

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, 2020–2023. Associate Professor, 2008–2014. Director, Bioinformatics Graduate Program, 2019–2020.
Chan Zuckerberg Biohub. Investigator, 2018–present.
Kavli Institute for Theoretical Physics. Visiting Professor. 2024.
Flatiron Institute. Visiting Professor. 2023.
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 / UC Berkeley, Summer Math Institute. 1994.

Honors & Awards

Elected Fellow, American Association for the Advancement of Science. 2024.
Elected Member, National Academy of Medicine. 2022.
Elected Fellow, American Institute for Medical and Biological Engineering. 2021.
Elected Fellow, International Society for Computational Biology. 2020.
UC Davis Storer Distinguished Lecture. 2020.
Gladstone Mentoring Award. 2019.
Chan Zuckerberg Biohub Investigator. 2017–present.
Elected Fellow, California Academy of Sciences. 2013.
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, Sophomore Math Prize, Pomona College. 1993 & 1995.

Teaching

UC San Francisco. Statistical Methods for Bioinformatics, other lectures. 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

National Academy of Medicine. 2022–present.
American Institute for Medical and Biological Engineering. 2020–present.
American Association for the Advancement of Science. 2019–present.
American Society of Human Genetics. 2012–present.
International Society for Computational Biology. 2005–present.
American Statistical Association. 2002–present.

Advisory Service

UC Santa Cruz Genome Browser. 2025–present.
Flatiron Institute. 2024–present.
Laboratory for Genomics Research (LGR). 2022–present.
Science Magazine Board of Reviewing Editors. 2019–present.
Helmsley Trust. 2022–2023.
Tabula Madagascar. 2021–2022.
SFARI Microbiome Initiative. 2020–2021.
EBI Metagenomics. 2016–2021.
Chan Zuckerberg Initiative. 2017–2022.
ENCODE Project. 2017–2022.
Phylagen Biosciences. 2016–2022.
Tenaya Therapeutics. 2016–2022.
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. K. Gjoni, S. Zhang, R.E. Yan, B. Zhang, D. Miller, A. Resnick, N. Dahmane, K.S. Pollard (2025). *Machine learning-predicted chromatin organization landscape across pediatric tumors*, **BioRxiv** (in review at **Scientific Reports** for a special issue).
2. Z.L. Grant, S. Kuang, S. Zhang, A.J. Horrillo, K.S. Rao, V. Kameswaran, C. Joubran, P.K. Lau, K. Dong, B. Yang, W.M. Bartosik, N.R. Zemke, B. Ren, I.S. Kathiriya, K.S. Pollard, B.G. Bruneau (2025). *Dose-dependent sensitivity of human 3D chromatin to a heart disease-linked transcription factor*, **BioRxiv** (in revision for **Science**).
3. K. Gjoni, X. Ren, A. Everitt, Y. Shen, K.S. Pollard (2024). *De novo structural variants in autism spectrum disorder disrupt distal regulatory interactions of neuronal genes*, **BioRxiv** (in review at **Genome Research**).

4. R. Sharma, K.M. Berendzen, A. Everitt, B. Wang, G. Williams, S. Wang, K. Quine, R.D. Larios, K.L. P. Long, N. Hoglen, B.A. Sulaman, M.C. Heath, M. Sherman, M. Kinkel, A. Cai, D. Galo, L.C. Caamal, N.L. Goodwin, A. Beery, K.L. Bales, K.S. Pollard, A.J. Willsey, D.S. Manoli (2024). *Oxytocin receptor controls distinct components of pair bonding and development in prairie voles*, **BioRxiv** (in review at **Cell**)
5. 4D Nucleome Consortium (2024). *An integrated view of the structure and function of the human 4D nucleome*, **BioRxiv** (in revision for **Nature**).
6. S. Drusinsky, S. Whalen, K.S. Pollard (2024). *Deep-learning prediction of gene expression from personal genomes*, **BioRxiv** (in revision for **Genome Biology**)
7. M. Goldman, C. Zhao, K.S. Pollard (2024). *Improved detection of microbiome-disease associations via population structure-aware generalized linear mixed effects models (microSLAM)*, **BioRxiv** (in revision for **PLoS Computational Biology**).
8. S.S. Ranade, S. Whalen, I. Zlatanova, T. Nishino, B. van Soldt, L. Ye, A. Pelonero, L.G. Wallace, Y. Huang, M. Alexanian, A. Padmanabhan, B. Gonzalez-Teran, P. Przytycki, M.W. Costa, C.A. Gifford, B.L. Black, K.S. Pollard, D. Srivastava (2022). *Single cell epigenetics reveal cell-cell communication networks in normal and abnormal cardiac morphogenesis*, **BioRxiv** (in revision for **Nature Cardiovascular Research**).
9. 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** (in revision for **Genome Research**).
10. 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** (in revision for **Cell**).
11. 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**.
12. J. Ladau, J.L. Green, K.S. Pollard (2017). *The geometry of the distance-decay of similarity in ecological communities*, **BioRxiv**.
13. 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. A. Lind, N.A. McDonald, E.R. Gerrick, A.S. Bhatt, K.S. Pollard (2025). *Hybrid assemblies of microbiome Blastocystis protists reveal evolutionary diversification reflecting host ecology*, **Genome Research** (In Press).
2. Z. Hu, P.F. Przytycki, K.S. Pollard (2025). *CellWalker2: multi-omic discovery of hierarchical cell type relationships and their associations with genomic annotations*, **Cell Genomics** (In Press).
3. X. Cui, H. Yang, C. Cai, C. Beaman, X. Yang, H. Liu, X. Ren, Z. Amador, I.R. Jones, K.C. Keough, M. Zhang, T. Fair, A. Abnoui, S. Mishra, Z. Ye, M. Hu, A.A. Pollen, K.S. Pollard, Y. Shen (2025). *Comparative characterization of human accelerated regions in neurons*, **Nature**, 640: 991–999.
4. L.M. Gunsalus, E. McArthur, K. Gjoni, S. Kuang, M. Pittman, J.A. Capra, K.S. Pollard (2025). *Comparing chromatin contact maps at scale: methods and insights*, **Nature Methods**, 22: 824–833.
5. B.J. Smith, C. Zhao, V. Dubinkina, X. Jin, J. Moltzau-Anderson, K.S. Pollard (2025). *Accurate estimation of intraspecific microbial gene content variation in metagenomic data with MIDAS v3 and StrainPGC*, **Genome Research**, 35: 1247-1260.
6. L.M. Gunsalus, M.J. Keiser, K.S. Pollard (2025). *ChromaFactor: deconvolution of single-molecule chromatin organization with non-negative matrix factorization*, **PLoS Computational Biology**, 21(2): e1012841.
7. X. Jin, A.G. Cheng, R. Chanin, F.B. Yu, A. Dimas, M. Jasper, A. Weakley, J. Yan, A.S. Bhatt, K.S. Pollard (2025). *Comprehensive profiling of genomic invertons in defined gut microbial community reveals associations with intestinal colonization and surface adhesion*, **Microbiome**, 13: 71.

8. K.R. Iyer, S.L. Clarke, R. Guarischi-Sousa, K. Gjoni, ...K.S. Pollard, B.D. Mitchell, R.J.F. Loos, M. Fornage, L. Hou, B.M. Psaty, K.A. Young, E.A. Regan, B.I. Freedman, R.S. Vasan, D. Levy, R.A. Mathias, P.A. Peyser, L.M. Raffield, C. Kooperberg, A.P. Reiner, J.I. Rotter, G. Jun, P.S. de Vries, T.L. Assimes (2025). *Unveiling the genetic landscape of coronary artery disease through common and rare structural variants*, **J American Heart Association**, 4(4): e036499.
9. A. Kundaje, K.S. Pollard, J. Ma, X. Chang, M. Chen, R. Rohs (2025). *Artificial intelligence in molecular biology*, **Molecular Cell**, 85(2): 193-198.
10. IGVF Consortium (2024). The Impact of Genomic Variation on Function (IGVF) Consortium, **Nature**, 633: 47–57.
11. C.M. Brand, S. Kuang, E.N. Gilbertson, E. McArthur, K.S. Pollard, T.H. Webster, J.A. Capra (2024). *Sequence-based machine learning reveals 3D genome differences between bonobos and chimpanzees*, **Genome Biology & Evolution**, 16(11): evae210.
12. P.F. Przytycki, K.S. Pollard (2024). *Hierarchical annotation of eQTLs by H-eQTL enables identification of genes with cell type-divergent regulation*, **Genome Biology**, 25: 299.
13. M. Alexanian, A. Padmanabhan, T. Nishino, J.G. Travers, L. Ye, A. Pelonero, C.Y. Lee, N. Sadagopan, Y. Huang, K. Auclair, A. Zhu, Y. An, C.A. Ekstrand, C. Martinez, B.G. Teran, W.R. Flanigan, C.K.S. Kim, K. Lumbao-Conradson, Z. Gardner, L. Li, M.W. Costa, R. Jain, I. Charo, A.J. Combes, S.M. Haldar, K.S. Pollard, R.J. Vagnozzi, T.A. McKinsey, P.F. Przytycki, D. Srivastava (2024). *Chromatin remodelling drives immune cell–fibroblast communication in heart failure*, **Nature**, 635: 434–443.
14. E.N. Gilbertson, C.M. Brand, E. McArthur, D.C. Rinker, S. Kuang, K.S. Pollard, J.A. Capra (2024). *Machine learning reveals the diversity of human 3D chromatin contact patterns*, **Molecular Biology & Evolution**, 41(10): msae209.
15. D. Häcker, K. Siebert, B.J. Smith, N. Köhler, H. Heimes, A. Metwaly, A. Mahapatra, H. Hölz, F. De Zen, J. Heetmeyer, K. Socas, G.L. Thi, C. Meng, K. Kleigrewe, J.K. Pauling, K. Neuhaus, M. List, K.S. Pollard, T. Schwerd, D. Haller (2024). *Exclusive enteral nutrition initiates individual protective microbiome changes to induce remission in pediatric Crohn’s disease*, **Cell Host & Microbe**, 32(11): 2019-2034.e8.
16. S. Shoer, L. Reicher, C. Zhao, K.S. Pollard, Y. Pilpel, E. Segal (2024). *Pangenomes of human gut microbiota uncover links between genetic diversity and stress response*, **Cell Host & Microbe**, 32(10): 1744-1757.
17. F.W. Lindhout, F.M. Krienen, K.S. Pollard, M.A. Lancaster (2024). *A molecular and cellular perspective on human brain evolution and tempo*, **Nature**, 630: 596–608.
18. B. Zhang, K.M. Magnaye, E. Stryker, J. Moltzau-Anderson, C.E. Porsche, S. Hertz, K.E. McCauley, B.J. Smith, M. Zydek, K.S. Pollard, A. Ma, N. El-Nachef, S.V. Lynch (2024). *Sustained mucosal colonization and fecal metabolic dysfunction by Bacteroides associates with fecal microbial transplant failure in ulcerative colitis patients*, **Scientific Reports**, 14: 18558.
19. L. Pasquini, F.L. Pereira, S. Seddighi, Y. Zeng, Y. Wei, I. Illán-Gala, S.C. Vatsavayai, A. Friedberg, A.J. Lee, J.A. Brown, S. Spina, L.T. Grinberg, D.W. Sirkis, L.W. Bonham, J.S. Yokoyama, A.L. Boxer, J.H. Kramer, H.J. Rosen, J. Humphrey, A.D. Gitler, B.L. Miller, K.S. Pollard, M.E. Ward, W.W. Seeley (2024). *Frontotemporal lobar degeneration targets brain regions linked to expression of recently evolved genes*, **Brain**, 147(9): 3032–3047.
20. S. Kuang, K.S. Pollard (2024). *Exploring the roles of RNAs in chromatin architecture using deep learning*, **Nature Communications**, 15: 6373.
21. K. Gjoni, K.S. Pollard (2024). *SuPreMo: a computational tool for streamlining in silico perturbation using sequence-based predictive models*, **Bioinformatics**: btae340.
22. C.T. Mowery, J.W. Freimer, Z. Chen, S. Casani-Galdón, J.M. Umhoefer, M.M. Arce, K. Gjoni, B. Daniel, K. Sandor, B.G. Gowen, V. Nguyen, D.R. Simeonov, C.M. Garrido, G.L. Curie, R. Schmidt, Z. Steinhart, A.T. Satpathy, K.S. Pollard, J.E. Corn, B.E. Bernstein, C.J. Ye, A. Marson (2024). *Systematic decoding of cis gene regulation defines context-dependent control of the multi-gene costimulatory receptor locus in human T cells*, **Nature Genetics**.
23. C. Deng, S. Whalen, M. Steyert, R. Ziffra, P.F. Przytycki, F. Inoue, D.A. Pereira, D. Caputo, S. Norton, F.M. Vaccarino, A. Pollen, T.J. Nowakowski, N. Ahituv, K.S. Pollard (2024). *Massively parallel characterization of regulatory elements in the developing human cortex*, **Science**, 384: eadh0559.

24. C. Wen, M. Margolis, R. Dai, P. Zhang, P.F. Przytycki, D.D. Vo, A. Bhattacharya, N. Matoba, C. Jiao, M. Kim, E. Tsai, C. Hoh, N. Aygün, R.L. Walker, C. Chatzinakos, D. Clarke, H. Pratt, PsychENCODE Consortium, M.A. Peters, M. Gerstein, N.P. Daskalakis, Z. Weng, A.E. Jaffe, J.E. Kleinman, T.M. Hyde, D.R. Weinberger, N.J. Bray, N. Sestan, D.H. Geschwind, K. Roeder, A. Gusev, B. Pasaniuc, J.L. Stein, M.I. Love, K.S. Pollard, C. Liu, M.J. Gandal (2024). *Cross-ancestry atlas of gene, isoform, and splicing regulation in the developing human brain*, **Science**, 384: eadh0829.
25. C. Martyn, B.M. Hayes, D. Lauko, E. Mithun, G. Castaneda, A. Bosco-Lauth, A. Kistler, K.S. Pollard, S. Chou (2024). *Metatranscriptomic investigation of single Ixodes pacificus ticks reveals diverse microbes, viruses, and novel mRNA-like endogenous viral elements*, **mSystems**.
26. L.M. Gunsalus, M.J. Keiser, K.S. Pollard (2023). *In silico discovery of repetitive elements as key sequence determinants of 3D genome folding*, **Cell Genomics**, 3(10): 100410.
27. A. Bustion, A. Agrawal, P.J. Turnbaugh, K.S. Pollard (2023). *A novel in silico method employs chemical and protein similarity algorithms to accurately identify chemical transformations in the human gut microbiome*, **ELife**, 12:e82401.
28. Z.J. Shi, S. Nayfach, K.S. Pollard (2023). *Maast: genotyping thousands of microbial strains efficiently*, **Genome Biology**, 24:186.
29. X. Jin, F.B. Yu, J. Yan, A. Weakley, K.S. Pollard (2023). *Culturing of a complex gut microbial community in mucin-hydrogel carriers reveals strain- and gene-associated spatial organization*, **Nature Communications**, 14: 3510.
30. K.C. Keough, S. Whalen, F. Inoue, P.F. Przytycki, T. Fair, C. Deng, M. Steyert, H. Ryu, K. Lindblad-Toh, E. Karlsson, Zoonomia Consortium, T.J. Nowakowski, N.J. Ahituv, A.A. Pollen, K.S. Pollard (2023). *Three-dimensional genome re-wiring in loci with Human Accelerated Regions*, **Science**, 380 (6643): amb1696.
31. P.F. Sullivan, J.R.S. Meadows, S. Gazal, B.D.N. Phan, X. Li, D.P. Genereux, M.X. Dong, M. Bianchi, G. Andrews, S. Sakthikumar, J. Nordin, A. Roy, M.J. Christmas, V.D. Marinescu, C. Wang, O. Wallerman, J.R. Xue, Y. Li, S. Yao, Q. Sun, J. Szatkiewicz, J. Wen, L.M. Huckins, A.J. Lawler, K.C. Keough, Z. Zheng, J. Zeng, N.R. Wray, J. Johnson, J. Chen, Zoonomia Consortium, B. Paten, S.K. Reilly, G.M. Hughes, Z. Weng, K.S. Pollard, A.R. Pfenning, K. Forsberg-Nilsson, E.K. Karlsson, K. Lindblad-Toh (2023). *Leveraging base pair mammalian constraint to understand genetic variation and human disease*, **Science**, 380 (6643): abn2937.
32. M.J. Christmas, I.M. Kaplow, D.P. Genereux, M.X. Dong, G.M. Hughes, X. Li, P.F. Sullivan, A.G. Hindle, G. Andrews, J.C. Armstrong, M. Bianchi, A.M. Breit, M. Diekhans, C. Fanter, N.M. Foley, D.B. Goodman, L. Goodman, K.C. Keough, B. Kirilenko, A. Kowalczyk, C. Lawless, A.L. Lind, J.R.S. Meadows, L.R. Moreira, R.W. Redlich, L. Ryan, R. Swofford, A. Valenzuela, F. Wagner, O. Wallerman, A.R. Brown, J. Damas, K. Fan, J. Gatesy, J. Grimshaw, J. Johnson, S.V. Kozyrev, A.J. Lawler, V.D. Marinescu, K.M. Morrill, A. Osmanski, N.S. Paulat, B.D.N. Phan, S.K. Reilly, D.E. Schäffer, C. Steiner, M.A. Supple, A.P. Wilder, M.E. Wirthlin, J.R. Xue, Zoonomia Consortium, B.W. Birren, S. Gazal, R.M. Hubley, K.-P. Koepfli, T. Marques-Bonet, W.K. Meyer, M. Nweeia, P.C. Sabeti, B. Shapiro, A.F.A. Smit, M. Springer, E. Teeling, Z. Weng, M. Hiller, D.L. Levesque, H.A. Lewin, W.J. Murphy, A. Navarro, B. Paten, K.S. Pollard, D.A. Ray, I. Ruf, O.A. Ryder, A.R. Pfenning, K. Lindblad-Toh, E.K. Karlsson (2023). *Evolutionary constraint and innovation across hundreds of placental mammals*, **Science**, 380 (6643): abn3943.
33. P.P. Shah, K.C. Keough, K. Gjoni, G.T. Santini, R.J. Abdill, N.M. Wickramasinghe, C.E. Dundes, A. Karnay, A. Chen, R.E.A. Salomon, P.J. Walsh, S.C. Nguyen, S. Whalen, E.F. Joyce, K.M. Loh, N. Dubois, K.S. Pollard, R. Jain (2023). *An atlas of lamina-associated chromatin across thirteen human cell types reveals cell-type-specific and multiple subtypes of peripheral heterochromatin*, **Genome Biology**, 24: 16.
34. S. Whalen, F. Inoue, H. Ryu, T. Fair, E. Markenscoff-Papadimitriou, K. Keough, M. Kircher, B. Martin, B. Alvarado, O. Elor, D. Laboy Cintron, A. Williams, Md.A.H. Samee, S. Thomas, R. Krencik, E.M. Ullian, A. Kriegstein, J. Shendure, A.A. Pollen, N. Ahituv, K.S. Pollard (2023). *Machine-learning dissection of Human Accelerated Regions in primate neurodevelopment*, **Neuron**, 11(6): 857-873.
35. 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 (2023). *Genetic determinants of*

- interventricular septal anatomy are linked to ventricular septal defects and hypertrophic cardiomyopathy*, **Circulation: Genomic and Precision Medicine**, e003708.
36. M. Yu, M. Aguirre, M. Jia, K. Gjoni, A. Cordova-Palomera, C. Munger, D. Amgalan, X. R. Ma, A. Pereira, C. Tcheandjieu, C. Seidman, J. Seidman, M. Tristani-Firouzi, W. Chung, E. Goldmuntz, D. Srivastava, R.J.F. Loos, N. Chami, H. Cordell, M. Dreßen, B. Mueller-Myhsok, H. Lahm, M. Krane, K.S. Pollard, J.M. Engreitz, S.A.G. Taliun, B.D. Gelb, J.R. Priest (2023). *Oligogenic architecture of rare noncoding variants distinguishes four congenital heart disease phenotypes*, **Circulation: Genomic and Precision Medicine**, 16(3): 258-266.
 37. C. Zhao, Z.J. Shi, K.S. Pollard (2023). *Pitfalls of genotyping microbial communities with rapidly growing genome collections*, **Cell Systems**, 14(2): 160-175.
 38. Z.J. Shi, S. Nayfach, K.S. Pollard (2023). *Identifying species-specific k-mers for fast and accurate metagenotyping with Maast and GT-Pro*, **STAR Protocols**, 4(1): 101964.
 39. C. Zhao, B. Dimitrov, M. Goldman, S. Nayfach, K.S. Pollard (2022). *MIDAS2: Metagenomic Intra-species Diversity Analysis System*, **Bioinformatics**, btac713.
 40. C. Zhao, M. Goldman, B.J. Smith, K.S. Pollard (2022). *Genotyping Microbial Communities with MIDAS2: From Metagenomic Reads to Allele Tables*, **Current Protocols**, 2: e604.
 41. S. Whalen, K.S. Pollard (2022). *Enhancer function and evolutionary roles of Human Accelerated Regions*, **Annual Review of Genetics**, 56.
 42. P. Spanogiannopoulos, P.H. Bradley, J. Melamed, Y.N.A. Malig, K.N. Lam, R.R. Gerona, K.S. Pollard, P.J. Turnbaugh (2022). *Host and gut bacteria share metabolic pathways for anti-cancer drug metabolism*, **Nature Microbiology**, 7: 1605–1620.
 43. 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*, **Bioinformatics Advances**, 2(1): vbac051.
 44. B.J. Smith, X. Li, A. Abate, Z.J. Shi, K.S. Pollard (2022). *Scalable microbial strain inference in metagenomic data using StrainFacts*, **Frontiers in Bioinformatics**.
 45. T. Sinha, K. Lammerts van Bueren, D.E. Dickel, I. Zlatanova, R. Thomas, C.O. Lizama. S.-M. Xu, A.C. Zovein, K. Ikegami, I.P. Moskowitz, K.S. Pollard, L.A. Pennacchio, B.L. Black (2022). *Differential Etv2 threshold requirement for endothelial and erythropoietic development*, **Cell Reports**, 39(9): 110881.
 46. M. Wagle, M. Zarei, M. Lovett-Barron, K.T. Poston, J. Xu, V. Ramey, K.S. Pollard, D.A. Prober, J. Schulkun, K. Deisseroth, S. Guo (2022). *Brain-wide perception of the emotional valence of light is regulated by distinct hypothalamic neurons*, **Molecular Psychiatry**, 27: 3777-3793.
 47. 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.
 48. 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.
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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 & Genome Structure

CellWalkR: Network model for integrating single-cell and bulk data
<https://github.com/PFPrzytycki/CellWalkR>
SuPreMo: Sequence mutator for predictive models
<https://github.com/ketringjoni/SuPreMo>
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

AcceleratedRegionsNF: NextFlow pipeline for identifying accelerated regions
<https://github.com/keoughkath/AcceleratedRegionsNF>
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/dglemay/G-NEST>

Metagenomics

MicroSLAM: metagenome-wide association studies adjusting for microbiome genetic relatedness
<https://github.com/miriam-goldman/microSLAM>
SIMMER: prediction of microbiome enzymes that metabolize drugs and dietary compounds
<https://github.com/aebustion/SIMMER>
Maast: discovery and genotyping of genetic variants in large numbers of genomes or reads
<https://github.com/zjshi/Maast>
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/czbiohub-sf/MIDAS>

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

Phylogenize: phylogenetic regression with traits and genes estimated from metagenomes

<https://phylogenize.org/>

PhyIOTU: taxonomic clustering

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

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/NIA

Human-specific vulnerabilities and compensatory adaptations to age-related stressors in selectively vulnerable midbrain dopaminergic neurons

Role: PI (jointly with Alex Pollen)

2024-2029

\$750,000 (Pollard component only)

NIH/NIMH

Discovering human divergent activity-regulated elements using comparative, computational, and functional approaches

Role: PI (jointly with Alex Pollen)

2023-2028

\$795,755 (Pollard component only)

NIH/NHLBI

Linking microbiome genetic variants with cardiovascular phenotypes in 50,000 individuals

Role: PI (jointly with Eran Segal)

2022-2026

\$1,837,735

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

2020-2025 (NCE)

\$1,604,695

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)

2019-2025 (NCE)

\$850,000 (Pollard component only)

COMPLETED

NIH/NIAID R01

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

Role: Co-Investigator

2019-2024

\$48,805

NIH Common Fund

Deciphering the 3D genome of pediatric brain tumors

Role: PI (jointly with Nadia Dahmane and Adam Resnick)

2022-2023

\$200,000

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/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 (No cost extension to 2023)

\$133,830 (Pollard component only)

NIH/NEI R01

Therapeutic genome editing to treat Best disease

Role: Co-Investigator

2017-2022

\$225,000

NIH/NIMH

Massively parallel dissection of psychiatric regulatory networks

Role: PI

2016-2022

\$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

\$846,540

NIH/NHLBI

The epigenetic landscape of heart development

Role: PI

2015-2021

\$2,500,000

NIH/NHLBI P01
Transcriptional networks during cardiac differentiation
Role: Core Director
2013-2018
\$393,041 (Pollard component only)

NIH/NINDS R01
Automated longitudinal single cell analysis
Role: Co-Investigator
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
2014-2016
\$500,000

NIH/NHLNI U01
Defining a comprehensive reference profile of circulating human extracellular RNA
Role: Consortium PI
2014-2016
\$95,455 (Pollard subcontract only)

NIH/NHLBI U01
The epigenetic landscape of heart development
Role: PI
2009-2015
\$4,429,581

NIH/NIGMS P01
Collaborative Center for an Enzyme Function Initiative

Role: Consortium PI
2014-2015
\$68,192 (Pollard subcontract only)

NIH/NIGMS R01
What made us human?
Role: PI
2008-2012
\$864,000

Gordon & Betty Moore Foundation
Integrating evolutionary, ecological and statistical approaches to metagenomics
Role: PI
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
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
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