

Theodore J Perkins

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

1,552

citations

20

h-index

38

g-index

69

ext. papers

1,921

ext. citations

7.2

avg, IF

4.52

L-index

#	Paper	IF	Citations
62	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa002	3.7	5
61	Establishment of macaque trophoblast stem cell lines derived from cynomolgus monkey blastocysts. <i>Scientific Reports</i> , 2020 , 10, 6827	4.9	6
60	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020 , 78, 960-974.e11	17.6	38
59	Myf6/MRF4 is a myogenic niche regulator required for the maintenance of the muscle stem cell pool. <i>EMBO Reports</i> , 2020 , 21, e49499	6.5	11
58	Absolute quantification of transcription factors in human erythropoiesis using selected reaction monitoring mass spectrometry. <i>STAR Protocols</i> , 2020 , 1, 100216	1.4	1
57	Accuracy and reproducibility of somatic point mutation calling in clinical-type targeted sequencing data. <i>BMC Medical Genomics</i> , 2020 , 13, 156	3.7	4
56	Preclinical rationale for entinostat in embryonal rhabdomyosarcoma. <i>Skeletal Muscle</i> , 2019 , 9, 12	5.1	9
55	RECAP reveals the true statistical significance of ChIP-seq peak calls. <i>Bioinformatics</i> , 2019 , 35, 3592-3598	7.2	5
54	High-resolution genome-wide expression analysis of single myofibers using SMART-Seq. <i>Journal of Biological Chemistry</i> , 2019 , 294, 20097-20108	5.4	13
53	Human gene expression variability and its dependence on methylation and aging. <i>BMC Genomics</i> , 2019 , 20, 941	4.5	9
52	Transcriptomically Guided Mesendoderm Induction of Human Pluripotent Stem Cells Using a Systematically Defined Culture Scheme. <i>Stem Cell Reports</i> , 2019 , 13, 1111-1125	8	2
51	Mtf2-PRC2 control of canonical Wnt signaling is required for definitive erythropoiesis. <i>Cell Discovery</i> , 2018 , 4, 21	22.3	24
50	Dynamics in Epistasis Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 878-891	3	
49	Cis-regulatory determinants of MyoD function. <i>Nucleic Acids Research</i> , 2018 , 46, 7221-7235	20.1	6
48	Targeting the MTF2-MDM2 Axis Sensitizes Refractory Acute Myeloid Leukemia to Chemotherapy. <i>Cancer Discovery</i> , 2018 , 8, 1376-1389	24.4	22
47	The HDAC3-SMARCA4-miR-27a axis promotes expression of the fusion oncogene in rhabdomyosarcoma. <i>Science Signaling</i> , 2018 , 11,	8.8	30
46	PCP and SAX-3/Robo Pathways Cooperate to Regulate Convergent Extension-Based Nerve Cord Assembly in <i>C. elegans</i> . <i>Developmental Cell</i> , 2017 , 41, 195-203.e3	10.2	19

45	Induction of senescence in primary glioblastoma cells by serum and TGF β . <i>Scientific Reports</i> , 2017 , 7, 2156	4.9	13
44	Reprogramming progeria fibroblasts re-establishes a normal epigenetic landscape. <i>Aging Cell</i> , 2017 , 16, 870-887	9.9	28
43	Epigenetic Activation of Pro-angiogenic Signaling Pathways in Human Endothelial Progenitors Increases Vasculogenesis. <i>Stem Cell Reports</i> , 2017 , 9, 1573-1587	8	30
42	Uncovering robust patterns of microRNA co-expression across cancers using Bayesian Relevance Networks. <i>PLoS ONE</i> , 2017 , 12, e0183103	3.7	5
41	Fully polynomial-time computation of maximum likelihood trajectories in Markov chains. <i>Information Processing Letters</i> , 2017 , 118, 53-57	0.8	
40	On cross-conditional and fluctuation correlations in competitive RNA networks. <i>Bioinformatics</i> , 2016 , 32, i790-i797	7.2	4
39	UTX inhibition as selective epigenetic therapy against TAL1-driven T-cell acute lymphoblastic leukemia. <i>Genes and Development</i> , 2016 , 30, 508-21	12.6	77
38	Bayesian Correlation Analysis for Sequence Count Data. <i>PLoS ONE</i> , 2016 , 11, e0163595	3.7	8
37	Control of glioblastoma tumorigenesis by feed-forward cytokine signaling. <i>Nature Neuroscience</i> , 2016 , 19, 798-806	25.5	62
36	Induction of Activating Transcription Factor 3 Is Associated with Cisplatin Responsiveness in Non-Small Cell Lung Carcinoma Cells. <i>Neoplasia</i> , 2016 , 18, 525-35	6.4	19
35	miR Profiling Identifies Cyclin-Dependent Kinase 6 Downregulation as a Potential Mechanism of Acquired Cisplatin Resistance in Non-Small-Cell Lung Carcinoma. <i>Clinical Lung Cancer</i> , 2015 , 16, e121-9	4.9	20
34	Integrative genomics positions MKRN1 as a novel ribonucleoprotein within the embryonic stem cell gene regulatory network. <i>EMBO Reports</i> , 2015 , 16, 1334-57	6.5	20
33	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. <i>Epigenetics and Chromatin</i> , 2015 , 8, 33	5.8	13
32	Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach. <i>Bioinformatics</i> , 2015 , 31, 2676-82	7.2	
31	A scaling law for random walks on networks. <i>Nature Communications</i> , 2014 , 5, 5121	17.4	16
30	Learning to Detect Contours with Dynamic Programming Snakes 2014 ,		2
29	Trichostatin A enhances vascular repair by injected human endothelial progenitors through increasing the expression of TAL1-dependent genes. <i>Cell Stem Cell</i> , 2014 , 14, 644-57	18	42
28	Pooled screening for synergistic interactions subject to blocking and noise. <i>PLoS ONE</i> , 2014 , 9, e85864	3.7	2

27	Chromatin tandem affinity purification sequencing. <i>Nature Protocols</i> , 2013 , 8, 1525-34	18.8	11
26	Adaptive bandwidth kernel density estimation for next-generation sequencing data. <i>BMC Proceedings</i> , 2013 , 7, S7	2.3	6
25	MaSC: mappability-sensitive cross-correlation for estimating mean fragment length of single-end short-read sequencing data. <i>Bioinformatics</i> , 2013 , 29, 444-50	7.2	23
24	Transcriptional dominance of Pax7 in adult myogenesis is due to high-affinity recognition of homeodomain motifs. <i>Developmental Cell</i> , 2012 , 22, 1208-20	10.2	107
23	Methods for Determining the Statistical Significance of Enrichment or Depletion of Gene Ontology Classifications under Weighted Membership. <i>Frontiers in Genetics</i> , 2012 , 3, 24	4.5	
22	What do molecules do when we are not looking? State sequence analysis for stochastic chemical systems. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 3411-25	4.1	1
21	Systematic discovery of Rab GTPases with synaptic functions in Drosophila. <i>Current Biology</i> , 2011 , 21, 1704-15	6.3	95
20	Quantitative epistasis analysis and pathway inference from genetic interaction data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002048	5	9
19	Stochastic Gene Expression and the Processing and Propagation of Noisy Signals in Genetic Networks. <i>Intelligent Systems Reference Library</i> , 2011 , 89-112	0.8	2
18	Maximum probability reaction sequences in stochastic chemical kinetic systems. <i>Frontiers in Physiology</i> , 2010 , 1, 170	4.6	2
17	A trade-off between sample complexity and computational complexity in learning Boolean networks from time-series data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010 , 7, 118-25	3	16
16	Estimating the stochastic bifurcation structure of cellular networks. <i>PLoS Computational Biology</i> , 2010 , 6, e1000699	5	25
15	Robust dynamics in minimal hybrid models of genetic networks. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010 , 368, 4961-75	3	18
14	Functional data analysis for identifying nonlinear models of gene regulatory networks. <i>BMC Genomics</i> , 2010 , 11 Suppl 4, S18	4.5	6
13	A general model of codon bias due to GC mutational bias. <i>PLoS ONE</i> , 2010 , 5, e13431	3.7	107
12	Strategies for cellular decision-making. <i>Molecular Systems Biology</i> , 2009 , 5, 326	12.2	210
11	Statistical lower bounds on protein copy number from fluorescence expression images. <i>Bioinformatics</i> , 2009 , 25, 2670-6	7.2	10
10	Implementing arithmetic and other analytic operations by transcriptional regulation. <i>PLoS Computational Biology</i> , 2008 , 4, e1000064	5	6

9	The gap gene system of <i>Drosophila melanogaster</i> : model-fitting and validation. <i>Annals of the New York Academy of Sciences</i> , 2007 , 1115, 116-31	6.5	3
8	Noisy information processing through transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7151-6	11.5	60
7	Reverse engineering the gap gene network of <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2006 , 2, e51	5	139
6	A fluctuation method to quantify in vivo fluorescence data. <i>Biophysical Journal</i> , 2006 , 91, 759-66	2.9	54
5	Dynamical properties of model gene networks and implications for the inverse problem. <i>BioSystems</i> , 2006 , 84, 115-23	1.9	8
4	Chaotic Dynamics in an Electronic Model of a Genetic Network. <i>Journal of Statistical Physics</i> , 2005 , 121, 969-994	1.5	15
3	Inferring models of gene expression dynamics. <i>Journal of Theoretical Biology</i> , 2004 , 230, 289-99	2.3	51
2	Bayesian Correlation is a robust similarity measure for single cell RNA-seq data		1
1	Myf6/MRF4 is a Myogenic Niche Regulator Required for the Maintenance of the Muscle Stem Cell Pool		1