

Stephen Bush

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2079544/stephen-bush-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

57
papers

824
citations

16
h-index

27
g-index

68
ext. papers

1,821
ext. citations

5.5
avg, IF

4.47
L-index

#	Paper	IF	Citations
57	Alternative splicing and the evolution of phenotypic novelty. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	88
56	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). <i>PLoS Genetics</i> , 2017 , 13, e1006997	6	79
55	Correcting for differential transcript coverage reveals a strong relationship between alternative splicing and organism complexity. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1402-13	8.3	79
54	Pleiotropic Impacts of Macrophage and Microglial Deficiency on Development in Rats with Targeted Mutation of the Locus. <i>Journal of Immunology</i> , 2018 , 201, 2683-2699	5.3	60
53	ADGRE1 (EMR1, F4/80) Is a Rapidly-Evolving Gene Expressed in Mammalian Monocyte-Macrophages. <i>Frontiers in Immunology</i> , 2018 , 9, 2246	8.4	51
52	Genomic diversity affects the accuracy of bacterial single-nucleotide polymorphism-calling pipelines. <i>GigaScience</i> , 2020 , 9,	7.6	42
51	Species-Specific Transcriptional Regulation of Genes Involved in Nitric Oxide Production and Arginine Metabolism in Macrophages. <i>ImmunoHorizons</i> , 2018 , 2, 27-37	2.7	31
50	The genomic architecture of mastitis resistance in dairy sheep. <i>BMC Genomics</i> , 2017 , 18, 624	4.5	28
49	Presence-absence variation in <i>A. thaliana</i> is primarily associated with genomic signatures consistent with relaxed selective constraints. <i>Molecular Biology and Evolution</i> , 2014 , 31, 59-69	8.3	28
48	Network analysis of transcriptomic diversity amongst resident tissue macrophages and dendritic cells in the mouse mononuclear phagocyte system. <i>PLoS Biology</i> , 2020 , 18, e3000859	9.7	28
47	Cross-species inference of long non-coding RNAs greatly expands the ruminant transcriptome. <i>Genetics Selection Evolution</i> , 2018 , 50, 20	4.9	24
46	Characterization of Subpopulations of Chicken Mononuclear Phagocytes That Express TIM4 and CSF1R. <i>Journal of Immunology</i> , 2019 , 202, 1186-1199	5.3	22
45	Characterisation of the British honey bee metagenome. <i>Nature Communications</i> , 2018 , 9, 4995	17.4	22
44	Optimization of next-generation sequencing transcriptome annotation for species lacking sequenced genomes. <i>Molecular Ecology Resources</i> , 2016 , 16, 446-58	8.4	20
43	A Gene Expression Atlas of the Domestic Water Buffalo (<i>Bubalus bubalis</i>). <i>Frontiers in Genetics</i> , 2019 , 10, 668	4.5	18
42	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. <i>BMC Bioinformatics</i> , 2017 , 18, 301	3.6	18
41	Combination of novel and public RNA-seq datasets to generate an mRNA expression atlas for the domestic chicken. <i>BMC Genomics</i> , 2018 , 19, 594	4.5	14

40	Functional Annotation of the Transcriptome of the Pig, , Based Upon Network Analysis of an RNAseq Transcriptional Atlas. <i>Frontiers in Genetics</i> , 2019 , 10, 1355	4.5	11
39	Species-Specificity of Transcriptional Regulation and the Response to Lipopolysaccharide in Mammalian Macrophages. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 661	5.7	11
38	Analysis of homozygous and heterozygous Csf1r knockout in the rat as a model for understanding microglial function in brain development and the impacts of human CSF1R mutations. <i>Neurobiology of Disease</i> , 2021 , 151, 105268	7.5	11
37	The Transcriptional Network That Controls Growth Arrest and Macrophage Differentiation in the Human Myeloid Leukemia Cell Line THP-1. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 498	5.7	10
36	CSF1R-dependent macrophages control postnatal somatic growth and organ maturation. <i>PLoS Genetics</i> , 2021 , 17, e1009605	6	10
35	Arginine to Glutamine Variant in Olfactomedin Like 3 () Is a Candidate for Severe Goniodysgenesis and Glaucoma in the Border Collie Dog Breed. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 943-954	3.2	9
34	Elimination of Reference Mapping Bias Reveals Robust Immune Related Allele-Specific Expression in Crossbred Sheep. <i>Frontiers in Genetics</i> , 2019 , 10, 863	4.5	9
33	Quantitative trait loci and transcriptome signatures associated with avian heritable resistance to <i>Campylobacter</i> . <i>Scientific Reports</i> , 2021 , 11, 1623	4.9	7
32	Transcriptomic Analysis of Rat Macrophages. <i>Frontiers in Immunology</i> , 2020 , 11, 594594	8.4	7
31	Genomic diversity affects the accuracy of bacterial SNP calling pipelines		6
30	A Mini-Atlas of Gene Expression for the Domestic Goat (). <i>Frontiers in Genetics</i> , 2019 , 10, 1080	4.5	6
29	Comprehensive Transcriptional Profiling of the Gastrointestinal Tract of Ruminants from Birth to Adulthood Reveals Strong Developmental Stage Specific Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 359-373	3.2	6
28	Environmentally enriched pigs have transcriptional profiles consistent with neuroprotective effects and reduced microglial activity. <i>Behavioural Brain Research</i> , 2018 , 350, 6-15	3.4	6
27	Lineage-specific sequence evolution and exon edge conservation partially explain the relationship between evolutionary rate and expression level in <i>A. thaliana</i> . <i>Molecular Ecology</i> , 2015 , 24, 3093-106	5.7	5
26	The Mononuclear Phagocyte System of the Rat. <i>Journal of Immunology</i> , 2021 , 206, 2251-2263	5.3	5
25	Analysis of the Progeny of Sibling Matings Reveals Regulatory Variation Impacting the Transcriptome of Immune Cells in Commercial Chickens. <i>Frontiers in Genetics</i> , 2019 , 10, 1032	4.5	5
24	Transcriptomic profiling of feline teeth highlights the role of matrix metalloproteinase 9 (MMP9) in tooth resorption. <i>Scientific Reports</i> , 2020 , 10, 18958	4.9	4
23	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	4

22	Genetic and genomic analyses underpin the feasibility of concomitant genetic improvement of milk yield and mastitis resistance in dairy sheep. <i>PLoS ONE</i> , 2019 , 14, e0214346	3.7	4
21	Network analysis of the social and demographic influences on name choice within the UK (1838-2016). <i>PLoS ONE</i> , 2018 , 13, e0205759	3.7	4
20	Characterisation of the UK honey bee (<i>Apis mellifera</i>) metagenome		3
19	A mini-atlas of gene expression for the domestic goat (<i>Capra hircus</i>) reveals transcriptional differences in immune signatures between sheep and goats		3
18	Generalizable characteristics of false-positive bacterial variant calls. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
17	Re-using the names of newborns: symbolic reincarnation in an age of infant mortality. <i>Names</i> , 2019 , 67, 100-112	0.2	2
16	Read trimming has minimal effect on bacterial SNP-calling accuracy. <i>Microbial Genomics</i> , 2020 , 6,	4.4	2
15	Evaluation of methods for detecting human reads in microbial sequencing datasets. <i>Microbial Genomics</i> , 2020 , 6,	4.4	2
14	CRISPR-Cas9 Editing of Human Histone Deubiquitinase Gene in Human Monocytic Leukemia Cell Line THP-1. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 679544	5.7	2
13	Comprehensive transcriptional profiling of the gastrointestinal tract of ruminants from birth to adulthood reveals strong developmental stage specific gene expression		1
12	Elimination of reference mapping bias reveals robust immune related allele-specific expression in crossbred sheep		1
11	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>)		1
10	Genetic control of <i>Campylobacter</i> colonisation in broiler chickens: genomic and transcriptomic characterisation		1
9	Gene expression in the cardiovascular system of the domestic sheep (<i>Ovis aries</i>); a new tool to advance our understanding of cardiovascular disease		1
8	CSF1R-dependent macrophages control postnatal somatic growth and organ maturation		1
7	Characterisation of subpopulations of chicken mononuclear phagocytes that express TIM4 and the macrophage colony-stimulating factor receptor (CSF1R)		1
6	Combination of novel and public RNA-seq datasets to generate an mRNA expression atlas for the domestic chicken		1
5	Expression of Calcification and Extracellular Matrix Genes in the Cardiovascular System of the Healthy Domestic Sheep (). <i>Frontiers in Genetics</i> , 2020 , 11, 919	4.5	1

4	MeDAS: a Metazoan Developmental Alternative Splicing database. <i>Nucleic Acids Research</i> , 2021 , 49, D144-D150.	4.1	0
3	Rats exhibit age-related mosaic loss of chromosome Y.. <i>Communications Biology</i> , 2021 , 4, 1418	6.7	1
2	Ambivalence, Avoidance, and Appeal: Alliterative Aspects of Anglo Anthroponyms. <i>Names</i> , 2020 , 68, 141-155	0.2	0
1	Generation and network analysis of an RNA-seq transcriptional atlas for the rat.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac017	3.7	0