

# Elissa J Chesler

## List of Publications by Year in descending order

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151  
papers

11,074  
citations

44069

48  
h-index

36028

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.	21.4	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.	21.4	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.	7.1	469
4	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. <i>Genetics</i> , 2012, 190, 437-447.	2.9	437
5	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	16.3	390
6	Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. <i>Nature Genetics</i> , 2005, 37, 225-232.	21.4	366
7	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	5.5	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.	6.1	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.	2.2	245
10	Influences of laboratory environment on behavior. <i>Nature Neuroscience</i> , 2002, 5, 1101-1102.	14.8	228
11	Host genetic and environmental effects on mouse intestinal microbiota. <i>ISME Journal</i> , 2012, 6, 2033-2044.	9.8	206
12	Prevalence of sexual dimorphism in mammalian phenotypic traits. <i>Nature Communications</i> , 2017, 8, 15475.	12.8	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.	2.2	199
14	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.	1.8	195
15	Comparing phenotypic variation between inbred and outbred mice. <i>Nature Methods</i> , 2018, 15, 994-996.	19.0	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.	7.1	181
17	WebQTL: rapid exploratory analysis of gene expression and genetic networks for brain and behavior. <i>Nature Neuroscience</i> , 2004, 7, 485-486.	14.8	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.	2.1	171

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19	Genetic analysis in the Collaborative Cross breeding population. <i>Genome Research</i> , 2011, 21, 1223-1238.	5.5	158
20	Reproducibility and replicability of rodent phenotyping in preclinical studies. <i>Neuroscience and Biobehavioral Reviews</i> , 2018, 87, 218-232.	6.1	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.	7.1	151
22	Mechanistic Differences in Neuropathic Pain Modalities Revealed by Correlating Behavior with Global Expression Profiling. <i>Cell Reports</i> , 2018, 22, 1301-1312.	6.4	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.	2.6	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.	5.5	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.	2.0	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.	2.8	118
27	High-Diversity Mouse Populations for Complex Traits. <i>Trends in Genetics</i> , 2019, 35, 501-514.	6.7	116
28	GeneWeaver: a web-based system for integrative functional genomics. <i>Nucleic Acids Research</i> , 2012, 40, D1067-D1076.	14.5	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.	2.2	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.	2.5	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.	7.1	89
33	Extracting Gene Networks for Low-Dose Radiation Using Graph Theoretical Algorithms. <i>PLoS Computational Biology</i> , 2006, 2, e89.	3.2	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.	2.9	85
35	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	2.9	82
36	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 157-165.	1.8	80

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37	Cisplatin-resistant triple-negative breast cancer subtypes: multiple mechanisms of resistance. BMC Cancer, 2019, 19, 1039.	2.6	77
38	Inferring gene transcriptional modulatory relations: a genetical genomics approach. Human Molecular Genetics, 2005, 14, 1119-1125.	2.9	76
39	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. PLoS Genetics, 2015, 11, e1004850.	3.5	76
40	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	5.6	75
41	Out of the bottleneck: the Diversity Outcross and Collaborative Cross mouse populations in behavioral genetics research. Mammalian Genome, 2014, 25, 3-11.	2.2	74
42	The Genetics of Neuropathic Pain from Model Organisms to Clinical Application. Neuron, 2019, 104, 637-653.	8.1	71
43	Systems genetics of intravenous cocaine self-administration in the BXD recombinant inbred mouse panel. Psychopharmacology, 2016, 233, 701-714.	3.1	70
44	Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. Mammalian Genome, 2015, 26, 511-520.	2.2	66
45	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. G3: Genes, Genomes, Genetics, 2016, 6, 3893-3902.	1.8	66
46	Male Infertility Is Responsible for Nearly Half of the Extinction Observed in the Mouse Collaborative Cross. Genetics, 2017, 206, 557-572.	2.9	66
47	Mouse Phenome Database: an integrative database and analysis suite for curated empirical phenotype data from laboratory mice. Nucleic Acids Research, 2018, 46, D843-D850.	14.5	65
48	Genotype-dependence of gabapentin and pregabalin sensitivity: the pharmacogenetic mediation of analgesia is specific to the type of pain being inhibited. Pain, 2003, 106, 325-335.	4.2	64
49	The Heritability of Antinociception II: Pharmacogenetic Mediation of Three Over-the-Counter Analgesics in Mice. Journal of Pharmacology and Experimental Therapeutics, 2003, 305, 755-764.	2.5	60
50	Architecture of energy balance traits in emerging lines of the Collaborative Cross. American Journal of Physiology - Endocrinology and Metabolism, 2011, 300, E1124-E1134.	3.5	58
51	A systematic comparison of genome-scale clustering algorithms. BMC Bioinformatics, 2012, 13, S7.	2.6	55
52	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. Molecular Biology and Evolution, 2016, 33, 1381-1395.	8.9	55
53	Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. Mammalian Genome, 2014, 25, 211-222.	2.2	54
54	Genome-level analysis of genetic regulation of liver gene expression networks. Hepatology, 2007, 46, 548-557.	7.3	49

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55	Robust mouse tracking in complex environments using neural networks. <i>Communications Biology</i> , 2019, 2, 124.	4.4	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.	14.5	48
57	KCNN Genes that Encode Small-Conductance Ca <sup>2+</sup> -Activated K <sup>+</sup> Channels Influence Alcohol and Drug Addiction. <i>Neuropsychopharmacology</i> , 2015, 40, 1928-1939.	5.4	47
58	Integration of mouse phenome data resources. <i>Mammalian Genome</i> , 2007, 18, 157-163.	2.2	44
59	Genetic Regulation of <i>Zfp30</i> , CXCL1, and Neutrophilic Inflammation in Murine Lung. <i>Genetics</i> , 2014, 198, 735-745.	2.9	44
60	Identification of quantitative trait loci for chemical/inflammatory nociception in mice. <i>Pain</i> , 2002, 96, 385-391.	4.2	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.	2.2	40
62	Association of novelty-related behaviors and intravenous cocaine self-administration in Diversity Outbred mice. <i>Psychopharmacology</i> , 2015, 232, 1011-1024.	3.1	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.	2.9	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.	2.9	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.	2.6	37
66	Genome Reshuffling for Advanced Intercross Permutation (GRAIP): Simulation and Permutation for Advanced Intercross Population Analysis. <i>PLoS ONE</i> , 2008, 3, e1977.	2.5	35
67	Ontological discovery environment: A system for integrating gene-phenotype associations. <i>Genomics</i> , 2009, 94, 377-387.	2.9	35
68	Host genetic control of gut microbiome composition. <i>Mammalian Genome</i> , 2021, 32, 263-281.	2.2	35
69	Identification of a novel gene regulating amygdala-mediated fear extinction. <i>Molecular Psychiatry</i> , 2019, 24, 601-612.	7.9	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.	3.6	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.	3.3	32
72	Sex-specific gene expression in the BXD mouse liver. <i>Physiological Genomics</i> , 2010, 42, 456-468.	2.3	30

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73	GeneWeaver: data driven alignment of cross-species genomics in biology and disease. Nucleic Acids Research, 2016, 44, D555-D559.	14.5	30
74	Computational, Integrative, and Comparative Methods for the Elucidation of Genetic Coexpression Networks. Journal of Biomedicine and Biotechnology, 2005, 2005, 172-180.	3.0	29
75	Supplementing High-Density SNP Microarrays for Additional Coverage of Disease-Related Genes: Addiction as a Paradigm. PLoS ONE, 2009, 4, e5225.	2.5	27
76	Sex and strain influence attribution of incentive salience to reward cues in mice. Behavioural Brain Research, 2015, 292, 305-315.	2.2	27
77	Cross-Species Analyses Identify Dlgap2 as a Regulator of Age-Related Cognitive Decline and Alzheimer's Dementia. Cell Reports, 2020, 32, 108091.	6.4	27
78	Combinatorial Genetic Regulatory Network Analysis Tools for High Throughput Transcriptomic Data. , 2005, , 150-165.		27
79	Mapping of a quantitative trait locus for morphine withdrawal severity. Mammalian Genome, 2004, 15, 610-617.	2.2	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. Genetics, 2014, 197, 1377-1393.	2.9	25
81	Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. Psychopharmacology, 2020, 237, 979-996.	3.1	25
82	Genetic variation regulates opioid-induced respiratory depression in mice. Scientific Reports, 2020, 10, 14970.	3.3	25
83	Quantitative trait loci for sensitivity to ethanol intoxication in a C57BL/6J—129S1/SvImJ inbred mouse cross. Mammalian Genome, 2012, 23, 305-321.	2.2	24
84	Systems Genetic Analysis in GeneNetwork.org. Current Protocols in Neuroscience, 2017, 79, 8.39.1-8.39.20.	2.6	24
85	An Informatics Approach to Systems Neurogenetics. Methods in Molecular Biology, 2007, 401, 287-303.	0.9	24
86	The Major Locus for Mouse Adenovirus Susceptibility Maps to Genes of the Hematopoietic Cell Surface-Expressed LY6 Family. Journal of Immunology, 2010, 184, 3055-3062.	0.8	23
87	Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population. BMC Genomics, 2015, 16, 633.	2.8	22
88	CbGRiTS: Cerebellar gene regulation in time and space. Developmental Biology, 2015, 397, 18-30.	2.0	22
89	Genetic mapping in Diversity Outbred mice identifies a <i>Trpa1</i> variant influencing late-phase formalin response. Pain, 2019, 160, 1740-1753.	4.2	22
90	Interpretation of psychiatric genome-wide association studies with multispecies heterogeneous functional genomic data integration. Neuropsychopharmacology, 2021, 46, 86-97.	5.4	22

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91	Brain Gene Expression: Genomics and Genetics. International Review of Neurobiology, 2004, 60, 59-95.	2.0	21
92	Acute progesterone can recruit sex-specific neurochemical mechanisms mediating swim stress-induced and $\mu$ -opioid analgesia in mice. Hormones and Behavior, 2004, 46, 467-473.	2.1	21
93	Reconstructing Generalized Logical Networks of Transcriptional Regulation in Mouse Brain from Temporal Gene Expression Data. Eurasip Journal on Bioinformatics and Systems Biology, 2009, 2009, 1-13.	1.4	21
94	Identification of Quantitative Trait Loci for Susceptibility to Mouse Adenovirus Type 1. Journal of Virology, 2005, 79, 11517-11522.	3.4	20
95	Genetic variation in hippocampal microRNA expression differences in C57BL/6 J X DBA/2 J (BXD) recombinant inbred mouse strains. BMC Genomics, 2012, 13, 476.	2.8	20
96	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics, 2020, 214, 719-733.	2.9	20
97	Genetics of body weight in the LXS recombinant inbred mouse strains. Mammalian Genome, 2005, 16, 764-774.	2.2	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. Psychopharmacology, 2011, 215, 631-642.	3.1	19
99	Genetic analysis of albuminuria in collaborative cross and multiple mouse intercross populations. American Journal of Physiology - Renal Physiology, 2012, 303, F972-F981.	2.7	19
100	Systems genetics of sensation seeking. Genes, Brain and Behavior, 2019, 18, e12519.	2.2	19
101	Complex Genetics of Interactions of Alcohol and CNS Function and Behavior. Alcoholism: Clinical and Experimental Research, 2005, 29, 1706-1719.	2.4	18
102	Neurobehavioral mutants identified in an ENU-mutagenesis project. Mammalian Genome, 2007, 18, 559-572.	2.2	18
103	Heritable variation in locomotion, reward sensitivity and impulsive behaviors in a genetically diverse inbred mouse panel. Genes, Brain and Behavior, 2021, 20, e12773.	2.2	17
104	Autism candidate genes via mouse phenomics. Journal of Biomedical Informatics, 2011, 44, S5-S11.	4.3	16
105	Genetic networks controlling retinal injury. Molecular Vision, 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. Neurotherapeutics, 2012, 9, 338-348.	4.4	15
107	Genome-wide microarray comparison reveals downstream genes of Pax6 in the developing mouse cerebellum. European Journal of Neuroscience, 2012, 36, 2888-2898.	2.6	15
108	Use of the Expanded Panel of BXD Mice Narrow QTL Regions in Ethanol-Induced Locomotor Activation and Motor Incoordination. Alcoholism: Clinical and Experimental Research, 2013, 37, 170-183.	2.4	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.	2.4	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.	4.1	13
111	Reply to "Normalization procedures and detection of linkage signal in genetical-genomics experiments". <i>Nature Genetics</i> , 2006, 38, 856-858.	21.4	13
112	Genome-wide association for testis weight in the diversity outbred mouse population. <i>Mammalian Genome</i> , 2018, 29, 310-324.	2.2	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.	2.2	13
114	Multi-omic and multi-species meta-analyses of nicotine consumption. <i>Translational Psychiatry</i> , 2021, 11, 98.	4.8	13
115	Genomic loci and candidate genes underlying inflammatory nociception. <i>Pain</i> , 2011, 152, 599-606.	4.2	12
116	GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. <i>Mammalian Genome</i> , 2015, 26, 556-566.	2.2	12
117	Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. <i>Genetics</i> , 2019, 212, 919-929.	2.9	12
118	Machine learning-based automated phenotyping of inflammatory nocifensive behavior in mice. <i>Molecular Pain</i> , 2020, 16, 174480692095859.	2.1	12
119	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	2.2	12
120	Testing Pleiotropy vs. Separate QTL in Multiparental Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2317-2324.	1.8	11
121	On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. <i>Algorithms</i> , 2019, 12, 23.	2.1	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.	2.2	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.	2.3	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.	0.7	8
125	Genetic Mapping of Vocalization to a Series of Increasing Acute Footshocks Using B6.A Consomic and B6.D2 Congenic Mouse Strains. <i>Behavior Genetics</i> , 2008, 38, 417-423.	2.1	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.	2.1	7



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127	The importance of open-source integrative genomics to drug discovery. <i>Current Opinion in Drug Discovery &amp; 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.	0.9	6
129	Performing Integrative Functional Genomics Analysis in GeneWeaver.org. <i>Methods in Molecular Biology</i> , 2014, 1101, 13-29.	0.9	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.	2.5	5
132	Curating gene sets: challenges and opportunities for integrative analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	5
133	Analysis of morphine responses in mice reveals a QTL on Chromosome 7. <i>F1000Research</i> , 2016, 5, 2156.	1.6	5
134	The dihydropyrimidine dehydrogenase gene contributes to heritable differences in sleep in mice. <i>Current Biology</i> , 2021, 31, 5238-5248.e7.	3.9	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.	2.4	5
136	Dynamic Visualization of Coexpression in Systems Genetics Data. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2008, 14, 1081-1095.	4.4	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.	2.6	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.	2.8	4
139	Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. <i>Pain</i> , 2022, 163, 1139-1157.	4.2	4
140	Analysis of morphine responses in mice reveals a QTL on Chromosome 7. <i>F1000Research</i> , 2016, 5, 2156.	1.6	4
141	Opportunities for Bioinformatics in the Classification of Behavior and Psychiatric Disorders. <i>International Review of Neurobiology</i> , 2012, 104, 183-211.	2.0	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.	1.3	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.	2.4	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.	2.0	1
147	Inferring gene coexpression networks for low dose ionizing radiation using graph theoretical algorithms and systems genetics. BMC Bioinformatics, 2010, 11, .	2.6	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.	1.3	0
150	Algorithmic tools for tripartite data analysis. BMC Bioinformatics, 2014, 15, P32.	2.6	0
151	Abstract 4387: Diversity Outbred: a new, highly diverse mouse stock for toxicology and cancer. , 2011, , .		0