

# William Valdar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3553767/publications.pdf>

Version: 2024-02-01

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  | 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  | Sex ratio of multiple sclerosis in Canada: a longitudinal study. <i>Lancet Neurology</i> , The, 2006, 5, 932-936.  | 4.9  | 785       |
| 3  | A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2009, 5, e1000551.   | 1.5  | 554       |
| 4  | Genome-wide genetic association of complex traits in heterogeneous stock mice. <i>Nature Genetics</i> , 2006, 38, 879-887.   | 9.4  | 508       |
| 5  | Strategies for mapping and cloning quantitative trait genes in rodents. <i>Nature Reviews Genetics</i> , 2005, 6, 271-286.   | 7.7  | 462       |
| 6  | High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. <i>Genetics</i> , 2012, 190, 437-447.  | 1.2  | 437       |
| 7  | Mutations in $\beta$ -Tubulin Cause Abnormal Neuronal Migration in Mice and Lissencephaly in Humans. <i>Cell</i> , 2007, 128, 45-57.   | 13.5 | 397       |
| 8  | Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.  | 2.4  | 327       |
| 9  | Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. <i>Nature Genetics</i> , 2015, 47, 353-360.                                  | 9.4  | 204       |
| 10 | Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.   | 0.8  | 195       |
| 11 | Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.  | 2.1  | 183       |
| 12 | Simulating the Collaborative Cross: Power of Quantitative Trait Loci Detection and Mapping Resolution in Large Sets of Recombinant Inbred Strains of Mice. <i>Genetics</i> , 2006, 172, 1783-1797. | 1.2  | 168       |
| 13 | Genetic and Environmental Effects on Complex Traits in Mice. <i>Genetics</i> , 2006, 174, 959-984.   | 1.2  | 161       |
| 14 | Reproducibility and replicability of rodent phenotyping in preclinical studies. <i>Neuroscience and Biobehavioral Reviews</i> , 2018, 87, 218-232.   | 2.9  | 153       |
| 15 | Autoimmune disease in families with multiple sclerosis: a population-based study. <i>Lancet Neurology</i> , The, 2007, 6, 604-610.   | 4.9  | 145       |
| 16 | Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. <i>PLoS Genetics</i> , 2015, 11, e1005504.   | 1.5  | 137       |
| 17 | Mapping in Structured Populations by Resample Model Averaging. <i>Genetics</i> , 2009, 182, 1263-1277.   | 1.2  | 133       |
| 18 | Detecting Major Genetic Loci Controlling Phenotypic Variability in Experimental Crosses. <i>Genetics</i> , 2011, 188, 435-447.   | 1.2  | 129       |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Recent developments in statistical methods for detecting genetic loci affecting phenotypic variability. <i>BMC Genetics</i> , 2012, 13, 63.  | 2.7 | 105       |
| 20 | A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. <i>Mammalian Genome</i> , 2006, 17, 129-146.   | 1.0 | 99        |
| 21 | Age of puberty and the risk of multiple sclerosis: a population based study. <i>European Journal of Neurology</i> , 2009, 16, 342-347.   | 1.7 | 86        |
| 22 | Association of Infectious Mononucleosis with Multiple Sclerosis. <i>Neuroepidemiology</i> , 2009, 32, 257-262.   | 1.1 | 85        |
| 23 | Maternal vitamin D depletion alters DNA methylation at imprinted loci in multiple generations. <i>Clinical Epigenetics</i> , 2016, 8, 107.   | 1.8 | 74        |
| 24 | Unlearned anxiety predicts learned fear: A comparison among heterogeneous rats and the Roman rat strains. <i>Behavioural Brain Research</i> , 2009, 202, 92-101.                                     | 1.2 | 73        |
| 25 | A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: The NIH heterogeneous stock. <i>Genome Research</i> , 2009, 19, 150-158.                        | 2.4 | 72        |
| 26 | Using the emerging Collaborative Cross to probe the immune system. <i>Genes and Immunity</i> , 2014, 15, 38-46.  | 2.2 | 71        |
| 27 | High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009, 19, 1133-1140.  | 2.4 | 69        |
| 28 | Genetic Fine-Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. <i>Obesity</i> , 2018, 26, 213-222.  | 1.5 | 64        |
| 29 | Content and Performance of the MiniMUGA Genotyping Array: A New Tool To Improve Rigor and Reproducibility in Mouse Research. <i>Genetics</i> , 2020, 216, 905-930.                                   | 1.2 | 58        |
| 30 | Fearfulness in a large N/Nih genetically heterogeneous rat stock: Differential profiles of timidity and defensive flight in males and females. <i>Behavioural Brain Research</i> , 2008, 188, 41-55. | 1.2 | 49        |
| 31 | Fine-mapping a locus for glucose tolerance using heterogeneous stock rats. <i>Physiological Genomics</i> , 2010, 41, 102-108.  | 1.0 | 47        |
| 32 | A General Bayesian Approach to Analyzing Diallel Crosses of Inbred Strains. <i>Genetics</i> , 2012, 190, 413-435.  | 1.2 | 47        |
| 33 | Candidate Risk Factors and Mechanisms for Tolvaptan-Induced Liver Injury Are Identified Using a Collaborative Cross Approach. <i>Toxicological Sciences</i> , 2017, 156, kfw269.                     | 1.4 | 46        |
| 34 | Fine-mapping diabetes-related traits, including insulin resistance, in heterogeneous stock rats. <i>Physiological Genomics</i> , 2012, 44, 1013-1026.  | 1.0 | 45        |
| 35 | Determinants of QTL Mapping Power in the Realized Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1707-1727.   | 0.8 | 45        |
| 36 | Plasma Levels of Soluble Interleukin-2 Receptor $\beta$ . <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2246-2253.   | 1.1 | 43        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 37 | Genome- and exome-wide association study of serum lipoprotein (a) in the Jackson Heart Study. <i>Journal of Human Genetics</i> , 2015, 60, 755-761.  | 1.1 | 42        |
| 38 | Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. <i>PLoS Genetics</i> , 2013, 9, e1003853.   | 1.5 | 41        |
| 39 | Bayesian Modeling of Haplotype Effects in Multiparent Populations. <i>Genetics</i> , 2014, 198, 139-156.   | 1.2 | 36        |
| 40 | Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. <i>PLoS Genetics</i> , 2020, 16, e1008537.   | 1.5 | 35        |
| 41 | Estimating the number of coding mutations in genotypic and phenotypic driven N-ethyl-N-nitrosourea (ENU) screens: revisited. <i>Mammalian Genome</i> , 2007, 18, 123-124.  | 1.0 | 30        |
| 42 | Genetics of Adverse Reactions to Haloperidol in a Mouse Diallel: A Drugâ€œPlacebo Experiment and Bayesian Causal Analysis. <i>Genetics</i> , 2014, 196, 321-347.   | 1.2 | 30        |
| 43 | Perinatal nutrition interacts with genetic background to alter behavior in a parentâ€œofâ€œoriginâ€œdependent manner in adult Collaborative Cross mice. <i>Genes, Brain and Behavior</i> , 2018, 17, e12438.                 | 1.1 | 30        |
| 44 | Midregional pro-adrenomedullin plasma concentrations are blunted in severe preeclampsia. <i>Placenta</i> , 2014, 35, 780-783.  | 0.7 | 29        |
| 45 | Bayesian Diallel Analysis Reveals <i>Mx1</i> -Dependent and <i>Mx1</i> -Independent Effects on Response to Influenza A Virus in Mice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 427-445.                                | 0.8 | 27        |
| 46 | Inbred Strain Variant Database (ISVdb): A Repository for Probabilistically Informed Sequence Differences Among the Collaborative Cross Strains and Their Founders. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1623-1630. | 0.8 | 26        |
| 47 | Dissecting the Genetic Architecture of Shoot Growth in Carrot ( <i>Daucus carota</i> ) Using a Diallel Mating Design. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 411-426.  | 0.8 | 25        |
| 48 | 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        |
| 49 | Reprioritizing Genetic Associations in Hit Regions Using LASSO-Based Resample Model Averaging. <i>Genetic Epidemiology</i> , 2012, 36, 451-462.  | 0.6 | 22        |
| 50 | Identification of Candidate Risk Factor Genes for Human Idelalisib Toxicity Using a Collaborative Cross Approach. <i>Toxicological Sciences</i> , 2019, 172, 265-278.  | 1.4 | 22        |
| 51 | Deciphering gene-environment interactions through mouse models of allergic asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2009, 123, 14-23.   | 1.5 | 21        |
| 52 | Genome-wide and species-wide dissection of the genetics of arthritis severity in heterogeneous stock mice. <i>Arthritis and Rheumatism</i> , 2011, 63, 2630-2640.  | 6.7 | 20        |
| 53 | High-resolution mapping of a complex disease, a model for rheumatoid arthritis, using heterogeneous stock mice. <i>Human Molecular Genetics</i> , 2011, 20, 3031-3041.   | 1.4 | 20        |
| 54 | Ovariectomy results in inbred strain-specific increases in anxiety-like behavior in mice. <i>Physiology and Behavior</i> , 2016, 167, 404-412.   | 1.0 | 19        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 55 | Genomewide SNP Screen to Detect Quantitative Trait Loci for Alcohol Preference in the High Alcohol Preferring and Low Alcohol Preferring Mice. <i>Alcoholism: Clinical and Experimental Research</i> , 2009, 33, 531-537. | 1.4 | 18        |
| 56 | Fine-Mapping Additive and Dominant SNP Effects Using Group-LASSO and Fractional Resample Model Averaging. <i>Genetic Epidemiology</i> , 2015, 39, 77-88.  | 0.6 | 18        |
| 57 | A Permutation Approach for Selecting the Penalty Parameter in Penalized Model Selection. <i>Biometrics</i> , 2015, 71, 1185-1194.   | 0.8 | 18        |
| 58 | Joint estimation of multiple dependent Gaussian graphical models with applications to mouse genomics. <i>Biometrika</i> , 2016, 103, 493-511.   | 1.3 | 15        |
| 59 | Inferring the Allelic Series at QTL in Multiparental Populations. <i>Genetics</i> , 2020, 216, 957-983.   | 1.2 | 14        |
| 60 | No Effect of Birth Weight on the Risk of Multiple Sclerosis. <i>Neuroepidemiology</i> , 2008, 31, 181-184.  | 1.1 | 13        |
| 61 | QTL Mapping on a Background of Variance Heterogeneity. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3767-3782.  | 0.8 | 13        |
| 62 | Sept8/SEPTIN8 involvement in cellular structure and kidney damage is identified by genetic mapping and a novel human tubule hypoxic model. <i>Scientific Reports</i> , 2021, 11, 2071.                                    | 1.6 | 13        |
| 63 | Reciprocal F1 Hybrids of Two Inbred Mouse Strains Reveal Parent-of-Origin and Perinatal Diet Effects on Behavior and Expression. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3447-3468.                                | 0.8 | 12        |
| 64 | Human-relevant mechanisms and risk factors for TAK-875-Induced liver injury identified via a gene pathway-based approach in Collaborative Cross mice. <i>Toxicology</i> , 2021, 461, 152902.                              | 2.0 | 12        |
| 65 | Impact of vitamin D depletion during development on mouse sperm DNA methylation. <i>Epigenetics</i> , 2018, 13, 959-974.  | 1.3 | 11        |
| 66 | A Diallel of the Mouse Collaborative Cross Founders Reveals Strong Strain-Specific Maternal Effects on Litter Size. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1613-1622.   | 0.8 | 11        |
| 67 | Mean-Variance QTL Mapping Identifies Novel QTL for Circadian Activity and Exploratory Behavior in Mice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3783-3790.   | 0.8 | 10        |
| 68 | Transcriptome-wide analyses of adipose tissue in outbred rats reveal genetic regulatory mechanisms relevant for human obesity. <i>Physiological Genomics</i> , 2022, 54, 206-219.   | 1.0 | 9         |
| 69 | vqtl: An R Package for Mean-Variance QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3757-3766.   | 0.8 | 8         |
| 70 | A Bayesian model selection approach to mediation analysis. <i>PLoS Genetics</i> , 2022, 18, e1010184.   | 1.5 | 8         |
| 71 | Maternal Liver Metabolic Response to Chronic Vitamin D Deficiency Is Determined by Mouse Strain Genetic Background. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa106.  | 0.1 | 5         |
| 72 | Bayesian modeling of skewed X inactivation in genetically diverse mice identifies a novel Xce allele associated with copy number changes. <i>Genetics</i> , 2021, 218, .  | 1.2 | 5         |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 73 | 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         |
| 74 | Title is missing!. , 2020, 16, e1008537.   |     | 0         |
| 75 | Title is missing!. , 2020, 16, e1008537.   |     | 0         |
| 76 | Title is missing!. , 2020, 16, e1008537.   |     | 0         |
| 77 | Title is missing!. , 2020, 16, e1008537.   |     | 0         |