Jacqueline K White

List of Publications by Year
in descending order

54 papers	5,734 citations	136950 32 h-index	155660 55 g-index
57 all docs	57 docs citations	57 times ranked	11503 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	The venous system of E14.5 mouse embryosâ€"reference data and examples for diagnosing malformations in embryos with gene deletions. Journal of Anatomy, 2022, 240, 11-22.	1.5	8
3	High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. Nature Immunology, 2020, 21, 86-100.	14.5	32
4	Machine learning-based automated phenotyping of inflammatory nocifensive behavior in mice. Molecular Pain, 2020, 16, 174480692095859.	2.1	12
5	T Cells from NOD-Perlg Mice Target Both Pancreatic and Neuronal Tissue. Journal of Immunology, 2020, 205, 2026-2038.	0.8	2
6	The occurrence of tarsal injuries in male mice of C57BL/6N substrains in multiple international mouse facilities. PLoS ONE, 2020, 15, e0230162.	2.5	1
7	Mouse mutant phenotyping at scale reveals novel genes controlling bone mineral density. PLoS Genetics, 2020, 16, e1009190.	3.5	19
8	Large-scale discovery of mouse transgenic integration sites reveals frequent structural variation and insertional mutagenesis. Genome Research, 2019, 29, 494-505.	5.5	130
9	Mouse screen reveals multiple new genes underlying mouse and human hearing loss. PLoS Biology, 2019, 17, e3000194.	5.6	84
10	FBXO7 sensitivity of phenotypic traits elucidated by a hypomorphic allele. PLoS ONE, 2019, 14, e0212481.	2.5	7
11	Identification of genetic elements in metabolism by high-throughput mouse phenotyping. Nature Communications, 2018, 9, 288.	12.8	59
12	Placentation defects are highly prevalent in embryonic lethal mouse mutants. Nature, 2018, 555, 463-468.	27.8	287
13	A synthesis approach of mouse studies to identify genes and proteins in arterial thrombosis and bleeding. Blood, 2018, 132, e35-e46.	1.4	29
14	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	12.8	200
15	Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. Nature Genetics, 2017, 49, 1231-1238.	21.4	216
16	Improving the Identification of Phenotypic Abnormalities and Sexual Dimorphism in Mice When Studying Rare Event Categorical Characteristics. Genetics, 2017, 205, 491-501.	2.9	8
17	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	21.4	391
18	Wbp2 is required for normal glutamatergic synapses in the cochlea and is crucial for hearing. EMBO Molecular Medicine, 2016, 8, 191-207.	6.9	41

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19	High-throughput discovery of novel developmental phenotypes. Nature, 2016, 537, 508-514.	27.8	1,001
20	Deficiency of the zinc finger protein ZFP106 causes motor and sensory neurodegeneration. Human Molecular Genetics, 2016, 25, 291-307.	2.9	19
21	MacroH2A1 isoforms are associated with epigenetic markers for activation of lipogenic genes in fatâ€induced steatosis. FASEB Journal, 2015, 29, 1676-1687.	0.5	41
22	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
23	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	5.6	75
24	A gene expression resource generated by genome-wide lacZ profiling in the mouse. DMM Disease Models and Mechanisms, 2015, 8, 1467-78.	2.4	12
25	Targeting of Slc25a21 Is Associated with Orofacial Defects and Otitis Media Due to Disrupted Expression of a Neighbouring Gene. PLoS ONE, 2014, 9, e91807.	2.5	30
26	Identification of Genes Important for Cutaneous Function Revealed by a Large Scale Reverse Genetic Screen in the Mouse. PLoS Genetics, 2014, 10, e1004705.	3.5	20
27	Spinster Homolog 2 (Spns2) Deficiency Causes Early Onset Progressive Hearing Loss. PLoS Genetics, 2014, 10, e1004688.	3.5	54
28	Histopathology reveals correlative and unique phenotypes in a high throughput mouse phenotyping screen. DMM Disease Models and Mechanisms, 2014, 7, 515-24.	2.4	44
29	Impact of Temporal Variation on Design and Analysis of Mouse Knockout Phenotyping Studies. PLoS ONE, 2014, 9, e111239.	2.5	46
30	High-fat feeding rapidly induces obesity and lipid derangements in C57BL/6N mice. Mammalian Genome, 2013, 24, 240-251.	2.2	71
31	A comparative phenotypic and genomic analysis of C57BL/6J and C57BL/6N mouse strains. Genome Biology, 2013, 14, R82.	9.6	403
32	Omi, a recessive mutation on chromosome 10, is a novel allele of Ostm1. Mammalian Genome, 2013, 24, 44-53.	2.2	3
33	Genome-wide Generation and Systematic Phenotyping of Knockout Mice Reveals New Roles for Many Genes. Cell, 2013, 154, 452-464.	28.9	449
34	Mcph1-Deficient Mice Reveal a Role for MCPH1 in Otitis Media. PLoS ONE, 2013, 8, e58156.	2.5	36
35	Rapid-Throughput Skeletal Phenotyping of 100 Knockout Mice Identifies 9 New Genes That Determine Bone Strength. PLoS Genetics, 2012, 8, e1002858.	3.5	73
36	Disruption of Mouse Cenpj, a Regulator of Centriole Biogenesis, Phenocopies Seckel Syndrome. PLoS Genetics, 2012, 8, e1003022.	3.5	84

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37	The Role of Sphingosine-1-Phosphate Transporter Spns2 in Immune System Function. Journal of Immunology, 2012, 189, 102-111.	0.8	90
38	Generation of the Sotos syndrome deletion in mice. Mammalian Genome, 2012, 23, 749-757.	2.2	13
39	Loss-of-function mutations in IGSF1 cause an X-linked syndrome of central hypothyroidism and testicular enlargement. Nature Genetics, 2012, 44, 1375-1381.	21.4	169
40	Largeâ€scale mouse knockouts and phenotypes. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 547-563.	6.6	6
41	The fallacy of ratio correction to address confounding factors. Laboratory Animals, 2012, 46, 245-252.	1.0	22
42	Deficiency for the Ubiquitin Ligase UBE3B in a Blepharophimosis-Ptosis-Intellectual-Disability Syndrome. American Journal of Human Genetics, 2012, 91, 998-1010.	6.2	82
43	Modeling Partial Monosomy for Human Chromosome 21q11.2-q21.1 Reveals Haploinsufficient Genes Influencing Behavior and Fat Deposition. PLoS ONE, 2012, 7, e29681.	2.5	24
44	Experimental and husbandry procedures as potential modifiers of the results of phenotyping tests. Physiology and Behavior, 2012, 106, 602-611.	2.1	38
45	Optimising experimental design for high-throughput phenotyping in mice: a case study. Mammalian Genome, 2010, 21, 467-476.	2.2	11
46	Influence ofSlc11a1(formerlyNramp1) on DSS-induced colitis in mice. Journal of Leukocyte Biology, 2009, 85, 703-710.	3.3	11
47	Slc11a1, Formerly Nramp1, Is Expressed in Dendritic Cells and Influences Major Histocompatibility Complex Class II Expression and Antigen-Presenting Cell Function. Infection and Immunity, 2007, 75, 5059-5067.	2.2	57
48	Slc11a1-mediated resistance toSalmonella entericaserovar Typhimurium andLeishmania donovaniinfections does not require functional inducible nitric oxide synthase or phagocyte oxidase activity. Journal of Leukocyte Biology, 2005, 77, 311-320.	3.3	47
49	Candidate gene association study of solute carrier family 11a members 1 (SLC11A1) and 2 (SLC11A2) genes in Alzheimer's disease. Neuroscience Letters, 2005, 374, 124-128.	2.1	32
50	Divalent cation transport and susceptibility to infectious and autoimmune disease: continuation of the Ity/Lsh/Bcg/Nramp1/Slc11a1 gene story. Immunology Letters, 2003, 85, 197-203.	2.5	132
51	SLC11A1 (formerly NRAMP1) and disease resistance. Microreview. Cellular Microbiology, 2001, 3, 773-784.	2.1	231
52	Huntingtin is required for neurogenesis and is not impaired by the Huntington's disease CAG expansion. Nature Genetics, 1997, 17, 404-410.	21.4	472
53	Genetic regulation of leishmanial and mycobacterial infections: the Lsh / Ity / Bcg gene story continues. Immunology Letters, 1994, 43, 99-107.	2.5	100
54	Genetic and Physical Mapping of 2q35 in the Region of the NRAMP and IL8R Genes: Identification of a Polymorphic Repeat in Exon 2 of NRAMP. Genomics, 1994, 24, 295-302.	2.9	59