

Karen H. Miga

Biomolecular Engineering Department, University of California, Santa Cruz
Phone (919) 323-0462 email: khmiga@ucsc.edu
www.karenmiga.org

EDUCATION

- 2011 Ph.D. University Program in Genetics and Genomics w/ Certification in Computational Biology and Bioinformatics, Duke University Durham, NC
- 2004 M.S. Department of Genetics, Case Western Reserve University
- 2000 B.S. University of Tennessee, Knoxville. Degree with honors in Biological Sciences: Biochemistry, Cellular, and Molecular Biology

RESEARCH INTERESTS

Chromosome structure and function; Functional impact of satellite DNAs; long-read technologies and computational tools to improve high-resolution maps of human peri/centromeric regions; assess clinical impact of satellite sequence variation; novel gene regulation mechanisms involving constitutive heterochromatin

RESEARCH EXPERIENCE

- 2017-present Assistant Research Scientist, University of California, Santa Cruz
- 2017-2019 Visiting Scientist, UW Medicine Pathology, University of Washington, Seattle
- 2012-2017 Postdoctoral fellow, University of California, Santa Cruz, Mentor: David Haussler
- 2011 Weizmann Institute, Eran Segal laboratory, collaborative project with Huntington F. Willard
- 2006-2011 Graduate Student, Doctoral Thesis, Duke University. University Program in Genetics and Genomics. Mentor: Huntington F. Willard
- 2005 Research technician. Duke University. Institute of Genome Sciences and Policy. Kristin Scott laboratory
- 2004 Data Archivist. Station D'Etudes des Gorilles et Chimpanzees (SEGC). Wildlife Conservation Society, Lope, Gabon. Dr. Kate Abernathy, Director
- 2001-2004 Graduate Student, Masters Thesis. Case Western Reserve University, Mentor: Evan E. Eichler

RESEARCH ACCOMPLISHMENTS

- Co-founder of the Telomere-to-telomere (T2T) Consortium: released the first complete T2T assembly of a human chromosome, including a structurally validated 3.1 Mb human centromere and a new mapping method for repeat polishing and methylation studies (Miga *et al* 2020), and the first release of a complete human genome (v1.0)
- Project Director of the Human Pangenome Reference Center and T2T Data Production at UCSC. Credited as the 'next human genome project' that aims to generate at least 350 high

- quality reference genomes to improve comprehensive variant detection. (1U01HG010971-01).
- Led the first assembly of a human centromere (Jain *et al* 2018) and demonstrated the use of ultra-long read data (100 kb+) on the nanopore platform to resolve the remaining gaps in the human reference genome (Jain *et al* 2018)
 - Developed initial reference models for all centromere-assigned gaps in the current human reference genome (GRCh38) (Miga *et al* 2014), and published new methods to study satellite variation and evolution (Altemose *et al* 2013, Miga *et al* 2014, Sevim *et al* 2016, Langley *et al* 2019)
 - Established new epigenetic profiles of human centromeric proteins within satellite DNAs (Hayden *et al* 2012; Hayden *et al* 2013; Nechemia-Arbely and Miga *et al.* 2019)

TEACHING EXPERIENCE

- 2013 Instructor, University of California, Santa Cruz. Department of Biomolecular Engineering (Fall Quarter BME110/BIO181), Computational Tools for Biologists
- As the primary instructor for BME110/BIO181, I designed and successfully implemented new course curriculum aimed to advance topics in genomics and computational biology. Students were introduced to applications of various sequencing technologies relevant in current industry and research, including genome-wide alignments of experimental datasets, short-read assembly, and metagenomics. I obtained an educational grant from Amazon to support cloud-based storage and compute for 56 students, thereby enabling students to design creative and innovative final projects using high throughput sequence analysis pipelines on publicly available genomic datasets.
- 2007, 2009 Lecturer: Institute for Genome Sciences and Policy Summer Fellowship. Duke University. Course teaching UCSC Genome Browser and Galaxy Basics
- 2007 Teaching Assistant. Duke University. BIO289 Advanced Topics in Genome Sciences

PUBLICATIONS

Leah Bury, Brittanica Moodie, Jimmy Ly, Liliana S McKay, **Karen H Miga**, Iain M Cheeseman. "Alpha-satellite RNA transcripts are repressed by centromere-nucleolus associations." *eLife* 2020;9:e59770 DOI: 10.7554/eLife.59770

Glennis A. Logsdon, Mitchell R. Vollger, PingHsun Hsieh, Yafei Mao, Mikhail A. Liskovoykh, Sergey Koren, Sergey Nurk, Ludovica Mercuri, Philip C. Dishuck, Arang Rhie, Leonardo G. de Lima, David Porubsky, Andrey V. Bzikadze, Milinn Kremitzki, Tina A. Graves-Lindsay, Chirag Jain, Kendra Hoekzema, Shwetha C. Murali, Katherine M. Munson, Carl Baker, Melanie Sorensen, Alexandra M. Lewis, Urvashi Surti, Jennifer L. Gerton, Vladimir Larionov, Mario Ventura, **Karen H. Miga**, Adam M. Phillippy, Evan E. Eichler. "The structure, function, and evolution of a complete human chromosome 8." (2020) *bioRxiv* 2020.09.08.285395; doi: <https://doi.org/10.1101/2020.09.08.285395>

Sergey Nurk, Brian P. Walenz, Arang Rhie, Mitchell R. Vollger, Glennis A. Logsdon, Robert Grothe, **Karen H. Miga**, Evan E. Eichler, Adam M. Phillippy, and Sergey Koren. "HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads." *Genome Res.* (2020)doi:10.1101/gr.263566.120

Mikheenko, Alla, Andrey V. Bzikadze, Alexey Gurevich, **Karen H. Miga**, and Pavel A. Pevzner. TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats." *Bioinformatics* 36, no. Supplement_1 (2020): i75-i83.

Karen H. Miga*†, Sergey Koren*, Arang Rhie, Mitchell R. Vollger, Ariel Gershman, Andrey Bzikadze, Shelise Brooks, Edmund Howe, David Porubsky, Glennis A. Logsdon, Valerie A. Schneider, Tamara Potapova, Jonathan Wood, William Chow, Joel Armstrong, Jeanne Fredrickson, Evgenia Pak, Kristof Tigyi, Milinn Kremitzki, Christopher Markovic, Valerie Maduro, Amalia Dutra, Gerard G. Bouffard, Alexander Chang, Nancy F. Hansen, Françoise Thibaud-Nissen, Anthony D. Schmitt, Jon-Matthew Belton, Siddarth Selvaraj, Megan Y. Dennis, Daniela C. Soto, Ruta Sahasrabudhe, Gulhan Kaya, Josh Quick, Nicholas J. Loman, Nadine Holmes, Matthew Loose, Urvashi Surti, Rosa ana Risques, Tina A. Graves Lindsay, Robert Fulton, Ira Hall, Benedict Paten, Kerstin Howe, Winston Timp, Alice Young, James C. Mullikin, Pavel A. Pevzner, Jennifer L. Gerton, Beth A. Sullivan, Evan E. Eichler, Adam M. Phillippy†. "Telomere-to-telomere assembly of a complete human X chromosome." *Nature* (2020). <https://doi.org/10.1038/s41586-020-2547-7>

(* denotes equal contribution, † denotes corresponding authorship)

Kishwar Shafin*, Trevor Pesout*, Ryan Lorig-Roach*, Marina Haukness*, Hugh E. Olsen, Colleen Bosworth, Joel Armstrong, Kristof Tigyi, Nicholas Maurer, Sergey Koren, Fritz J. Sedlazeck, Tobias Marschall, Simon Mayes, Vania Costa, Justin M. Zook, Kelvin J. Liu, Duncan Kilburn, Melanie Sorensen, Katy M. Munson, Mitchell R. Vollger, Evan E. Eichler, Sofie Salama, David Haussler, Richard E. Green, Mark Akeson, Adam Phillippy, **Karen H. Miga**, Paolo Carnevali, Miten Jain, Benedict Paten. "Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes." *Nature Biotechnology* (2020): 1-10.

Marie Dumont*, Riccardo Gamba *, Gestraud P. , Klaasen S., Worrall J.T. , De Vries S.G , Boudreau V., Paul S. Maddox, Lens S.M.A. , Kops G.J.P.L. , Sarah Mc Clelland, **Karen H. Miga**, Daniele Fachinetti. "Chromosome-specific aneuploidy in human is influenced by the inter-chromosomal heterogeneity of centromeric features" *EMBO J* (2019) *e102924*

Yael Nechemia-Arbely*, **Karen H. Miga***, Ofer Shoshani, Aaron Aslanian, Moira A. McMahon, Ah Young Lee, Daniele Fachinetti, John R. Yates III, Bing Ren, Don Cleveland. "DNA replication-mediated error correction of ectopic CENP-A deposition maintains centromere identity." *Nature Cell Biology* 21.6 (2019): 743.

Yannick Delpu, Thomas McNamara, Patrick Griffin, Suhail Kaleem, Shubhada Narayan, Carl Schildkraut, **Karen H. Miga**, Mamta Tahiliani. "Chromosomal rearrangements at hypomethylated Satellite 2 sequences are associated with impaired replication efficiency and increased fork stalling." *bioRxiv* doi: <https://doi.org/10.1101/554410>

Sasha A. Langley, **Karen H. Miga**, Gary H. Karpen, Charles H. Langley. "Diverse haplotypes span human centromeres and include archaic lineages within and out of Africa." *eLife*. 2019;8:e42989. doi: <https://doi.org/10.7554/eLife.42989>

Glennis A. Logsdon, Craig W. Gambogi, Mikhail A. Liskovyykh, Evelyne J. Barrey, Vladimir Larionov, **Karen H. Miga**, Patrick Heun, and Ben E. Black. "Human Artificial Chromosomes that Bypass Centromeric DNA". *Cell* 178.3 (2019): 624-639.

Quan Zhu, Nien Hoong, Aaron Aslanian, Toshiro Hara, Christopher Benner, Sven Heinz, **Karen H. Miga**, Eugene Ke, Sachin Verma, Jan Soroczynski, John R. Yates III, Tony Hunter, Inder M. Verma. "Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer." *Molecular Cell* (2018). Jun 7;70(5):842-853.e7. doi: 10.1016/j.molcel.2018.04.023

Miten Jain*, Hugh Olsen*, Dan Turner, David Stoddart, Benedict Paten, David Haussler, Huntington F. Willard, Mark Akeson, and **Karen H. Miga**†. "Linear assembly of a human centromere on the Y chromosome." *Nature Biotechnology* (2018) doi:10.1038/nbt.4109

Miten Jain*, Sergey Koren*, **Karen H Miga***, Josh Quick*, Arthur C Rand*, Thomas A Sasani, John R Tyson, Andrew D Beggs, Alexander T Dilthey, Ian T Fiddes, Sunir Malla, Hannah Marriott, Tom Nieto, Justin O'Grady, Hugh E Olsen, Brent S Pedersen, Arang Rhie, Hollian Richardson, Aaron Quinlan, Terrance P Snutch, Louise Tee, Benedict Paten, Adam M. Phillippy, Jared T Simpson, Nicholas James Loman, Matthew Loose. "Nanopore sequencing and assembly of a human genome with ultra-long reads." *Nature Biotechnology* (2018) doi:10.1038/nbt.4060

Yael Nechemia-Arbely, Daniele Fachinetti, **Karen H. Miga**, Nikolina Sekulic, Gautam Soni, Adeline Karwei Wong, Ah Young Lee, Kristen Nguyen, Cees Dekker, Bing Ren, Ben E. Black, and Don W. Cleveland. "Human centromeric CENP-A-containing chromatin is a homotypic, octameric nucleosome with loosely held DNA termini at all cell cycle points." *The Journal of Cell Biology* (2017): 216(3):607-621.

Adam M Novak, Glenn Hickey, Erik Garrison, Sean Blum, Abram Connelly, Alexander Dilthey, Jordan Eizenga, M. A. Saleh Elmohamed, Sally Guthrie, André Kahles, Stephen Keenan, Jerome Kelleher, Deniz Kural, Heng Li, Michael F Lin, **Karen H. Miga**, Nancy Ouyang, Goran Rakocevic, Maciek Smuga-Otto, Alexander Wait Zaranek, Richard Durbin, Gil McVean, David Haussler, Benedict Paten. "Community Genome Graphs." bioRxiv doi: <https://doi.org/10.1101/101378>

Karen H. Miga†. "Chromosome-specific centromere sequences provide an estimate of ancestral chromosome 2 fusion event in hominin genomes." *J Heredity* (2016): esw039

Volkan Sevim, Ali Bashir, Chen-Shan Chin, and **Karen H. Miga**. "Alpha-CENTAURI: assessing novel centromeric repeat sequence variation with long read sequencing." *Bioinformatics* (2016): btw101.

Karen H. Miga†, Christopher Eisenhart and W. James Kent. "Utilizing mapping targets of sequences underrepresented in the reference assembly to reduce false positive alignments." *Nucleic acids research* (2015): gkv671

Miten Jain, Ian T. Fiddes, **Karen H. Miga**, Hugh E. Olsen, Benedict Paten, and Mark Akeson. "Improved data analysis for the MinION nanopore sequencer." *Nature Methods* (2015); 12(4):351-6.

Kate R. Rosenbloom, Joel Armstrong, Galt P. Barber, Jonathan Casper, Hiram Clawson, Mark Diekhans, Timothy R. Dreszer, Pauline A. Fujita, Luvina Guruvadoo, Maximilian Haeussler, Rachel A. Harte, Steve Heitner, Glenn Hickey, Angie S. Hinrichs, Robert Hubley, Donna Karolchik, Katrina Learned, Brian T. Lee, Chin H. Li, **Karen H. Miga**, Ngan Nguyen, Benedict Paten, Brian J. Raney, Arian F. A. Smit, Matthew L. Speir, Ann S. Zweig, David Haussler, Robert M. Kuhn and W. James Kent. "The UCSC Genome Browser database: 2015 update." *Nucleic acids research* 43.D1 (2015): D670-D681

Indri Erliandri, Haiqing Fu, Megumi Nakano, Jung-Hyun Kim, **Karen H. Miga**, Mikhail Liskovykh, William C. Earnshaw, Hiroshi Masumoto, Natalay Kouprina, Mirit I. Aladjem, and Vladimir Larionov. "Replication of alpha-satellite DNA arrays in endogenous human centromeric regions and in human artificial chromosome." *Nucleic acids research* 42, no. 18 (2014): 11502-11516.

Nicolas Altemose, **Karen H. Miga**†, Mauro Maggioni, and Huntington F. Willard. Genomic "Characterization of Large Heterochromatic Gaps in the Human Genome Assembly." *PLOS Comput Biol.* 2014 May 15;10(5):e1003628.

Karen H. Miga, Yulia Newton, Miten Jain, Nicolas F. Altemose, Huntington F. Willard and W. James Kent. "Centromere reference models for human chromosomes X and Y satellite arrays." *Genome Res.* 2014 Apr;24(4):697-707.

(Karen E. Hayden is my maiden name)

Karen E. Hayden*, Erin D. Strome*, Stephanie E. Merrett, Hye-Ran Lee, and Huntington F. Willard. "Defining Centromere Competent Sequence Features in the Human Genome." *Mol Cell Biol.* 2013 Feb;33(4):763-7.

Karen E. Hayden† and Huntington F Willard. "Composition and organization of active centromere sequences in complex genomes." *BMC Genomics.* 2012 Jul 20;13(1):324

Hye-Ran Lee, **Karen E. Hayden**, and Huntington F. Willard. "Organization and molecular evolution of CENP-A-associated satellite DNA families in a basal primate genome." *Genome Biol Evol.* 2011 Aug 9

Kaitlin M. Stimpson, Ihn Young Song, Anna Jauch, Heidi Holtgreve-Grez, **Karen E. Hayden**, Joanna M. Bridger, and Beth A. Sullivan. "Telomere Disruption Results in Non-random Formation of De Novo Dicentric Human Chromosomes That Are Stabilized by Partial Centromeric Deletion." *PLOS Genet.* 2010 Aug 12;6(8)

Tera L. Newman, Eray Tuzun, V. Anne Morrison, **Karen E. Hayden**, Mario Ventura, Sean D. McGrath, Mariano Rocchi, and Evan E. Eichler. "A genome-wide survey of structural variation between human and chimpanzee." *Genome Res.* 2005 Oct;15(10):1344-56.

Chimpanzee Sequencing and Analysis Consortium. "Initial sequence of the chimpanzee genome and comparison with the human genome." (...**Karen E. Hayden** [authorship order 26 out of 67], ...) *Nature.* 2005 Sep 1;437(7055):69-87.

Chris T. Yohn, Zhaoshi Jiang, Sean D. McGrath, **Karen E. Hayden**, Philipp Khaitovich, Matthew E. Johnson, Marla Y. Eichler, John D McPherson, Shaying Zhao, Savante Pääbo, and Evan E. Eichler. "Lineage-specific expansions of retroviral insertions within the genomes of African great apes but not humans and orangutans." *PLOS Biol.* 2005 Apr;3(4):e110.

Undergraduate publications

Massimo Pigliucci and **Karen Hayden**. "Phenotypic plasticity is the major determinant of changes in phenotypic integration in Arabidopsis." *New Phytologist* 152.3 (2001): 419-430.

(University of Tennessee, Knoxville. Dept of Ecology and Evol. Biology. Massimo Pigliucci laboratory; In 2000 I was awarded the "Young Botanist: Certificate of Special Achievement" award from the Botanical Society of America for my undergraduate research work)

Guy D. Griffin, Waleed Khalaf, **Karen E. Hayden**, Estelle J. Miller, Vinay R. Dowray, Amy L. Creekmore, Carl W. Carruthers, M. Wendy Williams, and Paul C. Gailey. Power frequency magnetic field exposure and gap junctional communication in Clone 9 cells. *Bioelectrochemistry* 51, no. 2 (2000): 117-123.

(Oak Ridge National Laboratory, Energy Research Undergraduate Laboratory Fellowship (ERULF). Guy Griffin laboratory; I was also invited to join the Howard Hughes Threshold Program/Oak Ridge Institute for Science and Education (ORISE) Program. During this time, I was invited to join Beta Beta Beta National Biological Honor Society, 1999 Mu Zeta Chapter)

Invited book chapters and reviews

Karen H. Miga† and Adam M. Phillippy. "Repeat Paradise Lost: telomere-to-telomere assemblies and a new era of biological discovery." *Trends in Genetics* (2021). *In review*

Karen H. Miga†. "Bridging the abyss: a new era of genome exploration." *Nature News and Views* (2021). *In review*

Karen H. Miga and Ting Wang. "The Need for a Human Pangenome Reference." *Annuals Review Genomics and Human Genetics* (2021). *In review*

Karen H. Miga†. "Centromere studies in the era of 'telomere-to-telomere' genomics." *Experimental Cell Research* (2020): 112127.

Karen H. Miga†. Centromeric Satellite DNAs: Hidden Sequence Variation in the Human Population. *Genes* 10, no. 5 (2019): 352.

Karen H. Miga† (2017) The promises and challenges of genomic studies of human centromeres. Ben E. Black (Ed.), *Centromeres and Kinetochores, Progress in Molecular and Subcellular Biology*, © Springer-Verlag Berlin Heidelberg

Karen H. Miga†. Completing the human genome: progress and challenges of a satellite DNA assembly. *Chromosome Research* 23.3 (2015): 421-426.

Karen E. Hayden†. Human Centromere Genomics: This Time it's Personal. *Chromosome Res.* 2012 Jul;20(5):621-33.

INVITED CONFERENCE TALKS AND DEPARTMENTAL SEMINARS

- 2021 Stowers Research Conference Series on Chromosome Biology, Kansas City, MO
- 2021 Gordon Conference: Centromere Biology, West Dover, VT
- 2021 JAX - McKusick Short Course [Invited Instructor]; Bioscience Connecticut; Farmington, Conn
- 2021 Structural Variation and Function. Biological and Medical Research Center (BMFZ) Düsseldorf, Germany
- 2021 European Society of Human Genetics (ESHG), Glasgow, United Kingdom
- 2021 Advances in Genome Graphs [Keynote Speaker] Ascona, Switzerland
- 2021 Long-Read Sequencing [Keynote Speaker] NGI Sweden/SciLifeLab; Uppsala, Sweden
- 2021 Cell Symposium: Human Genome Project, San Diego, CA
- 2021 Revolutionizing Next-Generation Sequencing 2021, Ghent Belgium
- 2021 Program in Quantitative Genomics (PQG) seminar, Harvard School of Public Health; Boston, MA (*Virtual Meeting: COVID-19 Response*)
- 2021 5th University of Utah Precision Medicine Symposium, Salt Lake City, UT (*Virtual Meeting/Seminar: COVID-19 Response*)
- 2021 NHGRI Bold Predictions Seminar Series; National Human Genome Research Institute, NIH (*Virtual Meeting: COVID-19 Response*)
- 2020 Department of Biochemistry and Molecular Biology, Penn State; University Park, PA (*Virtual Two-Day Seminar and Departmental Meeting: COVID-19 Response*)
- 2020 The Australian Bioinformatics And Computational Biology Society (ABACBS) Annual Conference [International Keynote Speaker] (*Virtual Meeting: COVID-19 Response*)
- 2020 Johns Hopkins Center for Computational Genomics Symposium; Baltimore, MD [Keynote Speaker]. (*Virtual Meeting: COVID-19 Response*)
- 2020 T2T/HPRC Symposium, Co-lead Coordination Committee (*Virtual Meeting: COVID-19 Response; Partial funding: NHGRI, R13 PA-16-294, Miga (PI)*)

- 2020 Wellcome Genome Informatics, Session Co-Lead Sequencing Algorithms, Variant Discovery and Genome Assembly; Hinxton, UK (*Virtual Meeting: COVID-19 Response*)
- 2020 International Society for Computational Biology (ISCB)/High Throughput Sequencing (HiTSeq) 2020 [Keynote Speaker]. Montreal, Canada (*Virtual Meeting: COVID-19 Response*)
- 2020 The Socially Distant Centromere (Remote GRC Centromere Biology Online Conference Series) (*Virtual Meeting: COVID-19 Response*)
- 2020 CSHL Biology of Genomes: Nanopore Workshop; Cold Spring Harbor, NY (*Virtual Meeting: COVID-19 Response*)
- 2020 Stanford Genetics Conference on Structural Variants and DNA Repeats; Stanford, CA (*Virtual Meeting: COVID-19 Response*)
- 2020 Workshop: Long-Read Sequencing, The Jackson Laboratory. Farmington, CT (*Cancelled: COVID-19 Response*)
- 2020 Nature Conference on Human Genetics and Big Data, Beijing, China (*Cancelled: COVID-19 Response*)
- 2020 Human Genome Meeting 2020 (HUGO 2020), Perth, Australia (*Virtual Meeting: COVID-19 Response*)
- 2020 Case Western Reserve University: Genetics, Cleveland, OH
- 2020 4th International Brainstorm Symposium: Expanding Role of Repeats in Disease, Gainesville, FL
- 2020 Duke University: MGM Department and Women in Science Graduate Students, Durham, NC
- 2019 Guest Lecturer: CSHL Advanced Sequencing Technology course
- 2019 American Society of Human Genetics Genome in a Bottle and Genome Research Consortium Workshop Houston, TX
- 2019 UC Davis: Genetics Seminar Series, Davis, CA
- 2019 Workshop: Long-Read Sequencing, The Jackson Laboratory. Farmington, CT
- 2019 14th Heterochromatin Conference, Spoleto, Italy
- 2019 London Calling Plenary, Oxford Nanopore Community Conference, London, UK
- 2019 Workshop: Long-Read Sequencing, The Jackson Laboratory. Farmington, CT
- 2019 Frontiers in Bioinformatics and Systems Biology Seminar Series, University of California, San Diego (Invitation from student in the UCSD Bioinformatics and Systems Biology Graduate Program)
- 2019 Advance in Genome Biology and Technology (AGBT), Marco Island, FL
- 2019 Workshop: Transposable Elements at the crossroad of health and disease, McGill's Bellairs research institute, Barbados
- 2018 Molecular Biology Society of Japan, Yokohama, Japan
- 2018 Nanopore Day Seattle, Seattle, WA
- 2018 2nd Uppsala Transposon Symposium (Keynote Speaker), Uppsala, Sweden
- 2018 Second Joint Conference on Evolutionary Biology, Montpellier, France
- 2018 Gordon Conference: Centromere Biology, West Dover, VT

- 2018 Whitehead Institute, Boston, MA
- 2018 NIH/National Human Genome Research Institute (NHGRI); Bethesda, MD
- 2018 Department of Human Genetics, University of Utah, Salt Lake City, UT
- 2017 American Society of Human Genetics Genome Research Consortium Workshop
Orlando, FL
- 2017 GP-Write, New York City, NY
- 2017 Oxford Nanopore London Calling, London, UK
- 2017 Ludwig Maximilian University of Munich, Biology Dpt Seminar, Munich, Germany
- 2017 University of Rochester Biology Departmental Seminar, Rochester, NY
- 2017 Stanford University, CEHG Institute Evolgenome Seminar Series, Stanford, CA
- 2016 Gordon Conference: Centromere Biology, West Dover, VT
- 2016 Nuclear Dynamics and Genome Plasticity, Institut Curie, Paris, France
- 2016 Second Annual Stem Cell Genomics CIRM Retreat, Salk Institute, La Jolla, CA
- 2015 Emory University: Biology Departmental Seminar, Atlanta, GA
- 2015 Pacific Biosciences West Coast User Group Mtg; Stanford, CA
- 2015 American Genetics Association 2015: Chromosome Evolution: Molecular
Mechanisms and Evolutionary Consequences, Bainbridge Island, WA
- 2015 Gordon Conference: Epigenetics, Bentley University, MA
- 2014 Gordon Conference: Centromere Biology, Bentley University, MA
- 2013 Stowers Institute, Seminar and Hosted Genomics Workshop. Kansas City, MO
- 2013 Cold Spring Harbor Laboratory Genome Informatics, Cold Spring Harbor, NY
- 2013 American Society of Human Genetics Genome Research Consortium Workshop
Boston, MA
- 2013 University of Massachusetts Medical School, Biochemistry & Molecular
Pharmacology Departmental Seminar, Worcester, MA
- 2012 EMBO Workshop: Chromosome Segregation Centromeres and Kinetochores
Barcelona, Spain
- 2012 Nuclear Dynamics and Genome Plasticity, Institut Curie, Paris, France
- 2012 NCI/NIH Invited Speaker, Bethesda, MD
- 2010 Cold Spring Harbor Laboratory Genome Informatics, Hinxton, UK
- 2008 EMBO Workshop: Chromosome Segregation Centromeres and Kinetochores,
Archachon, Bordeaux, France

FELLOWSHIPS AND GRANTS

- 2020-24 National Human Genetics Research Institute (NHGRI, R01 PA-19-056). Telomere to
telomere assemblies of human genomes. (\$736,836); 1R01HG011274-01
PI: Karen Miga
- 2020-21 National Human Genetics Research Institute (NHGRI, R13 PA-16-294). Telomere-to-
Telomere (T2T) Symposium: Completing the Human Reference Genome. (\$12,700);
PI: Karen Miga

- 2019-24 National Human Genetics Research Institute (NHGRI, “Center for Human Reference Diversity” for the RFA “High Quality Human Reference Genomes” (HQRG) (U01) (RFA-HG-19-002).” (\$3,350,597/YR); 1U01HG010971-01
 PIs: David Haussler (UCSC, Contact PI), Co-PIs: Evan Eichler (UW), Ira Hall (WUSTL), Erich Jarvis (Rockefeller University)
 PD, Co-I: Karen Miga
- 2019-21 National Human Genetics Research Institute (NHGRI, R21). Improving throughput of long reads with high consensus base accuracy to resolve repetitive DNAs. (\$612,014); 1R21HG010548-01
 PI: Karen Miga
- 2018-19 National Institute of Standard and Technology (NIST). High coverage long read nanopore sequencing of reference human genomes (\$107,800); 70NANB18H224
 PI: Karen Miga
- 2014-15 California Institute for Regenerative Medicine (CIRM) Postdoctoral Fellowship. (\$73,100)
- 2013 Amazon Cloud Educational Grant, University of California, Santa Cruz (\$5600)
- 2012 Journal of Cell Science Travel Grant for collaboration at the Weizmann Institute (\$3000)

MENTORING EXPERIENCE

- 2013 - 2017 Miten Jain. University of California, Santa Cruz. BME Graduate Student
- 2014 Brittany Welence. University of California, Santa Cruz. Undergraduate researcher
- 2014 Kevin Brown. University of California, Santa Cruz. Undergraduate researcher
- 2013 Veronica Urabe. Women in Science and Engineering (WiSE) mentor. University of California, Santa Cruz. Undergraduate
- 2013 Elizabeth Wimmer. Women in Science and Engineering (WiSE) mentor. University of California, Santa Cruz. Undergraduate
- 2013 Yulia Newton. University of California, Santa Cruz. BME Graduate Student
- 2009-2011 Nicolas Altemose. Duke University, Howard Hughes Medical Institute EXROP Fellow
- 2010 Kelvin Gu, Duke University, Independent Study Undergraduate Research
- 2009 Brandon Roane, Duke University, Howard Hughes Medical Institute EXROP Fellow
- 2007-2009 Caitlin Milligan. Duke University, Independent Study Undergraduate Research

STUDY SECTIONS/GRANT REVIEW COMMITTEES

- 2020-2024 NIH/NHGRI G-GNOM Study Section
- 2020 NIH/NHGRI COVID Supplement Review
- 2020 NIH/NHGRI Sequencing Technology

PUBLIC OUTREACH AND PROFESSIONAL SERVICE

Ad hoc reviewer for *Nature*, *Genome Research*, *PLOS Genetics*, *Genome Biology and Evolution*, *PLOS ONE*, *Nucleic Acid Research*, *Genetics*, *Scientific Reports*, *Molecular Biology and Evolution*, *Journal of Molecular Evolution*, *Human Genetics*, *Leakey Foundation*, *Current Genomics*, *Cells*, *Bioinformatics*, *Chromosome Research*, *Bio-Protocol*

Society Member, American Association for the Advancement of Science (AAAS), American Society for Cell Biology (ASCB), American Genetics Association (AGA), International Society for Stem Cell Research (ISSCR)

Scientific American Guest Blog: Our First View into the “Blackout Zones” of the Human Genome (March 6 2014). <http://blogs.scientificamerican.com/guest-blog/2014/03/06/our-first-view-into-the-blackout-zones-of-the-human-genome/>

Short Course Training: Johns Hopkins Specialization: Genomic Data Science (2016), LifeTech Stem Cell Culturing Course (Life Tech 2015), Probability and Statistical Inference, Summer Institute in Statistical Genetics (SISG 2010), Teaching College Biology, Duke University/BIO390 (2010); Programming for Biology, Cold Spring Harbor Laboratory (2003)