CURRICULUM VITAE

Date of Revision: 04/06/2023

Name: Hang Zhou, Ph.D.

School: Yale University School of Medicine

Education:

2015	Ph.D. Computational Biology (focus on population genetics), CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences, Shanghai, China
2009	B.S. Bioinformatics, Shanghai Jiao Tong University, Shanghai, China

Career/Academic Appointments:

2023-present	Assistant Professor, Dept. of Biomedical Informatics & Data Science, Yale University School of Medicine, New Haven, CT
2023-present	Member, Center for Brain & Mind Health, Yale University School of Medicine, New Haven, CT
2022-present	Assistant Professor, Dept. of Psychiatry, Yale University School of Medicine, New Haven, CT
2018-21	Associate Research Scientist, Dept. of Psychiatry, Yale University School of Medicine, New Haven, CT
2015-18	Postdoctoral Associate, Dept. of Psychiatry, Yale University School of Medicine, New Haven, CT
2011	Visiting Scholar, Department of Evolutionary Genetics, Max-Planck Institute for Evolutionary Anthropology, Lepzig, Germany
2007-08	Student Research Program, Laboratory of Plant Developmental Biology, Shanghai Jiao Tong University, Shanghai, China

Professional Honors & Recognition:

International/National/Regional

2023: Annual Pilot Award, Yale Center for the Translational Neuroscience of Alcoholism
2023: Early Investigator Career Enhancement Program, Yale-SCORE Program for Sex Differences in Alcohol Use Disorder
2021: Early Investigators, Yale-SCORE Program for Sex Differences in Alcohol Use Disorder
2019: Early Career Investigator, Department of Veterans Affairs, Million Veteran Program
2018: NARSAD Young Investigator Grant, P&S Fund Investigator, Brain & Behavior Research Foundation
2013: Graduate Travel Award, Society for Molecular Biology and Evolution
2012: National Scholarship for Graduate Students, China
2012: Trainee full scholarship, The 13th International Meeting on Human Genome Variation and Complex Genome Analysis

University

2014: Best Poster Report Award, CAS-MPG PICB Scientific Exchange Meeting
2013: Best Oral Report Award, CAS-MPG PICB Scientific Exchange Meeting

Invited Speaking Engagements, Presentations, Symposia & Workshops:

International/National

2022: The American Society of Human Genetics Annual Meeting. Los Angeles, CA. Co-chair for platform “Genetics for substance use disorders”

2021: Million Veteran Program Statistical Genetics working group: “Revisiting Diversity - Differences between South Asian and East Asians +/- applications to HARE”

2021: Latin American Genomics Consortium, virtual: “Alcohol Use Disorder in the Million Veteran Program”

2020: Psychiatric Genomics Consortium Worldwide Lab Meeting, virtual: “Meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology, pleiotropy and causality”

2020: World Congress of Psychiatric Genetics, virtual, PGC-SUD working group update: “AUD differs from alcohol use genetically: a major discovery from the large-GWAS era” and “Comorbid AUD and MDD”

Regional

2023: Yale Neurogenomics RIP: “Progress of genetic research of alcohol use disorder in multiple populations”

2022: UT Health School of Biomedical Informatics, CPH Seminar in Precision Medicine: “Progress of genetic research of alcohol use disorder in multiple populations”

2019: Biological Sciences Training Program (BSTP), Yale Psychiatry: “Genetic Studies of Alcohol Drinking and Dependence: Results from Million Veteran Program and Others”

2018: Million Veteran Program (MVP) beta project annual meeting, West Haven: “GWAS of alcohol consumption and alcohol use disorder in MVP”

2014: Fudan University, Shanghai, China, Seminar: “Fine atlas of natural selection in human genome”

2013: The 2013 CAS-MPG PICB Scientific Exchange Meeting, Shanghai, China: “Natural selection in human genome”

Peer-Reviewed Presentations & Symposia Given at Meetings:

International/National

2023: Research Society on Alcoholism Scientific Meeting, Bellevue, WA. Co-chair for symposium “Leveraging genetics of alcohol use and alcohol use disorder to investigate genetic liabilities to alcohol-related outcomes in diverse populations”

2023: Research Society on Alcoholism Scientific Meeting, Bellevue, WA: “Mendelian Randomization Analysis of the Associations between Alcohol Use and Cancer Risk”

2022: Million Veteran Program (MVP) Science Conference, St. Petersburg, FL: "Investigate the Genetic Causality of Problematic Alcohol Use on Cancer Risk"

2022: Research Society on Alcoholism Scientific Meeting, Orlando, FL: "Advanced genetic study of problematic alcohol use in > 1 million subjects from multiple populations"

2022: NIDA Genetics and Epigenetics Cross Cutting Research Team (GECCRT), virtual, Session on Can Increasing Diversity Lead to Deeper Understanding of Addiction?: "Advanced genetic study of problematic alcohol use in > 1 million subjects from multiple populations"

2022: Society of Biological Psychiatry, New Orleans, LA: "Advanced genetic study of problematic alcohol use in > 1 million subjects from multiple populations"

2021: World Congress of Psychiatric Genetics, virtual: "Advanced Genetic Study of Problematic Alcohol Use in Multiple Populations in > 1 Million Subjects."

2021: Million Veteran Program (MVP) Science Conference, virtual: "Advanced Genetic Study of Problematic Alcohol Use in Multiple Populations in > 1 Million Subjects."

2021: Research Society on Alcoholism Scientific Meeting, virtual, Symposia on Asian drinking, genotypes, and public health: "Genome-wide meta-analysis of alcohol use disorder in East Asians."

2019: World Congress of Psychiatric Genetics, Los Angles, CA, Symposia on Genetic architecture of psychiatric and addiction traits in the Million Veteran Program: "Functional coding variant in *OPRM1* gene associated with opioid use disorder: evidence from GWAS on large cohorts."

2019: The American Society of Human Genetics, Huston, TX, Platform session on Genetics of addiction and behavior: "Genome-wide meta-analysis of alcohol use disorder and problematic alcohol use identifies 29 risk variants."

2019: Million Veteran Program (MVP) Science Conference, Philadelphia, PA: "Functional coding variant in *OPRM1* gene associated with opioid use disorder: evidence from GWAS on large cohorts."

2019: Annual Research Society on Alcoholism (RSA) Scientific Meeting, Minneapolis, MN, Symposia on Genome-wide association study findings inform the relationship between heavy drinking and alcohol use disorder: "Genome-wide Association Study of Alcohol Consumption and Use Disorder in Multiple Populations (N = 274,424)."

2018: Million Veteran Program (MVP) Science Conference, Nashville, NV: "Genomics of alcohol consumption and alcohol use disorder."

2012: The 13th International Meeting on Human Genome Variation and Complex Genome Analysis, Shanghai, China, Session on NGS research: "Fine Map of Human Positive Selection from 1000 Genomes Data."

Professional Service

Journal Service:

Editor/Associate Editor

2020-present Editorial Board, *Complex Psychiatry*
2022-present Editorial Board, *PLOS One*

Reviewer (2018-present)

Addiction
Alcohol
Alcoholism: Clinical and Experimental Research
Alcohol and Alcoholism
American Journal of Drug and Alcohol Abuse
Biological Psychiatry
BMC Medicine
Communications Biology
Drug and Alcohol Dependence
Drug and Alcohol Dependence Reports
European Addiction Research
Nature Human Behaviour
Nucleic Acids Research
PLOS One
Translational Psychiatry

Peer-Reviewed Original Research (*contributed equally, google scholar)

1. Li J, Zhang L, **Zhou H**, Stoneking M, Tang K. Global patterns of genetic diversity and signals of natural selection for human ADME genes. *Human Molecular Genetics* 2011, 20(3):528-40.

2. Peng S, Tan J, Hu S, **Zhou H**, Guo J, Jin L, Tang K. Detecting genetic association of common human facial morphological variation using high density 3D image registration. *PLoS Computational Biology* 2013, 9(12):e1003375.

3. Guo J, Tan J, Yang Y, **Zhou H**, Hu S, Hashan A, Bahaxar N, Xu S, Weaver TD, Jin L, Stoneking M, Tang K. Variation and signatures of selection on the human face. *Journal of Human Evolution* 2014, 75:143-52.

4. Valverde G*, **Zhou H***, Lippold S, de Filippo C, Tang K, López Herráez D, Li J, Stoneking M. A novel candidate region for genetic adaptation to high altitude in Andean populations. *PLoS One* 2015, 10(5):e0125444.

5. Qian W, **Zhou H**, Tang K. Recent coselection in human populations revealed by protein-protein interaction network. *Genome Biology and Evolution* 2014, 7(1):136-53.

6. Hou Z, Luo Y, Wang Z, Zheng H, Wang Y, **Zhou H**, Wu L, Jin L. Inferring the dynamics of effective population size using autosomal genomes. *Scientific Reports* 2016, 6:20079.

7. Andersen AM, Pietrzak RH, Kranzler HR, Ma L, **Zhou H**, Liu X, Kramer J, Kuperman S, Edenberg HJ, Nurnberger JI Jr, Rice JP, Tischfield JA, Goate A, Foroud TM, Meyers JL, Porjesz B, Dick DM, Hesselbrock V, Boerwinkle E, Southwick SM, Krystal JH, Weissman MM, Levinson DF, Potash JB, Gelernter J, Han S. Polygenic scores for major depressive disorder and risk of alcohol dependence. *JAMA Psychiatry* 2017, 74(11):1153-1160.

8. **Zhou H**, Polimanti R, Yang BZ, Wang Q, Han S, Sherva R, Nuñez YZ, Zhao H, Farrer LA, Kranzler HR, Gelernter J. Genetic risk variants associated with comorbid alcohol dependence and major depression. *JAMA Psychiatry* 2017, 74(12):1234-1241.

9. Qiao L, Yang Y, Fu P, Hu S, **Zhou H**, Tan J, Lu Y, Lou H, Lu D, Wu S, Guo J, Peng S, Jin L, Guan Y, Wang S, Xu S, Tang K. Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. *Journal of Genetics and Genomics* 2018, 45(8):419-432.

10. Zhang H, **Zhou H**, Lencz T, Farrer LA, Kranzler HR, Gelernter J. Genome-wide association study of cognitive flexibility assessed by Wisconsin Card Sorting Tests. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* 2018, 177(5):511-519.

11. Gelernter J, **Zhou H**, Nuñez YZ, Mutirangura A, Malison RT, Kalayasiri R. Genomewide association study of alcohol dependence and related traits in a Thai population. *Alcoholism: Clinical and Experimental Research* 2018, 42(5):861-868.

12. Montalvo-Ortiz JL, **Zhou H**, D'Andrea I, Maroteaux L, Lori A, Smith A, Ressler K, Nuñez Y, Farrer LA, Zhao H, Kranzler HR, Gelernter J. Translational studies support a role for serotonin 2B receptors in aggression-related cannabis response. *Molecular Psychiatry* 2018, 23(12):2277-2286.

13. Cheng Z, **Zhou H**, Sherva R, Farrer LA, Kranzler HR, Gelernter J. Genome-wide association study identifies a regulatory variant of *RGMA* associated with opioid dependence in European Americans. *Biological Psychiatry* 2018, 84(10):762-770.

14. **Zhou H**, Cheng Z, Bass N, Farrer LA, Krystal JH, Kranzler HR, Gelernter J. Genome-wide association study identifies glutamate ionotropic receptor *GRIA4* as a risk gene for comorbid nicotine dependence and major depression. *Translational Psychiatry* 2018, 8(1):208.

15. Sun Y, Chang S, Wang F, Sun H, Ni Z, Yue W, **Zhou H**, Gelernter J, Malison RT, Kalayasiri R, Wu P, Lu L, Shi J. Genome-wide association study of alcohol dependence in male Han Chinese and cross-ethnic polygenic risk score comparison. *Translational Psychiatry* 2019, 9(1):249.

16. Levey DF, Polimanti R, Cheng Z, **Zhou H**, Nuñez YZ, Jain S, He F, Sun X, Ursano RJ, Kessler RC, Smoller JW, Stein MB, Kranzler HR, Gelernter J. Genetic associations with suicide attempt severity and polygenic overlap with major depression. *Translational Psychiatry* 2019, 9(1):22.

17. Xiang B, Yang B, **Zhou H**, Kranzler HR, Gelernter J. GWAS and network analysis of co-occurring nicotine and alcohol dependence identifies significantly associated alleles and network. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* 2019, 180(1):3-11.

18. Yang BZ, **Zhou H***, Cheng Z*, Kranzler HR, Gelernter J. Genomewide gene-by-sex interaction scans identify *ADGRV1* for sex differences in opioid dependent African Americans. *Scientific Reports* 2019, 9(1):18070.

19. Kranzler HR*, **Zhou H***, Kember RL*, Smith RV, Justice AC, Damrauer S, Tsao PS, Klarin D, Baras A, Reid J, Overton J, Rader DJ, Cheng Z, Tate JP, Becker WC, Concato J, Xu K, Polimanti R, Zhao H, Gelernter J. Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. *Nature Communications* 2019, 10(1):1499.

20. Munn-Chernoff MA, Johnson EC, Chou YL, …, **Zhou H**, …Gelernter J, Edenberg HJ, Bulik CM, Agrawal A. Shared genetic risk between eating disorder- and substance-use-related phenotypes: Evidence from genome-wide association studies. *Addiction Biology* 2020, 26(1):e12880.

21. Levey DF, Gelernter J, Polimanti R, **Zhou H**, Cheng Z, Aslan M, Quaden R, Concato J, Radhakrishnan K, Bryois J, Sullivan PF, Million Veteran Program, Stein MB. Reproducible genetic risk loci for anxiety: Results from ~200,000 participants in the Million Veteran Program. *American Journal of Psychiatry* 2020, 177(3):223-232.

22. Cheng Z, Yang BZ, **Zhou H**, Nuñez Y, Kranzler HR, Gelernter J. Genome-wide scan identifies opioid overdose risk locus close to *MCOLN1*. *Addiction Biology* 2020, 25(2):e12811.

23. Cao H, **Zhou H**, Cannon TD. Functional connectome-wide associations of schizophrenia polygenic risk. *Molecular Psychiatry* 2020, doi: 10.1038/s41380-020-0699-3.

24. Xu K, Li B, McGinnis KA, Vickers-Smith R, Dao C, Sun N, Kember RL, **Zhou H**, Becker WC, Gelernter J, Kranzler HR, Zhao H, Justice AC; VA Million Veteran Program. Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. *Nature Communications* 2020, 11(1):5302.

25. **Zhou H**, Sealock JM, Sanchez-Roige S, Clarke TK, Levey DF, Cheng Z, Li B, Polimanti R, Kember RL, Smith RV, Thygesen JH, Morgan MY, Atkinson SR, Thursz MR, Nyegaard M, Mattheisen M, Børglum AD, Johnson EC, Justice AC, Palmer AA, McQuillin A, Davis LK, Edenberg HJ, Agrawal A, Kranzler HR, Gelernter J. Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. *Nature Neuroscience* 2020, 23(7):809-818.

26. **Zhou H**, Rentsch CT, Cheng Z, Kember RL, Nuñez YZ, Tate JP, Dao C, Xu K, Polimanti R, Farrer LA, Justice AC, Kranzler HR, Gelernter J, for the VA Million Veteran Program. Association of *OPRM1* functional coding variant with opioid use disorder: A genome-wide association study. *JAMA Psychiatry* 2020, 77(10):1072–80.

27. Johnson EC, Demontis D, Thorgeirsson TE, Walters RK, Polimanti R, Hatoum AS, Sanchez-Roige S, Paul SE, Wendt FR, Clarke TK, Lai D, Reginsson GW, **Zhou H**, …, Psychiatric Genomics Consortium Substance Use Disorders Workgroup, Davis LK, Bogdan R, Gelernter J, Edenberg HJ, Stefansson K, Børglum AD, Agrawal A. A large-scale genome-wide association study meta-analysis of cannabis use disorder. *Lancet Psychiatry* 2020, 7(12):1032-1045.

28. Johnson EC, Kapoor M, Hatoum AS, **Zhou H**, Polimanti R, Wendt FR, Walters RK, Lai D, Kember RL, Hartz S, Meyers JL, Peterson RE, Ripke S, Bigdeli TB, Fanous AH, Pato CN, Pato MT, Goate AM, Kranzler HR, O'Donovan MC, Walters JTR, Gelernter J, Edenberg HJ, Agrawal A. Investigation of convergent and divergent genetic influences underlying schizophrenia and

alcohol use disorder. *Psychological Medicine* 2021 Jul 7;1-9. doi: 10.1017/S003329172100266X. Online ahead of print.

29. Dao C, **Zhou H**, Small A, Gordon KS, Li B, Kember RL, Ye Y, Gelernter J, Xu K, Kranzler HR*, Zhao H*, Justice AC*. The Impact of Removing Former Drinkers from Genome-wide Association Studies of AUDIT-C. *Addiction* 2021 Nov;116(11):3044-3054. doi: 10.1111/add.15511.

30. Mullins N, Forstner AJ, O'Connell KS, Coombes B, Coleman JRI, Qiao Z, Als TD, Bigdeli TB, …, **Zhou H**, …, Nurnberger JI, Cichon S, Edenberg HJ, Stahl EA, McQuillin A, Florio AD, Ophoff RA, Andreassen OA. Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. *Nature Genetics* 2021 May 17. doi: 10.1038/s41588-021-00857-4. Online ahead of print.

31. Levey DF, Stein MB, Wendt F, Pathak G, **Zhou H**, Aslan M, Quaden R, Harrington KM, Nuñez YZ, Overstreet C, Radhakrishnan K, Sanacora G, McIntosh AM, Shi J, Shringarpure SS, 23andMe Research Team, Million Veteran Program, Concato J, Polimanti R, Gelernter J. Bi-ancestral depression GWAS in the Million Veteran Program and meta-analysis in >1.2 million individuals highlight new therapeutic directions. *Nature Neuroscience* 2021 Jul;24(7):954-963. doi: 10.1038/s41593-021-00860-2.

32. Karlsson Linnér R, Mallard TT, Barr PB, Sanchez-Roige S, Madole JW, Driver MN, Poore HE, de Vlaming R, Grotzinger AD, Tielbeek JT, Johnson EC, Liu M, Rosenthal SB, Ideker T, **Zhou H**, Kember RL, Pasman JA, Verweij KJH, Liu DJ, Vrieze S, COGA Collaborators, Kranzler HR, Gelernter J, Harris KM, Tucker-Drob EM, Waldman I, Palmer AA, Harden KP, Koellinger PD, Dick DM. Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. *Nature Neuroscience* 2021 Oct;24(10):1367-1376. doi: 10.1038/s41593-021-00908-3.

33. Hatoum AS, Johnson EC, Colbert SMC, Polimanti R, **Zhou H**, Walters RK, Gelernter J, Edenberg HJ, Bogdan R, Agrawal A. The addiction risk factor: A unitary genetic vulnerability characterizes substance use disorders and their associations with common correlates. *Neuropsychopharmacology* 2021 Nov 8. doi: 10.1038/s41386-021-01209-w.

34. Mullins N, Kang J, Campos AI, Coleman JRI, …, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium; Bipolar Disorder Working Group of the Psychiatric Genomics Consortium; Eating Disorders Working Group of the Psychiatric Genomics Consortium; German Borderline Genomics Consortium; MVP Suicide Exemplar Workgroup; VA Million Veteran Program, …, Ruderfer DM. Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. *Biological Psychiatry* 2022 Feb 1;91(3):313-327. doi: 10.1016/j.biopsych.2021.05.029.

35. **Zhou H**, Kalayasiri R, Sun Y, Nuñez YZ, Deng HW, Chen XD, Justice AC, Kranzler HR, Chang S, Lu L, Shi J, Sanichwankul K, Mutirangura A, Malison RT, Gelernter J. Genome-wide Meta-analysis of Alcohol Use Disorder in East Asian. *Neuropsychopharmacology* 2022 Jan 29. doi: 10.1038/s41386-022-01265-w. Online ahead of print.

36. Love T, Shabalin AA, Kember RL, Docherty AR, **Zhou H**, Koppelmans V, Gelernter J, Baker AK, Hartwell E, Dubroff J, Zubieta JK, Kranzler HR. Unique and joint associations of polygenic

risk for major depression and opioid use disorder with endogenous opioid system function. *Neuropsychopharmacology* 2022. https://doi.org/10.1038/s41386-022-01325-1

37. Montalvo-Ortiz JL, Gelernter J, Cheng Z, Girgenti MJ, Xu K, Zhang X, Gopalan S, **Zhou H**, Duman RS, Southwick SM, Krystal JH; Traumatic Stress Brain Research Study Group, Pietrzak RH. Epigenome-wide association study of posttraumatic stress disorder identifies novel loci in U.S. military veterans. *Translational Psychiatry* 2022 Feb 17;12(1):65. doi: 10.1038/s41398-022-01822-3.

38. Topiwala A, Taschler B, Ebmeier KP, Smith S, **Zhou H**, Levey DF, Codd V, Samani NJ, Gelernter J, Nichols TE, Burgess S. Alcohol consumption and telomere length: Mendelian randomization clarifies alcohol's effects. *Molecular Psychiatry* 2022 Jul 26. doi: 10.1038/s41380-022-01690-9. Epub ahead of print.

39. Deak JD, **Zhou H**, Galimberti M, Levey DF, Wendt FR, Sanchez-Roige S, Hatoum AS, Johnson EC, Nunez YZ, Demontis D, Børglum AD, Rajagopal VM, Jennings MV, Kember RL, Justice AC, Edenberg HJ, Agrawal A, Polimanti R, Kranzler HR, Gelernter J. Genome-wide association study in individuals of European and African ancestry and multi-trait analysis of opioid use disorder identifies 19 independent genome-wide significant risk loci. *Molecular Psychiatry* 2022 Oct;27(10):3970-3979. doi: 10.1038/s41380-022-01709-1.

40. Topiwala A, Wang C, Ebmeier KP, Burgess S, Bell S, Levey DF, **Zhou H**, McCracken C, Roca-Fernández A, Petersen SE, Raman B, Husain M, Gelernter J, Miller KL, Smith SM, Nichols TE. Associations between moderate alcohol consumption, brain iron, and cognition in UK Biobank participants: Observational and mendelian randomization analyses. *PLoS Medicine* 2022 Jul 14;19(7):e1004039. doi: 10.1371/journal.pmed.1004039.

41. Kember RL, Hartwell EE, Xu H, Rotenberg J, Almasy L, **Zhou H**, Gelernter J, Kranzler HR. Phenome-wide association analysis of substance use disorders in a deeply-phenotyped sample. *Biological Psychiatry* 2022, doi:https://doi.org/10.1016/j.biopsych.2022.08.010

42. Kember RL, Vickers-Smith R, Xu H, Toikumo S, Niarchou M, **Zhou H**, Hartwell EE, Crist RC, Rentsch CT, Davis LK, Justice AC, Sanchez-Roige S, Kampman KM, Gelernter J, Kranzler HR. Cross-ancestry meta-analysis of opioid use disorder uncovers novel loci with predominant effects on brain. *Nature Neuroscience* 2022 Oct;25(10):1279-1287. doi: 10.1038/s41593-022-01160-z.

43. Deak JD, Levey DF, Wendt FR, **Zhou H**, Galimberti M, Kranzler HR, Gaziano JM, Stein MB, Polimanti R, Gelernter J. Genome-wide investigation of maximum habitual alcohol intake (MaxAlc) in 247,755 European and African Ancestry U.S. Veterans informs the relationship between habitual alcohol consumption and alcohol use disorder. *JAMA Network Open* 2022 Oct 3;5(10):e2238880. doi: 10.1001/jamanetworkopen.2022.38880.

44. Gaddis N, Mathur R, …, Kranzler HR, **Zhou H**, …, Gelernter J, Edenberg H, Bierut L, Hancock DB, Johnson EO. Multi-trait genome-wide association study of opioid addiction: OPRM1 and Beyond. *Scientific Reports* 2022 Oct 7;12(1):16873. doi: 10.1038/s41598-022-21003-y.

45. Overstreet C, Levey DF, **Zhou H**, Harrington KM, Quaden R, Stein MB, Gelernter J, Pietrzak RH; Million Veteran Program. Factor structure of the posttraumatic stress disorder checklist

(PCL-17) in 279,897 million veteran program participants. *Psychiatry Research* 2023 Jan;319:114994. doi: 10.1016/j.psychres.2022.114994.

46. Kember RL, Vickers-Smith R, **Zhou H**, Xu H, Dao C, Justice AC, Gelernter J, Vujkovic M, Kranzler HR. Genetic underpinnings of the transition from alcohol consumption to alcohol use disorder: shared and unique genetic architectures in a cross-ancestry sample. *American Journal of Psychiatry* (in press).

47. Cheng Y, Dao C, Zhou H, Li B, Kember RL, Toikumo S, Zhao H, Gelernter J, Kranzler HR, Justice AC, Xu K. Multi-trait genome-wide association analyses leveraging alcohol use disorder findings identify novel loci for smoking behaviors in the Million Veteran Program. *Translational Psychiatry* (in press).

Chapters, Books, and Reviews

48. Kranzler HR, **Zhou H**, Kember RL. Identifying and Reducing Bias in Genome-Wide Association Studies of Alcohol-Related Traits. *American Journal of Psychiatry* 2022 Jan;179(1):14-16. doi: 10.1176/appi.ajp.2021.21111107.

49. **Zhou H**, Vasiliou V. Alcohol Use and Use Disorder and Cancer Risk: Perspective on Causal Inference. *Complex Psychiatry* 2022 Sep;8(1-2):9-12. doi: 10.1159/000526407.

Preprint (*contributed equally)

50. **Zhou H***, Hu S*, Matveev R, Yu Q, Li J, Khaitovich P, Jin L, Lachmann M, Stoneking M, Fu Q, Tang K. A chronological atlas of natural selection in the human genome during the past half-million years. *bioRxiv* 2015. doi:10.1101/018929.

51. **Zhou H***, Kember RL*, Deak JD, Xu H, Toikumo S, Yuan K, Lind PA, Farajzadeh L, Wang L, Hatoum AS, Johnson J, Lee H, Mallard TT, Xu J, Johnston KJA, Johnson EC, Galimberti M, Dao C, Levey DF, Overstreet C, Byrne EM, Gillespie NA, Gordon S, Hickie IB, Whitfield JB, Xu K, Zhao H, Huckins LM, Davis LK, Sanchez-Roige S, Madden PAF, Heath AC, Medland SE, Martin NG, Ge T, Smoller JW, Hougaard DM, Børglum AD, Demontis D, Krystal JH, Gaziano JM, Edenberg HJ, Agrawal A; Million Veteran Program; Justice AC, Stein MB, Kranzler HR, Gelernter J. Multi-ancestry study of the genetics of problematic alcohol use in >1 million individuals. *medRxiv,* doi: 10.1101/2023.01.24.23284960.

52. Toikumo S, Vickers-Smith R, Jinwala Z, Xu H, Saini D, Hartwell E, Pavicic M, Sullivan KA, Xu K, Jacobson D, Gelernter J, Rentsch CT, Stahl E, Cheatle M, Zhou H, Waxman S, Justice AC, Kember RL, Kranzler HR. The genetic architecture of pain intensity in a sample of 598,339 US veterans. *medRxiv*, doi: https://doi.org/10.1101/2023.03.09.23286958.

53. Toikumo S, Jennings Mv, Pham B, Lee H, Mallard TT, Bianchi SB, Meredith JJ, Vilar-Ribó L, Xu H, Hatoum AS, Johnson EC, Pazdernik V, Jinwala Z, Leger BS, Niarchou M, Ehinmowo M, Penn Medicine BioBank, Million Veteran Program, Jenkins GD, Batzler A, Pendegraft R, Palmer AA, Zhou H, Biernacka JM, Coombes BJ, Gelernter J, Xu K, Hancock DB, Cox NJ, Smoller JW, Davis LK, Justice AC, Kranzler HR, Kember RL, Sanchez-Roige S. Multi-ancestry meta-analysis of tobacco use disorders based on electronic health record data prioritizes novel candidate risk genes and reveals associations with numerous health outcomes. *medRxiv*, doi: https://doi.org/10.1101/2023.03.27.23287713.