

Elissa J Chesler

List of Publications by Year in descending order

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151
papers

11,074
citations

43973

48
h-index

35952

97
g-index

177
all docs

177
docs citations

177
times ranked

11082
citing authors

#	ARTICLE	IF	CITATIONS
1	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	9.4	1,034
2	Complex trait analysis of gene expression uncovers polygenic and pleiotropic networks that modulate nervous system function. <i>Nature Genetics</i> , 2005, 37, 233-242.	9.4	695
3	The melanocortin-1 receptor gene mediates female-specific mechanisms of analgesia in mice and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4867-4872.	3.3	469
4	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. <i>Genetics</i> , 2012, 190, 437-447.	1.2	437
5	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	7.7	390
6	Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. <i>Nature Genetics</i> , 2005, 37, 225-232.	9.4	366
7	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	2.4	327
8	Identification and ranking of genetic and laboratory environment factors influencing a behavioral trait, thermal nociception, via computational analysis of a large data archive. <i>Neuroscience and Biobehavioral Reviews</i> , 2002, 26, 907-923.	2.9	285
9	The Collaborative Cross at Oak Ridge National Laboratory: developing a powerful resource for systems genetics. <i>Mammalian Genome</i> , 2008, 19, 382-389.	1.0	245
10	Influences of laboratory environment on behavior. <i>Nature Neuroscience</i> , 2002, 5, 1101-1102.	7.1	228
11	Host genetic and environmental effects on mouse intestinal microbiota. <i>ISME Journal</i> , 2012, 6, 2033-2044.	4.4	206
12	Prevalence of sexual dimorphism in mammalian phenotypic traits. <i>Nature Communications</i> , 2017, 8, 15475.	5.8	200
13	High-throughput behavioral phenotyping in the expanded panel of BXD recombinant inbred strains. <i>Genes, Brain and Behavior</i> , 2010, 9, 129-159.	1.1	199
14	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.	0.8	195
15	Comparing phenotypic variation between inbred and outbred mice. <i>Nature Methods</i> , 2018, 15, 994-996.	9.0	192
16	Natural variation and genetic covariance in adult hippocampal neurogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 780-785.	3.3	181
17	WebQTL: rapid exploratory analysis of gene expression and genetic networks for brain and behavior. <i>Nature Neuroscience</i> , 2004, 7, 485-486.	7.1	176
18	Acute Administration of Estrogen and Progesterone Impairs the Acquisition of the Spatial Morris Water Maze in Ovariectomized Rats. <i>Hormones and Behavior</i> , 2000, 38, 234-242.	1.0	171

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19	Genetic analysis in the Collaborative Cross breeding population. <i>Genome Research</i> , 2011, 21, 1223-1238.	2.4	158
20	Reproducibility and replicability of rodent phenotyping in preclinical studies. <i>Neuroscience and Biobehavioral Reviews</i> , 2018, 87, 218-232.	2.9	153
21	Variable sensitivity to noxious heat is mediated by differential expression of the CGRP gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12938-12943.	3.3	151
22	Mechanistic Differences in Neuropathic Pain Modalities Revealed by Correlating Behavior with Global Expression Profiling. <i>Cell Reports</i> , 2018, 22, 1301-1312.	2.9	142
23	On finding bicliques in bipartite graphs: a novel algorithm and its application to the integration of diverse biological data types. <i>BMC Bioinformatics</i> , 2014, 15, 110.	1.2	131
24	Large-scale discovery of mouse transgenic integration sites reveals frequent structural variation and insertional mutagenesis. <i>Genome Research</i> , 2019, 29, 494-505.	2.4	130
25	Cross-Species Integrative Functional Genomics in GeneWeaver Reveals a Role for Pafah1b1 in Altered Response to Alcohol. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, 1.	1.0	123
26	Genetic Correlates of Gene Expression in Recombinant Inbred Strains: A Relational Model System to Explore Neurobehavioral Phenotypes. <i>Neuroinformatics</i> , 2003, 1, 343-358.	1.5	118
27	High-Diversity Mouse Populations for Complex Traits. <i>Trends in Genetics</i> , 2019, 35, 501-514.	2.9	116
28	GeneWeaver: a web-based system for integrative functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1067-D1076.	6.5	112
29	High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. <i>Genes, Brain and Behavior</i> , 2013, 12, 424-437.	1.1	110
30	The Heritability of Antinociception: Common Pharmacogenetic Mediation of Five Neurochemically Distinct Analgesics. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2003, 304, 547-559.	1.3	95
31	Aging Research Using Mouse Models. <i>Current Protocols in Mouse Biology</i> , 2015, 5, 95-133.	1.2	92
32	Functional coding variation in recombinant inbred mouse lines reveals multiple serotonin transporter-associated phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2047-2052.	3.3	89
33	Extracting Gene Networks for Low-Dose Radiation Using Graph Theoretical Algorithms. <i>PLoS Computational Biology</i> , 2006, 2, e89.	1.5	86
34	High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. <i>Genetics</i> , 2014, 197, 91-106.	1.2	85
35	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	1.2	82
36	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 157-165.	0.8	80

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37	Cisplatin-resistant triple-negative breast cancer subtypes: multiple mechanisms of resistance. <i>BMC Cancer</i> , 2019, 19, 1039.	1.1	77
38	Inferring gene transcriptional modulatory relations: a genetical genomics approach. <i>Human Molecular Genetics</i> , 2005, 14, 1119-1125.	1.4	76
39	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850.	1.5	76
40	Applying the ARRIVE Guidelines to an In Vivo Database. <i>PLoS Biology</i> , 2015, 13, e1002151.	2.6	75
41	Out of the bottleneck: the Diversity Outcross and Collaborative Cross mouse populations in behavioral genetics research. <i>Mammalian Genome</i> , 2014, 25, 3-11.	1.0	74
42	The Genetics of Neuropathic Pain from Model Organisms to Clinical Application. <i>Neuron</i> , 2019, 104, 637-653.	3.8	71
43	Systems genetics of intravenous cocaine self-administration in the BXD recombinant inbred mouse panel. <i>Psychopharmacology</i> , 2016, 233, 701-714.	1.5	70
44	Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. <i>Mammalian Genome</i> , 2015, 26, 511-520.	1.0	66
45	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3893-3902.	0.8	66
46	Male Infertility Is Responsible for Nearly Half of the Extinction Observed in the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 557-572.	1.2	66
47	Mouse Phenome Database: an integrative database and analysis suite for curated empirical phenotype data from laboratory mice. <i>Nucleic Acids Research</i> , 2018, 46, D843-D850.	6.5	65
48	Genotype-dependence of gabapentin and pregabalin sensitivity: the pharmacogenetic mediation of analgesia is specific to the type of pain being inhibited. <i>Pain</i> , 2003, 106, 325-335.	2.0	64
49	The Heritability of Antinociception II: Pharmacogenetic Mediation of Three Over-the-Counter Analgesics in Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2003, 305, 755-764.	1.3	60
50	Architecture of energy balance traits in emerging lines of the Collaborative Cross. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2011, 300, E1124-E1134.	1.8	58
51	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	1.2	55
52	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	3.5	55
53	Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals <i>Hydin</i> as a novel pain gene. <i>Mammalian Genome</i> , 2014, 25, 211-222.	1.0	54
54	Genome-level analysis of genetic regulation of liver gene expression networks. <i>Hepatology</i> , 2007, 46, 548-557.	3.6	49

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55	Robust mouse tracking in complex environments using neural networks. <i>Communications Biology</i> , 2019, 2, 124.	2.0	49
56	Mouse Phenome Database: a data repository and analysis suite for curated primary mouse phenotype data. <i>Nucleic Acids Research</i> , 2019, 48, D716-D723.	6.5	48
57	KCNN Genes that Encode Small-Conductance Ca ²⁺ -Activated K ⁺ Channels Influence Alcohol and Drug Addiction. <i>Neuropsychopharmacology</i> , 2015, 40, 1928-1939.	2.8	47
58	Integration of mouse phenome data resources. <i>Mammalian Genome</i> , 2007, 18, 157-163.	1.0	44
59	Genetic Regulation of <i>Zfp30</i> , CXCL1, and Neutrophilic Inflammation in Murine Lung. <i>Genetics</i> , 2014, 198, 735-745.	1.2	44
60	Identification of quantitative trait loci for chemical/inflammatory nociception in mice. <i>Pain</i> , 2002, 96, 385-391.	2.0	40
61	QTL and systems genetics analysis of mouse grooming and behavioral responses to novelty in an open field. <i>Genes, Brain and Behavior</i> , 2017, 16, 790-799.	1.1	40
62	Association of novelty-related behaviors and intravenous cocaine self-administration in Diversity Outbred mice. <i>Psychopharmacology</i> , 2015, 232, 1011-1024.	1.5	39
63	Integrative genetic analysis of transcription modules: towards filling the gap between genetic loci and inherited traits. <i>Human Molecular Genetics</i> , 2006, 15, 481-492.	1.4	38
64	Integrative Genetic Analysis of Allergic Inflammation in the Murine Lung. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 51, 436-445.	1.4	37
65	Kv7 channels in the nucleus accumbens are altered by chronic drinking and are targets for reducing alcohol consumption. <i>Addiction Biology</i> , 2016, 21, 1097-1112.	1.4	37
66	Genome Reshuffling for Advanced Intercross Permutation (GRAIP): Simulation and Permutation for Advanced Intercross Population Analysis. <i>PLoS ONE</i> , 2008, 3, e1977.	1.1	35
67	Ontological discovery environment: A system for integrating gene-phenotype associations. <i>Genomics</i> , 2009, 94, 377-387.	1.3	35
68	Host genetic control of gut microbiome composition. <i>Mammalian Genome</i> , 2021, 32, 263-281.	1.0	35
69	Identification of a novel gene regulating amygdala-mediated fear extinction. <i>Molecular Psychiatry</i> , 2019, 24, 601-612.	4.1	34
70	Accessing Data Resources in the Mouse Phenome Database for Genetic Analysis of Murine Life Span and Health Span. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2016, 71, 170-177.	1.7	32
71	Investigation of COVID-19 comorbidities reveals genes and pathways coincident with the SARS-CoV-2 viral disease. <i>Scientific Reports</i> , 2020, 10, 20848.	1.6	32
72	Sex-specific gene expression in the BXD mouse liver. <i>Physiological Genomics</i> , 2010, 42, 456-468.	1.0	30

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73	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. <i>Nucleic Acids Research</i> , 2016, 44, D555-D559.	6.5	30
74	Computational, Integrative, and Comparative Methods for the Elucidation of Genetic Coexpression Networks. <i>Journal of Biomedicine and Biotechnology</i> , 2005, 2005, 172-180.	3.0	29
75	Supplementing High-Density SNP Microarrays for Additional Coverage of Disease-Related Genes: Addiction as a Paradigm. <i>PLoS ONE</i> , 2009, 4, e5225.	1.1	27
76	Sex and strain influence attribution of incentive salience to reward cues in mice. <i>Behavioural Brain Research</i> , 2015, 292, 305-315.	1.2	27
77	Cross-Species Analyses Identify <i>Dlgap2</i> as a Regulator of Age-Related Cognitive Decline and Alzheimer's Dementia. <i>Cell Reports</i> , 2020, 32, 108091.	2.9	27
78	Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcriptomic Data. <i>Journal of Biomedical Research</i> , 2005, 150-165.		27
79	Mapping of a quantitative trait locus for morphine withdrawal severity. <i>Mammalian Genome</i> , 2004, 15, 610-617.	1.0	26
80	Identification of a QTL in <i>Mus musculus</i> for Alcohol Preference, Withdrawal, and <i>Ap3m2</i> Expression Using Integrative Functional Genomics and Precision Genetics. <i>Genetics</i> , 2014, 197, 1377-1393.	1.2	25
81	Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. <i>Psychopharmacology</i> , 2020, 237, 979-996.	1.5	25
82	Genetic variation regulates opioid-induced respiratory depression in mice. <i>Scientific Reports</i> , 2020, 10, 14970.	1.6	25
83	Quantitative trait loci for sensitivity to ethanol intoxication in a C57BL/6J- <i>Ap3m2</i> - <i>Ap3m2</i> 129S1/SvImJ inbred mouse cross. <i>Mammalian Genome</i> , 2012, 23, 305-321.	1.0	24
84	Systems Genetic Analysis in GeneNetwork.org. <i>Current Protocols in Neuroscience</i> , 2017, 79, 8.39.1-8.39.20.	2.6	24
85	An Informatics Approach to Systems Neurogenetics. <i>Methods in Molecular Biology</i> , 2007, 401, 287-303.	0.4	24
86	The Major Locus for Mouse Adenovirus Susceptibility Maps to Genes of the Hematopoietic Cell Surface-Expressed LY6 Family. <i>Journal of Immunology</i> , 2010, 184, 3055-3062.	0.4	23
87	Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population. <i>BMC Genomics</i> , 2015, 16, 633.	1.2	22
88	CbGRiTS: Cerebellar gene regulation in time and space. <i>Developmental Biology</i> , 2015, 397, 18-30.	0.9	22
89	Genetic mapping in Diversity Outbred mice identifies a <i>Trpa1</i> variant influencing late-phase formalin response. <i>Pain</i> , 2019, 160, 1740-1753.	2.0	22
90	Interpretation of psychiatric genome-wide association studies with multispecies heterogeneous functional genomic data integration. <i>Neuropsychopharmacology</i> , 2021, 46, 86-97.	2.8	22

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91	Brain Gene Expression: Genomics and Genetics. <i>International Review of Neurobiology</i> , 2004, 60, 59-95.	0.9	21
92	Acute progesterone can recruit sex-specific neurochemical mechanisms mediating swim stress-induced and μ -opioid analgesia in mice. <i>Hormones and Behavior</i> , 2004, 46, 467-473.	1.0	21
93	Reconstructing Generalized Logical Networks of Transcriptional Regulation in Mouse Brain from Temporal Gene Expression Data. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009, 2009, 1-13.	1.4	21
94	Identification of Quantitative Trait Loci for Susceptibility to Mouse Adenovirus Type 1. <i>Journal of Virology</i> , 2005, 79, 11517-11522.	1.5	20
95	Genetic variation in hippocampal microRNA expression differences in C57BL/6 J X DBA/2 J (BXD) recombinant inbred mouse strains. <i>BMC Genomics</i> , 2012, 13, 476.	1.2	20
96	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. <i>Genetics</i> , 2020, 214, 719-733.	1.2	20
97	Genetics of body weight in the LXS recombinant inbred mouse strains. <i>Mammalian Genome</i> , 2005, 16, 764-774.	1.0	19
98	Genotype-dependent effects of adolescent nicotine exposure on dopamine functional dynamics in the nucleus accumbens shell in male and female mice: a potential mechanism underlying the gateway effect of nicotine. <i>Psychopharmacology</i> , 2011, 215, 631-642.	1.5	19
99	Genetic analysis of albuminuria in collaborative cross and multiple mouse intercross populations. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, F972-F981.	1.3	19
100	Systems genetics of sensation seeking. <i>Genes, Brain and Behavior</i> , 2019, 18, e12519.	1.1	19
101	Complex Genetics of Interactions of Alcohol and CNS Function and Behavior. <i>Alcoholism: Clinical and Experimental Research</i> , 2005, 29, 1706-1719.	1.4	18
102	Neurobehavioral mutants identified in an ENU-mutagenesis project. <i>Mammalian Genome</i> , 2007, 18, 559-572.	1.0	18
103	Heritable variation in locomotion, reward sensitivity and impulsive behaviors in a genetically diverse inbred mouse panel. <i>Genes, Brain and Behavior</i> , 2021, 20, e12773.	1.1	17
104	Autism candidate genes via mouse phenomics. <i>Journal of Biomedical Informatics</i> , 2011, 44, S5-S11.	2.5	16
105	Genetic networks controlling retinal injury. <i>Molecular Vision</i> , 2005, 11, 958-70.	1.1	16
106	Accelerating Discovery for Complex Neurological and Behavioral Disorders Through Systems Genetics and Integrative Genomics in the Laboratory Mouse. <i>Neurotherapeutics</i> , 2012, 9, 338-348.	2.1	15
107	Genome-wide microarray comparison reveals downstream genes of Pax6 in the developing mouse cerebellum. <i>European Journal of Neuroscience</i> , 2012, 36, 2888-2898.	1.2	15
108	Use of the Expanded Panel of BXD Mice Narrow QTL Regions in Ethanol-Induced Locomotor Activation and Motor Incoordination. <i>Alcoholism: Clinical and Experimental Research</i> , 2013, 37, 170-183.	1.4	15

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109	Heritability of ethanol consumption and pharmacokinetics in a genetically diverse panel of collaborative cross mouse strains and their inbred founders. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 697-708.	1.4	15
110	P2P-R expression is genetically coregulated with components of the translation machinery and with PUM2, a translational repressor that associates with the P2P-R mRNA. <i>Journal of Cellular Physiology</i> , 2005, 204, 99-105.	2.0	13
111	Reply to "Normalization procedures and detection of linkage signal in genetical-genomics experiments". <i>Nature Genetics</i> , 2006, 38, 856-858.	9.4	13
112	Genome-wide association for testis weight in the diversity outbred mouse population. <i>Mammalian Genome</i> , 2018, 29, 310-324.	1.0	13
113	Prospects for finding the mechanisms of sex differences in addiction with human and model organism genetic analysis. <i>Genes, Brain and Behavior</i> , 2020, 19, e12645.	1.1	13
114	Multi-omic and multi-species meta-analyses of nicotine consumption. <i>Translational Psychiatry</i> , 2021, 11, 98.	2.4	13
115	Genomic loci and candidate genes underlying inflammatory nociception. <i>Pain</i> , 2011, 152, 599-606.	2.0	12
116	GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. <i>Mammalian Genome</i> , 2015, 26, 556-566.	1.0	12
117	Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. <i>Genetics</i> , 2019, 212, 919-929.	1.2	12
118	Machine learning-based automated phenotyping of inflammatory nocifensive behavior in mice. <i>Molecular Pain</i> , 2020, 16, 174480692095859.	1.0	12
119	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	1.1	12
120	Testing Pleiotropy vs. Separate QTL in Multiparental Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2317-2324.	0.8	11
121	On Finding and Enumerating Maximal and Maximum k -Partite Cliques in k -Partite Graphs. <i>Algorithms</i> , 2019, 12, 23.	1.2	10
122	Do gene expression findings from mouse models of cocaine use recapitulate human cocaine use disorder in reward circuitry?. <i>Genes, Brain and Behavior</i> , 2021, 20, e12689.	1.1	10
123	Identifying genetic loci and spleen gene coexpression networks underlying immunophenotypes in BXD recombinant inbred mice. <i>Physiological Genomics</i> , 2010, 41, 244-253.	1.0	9
124	A genetic approach to the prediction of drug side effects: bleomycin induces concordant phenotypes in mice of the collaborative cross. <i>Pharmacogenomics and Personalized Medicine</i> , 2011, 4, 35.	0.4	8
125	Genetic Mapping of Vocalization to a Series of Increasing Acute Footshocks Using B6.A Consonic and B6.D2 Congenic Mouse Strains. <i>Behavior Genetics</i> , 2008, 38, 417-423.	1.4	7
126	Whole-Genome Sequencing of Inbred Mouse Strains Selected for High and Low Open-Field Activity. <i>Behavior Genetics</i> , 2021, 51, 68-81.	1.4	7

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127	The importance of open-source integrative genomics to drug discovery. <i>Current Opinion in Drug Discovery & Development</i> , 2010, 13, 310-6.	1.9	7
128	Integrative Functional Genomics for Systems Genetics in GeneWeaver.org. <i>Methods in Molecular Biology</i> , 2017, 1488, 131-152.	0.4	6
129	Performing Integrative Functional Genomics Analysis in GeneWeaver.org. <i>Methods in Molecular Biology</i> , 2014, 1101, 13-29.	0.4	6
130	Phenotype screening for genetically determined age-onset disorders and increased longevity in ENU-mutagenized mice. <i>Age</i> , 2005, 27, 75-90.	3.0	5
131	Integration of heterogeneous functional genomics data in gerontology research to find genes and pathway underlying aging across species. <i>PLoS ONE</i> , 2019, 14, e0214523.	1.1	5
132	Curating gene sets: challenges and opportunities for integrative analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	5
133	Analysis of morphine responses in mice reveals a QTL on Chromosome 7. <i>F1000Research</i> , 2016, 5, 2156.	0.8	5
134	The dihydropyrimidine dehydrogenase gene contributes to heritable differences in sleep in mice. <i>Current Biology</i> , 2021, 31, 5238-5248.e7.	1.8	5
135	Genes identified in rodent studies of alcohol intake are enriched for heritability of human substance use. <i>Alcoholism: Clinical and Experimental Research</i> , 2021, 45, 2485-2494.	1.4	5
136	Dynamic Visualization of Coexpression in Systems Genetics Data. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2008, 14, 1081-1095.	2.9	4
137	Analysis of sleep traits in knockout mice from the large-scale KOMP2 population using a non-invasive, high-throughput piezoelectric system. <i>BMC Bioinformatics</i> , 2015, 16, P15.	1.2	4
138	Discovery of a Role for Rab3b in Habituation and Cocaine Induced Locomotor Activation in Mice Using Heterogeneous Functional Genomic Analysis. <i>Frontiers in Neuroscience</i> , 2020, 14, 721.	1.4	4
139	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. <i>Pain</i> , 2022, 163, 1139-1157.	2.0	4
140	Analysis of morphine responses in mice reveals a QTL on Chromosome 7. <i>F1000Research</i> , 2016, 5, 2156.	0.8	4
141	Opportunities for Bioinformatics in the Classification of Behavior and Psychiatric Disorders. <i>International Review of Neurobiology</i> , 2012, 104, 183-211.	0.9	3
142	Scalable multipartite subgraph enumeration for integrative analysis of heterogeneous experimental functional genomics data. , 2015, , .		3
143	A Systematic Comparison of Genome Scale Clustering Algorithms. <i>Lecture Notes in Computer Science</i> , 2011, , 416-427.	1.0	2
144	Genome-wide association mapping of ethanol sensitivity in the Diversity Outbred mouse population. <i>Alcoholism: Clinical and Experimental Research</i> , 2022, 46, 941-960.	1.4	2

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145	Combining Quantitative Trait and Gene-Expression Data. , 0, , 389-411.		1
146	Lost and Found in Behavioral Informatics. International Review of Neurobiology, 2012, 103, 1-18.	0.9	1
147	Inferring gene coexpression networks for low dose ionizing radiation using graph theoretical algorithms and systems genetics. BMC Bioinformatics, 2010, 11, .	1.2	0
148	Genetic Susceptibility To Allergen-Induced Airway Inflammation In Mice. , 2011, , .		0
149	A Context-Driven Gene Prioritization Method for Web-Based Functional Genomics. Lecture Notes in Computer Science, 2013, , 161-172.	1.0	0
150	Algorithmic tools for tripartite data analysis. BMC Bioinformatics, 2014, 15, P32.	1.2	0
151	Abstract 4387: Diversity Outbred: a new, highly diverse mouse stock for toxicology and cancer. , 2011, , .		0