homeostasis and Heart Failure. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	29
22	Prediction and Subtyping of Hypertension from Pan-Tissue Transcriptomic and Genetic Analyses. <i>Genetics</i> , 2017, 207, 1121-1134.	2.9	6
23	A network diffusion approach to inferring sample-specific function reveals functional changes associated with breast cancer. <i>PLoS Computational Biology</i> , 2017, 13, e1005793.	3.2	10
24	A pathway-centric view of spatial proximity in the 3D nucleome across cell lines. <i>Scientific Reports</i> , 2016, 6, 39279.	3.3	10
25	Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. <i>BMC Cancer</i> , 2016, 16, 88.	2.6	1
26	Heterogeneity of transcription factor binding specificity models within and across cell lines. <i>Genome Research</i> , 2016, 26, 1110-1123.	5.5	7
27	Chromatin and genomic determinants of alternative splicing. , 2015, 2015, 345-354.		3
28	Regulated CRISPR Modules Exploit a Dual Defense Strategy of Restriction and Abortive Infection in a Model of Prokaryote-Phage Coevolution. <i>PLoS Computational Biology</i> , 2015, 11, e1004603.	3.2	14
29	Phenotype-Dependent Coexpression Gene Clusters: Application to Normal and Premature Ageing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 30-39.	3.0	6
30	High-Throughput Identification of <i>Cis</i> -Regulatory Rewiring Events in Yeast. <i>Molecular Biology and Evolution</i> , 2015, 32, msv203.	8.9	13
31	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. <i>Nature Communications</i> , 2015, 6, 8555.	12.8	22
32	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , 2015, 105, 83-89.	2.9	220
33	Evolutionarily Conserved Network Properties of Intrinsically Disordered Proteins. <i>PLoS ONE</i> , 2015, 10, e0126729.	2.5	17
34	An evaluation of Monte-Carlo logic and logicFS motivated by a study of the regulation of gene expression in heart failure. <i>Journal of Applied Statistics</i> , 2014, 41, 1956-1975.	1.3	1
35	Determinants of expression variability. <i>Nucleic Acids Research</i> , 2014, 42, 3503-3514.	14.5	68
36	Conservation in first introns is positively associated with the number of exons within genes and the presence of regulatory epigenetic signals. <i>BMC Genomics</i> , 2014, 15, 526.	2.8	66

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37	Developmental expression of chicken FOXN1 and putative target genes during feather development. <i>International Journal of Developmental Biology</i> , 2014, 58, 57-64.	0.6	5
38	Next-Generation Sequencing and Epigenomics Research: A Hammer in Search of Nails. <i>Genomics and Informatics</i> , 2014, 12, 2.	0.8	47
39	Three Independent Determinants of Protein Evolutionary Rate. <i>Journal of Molecular Evolution</i> , 2013, 76, 98-111.	1.8	23
40	Intrinsically disordered proteins and conformational noise. <i>Cell Cycle</i> , 2013, 12, 26-31.	2.6	48
41	Enhancer networks revealed by correlated DNase hypersensitivity states of enhancers. <i>Nucleic Acids Research</i> , 2013, 41, 6828-6838.	14.5	29
42	Correlated Evolution of Positions within Mammalian cis Elements. <i>PLoS ONE</i> , 2013, 8, e55521.	2.5	2
43	Why Transcription Factor Binding Sites Are Ten Nucleotides Long. <i>Genetics</i> , 2012, 192, 973-985.	2.9	132
44	Genomic analysis of sleep deprivation reveals translational regulation in the hippocampus. <i>Physiological Genomics</i> , 2012, 44, 981-991.	2.3	123
45	EPIGENOMIC MODEL OF CARDIAC ENHANCERS WITH APPLICATION TO GENOME WIDE ASSOCIATION STUDIES. , 2012, , .		2
46	Transcriptional regulation via TF-modifying enzymes: an integrative model-based analysis. <i>Nucleic Acids Research</i> , 2011, 39, e78-e78.	14.5	7
47	Gene Coexpression Network Topology of Cardiac Development, Hypertrophy, and Failure. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 26-35.	5.1	88
48	Epigenomic and RNA structural correlates of polyadenylation. <i>RNA Biology</i> , 2011, 8, 529-537.	3.1	20
49	Genome-Wide Survey of Natural Selection on Functional, Structural, and Network Properties of Polymorphic Sites in <i>Saccharomyces paradoxus</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 2615-2627.	8.9	18
50	Genetic and Physiological Activation of Osmosensitive Gene Expression Mimics Transcriptional Signatures of Pathogen Infection in <i>C. elegans</i> . <i>PLoS ONE</i> , 2010, 5, e9010.	2.5	71
51	Correlated changes between regulatory cis elements and condition-specific expression in paralogous gene families. <i>Nucleic Acids Research</i> , 2010, 38, 738-749.	14.5	8
52	Young proteins experience more variable selection pressures than old proteins. <i>Genome Research</i> , 2010, 20, 1574-1581.	5.5	69
53	Hopx and Hdac2 Interact to Modulate Gata4 Acetylation and Embryonic Cardiac Myocyte Proliferation. <i>Developmental Cell</i> , 2010, 19, 450-459.	7.0	125
54	Gene Profiling of Human Adipose Tissue During Evoked Inflammation In Vivo. <i>Diabetes</i> , 2009, 58, 2211-2219.	0.6	57

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55	Evidence for Coregulation of Myocardial Gene Expression by MEF2 and NFAT in Human Heart Failure. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 212-219.	5.1	26
56	Resistin gene variation is associated with systemic inflammation but not plasma adipokine levels, metabolic syndrome or coronary atherosclerosis in nondiabetic Caucasians. <i>Clinical Endocrinology</i> , 2009, 70, 698-705.	2.4	33
57	The evolution of Fox genes and their role in development and disease. <i>Nature Reviews Genetics</i> , 2009, 10, 233-240.	16.3	550
58	Sex and Age Dimorphism of Myocardial Gene Expression in Nonischemic Human Heart Failure. <i>Circulation: Cardiovascular Genetics</i> , 2008, 1, 117-125.	5.1	48
59	Functional Diversification of Paralogous Transcription Factors via Divergence in DNA Binding Site Motif and in Expression. <i>PLoS ONE</i> , 2008, 3, e2345.	2.5	31
60	Computational Analysis of Constraints on Noncoding Regions, Coding Regions and Gene Expression in Relation to Plasmodium Phenotypic Diversity. <i>PLoS ONE</i> , 2008, 3, e3122.	2.5	8
61	Genome-Wide Analysis of Natural Selection on Human Cis-Elements. <i>PLoS ONE</i> , 2008, 3, e3137.	2.5	24
62	Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. <i>Nucleic Acids Research</i> , 2007, 35, 3203-3213.	14.5	52
63	TREMOR—a tool for retrieving transcriptional modules by incorporating motif covariance. <i>Nucleic Acids Research</i> , 2007, 35, 7360-7371.	14.5	6
64	A mammalian promoter model links cis elements to genetic networks. <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 166-177.	2.1	31
65	Differential transcriptional response to nonassociative and associative components of classical fear conditioning in the amygdala and hippocampus. <i>Learning and Memory</i> , 2006, 13, 135-142.	1.3	49
66	Functional Analysis of Hes-1 in Preadipocytes. <i>Molecular Endocrinology</i> , 2006, 20, 698-705.	3.7	46
67	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. <i>PLoS Pathogens</i> , 2006, 2, e60.	4.7	310
68	Selection of Target Sites for Mobile DNA Integration in the Human Genome. <i>PLoS Computational Biology</i> , 2006, 2, e157.	3.2	191
69	Transcriptional Genomics Associates FOX Transcription Factors With Human Heart Failure. <i>Circulation</i> , 2006, 114, 1269-1276.	1.6	210
70	Genome-wide analysis of retroviral DNA integration. <i>Nature Reviews Microbiology</i> , 2005, 3, 848-858.	28.6	390
71	A Note on Efficient Computation of Haplotypes via Perfect Phylogeny. <i>Journal of Computational Biology</i> , 2004, 11, 858-866.	1.6	28
72	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	7.1	164

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73	Transcriptional regulation of protein complexes and biological pathways. <i>Mammalian Genome</i> , 2003, 14, 611-619.	2.2	20
74	Predicting transcription factor synergism. <i>Nucleic Acids Research</i> , 2002, 30, 4278-4284.	14.5	72
75	Identification of transcription factor binding sites in the human genome sequence. <i>Mammalian Genome</i> , 2002, 13, 510-514.	2.2	105
76	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
77	Ligand-Receptor Pairing Via Tree Comparison. <i>Journal of Computational Biology</i> , 2000, 7, 59-70.	1.6	10
78	Hardness of Flip-Cut Problems from Optical Mapping. <i>Journal of Computational Biology</i> , 1997, 4, 119-125.	1.6	8
79	Local Rules for Protein Folding on a Triangular Lattice and Generalized Hydrophobicity in the HP Model. <i>Journal of Computational Biology</i> , 1997, 4, 275-296.	1.6	58
80	Polynomial-time algorithm for computing translocation distance between genomes. <i>Discrete Applied Mathematics</i> , 1996, 71, 137-151.	0.9	103
81	Genome Sequence Comparison and Scenarios for Gene Rearrangements: A Test Case. <i>Genomics</i> , 1995, 30, 299-311.	2.9	115