

DeannaMChurch

Genomics, Technology and Bioinformatics Leader

contact

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USA

(301) 233 2991

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skills

Leadership, Team Player,
Project Management (Jira),
Curiosity & Initiative

genomics

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

bioinformatics

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

languages

english, mother tongue

focus

Leading interdisciplinary teams to make genomics and technology accessible to all.

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 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. Led the development of knowledge bases built using automated data processing coupled with expert 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 For extraordinary effort in providing access to the 1000 genomes project data.	National Library of Medicine
1997-1999	Human Frontiers Postdoctoral Fellowship Awarded to early career scientist to enable them to broaden their skills in a new country.	Mt. Sinai Hospital
1986-1990	Echols Scholar Awarded to select undergraduates who exhibit academic independence.	University of Virginia

presentations

Selected highlights from over 50 presentations.

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, "High resolution biology with 10x"	Hobart, AUS

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	Standard, 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

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. 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 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

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 Zehnbauser, 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, Xinwei 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 Potamouisis, 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 Helmborg, 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 Mas-tro, 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
Mamm. Genome 4.9 pp. 466–474. 1993

Molecular basis of myotonic dystrophy: expansion of a trinucleotide (CTG) repeat at the 3' end of a transcript encoding a protein kinase family member

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