

Theodore J Perkins

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

2,129
citations

279487

23
h-index

253896

43
g-index

69
all docs

69
docs citations

69
times ranked

3716
citing authors

#	ARTICLE	IF	CITATIONS
1	Strategies for cellular decision-making. <i>Molecular Systems Biology</i> , 2009, 5, 326.	3.2	272
2	Reverse Engineering the Gap Gene Network of <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2006, 2, e51.	1.5	161
3	A General Model of Codon Bias Due to GC Mutational Bias. <i>PLoS ONE</i> , 2010, 5, e13431.	1.1	144
4	Transcriptional Dominance of Pax7 in Adult Myogenesis Is Due to High-Affinity Recognition of Homeodomain Motifs. <i>Developmental Cell</i> , 2012, 22, 1208-1220.	3.1	139
5	Systematic Discovery of Rab GTPases with Synaptic Functions in <i>Drosophila</i> . <i>Current Biology</i> , 2011, 21, 1704-1715.	1.8	122
6	UTX inhibition as selective epigenetic therapy against TAL1-driven T-cell acute lymphoblastic leukemia. <i>Genes and Development</i> , 2016, 30, 508-521.	2.7	104
7	Noisy information processing through transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7151-7156.	3.3	83
8	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	4.5	83
9	Control of glioblastoma tumorigenesis by feed-forward cytokine signaling. <i>Nature Neuroscience</i> , 2016, 19, 798-806.	7.1	82
10	A Fluctuation Method to Quantify In Vivo Fluorescence Data. <i>Biophysical Journal</i> , 2006, 91, 759-766.	0.2	69
11	Inferring models of gene expression dynamics. <i>Journal of Theoretical Biology</i> , 2004, 230, 289-299.	0.8	55
12	The HDAC3-SMARCA4-miR-27a axis promotes expression of the PAX3:FOXO1 fusion oncogene in rhabdomyosarcoma. <i>Science Signaling</i> , 2018, 11, .	1.6	51
13	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, 644-657.	5.2	48
14	Targeting the MTF2-MDM2 Axis Sensitizes Refractory Acute Myeloid Leukemia to Chemotherapy. <i>Cancer Discovery</i> , 2018, 8, 1376-1389.	7.7	40
15	Myf6/MRF4 is a myogenic niche regulator required for the maintenance of the muscle stem cell pool. <i>EMBO Reports</i> , 2020, 21, e49499.	2.0	40
16	Mtf2-PRC2 control of canonical Wnt signaling is required for definitive erythropoiesis. <i>Cell Discovery</i> , 2018, 4, 21.	3.1	37
17	PCP and SAX-3/Robo Pathways Cooperate to Regulate Convergent Extension-Based Nerve Cord Assembly in <i>C.Ælegans</i> . <i>Developmental Cell</i> , 2017, 41, 195-203.e3.	3.1	36
18	Epigenetic Activation of Pro-angiogenic Signaling Pathways in Human Endothelial Progenitors Increases Vasculogenesis. <i>Stem Cell Reports</i> , 2017, 9, 1573-1587.	2.3	36

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19	Reprogramming progeria fibroblasts reestablishes a normal epigenetic landscape. <i>Aging Cell</i> , 2017, 16, 870-887.	3.0	34
20	Estimating the Stochastic Bifurcation Structure of Cellular Networks. <i>PLoS Computational Biology</i> , 2010, 6, e1000699.	1.5	32
21	MaSC: mappability-sensitive cross-correlation for estimating mean fragment length of single-end short-read sequencing data. <i>Bioinformatics</i> , 2013, 29, 444-450.	1.8	31
22	Integrative genomics positions <i>MKRN1</i> as a novel ribonucleoprotein within the embryonic stem cell gene regulatory network. <i>EMBO Reports</i> , 2015, 16, 1334-1357.	2.0	28
23	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-e129.	1.1	25
24	Induction of Activating Transcription Factor 3 Is Associated with Cisplatin Responsiveness in Non-Small Cell Lung Carcinoma Cells. <i>Neoplasia</i> , 2016, 18, 525-535.	2.3	25
25	High-resolution genome-wide expression analysis of single myofibers using SMART-Seq. <i>Journal of Biological Chemistry</i> , 2019, 294, 20097-20108.	1.6	25
26	Human gene expression variability and its dependence on methylation and aging. <i>BMC Genomics</i> , 2019, 20, 941.	1.2	25
27	Robust dynamics in minimal hybrid models of genetic networks. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2010, 368, 4961-4975.	1.6	20
28	A scaling law for random walks on networks. <i>Nature Communications</i> , 2014, 5, 5121.	5.8	20
29	Chaotic Dynamics in an Electronic Model of a Genetic Network. <i>Journal of Statistical Physics</i> , 2005, 121, 969-994.	0.5	18
30	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, 118-125.	1.9	18
31	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.	1.8	17
32	Induction of senescence in primary glioblastoma cells by serum and TGF β ² . <i>Scientific Reports</i> , 2017, 7, 2156.	1.6	17
33	Preclinical rationale for entinostat in embryonal rhabdomyosarcoma. <i>Skeletal Muscle</i> , 2019, 9, 12.	1.9	17
34	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa002.	1.5	17
35	Statistical lower bounds on protein copy number from fluorescence expression images. <i>Bioinformatics</i> , 2009, 25, 2670-2676.	1.8	15
36	Quantitative Epistasis Analysis and Pathway Inference from Genetic Interaction Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002048.	1.5	15

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37	Chromatin tandem affinity purification sequencing. <i>Nature Protocols</i> , 2013, 8, 1525-1534.	5.5	13
38	Cis-regulatory determinants of MyoD function. <i>Nucleic Acids Research</i> , 2018, 46, 7221-7235.	6.5	11
39	Establishment of macaque trophoblast stem cell lines derived from cynomolgus monkey blastocysts. <i>Scientific Reports</i> , 2020, 10, 6827.	1.6	10
40	Bayesian Correlation Analysis for Sequence Count Data. <i>PLoS ONE</i> , 2016, 11, e0163595.	1.1	10
41	Dynamical properties of model gene networks and implications for the inverse problem. <i>BioSystems</i> , 2006, 84, 115-123.	0.9	9
42	Adaptive bandwidth kernel density estimation for next-generation sequencing data. <i>BMC Proceedings</i> , 2013, 7, S7.	1.8	9
43	Accuracy and reproducibility of somatic point mutation calling in clinical-type targeted sequencing data. <i>BMC Medical Genomics</i> , 2020, 13, 156.	0.7	8
44	Functional data analysis for identifying nonlinear models of gene regulatory networks. <i>BMC Genomics</i> , 2010, 11, S18.	1.2	7
45	RECAP reveals the true statistical significance of ChIP-seq peak calls. <i>Bioinformatics</i> , 2019, 35, 3592-3598.	1.8	7
46	Implementing Arithmetic and Other Analytic Operations By Transcriptional Regulation. <i>PLoS Computational Biology</i> , 2008, 4, e1000064.	1.5	6
47	Uncovering robust patterns of microRNA co-expression across cancers using Bayesian Relevance Networks. <i>PLoS ONE</i> , 2017, 12, e0183103.	1.1	6
48	On cross-conditional and fluctuation correlations in competitive RNA networks. <i>Bioinformatics</i> , 2016, 32, i790-i797.	1.8	4
49	Transcriptomically Guided Mesendoderm Induction of Human Pluripotent Stem Cells Using a Systematically Defined Culture Scheme. <i>Stem Cell Reports</i> , 2019, 13, 1111-1125.	2.3	4
50	Absolute quantification of transcription factors in human erythropoiesis using selected reaction monitoring mass spectrometry. <i>STAR Protocols</i> , 2020, 1, 100216.	0.5	4
51	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, 116-131.	1.8	3
52	Pooled Screening for Synergistic Interactions Subject to Blocking and Noise. <i>PLoS ONE</i> , 2014, 9, e85864.	1.1	3
53	BATL: Bayesian annotations for targeted lipidomics. <i>Bioinformatics</i> , 2022, 38, 1593-1599.	1.8	3
54	Maximum probability reaction sequences in stochastic chemical kinetic systems. <i>Frontiers in Physiology</i> , 2010, 1, 170.	1.3	2

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55	Learning to Detect Contours with Dynamic Programming Snakes. , 2014, , .		2
56	What do molecules do when we are not looking? State sequence analysis for stochastic chemical systems. Journal of the Royal Society Interface, 2012, 9, 3411-3425.	1.5	1
57	The potential power of dynamics in epistasis analysis. , 2015, , .		1
58	Methods for Determining the Statistical Significance of Enrichment or Depletion of Gene Ontology Classifications under Weighted Membership. Frontiers in Genetics, 2012, 3, 24.	1.1	0
59	Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach. Bioinformatics, 2015, 31, 2676-2682.	1.8	0
60	Fully polynomial-time computation of maximum likelihood trajectories in Markov chains. Information Processing Letters, 2017, 118, 53-57.	0.4	0
61	Analysis of Controls in ChIP-seq. , 2017, , .		0
62	Dynamics in Epistasis Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 878-891.	1.9	0