Elissa J. Chesler, Ph. D.

Professor
Ann Watson Symington Chair in Addiction Research
Senior Director, Integrative Data Science
The Jackson Laboratory
600 Main St
Bar Harbor, ME 04609
elissa.chesler@jax.org
207-288-6453

Curriculum Vitae

Institutional Affiliations:

University of Connecticut Department of Psychology
School of Biomedical Sciences, External Graduate Faculty, University of Maine
Tufts University School of Medicine, Genetics Program and Neuroscience Program
Emory University Department of Psychology

Positions Held:

2023 – Present	Senior Director, Integrative Data Science
2021 – Present	Ann Watson Symington Chair in Addiction Research
2018 – Present	The Jackson Laboratory, Bar Harbor, ME Professor
2012 – 2018	The Jackson Laboratory, Bar Harbor, ME Associate Professor, Bioinformatics and Computational Biology
2009 – 2012	The Jackson Laboratory, Bar Harbor, ME Assistant Professor, Bioinformatics and Computational Biology
2006 – 2009	Oak Ridge National Laboratory – UT-Battelle, LLC Group Leader, Systems Genetics Group (Former Mammalian Genetics and Genomics Group), Biosciences Division (Former Life Sciences Division)
2005 – 2006	Oak Ridge National Laboratory – UT-Battelle, LLC Staff Scientist, Mammalian Genetics and Genomics Group, Life Sciences Division
2005 – 2013	University of Tennessee, Knoxville, TN Adjunct Assistant Professor, Genome Science and Technology Program
2004 – 2005	University of Tennessee Health Science Center, Memphis, TN Assistant Professor (Non-tenure track) Department of Anatomy and Neurobiology, Center for Genomics and Bioinformatics
2002 – 2004	University of Tennessee Health Science Center, Memphis, TN Post-Doctoral Research Trainee, Department of Anatomy and Neurobiology, Center for Genomics and Bioinformatics. Advisors: Dr. Robert W. Williams, Dr. Daniel Goldowitz

Education:

2002	Doctor of Philosophy in Neuroscience, University of Illinois at Urbana-Champaign Neuroscience Program, Advisor: Dr. Jeffrey S. Mogil Thesis: Use of Inbred Strains for the Study of Individual Differences in Pain Related Phenotypes in the Mouse.
1997 – 1998	University of Illinois College of Medicine, First year medical curriculum, Medical Scholars Program University of Illinois at Urbana-Champaign
1997	Master of Science, University of Illinois at Urbana-Champaign Biological Psychology, Medical Scholars Program, Advisor: Dr. Janice M. Juraska Thesis: Sex and age effects on dendritic spine density of CA1 hippocampal pyramidal neurons
1995	Bachelor of Science, University of Connecticut Double Major in Psychology/Physiology and Neurobiology Honors in Psychology, Summa Cum Laude, University Scholar, Advisor: Dr. John D. Salamone Thesis: A rat model for anti-parkinsonian effects of Clozapine: Interactions of clozapine with cholinomimetic drugs

Honors & Awards:

1993	Summer Undergraduate Research Fellow, University of Connecticut School of Medicine
1994 – 1995	Julias A. Elias Scholarship, University of Connecticut
1995	Outstanding Woman Scholar from College of Liberal Arts & Sciences, University of Connecticut Phi Beta Kappa, Psi Chi, Phi Kappa Phi, and Alpha Lambda Delta Honor Societies
1995 – 1996	Fellow, Graduate College, University of Illinois at Urbana-Champaign
2006	Early Career Award for Scientific Accomplishment-UT-Battelle Oak Ridge National Laboratory
2007	Young Scientist Award, International Behavioral and Neurogenetics Society
2019	International Behavioral and Neural Genetics Society Fellow
2022	Distinguished Scientist Award International Behavioral and Neural Genetics Society.

Grant Review Panels:

2004	NIH Special emphasis panel for NIDCR and NINDS RFA-DE-05-004 "Mechanisms of orofacial pain: Anatomy, genomics, and proteomics"
2006	Israel Science Foundation, Ad Hoc Reviewer.
2006 – Present	National Science Foundation, Ad Hoc Reviewer
2007	NIH Special Emphasis Panel NIEHS Environmental stress centers U54 RFA-ES-06-012 and U01 RFA-ES-06-013 Biological response indicators of environmental stress.
2007	NIH Ad hoc reviewer "Biobehavioral Regulation, Learning and Ethology Study Section (BRLE)"
2007; 2009	Wellcome Trust, Ad Hoc Reviewer
2008	NIH Ad hoc reviewer "Genomics, Computational Biology and Technology Study Section (GCAT)"
2009	Biotechnology and Biological Sciences Research Council, UK, Ad Hoc Reviewer
2009	Genome Canada, Ad Hoc Reviewer

2009 – 2015	Member NIH: Genomics, Computational Biology and Technology Study Section (GCAT)
2015	NIH Ad hoc reviewer "Bioengineering Sciences and Technologies (BST)" member conflict panel
2015	NIH SEP reviewer "NHGRI Training Program Data Access and Coordinating Center (DACC)" RFA-HG-15-025
2016	NIH SEP reviewer NCI "Genomic Data Analysis Network (U24)"
2017; 2019	NIH SEP reviewer NIDA PAR-16-009 (P50 Research Center of Excellence) & PAR-14-186 (P30 Core Center of Excellence)
2018; 2019;2022	NIH SEP Phase II interviewer NIDA PAR-16-357 Avenir Award Program for Genetics or Epigenetics of Substance Use Disorders (DP1)
2021	NIH Ad hoc reviewer "Biological Data Management and Analysis (BDMA)

Committees and Additional Professional Activities:

1998 – 2001	Medical Scholars Program Advisory Committee, Co-Chair
2000	International Behavioral Neuroscience Society, Student Representative to Council.
2002	International Behavioral Neuroscience Society, Student Member of Program Committee
2003 – 2004	Consultant, Protocol power analysis, Uniformed Services University of the Health Sciences
2005	UT-Knoxville Genome Science and Technology Computational Biology & Bioinformatics Task Force
2005	International Phenome Database Integration Committee
2009 – 2010	Society for Neuroscience, Neuroinformatics Committee
2010 – 2013	International Behavioral and Neurogenetics Society (Executive Committee Member at Large)
2011	Scientific Advisory Committee, The Jackson Laboratory
2011 – 2023	External Advisory Board, NIH NIAAA Monkey Alcohol Tissue Research Resource.
2012 – 2013	International Mouse Phenotyping Consortium (IMPC) Statistical Working Group, Chair
2014 – Present	External Advisory Board, NIH NIDA P50 Center for GWAS in Outbred Rats
2012 – Present	Editorial Board, Genes, Brain, Behavior
2012 – Present	Editorial Board, Mammalian Genome
2013	External Advisor to SYSGENET European Union COST consortium
2013	NIH Big Data to Knowledge Workshop on Enhancing Training for Biomedical Big Data, Participant
2014	NIH Office of Behavioral and Social Sciences Research Workshop on Challenges in Replication of GXE, Workshop Speaker
2015 – 2017	International Behavioral and Neurogenetics Society (President-Elect, President, Past President)
2014 – 2017	International Behavioral and Neurogenetics Society (Program Committee)
2015	Phenotype Research Coordination Network Workshop on the Integration of Animal Behavior Ontology and Neurobehavioral Ontology (NBO-ABO), Participant.
2016	NIH National Advisory Mental Health Council (NAMHC) Workgroup on Future Directions of Genomics at NIMH
2017	Program Committee, 15th Annual Meeting Complex Trait Community.
2017 – 2018	International Mouse Phenotyping Consortium (IMPC) Behavioral Working Group, Co-Chair
2018 – 2020	External Advisory Board NSF Research Traineeship “Science of Learning and the Art of Communication (SLAC)”, University of Connecticut, Psychological Sciences, PI Jim Magnuson
2018 – Present	Associate Editor, Genetics
2020	Advisory Board, JAX Specialty Mouse Strain Resource P40
2023 – Present	Scientific Advisory Board, Monarch Initiative

Active Memberships:

1994 – Present	International Mouse Genome Society; Genetics Society of America
1996 – 2020	Society for Neuroscience
2002 – Present	Complex Trait Consortium
2003 – 2023	Research Society on Alcoholism
2003 – 2023	International Behavioral and Neurogenetics Society (IBANGS)
2009 – Present	International Society of Computational Biology

Manuscript Referee:

Genetics; Genome Research; Genomics; Alcoholism: Clinical and Experimental Research; Current Biology; Public Library of Science (PLOS) Biology; Public Library of Science (PLOS) Genetics; Genes, Brain, and Behavior; Bioinformatics; Nature; Nature Genetics; BMC Genomics; Mammalian Genome; Science, Biological Psychiatry; Biomedical Informatics

Post-Doctoral Trainees:

Dr. Roumyana Yordanova Kirova, 2005–2006. *Present Position*: Assistant Professor, Institute of Mathematics and Informatics, Bulgarian Academy of Sciences.

Dr. Ryan Logan, 2011–2012. *Present Position*: Associate Professor, University of Massachusetts, Worcester

Dr. Juliet Ndukum, 2012-2014. *Present Position*: Biostatistician, Arizona

Dr. Price Dickson, 2012-2020. Present Position: Assistant Professor, Marshall University

Dr. Michael Saul, 2018-2019. Present Position: Computational Scientist, The Jackson Laboratory

Dr. Udita Datta, 2018-2021. Present Position: Pharmaceutical Industry Position, France.

Doctoral Trainees:

Vivek M. Philip, Genome Science and Technology Program, Oak Ridge National Laboratory and University of Tennessee, Knoxville, TN, Major advisor, *Present Position*: Computational Science Service, The Jackson Laboratory.

Jeremy Jay, Electrical Engineering and Computer Science, University of Maine, Orono, ME, *Present Position:* Department of Bioinformatics and Genomics, UNC Charlotte.

Master's Trainees:

Tyler Roy, University of Maine, Orono

Ashley Olson, University of Maine, Orono

Troy Wilcox, University of Maine, Orono

Dissertation Committee Memberships:

Bhavesh Borate, Genome Science and Technology Program, Oak Ridge National Laboratory and University of Tennessee, Knoxville, TN, *Present Position*: Applied Statistics, Fred Hutchinson Cancer Research Center

Leslie Jellen, Department of Psychology, Pennsylvania State University, Happy Valley, PA

Yun Zhang, Computer Science Department, University of Tennessee, Knoxville, TN, *Present Position*: Pioneer Hybrids

Joshua R. New, Computer Science Department, University of Tennessee, Knoxville, TN, *Present Position:* Staff Scientist, Building Technologies Research and Integration Center, ORNL.

Suman Duvurru, Genome Science and Technology Program, Oak Ridge National Laboratory and University of Tennessee, Knoxville, TN, *Present Position:* Research Scientist, Eli Lilly

Leah Graham, Genetics, Tufts University and The Jackson Laboratory

Timothy Reynolds, Computer Science, Baylor University

Alexandra Goetjen, University of Connecticut School of Medicine

Uma Arora, Tufts University and The Jackson Laboratory

Lauren Kuffler, Tufts University and The Jackson Laboratory

Callan O'Connor, Tufts University and The Jackson Laboratory

Alexis Garretson, Tufts University and The Jackson Laboratory

Faculty Mentoring Committees:

Dr. Catherine Kaczorowski, The Jackson Laboratory

Dr. Zhenqing Ouyang, The Jackson Laboratory

High School and Undergraduate Trainees

Date	**Name**	**Institution**	**Present**
2007-2008	Sarah Jo Jenkins	Austin Peay State University	Research Assistant, Vanderbilt University
2008-2009	Boloye Gomero	Maryville College	The Bullis School, Upper School Mathematics Teacher
2010	Amanda Ackovitz	N Carolina School of Science and Maths	Assistant Vice-President, Bank of America
2010	Ashley Hunt	The Maine School of Science and Maths	Implementation Consultant, Avalara, Durham, NC
2011	Avner Maiberg	University of Maine	Carnegie Mellon

2011	Carter Harwood	The Groton School, Groton, MA	John Hopkins University
2011	Lillian Kang	North Carolina School of Science & Maths	Duke University
2012	David Wang	North Carolina School of Science & Maths	DevOps, Truecar, Inc.
2012	Eleonora Hubbell	Mount Desert Island High School	Bowdoin College, Brunswick, ME
2012	Axis Fuksman-Kumpa	Mount Desert Island High School	Bowdoin College, Brunswick, ME
2012-2014	Casey Acklin	College of the Atlantic, Bar Harbor, ME	AmeriCorps, VISTA at Dementia Friendly, NV
2012-2014	Courtney Vaughn	University of North Carolina, Chapel Hill	Churchill Fellowship
2012-2015	Andrew Gallup	Mount Desert Island High School	Software Engineer, MITRE
2012	Katie Long	University of Michigan	University of Chicago
2012	Joshua Higgins	Baylor University	Scientific Curator, Celmatix
2014-2015	Kathryn McNaughton*	Williams College	Graduate Student, Neuroscience and Cognitive Science, University of Maryland
2014	Lingfeng Hou	Harvard University	Harvard University
2014	Astrid Moore	Colby College	Software Engineer, NowPow
2014	Kathryn Toal	Dartmouth University	Consultant, Trinity
2015	Summit Liu	Colgate University	Molecular & Cell Biology Technician, The Jackson Laboratory, Bar Harbor, ME
2016	Nkima Stephenson**	Rockdale Magnet Science & Tech School	Student, bachelor's degree in Neuroscience, Columbia University, New York City
2017	Satre Nbedeneza	Patterson High School, Baltimore, MD	
2017	Padam Kumar	University of North Carolina, Chapel Hill	Medical Student, University of Tennessee Science Center
2017	Robbie Denegre	Mount Desert Island High School	
2018	Eleanor Bridges	Mount Desert Island High School	
2018	Ashley Greaves	New York University	Graduate Student and Research Assistance, New York University
2018	Xochitl Ortiz-Ross	College of the Atlantic	Seasonal Research Assistant/Avian Ecology Intern, Archbold Biological Station, Venus Florida
2018-2020	Christian Monroy-Hernandez	The Jackson Laboratory Postbaccalaureate Program	Washington University MD/PhD program
2019	Violet Kimble	Drew University, Madison, NJ	Undergraduate Research Assistant, Drew University
2019	Pura Ileana Arroya-Morales	University of Puerto Rico, Mayaguez, PR	
2021	Bailey West		Johns Hopkins University
2021	Addison Smith	Mount Desert Island High School	
2022-2023	Kuranosuke Yamada	Colby College	Colby College
2022	Matthew Kim	University of British Columbia	University of British Columbia
2023	Saathvika Diviti	Colby College	Colby College
2023	Jane Adams	Northeastern University	Northeastern University
2023	DeAnna James	Morgan State University	

*Council on Undergraduate Research, NSF Research Experience for Undergraduates Poster Presenter

**NIDA Intel Prize 2017

Teaching:

Courses:

08/96–12/97	Behavioral Science for Medical Students, University of Illinois at Urbana-Champaign, Teaching Assistant, Dept. of Psychology and College of Medicine
08/98–12/98	Gross Anatomy for Medical Students, University of Illinois at Urbana-Champaign, Teaching Assistant, College of Medicine
01/97–05/00	The Brain and the Mind, University of Illinois at Urbana-Champaign, Teaching Assistant, Dept. of Psychology
08/00–12/00	Psychopharmacology, University of Illinois at Urbana-Champaign, Teaching Assistant, Dept. of Psychology
08/06–05/09	Genome Science and Technology I-II, University of Tennessee, Lecturer, Complex Trait Analysis
2019-2020	Mammalian Genetics, Tufts University, Lecturer, Complex Trait Analysis

Short Courses and Guest Lectures: (out of 21 total courses, some given multiple years)

11/2003	Society for Neuroscience Annual Meeting, New Orleans, Louisiana Faculty— The Bioinformatics of Brains: From Genes and Proteins to Behaviors. Microarray Analysis
05/04-06	NIMH Workshop on Experimental Neurogenetics of the Mouse, Memphis, TN Faculty, Gene-Environment Interactions
08/2004	IBANGS 10th International Summer School in Neurobehavioral Genetics, Memphis, TN Faculty, Genetics of Gene Expression, WebQTL
09/2004	The Jackson Laboratory Short Course on Mathematical Approaches to Complex Phenotypes, Bar Harbor, ME. Faculty, Genetics of Gene Expression, WebQTL
07/2005	IBANGS 11th International Summer School in Neurobehavioral Genetics, Bordeaux, France Faculty, Bioinformatics, WebQTL
09/2005	IBANGS 12th International Summer School in Neurobehavioral Genetics, Moscow, Russia Faculty, Molecular Biology From QTL to Gene, Systems Genetics, WebQTL
2005-2009	The Jackson Laboratory Short Course on Complex Trait Analysis, Bar Harbor, ME Faculty, Genetics of Gene Expression, WebQTL
2010-Present	The Jackson Laboratory Short Course on the Genetics of Addiction, Bar Harbor, ME. Course Organizer
2011-2016	The Jackson Laboratory Short Course on Systems Genetics, Bar Harbor, ME Faculty, GeneWeaver
09/2011	The Jackson Laboratory Short Course on the Genomic and Proteomic Approaches to Complex Heart, Lung, Blood & Sleep Disorders, Bar Harbor, ME
2014-2016	The Jackson Laboratory McKusick Short Course on Medical and Experimental Genetics, Faculty, Studying behavior in the laboratory mouse
2016-2019	The Jackson Laboratory Short Course on Neurotools, Course faculty and organizing committee. "Complex Trait Analysis and Advanced Mouse Populations", Bar Harbor, ME
2016-2020	The Jackson Laboratory Short Course on 21st Century Mouse Genetics, Course faculty and organizing committee. "Complex Trait Analysis and Advanced Mouse Populations", Bar Harbor, ME

Invited Talks and Symposia (out of 119 total):

09/30/03	"Genetic Interactions with the Laboratory Environment" The Neuroscience Institute Neuroscience Seminar Series, University of Tennessee Health Science Center, Memphis TN. Host: Dr. Robyn Wallace
10/20/03	"Genetic modulation of gene expression and correlations with neurobehavioral traits" Behavioral Neuroscience Seminar, Department of Psychology, University of Connecticut, Storrs, CT. Host: Dr. Steve Maxson
03/03/04	"Relational genetics from base pair to behavior in WebQTL: Genetic analysis of gene transcription regulation and correlations with neurobehavioral phenotypes" Neuroscience Program Seminar, University of Illinois at Urbana-Champaign, Urbana, IL. Hosts: Graham Huesmann and Dr. David Clayton
08/23/04	"WebQTL: Genetics of Individual Differences in Gene Expression, Brain, and Behavior in the Mouse CNS." Oak Ridge National Laboratory, Oak Ridge, TN. Host: Dr. Dabney Johnson

08/28/04	“From Base Pair to Behavior: Use of Genetic Reference Populations for Genome-wide Analysis of Gene Expression and Systems Level Phenotypes,” CBI Seminar, Oak Ridge National Laboratory, Oak Ridge, TN. Host: Dr. Jay R. Snoddy
10/01/04	“From base pair to behavior: Use of reference populations for genetic analysis of gene expression and systems level phenotypes” University of Pittsburgh Medical College. Host: Dr. William R. Lariviere
10/04/04	“WebQTL demonstration workshop,” Penn State University, State College, PA. Host: Dr. Byron C. Jones
10/11/04	“WebQTL: Genetics of individual differences in gene expression, brain, and behavior,” Southern Illinois University, Springfield, IL. Host: Dr. Linda C. Toth
10/24/04	“Internet based genetic analysis from base-pair to behavior in inbred mice” in “Neurogenomics of Behavior,” Society for Neuroscience, San Diego, CA. Organizer and Chair: Dr. David Clayton
11/15/04	“WebQTL Tutorial,” Wake Forest University, Winston-Salem, NC. Host: Dr. Sara Jones
02/24/05	“From Base Pair to Behavior: Use of Genetic Reference Populations for Genome-wide Analysis of Gene Expression and Systems Level Phenotypes,” Virginia Institute for Psychiatric and Behavioral Genetics, Department of Pharmacology and Toxicology. Hosts: Dr. Kenneth Kendler and Dr. William Martin
06/27/05	“Progress on Using Mouse Inbred Strains, Consomics and Mutants to Identify Genes Related to Stress, Anxiety and Alcohol Phenotypes” RSA 28th Annual Meeting, Invited Speaker. Organizer: Kathleen Grant, Chair: Daniel Goldowitz
07/29/05	“WebQTL: Internet based genetic analysis from base-pair to behavior in inbred mice” University of Antwerp, Belgium. Hosts: Dr. Frank Kooy and Vanessa Errygers
10/24/05	“Systems Genetics: Building Gene to Phenotype Networks for Pain,” Wyeth Pharmaceuticals, Princeton, NJ. Host: Dr. Philip Jones
11/16/05	“Systems Genetics: Gene to phenotype networks in mouse reference populations” NCBI, Bethesda, MD. Host: Dr. Teresa Pryztych
11/18/05	“Fundamentals of Genomics in the Study of Pain” Special Session on Genomics and Pain, American Society of Regional Anesthesia and Pain Medicine Annual Fall Pain Meeting and Workshops, Miami, FL. Organizer and Chair: Dr. Sunil Panchal
02/15/06	“Gene to phenotype networks for brain and behavior” Gordon Research Conference on Genes and Behavior, Ventura, CA. Chairperson: Dr. Robert Hitzeman; Session Chairs: Dr. Tamara Phillips and Dr. Eric Schadt
03/27/06	“Extracting biological networks from basepair to behavior” Center for Alcohol Studies, University of North Carolina, NC. Host: Dr. Fulton Crews
06/27/06	“What can microarrays tell us about alcoholism that we don’t already know and how can we extract this information?” Research Society on Alcoholism, Workshop Organizer.
09/25/06	“Systems Genetics: the Systems Biology of Populations” University of Chicago Department of Genetics, Chicago, IL. Host: Justin Borevitz
09/29/06	“The Collaborative Cross at ORNL: Progress and Applications” Keynote Workshop on Complex Traits as Human Diseases, Oak Ridge National Laboratory, TN. Organizer: Dr. Brynn Voy
10/14/06	“Integrative bioinformatics for neurobehavioral genetics,” at “Meet the Experts,” Society for Neuroscience, Atlanta, GA.
11/28/06	“Systems Neurogenetics: Systems Biology of Populations for Brain and Behavior,” Neuroscience Program, University of Illinois-at Urbana Champaign, IL. Host: Justin Rhodes
12/07/06	“Rapid Compilation of Neurobiological Networks from Basepair to Behavior” American College of Neuropharmacology Annual Meeting, Hollywood, FL. Chairs: Dr. Adron Harris and Dr. Igor Ponomarov
01/26/07	“Interactions of the Laboratory Environment with Mouse Behavior” Appalachian Branch AALAS Winter Quarter Meeting, Knoxville, TN. Chair: Lee Barnett, Bionetics Corporation
02/19/07	“The collaborative cross at ORNL: a community resource for systems genetics” Gordon Research Conference in Quantitative Genetics and Genomics, Ventura, CA. Session Chairs: Dr. David Threadgill and Dr. Daniel Pomp
03/19/07	“Ontological Discovery from Genes to Behavior” Portland Alcohol Research Center, Oregon Health Sciences University, Portland Oregon. Host: Dr. Robert Hitzemann
03/21/07	“Systems Genetics, the systems biology of populations” Institute for Systems Biology, Seattle, WA. Host: Dr. David Galas
05/21/07	“Ontological Discovery from Genes to Behavior” Young Investigator Awardee Lecture, International Behavioral and Neurogenetics Society, Doorwerth, the Netherlands.
05/30/07	“The Collaborative Cross a reference population for the systems genetic analysis of addiction” NIH/NIDA Workshop on Addiction, Microarrays and Gene Discovery. Organizers: Dr. Jonathan Pollock and Dr. John Satterlee

06/15/07	"Using genetics and genomics to understand relations among anxiety-like behaviors and other traits" International Behavioral Neuroscience Society, Symposium. Organizer: Dr. Abraham Palmer
11/05/07	"1000 Mixed-up Mice: Behavioral Phenotyping in the Collaborative Cross—a large population of unprecedented genetic diversity," in speeding up behavioral testing of rodents and zebrafish: high-throughput solutions, challenges, and perspectives. Noldus Information Technology Satellite Symposium, Society for Neuroscience annual meeting 2007. Sponsoring SFN member: Dr. Robert Gerlai
06/03/08	"Comparison of linkage disequilibrium networks in genetic reference populations," Complex Trait Consortium Meeting, Montreal, QC.
06/08/09	"Multivariate genetic analysis for the functional genomics of behavior" International Behavioral and Neurogenetics Society, Dresden, Germany. Symposium Chair: Leo Schalkwyk
06/21/09	"Multidimensional trait assays for genetic prediction of alcohol addiction: Multidimensional analysis of mouse behavior for genetic analysis," RSA 32nd Annual Meeting, Symposium organizer, speaker. Chair: Daniel Goldowitz
05/05/09	"Extracting and validating gene-phenotype association networks using the ontological discovery environment" Complex Trait Consortium, Manchester UK.
04/23/10	"Identification of addiction related genes using integrative genetics and genomics" National Institute on Drug Abuse, Webinar.
05/13/10	"Behavior genetic analysis in the collaborative cross and related populations" International Behavioral and Neural Genetics Society, Halifax, Nova Scotia, Symposium Chair.
06/26/10	"A Computational System for Integrative Genomics," NIAAA Satellite Symposium: A Systems Biology Approach to Understanding the Effects of Alcohol on the Brain. San Antonio, TX.
07/08/10	"The Ontological Discovery Environment: Points to Consider When Populating and Using a Virtual Environment for the Application of High-Performance Computing to Discover Phenotypes Through Integrating Gene Sets Across Species, Tissue and Experimental Platform" NIDA Workshop: Informatics for Data and Resource Discovery, Rockville, MD.
10/04/10	"Discovering the organization of behavioral traits using integrative genetics and genomics" Children's Hospital Boston/Harvard Medical School. Host Dr. Clifford Woolf
11/12/10	"Systems genetics for identification of addiction-related genes using high-throughput behavioral phenotyping" NIDA Frontiers in Addiction Research Mini-Convention. Organizer: John Satterlee
11/18/10	"Integrative Genetics and Genomics for Pain Research" Amgen, Thousand Oaks, CA. Host: Sonya Lehto
12/03/10	"Discovering the organization of behavioral traits using integrative genetics and genomics" University of Maine Department of Psychology, Orono, ME, Host: Alan Rossenwasser
02/11/11	"OntologicalDiscovery.org: Building an interactive system for the integration of functional genomics data", University of Maine, Computer Science Department, Orono, ME Host: George Markowsky
05/19/11	"Target Identification Strategies in the Genomic Era" APS 30th Annual Meeting, Austin, TX. Organizer: Luda Diatchenko
06/28/11	"Integrative Genomics of Alcohol Use and Alcohol Response: Finding Convergent Evidence Across Species and Experimental Systems" RSA 34th Annual Meeting. Chairs: Mary-Anne Enoch and David Goldman
03/18/12	"Leveraging Different Genomes for Social Behavior" Gordon Research Seminar: Genes and Behavior, Galveston, TX, Discussant. Chairs: Zhengzheng S. Liang and Jesse N. Weber
03/30/12	"Accelerating discovery in behavioral genetics through integrative genetics and genomics." KBRIN Bioinformatics Summit 2012, Louisville, KY. Plenary Speaker.
09/09/12	"Cross Species Integrative Functional Genomics of Alcohol Related Behaviors in The Gene Weaver Web based Software System" in the "Neurogenomics of Alcoholism" 16th Congress of International Society for Biomedical Research on Alcoholism, Sapporo, Japan, Symposium Organizer and Speaker.
01/14/12	"Accelerating discovery for behavioral traits with integrative genetics and genomics" Department of Psychiatry, UConn Health Center. Host: Victor Hesselbrock
04/15/13	"High Precision Systems Genetic Analysis of Behavior in Advanced Mouse Populations" Human Genome Meeting and 21st International Congress on Genetics, Singapore, Invited speaker. Hosts: Edison T. Liu and Alfred Nordheim
05/29/13	"Genetics of Hippocampal Gene Expression in Diversity Outbred Mice" Complex Trait Consortium, Madison, WI.
11/02/13	"Integrative functional genomics using GeneWeaver.org" Maine Neuroscience Symposium, Colby College, ME, Keynote Speaker. Host: Allen Rosenwasser
11/23/13	"Cross-species integrative functional genomics of aging in the GeneWeaver web-based software system", Gerontological Society of America Meeting and Exposition, New Orleans LA.

11/25/13	"Advances in Discovery of Mouse Models for Genetics of Addiction" NIDA Genetics Consortium Meeting, Invited Guest. Host: Jonathan Pollock
12/12/13	"Conceptual comparison through integrative functional genomics in GeneWeaver.org" 11th Annual Rocky Mountain Bioinformatics Conference, Snowmass, CO, Invited Speaker. Chair: Lawrence Hunter
12/16/13	"Cross-species integrative functional genomics of alcoholism in GeneWeaver.org" Waggoner Center for Alcohol Studies, Austin TX. Host: Adron Harris
02/26/14	Integrative Genomics Strategies for the Cross-species Analysis and Classification of Psychiatric Disorders" "Research Education Program in Aspects of Statistical Genetics and Addiction Invited Speaker, Department of Psychiatry, Washington University St Louis. Host: Pamela Madden
02/28/14	"Integrative Genomics Strategies for the Cross-species Analysis and Classification of Psychiatric Disorders" Anatomy and Neurobiology Department, University of Tennessee Health Science Center. Host: Robert W. Williams
05/13/14	"Workshop on the Use of Advanced Mouse Populations" International Behavioral and Neurogenetics Society, Workshop Chair.
05/21/14	"Bioinformatics Strategies to Address GXE in the Study of Behavior" NIH Office of Behavioral and Social Sciences Research Workshop on Challenges in Replication of GXE, Workshop Speaker.
06/03/14	"Mouse Genetic Technologies" NIDA Genetics Consortium Meeting, Rockville, MD, Invited Speaker. Host: Jonathan Pollock
09/08/14	"Perspectives on Data Integration" Symposium on Data Integration from the Monkey Model of Alcohol Drinking, Oregon Health & Science University. Host: Kathy Grant
10/02/14	"Integrative Genetic and Genomic Strategies for the Classification of Psychiatric Disorders" Behavioral Neuroscience Seminar, University of Connecticut, Department of Psychology. Host: Ian Stevenson
01/05/15	"Beyond Replication and Reproducibility: Finding Consilience in Genetic and Genomic Analyses of Behavior" Workshop on Replicability and Reproducibility, Tel Aviv University. Host: Yoav Benjamini
01/23/15	"Integrative Genetics and Genomic Strategies for the Classification of Psychiatric Disorders" Transdisciplinary Training Program in Addiction Studies, Department of Pharmacology, Boston University. Host: Camron Bryant
02/23/15	"Improving the classification of psychiatric disorders through genetics and genomics" Research Center for Group Dynamics, University of Michigan, Ann Arbor, MI. Host: Richard Gonzalez
03/18/15	"Harnessing Diversity in the CC and DO Populations for the Study of Behavior NIEHS Population-Based Rodent Resources for Environmental Health Sciences Meeting, Invited Speaker.
04/17/15	"Genetic and Genomic Studies of Addiction in Model Organisms" Maine Medical Professionals Health Program Professionals Conference, Invited Speaker. Hosts: Mike Sloan, DDS, Cathryn Stratton.
05/14/15	"Integrative Genetic and Genomic Studies of Psychiatric Disorders in Model Organisms" University of Connecticut Health Center Medical Grand Rounds. Host: Steven Angus
06/18/15	"Behavioral Predictors of drug self-administration in diversity outbred mice" College on Problems of Drug Dependence Annual Meeting, Phoenix, AZ, Symposium Speaker. Chair: David Jentsch
06/24/15	"Computational Genomics" Frontline Genomics Festival of Genomics, Boston, MA, Panelist. Festival Director: James Bell
09/10/15	"Finding Cross-Species Phenomic Similarity Through Integration of Heterogeneous Functional Genomic Data", NIH Office of the Director Symposium on Linking Disease Model Phenotypes to Human Conditions, Invited speaker. Host: Oleg Mirochnitchenko
11/03/15	"Integrative Genetics and Genomic Strategies for the Classification of Psychiatric Disorders and Model Organism Phenotypes" Pharmacology and Systems Therapeutics Seminar Lecture ICAHN Mount Sinai School of Medicine, New York, New York. Host: Paul Kenny
11/11/15	Workshop on Gene Enrichment Analysis. International Mouse Genome Consortium, Yokohama, Japan. Co-organizer with Dr. Judith A. Blake.
01/04/16	"GeneWeaver: Finding relations among genes, phenotypes and diseases from heterogeneous functional genomics data" Pacific Symposium on Biocomputing, Big Island of Hawaii. Invited Speaker. Innovative approaches to combining genotype, phenotype, epigenetic and exposure data from precision diagnostics Session. Organizers: Melissa Haendel and Maricel Kann.
03/07/16	"Refining classification and characterization of behavior with integrative genetics and genomics" Bioinformatics Seminar Series. University of California-Los Angeles. Host: Eleazar Eskin, Wei Wang
06/26/16	"Integrating the Epigenome with Functional Genomic Studies of Alcoholism and Addiction" Research Society on Alcoholism New Orleans, LA, Symposium Speaker. Chair: Igor Ponomarev
06/27/16	"Integrating Heterogeneous Functional Genomics Studies of Alcoholism" Research Society on Alcoholism, New Orleans, LA Symposium Chair.

07/12/16	“GeneWeaver”, Technology Track, Intelligent Systems in Molecular Biology, Orlando FL.
12/05/16	University of Tennessee Health Science Center, Memphis, TN. Host: Robert W. Williams
03/16/17	“Integration of heterogeneous functional genomics data in GeneWeaver with applications in toxicology” in “Bioinformatics Tools for Accelerated Hypothesis Generation and Mechanistic Insights” Society of Toxicology, Baltimore, MD. Chairs: Susan Bello, Marc Gillespie
05/05/17	“Genetic and Genomic Studies in Addiction” Maine Medical Association, Medical Professionals Health Program, Portland, ME
05/17/17	“Advances in Bioinformatics resources for brain and behavior” Symposium Chair, IBANGS, Madrid, Spain
06/16/17	GeneWeaver Workshop. Complex Trait Consortium Meeting, Memphis, TN.
06/24/17	“The use of Model Organisms to Understand Human Genetics of Alcoholism” Research Society on Alcoholism, Denver, CO Symposium Chair and Discussant.
08/04/17	The Jackson Laboratory, Neuroscience Meets 3D Genome Biology Mini Symposium, “Integrative Genetics and Genomics of Alcohol Use Disorder Related Traits Reveals Functional Variation in the 3D Genome” organizer, Dr. Yijun Ruan
10/11/17	GeneWeaver. Protein Ontology Consortium Meeting, Bar Harbor ME Organizer: Barry Smith
10/19/17	“Understanding Behavioral Diversity Through Integrative Genetics and Genomics" John Belknap Memorial Symposium Plenary talk, Portland OR. Organizer: Dr. John C. Crabbe
12/01/17	“Understanding Behavioral Diversity through Integrative Genetics and Genomics” University of Tennessee Health Science Center, Memphis, TN. Host: Byron C. Jones
01/08/18	“Strategies to integrate developmental behavioral and genetic data”. NIDA Genetics Consortium Meeting, Bethesda, MD.
01/10/18	“Advanced Mouse Resources: The DO and CC” NIDA Genetics Animal Models Consortium Meeting, Bethesda, MD
03/12/18	“Integrative Genetic and Genomic Analysis of Addiction Related Behaviors” Icahn School of Medicine at Mount Sinai, New York, NY. Host: Dr. Eric Nestler
05/21/18	“Integrative Genomics Workshop” IBANGS, Rochester, Minnesota.
06/16/18	“Characterizing regulatory variants in humans and animals using GeneWeaver” NIDA Genetics Consortium Meeting. Coordinating Efforts Between Human and Animal Opioid Studies. Speaker
06/17/18	“Finding convergent behavioral features of Alcohol Use Disorder through functional genomic comparison across species” in “Data integration for characterization, prediction and treatment of alcohol use disorders, Speaker, Symposium Chair, Research Society on Alcoholism, San Diego, California
06/29/18	“Assessing replicability of mouse behavioral genetic studies through aggregated experimental results” in “Factors influencing replicability of behavioral neuroscience studies.” International Behavioral Neuroscience Society, Boca Raton, FL. Symposium Chairs: Drs. Polymnia Georgiou & Todd Gould
07/12/18	“Cross-species functional genomic data integration with GeneWeaver”, IMPC Data Analysis Working Group, London, UK.
08/07/18	“Personal Genetics and Addiction.” Jesup Memorial Library, Bar Harbor, ME
09/10/18	The Opioid Crisis Session Chair Genetics of Neuropathic Pain and its Comorbidities, Program Committee, IASP Genetics &Pain SIG and Neuropathic Pain SIG Joint meeting, Bar Harbor, ME
11/07/18	“Integrative Genetics and Genomics of Addiction and Predisposing Traits” Translational Research Day 2018: Addiction Research in the Lab, Clinic and Community, Speaker, Tufts CTSI, Boston, MA.
12/20/18	Seminar Speaker, Fujita Health University, Toyoake, Aichi, Host: Tsuyoshi Miyakawa
12/21/18	“Finding relations among genes, brain and behavior in heterogeneous functional genomics data” 6th INCF Japan Node International Workshop Advances in Neuroinformatics (AINI 2018) Keynote Speaker, RIKEN, Wako, Japan
02/18/19	“Finding relations among genes, brain and behavior with heterogeneous functional genomics” Institute for Behavioral Genetics, University of Colorado, Boulder, CO. Host: Marissa Ehringer
04/26/19	“Genetics of Addiction and the Opioid Crisis” 46th Maine Biological and Medical Sciences Symposium, MDI Biological Laboratory, Bar Harbor, ME, Symposium Chair: Karen Houseknecht.
	Panelist, NHGRI “Genetic Modifiers of Phenotype” Webinar and Discussion
01/13/20	“Interpreting human genetics of SUD using multi-species heterogeneous functional genomics data,” NIDA Genetics and Epigenetics Cross-Cutting Research Team Meeting; Rockville, MD
10/23/20	“Introduction to GeneWeaver: Integrating and analyzing heterogeneous function genomics data” Omics Portal for Addiction Research Webinar Series; Host: Laura Saba.
09/2021	“Network based prioritization of human GWAS candidates for Schizophrenia using IMPC behavioral phenotypes” International Mouse Phenotyping Consortium 10th Anniversary Symposium

12/2021	Panelist, NIDA/NSF workshop “Training in Computer and Addiction Science: Bringing Fields Together”
12/02/2021	NIDA workshop: “How can we leverage AI/ML, and omics data to better understand the genetics of addiction?”
12/09/2021	Congressional Staff Briefing “Genetics of Addiction: What can we learn from laboratory mice?”
01/28/2021	“Integrative Genetics and Genomics of Predisposing Addiction Risk” NIDA Science Friday Webinar.
03/17/2021	“Prioritization of human GWAS candidates for schizophrenia”, International Mouse Phenotyping Consortium Workshop on the Translational Value of Mouse Models in CNS Diseases”
05/25/2022	“What have you done for me lately? Integrative genetics and genomics for the study of human behavior.” Distinguished Scientist Award Talk. International Behavioral and Neural Genetics Society, Memphis, TN.
06/26/2022	“Understanding and characterizing alcohol related variation through cross-species genetic and genomic data integration” Research Society on Alcoholism, Symposium Speaker. Orlando, FL. Chair Dr. Jason Bubier
07/20/2023	“The state of addiction research in Maine” Governor Mills Annual Opioid Response Summit
06/19/2024	“NIDA Research Center of Excellence Grants: How these collaborative Centers Contribute to the Understanding and Treatment of Substance Use Disorders” College on Problems of Drug Dependence 86th Annual Scientific Meeting, Symposium Speaker. Montreal, Canada Chair Dr. Kevin Freeman

Extramural Research Support:

Active:

5 P50 DA039841 Chesler (PI) 08/15/16-06/30/27
NIH/NIDA
Center for Systems Neurogenetics of Addiction

The goal of this Center is to assess the impact of multiple, highly relevant behavioral and biological predictors of addiction using a deeply characterized mouse population. Collaborative research projects are supported by three research cores characterize the behavioral, genetic, and genomic basis of predisposition to psychostimulant abuse. Pilot projects and outreach activities support opportunities for trainees and investigators to gain access to systems genetics tools, resources, and methods in the study of the genetics of addiction.

Role: Principal Investigator

5 R01 DA037927 Chesler (PI) 04/01/15-05/31/26
NIH/NIDA
Discovery of Addiction Related Genes with Advanced Mouse Resources

The goal of this project is to identify biological mechanisms of addiction and predisposing novelty-seeking behavior by harnessing recent advances in mouse genetic resources, including the high precision Diversity Outbred (DO) mouse population, validation in genetically modified mice, gene expression quantitation through RNA sequence analysis, and computational and statistical method development in systems genetics. Previously we developed a canonical correlation strategy for combining behavioral and neurogenomic data through a common set of behavioral observations in a large population. In this renewal we are simultaneously evaluating multiple tissues and deconvolving bulk transcriptomics using founder single-cell data using novel extensions of the PMCA method.

Role: Principal Investigator

5 R25 DA051342 Berwin, Chesler (PI) 05/01/21-3/31/2026
NIH/NIDA
Growing the Genetics of Addiction Workforce with URM Faculty-Student Research Experiences

The goal of this project is to provide a unique research and training experience designed to encourage and assist members of groups that are under-represented in the biomedical and behavioral sciences to pursue or advance research or science-related careers in addiction related areas.

Role: PD/Principal Investigator

5 R13 DA052199 Chesler (PI) 07/01/20-06/30/25
NIH/NIDA
Short Course on Genetics of Addiction

In alignment with one of the missions of The Jackson Laboratory, the goal of this program is to provide training and educational opportunities in genetics, genomics, and systems biology to both students and professional scientists.

Role: Principal Investigator

5 R01 DA028420 Bogue (PI) 04/01/20-02/28/25
NIH/NIDA
Mouse Phenome Project
The goal of the Mouse Phenome Project is to support biomedical research by delivering a widely accessed and highly functional data repository for well-documented disease relevant phenotypic data from heterogeneous mouse populations along with a growing suite of analytics for integrative genetic analysis.
Role: Co-Investigator

5 P50DA054071 Johnson (PI) 09/15/22-5/31/27
NIH/NIDA
Integrative Omics Center for Accelerating Neurobiological Understanding of Opioid Addiction (ICAN)
The goal of this program is to integrate human genetic studies of opioid addiction across multiple omics and other modalities, and to extend and apply cross-species analysis methods to identify and prioritize relevant model organisms.
Role: Project MPI
5 U54OD030187 Lutz, Murray (PIs) 9/1/2020 - 8/31/2025NIH/ORIPThe Jackson Laboratory Center for Precision Genetics Bioinformatics Core The Bioinformatics Core will develop, implement, disseminate, apply, and validate data-driven approaches to the refinement of mouse models through the computational integration of genetic and phenotypic heterogeneity. Role: Core Lead

Completed:

5 UM1 OD02322-07 Braun/Murray/Svenson (PI) 8/2/16-7/31/22
NIH/NHGRI
The Jackson Laboratory KOMP2 Phenotyping Center
The specific goal of this project is to expand the JAX KOMP2 Center to produce and phenotype 1,500 novel lines of knockout mice on an isogenic C57BL/6N background, and to share these animal resources and data with the scientific community.
Role: Co-Investigator

5 R01DA045401 Bogue (PI) 07/01/15-04/30/20
NIH/NIDA
CRCNS: Computational Approach to Assess Replicability of Neurobehavior Phenotypes
This collaborative project with Dr. Yoav Benjamini integrates replicability analysis into the Mouse Phenome Database.
Role: Co-Investigator

1 U54 OD020351 Burgess (PI) 8/15/15-6/30/21
The Jackson Laboratory Center for Precision Genetics: From New Models to Novel Therapeutics.
The goal of the Center is to develop and disseminate new, precise animal models of incurable and genetically complex human diseases. Each of the center's projects address intractable or incurable diseases linked by genetic complexity, molecular genetic data and/or "humanization" that represent diverse stages of preclinical development. The JCPG will: Aim 1) Align investigator-initiated disease model research projects with institution-wide support to create efficient and goal-oriented preclinical pipelines; Aim 2) Use heuristic program development in the pilot center research projects and cores to position JAX to be a fully functional center in five years, while nevertheless achieving tangible outcomes during the pilot period; Aim 3) Embrace both realistic, cutting-edge technological platforms and ambitious high-risk, high-reward platforms as required to advance paths to therapies for heretofore incurable diseases; and Aim 4) Through JAX's many inter-institutional collaborations, identify and engage key clinical, foundation and corporate partners, who share its vision both for specific disease objectives, to help navigate larger center goals. Ultimately, the JCPG will generate new disease modeling processes and pipelines, data resources, research results and models that will be swiftly shared through JAX's proven dissemination pipelines to accelerate translation to medical benefit. Dr. Chesler is a member of the bioinformatics core, led by Dr. Judith A. Blake, which serves the center's projects through data analysis, integration and dissemination for the discovery and characterization of these models.
Role: Co-Investigator

5 R01 AA018776 Chesler (PI) 9/25/10-6/30/20

NIH/NIAAA

Data Structures, Algorithms and Tools for Ontological Discovery

The aims of this project are: 1) to develop a large data repository for behavioral neuroscience and data structures that more efficiently enable the use of databases to represent graphical network data; 2) to develop algorithms for the analysis of integrated gene centered data across species and experimental platforms to incorporate these developments into a Web-based software system; and 3) to use this tool to find genes underlying relationships between multiple abused substances and behavior.

Role: Principal Investigator

5 R01 DA028420-13 Bogue (PI) 07/01/15-04/30/20

NIH/NIDA

Mouse Phenome Project

The Mouse Phenome Database (MPD; phenome.jax.org) is a repository of expertly curated, highly integrated, and diverse mouse phenotype data, including significant amounts of data relevant to alcoholism, addiction, neurobehavioral processes, and other physiological domains. Goals for this cycle are to upgrade the MPD system and acquire new data and data types; incorporate evolving technologies for archiving, integrating, and analyzing data; expand activities that promote data reproducibility within and across resources; and ensure interoperability of MPD with other public databases.

Role: Co-Investigator

ANON-FY16-EJC Chesler (PI) 04/29/16-05/31/18

Anonymous (Industry)

GeneWeaver, Web-based system for integrative functional genomics

This collaborative research agreement enables the enhancement of the public release of GeneWeaver functionality in a manner that also meets specific needs for industry application.

Role: Principal Investigator

2 R13 DA032192 Chesler (PI) 7/1/11-6/30/20

NIH/NIDA

Workshop on the Genetics of Addiction

The goal of the annual workshop on the Genetics of Addiction proposed in this application is to provide students an opportunity to learn about genetic applications and approaches to drug addiction research.

Role: Principal Investigator

1 U54 HG006332-01 Braun/Svenson (PI) 9/16/11-7/31/16

NIH/NHGRI

The Jackson Laboratory KOMP2 Phenotyping Center

The Knockout Mouse Phenotyping Program (KOMP2) seeks to build a phenotype resource summarizing the function of 20,000 genes in the mouse and to ultimately create a resource for understanding gene function in humans. The Jackson Laboratory will contribute to this goal by efficiently generating and sharing functional data for 833 mouse genes and will enhance the value of these data by linking them with current genetic and biological knowledge, enabling the scientific community to discover the roles of these genes in human health and disease. A supplement to this funding validates addiction predictions from baseline phenotyping.

Role: Co-Investigator

5 P30 AG038070-02 Churchill (PI) 8/15/10-6/30/15

NIH/NIA

Shock Center for Aging Research at The Jackson Laboratory - Core 4: Healthspan Core

The Healthspan Core will: a) provide affordable phenotyping of aging mice by a variety of techniques using defined protocols; b) provide genotypic data for these resources to allow researchers to map genetic and phenotypic associations with aging in the mouse; and c) collect and store valuable tissues from CC strains for distribution to internal and external researchers for further pathology and biochemical studies.

Role: Core Leader

5 R01 DA021198-05 Chesler (PI) 8/1/09-7/31/12

NIH/NIDA

Genetics of Neuropathic and Inflammatory Hypersensitivity

The goal of this project is to determine novel genetic mechanisms of chronic neuropathic and inflammatory pain for predisposition assessment and treatment development. Dr. Chesler's role is to provide bioinformatics support to the project.

Role: Consortium PI

5 U01 AA016662-05 Miles (PI) 2/1/10-1/31/12

NIH/NIAAA

INIA-Stress: Information and Analysis Core

This project focuses on statistical analysis and web tools for data integration across methodologically diverse alcoholism research. This funding primary supports alcoholism specific application and database population for the ODE project.

Role: Consortium PI

5 P50 GM076468-05 Churchill (PI) 4/1/06-3/31/12

NIH/NIGMS

Genome Dynamics: Evolution, Organization and Function - Core 2 Subproject 2 (Chesler)

The goal of this subproject is to develop methods of extracting genotype and genetic map information from RNA-seq data for systems genetic analyses from a single source of molecular data in complex populations.

Role: Co-Core Leader

2 P50 GM076468-06 Churchill (PI) 7/15/11-6/30/16

NIH/NIGMS

Center for Genome Dynamics - Project E: Data Driven Systems Genetics Workflow for New Experimental Platforms

The goal of this project is the development and application of high throughput RNA sequencing technology (HTPS) as the sole source of transcription and polymorphism data for an expression QTL experiment.

Role: Co-Project Leader

1 R13 DA030036-01 Chesler (PI) 7/1/10-6/30/11

NIH/NIDA

Genetics of Drug Addiction

The short course on the Genetics of Addiction proposed in this application will provide students with an opportunity to learn about genetic applications and approaches to drug addiction research.

Role: Principal Investigator

7 U01 AA016669-04 Chesler (PI) 11/25/10-1/31/11

NIH/NIAAA

Ontological Discovery for Ethanol Research (INIA Project)

This funding supports development of a web-based software system for integration of ethanol related gene sets and develops methods to analyze the sets and their relationship to behavior using graph algorithms. This funding specifically supports the database and tool development.

Role: Principal Investigator

DOE ERKP 804 (Chesler) 10/1/06 – 9/30/09

DOE/Office of Science

Mouse Genetics and Mutagenesis for Functional Genomics

This funding provided the majority of the support for the develop and characterization of the Collaborative Cross reference population and included support for the genotyping and gene expression lab, behavioral, physiological, and morphological phenotyping labs, bioinformatics and biostatistics, breeding operations and Mouse Genetics Research Facility in the Systems Genetics Group at ORNL. External advisors: David Galas, Lisa Stubbs, Rick Woychik, Rudi Balling, Miriam Meisler, Randy Blakely, David Threadgill, John E. French, Robert Ullrich.

Role: Principal Investigator

Ellison Medical Foundation (Chesler) 2/2/06 – 1/10/10

A Genetic Reference Panel for the Systematic Analysis of Lifetime Factors that Alter Lifespan and Quality of Life

This funding, initially issued to DK Johnson, supported initiation and breeding of 500 lines of the Collaborative Cross. Dr. Chesler served as PI of this project from 7/2006-7/2009.
Role: Principle Investigator

ORNL Laboratory Directors' Research and Development Fund (Chesler) 10/1/07 – 9/30/09
This funding supported genetic analysis of microbial-host interactions in the Collaborative Cross including high throughput sequencing of the gut microbiome using 454, genome wide transcriptional profiling of the surrounding mouse intestine and SNP genotypes in collaborative cross mice and their progenitor strains.
Role: Principle Investigator

NIH/NIDA, NIAAA 5R01DA020677 (Goldowitz) 7/1/06- 6/30/09
Gene to Phenotype Networks for Alcohol and Drug Addiction
This project supported the characterization of the newly expanded BXD Recombinant Inbred strain panel on over 250 behavioral phenotypes using the Tennessee Mouse Genome Consortium's behavioral phenotyping labs. Dr. Chesler conceived of the project, devised and implemented analysis tools and data management procedures, collected pain related phenotypes, and led the preparation of manuscripts.
Role: Co-Investigator

NIH/NIMH 5 U01 MH61971-05 (Goldowitz) 9/2/00 – 8/31/06
Targeted Mutagenesis of the Mouse Genome and Neural Phenotypes
This funding supports the production and phenotyping of potentially mutant mice to identify mutant mice that serve as models to study human disease.
Role: Collaborator and biostatistician

NIH/NIAAA 5 U01AA013512-05 (Grant/Chesler) 8/1/05 – 12/31/06
The Integrative Neurosciences Initiative on Alcoholism (INIA): Informatics
This funding supports the statistical analysis and design of web tools for creation of data integration across methodologically diverse behavioral neuroscience research in the context of the INIA.
Role: Co-Investigator

NIH/NIAAA U01 AA13641-05 (Langston/Chesler) 1/1/06 – 12/31/06
Combinatorial Network Analysis of High Throughput Stress and Alcohol Data
INIA pilot project to apply the combinational algorithms to analysis of data related to stress and alcoholism.
Role: Pilot Principal Investigator

D06 -033 (Voy) 10/1/05 – 9/30/07
ORNL Laboratory Directed Research and Development Funds (LDRD)
A Model System for Analyzing Whole-body Toxicity of TICs, TIMs, and Chemical Warfare Agents
Impact of genetic diversity on response to toxic chemicals in mice.
This funding initially supported toxicology studies in the BXD Recombinant Inbred Strains and was redirected to the development of a genotyping array for the Collaborative Cross.
Role: Co-PI

S08-009 (Chesler) 10/1/07 – 9/30/08
ORNL Laboratory Directed Research and Systems Neurogenetics of Methyl Mercury Exposure
This project investigates the effects of genetic variability on the neurobehavioral and transcriptional response to an important environmental contaminant, Methyl Mercury.
Role: Principle Investigator

NIH/NICHD 1 R01 HD052472-05 (Hamre) 9/5/05 – 6/30/10
Mapping Cerebellar Development in Time and Space
This project examines developmental cerebella gene expression in mouse models including BXD RI lines. Dr. Chesler's lab provided time series analysis of mutant and BXD gene expression data through development and assisted in the design of databases and web resources for this project.
Role: Co-PI

ORNL Technology Transfer and Economic Development (TTED) Royalty Funds (Chesler) 5/15/06

Combination High Throughput Genotyping and Expression Analysis Equipment for Mammalian Systems Genetic Analysis

This equipment grant supported the purchase of an Illumina Infinium Beadstation for Dr. Chesler's group for gene expression genetics and genotyping of the Collaborative Cross using their custom designed genotyping array.

NIH/NCRR 5 U01 CA134240 (Threadgill) 9/30/07 – 9/29/12

Systems Genetics Resource Consortium

This funding supports the distribution of the collaborative cross lines for profiling. Originally developed as a P30 resource core at ORNL led by Dr. Chesler, this funding supported the provision of mice to UNC Chapel Hill for the Pre-CC proof of concept study.

NIAAA 1R01 AA014425-01A1 (Lu) 4/1/04 – 3/31/09

Genetic Analysis of Ethanol-mediated Stress Reduction

The major goal of this proposal is to extend transcriptome QTL mapping and trait association in RI strains to the hippocampus of the LXS mice under alcohol and stress exposure to test the role of shared genetic mediation of responses to both treatments. Dr. Chesler developed major aspects of this proposal and the methods used to execute the project.

Role: Co-Investigator

NSF IGERT (Peterson) 8/08-8/13

SCALE-IT:

This is a grant to develop a graduate program and curriculum in high-performance computing applications in the biological sciences including systems genetics.

Role: Co-Investigator

NOTES:

*Laboratory Director's Research and Development Funds are awarded annually on a competitive basis within the Oak Ridge National Laboratory. Applications are reviewed by a committee including external peer reviewers, lab scientific staff and management. Funding of up to $350,000 per year over a two-year period is awarded.

**ORNL Seed Money Funds are awarded on a competitive basis based on an internal review by Lab scientific staff.

***DOE funding is awarded via the Office of Biological and Environmental Research, Office of Science, US. Department of Energy, requiring annual peer reviewed Field Work Proposal. An external advisory board reviewed progress and directions on the Mouse Genetics Research Facility supported by these funds.

****ORNL Technology Transfer and Economic Development (TTED) Royalty Funds are awarded based on a competitive internal review by a committee consisting of the Director of Technology Transfer and Economic Development and three of the five Associate Lab Directors at ORNL.

Publications:

Review and Commentary:

1. Lariviere WR, **Chesler EJ**, Mogil JS. 2001. Transgenic studies of pain and analgesia: mutation or background genotype? *Journal of Pharmacology and Experimental Therapeutics*, 297:467-73.
2. **Chesler EJ**, Rodriguez-Zas SL, Mogil JS. 2001. In Silico Mapping of Mouse Quantitative Trait Loci. *Science*, 294:2423.
3. The Complex Trait Consortium: Flaherty L, Abiola O, Angel JM, Avner P, Bachmanov AA, Belknap JK, Bennett B, Blankenhorn EP, Blizard DA, Bolivar V, Brockmann GA, Buck KJ, Bureau J-F, Casley WL, **Chesler EJ,** Cheverud JM, Churchill GA, Cook M, Crabbe JC, Crusio WE, Darvasi A, de Haan G, Demant P, Doerge RW, Elliott RW, Farber CR, Flint J, Gershenfeld H, Gibson JP, Gu W, Himmelbauer H, Hitzemann R, Hsu H-C, Hunter K, Iraqi F, Jansen RC, Johnson, TE, Jones BC, Kempermann G, Lammert F, Lu L, Manly KF, Matthews DB, Medrano JF, Mehrabian M, Mittleman G, Mock BA, Mogil JS, Montagutelli X, Morahan G, Mountz JD, Nagase H, Nowakowski RS, O'Hara BF, Osadchuk AV, Paigen B, Palmer AA, Peirce JL, Pomp D, Rosemann M, Rosen GD, Schalkwyk L C, Seltzer Z, Settle S, Shimomura K, Shou S, Sikela JM, Siracusa LD, Spearow JL, Teuscher C, Threadgill DW, Toth LA, Toye AA, Vadasz C, Van Zant G,Wakeland E, Williams RW, Zhang H-G, Zou F. 2003. The nature and identification of quantitative trait loci: a community's view. *Nature Rev Genet*, 4(11):911-916.
4. Churchill GA, Airey DC, Allayee H, Angel JM, Attie AD, Beatty J, Beavis WD, Belknap JK, Bennett B, Berrettini W, Bleich A, Bogue M, Broman KW, Buck KJ, Buckler E, Burmeister M, **Chesler EJ,** Cheverud JM, Clapcote S, Cook MN, Cox RD, Crabbe JC, Crusio WE, Darvasi A, Deschepper CF, Doerge RW, Farber CR, Forejt J, Gaile D, Garlow SJ, Geiger H, Gershenfeld H, Gordon T, Gu J, Gu W, de Haan G, Hayes NL, Heller C, Himmelbauer H, Hitzemann R, Hunter K, Hsu HC, Iraqi FA, Ivandic B, Jacob HJ, Jansen RC, Jepsen KJ, Johnson DK, Johnson TE, Kempermann, G, Kendziorski C, Kotb M, Kooy RF, Llamas B, Lammert F, Lassalle JM, Lowenstein PR, Lu L, Lusis A, Manly KF, Marcucio R, Matthews D, Medrano JF, Miller DR, Mittleman G, Mock, BA, Mogil JS, Montagutelli X, Morahan G, Morris DG, Mott R, Nadeau JH, Nagase H, Nowakowski RS, O'Hara BF, Osadchuk AV, Page GP, Paigen B, Paigen K, Palmer AA, Pan HJ, Peltonen-Palotie L, Peirce J, Pomp D, Pravenec M, Prows DR, Qi Z, Reeves RH, Roder J, Rosen GD, Schadt EE, Schalkwyk LC, Seltzer Z, Shimomura K, Shou S, Sillanpaa MJ, Siracusa LD, Snoeck HW, Spearow JL, Svenson K, Tarantino LM, Threadgill D, Toth LA, Valdar W, de Villena, FP, Warden C, Whatley S, Williams RW, Wiltshire T, Yi N, Zhang D, Zhang M, Zou, F. 2004. Complex Trait Consortium. The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nat Genet*, 36:1133-1137.
5. Chesler **EJ,** Bystrykh L, de Haan G, Cooke MP, Su A, Manly KF, Williams RW. 2006. Reply to "Normalization procedures and detection of linkage signal in genetical-genomics experiments". Nat Genet 38(8):856-8.
6. **Chesler, EJ.** 2006. "Book Review: *Mutagenesis of the Mouse Genome*" M. Justice and M. Bedell, Eds. *Genes, Brain and Behavior*, 5(2): 207.
7. The Mouse Phenotype Database Integration Consortium: Hancock JM, Adams NC, Aidinis V, Blake A, Blake JA, Bogue M, Brown SDM, **Chesler E**, Davidson D, Duran C, Eppig JT, Gailus-Durner V, Gates H, Gkoutos GV, Greenaway S, Hrabe´ De Angelis M, Kollias, Leblanc GS, Lee K, Lengger C, Maier H, Mallon A-M, Masuya H, Melvin DG, Muller W, Parkinson H, Proctor G, Reuveni E, Schofield P, Shukla A, Smith C, Toyoda T, Vasseur L, Wakana S, Walling A, White J, Wood J, Zouberakis M. 2007. Integration of mouse phenome data resources. Mammalian Genome, 2007 Mar;18(3):157-63.
8. **Chesler EJ** (2013) Out of the bottleneck: The Diversity Outcross and Collaborative Cross Mouse populations in Behavioral Genetics Research. Invited Review Mammalian Genome Special Issue
9. Bubier JA, Phillips CA, Langston MA, Baker EJ, **Chesler EJ**. GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. Mamm Genome. 2015 Jun 20. PubMed PMID: 26092690.
10. Bogue MA, Churchill GA, **Chesler EJ**. Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. Mamm Genome. 2015 Oct;26(9-10):511-20.
11. Saul MC, Philip VM, Reinholdt LG, Center for Systems Neurogenetics of Addiction, **Chesler EJ**. High-Diversity Mouse Populations for Complex Traits. Trends Genet. 2019 May 24; pii: S0168-9525(19)30065-4. doi: 10.1016/j.tig.2019.04.003.

Research Papers:

1. **Chesler EJ,** Salamone JD. 1996. Effects of acute and repeated clozapine injections on cholinomimetic induced vacuous jaw movements. Pharmacol Biochem Behav 54(3):619-624.
2. Mogil JS, **Chesler EJ,** Wilson SG, Juraska JM, Sternberg WF. 2000. Sex differences in thermal nociception and morphine antinociception in rodents depend on genotype. Neurosci Biobehav Rev 24(3):375-389.
3. **Chesler EJ,** Juraska JM. 2000. Acute administration of estrogen and progesterone impairs the acquisition of the spatial morris water maze in ovariectomized rats. Horm Behav 38(4):234-242.

4. Wilson SG, **Chesler EJ,** Hain H, Rankin AJ, Schwarz JZ, Call SB, Murray MR, West EE, Teuscher C, Rodriguez-Zas S, Belknap JK, Mogil JS. 2002. Identification of quantitative trait loci for chemical/inflammatory nociception in mice. Pain 96(3):385-391.
5. **Chesler EJ,** Wilson SG, Lariviere WR, Rodriguez-Zas SL, Mogil JS. 2002. Influences of laboratory environment on behavior. Nat Neurosci 5(11):1101-1102.
6. **Chesler EJ,** Wilson SG, Lariviere WR, Rodriguez-Zas SL, Mogil JS. 2002. Identification and ranking of genetic and laboratory environment factors influencing a behavioral trait, thermal nociception, via computational analysis of a large data archive. Neurosci Biobehav Rev 26(8):907-923.
7. Wilson SG, Smith SB, **Chesler EJ,** Melton KA, Haas JJ, Mitton B, Strasburg K, Hubert L, Rodriguez-Zas SL, Mogil JS. 2003. The heritability of antinociception: common pharmacogenetic mediation of five neurochemically distinct analgesics. J Pharmacol Exp Ther 304(2):547-559.
8. Wilson SG, Bryant CD, Lariviere WR, Olsen MS, Giles BE, **Chesler EJ,** Mogil JS. 2003. The heritability of antinociception II: pharmacogenetic mediation of three over-the-counter analgesics in mice. J Pharmacol Exp Ther 305(2):755-764.
9. Mogil JS, Wilson SG, **Chesler EJ**, Rankin AL, Nemmani KV, Lariviere WR, Groce MK, Wallace MR, Kaplan L, Staud R, Ness TJ, Glover TL, Stankova M, Mayorov A, Hruby VJ, Grisel JE, Fillingim RB. 2003. The melanocortin-1 receptor gene mediates female-specific mechanisms of analgesia in mice and humans. Proc Natl Acad Sci USA 100(8):4867-4872. PMC153647
10. Peirce JL, **Chesler EJ**, Williams RW, Lu L. 2003. Genetic architecture of the mouse hippocampus: identification of gene loci with selective regional effects. Genes Brain Behav 2(4):238-252.
11. **Chesler EJ**, Wang J, Lu L, Qu Y, Manly KF, Williams RW. 2003. Genetic correlates of gene expression in recombinant inbred strains: a relational model system to explore neurobehavioral phenotypes. Neuroinformatics 1(4):343-357.
12. **Chesler EJ**, Ritchie J, Kokayeff A, Lariviere WR, Wilson SG, Mogil JS. 2003. Genotype-dependence of gabapentin and pregabalin sensitivity: the pharmacogenetic mediation of analgesia is specific to the type of pain being inhibited. Pain 106(3):325-335.
13. Sternberg WF, **Chesler EJ,** Wilson SG, Mogil JS. 2004. Acute progesterone can recruit sex-specific neurochemical mechanisms mediating swim stress-induced and kappa-opioid analgesia in mice. Horm Behav 46(4):467-473.
14. Kest B, Palmese CA, Juni A, **Chesler EJ**, Mogil JS. 2004. Mapping of a quantitative trait locus for morphine withdrawal severity. Mamm Genome 15(8):610-617.
15. **Chesler EJ**, Lu L, Wang J, Williams RW, Manly KF. 2004. WebQTL: rapid exploratory analysis of gene expression and genetic networks for brain and behavior. Nat Neurosci 7(5):485-486.
16. Mhyre TR, **Chesler EJ**, Thiruchelvam M, Lungu C, Cory-Slechta DA, Fry JD, Richfield EK. 2005. Heritability, correlations and in silico mapping of locomotor behavior and neurochemistry in inbred strains of mice. Genes Brain Behav 4(4):209-228.
17. Baldwin NE, **Chesler EJ**, Kirov S, Langston MA, Snoddy JR, Williams RW, Zhang B. 2005. Computational, integrative, and comparative methods for the elucidation of genetic coexpression networks. J Biomed Biotechnol (2)172-180. PMC1184052
18. Jablonski MM, Lu L, Wang X, **Chesler EJ**, Carps E, Qi S, Gu J, Williams RW. 2004. The ldis1 lens mutation in RIIIS/J mice maps to chromosome 8 near cadherin 1. Mol Vis 10:577-587.
19. Scott RE, White-Grindley E, Ruley HE, **Chesler EJ**, Williams RW. 2005. 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. J Cell Physiol 204(1):99-105.
20. Bystrykh L, Weersing E, Dontje B, Sutton S, Pletcher MT, Wiltshire T, Su AI, Vellenga E, Wang J, Manly KF, Lu L, **Chesler EJ**, Alberts R, Jansen RC, Williams RW, Cooke MP, de Haan G. 2005. Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. Nat Genet 37(3):225-232.
21. **Chesler EJ**, Lu L, Shou S, Qu Y, Gu J, Wang J, Hsu HC, Mountz JD, Baldwin NE, Langston MA, Threadgill DW, Manly KF, Williams RW. 2005. Complex trait analysis of gene expression uncovers polygenic and pleiotropic networks that modulate nervous system function. Nat Genet 37(3):233-242.
22. Carlborg O, De Koning DJ, Manly KF, **Chesler E**, Williams RW, Haley CS. 2005. Methodological aspects of the genetic dissection of gene expression. Bioinformatics 21(10):2383-2393.
23. Lariviere WR, **Chesler EJ**, Li Z, Shang GW, Chen YN, Yu YQ, Lu ZM, Chang Y, Luo C, Li KC, Chen J. 2005. Correlations between edema and the immediate and prolonged painful consequences of inflammation: therapeutic implications? Acta Physiologica Sinica 57(3):278-288.
24. Li H, Lu L, Manly KF, **Chesler EJ**, Bao L, Wang J, Zhou M, Williams RW, Cui Y. 2005. Inferring gene transcriptional modulatory relations: a genetical genomics approach. Hum Mol Genet 14(9):1119-1125.
25. Welton AR, **Chesler EJ**, Sturkie C, Jackson AU, Hirsch GN, Spindler KR. 2005. Identification of quantitative trait loci for susceptibility to mouse adenovirus type 1. J Virol 79(17):11517-11522. PMC1193630

26. Bennett B, Carosone-Link PJ, Lu L, **Chesler EJ**, Johnson TE. 2005. Genetics of body weight in the LXS recombinant inbred mouse strains. Mamm Genome 16(10):764-774.
27. Johnson DK, Rinchik EM, Moustaid-Moussa N, Miller DR, Williams RW, Michaud EJ, Jablonski MM, Elberger A, Hamre K, Smeyne R, **Chesler EJ**, Goldowitz D. 2005. Phenotype screening for genetically determined age-onset disorders and increased longevity in ENU-mutagenized mice. Age 27:75-90.
28. Mogil JS, Miermeister F, Seifert F, Strasburg K, Zimmermann K, Reinold H, Austin JS, Bernardini N, **Chesler EJ**, Hofmann HA, Hordo C, Messlinger K, Nemmani KV, Rankin AL, Ritchie J, Siegling A, Smith SB, Sotocinal S, Vater A, Lehto SG, Klussmann S, Quirion R, Michaelis M, Devor M, Reeh PW. 2005. Variable sensitivity to noxious heat is mediated by differential expression of the CGRP gene. Proc Natl Acad Sci USA 102(36):12938-12943. PMC1200271
29. Matthews DB, Bhave SV, Belknap JK, Brittingham C, **Chesler EJ**, Hitzemann RJ, Hoffmann PL, Lu L, McWeeney S, Miles MF, Tabakoff B, Williams RW. 2005. Complex genetics of interactions of alcohol and CNS function and behavior. Alcohol Clin Exp Res 29(9):1706-1719.
30. Vázquez-Chona FR, Khan AN, Chan CK, Moore AN, Dash PK, Hernandez MR, Lu L, **Chesler EJ**, Manly KF, Williams RW, Geisert EE Jr. 2005. Genetic networks controlling retinal injury. Mol Vis 11:958-970.
31. Kempermann G, **Chesler EJ**, Lu L, Williams RW, Gage FH. 2006. Natural variation and genetic covariance in adult hippocampal neurogenesis. Proc Natl Acad Sci USA 103(3):780-785. PMC1325968
32. Li H, Chen H, Bao L, Manly KF, **Chesler EJ**, Lu L, Wang J, Zhou M, Williams RW, Cui Y. 2006. Integrative genetic analysis of transcription modules: towards filling the gap between genetic loci and inherited traits. Hum Mol Genet 15(3):481-492.
33. Goldowitz D, Matthews DB, Hamre KM, Mittleman G, **Chesler EJ**, Becker HC, Lopez MF, Jones SR, Mathews TA, Miles MF, Kerns R, Grant KA. 2006. Progress in using mouse inbred strains, consomics, and mutants to identify genes related to stress, anxiety, and alcohol phenotypes. Alcohol Clin Exp Res 30(6):1066-1078.
34. Voy BH, Scharff JA, Perkins AD, Saxton AM, Borate B, **Chesler EJ**, Branstetter LK, Langston MA. 2006. Extracting gene networks for low-dose radiation using graph theoretical algorithms. PLos Comput Biol 2(7): e89. PMC1513268
35. Gatti D, Maki A, **Chesler EJ**, Kirova R, Kosyk O, Lu L, Manly KF, Williams RW, Perkins A, Langston MA, Threadgill DW, Rusyn I. 2007. Genome-level analysis of genetic regulation of liver gene expression networks. Hepatology 46(2):548-557.
36. Cook MN, Dunning JP, Wiley RG, **Chesler EJ**, Johnson DK, Miller DR, Goldowitz D. 2007. Neurobehavioral mutants identified in an ENU-mutagenesis project. Mamm Genome 18(8):559-572.
37. Rosen GD, **Chesler EJ**, Manly KF, Williams RW. 2007. An informatics approach to systems neurogenetics. Methods Mol Biol 401:287-303.
38. New J, Kendall W, Huang J, **Chesler EJ**. 2008. Dynamic visualization of coexpression in systems genetics data. IEEE Trans Vis Comput Graph 14(5):1081-1094.
39. Peirce JL, Broman KW, Lu L, **Chesler EJ**, Zhou G, Airey DC, Birmingham AE, Williams RW. 2008. Genome Reshuffling for Advanced Intercross Permutation (GRAIP): simulation and permutation for advanced intercross population analysis. PLoS One 3(4): e1977. PMC2295257
40. Matthews DB, **Chesler EJ**, Cook MN, Cockroft J, Philip VM, Goldowitz D. 2008. Genetic mapping of vocalization to a series of increasing acute footshocks using B6.A consomic and B6.D2 congenic mouse strains. Behav Genet 38(4):417-423. PMC2504763
41. **Chesler EJ**, Miller DR, Branstetter LR, Galloway LD, Jackson BL, Philip VM, Voy BH, Culiat CT, Threadgill DW, Williams RW, Churchill GA, Johnson DK, Manly KF. 2008. The Collaborative Cross at Oak Ridge National Laboratory: developing a powerful resource for systems genetics. Mamm Genome 19(6):382-389. PMC2745091
42. Baker EJ, Jay JJ, Philip VM, Zhang Y, Li Z, Kirova R, Langston MA, **Chesler EJ**. 2009. Ontological discovery environment: a system for integrating gene-phenotype associations. Genomics 94(6):377-387. PMC2783409
43. Borate BR, **Chesler EJ**, Langston MA, Saxton AM, Voy BH. 2009. Comparison of threshold selection methods for microarray gene co-expression matrices. BMC Res Notes 2:240. PMC2794870
44. Carneiro AM, Airey DC, Thompson B, Zhu CB, Lu L, **Chesler EJ**, Erikson KM, Blakely RD. 2009. Functional coding variation in recombinant inbred mouse lines reveals multiple serotonin transporter associated phenotypes. Proc Natl Acad Sci USA 106(6):2047-2052. PMC2632716
45. Saccone SF, Bierut LJ, **Chesler EJ**, Kalivas PW, Lerman C, Saccone NL, Uhl GR, Li CY, Philip VM, Edenberg HJ, Sherry ST, Feolo M, Moyzis RK, Rutter JL. 2009. Supplementing high-density SNP microarrays for additional coverage of disease-related genes: addiction as a paradigm. PLos One 4(4): e5225. PMC2668711
46. Song MJ, Lewis CK, Lance ER, **Chesler EJ**, Yordanova RK, Langston MA, Lodowski KH, Bergeson SE. 2009. Reconstructing generalized logical networks of transcriptional regulation in mouse brain from temporal gene expression data. EURASIP J Bioinform Syst Biol epub:545176. PMC3171431
47. **Chesler EJ**, Baker EJ. 2010. The importance of open-source integrative genomics to drug discovery. Curr Opin Drug Discov Devel 13(3):310-316.

48. Gatti DM, Zhao N, **Chesler EJ**, Bradford BU, Shabalin AA, Yordanova R, Lu L, Rusyn I. 2010. Sex specific Gene Expression in BXD Mouse Liver. Physiol Genomics Aug;42(3):456-468. PMC2929887
49. Lynch RM, Naswa S, Rogers GL Jr, Kania SA, Das S, **Chesler EJ**, Saxton AM, Langston MA, Voy BH. 2010. Identifying genetic loci and spleen gene coexpression networks underlying immunophenotypes in BXD recombinant inbred mice. Physiol Genomics 41:244-253.
50. Philip VM, Duvvuru S, Gomero B, Ansah TA, Blaha CD, Cook MN, Hamre KM, Lariviere WR, Matthews DB, Mittleman G, Goldowitz D, **Chesler EJ**. 2010. High-throughput behavioral phenotyping in the expanded panel of BXD recombinant inbred strains. Genes Brain Behav 9(2):129-159. PMC2855868
51. Spindler KR, Welton AR, Lim ES, Duvvuru S, Althaus IW, Imperiale JE, Daoud AI, **Chesler EJ**. 2010. The major locus for mouse adenovirus susceptibility maps to genes of the hematopoietic cell surface expressed Ly6 family. J Immunol 184(6):3055-3062. PMC2832721
52. Nair HK, Hain H, Quock RM, Philip VM, **Chesler EJ**, Belknap JK, Lariviere WR. Genomic loci and candidate genes underlying inflammatory nociception. Pain. 2011 Mar;152(3):599-606. doi: 10.1016/j.pain.2010.11.029. Epub 2010 Dec 30. PMID: 21195549
53. Dickson P, Rogers T, Lester D, Miller M, Matta S, **Chesler EJ**, Goldowitz D, Blaha C, Mittleman G. 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 Jun;215(4):631-42. doi: 10.1007/s00213-010-2159-2. Epub 2011 Jan 7. PMID: 21212937
54. Aylor DL, Valdar W, Foulds-MathesW, Buus RJ, Verdugo RA, Baric RS, Ferris MT, Frelinger JA, Heise M, Frieman MB, Gralinski LE, Bell TA, Didion JD, Hua K, Nehrenberg DL, Powell CL, Steigerwalt J, Yuying Xie1, Kelada SNP, Collins F, Yang IV , Schwartz DA, Branstetter LA, **Chesler EJ,** Miller DR, Spence J, Eric Yi Liu9, McMillan L, Sarkar A, Wang J, Wang W, Zhang Q, Broman KW, Korstanje R, Durrant C, Mott R, Iraqi1 FA, Pomp D, Threadgill D, Pardo-Manuel de Villena F, and Churchill GA. 2011. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. Genome Research 21(8):1213-1222. PMC3149489
55. Gelinas R, **Chesler EJ**, Vasconcelos D, Miller DR, Yuan Y, Wang K, Galas D. 2011. A genetic approach to the prediction of drug side effects: bleomycin induces concordant phenotypes in mice of the collaborative cross. Pharm Person Med 4:35-45.
56. Mathes WF, Aylor DL, Miller DR, Churchill GA, **Chesler EJ,** Pardo Manuel de Villena F, Threadgill DW, Pomp D. 2011. Architecture of energy balance traits in emerging lines of the Collaborative Cross. Am J Physiol Endocrinol Metab 300(6): E1124-1134. PMC3118585
57. Meehan TF, Carr CJ, Jay JJ, Bult CJ, **Chesler EJ,** Blake JA. 2011. Autism candidate genes via mouse phenomics. J Biomed Inform 44 Suppl 1:S5-11. PMC3263820
58. Philip VM, Sokoloff G, Ackert-Bicknell CL, Striz M, Branstetter L, Beckmann MA, Spence JS, Jackson BL, Galloway LD, Barker P, Wymore AM, Hunsicker PR, Durtschi DC, Shaw GS, Shinpock S, Manly KF, Miller DR, Donohue KD, Culiat CT, Churchill GA, Lariviere WR, Palmer AA, O'Hara BF, Voy BH, **Chesler EJ.** 2011. Genetic analysis in the Collaborative Cross breeding population. Genome Res 21(8):1223-1238. PMC3149490.
59. Baker EJ, Jay JJ, Bubier JA, Langston MA, **Chesler EJ.** 2011.GeneWeaver: a web-based system for integrative functional genomics. Nucleic Acids Res. 2012 Jan;40(Database issue):D1067-76. Epub 2011 Nov 12. PMC3245070
60. **Chesler EJ,** Plitt A, Fisher D, Hurd B, Lederle L, Bubier JA, Kiselycznk C, Holmes A. 2012. Quantitative trait loci for sensitivity to ethanol intoxication in a C57BL/6J x 129S1/SvImJ inbred mouse cross. Mamm Genome Feb 28. PMC3357470
61. Svenson KL, Gatti DM, Valdar W, Welsh CE, Cheng R, **Chesler EJ,** Palmer AA, McMillan L, Churchill GA. 2012. High-resolution genetic mapping using the mouse diversity outbred population. Genetics 190(2):437-447. PMC3276626
62. Collaborative Cross Consortium. 2012. The genome architecture of the collaborative cross mouse genetic reference population. Genetics 190(2):389-401. PMC3276630
63. Kelada SN, Aylor DL, Peck BCE, Ryan JF, Tavarez U, Buus RJ, Miller DR, **Chesler EJ,** Threadgill DW, Churchill GA, Pardo-Manuel de Villena F, Collins FS. 2012. Genetic analysis of hematological parameters in incipient lines of the Collaborative Cross. G3 (Bethesda) 2(2):157-165. PMC3284323
64. Bubier JJ, **Chesler EJ.** 2012. Accelerating discovery for complex neurological and behavioral disorders through systems genetics and integrative genomics in the laboratory mouse. Neurotherapeutics 9(2):338-348. PMC3325414
65. Campbell JH, Foster CM, Vishnivetskaya T, Campbell AG, Yang ZK, Wymore A, Palumbo AV, **Chesler EJ**, Podar M. Host genetic and environmental effects on mouse intestinal microbiota. ISME J. 2012 Nov;6(11):2033-44.
66. Jay JJ, Eblen JD, Zhang Y, Benson M, Perkins AD, Saxton AM, Voy BH, **Chesler EJ**, Langston MA. A systematic comparison of genome-scale clustering algorithms. BMC Bioinformatics. 2012 Jun 25;13 Suppl 10:S7. PMC3382433
67. Ha TJ, Swanson DJ, Kirova R, Yeung J, Choi K, Tong Y, **Chesler EJ**, Goldowitz D. Genome-wide microarray comparison reveals downstream genes of Pax6 in the developing mouse cerebellum. Eur J Neurosci. 2012 Oct;36(7):2888-98. PMC4189819

68. 69.Thaisz J, Tsaih SW, Feng M, Philip VM, Zhang Y, Yanas L, Sheehan S, Xu L, Miller DR, Paigen B, **Chesler EJ**, Churchill GA, Dipetrillo K. Genetic analysis of albuminuria in collaborative cross and multiple mouse intercross populations. Am J Physiol Renal Physiol. 2012 Oct;303(7):F972-81. PMC3469684
69. Parsons MJ, Grimm C, Paya-Cano JL, Fernandes C, Liu L, Philip VM, **Chesler EJ,** Nietfeld W, Lehrach H, Schalkwyk LC. Genetic variation in hippocampal microRNA expression differences in C57BL/6 J X DBA/2 J (BXD) recombinant inbred mouse strains. BMC Genomics. 2012 Sep 13;13:47671. PMC3496628
70. Dubose, CS, **Chesler EJ**, Goldowitz D, Hamre K. 2013. Use of the Expanded Panel of BXD Mice Narrow QTL Regions in Ethanol-Induced Locomotor Activation and Motor Incoordination. Alcohol Clin Exp Res, 37(1):170-83
71. Logan RW, Robledo RF, Recla JM, Philip VM, Bubier JA, Jay JJ, Harwood C, Wilcox T, Gatti DM, Bult CJ, Churchill GA, **Chesler EJ**. High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. Genes Brain Behav. 2013 Feb 21.
72. Liu EY, Morgan AP, **Chesler EJ**, Wang W, Churchill GA, Pardo-Manuel de Villena F. High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. Genetics. 2014 Feb 27.
73. Recla JM, Robledo RF, Gatti DM, Bult CJ, Churchill GA, **Chesler EJ**. Precise genetic mapping and integrative bioinformatics in Diversity Outbred Mice reveals Hydin as a novel pain gene. Mammalian Genome. 2014 Apr 5. PMC4032469.
74. Kelada SN, Carpenter DE, Aylor DL, Chines P, Rutledge H, **Chesler EJ**, Churchill GA, Pardo-Manuel de Villena F, Schwartz DA, Collins FS. Integrative Genetics of Allergic Inflammation in the Murine Lung. Am J Respir Cell Mol Biol. 2014.
75. Dickson PE, Ndukum J, Wilcox T, Clark J, Roy B, Zhang L, Li Y, Lin DT, **Chesler EJ**. Association of novelty-related behaviors and intravenous cocaine self-administration in Diversity Outbred mice. Psychopharmacology (Berl). 2014 Sep 20. [Epub ahead of print] PubMed PMID: 25238945.
76. Gatti DM, Svenson KL, Shabalin A, Wu LY, Valdar W, Simecek P, Goodwin N, Cheng R, Pomp D, Palmer A, **Chesler EJ,** Broman KW, Churchill GA. Quantitative trait locus mapping methods for diversity outbred mice. G3 (Bethesda). 2014 Sep 18;4(9):1623-33. doi: 10.1534/g3.114.013748. PubMed PMID: 25237114; PubMed Central PMCID: PMC4169154.
77. Munger SC, Raghupathy N, Choi K, Simons AK, Gatti DM, Hinerfeld DA, Svenson KL, Keller MP, Attie AD, Hibbs MA, Graber JH, **Chesler EJ**, Churchill GA. RNA-Seq alignment to individualized genomes improves transcript abundance estimates in multiparent populations. Genetics. 2014 Sep;198(1):59-73. doi: 10.1534/genetics.114.165886. PubMed PMID: 25236449; PubMed Central PMCID:PMC4174954.
78. Rutledge H, Aylor DL, Carpenter DE, Peck BC, Chines P, Ostrowski LE, **Chesler EJ,** Churchill GA, de Villena FP, Kelada SN. Genetic regulation of Zfp30, CXCL1, and neutrophilic inflammation in murine lung. Genetics. 2014 Oct;198(2):735-45. doi: 10.1534/genetics.114.168138. Epub 2014 Aug 11. PubMed PMID: 25114278; PubMed Central PMCID: PMC4196624.
79. Bubier JA, Jay JJ, Baker CL, Bergeson SE, Ohno H, Metten P, Crabbe JC, **Chesler EJ.** Identification of a QTL in Mus musculus for alcohol preference, withdrawal, and Ap3m2 expression using integrative functional genomics and precision genetics. Genetics. 2014 Aug;197(4):1377-93. doi: 10.1534/genetics.114.166165. Epub 2014 Jun 11. PubMed PMID: 24923803; PubMed Central PMCID: PMC4125407.
80. 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;11(2):e1004850. doi: 10.1371/journal.pgen.1004850. eCollection 2015 Feb. PubMed PMID: 25679959.
81. Padula AE, Griffin WC 3rd, Lopez MF, Nimitvilai S, McGuier NS, **Chesler EJ**, Miles MF, Williams RW, Randall PK, Woodward JJ, Becker HC, Mulholland PJ. KCNN genes That Encode Small-Conductance Ca(2+)-Activated K(+) Channels Influence Alcohol and Drug Addiction. Neuropsychopharmacology. 2015 Feb 9. doi: 10.1038/npp.2015.42. PubMed PMID: 25662840.
82. McGuier NS, Griffin WC 3rd, Gass JT, Padula AE, **Chesler EJ**, Mulholland PJ. Kv7 channels in the nucleus accumbens are altered by chronic drinking and are targets for reducing alcohol consumption. Addict Biol. 2016 Nov;21(6):1097-1112.
83. Dickson PE, McNaughton KA, Hou L, Anderson LC, Long KH, **Chesler EJ**. Sex and strain influence attribution of incentive salience to reward cues in mice. Behav Brain Res. 2015 Jun 20. pii: S0166-4328(15)30005-X. doi:10.1016/j.bbr.2015.05.039. PubMed PMID: 26102561.
84. 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;5(2):95-133. doi: 10.1002/9780470942390.mo140195. PubMed PMID: 26069080.
85. Karp NA, Meehan TF, Morgan H, Mason JC, Blake A, Kurbatova N, Smedley D, Jacobsen J, Mott RF, Iyer V, Matthews P, Melvin DG, Wells S, Flenniken AM, Masuya H, Wakana S, White JK, Lloyd KC, Reynolds CL, Paylor R,

West DB, Svenson KL, **Chesler EJ**, de Angelis MH, Tocchini-Valentini GP, Sorg T, Herault Y, Parkinson H, Mallon AM, Brown SD. Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biol. 2015 May 20;13(5):e1002151.

86. Rutledge H, Baran-Gale J, Pardo Manuel de Villena F, **Chesler EJ**, Churchill GA, Sethupathy P, Kelada S. Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population, BMC Genomics 2015 Aug 25;16:633.
87. Dickson PE, Miller MM, Calton MA, Bubier JA, Cook MN, Goldowitz D, **Chesler EJ**, Mittleman G. Systems genetics of intravenous cocaine self-administration in the BXD recombinant inbred mouse panel. Psychopharmacology (Berl). 2015 Nov 19.
88. Baker E, Bubier JA, Reynolds T, Langston MA, **Chesler EJ**. GeneWeaver: data driven alignment of cross-species genomics in biology and disease. Nucleic Acids Res. 2016 Jan 4;44(D1):D555-9.
89. Bubier JA, Wilcox TD, Jay JJ, Langston MA, Baker EJ, Chesler EJ. Cross-species integrative functional genomics in GeneWeaver reveals a role for Pafah1b1 in altered response to alcohol. Frontiers in Behavioral Neuroscience, 2016.
90. Putman AH, Wolen AR, Harenza JL, Yordanova RK, Webb BT, Chesler EJ, Miles MF. Identification of quantitative trait loci and candidate genes for an anxiolytic-like response to ethanol in BXD recombinant inbred strains. Genes Brain Behav. 2016 Apr;15(4):367-81.
91. **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;6(12):3893-3902. doi: 10.1534/g3.116.035527. PubMed PMID: 27694113; PubMed Central PMCID: PMC5144960.
92. Crusio WE, Dhawan E, **Chesler EJ,** Delprato A. Analysis of morphine responses in mice reveals a QTL on Chromosome 7. Version 2. F1000Res. 2016 Sep 2 [revised 2016 Jan 1];5:2156. PubMed PMID: 27746909; PubMed Central PMCID: PMC5043443.
93. Young EE, Bryant CD, Lee SE, Peng X, Cook B, Nair HK, Dreher KJ, Zhang X, Palmer AA, Chung JM, Mogil JS, **Chesler EJ**, Lariviere WR. Systems genetic and pharmacological analysis identifies candidate genes underlying mechanosensation in the von Frey test. Genes Brain Behav. 2016 Jul;15(6):604-15. doi:10.1111/gbb.12302. PubMed PMID: 27231153; PubMed Central PMCID: PMC4955286.
94. Bogue MA, Peters LL, Paigen B, Korstanje R, Yuan R, Ackert-Bicknell C, Grubb SC, Churchill GA, **Chesler EJ**. Accessing Data Resources in the Mouse Phenome Database for Genetic Analysis of Murine Life Span and Health Span. J Gerontol A Biol Sci Med Sci. 2016 Feb;71(2):170-7. doi: 10.1093/gerona/glu223. PubMed PMID: 25533306; PubMed Central PMCID: PMC4707687.
95. 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;33(6):1381-95. doi: 10.1093/molbev/msw036. PubMed PMID: 26882987; PubMed Central PMCID: PMC4868115.
96. Shorter JR, Odet F, Aylor DL, Pan W, Kao CY, Fu CP, Morgan AP, Greenstein S, Bell TA, Stevans AM, Feathers RW, Patel S, Cates SE, Shaw GD, Miller DR, **Chesler EJ**, McMillian L, O'Brien DA, Villena FP. Male Infertility Is Responsible for Nearly Half of the Extinction Observed in the Mouse Collaborative Cross. Genetics. 2017 Jun;206(2):557-572. doi: 10.1534/genetics.116.199596. PubMed PMID: 28592496; PubMed Central PMCID: PMC5499172.
97. Karp NA, Mason J, Beaudet AL, Benjamini Y, Bower L, Braun RE, Brown SDM, **Chesler EJ**, Dickinson ME, Flenniken AM, Fuchs H, Angelis MH, Gao X, Guo S, Greenaway S, Heller R, Herault Y, Justice MJ, Kurbatova N, Lelliott CJ, Lloyd KCK, Mallon AM, Mank JE, Masuya H, McKerlie C, Meehan TF, Mott RF, Murray SA, Parkinson H, Ramirez-Solis R, Santos L, Seavitt JR, Smedley D, Sorg T, Speak AO, Steel KP, Svenson KL; International Mouse Phenotyping Consortium, Wakana S, West D, Wells S, Westerberg H, Yaacoby S, White JK. Prevalence of sexual dimorphism in mammalian phenotypic traits. Nat Commun. 2017 Jun 26;8:15475. doi: 10.1038/ncomms15475. Pubmed PMID:28650954
98. Delprato A, Algéo MP, Bonheur B, Bubier JA, Lu L, Williams RW, **Chesler EJ**, Crusio WE. QTL and systems genetics analysis of mouse grooming and behavioral responses to novelty in an open field. Genes Brain Behav. 2017 Nov;16(8):790-799. doi: 10.1111/gbb.12392. Epub 2017 Jun 22. PubMed PMID: 28544613.
99. Bogue MA, Grubb SC, Walton DO, Philip VM, Kolishovski G, Stearns T, Dunn MH, Skelly DA, Kadakkuzha B, TeHennepe G, Kunde-Ramamoorthy G, **Chesler EJ**. Mouse Phenome Database: an integrative database and analysis suite for curated empirical phenotype data from laboratory mice. Nucleic Acids Res. 2018 Jan 4;46(D1):D843-D850. doi: 10.1093/nar/gkx1082. PubMed PMID: 29136208; PubMed Central PMCID: PMC5753241.
100. Gunduz-Cinar O, Brockway E, Lederle L, Wilcox T, Halladay LR, Ding Y, Oh H, Busch EF, Kaugars K, Flynn S, Limoges A, Bukalo O, MacPherson KP, Masneuf S, Pinard C, Sibille E, **Chesler EJ**, Holmes A. Identification of a novel

gene regulating amygdala-mediated fear extinction. Mol Psychiatry. 2018 Jan 8. doi: 10.1038/s41380-017-0003-3. [Epub ahead of print] PubMed PMID: 29311651.

101. Kafkafi N, Agassi J, **Chesler EJ**, Crabbe JC, Crusio WE, Eilam D, Gerlai R, Golani I, Gomez-Marin A, Heller R, Fuad Iraqi F, Jaljuli I, Karp NA, Morgan H, Nicholson G, Pfaff DW, Richter SH, Stark PB, Stiedl O, Stodden V, Tarantino LM, Tucci V, Valdar W, Williams RW, Würbel H, Benjamini Y. Reproducibility and replicability of rodent phenotyping in preclinical studies. Neurosci Biobehav Rev 2018 Apr;87:218-232. doi: 10.1016/j.neubiorev.2018.01.003. Epub 2018 Jan 31. Review. PubMed PMID: 29357292; PubMed Central PMCID: PMC6071910.
102. Cobos EJ, Nickerson C, Gao F, Chandran V, Bravo-Caparro´ I, lez-Cano RG, Riva P, Andrews N, Latremoliere A, Seehus C, Perazzoli G, Nieto FR, Joller N, Painter M, Ma CHE, Omura T, **Chesler EJ**, Geschwind DH, Giovanni Coppola G, Rangachari M, Woolf CJ and Costigan M. Mechanistic Differences in Neuropathic Pain Modalities Revealed by Correlating Behavior with Global Expression Profiling. Cell Rep. 2018 Jan 30;22(5):1301-1312. doi: 10.1016/j.celrep.2018.01.006. PubMed PMID: 29386116; PubMed Central PMCID: PMC5908229.
103. Dickson PE, Roy TA, McNaughton KA, Wilcox TD, Kumar P, **Chesler EJ.** Systems genetics of sensation seeking. Genes Brain Behav. 2018 Sep 17:e12519. doi: 10.1111/gbb.12519. [Epub ahead of print] PubMed PMID: 30221471
104. Yuan JT, Gatti DM, Philip VM, Kasparek S, Kreuzman AM, Mansky B, Sharif K, Taterra D, Taylor WM, Thomas M, Ward JO, Holmes A, **Chesler EJ**, Parker CC. Genome-wide association for testis weight in the diversity outbred mouse population. Mamm Genome. 2018 Jun;29(5-6):310-324. doi:10.1007/s00335-018-9745-8. Epub 2018 Apr 24. PubMed PMID: 29691636.
105. Tuttle AH, Philip VM, **Chesler EJ**, Mogil JS. Comparing phenotypic variation between inbred and outbred mice. Nat Methods. 2018 Dec;15(12):994-996. PubMed PMID: 3050487
106. Phillips C, Wang K, Baker, EJ, Bubier JA, **Chesler EJ,** Langston MA. On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. Algorithms, 2019.
107. Goodwin LO, Splinter E, Davis TL, 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, Murray SA. Large-scale discovery of mouse transgenic integration sites reveals frequent structural variation and insertional mutagenesis. Genome Res.2019 Jan 18. pii: gr.233866.117. doi: 10.1101/gr.233866.117. PubMed PMID: 30659012
108. Bubier J, Hill D, Mukherjee G., Reynolds, T, Baker EJ, Berger A, Emerson J, Blake J, **Chesler EJ**. Curating Gene Sets: Challenges and Opportunities for Integrative Analysis. Database, 2019 Jan 1. pii: baz036. doi: 10.1093/database/baz036
109. Recla JM, Bubier JA, Gatti DM, Ryan JL, Long KH, Robledo RF, Glidden N, Hou G, Churchill GA, Maser RS, Zhang ZW, Young YE, **Chesler EJ*,** Bult CJ*. Genetic mapping in diversity outbred mice identifies a Trpa1 variant influencing late phase formalin response. Pain. 2019 Mar 27. doi:10.1097/j.pain.0000000000001571. [Epub ahead of print] PubMed PMID: 30925521
110. Skelly D, Raghupathy N, Robledo J, Graber JH, **Chesler EJ**. Reference Trait Analysis Reveals Correlations Between Gene Expression and Quantitative Traits in Disjoint Samples. Genetics. 2019 May 21. pii: genetics.301865.2018. doi: 10.1534/genetics.118.301865. [Epub ahead of print]
111. Boehm FJ, **Chesler EJ**, Yandell BS, Broman KW. Testing Pleiotropy vs. Separate QTL in Multiparental Populations. G3 (Bethesda). 2019 May 15. pii: g3.400098.2019. doi: 10.1534/g3.119.400098. [Epub ahead of print] PubMed PMID: 31092608.
112. Bubier JA, Sutphin GL, Reynolds TJ, Korstanje R, Fuksman-Kumpa A, Baker EJ, Langston MA, **Chesler EJ**. Integration of heterogeneous functional genomics data in gerontology research to find genes and pathway underlying aging across species. PLoS One. 2019 Apr 12;14(4):e0214523. doi: 10.1371/journal.pone.0214523. eCollection 2019. PubMed PMID: 30978202; PubMed Central PMCID: PMC6461221.
113. Geuther BQ, Deats SP, Fox KJ, Murray SA, Braun RE, White JK, **Chesler EJ**, Lutz CM, Kumar V. Robust mouse tracking in complex environments using neural networks. Commun Biol. 2019 Mar 29;2:124. doi: 10.1038/s42003-019-0362-1. eCollection 2019. PubMed PMID: 30937403; PubMed Central PMCID: PMC6440983.
114. Datta U, Schoenrock SE, Bubier JA, Bogue MA, Jentsch JD, Logan RW, Tarantino LM, Chesler EJ. Prospects for finding the mechanisms of sex differences in addiction with human and model organism genetic analysis. Genes Brain Behav. 2020 Mar;19(3):e12645. doi: 10.1111/gbb.12645. Epub 2020 Feb 11. PMID: 32012419; PMCID: PMC7060801.
115. Calvo M, Davies AJ, Hébert HL, Weir GA, **Chesler EJ**, Finnerup NB, Levitt RC, Smith BH, Neely GG, Costigan M, Bennett DL. The Genetics of Neuropathic Pain from Model Organisms to Clinical Application. Neuron. 2019 Nov 20;104(4):637-653. doi: 10.1016/j.neuron.2019.09.018. PMID: 31751545; PMCID:PMC6868508.
116. Bogue MA, Philip VM, Walton DO, Grubb SC, Dunn MH, Kolishovski G, Emerson J, Mukherjee G, Stearns T, He H, Sinha V, Kadakkuzha B, Kunde-Ramamoorthy G, **Chesler EJ**. Mouse Phenome Database: a data repository and analysis suite for curated primary mouse phenotype data. Nucleic Acids Res. 2020 Jan 8;48(D1):D716-D723. doi: 10.1093/nar/gkz1032. PMID: 31696236; PMCID: PMC7145612.
117. Thomas AL, Evans LM, Nelsen MD, **Chesler EJ**, Powers MS, Booher WC, Lowry CA, DeFries JC, Ehringer MA. Whole-Genome Sequencing of Inbred Mouse Strains Selected for High and Low Open-Field Activity. Behav Genet. 2020 Sep 16. doi: 10.1007/s10519-020-10014-y. Epub ahead of print. PMID: 32939625.
118. Wotton JM, Peterson E, Anderson L, Murray SA, Braun RE, **Chesler EJ**, White JK, Kumar V. Machine learning-based automated phenotyping of inflammatory nocifensive behavior in mice. Mol Pain. 2020 Jan-Dec;16:1744806920958596. doi: 10.1177/1744806920958596. PMID: 32955381; PMCID: PMC7509709.

119. Bubier JA, He H, Philip VM, Roy T, Hernandez CM, Bernat R, Donohue KD, O'Hara BF, **Chesler EJ**. Genetic variation regulates opioid-induced respiratory depression in mice. Sci Rep. 2020 Sep 11;10(1):14970. doi: 10.1038/s41598-020-71804-2. PMID: 32917924; PMCID: PMC7486296.
120. Schoenrock SA, Kumar P, Gómez-A A, Dickson PE, Kim SM, Bailey L, Neira S, Riker KD, Farrington J, Gaines CH, Khan S, Wilcox TD, Roy TA, Leonardo MR, Olson AA, Gagnon LH, Philip VM, Valdar W, de Villena FP, Jentsch JD, Logan RW, McClung CA, Robinson DL, **Chesler EJ**, Tarantino LM. Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. Psychopharmacology (Berl). 2020 Apr;237(4):979-996. doi: 10.1007/s00213-019-05429-3. Epub 2020 Jan 3. PMID: 31897574.
121. Bubier JA, Philip VM, Quince C, Campbell J, Zhou Y, Vishnivetskaya T, Duvvuru S, Blair RH, Ndukum J, Donohue KD, Foster CM, Mellert DJ, Weinstock G, Culiat CT, O'Hara BF, Palumbo AV, Podar M, **Chesler EJ**. A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics. 2020 Mar;214(3):719-733. doi: 10.1534/genetics.119.303013. Epub 2020 Jan 2. PMID: 31896565; PMCID: PMC7054020.
122. Reynolds T, Johnson EC, Huggett SB, Bubier JA, Palmer RHC, Agrawal A, Baker EJ, **Chesler EJ**. Interpretation of psychiatric genome-wide association studies with multispecies heterogeneous functional genomic data integration. Neuropsychopharmacology. 2020 Aug 13. doi: 10.1038/s41386-020-00795-5. Epub ahead of print. PMID: 32791514.
123. Huggett SB, Bubier JA, **Chesler EJ**, Palmer RHC. Do gene expression findings from mouse models of cocaine use recapitulate human cocaine use disorder in reward circuitry? Genes Brain Behav. 2020 Jul 27:e12689. doi: 10.1111/gbb.12689. Epub ahead of print. PMID: 32720468.
124. Yang JH, Presby RE, Cayer S, Rotolo RA, Perrino PA, Fitch RH, Correa M, **Chesler EJ**, Salamone JD. Effort-related decision making in humanized COMT mice: Effects of Val^{158}Met polymorphisms and possible implications for negative symptoms in humans. Pharmacol Biochem Behav. 2020 Sep;196:172975. doi: 10.1016/j.pbb.2020.172975. Epub 2020 Jun 25. PMID: 32593787.
125. Bubier JA, Philip VM, Dickson PE, Mittleman G, **Chesler EJ**. Discovery of a Role for *Rab3b* in Habituation and Cocaine Induced Locomotor Activation in Mice Using Heterogeneous Functional Genomic Analysis. Front Neurosci. 2020 Jul 9;14:721. doi: 10.3389/fnins.2020.00721. PMID: 32742255; PMCID: PMC7364128.
126. Cacheiro P, Muñoz-Fuentes V, Murray SA, Dickinson ME, Bucan M, Nutter LMJ, Peterson KA, Haselimashhadi H, Flenniken AM, Morgan H, Westerberg H, Konopka T, Hsu CW, Christiansen A, Lanza DG, Beaudet AL, Heaney JD, Fuchs H, Gailus-Durner V, Sorg T, Prochazka J, Novosadova V, Lelliott CJ, Wardle-Jones H, Wells S, Teboul L, Cater H, Stewart M, Hough T, Wurst W, Sedlacek R, Adams DJ, Seavitt JR, Tocchini-Valentini G, Mammano F, Braun RE, McKerlie C, Herault Y, de Angelis MH, Mallon AM, Lloyd KCK, Brown SDM, Parkinson H, Meehan TF, Smedley D; Genomics England Research Consortium; International Mouse Phenotyping Consortium. Human and mouse essentiality screens as a resource for disease gene discovery. Nat Commun. 2020 Jan 31;11(1):655. doi: 10.1038/s41467-020-14284-2. PMID: 32005800; PMCID: PMC6994715.
127. Hill DP, Harper A, Malcolm J, McAndrews MS, Mockus SM, Patterson SE, Reynolds T, Baker EJ, Bult CJ, **Chesler EJ**, Blake JA. Cisplatin-resistant triple-negative breast cancer subtypes: multiple mechanisms of resistance. BMC Cancer. 2019 Nov 4;19(1):1039. doi: 10.1186/s12885-019-6278-9. PMID: 31684899; PMCID: PMC6829976.
128. Ouellette AR, Neuner SM, Dumitrescu L, Anderson LC, Gatti DM, Mahoney ER, Bubier JA, Churchill G, Peters L, Huentelman MJ, Herskowitz JH, Yang HS, Smith AN, Reitz C, Kunkle BW, White CC, De Jager PL, Schneider JA, Bennett DA, Seyfried NT, **Chesler EJ**, Hadad N, Hohman TJ, Kaczorowski CC. Cross-Species Analyses Identify Dlgap2 as a Regulator of Age-Related Cognitive Decline and Alzheimer's Dementia. Cell Rep. 2020 Sep 1;32(9):108091. doi: 10.1016/j.celrep.2020.108091. PubMed PMID: 32877673; PubMed Central PMCID: PMC7502175.
129. Yuan R, Musters CJM, Zhu Y, Evans TR, Sun Y, **Chesler EJ**, Peters LL, Harrison DE, Bartke A. Genetic differences and longevity-related phenotypes influence lifespan and lifespan variation in a sex-specific manner in mice. Aging Cell. 2020 Oct 26;:e13263. doi: 10.1111/acel.13263. [Epub ahead of print] PubMed PMID: 33105070.
130. Palmer, R. H. C. et al. Integration of Evidence across Human and Model Organism Studies: A Meeting Report. Genes Brain Behav, e12738, doi:10.1111/gbb.12738 (2021).
131. Bagley, J. R., **Chesler, E. J.**, Philip, V. M., Center for the Systems Genetics o Addiction & Jentsch, J. D. Heritability of ethanol consumption and pharmacokinetics in a genetically diverse panel of collaborative cross mouse strains and their inbred founders. Alcohol Clin Exp Res 45, 697-708, doi:10.1111/acer.14582 (2021) PubMed PMID:3361752.
132. Dolan ME, Hill DP, Mukherjee G, McAndrews MS, **Chesler EJ**, Blake JA of COVID-19 comorbidities reveals genes and pathways coincident with the SARS-CoV-2 viral disease. Sci Rep. 2020 Nov 30;10, (1):20848, doi:10.1038/s41598-020-77632-8 (2020). PubMed PMID: 33257774; PubMed Central PMCID: PMC7704638.
133. Huggett SB, Johnson EC, Hatoum AS, Lai D, Srijeyanthan J, Bubier JA, **Chesler EJ**, Agrawal A, Palmer AA, Edenberg HJ, Palmer RHC. Genes identified in rodent studies of alcohol intake are enriched for heritability of human substance use. Alcohol Clin Exp Res. 2021 Nov 9. doi: 10.1111/acer.14738. Epub ahead of print. PMID: 34751961.
134. Bailey LS, Bagley JR, Dodd R, Olson A, Bolduc M, Philip VM, Reinholdt LG, Sukoff Rizzo SJ, Tarantino L, Gagnon L, **Chesler EJ**, Jentsch JD. Heritable variation in locomotion, reward sensitivity and impulsive behaviors in a genetically diverse inbred mouse panel. Genes Brain Behav. 2021 Nov;20(8):e12773. doi: 10.1111/gbb.12773. Epub 2021 Oct 21. PMID: 34672075.

135. 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 Dec 6;31(23):5238-5248.e7. doi: 10.1016/j.cub.2021.09.049. Epub 2021 Oct 14. PMID: 34653361.
136. Kim SM, Vadnie CA, Philip VM, Gagnon LH, Chowdari KV, **Chesler EJ**, McClung CA, Logan RW. High-throughput measurement of fibroblast rhythms reveals genetic heritability of circadian phenotypes in diversity outbred mice and their founder strains. Sci Rep. 2021 Jan 28;11(1):2573. doi: 10.1038/s41598-021-82069-8. PMID: 33510298; PMCID: PMC7843998.
137. Phillips TJ, Roy T, Aldrich SJ, Baba H, Erk J, Mootz JRK, Reed C, **Chesler EJ**. Confirmation of a Causal Taar1 Allelic Variant in Addiction-Relevant Methamphetamine Behaviors. Front Psychiatry. 2021 Aug 26;12:725839. doi: 10.3389/fpsyt.2021.725839. PMID: 34512422; PMCID: PMC8428522.
138. Hitzemann R, Bergeson SE, Berman AE, Bubier JA, **Chesler EJ**, Finn DA, Hein M, Hoffman P, Holmes A, Kisby BR, Lockwood D, Lodowski KH, McManus M, Owen JA, Ozburn AR, Panthagani P, Ponomarev I, Saba L, Tabakoff B, Walchale A, Williams RW, Phillips TJ. Sex Differences in the Brain Transcriptome Related to Alcohol Effects and Alcohol Use Disorder. Biol Psychiatry. 2022 Jan 1;91(1):43-52. Doi 10.1016/j.biopsych.2021.04.016. Epub 2021 May 1. PMID: 34274109; PMCID: PMC8558111.
139. Bubier JA, **Chesler EJ**, Weinstock GM. Host genetic control of gut microbiome composition. Mamm Genome. 2021 Aug;32(4):263-281. doi: 10.1007/s00335-021-09884-2. Epub 2021 Jun 22. PMID: 34159422; PMCID: PMC8295090.
140. Palmer RHC, Johnson EC, Won H, Polimanti R, Kapoor M, Chitre A, Bogue MA,Benca-Bachman CE, Parker CC, Verma A, Reynolds T, Ernst J, Bray M, Kwon SB, Lai D, Quach BC, Gaddis NC, Saba L, Chen H, Hawrylycz M, Zhang S, Zhou Y, Mahaffey S, Fischer C, Sanchez-Roige S, Bandrowski A, Lu Q, Shen L, Philip V, Gelernter J, Bierut LJ, Hancock DB, Edenberg HJ, Johnson EO, Nestler EJ, Barr PB, Prins P, Smith DJ, Akbarian S, Thorgeirsson T, Walton D, Baker E, Jacobson D, Palmer AA, Miles M, **Chesler EJ**, Emerson J, Agrawal A, Martone M, Williams RW. Integration of evidence across human and model organism studies: A meeting report. Genes Brain Behav. 2021 Apr 23;20(6):e12738. doi: 10.1111/gbb.12738. Epub ahead of print. PMID: 33893716; PMCID: PMC8365690.
141. Palmer RHC, Benca-Bachman CE, Huggett SB, Bubier JA, McGeary JE, Ramgiri N, Srijeyanthan J, Yang J, Visscher PM, Yang J, Knopik VS, **Chesler EJ**. Multi-omic and multi-species meta-analyses of nicotine consumption. Transl Psychiatry. 2021 Feb 4;11(1):98. doi: 10.1038/s41398-021-01231-y. PMID: 33542196; PMCID: PMC7862377.
142. Wotton JM, Peterson E, Flenniken AM, Bains RS, Veeraragavan S, Bower LR, Bubier JA, Parisien M, Bezginov A, Haselimashhadi H, Mason J, Moore MA, Stewart ME, Clary DA, Delbarre DJ, Anderson LC, D'Souza A, Goodwin LO, Harrison ME, Huang Z, Mckay M, Qu D, Santos L, Srinivasan S, Urban R, Vukobradovic I, Ward CS, Willett AM, Braun RE, Brown SDM, Dickinson ME, Heaney JD, Kumar V, Lloyd KCK, Mallon AM, McKerlie C, Murray SA, Nutter LMJ, Parkinson H, Seavitt JR, Wells S, Samaco RC, **Chesler EJ**, Smedley D, Diatchenko L, Baumbauer KM, Young EE, Bonin RP, Mandillo S, White JK; International Mouse Phenotyping Consortium. Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain. 2022 Jun 1;163(6):1139-1157. doi:10.1097/j.pain.0000000000002481. Epub 2021 Sep 13. PMID: 35552317; PMCID: PMC9100450.
143. Parker CC, Philip VM, Gatti DM, Kasparek S, Kreuzman AM, Kuffler L, Mansky B, Masneuf S, Sharif K, Sluys E, Taterra D, Taylor WM, Thomas M, Polesskaya O, Palmer AA, Holmes A, Chesler EJ. Genome-wide association mapping of ethanol sensitivity in the Diversity Outbred mouse population. Alcohol Clin Exp Res. 2022 Jun;46(6):941-960. doi: 10.1111/acer.14825. Epub 2022 Apr 17. PMID: 35383961; PMCID: PMC9246903.
144. Schoenrock SA, Gagnon L, Olson A, Leonardo M, Philip VM, He H, Reinholdt LG, Sukoff Rizzo SJ, Jentsch JD, **Chesler EJ**, Tarantino LM. The collaborative cross strains and their founders vary widely in cocaine-induced behavioral sensitization. Front Behav Neurosci. 2022 Oct 5;16:886524. doi:10.3389/fnbeh.2022.886524. PMID: 36275853; PMCID: PMC9580558.
145. Tran TDB, Monroy Hernandez C, Nguyen H, Wright S; Center for Systems Neurogenetics of Addiction; Tarantino LM, **Chesler EJ**, Weinstock GM, Zhou Y, Bubier JA. The microbial community dynamics of cocaine sensitization in two behaviorally divergent strains of collaborative cross mice. Genes Brain Behav. 2023 Jun;22(3):e12845. doi: 10.1111/gbb.12845. Epub 2023 Apr 27. PMID: 37114320; PMCID: PMC10242200.
146. Jaljuli I, Kafkafi N, Giladi E, Golani I, Gozes I, **Chesler EJ**, Bogue MA, Benjamini Y. A multi-lab experimental assessment reveals that replicability can be improved by using empirical estimates of genotype-by-lab interaction. PLoS Biol. 2023 May 1;21(5):e3002082. doi: 10.1371/journal.pbio.3002082. PMID: 37126512; PMCID: PMC10174519.
147. Binh Tran TD, Nguyen H, Sodergren E, Addiction CFSNO, Dickson PE, Wright SN, Philip VM, Weinstock GM, **Chesler EJ**, Zhou Y, Bubier JA. Microbial glutamate metabolism predicts intravenous cocaine self-administration in diversity outbred mice. Neuropharmacology. 2023 Mar 15;226:109409. doi: 10.1016/j.neuropharm.2022.109409. Epub 2022 Dec 30. PMID: 36592885; PMCID: PMC9943525.
148. Raza A, Diehl SA, Krementsov DN, Case LK, Li D, Kost J, Ball RL, **Chesler EJ**, Philip VM, Huang R, Chen Y, Ma R, Tyler AL, Mahoney JM, Blankenhorn EP, Teuscher C. A genetic locus complements resistance to Bordetella pertussis-induced histamine sensitization. Commun Biol. 2023 Mar 6;6(1):244. doi: 10.1038/s42003-023-04603-w. PMID: 36879097; PMCID: PMC9988836.
149. Bailey LS, Bagley JR, Wherry JD, **Chesler EJ**, Karkhanis A, Jentsch JD, Tarantino LM. Repeated dosing with cocaine produces strain-dependent effects on responding for conditioned reinforcement in Collaborative Cross mice. Psychopharmacology (Berl). 2023 Mar;240(3):561-573. doi: 10.1007/s00213-022-06256-9. Epub 2022 Oct 14. PMID: 36239767; PMCID: PMC10083021.

150. Chee JM, Lanoue L, Clary D, Higgins K, Bower L, Flenniken A, Guo R, Adams DJ, Bosch F, Braun RE, Brown SDM, Chin HG, Dickinson ME, Hsu CW, Dobbie M, Gao X, Galande S, Grobler A, Heaney JD, Herault Y, de Angelis MH, Mammano F, Nutter LMJ, Parkinson H, Qin C, Shiroishi T, Sedlacek R, Seong JK, Xu Y; International Mouse Phenotyping Consortium; Brooks B, McKerlie C, Lloyd KCK, Westerberg H, Moshiri A. Genome-wide screening reveals the genetic basis of mammalian embryonic eye development. BMC Biol. 2023 Feb 3;21(1):22. doi: 10.1186/s12915-022-01475-0. PMID: 36737727; PMCID: PMC9898963.
151. Bogue MA, Ball RL, Philip VM, Walton DO, Dunn MH, Kolishovski G, Lamoureux A, Gerring M, Liang H, Emerson J, Stearns T, He H, Mukherjee G, Bluis J, Desai S, Sundberg B, Kadakkuzha B, Kunde-Ramamoorthy G, **Chesler EJ**. Mouse Phenome Database: towards a more FAIR-compliant and TRUST-worthy data repository and tool suite for phenotypes and genotypes. Nucleic Acids Res. 2023 Jan 6;51(D1):D1067-D1074. doi: 10.1093/nar/gkac1007. PMID: 36330959; PMCID: PMC9825561.
152. Bagley JR, Bailey LS, Gagnon LH, He H, Philip VM, Reinholdt LG, Tarantino LM, **Chesler EJ**, Jentsch JD. Behavioral phenotypes revealed during reversal learning are linked with novel genetic loci in diversity outbred mice. Addict Neurosci. 2022 Dec;4:100045. doi: 10.1016/j.addicn.2022.100045. Epub 2022 Nov 4. PMID:36714272; PMCID: PMC9879139.
153. Bogue MA, Ball RL, Walton DO, Dunn MH, Kolishovski G, Berger A, Lamoureux A, Grubb SC, Gerring M, Kim M, Liang H, Emerson J, Stearns T, He H, Mukherjee G, Bluis J, Davis S, Desai S, Sundberg B, Kadakkuzha B, Kunde-Ramamoorthy G, Philip VM, **Chesler EJ**. Mouse phenome database: curated data repository with interactive multi-population and multi-trait analyses. Mamm Genome. 2023 Dec;34(4):509-519. doi: 10.1007/s00335-023-10014-3. Epub 2023 Aug 15. PMID: 37581698; PMCID: PMC10627943.
154. Stefancsik R, Balhoff JP, Balk MA, Ball RL, Bello SM, Caron AR, **Chesler EJ**, de Souza V, Gehrke S, Haendel M, Harris LW, Harris NL, Ibrahim A, Koehler S, Matentzoglu N, McMurry JA, Mungall CJ, Munoz-Torres MC, Putman T, Robinson P, Smedley D, Sollis E, Thessen AE, Vasilevsky N, Walton DO, Osumi-Sutherland D. The Ontology of Biological Attributes (OBA)-computational traits for the life sciences. Mamm Genome. 2023 Sep;34(3):364-378. doi: 10.1007/s00335-023-09992-1. Epub 2023 Apr 19. PMID: 37076585; PMCID: PMC10382347.
155. Ball RL, Bogue MA, Liang H, Srivastava A, Ashbrook DG, Lamoureux A, Gerring MW, Hatoum AS, Kim M, He H, Emerson J, Berger AK, Walton DO, Sheppard K, Kassaby BE, Castellanos F, Kunde-Ramamoorthy G, Lu L, Bluis J, Desai S, Sundberg BA, Peltz G, Fang Z, Churchill GA, Williams RW, Agrawal A, Bult CJ, Philip VM, **Chesler EJ**. GenomeMUSter mouse genetic variation service enables multi-trait, multi-population data integration and analyses. bioRxiv [Preprint]. 2023 Aug 10:2023.08.08.552506. doi: 10.1101/2023.08.08.552506. PMID: 37609331; PMCID: PMC10441370. In press at Genome Research
156. Philip VM, He H, Saul MC, Dickson PE, Bubier JA, **Chesler EJ**. Gene expression genetics of the striatum of Diversity Outbred mice. Sci Data. 2023 Aug 5;10(1):522. doi: 10.1038/s41597-023-02426-2. PMID: 37543624; PMCID: PMC10404230.
157. Roy TA, Bubier JA, Dickson PE, Wilcox TD, Ndukum J, Clark JW, Rizzo SJS, Crabbe JC, Denegre JM, Svenson KL, Braun RE, Kumar V, Murray SA, White JK, Philip VM, **Chesler EJ**. Discovery and validation of genes driving drug-intake and related behavioral traits in mice. Genes Brain Behav 2024 Jan 2:e12875. doi: 10.1111/gbb.12875_PMID: 38164795**.**
158. Poirion OB, Zuo W, Spruce C, Daigle SL, Olson A, Skelly DA, **Chesler EJ**, Baker CL, White BS. Enhlink infers distal and context-specific enhancer-promoter linkages. bioRxiv [Preprint]. 2023 May 11:2023.05.11.540453. doi: 10.1101/2023.05.11.540453. PMID: 37214950; PMCID: PMC10197707.
159. Mitra A, Deats S, Dickson P, Zhu J, Gardin J, Nieman B, Henkelman RM, Tsai NP, **Chesler EJ**, Zhang ZW, and Kumar V Tmod2 is a regulator of cocaine responses through control of striatal and cortical excitability, and drug-induced plasticity. [Preprint] bioRxiv 648295; doi: https://doi.org/10.1101/648295, in press at J. Neuroscience

Refereed Computer Science Conference Papers:

1. Zhang Y, Abu-Khzam FN, Baldwin NE, **Chesler EJ,** Langston MA, Samatova NF. 2005. Genome-Scale Computational Approaches to Memory-Intensive Applications in Systems Biology. *Super Computing*.
2. **Chesler EJ,** Langston MA. 2005. Combinatorial genetic regulatory network analysis tools for high throughput transcriptomic data. *RECOMB First Annual RECOMB Satellite Workshop on Systems Biology and the Second Annual RECOMB Satellite Workshop on Regulatory genomics*.
3. Kirova R, Langston MA, Peng X, Perkins A, **Chesler EJ.** 2006. A Systems Genetic Analysis of Chronic Fatigue Syndrome: Combinatorial Data Integration from SNPs to Differential Diagnosis of Disease. *Critical Assessment of Microarray Data,* Durham, NC.
4. Song J, Lewis C, Lance E, **Chesler EJ**, Kirova R, Langston MA, Bergeson S. 2007. Inferring Transcriptional Regulation through Logical Networks from Temporal Mouse Brain Gene Expression Data. FOSBE, Stuttgart, Germany.
5. Zhang Y, **Chesler EJ,** Langston MA. 2007. On Finding Bicliques in Bipartite Graphs: a Novel Algorithm with Application to the Integration of Diverse Biological Data Types. Hawaii International Conference on System Sciences, Waikoloa, HI.

6. Meehan TF, Carr CJ, Bult CJ, **Chesler EJ**, Blake JA. 2011. Autism Candidate Genes via Mouse Phenomics. AMIA Summit on Translational Bioinformatics. San Francisco, CA.
7. Jay JJ, Eblen JD, Zhang Y, Benson M, Perkins AD, Saxton AM, Voy BH, **Chesler EJ** and Langston MA, "A Systematic Comparison of Genome Scale Clustering Algorithms," Proceedings, International Symposium on Bioinformatics Research and Applications, Changsha, China, May 2011. Proceedings published as Lecture Notes in Bioinformatics 6674 (Jianer Chen, Jianxin Wang and Alexander Zelikovsky, editors), Springer, pages 416-427.
8. Jay JJ, Baker EJ, **Chesler EJ**. A Context-Driven Gene Prioritization Method for Web-based Functional Genomics. ISBRA, 2013, Charlotte, NC.
9. Baker E, Culpepper C, Philips C, Bubier J, Langston M, **Chesler E.** Identifying common components across biological network graphs using a bipartite data model. BMC Proc. 2014 Oct 13;8(Suppl 6 Proceedings of the Great Lakes Bioinformatics Confer):S4. doi: 10.1186/1753-6561-8-S6-S4. eCollection 2014. PubMed PMID: 25374613; PubMed Central PMCID: PMC4202189.
10. Lu Y, Phillips C, **Chesler EJ**, Langston M. Clique Selection and its Effect on Paraclique Enrichment: An Experimental Study. Proceedings, International Conference on Bioinformatics and Computational Biology (BICOB), San Francisco, CA, USA, March 2020.

Book Chapters:

1. Chesler, EJ. (2003) "Design and Analysis of Microarray Experiments" in *The Bioinformatics of Brains: From Genes and Proteins to Behaviors,* (Williams RW, ed), Washington, DC, Society for Neuroscience.

2. Chesler, EJ, Williams RW. (2004) Brain gene expression: genomics and genetics. *Int Rev Neurobiol.* (Miles MF, ed) 60, 59-95.

3. Chesler, EJ. (2006) "Bioinformatics of Behavior" in Neurobehavioral Genetics. (Jones B, Mormede P, eds), CRC press.

4. Chesler, EJ. (2007) "*Combining quantitative trait and gene expression data*" in Bioinformatics for Geneticists. (Barnes MG, Gray IC, eds)

5. Haendel MA, **Chesler EJ**. Lost and found in behavioral informatics. *Int Rev Neurobiol.* (Chesler EJ, Haendel MA, eds.) 2012;103:1-18.

6. Chesler EJ, Haendel MA. The field of bioinformatics. Preface. *Int Rev Neurobiol.* (Chesler EJ, Haendel MA, eds.) 2012;103:xi-xii.

7. Chesler EJ, Logan RW. Opportunities for bioinformatics in the classification of behavior and psychiatric disorders. *Int Rev Neurobiol.* (Chesler EJ, Haendel MA, eds.) 2012;104:183-211.

8. Chesler EJ, Baker EJ "Contributions of genomic and informatics approaches to understanding alcohol dependence: from genes to networks" Neurobiology of Alcohol Dependence. (Cui, Crabbe, Noronha, eds.) in press

9. Jay, J. and **Chesler EJ** (2014) Performing Integrative Functional Genomics Analysis in GeneWeaver.org Methods in Molecular biology. Springer, 1101:13-29.

10. Bubier JA, **Chesler EJ** (2015) Integrative Functional Genomics for Systems Genetics in GeneWeaver.org. Systems Genetics. Methods in Molecular Biology. Springer. Methods Mol Biol. 2017;1488:131-152.

11. Parker CC, Dickson PE, Philip VM, Thomas M, **Chesler EJ.** Systems Genetic Analysis in GeneNetwork.org. Curr Protoc Neurosci. 2017 Apr 10;79:8.39.1-8.39.20. doi: 10.1002/cpns.23. PubMed PMID: 28398643; PubMed Central PMCID: PMC5548442.

Internet Resources:

WebQTL/GeneNetwork. www.webqtl.org, www.genenetwork.org Design of tools for multi-trait and genetic correlation analysis including Cluster Map, Associative Network, Genetic Correlation and Principal Component Analysis.

Mutrack/MouseTrack. www.tnmouse.org; http://mouse.ornl.gov Design of robust methods for mutant detection, mutant comparison analysis and tools for complex trait analysis for the Tennessee Mouse Genome Consortium and Integrative Neuroscience Initiative on Alcoholism.

GeneWeaver http://geneweaver.org formerly the Ontological Discovery Environment. http://ontologicaldiscovery.org Combinatorial analysis of user submitted and curated experimental results in functional genomics.

Mouse Phenome Database. https://phenome.jax.org Redesign of the Mouse Phenome Database to a modern framework, design of an integrative genetics tool set and incorporation of advanced genetic population data for integrative genetic analysis.

GenomeMUSter. A harmonized SNP resource consisting of observed and imputed variant states for 657 strains at over 100M loci connected to the Mouse Phenome Database for trait metanalysis and other applications. https://mpd.jax.org/genotypes

VariantGraphDB A Neo4J graph database for translation of variant effects from mouse to human.

Outreach Resources.

LEGO operant chamber.

https://www.jax.org/news-and-insights/2015/july/thinking-outside-the-blocks

“A LEGO box to study drug addiction”. Bethany Brookshire, Student Science Eureka! Lab. 11/2/14.

Featured at University of Chicago 4th annual Conte Center for Computational Neuropsychiatric Genomics Brain Awareness Day 2015.

Featured at Sciencia: Blue Hill Teen Science Café, Blue Hill, Maine, November 18, 2015.

Community.

Acadia Night Sky Festival, Organizing Committee member and volunteer. 2009-2021.
Town of Bar Harbor Conservation Commission. 2014-2017
Town of Bar Harbor Planning Board. 2021-present; secretary 2022-present
Town of Bar Harbor Comprehensive Plan Committee. 2021-present
Acadia Family Center, Board member, Task force committee member, 2022-present
Jesup Memorial Library. Volunteer, science programming, 2012-2020