JONATHAN K. PRITCHARD

Bing Professor of Population Studies
Departments of Biology and Genetics
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Employment History

2020–Present	Bing Professor of Population Studies, Stanford University
2013–Present	Professor, Departments of Genetics and Biology, Stanford University
2008–2019	Investigator, Howard Hughes Medical Institute
2006–2013	Professor, Department of Human Genetics, The University of Chicago
2001–2005	Assistant Professor, Department of Human Genetics, The University of Chicago

Education

1998–2001	Postdoctoral Fellow, Statistics University of Oxford Advised by Peter Donnelly
1994–1998	Ph.D., Biology Stanford University Advised by Marcus Feldman
1989–1994	B.Sc., Biology and Mathematics Pennsylvania State University

Personal Statement

My group has expertise in the development of new statistical methods for genetic analysis and in their application to genomic data from humans and other organisms. We focus on questions relating to genetic variation and evolution. What are the major evolutionary forces shaping genetic variation? How does genetic variation impact phenotypic traits and evolution, both at the organismal and cellular level?

Currently the central focus of my group is on understanding how genetic variation affects gene regulation, and how these effects flow through regulatory networks to drive complex phenotypes. One major motivating question is to understand why so much of the genome can be implicated in affecting any given complex trait, and secondly how we can better extract biological insight from association studies. Our primary tools for this include a mixture of population genetics, statistical and computational approaches, and collaborative work in regulatory genomics and specifically in high-throughput perturbation experiments.

We generally work on problems where there are no off-the-shelf statistical methods. Thus, an important part of our work is in developing appropriate statistical and computational approaches that can yield new insights into biological data. In the past, we have made important contributions to a variety of problems in human population genetics, including methods for complex trait mapping, inference of population structure and history, studies of natural selection, and understanding the architecture of complex traits.

We have a strong track record of producing user-friendly, open-source resources that are widely used for applied data analysis to tackle important biological questions. Our software packages (including Structure and TreeMix) have been applied to a broad range of applications. I'm also actively committed to education, including my free online textbook on human genetics, "An Owner's Guide to the Human Genome".

Awards and honors

2025	Elected to the US National Academy of Sciences
2020	Appointed as the Bing Professor of Population Studies at Stanford University
2019	Fabio Frassetto International Prize in Physical Anthropology from the Lincean Academy of Italy
2016	Review of Pritchard et al. (2000) in the Classic Papers series for the centennial year of *Genetics* by John Novembre (PMID 27729489). P. et al. has now been cited ∼40,000 times (G Scholar)
2015	Kistler Prize in Population Genetics and Society
2013	Selected as a Fellow of the American Academy of Arts and Sciences
2013	Edward Novitski Prize from the Genetics Society of America; this award recognizes "creativity and intellectual ingenuity in the solution of significant problems in genetics"
2013	Outstanding Alumni Award, Eberly College of Science, Penn State University
2008	Selected as an investigator of the Howard Hughes Medical Institute
2004	Selected Packard Fellow
2004	Selected Alfred P. Sloan Fellow
2003	Lancet's *Paper of the Year* (for any biomedical journal) was awarded to the paper of Rosenberg, Pritchard et al. (Science 2002) on human population structure (editorial in Lancet 362:2101-2103).
2002	Mitchell Prize from the American Statistical Association and the International Society of Bayesian Analysis, presented annually for "an outstanding paper describing how a Bayesian analysis has solved an important applied problem."
1994-1998	Howard Hughes Medical Institute Predoctoral Fellowship
1994	McCoy Award, given to the Penn State Outstanding Scholar-Athlete
1992	Stecker Award, given to a Penn State undergraduate in Mathematics
1989-1993	Penn State Braddock Scholarship and Academic Excellence Scholarship

Selected Professional Activities

2021–2025	Co-Director of Graduate Studies, Dept of Biology, Stanford
2017–present	Co-Director: Stanford Center for Computational, Evolutionary and Human Genomics
2017–2021	External Advisory Board to Wellcome Trust Sanger Institute
2016–2020	NHGRI (NIH) Council Member
2016–2018	Lead organizing committee for "Biology of Genomes" meeting, Cold Spring Harbor
2015–2022	Science Magazine Board of Reviewing Editors
2013	Scientific Advisory Board, Cellular Genomics Program, Wellcome Trust Sanger Institute
2012–2015	Editorial Board: Current Biology
2008–2012	Associate Editor: Molecular Biology and Evolution
2006–2014	Associate Editor: PLOS Genetics

Research Support [for brevity only listing grants where I am PI]

2025-2029	RO1 HG014005: "Bayesian estimation of gene effects on traits from coding variants"
2016-2025	RO1 HG008140: "Integration of functional data and GWAS to elucidate genetic basis of diseases"; renewal pending
2025-2026	Arc Institute Ignite award.

Previous grants/fellowships:

2020-2024	RO1 HG011432: "New methods for constructing and evaluating polygenic scores."
2017-2020	UO1 HG009431: "Decoding the regulatory architecture of the human genome across cell types, individuals and disease." [Supplement to 2021]
2008-2019	Investigator, Howard Hughes Medical Institute.
2014-2017	RO1 ES025009: "Computational methods for modeling lineage-specific gene regulation." Administrative supplement for 2016-2017.
2012-2016	U01 HG007036: "Genetic and epigenetic controls of gene regulation." Includes administrative supplement for 2015-2016.
2010-2013	RO1 MH090951: "Statistical analysis of gene expression quantitative trait loci (eQTL)." Includes administrative supplement for 2012-2013.
2008-2016	RO1 MH084703: "Analysis and interpretation of DNA sequence data in association studies."
2003-2008	RO1 HG002772: "Linkage Disequilibrium Methods for Complex Trait Mapping."
2004–2009	Packard Foundation Fellowship: "Population genetics of genomic rearrangements."
2004-2006	Sloan Foundation Fellowship
1999-2003	Burroughs-Wellcome Fund Hitchings-Elion Postdoc-Faculty Award "Population structure and linkage disequilibrium in association mapping."
1998	NIH (NRSA) 3-year Postdoctoral Award (replaced by BWF award) "The impact of population history on association mapping."
1994-1998	Howard Hughes Medical Institute Predoctoral Fellowship
1994	NSF Predoctoral Fellowship (declined)
1989-1993	Penn State Braddock Scholarship (four-year full-tuition award)
1989-1993	Penn State Academic Excellence Scholarship

Mentoring:

2025–Present	Sayali Alatkar (postdoc)
2025–Present	Jiacheng Miao (postdoc; joint with James Zou)
2025–Present	Xinyi Li (postdoc)
2024–Present	Yun Deng (postdoc)
2024–Present	Emma Dann (postdoc; joint with Alex Marson)
2022–Present	Ronghui Zhu (postdoc; joint with Alex Marson)

2025–Present	Ryan Goto (PhD student, BMDS; joint with Rob Tibshirani)
2023–Present	Tami Gjorgjieva (PhD student, Genetics)
2023–Present	Nikhil Milind (PhD student, Genetics)
2023–Present	Julie (Huisheng) Zhu (PhD student, Biology)
2022–Present	Alvina Adimoelja (PhD student, Genetics; joint with Christina Curtis)
2022–Present	Tony Zeng (PhD student, Genetics; joint with Jesse Engreitz)

Previous Postdocs:

2021–2025	Mineto Ota (postdoc; joint with Alex Marson); now Assistant Professor, University of Tokyo

2021–2025	Romain Lopez (postdoc; joint with Aviv Regev); now Assistant Professor, NYU
2020–2025	Daphna Rothschild (postdoc; joint with Maria Barna); now staff scientist Barna lab
2022–2024	Wilder Wohns; concurrent postdoc–MD student; now completing MD
2019–2024	Sahin Naqvi (postdoc; joint with Joanna Wysocka); now Assistant Professor, Harvard Medical School
2021–2023	Josh Weinstock (postdoc; joint with Alexis Battle); now Assistant Professor, Emory
2019–2023	Hakhamanesh Mostafavi (postdoc); now Assistant Professor, NYU Langone
2019–2023	Clemens Weiss (postdoc); now staff scientist, Curtis lab, Stanford
2019–2023	Jeff Spence (postdoc); 2023-25 staff scientist, Pritchard lab; now Asst Professor, UCSF
2018–2023	Yuval Simons (postdoc); now Assistant Professor, University of Chicago
2019–2022	Shaila Musharoff (postdoc); now Assistant Professor, Cornell
2018–2022	Jake Freimer (postdoc; joint with Alex Marson); now staff scientist at Genentech
2018–2019	Hanna Ollila (postdoc); now Group Leader, University of Helsinki
2016–2020	Harold Pimentel (postdoc); now Assistant Professor, UCLA
2015–2020	Ziyue Gao (postdoc); now Assistant Professor, Univ Pennsylvania
2015–2018	David Knowles (postdoc); joint w/ Sylvia Plevritis; now asst prof, NY Genome Center/ Columbia
2014–2018	Eilon Sharon (postdoc); joint with Hunter Fraser; now staff scientist, Insitro
2012–2018	Yair Field (postdoc; now staff scientist, Illumina)
2015–2017	Kelley Harris (postdoc; now assistant professor, U Washington)
2012–2017	Xun Lan (postdoc; now assistant professor, Tsinghua University)
2014–2017	Yang Li (postdoc; now assistant professor, U Chicago)
2014–2017	Anand Bhaskar (postdoc); now data scientist, Facebook
2011–2016	Anil Raj (postdoc); now staff scientist, Calico
2014–2016	David Golan (postdoc); cofounder of Viz.ai
2014–2015	Audrey Fu (visiting postdoc); now assistant professor, Univ of Idaho
2014–2015	Towfique Raj (visiting postdoc); now assistant professor, Mt Sinai
2014–2015	Kyle Gaulton (visiting postdoc); now assistant professor, UCSD
2010–2015	Graham McVicker (postdoc); now assistant professor, Salk Institute
2013–2014	Alexis Battle (postdoc); now associate professor, Johns Hopkins
2011–2014	Stoyan Georgiev (postdoc); now data scientist, Google
2011–2013	Zia Khan (postdoc; joint with Y Gilad); assistant professor, University of Maryland; now Genentech
2011–2013	Shyam Gopalakrishnan (postdoc; joint with Abe Palmer); now Assoc Prof, U Copenhagen
2012–2013	Allegra Petti (postdoc; joint with Y Gilad); now staff scientist, Wash U St Louis
2009–2012	Roger Pique-Regi (postdoc); now associate professor, Wayne State, MI
2008–2011	Daniel Gaffney (postdoc); G.L. at Sanger Institute; now head of Cellular Genetics, Genomics PLC
2009–2011	Pall Melsted (postdoc); now assistant professor, University of Iceland
2009–2011	Ying Wang (postdoc); now junior faculty, Beijing Institute of Genomics
2008–2009	Jordana Bell (postdoc); now Senior Lecturer, Kings College London
2006–2007	Jean-Baptiste Veyrieras (postdoc); now group leader at bioMerieux
2004–2008	Graham Coop (postdoc); now professor, U. of California, Davis
2001–2005	Sebastian Zöllner (postdoc); now professor, Biostatistics, U. of Michigan
2002–2004	Giovanni Montana (postdoc); now professor of Biostatistics, Imperial College London
2002–2003	Jeffrey Wall (postdoc); now professor of Epidemiology and Biostats, UCSF

Previous PhD Students:

2022–2025	Jon Judd (PhD student, Genetics; joint with John Witte, Linda Kachuri); postdoc science policy
2020–2025	Matthew Aguirre (PhD student, BMI); now postdoc McCarthy/Regev labs, Genentech
2020–2024	Courtney Smith (MSTP student, Genetics); now completing MD
2019–2024	Roshni Patel (PhD student, Genetics); postdoc Doc Edge lab, USC; now Asst Prof U Oregon
2019–2023	Alyssa Lyn Fortier (PhD student, Biology); postdoc Pritchard lab 2023-24

2018–2022	Adele Xu (MSTP; primary lab Maria Barna); now MD student
2017–2022	Margaret Antonio (PhD student, BMI); now staff scientist at Grail
2017–2022	Nasa Sinnott-Armstrong (PhD student, Genetics); now Asst Prof, Fred Hutch
2017–2021	Hannah Moots (PhD student, Archaeology); postdoc U Chicago; postdoc Sweden
2015–2019	Jessica Ribado (PhD student, Genetics, joint w/ Ami Bhatt); now PD at Centers for Disease Modeling
2015–2019	Evan Boyle (PhD student, Genetics; joint with Will Greenleaf); postdoc with Gene Yeo, UCSD, now indus
2014–2019	Diego Calderon (PhD student, BMI); postdoc with Trapnell/Shendure at U Washington, Asst Prof UCSF
2014–2019	Emily Glassberg (PhD student, Biology); now at Boston Consulting Group
2014–2018	Arbel Harpak (PhD student, Biology); postdoc with Molly Przeworski, Columbia, Asst Prof U Texas
2014–2018	Natalie Telis (PhD student, BMI); now industry scientist
2011–2015	Bryce van de Geijn (PhD student, Chicago GGSB); postdoc with Alkes Price, Harvard, now industry scien
2014–2015	Cristina Pop (PhD, CS with Daphne Koller; mentored by me 2014-5); data scientist at Google
2011–2014	Paul Grabowski (PhD student, Ecology and Evolution; joint with J. Borevitz); postdoc at USDA
2012–2013	Carolyn Jumper (PhD student, Human Genetics); switched to Cox lab due to Stanford move
2012–2013	Michael Turchin (PhD student, Human Genetics); switched to Stephens lab due to Stanford move
2008–2012	Jack Degner (PhD, GGSB); postdoc with Eileen Furlong, EMBL; now Senior Scientist at AbbVie
2007–2011	Joseph Pickrell (PhD, Human Genetics); postdoc with David Reich, Harvard; asst prof NY Genome Center/Columbia Univ; now founder/CEO of GenCove
2004–2008	Sridhar Kudaravalli (PhD, Human Genetics, 2008)
2004–2008	Su Yeon Kim (PhD, Statistics, 2008; joint with P. McCullagh) postdoc with Rasmus Nielsen, Terry Speed at UC Berkeley; now Bioinformatician Veracyte
2004–2006	Daniel Davison (PhD, Comm Ev. Biol., 2006; joint with S. Hackett) postdoc in Statistics with Peter Donnelly, U. of Oxford; now at Counsyl
2003–2007	Donald Conrad (PhD, Human Genetics, 2008) postdoc with Matt Hurles, Sanger Institute; now assoc. prof. Wash U.
2002–2006	Benjamin Voight (PhD, Human Genetics, 2006; joint with N. Cox) postdoc with Mark Daly, Broad Institute; now assoc. prof., Univ of Pennsylvania

Selected other lab members:

2023–2025	Jeff Spence staff scientist, Pritchard lab
2016–2017	Ben Lehmann (programmer); PhD in astrophysics UCSC, now Postdoc MIT
2011-2012	Andy Dahl (Honors Thesis, Statistics); DPhil student, Oxford; PD UCSF; now asst Prof U Chicago
2006–2008	Melissa Hubisz (M.S., Human Genetics); PhD student, Cornell; staff scientist Cornell
2001–2007	Xiaoquan William Wen (programmer); now Associate Professor Biostatistics, Michigan

Free Online TextBook:

2023–Present *An Owner's Guide to the Human Genome:*
an introduction to human population genetics, variation and disease
Link: http://web.stanford.edu/group/pritchardlab/HGbook.html

Publications

[191] R Zhu, E Dann, J Yan, J Reyes Retana, R Goto, RC Guitche, LK Petersen, M Ota, JK Pritchard, and A Marson. Genome-scale perturb-seq in primary human CD4+ T cells maps context-specific regulators of T cell programs and human immune traits. *bioRxiv*, 2025.

[190] PA Gerlach, N Milind, JP Spence, and JK Pritchard. High false sign rates in transcriptome-wide association studies. *bioRxiv*, 2025.

[189] M Ota, JP Spence, T Zeng, E Dann, N Milind, A Marson, and JK Pritchard. Causal modelling of gene effects from regulators to programs to traits. *Nature*, pages 1–10, 2025.

[188] J Judd, JP Spence, N Milind, L Kachuri, JS Witte, and JK Pritchard. Allele frequencies at recessive disease genes are mainly determined by pleiotropic effects in heterozygotes. *bioRxiv*, 2025.

[187] AL Fortier and JK Pritchard. The primate major histocompatibility complex as a case study of gene family evolution. *eLife*, 14:RP103545, 2025.

[186] JP Spence, H Mostafavi, M Ota, N Milind, T Gjorgjieva, CJ Smith, YB Simons, G Sella, and JK Pritchard. Specificity, length and luck drive gene rankings in association studies. *Nature*, pages 1–8, 2025.

[185] YB Simons, H Mostafavi, H Zhu, CJ Smith, JK Pritchard, and G Sella. Simple scaling laws control the genetic architectures of human complex traits. *PLoS Biology*, 23(10):e3003402, 2025.

[184] J Judd, JP Spence, JK Pritchard, L Kachuri, and JS Witte. Investigating the role of neighborhood socioeconomic status and germline genetics on prostate cancer risk. *Human Genetics and Genomics Advances*, 6(4), 2025.

[183] AL Fortier and JK Pritchard. Ancient trans-species polymorphism at the major histocompatibility complex in primates. *Elife*, 14:RP103547, 2025.

[182] J Miao, JR Davis, Y Zhang, JK Pritchard, and J Zou. Paper2agent: Reimagining research papers as interactive and reliable ai agents. *arXiv preprint arXiv:2509.06917*, 2025.

[181] D Rothschild, A Raj, J Brown, N Thayer, M Hotz, D Hendrickson, JK Pritchard, and M Barna. Ribosome heterogeneity arising from common and rare rRNA sequence variants affects diverse human phenotypes. *medRxiv*, pages 2025–09, 2025.

[180] M Aguirre, JP Spence, G Sella, and JK Pritchard. Gene regulatory network structure informs the distribution of perturbation effects. *PLOS Computational Biology*, 21(9):e1013387, 2025.

[179] M Aguirre, JP Spence, G Sella, and JK Pritchard. Regulatory network topology and the genetic architecture of gene expression. *bioRxiv*, 2025.

[178] CJ Smith, S Strausz, JP Spence, HM Ollila, and JK Pritchard. Haplotype analysis reveals pleiotropic disease associations in the HLA region. *The American Journal of Human Genetics*, 112(8):1833–1851, 2025.

[177] RA Patel, CL Weiß, H Zhu, H Mostafavi, YB Simons, JP Spence, and JK Pritchard. Characterizing selection on complex traits through conditional frequency spectra. *Genetics*, 229(4):iyae210, 2025.

[176] Sahin Naqvi, Seungsoo Kim, Saman Tabatabaee, Anusri Pampari, Anshul Kundaje, Jonathan K Pritchard, and Joanna Wysocka. Transfer learning reveals sequence determinants of the quantitative response to transcription factor dosage. *Cell Genomics*, 5(3), 2025.

[175] MM Arce, JM Umhoefer, N Arang, S Kasinathan, JW Freimer, Z Steinhart, H Shen, Minh TN Pham, M Ota, A Wadhera, [others], JK Pritchard, and A. Marson. Central control of dynamic gene circuits governs T cell rest and activation. *Nature*, 637(8047):930–939, 2025.

[174] JS Weinstock, MM Arce, JW Freimer, M Ota, A Marson, A Battle, and JK Pritchard. Gene regulatory network inference from CRISPR perturbations in primary CD4+ T cells elucidates the genomic basis of immune disease. *Cell Genomics*, 4(11), 2024.

[173] N Milind, CJ Smith, H Zhu, JP Spence, and JK Pritchard. Buffering and non-monotonic behavior of gene dosage response curves for human complex traits. *medRxiv*, pages 2024–11, 2024.

[172] D Rothschild, TT Susanto, X Sui, JP Spence, R Rangan, NR Genuth, N Sinnott-Armstrong, X Wang, JK Pritchard, and M Barna. Diversity of ribosomes at the level of rRNA variation associated with human health and disease. *Cell Genomics*, 4(9), 2024.

[171] T Zeng, JP Spence, H Mostafavi, and JK Pritchard. Bayesian estimation of gene constraint from an evolutionary model with gene features. *Nature Genetics*, pages 1–12, 2024.

[170] R Lopez, J-C Huetter, E Hajiramezanali, JK Pritchard, and A Regev. Toward the identifiability of comparative deep generative models. In *Causal Learning and Reasoning*, pages 868–912. PMLR, 2024.

[169] O Naret, Y Simons, J Fellay, and JK Pritchard. Is competition for cellular resources a driver of complex trait heritability? *eLife*, 12, 2024.

[168] ML Antonio, CL Weiß, Z Gao, S Sawyer, V Oberreiter, HM Moots, JP Spence, O Cheronet, B Zagorc, E Praxmarer, [about 100 others], and Pritchard JK. Stable population structure in Europe since the Iron Age, despite high mobility. *Elife*, 13:e79714, 2024.

[167] Ralf Schmidt, Carl C Ward, Rama Dajani, Zev Armour-Garb, Mineto Ota, Vincent Allain, Rosmely Hernandez, Madeline Layeghi, Galen Xing, [others], JK Pritchard, SE Dodgson, and A Marson. Base-editing mutagenesis maps alleles to tune human T cell functions. *Nature*, 625(7996):805–812, 2024.

[166] H Pimentel, J Freimer, MM Arce, CM Garrido, A Marson, and JK Pritchard. A model for accurate quantification of CRISPR effects in pooled FACS screens. *bioRxiv*, pages 2024–06, 2024.

[165] H Mostafavi, JP Spence, S Naqvi, and JK Pritchard. Systematic differences in discovery of genetic effects on gene expression and complex traits. *Nature Genetics*, 55(11):1866–1875, 2023.

[164] JP Spence, T Zeng, H Mostafavi, and JK Pritchard. Scaling the discrete-time Wright–Fisher model to biobank-scale datasets. *Genetics*, 225(3):iyad168, 2023.

[163] HM Moots, ML Antonio, S Sawyer, JP Spence, [20 others], JK Pritchard, and R Pinhasi. A genetic history of continuity and mobility in the Iron Age Central Mediterranean. *Nature Ecology & Evolution*, 7(9):1515–1524, 2023.

[162] VK Bajpai, T Swigut, J Mohammed, S Naqvi, M Arreola, J Tycko, TC Kim, JK Pritchard, MC Bassik, and J Wysocka. A genome-wide genetic screen uncovers determinants of human pigmentation. *Science*, 381(6658):eade6289, 2023.

[161] R Lopez, N Tagasovska, S Ra, K Cho, JK Pritchard, and A Regev. Learning causal representations of single cells via sparse mechanism shift modeling. In *Conference on Causal Learning and Reasoning*, pages 662–691. PMLR, 2023.

[160] JA Mooney, L Agranat-Tamir, JK Pritchard, and NA Rosenberg. On the number of genealogical ancestors tracing to the source groups of an admixed population. *Genetics*, 224(3):iyad079, 2023.

[159] AF Xu, R Molinuevo, E Fazzari, H Tom, Z Zhang, J Menendez, KM Casey, D Ruggero, L Hinck, JK Pritchard, and Barna M. Subfunctionalized expression drives evolutionary retention of ribosomal protein paralogs Rps27 and Rps27l in vertebrates. *Elife*, 12:e78695, 2023.

[158] MO Maksimov, C Wu, DG Ashbrook, F Villani, V Colonna, N Mousavi, N Ma, L Lu, JK Pritchard, A Goren, RW Williams, AA Palmer, and M Gymrek. A novel quantitative trait locus implicates msh3 in the propensity for genome-wide short tandem repeat expansions in mice. *Genome Research*, 2023.

[157] S Naqvi, S Kim, H Hoskens, HS Matthews, RA Spritz, OD Klein, B Hallgrímsson, T Swigut, P Claes, JK Pritchard, and Wysocka J. Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. *Nature Genetics*, pages 1–11, 2023.

[156] R Lopez, J-C Hütter, JK Pritchard, and A Regev. Large-scale differentiable causal discovery of factor graphs. *Advances in Neural Information Processing Systems*, 35:19290–19303, 2022.

[155] CJ Smith, N Sinnott-Armstrong, A Cichońska, H Julkunen, EB Fauman, P Würtz, and JK Pritchard. Integrative analysis of metabolite GWAS illuminates the molecular basis of pleiotropy and genetic correlation. *Elife*, 11:e79348, 2022.

[154] Q Li, MJ Gloudemans, JM Geisinger, B Fan, F Aguet, T Sun, G Ramaswami, YI Li, J-B Ma, JK Pritchard, Montgomery SB, and Li JB. RNA editing underlies genetic risk of common inflammatory diseases. *Nature*, 608:1–9, 2022.

[153] JW Freimer, O Shaked, S Naqvi, N Sinnott-Armstrong, A Kathiria, CM Garrido, AF Chen, JT Cortez, WJ Greenleaf, JK Pritchard, and A Marson. Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. *Nature Genetics*, 54(8):1133–1144, 2022.

[152] RA Patel, SA Musharoff, JP Spence, H Pimentel, C Tcheandjieu, H Mostafavi, Nasa Sinnott-Armstrong, [17 others], and Pritchard JK. Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. *The American Journal of Human Genetics*, 109(7):1286–1297, 2022.

[151] DG Ashbrook, T Sasani, M Maksimov, MH Gunturkun, N Ma, F Villani, Y Ren, D Rothschild, H Chen, L Lu, [4 others], Pritchard JK, Palmer AA, and Williams RW. Private and sub-family specific mutations of founder haplotypes in the BXD family reveal phenotypic consequences relevant to health and disease. *bioRxiv*, 2022.

[150] TA Sasani, DG Ashbrook, AC Beichman, L Lu, AA Palmer, RW Williams, JK Pritchard, and K Harris. A natural mutator allele shapes mutation spectrum variation in mice. *Nature*, 605(7910):497–502, 2022.

[149] Sahin Naqvi, Yoeri Sleyp, Hanne Hoskens, Karlijne Indencleef, Jeffrey P Spence, [9 others], Jonathan K Pritchard, S Sunaert, H Peeters, J Wysocka, and P Claes. Shared heritability of human face and brain shape. *Nature Genetics*, 53:1–10, 2021.

[148] N Sinnott-Armstrong, S Naqvi, M Rivas, and JK Pritchard. GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. *Elife*, 10:e58615, 2021.

[147] N Sinnott-Armstrong, IS Sousa, S Laber, E Rendina-Ruedy, SEN Dankel, T Ferreira, G Mellgren, D Karasik, M Rivas, JK Pritchard, [9 others], and M Claussnitzer. A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. *Cell Metabolism*, 33(3):615–628, 2021.

[146] N Sinnott-Armstrong, Y Tanigawa, D Amar, N Mars, C Benner, M Aguirre, GR Venkataraman, M Wainberg, HM Ollila, T Kiiskinen, JP Pirruccello, J Qian, [8 others], JK Pritchard, MJ Daly, and MA Rivas. Genetics of 35 blood and urine biomarkers in the UK Biobank. *Nature Genetics*, 53(2):185–194, 2021.

[145] S Catania, PA Dumesic, H Pimentel, A Nasif, CI Stoddard, JE Burke, JK Diedrich, S Cook, T Shea, E Geinger, Lintner R, Yates JR 3rd, Hajkova P, GJ Narlikar, CA Cuomo, JK Pritchard, and HD. Madhani. Evolutionary persistence of DNA methylation for millions of years after ancient loss of a de novo methyltransferase. *Cell*, 2020.

[144] H Mostafavi, A Harpak, I Agarwal, D Conley, JK Pritchard, and M Przeworski. Variable prediction accuracy of polygenic scores within an ancestry group. *Elife*, 9:e48376, 2020.

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[141] D Calderon, MLT Nguyen, A Mezger, A Kathiria, F Müller, V Nguyen, N Lescano, B Wu, J Trombetta, JV Ribado, DA Knowles, Z Gao, F Blaeschke, AV Parent, TD Burt, MS Anderson, LA Criswell, WJ Greenleaf, A Marson, and JK. Pritchard. Landscape of stimulation-responsive chromatin across diverse human immune cells. *Nature Genetics*, pages 1–12, 2019.

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