

Jeremy C Mason

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

3,693
citations

430874

18
h-index

526287

27
g-index

35
all docs

35
docs citations

35
times ranked

10248
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. <i>Pain</i> , 2022, 163, 1139-1157.	4.2	4
2	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
3	The EurOPDX Data Portal: an open platform for patient-derived cancer xenograft data sharing and visualization. <i>BMC Genomics</i> , 2022, 23, 156.	2.8	10
4	Pleiotropy data resource as a primer for investigating co-morbidities/multi-morbidities and their role in disease. <i>Mammalian Genome</i> , 2021, , 1.	2.2	2
5	Soft windowing application to improve analysis of high-throughput phenotyping data. <i>Bioinformatics</i> , 2020, 36, 1492-1500.	4.1	9
6	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. <i>Nature Immunology</i> , 2020, 21, 86-100.	14.5	32
7	A dynamic COVID-19 immune signature includes associations with poor prognosis. <i>Nature Medicine</i> , 2020, 26, 1623-1635.	30.7	765
8	A comprehensive and comparative phenotypic analysis of the collaborative founder strains identifies new and known phenotypes. <i>Mammalian Genome</i> , 2020, 31, 30-48.	2.2	22
9	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. <i>PLoS Genetics</i> , 2020, 16, e1009190.	3.5	19
10	Sexual dimorphism in trait variability and its eco-evolutionary and statistical implications. <i>ELife</i> , 2020, 9, .	6.0	64
11	OpenStats: A robust and scalable software package for reproducible analysis of high-throughput phenotypic data. <i>PLoS ONE</i> , 2020, 15, e0242933.	2.5	12
12	PDX Finder: A portal for patient-derived tumor xenograft model discovery. <i>Nucleic Acids Research</i> , 2019, 47, D1073-D1079.	14.5	75
13	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. <i>Nature Communications</i> , 2018, 9, 288.	12.8	59
14	Identification of genes required for eye development by high-throughput screening of mouse knockouts. <i>Communications Biology</i> , 2018, 1, 236.	4.4	37
15	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. <i>Nature Communications</i> , 2017, 8, 886.	12.8	116
16	Prevalence of sexual dimorphism in mammalian phenotypic traits. <i>Nature Communications</i> , 2017, 8, 15475.	12.8	200
17	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. <i>Nature Genetics</i> , 2017, 49, 1231-1238.	21.4	216
18	High-throughput discovery of novel developmental phenotypes. <i>Nature</i> , 2016, 537, 508-514.	27.8	1,001

#	ARTICLE	IF	CITATIONS
19	PhenStat: A Tool Kit for Standardized Analysis of High Throughput Phenotypic Data. PLoS ONE, 2015, 10, e0131274.	2.5	51
20	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	5.6	75
21	A mouse informatics platform for phenotypic and translational discovery. Mammalian Genome, 2015, 26, 413-421.	2.2	27
22	The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data. Nucleic Acids Research, 2014, 42, D802-D809.	14.5	252
23	The mammalian gene function resource: the international knockout mouse consortium. Mammalian Genome, 2012, 23, 580-586.	2.2	292
24	BioMart Central Portal: an open database network for the biological community. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar041-bar041.	3.0	145
25	The IKMC web portal: a central point of entry to data and resources from the International Knockout Mouse Consortium. Nucleic Acids Research, 2011, 39, D849-D855.	14.5	83