Theodore J Perkins

List of Publications by Citations

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	Strategies for cellular decision-making. *Molecular Systems Biology*, **2009**, 5, 326	12.2	210
61	Reverse engineering the gap gene network of Drosophila melanogaster. *PLoS Computational Biology*, **2006**, 2, e51	5	139
60	Transcriptional dominance of Pax7 in adult myogenesis is due to high-affinity recognition of homeodomain motifs. *Developmental Cell*, **2012**, 22, 1208-20	10.2	107
59	A general model of codon bias due to GC mutational bias. *PLoS ONE*, **2010**, 5, e13431	3.7	107
58	Systematic discovery of Rab GTPases with synaptic functions in Drosophila. *Current Biology*, **2011**, 21, 1704-15	6.3	95
57	UTX inhibition as selective epigenetic therapy against TAL1-driven T-cell acute lymphoblastic leukemia. *Genes and Development*, **2016**, 30, 508-21	12.6	77
56	Control of glioblastoma tumorigenesis by feed-forward cytokine signaling. *Nature Neuroscience*, **2016**, 19, 798-806	25.5	62
55	Noisy information processing through transcriptional regulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 7151-6	11.5	60
54	A fluctuation method to quantify in vivo fluorescence data. *Biophysical Journal*, **2006**, 91, 759-66	2.9	54
53	Inferring models of gene expression dynamics. *Journal of Theoretical Biology*, **2004**, 230, 289-99	2.3	51
52	Trichostatin A enhances vascular repair by injected human endothelial progenitors through increasing the expression of TAL1-dependent genes. *Cell Stem Cell*, **2014**, 14, 644-57	18	42
51	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. *Molecular Cell*, **2020**, 78, 960-974.e11	17.6	38
50	Epigenetic Activation of Pro-angiogenic Signaling Pathways in Human Endothelial Progenitors Increases Vasculogenesis. *Stem Cell Reports*, **2017**, 9, 1573-1587	8	30
49	The HDAC3-SMARCA4-miR-27a axis promotes expression of the fusion oncogene in rhabdomyosarcoma. *Science Signaling*, **2018**, 11,	8.8	30
48	Reprogramming progeria fibroblasts re-establishes a normal epigenetic landscape. *Aging Cell*, **2017**, 16, 870-887	9.9	28
47	Estimating the stochastic bifurcation structure of cellular networks. *PLoS Computational Biology*, **2010**, 6, e1000699	5	25
46	Mtf2-PRC2 control of canonical Wnt signaling is required for definitive erythropoiesis. *Cell Discovery*, **2018**, 4, 21	22.3	24

45	MaSC: mappability-sensitive cross-correlation for estimating mean fragment length of single-end short-read sequencing data. *Bioinformatics*, **2013**, 29, 444-50	7.2	23
44	Targeting the MTF2-MDM2 Axis Sensitizes Refractory Acute Myeloid Leukemia to Chemotherapy. *Cancer Discovery*, **2018**, 8, 1376-1389	24.4	22
43	miR Profiling Identifies Cyclin-Dependent Kinase 6 Downregulation as a Potential Mechanism of Acquired Cisplatin Resistance in Non-Small-Cell Lung Carcinoma. *Clinical Lung Cancer*, **2015**, 16, e121-9	4.9	20
42	Integrative genomics positions MKRN1 as a novel ribonucleoprotein within the embryonic stem cell gene regulatory network. *EMBO Reports*, **2015**, 16, 1334-57	6.5	20
41	PCP and SAX-3/Robo Pathways Cooperate to Regulate Convergent Extension-Based Nerve Cord Assembly in C. elegans. *Developmental Cell*, **2017**, 41, 195-203.e3	10.2	19
40	Induction of Activating Transcription Factor 3 Is Associated with Cisplatin Responsiveness in Non-Small Cell Lung Carcinoma Cells. *Neoplasia*, **2016**, 18, 525-35	6.4	19
39	Robust dynamics in minimal hybrid models of genetic networks. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2010**, 368, 4961-75	3	18
38	A scaling law for random walks on networks. *Nature Communications*, **2014**, 5, 5121	17.4	16
37	A trade-off between sample complexity and computational complexity in learning Boolean networks from time-series data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2010**, 7, 118-25	3	16
36	Chaotic Dynamics in an Electronic Model of a Genetic Network. *Journal of Statistical Physics*, **2005**, 121, 969-994	1.5	15
35	Induction of senescence in primary glioblastoma cells by serum and TGF *Scientific Reports*, **2017**, 7, 2156	4.9	13
34	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. *Epigenetics and Chromatin*, **2015**, 8, 33	5.8	13
33	High-resolution genome-wide expression analysis of single myofibers using SMART-Seq. *Journal of Biological Chemistry*, **2019**, 294, 20097-20108	5.4	13
32	Chromatin tandem affinity purification sequencing. *Nature Protocols*, **2013**, 8, 1525-34	18.8	11
31	Myf6/MRF4 is a myogenic niche regulator required for the maintenance of the muscle stem cell pool. *EMBO Reports*, **2020**, 21, e49499	6.5	11
30	Statistical lower bounds on protein copy number from fluorescence expression images. *Bioinformatics*, **2009**, 25, 2670-6	7.2	10
29	Preclinical rationale for entinostat in embryonal rhabdomyosarcoma. *Skeletal Muscle*, **2019**, 9, 12	5.1	9
28	Quantitative epistasis analysis and pathway inference from genetic interaction data. *PLoS Computational Biology*, **2011**, 7, e1002048	5	9

27	Human gene expression variability and its dependence on methylation and aging. *BMC Genomics*, **2019**, 20, 941	4.5	9
26	Dynamical properties of model gene networks and implications for the inverse problem. *BioSystems*, **2006**, 84, 115-23	1.9	8
25	Bayesian Correlation Analysis for Sequence Count Data. *PLoS ONE*, **2016**, 11, e0163595	3.7	8
24	Establishment of macaque trophoblast stem cell lines derived from cynomolgus monkey blastocysts. *Scientific Reports*, **2020**, 10, 6827	4.9	6
23	Cis-regulatory determinants of MyoD function. *Nucleic Acids Research*, **2018**, 46, 7221-7235	20.1	6
22	Adaptive bandwidth kernel density estimation for next-generation sequencing data. *BMC Proceedings*, **2013**, 7, S7	2.3	6
21	Functional data analysis for identifying nonlinear models of gene regulatory networks. *BMC Genomics*, **2010**, 11 Suppl 4, S18	4.5	6
20	Implementing arithmetic and other analytic operations by transcriptional regulation. *PLoS Computational Biology*, **2008**, 4, e1000064	5	6
19	RECAP reveals the true statistical significance of ChIP-seq peak calls. *Bioinformatics*, **2019**, 35, 3592-3598	7.2	5
18	Bayesian correlation is a robust gene similarity measure for single-cell RNA-seq data. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa002	3.7	5
17	Uncovering robust patterns of microRNA co-expression across cancers using Bayesian Relevance Networks. *PLoS ONE*, **2017**, 12, e0183103	3.7	5
16	On cross-conditional and fluctuation correlations in competitive RNA networks. *Bioinformatics*, **2016**, 32, i790-i797	7.2	4
15	Accuracy and reproducibility of somatic point mutation calling in clinical-type targeted sequencing data. *BMC Medical Genomics*, **2020**, 13, 156	3.7	4
14	The gap gene system of Drosophila melanogaster: model-fitting and validation. *Annals of the New York Academy of Sciences*, **2007**, 1115, 116-31	6.5	3
13	Learning to Detect Contours with Dynamic Programming Snakes **2014**,		2
12	Maximum probability reaction sequences in stochastic chemical kinetic systems. *Frontiers in Physiology*, **2010**, 1, 170	4.6	2
11	Pooled screening for synergistic interactions subject to blocking and noise. *PLoS ONE*, **2014**, 9, e85864	3.7	2
10	Stochastic Gene Expression and the Processing and Propagation of Noisy Signals in Genetic Networks. *Intelligent Systems Reference Library*, **2011**, 89-112	0.8	2

List of Publications

9	Transcriptomically Guided Mesendoderm Induction of Human Pluripotent Stem Cells Using a Systematically Defined Culture Scheme. *Stem Cell Reports*, **2019**, 13, 1111-1125	8	2
8	What do molecules do when we are not looking? State sequence analysis for stochastic chemical systems. *Journal of the Royal Society Interface*, **2012**, 9, 3411-25	4.1	1
7	Bayesian Correlation is a robust similarity measure for single cell RNA-seq data		1
6	Absolute quantification of transcription factors in human erythropoiesis using selected reaction monitoring mass spectrometry. *STAR Protocols*, **2020**, 1, 100216	1.4	1
5	Myf6/MRF4 is a Myogenic Niche Regulator Required for the Maintenance of the Muscle Stem Cell Pool		1
4	Dynamics in Epistasis Analysis. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2018**, 15, 878-891	3	
3	Fully polynomial-time computation of maximum likelihood trajectories in Markov chains. *Information Processing Letters*, **2017**, 118, 53-57	0.8	
2	Gene selection for the reconstruction of stem cell differentiation trees: a linear programming approach. *Bioinformatics*, **2015**, 31, 2676-82	7.2	
1	Methods for Determining the Statistical Significance of Enrichment or Depletion of Gene Ontology Classifications under Weighted Membership. *Frontiers in Genetics*, **2012**, 3, 24	4.5	