Calvin Pan

List of Publications by Year in descending order

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		126907	118850
58	4,738	33	62
papers	citations	h-index	g-index
63	63	63	8934
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. Cell Metabolism, 2013, 17, 141-152.	16.2	464
2	A high-resolution association mapping panel for the dissection of complex traits in mice. Genome Research, 2010, 20, 281-290.	5.5	299
3	Genetic and environmental control of host-gut microbiota interactions. Genome Research, 2015, 25, 1558-1569.	5.5	288
4	Flavin containing monooxygenase 3 exerts broad effects on glucose and lipid metabolism and atherosclerosis. Journal of Lipid Research, 2015, 56, 22-37.	4.2	254
5	Influenza Virus Affects Intestinal Microbiota and Secondary Salmonella Infection in the Gut through Type I Interferons. PLoS Pathogens, 2016, 12, e1005572.	4.7	213
6	Genetic Architecture of Insulin Resistance in the Mouse. Cell Metabolism, 2015, 21, 334-347.	16.2	196
7	The TMAO-Producing Enzyme Flavin-Containing Monooxygenase 3 Regulates Obesity and the Beiging of White Adipose Tissue. Cell Reports, 2017, 19, 2451-2461.	6.4	194
8	Applications and Limitations of Mouse Models for Understanding Human Atherosclerosis. Cell Metabolism, 2017, 25, 248-261.	16.2	161
9	The Hybrid Mouse Diversity Panel: a resource for systems genetics analyses of metabolic and cardiovascular traits. Journal of Lipid Research, 2016, 57, 925-942.	4.2	143
10	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	21.4	143
11	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	6.2	141
12	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. Mammalian Genome, 2012, 23, 680-692.	2.2	134
13	Integration of Multi-omics Data from Mouse Diversity Panel Highlights Mitochondrial Dysfunction in Non-alcoholic Fatty Liver Disease. Cell Systems, 2018, 6, 103-115.e7.	6.2	124
14	Genetic Architecture of Atherosclerosis in Mice: A Systems Genetics Analysis of Common Inbred Strains. PLoS Genetics, 2015, 11, e1005711.	3.5	124
15	Genome-wide analysis highlights contribution of immune system pathways to the genetic architecture of asthma. Nature Communications, 2020, 11, 1776.	12.8	119
16	Natural variation of macrophage activation as disease-relevant phenotype predictive of inflammation and cancer survival. Nature Communications, 2017, 8, 16041.	12.8	113
17	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
18	<i>RIPK1</i> Expression Associates With Inflammation in Early Atherosclerosis in Humans and Can Be Therapeutically Silenced to Reduce NF-ÎB Activation and Atherogenesis in Mice. Circulation, 2021, 143, 163-177.	1.6	102

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19	An integrative systems genetic analysis of mammalian lipid metabolism. Nature, 2019, 567, 187-193.	27.8	101
20	The genetic architecture of NAFLD among inbred strains of mice. ELife, 2015, 4, e05607.	6.0	96
21	Obesity-linked suppression of membrane-bound O-acyltransferase 7 (MBOAT7) drives non-alcoholic fatty liver disease. ELife, 2019, 8, .	6.0	93
22	Gene-by-Sex Interactions in Mitochondrial Functions and Cardio-Metabolic Traits. Cell Metabolism, 2019, 29, 932-949.e4.	16.2	79
23	Impact of Individual Traits, Saturated Fat, and Protein Source on the Gut Microbiome. MBio, 2018, 9, .	4.1	70
24	Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. Molecular Phylogenetics and Evolution, 2015, 92, 140-146.	2.7	68
25	Tissue-specific pathways and networks underlying sexual dimorphism in non-alcoholic fatty liver disease. Biology of Sex Differences, 2018, 9, 46.	4.1	65
26	Genome-Wide Association Study Identifies Nox3 as a Critical Gene for Susceptibility to Noise-Induced Hearing Loss. PLoS Genetics, 2015, 11, e1005094.	3.5	64
27	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. Cell Metabolism, 2018, 27, 1138-1155.e6.	16.2	58
28	Metabolic reprogramming and epigenetic changes of vital organs in SARS-CoV-2–induced systemic toxicity. JCI Insight, 2021, 6, .	5.0	57
29	Genetic regulation of mouse liver metabolite levels. Molecular Systems Biology, 2014, 10, 730.	7.2	55
30	The Genetic Architecture of Dietâ€Induced Hepatic Fibrosis in Mice. Hepatology, 2018, 68, 2182-2196.	7.3	51
31	Genetic and hormonal control of hepatic steatosis in female and male mice. Journal of Lipid Research, 2017, 58, 178-187.	4.2	46
32	Sex-specific metabolic functions of adipose Lipocalin-2. Molecular Metabolism, 2019, 30, 30-47.	6.5	41
33	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. Human Molecular Genetics, 2019, 28, 4161-4172.	2.9	41
34	Epigenome-wide association in adipose tissue from the METSIM cohort. Human Molecular Genetics, 2018, 27, 1830-1846.	2.9	38
35	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. ELife, 2016, 5, .	6.0	35
36	RIPK1 gene variants associate with obesity in humans and can be therapeutically silenced to reduce obesity in mice. Nature Metabolism, 2020, 2, 1113-1125.	11.9	34

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37	Sex-specific genetic regulation of adipose mitochondria and metabolic syndrome by Ndufv2. Nature Metabolism, 2021, 3, 1552-1568.	11.9	32
38	Sex differences in heart mitochondria regulate diastolic dysfunction. Nature Communications, 2022, 13, .	12.8	30
39	Genetic, dietary, and sex-specific regulation of hepatic ceramides and the relationship between hepatic ceramides and IR [S]. Journal of Lipid Research, 2018, 59, 1164-1174.	4.2	26
40	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. Basic Research in Cardiology, 2022, 117, 6.	5.9	22
41	Genomewide Association Study Identifies Cxcl Family Members as Partial Mediators of LPS-Induced Periodontitis. Journal of Bone and Mineral Research, 2018, 33, 1450-1463.	2.8	21
42	Integrative analysis of liver-specific non-coding regulatory SNPs associated with the risk of coronary artery disease. American Journal of Human Genetics, 2021, 108, 411-430.	6.2	20
43	Placental genomics mediates genetic associations with complex health traits and disease. Nature Communications, 2022, 13, 706.	12.8	20
44	The Genetic Architecture of Carbon Tetrachloride-Induced Liver Fibrosis in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 199-220.	4.5	19
45	The Genetic Architecture of Hearing Impairment in Mice: Evidence for Frequency-Specific Genetic Determinants. G3: Genes, Genomes, Genetics, 2015, 5, 2329-2339.	1.8	16
46	Genetic regulation of liver lipids in a mouse model of insulin resistance and hepatic steatosis. Molecular Systems Biology, 2021, 17, e9684.	7.2	16
47	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. MSystems, 2021, 6, .	3.8	13
48	The Systems Genetics Resource: A Web Application to Mine Global Data for Complex Disease Traits. Frontiers in Genetics, 2013, 4, 84.	2.3	12
49	Collaborative interactions of heterogenous ribonucleoproteins contribute to transcriptional regulation of sterol metabolism in mice. Nature Communications, 2020, 11, 984.	12.8	10
50	Mouse genome-wide association studies and systems genetics uncover the genetic architecture associated with hepatic pharmacokinetic and pharmacodynamic properties of a constrained ethyl antisense oligonucleotide targeting Malat1. PLoS Genetics, 2018, 14, e1007732.	3.5	7
51	Maternal High-Protein and Low-Protein Diets Perturb Hypothalamus and Liver Transcriptome and Metabolic Homeostasis in Adult Mouse Offspring. Frontiers in Genetics, 2018, 9, 642.	2.3	6
52	Dietary and Pharmacologic Manipulations of Host Lipids and Their Interaction With the Gut Microbiome in Non-human Primates. Frontiers in Medicine, 2021, 8, 646710.	2.6	6
53	Identification of DNA Damage Repair Enzyme <i>Ascc2</i> as Causal for Heart Failure With Preserved Ejection Fraction. Circulation, 2022, 145, 1102-1104.	1.6	6
54	A Suite of Tools for Biologists That Improve Accessibility and Visualization of Large Systems Genetics Datasets: Applications to the Hybrid Mouse Diversity Panel. Methods in Molecular Biology, 2017, 1488, 153-188.	0.9	5

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55	Identifying fenofibrate responsive CpG sites. BMC Proceedings, 2018, 12, 43.	1.6	4
56	Hybrid Mouse Diversity Panel Identifies Genetic Architecture Associated with the Acute Antisense Oligonucleotide-Mediated Inflammatory Response to a 2′-O-Methoxyethyl Antisense Oligonucleotide. Nucleic Acid Therapeutics, 2019, 29, 266-277.	3.6	4
57	GNAI3: Another Candidate Gene to Screen in Persons with Ocular Albinism. PLoS ONE, 2016, 11, e0162273.	2.5	3
58	Genetic complexity at expression quantitative trait loci. BMC Proceedings, 2016, 10, 85-89.	1.6	1