

# Jeremy C Mason

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9577202/publications.pdf>

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	High-throughput discovery of novel developmental phenotypes. <i>Nature</i> , 2016, 537, 508-514.	27.8	1,001
2	A dynamic COVID-19 immune signature includes associations with poor prognosis. <i>Nature Medicine</i> , 2020, 26, 1623-1635.	30.7	765
3	The mammalian gene function resource: the international knockout mouse consortium. <i>Mammalian Genome</i> , 2012, 23, 580-586.	2.2	292
4	The International Mouse Phenotyping Consortium Web Portal, a unified point of access for knockout mice and related phenotyping data. <i>Nucleic Acids Research</i> , 2014, 42, D802-D809.	14.5	252
5	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
6	Prevalence of sexual dimorphism in mammalian phenotypic traits. <i>Nature Communications</i> , 2017, 8, 15475.	12.8	200
7	BioMart Central Portal: an open database network for the biological community. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar041-bar041.	3.0	145
8	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
9	The IKMC web portal: a central point of entry to data and resources from the International Knockout Mouse Consortium. <i>Nucleic Acids Research</i> , 2011, 39, D849-D855.	14.5	83
10	Applying the ARRIVE Guidelines to an In Vivo Database. <i>PLoS Biology</i> , 2015, 13, e1002151.	5.6	75
11	PDX Finder: A portal for patient-derived tumor xenograft model discovery. <i>Nucleic Acids Research</i> , 2019, 47, D1073-D1079.	14.5	75
12	Sexual dimorphism in trait variability and its eco-evolutionary and statistical implications. <i>ELife</i> , 2020, 9, .	6.0	64
13	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. <i>Nature Communications</i> , 2018, 9, 288.	12.8	59
14	PhenStat: A Tool Kit for Standardized Analysis of High Throughput Phenotypic Data. <i>PLoS ONE</i> , 2015, 10, e0131274.	2.5	51
15	Identification of genes required for eye development by high-throughput screening of mouse knockouts. <i>Communications Biology</i> , 2018, 1, 236.	4.4	37
16	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. <i>Nature Immunology</i> , 2020, 21, 86-100.	14.5	32
17	A mouse informatics platform for phenotypic and translational discovery. <i>Mammalian Genome</i> , 2015, 26, 413-421.	2.2	27
18	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

#	ARTICLE	IF	CITATIONS
19	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
20	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	3.5	19
21	OpenStats: A robust and scalable software package for reproducible analysis of high-throughput phenotypic data. PLoS ONE, 2020, 15, e0242933.	2.5	12
22	The EurOPDX Data Portal: an open platform for patient-derived cancer xenograft data sharing and visualization. BMC Genomics, 2022, 23, 156.	2.8	10
23	Soft windowing application to improve analysis of high-throughput phenotyping data. Bioinformatics, 2020, 36, 1492-1500.	4.1	9
24	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain, 2022, 163, 1139-1157.	4.2	4
25	Pleiotropy data resource as a primer for investigating co-morbidities/multi-morbidities and their role in disease. Mammalian Genome, 2021, , 1.	2.2	2