Ann-Marie Mallon

List of Publications by Year
in descending order

51	4,223	218677	233421
papers	citations	26 h-index	45 g-index

57	57	57	9382
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain, 2022, 163, 1139-1157.	4.2	4
2	Making sense of the linear genome, gene function and TADs. Epigenetics and Chromatin, 2022, 15, 4.	3.9	15
3	Introduction to Mammalian Genome Special Issue: Mammalian Genetic Resources. Mammalian Genome, 2022, 33, 1-3.	2.2	0
4	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
5	Modelling the genetic aetiology of complex disease: humanâ€“mouse conservation of noncoding features and disease-associated loci. Biology Letters, 2022, 18, 20210630.	2.3	4
6	LAMA: automated image analysis for the developmental phenotyping of mouse embryos. Development (Cambridge), 2021, 148, .	2.5	7
7	A resource of targeted mutant mouse lines for 5,061 genes. Nature Genetics, 2021, 53, 416-419.	21.4	60
8	Advancing data science in drug development through an innovative computational framework for data sharing and statistical analysis. BMC Medical Research Methodology, 2021, 21, 250.	3.1	9
9	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. BMC Genomics, 2020, 21, 754.	2.8	3
10	Protection Against XY Gonadal Sex Reversal by a Variant Region on Mouse Chromosome 13. Genetics, 2020, 214, 467-477.	2.9	6
11	The Deep Genome Project. Genome Biology, 2020, 21, 18.	8.8	30
12	Human and mouse essentiality screens as a resource for disease gene discovery. Nature Communications, 2020, 11, 655.	12.8	64
13	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	3.5	19
14	Genetic background influences tumour development in heterozygous Men1 knockout mice. Endocrine Connections, 2020, 9, 426-437.	1.9	5
15	Genomic Mutation Identification in Mice Using Illumina Sequencing and Linuxâ€Based Computational Methods. Current Protocols in Mouse Biology, 2019, 9, e64.	1.2	0
16	TarGo: network based target gene selection system for human disease related mouse models. Laboratory Animal Research, 2019, 35, 23.	2.5	0
17	An N-Ethyl-N-Nitrosourea (ENU)-Induced Tyr265Stop Mutation of the DNA Polymerase Accessory Subunit Gamma 2 (Polg2) Is Associated With Renal Calcification in Mice. Journal of Bone and Mineral Research, 2019, 34, 497-507.	2.8	3
18	A bioimage informatics platform for high-throughput embryo phenotyping. Briefings in Bioinformatics, 2018, 19, bbw101.	6.5	9

#	Article	IF	Citations
19	High-throughput mouse phenomics for characterizing mammalian gene function. Nature Reviews Genetics, 2018, 19, 357-370.	16.3	78
20	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	12.8	59
21	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	4.4	37
22	The International Mouse Phenotyping Consortium (IMPC): a functional catalogue of the mammalian genome that informs conservation. Conservation Genetics, 2018, 19, 995-1005.	1.5	82
23	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. Nature Communications, 2017, 8, 886.	12.8	116
24	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	12.8	200
25	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	21.4	216
26	A mutation in Nischarin causes otitis media via LIMK1 and NF-Î¹B pathways. PLoS Genetics, 2017, 13, e1006969.	3.5	36
27	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	27.8	1,001
28	Correction of the auditory phenotype in C57BL/6N mice via CRISPR/Cas9-mediated homology directed repair. Genome Medicine, 2016, 8, 16.	8.2	113
29	Introduction to Mammalian Genome special issue: Informatics and Integrative Genomicsâ€"Part 1. Mammalian Genome, 2015, 26, 271-271.	2.2	0
30	Comparative visualization of genotype-phenotype relationships. Nature Methods, 2015, 12, 698-699.	19.0	2
31	Analysis of mammalian gene function through broad-based phenotypic screens across a consortium of mouse clinics. Nature Genetics, 2015, 47, 969-978.	21.4	137
32	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	5.6	75
33	Introduction to Mammalian Genome special issue: Informatics and Integrative Genomicsâ€"Part 2. Mammalian Genome, 2015, 26, 365-365.	2.2	0
34	A mouse informatics platform for phenotypic and translational discovery. Mammalian Genome, 2015, 26, 413-421.	2.2	27
35	Current strategies for mutation detection in phenotype-driven screens utilising next generation sequencing. Mammalian Genome, 2015, 26, 486-500.	2.2	28
36	Genetic Factors Regulating Lung Vasculature and Immune Cell Functions Associate with Resistance to Pneumococcal Infection. PLoS ONE, 2014, 9, e89831.	2.5	15

#	Article	IF	Citations
37	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
38	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. Genome Biology, 2013, 14, R82.	9.6	403
39	Accessing and Mining Data from Large-Scale Mouse Phenotyping Projects. International Review of Neurobiology, 2012, 104, 47-70.	2.0	9
40	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. Mammalian Genome, 2012, 23, 641-652.	2.2	37
41	High-throughput mouse phenotyping. Methods, 2011, 53, 394-404.	3.8	31
42	Anatomy ontologies and potential users: bridging the gap. Journal of Biomedical Semantics, 2011, 2, S3.	1.6	6
43	EMMA--mouse mutant resources for the international scientific community. Nucleic Acids Research, 2010, 38, D570-D576.	14.5	39
44	EuroPhenome: a repository for high-throughput mouse phenotyping data. Nucleic Acids Research, 2010, 38, D577-D585.	14.5	75
45	MouseBook: an integrated portal of mouse resources. Nucleic Acids Research, 2010, 38, D593-D599.	14.5	18
46	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. BMC Bioinformatics, 2009, 10, S2.	2.6	39
47	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian Genome, 2009, 20, 457-461.	2.2	21
48	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
49	EuroPhenome and EMPReSS: online mouse phenotyping resource. Nucleic Acids Research, 2007, 36, D715-D718.	14.5	68
50	Integration of mouse phenome data resources. Mammalian Genome, 2007, 18, 157-163.	2.2	44
51	Using ontologies to describe mouse phenotypes. Genome Biology, 2004, 6, R8.	9.6	191