The Faculty of Medicine of Harvard University
Curriculum Vitae

Date Prepared:	March 27, 2023
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Education:

09/1999-06/2003	B.S. Highest Honors	Physics	Nanjing University
09/2003-05/2005	M.A.	Physics	Johns Hopkins University
09/2005-03/2012	Ph.D.	Biomedical Engineering (Advisor: Dr. Joel Bader)	Johns Hopkins School of Medicine

Postdoctoral Training:

04/12-01/17	Research Fellow	Analytic and Translational Genetics Unit (Advisor: Dr. Mark Daly)	Massachusetts General Hospital/Harvard Medical School

Faculty Academic Appointments:

2017-2020	Instructor	Department of Medicine	Harvard Medical School
2020-	Assistant Professor	Department of Medicine	Harvard Medical School

2022-	Faculty	Bioinformatics and Integrative Genomics	Harvard Medical School

Appointments at Hospitals/Affiliated Institutions:

2017-2019	Instructor in Investigation	Analytic and Translational Genetics Unit, Department of Medicine	Massachusetts General Hospital
2017-2019	Associated Scientist	Stanley Center for Psychiatric Research	Broad Institute of MIT and Harvard
2019-2023	Associate Member	Stanley Center for Psychiatric Research	Broad Institute of MIT and Harvard
2019-	Assistant Investigator	Analytic and Translational Genetics Unit, Department of Medicine	Massachusetts General Hospital
2023-	Institute Member	Stanley Center for Psychiatric Research	Broad Institute of MIT and Harvard

Faculty Membership in Harvard Initiatives, Programs, Centers, and Institutes:

2020-	Faculty	Program in Quantitative Genomics	Harvard T.H. Chan School of Public Health

Other Professional Positions:

2011	Intern	Healthcare Informatics, IBM Research
2017	Intern	Systems Toxicology, Merck & Co., Inc.

Major Administrative Leadership Positions:

Local

2017-	Director, Stanley Global Asia Initiatives	Broad Institute of MIT and Harvard

International

2018-	Co-chair, Cross-Population Workgroup	Psychiatric Genomics Consortium

Committee Service:

Local

2019-	Steering Committee	Medical and Population Genetics, Broad Institute of MIT and Harvard
2020-	Seminar Series Co-organizers	Program in Quantitative Genomics, Harvard T.H. Chan School of Public Health
2021-	Faculty Advancement Executive Committee	Department of Medicine, Massachusetts General Hospital

International

2018, 2022	Program Committee	Pan-Asia Symposium on the Genetics of Brain Disorders

Professional Societies:

2010-	American Society of Human Genetics (ASHG)	
	2010-	Member
	2017-2018	Abstract Reviewer, ASHG Annual Meeting
	2022-2024	Program Committee, ASHG Annual Meeting
2017-	International Society of Psychiatric Genetics	
	2017-	Member
	2020-2024	Board of Directors

Grant Review Activities:

2017	Fellows Award	The MQ Foundation
2021, 2022	Research Grant	Medical Research Council, United Kingdom
2021	NIH Director's New Innovator Award Program (DP2)	National Institute of Health (NIH) Stage I (mail-in) reviewer

Editorial Activities:

Ad hoc Reviewer

Bioinformatics
Biological Psychiatry
Cancer Informatics
Cancer Medicine
Clinical Epigenetics
Genetics
Hereditas
Human Molecular Genetics
Inflammatory Bowel Diseases
JAMA Psychiatry
Journal of Cardiovascular Disease Research
Journal of Medical Genetics
Nature Genetics
Neuropsychopharmacology
Nucleic Acid Research
Pacific Symposium on Biocomputing 2013
PLoS Computational Biology
PLoS Genetics
PLoS ONE
PMC Genetics
Proceedings of the National Academy of Sciences
The British Journal of Psychiatry
The Pharmacogenomics Journal
Translational Psychiatry
Science Advances
Molecular Psychiatry

Other Editorial Roles

2020-	Editor	Journal of Genetics and Genomics

Honors and Prizes:

2003	National Challenge Cup award/3rd place	Ministry of Education, China
2006	Travel award	Center for Discrete Mathematics and Theoretical Computer Science (DIMACS) Workshop
2006	Travel award	Research in Computational Molecular Biology (RECOMB) Satellite Conference on Systems Biology
2012	Award for Outstanding Self-financed Students Abroad	China Scholarship Council
2013	Bristol-Myers Squibb Scholar-in-Training Award	The American Association for Cancer Research
2013	Magna Cum Laude	International Society for Magnetic Resonance in Medicine
2015	Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist	American Society of Human Genetics
2017	Harvard Chinese Life Sciences Yongjin Distinguished Research Award	Harvard Medical School Chinese Scientists and Scholars Association
2023	Celebration of Science Recognition Award	Massachusetts General Hospital

Report of Funded and Unfunded Projects

Past

2016-2021	2/7 Psychiatric Genomics Consortium: Finding Actionable Variation-Supplement NIH/NIMH; U01MH109539 Sub-Contract PI ($148,700) We propose a supplement to the parent award to support an effort to compile a sample of over 30,000 schizophrenia patients and similar number of matched controls of East Asian ancestry. We will leverage this sample to identify novel genetic loci associated with schizophrenia in the East Asian ancestry and across the world, to evaluate the transferability of the polygenic risk score, and to elucidate the contribution of the major histocompatibility complex locus to schizophrenia. Findings from this supplement will provide additional insights into the schizophrenia genetic architecture, especially in its genetic epidemiology across the word populations. This supplement will be a critical enhancement to the existing PGC efforts and the parent award.
2017-2022	Genetics and gene regulation in the inflammatory bowel diseases NIH/NIDDK; K01DK114379 PI ($579,292) Inflammatory bowel diseases (IBD) are a group of inheritable, chronic disorders of the gastrointestinal tract affecting more than 1.4 million people in the U.S. with a direct healthcare cost of $6.3 billion/year. Many causal variants for IBD are non-coding with no well-characterized functions. This proposal will investigate the regulatory functions of these non-coding causal variants and provide insights into how they contribute to the IBD disease etiology.
2018-2020	Mitochondrial-Nuclear Genetic Interactions in Spontaneous HCV Clearance NIH/NIAID; R21AI139012 Co-Investigator (PI: Hulgan, Todd) The goal of this project is to investigate the connection between mitochondrial genetic factors and the spontaneous HCV clearance
2020-2020	Finding rare protective variants for the inflammatory bowel diseases using polygenic signatures in large population controls NIH/NIDDK; Center for the study of IBD (MGH) -- Pilot/Feasibility Study, P30DK043351 PI ($50,000) The goal of this project is to develop and implement a novel test using population controls and known genetic risk profiles to identify rare protective variants for IBD.

2020-2022 Contribution of major histocompatibility complex locus to schizophrenia in the East Asian populations
Brain & Behavior Research Foundation; 28450
PI ($70,000)
The goal of this project is to investigate the contribution of major histocompatibility complex to schizophrenia in the East Asian populations.

2020-2022 2nd Pan-Asian Symposium on the Genetics of Brain Disorders
Biogen Inc.; Industry funding: conference development
PI ($10,000)
Support for the 2nd Pan-Asia Symposium on the Genetics of Brain Disorders, jointly organized by Stanley Center for Psychiatric Research and National University of Singapore in 2022 (postponed from 2020).

2021-2022 Genetics and gene regulation in the inflammatory bowel diseases.
NIH/NIDDK; K01DK114379-04S1
PI ($49,005)
This supplement employs exome-sequencing analyses to identify genes underlying IBD for insights into the disease pathogenesis.

Current

2018- Philanthropic Gift
Zhengxu & Ying He Foundation; Philanthropic Gift
PI ($261,363)
This grant supported my psychiatric genetics studies in East Asia.

2018- Stanley Global Asia Initiatives
Stanley Medical Research Institute, The Broad Institute of MIT and Harvard; Institutional Grant
PI ($5,378,636)
This grant supports me to supervise a collaboration with colleagues in East Asia to recruit study participants, generate genetics data and perform analysis to pinpoint genetic factors underlying psychiatric disorders in the East Asian populations. The funding pays multiple subawards to our collaborators to cover the patient recruitment expenses, the salary of two project managers under my supervision to manage the recruitment, a capacity building program for trainees from the collaborators' laboratory, and project related travels.

2019- Startup
Stanley Medical Research Institute, The Broad Institute of MIT and Harvard; NA

PI ($340,000)
Startup provided by the Broad Institute, including sundry and salary to cover my efforts and salary gap.

2020-2026 2/7 Psychiatric Genomics Consortium: Advancing Discovery and Impac
NIH/NIMH; R01MH124851
Co-Investigator (PI: Neale, Benjamin)
Now in its 13th year, the Psychiatric Genomics Consortium is perhaps the most innovative and productive experiment in the history of psychiatry. We propose to expand the work of the PGC so we can learn key lessons about the fundamental basis of major psychiatric disorders.

2020-2025 Identifying mechanism-focused targets for therapeutic development
GlaxoSmithKline; Industry Grant
Co-Investigator (PI: Xavier, Ramnik)
Here, we propose to leverage leads from human genetics to identify mechanism-focused targets for therapeutic development. Specifically, we will focus on (1) Protective variants and mechanisms in autoimmune disease, and (2) Disease pathways implicated by genetics that are underexploited by therapeutics.

2020-2025 Identifying mechanism-focused targets for therapeutic development
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Co-Investigator (PI: Xavier, Ramnik)
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2021-2023 Sex Chromosome GWAS of Post-Traumatic Stress Disorder (PTSD)
NIH/NIMH; R21MH125358
Sub-Contract PI (PI: Duncan, Laramie, $118,036)
Major goals of this project include genome-wide association studies (GWAS) of the X and Y chromosomes and tests for disproportionate effects of sex chromosomes on PTSD.

2022-2027 Identification and characterization of inflammatory bowel disease causal variants
NIH/NIDDK; R01DK129364
PI ($2,889,211)
Inflammatory bowel diseases (IBD) are a group of inheritable, chronic disorders of the gastrointestinal tract affecting more than 3 million people in

the U.S. with a direct healthcare cost of $6.3 billion/year. The pathogenesis of IBD is poorly understood though genetic factors are known to strongly influence the IBD risk. This proposal will identify and functionally characterize novel putative causal genetic variants for IBD through aggregating, harmonizing and fine-mapping genomic resources at population scale, with the goal to reveal major elements in IBD pathogenesis.

2022-2027

1/4 Asian Bipolar Genetics Network (A-BIG-NET)
NIH/NIMH; R01MH130675
PI ($8,008,107)
This proposal will leverage the Asian Bipolar Genetics Network (A-BIG-NET), an international collaboration of investigators from the U.S., Taiwan, Japan, South Korea, Singapore, India and Pakistan, to carry out a genetics study of bipolar disorder in East and South Asia. It will establish a valuable genetics resource with 4x low-pass whole genome sequence and rich phenotype data that will dramatically increase the worldwide diversity of genetics data on bipolar disorder, an important step to accelerate gene discovery in this disorder and advance global mental health equity.

2022-2027

Improving Methods and Practices for Trans-Ethnic Genetic Studies
NIH/NHGRI; R01HG012354
Co-Investigator (PI: Ge, Tian)
Trans-ethnic genetic analysis can facilitate genomic discoveries and is critical for equal delivery of precision healthcare globally. However, current trans-ethnic genetic research is impeded by limited genomic resources for non-European populations and limited statistical methods that can appropriately integrate multi- ethnic genomic data. This project will address these challenges by capitalizing on the rich phenotypic and ge- nomic resources in the Taiwan Biobank, and by developing novel statistical methods that can integrate multi- ethnic multi-omic data for improved trans-ethnic fine-mapping and polygenic prediction.

2023-2026

Uncovering Crohn’s genetic risk in African-American and Hispanic/Latino populations
Helmsley Charitable Trust
Co-PI (Co-PI: Mark Daly, Ramnik Xavier and Hailiang Huang, $2,779,493)
We propose here a CD sequencing and analysis effort in the Hispanic/Latino and African Ameri- can population. We anticipate identifying and pursuing new biological insights missed by less representative genetic studies, ensuring more equitable insights from genetic research and building a computational resource for researchers to use the data.

Training Grants and Mentored Trainee Grants

2016-2017	A novel trans-ethnicity fine-mapping method for complex traits in human and animal China Scholarship Council Mentor (PI: Ruize Liu) The major goal is to design a novel fine-mapping algorithm that leverages the genetic diversity to improve the resolution to isolate the causal allele for the complex diseases and traits.
2019-2020	A study of the genetic association between schizophrenia and immune response of gluten or casein China Scholarship Council Mentor (PI: Baijia Li) The goal of this study is to elucidate the connection between genetic factors, immune response to gluten and casein and schizophrenia

Report of Local Teaching and Training

Teaching of Students in Courses:

2022	Seminar, Bioinformatics and Integrative Genomics Graduate student	Harvard Medical School 0.5 hours / year

Formal Teaching of Residents, Clinical Fellows and Research Fellows (post-docs):

2016	Statistical Genetics workshop (BroadE series) Trainees in the Harvard-MIT community	Broad Institute 1 hour / year
2017-2019	Global Initiative for Neuropsychiatric Genetics Education in Research Fellows in the program	Harvard T.H. Chan School of Public Health 2 hours / year (4 hours in 2017, 2 hours in 2018 and 2019 respectively)
2019-2021	A Practical Introduction to Statistical Genetics Residents, Clinical Fellows, and Research Fellows	Massachusetts General Hospital 3 hours / year

Research Supervisory and Training Responsibilities:

2016-2017, 2019-2020, 2021-	1:1 supervision Visiting graduate student	The Broad Institute 1 hour / week
2017-2020	1:1 supervision Research fellow	Massachusetts General Hospital 1 hour / week
2018-	1:1 supervision Research fellows	The Broad Institute 4.5 hours / week
2018-	1:1 supervision Research fellows	Massachusetts General Hospital 2.5 hours / week
2019-2020	1:1 supervision Undergraduate student, Harvard University	The Broad Institute 1 hour / week
2022-2022	1:1 supervision Undergraduate student, Middlebury Colleague	The Broad Institute 1 hour / week

Formally Mentored Harvard Students (Medical, Dental, Graduate, and Undergraduate):

2022-	Computational Biology and Quantitative Genetics Master thesis project in progress.

Other Mentored Trainees and Faculty:

2017-2020	Wenyu Song, Ph.D. Current Position: Instructor, Brigham and Women's Hospital Career stage: Research Fellow Mentoring role: Research advisor Manuscripts published and grants in review.
2018-2022	Max Lam, Ph.D. Current Position: Principal Investigator, Neuropsychiatric Genomics Laboratory, Institute of Mental Health, Singapore Career stage: Research Fellow Mentoring role: Research advisor Manuscripts published and grants in review.

Local Invited Presentations:

☒ *No presentations below were sponsored by 3rd parties/outside entities*

2009	HistoneHits-A database for histone mutations and their phenotypes / Monthly Colloquium Department of Molecular Biology & Genetics, Johns Hopkins School of Medicine
2011	GWiS: a novel gene-based test of association for the identification of multiple independent effects / Monthly Colloquium High-Throughput Biology Center, Johns Hopkins School of Medicine
2013	Fine-mapping of inflammatory bowel disease risk loci using immunochip / Seminar Series Center for Human Genetics Research, Massachusetts General Hospital
2015	Association mapping of inflammatory bowel disease loci to single variant resolution / Seminar Series Center for Human Genetics Research, Massachusetts General Hospital
2015	Fine-mapping genome-wide association loci / Program Meeting Medical and Population Genetics, the Broad Institute
2017	Fine-mapping genetic risk loci to single-variant resolution / Invited Lecture Chinese Scientists and Scholars Association, Harvard Medical School
2018	Fine-mapping genetic associations to single-variant resolution / Invited Lecture Channing Division of Network Medicine, Brigham and Women's Hospital
2018	Fine-mapping genetic associations to single-variant resolution / Seminar Series Program in Genetic Epidemiology and Statistical Genetics, Harvard T.H. Chan School of Public Health
2019	Fine-mapping genetic loci associated with human complex disorders / Primer Series Stanley Center for Psychiatric Research, the Broad Institute
2020	Genetics studies in diverse ancestral populations / Program Meeting Stanley Center for Psychiatric Research, the Broad Institute
2021	Large-scale sequencing and multi-ancestry genetic analyses identify novel genes and variants associated with IBD / Invited Lecture

	31st Center for the Study of Inflammatory Bowel Disease Workshop, the Broad Institute
2022	Inclusive analytical methods for globally representative data sets Broad Scientific Equity Symposium, the Broad Institute
2022	Genetic discovery to disease pathogenesis / Invited Lecture Bioinformatics and Integrative Genomics, Department of Biomedical Informatics at Harvard Medical School

Report of Regional, National and International Invited Teaching and Presentations

☒ *No presentations below were sponsored by 3rd parties/outside entities*

Regional

2016	Genomics and human diseases / Invited Lecture Longwood Translational Medicine China Initiative, Boston, MA
2018	Fine-map genetic risk loci to single-variant resolution / Invited Lecture Genetics Department Seminar Series, Yale School of Medicine

National

2006	Group tests for protein interactions / Workshop DIMACS workshop, Piscataway, NJ
2010	GWiS: a novel gene-based test of association for the identification of multiple independent effects / Selected oral abstract American Society of Human Genetics annual meeting, Washington DC
2014	Fine-mapping of inflammatory bowel disease risk loci using immunochip / Symposium The Biology of Genome, Cold Spring Harbor, NY
2015	Single variant resolution association mapping of inflammatory bowel disease loci / Selected oral abstract American Society of Human Genetics annual meeting, Baltimore, MD
2018	Comparative genetic architectures of schizophrenia in East Asian and European populations. / Selected oral abstract American Society of Human Genetics annual meeting, San Diego, CA

2021	Genetic architecture of complex traits across East Asian and European ancestries: Insights from novel methods and emerging resources / Invited Lecture Center for Genetic Epidemiology, University of Southern California, Los Angeles, CA (virtual)

International

2006	Probabilistic paths for protein complex inference / Symposium RECOMB Satellite Conference on Systems Biology, San Diego, CA
2008	Biological network and regulation / Invited Lecture Nanjing University, Jiangsu, China
2013	Computational approaches to study the relation between genomic variations and phenotypes / Invited Lecture Chinese Academy of Science, Beijing, China
2013	Using paired tissue and serum samples to characterize human lung cancer metabolomics with ex vivo 1H HRMAS MRS / Platform International Society for Magnetic Resonance in Medicine annual meeting, Salt Lake City, UT
2014	Fine-mapping of the genetic risk loci underlying human disorders / Platform The Sixth National Conference on Bioinformatics and Systems Biology, Jiangsu, China
2015, 2016, 2017, 2018, 2019	Annual Genetic Epidemiology Workshop / Invited Lecture Academia Sinica, Taipei, ROC
2015	Fine-mapping of inflammatory bowel disease risk loci using immunochip / Invited Lecture Gordon conference on Quantitative Genetics & Genomics, Lucca (Barga), Italy
2015	Statistical Genomics Workshop / Invited Lecture Shanghai Jiaotong University, Shanghai, China
2016	Fine-mapping of disease associated loci / Invited Lecture Shanghai Jiaotong University, Shanghai, China

2017	Fine-mapping of genetic loci underlying human complex disorders / Invited Lecture Advanced Technologies in Precision Medicine, Shanghai, China
2017, 2018	Statistical Genomics Workshop / Invited Lecture Beijing Computing Center, Beijing, China
2018	Diversity and psychiatric genetics: why do genetics in a global setting / Invited Lecture The 5th Summit on Chinese Psychiatric Genetics, Suzhou, China
2018	Diversity and psychiatric genetics: why do genetics in a global setting / Invited Lecture Pan-Asia Symposium on the Genetics of Brain Disorders, Shanghai, China
2019	Comparative genetic architectures of schizophrenia in East Asian and European populations / Symposium Asian College of Neuropsychopharmacology, Fukuoka, Japan
2019	Fine-map genetic loci associated with human complex disorders to single-variant resolution / Platform The 4th Global Conference of Chinese Geneticists, Shanghai, China
2019	Fine-mapping genetic risk loci to single variant resolution / Invited Lecture Symposium on Precision Medicine and Mental Health, Hong Kong SAR, China
2019	Increasing ancestry diversity in psychiatric genomics research / Symposium World Congress of Psychiatric Genetics, Anaheim, CA
2020	Novel methods leveraging genomic diversity / PGC Worldwide Lab Meeting PGC Worldwide Lab meeting, Psychiatric Genomics Consortium (virtual)
2021	Genetic architecture of the inflammatory bowel diseases / Invited Lecture 14th Janssen Immunology Summit: Back to Normal Life with IBD (Shanghai, talk delivered virtually)
2021	Quality control in genome-wide association studies / Invited Lecture World Congress of Psychiatric Genetics (virtual)
2021	Large-scale sequencing and genetic analyses identify novel genes and variants underlying the inflammatory bowel disease / Invited Lecture Shanghai Inflammatory Bowel Diseases Research Forum (Shanghai, talk delivered virtually)

2022	Decolonization of psychiatric genetics / Plenary panel discussion World Congress of Psychiatric Genetics, Florence Italy
2022	Genetics of human complex disorders / Invited Lecture Pan-Asia Symposium on the Genetics of Brain Disorders, Singapore

Report of Education of Patients and Service to the Community

☒ *No presentations below were sponsored by 3rd parties/outside entities*

Activities

2016	MIT-China Innovation and Entrepreneurship Forum / Panelist, Healthcare Panel An annual forum to address key issues in technology, innovation, and entrepreneurship in China and US, providing a platform upon which high-impact discussions and collaborations can take place.
2017	STEP Forum / Invited Speaker A platform for young elites across the world to exchange ideas
2018-2019	Broad Institute outreaching activities Speak at various outreaching activities to introduce psychiatric genetics
2022	The MRCT Center of Brigham and Women's Hospital / invited speaker This is a program to provide advanced learning for public and private university lecturers who teach in undergraduate and graduate biotechnology degree programs in Indonesia. I gave a talk in advanced genomics and gene sequencing and participated in a panel discussion.

Report of Scholarship

ORCID: 0000-0003-1461-5762

Peer-Reviewed Scholarship in print or other media:

Research Investigations

1. **Huang H**, Zhang LV, Roth FP, Bader JS. Probabilistic Paths for Protein Complex Inference. Syst. Biol. and Comput. Proteomics Ws. 2006

2. Stuart LM, Boulais J, Charriere GM, Hennessy EJ, Brunet S, Jutras I, Goyette G, Rondeau C, Letarte S, **Huang H**, Ye P, Morales F, Kocks C, Bader JS, Desjardins M, Ezekowitz RA. A systems biology analysis of the Drosophila phagosome. Nature. 2007 Jan 4;445(7123):95-9101. PMID: 17151602

3. **Huang H**, Jedynak BM, Bader JS. Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. PLoS Comput Biol. 2007 Nov;3(11):e214. PMID: 18039026, PMCID: PMC2082503, https://doi.org/e214

4. Dai J, Hyland EM, Yuan DS, **Huang H**, Bader JS, Boeke JD. Probing nucleosome function: a highly versatile library of synthetic histone H3 and H4 mutants. Cell. 2008 Sep 19;134(6):1066-1078. PMID: 18805098, PMCID: PMC2701395, https://doi.org/10.1016/j.cell.2008.07.019

5. **Huang H**, Bader JS. Precision and recall estimates for two-hybrid screens. Bioinformatics. 2009 Feb 1;25(3):372-378. PMID: 19091773, PMCID: PMC2639075, https://doi.org/10.1093/bioinformatics/btn640

6. **Huang H**, Maertens AM, Hyland EM, Dai J, Norris A, Boeke JD, Bader JS. HistoneHits: a database for histone mutations and their phenotypes. Genome Res. 2009 Apr;19(4):674-681. PMID: 19218532, PMCID: PMC2666297, https://doi.org/10.1101/gr.083402.108

7. Zhong J, Krawczyk SA, Chaerkady R, **Huang H**, Goel R, Bader JS, Wong GW, Corkey BE, Pandey A. Temporal profiling of the secretome during adipogenesis in humans. J Proteome Res. 2010 Oct 1;9(10):5228-5238. PMID: 20707391, PMCID: PMC2948433, https://doi.org/10.1021/pr100521c

8. **Huang H**, Chanda P, Alonso A, Bader JS, Arking DE. Gene-based tests of association. PLoS Genet. 2011 Jul;7(7):e1002177. PMID: 21829371, PMCID: PMC3145613, https://doi.org/e1002177

9. **Huang H**, Tata S, Prill RJ. BlueSNP: R package for highly scalable genome-wide association studies using Hadoop clusters. Bioinformatics. 2013 Jan 1;29(1):135-136. PMID: 23202745, https://doi.org/10.1093/bioinformatics/bts647

10. Early RJ, Yu H, Mu XP, Xu H, Guo L, Kong Q, Zhou J, He B, Yang X, **Huang H**, Hu E, Jiang Y. Repeat oral dose toxicity studies of melamine in rats and monkeys. Arch Toxicol. 2013 Mar;87(3):517-527. PMID: 23052191, https://doi.org/10.1007/s00204-012-0939-7

11. Chanda P, **Huang H**, Arking DE, Bader JS. Fast association tests for genes with FAST. PLoS One. 2013;8(7):e68585. PMID: 23935874, PMCID: PMC3720833, https://doi.org/e68585

12. Chiu YL, Shan L, **Huang H**, Haupt C, Bessell C, Canaday DH, Zhang H, Ho YC, Powell JD, Oelke M, Margolick JB, Blankson JN, Griffin DE, Schneck JP. Sprouty-2

regulates HIV-specific T cell polyfunctionality. J Clin Invest. 2014 Jan;124(1):198-208. PMID: 24292711, PMCID: PMC3871241

13. Ananthakrishnan AN, **Huang H**, Nguyen DD, Sauk J, Yajnik V, Xavier RJ. Differential effect of genetic burden on disease phenotypes in Crohn's disease and ulcerative colitis: analysis of a North American cohort. Am J Gastroenterol. 2014 Mar;109(3):395-400. PMID: 24419484, PMCID: PMC4225079, https://doi.org/10.1038/ajg.2013.464

14. Li X, Yang H, **Huang H**, Zhu T. CELLCOUNTER: novel open-source software for counting cell migration and invasion in vitro. Biomed Res Int. 2014;2014:863564. PMID: 25054152, PMCID: PMC4099152, https://doi.org/863564

15. Arking DE, Pulit SL, Crotti L, van der Harst P, Munroe PB, Koopmann TT, Sotoodehnia N, Rossin EJ, Morley M, Wang X, Johnson AD, Lundby A, Gudbjartsson DF, Noseworthy PA, Eijgelsheim M, Bradford Y, Tarasov KV, Dörr M, Müller-Nurasyid M, Lahtinen AM, Nolte IM, Smith AV, Bis JC, Isaacs A, Newhouse SJ, Evans DS, Post WS, Waggott D, Lyytikäinen LP, Hicks AA, Eisele L, Ellinghaus D, Hayward C, Navarro P, Ulivi S, Tanaka T, Tester DJ, Chatel S, Gustafsson S, Kumari M, Morris RW, Naluai ÅT, Padmanabhan S, Kluttig A, Strohmer B, Panayiotou AG, Torres M, Knoflach M, Hubacek JA, Slowikowski K, Raychaudhuri S, Kumar RD, Harris TB, Launer LJ, Shuldiner AR, Alonso A, Bader JS, Ehret G, **Huang H**, Kao WH, Strait JB, Macfarlane PW, Brown M, Caulfield MJ, Samani NJ, Kronenberg F, Willeit J, CARe Consortium, COGENT Consortium, Smith JG, Greiser KH, Meyer Zu Schwabedissen H, Werdan K, Carella M, Zelante L, Heckbert SR, Psaty BM, Rotter JI, Kolcic I, Polašek O, Wright AF, Griffin M, Daly MJ, DCCT/EDIC, Arnar DO, Hólm H, Thorsteinsdottir U, eMERGE Consortium, Denny JC, Roden DM, Zuvich RL, Emilsson V, Plump AS, Larson MG, O'Donnell CJ, Yin X, Bobbo M, D'Adamo AP, Iorio A, Sinagra G, Carracedo A, Cummings SR, Nalls MA, Jula A, Kontula KK, Marjamaa A, Oikarinen L, Perola M, Porthan K, Erbel R, Hoffmann P, Jöckel KH, Kälsch H, Nöthen MM, HRGEN Consortium, den Hoed M, Loos RJ, Thelle DS, Gieger C, Meitinger T, Perz S, Peters A, Prucha H, Sinner MF, Waldenberger M, de Boer RA, Franke L, van der Vleuten PA, Beckmann BM, Martens E, Bardai A, Hofman N, Wilde AA, Behr ER, Dalageorgou C, Giudicessi JR, Medeiros-Domingo A, Barc J, Kyndt F, Probst V, Ghidoni A, Insolia R, Hamilton RM, Scherer SW, Brandimarto J, Margulies K, Moravec CE, del Greco M F, Fuchsberger C, O'Connell JR, Lee WK, Watt GC, Campbell H, Wild SH, El Mokhtari NE, Frey N, Asselbergs FW, Mateo Leach I, Navis G, van den Berg MP, van Veldhuisen DJ, Kellis M, Krijthe BP, Franco OH, Hofman A, Kors JA, Uitterlinden AG, Witteman JC, Kedenko L, Lamina C, Oostra BA, Abecasis GR, Lakatta EG, Mulas A, Orrú M, Schlessinger D, Uda M, Markus MR, Völker U, Snieder H, Spector TD, Ärnlöv J, Lind L, Sundström J, Syvänen AC, Kivimaki M, Kähönen M, Mononen N, Raitakari OT, Viikari JS, Adamkova V, Kiechl S, Brion M, Nicolaides AN, Paulweber B, Haerting J, Dominiczak AF, Nyberg F, Whincup PH, Hingorani AD, Schott JJ, Bezzina CR,

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Scholarship without named authorship

1. Schizophrenia Working Group of the Psychiatric Genomics Consortium. Biological insights from 108 schizophrenia-associated genetic loci. Nature. 2014 Jul 24;511(7510):421-427. PMID: 25056061, PMCID: PMC4112379, https://doi.org/10.1038/nature13595

   I am an analyst in this project responsible for fine-mapping and the co-localization analysis with brain eQTL.

2. Autism Spectrum Disorders Working Group of The Psychiatric Genomics Consortium. Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. Mol Autism. 2017;8:21. PMID: 28540026, PMCID: PMC5441062, https://doi.org/21

   I am an analyst in this project responsible for the gene-based tests.

3. Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium. Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell. 2018 Jun 14;173(7):1705-1715.e16. PMID: 29906448, PMCID: PMC6432650, https://doi.org/S0092-8674(18)30658-5

   I am an analyst in this project responsible for performing analyses on a subset of the data.

4. Cross-Disorder Group of the Psychiatric Genomics Consortium. Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell. 2019 Dec 12;179(7):1469-1482.e11. PMID: 31835028, PMCID: PMC7077032, https://doi.org/S0092-8674(19)31276-0

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5. Satterstrom FK, Kosmicki JA, Wang J, Breen MS, De Rubeis S, An JY, Peng M, Collins R, Grove J, Klei L, Stevens C, Reichert J, Mulhern MS, Artomov M, Gerges S, Sheppard B, Xu X, Bhaduri A, Norman U, Brand H, Schwartz G, Nguyen R, Guerrero EE, Dias C, Autism Sequencing Consortium, iPSYCH-Broad Consortium, Betancur C, Cook EH, Gallagher L, Gill M, Sutcliffe JS, Thurm A, Zwick ME, Børglum AD, State MW, Cicek AE, Talkowski ME, Cutler DJ, Devlin B, Sanders SJ, Roeder K, Daly MJ, Buxbaum JD. Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell. 2020 Feb 6;180(3):568-584.e23. PMID: 31981491, PMCID: PMC7250485, https://doi.org/10.1016/j.cell.2019.12.036

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6. Blokland GAM, Grove J, Chen CY, Cotsapas C, Tobet S, Handa R, Schizophrenia Working Group of the Psychiatric Genomics Consortium, St Clair D, Lencz T, Mowry BJ, Periyasamy S, Cairns MJ, Tooney PA, Wu JQ, Kelly B, Kirov G, Sullivan PF, Corvin A, Riley BP, Esko T, Milani L, Jönsson EG, Palotie A, Ehrenreich H, Begemann M, Steixner-Kumar A, Sham PC, Iwata N, Weinberger DR, Gejman PV, Sanders AR, Buxbaum JD, Rujescu D, Giegling I, Konte B, Hartmann AM, Bramon E, Murray RM, Pato MT, Lee J, Melle I, Molden E, Ophoff RA, McQuillin A, Bass NJ, Adolfsson R, Malhotra AK, Bipolar Disorder Working Group of the Psychiatric Genomics Consortium, Martin NG, Fullerton JM, Mitchell PB, Schofield PR, Forstner AJ, Degenhardt F, Schaupp S, Comes AL, Kogevinas M, Guzman-Parra J, Reif A, Streit F, Sirignano L, Cichon S, Grigoroiu-Serbanescu M, Hauser J, Lissowska J, Mayoral F, Müller-Myhsok B, Świątkowska B, Schulze TG, Nöthen MM, Rietschel M, Kelsoe J, Leboyer M, Jamain S, Etain B, Bellivier F, Vincent JB, Alda M, O'Donovan C, Cervantes P, Biernacka JM, Frye M, McElroy SL, Scott LJ, Stahl EA, Landén M, Hamshere ML, Smeland OB, Djurovic S, Vaaler AE, Andreassen OA, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, Baune BT, Air T, Preisig M, Uher R, Levinson DF, Weissman MM, Potash JB, Shi J, Knowles JA, Perlis RH, Lucae S, Boomsma DI, Penninx BWJH, Hottenga JJ, de Geus EJC, Willemsen G, Milaneschi Y, Tiemeier H, Grabe HJ, Teumer A, Van der Auwera S, Völker U, Hamilton SP, Magnusson PKE, Viktorin A, Mehta D, Mullins N, Adams MJ, Breen G, McIntosh AM, Lewis CM, Sex Differences Cross-Disorder Analysis Group of the

Psychiatric Genomics Consortium, iPSYCH, Hougaard DM, Nordentoft M, Mors O, Mortensen PB, Werge T, Als TD, Børglum AD, Petryshen TL, Smoller JW, Goldstein JM. Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biol Psychiatry. 2022 Jan 1;91(1):102-117. PMID: 34099189, PMCID: PMC8458480, https://doi.org/S0006-3223(21)01139-2

I am an analyst in this project responsible for performing analyses on a subset of the data.

Non-peer reviewed scholarship in print or other media:

Reviews, chapters, and editorials

1. Muise A and **Huang H**. Sequencing and Mapping IBD Genes to Individual Causative Variants and Their Clinical Relevance. Molecular Genetics of Inflammatory Bowel Disease (Editor: Mauro D'Amato)

2. Mullins N, **Huang H**. Genetic Architecture of Bipolar Disorder in Individuals of Han Chinese and European Ancestries. JAMA Psychiatry. 2021 Mar 1;78(3):248-249. PMID: 33263741, https://doi.org/10.1001/jamapsychiatry.2020.3639

3. Wang QS, **Huang H**. Methods for statistical fine-mapping and their applications to auto-immune diseases. Semin Immunopathol. 2022 Jan;44(1):101-113. PMID: 35041074, PMCID: PMC8837575, https://doi.org/10.1007/s00281-021-00902-8

Professional educational materials or reports, in print or other media:

1. Population structure in genetic association studies / Course video

   I created and used this video to teach a course for the “Global Initiative for Neuropsychiatric Genetics Education in Research” at the Harvard T.H. Chan School of Public Health. (2019)

2. Post-GWAS analyses: heritability, genetic correlation and annotation / Course video

   I created and used this video to teach a course for the “Global Initiative for Neuropsychiatric Genetics Education in Research” at the Harvard T.H. Chan School of Public Health. (2019)

Thesis:

1. Huang, H. "Computational Approaches to Study the Relation Between Genomic Variations and Phenotypes". Ph.D. dissertation, Johns Hopkins University, 2012.

* Co-author, ** Mentee

Narrative Report

I am a statistical geneticist with special interests in the genetics of human complex disorders. I received my Ph.D. training in Dr. Joel Bader's lab at the Johns Hopkins School of Medicine, with focuses on biological pathways and networks, statistical genetics and bioinformatics. One major component in my dissertation was the development of a new gene-based method for genome-wide association studies that combined multiple independent associations within a gene and had greater power than all other existing methods. This method has been used widely in consortia of psychiatric, autoimmune, and cardiovascular diseases. Due to the burgeoning commercial interests in this method, a U.S. patent (pending) was filed, and I was also hired by the IBM Healthcare Informatics group as a summer intern to extend this method in their parallel computing environment.

After receiving my Ph.D., I joined Dr. Mark J. Daly's lab at the Massachusetts General Hospital. I focused on developing methods and analyses to investigate the genetics of common disorders, especially the inflammatory bowel diseases (IBD) and schizophrenia. I have been heavily involved in international IBD genetics consortia and contributed to several major studies. I led the fine-mapping project and developed a Bayesian approach to resolve known genetic associations to much smaller sets of variants with high causal probabilities. This project mapped IBD associations down to a single variant and significantly advanced our knowledge of IBD genetics. Moreover, a simplified implementation of this method that only requires summary data has been widely used for other disorders including schizophrenia and migraines. In addition to this fine-mapping project, I have led or participated in the study design, method development, or analysis of other IBD studies covering a broad range of topics, including IBD genetic associations, clinical sub-phenotyping, functional studies of *CARD9* and *GPR65*, and the interaction between the microbiome and host genetics in IBD.

In addition to IBD genetics, I have led a workgroup in Psychiatric Genomics Consortium (PGC) to understand the genetic contributions to schizophrenia in Asian populations. Working with over 40 participants across 10 countries, I have built a large Asian schizophrenia cohort. Together, we are working to identify new schizophrenia genetic loci, evaluate the genetic correlations between Asian and European populations, and understand whether or how the schizophrenia genetic effects differ between the two populations. With support from the Stanley Center at the Broad Institute, I am also spearheading new major research collaborations with institutes and hospital networks in East Asia and the Broad Institute to expand our psychiatric genetics initiatives in Asia. As part of this, I am organizing and teaching an annual statistical genetics workshop series in Shanghai (2015), Beijing (2017 and 2018) and Taipei (2015-2019). These workshops have been attended by over 600 participants from more than 70 institutions and helped to build global genetics research capacity.

In parallel with my research activities, I am committed to teaching and mentoring. I am one of the teaching fellows for the Harvard T.H. Chan School of Public Health (HSPH) *Global Initiative for Neuropsychiatric Genetics Education in Research*, a training program that aims to boost global capacity to conduct neuropsychiatric genetics research. I participated in the initial curriculum design in 2017, and

since then taught annually in person (Boston and London), in virtual classroom and as recorded course lectures. My lectures have covered genome-wide association studies, population structure, genetic correlations, career development and grant writing. In 2019 and 2020, I co-taught a new MGH course with Dr. Tian Ge (Assistant Professor, HMS and MGH) entitled *A Practical Introduction to Statistical Genetics*. Over 50 participants with Harvard affiliations attended this course. I taught sessions in the genome-wide association studies and fine-mapping studies. Lastly, I have mentored or co-mentored 6 research fellows and 3 visiting fellows from Harvard affiliated hospitals and institutions (MGH, BWH and the Broad Institute). I met with them regularly, worked closely with them on statistical genetics, psychiatric genetics, or computational biology projects, and assisted them in career development and grant writing. Our work together has led to manuscripts in publication and in preparation and grant in review.