Ann-Marie Mallon

List of Publications by Year
in descending order

51 papers	4,223 citations	218677 26 h-index	233421 45 g-index
57 all docs	57 docs citations	57 times ranked	9382 citing authors

#	Article	IF	Citations
1	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	27.8	1,001
2	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
3	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. Genome Biology, 2013, 14, R82.	9.6	403
4	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
5	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	21.4	216
6	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	12.8	200
7	Using ontologies to describe mouse phenotypes. Genome Biology, 2004, 6, R8.	9.6	191
8	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
9	A large scale hearing loss screen reveals an extensive unexplored genetic landscape for auditory dysfunction. Nature Communications, 2017, 8, 886.	12.8	116
10	Correction of the auditory phenotype in C57BL/6N mice via CRISPR/Cas9-mediated homology directed repair. Genome Medicine, 2016, 8, 16.	8.2	113
11	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
12	High-throughput mouse phenomics for characterizing mammalian gene function. Nature Reviews Genetics, 2018, 19, 357-370.	16.3	78
13	EuroPhenome: a repository for high-throughput mouse phenotyping data. Nucleic Acids Research, 2010, 38, D577-D585.	14.5	75
14	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	5.6	75
15	EuroPhenome and EMPReSS: online mouse phenotyping resource. Nucleic Acids Research, 2007, 36, D715-D718.	14.5	68
16	Human and mouse essentiality screens as a resource for disease gene discovery. Nature Communications, 2020, 11, 655.	12.8	64
17	A resource of targeted mutant mouse lines for 5,061 genes. Nature Genetics, 2021, 53, 416-419.	21.4	60
18	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	12.8	59

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19	Integration of mouse phenome data resources. Mammalian Genome, 2007, 18, 157-163.	2.2	44
20	Practical application of ontologies to annotate and analyse large scale raw mouse phenotype data. BMC Bioinformatics, 2009, 10, S2.	2.6	39
21	EMMA--mouse mutant resources for the international scientific community. Nucleic Acids Research, 2010, 38, D570-D576.	14.5	39
22	Accessing data from the International Mouse Phenotyping Consortium: state of the art and future plans. Mammalian Genome, 2012, 23, 641-652.	2.2	37
23	Identification of genes required for eye development by high-throughput screening of mouse knockouts. Communications Biology, 2018, 1, 236.	4.4	37
24	A mutation in Nischarin causes otitis media via LIMK1 and NF-κB pathways. PLoS Genetics, 2017, 13, e1006969.	3.5	36
25	High-throughput mouse phenotyping. Methods, 2011, 53, 394-404.	3.8	31
26	The Deep Genome Project. Genome Biology, 2020, 21, 18.	8.8	30
27	Current strategies for mutation detection in phenotype-driven screens utilising next generation sequencing. Mammalian Genome, 2015, 26, 486-500.	2.2	28
28	A mouse informatics platform for phenotypic and translational discovery. Mammalian Genome, 2015, 26, 413-421.	2.2	27
29	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
30	Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. Mammalian Genome, 2009, 20, 457-461.	2.2	21
31	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	3.5	19
32	MouseBook: an integrated portal of mouse resources. Nucleic Acids Research, 2010, 38, D593-D599.	14.5	18
33	Genetic Factors Regulating Lung Vasculature and Immune Cell Functions Associate with Resistance to Pneumococcal Infection. PLoS ONE, 2014, 9, e89831.	2.5	15
34	Making sense of the linear genome, gene function and TADs. Epigenetics and Chromatin, 2022, 15, 4.	3.9	15
35	Accessing and Mining Data from Large-Scale Mouse Phenotyping Projects. International Review of Neurobiology, 2012, 104, 47-70.	2.0	9
36	A bioimage informatics platform for high-throughput embryo phenotyping. Briefings in Bioinformatics, 2018, 19, bbw101.	6.5	9

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37	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
38	LAMA: automated image analysis for the developmental phenotyping of mouse embryos. Development (Cambridge), 2021, 148, .	2.5	7
39	Anatomy ontologies and potential users: bridging the gap. Journal of Biomedical Semantics, 2011, 2, S3.	1.6	6
40	Protection Against XY Gonadal Sex Reversal by a Variant Region on Mouse Chromosome 13. Genetics, 2020, 214, 467-477.	2.9	6
41	Genetic background influences tumour development in heterozygous Men1 knockout mice. Endocrine Connections, 2020, 9, 426-437.	1.9	5
42	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain, 2022, 163, 1139-1157.	4.2	4
43	Modelling the genetic aetiology of complex disease: human–mouse conservation of noncoding features and disease-associated loci. Biology Letters, 2022, 18, 20210630.	2.3	4
44	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
45	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. BMC Genomics, 2020, 21, 754.	2.8	3
46	Comparative visualization of genotype-phenotype relationships. Nature Methods, 2015, 12, 698-699.	19.0	2
47	Introduction to Mammalian Genome special issue: Informatics and Integrative Genomics–Part 1. Mammalian Genome, 2015, 26, 271-271.	2.2	0
48	Introduction to Mammalian Genome special issue: Informatics and Integrative Genomics–Part 2. Mammalian Genome, 2015, 26, 365-365.	2.2	0
49	Genomic Mutation Identification in Mice Using Illumina Sequencing and Linux–Based Computational Methods. Current Protocols in Mouse Biology, 2019, 9, e64.	1.2	0
50	TarGo: network based target gene selection system for human disease related mouse models. Laboratory Animal Research, 2019, 35, 23.	2.5	0
51	Introduction to Mammalian Genome Special Issue: Mammalian Genetic Resources. Mammalian Genome, 2022, 33, 1-3.	2.2	0