DeannaMChurch

Genomics and Bioinformatics Leader

contact

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languages

english, mother tongue

Genomics

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

Bioinformatics

Python, R, HTML, XML/XSLT, Javascript, CSS3, SQL & Perl

focus

Leading interdisciplinary teams using genomics and computation to improve human health.

experience

2016–Present **10x Genomics** Pleasant, California
Senior Director of Applications
Leads an interdisciplinary team of top rate scientists in demonstrating the scientific value of the full 10x product suite. This work covers a variety of scientific areas including genome assembly, genome analysis, tumor microenvironment analysis, tumor heterogeneticy and immune profiling.

2014-2016 **Personalis, Inc** Menlo Park, CA
Senior Director of Genomics and Content
Led a team developing novel genome analysis algorthms and pipelines. Led the development of knowledge bases built using automated data processing coupled with data curation to support genome interpretation.

2001-2014 **National Center for Biotechnology Information, NIH** Bethesda, MA
Staff Scientist
Led a team of biologists and software developers in developing databases and tools to make genomic data accessible to the research and clinical communities. Participated in numerous international collaborations including helping to found the Genome Reference Consortium, the group tasked with maintaining the human reference assembly.

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 Coordinated mouse genome resources.

1997-1999 **Laboratory of Janet Rossant, Mt. Sinai Hospital** Toronto, Ontario
Postdoctoral fellow Applying genomics methods to understanding mouse developmental biology

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

additional training

2010	**Client-Side Web Development**	University of Illinois (O'Reilly)
2009	**XSLT/XPATH: Introduction and Syntax**	Mulberry Technologies
2007	**Introduction to XML**	University of Illinois (O'Reilly)

advisory boards and professional service

2018-present	**Genome Quebec**	Scientific Advisory Board
2018-present	**American Association for Cancer Research**	Member
2012-present	**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

awards

2012 **Special Service Award** — National Library of Medicine
For extraordinary effort in providing access to the 1000 genomes project data.

1997-1999 **Human Frontiers Postdoctoral Fellowship** — Mt. Sinai Hospital
Awarded to early career scientist to enable them to broaden their skills in a new country.

1986-1990 **Echols Scholar** — University of Virginia
Awarded to select undergraduates who exhibit academic independence.

presentations

Selected highlights from over 50 presentations.

2018-Feb **Beckman Symposium, Technology Innovation and Human Genomics** — Palo Alto, CA
Invited Speaker, "The impact of technology on our view of biology"

2017-Nov **Australasian Genomic Technologies Association Annual Meeting** — Hobart, AUS
Keynote, "High resolution biology with 10x"

2017-Nov	**Australasian Genomic Technologies Association Annual Meeting** Keynote, "The impact of technology on biology"	Hobart, AUS
2017-Apr	**NGS Barcelona** Keynote, "Advancing genomics drop by drop"	Barcelona, SP
2017-Feb	**Advance in Genomics and Biotechnology** Abstract Selected, "More complete genome analysis"	Hollywood, FL
2017-Jan	**Plant and Animal Genome Conference** Invited Speaker, "Quantitative profiling of large and complex populations by single cell RNA-sequencing"	San Diego, CA
2016-Oct	**American Society of Human Genetics** Abstract Selected, "De novo assembly of individual human haplotypes from diploid samples"	Vancouver, CA
2016-Sep	**Genome Informatics** Abstract Selected, "Improving genome analysis using Linked-Reads"	Hinxton, UK
2016-Aug	**Cancer Genomics Consortium** Invited Speaker, "Complete genome analysis"	Denver, CO
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
2015-Mar	**American College of Medical Genetics Annual Meeting** Invited Speaker, "Technical limitations of variant identification and annotation"	Salt Lake City, UT
2014-Nov	**Biological Data Sciences** Keynote Speaker, "Analog reporting in a digital age"	Cold Spring Harbor, NY
2014-Oct	**American Society of Human Genetics** Abstract Selected, "The impact of GRCh38 on clinical sequencing"	San Diego, CA
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
2012-Nov	**American Society of Human Genetics** Invited Speaker, "Improving the accuracy of variant identification"	San Francisco, CA
2012-Apr	**Generic Model Organism Database Conference** Keynote Address, "Navigating genome resources at NCBI"	Washington, DC
2011-Jul	**BIO-IT APAC Conference and Expo** Keynote Speaker, "The evolution of the reference human genome"	Shenzhen, China
2011-Jan	**Plant and Animal Genome Conference** Keynote Address, "The evolution of the reference human genome"	San Diego, CA
2008-May	**Finishing in the Future** Keynote Speaker, "Great expectations: fulfilling the promises of the human genome project"	Santa Fe, NM
2006-Jun	**Human Genome Variation Society** Keynote Speaker, "The evolution of the reference human genome"	Someplace, WO

teaching

Selected courses and lectures.

2017 **Standord, 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 in peer-reviewed journals

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. 2018

Genomes for all
Deanna M Church
Nat. Biotechnol. 36 p. 815. Nature Publishing Group, a division of Macmillan Publishers Limited. All Rights Reserved., 2018

Reference quality assembly of the 3.5-Gb genome of Capsicum annum 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

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

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

Database resources of the National Center for Biotechnology Information
Ncbi Resource Coordinators
Nucleic Acids Res. 41.Database issue pp. D8–D20. 2013

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

Database resources of the National Center for Biotechnology Information

David L Wheeler, Tanya Barrett, Dennis A Benson, Stephen H Bryant, Kathi Canese, Vyacheslav Chetvernin, Deanna M Church, Michael DiCuccio, Ron Edgar, Scott Federhen, Lewis Y Geer, Wolfgang Helmberg, Yuri Kapustin, David L Kenton, Oleg Khovayko, David J Lipman, Thomas L Madden, Donna R Maglott, James Ostell, Kim D Pruitt, Gregory D Schuler, Lynn M Schriml, Edwin Sequeira, Stephen T Sherry, Karl Sirotkin, Alexandre Souvorov, Grigory Starchenko, Tugba O Suzek, Roman Tatusov, Tatiana A Tatusova, Lukas Wagner, and Eugene Yaschenko

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
David L Wheeler, Deanna M Church, Scott Federhen, Alex E Lash, Thomas L Madden, Joan U Pontius, Gregory D Schuler, Lynn M Schriml, Edwin Sequeira, Tatiana A Tatusova, and Lukas Wagner
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
P R Cooper, N J Nowak, M J Higgins, D M Church, and T B Shows
Genomics 49.3 pp. 419–429. 1998

A High-Resolution Physical and Transcript Map of the Cri du Chat A High-Resolution Physical and Transcript Map of the Cri du Chat Region of Human Chromosome 5p
Deanna M Church, Julie Yang, Maureen Bocian, Rita Shiang, and John J Wasmuth
Genome Res. 7.8 pp. 787–801. 1997

A Radiation Hybrid Map of Human Chromosome 5 with Integration of Cytogenetic , Genetic , and Transcript Maps
John D Mcpherson, Barbara Apostol, Caryn B Wagner-mcpherson, Simin Hakim, Richard G Del Mastro, Naeema Aziz, Elizabeth Baer, Genalyn Gonzales, Mary Carol Krane, Rachelle Markovich, Peter Masny, Miguel Ortega, John Vu, Marco Vujicic, Deanna M Church, Allan Segal, Deborah L Grady, Robert K Moyzis, M Anne Spence, Michael Lovett, and John J Wasmuth
Genome Res. 7.9 pp. 897–909. 1997

Exon trapping and sequence-based methods of gene finding in transcript mapping of human 4p16.3
I Pribill, G T Barnes, J Chen, D Church, A Buckler, S Baxendale, G P Bates, H Lehrach, M J Gusella, M P Duyao, C M Ambrose, J F Gusella, and M E MacDonald
Somat. Cell Mol. Genet. 23.6 pp. 413–427. 1997

The Ras GTPase-activating-protein-related human protein IQGAP2 harbors a potential actin binding domain and interacts with calmodulin and Rho family GTPases
S Brill, S Li, C W Lyman, D M Church, J J Wasmuth, L Weissbach, A Bernards, and a J Snijders
Mol. Cell. Biol. 16.9 pp. 4869–4878. 1996

Identification and characterization of two novel tetratricopeptide repeat-containing genes
A E Murthy, A Bernards, D Church, J Wasmuth, and J F Gusella
DNA Cell Biol. 15.9 pp. 727–735. 1996

Molecular definition of deletions of different segments of distal 5p that result in distinct phenotypic features
D M Church, U Bengtsson, K V Nielsen, J J Wasmuth, and E Niebuhr
Am. J. Hum. Genet. 56.5 pp. 1162–1172. 1995

Isolation of genes from complex sources of mammalian genomic DNA using exon amplification
Deanna M Church, Christy J Stotler, Joni L Rutter, Jill R Murrell, James A Trofatter, and Alan J Buckler
Nat. Genet. 6.1 pp. 98–105. 1994

Mutations in the transmembrane domain of FGFR3 cause the most common genetic form of dwarfism, achondroplasia
R Shiang, L M Thompson, Y Z Zhu, D M Church, T J Fielder, M Bocian, S T Winokur, and J J Wasmuth
Cell 78.2 pp. 335–342. 1994

A novel gene containing a trinucleotide repeat that is expanded and unstable on Huntington's disease chromosomes. The Huntington's Disease Collaborative Research Group
Cell 72.6 pp. 971–983. 1993

Identification of human chromosome 9 specific genes using exon amplification
D M Church, L T Banks, a C Rogers, S L Graw, D E Housman, J F Gusella, and a J Buckler
Hum. Mol. Genet. 2.11 pp. 1915–1920. 1993

A gene from chromosome 4p16.3 with similarity to a superfamily of transporter proteins
Mabel P Duyao, Sherryl A M Tayler, Alan J Buckler, Christine M Ambrose, Carol Lin, Nicolet Groot, Deanna Church, Glenn Barnes, John J Wasmuth, David E Housman, Marcy E MacDonald, and James F Gusella
Hum. Mol. Genet. 2.6 pp. 673–676. 1993

Efficiency and specificity of gene isolation by exon amplification

M A North, P Sanseau, A J Buckler, D Church, A Jackson, K Patel, J Trowsdale, and H Lehrach

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