

DeannaMChurch

Genomics, Technology and Bioinformatics Leader

contact

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USA

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skills

Leadership, Mentorship,
Product
Commercialization,
Team Player,
Project Management,
Curiosity & Initiative

genomics

Genome editing,
Genome assembly,
Genome annotation,
variant analysis &
Single-cell 'omics

bioinformatics

Python, R, Git,
HTML, XML/XSLT,
Javascript,
CSS3, SQL & Perl
github.com/deannachurch

languages

english, mother tongue

focus

Leading interdisciplinary teams to deliver cutting edge life sciences tools.

experience

2021–present **Inscripta, Inc**

Boulder, CO

Vice President, Mammalian Business Area and Software Strategy

Driving customer voice and commercialization of our mammalian editing platform. Ensuring our software platform supports all of our platforms and provides customers with an excellent experience.

2019–2021 **Inscripta, Inc**

Boulder, CO

Senior Director, Applications Mammalian

Driving customer voice of our mammalian editing platform.

2016–2018 **10x Genomics**

Pleasant, CA

Senior Director of Applications

Led an interdisciplinary team of top scientists in demonstrating the scientific value of the full 10x product suite. This work covers a variety of scientific areas including single cell 'omics, genome assembly, genome analysis, tumor microenvironment analysis, tumor heterogeneity and immune profiling.

2014–2016 **Personalis, Inc**

Menlo Park, CA

Senior Director of Genomics and Content

Led a team developing novel genome analysis algorithms and pipelines and knowledge bases built to support genome interpretation.

2001–2014 **National Center for Biotechnology Information, NIH**

Bethesda, MA

Staff Scientist

Participated in and led numerous international collaborations including helping to found the Genome Reference Consortium. Developed tools and resources for the scientific community.

1990–1992 **MIT and MGH**

Boston, MA

Laboratory Technician

Managed laboratory and performed experiments, including helping to develop the exon amplification protocol.

education

1999–2001 **National Center for Biotechnology Information, NIH**

Bethesda, MD

Postdoctoral fellow

1997–1999 **Laboratory of Janet Rossant, Mt. Sinai Hospital**

Toronto, Ontario

Postdoctoral fellow

1992–1997 **PhD of Biological Sciences**

The University of California, Irvine

Phenotype-genotype correlation in the Cri-du-Chat region of chromosome 5

1986–1990 **Bachelor of Liberal Arts**

University of Virginia

Research project focused on cell cycle regulation using yeast

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

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

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

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, Fereydown 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, Zeichen 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 Bhargava, 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

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 Christopher 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 of *Capsicum annuum* from 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

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, and Javier Herrero

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 Zehnbauser, Justin M Zook, and Ira M Lubin
Nat. Biotechnol. 33.7 pp. 689–693. 2015

Assembly: a resource for assembled genomes at NCBI

P A Kitts, D M Church, F Thibaud-Nissen, J Choi, V Hem, V Sapojnikov, R G Smith, T Tatusova, C Xiang, A Zherikov, M DiCuccio, T D Murphy, K D Pruitt, and A Kimchi
Nucleic Acids Res. Pp. 1–8. 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 Tirsch, 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 Potamiosis, 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 Mizrahi, 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

Database resources of the National Center for Biotechnology Information

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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

Genome Res. 14.216 pp. 789–801. 2004

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

Nucleic Acids Res. 32.Database issue pp. D35–40. 2004

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

Cross-Species Sequence Comparisons : A Review of Methods and Available Resources

Kelly A Frazer, Laura Elnitski, Deanna M Church, Inna Dubchak, and Ross C Hardison

Genome Res. 13.1 pp. 1–12. 2003

Database resources of the National Center for Biotechnology

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Nucleic Acids Res. 31.1 pp. 28–33. 2003

Initial sequencing and comparative analysis of the mouse genome

Robert H Waterston et al.

Nature 420.6915 pp. 520–562. 2002

Database resources of the National Center for Biotechnology Information: 2002 update

David L Wheeler, Deanna M Church, Alex E Lash, Detlef D Leipe, Thomas L Madden, Joan U Pontius, Gregory D Schuler, Lynn M Schriml, Tatiana a Tatusova, Lukas Wagner, and Barbara a Rapp

Nucleic Acids Res. 30.1 pp. 13–16. 2002

A radiation hybrid map of mouse genes

T J Hudson, D M Church, S Greenaway, H Nguyen, A Cook, R G Steen, W J Van Etten, a B Castle, M a Strivens, P Trickett, C Heuston, C Davison, A Southwell, R Hardisty, A Varela-Carver, a R Haynes, P Rodriguez-Tome, H Doi, M S Ko, J Pontius, L Schriml, L Wagner, D Maglott, S D Brown, E S Lander, G Schuler, and P Denny

Nat. Genet. 29.2 pp. 201–205. 2001

Initial sequencing and analysis of the human genome

E S Lander et al.
Nature 409.6822 pp. 860–921. 2001

Generation of RCAS vectors useful for functional genomic analyses
S K Loftus, D M Larson, D Watkins-Chow, D M Church, and W J Pavan
DNA Res. 8.5 pp. 221–226. 2001

Spidey : A Tool for mRNA-to-Genomic Alignments
Sarah J Wheelan, Deanna M Church, and James M Ostell
Genome Res. 11.11 pp. 1952–1957. 2001

Rapid generation of nested chromosomal deletions on mouse chromosome 2
D F LePage, D M Church, E Millie, T J Hassold, and R a Conlon
Proc. Natl. Acad. Sci. U. S. A. 97.19 pp. 10471–10476. 2000

Gene identification by exon amplification
D M Church and A J Buckler
Methods Enzymol. 303 pp. 83–99. 1999

Transcript mapping of the human chromosome 11q12-q13.1 gene-rich region identifies several newly described conserved genes
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