Curriculum Vitae

Mark Zlojutro Kos, Ph.D.

Associate Research Professor
Division of Human Genetics
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Contact Information

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Education

Ph.D., Anthropology, University of Kansas, Lawrence, KS, 2008

- Concentration in Anthropological Genetics
- Dissertation: “Mitochondrial DNA and Y-Chromosome Variation in Aleut Populations: Genetic Implications of Founder Effect, Asymmetrical Gene Flow and the Original Peopling of the Aleutian Archipelago”
- Ph.D. advisor and committee chair: Dr. Michael H. Crawford

M.A., Anthropology, University of Kansas, Lawrence, KS, 2006

- Thesis: “Mitochondrial DNA Variation in Yakutia: The Genetic Structure of an Expanding Population”

B.S., Biology, McMaster University, Hamilton, ON, Canada, 1997

- Minor in History
- Senior thesis: “A Population Genetic Study of Three Microsatellite Loci in the Indian Subcontinent”

Employment History

2023-Present	Associate Research Professor, South Texas Diabetes and Obesity Institute, The University of Texas Rio Grande Valley SOM
2015-2023	Assistant Research Professor, South Texas Diabetes and Obesity Institute, The University of Texas Rio Grande Valley SOM

2012-2015	Staff Scientist I, Texas Biomedical Research Institute
2008-2012	Post-Doctoral Scientist, Texas Biomedical Research Institute
2006-2008	Laboratory Supervisor, Laboratory of Biological Anthropology (LBA), University of Kansas
2004-2006	Graduate Teaching Assistant, University of Kansas
2003-2004	Visiting Researcher, Integrated DNA Technologies, Coralville, IA
2001	Intern, Kansas Health Institute, Topeka, Kansas
2000-2004	Research Assistant, Laboratory of Biological Anthropology, University of Kansas

Honors and Fellowships

2016	Junior Faculty Travel Support Program Award (UTRGV) to attend the 39th Research Society on Alcoholism, New Orleans, LA, USA
2012	Travel award and poster presentation award finalist for the 20th World Congress of Psychiatric Genetics in Hamburg, Germany
2009	Cowles Memorial Trust Fellowship for Postdoctoral Research, Southwest Foundation for Biomedical Research, San Antonio, TX
2008	Dissertation honors pass for Mitochondrial DNA and Y-Chromosome Variation of Eastern Aleut Populations: Implications for the Genetic Structure and Peopling of the Aleutian Archipelago, University of Kansas, Lawrence, KS
2007	The Midwestern Association of Graduate Schools (MAGS) & UMI Dissertation Publishing's Distinguished Masters Thesis Award for the MA thesis entitled Mitochondrial DNA Variation in Yakutia: The Genetic Structure of an Expanding Population, Indianapolis, IN
2005	Carroll D. Clark Research Award, University of Kansas, Lawrence, KS
2004	American Association of Anthropological Genetics (AAAG) Best Graduate Student Presentation. Awarded for Mitochondrial DNA Variation in Yakutia: The Genetic Structure of an Expanding Population presented at Human Biology Association's annual meeting, Tampa, FL

Teaching

Ph.D Program in Human Genetics, UTRGV, Brownsville, TX

2022-2023	HGEN 8301 Molecular Genetics
2022-2024	HGEN 8310 Genetic Epidemiology and Statistical Genetics
2023-2024	HGEN 8215 Current Topics in Human Genetics

2023-2024	HGEN 8305 Genetic Basis of Human Disease
2023	HGEN 8355 Advanced Topics in Omics Research
2023	HGEN 8380 Advanced Topics in Neurogenetics
2024	HGEN 8395 Directed Research

UTRGV School of Medicine, Edinburg, TX

2020-2021	Endocrine & Female Reproduction Module: Endocrine Disruptors
2017-2022	Endocrine & Female Reproduction Module: Endocrine Genetics
2019-2023	Molecules to Medicine Module: Epigenetics

The University of Texas Health Science Center, San Antonio, TX

2015-2018	CSBL5024-001: Genomics (Graduate Level)

University of Kansas, Lawrence, KS

2004-2006	ANTH 104: Fundamentals of Physical Anthropology

Other Teaching Activities:

University of Kansas, Lawrence, KS

2012	Reviewed Ph.D. dissertation by Christine Phillips-Krawczak: “Origins and Genetic Structure of the Garifuna Population of Central America”
2016	Adviser for Masters’ thesis by Sarah Dale Alden; examining population genetic structure in the Aleutian Islands

Texas Biomedical Research Institute, San Antonio, TX

2012-2013	Organized workshop for visiting researchers from the Collaborative Study on the Genetics of Alcoholism (COGA) on the use and applications of SOLAR, a genetic statistical software package

Queensland University of Technology, Brisbane, QLD, Australia

2018	Served as examiner for Ph.D. dissertation by Seyyed Reza: “Investigation of Cardiovascular Disease Susceptibility Markers in the Norfolk Island Population Isolate and an Australian Hypertensive-Normotensive Cohort”

University of Applied Sciences, FH Campus Wien, Vienna, Austria

2018	Advised and assisted on undergraduate research thesis by Vanessa Feuerer: “Identification of Potential Peripheral miRNA Biomarkers for Brain-Related Disease”

Gomal University, Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan

2020	Served as examiner for Ph.D. dissertation by Hadia Gul: “Genetic Dissection of Pakistani Families Segregating Autosomal Recessive Albinism”

Research Interests

My areas of research interest include statistical genetics, genetic epidemiology, bioinformatics, methods and software development, and genetics of complex traits. My research has mostly focused on identifying the genetic and epigenetic determinants of psychiatric and neurological disorders (e.g., schizophrenia, epilepsy) and brain-related correlates (e.g., electrophysiology, neurocognition), as well as diabetes and obesity. I have worked on both case-control and family-based study designs, including genome-wide association studies (GWAS), linkage analysis, pathway enrichment tests, hierarchical clustering and network construction, and polygenic risk scoring routines. Currently, my research is investigating the genetics of generalized epilepsy in the baboon colony at the Southwest National Primate Research Center (SNPRC; San Antonio, TX), with the objective of identifying key pathophysiological mechanisms underlying the disease. The primary goal from this work is to develop a multi-omic, preclinical platform for developing and testing novel therapies in the baboon that can translate to human applications and serve as a unique resource for the wider epilepsy research community.

I also have a strong interest in molecular anthropology and human evolution, which was the area of research for my graduate work at the University of Kansas. I have published studies about the population genetics of Native American and Siberian populations and the peopling of the Americas, with a focus on the native communities of the Aleutian archipelago and the consequences of male-biased gene flow from European populations.

My technical skills include R statistical programming; Perl and Unix shell scripting; SOLAR software package for genetic variance components analysis; PLINK program for genome-wide association testing and polygenic risk scoring; pathway enrichment analysis; weighted gene co-expression network analysis (WGCNA); and bioinformatics pipelines for processing, aligning, and annotating variant calls from whole-genome sequence (WGS), RNA-seq, and Meth-seq data.

Research Grants

Current Research Support

2018-2025	1 R01 DK118630-01 (Carless) “Epigenetics of energy homeostasis, bioenergetics and obesity” The major goal of this project is to identify epigenetic factors which are associated with energy balance and obesity and define their role in transcriptional regulation and cellular energy metabolism.	NIH/NIDDK

Role: Co-Investigator, PI of Subcontract to UTRGV

2023-2025 R21 AG085428 (Carless) NIH
“DNA methylation signatures of Alzheimer’s disease in aged astrocytes”
Role: Co-Investigator, PI of Subcontract to UTRGV

Completed Research Support

2011-2012 Forum Foundation Grant (TX Biomed), $35,000
“Application of Exome Sequencing to Identify Genetic Variants Contributing to Schizophrenia and Related Phenotypes”

Grant Applications Submitted

Title: Preclinical modeling of neural regulatory networks in baboon epilepsy; Grant Period: 12/01/2024-11/30/2029; Funding Agency: NIH (R01); Direct Costs: $391,083.00; Indirect Costs: $178,119.00; Total Costs: $569,202.00; Role: MPI.

Title: miRNA profiling of neural-derived plasma exosomes in bipolar disorder; Grant Period: 04/01/2024-03/31/2026; Funding Agency: NIH (R21); Direct Costs: $18,367.00; Indirect Costs: $8,816.00; Total Costs: $27,183.00; Role: Co-I.

Title: Pedigree-based analytical methods for studying the genome, the exposome, and their interaction; Grant Period: 04/01/2024-03/31/2029; Funding Agency: NIH (R01); Direct Costs: $2,120,143.00; Indirect Costs: $970,424.00; Total Costs: $3,090,567.00; Role: Co-I.

Title: Pedigree-based analytical methods for studying the genome, the exposome, and their interaction; Grant Period: 09/01/2024-08/31/2029; Funding Agency: NIH (R01); Direct Costs: $2,281,021.00; Indirect Costs: $1,047,645.00; Total Costs: $3,328,666.00; Role: Co-I.

Title: Integrative Lipidomic and Proteomic Analysis of ADRD in Hispanics; Grant Period: 09/01/2024-08/31/2029; Funding Agency: NIH (R01); Direct Costs: $2,032,949.00; Indirect Costs: $987,817.00; Total Costs: $3,020,766.00; Role: Assoc. Prof. Research.

Publications and Manuscripts

Note: Includes publications under former name **Mark Zlojutro**

Scientific Articles:

1. Kumar A*****, **Kos MZ***, Roybal D, and Carless MA (2023) A pilot investigation of differential hydroxymethylation levels in patient-derived neural stem cells

implicates altered cortical development in bipolar disorder. *Frontiers in Psychiatry* 14: 1077415. *****Equally contributing first authors.

2. **Kos MZ**, Puppala S, Cruz D, Neary JL, Ashish K, Dalan E, Li C, Nathanielsz P, and Carless MA (2022) Blood-based miRNA biomarkers as correlates of brain-based miRNA expression. *Frontiers in Molecular Neuroscience* 15: 817290.

3. **Kos MZ**, Carless MA, Blondell L, Leland MM, Knape KD, Göring HHH, and Szabó CA (2021) Whole genome sequence data from captive baboons implicate *RBFOX1* in epileptic seizure risk. *Frontiers in Genetics* 12: 714282.

4. Blondell L, **Kos MZ**, Blangero J, and Göring HHH (2021) Genz and Mendell-Elston estimation of the high-dimensional multivariate normal distribution. *Algorithms* 14: 296.

5. Blackburn AN, Blondell L, **Kos MZ**, Blackburn N, Peralta JM, Stevens PT, Lehman DM, Blangero J, and Göring HHH (2020) Genotype phasing in pedigrees using whole genome sequence data. *European Journal of Human Genetics* 28(6): 790-803.

6. **Kos MZ**, Duan J, Sanders AR, Blondell L, Drigalenko EI, Carless MA, MGS, Gejman PV, and Göring HHH (2018) Dopamine perturbation of gene co-expression networks reveals differential response in schizophrenia for translational machinery. *Translational Psychiatry* 8(1): 278.

7. Arya R, Escalante A, Farook V, Restrepo JF, Battafarano DF, Almeida M, **Kos MZ**, Fourcaudot MJ, Mummidi S, Kumar S, Curran JE, Jenkinson CP, Blangero J, Duggirala R, and del Rincon I (2018) Data on genetic associations of carotid atherosclerosis markers in Mexican American and European American rheumatoid arthritis subjects. *Data in Brief* 17: 820-829.

8. Arya R, Escalante A, Farook V, Restrepo JF, Battafarano DF, Fourcaudot MJ, Almeida M, **Kos MZ**, Kumar S, Curran JE, Jenkinson CP, Blangero J, Duggirala R, and del Rincon I (2018) A genetic association study of carotid intima-media thickness (CIMT) and plaque in Mexican Americans and European Americans with rheumatoid arthritis. *Atherosclerosis* 271: 92-101.

9. Blondell L, Blackburn A, **Kos MZ**, Blangero J, and Göring HHH (2018) Contribution of inbred singletons to variance component estimation of heritability and linkage. *Human Heredity* 83(2): 92-99.

10. Duan J, Göring HHH, Sanders AR, Moy W, Freda J, Drigalenko EI, **Kos M**, He D, and Gejman PV (2018) Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. *Translational Psychiatry* 8(1): 158.

11. **Kos MZ**, Carless MA, Peralta J, Curran JE, Quillen EE, Almeida M, Blackburn, A, Blondell L, Roalf DR, Pogue-Geile MF, Prasad K, Gur RC, Göring HHH, Nimgaonkar V, Gur RE, and Almasy L (2017) Exome sequences of multiplex, multigenerational families reveal schizophrenia risk loci with potential implications for neurocognitive performance. *American Journal of Medical Genetics Part B* 174(8): 817-827.

12. Mathies LD, Aliev F, Porjesz B, Hesselbrock V, Edenberg H, Bierut L, Nurnberger J Jr, Foroud T, Kuperman S, Kramer J, Porjesz B, Bierut L, Rice J, Bucholz K, Agrawal A, Schuckit M, Tischfield J, Brooks A, Almasy L, Goate A, Taylor R, Bauer L, McClintick J, Wetherill L, Xuei X, Liu Y, Lai D, O'Connor S, Plawecki M, Lourens S, Chan G, Meyers J, Chorlian D, Kamarajan C, Pandey A, Zhang J, Wang JC, Kapoor M, Bertelsen S, Anokhin A, McCutcheon V, Saccone S, Salvatore J, Cho B, **Kos M**, Parsian A, Reilly M, Davies AG, Dick DM, and Bettinger JC (2017) Variation in SWI/SNF chromatin remodeling complex proteins is associated with alcohol dependence and antisocial behavior in human populations. *Alcoholism: Clinical and Experimental Research* 41(12): 2033-2040.

13. **Kos MZ**, Carless MA, Peralta J, Blackburn A, Almeida M, Roalf D, Pogue-Geile MF, Prasad K, Gur RC, Nimgaonkar V, Curran JE, Duggirala R, Glahn DC, Blangero J, Gur RE, and Almasy L (2016) Exome sequence data from multigenerational families implicate AMPA receptor trafficking in neurocognitive impairment and schizophrenia risk. *Schizophrenia Bulletin* 42(2): 288-300.

14. Kulkarni H, **Kos MZ**, Neary J, Dyer TD, Kent JW Jr, Göring HH, Cole SA, Comuzzie AG, Almasy L, Mahaney MC, Curran JE, Blangero J, and Carless MA (2015) Novel epigenetic determinants of type 2 diabetes in Mexican-American families. *Human Molecular Genetics* 24(18): 5330-5344.

15. **Kos MZ**, Glahn DC, Carless MA, Olvera R, McKay DR, Quillen EE, Gelernter J, Chen X-D, Deng H-W, Kent JW, Dyer TD, Göring HHH, Curran JE, Duggirala R, Blangero J, and Almasy L (2014) Novel QTL at chromosome 6p22 for alcohol consumption: Implications for the genetic liability of alcohol use disorders. *American Journal of Medical Genetics B* 165B: 294-302.

16. Yan J, Aliev F, Webb BT, Kendler KS, Williamson VS, Edenberg HJ, Agrawal A,

Kos MZ, Almasy L, Nurnberger JI Jr, Schuckit MA, Kramer JR, Rice JP, Kuperman S, Goate AM, Tischfield JA, Porjesz B, and Dick DM (2014) Using genetic information from candidate gene and genome-wide association studies in risk prediction for alcohol dependence. *Addiction Biology* 19:708-721.

17. **Kos MZ**, Yan J, Dick DM, Agrawal A, Bucholz KK, Rice JP, Johnson EO, Schuckit M, Kuperman S, Kramer J, Goate AM, Tischfield JA, Foroud T, Nurnberger J Jr, Hesselbrock V, Porjesz B, Bierut LJ, Edenberg HJ, and Almasy L (2013) Common biological networks underlie genetic risk for alcoholism in African- and European-American populations. *Genes, Brain and Behavior* 12: 532-542.

18. Anderson-Schmidt H, Beltcheva O, Brandon MD, Byrne EM, Diehl EJ, Duncan L, Gonzalez SD, Hannon E, Kantojärvi K, Karagiannidis I, **Kos MZ**, Kotyuk E, Laufer BI, Mantha K, McGregor NW, Meier S, Nieratschker V, Spiers H, Squassina A, Thakur GA, Tiwari Y, Viswanath B, Way MJ, Wong CC, O'Shea A, and DeLisi LE (2013) Selected rapporteur summaries from the XX World Congress of Psychiatric Genetics, Hamburg, Germany, October 14-18, 2012. *American Journal of Medical Genetics B* 162B: 96-121.

19. Carless MA, Kulkarni H, **Kos MZ**, Charlesworth J, Peralta JM, Göring HHH, Curran JE, Almasy L, Dyer TD, Comuzzie AG, Mahaney MC, and Blangero J (2013) Genetic effects on DNA methylation and its potential relevance for obesity in Mexican Americans. *PLoS One* 8: e73950.

20. **Zlojutro M**, Manz N, Rangaswamy M, Xuei X, Flury-Wetherill L, Koller D, Beirut L, Cloninger R, Goate A, Hesselbrock V, Kuperman S, Nurnberger J, Rice J, Schuckit M, Foroud T, Edenberg HJ, Porjesz B, and Almasy L (2011) Genome-wide association study of theta band event-related oscillations identifies serotonin receptor gene *HTR7* influencing risk of alcohol dependence. *American Journal of Medical Genetics: Part B* 156B: 44-58.

21. Kumar S, Bellis C, **Zlojutro M**, Melton PE, Blangero J, and Curran J (2011) Large scale mitochondrial sequencing in Mexican Americans suggests a reappraisal of Native American origins. *BMC Evolutionary Biology* Oct. 7: 293.

22. Crawford MH, Rubicz RC, and **Zlojutro M** (2010) Origins of Aleuts and the genetic structure of populations of the archipelago: molecular and archaeological perspectives. *Human Biology* 82: 695-717.

23. Graf OM, **Zlojutro M**, Rubicz R, and Crawford MH (2010) Surname distributions and their association with Y-chromosome markers in the Aleutian Islands. *Human Biology* 82: 745-757.

24. Melton PE, Mosher MJ, Rubicz R, **Zlojutro M**, and Crawford MH (2010) Mitochondrial DNA diversity in Mennonite communities from the Midwestern United States. *Human Biology* 82: 267-289.

25. Rubicz R, **Zlojutro M**, Sun G, Spitsyn V, Deka R, Young K, and Crawford MH (2010) Genetic architecture of a small, recently aggregated Aleut population: Bering Island, Russia. *Human Biology* 82: 719-736.

26. **Zlojutro M**, Rubicz R, and Crawford MH (2009) Mitochondrial DNA and Y-chromosome variation in five eastern Aleut communities: evidence for genetic substructure in the Aleut population. *Annals of Human Biology* 36 (5): 511-526.

27. **Zlojutro M**, Tarskaia LA, Sorensen M, Snodgrass JJ, Leonard WR, and Crawford MH (2009) Coalescent simulations of Yakut mtDNA diversity suggest small founding population. *American Journal of Physical Anthropology* 139 (4): 474-482.

28. Devor EJ, Abdurakhmonov I, **Zlojutro M**, Millis MP, Galbraith JJ, Crawford MH, Shermatov S, Buriev Z, and Abdukarimov A (2009) Gene flow at the crossroads of humanity: mtDNA sequence diversity and *Alu* insertion polymorphism frequencies in Uzbekistan. *The Open Genomics Journal* 2: 1-11.

29. **Zlojutro M**, Tarskaia LA, Sorensen M, Snodgrass JJ, Leonard WR, and Crawford MH (2008) The origins of the Yakut People: Evidence from mitochondrial DNA diversity. *International Journal of Human Genetics* 8 (1-2): 119-130.

30. Moscoso J, Crawford MH, Vicario JL, **Zlojutro M**, Serrano-Vela JI, Reguera R, and Arnaiz-Villena A (2008) HLA genes of Aleutian Islanders living between Alaska (USA) and Kamchatka (Russia) suggest a possible southern Siberia origin. *Molecular Immunology* 45 (4): 1018-1026.

31. **Zlojutro M**, Roy R, Palikij J, and Crawford MH (2006) Autosomal STR variation in a Basque population. *Human Biology* 78 (5): 599-618.

32. **Zlojutro M**, Rubicz R, Devor E, Spitsyn V, Wilson K, and Crawford MH (2006) Genetic structure of the Aleuts and circumpolar populations Based on mitochondrial DNA Sequence: A Synthesis. *American Journal of Physical Anthropology* 129 (3): 446-464.

33. Melton PE, **Zlojutro M**, Kimminau K, and Crawford MH (2006) Biological aging and Cox hazard analysis of mortality trends in a Mennonite community from south-central Kansas. *American Journal of Human Biology* 18 (3): 387-401.

34. Phillips-Krawczak C, Devor E, **Zlojutro M**, and Crawford MH (2006) mtDNA variation in the Altai-Kizhi population of Southern Siberia: A synthesis of genetic variation. *Human Biology* 78 (4): 477-494.

35. Crawford MH, Banerjee P, Demarchi DA, **Zlojutro M**, McComb J, Livshits G, Henneberg M, Mosher MJ, Schanfield MS, and Knowles JA (2005) Applications of pooled DNA samples to the assessment of population affinities: Short tandem repeats. *Human Biology* 77 (6): 723-733.

Book Chapters:

36. Almasy L, **Kos MZ**, and Blangero J (2015) Linkage mapping: Localizing the genes that shape human variation. In *Genome Mapping and Genomics in Human and non-Human Primates*, R Duggirala, L Almasy, S Williams-Blangero, SFD Paul, and C Kole eds. Heidelberg, Germany: Springer-Verlag.

Preprints:

37. Bhaskar U, Shrimpton E, Ayo J, Prasla A, **Kos MZ**, and Carless MA (2024) An Efficient Direct Conversion Strategy to Generate Functional Astrocytes from Human Adult Fibroblasts. *bioXriv*. DOI: 10.1101/2024.09.02.610876

Submissions:

38. Bhaskar U, **Kos MZ**, and Carless MA. Direct conversion of human fibroblasts to induced astrocytes using small molecules. Submitted to *Stem Cell Reports*.

In Preparation:

39. **Kos MZ**, Blackburn AN, Stevens P, Blondell L, and Göring HHH. Software for peak alignment and quantification of comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry metabolomics data.

Presentations

Invited Presentations:

1. **Kos MZ**, Salinas F, and Szabó CA (2021) Back to the baboon: New insights into the epilepsy model and their implications for future studies. Presentation given for the Neuroscience Grand Rounds at the Department of Neurology at UT Health, San Antonio, TX, USA.

2. **Kos MZ**, Bierut L, Porjesz B, Almasy L, COGEND Authors, and COGA Authors (2016) Investigation of the P300 genetic component in the risk of alcohol dependence among European- and African-American subjects via multimarker scoring. Podium presentation given at the 39th Research Society on Alcoholism, New Orleans, LA, USA.

3. **Kos MZ** (2016) Genetic architecture of the P300 brain potential and its role in alcohol dependence. Invited speaker to the Department of Cellular and Structural Biology (CSB) Seminar Series, University of Texas Health Science Center at San Antonio, San Antonio, TX, USA.

4. **Zlojutro M** (2010) Why did I become an anthropologist? Podium presentation given at the 79th annual meeting of the American Association of Physical Anthropologists, Albuquerque, NM.

5. **Zlojutro M**, Rubicz R, and Crawford M (2006) The genetic structure of the Aleuts and circumarctic populations and its implications for the peopling of North America. Podium presentation given at the 75th annual meeting of American Association of Physical Anthropologists, Anchorage, AK.

Conference Presentations:

6. **Kos MZ**, Carless MA, Blondell L, Leland MM, Knape KD, Göring HHH, and Szabó CA (2021) Whole genome sequence data implicate RBFOX1 in epilepsy risk in baboons. Poster presentation given at the 34th International Epilepsy Congress (conducted virtually).

7. **Kos MZ**, Blackburn A, Stevens P, Truax K, Blondell L, and Göring H (2019) Computational software for peak alignment and quantification of comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry metabolomics data. Poster presentation given at the 69th American Society of Human Genetics conference, Houston, TX, USA.

8. **Kos MZ**, Blackburn A, Stevens P, Truax K, Blondell L, and Göring H (2019) Software for peak alignment and quantification of comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry metabolomics data. Poster presentation given at the 3rd UTRGV Research Symposium, McAllen, TX, USA.

9. **Kos M**, Duan J, Sanders A, Blondell L, Drigalenko E, Carless M, Gejman P, and Göring H (2018) Dopamine perturbation of gene co-expression networks reveals differential response among schizophrenia subjects for translational machinery. Poster presentation given at the 2nd UTRGV Research Symposium, Edinburg, TX, USA.

10. **Kos MZ**, Duan J, Sanders AR, Moy W, Freda J, Drigalenko EI, He D, MGS, Gejman PV, and Göring HHH (2017) Dopamine-induced gene expression signatures of schizophrenia in lymphoblastoid cell lines. Poster presentation given at the 1st UTRGV Research Symposium, Edinburg, TX, USA.

11. **Kos MZ**, Bierut L, Porjesz B, Almasy L, COGEND Authors, and COGA Authors (2015) Multimarker scoring routines based on P300 neuroelectrical measurements show association with alcohol dependence in independent subjects, with significant enrichment in axon guidance pathways. Poster presentation given at the 23rd World Congress of Psychiatric Genetics, Toronto, Canada.

12. **Kos MZ**, Blackburn AN, and Almasy L (2014) Assessment of Type I error rates and power for pathway analysis in family-based samples: Comparison of GWAS and exome sequence datasets from GAW19. Presentation given at the Genetic Analysis Workshop (GAW) 19, Vienna, Austria.

13. **Kos MZ**, Carless M, Peralta J, Almeida M, Gur RC, Pogue-Geile MF, Roalf D, Nimgaonkar V, Curran JE, Duggirala R, Glahn D, Blangero J, Gur RE, and Almasy L (2014) Exome sequence data from multigenerational families implicate AMPA receptor trafficking in neurocognitive impairment and schizophrenia risk. Poster presentation given at the 22nd World Congress of Psychiatric Genetics, Copenhagen, Denmark.

14. **Kos MZ**, Peralta J, Carless MA, Almeida M, Gur RC, Pogue-Geile MF, Calkins ME, Nimgaonkar V, Gur RE, and Almasy L (2013) Dissection of QTL for neurocognitive performance on chromosome 5q: Identification of two schizophrenia susceptibility loci from exome sequence data. Poster presentation given at the 21st World Congress of Psychiatric Genetics, Boston, MA.

15. **Kos MZ**, Peralta J, Carless MA, Almeida M, Gur RC, Pogue-Geile MF, Roalf D, Nimgaonkar V, Gur RE, and Almasy L (2013) Exome sequences of multiplex, multigenerational families reveal schizophrenia risk loci involved in fatty acid oxidation. Poster presentation given at the 63rd American Society of Human Genetics conference, Boston, MA.

16. **Kos MZ**, Neary J, Cruz DA, Kulkarni H, Curran JE, Almasy L, Olvera R, Duggirala R, Thompson PM, Glahn D, Blangero J, and Carless MA (2012) Association of microRNA expression with diagnoses of major depression (MDD) and the Beck Depression Inventory (BDI) test. Podium presentation given at the 9th GeneMappers conference, Port Douglas, Australia.

17. **Kos MZ**, Glahn D, Carless M, Olvera R, Kent J, Dyer T, Göring HHH, Curran JE, Duggirala R, Blangero J, and Almasy L (2012) Novel quantitative trait locus for an alcoholism-related phenotype. Poster presentation given at the 20th World Congress of Psychiatric Genetics, Hamburg, Germany.

18. **Kos MZ**, Carless MA, Peralta J, Quillen EE, Gur RC, Pogue-Geile MF, Prasad K, Blangero J, Nimgaonkar VL, Gur RE, and Almasy L (2012) Exome sequencing of multiplex, schizophrenic families implicates variants from chromosome 5q in neurocognitive performance. Poster presentation given at the 62nd American Society of Human Genetics conference, San Francisco, CA.

19. **Zlojutro M**, Dick DM, Agrawal A, Bucholz KK, Schuckit M, Kuperman S, Kramer J, Tischfield JA, Nurnberger Jr JI, Hesselbrock V, Porjesz B, Bierut L, Edenberg HJ, and Almasy L (2011) GWAS scoring routines and serial, permutated enrichment analyses reveal a substantial polygenic component to the risk of alcohol dependence, with biological ontologies implicated in both European-American and African-American subjects. Poster presentation given at the 12th meeting of the International Congress of Human Genetics, Montreal, Canada.

20. **Zlojutro M**, Kent Jr JW, Dyer T, Blangero J, and Almasy L (2010) Application of endophenotype-based genetic scoring routines for assessing the polygenic architecture of complex disease and its underlying biological pathways in the

Genetic Analysis Workshop 17 exome sequence data. Presentation given at the 17th Genetic Analysis Workshop, Boston, MA.

21. **Zlojutro M**, Tarskaia LA, Sorensen M, Snodgrass JJ, Leonard WR, and Crawford MH (2010) Coalescent modeling of Yakut origins points to small founding population based on mtDNA variation. Poster presentation given at the 79th annual meeting of the American Association of Physical Anthropologists, Albuquerque, NM.

22. **Zlojutro M**, Gur RC, Pogue-Geile M, Hare E, Calkins ME, Prasad K, Glahn D, Blangero J, Nimgaonkar V, Gur RE, and Almasy L (2010) Evaluating endophenotypes for schizophrenia with endophenotype ranking value statistic. Poster presentation given at the 60th annual meeting of the American Society of Human Genetics, Washington, DC.

23. **Zlojutro M**, Rangaswamy M, Manz N, Derringer J, Edenberg HJ, Kramer J, Krueger R, Nurnberger Jr J, Schuckit MA, Bierut LA, Porjesz B, and Almasy L (2010) Identification of genes influencing alcohol dependence via electrophysiological mechanisms using GWAS scoring and pathway-oriented analysis. Poster presentation given at the 18th World Congress on Psychiatric Genetics, Athens, Greece.

24. **Zlojutro M**, Glahn D, Escamilla M, Carless M, Olvera R, Dyer T, Göring H, Curran J, Duggirala R, Blangero J, and Almasy L (2010) Identifying endophenotypes for alcohol dependence: the endophenotype ranking value (ERV). Poster presentation given at the 33rd annual meeting of the Research Society on Alcoholism, San Antonio, TX.

25. **Zlojutro M**, Manz N, Rangaswamy M, Xuei X, Flury-Wetherill L, Koller D, Bierut LJ, Goate A, Hesselbrock V, Kuperman S, Nurnberger Jr J, Rice JP, Schuckit MA, Foroud T, Edenberg HJ, Porjesz B, and Almasy L (2010) Pathway-oriented analysis of genome-wide association studies of neuroelectrical measurements for African- and European-American case-control subjects with alcohol dependence. Poster presentation given at the 35th annual meeting of the Human Biology Association, Albuquerque, NM.

26. **Zlojutro M**, Glahn D, Carless M, Olvera R, Dyer T, Göring H, Curran J, Nimgaonkar VL, Pogue-Geile M, Gur R, Duggirala R, Blangero J, and Almasy L (2009) *KIBRA* and *ODZ2* gene polymorphisms from chromosome region 5q32-34 associated with neurocognitive performance. Poster presentation given at the 17th World Congress on Psychiatric Genetics, San Diego, CA.

27. **Zlojutro M**, Manz N, Rangaswamy M, Xuei X, Bierut L, Edenberg HJ, Foroud T, Goate A, Hesselbrock V, Kuperman S, Nurnberger Jr J, Rice JP, Schuckit MA, Porjesz B, Almasy L, and COGA collaborators (2009) Multi-stage genome-wide association study uncovers genetic factors influencing the P300 event-related brain potential. Poster presentation given at the 59th annual meeting of the American Society of Human Genetics, Honolulu, HI.

28. **Zlojutro M**, Sorensen M, Snodgrass JJ, Tarskia LA, and Crawford MH (2004) Mitochondrial DNA variation in Yakutia: The genetic structure of an expanding population. Poster presentation given at the 29th annual meeting of the Human Biology Association, Tampa, FL.

29. **Zlojutro M**, Sorensen M, Snodgrass JJ, Tarskia LA, Crawford MH (2003) Mitochondrial DNA analysis in Yakutia: Implications for the genetic history of northern Siberia. Poster Presentation given at the 28th annual meeting of the Human Biology Association, Tempe, AZ.

Other Presentations:

30. **Kos MZ** (2012) Synthetic association: Implications for GWAS association and the search for causality. Invited speaker to the Department of Genetics Seminar Series, Texas Biomedical Research Institute, San Antonio, TX, USA.

31. **Zlojutro M** (2007) Mitochondrial DNA variation in Yakutia: The genetic structure of an expanding population. Podium presentation given at the 63rd annual meeting of the Midwestern Association of Graduate Schools (MAGS), Indianapolis, IN.

32. **Zlojutro M** (2004) Coalescent theory: The new population genetics and its application in molecular anthropology. Paper presented for Laboratory of Biological Anthropology colloquium, Lawrence, KS.

33. **Zlojutro M** (2001) Data mining for predictors of causes of mortality in Kansas Mennonite populations. Presented to the executive board at the Kansas Health Institute, Topeka, KS.

Professional Activities

Editorial Boards:

2011-Present	Review Editor, *Frontiers in Genetics*

University Committees:

2020-2024	Optimal Learning Environment Committee (OLEC), UTRGV School of Medicine
2020-2023	Jean W. MacCluer and Bennett Dyke Lectureship, STDOI, UTRGV School of Medicine

Conference Engagement:

2010	Program Committee, American Association of Physical Anthropologists, Albuquerque, NM
2010	Student Prize Committee, American Association of Anthropological Genetics
2014	Manuscript Reviewer, Genetic Analysis Workshop, Vienna, Austria
2017	Manuscript Reviewer, Genetic Analysis Workshop, San Diego, CA

Professional Society Committees:

2011-2012	Elections and Nominations Committee, American Association of Anthropological Genetics (AAAG)

Manuscript Reviews (Ad Hoc):

American Journal of Physical Anthropology
Archives of General Psychiatry
Behavioral and Brain Functions
Bipolar Disorders
BMC Psychiatry
Computers in Biology and Medicine
Current HIV Research
European Journal of Epilepsy

European Journal of Medical Research
Frontiers in Applied Genetic Epidemiology
Frontiers in Biology
Frontiers in Genetics
Frontiers in Molecular Neuroscience
Human Biology
Human Genetics
JAMA
JAMA Network Open
Journal of Clinical Endocrinology and Metabolism
Journal of Clinical Psychopharmacology
Journal of Orthopedics and Orthopedic Surgery
Journal of Translational Medicine
Molecular Psychiatry
Nature Human Behavior
PLOS One
Schizophrenia Bulletin
Scientific Reports