

CURRICULUM VITAE

NAME Christina Kendziorski

TITLE Professor

ADDRESS Department of Biostatistics and Medical Informatics
University of Wisconsin - Madison
1300 University Avenue (4715 MSC)
Madison, Wisconsin 53706
Phone: (608) 262-3146
Email: kendzior@biostat.wisc.edu
URL: <http://www.biostat.wisc.edu/~kendzior>

EDUCATION

1998 Ph.D. Mathematics, with emphasis in Biomathematics
Marquette University, Milwaukee, Wisconsin

1992 B.S. Mathematics
University of Wisconsin, Eau Claire, Wisconsin

PROFESSIONAL POSITIONS

June 2013 – present Professor. Department of Biostatistics and Medical Informatics.
University of Wisconsin, Madison, WI

July 2007 – May 2013 Associate Professor. Department of Biostatistics and Medical
Informatics. University of Wisconsin, Madison, WI.

September 2001 – June 2007 Assistant Professor. Department of Biostatistics and Medical
Informatics. University of Wisconsin, Madison, WI.

August 1998 - Sept 2001 Postdoctoral Research Fellow. Department of Biostatistics and
Medical Informatics, University of Wisconsin, Madison, WI.

PROFESSIONAL APPOINTMENTS

Head, Statistical Genetics and Genomics, Institute for Translational and Clinical Research (ICTR).
University of Wisconsin, Madison, WI
September 2010 - present

Member, Cancer Genetics Program. Comprehensive Cancer Center. University of Wisconsin, Madison, WI
September 2003 – present

Affiliate Faculty Member, Department of Statistics, University of Wisconsin, Madison, WI
January 2003 – present

Affiliate Faculty Member, University of Wisconsin Genome Center, Madison, WI
January 2005 - present

Member, Waisman Center. University of Wisconsin, Madison, WI
February 2006 – 2009

EDITORIAL ACTIVITIES

Member, NIH Genomics Computational Biology and Technology (GCAT) Study Section
October 2010-2016.

Member, External Advisory Committee for NHLBI's Pediatric Cardiac Translational Research Program, titled "Bench to Bassinet" June 2011- 2015.

Editorial Board

Genomics, Bioinformatics, and Systems Biology Section of Biology Direct, January 2008-present

Associate Editor

Biometrics, March 2006 – December 2008; June 2010- December 2012;
Journal of the American Statistical Association Book Reviews, October 2008-September 2012
Bayesian Analysis, November 2008-present
Annals of Applied Statistics, January 2012 – present
Genetics, January 2013 - present

Referee for manuscripts submitted to:

Annals of Statistics, Archives of Ophthalmology, Bioinformatics, Biometrics, Biostatistics, Biometrical Journal, Biotechniques, Computational Statistics and Data Analysis, Genetics, Genome Research, Journal of the American Statistical Association, Journal of the Royal Statistical Society Series C, Lancet, Mammalian Genome, Nature Biotechnology, Nature Communications, Nature Genetics, Nature Protocols, Nucleic Acids Research, Plant Cell, PLOS Genetics, Statistical Applications in Genetics and Molecular Biology, and Trends in Genetics

Ad hoc member for:

NIH- National Institute of Arthritis and Musculoskeletal and Skin Disease Special Emphasis Panel for Microarray Awards August 21-23, 2003
NIH Biostatistical Methods and Research Design (BMRD) Study Section February 19-20, 2004
NIH Genomics Computational Biology and Technology (GCAT) Study Section October 5-6, 2006.
NIH Genomics Computational Biology and Technology (GCAT) Study Section June 3-4, 2008
NIH Center for Inherited Disease Research (CIDR) November 2009
NIH- National Institute of Mental Health Special Emphasis Panel July 2010

AWARDS AND HONORS

- 1992 James Graham Brown Cancer Research Center, Louisville, KY, student fellowship
- provided full summer support, 1992.
- 1993 Harris Fellowship, US Department of Education, for graduate studies in mathematics
- provided full academic year support, 1993-1998.
- 1994 Center for Research Mathematicians program in mathematical biology student fellowship
- provided full summer support, 1994.
- 1997 Swokowsky fellowship, Marquette University, for top graduate student in mathematical biology
- provided full summer support, 1997.
- 2005 The efficiency of pooling mRNA in microarray experiments by Kendziorski, Zhang, Lan, and Attie, *Biostatistics* 2003, is a Thomson ISI fast breaking paper
(<http://www.esi-topics.com/fbp/fbp-june2005.html>)
- 2006 Kendziorski and Wang. A Review of Statistical Methods for Expression Quantitative Trait Loci Mapping. *Mammalian Genome* 17(6):509-17, 2006. Most viewed article over 90 days, December 2006.
- 2006 Yuan and Kendziorski. Hidden Markov models for microarray time course data in multiple biological conditions. *JASA Discussion and ASA/JSM session paper*.

- 2007 Chen and Kendziorski. A statistical framework for expression Quantitative Trait Loci (eQTL) Mapping. *Genetics* 177:761-771, 2007. Genetics highlighted paper.
- 2010 Vilas Associate Award
- 2014 Leng et al. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq experiments, *Bioinformatics* 29(8), 1035-1043, 2013. In the Top 10 list of *Bioinformatics* highly cited papers of 2014.

TEACHING AND ADVISING

Short Courses and Workshops

- Microarray Methods and Data Analysis. Agricultural University of Norway. Lillehammer, Norway, Summer 2003
- Statistical Approaches to Analyzing Gene Expression Data. Promega. Madison, WI
Summer 2003, 2006, 2008-present
- Mathematical Approaches to Complex Traits. The Jackson Laboratory. Bar Harbor, ME
Fall 2003, 2004, 2006, 2008
- First Short Course on Statistical Genetics and Genomics, Department of Biostatistics, University of Alabama, Birmingham, AL, Summer 2011
- Webinar on Statistical Methods for Genomic Based Studies of Disease,
Section on Bayesian Statistical Science (SBSS), Summer 2013
- Short Course on Systems Genetics. The Jackson Laboratory. Bar Harbor, ME
Fall 2009, 2010, 2012-2014, 2016

Classroom Instruction

- Mathematical Statistics, Summer Minority Internship Program, 2002-2005
- Statistical Methods for Microarrays, STAT 992, 2003
- Introduction to Biostatistics, STAT 541, 2001, 2002, 2004, 2005
- Statistical Methods for Molecular Biometry, STAT 877, Spring 2014, Spring 2017

Postdoctoral Scholars

- Ming Yuan, Ph.D., 2004-2005
- Alina Andrei, Ph.D. 2006-2008
- Oleg Moskvina, Ph.D., 2010-2013
- Kevin Eng, Ph.D., 2011-2013

Ph.D. Students

- Meng Chen, Ph.D. conferred August 2006
- YounJeong Choi, Ph.D. conferred August 2009
- Ping Wang, Ph.D. conferred December 2009
- John Dawson Ph.D. conferred May 2012
- Ning Leng Ph.D. conferred August 2014
- Keegan Korthaur Ph.D. conferred May 2015
- Shuyun Ye Ph.D. conferred August 2015
- Jeea Choi Ph.D. expected May 2017
- Rhonda Bacher Ph.D. expected August 2017

Ph.D. Committees

- Yuan Ji, Statistics, Ph.D. conferred 2003
- David Dahl, Statistics, Ph.D. conferred 2004
- Ming Yuan, Statistics, Ph.D. conferred 2004
- Yang Song, Statistics, Ph.D. conferred 2005
- Stephan Woditschka, Genetics, Ph.D. conferred 2008
- Lisa Chung, Statistics, Ph.D. conferred 2010

Elias Chaibub Neto, Statistics, Ph.D. conferred 2010
Amanda Esch, Cancer Biology, Ph.D. conferred 2011
JeeYoung Moon, Statistics, Ph.D. conferred 2013
Bo Li, Computer Science, Ph.D. conferred 2013
Rebecca Bartlett, Department of Surgery-Otolaryngology, Ph.D. conferred 2014
Xin Zeng, Department of Statistics, Ph.D. conferred 2014
Il-youp Kwak, Department of Statistics, Ph.D. conferred 2014
Kelly Werner, Department of Biochemistry, Ph.D. conferred 2014
Joel Gaston, Department of Surgery-Otolaryngology, Ph.D. conferred 2015
Zhishi Wang, Department of Statistics, Ph.D. conferred 2016
Ryan Donahue, Department of Ophthalmology and Visual Sciences, expected 2017
Mary O'Neill, Department of Medical Microbiology and Immunology, expected 2017

Undergraduate Mentoring

Jacquis Casher, Summer Research Program in Biostatistics, 2000
Jamilla Williams, Summer Research Program in Biostatistics, 2001
Chris Klundt, Hilldale Fellow, 2002 - 2003
Kevin Eng, Summer Research Program in Biostatistics, 2004
Linda Wu, Science Research Internship Program, Madison Metropolitan School District, 2010-2011

Other Training Program Activity

Trainer, Interdisciplinary Biostatistics Training Program, 2003-present
Trainer, Cardiovascular Biostatistics Training Programs, 2003-present
Trainer, Computation and Informatics in Biology and Medicine Training Program, 2004-present
Trainer, Genomic Sciences Training Program, 2006-present
Management Committee, Genomic Sciences Training Program, 2012-present

SERVICE

Department

Graduate Student Admissions Committee, 2003, 2005, 2007, 2008, 2013-2014, 2017
Organizer of the Biostatistics and Medical Informatics weekly seminar series, 2001-2003
Mentor for Summer Research Program in Biostatistics, 2000, 2001, 2004
Organizer for Statistical Genomics Series, Summer Institute for Training in Biostatistics (SIBS) 2012
Chair, Website Redevelopment Committee, 2013-2014

University

Faculty Mentor for Hilldale Fellow, 2002 - 2003
Organizer of the gene expression data analysis (GEDA) group, 2000-2002
Member, Wisconsin Genomics Initiative (WGI) Management Committee, 2008-2011
Chair, Hiring Committee for Human Genetics Cluster positions, 2010
Member, Department of Genetics ten-year review, 2010
Member, Hiring Committee for Chair of Genetics and Medical Genetics Departments, 2013-2014
Member, UW Committee on Undergraduate Recruitment, Admissions, and Financial Aid, 2013-2014
Member, Hiring Committee for Chair of Department of Oncology, 2014
Member, UWSMPH Basic Sciences Strategic Planning Committee, 2014
Member, Information Technology Committee, 2014-present
Chair, UW Committee on Undergraduate Recruitment, Admissions, and Financial Aid, 2014-2016

Community

Member of the organizing committee for the Workshop for Junior Researchers preceding the annual ENAR meeting, 2004

Member of the steering committee for Lilith Computing Group, an organization for middle school students interested in technical careers and computing, 2000-2003

Member of the executive committee for the Conference on Integrative Genomics, Imaging, Biosstatistics & Personalized Medicine, MD Anderson, 2015.

Memberships

American Statistical Association, International Biometric Society
Institute of Mathematical Statistics

Consulting

St. Mary's Hospital, Madison, WI, 1999 - 2001
Southern Wisconsin Radiotherapy Center, Madison, WI, 1999 - 2002
Third Wave Technologies, Madison, WI, 2000 - 2001
Nimblegen, 2002-2003
Epicentre Technologies, Madison, WI, 2005
Stratatech Corporation, Madison, WI, 2004 – 2005, 2008, 2011
Eli Lilly, Indianapolis, IN, July 2012-2014

Invited Conference Presentations

- International Association for Mathematics and Computers in Simulation (IMACS): International Conference on Scientific Computing and Mathematical Modeling. Milwaukee, WI, May 1999
- Wisconsin Symposium I: Genetics, Genomics, and Molecules. Madison, WI, May 1999
- Upper Midwest Biostatistics Symposium. Rochester, MN, August 1999
- Wisconsin Symposium II: The Analysis of Human Biology Genes, Genomes, and Molecules. Madison, WI, June 2001
- Joint Statistics Meetings. New York, NY, August 2002
- Frontiers of Statistical Research: A Celebration of the 40th Anniversary of the Department of Statistics at Texas A&M University. College Station, TX, October 2002
- Gordon Research Conference on Quantitative Genetics and Genomics. Ventura, CA, February 2003
- Overview Lecture. Joint Statistics Meetings. San Francisco, CA, August 2003
- WNAR Session. Joint Statistics Meetings. San Francisco, CA, August 2003
- Proteomics and Microarrays. Institute for Mathematics and Its Applications, Minneapolis, Minnesota, September 2003
- Cold Spring Harbor Laboratory Rat Genome & Biology Meeting. Cold Spring Harbor, New York, December 2003
- Joint Statistics Annual Meeting. Toronto, August 2004
- Statistical Science for Genome Biology Meeting. Banff International Research Station, Banff, Alberta, Canada, August 2004
- Analysis of Gene Expression Data: Principles and Applications. Mathematical Biosciences Institute. Ohio State University, Columbus, Ohio, October 2004
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Austin, Texas, March 2005
- Joint Statistics Annual Meeting. Minneapolis, Minnesota, August 2005
- Second International Symposium on Animal Functional Genomics. Michigan State University, East Lansing, Michigan, May 2006
- Summer Program on Multiplicity and Reproducibility in Scientific Studies. Statistical and Applied Mathematical Sciences Institute (SAMSI). Research Triangle Park, North Carolina, July 2006
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Atlanta, Georgia, March 2007
- BIOCOMP 2008, part of WORLDCOMP 2008, the 2008 World Congress in Computer Science, Computer Engineering, and Applied Computing. Las Vegas, July 2008

- Integration of the Mathematical and Biological Sciences Symposium, Morgridge Research Institute, Madison, Wisconsin, September 2008
- Biostatistics, Bioinformatics, and Nutrition Training Program Conference, Keynote Address. The Center for Statistical Bioinformatics, Texas A&M, October 2008
- Statistical Advances in Genome-scale Data Analysis Workshop, Ascona, Switzerland, May 2009.
- Systems Genetics Workshop, University of North Carolina, April 2010
- American Society of Pediatric Hematology/Oncology Annual Meeting, Montreal, Canada, April 2010.
- MCMSki III, Utah, January 2011
- Workshop on Computational Statistical Methods for Genomics and Systems Biology, Centre de Recherches Mathematiques, Montreal, April 2011
- Transcriptomics and Epigenomics, Institute for Pure and Applied Mathematics (IPAM) UCLA, October 2011
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Washington DC April 2012
- Second Biostatistics Symposium, Session on Biostatistics for Genetics and Bioinformatics, Beijing, July 2012
- Joint Statistics Annual Meeting. San Diego, CA, August 2012
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Orlando, March 2013
- Statistical Society of Canada (SSC) Annual Meeting, Alberta, May 2013
- International Biometric Society Western North American Region (WNAR) Annual Meeting. Los Angeles, June 2013
- Workshop on Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine. Banff International Research Station, August 2013
- 7th Annual Bayesian Biostatistics Conference, MD Anderson, Houston, February 2014
- Translational Science Annual Meeting, Washington DC, April 2014
- Joint Statistics Annual Meeting. Boston, MA, August 2014
- Joint Statistics Annual Meeting, Seattle, WA, August 2015
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Austin, TX, March 2016
- AAAS Annual Meeting, Boston, February 2017
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Washington, DC, March 2017
- Joint Statistics Annual Meeting, Baltimore, MD, August 2017

Invited Presentations

- Department of Physics: Chaos and Complex Systems Seminar Series. University of Wisconsin, Madison, WI, September 1999
- Cancer Genetics Seminar Series. University of Wisconsin, Madison, WI, February 2000
- Statistical Genetics Seminar Series. Purdue University, Lafayette, IN, October 2000
- Department of Biostatistics Seminar Series. Medical College of Wisconsin, Milwaukee, WI, November 2000
- Statistical Genetics Seminar Series. Purdue University, Lafayette, IN, November 2001
- Department of Statistics, University of British Columbia, Vancouver, BC, March 2002
- Cancer Genetics Seminar Series. University of Wisconsin, Madison, WI, April 2002
- Department of Botany and Plant Sciences Seminar Series. University of California -Riverside, April 2002
- Department of Statistics Seminar Series, University of Wisconsin, Madison, WI, Jan 2003
- Department of Animal Sciences Seminar Series, University of Wisconsin, Madison, WI, April 2003
- Statistical Genetics Seminar Series, University of Alabama, Birmingham, AL, April 2003
- Department of Biostatistics Seminar Series, University of Minnesota, Minneapolis, MN, December 2003
- Department of Biostatistics Seminar Series, M.D. Anderson Cancer Center, Houston, TX, April 2004
- Department of Molecular Genetics Seminar Series, University of Toronto, Toronto, ON, August 2004
- Department of Genetics Seminar Series. University of Wisconsin, Madison, WI, Feb 2005

- Computation and Informatics in Biology and Medicine Seminar Series. University of Wisconsin, Madison, WI, February 2005
- Department of Biostatistics Seminar Series, Johns Hopkins University, March 2005
- WiCell. Madison, WI, April 2005
- Computation and Informatics in Biology and Medicine Annual Retreat. University of Wisconsin, Madison, WI, May 2006
- Department of Biostatistics Seminar Series, University of Michigan, Ann Arbor, MI, November 2007
- UW Department of Genetics Annual Retreat, Devil's Head Resort, Merrimac, WI, September 2011
- Department of Genetics Seminar Series, University of Wisconsin, Madison, WI, March 2012
- Department of Statistics Seminar Series, Yale, New Haven, CT, April 2012
- UW Biotechnology Drug Discovery Course, September 2012
- Bioinformatics Seminar Series, University of Iowa, Iowa City, IA, November 2012
- Computational Informatics in Biology and Medicine (CIBM) Seminar Series, Madison, February 2013
- UW Biotechnology Drug Discovery Course, September 2013
- Morgridge Institute for Research (MIR) Crossroads of Ideas Seminar Series, Madison, April 2014
- East High School STEM Program, Madison, WI, May 2014
- Genomic Sciences Training Program Retreat, Madison, WI, May 2014
- UW Biotechnology Drug Discovery Course, September 2014
- Department of Statistics Seminar Series, Michigan State, April 2015
- Medical Research Council Biostatistics seminar, Cambridge, UK, April 2016
- EMBL-European Bioinformatics Institute seminar, Hinxton, UK, May 2016
- Department of Biostatistics Seminar Series, Johns Hopkins University, November 2016
- qBio2017, University of Wisconsin-Madison and the Morgridge Institute for Research, March 2017
- Penn Bioinformatics Forum, student-selected speaker, University of Pennsylvania, April 2017

Contributed Presentations

- Joint Statistics Meetings. Baltimore, MD, August 1999
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Chicago, IL, March 2000
- Center for Statistics. ETH, Zurich, August 2001
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Arlington, VA, March 2002
- International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Pittsburgh, PA, March 2004
- Joint Statistics Meetings, Chicago, August 2016

PUBLICATIONS

1. Bansal, N., N. Casper, **C.M. Kendziorski**, and G.G. Hamedani. A class of non-inverse Gaussian distributions with finite positive and negative moments. *Journal of Applied Statistical Science* 4(2-3): 203-214, 1996.
2. **Kendziorski, C.M.**, J.B. Basingthwaighte, and P.J. Tonellato. Evaluating maximum likelihood estimation methods to determine the Hurst coefficient. *Physica A* 273(3-4): 439-451, 1999.
3. Lan, H., **C.M. Kendziorski**, L.A. Shepel, J.D. Haag, M.A. Newton, and M.N. Gould. Genetic loci controlling breast cancer susceptibility in the Wistar-Kyoto rat. *Genetics* 157: 331-339, 2001.

4. Newton, M.A., **C.M. Kendziorski**, C.S. Richmond, F.R. Blattner, and K.W. Tsui. On differential variability of expression ratios: Improving statistical inference about gene expression changes from microarray data. *Journal of Computational Biology* 8: 37-52, 2001.
5. Ntambi, J.M., M. Miyazaki, J.P. Stoehr, H. Lan, **C.M. Kendziorski**, B.S. Yandell, Y. Song, P. Cohen, J.M. Friedman, and A.D. Attie. Loss of stearyl-CoA desaturase-1 function protects mice against adiposity. *Proceedings of the National Academy of Sciences* 99(17): 11482-11486, 2002.
6. **Kendziorski, C.M.**, A.W. Cowley, Jr., A.S. Greene, H. Salgado, H.J. Jacob, and P.J. Tonellato. Mapping baroreceptor function to the genome: A mathematical modeling approach. *Genetics* 160: 1687-1695, 2002.
7. Djamali, A., **C.M. Kendziorski**, P.C. Brazy, B.N. Becker. Disease Progression and Outcomes in Chronic Kidney Disease and Renal Transplantation. *Kidney International* 64(5): 1800-1807, 2003.
8. Attie, A. and **C.M. Kendziorski**. PGC-1 α at the crossroads of type 2 diabetes. *Nature Genetics* 34: 244-245, 2003.
9. **Kendziorski, C.M.**, Y. Zhang, H. Lan, and A. Attie. The efficiency of mRNA pooling in microarray experiments. *Biostatistics* 4: 465-477, 2003.
10. **Kendziorski, C.M.**, M.A. Newton, H. Lan, and M.N. Gould. On parametric empirical Bayes methods for comparing multiple groups using replicated gene expression profiles. *Statistics in Medicine* 22: 3899-3914, 2003.
11. The Complex Trait Consortium [113 authors]. The Collaborative Cross, a community resource for the genetic analysis of complex traits. *Nature Genetics* 36: 1133-1137, 2004.
12. Holzmacher, R., **C. Kendziorski**, R.M. Hoffman, J. Jaffery, B. Becker, and A. Djamali. Low Serum Magnesium is Associated with Decreased Graft Survival in Patients with Chronic Cyclosporine Nephrotoxicity. *Nephrology Dialysis Transplantation* 20(7): 1456-1462, 2005.
13. Minn, A.H., C.A. Pise-Masison, M. Radonovich, M.N. Brady, P. Wang, **C. Kendziorski**, and A. Shalev. Gene Expression Profiling in INS-1 Cells Overexpressing Thioredoxin-Interacting Protein. *Biochemical and Biophysical Research Communications* 336(3): 770-778, 2005.
14. **Kendziorski, C.**, R.A. Irizarry, K. Chen, J.D. Haag, and M.N. Gould. On the utility of pooling biological samples in microarray experiments. *Proceedings of the National Academy of Sciences* 102(12): 4252-4257, 2005.
15. Lan, H., M. Chen*, J.E. Byers, B.S. Yandell, D.S. Stapleton, C.M. Mata, E. Ton-Keen Mui, M.T. Flowers, K.L. Schueler, K.F. Manly, R.W. Williams, **C. Kendziorski**, and A.D. Attie. Combined Expression Trait Correlations and Expression Quantitative Trait Locus Mapping. *PLoS Genetics* 2(1):e6, 2006.
16. Flowers, M.T., A. K. Groen, A.T. Oler, M.P. Gray-Keller, Y. Choi*, K.L. Schueler, O.C. Richards, H. Lan, M. Miyazaki, F. Kuipers, **C. Kendziorski**, J. Ntambi, and A.D. Attie. Cholestasis and Hypercholesterolemia in SCD1-Deficient Mice Fed a Low-Fat, High-Carbohydrate Diet. *Journal of Lipid Research* 47: 2668-2680, 2006.
17. Yuan, M*. and **C. Kendziorski**. Hidden Markov Models for Microarray Time Course Data in Multiple Biological Conditions (with Discussion). *Journal of the American Statistical Association* 101(476): 1323-1332; Discussion 1332-1340, 2006.

18. Yuan, M*. and **C.Kendziorski**. A Unified Approach for Simultaneous Gene Clustering and Differential Expression Identification, *Biometrics* 62(4): 1089-1098, 2006.
19. **Kendziorski, C.**, and P. Wang*. A Review of Statistical Methods for Expression Quantitative Trait Loci Mapping. *Mammalian Genome* 17(6): 509-517, 2006.
20. **Kendziorski, C.**, M. Chen*, M. Yuan*, H. Lan, and A.D. Attie. Statistical Methods for Expression Quantitative Trait Loci (eQTL) Mapping. *Biometrics* 62: 19-27, 2006.
21. Burleigh, D.W., C. Kendziorski, Y.J. Choi*, K.M. Grindle, R.L. Grendell, R.R. Magness, and T.G. Golos. Microarray Analysis of BeWo and JEG3 Trophoblast Cell Lines: Identification of Differentially Expressed Transcripts. *Placenta* 28(5-6): 383-389, 2007.
22. Chen, M*. and **C. Kendziorski**. A Statistical Framework for Expression Quantitative Trait Loci (eQTL) Mapping. *Genetics* 177: 761-771, 2007. Genetics highlighted paper.
23. Amos-Landgraf, J.M., L.N. Kwong, **C. Kendziorski**, M. Reichelderfer, J. Torrealba, J.P. Weichert, J.D. Haag, K.S. Chen, J.L. Waller, M.N. Gould, and W.F. Dove. A target-selected Apc-mutant rat kindred enhances the modeling of familial human colon cancer. *Proceedings of the National Academy of Sciences* 104(10): 4036-4041, 2007. *co-first authors.
24. Chen, D., P. Wang*, R.L. Lewis, C.A. Daigh, C. Ho, X. Chen, J.A. Thomson, and **C. Kendziorski**. A Microarray Analysis of the Emergence of Embryonic Definitive Hematopoiesis. *Experimental Hematology* 35(9): 1344-1357, 2007.
25. Couto, F., A.H. Minn, C.A. Pise-Masison, M. Radonovich, J.N. Brady, M. Hanson, L.A. Fernandez, P. Wang*, **C. Kendziorski**, and A. Shalev. Exenatide blocks JAK1-STAT1 in pancreatic beta cells. *Metabolism: Clinical and Experimental* 56(7): 915-918, 2007.
26. Flowers, J.B., A.T. Oler, S.T. Nadler, Y.J. Choi*, K.L. Schueler, B.S. Yandell, **C. Kendziorski**, and A.D. Attie. Abdominal obesity in BTBR male mice is associated with peripheral but not hepatic insulin resistance. *American Journal of Physiology Endocrinology and Metabolism*, 292(3): E936-945, 2007.
27. Wang H., D. Teske, A. Tess, R. Kohlhepp, Y.J. Choi*, **C. Kendziorski**, and A.R. Moser. Identification of novel modifier loci of Apc Min affecting mammary tumor development. *Cancer Research* 67(23): 11226-11233, 2007.
28. Edwards, M.G., R. Anderson, M. Yuan*, **C. Kendziorski**, R. Weindruch, and T. Prolla. Gene Expression Profiling of Aging Reveals Activation of a p53-Mediated Transcriptional Program. *BMC Genomics* 8:80, 2007.
29. Mellman,D.L., M.L. Gonzales, C.A. Barlow, P. Wang*, **C. Kendziorski**, and R.A. Anderson. A Novel PI4, 5P2 Regulated Nuclear Poly(A) Polymerase Controls Expression of Select mRNAs. *Nature*,451(7181): 1013-1017, 2008.
30. Keller, M.P., Y.J. Choi*, P. Wang*, D.B. Davis, M.E. Rabaglia, A.T. Oler, D.S. Stapleton, C. Argmann, K.L. Schueler, S. Edwards, H.A. Steinberg, E. Chaibub Neto, R. Kleinhanz, S. Turner, M.K. Hellerstein, E.E. Schadt, B. Yandell, **C. Kendziorski**, and A.D. Attie. A Gene Expression Network Model of Type II Diabetes Establishes a Relationship Between Cell Cycle Regulation in Islets and Diabetes Susceptibility. *Genome Research*, 18(5): 706-716, 2008.

31. Flowers M.T., M.P. Keller, Y.J. Choi*, H. Lan, **C. Kendziorski**, J.M. Ntambi, and A.D. Attie. Liver gene expression analysis reveals endoplasmic reticulum stress and metabolic dysfunction in SCD1-deficient mice fed a very low-fat diet. *Physiological Genomics*, 33(3): 361-372, 2008.
32. Ferrara, C.T., P. Wang*, E. Chaibub Neto, R.D. Stevens, J.R. Bain, B.R. Wenner, O.R. Ilkayeva, M.P. Keller, D.A. Blasiolo, **C. Kendziorski**, B.S. Yandell, C.B. Newgard, and A.D. Attie. Genetic Networks of Liver Metabolism Revealed by Integration of Metabolic and Transcriptomic Profiling. *PLoS Genetics*, 4(3):e1000034, 2008.
33. Zhao E., M.P. Keller, M.E. Rabaglia, A.T. Oler, D.S. Stapleton, K.L. Schueler, E.C. Neto, J.Y. Moon, P. Wang, I.M. Wang, P.Y. Lum, I. Ivanovska, M. Cleary, D. Greenawalt, J. Tsang, Y.J. Choi*, R. Kleinhanz, J. Shang, Y.P. Zhou, A.D. Howard, B.B. Zhang, **C. Kendziorski**, N.A. Thornberry, B.S. Yandell, E.E. Schadt, and A.D. Attie. Obesity and genetics regulate microRNAs in islets, liver, and adipose of diabetic mice. *Mammalian Genome*, 20(8):476-85, 2009.
34. Hopkins WJ, Elkahwaji J, **Kendziorski C**, Moser AR, Briggs PM, Suhs KA. Quantitative trait loci associated with susceptibility to bladder and kidney infections induced by Escherichia coli in female C3H/HeJ mice. *J Infect Dis* 199(3):355-61, 2009.
35. Andrei, A.* , and **C. Kendziorski**. An Efficient Method for Identifying Statistical Interactors in Gene Association Networks. *Biostatistics*, 10(4): 706-718, 2009.
36. Choi, Y.J.* , and **C. Kendziorski**. Statistical Methods for Gene Set Co-Expression Analysis. *Bioinformatics* 25(21):2780-2786, 2009.
37. Zhong, H., J. Beaulaurier, P.Y. Lum, C. Molony, X. Yang, D.J. Macneil, D.T. Weingarh, B. Zhang, D. Greenawalt, R. Dobrin, K. Hao, S. Woo, C. Fabre-Suver, S. Qian, M.R. Tota, M.P. Keller, **C. Kendziorski**, B.S. Yandell, V. Castro, A.D. Attie, L.M. Kaplan, and E.E. Schadt. Liver and adipose expression associated SNPs are enriched for association to type 2 diabetes. *PLoS Genetics* 6(5): e1000932, 2010.
38. Wang, P.* , J.A. Dawson*, M.P. Keller, B.S. Yandell, N.A. Thornberry, B.B. Zhang, I.M. Wang, E.E. Schadt, A.D. Attie, and **C. Kendziorski**. A model selection approach for expression quantitative trait loci (eQTL) mapping. *Genetics* 187(2): 611-621, 2011.
39. Flowers, M.T., C.M. Paton, S.M. O'Byrne, K. Schiesser, J.A. Dawson*, W.S. Blaner, **C. Kendziorski**, and J.M. Ntambi. Metabolic changes in skin caused by scd1 deficiency: a focus on retinol metabolism. *PLoS One*, May 9;6(5):e19734, 2011.
40. Dawson, J.A.* and **C. Kendziorski**. An Empirical Bayesian Approach for Identifying Differential Co-expression in High-throughput Experiments. *Biometrics* 68(2): 455-465, 2011.
41. Newton, M.A., Q. He and **C. Kendziorski**. A model-based analysis to infer the functional content of a gene list. *Statistical Applications in Genetics and Molecular Biology* 11(2): Article 9, 2012.
42. Wang C.Y., D.S. Stapleton, K.L. Schueler, M.E. Rabaglia, A.T. Oler, M.P. Keller MP, **C. Kendziorski, C.**, K.W. Broman, B.S. Yandell, E.E. Schadt, and A.D. Attie. Tsc2, a positional candidate gene underlying a quantitative trait locus for hepatic steatosis. *Journal of Lipid Research* 53(8):1493-1501, 2012.
43. Bagley, B.N., T.M. Keane, V.I. Maklakova, J.G. Marshall, R.A. Lester, M.M. Cancel, L.E. Bendzick, R.A. Been, S.C. Kogan, R.T. Cormier, **C. Kendziorski**, D.J. Adams, and L.S. Collier. A dominantly acting allele of Mcm4 causes chromosomal abnormalities and promotes tumorigenesis. *PLOS Genetics*, 8(11):e1003034, 2012.

44. Tu, Z., Keller, M.P., Zhang, C., Rabaglia, M.E., Greenawalt, D.M., Yang, X., Wang, I-M., Dai, H., Bruss, M.D., Lum, P.Y., Zhou, Y-P., Kemp, D.M., **Kendziorski, C.**, Yandell, B.S., Attie, A.D., Schadt, E.S., and Zhu, J. Integrative Analysis of a Cross-loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. *PLoS Genetics* 8(12):e1003107, 2012.
45. Dawson, J.A.* , S. Ye*, and **C. Kendziorski**. R/EBcoexpress: An R package for Discovering Differential Co-expression. *Bioinformatics*, Jul 15;28(14):1939-40, 2012.
46. Leng, N.* , J.A. Dawson*, R. M. Stewart, V. Ruotti, A. Rissman, B. Smits, J. Haag, M.N. Gould, J.A. Thomson, and **C. Kendziorski**. EBSeq: An empirical Bayes hierarchical model for inference in RNA-seq Experiments. *Bioinformatics* 29(8): 1035-1043, 2013.
47. Eng, K.E.* , S. Wang, W.H. Bradley, J.S. Rader, and **C. Kendziorski**. Pathway-Index Models for Construction of Patient-Specific Risk Profiles. *Statistics in Medicine*, 32(9): 1524-1535, 2013.
48. Anderson, S.A., Nizzi, C., Chang, Y.I., Deck, K.M., Schmidt, P., Galy, B. Broman, A.T., **Kendziorski, C.**, Hentze, M.W., Fleming, M.D., Zhang, J., and Eisenstein, R.S. The IRP1-HIF-2 α axis coordinates iron and oxygen sensing with erythropoiesis and iron absorption. *Cell Metabolism*, 17(2): 282-290, 2013.
49. Smits, B., Haag, J.D., Rissman, A.I., Sharman, D., Tran, A., Schoenborn, A., Baird, R., Peiffer, D., Leinweber, M., Muelbl, M., Meilahn, A., Eichelberg, M.R., Leng, N.* , **Kendziorski, C.**, Manorama, J., Powers, P., Alexander, C., and Gould, M.N.. The Gene Desert Mammary Carcinoma Susceptibility Locus Mcs1a Regulates Nr2f1 Modifying Mammary Epithelial Cell Differentiation and Proliferation. *PLoS Genetics* 9(6): e1003549, 2013.
50. Ray, M., Goldstein, S., Zhou, S., Potamouis, K., Sarkar, D., Newton, M. A., Esterberg, E.* , **Kendziorski, C.**, Bogler, O., and Schwartz, D. C. Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. *BMC genomics*, 14(1), 505, 2013.
51. Jiang, Y.Z., Wang, K., Li, Y., Dai, C.F., Wang, P*., **Kendziorski, C.**, Chen, D.B., and Zheng, J. Transcriptional and Functional Adaptations of Human Endothelial Cells to Physiological Chronic Low Oxygen. *Biology of Reproduction* 88(5): Article 114, 1-11, 2013.
52. Iruetagoiena J.I., Davis, W., Bird, C., Olsen, J., Radue, R., Broman, A.T.* , **Kendziorski, C.**, Bondurant, S.S., Golos, T., Bird, I., and Shah, D. Differential Changes in Gene Expression in Human Heart during Late First Trimester and Early Second Trimester of Pregnancy. *Prenatal Diagnosis* 34 (5), 431-437, 2014.
53. Kennedy-Darling, J., Guillen-Ahlers, H., Shortreed, M.R., Scalf, M., Knoener, R., Frey, B.L., **Kendziorski, C.**, Olivier, M., Gasch, A.P., and Smith, L.M. Discovery of chromatin-associated proteins via sequence-specific capture and mass spectrometric protein identification in *Saccharomyces cerevisiae*, *Journal of Proteome Research* 13(8): 3810–3825, 2014.
54. Iruetagoiena J.I., Davis, W., Bird, C., Olsen, J., Radue, R., Broman, A.T.* , **Kendziorski, C.**, Bondurant, S.S., Golos, T., Bird, I., and Shah, D. Metabolic gene profile in early human fetal heart development. *Molecular Human Reproduction* 20(7): 690-700, 2014.
55. Christopherson, M.R. Dawson, J.A.* , Stevenson, D., Cunningham, A., Bramhacharya, S., Weimer, P.J., **Kendziorski, C.**, and G. Suen. Unique aspects of fiber degradation by the ruminal ethanologen *Ruminococcus albus* 7 revealed by physiological and transcriptomic analysis. *BMC genomics* 15(1): 1066, 2014.

56. Hines, E.A., Szakaly, R.J., Leng, N.*, Webster, A.T., Verheyden, J.M., Lashua, A.J. **Kendziorski, C.**, Rosenthal, L.A., Gern, J.E., Sorkness, R.L., Sun, X., and R.F. Lemanske Jr. Comparison of Temporal Transcriptomic Profiles from Immature Lungs of Two Rat Strains Reveals a Viral Response Signature Associated with Chronic Lung Dysfunction. *PLoS One* 9(12): e112997, 2014.
57. St. John, H.C, Bishop, K.A., Meyer, M.B. Benkusky, N.A., Leng, N.*, **Kendziorski, C.**, Bonewald, L.F., and J.W. Pike. The osteoblast to osteocyte transition: epigenetic changes and response to the vitamin D3 hormone. *Molecular Endocrinology* 28(7):1150-65, 2014.
58. Ye, S.*, Dawson, J.A.*, and **C. Kendziorski**. Extending information retrieval methods to personalized genomic based studies of disease. *Cancer Informatics*, 13(7): 85-95, 2014.
59. Song, C., Chung, L., Xiaokang, P., Zhanjun, L., Ding, Y., Sachdev, M., Muthusami, S., Gowda, C.S., Ge, Z., Steffens, S., Tan, B-H., **Kendziorski, C.**, Newton, M.A., and S. Dovat. Chromatin State Shaping the Gene Expression Profiling in the Inducible Differentiation of Promyelocytic Leukemia Cells. *Blood* 124(21), 2014.
60. Tran, K.A., Jackson, S.A., Olufs, Z.P.G., Leng, N. *, **Kendziorski, C.**, Roy, S., and R. Sridharan. Collaborative rewiring of the pluripotency network by chromatin and signaling modulating pathways. *Nature Communications*, 6(6188): doi:10.1038/ncomms7188, 2015.
61. Welham, N.V., Ling, C., Dawson, J.A.*, **Kendziorski, C.**, Thibeault, S.L., and Yamashita, M. Microarray-based characterization of differential gene expression during vocal fold wound healing. *Disease Models and Mechanisms*, 8(3):311-321, 2015.
62. Korthauer, K. *, and **C. Kendziorski**. MADGiC: a model-based approach for identifying driver genes in cancer. *Bioinformatics*, 31(10): 1526-1535, 2015.
63. Marty, A.J., Broman, A.T.*, **Kendziorski, C.**, Zarnowski, R. Dwyer, T., Bond, L.M., Ntambi, J.M., Lounes-Hadj Sahraoui, A., Fontaine, J., and Gauthier, G.M. Fungal morphology, iron homeostasis, and lipid metabolism regulated by a GATA transcription factor in *Blastomyces dermatitidis*. *PLoS Pathogens*, 11(6):e1004959, 2015.
64. Leng, N.*, Li, Y., McIntosh, B.E., Nguyen, B.K., Duffin, B., Tian, S., Thomson, J.A., Dewey, C., Stewart, R., and **Kendziorski, C.** EBSeq-HMM: A Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. *Bioinformatics* 31(16): 2614-2622, 2015.
65. Leng, N.*, Chu, L-F., Barry, C., Li, Y.*, Choi, J.*, Li, X.*, Jiang, P., Stewart, R.M., Thomson, J.A., and **Kendziorski, C.** Oscope identifies oscillatory genes in unsynchronized single cell RNA-Seq experiments. *Nature Methods* 12(10): 947-950, 2015.
66. Bartlett, R.S., Gaston, J.D., Yen, T.Y., **Kendziorski, C.**, and Thibeault, S.L. Biomechanical screening of cell therapies for vocal fold scar. *Tissue Engineering Part A* 21 (17-18): 2437-2447, 2015.
67. Bradley, W.H., Eng, K. *, Mutch, D.G., MacKinnon, C., **Kendziorski, C.**, and Rader, J. Comparing gene expression data from FFPE tissue and qPCR with that from snap-frozen tissue and microarrays for modeling outcomes of patients with ovarian carcinoma. *BMC clinical pathology* 15 (1): 17, 2015.
68. Broman, K.W., Keller, M.P., Broman, A.T., **Kendziorski, C.**, Yandell, B.S., Sen, S., and Attie, A.D. Identification and correction of sample mix-ups in expression genetic data. *G3: Genes, Genomes, Genetics* 5 (10): 2177-2186, 2015.

69. Tian, J., Keller, M.P., Oler, A., Rabaglia, M., Schueler, K., Stapleton, D., Broman, A.T., Zhao, W., **Kendziorski, C.**, Yandell, B.S., Hagenbuch, B., Broman, K.W., and Attie, A.D. Identification of *Slco1a6* as a candidate gene that broadly affects gene expression in mouse pancreatic islets. *Genetics* 201(3): 1253-1262, 2015.
70. Paul, P.K., Rabaglia, M.E., Stapleton, D.S., Wang, C-Y., Leng, N.*, **Kendziorski, C.**, Lewis, P., Newgard, C.B., Keller, M.P., and A.D. Attie. ASF1B Promotes Proliferation in Human Pancreatic β -cells. *Cell Cycle* 15: 3191-3202, 2016.
71. Keller, M.P., Paul, P.K., Rabaglia, M.E., Stapleton, D.S., Schueler, K.L., Broman, A.T., Ye, S.*, Leng, N.*, Brandon, C.J., Chaibub Neto, E., Plaisier, C.L. Simonett, S.P., Kebede, M.A., Sheynkman, G.M., Klein, M.A., Baliga, N.S., Smith, L.M., Broman, K.W., Yandell, B.S., **Kendziorski, C.**, and Attie, A.D. The Transcription Factor *Nfatc2* Regulates β -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. *PLoS Genetics* 12(12): e1006466, 2016.
72. Chu, L-F., Leng, N., Zhang, J., Hou, Z., Mamott, D., Vereide, D.T., Choi, J.*, **Kendziorski, C.**, Stewart, R., and Thomson, J.A. Single-cell RNA-seq reveals novel regulators of human embryonic stem cell differentiation to definitive endoderm. *Genome Biology* 17: 173-178, 2016.
73. Kishimoto, Y., Kishimoto, A.O., Ye, S.*, **Kendziorski, C.**, and Welham, N.V. Modeling fibrosis using fibroblasts isolated from scarred rat vocal folds. *Laboratory Investigation* 96: 807-816, 2016.
74. Bacher, R.*, and **Kendziorski, C.** Design and computational analysis of single-cell RNA-sequencing experiments. *Genome Biology* 17: 63-67, 2016.
75. Korthauer, K.D*., Chu, L-F., Newton, M.A., Li, Y.*, Thomson, J.A., Stewart, R., and **Kendziorski, C.** A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. *Genome Biology* 17: 222-227, 2016.
76. Choi, J., Ye, S.*, Eng, K.*, Korthauer, K.*, Bradley, W.H., Rader, J.S., and **Kendziorski, C.** IPI59: An Actionable Biomarker to Improve Treatment Response in Serous Ovarian Carcinoma Patients. *Statistics in Biosciences* 8: 1-12, 2016.
77. Leng, N.*, Choi, J.*, Chu, L-F., Thomson, J.A., **Kendziorski, C.**, and Stewart, R. OEFinder: a user interface to identify and visualize ordering effects in single-cell RNA-seq data. *Bioinformatics* 32 (9): 1408-1410, 2016.
78. Tian, J., Keller, M.P., Broman, A.T., **Kendziorski, C.**, Yandell, B.S., Attie, A.D., and Broman, K.W. The Dissection of Expression Quantitative Trait Locus Hotspots. *Genetics* 202(4): 1563-1574, 2016.
79. Bacher, R., Chu, L-F., Leng, N., Gasch, A.P., Thomson, J.A., Stewart, R., Newton, M.A., and **Kendziorski, C.** SCnorm: A quantile-regression based approach for robust normalization of single-cell RNA-seq data. *Nature Methods*, invited revision, 2017.
80. Ye, S.*, Bacher, R.*, Keller, M.P., Attie, A.D., and **Kendziorski, C.** Statistical Methods for Latent Class Quantitative Trait Loci Mapping. *Genetics*, invited revision, 2017.
81. Bradley, R.A., Shireman, J., McFalls, C., Choi, J.*, Chiang, M.S., Dong, Y., Canfield, S., Jones, J.R., Petersen, A., Palacek, S., Shusta, E., **Kendziorski, C.**, Yang, Y., Zhang, S-C. Regionally Specified Human Astrocytes Exhibit Differential Molecular Signatures and Functional Properties. Submitted, 2017.
82. Palatnik, A., Ye, S.*, **Kendziorski, C.**, Iden, M., Zigman, J.S., Hessner, M.J., Rader, J.S. Identification of a serum-induced transcriptional signature associated with metastatic cervical cancer. Submitted, 2017.

BOOK CHAPTERS, DISCUSSIONS, OPEN LETTERS

1. **Kendziorski, C.M.** Pooling Biological Samples in Microarray Studies in DNA Microarrays and Statistical Genomics Techniques: Design, Analysis, and Interpretation of Experiments Eds. D.B. Allison, G. Page, T.M. Beasley, J.W. Edwards, New York: Marcel Dekker, 2003.
2. Newton, M.A. and **C.M. Kendziorski**. Parametric Empirical Bayes Methods for Microarrays in The analysis of gene expression data: methods and software. Eds. G. Parmigiani, E.S. Garrett, R. Irizarry and S.L. Zeger, New York: Springer Verlag, 2003.
3. **Kendziorski, C.M.** A Discussion of Resampling-based multiple testing for microarray data analysis" by Y. Ge, S. Dudoit, and T.P. Speed. *Test: A Journal of the Spanish Society of Statistics and Operations Research* 12:1, 1-77, 2003.
4. Newton, M., P. Wang*, and **C. Kendziorski**. Hierarchical Mixture Models for Expression Profiles in Bayesian Inference for Gene Expression and Proteomics. Eds. Kim-Anh Do, Peter Mueller, and Marina Vanucci. Cambridge University Press, 2006.
5. Chen, M.* and **C. Kendziorski**. Interval Mapping for Expression Quantitative Trait Loci in Bayesian Inference for Gene Expression and Proteomics. Eds. Kim-Anh Do, Peter Mueller, and Marina Vanucci. Cambridge University Press, 2006.
6. **Kendziorski, C.M.** and M. Chen*. An Overview of Statistical Approaches for Expression Trait Loci Mapping in Meta-Analysis and Combining Information in Genetics. Eds. Rudy Guerra and David Allison. Chapman and Hall, 2007.
7. "31 Nerds Letter". Letter to Harold Varmus, head of NCI regarding concerns about prediction models used in Duke clinical trials. <http://news.sciencemag.org/scienceinsider/DukeTrialLetter.pdf> and <http://dukefactchecker.blogspot.com/2010/07/whos-who-from-genetics-demands-federal.html> July, 2010.
8. Korthauer, K.* , J.A. Dawson*, and **C. Kendziorski**. Predicting Cancer Subtypes Using Survival-Supervised Latent Dirichlet Allocation Models in Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data. Eds. Kim Anh-Do, Steve Qin, and Marina Vanucci. Cambridge University Press, 2012.

*Denotes one of C. Kendziorski's Ph.D. Students or Postdoctoral Scholars

RESEARCH GRANTS (CK PI)

Title: Statistical Methods for Analysis and Integration in Genomic Studies of Disease

Category: R01

Principal Investigator: Christina Kendziorski

Period: July 2012 – June 2016

Agency: NIH/NIGMS

Title: Statistical Modeling and Inference of Vast Matrices for Complex Problems

Principal Investigators: Yazhen Wang, Christina Kendziorski, and Ming Yuan

Period: September 2013 – May 2017

Agency: NSF

PRIOR RESEARCH GRANTS (CK PI)

Title: Statistical Methods for the Genomic Analysis of Gene Expression Data

Category: R01

Principal Investigator: Christina Kendziorski

Period: July 2006 - July 2012

Agency: NIH/NIGMS

Title: Validation of a genomics based assay for personalized treatment of patients with recurrent ovarian cancer
Category: UWCCC-investigator initiated translational award
Principal Investigator: Christina Kendziorski
Period: May 2011 – May 2013
Agency: UWCCC

Title: Pooling Designs for Microarray Studies
Category: R03
Principal Investigator: Christina Kendziorski
Period: July 2003- June 2005
Agency: NIH/NCI

COLLABORATIVE RESEARCH GRANTS

Title: A Multi-Scale, Systems-based Approach to Quantify Soft Tissue Healing
Category: R01
Principal Investigator: Susan Thibeault
Co-Investigator: Christina Kendziorski
Period: September 2012 – August 2017
Agency: NIH/NIDCD

Title: STAT3 and astrogliosis in Alexander disease
Category: R21
Principal Investigator: Tracy Hagemann
Co-Investigator: Christina Kendziorski
Period: July 2015 – June 2017
Agency: NIH/NINDS

Title: Institute for Clinical and Translational Research
Category: UL1
Principal Investigator: Marc Drezner
Period: October 2007 – September 2017
CK Role: Head of Statistical Genetics and Genomics
Agency: NIH

Title: Epithelial-mesenchyme interactions in a novel 3D model of vocal fold injury
Category: R01
Principal Investigator: Susan Thibeault
Co-Investigator: Christina Kendziorski
Period: September 2014 – August 2018
Agency: NIH/NIDCD

Title: BD2K Center for Predictive Computational Phenotyping
Category: U54
Principal Investigator: Mark Craven
Co-PIs on transcriptome based sub-project: Colin Dewey and Christina Kendziorski
Period: September 2015-August 2019
Agency: NIH/NIAID

Title: Post exertion malaise in GWI: Brain autonomic and behavioral interaction
Category: Merit award
Principal Investigator: Dane Cook
Co-Investigator: Christina Kendziorski
Period: May 2016 – April 2020
Agency: VA

Title: Global mass spectrometry-based analysis of covalent modifications in proteomes after radiation
Category: DTRA
Principal Investigator: Michael Sussman
Period: May 2016-April 2021
Co-Investigator: Christina Kendziorski
Agency: DOD