Updated 010/15/2023

BARAK A. COHEN, PhD

1. Personal Information

Gender:	Male
Date of birth:	11/28/1970
Place of birth:	Israel

2. Citizenship: USA

3. Address and Telephone Numbers

Office: Department of Genetics, Box 8510
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University City, MO 63130
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4. Present position

2014-Present	Professor of Genetics, Washington University School of Medicine,
2014-Present	Alvin J. Goldfarb Distinguished Professor of Computational Biology

5. Education

Undergraduate	1992	B.S.	Cornell University
Graduate	1998	Ph.D.	Harvard University
Postdoctoral	1998 – 2001		Harvard University

6. Academic Positions/Employment

2002-2008	Assistant Professor of Genetics, Washington University School of Medicine
2009-2013	Associate Professor of Genetics, Washington University School of Medicine
2014- present	Professor of Genetics, Washington University School of Medicine

7. Clinical Title and Responsibilities: None.

8. Teaching Title and Responsibilities:

2003-2011	Bio5488, Introduction to Genomics, Course Master (developed this course and its computer lab from scratch)
2010-2017	Bio5496, Computational Biology Journal Club, Co-course master
2008-2010	Bio5924, Molecular Basis of Heredity, Lecturer
2002-2003	Bio5495, Computational Molecular Biology, Lecturer

2002-2004	Bio548, Nucleic Acids and Protein Biosynthesis, Discussion Section Leader

9. University, School of Medicine, Hospital Appointments, and Committees:

2024	Faculty Search Committee, Department of Genetics
2024	Faculty Search Committee, Department of Biology
2023	Chair, Faculty Search Committee, Department of Genetics
2022 – present	Co-director, High-Performance Computing Facility
2017 – 2023	Medical Scientist Training Program (MSTP) Admissions Committee
2012	Faculty Search Committee, Department of Genetics
2012 - 2017	New Investigator Internal Competitions Award Committee
2010	Faculty Search Committee, Department of Genetics
2009 - 2016	Director, Computational and Systems Biology Graduate Program
2008 - 2009	Organizing Committee, Tetra-Departmental Seminar Series
2008 – present	Steering Committee, Computational and Systems Biology Graduate Program
2006	Faculty Search Committee, Department of Genetics
2006	Faculty Search Committee, Department of Energy, Environmental, and Chemical Engineering
2006 – present	Director, Genome Analysis Training Program (GATP) T32 Training Grant
2002-present	Thesis Advisory Committees, (15 present, >40 total)
2002-present	Qualifying Exam Committees, (>40 total)

10. Medical Licensure and Board Certification: None.

11. Military Service: None.

12. Honors and Awards:

1991	Howard Hughes Scholar Undergraduate Research Fellow
1994-1996	Ryan Fellow, Harvard University
1998-2000	American Cancer Society, Postdoctoral Fellowship
2006	Recognition for Outstanding Mentorship, Washington University Graduate School of Arts and Sciences
2006	American Cancer Society Hope Award
2011	Recognition for Outstanding Mentorship, Washington University Graduate School of Arts and Sciences
2012	Named Alvin J. Goldfarb Distinguished Professor of Computational Biology
2013	Recognition for Outstanding Mentorship, Washington University Graduate School of Arts and Sciences

13. Editorial Responsibilities:

2019-present	Editorial Board, *Cell Systems Biology*
2011-present	Editorial Board, *G3, Genes, Genomes, and Genetics*
2007-2019	Editorial Board, *Genome Research*
ad hoc editor	*PLoS Genetics, ELife*

14. National Panels, Committees, Boards:

2026	Maximizing Investigators' Research Award (MIRA), NIH Study Section (ZRG1 MGG-F)

2025	Maximizing Investigators' Research Award (MIRA), NIH Study Section (ZRG1 MGG-D)
2024	Director's Transformative Research Awards, NIH Study Section (ZRG1 MGG-P)
2021-2023	Chairman: Genomics, Computation, and Technology (GCAT) NIH Study Section
2018 - 2021	Standing Member, Genomics, Computation, and Technology (GCAT) NIH Study Section
2019 - Present	Standing Member, Israel Cancer Research Foundation Review Panel
2021	NHGRI Functional Characterization Review Panel
2014, 2015	Genomics, Computation, and Technology NIH Study Section, *ad hoc* member
2008-2010	NSF Review Panels on Eukaryotic Genetics
2008-2009	Genes, Genetics, and Genomics NIH Study Section, *ad hoc* member
2008	Genetic Mechanisms of Cancer Peer Review Group, American Cancer Society

15. Community Service Contributions

Committees and Activities

2015-2018	Meeting Organizer, Cold Spring Harbor Laboratory Conference on Systems Biology
2016	External Academic Reviewer, Center for Genetics and Molecular Medicine, Wayne State University, Detroit, MI, USA
2017	External Academic Reviewer, Human Genetics Unit of the Medical Research Council, Edinburgh, UK
2018-present	External Advisory Board, Center for Genetics and Molecular Medicine, Wayne State University, Detroit, MI, USA
2023	External Academic Reviewer, Center for Genetics and Molecular Medicine, Wayne State University, Detroit, MI, USA
2008	External Advisory Board, Institute for Systems Biology, Seattle, WA, USA

Professional Societies and Organizations

2002-present	Genetics Society of America
2016-present	American Society for Human Genetics

Media Activities

2015	Interviewed for "Hold That Thought" podcast
2017	Interviewed for "The Naked Scientist" podcast

16. Invited Professorships and Lectureships:

2002 Wayne State University, Detroit, MI
2003 Cambridge University, Cambridge, UK
2003 Department of Biostatistics, WUSM
2004 Cold Spring Harbor Banbury Center, Func. Elements of the Genome
2004 Department of Molecular Biology and Pharmacology, WUSM
2006 Department of Microbiology, WUSM

2007 University of Missouri, Kansas City, MO
2007 Cold Spring Harbor Systems Biology Meeting
2007 Cold Spring Harbor Biology of Genomes Meeting
2007 Columbia University, New York, NY
2007 Welcome Trust Func. Genomics and Sys. Biol. Meeting, Hinxton, UK
2007 Biophysical Evenings, WUSM
2008 Harvard Medical School, Boston, MA
2008 Monsanto Corporation, St. Louis, MO
2008 Institute for Systems Biology, Seattle, WA
2009 University of Washington, Seattle, WA
2009 University of Chicago, Chicago, Il
2009 NHGRI Genomics of Gene Regulation Workshop, Washington, D.C.
2009 University of California at Berkeley, Berkeley, CA
2009 University of Colorado at Denver, Denver, CO
2010 NHGRI Planning the Future of Genomics: Foundational Research and Applications in Genomic Medicine, Warrenton, VA
2010 Cold Spring Harbor Biology of Genomes Meeting
2010 New York University, New York, NY
2010 Princeton University, Princeton, NJ
2010 University of Chicago, Chicago, Il
2010 Johns Hopkins University, Baltimore, MD
2011 University of Colorado, Denver, CO
2011 Keystone Symposium on Quantitative Genetics, Galveston, TX
2011 Cold Spring Harbor Biology of Genomes Meeting
2011 Stanford University, Palo Alto, CA
2012 Cold Spring Harbor Systems Biology Meeting
2012 Cold Spring Harbor Biology of Genomes Meeting
2012 NHGRI Planning Meeting: Integrating Functional Data for Connecting Genotype to Phenotype, Bethesda, MD
2012 Hudson Alpha Institute for Biotechnology, Huntsville, AB
2012 Harvard Medical School, Boston, MA
2012 University of Southern California (USC), Los Angeles, CA
2013 University of Iowa, Cedar Rapids, IA
2013 Invited Speaker, ASBMB Meeting on Core Processes in Transcription, Chicago,
2013 University of Geneva, Switzerland
2013 Weizmann Institute of Science, Israel
2014 University of Toronto, Canada
2014 Platform Talk, Cold Spring Harbor Biology of Genomes Meeting
2014 North Carolina State University, Raleigh, NC
2014 Boston University, Boston, MA
2014 University of California San Francisco (UCSF), San Francisco, CA
2015 University of Lausanne, Switzerland
2015 Invited Speaker, BIRS Workshop on Protein-DNA Recognition, Oaxaca, Mexico
2015 Duke University, Durham, NC
2015 Invited Speaker, ASBMB Meeting on Core Processes in Transcription, St. Louis, MO
2015 Invited Speaker, Radcliffe Institute for Advanced Studies, “Gene Expression by the Numbers”, Boston, MA
2015 Stowers Institute, Kansas City, MO
2015 Donald Danforth Plant Sciences Center, St. Louis, MO
2016 Invited speaker, CHARGE Consortium Meeting, Houston, TX

2016 University of Southern California (USC), Los Angeles, CA
2016 Invited speaker, Keystone Symposium, Understanding the function of human genetic variation, Uppsala, Sweden
2016 Invited speaker, Genetics Society Meeting: Functional genetic variation in the non-coding genome. The Royal Society, London, UK
2016 Invited Speaker, The 15th International Conference on Bioinformatics, Singapore
2016 University of Michigan, Ann Arbor, MI
2017 University of California Los Angeles (UCLA), Los Angeles, CA
2017 University of Minnesota, Minneapolis, MN
2018 Department of Ophthalmology, Washington University, St. Louis, MO
2018 ICTS Symposium on Translational Medicine, Washington University, St. Louis, MO
2018 Cold Spring Harbor Lab Systems Biology Meeting: Global Analysis of Gene Expression, Platform Talk
2018 Invited Speaker, BIRS Workshop on Protein-DNA Recognition, Oaxaca, Mexico
2018 Invited Speaker, Cold Spring Harbor Asia, Systems Biology of Gene Regulation, Suzhou, China
2018 Institute for Molecular Pathology, Vienna, Austria
2018 Invited Speaker, EMBL Conference, From Functional Genomics to Systems Biology, Heidelberg, Germany
2019 Invited Speaker, Single Cell and Massively Parallel Approaches Meeting, McGill University's Bellairs Research Station, Barbados
2019 University of Massachusetts, Worcester, MA
2020 KU Leuven, Belgium
2021 University of Texas, Galveston, TX
2022 Cold Spring Harbor Lab Systems Biology Meeting: Global Analysis of Gene Expression, Platform Talk
2022 University of California, San Diego, CA
2022 University of Toronto, Toronto, Ontario, Canada
2023 Single-Cell Network Netherlands, Netherlands
2023 Gordon Research Conference: Human Genetics and Genomics, Invited Talk, Waterville Valley, NH
2023 University of Washington, Seattle, WA
2023 Harvard University/Mass General Hospital, Boston, MA
2024 New York University, Langone, New York, NY
2024 Invited Speaker, International Union of Pure and Applied Biophysics Annual Conference, Kyoto, Japan
2024 Invited Speaker, Building to Understand: The Constructionist Approach to Studying Gene Regulation, Company of Biologists Workshop, Buxted Park, UK
2024 University of Wisconsin, Madison, WI
2024 Bayer Inc, Chesterfield, MO
2025 University of Washington, Seattle, WA
2025 Cold Spring Harbor Laboratory Mechanisms of Eukaryotic Transcription Meeting, Platform Talk
2025 University of California, San Francisco, CA
2026 University of California, Berkeley, CA

17. Consulting Relationships and Board Memberships

2011 Fidelity Biosciences
2021- 2024 Patch Biosciences

18. Research Support

Active

09/01/26-04/30/27 NIH , R35GM161206 (Cohen)
Analysis of combinatorial cis-regulation in synthetic and genomic promoters
The main goal of this grant is to understand how combinations of transcription factor binding sites control cell-type-specific gene expression.
Role: PI

08/01/23-07/31/27 NIH , R01HG014139 (Cohen)
High-throughput interrogation of long-range enhancers
The primary goal of this proposal is to introduce a high-throughput reporter gene system for studying the sequence features of long-range enhancers.
Role: PI

09/01/26-05/30/2030 NIH, R01HL181047 (Siggers/Munshi)
Decoding regulatory variants in cardiovascular disease
Major Goals: Aim 1: To characterize the biophysical mechanism of heart disease-associated non-coding variants. Aim 2: To characterize the impact of heart disease-associated non-coding variants on gene expression. Aim 3: To characterize the biological effect of heart disease-associated elements and non-coding variants.
Role: Co-Investigator

07/01/22-06/30/2027 NIH, R01MH126933 (Turner)
Noncoding mutations in neurodevelopmental disorders
Major Goals: This major goal of this project is to provide integral work to the genetic understanding of NDDs and the consequences of noncoding variation. It will also provide key insights into their role in the overall genetic architecture of NDDs.
Role: Co-Investigator

06/19/2024-01/31/2029 NIH, R01MH116999 (Dougherty)
Highly parallel analysis of 5' and 3' UTR variants in Autism Spectrum Disorders
Major Goals: We propose to detect and analyze new NDD mutations by bringing to bear a unique set of tools specifically designed to study translational regulation by UTRs, extending the utility of ongoing efforts to sequence the genomes of tens of thousands of NDD cases across the US and the world.
Role: Co-Investigator

PENDING

04/01/2027-03/30/2032 NIH, R01HD121704 (White, Baldrdge)
Normal and Pathogenic GLI-Dependent cis- Regulatory Responses to Sonic Hedgehog
Major Goals: Sonic Hedgehog (Shh) signaling is critical throughout development. The response to Shh signal is governed by three related regulatory genes, GLI1, GLI2, and GLI3, and variants in these genes cause a range of congenital malformation syndromes. We propose to decipher the logic that underlies the regulatory responses of wild-type GLI genes and their pathogenic variants.
Role: Co-PI

07/01/2026-06/30/2030 NIH, R01HG014829 (White, Baldridge)
A scalable system for relating transcription factor occupancy states to gene regulation
Major Goals: The major goal is to develop a scalable system for relating transcription factor occupancy states to gene regulation.
Role: PI

COMPLETED

02/16/22-01/31/26 NIH , R01HG012304 (Cohen)
High-throughput analysis of the effects of gene promoters and chromosomal environments on single-cell gene expression
The aim of this proposal is to develop a technology that allows us to understand the properties of the genome that control single-cell variability of mRNA expression
Role: PI

05/01/21-02/28/25 NIH , R01GM140711 (Cohen)
Molecular properties of transcription factors that control cell-to-cell variability in gene expression
The major goal of this proposal is to quantify and model how different chromosomal locations and transcription factors influence patterns of cell-to-cell variation in gene expression
Role: PI

7/1/2017-6/30/2023 NIH, R01GM121755 (White)
Discovery of DNA Determinants of Transcription Factor Binding and Function in PHO
The aim of this proposal is to understand the DNA sequence properties that define a functional CRX binding site in photoreceptors.
Role: Co-Investigator

09/01/18-08/31/23 NIH, R01HG007175 (Wang)
Decoding the impact of transposable elements on gene regulation
Major Goals: This project develops the computational and experimental infrastructure to investigate the contribution of transposable elements on the evolution of mammalian regulatory networks.
Role: Co-Investigator

09/01/21-08/31/23 NIH, R21HG012146 (Cohen)
Cell-based assays for Deep Mutational Scans of Transcription Factors
The major goal of this proposal is to improve the functionality and reliability of DMS by improving its methodologies and expanding the range of appropriate cell types
Role: PI

08/01/19-07/31/23 NIH , R01GM092910 (Cohen)
Analysis of combinatorial cis-regulation in synthetic and genomic promoters
The main goal of this grant is to understand how the cell integrates information from cis-regulatory elements and their surrounding chromatin environments to control average levels of gene expression.
Role: PI

2/1/2017-1/31/2023 NIH, 5U01HG009391-02 (Wang, Cohen, Feschotte)
Connecting transposable elements and regulatory innovation using ENCODE data

The goal of this project is to develop and apply computational and systems biology methods specifically for analyzing transposable elements as a source of regulatory sequences using ENCODE data.
Role: Multi PD/PI

07/01/18-06/30/23 NIH, 1R01MH116999-01 (Dougherty)
Highly parallel analysis of 5' and 3' UTR variants in Autism Spectrum Disorders
The aim of this proposal is to use a massively parallel reporter assay to measure the effects of genetic variation in the 3' UTRs of genes involved in Autism Spectrum Disorders. We propose to measure the effects of these variants in human primary neural cells and in specific cell types in mouse brains.
Role: Co-Investigator

04/01/17-03/31/21 NIH , 5R01EY027784-02 (Cohen, Chen)
Cis-regulatory mechanisms underlying retinopathy
The aim of this proposal is to understand how different mutations in the Crx transcription factors impact gene expression in models of retinopathy.
Role: Multi PI, Contact PI

07/01/18-06/30/21 CDI-LI-2018-765 (Baldridge, Cohen)
Children's Discovery Institute
High-Throughput, Large-Scale Functional Genomics of Genetic Variation in Pediatric Cancer
The aim of this proposal is to develop a high-throughput framework for assessing the impact of specific genetic variants in two pediatric cancer genes, *TP53* and *SMAD4*. We propose to perform Deep Mutational Scanning on these two genes using massively parallel reporter genes to measure the impact of all possible mutations in the coding regions of these two genes. We propose a battery of different functional assays to measure the effects of mutations in these on different cellular functions. Finally, we propose to use the results of these assays to build a computational classifier that will distinguish benign from pathogenic genetic variants in these two genes.
Role: Co-PI

08/01/18-07/31/21 SAFRI Simons Foundation (Dougherty)
4/4 SSC-ASC Whole Genome Sequencing Consortium: UTR Mutation Analysis
The primary goal of the pipeline is to identify de novo mutations in UTRs that result in functional haplo insufficiency in the brain and likely cause ASD.
Role: Co-Investigator

01/01/2011-05/31/2019 NIH, 5R01GM092910-08 (Cohen)
Analysis of combinatorial cis-regulation in synthetic and genomic promoters
The aim of this proposal is to understand how combinations of transcription factor binding sites specify specific patterns of gene expression in mammalian cells.
Role: Principal Investigator

08/17/15 - 06/30/2018 NIH, 5 R01 HG008687-02 (Cohen)
Massively parallel characterization of cis-regulatory elements in the brain.
The aim of this proposal is to develop a novel high-throughput technology for assaying the *in vivo* activity of *cis*-regulatory elements.
Role: Principal Investigator

04/24/12-02/29/16 NIH, R01 HG006790 (Cohen)

M*assively parallel cis-regulatory element analysis in mammalian cells*
Role: Principal Investigator (along with Joe Corbo as the other PI)
The aims of this project are 1) to develop a massively parallel technology for evaluating the regulatory potential of ChIP-seq peaks, and 2) to map human *cis*-regulatory polymorphisms onto changes in gene expression in a genome-wide fashion.
Role: Principal Investigator

03/01/2011 – 02/28/2015 NIH, R01 RGM092910A (Cohen)
Title: Analysis of combinatorial *cis*-regulation in synthetic and genomic promoters.
The aims of this proposal are 1) To understand the role that differences in promoter occupancy by TFs play in generating differences in gene expression in yeast, and 2) To understand the effects of basal promoter strength, chromosomal position, and chromatin modifications on the combinatorial interactions among TFBS in yeast.
Role: Principal Investigator

04/01/2012– 03/31/2015 NIH, R01 HG006790-01 (Cohen and Corbo (PIs)
Title: Massively parallel *cis*-regulatory analysis in mammalian cells
The aim of this proposal is to develop a technology for assaying thousands of *cis*-regulatory variants in mammalian cells.
Role: Principal Investigator

06/01/2012-05/30/2016 NSF, (MCB-0948512) Barolo (PI)
Title: Interpreting Hedgehog Signaling Gradients With Cis-Regulatory DNA: A Quantitative In Vivo/Computational Approach
The aim of this project is to understand the cis-regulatory logic underlying the response of Gli transcription factors to gradients of the Hedgehog morphogen. In particular we aim to quantify and model the effects of binding site affinity, and cooperativity between Gli monomers on interpreting positional information within Hedgehog gradients
Role: Co-Investigator

03/01/2010-02/28/2014 NSF, (MCB-0948512) Cohen (PI)
Title: Genetic and Genomic Analysis of Natural Variation in Yeast.
The aims of this project are to 1) Identify naturally occurring polymorphisms that directly contribute to differences in sporulation efficiency between wild isolates of yeast, and 2) Determine whether changes in gene expression are responsible for differences in sporulation efficiency between wild isolates of yeast.
Role: Principal Investigator

03/01/2011 – 02/28/2013 NIH,(R21 HG006346-01) Cohen and Corbo (PIs)
Title: Analysis of combinatorial *cis*-regulation in synthetic and genomic promoters.
The aims of this proposal are 1) To understand the functional architecture of the *Rho* proximal promoter at single nucleotide resolution, and 2) To elucidate the *cis*-regulatory grammar of photoreceptor gene expression.
Role: Co-Investigator

05/01/2007-04/30/2011 NIH, (R01 GM078222-01A1) Stormo (PI)
Title: Deciphering the regulatory code of a cell.
Responsible for Aim 4 (of four Aims). The aim of this project is to identify the specific DNA binding sites for all yeast transcription factors. The responsibility of the Cohen Lab is to model the interactions between transcription factor binding sites that regulate glucose metabolism.
Role: Co-Investigator

09/15/2006-08/31/2010 NSF, (MCB-0543156) Cohen (PI)
Title: Genetic and Genomic Analysis of Natural Variation in Yeast.
The aims of this project are to 1) Identify naturally occurring polymorphisms that directly contribute to differences in sporulation efficiency between wild isolates of yeast, and 2) Determine whether changes in gene expression are responsible for differences in sporulation efficiency between wild isolates of yeast.
Role: Principal Investigator

01/2006 –12/2006 Washington University Sequencing Center Pilot and Feasibility Study Cohen (PI)
Title: High Throughput SNP Discovery.
The aim of this project was to develop methodologies for using "Next Generation" sequencing technologies for SNP discovery.
Role: Principal Investigator

01/01/2006 –12/31/2009 American Cancer Society Research Scholar Grant (RSG-06-039-01-GMC) Cohen (PI)
Title: Cell Cycle Networks in Yeast.
The aims of this project were to 1) identify all single gene disruptions that have quantitative effects on cell cycle progression, and 2) identify the *cis*-regulatory sites and downstream targets of transcription factors that affect cell cycle progression.
Role: Principal Investigator

02/01/2008-01/31/2010 Children's Discovery Institute (MD-II-2008-2) Cohen (PI)
Title: Genetic analysis of human variation in B-cell activation.
Role: PI
The aims of this project were to 1) map the genetic basis of differences in the expression of cell surface molecules involved in B-cell activation, and 2) map the genetic basis of the efficiency of signaling pathways involved in B-cell activation.

19. **Trainee/ Mentee/Sponsorship Record**

Previous Fellows/Trainees:

Justin Gerke, PhD	predoctoral	Group Leader, Computational Biology Corteva, Des Moines, IA
Christina Chen, PhD	predoctoral	Senior Scientist, Fred Hutchinson Cancer Research Center, Seattle, WA
Jay Gertz, PhD	predoctoral	Associate Professor, University of Utah, Salt Lake City, UT
Josh Witten, PhD	predoctoral	Consultant, Finch & Pea Group,LTD Hartsville, SC
Robert Zeigler, PhD	predoctoral	Scientist, Assuregen, Austin, TX
Jamie Kwasnieski, PhD	predoctoral	Dyno Therapeutics, Boston, MA
Marc Sherman, MD/PhD	predoctoral	Instructor, Dept of Gastroenterology, Mass General Hospital, Boston, MA
Ilaria Mogno, PhD	postdoctoral	Instructor, Albert Einstein

		College of Medicine, New York, NY
Kim Lorenz, PhD	predoctoral	Staff Scientist, University of Pennsylvania
Priya Sudarsanam, PhD	postdoctoral	Digital Strategy Lead, Bayer Co., St. Louis, MO
Chris Fiore, PhD	predoctoral	Scientist, Syros Pharmaceuticals, Cambridge, MA
Brett Maricque, PhD	predoctoral	Assistant Professor, Washington University, St. Louis, MO
Devi Swain, PhD	postdoctoral	Assistant Professor, Duke University, Raleigh, NC
Hemangi Chaudhari, PhD	predoctoral	Scientist, CRISPR Therapeutics, Cambridge, MA
Mike White, PhD	postdoctoral	Associate Professor, Department of Genetics, Washington University, School of Medicine
Ivy Zhang	undergraduate	Graduate Student, Cornell University Medical School New York, NY
Mary Richardson	undergraduate	Graduate Student, Systems Biology, Harvard Medical School Boston, MA
Dana King, PhD	predoctoral	Bioinformatics Support Specialist, University of Michigan Bioinformatics Core, Ann Arbor, MI
Ellie Degen	undergraduate	Graduate Student, Northwestern University, Chicago, Il
Max Staller, PhD	postdoctoral	Assistant Professor, University of California, Berkeley
Jeff Hansen, PhD	predoctoral	MSTP fellow, Washington University in St. Louis, School of Medicine
Siqi Zhao, PhD	predoctoral	Scientist, Gingko Bioworks, Boston, MA
Dustin Baldridge, MD/PhD	postdoctoral	Assistant Professor, Department of Pediatrics, Washington University in St. Louis, School of Medicine
Clarice Hong, PhD	predoctoral	Postdoctoral Fellow, MIT, Boston, MA
Kai Loell	predoctoral	Postdoctoral Fellow, Cold Spring Harbor Lab, NY
Ryan Friedman	predoctoral	Postdoctoral Fellow, University of Washington, Seattle, WA
Avinash Ramu	predoctoral	Verily Life Sciences, San Francisco, CA
Sara Lichtarge	undergraduate	Pfizer, San Diego, CA
James Shepherdson	predoctoral	MD/PhD training, Washington University in St. Louis

Current Fellows/Trainees

Xilin Hou	predoctoral
Yawei Wu	predoctoral
Emma Bartley-Dier	predoctoral
Yuning Zhang	postdoctoral
Zara Shariff	undergraduate
Nikita Gupta	predoctoral
Yuelai Wang	predoctoral

20. Patents Granted/Applied For:

2010: Invention Disclosure Form filed with OTM for “Multiplex Analysis of Promoters.”
2021: US patent “A Method to Perform Single-Cell Massively Parallel Reporter Gene Assays

21. Bibliography:

Preprints:

1. Wu, Y., Li, J., Bartley-Dier, E.L., Pitts, C. and **Cohen, B.A.** (2025) Long-range massively parallel reporter assay reveals rules of distal enhancer-promoter interactions (bioRxiv 10.1101/2025.04.21.649048)

Peer reviewed manuscripts:

1. Swanson, E.G., Mao, Y., Mallory, B.J., Vollger, M.R., Ranchallis, J., Bohaczuk, S.C., Lyon, D.B., Oliveira, C.B., Parmalee, N.L., **Cohen, B.A**., Bennett, J.T., and Stergachis, A.B (2025) Comprehensive single-cell diploid chromatin fiber architectures using DAF-seq. *Nature Biotechnol. doi:10.1038/s41587-025-02914-3*
2. Friedman R.Z., Ramu A., Lichtarge S., Wu Y., Tripp L., Lyon D., Myers, C.A., Granas, D.M., Gause, M., Corbo, J.C., **Cohen, B.A.,** and White, M.A. (2025) Active learning of enhancers and silencers in the developing neural retina. *Cell Syst* 2025:101163.
3. Shepherdson, J.L., Granas D.M., Li J., Shariff, Z., Plassmeyer, S.P., Holehouse, A.S., White, M.A. and **Cohen, B.A.** (2024) Mutational scanning of CRX classifies clinical variants and reveals biochemical properties of the transcriptional effector domain. *Genome Res*. doi:10.1101/gr.279415.124
4. Shepherdson, J.L, Friedman, R.Z, Zheng Y., Sun, C., Oh, I.Y., Granas, D.M., **Cohen, B.A.**, Chen S, White MA. (2024) Pathogenic variants in CRX have distinct cis-regulatory effects on enhancers and silencers in photoreceptors. *Genome Res* 34:243-255.
5. Loell, K.J., Friedman, R.Z., Myers, C.A., Corbo, J.C., **Cohen, B.A.** and White, M.A. (2024) Transcription factor interactions explain the context-dependent activity of CRX binding sites. *PLoS Comput Biol* 16;20(1):e1011802
6. Hong, C.K.Y., Erickson, A., Li, J., Federico, A.J., and **Cohen, B.A.** (2024) Massively parallel characterization of insulator function across the genome. *Nat Commun* 27:8350.

7. Hong, C.K.Y., Ramu, A., Zhao, S., and **Cohen, B.A.** (2024) A method to measure the impact of genomic and cellular environments on gene expression noise. *Genome Biol* 25:137.
8. Zhao, S., Hong, C.K.Y., Granas, D. and **Cohen, B.A.** (2023) A single-cell massively parallel reporter assay detects cell type specific cis-regulatory activity. *Nat. Genet.,* 55:346–354
9. Rockweiler, N., Ramu, A., Nagrinaja, L., Wong, W.H., Noordam, M., Drubin, C., Huang, N., Miller, B., Todres, E., Vigh-Conrad, K., Zito, A, Small, K., Ardlie, K., **Cohen, B.A.,** Conrad, D. (2023) The origins and functional effects of postzygotic mutations throughout the human lifespan. *Science.* 380, eabn7113.
10. Ramu, A. and **Cohen, B.A.** (2023) Transcription factor fluctuations underlie cell-to-cell variability in the Hedgehog response. *Genetics,* 224, iyad094.
11. Lagunas Jr., T, Plassmeyer, S.P., Friedman, R.Z., Rieger, M.A., Fischer, A.D., Aguilar Lucero, A.F., An, J.-Y., Sanders, S.J., **Cohen, B.A.,** and Dougherty, J.D. (2023) A Cre-dependent massively parallel reporter assay allows for cell-type specific assessment of the functional effects of genetic variants *in vivo*. *Communications Biology* 6:1151.
12. Hansen, J. L. and **Cohen, B.A.** (2022) A quantitative metric of pioneer activity reveals that HNF4A has stronger in vivo pioneer activity than FOXA1. *Genome Biol.,* 23:221
13. Loell, K.J., Wu, Y., Staller, M. V., and **Cohen, B.A.** (2022) Activation domains can decouple the mean and noise of gene expression. *Cell Reports,* 40, 111118
14. Hansen, J.L., Loell, K.J., **Cohen, B.A.** (2022). The pioneer factor hypothesis is not necessary to explain ectopic liver gene activation. *Elife* 11, e73358.
15. Hong, C.K.Y. and **Cohen, B.A**. (2022) Genomic environments scale the activities of diverse core promoters. *Genome Res*. 32:85-96.
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