Thomas Freeman

List of Publications by Year in descending order

87 papers	13,407 citations	50276 46 h-index
103 all docs	103 docs citations	103 times ranked

48315 88 g-index

24629 citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
2	Transcriptome-Based Network Analysis Reveals a Spectrum Model of Human Macrophage Activation. Immunity, 2014, 40, 274-288.	14.3	1,692
3	Microglial brain regionâˆ'dependent diversity and selective regional sensitivities to aging. Nature Neuroscience, 2016, 19, 504-516.	14.8	919
4	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828
5	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
6	Fulminant Jejuno-Ileitis following Ablation of Enteric Glia in Adult Transgenic Mice. Cell, 1998, 93, 189-201.	28.9	530
7	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
8	Tissue distribution of adenosine receptor mRNAs in the rat. British Journal of Pharmacology, 1996, 118, 1461-1468.	5.4	503
9	Network visualization and analysis of gene expression data using BioLayout Express3D. Nature Protocols, 2009, 4, 1535-1550.	12.0	443
10	An expression atlas of human primary cells: inference of gene function from coexpression networks. BMC Genomics, 2013, 14, 632.	2.8	347
11	Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance. PLoS Genetics, 2016, 12, e1005846.	3.5	267
12	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. PLoS Computational Biology, 2007, 3, e206.	3.2	261
13	A high resolution atlas of gene expression in the domestic sheep (Ovis aries). PLoS Genetics, 2017, 13, e1006997.	3.5	210
14	Structural and functional annotation of the porcine immunome. BMC Genomics, 2013, 14, 332.	2.8	203
15	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	3.8	199
16	Mapping macrophage polarization over the myocardial infarction time continuum. Basic Research in Cardiology, 2018, 113, 26.	5.9	189
17	Immune Cell Gene Signatures for Profiling the Microenvironment of Solid Tumors. Cancer Immunology Research, 2018, 6, 1388-1400.	3.4	169
18	Replicable and Coupled Changes in Innate and Adaptive Immune Gene Expression in Two Case-Control Studies of Blood Microarrays in Major Depressive Disorder. Biological Psychiatry, 2018, 83, 70-80.	1.3	158

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19	The Genome of a Pathogenic Rhodococcus: Cooptive Virulence Underpinned by Key Gene Acquisitions. PLoS Genetics, 2010, 6, e1001145.	3.5	143
20	The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle. Microbiome, 2017, 5, 159.	11.1	128
21	The Genes Induced by Signal Transducer and Activators of Transcription (STAT)3 and STAT5 in Mammary Epithelial Cells Define the Roles of these STATs in Mammary Development. Molecular Endocrinology, 2006, 20, 675-685.	3.7	118
22	Fibroblast polarization over the myocardial infarction time continuum shifts roles from inflammation to angiogenesis. Basic Research in Cardiology, 2019, 114, 6.	5.9	118
23	Sertoli cells control peritubular myoid cell fate and support adult Leydig cell development in the prepubertal testis. Development (Cambridge), 2014, 141, 2139-2149.	2.5	110
24	Sertoli Cells Maintain Leydig Cell Number and Peritubular Myoid Cell Activity in the Adult Mouse Testis. PLoS ONE, 2014, 9, e105687.	2.5	109
25	An oligonucleotide microarray for transcriptome analysis of Schistosoma mansoni and its application/use to investigate gender-associated gene expression. Molecular and Biochemical Parasitology, 2005, 141, 1-13.	1.1	100
26	Oncogenic Properties of Apoptotic Tumor Cells in Aggressive B Cell Lymphoma. Current Biology, 2015, 25, 577-588.	3.9	96
27	An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. Nucleic Acids Research, 2006, 34, e87-e87.	14.5	89
28	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. BMC Genomics, 2013, 14, 581.	2.8	83
29	Meta-analysis of lineage-specific gene expression signatures in mouse leukocyte populations. Immunobiology, 2010, 215, 724-736.	1.9	81
30	Assembly of a parts list of the human mitotic cell cycle machinery. Journal of Molecular Cell Biology, 2019, 11, 703-718.	3.3	80
31	Expression profiling of the Leishmania life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. Molecular and Biochemical Parasitology, 2004, 136, 87-100.	1.1	76
32	Characterization of DRP2, a novel human dystrophin homologue. Nature Genetics, 1996, 13, 223-226.	21.4	73
33	Improved grading and survival prediction of human astrocytic brain tumors by artificial neural network analysis of gene expression microarray data. Molecular Cancer Therapeutics, 2008, 7, 1013-1024.	4.1	72
34	Defining the Microglia Response during the Time Course of Chronic Neurodegeneration. Journal of Virology, 2016, 90, 3003-3017.	3.4	71
35	A core transcriptional signature of human microglia: Derivation and utility in describing region†dependent alterations associated with Alzheimer's disease. Glia, 2019, 67, 1240-1253.	4.9	67
36	Can DCs be distinguished from macrophages by molecular signatures?. Nature Immunology, 2013, 14, 187-189.	14.5	64

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37	Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse Bos Taurus Breeds and Basal Diets. Frontiers in Microbiology, 2017, 8, 2642.	3.5	64
38	The Human Family of Deafness/Dystonia Peptide (DDP) Related Mitochondrial Import Proteins. Genomics, 1999, 61, 259-267.	2.9	63
39	Transcriptomic analysis of mononuclear phagocyte differentiation and activation. Immunological Reviews, 2014, 262, 74-84.	6.0	62
40	Human Conjunctival Transcriptome Analysis Reveals the Prominence of Innate Defense in<i>Chlamydia trachomatis</i>Infection. Infection and Immunity, 2010, 78, 4895-4911.	2.2	58
41	A logic-based diagram of signalling pathways central to macrophage activation. BMC Systems Biology, 2008, 2, 36.	3.0	56
42	Analysis of the transcriptional networks underpinning the activation of murine macrophages by inflammatory mediators. Journal of Leukocyte Biology, 2014, 96, 167-183.	3.3	54
43	A graphical and computational modeling platform for biological pathways. Nature Protocols, 2018, 13, 705-722.	12.0	53
44	COVID19 Disease Map, a computational knowledge repository of virusâ€"host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
45	Distribution of Misfolded Prion Protein Seeding Activity Alone Does Not Predict Regions of Neurodegeneration. PLoS Biology, 2016, 14, e1002579.	5.6	52
46	Modulation of macrophage antitumor potential by apoptotic lymphoma cells. Cell Death and Differentiation, 2017, 24, 971-983.	11.2	51
47	Characterisation of the British honey bee metagenome. Nature Communications, 2018, 9, 4995.	12.8	51
48	Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine. Frontiers in Microbiology, 2020, 11, 659.	3.5	51
49	Expression of mesenchyme-specific gene signatures by follicular dendritic cells: insights from the meta-analysis of microarray data from multiple mouse cell populations. Immunology, 2011, 133, 482-498.	4.4	50
50	Network Analysis Reveals Distinct Clinical Syndromes Underlying Acute Mountain Sickness. PLoS ONE, 2014, 9, e81229.	2.5	48
51	Correlating Physiology with Gene Expression in Striatal Cholinergic Neurones. Journal of Neurochemistry, 2001, 74, 839-846.	3.9	47
52	Distinct Molecular Signature of Human Skin Langerhans Cells Denotes Critical Differences in Cutaneous Dendritic Cell Immune Regulation. Journal of Investigative Dermatology, 2014, 134, 695-703.	0.7	46
53	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. Frontiers in Genetics, 2019, 10, 701.	2.3	43
54	Identification and characterisation of human apoptosis inducing proteins using cell-based transfection microarrays and expression analysis. BMC Genomics, 2006, 7, 145.	2.8	42

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55	Transcription Analysis of the Myometrium of Labouring and Non-Labouring Women. PLoS ONE, 2016, 11, e0155413.	2.5	40
56	Coexpression analysis of large cancer datasets provides insight into the cellular phenotypes of the tumour microenvironment. BMC Genomics, 2013, 14, 469.	2.8	39
57	Co-ordinate regulation of the cystic fibrosis and multidrug resistance genes in cystic fibrosis knockout mice. Human Molecular Genetics, 1997, 6, 527-537.	2.9	37
58	Modelling the Structure and Dynamics of Biological Pathways. PLoS Biology, 2016, 14, e1002530.	5.6	37
59	The transcriptional signature associated with human motile cilia. Scientific Reports, 2020, 10, 10814.	3.3	37
60	Endothelial cells preparing to die by apoptosis initiate a program of transcriptome and glycome regulation. FASEB Journal, 2004, 18, 188-190.	0.5	35
61	Construction of a large scale integrated map of macrophage pathogen recognition and effector systems. BMC Systems Biology, 2010, 4, 63.	3.0	35
62	Analysis of gene expression in single cells. Current Opinion in Biotechnology, 1999, 10, 579-582.	6.6	33
63	Adenosine receptor expression and function in rat striatal cholinergic interneurons. British Journal of Pharmacology, 2000, 130, 886-890.	5.4	32
64	Pre/pro-B cells generate macrophage populations during homeostasis and inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3954-E3963.	7.1	32
65	Bioinformatic analysis of primary endothelial cell gene array data illustrated by the analysis of transcriptome changes in endothelial cells exposed to VEGF-A and PlGF. Angiogenesis, 2004, 7, 143-156.	7.2	29
66	Parallel patterns of cell-specific gene expression during enterocyte differentiation and maturation in the small intestine of the rabbit. Differentiation, 1995, 59, 179-192.	1.9	28
67	Meta-analysis reveals conserved cell cycle transcriptional network across multiple human cell types. BMC Genomics, 2017, 18, 30.	2.8	28
68	Effects of anti-inflammatory drugs on the expression of tryptophan-metabolism genes by human macrophages. Journal of Leukocyte Biology, 2018, 103, 681-692.	3.3	27
69	High sample throughput genotyping for estimating C-lineage introgression in the dark honeybee: an accurate and cost-effective SNP-based tool. Scientific Reports, 2018, 8, 8552.	3.3	27
70	Macrophage Gene Expression Associated with Remodeling of the Prepartum Rat Cervix: Microarray and Pathway Analyses. PLoS ONE, 2015, 10, e0119782.	2.5	27
71	Petri Net computational modelling of Langerhans cell Interferon Regulatory Factor Network predicts their role in T cell activation. Scientific Reports, 2017, 7, 668.	3.3	26
72	Setting the basis of best practices and standards for curation and annotation of logical models in biologyâ€"highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. Briefings in Bioinformatics, 2021, 22, 1848-1859.	6.5	25

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73	Derivation of marker gene signatures from human skin and their use in the interpretation of the transcriptional changes associated with dermatological disorders. Journal of Pathology, 2017, 241, 600-613.	4.5	22
74	Expression of the dystrophin-related protein 2 (Drp2) transcript in the mouse 1 1Edited By J.Karn. Journal of Molecular Biology, 1997, 270, 551-558.	4.2	18
75	The mEPN scheme: an intuitive and flexible graphical system for rendering biological pathways. BMC Systems Biology, 2010, 4, 65.	3.0	18
76	Transcriptomics Analysis of Porcine Caudal Dorsal Root Ganglia in Tail Amputated Pigs Shows Long-Term Effects on Many Pain-Associated Genes. Frontiers in Veterinary Science, 2019, 6, 314.	2.2	18
77	Macrophages.com: An on-line community resource for innate immunity research. Immunobiology, 2011, 216, 1203-1211.	1.9	17
78	Identification of Novel Genes Selectively Expressed in the Follicle-Associated Epithelium from the Meta-Analysis of Transcriptomics Data from Multiple Mouse Cell and Tissue Populations. DNA Research, 2012, 19, 407-422.	3.4	17
79	Visualisation of BioPAX Networks using BioLayout Express3D. F1000Research, 2014, 3, 246.	1.6	16
80	Network analysis of the social and demographic influences on name choice within the UK (1838-2016). PLoS ONE, 2018, 13, e0205759.	2.5	11
81	Network analysis of canine brain morphometry links tumour risk to oestrogen deficiency and accelerated brain ageing. Scientific Reports, 2019, 9, 12506.	3.3	11
82	Single-cell RNA-seq reveals CD16- monocytes as key regulators of human monocyte transcriptional response to Toxoplasma. Scientific Reports, 2020, 10, 21047.	3.3	8
83	A Systems-Level Analysis of Total-Body PET Data Reveals Complex Skeletal Metabolism Networks in vivo. Frontiers in Medicine, 2021, 8, 740615.	2.6	8
84	Visualization and analysis of RNA-Seq assembly graphs. Nucleic Acids Research, 2019, 47, 7262-7275.	14.5	4
85	Large-Scale Cell-Based Microarrays and Their Use with HEK293T Cells and Downstream Apoptotic Assays. Methods in Molecular Biology, 2011, 706, 27-40.	0.9	2
86	Modelling steroidogenesis: a framework model to support hypothesis generation and testing across endocrine studies. BMC Research Notes, 2018, 11, 252.	1.4	1
87	Assembly of Logic-Based Diagrams of Biological Pathways. Systems Biology, 2010, , 139-157.	0.1	0