DeannaMChurch

Genomics, Technology and Bioinformatics Leader

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leadership skills

Empathy, Communication, Mentorship, Team Player, Curiosity, Initiative & Strategic and Critical Thinking

product skills

Product definition, Product commercialization, Product management, Applications, Writing & Presentations

genomics

Genome assembly, Genome annotation, Variant analysis, Functional genomics & Genome editing

bioinformatics

Python, Data Science, R, Git, HTML, XML/XSLT, Javascript, CSS3 & SQL

focus

Leading interdisciplinary teams that match new technology to research needs. A systems level thinker comfortable diving deep into the data and delivering high level strategic plans.

experience

2023 - Present — **General Inception** — Remote
Executive-in-Residence
Driving diligence, operational excellence and providing executive leadership for General Inception companies.

2022 - Present — **dmchurch bio, llc** — Boulder, CO
Principal
Independent consultant with a focus on genomics, funcational genomes and data analysis.

2021–2022 — **Inscripta, Inc** — Boulder, CO
Vice President, Mammalian Business Area and Software Strategy
Reported to the CEO. Established requirements and drove software changes required to scale from 10s of genomes to 1000s of genomes (80% of customer base). Led a functional genomics team to establish single cell measurements to accelerate product development. Led a Data Science team developing new analysis methods critical for customer success.

2019–2021 — **Inscripta, Inc** — Boulder, CO
Senior Director, Applications Mammalian
Reported to the CEO. Established customer requirements for the mammalian platform to enter a multimillion dollar market. Communicated requirements to a multidisciplinary product team. Contributed to three patents critical for application success.

2016–2018 — **10x Genomics** — Pleasant, CA
Senior Director of Applications
Led a team of scientists demonstrating the value of the 10x platforms, contributing to 14 published manuscripts and a dozen Application notes across the product portfolio. Presented at over 40 conferences and meetings, leading to wide spread adoption of 10x products.

2014-2016 — **Personalis, Inc** — Menlo Park, CA
Senior Director of Genomics and Content
Led a team developing novel genome analysis algorithms, pipelines and knowledge bases built to support genome interpretation, cutting report generation by half. Worked collaboratively with partners and government agencies to establish best practices for genome analysis and interpretation.

2001-2014 — **National Center for Biotechnology Information, NIH** — Bethesda, MA
Staff Scientist
Led large international collaborations and led the development teams for NCBI systems serving 1000s of users daily. Contributed to or led the development of over 10 public resources, including the Genome Reference Consortium and Clinvar.

education

2024-2025	**Springboard Data Science Program**	Boulder, CO
1999-2001	**National Center for Biotechnology Information, NIH** *Postdoctoral fellow*	Bethesda, MD
1997-1999	**Laboratory of Janet Rossant, Mt. Sinai Hospital** *Postdoctoral fellow*	Toronto, Ontario
1992-1997	**PhD** of Biological Sciences *Phenotype-genotype correlation in the Cri-du-Chat region of chromosome 5*	The University of California, Irvine
1986-1990	**Bachelor** of Liberal Arts *Research project focused on cell cycle regulation using yeast*	University of Virginia

advisory boards and professional service

2020-present	**Human Pangenome Reference Consortium**	Scientific Advisory Board
2018-2022	**Genome Quebec**	Scientific Advisory Board
2018-2020	**American Association for Cancer Research**	Member
2012-2019	**Ensembl**	Scientific Advisory Board
2014-2016	**American College of Medical Genetics**	Member
2013-2016	**The Genome Analysis Center/Earlham Institute**	Scientific Advisory Board
2010-2014	**Database of Genomic Variants**	Scientific Advisory Board
2010-present	**American Society of Human Genetics**	Member
2008-2013	**Advances in Genome Biology and Technology**	Organizing Committee Member
2008-2013	**International Standards Cytogenomic Arrays**	Committee Member
2008-2012	**International Mammalian Genome Society**	Nomenclature Committee Member
2004-2012	**International Mammalian Genome Society**	Member
2006-2011	**European Conditional Mouse Mutagenesis Program**	Scientific Advisory Board
2006-2009	**Genome Canada-MORGEN project**	Scientific Advisory Board
2005	**Mouse Genome Finishing Meeting**	Organizer

presentations

Selected highlights from over 50 presentations.

2019-Nov	**Rosalind Franklin Society** Invited Speaker, "The impact of technology on our view of biology"	Philadelphia, PA
2018-Feb	**Beckman Symposium, Technology Innovation and Human Genomics** Invited Speaker, "The impact of technology on our view of biology"	Palo Alto, CA
2017-Nov	**Australasian Genomic Technologies Association Annual Meeting** Keynote, "The impact of technology on biology"	Hobart, AUS
2016-Feb	**Stanford Big Data in Genomics** Invited Speaker, "Truly personalized genomics"	Palo Alto, CA
2015-Oct	**Genome informatics** Invited Speaker, "The Rumsfeldian challenge of developing clinical sequencing tests"	Cold Spring Harbor, NY
2014-Nov	**Biological Data Sciences** Keynote Speaker, "Analog reporting in a digital age"	Cold Spring Harbor, NY
2013-Oct	**American Society of Human Genetics** Invited Speaker, "Navigating clinical genomic resources at NCBI"	Boston, MA
2013- May	**Sequencing Finishing and Analysis in the Future** Keynote Address, "Keep calm and carry on sequencing"	Santa Fe, NM
2011-Jul	**BIO-IT APAC Conference and Expo** Keynote Speaker, "The evolution of the reference human genome"	Shenzhen, China
2008-May	**Finishing in the Future** Keynote Speaker, "Great expectations: fulfilling the promises of the human genome project"	Santa Fe, NM

teaching

Selected courses and lectures.

2017	**Stanford, Informatics in Industry** Prepared lecture for 50 students.
2013	**54th Annual Short Course on Medical and Experimental Mammalian Genetics** Prepared 6 hours of lecture and online tutorials for 75 students.
2012, 2008	**Genome Reference Consortium Workshop at ASHG** Prepared 4 hours of lecture on the human reference assembly for 250 people.
2011-2012	**Frontiers in Reproduction** Prepared 4 hours of lecture on online tutorials for 25 students.
2003-2012	**International Mammalian Genome Conference** Co-organized and prepared 4 hours of lecture and online tutorials for 50-75 students.
2008	**NIDA Short Course on Genetics and Epigenetics** Prepared 2 hours of lecture for 100 students
2004-2005	**AGBT workshop** Prepared 1 hour lecture for the pre-meeting workshop.
2003-2005	**The Jackson Laboratory Bioinformatics for Bench Scientists** Co-organized this two week course to introduce bench scientists to bioinformatics.

publications

Articles

A next-generation human genome sequence
Deanna M Church
Science *376.6588 pp. 34–35. 2022*

A Chromosome-Length Assembly of the Hawaiian Monk Seal (Neomonachus schauinslandi): A History of “Genetic Purging” and Genomic Stability
David W Mohr, Stephen J Gaughran, Justin Paschall, Ahmed Naguib, Andy Wing Chun Pang, Olga Dudchenko, Erez Lieberman Aiden, Deanna M Church, and Alan F Scott
Genes *13.7 p. 1270. Multidisciplinary Digital Publishing Institute, 2022*

De novo assembly of the olive fruit fly (Bactrocera oleae) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly
Anthony Bayega, Haig Djambazian, Konstantina T Tsoumani, Maria-Eleni Gregoriou, Efthimia Sagri, Eleni Drosopoulou, Penelope Mavragani-Tsipidou, Kristina Giorda, George Tsiamis, Kostas Bourtzis, Spyridon Oikonomopoulos, Ken Dewar, Deanna M Church, Alexie Papanicolaou, Kostas D Mathiopoulos, and Jiannis Ragoussis
BMC Genomics *21.1 p. 259. 2020*

Thousands of human sequences provide deep insight into single genomes
Deanna M Church
Nature *581.7809 pp. 385–386. 2020*

Single-Cell Transcriptomics Reveals Early Emergence of Liver Parenchymal and Non-parenchymal Cell Lineages
Jeremy Lotto, Sibyl Drissler, Rebecca Cullum, Wei Wei, Manu Setty, Erin M Bell, Stéphane C Boutet, Sonja Nowotschin, Ying-Yi Kuo, Vidur Garg, Dana Pe’er, Deanna M Church, Anna-Katerina Hadjantonakis, and Pamela A Hoodless
Cell *183.3 702–716.e14. 2020*

The effects of common structural variants on 3D chromatin structure
Omar Shanta, Amina Noor, Human Genome Structural Variation Consortium (HGSVC), and Jonathan Sebat
BMC Genomics *21.1 p. 95. 2020*

Haplotyping the Vitis collinear core genome with rhAmpSeq improves marker transferability in a diverse genus
Cheng Zou, Avinash Karn, Bruce Reisch, Allen Nguyen, Yongming Sun, Yun Bao, Michael S Campbell, Deanna Church, Stephen Williams, Xia Xu, Craig A Ledbetter, Sagar Patel, Anne Fennell, Jeffrey C Glaubitz, Matthew Clark, Doreen Ware, Jason P Londo, Qi Sun, and Lance Cadle-Davidson
Nat. Commun. *11.1 p. 413. 2020*

Multi-platform discovery of haplotype-resolved structural variation in human genomes
Mark J P Chaisson, Ashley D Sanders, Xuefang Zhao, Ankit Malhotra, David Porubsky, Tobias Rausch, Eugene J Gardner, Oscar L Rodriguez, Li Guo, Ryan L Collins, Xian Fan, Jia Wen, Robert E Handsaker, Susan Fairley, Zev N Kronenberg, Xiangmeng Kong, Fereydoun Hormozdiari, Dillon Lee, Aaron M Wenger, Alex R Hastie, Danny Antaki, Thomas Anantharaman, Peter A Audano, Harrison Brand, Stuart Cantsilieris, Han Cao, Eliza Cerveira, Chong Chen, Xintong Chen, Chen-Shan Chin, Zechen Chong, Nelson T Chuang, Christine C Lambert, Deanna M Church, Laura Clarke, Andrew Farrell, Joey Flores, Timur Galeev, David U Gorkin, Madhusudan Gujral, Victor Guryev, William Haynes Heaton, Jonas Korlach, Sushant Kumar, Jee Young Kwon, Ernest T Lam, Jong Eun Lee, Joyce Lee, Wan-Ping Lee, Sau Peng Lee, Shantao Li, Patrick Marks, Karine Viaud-Martinez, Sascha Meiers, Katherine M Munson, Fabio C P Navarro, Bradley J Nelson, Conor Nodzak, Amina Noor, Sofia Kyriazopoulou-Panagiotopoulou, Andy W C Pang, Yunjiang Qiu, Gabriel Rosanio, Mallory Ryan, Adrian Stütz, Diana C J Spierings, Alistair Ward, Annemarie E Welch, Ming Xiao, Wei Xu, Chengsheng Zhang, Qihui Zhu, Xiangqun Zheng-Bradley, Ernesto Lowy, Sergei Yakneen, Steven McCarroll, Goo Jun, Li Ding, Chong Lek Koh, Bing Ren, Paul Flicek, Ken Chen, Mark B Gerstein, Pui-Yan Kwok, Peter M Lansdorp, Gabor T Marth, Jonathan Sebat, Xinghua Shi, Ali Bashir, Kai Ye, Scott E Devine, Michael E Talkowski, Ryan E Mills, Tobias Marschall, Jan O Korbel, Evan E Eichler, and Charles Lee
Nat. Commun. *10.1 p. 1784. Nature Publishing Group, 2019*

Resolving the full spectrum of human genome variation using Linked-Reads

Patrick Marks, Sarah Garcia, Alvaro Martinez Barrio, Kamila Belhocine, Jorge Bernate, Rajiv Bharadwaj, Keith Bjornson, Claudia Catalanotti, Josh Delaney, Adrian Fehr, Ian T Fiddes, Brendan Galvin, Haynes Heaton, Jill Herschleb, Christopher Hindson, Esty Holt, Cassandra B Jabara, Susanna Jett, Nikka Keivanfar, Sofia Kyriazopoulou-Panagiotopoulou, Monkol Lek, Bill Lin, Adam Lowe, Shazia Mahamdallie, Shamoni Maheshwari, Tony Makarewicz, Jamie Marshall, Francesca Meschi, Christopher J O'Keefe, Heather Ordonez, Pranav Patel, Andrew Price, Ariel Royall, Elise Ruark, Sheila Seal, Michael Schnall-Levin, Preyas Shah, David Stafford, Stephen Williams, Indira Wu, Andrew Wei Xu, Nazneen Rahman, Daniel MacArthur, and Deanna M Church

Genome Res. *29.4 pp. 635–645. 2019*

The emergent landscape of the mouse gut endoderm at single-cell resolution

Sonja Nowotschin, Manu Setty, Ying-Yi Kuo, Vincent Liu, Vidur Garg, Roshan Sharma, Claire S Simon, Nestor Saiz, Rui Gardner, Stéphane C Boutet, Deanna M Church, Pamela A Hoodless, Anna-Katerina Hadjantonakis, and Dana Pe'er

Nature*. 2019*

A general approach for detecting expressed mutations in AML cells using single cell RNA-sequencing

Allegra A Petti, Stephen R Williams, Christopher A Miller, Ian T Fiddes, Sridhar N Srivatsan, David Y Chen, Catrina C Fronick, Robert S Fulton, Deanna M Church, and Timothy J Ley

Nat. Commun. *10.1 p. 3660. 2019*

Birth, expansion, and death of VCY-containing palindromes on the human Y chromosome

Wentao Shi, Andrea Massaia, Sandra Louzada, Juliet Handsaker, William Chow, Shane McCarthy, Joanna Collins, Pille Hallast, Kerstin Howe, Deanna M Church, Fengtang Yang, Yali Xue, and Chris Tyler-Smith

Genome Biol. *20.1 p. 207. 2019*

Human-specific tandem repeat expansion and differential gene expression during primate evolution

Arvis Sulovari, Ruiyang Li, Peter A Audano, David Porubsky, Mitchell R Vollger, Glennis A Logsdon, Human Genome Structural Variation Consortium, Wesley C Warren, Alex A Pollen, Mark J P Chaisson, and Evan E Eichler

Proc. Natl. Acad. Sci. U. S. A. *116.46 pp. 23243–23253. 2019*

Dissecting the Causal Mechanism of X-Linked Dystonia-Parkinsonism by Integrating Genome and Transcriptome Assembly

Tatsiana Aneichyk, William T Hendriks, Rachita Yadav, David Shin, Dadi Gao, Christine A Vaine, Ryan L Collins, Aloysius Domingo, Benjamin Currall, Alexei Stortchevoi, Trisha Multhaupt-Buell, Ellen B Penney, Lilian Cruz, Jyotsna Dhakal, Harrison Brand, Carrie Hanscom, Caroline Antolik, Marisela Dy, Ashok Ragavendran, Jason Underwood, Stuart Cantsilieris, Katherine M Munson, Evan E Eichler, Patrick Acuña, Criscely Go, R Dominic G Jamora, Raymond L Rosales, Deanna M Church, Stephen R Williams, Sarah Garcia, Christine Klein, Ulrich Müller, Kirk C Wilhelmsen, H T Marc Timmers, Yechiam Sapir, Brian J Wainger, Daniel Henderson, Naoto Ito, Neil Weisenfeld, David Jaffe, Nutan Sharma, Xandra O Breakefield, Laurie J Ozelius, D Cristopher Bragg, and Michael E Talkowski

Cell *172.5 897–909.e21. Cold Spring Harbor Laboratory, 2018*

Genomes for all

Deanna M Church

Nat. Biotechnol. *36.9 pp. 815–816. 2018*

Reference quality assembly of the 3.5-Gb genome ofCapsicum annuumfrom a single linked-read library

Amanda M Hulse-Kemp, Shamoni Maheshwari, Kevin Stoffel, Theresa A Hill, David Jaffe, Stephen R Williams, Neil Weisenfeld, Srividya Ramakrishnan, Vijay Kumar, Preyas Shah, Michael C Schatz, Deanna M Church, and Allen Van Deynze

Hortic Res *5 p. 4. 2018*

Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings

Ira M Lubin, Nazneen Aziz, Lawrence J Babb, Dennis Ballinger, Himani Bisht, Deanna M Church, Shaun Cordes, Karen Eilbeck, Fiona Hyland, Lisa Kalman, Melissa Landrum, Edward R Lockhart, Donna Maglott,

Gabor Marth, John D Pfeifer, Heidi L Rehm, Somak Roy, Zivana Tezak, Rebecca Truty, Mollie Ullman-Cullere, Karl V Voelkerding, Elizabeth A Worthey, Alexander W Zaranek, and Justin M Zook
J. Mol. Diagn. *19.3 pp. 417–426. 2017*

Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly
Valerie A Schneider, Tina Graves-Lindsay, Kerstin Howe, Nathan Bouk, Hsiu-Chuan Chen, Paul A Kitts, Terence D Murphy, Kim D Pruitt, Françoise Thibaud-Nissen, Derek Albracht, Robert S Fulton, Milinn Kremitzki, Vincent Magrini, Chris Markovic, Sean McGrath, Karyn Meltz Steinberg, Kate Auger, William Chow, Joanna Collins, Glenn Harden, Timothy Hubbard, Sarah Pelan, Jared T Simpson, Glen Threadgold, James Torrance, Jonathan M Wood, Laura Clarke, Sergey Koren, Matthew Boitano, Paul Peluso, Heng Li, Chen-Shan Chin, Adam M Phillippy, Richard Durbin, Richard K Wilson, Paul Flicek, Evan E Eichler, and Deanna M Church
Genome Res. *27.5 pp. 849–864. 2017*

Building and Improving Reference Genome Assemblies
K Meltz Steinberg, V A Schneider, C Alkan, M J Montague, W C Warren, D M Church, and R K Wilson
Proc. IEEE *105.3 pp. 422–435. 2017*

Direct determination of diploid genome sequences
Neil I Weisenfeld, Vijay Kumar, Preyas Shah, Deanna M Church, and David B Jaffe
Genome Res. *27.5 pp. 757–767. 2017*

A variant by any name: quantifying annotation discordance across tools and clinical databases
Jennifer L Yen, Sarah Garcia, Aldrin Montana, Jason Harris, Stephen Chervitz, Massimo Morra, John West, Richard Chen, and Deanna M Church
Genome Med. *9.1 p. 7. 2017*

Alternate-locus aware variant calling in whole genome sequencing
Marten Jäger, Max Schubach, Tomasz Zemojtel, Knut Reinert, Deanna M Church, and Peter N Robinson
Genome Med. *8.1 p. 130. 2016*

Assembly: a resource for assembled genomes at NCBI
Paul A Kitts, Deanna M Church, Françoise Thibaud-Nissen, Jinna Choi, Vichet Hem, Victor Sapojnikov, Robert G Smith, Tatiana Tatusova, Charlie Xiang, Andrey Zherikov, Michael DiCuccio, Terence D Murphy, Kim D Pruitt, and Avi Kimchi
Nucleic Acids Res. *44.D1 pp. D73–80. 2016*

A global reference for human genetic variation
Adam Auton et al.
Nature *526.7571 pp. 68–74. 2015*

Extending reference assembly models
Deanna M Church, Valerie A Schneider, Karyn Meltz Steinberg, Michael C Schatz, Aaron R Quinlan, Chen-Shan Chin, Paul A Kitts, Bronwen Aken, Gabor T Marth, Michael M Hoffman, Javier Herrero, M Lisandra Zepeda Mendoza, Richard Durbin, and Paul Flicek
Genome Biol. *16.13 pp. 2–6. 2015*

Good laboratory practice for clinical next-generation sequencing informatics pipelines
Amy S Gargis, Lisa Kalman, David P Bick, Cristina da Silva, David P Dimmock, Birgit H Funke, Sivakumar Gowrisankar, Madhuri R Hegde, Shashikant Kulkarni, Christopher E Mason, Rakesh Nagarajan, Karl V Voelkerding, Elizabeth A Worthey, Nazneen Aziz, John Barnes, Sarah F Bennett, Himani Bisht, Deanna M Church, Zoya Dimitrova, Shaw R Gargis, Nabil Hafez, Tina Hambuch, Fiona C L Hyland, Ruth Ann Luna, Duncan MacCannell, Tobias Mann, Megan R McCluskey, Timothy K McDaniel, Lilia M Ganova-Raeva, Heidi L Rehm, Jeffrey Reid, David S Campo, Richard B Resnick, Perry G Ridge, Marc L Salit, Pavel Skums, Lee-Jun C Wong, Barbara A Zehnbauer, Justin M Zook, and Ira M Lubin
Nat. Biotechnol. *33.7 pp. 689–693. 2015*

Achieving high-sensitivity for clinical applications using augmented exome sequencing
Anil Patwardhan, Jason Harris, Nan Leng, Gabor Bartha, Deanna M Church, Shujun Luo, Christian Haudenschild, Mark Pratt, Justin Zook, Marc Salit, Jeanie Tirch, Massimo Morra, Stephen Chervitz, Ming Li,

Michael Clark, Sarah Garcia, Gemma Chandratillake, Scott Kirk, Euan Ashley, Michael Snyder, Russ Altman, Carlos Bustamante, Atul J Butte, John West, and Richard Chen
Genome Med. *7.1 p. 71. Genome Medicine, 2015*

ClinVar: public archive of relationships among sequence variation and human phenotype
Melissa J Landrum, Jennifer M Lee, George R Riley, Wonhee Jang, Wendy S Rubinstein, Deanna M Church, and Donna R Maglott
Nucleic Acids Res. *42.Database issue pp. D980–5. 2014*

Database resources of the National Center for Biotechnology Information
NCBI Resource Coordinators
Nucleic Acids Res. *42.Database issue pp. D7–17. 2014*

Single haplotype assembly of the human genome from a hydatidiform mole
Karyn Meltz Steinberg, Valerie A Schneider, Tina A Graves-Lindsay, Robert S Fulton, Richa Agarwala, John Huddleston, Sergey A Shiryev, Aleksandr Morgulis, Urvashi Surti, Wesley C Warren, Deanna M Church, Evan E Eichler, and Richard K Wilson
Genome Res. *24.12 pp. 2066–2076. 2014*

DbVar and DGVa: public archives for genomic structural variation
Ilkka Lappalainen, John Lopez, Lisa Skipper, Timothy Hefferon, J Dylan Spalding, John Garner, Chao Chen, Michael Maguire, Matt Corbett, George Zhou, Justin Paschall, Victor Ananiev, Paul Flicek, and Deanna M Church
Nucleic Acids Res. *41.Database issue pp. D936–41. 2013*

Clone DB: an integrated NCBI resource for clone-associated data
Valerie A Schneider, Hsiu-Chuan Chen, Cliff Clausen, Peter A Meric, Zhigang Zhou, Nathan Bouk, Nora Husain, Donna R Maglott, and Deanna M Church
Nucleic Acids Res. *41.Database issue pp. D1070–8. 2013*

Towards an evidence-based process for the clinical interpretation of copy number variation
E R Riggs, D M Church, K Hanson, V L Horner, E B Kaminsky, R M Kuhn, K E Wain, E S Williams, S Aradhya, H M Kearney, D H Ledbetter, S T South, E C Thorland, and C L Martin
Clin. Genet. *81(5).November pp. 403–412. 2012*

Online resources for genomic structural variation
Tam P Sneddon and Deanna M Church
Methods Mol. Biol. *838 pp. 273–289. 2012*

Modernizing Reference Genome Assemblies
Deanna M Church, Valerie a Schneider, Tina Graves, Katherine Auger, Fiona Cunningham, Nathan Bouk, Hsiu-Chuan Chen, Richa Agarwala, William M McLaren, Graham R S Ritchie, Derek Albracht, Milinn Kremitzki, Susan Rock, Holland Kotkiewicz, Colin Kremitzki, Aye Wollam, Lee Trani, Lucinda Fulton, Robert Fulton, Lucy Matthews, Siobhan Whitehead, Will Chow, James Torrance, Matthew Dunn, Glenn Harden, Glen Threadgold, Jonathan Wood, Joanna Collins, Paul Heath, Guy Griffiths, Sarah Pelan, Darren Grafham, Evan E. Eichler, George Weinstock, Elaine R Mardis, Richard K Wilson, Kerstin Howe, Paul Flicek, and Tim Hubbard
PLoS Biol. *9.7 e1001091. 2011*

An evidence-based approach to establish the functional and clinical significance of copy number variants in intellectual and developmental disabilities
Erin B Kaminsky, Vineith Kaul, Justin Paschall, Deanna M Church, Brian Bunke, Dawn Kunig, Daniel Moreno-De-Luca, Andres Moreno-De-Luca, Jennifer G Mulle, Stephen T Warren, Gabriele Richard, John G Compton, Amy E Fuller, Troy J Gliem, Shuwen Huang, Morag N Collinson, Sarah J Beal, Todd Ackley, Diane L Pickering, Denae M Golden, Emily Aston, Heidi Whitby, Shashirekha Shetty, Michael R Rossi, M Katharine Rudd, Sarah T South, Arthur R Brothman, Warren G Sanger, Ramaswamy K Iyer, John a Crolla, Erik C Thorland, Swaroop Aradhya, David H Ledbetter, and Christa L Martin
Genet. Med. *13.9 pp. 777–784. 2011*

Public data archives for genomic structural variation
Deanna M Church, Ilkka Lappalainen, Tam P Sneddon, Jonathan Hinton, John Lopez, John Garner, Justin Paschall, Michael Dicuccio, Stephen W Scherer, Lars Feuk, and Paul Flicek

Nat. Genet. *42.10 pp. 813–814. 2010*

Consensus statement: chromosomal microarray is a first-tier clinical diagnostic test for individuals with developmental disabilities or congenital anomalies

David T Miller, Margaret P Adam, Swaroop Aradhya, Leslie G Biesecker, Arthur R Brothman, Nigel P Carter, Deanna M Church, John a Crolla, Evan E Eichler, Charles J Epstein, W Andrew Faucett, Lars Feuk, Jan M Friedman, Ada Hamosh, Laird Jackson, Erin B Kaminsky, Klaas Kok, Ian D Krantz, Robert M Kuhn, Charles Lee, James M Ostell, Carla Rosenberg, Stephen W Scherer, Nancy B Spinner, Dimitri J Stavropoulos, James H Tepperberg, Erik C Thorland, Joris R Vermeesch, Darrel J Waggoner, Michael S Watson, Christa Lese Martin, and David H Ledbetter

Am. J. Hum. Genet. *86.5 pp. 749–764. The American Society of Human Genetics, 2010*

Completing the map of human genetic variation

David Altshuler, Anne M Bowcock, Lisa D Brooks, Nigel P Carter, M Church, Adam Felsenfeld, Mark Guyer, Charles Lee, James R Lupski, C James, Jonathan K Pritchard, Jonathan Sebat, Stephen T Sherry, David Valle, and Robert H Waterston

Nature *447.7141 pp. 161–165. 2009*

Lineage-specific biology revealed by a finished genome assembly of the mouse

Deanna M Church, Leo Goodstadt, Ladeana W Hillier, Michael C Zody, Steve Goldstein, Xinwe She, Carol J Bult, Richa Agarwala, Joshua L Cherry, Michael DiCuccio, Wratko Hlavina, Yuri Kapustin, Peter Meric, Donna Maglott, Zoë Birtle, Ana C Marques, Tina Graves, Shiguo Zhou, Brian Teague, Konstantinos Potamousis, Christopher Churas, Michael Place, Jill Herschleb, Ron Runnheim, Daniel Forrest, James Amos-Landgraf, David C Schwartz, Ze Cheng, Kerstin Lindblad-Toh, Evan E Eichler, and Chris P Ponting

PLoS Biol. *7.5 e1000112. 2009*

Back to Bermuda: how is science best served?

Deanna M Church and Ladeana W Hillier

Genome Biol. *10.4 p. 105. 2009*

Database resources of the National Center for Biotechnology Information

Eric W Sayers, Tanya Barrett, Dennis a Benson, Stephen H Bryant, Kathi Canese, Vyacheslav Chetvernin, Deanna M Church, Michael DiCuccio, Ron Edgar, Scott Federhen, Michael Feolo, Lewis Y Geer, Wolfgang Helmberg, Yuri Kapustin, David Landsman, David J Lipman, Thomas L Madden, Donna R Maglott, Vadim Miller, Ilene Mizrachi, James Ostell, Kim D Pruitt, Gregory D Schuler, Edwin Sequeira, Stephen T Sherry, Martin Shumway, Karl Sirotkin, Alexandre Souvorov, Grigory Starchenko, Tatiana a Tatusova, Lukas Wagner, Eugene Yaschenko, and Jian Ye

Nucleic Acids Res. *37.Database issue pp. D5–15. 2009*

Mouse segmental duplication and copy number variation

Xinwei She, Ze Cheng, Sebastian Zöllner, Deanna M Church, and Evan E Eichler

Nat. Genet. *40.7 pp. 909–914. 2008*

Candidate single nucleotide polymorphism selection using publicly available tools: a guide for epidemiologists

Parveen Bhatti, Deanna M Church, Joni L Rutter, Jeffery P Struewing, and Alice J Sigurdson

Am. J. Epidemiol. *164.8 pp. 794–804. 2006*

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Nucleic Acids Res. *34.Database issue pp. D173–80. 2006*

A genome-wide comparison of recent chimpanzee and human segmental duplications

Ze Cheng, Mario Ventura, Xinwei She, Philipp Khaitovich, Tina Graves, Kazutoyo Osoegawa, Deanna Church, Pieter DeJong, Richard K Wilson, Svante Pääbo, Mariano Rocchi, and Evan E Eichler

Nature *437.7055 pp. 88–93. 2005*

Analysis of Segmental Duplications and Genome Assembly in the Mouse
Jeffrey A Bailey, Deanna M Church, Mario Ventura, Mariano Rocchi, and Evan E Eichler
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Shotgun sequence assembly and recent segmental duplication within the human genome
Xinwei She, Zhaoshi Jiang, Royden A Clark, Ge Liu, Ze Cheng, Eray Tuzun, Deanna M Church, Granger Sutton, Aaron L Halpern, and Evan E Eichler
Nature *431.7011 pp. 927–930. 2004*

Database resources of the National Center for Biotechnology Information: update
David L Wheeler, Deanna M Church, Ron Edgar, Scott Federhen, Wolfgang Helmberg, Thomas L Madden, Joan U Pontius, Gregory D Schuler, Lynn M Schriml, Edwin Sequeira, Tugba O Suzek, Tatiana a Tatusova, and Lukas Wagner
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Connecting Sequence and Biology in the Laboratory Mouse
Richard M Baldarelli, David P Hill, Judith A Blake, Jun Adachi, Masaaki Furuno, Dirck Bradt, Lori E Corbani, Sharon Cousins, Kenneth S Frazer, Dong Qi, Longlong Yang, Sridhar Ramachandran, Deborah Reed, Yunxia Zhu, Takeya Kasukawa, Martin Ringwald, Benjamin L King, Lois J Maltais, Louise M Mckenzie, Lynn M Schriml, Donna Maglott, Deanna M Church, Kim Pruitt, Janan T Eppig, Joel E Richardson, Jim A Kadin, and Carol J Bult
Genome Res. *13.6b pp. 1505–1519. 2003*

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