William Valdar

List of Publications by Year
in descending order

77 papers	8,028 citations	101384 36 h-index	76769 74 g-index
97 all docs	97 docs citations	97 times ranked	8896 citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-wide analyses of adipose tissue in outbred rats reveal genetic regulatory mechanisms relevant for human obesity. Physiological Genomics, 2022, 54, 206-219.	1.0	9
2	A Bayesian model selection approach to mediation analysis. PLoS Genetics, 2022, 18, e1010184.	1.5	8
3	Bayesian modeling of skewed X inactivation in genetically diverse mice identifies a novel *Xce* allele associated with copy number changes. Genetics, 2021, 218, .	1.2	5
4	Human-relevant mechanisms and risk factors for TAK-875-Induced liver injury identified via a gene pathway-based approach in Collaborative Cross mice. Toxicology, 2021, 461, 152902.	2.0	12
5	Sept8/SEPTIN8 involvement in cellular structure and kidney damage is identified by genetic mapping and a novel human tubule hypoxic model. Scientific Reports, 2021, 11, 2071.	1.6	13
6	Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. Psychopharmacology, 2020, 237, 979-996.	1.5	25
7	Maternal Liver Metabolic Response to Chronic Vitamin D Deficiency Is Determined by Mouse Strain Genetic Background. Current Developments in Nutrition, 2020, 4, nzaa106.	0.1	5
8	Content and Performance of the MiniMUGA Genotyping Array: A New Tool To Improve Rigor and Reproducibility in Mouse Research. Genetics, 2020, 216, 905-930.	1.2	58
9	Inferring the Allelic Series at QTL in Multiparental Populations. Genetics, 2020, 216, 957-983.	1.2	14
10	Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. PLoS Genetics, 2020, 16, e1008537.	1.5	35
11	Title is missing!. , 2020, 16, e1008537.		0
12	Title is missing!. , 2020, 16, e1008537.		0
13	Title is missing!. , 2020, 16, e1008537.		0
14	Title is missing!. , 2020, 16, e1008537.		0
15	Identification of Candidate Risk Factor Genes for Human Idelalisib Toxicity Using a Collaborative Cross Approach. Toxicological Sciences, 2019, 172, 265-278.	1.4	22
16	Determinants of QTL Mapping Power in the Realized Collaborative Cross. G3: Genes, Genomes, Genetics, 2019, 9, 1707-1727.	0.8	45
17	A Diallel of the Mouse Collaborative Cross Founders Reveals Strong Strain-Specific Maternal Effects on Litter Size. G3: Genes, Genomes, Genetics, 2019, 9, 1613-1622.	0.8	11
18	Perinatal nutrition interacts with genetic background to alter behavior in a parent‐of‐origin‐dependent manner in adult Collaborative Cross mice. Genes, Brain and Behavior, 2018, 17, e12438.	1.1	30

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19	Bayesian Diallel Analysis Reveals *Mx1*-Dependent and *Mx1*-Independent Effects on Response to Influenza A Virus in Mice. G3: Genes, Genomes, Genetics, 2018, 8, 427-445.	0.8	27
20	Dissecting the Genetic Architecture of Shoot Growth in Carrot (*Daucus carota* L.) Using a Diallel Mating Design. G3: Genes, Genomes, Genetics, 2018, 8, 411-426.	0.8	25
21	Genetic Fine‐Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. Obesity, 2018, 26, 213-222.	1.5	64
22	Mean-Variance QTL Mapping Identifies Novel QTL for Circadian Activity and Exploratory Behavior in Mice. G3: Genes, Genomes, Genetics, 2018, 8, 3783-3790.	0.8	10
23	Reciprocal F1 Hybrids of Two Inbred Mouse Strains Reveal Parent-of-Origin and Perinatal Diet Effects on Behavior and Expression. G3: Genes, Genomes, Genetics, 2018, 8, 3447-3468.	0.8	12
24	vqtl: An R Package for Mean-Variance QTL Mapping. G3: Genes, Genomes, Genetics, 2018, 8, 3757-3766.	0.8	8
25	QTL Mapping on a Background of Variance Heterogeneity. G3: Genes, Genomes, Genetics, 2018, 8, 3767-3782.	0.8	13
26	Impact of vitamin D depletion during development on mouse sperm DNA methylation. Epigenetics, 2018, 13, 959-974.	1.3	11
27	Reproducibility and replicability of rodent phenotyping in preclinical studies. Neuroscience and Biobehavioral Reviews, 2018, 87, 218-232.	2.9	153
28	Candidate Risk Factors and Mechanisms for Tolvaptan-Induced Liver Injury Are Identified Using a Collaborative Cross Approach. Toxicological Sciences, 2017, 156, kfw269.	1.4	46
29	Inbred Strain Variant Database (ISVdb): A Repository for Probabilistically Informed Sequence Differences Among the Collaborative Cross Strains and Their Founders. G3: Genes, Genomes, Genetics, 2017, 7, 1623-1630.	0.8	26
30	Maternal vitamin D depletion alters DNA methylation at imprinted loci in multiple generations. Clinical Epigenetics, 2016, 8, 107.	1.8	74
31	Joint estimation of multiple dependent Gaussian graphical models with applications to mouse genomics. Biometrika, 2016, 103, 493-511.	1.3	15
32	Ovariectomy results in inbred strain-specific increases in anxiety-like behavior in mice. Physiology and Behavior, 2016, 167, 404-412.	1.0	19
33	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. PLoS Genetics, 2015, 11, e1005504.	1.5	137
34	Fine‐Mapping Additive and Dominant SNP Effects Using Group‐LASSO and Fractional Resample Model Averaging. Genetic Epidemiology, 2015, 39, 77-88.	0.6	18
35	A Permutation Approach for Selecting the Penalty Parameter in Penalized Model Selection. Biometrics, 2015, 71, 1185-1194.	0.8	18
36	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature Genetics, 2015, 47, 353-360.	9.4	204

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37	Plasma Levels of Soluble Interleukin-2 Receptor Î±. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2246-2253.	1.1	43
38	Genome- and exome-wide association study of serum lipoprotein (a) in the Jackson Heart Study. Journal of Human Genetics, 2015, 60, 755-761.	1.1	42
39	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. G3: Genes, Genomes, Genetics, 2014, 4, 1623-1633.	0.8	195
40	Using the emerging Collaborative Cross to probe the immune system. Genes and Immunity, 2014, 15, 38-46.	2.2	71
41	Genetics of Adverse Reactions to Haloperidol in a Mouse Diallel: A Drugâ€"Placebo Experiment and Bayesian Causal Analysis. Genetics, 2014, 196, 321-347.	1.2	30
42	Bayesian Modeling of Haplotype Effects in Multiparent Populations. Genetics, 2014, 198, 139-156.	1.2	36
43	Midregional pro-adrenomedullin plasma concentrations are blunted in severe preeclampsia. Placenta, 2014, 35, 780-783.	0.7	29
44	Quantitative trait loci for energy balance traits in an advanced intercross line derived from mice divergently selected for heat loss. PeerJ, 2014, 2, e392.	0.9	3
45	Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. PLoS Genetics, 2013, 9, e1003853.	1.5	41
46	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. PLoS Pathogens, 2013, 9, e1003196.	2.1	183
47	Fine-mapping diabetes-related traits, including insulin resistance, in heterogeneous stock rats. Physiological Genomics, 2012, 44, 1013-1026.	1.0	45
48	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. Genetics, 2012, 190, 437-447.	1.2	437
49	A General Bayesian Approach to Analyzing Diallel Crosses of Inbred Strains. Genetics, 2012, 190, 413-435.	1.2	47
50	Recent developments in statistical methods for detecting genetic loci affecting phenotypic variability. BMC Genetics, 2012, 13, 63.	2.7	105
51	Reprioritizing Genetic Associations in Hit Regions Using LASSOâ€"Based Resample Model Averaging. Genetic Epidemiology, 2012, 36, 451-462.	0.6	22
52	Genomeâ€"wide and speciesâ€"wide dissection of the genetics of arthritis severity in heterogeneous stock mice. Arthritis and Rheumatism, 2011, 63, 2630-2640.	6.7	20
53	Detecting Major Genetic Loci Controlling Phenotypic Variability in Experimental Crosses. Genetics, 2011, 188, 435-447.	1.2	129
54	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	2.4	327

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55	High-resolution mapping of a complex disease, a model for rheumatoid arthritis, using heterogeneous stock mice. Human Molecular Genetics, 2011, 20, 3031-3041.	1.4	20
56	Fine-mapping a locus for glucose tolerance using heterogeneous stock rats. Physiological Genomics, 2010, 41, 102-108.	1.0	47
57	A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: The NIH heterogeneous stock. Genome Research, 2009, 19, 150-158.	2.4	72
58	A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in Arabidopsis thaliana. PLoS Genetics, 2009, 5, e1000551.	1.5	554
59	Association of Infectious Mononucleosis with Multiple Sclerosis. Neuroepidemiology, 2009, 32, 257-262.	1.1	85
60	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. Genome Research, 2009, 19, 1133-1140.	2.4	69
61	Mapping in Structured Populations by Resample Model Averaging. Genetics, 2009, 182, 1263-1277.	1.2	133
62	Genomewide SNP Screen to Detect Quantitative Trait Loci for Alcohol Preference in the High Alcohol Preferring and Low Alcohol Preferring Mice. Alcoholism: Clinical and Experimental Research, 2009, 33, 531-537.	1.4	18
63	Age of puberty and the risk of multiple sclerosis: a population based study. European Journal of Neurology, 2009, 16, 342-347.	1.7	86
64	Unlearned anxiety predicts learned fear: A comparison among heterogeneous rats and the Roman rat strains. Behavioural Brain Research, 2009, 202, 92-101.	1.2	73
65	Deciphering gene-environment interactions through mouse models of allergic asthma. Journal of Allergy and Clinical Immunology, 2009, 123, 14-23.	1.5	21
66	Fearfulness in a large N/Nih genetically heterogeneous rat stock: Differential profiles of timidity and defensive flight in males and females. Behavioural Brain Research, 2008, 188, 41-55.	1.2	49
67	No Effect of Birth Weight on the Risk of Multiple Sclerosis. Neuroepidemiology, 2008, 31, 181-184.	1.1	13
68	Mutations in Î±-Tubulin Cause Abnormal Neuronal Migration in Mice and Lissencephaly in Humans. Cell, 2007, 128, 45-57.	13.5	397
69	Autoimmune disease in families with multiple sclerosis: a population-based study. Lancet Neurology, The, 2007, 6, 604-610.	4.9	145
70	Estimating the number of coding mutations in genotypic and phenotypic driven N-ethyl-N-nitrosourea (ENU) screens: revisited. Mammalian Genome, 2007, 18, 123-124.	1.0	30
71	Genome-wide genetic association of complex traits in heterogeneous stock mice. Nature Genetics, 2006, 38, 879-887.	9.4	508
72	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. Mammalian Genome, 2006, 17, 129-146.	1.0	99

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73	Sex ratio of multiple sclerosis in Canada: a longitudinal study. Lancet Neurology, The, 2006, 5, 932-936.	4.9	785
74	Genetic and Environmental Effects on Complex Traits in Mice. Genetics, 2006, 174, 959-984.	1.2	161
75	Simulating the Collaborative Cross: Power of Quantitative Trait Loci Detection and Mapping Resolution in Large Sets of Recombinant Inbred Strains of Mice. Genetics, 2006, 172, 1783-1797.	1.2	168
76	Strategies for mapping and cloning quantitative trait genes in rodents. Nature Reviews Genetics, 2005, 6, 271-286.	7.7	462
77	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	9.4	1,034