

Thomas Freeman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/112863/publications.pdf>

Version: 2024-02-01

87
papers

13,407
citations

50276

46
h-index

48315

88
g-index

103
all docs

103
docs citations

103
times ranked

24629
citing authors

#	ARTICLE	IF	CITATIONS
1	Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLoMoTo/SysMod Workshop. <i>Briefings in Bioinformatics</i> , 2021, 22, 1848-1859.	6.5	25
2	A Systems-Level Analysis of Total-Body PET Data Reveals Complex Skeletal Metabolism Networks in vivo. <i>Frontiers in Medicine</i> , 2021, 8, 740615.	2.6	8
3	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
4	Single-cell RNA-seq reveals CD16- monocytes as key regulators of human monocyte transcriptional response to <i>Toxoplasma</i> . <i>Scientific Reports</i> , 2020, 10, 21047.	3.3	8
5	The transcriptional signature associated with human motile cilia. <i>Scientific Reports</i> , 2020, 10, 10814.	3.3	37
6	Identification of Complex Rumen Microbiome Interaction Within Diverse Functional Niches as Mechanisms Affecting the Variation of Methane Emissions in Bovine. <i>Frontiers in Microbiology</i> , 2020, 11, 659.	3.5	51
7	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019, 47, 7262-7275.	14.5	4
8	Transcriptomics Analysis of Porcine Caudal Dorsal Root Ganglia in Tail Amputated Pigs Shows Long-Term Effects on Many Pain-Associated Genes. <i>Frontiers in Veterinary Science</i> , 2019, 6, 314.	2.2	18
9	Identification of Rumen Microbial Genes Involved in Pathways Linked to Appetite, Growth, and Feed Conversion Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 701.	2.3	43
10	Network analysis of canine brain morphometry links tumour risk to oestrogen deficiency and accelerated brain ageing. <i>Scientific Reports</i> , 2019, 9, 12506.	3.3	11
11	A core transcriptional signature of human microglia: Derivation and utility in describing region–dependent alterations associated with Alzheimer's disease. <i>Glia</i> , 2019, 67, 1240-1253.	4.9	67
12	Assembly of a parts list of the human mitotic cell cycle machinery. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 703-718.	3.3	80
13	Fibroblast polarization over the myocardial infarction time continuum shifts roles from inflammation to angiogenesis. <i>Basic Research in Cardiology</i> , 2019, 114, 6.	5.9	118
14	Effects of anti-inflammatory drugs on the expression of tryptophan-metabolism genes by human macrophages. <i>Journal of Leukocyte Biology</i> , 2018, 103, 681-692.	3.3	27
15	A graphical and computational modeling platform for biological pathways. <i>Nature Protocols</i> , 2018, 13, 705-722.	12.0	53
16	Replicable and Coupled Changes in Innate and Adaptive Immune Gene Expression in Two Case-Control Studies of Blood Microarrays in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2018, 83, 70-80.	1.3	158
17	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018, 9, 4995.	12.8	51
18	Network analysis of the social and demographic influences on name choice within the UK (1838-2016). <i>PLoS ONE</i> , 2018, 13, e0205759.	2.5	11

#	ARTICLE	IF	CITATIONS
19	Immune Cell Gene Signatures for Profiling the Microenvironment of Solid Tumors. <i>Cancer Immunology Research</i> , 2018, 6, 1388-1400.	3.4	169
20	High sample throughput genotyping for estimating C-lineage introgression in the dark honeybee: an accurate and cost-effective SNP-based tool. <i>Scientific Reports</i> , 2018, 8, 8552.	3.3	27
21	Modelling steroidogenesis: a framework model to support hypothesis generation and testing across endocrine studies. <i>BMC Research Notes</i> , 2018, 11, 252.	1.4	1
22	Mapping macrophage polarization over the myocardial infarction time continuum. <i>Basic Research in Cardiology</i> , 2018, 113, 26.	5.9	189
23	Meta-analysis reveals conserved cell cycle transcriptional network across multiple human cell types. <i>BMC Genomics</i> , 2017, 18, 30.	2.8	28
24	Modulation of macrophage antitumor potential by apoptotic lymphoma cells. <i>Cell Death and Differentiation</i> , 2017, 24, 971-983.	11.2	51
25	Pre/pro-B cells generate macrophage populations during homeostasis and inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3954-E3963.	7.1	32
26	Derivation of marker gene signatures from human skin and their use in the interpretation of the transcriptional changes associated with dermatological disorders. <i>Journal of Pathology</i> , 2017, 241, 600-613.	4.5	22
27	Petri Net computational modelling of Langerhans cell Interferon Regulatory Factor Network predicts their role in T cell activation. <i>Scientific Reports</i> , 2017, 7, 668.	3.3	26
28	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). <i>PLoS Genetics</i> , 2017, 13, e1006997.	3.5	210
29	The rumen microbiome as a reservoir of antimicrobial resistance and pathogenicity genes is directly affected by diet in beef cattle. <i>Microbiome</i> , 2017, 5, 159.	11.1	128
30	Identification, Comparison, and Validation of Robust Rumen Microbial Biomarkers for Methane Emissions Using Diverse <i>Bos Taurus</i> Breeds and Basal Diets. <i>Frontiers in Microbiology</i> , 2017, 8, 2642.	3.5	64
31	Modelling the Structure and Dynamics of Biological Pathways. <i>PLoS Biology</i> , 2016, 14, e1002530.	5.6	37
32	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. <i>PLoS Genetics</i> , 2016, 12, e1005846.	3.5	267
33	Transcription Analysis of the Myometrium of Labouring and Non-Labouring Women. <i>PLoS ONE</i> , 2016, 11, e0155413.	2.5	40
34	Microglial brain region-dependent diversity and selective regional sensitivities to aging. <i>Nature Neuroscience</i> , 2016, 19, 504-516.	14.8	919
35	Defining the Microglia Response during the Time Course of Chronic Neurodegeneration. <i>Journal of Virology</i> , 2016, 90, 3003-3017.	3.4	71
36	Distribution of Misfolded Prion Protein Seeding Activity Alone Does Not Predict Regions of Neurodegeneration. <i>PLoS Biology</i> , 2016, 14, e1002579.	5.6	52

#	ARTICLE	IF	CITATIONS
37	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	12.6	517
38	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
39	Oncogenic Properties of Apoptotic Tumor Cells in Aggressive B Cell Lymphoma. <i>Current Biology</i> , 2015, 25, 577-588.	3.9	96
40	Macrophage Gene Expression Associated with Remodeling of the Parturient Rat Cervix: Microarray and Pathway Analyses. <i>PLoS ONE</i> , 2015, 10, e0119782.	2.5	27
41	Sertoli Cells Maintain Leydig Cell Number and Peritubular Myoid Cell Activity in the Adult Mouse Testis. <i>PLoS ONE</i> , 2014, 9, e105687.	2.5	109
42	Transcriptomic analysis of mononuclear phagocyte differentiation and activation. <i>Immunological Reviews</i> , 2014, 262, 74-84.	6.0	62
43	Distinct Molecular Signature of Human Skin Langerhans Cells Denotes Critical Differences in Cutaneous Dendritic Cell Immune Regulation. <i>Journal of Investigative Dermatology</i> , 2014, 134, 695-703.	0.7	46
44	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
45	Analysis of the transcriptional networks underpinning the activation of murine macrophages by inflammatory mediators. <i>Journal of Leukocyte Biology</i> , 2014, 96, 167-183.	3.3	54
46	Sertoli cells control peritubular myoid cell fate and support adult Leydig cell development in the prepubertal testis. <i>Development (Cambridge)</i> , 2014, 141, 2139-2149.	2.5	110
47	Transcriptome-Based Network Analysis Reveals a Spectrum Model of Human Macrophage Activation. <i>Immunity</i> , 2014, 40, 274-288.	14.3	1,692
48	Visualisation of BioPAX Networks using BioLayout Express3D. <i>F1000Research</i> , 2014, 3, 246.	1.6	16
49	Network Analysis Reveals Distinct Clinical Syndromes Underlying Acute Mountain Sickness. <i>PLoS ONE</i> , 2014, 9, e81229.	2.5	48
50	Coexpression analysis of large cancer datasets provides insight into the cellular phenotypes of the tumour microenvironment. <i>BMC Genomics</i> , 2013, 14, 469.	2.8	39
51	Structural and functional annotation of the porcine immunome. <i>BMC Genomics</i> , 2013, 14, 332.	2.8	203
52	An expression atlas of human primary cells: inference of gene function from coexpression networks. <i>BMC Genomics</i> , 2013, 14, 632.	2.8	347
53	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. <i>BMC Genomics</i> , 2013, 14, 581.	2.8	83
54	Can DCs be distinguished from macrophages by molecular signatures?. <i>Nature Immunology</i> , 2013, 14, 187-189.	14.5	64

#	ARTICLE	IF	CITATIONS
55	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. <i>DNA Research</i> , 2012, 19, 407-422.	3.4	17
56	A gene expression atlas of the domestic pig. <i>BMC Biology</i> , 2012, 10, 90.	3.8	199
57	Macrophages.com: An on-line community resource for innate immunity research. <i>Immunobiology</i> , 2011, 216, 1203-1211.	1.9	17
58	Expression of mesenchyme-specific gene signatures by follicular dendritic cells: insights from the meta-analysis of microarray data from multiple mouse cell populations. <i>Immunology</i> , 2011, 133, 482-498.	4.4	50
59	Large-Scale Cell-Based Microarrays and Their Use with HEK293T Cells and Downstream Apoptotic Assays. <i>Methods in Molecular Biology</i> , 2011, 706, 27-40.	0.9	2
60	Construction of a large scale integrated map of macrophage pathogen recognition and effector systems. <i>BMC Systems Biology</i> , 2010, 4, 63.	3.0	35
61	The mEPN scheme: an intuitive and flexible graphical system for rendering biological pathways. <i>BMC Systems Biology</i> , 2010, 4, 65.	3.0	18
62	The Genome of a Pathogenic <i>Rhodococcus</i> : Cooptive Virulence Underpinned by Key Gene Acquisitions. <i>PLoS Genetics</i> , 2010, 6, e1001145.	3.5	143
63	Human Conjunctival Transcriptome Analysis Reveals the Prominence of Innate Defense in <i>Chlamydia trachomatis</i> Infection. <i>Infection and Immunity</i> , 2010, 78, 4895-4911.	2.2	58
64	Meta-analysis of lineage-specific gene expression signatures in mouse leukocyte populations. <i>Immunobiology</i> , 2010, 215, 724-736.	1.9	81
65	Assembly of Logic-Based Diagrams of Biological Pathways. <i>Systems Biology</i> , 2010, , 139-157.	0.1	0
66	The Systems Biology Graphical Notation. <i>Nature Biotechnology</i> , 2009, 27, 735-741.	17.5	828
67	Network visualization and analysis of gene expression data using BioLayout Express3D. <i>Nature Protocols</i> , 2009, 4, 1535-1550.	12.0	443
68	A logic-based diagram of signalling pathways central to macrophage activation. <i>BMC Systems Biology</i> , 2008, 2, 36.	3.0	56
69	Improved grading and survival prediction of human astrocytic brain tumors by artificial neural network analysis of gene expression microarray data. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 1013-1024.	4.1	72
70	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. <i>PLoS Computational Biology</i> , 2007, 3, e206.	3.2	261
71	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. <i>Molecular Endocrinology</i> , 2006, 20, 675-685.	3.7	118
72	Identification and characterisation of human apoptosis inducing proteins using cell-based transfection microarrays and expression analysis. <i>BMC Genomics</i> , 2006, 7, 145.	2.8	42

#	ARTICLE	IF	CITATIONS
73	An open-access long oligonucleotide microarray resource for analysis of the human and mouse transcriptomes. <i>Nucleic Acids Research</i> , 2006, 34, e87-e87.	14.5	89
74	An oligonucleotide microarray for transcriptome analysis of <i>Schistosoma mansoni</i> and its application/use to investigate gender-associated gene expression. <i>Molecular and Biochemical Parasitology</i> , 2005, 141, 1-13.	1.1	100
75	Endothelial cells preparing to die by apoptosis initiate a program of transcriptome and glycome regulation. <i>FASEB Journal</i> , 2004, 18, 188-190.	0.5	35
76	Expression profiling of the <i>Leishmania</i> life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 87-100.	1.1	76
77	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. <i>Angiogenesis</i> , 2004, 7, 143-156.	7.2	29
78	Correlating Physiology with Gene Expression in Striatal Cholinergic Neurons. <i>Journal of Neurochemistry</i> , 2001, 74, 839-846.	3.9	47
79	Adenosine receptor expression and function in rat striatal cholinergic interneurons. <i>British Journal of Pharmacology</i> , 2000, 130, 886-890.	5.4	32
80	Analysis of gene expression in single cells. <i>Current Opinion in Biotechnology</i> , 1999, 10, 579-582.	6.6	33
81	The Human Family of Deafness/Dystonia Peptide (DDP) Related Mitochondrial Import Proteins. <i>Genomics</i> , 1999, 61, 259-267.	2.9	63
82	Fulminant Jejuno-ileitis following Ablation of Enteric Glia in Adult Transgenic Mice. <i>Cell</i> , 1998, 93, 189-201.	28.9	530
83	Co-ordinate regulation of the cystic fibrosis and multidrug resistance genes in cystic fibrosis knockout mice. <i>Human Molecular Genetics</i> , 1997, 6, 527-537.	2.9	37
84	Expression of the dystrophin-related protein 2 (Drp2) transcript in the mouse 1 Edited By J.Karn. <i>Journal of Molecular Biology</i> , 1997, 270, 551-558.	4.2	18
85	Tissue distribution of adenosine receptor mRNAs in the rat. <i>British Journal of Pharmacology</i> , 1996, 118, 1461-1468.	5.4	503
86	Characterization of DRP2, a novel human dystrophin homologue. <i>Nature Genetics</i> , 1996, 13, 223-226.	21.4	73
87	Parallel patterns of cell-specific gene expression during enterocyte differentiation and maturation in the small intestine of the rabbit. <i>Differentiation</i> , 1995, 59, 179-192.	1.9	28