Stephen C. J. Parker

100 Washtenaw Avenue Ann Arbor, MI 48109 734-647-3144 scjp@umich.edu http://theparkerlab.org

PROFESSIONAL EXPERIENCE

2014 – present Assistant Professor, Department of Computational Medicine &

Bioinformatics

Assistant Professor, Department of Human Genetics **Member**, Genome Sciences Training Program (GSTP)

2016 – present
 2017 – present
 Member, Center for RNA Biomedicine
 Member, Genetics Training Program (GTP)

University of Michigan

Ann Arbor, MI

2012 – 2014 Pharmacology Research Associate (PRAT) Fellow

National Institute of General Medical Sciences

National Institutes of Health

Bethesda, MD

Advisor: Francis S. Collins, M.D., Ph.D.

2009 – 2011 Postdoctoral Fellow

National Human Genome Research Institute

National Institutes of Health

Bethesda, MD

Advisor: Elliott H. Margulies, Ph.D.

EDUCATION

2004 – 2009 Ph.D. in Bioinformatics and Systems Biology

Boston University Boston, MA

Advisor: Thomas D. Tullius, Ph.D.

1998 – 2000 M.S. in Molecular Biology and Biotechnology

Advisor: Edmund J. Stellwag, Ph.D.

1994 – 1998 B.S. in Biology, concentration in Molecular Biology

East Carolina University

Greenville, NC

RESEARCH EXPERIENCE

Assistant Professor

September 2014-present

University of Michigan, Departments of Computational Medicine & Bioinformatics and Human Genetics

The major goal of the lab is to generate mechanistic knowledge about how disease susceptibility is encoded in the non-coding portion of the genome, with a focus on type 2

diabetes. We accomplish this through an interdisciplinary combination of molecular/cellular and computational approaches. Specifically, we generate multiple high-throughput data sets on the genome, epigenome, transcriptome, and proteome across species and in disease-relevant tissues/cells and use computational approaches to integrate and analyze this data.

Postdoctoral Fellow

August 2009-August 2014

National Human Genome Research Institute, National Institutes of Health, Bethesda, MD Utilize high-performance computing platforms and high-throughput DNA sequencing technologies to address health-related biological problems.

Bioinformatics Consultant

March 2009-August 2009

BD TriPath, RTP, NC

Performed various computational gene expression microarray analyses to help establish new cancer biomarker research projects.

Research Assistant

August 2004-May 2009

Boston University, Boston, MA

Initiated various analyses to explore the relationship between DNA structure, evolutionary constraint, and genome function. Developed various computational algorithms and statistical approaches to investigate these relationships.

Genome Closure Data Analyst

July 2002-August 2004

The Broad Institute & MIT Center for Genome Research, Cambridge, MA

Measured and monitored the quality and accuracy of human genome closure data using various computational tools. Designed and implemented new computational tools using Unix and Perl programming knowledge.

Associate Scientist

January 2001-June 2002

Cogent Neuroscience Inc., Durham, NC

Responsible for all duties associated with operating the core sequencing facility. Simultaneously managed several side projects involving hit characterization. Developed and executed strategies to clone genes of interest for functional analysis.

M.S. Thesis Degree Research Project

January 1998-December 2000

East Carolina University, Greenville, NC

Employed molecular biology-based techniques to obtain the genomic sequence of a *Hox* gene region on the *HoxBa* cluster in the *Teleost* fish *Morone saxatilis*. Performed various evolutionary analyses using multiple bioinformatics techniques with the resulting data.

Research Associate

May-August 1998

Novartis Biotechnology Inc., RTP, NC

Research associate in Bioinformatics lab. Responsible for PCR amplifying an *Arabadopsis thaliana* EST library to be put on micro array chips. Performed standard molecular techniques using 96 well format protocols in order to achieve high-throughput results.

Research Assistant

May-August 1997 and May-August 1996

Glaxo Wellcome (currently GSK), RTP, NC

Completed two clinical studies for 5-alpha reductase inhibitor class drug using high-throughput robotic sample processing and HPLC/APCI/MS/MS detection. Assisted in the completion of several other clinical studies for various other compounds. Analyzed the resulting data and co-authored the Bioanalytical Reports resulting from these studies.

GRANT FUNDING

Current

- American Diabetes Association Pathway to Stop Diabetes Program, Career Initiator Award, Grant #1-14-INI-07 (2014-2020) \$1.625M total.
 "Deconstructing type 2 diabetes using genome-wide high-density multi-tissue 'omics' profiling"
- NIH/NIDDK 1U01DK105561-01(Co-I; PI Mohlke) (2015-2020) \$120k total directs. "Functional genetic variants for type 2 diabetes"
- NIH/NIDDK R00DK099240 (2013-2018) \$750k total over three years during R00 phase. "Synthesizing genome, epigenome, and transcriptome datasets in type 2 diabetes."
- NIH/NIDA R21DA041202 (Co-I; PI Burmeister) (2016-2018) \$275k total directs. "Molecular basis of GABRA2 haplotypes associated with behavior and addiction"
- NIH U24DK112342 (Co-I; PI Burant) (2016-2022) \$8.239M total. "Michigan MoTrPAC Chemical Analysis Site (MiCAS)"
- NIH/NHLBI 1U01HL137182 (Co-I; PI Kang) (2017-2020) \$1.629M total.
 "Scalable and Translational Analysis Tools on the Cloud for Deep Integrative Omics Data"
- NIH/NIDDK 2R01DK093757-06 (Co-I; PI Mohlke) (2017-2022) \$152k total directs. "Genetic epidemiology of rare and regulatory variants for metabolic traits"

Completed

- NIH/NIGMS Pharmacology Research Associate (PRAT) Fellowship (2011-2014) \$285k
- NIH/NHGRI/NISC Pilot Project Sequencing Award (2014) \$10k "Cell-type specific epigenome and transcriptome signatures of alpha and beta cells in rat islets." Co-author
- NIH/NHGRI/NISC Pilot Project Sequencing Award (2014) \$10k "Allelic and cross-species signatures of functional chromatin architecture in diabetes relevant cells." Primary author
- NIH/NHGRI/NISC Pilot Project Sequencing Award (2013) \$10k
 "Genome-wide regulatory element mapping at DNA binding site resolution in frozen samples." Primary author
- NIH/NHGRI/NISC Pilot Project Sequencing Award (2013) \$10k
 "Enhancer RNA-seq to measure regulatory element activity in type 2 diabetes." Primary author
- NIH/NHGRI/NISC Flagship Project Sequencing Award (2012) \$175k
 "Determining effects of diabetes variants on the transcriptome of human pancreatic islets." Co-author

RESEARCH SKILLS

- Utilization of high-performance UNIX computing environments.
- Proficient at operating large parallel computing clusters for bioinformatics analyses.

• Skilled at performing various molecular-based laboratory techniques.

Programming LanguagesOperating SystemsPerlLinux/UNIXRMac OS X

UNIX shell Windows NT/2000/XP

MySQL

HTML, XHTML, CSS, CGI

HONORS AND AWARDS

- Editorial Board, *eLife* (2017)
- Distinguished Postbac Mentor Award, NIH (2014)
- Trainee of the Year Award, NIH/NHGRI (2013)
- Selected participant to invitation-only Cold Spring Harbor Banbury conference on "Enhancer Biology in Health and Disease" (2013)
- Fellows Award for Research Excellence (FARE), NIH (2013)
- Pharmacology Research Associate (PRAT) Program Fellow, NIH/NIGMS (2011-2014)
- Genome Technology Young Investigators of the Year Award (2010)
- Boston University Bioinformatics Innovative Teaching Award (2009)
- Associate Faculty Member, Faculty of 1000 Biology (2008 present)
- National Academies, Ford Foundation Dissertation Fellowship (2008 2009)
- Genome Research Best Poster Award (Biology of Genomes Meeting, 2007)
- Boston University Presidential Fellowship (2004 2005)
- East Carolina University Mary C. Helms Scholarship for outstanding graduate student (2000)
- East Carolina University Research Day Best Poster Presentation Award (2000)
- East Carolina University James S. McDaniel Scholarship for outstanding graduate student (1999)
- East Carolina University Chancellor's List, Dean's List, and Honor Roll (1994 1998)
- East Carolina University soccer team

SCIENTIFIC SERVICE

- Abstract review committee, Bioinformatics and Computational Approaches section for American Society for Human Genetics (2017)
- Abstract review committee, American Diabetes Association (2017)
- Panel member, American Diabetes Association Focus on Fellows panel discussion on "Careers in Research: How to Get and Keep the World's Best Job" (2017)
- Study Section Member, National Human Genome Research Institute, H3Africa Research Projects (2017)
- Study Section Member, University of Michigan Center for RNA Biomedicine Pilot Grants (2017)
- Workshop Organizer, Harnessing Big Data for Precision Medicine: Infrastructures and Applications, Pacific Symposium on Biocomputing (2017)
- American Diabetes Association Scientific Sessions Content planning subcommittee: Genetics and Gene Regulation (2016 2017)
- Study Section Member, University of Michigan Medical School and Peking University Health Sciences Center Joint Institute grant review (2016)

- Executive Committee, Center for RNA Biomedicine, University of Michigan (2016 present)
- Bioinformatics Core Scientific Advisory Committee, University of Michigan (2016 present)
- External Reviewer for GrantSeeker Program at University of Texas Health Science Center at San Antonio (UTHSCSA) (2016)
- Abstract review committee, American Diabetes Association (2016)
- Manuscript review committee, Great Lakes Bioinformatics and the Canadian Computational Biology Conference (2016)
- Co-Chair, Admissions Committee, University of Michigan Department of Computational Medicine and Bioinformatics (2015 present)
- Grant reviewer for Diabetes UK (2015 2016)
- *Ad hoc* reviewer, Admissions Committee, University of Michigan Department of Computational Medicine and Bioinformatics (2014)
- Panel member, University of Michigan BF 527 discussion about the future of bioinformatics as a domain of data science (2014)
- Panel member, University of Michigan BF 527 discussion about the future of genomics (2014)
- Panel member, NHGRI Advances in Genomics Research Summer Program (2014)
- Reviewer, Fellows Award for Research Excellence (FARE), NIH (2014)
- Member, NHGRI, NIH Retreat Planning Committee (2013)
- Panel member, NHGRI, NIH Summer Intern Career Development Panel Discussion (2012)
- Member, NHGRI, NIH Genome Trainee Advisory Committee (GTAC) (2011 2013)
- Scientific Judge, NIH Graduate Student Research Symposium (2011 2013)
- Scientific Ambassador, DNA Day (2010 2013)
- Graduate Student Organization Travel Grant Review Committee Member (2009)
- National Center for Scientific Education, Project Steve Member (2009 present)
- Manuscript reviewer: Nature, Nature Genetics, Nature Communications, Bioinformatics, American Journal of Human Genetics, Genome Research, Genome Biology, Nucleic Acids Research, BMC Genomics, BMC Bioinformatics, PeerJ, PloS ONE, Genomics Data, Computers in Biology and Medicine, Diabetes, Gene, Trends in Genetics, Database, Human Heredity, and Advances in Nutrition
- Scientific Judge and Moderator, Boston University Regional High School Science Bowl (2007 – 2009)
- Organizing Committee Member, Boston University student-run Bioinformatics and Systems Biology Research Symposium (2007)

TEACHING EXPERIENCE

Mentor

University of Michigan, Ann Arbor, MI

Beth Ames Pediatric and Medical Genetics Fellow. Starts September 2017.

Daniel Quang Postdoctoral Fellow joint with Yuanfang Guan lab. Starts

August 2017.

Jessica Ebeling
Iyana Whalen
Shuze Wang
Biology UROP student. September 2017-present.
Biology UROP student. September 2017-present.
M.S. Student. Bioinformatics. September 2017-present.

Renaid Kim MSTP Rotation Student. August 2017.

Kevin Hu
Ph.D. Rotation Student. Bioinformatics. May-July 2017.
Alexandra Weber
Ph.D. Rotation Student. Bioinformatics. January-April 2017.
Maximilian Wehner
Biomedical Engineering UROP student. October 2016-present.

Sophia Manduca Biology UROP student. October 2016-present.

Collin Wang Summer intern. First place poster prize in Computational

Biology and Bioinformatics category at Detroit Science Fair.

June-September 2016, June-September 2017.

Adrienne Niederriter MSTP Rotation Student. Human Genetics. May-June 2016. Peter Orchard Ph.D. Student. Bioinformatics. T32 Fellowship. January 2016-

present.

Yoshi Kyono Postdoctoral Fellow joint with Jacob Kitzman laboratory. T32

Fellowship. July 2015-present.

Arushi Varshney Ph.D. Student. Human Genetics. AAUW Fellowship. Barbour

Scholar. May 2015-present.

Ricardo Albanus Ph.D. Student. Bioinformatics. May 2015-present.

Hadley VanRenterghem Summer intern. June-October 2015.

National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

Daniel Quang July 2014-July 2015; Best Speaker Award at Tsukuba Global

Science week in Tuskuba, Japan; co-authored manuscript.

Brooke Wolford August 2013-August 2015; Best Poster Award at NIH Postbac

Research Day; Best Poster Award at NHGRI Research

Symposium; primary author for successful NHGRI pilot grant; awarded NSF fellowship; co-author on manuscripts in review

and in preparation.

Leland Taylor August 2012-2013; awarded NSF Fellowship; accepted to

NIH-Oxford/Cambridge Doctoral Program; co-author on

manuscript.

Rachel Goldfeder 2010-2011; co-authored manuscript, currently Ph.D. student at

Stanford.

Boston University, Boston, MA

May 2005-May 2009

Mentored research projects for high school and undergraduate students. Supervised the research for eight students. Designed the project, performed interviews and screened applications, and helped select candidates. Trained all students the required molecular biology, chemistry, and computer science skills.

Doctoral Thesis Committees

2017 – present	Yeji Lee (Biostatistics, University of Michigan)
2017 – present	Tongyu Liu (Cell & Developmental Biology, University of Michigan)
2016 – present	Owen Funk (Human Genetics, University of Michigan)
2016 – present	Alexandre Daly (Human Genetics, University of Michigan)
2016 – present	Wei Zhou (Bioinformatics, University of Michigan)
2015 – present	Hongjiu Zhang (Bioinformatics, University of Michigan)
2015 – present	Christina Vallianatos (Human Genetics, University of Michigan)
2015 – present	Patricia Garay (Neuroscience, University of Michigan)
2015 - 2016	Chee Lee (Bioinformatics, University of Michigan)

Doctoral Qualifying Exam Committees

2017	Christopher Castro (Bioinformatics, University of Michigan)
2017	Jun Chen (Bioinformatics, University of Michigan)
2017	Marcus Sherman (Bioinformatics, University of Michigan)
2017	Li Guan (Bioinformatics, University of Michigan)
2016	Yaya Zhai (Bioinformatics, University of Michigan)
2016	Shriya Sethuraman (Bioinformatics, University of Michigan)
2015	Wei Zhou (Bioinformatics, University of Michigan)

Instructor Spring and Fall 2008

Boston University, Boston, MA

Co-developed, organized, and taught course material for a semester-long graduate-level Bioinformatics Applications course (ENG BF 527) designed to introduce students to concepts and tools used for genomic and computational biology research.

Head Graduate Teaching Assistant 1999 **Graduate Teaching Assistant** 1998

East Carolina University, Greenville, NC

Performed all duties associated with teaching freshman level biology labs and served as a mentor to novice teaching assistants.

Independent Teaching Lectures

- 1. "Conducting Interdisciplinary Research" University of Michigan Undergraduate Research Opportunities Program (UROP) class lecture, Ann Arbor, MI, February 7, 2017.
- 2. "Faculty Search Advice" National Institutes of Health, PRAT Fellow Program, webinar, November 28, 2016.
- 3. "Integrative analyses: Integrating genome, epigenome, and transcriptome data to detect functional signatures" University of Michigan Bioinf 545 / Biostat 646 / Stats 545 class on High-throughput molecular genomic and epigenomic data analysis. April 10, 2015.
- 4. "How to give a successful chalk talk" S.C.J. Parker. Invited seminar sponsored by NHGRI/NIH, Bethesda, MD. October 20, 2014.
- 5. "Computational Comparative Genomics: Insights into Human Disease" S. C. J. Parker. Invited DNA Day lecture for the Smithsonian National Museum of Natural History, Washington, DC. April 25, 2014.
- 6. "Comparative genomics: insights into biological variation (with a focus on non-coding regions)" S. C. J. Parker. Invited lecture at Mt. Vernon High School, Alexandria, VA. February 26, 2013.
- 7. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 16, 2013.
- 8. "Comparative genomics: insights into biological variation (with a focus on non-coding regions)" S. C. J. Parker. DNA Day lecture at Annandale High School, Annandale, VA. April 24, 2012.

- 9. "Comparative genomics: insights into biology (with a focus on non-coding DNA)" S. C. J. Parker. Hood College Department of Biology. Frederick, MD. March 1, 2012.
- 10. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 18, 2012.
- 11. "Genome Sequencing" S. C. J. Parker. University of the District of Columbia, Washington DC. September 21, 2011.
- 12. "Beyond genes: The hidden landscapes of your DNA. (non-coding DNA is important!)"
 S. C. J. Parker. DC Science Café Lecture Series at Busboys and Poets, Washington DC. August 8, 2011.
- 13. "Comparative Genomics: Evolution to Human Disease" S. C. J. Parker. DNA Day lecture at Annandale High School, Annandale, VA. April 11, 2011.
- 14. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 19, 2011.
- 15. "Comparative Genomics: From Evolution to Human Disease" S. C. J. Parker. DNA Day lecture at Wilde Lake High School, Columbia, MD. April 23, 2010.
- 16. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 19, 2010.

RESEARCH ACTIVITY

Publications

- "Interactions between genetic variation and cellular environment in skeletal muscle gene expression" D. L. Taylor, D. A. Knowles, L. J. Scott, A. H. Ramirez, F. Paolo Casale, B. N. Wolford, L. Guan, A. Varshney, R. D'Oliveira Albanus, S. C. J. Parker, N. Narisu, P. S. Chines, M. R. Erdos, R. P. Welch, M. Laakso, J. Tuomilehto, H. A. Koistinen, O. Stegle, M. Boehnke, E. Birney*, and F. S. Collins* (in review)
 [* equal contributor]
- 2. "A common type 2 diabetes risk variant potentiates activity of an evolutionarily conserved islet stretch enhancer and increases C2CD4A/B expression" I. Kycia, B. N. Wolford, J. R. Huyghe, C. Fuchsberger, S. Vadlamudi, R. Kursawe, A. Uyar, S. Khetan, M. Bolisetty, A. Mathur, J. Kuusisto, M. Laakso, D. Ucar, K. L. Mohlke, M. Boehnke, F. S. Collins, S. C.J. Parker, and M. L. Stitzel (*in review*)
- 3. "Large meta-analysis of genome wide association studies identifies five loci for lean body mass" MC Zillikens, S Demissie, YH Hsu, LM Yerges-Armstrong, WC Chou, L Stolk, *et al. Nature Communications* (2017) *Pubmed link*
- 4. "A type 2 diabetes-associated functional regulatory variant in a pancreatic islet enhancer at the ADCY5 locus" T. S. Roman, M. E. Cannon, S. Vadlamudi, M. L. Buchkovich, B.

- N. Wolford, R. P. Welch, M. A. Morken, G. J. Kwon, A. Varshney, R. Kursawe, Y. Wu, A. U. Jackson, NISC Comparative Sequencing Program, M. R. Erdos, J. Kuusisto, M. Laakso, L. J. Scott, M. Boehnke, F. S. Collins, S. C. J. Parker, M. L. Stitzel, and K. L. Mohlke. *Diabetes* (2017) *Pubmed link*
- 5. "Genetic regulatory signatures underlying islet gene expression and type 2 diabetes" A. Varshney*, L. J. Scott*, R. Welch*, M. R. Erdos*, P. S. Chines, N. Narisu, R. D'Oliveira Albanus, P. Orchard, B. N. Wolford, R. Kursawe, S. Vadlamudi, M. E. Cannon, J. Didion, J. Hensley, A. Kirilusha, NISC Comparative Sequencing Program, L. L. Bonnycastle, D. L. Taylor, R. M. Watanabe, K. L. Mohlke, M. Boehnke*, F. S. Collins*#, S. C. J. Parker*#, M. L. Stitzel* *PNAS* (2017) *Pubmed link* [# corresponding author, * equal contributor]
- 6. "The genetic regulatory signature of type 2 diabetes in human skeletal muscle" L.J. Scott*, M.R. Erdos*, J.R. Huyghe*, R.P. Welch*, A.T. Beck, B.N. Wolford, P.S. Chines, J.P. Didion, N. Narisu, H.M. Stringham, D.L. Taylor, A.U. Jackson, S. Vadlamudi, L.L. Bonnycastle, L. Kinnunen, J. Saramies, J. Sundvall, R. Albanus, A. Kiseleva, J. Hensley, G. Crawford, H. Jiang, X. Wen, R.M. Watanabe, T.A. Lakka, K.L. Mohlke, M. Laakso, J. Tuomilehto, H.A. Koistinen, M. Boehnke*, F.S. Collins*, S.C.J. Parker* Nature Communications (2016) Pubmed link
 [* equal contributor]
- 7. "The genetic architecture of type 2 diabetes" Christian Fuchsberger*, Jason Flannick*, Tanya M Teslovich*, Anubha Mahajan*, Vineeta Agarwala*, Kyle J Gaulton*, Clement Ma, Pierre Fontanillas, Loukas Moutsianas, Davis J McCarthy, Manuel A Rivas, John R B Perry, Xueling Sim, Thomas W Blackwell, Neil R Robertson, N William Rayner, Pablo Cingolani, Adam E Locke, Juan Fernandez Tajes, Heather M Highland, Josee Dupuis, Peter S Chines, Cecilia M Lindgren, Christopher Hartl, Anne U Jackson, Han Chen, Jeroen R Huvghe, Martijn van de Bunt, Richard D Pearson, Ashish Kumar, Martina Müller- Nurasyid, Niels Grarup, Heather M Stringham, Eric R Gamazon, Jaehoon Lee, Yuhui Chen, Robert A Scott, Jennifer E Below, Peng Chen, Jinyan Huang, Min Jin Go, Michael L Stitzel, Dorota Pasko, Stephen CJ Parker, Tibor V Varga, Todd Green, Nicola L Beer, Aaron G Day- Williams, Teresa Ferreira, Tasha Fingerlin, Momoko Horikoshi, Cheng Hu, Iksoo Huh, Mohammad Kamran Ikram, Bong- Jo Kim, Yongkang Kim, Young Jin Kim, Min-Seok Kwon, Juyoung Lee, Selyeong Lee, Keng-Han Lin, Taylor J Maxwell, Yoshihiko Nagai, Xu Wang, Ryan P Welch, Joon Yoon, Weihua Zhang, Nir Barzilai, Benjamin F Voight, Bok- Ghee Han, Christopher P Jenkinson, Teemu Kuulasmaa, Johanna Kuusisto, Alisa Manning, Maggie C Y Ng, Nicholette D Palmer, Beverley Balkau, Alena Stančáková, Hanna E Abboud[†], Heiner Boeing, Vilmantas Giedraitis, Dorairaj Prabhakaran, Omri Gottesman, James Scott, Jason Carey, Phoenix Kwan, George Grant, Joshua D Smith, Benjamin M Neale, Shaun Purcell, Adam S Butterworth, Joanna M M Howson, Heung Man Lee, Yingchang Lu, Soo- Heon Kwak, Wei Zhao, John Danesh, Vincent K L Lam, Kyong Soo Park, Danish Saleheen, Wing Yee So, Claudia H T Tam, Uzma Afzal, David Aguilar, Rector Arya, Tin Aung, Edmund Chan, Carmen Navarro, Ching- Yu Cheng, Domenico Palli, Adolfo Correa, Joanne E Curran, Denis Rybin, Vidya S Farook, Sharon P Fowler, Barry IFreedman, Michael Griswold, Daniel Esten Hale, Pamela J Hicks, Chiea- Chuen Khor, Satish Kumar, Benjamin Lehne, Dorothée Thuillier, Wei Yen Lim, Jianjun Liu, Yvonne T van der Schouw, Marie Loh, Solomon K Musani, Sobha Puppala, William R Scott,

Loïc Yengo, Sian-Tsung Tan, Herman A Taylor Jr, Farook Thameem, Gregory Wilson Sr, Tien Yin Wong, Pål Rasmus Njølstad, Jonathan C Levy, Massimo Mangino, Lori L Bonnycastle, ThomasSchwarzmayr, João Fadista, Gabriela L Surdulescu, Christian Herder, Christopher J Groves, Thomas Wieland, Jette Bork-Jensen, Ivan Brandslund, Cramer Christensen, Heikki A Koistinen, Alex S F Doney, Leena | PageKinnunen, Tõnu Esko, Andrew J Farmer, Liisa Hakaste, Dylan Hodgkiss, Jasmina Kravic, Valeriya Lyssenko, Mette Hollensted, Marit E Jørgensen, Torben Jørgensen, Claes Ladenvall, Johanne Marie Justesen, Annemari Käräjämäki, Jennifer Kriebel, Wolfgang Rathmann, Lars Lannfelt, Torsten Lauritzen, Narisu Narisu, Allan Linneberg, Olle Melander, Lili Milani, Matt Neville, Marju Orho-Melander, Lu Qi, Qibin Qi, Michael Roden, Olov Rolandsson, Amy Swift, Anders H Rosengren, Kathleen Stirrups, Andrew R Wood, Evelin Mihailov, Christine Blancher, Mauricio O Carneiro, Jared Maguire, Ryan Poplin, Khalid Shakir, Timothy Fennell, Mark DePristo, Martin Hrabé de Angelis, Panos Deloukas, Anette P Gjesing, Goo Jun, Peter Nilsson, Jacquelyn Murphy, Robert Onofrio, Barbara Thorand, Torben Hansen, Christa Meisinger, Frank B Hu, Bo Isomaa, Fredrik Karpe, Liming Liang, Annette Peters, Cornelia Huth, Stephen P O'Rahilly, Colin N A Palmer, Oluf Pedersen, Rainer Rauramaa, Jaakko Tuomilehto, Veikko Salomaa, Richard M Watanabe, Ann-Christine Syvänen, Richard N Bergman, Dwaipayan Bharadwaj, Erwin P Bottinger, Yoon Shin Cho, Giriraj R Chandak, Juliana C N Chan, Kee Seng Chia, Mark J Daly, Shah B Ebrahim, Claudia Langenberg, Paul Elliott, Kathleen A Jablonski, Donna M Lehman, Weiping Jia, Ronald C W Ma, Toni I Pollin, Manjinder Sandhu, Nikhil Tandon, Philippe Froguel, Inês Barroso, Yik Ying Teo, Eleftheria Zeggini, Ruth J F Loos, Kerrin S Small, Janina S Ried, Ralph A DeFronzo, Harald Grallert, Benjamin Glaser, Andres Metspalu, Nicholas J Wareham, Mark Walker, Eric Banks, Christian Gieger, Erik Ingelsson, Hae Kyung Im, Thomas Illig, Paul W Franks, Gemma Buck, Joseph Trakalo, David Buck, Inga Prokopenko, Reedik Mägi, Lars Lind, Yossi Farjoun, Katharine R Owen, Anna L Gloyn, Konstantin Strauch, Tiinamaija Tuomi, Jaspal Singh Kooner, Jong-Young Lee, Taesung Park, Peter Donnelly, Andrew D Morris, Andrew T Hattersley, Donald W Bowden, Francis S Collins, Gil Atzmon, John C Chambers, Timothy D Spector, Markku Laakso, Tim M Strom, Graeme I Bell, John Blangero, Ravindranath Duggirala, E Shyong Tai, Gilean McVean, Craig L Hanis, James G Wilson, Mark Seielstad, Timothy M Frayling, James B Meigs, Nancy J Cox, Rob Sladek, Eric S Lander, Stacey Gabriel, Noël P Burtt, Karen L Mohlke, Thomas Meitinger, Leif Groop, Goncalo Abecasis, Jose C Florez, Laura J Scott, Andrew P Morris, Hyun Min Kang, Michael Boehnke, David Altshuler, Mark I McCarthy (accepted) Nature [* equal contributor]

- 8. "Super Enhancers in cancers, complex disease, and developmental disorders." A. R. Niederriter, A. Varshney, S. C. J. Parker, and D. M. Martin. *Genes* (2015) *Pubmed link*
- "Motif signatures in stretch enhancers refine disease-associated genetic variants." D. X. Quang, M. R. Erdos, S. C. J. Parker*#, and F. S. Collins.* *Epigenetics & Chromatin* (2015) *Pubmed link* [# corresponding author, * equal contributor]
- 10. "Super-enhancers delineate disease-associated regulatory nodes in T cells." J. O'Shea, G. Vahedi, Y. Kanno, Y. Furumoto, K. Jiang, S. C. J. Parker, M. Erdos, S.

- Davis, R. Roychoudhuri, N. Restifo, M. Gadina, Z. Tang, Y. Ruan, F. S. Collins, and V. Sartorelli. *Nature* (2015) *Pubmed link*
- 11. "GBshape: a genome browser database for DNA shape annotations." T. P. Chiu, L. Yang, T. Zhou, B. J. Main, **S. C. J. Parker**, S. V. Nuzhdin, T. D. Tullius, and R. Rohs. *Nucleic Acids Res.* (2014) *Pubmed link*
- 12. "Comparative analysis of metazoan chromatin architecture" The modENCODE Project Consortium*. *Nature* (2014) *Pubmed link* [* lead analyst]
- 13. "Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants" S. C. J. Parker*, M. L. Stitzel*, D. L. Taylor, J. M. Orozco, M. R. Erdos, J. A. Akiyama, K. Lammerts van Bueren, P. S. Chines, N. Narisu, NISC Comparative Sequencing Program, B. L. Black, A. Visel, L. A. Pennacchio, F. S. Collins. *PNAS* (2013) *Pubmed link* [* co first author]
- 14. "Somatic Mutations in MAP3K5 Attenuate Its Proapoptotic Function in Melanoma through Increased Binding to Thioredoxin." T. D. Prickett*, B. Zerlanko*, J. J. Gartner, S. C. J. Parker, K. Dutton-Regester, J. C. Lin, J. K.Teer, X. Wei, J. Jiang, NISC Comparative Sequencing Program, G. Chen, M. A. Davies, J. E. Gershenwald, W. Robinson, S. Robinson, N. K. Hayward, S. A. Rosenberg, E. H. Margulies, Y. Samuels. *Journal of Investigative Dermatology* (2013) <u>Pubmed link</u>
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- 17. "Mutational signatures of de-differentiation in functional non-coding regions of melanoma genomes." **S. C. J. Parker**, J. Gartner, I. Cardenas-Navia, X. Wei, H. Ozel Abaan, S. S. Ajay, N. F. Hansen, L. Song, U. K. Bhanot, J. K. Killian, Y. Gindin, R. Walker, P. S. Meltzer, J. C. Mullikin, T. S. Furey, G. E. Crawford, S. A. Rosenberg, Y. Samuels, and E. H. Margulies. *PLoS Genetics* 8(8) (2012) *Pubmed link*
- 18. "Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection." Y. Shibata*, N. C. Sheffield*, O. Fedrigo, C. C. Babbitt, M. Wortham, D. London, L. Song, A. K. Tewari, S. C. J. Parker, E. H. Margulies, G. A. Wray, T. S. Furey, and G. E. Crawford. *PLoS Genetics* 8(6) (2012) *Pubmed link*

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- 20. "Accurate and comprehensive sequencing of personal genomes." S. S. Ajay, S. C. J. Parker, H. Ozel Abaan, K. Fuentes Fajardo, and E. H. Margulies. *Genome Research* (2011) *Pubmed link*
- 21."A computational method to search for DNA structural motifs in functional genomic elements." **S. C. J. Parker**, A. Harlap, and T. D. Tullius. *Methods in Molecular Biology: Yeast Systems Biology, Humana Press, USA* (2011) *Pubmed link*
- 22. "Evolutionary constraint on DNA shape in the human genome." T. D. Tullius, S. C. J. Parker, and E. H. Margulies. Evolutionary Biology: 14th Meeting 2010, P. Pontarotti, ed. Springer Heidelberg (2011) <u>Book chapter link</u>
- 23."A bioinformatics approach to determining sample identity from pooled lanes of high-throughput sequencing data." R. L. Goldfeder*, **S. C. J. Parker***, S. S. Ajay, H. Ozel Abaan, and E. H. Margulies. *PLoS ONE* (2011) *Pubmed link* [* co first author]
- 24. "A User's Guide to the Encyclopedia of DNA Elements (ENCODE)." The ENCODE Project Consortium. *PLoS Biology*. 9(4):e1001046 (2011) *Pubmed link*
- 25. "DNA shape, genetic codes, and evolution." **S. C. J. Parker** and T. D. Tullius. *Current Opinion in Structural Biology*. Advanced online publication (2011) *Pubmed link*
- 26. "Global epigenomic analysis of primary human pancreatic islets provides insights into type 2 diabetes susceptibility loci" M. L. Stitzel, P. Sethupathy, D. S. Pearson, P. S. Chines, L. Song, M. R. Erdos, R. Welch, S. C. J. Parker, A. P. Boyle, L. J. Scott, NISC Comparative Sequencing Program, E. H. Margulies, M. Boehnke, T. S. Furey, G. E. Crawford, and F. S. Collins. *Cell Metabolism* 12(5):443-55 (2010) *Pubmed link*
- 27. "Human NPY Promoter Variation rs16147 as a Moderator of Prefrontal NPY Gene Expression and Negative Affect" W. H. Sommer, J. Lidström, H. Sun, D. Passer, R. Eskay, **S. C. J. Parker**, S. H. Witt, U. Zimmermann, V. Nieratschker, M. Rietschel, E. H. Margulies, M. Palkovits, M. Laucht, and M. Heilig. *Human Mutation*. Online publication (2010) *Pubmed link*
- 28. "Family-based analysis of candidate genes for polycystic ovary syndrome" K. G. Ewens, D. R. Stewart, W. Ankener, M. Urbanek, J. M. McAllister, C. Chen, K. M. Baig, S. C. J. Parker, E. H. Margulies, R. S. Legro, A. Dunaif, J. F. Strauss III, and R. S. Spielman. *Journal of Clinical Endocrinology and Metabolism* 95:2306-2315 (2010) *Pubmed link*
- 29. "Local DNA Topography Correlates with Functional Non-coding Regions of the Human Genome" **S. C. J. Parker**, L. Hansen, H. Ozel Abaan, T. D. Tullius, and E. H. Margulies. *Science* 324:389-392 (2009) *Pubmed link*
- 30. "The Relationship Between Fine Scale DNA Structure, GC Content, and Functional Elements in 1% of the Human Genome" **S. C. J. Parker**, E. H. Margulies, and T. D. Tullius. *Genome Informatics* 20:199-211 (2008) *Pubmed link*

- 31."Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project" The ENCODE Project Consortium. *Nature* 447:799-816 (2007) *Pubmed link*
- 32."Detection of DNA structural motifs in functional genomic elements" J.A. Greenbaum, S. C. J. Parker, and T.D. Tullius. *Genome Research* 17:940-6 (2007) *Pubmed link*
- 33."Towards the identification of essential genes using targeted genome sequencing and comparative analysis" A. Gustafson, E. Snitkin, S. C. J. Parker, C. DeLisi and S. Kasif. *BMC Genomics* 7:265 (2006) *Pubmed link*
- 34."DNA Sequence and Analysis of Human Chromosome 8" C. Nusbaum, *et al. Nature* 439:331-5 (2006) *Pubmed link*
- 35."Finishing the euchromatic sequence of the human genome" International Human Genome Sequencing Consortium. *Nature* 431:931-45 (2004) *Pubmed link*

Selected Oral Presentations

- 1. American Diabetes Association 77th Scientific Sessions, San Diego, CA, June 11, 2017.
- 2. University of Michigan, T32 Lecture Series: Multidisciplinary training program in basic diabetes research, Ann Arbor, MI, May 17, 2017.
- 3. University of Southern California, Diabetes and Obesity Research Institute (DORI) annual symposium, Los Angeles, CA, February 28, 2017.
- 4. University of Michigan, Center for RNA Biomedicine seminar series, Ann Arbor, MI, December 15, 2016.
- 5. Michigan State University, Science at the Edge seminar series, East Lansing, MI, December 9, 2016.
- 6. University of Michigan, High Throughput Sequencing Special Interest Group, Ann Arbor, MI, June 16, 2016.
- 7. Genomics@Wayne Research Symposium, Detroit, MI, October 28, 2016.
- 8. American Diabetes Association 76th Scientific Sessions, New Orleans, LA, June 14, 2016.
- 9. University of Michigan Center for RNA Biomedicine Research Symposium, Ann Arbor, MI, March 25, 2016.
- 10. The University of Michigan, National Center for Integrative Biomedical Informatics (NCIBI) Tools & Technology talk, Ann Arbor, MI, April 16, 2015.
- 11. The University of Rochester, Graduate Student Society, Rochester, NY. January 13, 2015.

- 12. The University of Michigan, Bioinformatics Workshop, Ann Arbor, MI. October 13, 2014.
- 13. The University of Michigan, Department of Human Genetics, Ann Arbor, MI. September 9, 2014.
- 14. The American Diabetes Association 74th Scientific Sessions, San Francisco, CA, June 13-17, 2014.
- 15. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 6-10, 2014.
- 16. The Jackson Laboratory, Bar Harbor, ME. March 13, 2014.
- 17. Vanderbilt University School of Medicine, Department of Medicine, Nashville, TN. March 4, 2014.
- 18. The National Institutes of Health, National Institute on Aging, Earl Stadtman Investigator talk, Baltimore, MD. February 24, 2014.
- 19. Case Western Reserve University, Department of Genetics and Genome Sciences, Cleveland, OH. February 19, 2014.
- 20. The University of Massachusetts Medical School, Program in Bioinformatics & Integrative Biology, Worcester, MA. February 3, 2014.
- 21. The Jackson Laboratory for Genomic Medicine, Farmington, CT. January 29, 2014.
- 22. The University of Michigan, Department of Computational Medicine & Bioinformatics, Ann Arbor, MI. January 15, 2014.
- 23. Duke University, Department of Biostatistics and Bioinformatics, Durham, NC. January 8, 2014.
- 24. The National Institutes of Health, Earl Stadtman tenure track investigator search: Symposium on Computational Biology, Bioinformatics, Biostatistics, and Mathematics. Bethesda, MD. December 2, 2013.
- 25. Banbury Meeting on Enhancer Biology in Health and Disease, Cold Spring Harbor, NY. October 27-30, 2013.
- 26. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 7-11, 2013.
- 27. FUSION Study Meeting. Ann Arbor, MI. November 27, 2012.
- 28. The National Institutes of Health, Chromatin DECODE Meeting, Bethesda, MD. November 13, 2012.
- 29. The 17th Conversation: Journal of Biomolecular Structure and Dynamics; Invited under young investigator program. Albany, NY. June 14-18, 2011.
- 30. Annual Retreat for the National Human Genome Research Institute, National Institutes of Health, Cambridge, MD. November 15-16, 2010.
- 31. The ENCODE Consortium Meeting, Bethesda, MD. March 11, 2010.

- 32. Friday Floor Forums at the National Human Genome Research Institute, National Institutes of Health, Bethesda, MD. January 29, 2010.
- 33. Helicos BioSciences Corporation, Cambridge, MA. May 14, 2009.
- 34. Doctoral Dissertation Defense. Boston University, Boston, MA. April 9, 2009.
- 35. 8th International Workshop on Bioinformatics and Systems Biology. Zeuthen, Germany. June 9-11, 2008
- 36. Boston University Chemistry and Biology Seminar Series. April 23, 2008.
- 37. The ENCODE Consortium Chromatin and Replication Subgroup Meeting. Seattle, WA. October 28-30, 2005.
- 38. Master of Science Thesis Seminar. East Carolina University, Greenville, NC. February 16, 2001
- 39. NCAS (North Carolina Academy of Sciences) Meeting. Raleigh, NC. March 31-April 2, 2000

Selected Poster Presentations

- 1. The ENCODE and modENCODE Consortia Meeting, Crystal City, VA. May 23-25, 2011
- 2. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 10-14, 2010
- 3. The Genome Informatics Meeting, Hinxton, UK. September 14-18, 2010
- 4. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 11-15, 2010
- 5. The ENCODE Consortium Meeting. Bethesda, MD. March 12, 2010.
- 6. National Human Genome Research Institute, National Institutes of Health, Scientific Retreat, Gettysburg, PA. November 17-18, 2009.
- 7. The 16th Conversation: Journal of Biomolecular Structure and Dynamics. Albany, NY. June 16-20, 2009
- 8. National Institutes of Health, National Graduate Student Research Festival. Bethesda, MD. September 10-12, 2008
- 9. Boston University Science and Engineering Symposium. Boston, MA. March 31, 2008
- 10. The 15th Conversation: Journal of Biomolecular Structure and Dynamics 24(6):716. Albany, NY. June 19-23, 2007
- 11. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 8-12, 2007 (Genome Research Best Poster Award)
- 12. 6th International Workshop on Bioinformatics and Systems Biology. Boston, MA. July 24-26, 2006
- 13. ENCODE Consortium Meeting. Bethesda, MD. July 5-7, 2006 (two posters)

- 14. 5th International Workshop on Bioinformatics and Systems Biology. Berlin, Germany. August 22-25, 2005
- 15. ENCODE Consortium Meeting. Gaithersburg, MD. July 18-19, 2005
- 16. The 14th Conversation: Journal of Biomolecular Structure and Dynamics 22(6):828. Albany, NY. June 14-17, 2005
- 17. SICB (Society for Integrative and Comparative Biology) meeting. Chicago, IL. January 3-7, 2001
- 18. East Carolina University Research Day. Greenville. NC, April 3, 2000 (Best Poster Award)
- 19. SICB (Society for Integrative and Comparative Biology) meeting. Atlanta, GA. January 4-8, 2000