

Raja Jothi

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

5,937
citations

94269

37
h-index

133063

59
g-index

63
all docs

63
docs citations

63
times ranked

10467
citing authors

#	ARTICLE	IF	CITATIONS
1	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. <i>Genome Research</i> , 2009, 19, 24-32.	2.4	587
2	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from ChIP-Seq data. <i>Nucleic Acids Research</i> , 2008, 36, 5221-5231.	6.5	500
3	An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5187-5191.	3.3	374
4	Global Phosphoproteomic Analysis of Human Skeletal Muscle Reveals a Network of Exercise-Regulated Kinases and AMPK Substrates. <i>Cell Metabolism</i> , 2015, 22, 922-935.	7.2	333
5	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. <i>Immunity</i> , 2011, 35, 299-311.	6.6	293
6	esBAF facilitates pluripotency by conditioning the genome for LIF/STAT3 signalling and by regulating polycomb function. <i>Nature Cell Biology</i> , 2011, 13, 903-913.	4.6	238
7	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012, 28, 221-232.	2.9	235
8	DNMT1 is essential for mammary and cancer stem cell maintenance and tumorigenesis. <i>Nature Communications</i> , 2015, 6, 6910.	5.8	204
9	DOMINE: a comprehensive collection of known and predicted domain-domain interactions. <i>Nucleic Acids Research</i> , 2011, 39, D730-D735.	6.5	167
10	Histone-Fold Domain Protein NF-Y Promotes Chromatin Accessibility for Cell Type-Specific Master Transcription Factors. <i>Molecular Cell</i> , 2014, 55, 708-722.	4.5	149
11	INO80 Facilitates Pluripotency Gene Activation in Embryonic Stem Cell Self-Renewal, Reprogramming, and Blastocyst Development. <i>Cell Stem Cell</i> , 2014, 14, 575-591.	5.2	148
12	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. <i>Molecular Systems Biology</i> , 2009, 5, 294.	3.2	146
13	Fip1 regulates mRNA alternative polyadenylation to promote stem cell self-renewal. <i>EMBO Journal</i> , 2014, 33, 878-889.	3.5	136
14	Chromatin poises miRNA- and protein-coding genes for expression. <i>Genome Research</i> , 2009, 19, 1742-1751.	2.4	135
15	Diverse stresses dramatically alter genome-wide p53 binding and transactivation landscape in human cancer cells. <i>Nucleic Acids Research</i> , 2013, 41, 7286-7301.	6.5	135
16	ROR β directly regulates the circadian expression of clock genes and downstream targets <i>in vivo</i> . <i>Nucleic Acids Research</i> , 2012, 40, 8519-8535.	6.5	130
17	Co-evolutionary Analysis of Domains in Interacting Proteins Reveals Insights into Domain-Domain Interactions Mediating Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2006, 362, 861-875.	2.0	123
18	DOMINE: a database of protein domain interactions. <i>Nucleic Acids Research</i> , 2008, 36, D656-D661.	6.5	122

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19	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10.	2.9	111
20	Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. <i>Nature Immunology</i> , 2011, 12, 129-136.	7.0	91
21	mTORC1 Is a Major Regulatory Node in the FGF21 Signaling Network in Adipocytes. <i>Cell Reports</i> , 2016, 17, 29-36.	2.9	88
22	Intragenic Enhancers Attenuate Host Gene Expression. <i>Molecular Cell</i> , 2017, 68, 104-117.e6.	4.5	85
23	Acute depletion of Tet1-dependent 5-hydroxymethylcytosine levels impairs LIF/Stat3 signaling and results in loss of embryonic stem cell identity. <i>Nucleic Acids Research</i> , 2012, 40, 3364-3377.	6.5	84
24	Ldb1-nucleated transcription complexes function as primary mediators of global erythroid gene activation. <i>Blood</i> , 2013, 121, 4575-4585.	0.6	78
25	Retinoic Acid-Related Orphan Receptor $\hat{1}^3$ (ROR $\hat{1}^3$): A Novel Participant in the Diurnal Regulation of Hepatic Gluconeogenesis and Insulin Sensitivity. <i>PLoS Genetics</i> , 2014, 10, e1004331.	1.5	76
26	Predicting domain-domain interactions using a parsimony approach. <i>Genome Biology</i> , 2006, 7, R104.	13.9	73
27	Discovering functional linkages and uncharacterized cellular pathways using phylogenetic profile comparisons: a comprehensive assessment. <i>BMC Bioinformatics</i> , 2007, 8, 173.	1.2	71
28	GABP controls a critical transcription regulatory module that is essential for maintenance and differentiation of hematopoietic stem/progenitor cells. <i>Blood</i> , 2011, 117, 2166-2178.	0.6	69
29	Predicting protein-protein interaction by searching evolutionary tree automorphism space. <i>Bioinformatics</i> , 2005, 21, i241-i250.	1.8	68
30	Cnot1, Cnot2, and Cnot3 Maintain Mouse and Human ESC Identity and Inhibit Extraembryonic Differentiation. <i>Stem Cells</i> , 2012, 30, 910-922.	1.4	63
31	COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations. <i>Bioinformatics</i> , 2006, 22, 779-788.	1.8	61
32	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	1.5	58
33	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. <i>Nature Communications</i> , 2019, 10, 3072.	5.8	53
34	Decoding the function of bivalent chromatin in development and cancer. <i>Genome Research</i> , 2021, 31, 2170-2184.	2.4	48
35	GLIS3 is indispensable for TSH/TSHR-dependent thyroid hormone biosynthesis and follicular cell proliferation. <i>Journal of Clinical Investigation</i> , 2017, 127, 4326-4337.	3.9	47
36	Genome-Wide Characterization of Menin-Dependent H3K4me3 Reveals a Specific Role for Menin in the Regulation of Genes Implicated in MEN1-Like Tumors. <i>PLoS ONE</i> , 2012, 7, e37952.	1.1	46

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37	Decomposition of overlapping protein complexes: a graph theoretical method for analyzing static and dynamic protein associations. <i>Algorithms for Molecular Biology</i> , 2006, 1, 7.	0.3	43
38	Predicting protein domain interactions from coevolution of conserved regions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 811-820.	1.5	42
39	Approximation algorithms for the capacitated minimum spanning tree problem and its variants in network design. <i>ACM Transactions on Algorithms</i> , 2005, 1, 265-282.	0.9	38
40	ChIP-Seq Data Analysis: Identification of Protein-DNA Binding Sites with SISSRs Peak-Finder. <i>Methods in Molecular Biology</i> , 2012, 802, 305-322.	0.4	38
41	Positive-unlabeled ensemble learning for kinase substrate prediction from dynamic phosphoproteomics data. <i>Bioinformatics</i> , 2016, 32, 252-259.	1.8	34
42	Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004403.	1.5	32
43	CNOT3-Dependent mRNA Deadenylation Safeguards the Pluripotent State. <i>Stem Cell Reports</i> , 2016, 7, 897-910.	2.3	29
44	Approximating the k-traveling repairman problem with repair times. <i>Journal of Discrete Algorithms</i> , 2007, 5, 293-303.	0.7	28
45	KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. <i>Proteomics</i> , 2016, 16, 1868-1871.	1.3	27
46	Integrative framework for identification of key cell identity genes uncovers determinants of ES cell identity and homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1581-90.	3.3	26
47	Critical Requirement of GABP± for Normal T Cell Development. <i>Journal of Biological Chemistry</i> , 2010, 285, 10179-10188.	1.6	25
48	Knowledge-guided inference of domain-domain interactions from incomplete protein-protein interaction networks. <i>Bioinformatics</i> , 2009, 25, 2492-2499.	1.8	24
49	GLIS3 Transcriptionally Activates WNT Genes to Promote Differentiation of Human Embryonic Stem Cells into Posterior Neural Progenitors. <i>Stem Cells</i> , 2019, 37, 202-215.	1.4	21
50	Improved Approximation Algorithms for the Single-Sink Buy-at-Bulk Network Design Problems. <i>Lecture Notes in Computer Science</i> , 2004, , 336-348.	1.0	21
51	Degree-bounded minimum spanning trees. <i>Discrete Applied Mathematics</i> , 2009, 157, 960-970.	0.5	20
52	Transcriptional network dynamics during the progression of pluripotency revealed by integrative statistical learning. <i>Nucleic Acids Research</i> , 2020, 48, 1828-1842.	6.5	14
53	Fine-tuning of epigenetic regulation with respect to promoter CpG content in a cell type-specific manner. <i>Epigenetics</i> , 2014, 9, 747-759.	1.3	11
54	Survivable network design: the capacitated minimum spanning network problem. <i>Information Processing Letters</i> , 2004, 91, 183-190.	0.4	8

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55	Approximation Algorithms for the Capacitated Minimum Spanning Tree Problem and Its Variants in Network Design. Lecture Notes in Computer Science, 2004, , 805-818.	1.0	7
56	Minimum Latency Tours and the k-Traveling Repairmen Problem. Lecture Notes in Computer Science, 2004, , 423-433.	1.0	6
57	Improved approximation algorithms for the single-sink buy-at-bulk network design problems. Journal of Discrete Algorithms, 2009, 7, 249-255.	0.7	5
58	Differences in evolutionary pressure acting within highly conserved ortholog groups. BMC Evolutionary Biology, 2008, 8, 208.	3.2	4
59	Computational Approaches to Predict Protein-Protein and Domain-Domain Interactions. , 2007, , 465-491.		3
60	Load-balanced agent activation for value-added network services. Computer Communications, 2006, 29, 1905-1916.	3.1	1