GARY A. CHURCHILL, PROFESSOR
CURRICULUM VITAE

Place of Birth:	Bangor, ME
Citizenship:	USA
Work Address:	The Jackson Laboratory 600 Main Street Bar Harbor, ME 04609
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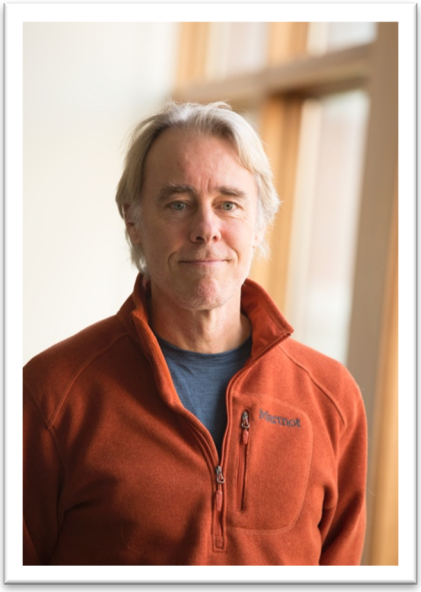
Marital Status:	Married



Education

1983 - 1988	University of Washington, Ph.D., Biostatistics
1979 - 1983	Massachusetts Institute of Technology, S.B., Mathematics

Appointment History

2003 - Present	Professor, The Jackson Laboratory, Bar Harbor, ME
1998 - 2003	Associate Professor, The Jackson Laboratory, Bar Harbor, ME
1997 - 1998	Visiting Investigator, The Jackson Laboratory, Bar Harbor, ME
1996 - 1999	Associate Professor, Biometrics Unit, Cornell University, Ithaca, NY
1990 - 1996	Assistant Professor, Biometrics Unit, Cornell University, Ithaca, NY
1981-1983	Research Assistant, Department of Psychology, Massachusetts Institute of Technology, Cambridge, MA
1989 - 1990	Visiting Assistant Professor, Department of Mathematics, University of Southern California, Los Angeles, CA
1988 - 1989	Research Associate, Department of Mathematics, University of Southern California, Los Angeles, CA
1983 - 1986	Research Assistant, Fred Hutchinson Cancer Research Center, Seattle, WA

Current Position

Professor, The Jackson Laboratory

Dr. Churchill is a statistical geneticist at The Jackson Laboratory (http://churchill.jax.org) where he has made major contributions to understanding the genetics of health and disease using the mouse as a model system. He has and continues to play a central role in the development of the Collaborative Cross and the Diversity Outbred mouse reference populations. Dr. Churchill is co-director of the Jackson Aging Center, a Nathan Shock Center of Excellence in the Basic Biology of Aging. The Churchill lab develops state-of-the-art bioinformatics, biostatistics, and computational methods as well as generating phenotype and molecular profiling data from genetically diverse mouse models.

Editorial Boards

2012 - Present	Genetics, Senior Editor
2011 - 2012	Genetics, Associate Editor
2010 - Present	Genome Research, Associate Editor
2002 - 2012	Statistical Applications in Genetics and Molecular Biology, Editor
2001 - Present	Mammalian Genome, Associate Editor
1998 - 2004	Genetics, Associate Editor
1997 - 2003	Journal of Computational Biology, Associate Editor
1997 - 2000	Biometrics, Associate Editor
1994 - 2000	Theoretical Population Biology, Associate Editor

Advisory Boards

2009 - 2016	Canadian Institute for Advanced Research, Advisory Committee Member
2002 - 2006	Diabetes Genome Project, (DGAP) Scientific Advisory Board
2003 - 2005	ENCODE Project, NHGRI, Scientific Advisory Board
2000 - Present	Computational Biology Resource, JAX, Scientific Director

Awards

2020	Changemaker of Public Health, University of Washington School of Public Health
2019	Fellow, American Academy for the Advancement of Science
2015	Karl Gunner Johansson Chair for Genomics and Computational Biology
2013	Science Prize for Inquiry-Based Instruction
2010	The Ellison Senior Scholar Award

Professional Organizations

2017 - Present	American Aging Association (AGE)
2016 - Present	American Society of Human Genetics (ASHG)
2000 - Present	International Mammalian Society (IMGS)
1997 - Present	Genetics Society of America (GSA)

1993 - Present	American Association for Advancement of Science (AAAS)
1990 - 2016	American Statistical Association (ASA)
1990 - 2016	International Biometrics Society (IBS)
1990 - 2016	Institute of Mathematical Statistics (IMS)

Teaching

2006 - 2016	Independent Studies in Computational Biology
2000 - 2016	Short Course on Systems Genetics

Publications

2021

- Dong C, Simonett SP, Shin S, Stapleton DS, Schueler KL, Churchill GA, Lu L, Liu X, Jin F, Li Y, Attie AD, Keller MP, Keleş S. INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. Genome Biol. 2021 Aug 23;22(1):241. doi: 10.1186/s13059-021-02450-8. PMID: 34425882
- Gould RL, Craig SW, McClatchy S, Churchill GA, Pazdro R. Genetic mapping of renal glutathione suggests a novel regulatory locus on the murine X chromosome and overlap with hepatic glutathione regulation. Free Radic Biol Med. 2021 Oct;174:28-39. doi: 10.1016/j.freeradbiomed.2021.07.035. Epub 2021 Jul 26. PMID: 34324982
- Gould RL, Craig SW, McClatchy S, Churchill GA, Pazdro R. Quantitative trait mapping in Diversity Outbred mice identifies novel genomic regions associated with the hepatic glutathione redox system. Redox Biol. 2021 Oct;46:102093. doi: 10.1016/j.redox.2021.102093. Epub 2021 Aug 5. PMID: 34418604
- Keele GR, Zhang T, Pham DT, Vincent M, Bell TA, Hock P, Shaw GD, Paulo JA, Munger SC, Pardo-Manuel de Villena F, Ferris MT, Gygi SP, Churchill GA. Regulation of protein abundance in genetically diverse mouse populations. Cell Genomics. 2021 August; 1(1). doi: xdoi: 10.1101/2020.09.18.296657.
- Keenan BT, Galante RJ, Lian J, Zhang L, Guo X, Veatch OJ, Chesler EJ, O'Brien WT, Svenson KL, Churchill GA, Pack AI. The dihydropyrimidine dehydrogenase gene contributes to heritable differences in sleep in mice. Curr Biol. 2021 Oct 8:S0960-9822(21)01289-6. doi: 10.1016/j.cub.2021.09.049. Online ahead of print. PMID: 34653361
- Keenan BT, Webster JC, Wiemken AS, Lavi-Romer N, Nguyen T, Svenson KL, Galante RJ, Churchill GA, Pickup S, Pack AI, Schwab RJ. Heritability of Fat Distributions in Male Mice from the Founder Strains of the Diversity Outbred Mouse Population. G3 (Bethesda). 2021 Mar 15:jkab079. doi: 10.1093/g3journal/jkab079. Online ahead of print. PMID: 33720343
- Korstanje R, Peters LL, Robinson LL, Krasinski SD, Churchill GA. The Jackson Laboratory Nathan Shock Center: impact of genetic diversity on aging. Geroscience. 2021 Jul 23. doi: 10.1007/s11357-021-00421-2. Online ahead of print. PMID: 34297313
- Palliyaguru DL, Shiroma EJ, Nam JK, Duregon E, Vieira Ligo Teixeira C, Price NL, Bernier M, Camandola S, Vaughan KL, Colman RJ, Deighan A, Korstanje R, Peters LL, Dickinson SL, Ejima K, Simonsick EM, Launer LJ, Chia CW, Egan J, Allison DB, Churchill GA, Anderson RM, Ferrucci L, Mattison JA, de Cabo R. Fasting blood glucose as a predictor of mortality: Lost in translation. Cell Metab. 2021 Sep 8:S1550-

4131(21)00376-4. doi: 10.1016/j.cmet.2021.08.013. Online ahead of print. PMID: 34508697

- Starcher AE, Peissig K, Stanton JB, Churchill GA, Cai D, Maxwell JT, Grider A, Love K, Chen SY, Coleman AE, Strauss E, Pazdro R. A systems approach using Diversity Outbred mice distinguishes the cardiovascular effects and genetics of circulating GDF11 from those of its homolog, myostatin. G3 (Bethesda). 2021 Sep 2;11(11):jkab293. doi: 10.1093/g3journal/jkab293. Online ahead of print. PMID: 34510201
- Takemon Y, Chick JM, Gerdes Gyuricza I, Skelly DA, Devuyst O, Gygi SP, Churchill GA, Korstanje R. Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. Elife. 2021 Mar 9;10:e62585. doi: 10.7554/eLife.62585. Online ahead of print. PMID: 33687326
- Zhang T, Keele GR, Churchill GA, Gygi SP, Paulo JA. Strain-Specific Peptide (SSP) Interference Reference Sample: A Genetically Encoded Quality Control for Isobaric Tagging Strategies. Anal Chem. 2021 Mar 30;93(12):5241-5247. doi: 10.1021/acs.analchem.0c05483. Epub 2021 Mar 18. PMID: 33735571

2020

- Choi K, Chen Y, Skelly DA, Churchill GA. Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. Genome Biol. 2020 Jul 27. Erratum in: Genome Biol. 2020 Nov 3. PMCID: PMC7384222.
- Keenan BT, Galante RJ, Lian J, Simecek P, Gatti DM, Zhang L, Lim DC, Svenson KL, Churchill GA, Pack AI. High-throughput sleep phenotyping produces robust and heritable traits in Diversity Outbred mice and their founder strains. Sleep. 2020 May 12. PMCID: PMC7215270.
- Linke V, Overmyer KA, Miller IJ, Brademan DR, Hutchins PD, Trujillo EA, Reddy TR, Russell JD, Cushing EM, Schueler KL, Stapleton DS, Rabaglia ME, Keller MP, Gatti DM, Keele GR, Pham D, Broman KW, Churchill GA, Attie AD, Coon JJ. A large- scale genome-lipid association map guides lipid identification. Nat Metab. 2020 Oct 2. Epub 2020 Sep 21. PMCID: PMC7572687.
- McClatchy S, Bass KM, Gatti DM, Moylan A, Churchill G. Nine quick tips for efficient bioinformatics curriculum development and training. PLoS Comput Biol. 2020 Jul 23. PMCID: PMC7377369.
- Ortmann D, Brown S, Czechanski A, Aydin S, Muraro D, Huang Y, Tomaz RA, Osnato A, Canu G, Wesley BT, Skelly DA, Stegle O, Choi T, Churchill GA, Baker CL, Rugg-Gunn PJ, Munger SC, Reinholdt LG, Vallier L. Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. Cell Stem Cell. 2020 Sep 3. Epub 2020 Aug 13. PMCID: PMC7487768.
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Cognitive Decline and Alzheimer's Dementia. Cell Rep. 2020 Sep 1. PMCID: PMC7502175.

- Skelly DA, Czechanski A, Byers C, Aydin S, Spruce C, Olivier C, Choi K, Gatti DM, Raghupathy N, Keele GR, Stanton A, Vincent M, Dion S, Greenstein I, Pankratz M, Porter DK, Martin W, O'Connor C, Qin W, Harrill AH, Choi T, Churchill GA, Munger SC, Baker CL, Reinholdt LG. Mapping the Effects of Genetic Variation on Chromatin State and Gene Expression Reveals Loci That Control Ground State Pluripotency. Cell Stem Cell. 2020 Sep 3. PMCID: PMC7484384.

2019

- Broman KW, Gatti DM, Simecek P, Furlotte NA, Prins P, Sen S, Yandell BS, Churchill GA. R/qtl2: Software for Mapping Quantitative Trait Loci with High-Dimensional Data and Multiparent Populations. *Genetics*. 2019 Feb. PMCID: PMC6366910.
- Broman KW, Gatti DM, Svenson KL, Sen Ś, Churchill GA. Cleaning Genotype Data from Diversity Outbred Mice. *G3* (Bethesda). 2019 May 7. PMCID: PMC6505173.
- Choi K, Raghupathy N, Churchill GA. A Bayesian mixture model for the analysis of allelic expression in single cells. *Nature Communications*. 2019 Nov 15. PMID: 31729374.
- Keenan BT, Galante RJ, Lian J, Simecek P, Gatti DM, Zhang L, Lim DC, Svenson KL, Churchill GA, Pack AI. High-throughput sleep phenotyping produces robust and heritable traits in diversity outbred mice and their founder strains. *Sleep Research Society*. Jan 2019 17. DOI: 10.1093/sleep/zsz061.324. (in press)
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- Recla JM, Bubier JA, Gatti DM, Ryan JL, Long KH, Robledo RF, Glidden NC, Hou G, Churchill GA, Maser RS, Zhang ZW, Young EE, Chesler EJ, Bult CJ. Genetic mapping in Diversity Outbred mice identifies a Trpa1 variant influencing late-phase formalin response. Pain. *OVID* 2019 Aug. PMCID: PMC6668363.
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2018

- Keller MP, Gatti DM, Schueler KL, Rabaglia ME, Stapleton DS, Simecek P, Vincent M, Allen S, Broman AT, Bacher R, Kendziorski C, Broman KW, Yandell BS, Churchill GA, Attie AD. Genetic Drivers of Pancreatic Islet Function. *Genetics*. 2018 May. Epub 2018 Mar 22. PMCID: PMC5937189.
- Morton NM, Beltram J, Carter RN, Michailidou Z, Gorjanc G, McFadden C, Barrios-Lierena ME,Rodriguez-Cuenca S, Gibbins MTG, Aird RE, Moreno-Navarrete JM, Munger SC, Svenson KL, Gastaldello A, Ramage L, Naredo G, Zeyda M, Wang ZV, Howie AF, Saari A, Sipila P, Stulnig TM, Gudnason V, Kenyon CJ, Seckl JR, Walker BR, Webster SP, Dunbar DR, Churchill GA, Vidal-Puig A, Fernandez-Real JM, Emilsson V, Horvat S. Corrigendum: Genetic identification of thiosulfate sulfurtransferase as an adipocyte-expressed antidiabetic target in mice selected for leanness. *Nat Med*. 2018 Apr 10. PMCID: PMC29634685.
- Raghupathy N, Choi K, Vincent MJ, Beane GL, Sheppard K, Munger SC, Korstanje R, Pardo-Manual de Villena F, Churchill GA, Valencia A. Hierarchical analysis of RNA-seq reads improves the accuracy of allele-specific expression. *Bioinformatics* 2018 Feb 12. PMCID: PMC6022640.
- Thompson MJ, Chwiałkowska K, Rubbi L, Lusis AJ, Davis RC, Srivastava A, Korstanje R, Churchill GA, Horvath S, Pellegrini M. A multi-tissue full lifespan epigenetic clock for mice. *Aging* (Albany NY). 2018 Oct 21. PMCID: PMC6224226.

2017

- Ackert-Bicknell CL, Anderson LC, Sheehan S, Hill WG, Chang B, Churchill GA, Chesler EJ, Korstanje R, Peters LL. Aging Research Using Mouse Models. *Curr Protoc Mouse Biol.* 2015 Jun 1. PMCID: PMC4590775.
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- Gatti DM, Weber SN, Goodwin NC, Lammert F, Churchill GA. Genetic background influences susceptibility to chemotherapy-induced hematotoxicity. *Pharmacogenomics* J. 2017 Jun 13. PMCID: PMC5729066.
- Morgan AP, Gatti DM, Najarian ML, Keane TM, Galante RJ, Pack AI, Mott R, Churchill GA, de Villena FP. Structural Variation Shapes the Landscape of Recombination in Mouse. *Genetics.* 2017 Jun. PMCID: PMC5499175.

- Simecek P, Forejt J, Williams RW, Shiroishi T, Takada T, Lu L, Johnson TE, Bennett B, Deschepper CF, Scott-Boyer MP, Pardo-Manuel de Villena F, Churchill GA. High-Resolution Maps of Mouse Reference Populations. *G3 (Bethesda)*. 2017 Oct 5. PMCID: PMC5633391.
- Srivastava A, Morgan AP, Najarian ML, Sarsani VK, Sigmon JS, Shorter JR, Kashfeen A, McMullan RC, Williams LH, Giusti-Rodríguez P, Ferris MT, Sullivan P, Hock P, Miller DR, Bell TA, McMillan L, Churchill GA, de Villena FP. Genomes of the Mouse Collaborative Cross. *Genetics*. 2017 Jun. PMCID: PMC5499171.
- Tyler AL, Ji B, Gatti DM, Munger SC, Churchill GA, Svenson KL, Carter GW. Epistatic Networks Jointly Influence Phenotypes Related to Metabolic Disease and Gene Expression in Diversity Outbred Mice. *Genetics*. 2017 Jun. PMCID: PMC5499176.
- Winter JM, Gildea DE, Andreas JP, Gatti DM, Williams KA, Lee M, Hu Y, Zhang S; NISC Comparative Sequencing Program., Mullikin JC, Wolfsberg TG, McDonnell SK, Fogarty ZC, Larson MC, French AJ, Schaid DJ, Thibodeau SN, Churchill GA, Crawford NP. Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. *Cell Syst*. 2017 Jan 25. PMCID: PMC5269474.

2016

- Chesler EJ, Gatti DM, Morgan AP, Strobel M, Trepanier L, Oberbeck D, McWeeney S, Hitzemann R, Ferris M, McMullan R, Clayshultle A, Bell TA, Manuel de Villena FP, Churchill GA. Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. *G3 (Bethesda)*. 2016 Dec 7. PMCID: PMC5144960.
- Chick JM, Munger SC, Simecek P, Huttlin EL, Choi K, Gatti DM, Raghupathy N, Svenson KL, Churchill GA, Gygi SP. Defining the consequences of genetic variation on a proteome-wide scale. *Nature*. 2016 Jun 15. PMCID: PMC5292866.
- Didion JP, Morgan AP, Yadgary L, Bell TA, McMullan RC, Ortiz de Solorzano L, Britton-Davidian J, Bult CJ, Campbell KJ, Castiglia R, Ching YH, Chunco AJ, Crowley JJ, Chesler EJ, Förster DW, French JE, Gabriel SI, Gatti DM, Garland T Jr, Giagia-Athanasopoulou EB, Giménez MD, Grize SA, Gündüz İ, Holmes A, Hauffe HC, Herman JS, Holt JM, Hua K, Jolley WJ, Lindholm AK, López-Fuster MJ, Mitsainas G, da Luz Mathias M, McMillan L, Ramalhinho Mda G, Rehermann B, Rosshart SP, Searle JB, Shiao MS, Solano E, Svenson KL, Thomas-Laemont P, Threadgill DW, Ventura J, Weinstock GM, Pomp D, Churchill GA, Pardo-Manuel de Villena F. R2d2 Drives Selfish Sweeps in the House Mouse. *Mol Biol Evol*. 2016 Jun. PMCID: PMC4868115.
- Morton NM, Beltram J, Carter RN, Michailidou Z, Gorjanc G, McFadden C, Barrios-Llerena ME, Rodriguez-Cuenca S, Gibbins MT, Aird RE, Moreno-Navarrete JM, Munger SC, Svenson KL, Gastaldello A, Ramage L, Naredo G, Zeyda M, Wang ZV, Howie AF, Saari A, Sipilä P, Stulnig TM, Gudnason V, Kenyon CJ, Seckl JR, Walker BR, Webster SP, Dunbar DR, Churchill GA, Vidal-Puig A, Fernandez-Real JM, Emilsson V, Horvat S. Genetic Identification of thiosulfate Sulfurtransferase as an Adipocyte-expressed Anti-diabetic Target in Mice Selected for Leanness. *Nat Med*. 2016 Jul. PMCID: PMC5524189.

- Gu T, Gatti DM, Srivastava A, Snyder EM, Raghupathy N, Simecek P, Svenson KL, Dotu I, Chuang JH, Keller MP, Attie AD, Braun RE, Churchill GA. Genetic Architectures of Quantitative Variation in RNA Editing Pathways. *Genetics*. 2016 Feb. PMCID: PMC4788250.
- Tyler AL, Donahue LR, Churchill GA, Carter GW. Weak Epistasis Generally Stabilizes Phenotypes in a Mouse Intercross. *PLOS Genet*. 2016 Feb 1. PMCID: PMC4734753.

2015

- Didion JP, Morgan AP, Clayshulte AM, Mcmullan RC, Yadgary L, Petkov PM, Bell TA, Gatti DM, Crowley JJ, Hua K, Aylor DL, Bai L, Calaway M, Chesler EJ, French JE, Geiger TR, Gooch TJ, Garland T Jr, Harrill AH, Hunter K, McMillan L, Holt M, Miller DR, O'Brien DA, Paigen K, Pan W, Rowe LB, Shaw GD, Simecek P, Sullivan PF, Svenson KL, Weinstock GM, Threadgill DW, Pomp D, Churchill GA, Pardo-Manuel de Villena F. A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. *PLoS Genet.* 2015 Feb 13. PMCID: PMC4334553.
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2014

- Church RJ, Gatti DM, Urban TJ, Long N, Yang X, Shi Q, Eaddy JS, Mosedale M, Ballard S, Churchill GA, Navarro V, Watkins PB, Threadgill DW, Harrill AH. Sensitivity to hepatotoxicity due to epigallocatechin gallate is affected by genetic background in diversity outbred mice. *Food Chem Toxicol*. 2015 Feb. PMCID: PMC4324012.

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2013

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Key Invited Lectures (2016-2019)

1. June 2016. 5th International Conference on Quantitative Genetics. Title: Post-translational mechanisms buffer protein expression against transcriptional variation.
2. July 2016. The Allied Genetics Conference. Title: Post-translational mechanisms buffer protein expression against transcriptional variation.
3. November 2016. Inaugural Roux Family Center for Genomics and Computational Biology Symposium. Title: The effects of aging interventions on generically diverse mice.
4. June 2017. National Institutes of Aging Summer Scientific Retreat. Title: Genetically diverse mice in aging research.
5. July 2017. Gordon Research Conference: Human Genetics and Genomics. Title: Post-translational mechanisms buffer protein expression against transcriptional variation.
6. May 2018. Population, Evolutionary and Quantitative Genetic Conference. Title: The aging Proteome: Is aging programmed in our genes?
7. July 2018. Environmental Genomics 2018. Title: Genetically diverse mice in toxicology research.
8. October 2018. International Mouse Phenotyping Consortium (IMPC) Annual Meeting. Title: Leveraging genetic diversity as a tool for understanding gene function.
9. November 2018. International Mammalian Genome Conference. Title: Updating the mouse genomes: The impact of mutation and drift on C57BL/6J.
10. July 2019. Complex Trait Consortium / Rat Genomics 17th Annual Meeting. Title: The Genetic Architecture of Insulin Secretion.
11. July 2019. Inaugural Interdisciplinary Nutrition Sciences Symposium at University of North Carolina Chapel Hill. Title: Finding the Perfect Mouse.
12. July 22 2019. National Institute for Environmental Health & Science Seminar. Title: Bringing Genetic Diversity into Toxicology Research.

Current Research Support

5 P01 HL094307-09 Pack (PI) 05/01/17-04/30/21
NIH/NHLBI
Individual Differences in Obstructive Sleep Apnea: Project 3 - Genetics of Sleep Apnea and its Consequences
This project will use DO mice to investigate the genetic determinants of local fat deposition and susceptibility to sleep apnea.
Role: Consortium Investigator

5 P30 AG038070-10 Churchill, Korstanje, Peters (PI) 07/15/15-06/30/20
NIH/NIA
The Jackson Laboratory Nathan Shock Center of Excellence in the Basic Biology of Aging
The goal of the JAX Nathan Shock Center is to develop and disseminate the next generation of genetic, statistical and information resources necessary to enable a systems-wide approach to

understanding healthy aging.
Role: Principal Investigator

5 P30 AG038070-10 Churchill, Korstanje, Peters (PI) 07/15/15-06/30/20
NIH/NIA
The Jackson Laboratory Nathan Shock Center of Excellence in the Basic Biology of Aging
The goal of this project is to develop and disseminate the next generation of genetic, statistical and information resources necessary to enable a systems-wide approach to understanding healthy aging.
Role: Principal Investigator

5 P50 DA039841-04 Chesler (PI) 08/15/16-04/30/21
NIH/NIDA
Center for Systems Neurogenetics of Addiction - Core 1: Integrative Genetics and Genomics
The Integrative Genetics and Genomics Core (IGGC) for the Center for Systems Neurogenetics of Addiction (CSNA) forms the backbone of the center's integrative study of predisposition to psychostimulant abuse, providing management and systems genetic analysis of experimental data collected from the recently developed Collaborative Cross and Diversity Outbred mouse populations.
Role: Co-Investigator

1 R01 ES029916-01 Churchill, Korstanje, Reinholdt (PI) 02/01/19-01/31/24
NIH/NIEHS
Genetic Factors that Influence Arsenic Toxicity
The project goals to capitalize on the potential of two powerful population-based model organism resources, the Collaborative Cross (CC) and Diversity Outbred (DO) mice, to study the role of genetics in conferring susceptibility to chemical exposures.
Role: Principal Investigator

2 R01 GM070683-13 Broman, Churchill (PI) 09/14/19-06/30/23
NIH/NIGMS
Systems Genetic Analysis of Multiparent Crosses
The goal of this project is to develop improved statistical methods and software for the analysis of systems of molecular and clinical traits in multi-parent populations of model organisms.
Role: Principal Investigator

5 R01 GM121551-03 Pazdro (PI) 08/01/17-07/31/22
NIH/NIGMS
Defining the Genetic Architecture of the Glutathione Redox System
The goal of this project is to define the genetic control of glutathione (GSH) and we to identify and validate novel genes that govern the broader GSH system.
Role: Consortium PI

5 R25 GM123516-03 Churchill (PI) 09/16/16-07/31/20
NIH/NIGMS
Curriculum Development and Training for Systems Genetics
The goal of this project is to develop, test and disseminate a curriculum to train biomedical researchers in advanced statistical methods for genomic data analysis and to nurture interdisciplinary collaboration.
Role: Principal Investigator

JAX-DIF-FY18-Beck Beck, Churchill, Lee, Reinholdt, Robson, Rosenthal, Srivastava (PI) 09/18/18-09/17/20
The Jackson Laboratory Director's Innovation Fund
Structural Variation Discovery as a Resource for the Collaborative Cross
The overall goal of this project is to transform the JAX KOMP2 Phenotyping pipeline to a generalized High-Throughput Phenotyping pipeline to serve other projects and programs, including the JAX Diversity Initiative.
Role: Principal Investigator

JAX-CUBE-FY19-GAC Churchill (PI) 07/15/19-07/14/21
The Jackson Laboratory Competitive Internal Awards
Cube Proof of Concept Aim 2.1. Complete transcriptome profiling of non-islet metabolic tissues in ~500 HFHS-treated DO mice
The goal of this project is to perform RNAseq with existing frozen mouse DO tissues from the Keller et al. (Genetics, 2018) experiments, in which ~500 DO mice were sensitized on a HFHS diet.
Role: Principal Investigator

CALICO-FY19-GAC-01 Churchill (PI) 02/20/19-02/19/23
Calico Life Sciences, LLC
Dietary Interverntion Of Aging In Genetically Diverse Mice
The proposed work is the continuation and completion of the Diversity Outbred (DO) mouse lifespan intervention study.
Role: Principal Investigator

Completed Research Support

5 R01 HL111725-04 Pack (PI) 08/15/12-06/30/17
NIH/NHLBI
Genetic Approaches to Sleep/Wake and Response to Sleep Loss in Mice
The goal of this proposal is to use the newly developed Diversity Outbred mouse resource to identify gene variants in mice that determine the duration of wakefulness that a mouse can sustain and other gene variants that determine the response to sleep deprivation. Genes identified in mice will be further interrogated in human populations including comparisons to human genome-wide association studies.
Role: Co-Investigator

1 R56 AG053309-01A1 Pazdro (PI) 09/30/17-08/31/18
NIH/NIA
A Systems Approach to GDF11 and its Effects on Cardiac Hypertrophy
This project will use a novel systems approach to clarify the relationship between growth differentiation factor 11 (GDF11) and cardiac hypertrophy and to determine the genetic contributions to that relationship. Work to be done on this project at The Jackson Laboratory includes mapping and statistical analysis of loci that regulate GDF11, MSTN, cardiovascular phenotypes, and lifespan from Diversity Outbred mice.
Role: Consortium PI

1 R56 AG050645-01 Peters (PI) 09/15/15-08/31/18
NIH/NIA
Aging KOMP: Genetic Regulation of Lifespan and Healthspan
The goal of this project is to measure lifespan and disease phenotypes relevant to human aging in inbred mouse strains carrying single gene knockout (KO) mutations.
Role: Co-Investigator

5 R01 AG038560-05 Harrison (PI) 08/01/11-04/30/18
NIH/NIA
Genetic Definition of Mechanisms by which Rapamycin Retards Mammalian Aging
The goal of this project is to identify genes regulating health benefits of rapamycin treatment, as well as key genes controlling normal mouse aging.
Role: Co-Investigator

5 R01 DK101573-05 Attie (PI) 04/01/14-01/31/19
NIH/NIDDK
Collaborative Cross of Diabetes and Obesity
The goal of this project is to develop metabolic phenotype systems using collaborative cross and diversity outbred mice.
Role: Consortium PI

Churchill (PI) 07/24/15-06/30/17
NIH/NIGMS
Short Course on Systems Genetics
This is an annual course held at The Jackson Laboratory which covers computational and experimental approaches to genetic studies that utilize whole genome approaches.
Role: Principal Investigator

5 R01 GM070683-12, -12S1 Broman, Churchill (PI) 04/01/15-03/31/19
NIH/NIGMS
Systems Genetic Analysis of Multi-parent Crosses
The goal of this project is to develop statistical methods and modular, extensible software,

including tools for interactive data visualization that empower researchers to explore systems genetics data on multi-parent populations.
Role: Principal Investigator

5 P50 GM076468-10 Churchill (PI) 07/15/11-06/30/17
NIH/NIGMS
Center for Genome Dynamics
The goal of the CGD, using a variety of model phenotypes, is to pioneer improved prediction, prevention and intervention strategies for complex diseases, with broad implication for multiple areas of human disease.
Role: Principal Investigator

CALICO-FY16-GAC-01 Churchill (PI) 02/20/16-02/19/19
Calico Life Sciences, LLC
Dietary Intervention of Aging in Genetically Diverse Mice
The goal of this project is to leverage the natural genetic variation in the Diversity Outbred (DO) mouse population to gain new insights into the fundamental biology of aging.
Role: Principal Investigator

HHSF223201400183C Koturbash (PI) 09/30/14-09/29/17
Food and Drug Administration
The Diversity Outbred: A Tool to Improve Preclinical Safety Testing and Pharmacogenomic Analysis
The overall goal of this project is to evaluate the performance of Diversity Outbred mice in predicting human toxicity responses to pharmaceutical compounds and to determine the underlying genetics of this response.
Role: Consortium PI

JAX-DIF-FY18-GAC Churchill (PI) 04/01/18-03/31/19
The Jackson Laboratory Director's Innovation Fund
JAX Supplement to NIGMS grant R01 GM070683-1251, “Computing Infrastructure for Interactive Data Analysis”
NEEDS AIMS
Role: Principal Investigator

JAX-DIF-FY17-CB-SCM Baker, Churchill, Munger, Reinholdt (PI) 04/01/17-10/31/18
The Jackson Laboratory Director's Innovation Fund
DO and CC RIX mESCs. An Advanced Platform for Cellular Systems Genetics
The goal of this proposal is to demonstrate the power of the founder strain, DO, and CCRIX mESC lines as a platform for cellular systems genetics by profiling the chromatin landscape and cellular proteomes of undifferentiated mESC lines comprising the eight DO/CC founder strains, 150 individual outbred DO cell lines, and 10 F1 progeny from crosses of CC strains (CC-RIX).
Role: Principal Investigator

TJL-DIF-FY14-GWC Carter (PI) 05/01/14-12/31/16
The Jackson Laboratory Director's Innovation Fund
Genetics of Molecular Epigenetics
This project takes a focused, integrated approach to understanding the consequences of genetic variation on genome-wide transcript regulation. Our plan includes two components: a workshop to assess opportunities, and a research project to pilot a comprehensive approach.
Role: Co-Investigator

JAX-SSIF-FY17-GAC Churchill (PI) 03/01/17-02/28/18
The Jackson Laboratory Scientific Services Innovation Fund
Interactive Analysis Tools for CC and DO Mice
This project will develop web-based interactive tools and shared database resources for projects that use Diversity Outbred and Collaborative Cross mice.
Role: Principal Investigator

ISG-ARC-FY13-GAC Churchill, Gillan, Isakoff, Liang, Manautou, Morris, Orsey, Toro-Salazar (PI) 10/01/13-09/30/18
The Jackson Laboratory Competitive Internal Awards
Use of Diversity Outbred Mice to Study Cardiotoxicity of Chemotherapeutic Agents
The goal of this project is to develop the Diversity Outbred (DO) mice as a model system to screen for the cardiotoxicity of anthracycline chemotherapy.
Role: Principal Investigator