

In the name of God

Zoha Kamali

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Ph.D. Fellow, UMCG

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EXPERIENCE

IUMS, Isfahan — *Research assistant*

September 2016 – September 2025

A collaboration with National Elites Foundation

IUMS, Isfahan — *Teacher assistant*

September 2016 – October 2024

A collaboration with National Elites Foundation

EDUCATION

UMCG, Groningen, Netherlands — *Doctor of Philosophy*

March 2020 – PRESENT

Department of Genetic Epidemiology and Bioinformatics

IUMS, Isfahan, Iran — *Doctor of Philosophy*

September 2019 – October 2024

Department of Bioinformatics

IUMS, Isfahan, Iran — *Master of science*

September 2016 – 2019

Department of genetics and molecular biology

Alzahra, Tehran, Iran — *Bachelor of science*

September 2012 – January 2016

Department of Biotechnology

SKILLS

Bioinformatics

Systems biology

Genetic Epidemiology

Biotechnology

Research, Teaching

AWARDS

Top student at the univ– Alzahra Uni, Tehran

Top student – IUMS, Isfahan

Top publication award – Groningen, NL

Top 10% KANS award - International

Jahat/Shahriari Award – NEF, Iran

Dastavard festival – NEF, Iran

Motahtari festival –Isfahan

Top TED talk - AMT, IUMS, Isfahan

LANGUAGES

Persian

English

Arabic

Publications

22 international journal papers

20 papers in international/national congresses

PROJECTS

Roadmap of developing systems biology in Iran— We wrote a 10-years roadmap for the development of systems biology approach in Iran, which was ordered by the Biotechnology Development Headquarters and conducted under the supervision of the Iranian Systems Biology Association

Kidney Meta- eQTL Project— We are conducting the largest expression quantitative trait loci (eQTL) mapping study on kidney gene expression patterns through a collaboration with international expert teams.

ICBP partitioned PRS Project— We are clustering BP SNPs to different functional groups based on their associations with other related complex traits and diseases. By partitioning the BP polygenic scores (PRS) into functional clusters, we aim to increase the transferability of PRS across ancestries.

Post-GWAS project—GWASs identify the associated genomic loci for complex traits. We analyze these data to find the biological interpretation of the associated loci. We have applied our pipeline on different complex traits/diseases through international projects which their publications are already available online.

PAPERS

Journal papers

Kamali Z, Jalilvandnejad A, Falenji B, Zarei P, Lotfi M, Hadizadeh F, Vaez A. Roadmap for a Systems Biology Initiative in Iran. *Journal of Medical Signals & Sensors*. 2025. 15(9):26. doi: 10.4103/jmss.jmss_66_24.

Zarei P, Kamali Z, Hassanzadeh Keshteli A, Adibi Sedeh P, Vaez A. Investigating Causal Links between Metabolite Profiles and Ulcerative Colitis: A Bidirectional Mendelian Randomization Study. *Journal of Medical Signals & Sensors*. 2025. 15(9):27. doi: 10.4103/jmss.jmss_16_25.

Rosenberg FM, van der Most PJ, Loman L, Kamali Z, et al. A genome-wide association study of hand eczema identifies locus 20q13.33 and reveals genetic overlap with atopic dermatitis. *Contact Dermatitis*. 2024; 91(3): 190-202. doi:10.1111/cod.14619.

Kamali Z, Esmaeil N, Thio CHL, Vaez A, Snieder H. Pathway-Based Mendelian Randomization for Pre-Infection IL-6 Levels Highlights Its Role in Coronavirus Disease. *Genes*. 2024; 15(7):889. doi: 10.3390/genes15070889

Keaton J, Kamali Z, Xie T, Vaez A, Williams A, et al. Genome-wide analysis in over 1 million individuals of European ancestry yields improved polygenic risk scores for blood pressure traits. *Nature Genetics*. 2024. 56: 778–791. doi: 10.21203/rs.3.rs-1409164/v1.

Riesmeijer S, Kamali Z, Ng Michael, Drichel D, Layton T, et al. A genome-wide association meta-analysis implicates Hedgehog and Notch signaling in Dupuytren's disease. *Nature Communications*. 2024. 15: 199. doi: 10.1038/s41467-023-44451-0.

Lu X, van der Meer TP, Kamali Z, van Faassen M, Kema IP, van Beek AP, et al. A genome-wide association study of 24-hour urinary excretion of endocrine disrupting chemicals. *Environment International*. 2024. 183:108396.

Mathieson I, Day FR, Barban N, Tropf FC, Brazel DM, ..., Kamali Z, et al. Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus. *Nature human behaviour*. 2023. 7(5): 790-801.

Suzuki K, Hatzikotoulas K, Southam L, Taylor HJ, Yin X, ... Kamali Z, et al. Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. *Nature*. 2024. doi: 10.1038/s41586-024-07019-6.

Kamali Z, Vonk JM, Thio CHL, Vaez A, Snieder H. A Mendelian randomization cytokine screen reveals IL-13 as causal factor in risk of severe COVID-19. *Journal of Infection*. 2022. 85(3):334-363.

Kamali Z, Keaton JM, Haghjooy Javanmard S, International Consortium of Blood Pressure, Million Veteran Program, eQTLGen Consortium, et al. Large-Scale Multi-Omics Studies Provide New Insights into Blood Pressure Regulation. *International Journal of Molecular Sciences*. 2022;23(14):7557.

Ganji Arjenaki M, Kamali Z, International Consortium of Blood pressure, Sardari S, de Borst M, Snieder H, Vaez A. Prioritization of kidney cell types highlights myofibroblast cells in regulating human blood pressure. *Kidney International Reports* [Accepted]. 2024.

Amare AT, Vaez A, Hsu YH, Direk N, Kamali Z, Howard DM, et al. Bivariate genome-wide association analyses of the broad depression phenotype combined with major depressive disorder, bipolar disorder or schizophrenia reveal eight novel genetic loci for depression. *Molecular Psychiatry*. 2020 Jul;25(7):1420-1429.

Mills MC, Tropf FC, Brazel DM, van Zuydam N, Vaez A, Pers TH, et al. Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. *Nature Human Behavior*. 2021; 5(12): 1717-1730.

de Haan A, Ahmadizar F, van der Most PJ, Thio CHL, Kamali Z, Ani A, et al. Genetic Determinants of Serum Calcification Propensity and Cardiovascular Outcomes in the General Population. *Frontiers in Cardiovascular Medicine*. 2022 Jan 14;8:809717.

Sas AA, Vaez A, Jamshidi Y, et al. Genetic and environmental influences on stability and change in baseline levels of C-reactive protein: A longitudinal twin study. *Atherosclerosis*. 2017;265:172-178.

Thio CHL, Reznichenko A, van der Most PJ, et al. Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. *American Journal of Nephrology*. 2019;49(3):193-202.

Rosenberg FM, Z Kamali, Voorberg AN, et al. Transcriptomics-and Genomics-Guided Drug Repurposing for the Treatment of Vesicular Hand Eczema. *Pharmaceutics*. 2024; 16(4): 476.

Poursafa P, Kamali Z, Fraszczyk E, et al. DNA methylation: a potential mediator between air pollution and metabolic syndrome. *Clinical epigenetics*. 2022; 14(1): 82.

Asefa NG, Kamali Z, Pereira S, Vaez A, Jansonius N, Bergen AA, et al. Bioinformatic Prioritization and Functional Annotation of GWAS-Based Candidate Genes for Primary Open-Angle Glaucoma. *Genes*. 2022 Jun 13;13(6):1055.

Asefa N, Pereira SD, Kamali Z, et al. Functional characteristics and relationships between GWAS-based candidate genes of primary open-angle glaucoma. *Investigative Ophthalmology & Visual Science*. 2020; 61(7): 1246.

Zhang W, van der Most PJ, Wang S, Kamali Z, Giontella A, Enhörning S, Gansevoort RT, van der Harst P, Bakker SJL, Melander O, Keus F, Lunter G, Snieder H. A Genome- and Phenome-Wide Association Study of Serum Procalcitonin Concentrations in Individuals of European Ancestry. SSRN. Doi: 10.2139/ssrn.5116033.

Kamali Z, Tarverdi S, Afzalan Z, Shariat Nabavi NS. Comparison of traditional and modern medicine in TB Treatment. *jiitm*. 2017 Mar 1;7(4):415–29.

Congress papers

Kamali Z, Haghjooy Javanmard S, Snieder H, Vaez A. Systems Genetics approaches reveal new targets and mediating mechanisms for blood pressure. *WEON*. In Amsterdam, the Netherlands; 2021.

Asefa N; Pereira SD; Kamali Z; Vaez A; Bergen A; Snieder H. Functional characteristics and relationships between GWAS-based candidate genes of primary open-angle glaucoma. *ARVO*. In US (Virtual); 2020.

Kamali Z, Haghjooy Javanmard S, ICBP Consortium, eQTLGen Consortium, BIOS Consortium, Snieder H, et al. Systems Genetics approaches reveal new targets and mediating mechanisms for blood pressure. *ASHG*. In California, US.; 2020.

Kamali Z, Vaez A. Linking cancer genomics to metabolites: a Mendelian randomization study. *ICIBS*. In Isfahan, Iran.; 2021.

Kamali Z, Vaez A. Genomic instruments help to find Driver nodes in co-expression networks. *ICIBS*. In Isfahan, Iran; 2021.

Kamali Z, Vaez A. Computational genomics of type 2 diabetes: an integrative approach to shed light on genome-wide statistics. *3rd international and 15th national genetics congress of Iran*. In Tehran, Iran; 2019.

Kamali Z, Haghjooy Javanmard S, Snieder H, Vaez A. Unravelling regulation of blood pressure: a large-scale multi-omics approach. *4th ICSB*. In Tehran, IR; 2020.

Kamali Z, Asefa N.G., Pereira S.D., Bergen A., Snieder H., Vaez A. Prioritization and follow up of primary open-angle glaucoma associated genes. *4th ICSB*. In Tehran, IR; 2020.

Kamali Z, Vaez A. Mendelian randomization analyses refer to a protective role for VLDL concentration against type 2 diabetes. *4th ICSB*. In Tehran, IR; 2020.

Kamali Z, Vaez A. Genomic instruments help to find Driver nodes in co-expression networks. *4th ICSB*. In Tehran, IR; 2020.

Kamali Z, Vaez A. Identification of relevant genes and tissues for blood pressure. *3rd ICSB*. In Tehran, IR; 2018.

Kamali Z. How to apply a genetic method to investigate causality of associations at the omics level. *USERN mTalks*. In Tehran, Iran; 2018.

de Haan A, Ahmadizar F, Van der Most PJ, Kamali Z, et al. Genetic Determinants of Serum Calcification Propensity and Mortality Risk in CKD: FR-OR59. *Journal of the American Society of Nephrology*. 2021; 32(10S): 38.

Asefa N, Pereira SD, Kamali Z, et al. Functional characteristics and relationships between GWAS-based candidate genes of primary open-angle glaucoma. *Investigative Ophthalmology & Visual Science*. 2020; 61(7): 1246.

Keaton JM, Xie T, Kamali Z, et al. Genetic analyses in over 1 million individuals yields improved polygenic risk scores for blood pressure enabling patient stratification of hypertension risk in both European and African ancestry populations. BIHS. UK; 2024.

Warren HR, Keaton JM, Kamali Z, et al. Genome-wide analysis in over 1 million individuals reveals over 2,000 independent genetic signals for blood pressure. BIHS. UK; 2022.

Keaton JM, Kamali Z, Vaez A, et al. Genome-wide analysis in over 1 million individuals reveals over 2,000 independent genetic signals for blood pressure. CHARGE. US; 2023.

Keaton JM, Xie T, Kamali Z, et al. SBayesRC improves polygenic risk score performance for blood pressure and hypertension in a large population cohort. CHARGE. US; 2024.

Keaton JM, Kamali Z, Vaez A, et al. Genome-wide analysis in over 1 million individuals reveals over 2,000 independent genetic signals for blood pressure. ASHG. US; 2022.