

Katherine S. Pollard

Gladstone Institutes • University of California • Chan Zuckerberg Biohub
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Research Positions

Gladstone Institutes. Director, Institute of Data Science & Biotechnology, 2016–present.

Senior Investigator, 2014–present. Associate Investigator, 2008–2014.

UC San Francisco. Professor, 2014–present. Division of Bioinformatics Chief, 2020–present.

Associate Professor, 2008–2014. Director, Bioinformatics Graduate Program, 2019–2020.

Chan Zuckerberg Biohub. Investigator, 2018–present.

Simons Institute for the Theory of Computing. Visiting Professor. 2016.

UC Davis. Assistant Professor. 2005–2008.

UC Santa Cruz. Postdoctoral Fellow. 2003–2005. *Mentors:* David Haussler & Todd Lowe.

UC Berkeley. Graduate Student. 1998–2003. *Mentors:* Mark van der Laan & Sandrine Dudoit.

Chiron Corporation. Intern. 1999–2003.

U of Bristol and United Medical & Dental Schools, UK. Research Assistant. 1996–1998.

Education

UC Berkeley, MA and PhD in Biostatistics. 1998–2003.

Pomona College, BA *Summa Cum Laude* in Anthropology and Mathematics. 1991–1995.

Johns Hopkins School of Public Health, Summer Graduate Program in Epidemiology. 1995.

Mills College, Summer Math Institute. 1994.

Honors & Awards

Fellow, American Institute for Medical and Biological Engineering. 2021.

Fellow, International Society for Computational Biology. 2020.

UC Davis Storer Distinguished Lecture. 2020.

Gladstone Mentoring Award. 2019.

Chan Zuckerberg Biohub Investigator. 2017–present.

Fellow, California Academy of Sciences. 2013–present.

Women Who Lead in the Life Sciences. SF Business Times. 2018.

75 Most Influential Alumni, UC Berkeley School of Public Health. 2018.

Best Scientific Visualizations of the Year, Wired Magazine. 2013.

Alumna of the Year, UC Berkeley School of Public Health. 2013.

Life Sciences Distinguished Lecturer, Brandeis University, 2013.

Edward H. Birkenmeier Distinguished Lecturer, Jackson Laboratory, 2013.

Breakthrough Biomedical Research Award, UCSF. 2009–2010.

Sloan Research Fellowship, Alfred P. Sloan Foundation. 2008–2010.

Faculty Development Award, UC Davis. 2007.

NIH Postdoctoral Fellowship, NIGMS/NIH NRSA. 2003–2005.

Evelyn Fix Prize, Chin Long Chiang Biostatistics Student of the Year, UC Berkeley. 2003.

Berkeley Fellowship, UC Berkeley. 1998–2000.

Thomas J. Watson Fellowship, New Zealand, Indonesia, and Australia. 1995–1996.

Valedictorian, High Scholarship Prize, Math Prize, Anthropology Prize, Phi Beta Kappa Award, Pomona College. 1995.

Sophomore Math Prize, Pomona College. 1993.

Teaching

UC San Francisco. Statistical Methods for Bioinformatics, Computational Genomics, Computational Immunology, Microbiome Precision Medicine. 2008–present.
UC Davis. Categorical Data, Bioinformatics, Intro Statistics, Biostatistics Seminar. 2005–2008.
Instructor. Coursera and Henry Stewart Talks online courses. Recorded 2013–2014.
Workshop Instructor. R/Bioconductor statistical programming. 2003–2007.

Professional Memberships

American Statistical Association. 2002–present.
International Society for Computational Biology. 2005–present.
American Society of Human Genetics. 2012–present.
American Association for the Advancement of Science. 2019–present.
American Institute for Medical and Biological Engineering. 2020–present.

Advisory Service

Laboratory for Genomics Research (LGR). 2022–present.
Helmsley Trust. 2022–present.
Tabula Madagascar. 2021–present.
SFARI Microbiome Initiative. 2020–present.
Science Board of Reviewing Editors. 2019–present.
Chan Zuckerberg Initiative. 2017–present.
ENCODE Project. 2017–present.
EBI Metagenomics. 2016–present.
Phylagen Biosciences. 2016–present.
Tenaya Therapeutics. 2016–present.
NCBI. 2018–2021.
NHGRI. 2018–2020.
Bigalow Single Cell Genomics Center. 2017–2020.
Third Rock Ventures. 2018–2019.
uBiome. 2018–2019.
UC San Diego Center for Systems Biology. 2015–2016.
California Academy of Sciences. 2009–2018.

Publications

Pre-prints

1. M. Pittman, K. Lee, D. Srivastava, K.S. Pollard (2022). *An oligogenic inheritance test detects risk genes and their interactions in congenital heart defects and developmental comorbidities*, **BioRxiv**.
2. E. McArthur, D.C. Rinker, E.N. Gilbertson, G. Fudenberg, M. Pittman, K. Keough, K.S. Pollard, J.A. Capra (2022). *Reconstructing the 3D genome organization of Neanderthals reveals that chromatin folding shaped phenotypic and sequence divergence*, **BioRxiv**.
3. B.J. Smith, X. Li, A. Abate, Z.J. Shi, K.S. Pollard (2022). *Scalable microbial strain inference in metagenomic data using StrainFacts*, **BioRxiv**.
4. M. Yu, A.R. Harper, M. Aguirre, M. Pittman, C. Tcheandjieu, D. Amgalan, C. Grace, A. Goel, M. Farrall, K. Xiao, J. Engreitz, K.S. Pollard, H. Watkins, J.R. Priest (2021). *Genetic determinants of interventricular septal anatomy and the risk of ventricular septal defects and hypertrophic cardiomyopathy*, **MedRxiv**.

5. A.P. Blair, R.K. Hu, E.N. Farah, N.C. Chi, K.S. Pollard, P.F. Przytycki, I.S. Kathiriya, B.G. Bruneau (2021). *Cell Layers: Uncovering clustering structure and knowledge in unsupervised single-cell transcriptomic analysis*, **BioRxiv**.
6. A.R. Norman, A.H. Ryu, K. Jamieson, S. Thomas, Y. Shen, N. Ahituv, K.S. Pollard, J.F. Reiter (2021). *A Human Accelerated Region is a Leydig cell GLI2 enhancer that affects male-typical behavior*, **BioRxiv**.
7. K.C. Keough, P.P. Shah, N.M. Wickramasinghe, C.E. Dundes, A. Chen, R.E.A. Salomon, S. Whalen, K.M. Loh, N. Dubois, K.S. Pollard, R. Jain (2020). *An atlas of lamina-associated chromatin across thirteen human cell types reveals cell-type-specific and multiple subtypes of peripheral heterochromatin*, **BioRxiv**.
8. P. Spanogiannopoulos, P.H. Bradley, J. Melamed, Y.N.A. Malig, K.N. Lam, R.R. Gerona, K.S. Pollard, P.J. Turnbaugh (2019). *Drug resistant gut bacteria mimic a host mechanism for anticancer drug clearance*, **BioRxiv**.
9. H. Ryu, F. Inoue, S. Whalen, A. Williams, M. Kircher, B. Martin, B. Alvarado, M.A.H. Samee, K. Keough, S. Thomas, A. Kriegstein, J. Shendure, A. Pollen, N. Ahituv, K.S. Pollard (2018). *Massively parallel dissection of human accelerated regions in human and chimpanzee neural progenitors*, **BioRxiv**.
10. K.S. Smith, D. Ghosh, K.S. Pollard, S. De (2017). *A computational framework for detecting signatures of accelerated somatic evolution in cancer genomes*, **BioRxiv**.

Peer-reviewed journals

1. M. Wagle, M. Zarei, M. Lovett-Barron, K.T. Poston, J. Xu, V. Ramey, K.S. Pollard, D.A. Prober, J. Schulkin, K. Deisseroth, S. Guo (2022). *Brain-wide perception of the emotional valence of light is regulated by distinct hypothalamic neurons*, **Molecular Psychiatry**.
2. S. Lyalina, R. Stepanauskas, F. Wu, S. Sanjabi, K.S. Pollard (2022). *Single cell genome sequencing of laboratory mouse microbiota improves taxonomic and functional resolution of this model microbial community*, **PLoS ONE**, 17(4): e0261795.
3. B.J. Smith, Y. Piceno, M. Zydek, B. Zhang, L.A. Syriani, J.P. Terdiman, Z. Kassam, A. Ma, S.V. Lynch, K.S. Pollard, N. El-Nachef (2022). *Clinical efficacy and increased donor strain engraftment after antibiotic pretreatment in a randomized trial of ulcerative colitis patients receiving fecal microbiota transplant*, **Scientific Reports**, 12: 5517.
4. P.F. Przytycki, K.S. Pollard (2022). *CellWalkR: An R Package for integrating single-cell and bulk data to resolve regulatory elements*, **Bioinformatics**, 38(9): 2621–2623.
5. B. Gonzalez-Teran, M. Pittman, F. Felix, D. Richmond-Buccola, R. Thomas, K. Choudhary, E. Moroni, G. Colombo, M. Alexanian, B. Cole, K. Samse-Knapp, M. McGregor, C.A. Gifford, R. Huttenhain, B.D. Gelb, B. Conklin, B.L. Black, B.G. Bruneau, N.J. Krogan, K.S. Pollard, D. Srivastava (2022). *Integration of protein interactome networks with congenital heart disease variants reveals candidate disease genes*, **Cell**, **185**: 1–21.
6. S. Whalen, J. Schreiber, W.S. Noble, K.S. Pollard (2022). *Navigating the pitfalls of applying machine learning in genomics*, **Nature Reviews Genetics**, 23: 169-181.
7. M. Alexander, Q.Y. Ang, R.R. Nayak, A.E. Bustion, V. Upadhyay, K.S. Pollard, P.J. Turnbaugh (2022). *A diet-dependent enzyme from the human gut microbiome promotes Th17 cell accumulation and colitis*, **Cell Host & Microbe**, 30(1): 17-30.e9.
8. E. Markenscoff-Papadimitriou, F. Binyameen, S. Whalen, J. Price, K. Lim, R. Catta-Preta, E.L. Pai, X. Mu, D. Xu, K.S. Pollard, A. Nord, M.W. State, J.L. Rubenstein (2021). *Autism risk gene POGZ promotes chromatin accessibility and expression of clustered synaptic genes*, **Cell Reports**, 37(10): 110089.
9. Z.J. Shi, B. Dimitrov, C. Zhao, S. Nayfach, K.S. Pollard (2021). *Ultra-rapid metagenotyping of the human gut microbiome*, **Nature Biotechnology**, 40: 507–516.
10. R.S. Ziffra, C.N. Kim, A. Wilfert, T.N. Turner, M. Haeussler, A.M. Casella, P.F. Przytycki, A. Kreimer, K.S. Pollard, S.A. Ament, E.E. Eichler, N. Ahituv, T.J. Nowakowski (2020). *Single cell epigenomic atlas of the developing human brain and organoids*, **Nature**, 598: 205–213.
11. L. Chumpitaz-Diaz, Md.A.H. Samee, K.S. Pollard (2021). *Systematic identification of non-canonical transcription factor motifs*, **BMC Molecular and Cell Biology**, 22: 44.

12. T.Y. Liu, G.J. Knott, D.C.J. Smock, J.J. Desmarais, S. Son, A. Bhuiya, S. Jakhanwal, N. Prywes, S. Agrawal, M. Díaz de León Derby, N.A. Switz, M. Armstrong, A.R. Harris, E.J. Charles, B.W. Thornton, P. Fozouni, J. Shu, S.I. Stephens, G.R. Kumar, C. Zhao, A. Mok, A.T. Iavarone, A.M. Escajeda, R. McIntosh, S.E. Kim, E.J. Dugan, IGI Testing Consortium, K.S. Pollard, M.X. Tan, M. Ott, D.A. Fletcher, L.F. Lareau, P.D. Hsu, D.F. Savage, J.A. Doudna (2021). *Accelerated RNA detection using tandem CRISPR nucleases*, **Nature Chemical Biology**, 17: 982–988.
13. X. Jin, G. Fudenberg, K.S. Pollard (2021). *Genome-wide variability in recombination activity is associated with meiotic chromatin organization*, **Genome Research**, 31: 1561-1572.
14. M. Roodgar, B.H. Good, N.R. Garud, S. Martis, M. Avula, W. Zhou, S. Lancaster, H. Lee, A. Babveyh, S. Nesamoney, K.S. Pollard, M.P. Snyder (2021). *Longitudinal linked read sequencing reveals ecological and evolutionary responses of a human gut microbiome during antibiotic treatment*, **Genome Research**, 31: 1433-1446.
15. R.J. von Schwartzberg, J.E. Bisanz, S. Lyalina, P. Spanogiannopoulos, Q.Y. Ang, J. Cai, S. Dickmann, M. Friedrich, S.-Y. Liu, S.L. Collins, D. Ingebrigtsen, S. Miller, J.A. Turnbaugh, A.D. Patterson, K.S. Pollard, K. Mai, J. Spranger, P.J. Turnbaugh (2021). *Caloric restriction disrupts the microbiota and colonization resistance*, **Nature**, 595: 272–277.
16. M. Alexanian, P.F. Przytycki, R. Micheletti, A. Padmanabhan, L. Ye, J.G. Travers, B.G. Teran, Q. Duan, S.S. Ranade, F. Felix, R. Linares-Saldana, Y. Huang, G. Andreoletti, J. Yang, K.N. Ivey, R. Jain, T.A. McKinsey, M.G. Rosenfeld, C. Gifford, K.S. Pollard, S.M. Haldar, D. Srivastava (2021). *A transcriptional switch governing fibroblast plasticity underlies reversibility of chronic heart disease*, **Nature**, 595: 438–443.
17. P.B. Cooch, A. Watson, A. Olarte, E.D. Crawford, J.L. DeRisi, B. Greenhouse, J. Hakim, K. Turcios, K.S. Pollard, L.R. Atkinson-McEvoy, R. Hirsch, R.L. Keller, T.D. Ruel, A. Cohen-Ross, A. Leon, N.S. Bardach (2021). *Supervised self-collected SARS-Cov-2 testing in classroom-based summer camps to inform safe in-person learning*, **Journal of Pediatrics, Perinatology & Child Health**, 5: 75-93.
18. M. Pittman, K.S. Pollard (2021). *Ultraconservation of enhancers is not ultranecessary*, **Nature Genetics**, 53: 29–430.
19. A.L. Lind, K.S. Pollard (2021). *The gut microbiomes of 180 species*, **Science**, 372: 238-239.
20. A.L. Lind, K.S. Pollard (2021). *Accurate and sensitive detection of microbial eukaryotes from metagenomic shotgun sequencing data*, **Microbiome**, 9: 58.
21. P.F. Przytycki, K.S. Pollard (2021). *CellWalker integrates single-cell and bulk data to resolve regulatory elements across cell types in complex tissues*, **Genome Biology**, 22: 61.
22. P. Fozouni, S. Son, M.D.L. Derby, G.J. Knott, C.N. Gray, M.V. D'Ambrosio, C. Zhao, N.A. Switz, G.R. Kumar, S.I. Stephens, D. Boehm, C.-L. Tsou, J. Shu, A. Bhuiya, M. Armstrong, A.R. Harris, P.-Y. Chen, J.M. Osterloh, A. Meyer-Franke, B. Joehnk, K. Walcott, A. Sil, C. Langelier, K.S. Pollard, E.D. Crawford, A.S. Puschnik, M. Phelps, A. Kistler, J.L. DeRisi, J.A. Doudna, D.A. Fletcher, M. Ott (2020). *Amplification-free detection of SARS-CoV-2 with CRISPR-Cas13a and mobile phone microscopy*, **Cell**, 184: 1-11.
23. P.H. Bradley, K.S. Pollard (2020). *Building a chemical blueprint for human blood*, **Nature**, 588(7836): 36-37.
24. Zoonomia Consortium (2020). *A comparative genomics multitool for scientific discovery and conservation*, **Nature**, 587: 240-245.
25. E.P. Nora, L. Caccianini, G. Fudenberg, V. Kameswaran, A. Nagle, A. Uebersohn, K. So, B. Hajj, A.L. Saux, A. Coulon, L.A. Mirny, K.S. Pollard, M. Dahan, B.G. Bruneau (2020). *Molecular basis of CTCF binding polarity in genome folding*, **Nature Communications**, 11: 5612.
26. D.E. Gordon, J. Hiatt, ..., K.C. Keough, A.L. Lind, ... K.S. Pollard, ... N. Krogan (2020). *Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms*, **Science**: eabe9403.
27. G. Fudenberg, D.R. Kelley, K.S. Pollard (2020). *Predicting 3D genome folding from DNA sequence*, **Nature Methods**, 17: 1111-1117.
28. J. Damas, G.M. Hughes, K.C. Keough, C.A. Painter, N.S. Persky, M. Corbo, M. Hiller, K.-P. Koepfli, A.R. Pfenning, H. Zhao, D.P. Genereux, R. Swofford, K.S. Pollard, O.A. Ryder, M.T. Nweeia, K. Lindblad-Toh, E.C. Teeling, E.K. Karlsson, H.A. Lewin (2020). *Broad host range of*

- SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates*, **Proceedings of the National Academy of Sciences**, 117(36): 22311-22322.
29. M.G. Gordon, F. Inoue, B. Martin, M. Schubach, V. Agarwal, S. Whalen, S. Feng, J. Zhao, T. Ashuach, R. Ziffra, A. Kreimer, I. Georgakopoulos-Soares, N. Yosef, C.J. Ye, K.S. Pollard, J. Shendure, M. Kircher, N. Ahituv (2020). *lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements*, **Nature Protocols**, 15: 2387-2412.
 30. E. Markenscoff-Papadimitriou, S. Whalen, P. Przytycki, R. Thomas, F. Binyameen, T.J. Nowakowski, S.J. Sanders, M.W. State, K.S. Pollard, J.L. Rubenstein (2020). *A chromatin accessibility atlas of the developing human telencephalon*, **Cell**, 182(3): 754-769.
 31. A. Almeida, S. Nayfach, M. Boland, F. Strozzi, M. Beracochea, Z.J. Shi, K.S. Pollard, D.H. Parks, P. Hugenholtz, N. Segata, N.C. Kyrpides, R.D. Finn (2020). *A unified sequence catalogue of over 280,000 genomes obtained from the human gut microbiome*, **Nature Biotechnology**, 39: 105-114.
 32. P.H. Bradley, K.S. Pollard (2020). *phylogenize: a web tool to identify microbial genes underlying environment associations*, **Bioinformatics**, 36(4): 1289-1290.
 33. I. Kostic, S. Lyalina, K.S. Pollard, A.J. Butte, M. Sirota (2020). *Meta-Analysis of vaginal microbiome data provides new insights into preterm birth*, **Frontiers in Microbiology**, 11:476.
 34. N.G. Garud, K.S. Pollard (2019). *Population Genetics in the Human Microbiome*, **Trends in Genetics**, 36: 53-67.
 35. S.A. Schalbetter, G. Fudenberg, J. Baxter, K.S. Pollard, M.J. Neale (2019). *Principles of meiotic chromosome assembly*, **Nature Communications**, 10: article 4795.
 36. A. Hoarfrost, S. Nayfach, J. Ladau, S. Yooseph, C. Arnosti, C.L. Dupont, K.S. Pollard (2019). *Global ecotypes in the ubiquitous marine clade SAR86*, **ISME Journal**, 14: 178-188.
 37. R.N. Carmody, J.E. Bisanz, B.P. Bowen, C.F. Maurice, S. Lyalina, K.B. Louie, D. Treen, K.S. Chadaideh, V.M. Rekdal, E.N. Bess, P. Spanogiannopoulos, Q.Y. Ang, K.C. Bauer, T.W. Balon, K.S. Pollard, T.R. Northen, P.J. Turnbaugh (2019). *Cooking shapes the structure and function of the gut microbiome*, **Nature Microbiology**, 4: 2052–2063.
 38. K.C. Keough, S. Lyalina, M.P. Olvera, S. Whalen, B.R. Conklin, K.S. Pollard (2019). *Leveraging genetic variants for personalized and allele-specific sgRNA design*, **Genome Biology**, 20: article 167.
 39. S. Whalen, K.S. Pollard (2019). *Reply to ‘Inflated performance measures in enhancer–promoter interaction-prediction methods’*, **Nature Genetics**, 51: 1198–1200.
 40. A. Lind, Y.Y.Y. Lai, Y. Mostovoy, A.K. Holloway, A. Iannucci, A.C.Y. Mak, M. Fondi, V. Orlandini, W.L. Eckalbar, M. Milan, M. Rovatsos, I.G. Kichigin, A.I. Makunin, V. Trifonov, E. Schijlen, L. Kratochvil, R. Fani, T.S. Jessop, T. Patarnello, J.W. Hicks, O.A. Ryder, J.R. Mendelson III, C. Ciofi, P.-Y.A. Kwok, K. S. Pollard, B. Bruneau (2019). *A high-resolution, chromosome-assigned Komodo dragon genome reveals adaptations in the cardiovascular, muscular, and chemosensory systems of monitor lizards*, **Nature Evolution & Ecology**, 3: 1241-1252.
 41. N.R. Stone, C.A. Gifford, R. Thomas, K.J.B. Pratt, K. Samse-Knapp, T.M.A. Mohamed, E.M. Radzinsky, A. Schrick, P. Yu, K.N. Ivey, K.S. Pollard, D. Srivastava (2019). *Unique transcription factor functions regulate epigenetic and transcriptional dynamics during cardiac reprogramming*, **Cell Stem Cell**, 25(1): 87-102.
 42. D.A. Pollard, T.D. Pollard, K.S. Pollard (2019). *Empowering statistical methods for cellular and molecular biologists*, **Molecular Biology of the Cell**, 30(12).
 43. D.D. Engle, H. Tiriach, K.D. Rivera, A. Pommier, S. Whalen, T.E. Oni, B. Alagesan, E.J. Lee, M.A. Yao, M.S. Lucito, B. Spielman, B. Da Silva, C. Schoepfer, K. Wright, B. Creighton, L. Afinowicz, K.H. Yu, R. Grützmann, D. Aust, P.A. Gimotty, K.S. Pollard, R.H. Hruban, M.G. Goggins, C. Pilarsky, Y. Park, D.J. Pappin, M.A. Hollingsworth, D.A. Tuveson (2019). *The glycan CA19-9 promotes pancreatitis and pancreatic cancer in mice*, **Science**, 364(6446): 1156-1162.
 44. C.R. Armour, S. Nayfach, K.S. Pollard, T.J. Sharpton (2019). *A metagenomic meta-analysis reveals functional signatures of health and disease in the human gut microbiome*, **mSystems**, 4: e00332-18.
 45. O.M. Ahmed, A. Avila-Herrera, K.M. Tun, G.W. Davis, K.S. Pollard, N.M. Shah (2019). *Evolution of mechanisms that control mating in Drosophila males*, **Cell Reports**, 27(9): P2527-2536.E4.

46. I.M. Cristea, P.C. Dorrestein, J.A. Eisen, J.A. Gilbert, J.A. Huber, J.K. Jansson, R. Knight, K.S. Pollard, J. Raes, P.A. Silver, N.S. Webster, J. Xu (2019). *Early-career scientists shaping the world*, **mSystems**, 4: e00196-19.
47. The 2017 NIH-wide microbiome workshop writing team (2019). *The Human Microbiome: Emerging Themes at the Horizon of the 21st Century*, **Microbiome**, 7:32.
48. S. Nayfach, Z.J. Shi, R. Seshadri, K.S. Pollard, N. Kyrpides (2019). *Novel insights from uncultivated genomes of the global human gut microbiome*, **Nature**, 568: 505–510.
49. Md. A.H. Samee, B.G. Bruneau, K.S. Pollard (2019). *A De Novo Shape Motif Discovery Algorithm Reveals Preferences of Transcription Factors for DNA Shape Beyond Sequence Motifs*, **Cell Systems**, 8(1): 27-42.e6.
50. S. Whalen, K.S. Pollard (2019). *Most regulatory interactions are not in linkage disequilibrium*, **Genome Research**, 29: 334-343.
51. R.I. Amann, S. Baichoo, B.J. Blencowe, P. Bork, M. Borodovsky, C. Brooksbank, P.S.G. Chain, R.R. Colwell, D.G. Daffonchio, A. Danchin, V. de Lorenzo, P.C. Dorrestein, R.D. Finn, C.M. Fraser, J.A. Gilbert, S.J. Hallam, P. Hugenholtz, J.P.A. Ioannidis, J.K. Jansson, J.F. Kim, H.-P. Klenk, M.G. Klotz, R. Knight, K.T. Konstantinidis, N.C. Kyrpides, C.E. Mason, A.C. McHardy, F. Meyer, C.A. Ouzounis, A.A.N. Patrinos, M. Podar, K.S. Pollard, J. Ravel, A. Reyes Muñoz, R.J. Roberts, R. Rosselló-Móra, S.-A. Sansone, P.D. Schloss, L.M. Schriml, J.C. Setubal, R. Sorek, R.L. Stevens, J.M. Tiedje, A. Turjanski, G.W. Tyson, D.W. Ussery, G.M. Weinstock, O. White, W.B. Whitman, I. Xenarios (2019). *Toward unrestricted use of public data*, **Science**, 363(6425): 350-352.
52. G. Fudenberg, K.S. Pollard (2019). *Chromatin features constrain structural variation across evolutionary timescales*, **Proceedings of the National Academy of Sciences**, 116(6): 2175-218.
53. N.R. Garud, B.H. Good, O. Hallatschek, K.S. Pollard (2019). *Evolutionary dynamics of bacteria in the gut microbiome within and across hosts*, **PLoS Biology**, 17(1): e3000102.
54. C. Langelier, K.L. Kalantar, F. Moazed, M.R. Wilson, E.D. Crawford, T. Deiss, A. Belzer, S. Bolourchi, S. Caldera, M. Fung, A. Jauregui, K. Malcolm, A. Lyden, L. Khan, K. Vessel, J. Quan, M. Zinter, C.Y. Chiu, E.D. Chow, J. Wilson, S. Miller, M.A. Matthay, K.S. Pollard, S. Christenson, C.S. Calfee, J.L. DeRisi (2018). *Integrating host response and unbiased microbe detection for lower respiratory tract infection diagnosis in critically ill adults*, **Proceedings of the National Academy of Sciences**, 115(52): E12353-E12362.
55. P.S. Shah, N. Link, G.M. Jang, P.P. Sharp, T. Zhu, D.L. Swaney, J.R. Johnson, J. Von Dollen, H.R. Ramage, L. Satkamp, B. Newton, R. Hüttenhain, M.J. Petit, T. Baum, A. Everitt, O. Laufman, M. Tassetto, M. Shales, E. Stevenson, G.N. Iglesias, L. Shokat, S. Tripathi, V. Balasubramaniam, L.G. Webb, S. Aguirre, A.J. Willsey, A. Garcia-Sastre, K.S. Pollard, S. Cherry, A.V. Gamarnik, I. Marazzi, J. Taunton, A. Fernandez-Sesma, H.J. Bellen, R. Andino, N.J. Krogan (2018). *Comparative flavivirus-host protein interaction mapping reveals mechanisms of dengue and zika virus pathogenesis*, **Cell**, 175(7): 1931-1945.e18.
56. J. Ladau, Y. Shi, X. Jing, J.-S. He, L. Chen, X. Lin, N. Fierer, J.A. Gilbert, K.S. Pollard, H. Chu (2018). *Climate change will lead to pronounced shifts in the diversity of soil microbial communities*, **mSystems**, 3(5): e00167-18.
57. S.K. Wyman, A. Avila-Herrera, S. Nayfach, K.S. Pollard (2018). *A most wanted list of conserved protein families with no known domains*, **PLoS ONE**, 13(10): e0205749.
58. P.H. Bradley, S. Nayfach, K.S. Pollard (2018). *Phylogeny-corrected identification of microbial gene families relevant to human gut colonization*, **PLoS Computational Biology**, 14(8): e1006242.
59. D. Kostka, A.K. Holloway, K.S. Pollard (2018). *Developmental loci harbor clusters of accelerated regions that evolved independently in ape lineages*, **Molecular Biology and Evolution**, 35(8): 2034–2045.
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Software Projects

Clustering Algorithms

hopach: hybrid hierarchical clustering with bootstrap

<http://cran.fhcrc.org/web/packages/hopach/index.html>

pamsil: partitioning algorithm

<http://docpollard.org/pamsil.tar.gz>

Multiple Hypothesis Testing Procedures

multtest: multiple testing procedures

<http://cran.fhcrc.org/web/packages/multtest/index.html>

Genome Browsers

Conservation and multiple sequence alignment tracks

<http://genome.ucsc.edu/>

<http://archaea.ucsc.edu/>

Regulatory Genomics

Akita: Deep learning prediction of 3D genome folding from sequence

<https://github.com/calico/basenji>

ShapeMF: Gibbs sampling algorithm for de novo discovery of DNA shape motifs

<https://github.com/h-samee/shape-motif/>

TargetFinder: predicting enhancer-promoter interactions

<https://github.com/shwhalen/targetfinder>

Comparative & Population Genomics

AlleleAnalyzer Genetic variation-aware CRISPR gRNA design tool

<https://github.com/keoughkath/AlleleAnalyzer>

PHAST: Phylogenetic Analysis with Space/Time Models

<http://compgen.bscb.cornell.edu/phast/>

<http://cran.r-project.org/web/packages/rphast/index.html>

ProteinHistorian: gene origin and evolution analysis

<http://lighthouse.ucsf.edu/ProteinHistorian/>

G-NEST: gene co-expression and synteny across species

<https://github.com/dgлемay/G-NEST>

Metagenomics

EukDetect: marker gene based detection of microbial eukaryotes in shotgun metagenomes

<https://github.com/allind/EukDetect>

gt-pro: k-mer based metagenotyping of microbiome species from shotgun metagenomes with code that runs on a laptop

<https://github.com/zjshi/gt-pro>

MIDAS: population genetic analysis

<https://github.com/snayfach/MIDAS>

<http://lighthouse.ucsf.edu/MIDAS/>

PhylOTU: taxonomic clustering

<https://github.com/sharpton/PhylOTU>

SFam: diverse protein database

http://edhar.genomecenter.ucdavis.edu/sifting_families/

VFam: viral protein database

<http://derisilab.ucsf.edu/software/price/vFam/>

Shotmap: quantification of gene abundance

<https://github.com/sharpton/shotmap>

MetaQuery: webserver for microbiome-host associations

<http://metaquery.docpollard.org>

MicrobeCensus: average genome and normalization

<https://github.com/snayfach/MicrobeCensus>

MetaPASSAGE: simulating metagenomics data

<https://github.com/sriesenfeld/MetaPASSAGE>

Species Distribution Modeling: mapping spatial distributions of microbes

<https://github.com/jladau/SpeciesDistributionModeling>

Grants

* Dollar amounts are total direct costs for the funding period.

ACTIVE

NIH Common Fund

Genetic determinants of 4D genome folding in human cardiac development

Role: PI (jointly with Benoit Bruneau)

2020-2025

\$1,002,590

NIH/NIMH

Resolving single-cell brain regulatory elements with bulk data supervised models

Role: PI

2020-2024

\$1,604,695

NIH/NIMH

Massively parallel characterization of psychiatric disease associated regulatory elements in defined cell types

Role: PI (jointly with Nadav Ahituv)

2018-2023

\$2,488,033

NIH/NIMH

Massively parallel dissection of psychiatric regulatory networks

Role: PI (jointly with Nadav Ahituv)

2016-2022 (NCE)

\$1,774,368

NSF/DMS (Joint program in Mathematical Biology with NIH/NIGMS)

Decoding strain-level variation in the human microbiome

Role: PI

2016-2022 (NCE)

\$846,540

NIH/NIA P01

Decoding the Multifactorial Etiology of Neural Network Dysfunction in Alzheimer's Disease

Role: Core Director (PI: Lennart Mucke)

2022-2026

\$1,545,809 (Pollard component only)

NIH/NHLBI P01

Combinatorial Regulation of Gene Networks During Cardiac Development and Disease

Role: Core Director (PI: Deepak Srivastava)

2019-2024

\$850,000 (Pollard component only)

NIH/NIAMS

Exploiting the Host-HIV Interface to Identify Biomarkers Predicting Time to Viral Rebound after Treatment Interruption

Role: Core Lead (PI: Warner Greene)

2017-2022

\$133,830 (Pollard component only)

NIH/NEI R01

Therapeutic genome editing to treat Best disease

Role: Co-Investigator

2017-2022

\$225,000

NIH/NIAID R01

Employing the Gut Microbiome to Accelerate Effective Initiation of Rheumatoid Arthritis Therapy

Role: Co-Investigator

2019-2024

\$48,805

COMPLETED

NIH/NHLBI

The epigenetic landscape of heart development

Role: PI (jointly with Benoit Bruneau, Deepak Srivastava)

2015-2021

\$2,500,000

NIH/NHLBI P01

Transcriptional networks during cardiac differentiation

Role: Core Director (PIs: Deepak Srivastava, Benoit Bruneau, Brian Black)

2013-2018

\$393,041 (Pollard component only)

NIH/NINDS R01

Automated longitudinal single cell analysis

Role: Co-Investigator (PI: Steve Finkbeiner)

2013-2017

\$214,971

NIH/NIAID R21

Longitudinal and functional dynamics of the autoimmune microbiome

Role: PI

2014-2017

\$290,630

Gordon & Betty Moore Foundation

Global mapping of microbial functions

Role: PI

2012-2017

\$1,377,312

NSF/DMS (Joint program in Mathematical Biology with NIH/NIGMS)

Exploring the niche space of human microbiome functions through convex geometry and evolutionary genomics

Role: PI

2011-2016

\$789,809

NIH/NHLBI U01 ancillary study

Dissecting the role of RBM20 in dilated cardiomyopathy using isogenic iPSCs

Role: Co-Investigator (PI: Bruce Conklin; U01 Contact PI: Deepak Srivastava)

2014-2016

\$500,000

NIH/NHLNI U01

Defining a comprehensive reference profile of circulating human extracellular RNA

Role: Consortium PI (Contact PI: Prescott Woodruff)

2014-2016

\$95,455 (Pollard subcontract only)

NIH/NHLBI U01

The epigenetic landscape of heart development

Role: PI (jointly with Benoit Bruneau, Bruce Conklin, Deepak Srivastava, Shinya Yamanaka, and Laurie Boyer)

2009-2015

\$4,429,581

NIH/NIGMS P01

Collaborative Center for an Enzyme Function Initiative

Role: Consortium PI (Contact PI: John Gerlt)

2014-2015

\$68,192 (Pollard subcontract only)

NIH/NIGMS R01

What made us human?

Role: PI (Adam Siepel, co-PI)

2008-2012

\$864,000

Gordon & Betty Moore Foundation

Integrating evolutionary, ecological and statistical approaches to metagenomics

Role: PI (jointly with Jonathan Eisen and Jessica Green)

2008-2012

\$1,791,500

Sloan Research Fellowship in Computational & Evolutionary Molecular Biology

Role: PI

2009-2010

\$45,000

UCSF Program for Breakthrough Biomedical Research (PBBR) Integrative Research Award

In vivo characterization of the vertebrate regulatory code

Role: PI (jointly with Nadav Ahituv)

2009-2010
\$197,387

UC Davis Faculty Development Award
Role: PI
2007-2008
\$16,000

NIH Individual National Research Service Award
Defining the Topography of Gene Expression
Role: PI (Postdoctoral Fellow)
2003-2005
\$39,700

University of California Discovery Grant
Computationally Intensive Statistical Inference for Microarray Based Drug Discovery
Role: Graduate student researcher (PI: Mark J. van der Laan)
2001-2003
\$334,000