Sridhar Hannenhalli

List of Publications by Year
in descending order

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	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
2	The evolution of Fox genes and their role in development and disease. Nature Reviews Genetics, 2009, 10, 233-240.	16.3	550
3	Genome-wide analysis of retroviral DNA integration. Nature Reviews Microbiology, 2005, 3, 848-858.	28.6	390
4	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. PLoS Pathogens, 2006, 2, e60.	4.7	310
5	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. Genomics, 2015, 105, 83-89.	2.9	220
6	Transcriptional Genomics Associates FOX Transcription Factors With Human Heart Failure. Circulation, 2006, 114, 1269-1276.	1.6	210
7	Selection of Target Sites for Mobile DNA Integration in the Human Genome. PLoS Computational Biology, 2006, 2, e157.	3.2	191
8	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. Cell, 2018, 174, 1559-1570.e22.	28.9	183
9	Whole-genome shotgun assembly and comparison of human genome assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1916-1921.	7.1	164
10	Why Transcription Factor Binding Sites Are Ten Nucleotides Long. Genetics, 2012, 192, 973-985.	2.9	132
11	Hopx and Hdac2 Interact to Modulate Gata4 Acetylation and Embryonic Cardiac Myocyte Proliferation. Developmental Cell, 2010, 19, 450-459.	7.0	125
12	Genomic analysis of sleep deprivation reveals translational regulation in the hippocampus. Physiological Genomics, 2012, 44, 981-991.	2.3	123
13	Genome Sequence Comparison and Scenarios for Gene Rearrangements: A Test Case. Genomics, 1995, 30, 299-311.	2.9	115
14	Identification of transcription factor binding sites in the human genome sequence. Mammalian Genome, 2002, 13, 510-514.	2.2	105
15	Polynomial-time algorithm for computing translocation distance between genomes. Discrete Applied Mathematics, 1996, 71, 137-151.	0.9	103
16	Harnessing synthetic lethality to predict the response to cancer treatment. Nature Communications, 2018, 9, 2546.	12.8	97
17	Gene Coexpression Network Topology of Cardiac Development, Hypertrophy, and Failure. Circulation: Cardiovascular Genetics, 2011, 4, 26-35.	5.1	88
18	Analysis and correction of compositional bias in sparse sequencing count data. BMC Genomics, 2018, 19, 799.	2.8	85

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19	Predicting transcription factor synergism. Nucleic Acids Research, 2002, 30, 4278-4284.	14.5	72
20	Genetic and Physiological Activation of Osmosensitive Gene Expression Mimics Transcriptional Signatures of Pathogen Infection in C. elegans. PLoS ONE, 2010, 5, e9010.	2.5	71
21	Young proteins experience more variable selection pressures than old proteins. Genome Research, 2010, 20, 1574-1581.	5.5	69
22	Determinants of expression variability. Nucleic Acids Research, 2014, 42, 3503-3514.	14.5	68
23	Conservation in first introns is positively associated with the number of exons within genes and the presence of regulatory epigenetic signals. BMC Genomics, 2014, 15, 526.	2.8	66
24	Local Rules for Protein Folding on a Triangular Lattice and Generalized Hydrophobicity in the HP Model. Journal of Computational Biology, 1997, 4, 275-296.	1.6	58
25	Gene Profiling of Human Adipose Tissue During Evoked Inflammation In Vivo. Diabetes, 2009, 58, 2211-2219.	0.6	57
26	Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. Nucleic Acids Research, 2007, 35, 3203-3213.	14.5	52
27	Single-Cell Profiling Defines Transcriptomic Signatures Specific to Tumor-Reactive versus Virus-Responsive CD4+ T Cells. Cell Reports, 2019, 29, 3019-3032.e6.	6.4	50
28	Predicting tissue-specific gene expression from whole blood transcriptome. Science Advances, 2021, 7, .	10.3	50
29	Differential transcriptional response to nonassociative and associative components of classical fear conditioning in the amygdala and hippocampus. Learning and Memory, 2006, 13, 135-142.	1.3	49
30	Sex and Age Dimorphism of Myocardial Gene Expression in Nonischemic Human Heart Failure. Circulation: Cardiovascular Genetics, 2008, 1, 117-125.	5.1	48
31	Intrinsically disordered proteins and conformational noise. Cell Cycle, 2013, 12, 26-31.	2.6	48
32	Next-Generation Sequencing and Epigenomics Research: A Hammer in Search of Nails. Genomics and Informatics, 2014, 12, 2.	0.8	47
33	Functional Analysis of Hes-1 in Preadipocytes. Molecular Endocrinology, 2006, 20, 698-705.	3.7	46
34	Comprehensive map of age-associated splicing changes across human tissues and their contributions to age-associated diseases. Scientific Reports, 2018, 8, 10929.	3.3	46
35	Resistin gene variation is associated with systemic inflammation but not plasma adipokine levels, metabolic syndrome or coronary atherosclerosis in nondiabetic Caucasians. Clinical Endocrinology, 2009, 70, 698-705.	2.4	33
36	Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal promoters. Genome Research, 2017, 27, 553-566.	5.5	32

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37	A mammalian promoter model links cis elements to genetic networks. Biochemical and Biophysical Research Communications, 2006, 347, 166-177.	2.1	31
38	Functional Diversification of Paralogous Transcription Factors via Divergence in DNA Binding Site Motif and in Expression. PLoS ONE, 2008, 3, e2345.	2.5	31
39	Enhancer networks revealed by correlated DNAse hypersensitivity states of enhancers. Nucleic Acids Research, 2013, 41, 6828-6838.	14.5	29
40	New Role for Interleukin–13 Receptor α1 in Myocardial Homeostasis and Heart Failure. Journal of the American Heart Association, 2017, 6, .	3.7	29
41	Beyond Synthetic Lethality: Charting the Landscape of Pairwise Gene Expression States Associated with Survival in Cancer. Cell Reports, 2019, 28, 938-948.e6.	6.4	29
42	A Note on Efficient Computation of Haplotypes via Perfect Phylogeny. Journal of Computational Biology, 2004, 11, 858-866.	1.6	28
43	Migration rather than proliferation transcriptomic signatures are strongly associated with breast cancer patient survival. Scientific Reports, 2019, 9, 10989.	3.3	28
44	Evidence for Coregulation of Myocardial Gene Expression by MEF2 and NFAT in Human Heart Failure. Circulation: Cardiovascular Genetics, 2009, 2, 212-219.	5.1	26
45	Genome–wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. Molecular Systems Biology, 2019, 15, e8323.	7.2	25
46	Genome-Wide Analysis of Natural Selection on Human Cis-Elements. PLoS ONE, 2008, 3, e3137.	2.5	24
47	Three Independent Determinants of Protein Evolutionary Rate. Journal of Molecular Evolution, 2013, 76, 98-111.	1.8	23
48	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. Nature Communications, 2015, 6, 8555.	12.8	22
49	Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. Nature Communications, 2019, 10, 2760.	12.8	22
50	Transcriptional regulation of protein complexes and biological pathways. Mammalian Genome, 2003, 14, 611-619.	2.2	20
51	Epigenomic and RNA structural correlates of polyadenylation. RNA Biology, 2011, 8, 529-537.	3.1	20
52	Ligand dependent gene regulation by transient ERα clustered enhancers. PLoS Genetics, 2020, 16, e1008516.	3.5	20
53	Genome-Wide Survey of Natural Selection on Functional, Structural, and Network Properties of Polymorphic Sites in Saccharomyces paradoxus. Molecular Biology and Evolution, 2011, 28, 2615-2627.	8.9	18
54	Evolutionarily Conserved Network Properties of Intrinsically Disordered Proteins. PLoS ONE, 2015, 10, e0126729.	2.5	17

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55	Regulated CRISPR Modules Exploit a Dual Defense Strategy of Restriction and Abortive Infection in a Model of Prokaryote-Phage Coevolution. PLoS Computational Biology, 2015, 11, e1004603.	3.2	14
56	High-Throughput Identification of *Cis*-Regulatory Rewiring Events in Yeast. Molecular Biology and Evolution, 2015, 32, msv203.	8.9	13
57	Orphan CpG islands as alternative promoters. Transcription, 2018, 9, 171-176.	3.1	11
58	Ligand-Receptor Pairing Via Tree Comparison. Journal of Computational Biology, 2000, 7, 59-70.	1.6	10
59	A pathway-centric view of spatial proximity in the 3D nucleome across cell lines. Scientific Reports, 2016, 6, 39279.	3.3	10
60	A network diffusion approach to inferring sample-specific function reveals functional changes associated with breast cancer. PLoS Computational Biology, 2017, 13, e1005793.	3.2	10
61	ChIPulate: A comprehensive ChIP-seq simulation pipeline. PLoS Computational Biology, 2019, 15, e1006921.	3.2	9
62	A Transcriptionally Distinct Subpopulation of Healthy Acinar Cells Exhibit Features of Pancreatic Progenitors and PDAC. Cancer Research, 2021, 81, 3958-3970.	0.9	9
63	Hardness of Flip-Cut Problems from Optical Mapping. Journal of Computational Biology, 1997, 4, 119-125.	1.6	8
64	Computational Analysis of Constraints on Noncoding Regions, Coding Regions and Gene Expression in Relation to Plasmodium Phenotypic Diversity. PLoS ONE, 2008, 3, e3122.	2.5	8
65	Correlated changes between regulatory cis elements and condition-specific expression in paralogous gene families. Nucleic Acids Research, 2010, 38, 738-749.	14.5	8
66	Transcriptional regulation via TF-modifying enzymes: an integrative model-based analysis. Nucleic Acids Research, 2011, 39, e78-e78.	14.5	7
67	Heterogeneity of transcription factor binding specificity models within and across cell lines. Genome Research, 2016, 26, 1110-1123.	5.5	7
68	Putative functional genes in idiopathic dilated cardiomyopathy. Scientific Reports, 2018, 8, 66.	3.3	7
69	A transcription-centric model of SNP-age interaction. PLoS Genetics, 2021, 17, e1009427.	3.5	7
70	TREMOR—a tool for retrieving transcriptional modules by incorporating motif covariance. Nucleic Acids Research, 2007, 35, 7360-7371.	14.5	6
71	Phenotype-Dependent Coexpression Gene Clusters: Application to Normal and Premature Ageing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 30-39.	3.0	6
72	Prediction and Subtyping of Hypertension from Pan-Tissue Transcriptomic and Genetic Analyses. Genetics, 2017, 207, 1121-1134.	2.9	6

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73	Cross-species identification of PIP5K1-, splicing- and ubiquitin-related pathways as potential targets for RB1-deficient cells. PLoS Genetics, 2021, 17, e1009354.	3.5	5
74	Developmental expression of chicken FOXN1 and putative target genes during feather development. International Journal of Developmental Biology, 2014, 58, 57-64.	0.6	5
75	Prioritizing and characterizing functionally relevant genes across human tissues. PLoS Computational Biology, 2021, 17, e1009194.	3.2	4
76	Chromatin and genomic determinants of alternative splicing. , 2015, 2015, 345-354.		3
77	Allele-specific enhancers mediate associations between LCAT and ABCA1 polymorphisms and HDL metabolism. PLoS ONE, 2019, 14, e0215911.	2.5	3
78	Correlated Evolution of Positions within Mammalian cis Elements. PLoS ONE, 2013, 8, e55521.	2.5	2
79	EPIGENOMIC MODEL OF CARDIAC ENHANCERS WITH APPLICATION TO GENOME WIDE ASSOCIATION STUDIES. , 2012, , .		2
80	An evaluation of Monte-Carlo logic and logicFS motivated by a study of the regulation of gene expression in heart failure. Journal of Applied Statistics, 2014, 41, 1956-1975.	1.3	1
81	Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. BMC Cancer, 2016, 16, 88.	2.6	1