Department of Molecular and Systems Biology
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Aaron McKenna

Education

Genome Sciences, University of Washington, *Seattle, Washington* — *August, 2017*
Ph.D. in Genome Sciences,
Certificates in Computational Biology and Statistical Genetics
Advisor: Jay Shendure M.D. Ph.D.

Boston University, *Boston, MA* — *December, 2008*
M.S. in Bioinformatics

Worcester Polytechnic Institute, *Worcester, MA* — *May, 2003*
B.S. in Computer Science

Employment

Assistant Professor — *May, 2019 –*
Dartmouth College. Hanover, NH, USA
Department of Molecular and Systems Biology, Geisel School of Medicine.

Senior Fellow — *August, 2017 - April, 2019*
University of Washington. Seattle, WA
Department of Genome Sciences
Advisor: Jay Shendure M.D. Ph.D.

Software Engineer / Computational Biologist — *September 2008 - July 2012*
The Broad Institute of Harvard and MIT, *Cambridge, MA*

I designed and implemented the Genome Analysis Toolkit (GATK) a Java framework for next-generation sequencing projects, which is now used at the Broad and other large sequencing centers. This was published as first author in *Genome Research*. In addition, I implemented a method for detecting inter-sample contamination in next generation sequencing samples, published as a first author in *Bioinformatics*, while leading the analysis of The Cancer Genome Atlas (TCGA) Glioblastoma project, published as a first author in *Cell*.

Software Engineer — *September 2006 – September 2008*
Adaptive Optic Associates, *Cambridge, MA*

I design, implemented, and tested a measurement and control system for a portable fiber-optic interrogation platform in Java. I also designed, implemented, and tested an embedded Linux system to control a fiber optic dispersion compensator, coded in assembly and C++.

Software Engineer — *July 2003 - September 2006*
General Dynamics C4 Systems, *Needham, MA*

I was part of a team that designed, implemented, and tested a packet processor engine for TACLANE inline gigabit IP encryption device under National Security Agency contract, coding in Assembly and C/C++. I developed a prototype Java application for the National Security Agency, incorporating their HMI device interface requirements into a rapid prototype, and I developed an application to automate configuration of encryption devices, greatly reducing production testing schedules. This program selected for excellence, receiving 100% award fee from the National Security Agency.

Software Engineer Intern *Summer 1999, 2000, 2001*
International Business Machines (IBM), *Essex, VT*
I worked on a team to develop timing analysis and noise prediction tools for ASIC circuit design on IBM AIX UNIX. I also migrated IBM Circuit Design Tools from AIX UNIX to the Linux platform. Lastly I was nominated for IBM Extreme Blue program.

Patents

Methods and Apparatus for Analyzing and Quantifying DNA Alterations in Cancer.
Scott L. Carter, Gad Getz, ***Aaron McKenna****, and Matthew Meyerson, inventor. The Broad Institute, Inc., Dana-Farber Cancer Institute, Inc, applicant. Patent WO2014026096 A1*

Whole-organism lineage tracing by combinatorial and cumulative genome editing.
Aaron McKenna*, Gregory M. Findlay, James A. Gagnon, Alexander F. Schier, Jay Shendure, inventor. Harvard University and University of Washington, applicant. Provisional Patent*

First Author Publications

FlashFry: a fast and flexible tool for large-scale CRISPR target design
Aaron McKenna and Jay Shendure
BMC Biology 2018 Jul 5;16(1):74.

Whole-organism lineage tracing by combinatorial and cumulative genome editing
McKenna A*, Findlay GM*, Gagnon JA*, Horwitz MS, Schier AF, Shendure J
Science 2016 Jul 29;353(6298):aaf7907

The somatic genomic landscape of glioblastoma
Brennan CW*, Verhaak RG*, **McKenna A***, Campos B, Noushmehr H, Salama SR, Zheng S, Chakravarty D, Sanborn JZ, Berman SH, Beroukhim R, Bernard B, Wu CJ, Genovese G, Shmulevich I, Barnholtz-Sloan J, Zou L, Vegesna R, Shukla SA, Ciriello G, Yung WK, Zhang W, Sougnez C, Mikkelsen T, Aldape K, Bigner DD, Van Meir EG, Prados M, Sloan A, Black KL, Eschbacher J, Finocchiaro G, Friedman W, Andrews DW, Guha A, Iacocca M, O'Neill BP, Foltz G, Myers J, Weisenberger DJ, Penny R, Kucherlapati R, Perou CM, Hayes DN, Gibbs R, Marra M, Mills GB, Lander E, Spellman P, Wilson R, Sander C, Weinstein J, Meyerson M, Gabriel S, Laird PW, Haussler D, Getz G, Chin L; TCGA Research Network
Cell 2013 Oct 10;155(2):462-77

ContEst: estimating cross-contamination of human samples in next-generation sequencing data
Cibulskis K*, **McKenna A***, Fennell T, Banks E, DePristo M, Getz G
Bioinformatics 2011 Sep 15;27(18):2601-2

Publications

The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data
McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, Garimella K, Altshuler D, Gabriel S, Daly M, DePristo MA
Genome Res 2010 Sep;20(9):1297-303

Estimation of cell lineage trees by maximum-likelihood phylogenetics
Jean Feng, William S DeWitt III, **Aaron McKenna**, Noah Simon, Amy Willis, Frederick A Matsen IV
BioRxiv March, 2019

Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair
Wei Chen, **Aaron McKenna**, Jacob Schreiber, Yi Yin, Vikram Agarwal, William Stafford Noble, Jay Shendure
BioRxiv November, 2018

Simultaneous single-cell profiling of lineages and cell types in the vertebrate brain
Raj B, Wagner DE, **McKenna A**, Pandey S, Klein AM, Shendure J, Gagnon JA, Schier AF
Nat Biotechnology 2018 Jun;36(5):442-450

CRISPR/Cas9-Mediated Scanning for Regulatory Elements Required for HPRT1 Expression via Thousands of Large, Programmed Genomic Deletions
Gasperini M, Findlay GM, **McKenna A**, Milbank JH, Lee C, Zhang MD, Cusanovich DA, Shendure J
Am J Hum Genetics 2017 Aug 3;101(2):192-205

Systematic genomic and translational efficiency studies of uveal melanoma
Johnson CP, Kim IK, Esmaeli B, Amin-Mansour A, Treacy DJ, Carter SL, Hodis E, Wagle N, Seepo S, Yu X, Lane AM, Gragoudas ES, Vazquez F, Nickerson E, Cibulskis K, **McKenna A**, Gabriel SB, Getz G, Van Allen EM, 't Hoen PAC, Garraway LA, Woodman SE
PLoS One 2017 Jun 8;12(6):e0178189 **A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine**
Van Allen EM, Robinson D, Morrissey C, Pritchard C, Imamovic A, Carter S, Rosenberg M, **McKenna A**, Wu YM, Cao X, Chinnaiyan A, Garraway L, Nelson PS
Oncotarget 2016 Aug 16;7(33):52888-52899

Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets
Brastianos PK, Carter SL, Santagata S, Cahill DP, Taylor-Weiner A, Jones RT, Van Allen EM, Lawrence MS, Horowitz PM, Cibulskis K, Ligon KL, Tabernero J, Seoane J, Martinez-Saez E, Curry WT, Dunn IF, Paek SH, Park SH, **McKenna A**, Chevalier A, Rosenberg M, Barker FG 2nd, Gill CM, Van Hummelen P, Thorner AR, Johnson BE, Hoang MP, Choueiri TK, Signoretti S, Sougnez C, Rabin MS, Lin NU, Winer EP, Stemmer-Rachamimov A, Meyerson M, Garraway L, Gabriel S, Lander ES, Beroukhim R, Batchelor TT, Baselga J, Louis DN, Getz G, Hahn WC
Cancer Discovery 2015 Nov;5(11):1164-1177

Paired exome analysis of Barrett's esophagus and adenocarcinoma
Stachler MD, Taylor-Weiner A, Peng S, **McKenna A**, Agoston AT, Odze RD, Davison JM, Nason KS, Loda M, Leshchiner I, Stewart C, Stojanov P, Seepo S, Lawrence MS, Ferrer-Torres D, Lin J, Chang AC, Gabriel SB, Lander ES, Beer DG, Getz G, Carter SL, Bass AJ
Nat Genetics 2015 Sep;47(9):1047-55

Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma
Van Allen EM, Lui VW, Egloff AM, Goetz EM, Li H, Johnson JT, Duvvuri U, Bauman JE, Stransky N, Zeng Y, Gilbert BR, Pendleton KP, Wang L, Chiosea S, Sougnez C, Wagle N, Zhang F, Du Y, Close D, Johnston PA, **McKenna A**, Carter SL, Golub TR, Getz G, Mills GB, Garraway LA, Grandis JR
JAMA Oncology 2015 May;1(2):238-44

Prospective derivation of a living organoid biobank of colorectal cancer patients
van de Wetering M, Francies HE, Francis JM, Bounova G, Iorio F, Pronk A, van Houdt W, van Gorp J, Taylor-Weiner A, Kester L, McLaren-Douglas A, Blokker J, Jaksani S, Bartfeld S, Volckman R, van Sluis P, Li VS, Seepo S, Sekhar Pedamallu C, Cibulskis K, Carter SL, **McKenna A**, Lawrence MS, Lichtenstein L, Stewart C, Koster J, Versteeg R, van Oudenaarden A, Saez-Rodriguez J, Vries RG, Getz G, Wessels L, Stratton MR, McDermott U, Meyerson M, Garnett MJ, Clevers H
Cell 2015 May 7;161(4):933-45

Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma
Perry JA, Kiezun A, Tonzi P, Van Allen EM, Carter SL, Baca SC, Cowley GS, Bhatt AS, Rheinbay E, Pedamallu CS, Helman E, Taylor-Weiner A, **McKenna A**, DeLuca DS, Lawrence MS, Ambrogio L, Sougnez C, Sivachenko A, Walensky LD, Wagle N, Mora J, de Torres C, Lavarino C, Dos Santos Aguiar S, Yunes JA, Brandalise SR, Mercado-Celis GE, Melendez-Zajgla J, C□rdenas-Card□s R, Velasco-Hidalgo L, Roberts CW, Garraway LA, Rodriguez-Galindo C, Gabriel SB, Lander ES, Golub TR, Orkin SH, Getz G, Janeway KA
Proc Natl Acad Sci U S A 2014 Dec 23;111(51):E5564-73

The genomic landscape of pediatric Ewing sarcoma
Crompton BD, Stewart C, Taylor-Weiner A, Alexe G, Kurek KC, Calicchio ML, Kiezun A, Carter SL, Shukla SA, Mehta SS, Thorner AR, de Torres C, Lavarino C, Su□ol M, **McKenna A**, Sivachenko A, Cibulskis K, Lawrence MS, Stojanov P, Rosenberg M, Ambrogio L, Auclair D, Seepo S, Blumenstiel B, DeFelice M, Imaz-Rosshandler I, Schwarz-Cruz Y Celis A, Rivera MN, Rodriguez-Galindo C, Fleming MD, Golub TR, Getz G, Mora J, Stegmaier K
Cancer Discovery 2014 Nov;4(11):1326-41

Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin- embedded tumor samples to guide precision cancer medicine
Van Allen EM, Wagle N, Stojanov P, Perrin DL, Cibulskis K, Marlow S, Jane-Valbuena J, Friedrich DC, Kryukov G, Carter SL, **McKenna A**, Sivachenko A, Rosenberg M, Kiezun A, Voet D, Lawrence M, Lichtenstein LT, Gentry JG, Huang FW, Fostel J, Farlow D, Barbie D, Gandhi L, Lander ES, Gray SW, Joffe S, Janne P, Garber J, MacConaill L, Lindeman N, Rollins B, Kantoff P, Fisher SA, Gabriel S, Getz G, Garraway LA
Nat Med 2014 Jun;20(6):682-8

Genetic and clonal dissection of murine small cell lung carcinoma progression by genome sequencing
McFadden DG, Papagiannakopoulos T, Taylor-Weiner A, Stewart C, Carter SL, Cibulskis K, Bhutkar A, **McKenna A**, Dooley A, Vernon A, Sougnez C, Malstrom S, Heimann M, Park J, Chen F, Farago AF, Dayton T, Shefler E, Gabriel S, Getz G, Jacks T
Cell 2014 Mar 13;156(6):1298-1311

Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy
Lohr JG, Stojanov P, Carter SL, Cruz-Gordillo P, Lawrence MS, Auclair D, Sougnez C, Knoechel B, Gould J, Saksena G, Cibulskis K, **McKenna A**, Chapman MA, Straussman R, Levy J, Perkins LM, Keats JJ, Schumacher SE, Rosenberg M; Multiple Myeloma Research Consortium, Getz G, Golub TR
Cancer Cell 2014 Jan 13;25(1):91-101

Landscape of genomic alterations in cervical carcinomas
Ojesina AI, Lichtenstein L, Freeman SS, Pedamallu CS, Imaz-Rosshandler I, Pugh TJ, Cherniack AD, Ambrogio L, Cibulskis K, Bertelsen B, Romero-Cordoba S, Trevi□o V, Vazquez-Santillan K, Guadarrama AS, Wright AA, Rosenberg MW, Duke F, Kaplan B, Wang R, Nickerson E, Walline HM, Lawrence MS, Stewart C, Carter SL, **McKenna A**, Rodriguez-Sanchez IP, Espinosa-Castilla M, Woie K, Bjorge L, Wik E, Halle MK, Hoivik EA, Krakstad C, Gabi□o NB, G□mez-Mac□as GS, Valdez-Chapa LD, Garza-Rodr□guez ML, Maytorena G, Vazquez J, Rodea C, Cravioto A, Cortes ML, Greulich H, Crum CP, Neuberg DS, Hidalgo-Miranda A, Escareno CR, Akslen LA, Carey TE, Vintermyr OK, Gabriel SB, Barrera-Salda□a HA, Melendez-Zajgla J, Getz G, Salvesen HB, Meyerson M
Nature 2014 Feb 20;506(7488):371-5

Integrative and comparative genomic analysis of lung squamous cell carcinomas in East Asian patients
Kim Y, Hammerman PS, Kim J, Yoon JA, Lee Y, Sun JM, Wilkerson MD, Pedamallu CS, Cibulskis K, Yoo YK, Lawrence MS, Stojanov P, Carter SL, **McKenna A**, Stewart C, Sivachenko AY, Oh IJ, Kim HK, Choi YS, Kim K, Shim YM, Kim KS, Song SY, Na KJ, Choi YL, Hayes DN, Kim J, Cho S, Kim YC, Ahn JS, Ahn MJ, Getz G, Meyerson M, Park K
J Clin Oncology 2014 Jan 10;32(2):121-8

MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition
Wagle N, Van Allen EM, Treacy DJ, Frederick DT, Cooper ZA, Taylor-Weiner A, Rosenberg M, Goetz EM, Sullivan RJ, Farlow DN, Friedrich DC, Anderka K, Perrin D, Johannessen CM, **McKenna A**, Cibulskis K, Kryukov G, Hodis E, Lawrence DP, Fisher S, Getz G, Gabriel SB, Carter SL, Flaherty KT, Wargo JA, Garraway LA
Cancer Discovery 2014 Jan;4(1):61-8

The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma
Van Allen EM, Wagle N, Sucker A, Treacy DJ, Johannessen CM, Goetz EM, Place CS, Taylor-Weiner A, Whittaker S, Kryukov GV, Hodis E, Rosenberg M, **McKenna A**, Cibulskis K, Farlow D, Zimmer L, Hillen U, Gutzmer R, Goldinger SM, Ugurel S, Gogas HJ, Egberts F, Berking C, Trefzer U, Loquai C, Weide B, Hassel JC, Gabriel SB, Carter SL, Getz G, Garraway LA, Schadendorf D; Dermatologic Cooperative Oncology Group of

Germany (DeCOG)
Cancer Discovery 2014 Jan;4(1):94-109

Somatic mutation of CDKN1B in small intestine neuroendocrine tumors
Francis JM, Kiezun A, Ramos AH, Serra S, Pedamallu CS, Qian ZR, Banck MS, Kanwar R, Kulkarni AA, Karpathakis A, Manzo V, Contractor T, Philips J, Nickerson E, Pho N, Hooshmand SM, Brais LK, Lawrence MS, Pugh T, **McKenna A**, Sivachenko A, Cibulskis K, Carter SL, Ojesina AI, Freeman S, Jones RT, Voet D, Saksena G, Auclair D, Onofrio R, Shefler E, Sougnez C, Grimsby J, Green L, Lennon N, Meyer T, Caplin M, Chung DC, Beutler AS, Ogino S, Thirlwell C, Shivdasani R, Asa SL, Harris CR, Getz G, Kulke M, Meyerson M
Nat Genetics 2013 Dec;45(12):1483-6

A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival
Zheng S, Fu J, Vegesna R, Mao Y, Heathcock LE, Torres-Garcia W, Ezhilarasan R, Wang S, **McKenna A**, Chin L, Brennan CW, Yung WK, Weinstein JN, Aldape KD, Sulman EP, Chen K, Koul D, Verhaak RG
Genes Dev 2013 Jul 1;27(13):1462-72

Mutational heterogeneity in cancer and the search for new cancer-associated genes
Lawrence MS, Stojanov P, Polak P, Kryukov GV, Cibulskis K, Sivachenko A, Carter SL, Stewart C, Mermel CH, Roberts SA, Kiezun A, Hammerman PS, **McKenna A**, Drier Y, Zou L, Ramos AH, Pugh TJ, Stransky N, Helman E, Kim J, Sougnez C, Ambrogio L, Nickerson E, Shefler E, Cort□s ML, Auclair D, Saksena G, Voet D, Noble M, DiCara D, Lin P, Lichtenstein L, Heiman DI, Fennell T, Imielinski M, Hernandez B, Hodis E, Baca S, Dulak AM, Lohr J, Landau DA, Wu CJ, Melendez-Zajgla J, Hidalgo-Miranda A, Koren A, McCarroll SA, Mora J, Crompton B, Onofrio R, Parkin M, Winckler W, Ardlie K, Gabriel SB, Roberts CWM, Biegel JA, Stegmaier K, Bass AJ, Garraway LA, Meyerson M, Golub TR, Gordenin DA, Sunyaev S, Lander ES, Getz G
Nature 2013 Jul 11;499(7457):214-218

Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1
Ramkissoon LA, Horowitz PM, Craig JM, Ramkissoon SH, Rich BE, Schumacher SE, **McKenna A**, Lawrence MS, Bergthold G, Brastianos PK, Tabak B, Ducar MD, Van Hummelen P, MacConaill LE, Pouissant-Young T, Cho YJ, Taha H, Mahmoud M, Bowers DC, Margraf L, Tabori U, Hawkins C, Packer RJ, Hill DA, Pomeroy SL, Eberhart CG, Dunn IF, Goumnerova L, Getz G, Chan JA, Santagata S, Hahn WC, Stiles CD, Ligon AH, Kieran MW, Beroukhim R, Ligon KL
Proc Natl Acad Sci U S A 2013 May 14;110(20):8188-93

Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity
Dulak AM, Stojanov P, Peng S, Lawrence MS, Fox C, Stewart C, Bandla S, Imamura Y, Schumacher SE, Shefler E, **McKenna A**, Carter SL, Cibulskis K, Sivachenko A, Saksena G, Voet D, Ramos AH, Auclair D, Thompson K, Sougnez C, Onofrio RC, Guiducci C, Beroukhim R, Zhou Z, Lin L, Lin J, Reddy R, Chang A, Landrenau R, Pennathur A, Ogino S, Luketich JD, Golub TR, Gabriel SB, Lander ES, Beer DG, Godfrey TE, Getz G, Bass AJ
Nat Genetics 2013 May;45(5):478-86

Evolution and impact of subclonal mutations in chronic lymphocytic leukemia
Landau DA, Carter SL, Stojanov P, **McKenna A**, Stevenson K, Lawrence MS, Sougnez C, Stewart C, Sivachenko A, Wang L, Wan Y, Zhang W, Shukla SA, Vartanov A, Fernandes SM, Saksena G, Cibulskis K, Tesar B, Gabriel S, Hacohen N, Meyerson M, Lander ES, Neuberg D, Brown JR, Getz G, Wu CJ
Cell 2013 Feb 14;152(4):714-26

Integrative eQTL-based analyses reveal the biology of breast cancer risk loci
Li Q, Seo JH, Stranger B, **McKenna A**, Pe'er I, Laframboise T, Brown M, Tyekucheva S, Freedman ML
Cell 2013 Jan 31;152(3):633-41

Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations
Brastianos PK, Horowitz PM, Santagata S, Jones RT, **McKenna A**, Getz G, Ligon KL, Palescandolo E, Van Hummelen P, Ducar MD, Raza A, Sunkavalli A, Macconaill LE, Stemmer-Rachamimov AO, Louis DN, Hahn WC, Dunn IF, Beroukhim R
Nat Genetics 2013 Mar;45(3):285-9

The genetic landscape of high-risk neuroblastoma
Pugh TJ, Morozova O, Attiyeh EF, Asgharzadeh S, Wei JS, Auclair D, Carter SL, Cibulskis K, Hanna M, Kiezun A, Kim J, Lawrence MS, Lichenstein L, **McKenna A**, Pedamallu CS, Ramos AH, Shefler E, Sivachenko A, Sougnez C, Stewart C, Ally A, Birol I, Chiu R, Corbett RD, Hirst M, Jackman SD, Kamoh B, Khodabakshi AH, Krzywinski M, Lo A, Moore RA, Mungall KL, Qian J, Tam A, Thiessen N, Zhao Y, Cole KA, Diamond M, Diskin SJ, Mosse YP, Wood AC, Ji L, Sposto R, Badgett T, London WB, Moyer Y, Gastier-Foster JM, Smith MA, Guidry Auvil JM, Gerhard DS, Hogarty MD, Jones SJ, Lander ES, Gabriel SB, Getz G, Seeger RC, Khan J, Marra MA, Meyerson M, Maris JM
Nat Genetics 2013 Mar;45(3):279-84

Whole-exome sequencing identifies a recurrent NAB2-STAT6 fusion in solitary fibrous tumors
Chmielecki J, Crago AM, Rosenberg M, O'Connor R, Walker SR, Ambrogio L, Auclair D, **McKenna A**, Heinrich MC, Frank DA, Meyerson M
Nat Genetics 2013 Feb;45(2):131-2

Comprehensive genomic characterization of squamous cell lung cancers
Cancer Genome Atlas Research Network
Nature 2012 Sep 27;489(7417):519-25

Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations
Pugh TJ, Weeraratne SD, Archer TC, Pomeranz Krummel DA, Auclair D, Bochicchio J, Carneiro MO, Carter SL, Cibulskis K, Erlich RL, Greulich H, Lawrence MS, Lennon NJ, **McKenna A**, Meldrim J, Ramos AH, Ross MG, Russ C, Shefler E, Sivachenko A, Sogoloff B, Stojanov P, Tamayo P, Mesirov JP, Amani V, Teider N, Sengupta S, Francois JP, Northcott PA, Taylor MD, Yu F, Crabtree GR, Kautzman AG, Gabriel SB, Getz G, J□ger N, Jones DT, Lichter P, Pfister SM, Roberts TM, Meyerson M, Pomeroy SL, Cho YJ
Nature 2012 Aug 2;488(7409):106-10

Comprehensive molecular characterization of human colon and rectal cancer

Cancer Genome Atlas Network
Nature 2012 Jul 18;487(7407):330-7

Absolute quantification of somatic DNA alterations in human cancer
Carter SL, Cibulskis K, Helman E, **McKenna A**, Shen H, Zack T, Laird PW, Onofrio RC, Winckler W, Weir BA, Beroukhim R, Pellman D, Levine DA, Lander ES, Meyerson M, Getz G
Nat Biotechnology 2012 May;30(5):413-21

The 1000 Genomes Project: data management and community access
Clarke L, Zheng-Bradley X, Smith R, Kulesha E, Xiao C, Toneva I, Vaughan B, Preuss D, Leinonen R, Shumway M, Sherry S, Flicek P; 1000 Genomes Project Consortium
Nat Methods 2012 Apr 27;9(5):459-62

The functional spectrum of low-frequency coding variation
Marth GT, Yu F, Indap AR, Garimella K, Gravel S, Leong WF, Tyler-Smith C, Bainbridge M, Blackwell T, Zheng-Bradley X, Chen Y, Challis D, Clarke L, Ball EV, Cibulskis K, Cooper DN, Fulton B, Hartl C, Koboldt D, Muzny D, Smith R, Sougnez C, Stewart C, Ward A, Yu J, Xue Y, Altshuler D, Bustamante CD, Clark AG, Daly M, DePristo M, Flicek P, Gabriel S, Mardis E, Palotie A, Gibbs R; 1000 Genomes Project
Genome Biol 2011 Sep 14;12(9):R84

The mutational landscape of head and neck squamous cell carcinoma
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Science 2011 Aug 26;333(6046):1157-60

Demographic history and rare allele sharing among human populations
Gravel S, Henn BM, Gutenkunst RN, Indap AR, Marth GT, Clark AG, Yu F, Gibbs RA; 1000 Genomes Project, Bustamante CD
Proc Natl Acad Sci U S A 2011 Jul 19;108(29):11983-8

Variation in genome-wide mutation rates within and between human families
Conrad DF, Keebler JE, DePristo MA, Lindsay SJ, Zhang Y, Casals F, Idaghdour Y, Hartl CL, Torroja C, Garimella KV, Zilversmit M, Cartwright R, Rouleau GA, Daly M, Stone EA, Hurles ME, Awadalla P; 1000 Genomes Project
Nat Genetics 2011 Jun 12;43(7):712-4

The variant call format and VCFtools
Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST, McVean G, Durbin R; 1000 Genomes Project Analysis Group
Bioinformatics 2011 Aug 1;27(15):2156-8

A framework for variation discovery and genotyping using next-generation DNA sequencing data

DePristo MA, Banks E, Poplin R, Garimella KV, Maguire JR, Hartl C, Philippakis AA, del Angel G, Rivas MA, Hanna M, **McKenna A**, Fennell TJ, Kernytsky AM, Sivachenko AY, Cibulskis K, Gabriel SB, Altshuler D, Daly MJ
Nat Genetics 2011 May;43(5):491-8

Mapping copy number variation by population-scale genome sequencing
Mills RE, Walter K, Stewart C, Handsaker RE, Chen K, Alkan C, Abyzov A, Yoon SC, Ye K, Cheetham RK, Chinwalla A, Conrad DF, Fu Y, Grubert F, Hajirasouliha I, Hormozdiari F, Iakoucheva LM, Iqbal Z, Kang S, Kidd JM, Konkel MK, Korn J, Khurana E, Kural D, Lam HY, Leng J, Li R, Li Y, Lin CY, Luo R, Mu XJ, Nemesh J, Peckham HE, Rausch T, Scally A, Shi X, Stromberg MP, St⊠tz AM, Urban AE, Walker JA, Wu J, Zhang Y, Zhang ZD, Batzer MA, Ding L, Marth GT, McVean G, Sebat J, Snyder M, Wang J, Ye K, Eichler EE, Gerstein MB, Hurles ME, Lee C, McCarroll SA, Korbel JO; 1000 Genomes Project
Nature 2011 Feb 3;470(7332):59-65

Diversity of human copy number variation and multicopy genes
Sudmant PH, Kitzman JO, Antonacci F, Alkan C, Malig M, Tsalenko A, Sampas N, Bruhn L, Shendure J; 1000 Genomes Project, Eichler EE
Science 2010 Oct 29;330(6004):641-6

A map of human genome variation from population-scale sequencing
1000 Genomes Project Consortium, Abecasis GR, Altshuler D, Auton A, Brooks LD, Durbin RM, Gibbs RA, Hurles ME, McVean GA
Nature 2010 Oct 28;467(7319):1061-73

Honors and Funding

NIH Pathway to Independence Award K99/R00 (1K99HG010152-01) *2018-2023*

Graduate School's Distinguished Dissertation Award Winner *2018*

National Institute of Health (NIH) National Research Service Award (T32) Trainee for Experimental Pathology of Cardiovascular Disease (5T32HL007312-37) *2015-2017*

National Institute of Health (NIH) Institutional National Research Service Award (T32) (5T32HG000035-20) *2012-2014*

Select Talks

"Improvements to CRISPR-based lineage tracing: A potpourri of success, challenges, and opportunities". High-Throughput Dense Reconstruction of Cell Lineages meeting, Janelia Farms / HHMI. *April, 2019*

"Whole organism lineage tracing in Drosophila with GESTALT". Second Fly Cell Atlas meeting. *March, 2019*

Cellular 'phylogenetics' - decoding the developmental history and relationships among individual cells. Phylogenetics seminar. *March, 2019*

Single cell state and fate: application to tumor heterogeneity and metastasis. National Cancer Institute Workshop on Linear and Non-Linear Metastases. *September, 2018*

Capturing high-dimensional cell state and cell fate from single cells. Machine Learning Strategies for Disease Prediction. Technical University of Denmark. *May, 2018*

Recovering single-cell state in conjunction with lineage in Drosophila. Fly Cell Atlas meeting. University of Leuven. *December, 2017*

Information storage and recovery using a diversity of second-generation sequencing technologies. Genome 10K and Genome Science 2017. Earlham Institute. *September, 2017*

Whole-organism lineage tracing with CRISPR-Cas9 barcodes. Genome Engineering Workshop 5.0. The Broad Institute of Harvard and MIT. *May, 2017*

Contiguity in Genome Sequencing – Methods and Applications. NHGRI Sequencing Technology Development Meeting. *May, 2015*

Mutation discovery in tumor sequencing. Our team led a two-day training on cancer genomics at the Carlos Slim Institute of Health in Mexico City. *June, 2012*

Service

Reviewed for: *Science*, *Cell*, *Bioinformatics*, *Molecular Oncology*, *BMC Medical Genomics*, *eLife*, *GigaScience*, *Nucleotide Acids Research*, *PLOS Computational Biology*

Program committee for:

AlCoB 2019, May 2019, University of California, Berkeley, CA

Other professional service:

Co-founder of the Young Alliance Against Cancer (YAAC), a Germany-based non-profit focused on bridging the gap between basic science and clinical training for young cancer researchers

Teaching Experience

Lecturer *Spring 2019*
QBS.146.01: Molecular and Computational Genomics *Dartmouth College*

Teaching Assistant *Winter 2016*
Genome Sciences 466: Cancer Genetics *University of Washington*

Teaching Assistant *Fall 2015*
Genome 371: Introductory Genetics *University of Washington*