LAURA GARVEY REINHOLDT, PhD

Associate Professor
The Jackson Laboratory
600 Main Street
Bar Harbor, ME 04609

laura.reinholdt@jax.org
@Laura_Reinholdt
office: 207.288.6693
cell: 207.801.1343

EDUCATION

2001-05	Post-doctoral training, Mammalian Genetics	The Jackson Laboratory, ME (mentor: Dr. John Schimenti)
2001	Ph.D., Genetics	University of Connecticut, CT (mentor: Dr. Hallie Krider)
1999	M.S., Genetics	University of Connecticut, CT
1995	B.S., Biology, Molecular and Cellular Biology	Roger Williams College, RI

RESEARCH EXPERIENCE AND APPOINTMENTS

2018-present	Associate Professor, co-Director, Genetic Resource Sciences, co-Director of The Mutant Mouse Resource and Research Center (MMRRC), The Jackson Laboratory, Bar Harbor ME
2018-present	Graduate Faculty, School of Biomedical Science and Engineering, University of Maine, Orono, ME
2016-2018	Senior Management Team, *ad hoc* member, The Jackson Laboratory, Bar Harbor
2015-2018	Senior Research Scientist, co-Director, Genetic Resource Sciences, The Jackson Laboratory, Bar Harbor, ME
2014-2015	Research Scientist, co-Director, Genetic Resource Sciences, The Jackson Laboratory, Bar Harbor, ME
2007-2014	Research Scientist, Core Management Team, Genetic Resource Sciences, The Jackson Laboratory, Bar Harbor, ME
2005-2007	Associate Research Scientist Dr. Mary Ann Handel, The Jackson Laboratory, Bar Harbor, ME

INSTITUTIONAL SERVICE (The Jackson Laboratory)

2011-2012	Member, Genetic Resource Committee
2011-present	Member, Genetic Quality Control Committee
2010-2013	Advisor, High Throughput Sequencing Advisory Committee
2013-2015	Organizer, Reproductive and Developmental Biology Interest Group
2015	Bar Harbor Master Campus Planning Committee
2016-2018	Scientific Advisory Council, Bar Harbor Chair

2017-2019	Member, Bar Harbor Faculty Candidate Triage Committee
2018-present	Genetic Diversity Initiative Committees, Bar Harbor
2018-present	Internal grant review, Director's Innovation Fund (standing member – GeDI related proposals), Scientific Service Innovation Fund (*ad hoc*)
2018-present	Member, Bar Harbor Campus Master Planning Committee
2019-present	CUBE Leadership Team, member
2019-present	JAX Center for 3D Genomics and Biology, core member
2019-present	JAX Center for Addiction Biology, core member

TEACHING EXPERIENCE

1995-2001	Graduate teaching assistant, University of Connecticut, Storrs, Department of Molecular and Cell Biology. Courses: Developmental Biology, Human Genetics (for non-majors), Introduction to Biochemistry, Biochemistry, DNA Analysis.
1999-2000	Instructor, Investigation of Special Topics: DNA Analysis University of Connecticut, Storrs, Department of Molecular and Cell Biology.
2006-2010	Instructor, The Genome Access Course, Cold Spring Harbor Laboratory, Cold Spring, NY.
2010-2011	Instructor, The Jackson Laboratory Workshop on Current Protocols in Stem Cell Biology
2013-2015	Instructor, The Jackson Laboratory Workshop on Modern Approaches to High Throughput Sequencing
2014-2016	Instructor, The Mouse as a Model System for Biomedicine, Bates College and The Jackson Laboratory
2014-2017	Instructor, The Colby College Genomics Institute, Jackson Laboratory
2014-2015	Instructor, The Whole Scientist, Mount Desert Biological Laboratory and The Jackson Laboratory
2014	Mentor, University of Maine Master of Science in Teaching Program
2004-2016	Mentor, The Jackson Laboratory Summer Student Program
2018-2020	Course Director, GENE 0208 Medical & Experimental Mammalian Genetics at The Jackson Laboratory
2019-present	Faculty lecturer, Mammalian Genetics Course, Tufts and University of Maine

TRAINEES

Current trainees: Callan O'Connor (predoc, Tufts Genetics, Ph.D.)
Emily Swanzey, Ph.D. (postdoc, The Jackson Laboratory)

Past trainees / lab members:

Griff Gilbert, IDEXX
Heather Fairfield, Research Laboratory Manager, MMCRI
Candice Byers, Tufts Mammalian Genetics, Ph.D. Program
Ian Greenstein, Pharm.D., University of New England
Herb Pratt, Research Project Manager/Research Scientist
Grace Gonella, University of Maine, Masters of Science in teaching program

Current graduate thesis committees:

Candice Byers, Tufts Mammalian Genetics Ph.D. program
Leslie Sepaniac, University of Vermont, Department of Molecular Physiology & Biophysics
Lauren Kuffler, Tufts Mammalian Genetics Ph.D. program
Uma Arora, Tufts Mammalian Genetics Ph.D. program

Aidan Burn, Tufts Mammalian Genetics Ph.D. program
Monique Mills, University of Maine GSBSE Ph.D. program

PROFESSIONAL ACTIVITIES, SERVICE, and AWARDS

2000	Dr. Claire M. Berg Memorial Fellowship in Genetics, University of Connecticut, Storrs, CT.
2001	The Jackson Laboratory Institutional Training Grant (T32)
2002	NIH Individual Ruth L. Kirschstein National Research Service Award (F32)
2013-2015	International Mammalian Genome Society, Nominations and Elections Committee
2017–present	Secretariat, International Mammalian Genome Society
2018-present	*Ad hoc* member, Institute for Systems Genomics Education Committee, University of Connecticut
2015-present	Advisory Board Member, Mouse Genome Database / MGI
2010-present	Grant review • NIH/NIEHS, SBIR, Special emphasis panel • NIH/NHGRI *ad hoc* scientific review R24 genomic resources (invitee) • NIH/CSR Genetics of Health and Disease, temporary member (invitee) • Maine Cancer Foundation
2008-present	Member, International Mammalian Genome Society
2014-present	Member, American Society of Human Genetics
2016-2018	Member, American Society for Cell Biology
2019-present	Member, International Society for Stem Cell Research
2019-present	Associate Member, Society of Toxicology
2008-present	*Ad Hoc* reviewer, American Journal of Human Genetics, Development, Molecular and Cellular Biology, Genome Research, Biology of Reproduction, Reproduction, Mammalian Genome, PLoS One, Journal of Cell Biology, Nucleic Acids Research, Cell Stem Cell, Molecular Reproduction and Development, BMC Genomics, Mammalian Genome, Human Mutation, Developmental Biology, Nature Protocols, Nature Communications, Genetics, Genome Research, Journal of Cell Science, PLoS Genetics

COMPLETE BIBLIOGRAPHY (h-index: 22; citations: 3074)

IN REVISION

Swanzey E., O'Connor C, and Reinholdt LG. Mouse Genetic Reference Populations: Cellular Platforms for Integrated Systems Genetics, Trends Genet., *in revision*.

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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. Cell Stem Cell. 2020 Aug 7;. doi: 10.1016/j.stem.2020.07.005. [Epub ahead of print] PubMed PMID: 32795400; NIHMSID:NIHMS1620410

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. Naïve Pluripotent Stem Cells Exhibit Phenotypic Variability that is Driven by Genetic Variation. Cell Stem Cell. 2020 Aug 11;. Doi 10.1016/j.stem.2020.07.019. [Epub ahead of print] PubMed PMID: 32795399

Slone JD, Yang L, Peng Y, Queme LF, Harris B, Rizzo SJS, Green T, Ryan JL, Jankowski MP, **Reinholdt LG,** Huang T. Integrated analysis of the molecular pathogenesis of FDXR-associated disease. Cell Death Dis. 2020 Jun 4;11(6):423. doi: 10.1038/s41419-020-2637-3. PMID: 32499495; PMCID: PMC7272433.

Gan P, Patterson M, Watanabe H, Wang K, Edmonds RA, **Reinholdt LG**, Sucov HM. Allelic variants between mouse substrains BALB/cJ and BALB/cByJ influence mononuclear cardiomyocyte composition and cardiomyocyte nuclear ploidy. Sci Rep. 2020 May 5;10(1):7605. doi: 10.1038/s41598-020-64621-0. PMID: 32371981; PMCID: PMC7200697.

Saul MC, Philip VM, **Reinholdt LG**; Center for Systems Neurogenetics of Addiction, Chesler EJ. High-Diversity Mouse Populations for Complex Traits. Trends Genet. 2019 Jul;35(7):501-514.

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Hu J, Lessard C, Longstaff C, O'Brien M, Palmer K, **Reinholdt L**, Eppig J, Schimenti J, Handel MA. ENU-induced mutant allele of Dnah1, ferf1, causes abnormal sperm behavior and fertilization failure in mice. Mol Reprod Dev. 2019 Apr;86(4):416-425.

Fonseca CL, Malaby HLH, Sepaniac LA, Martin W, Byers C, Czechanski A, Messinger D, Tang M, Ohi R, **Reinholdt LG***, Stumpff J*. Mitotic chromosome alignment ensures mitotic fidelity by promoting interchromosomal compaction during anaphase. J Cell Biol. 2019 Apr 1;218(4):1148-1163. ***equal contribution**

Goodwin LO, Splinter E, Davis T-L, Urban R, He H, Braun RE, Chesler EJ, Kumar V, van Min M, Ndukum J, Philip VM, **Reinholdt LG**, Svenson K, White JK, Sasner M, Lutz C, and Murray SA Large-scale discovery of mouse transgenic integration sites reveals frequent structural variation and insertional mutagenesis *Genome Res.* 2019 Mar;29(3):494-505. doi: 10.1101/gr.233866.117

Lilue J, Doran AG, Fiddes IT, Abrudan M, Armstrong J, Bennett R, Chow W, Collins J, Collins S, Czechanski A, Danecek P, Diekhans M, Dolle DD, Dunn M, Durbin R, Earl D, Ferguson-Smith A, Flicek P, Flint J, Frankish A, Fu B, Gerstein M, Gilbert J, Goodstadt L, Harrow J, Howe K, Ibarra-Soria X, Kolmogorov M, Lelliott CJ, Logan DW, Loveland J, Mathews CE, Mott R, Muir P, Nachtweide S, Navarro FCP, Odom DT, Park N, Pelan S, Pham SK, Quail M, **Reinholdt L**, Romoth L, Shirley L, Sisu C, Sjoberg-Herrera M, Stanke M, Steward C, Thomas M, Threadgold G, Thybert D, Torrance J, Wong K, Wood J, Yalcin B, Yang F, Adams DJ, Paten B, Keane TM. Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nat Genet.* 2018 Nov;50(11):1574-1583

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Handel MA, Lessard C, **Reinholdt LG**, Schimenti J, Eppig JJ. (2006) Mutagenesis as an unbiased approach to identify novel contraceptive targets. *Mol Cell Endocrinol*. 250(1-2):201-5.

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ACTIVE AND PENDING FUNDING

19-036-ASP (Liu, Reinholdt, Serreze) 9/1/2019 - 4/30/2022
Mark Foundation for Cancer Research Annual Direct: $603,572 Total: $2,533,684
Dissecting the Genetic Control of Response to Immune Checkpoint Inhibitors in Cancer
The overall goal is to determine the contribution of host genotype to tumor responses to immune checkpoint inhibitors (ICI) agents.
Role: Principal Investigator

5 R24 OD021325-05 (Reinholdt) 6/1/2016 - 4/30/2024
NIH/OD Annual Direct: $489,052 Total: $3,395,771
Resources for Comparative Mendelian Disease Genomics
The objectives of this project are to expand the scope of gene discovery beyond exome-imposed limitations, and to use these data to develop a mouse genome variation database, and other optimized resources, that will deliver improved mutation discovery success rates. Moreover, we will apply these new technologies to explore de novo mutations and perinatal lethal phenotypes in a large population of mouse neonates, as well as identifying the heritable molecular lesions in established, genetically defined Mendelian disease models.
Role: Principal Investigator

2 U42 OD010921-11 (Lutz, Reinholdt) 1/1/2020 - 12/31/2024
NIH/OD Annual Direct: $659,616 Total: $5,606,735
The Mutant Mouse Resource and Research Center at The Jackson Laboratory
The goals importation, archiving (through cryopreservation of sperm and/or embryos) and distribution of biomedically important strains of mice and related materials.
Role: Principal Investigator

5 R13 OD023013-03 (Reinholdt, Lutz) 4/1/2017 - 3/31/2021
NIH/OD Annual Direct: $19,058 Total: $59,928
Mutant Mouse Resource and Research Center Annual Meeting

The goal of this project is to convene an in-person meeting of the Mutant Mouse Resource and Research Center directors and key staff annually from 2017 to 2020.
Role: Principal Investigator

1 R01 ES029916-01 (Churchill, Korstanje, Reinholdt) 2/1/2019 - 1/31/2024
NIH/NIEHS Annual Direct: $451,799 Total: $3,582,956
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

5 P50 DA039841-04 (Chesler) 8/15/2016 - 4/30/2021
NIH/NIDA Annual Direct: $163,664 Total: $1,484,214
Center for Systems Neurogenetics of Addiction - Core 3: Mouse Resources and Validation
The goals of this core are to provide cohorts of Collaborative Cross (CC), Diversity Outbred (DO) and inbred strains of mice for neurobehavioral screening and biobanking and capacity for variant validation through the creation of novel variants in mouse iPS/ES cells, in vitro screening of the engineered cell lines for functional testing and, for a subset of promising functional variants, capacity for in vivo validation through CRISPR/Cas9 technology. The core will also provide expertise and infrastructure to create new mouse models for gene variants, which will be archived at JAX for distribution to the global research. Finally, the Core will conduct primary research on tools and technologies for cloning DO mice with the ultimate goal of developing best practices for functional validation of extreme, highly polygenetic phenotypes found in the DO genomes.
Role: Co-Investigator, Core Lead

5 P40 OD011102-19 (Lutz, Reinholdt) 5/1/2016 - 1/31/2021
NIH/OD Annual Direct: $446,753 Total: $3,938,596
Special Mouse Strains Resource
The overall goal of the Special Mouse Strains Resource (SMSR) is to provide biological resources for analysis of genetically complex traits.
Role: Principal Investigator

5 UM1 HG009409-03 (Ruan) 2/1/2017 - 1/31/2021
NIH/NHGRI Salary Only
Comprehensive Mapping of Long-Range Chromatin Interactions in Human and Mouse Genomes
Our major goal is to produce high quality, high resolution and comprehensive maps of long-range chromatin interactions between the structural and functional elements in human and mouse genomes. Dr. Reinholdt's project involves the provision of mESCs, in vitro differentiated early germ lineages, and select mouse tissues from select inbred mouse strains and disease models.
Role: Co-Investigator

HHSN275201500004C (Lutz) 9/22/2015 - 9/21/2020
NIH/NICHD Salary Only
A Repository of Mouse Models for Cytogenetic Disorders
The objective of this contract is to produce, maintain, and distribute mouse strains with specific aneuploidies with a primary emphasis on models of human trisomy for chromosome 21.
Role: Co-Investigator

5 R01 HL132024-04 (Lo) 4/15/2016 - 3/31/2021

NIH/NHLBI Annual Direct: $54,052 Total: $472,955
Modeling Complex Genetics of Congenital Heart Disease in Mice
The goal of this project is to model congenital heart disease through implementation of a dominant modifier screen in mice.
Role: Consortium PI

JAX-DIF-FY18-Beck 9/18/2018 – 9/17/2020
Director's Innovation Fund Annual Direct: $195,310 Total: $195,310
Structural Variation Discovery as a Resource for the Collaborative Cross
This pilot will accomplish characterization of the variation present in the 8 inbred strains used to create the Collaborative Cross (CC; 129S1/SvImJ, A/J, C57BL/6J, NOD/ShiLtJ, NZO/HlLtJ, CAST/EiJ, PWK/PhJ, and WSB/EiJ), as well as 8 resultant CC strains of interest using long read sequencing and Strand-seq technologies.
Role: Co-Investigator

JAX-DIF-FY19- REINHOLDT - SYSTEMS GEN 4/15/2019 - 4/14/2020
Director's Innovation Fund Annual Direct: $75,370 Total: $75,370
A Platform for Rapid Creation of Diversity Tool Strains for Systems Genetics
The overall goal of this pilot project is to create Bxb1 recombinase docking sites across a diverse panel of inbred strains including the some of the founder strains of the Collaborative Cross and BXD RI lines. These engineered inbred strains will serve as a broadly applicable platform for efficient, targeted integration of complex disease and/or 'tool strain' alleles into a ubiquitously expressed, non-essential safe harbor locus.
Role: Principal Investigator

JAX-DIF-FY19- REINHOLDT - IPSC RESOURCE 4/19/2019 - 10/18/2020
Director's Innovation Fund Annual Direct: $180,000 Total: $180,000
iPSC Resource for Systems Cellular Genetics
The overall goal of this pilot project is to create and credential a panel iPS cell lines (iPSCs) from Diversity Outcross and 24 iPSC lines from the 8 CC/DO founder inbred strains.
Role: Principal Investigator

JAX-SSIF-FY19-AS FUSORSV-M 5/13/2019 - 5/12/2020
Director's Innovation Fund Annual Direct: $94,165 Total: $94,165
Development of FusorSV-M an Algorithm to Optimally Detect SVs
The goals of this project are to extend the FusorSV algorithm to discover SVs by integrating data from long-reads (PacBio), linked-reads (10x Genomics), and Paired-End / Mate-Pair reads (Illumina), and to build a FusorSV SV detection model for the mouse genome.
Role: Principal Investigator

Domestic Pending Grant Support

1 R24 OD030037-01 (Baker, Munger, Reinholdt) 09/01/2020-08/31/2024
NIH/OD *Annual Direct: $494,858* Total: $3,341,326
Genetically Diverse Mouse Embryonic Stem Cells: A Platform for Cellular Systems Genetics
The objective of this application is to generate a thoroughly-validated panel of genetically diverse mouse embryonic stem cells (mESC) that will enable widespread adoption of cellular systems genetics.

5 P40 OD011102 (Lutz, Reinholdt) 2/1/2021 - 1/31/2025
NIH/OD Annual Direct: $446,753 Total: $3,938,596
Special Mouse Strains Resource
The overall goal of the Special Mouse Strains Resource (SMSR) is to provide biological resources for analysis of genetically complex traits.
Role: Principal Investigator

INACTIVE

DO and CC RIX mESCs. An Advanced Platform for Cellular Systems Genetics
JAX DIF FY17 CB SCM 04/01/2017-10/31/2018
The Jackson Laboratory Director's Innovation Fund $178,000

A better mouse strain for microbiome research
JAX DIF FY17 GMW 01 (Weinstock) 03/01/2017-08/31/2018
The Jackson Laboratory Director's Innovation Fund Salary Only

High Throughput Production and Cryopreservation of Knockout Mice
5 U42 OD011185-05 (Murray, Taft) 09/07/2011 - 07/31/2017
NIH/OD Salary Only (No Cost Extension)
Role: Co-I

Mouse Mutant Resource
5 P40 OD010972-38 (Bergstrom, Reinholdt) 05/20/2013 - 04/30/2016
NIH/OD $332,173

Single Molecule Sequencing of C57BL/6J Eve
TJLINT-LGR-FY15 (Reinholdt) 01/01/2015 - 12/31/2015
The Jackson Laboratory Competitive Internal Awards $105,000

Establishing a Role for Kinesin-8 in Mammalian Germ Line Development
5 R03 HD078485-02 (Reinholdt) 09/17/2014 - 08/31/2016
NIH/NICHD $50,000

INVITED TALKS, SELECTED ABSTRACTS (5 years)

Genetic variation influences pluripotent ground state stability in mouse embryonic stem cells through a hierarchy of molecular phenotypes, Invited lecture, Vanderbilt School of Medicine, Center for Stem Cell Biology, 2020.

Genetic variation influences pluripotent ground state stability in mouse embryonic stem cells through a hierarchy of molecular phenotypes, Invited lecture, University of Utah, Department of Genetics, 2019

Genetic variation influences pluripotent ground state stability in mouse embryonic stem cells through a hierarchy of molecular phenotypes, Selected abstract, 33rd International Mammalian Genome Conference, 2019

Genetic quality control in mouse model development. Invited lecture, Precision Mouse Modeling: Translation to Human Disease Symposium, University of Missouri, 2019

Genetically diverse mice and cancer model development, Invited lecture, 28th Annual Short Course on Experimental Models of Human Cancer, The Jackson Laboratory, 2019

Comparative Mendelian genomics and disease modeling in mice, Invited lecture, Big Genomic Data Course, The Jackson Laboratory, 2018

A potential role for the kinetochore protein, Kinetochore associated 1 (KNTC1) in ciliary signaling. Selected abstract, EMBL Mammalian Genetics and Genomics, 2017.

Comparative Mendelian genomics and disease modeling in mice. Invited lecture, Research Fellows Association Seminar, Maine Medical Research Institute, 2017

Comparative Mendelian genomics and disease modeling in mice. Invited lecture, Department of Biomedical Sciences, Cornell University, 2017.

Comparative Mendelian genomics and disease modeling in mice. Selected abstract, Genetics Society of America, Allied Genetic Conference, 2016, Orlando USA

Comparative Mendelian genomics and disease modeling in mice. Invited lecture, Boston University Genome Sciences Institute, 2016, Boston, MA.

Forward Genetic Approaches for Modeling Mendelian Diseases in Mice. Invited lecture, National Institute of Genetics, Mishima, Japan, 2016.

Forward Genetic Approaches for Modeling Mendelian Diseases in Mice. Invited lecture, Riken BioResource Center, Experimental Animal Division, Japan 2016.

Forward Genetic Approaches for Modeling Mendelian Diseases in Mice. Invited lecture, Welcome Trust Sanger Sequencing Bioinformatics Course, 2015. Hinxton, UK.

Mouse Model Resources for Comparative Mendelian Genomics. Selected abstract, American Society for Human Genetics, Annual Meeting, 2015, Baltimore, MD.

Forward genetic approaches for modeling Mendelian disease in mice. Invited talk, EWHA-JAX Joint Symposium on Genomic Medicine, 2015. EWHA Womans University, Seoul Korea.

The JAX CRISPR-cas9 mouse model core. Invited Talk. NHLBI, Bench to Bassinet Annual Meeting, 2015 Bethesda, MD.

Mendelian disease gene discovery by exome sequencing in mice: Is forward genetics obsolete? Invited lecture, The University of Vermont, Department of Molecular Physiology and Biophysics, 2015.