

**BIOGRAPHICAL SKETCH**

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NAME: Krauter, Kenneth S.

eRA COMMONS USER NAME (credential, e.g., agency login): Krauter

POSITION TITLE: Professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
SUNY at Stony Brook, NY	B.Sc.	1974	Biochemistry
Albert Einstein College of Medicine	Ph.D.	1980	Cell Biology
Rockefeller University	Postdoc	1984	Mol. Cell Biology

**A. Personal Statement**

My current research involves next-generation sequencing of microbial populations for metagenomic studies (gut and oral) as well as in GWAS and heritability studies to discover genes involved in complex human traits. Our overall motivation is to understand interactions between microbes and human genes and environment. Especially how changes in microbes over time or in response to environment can affect human complex phenotypes like behavior, mood, obesity, metabolism and oral diseases. I am the director of the Departmental Computing Facility, the University Genotyping Facility. I bring a background in molecular genetics, biochemistry, computation and experience managing large human sample sets to this project.

**B. Positions and honors**

1985-1990 Assistant Professor, Department of Cell Biology, Albert Einstein College of Medicine  
1990-1995 Associate Professor, Department of Cell Biology, Albert Einstein Coll. Of Med.  
1995-present Professor, Department of Molec. Cell. and Dev. Biology, U. of Colorado, Boulder  
2000-present Faculty Fellow, The Institute for Behavioral Genetics, U. of Colorado, Boulder  
1999-2004 NIH Training Grant Review Panel  
2005-2009 NIH K99/R00 Pathway to Independence Panel  
2007-2008 National Academies Education Fellow in the Life Sciences

**Other Experience and Professional Memberships**

1995-present Director CU DNA Sequencing facility  
1997-present Director CU Genotyping facility  
2002-present Co-director Gene Chip facility  
2004-2008 Director of MCDB Graduate Program  
2008-present Biofrontiers Institute Task Force  
2010-2019 Director of MCDB Graduate Program  
2010-present MCDB Executive Committee  
2010-2013 Promotions and Tenure Committee, CU College of Arts and Sciences  
2019-present Associate Chair MCDB

**C. Contributions to Science**

1. My early research was in the broad area of mammalian gene regulation. Our efforts were among the first groups to utilize in vitro nuclear run-on experiments to assess rates of gene transcription in animal tissues. We used this work to examine the regulation of tissue-specific gene expression in a variety of mouse model systems including liver and xenobiotic responses.
  - a. Derman, E, **KS Krauter**, L Walling, C Weinberger, M Ray, and JE Darnell, Jr.. "Transcriptional Control of Liver Specific mRNAs," *Cell* 23:731-739 1981. PMID: 7226226
  - b. Silver G and **KS Krauter**. "Expression of Cytochromes P-450c and P-450d mRNAs in Cultured Rat Hepatocytes: MCA Induction is Regulated Primarily at the Post-transcriptional Level." *J. Biol. Chem.* 263:11802-11807 1988. PMID: 3403555
  - c. Borriello F and **KS Krauter**. "The Duplicated Murine  $\alpha_1$ -Protease Inhibitor Genes Show Unusual Evolutionary Divergence." *Proc. Natl. Acad. Sci. USA.* 88:9417-9421 1991. PMID: 1946354
2. In the early 1990s, I made the decision to turn my research in an entirely new direction and began work on the Human Genome Project, and in particular high-throughput approaches to creating integrated genetic and physical maps of human chromosomes for the purpose of complete genome sequencing. We established one of the original 4 or 5 Human Genome Institute Chromosome centers focused on chromosome 12. We implemented and improved computational and molecular approaches to carrying out this mapping accurately and efficiently.
  - a. **Krauter, KS**, K Montgomery, S-J Yoon, Janine LeBlanc-Straceski, B Renault, I Marondel, I Herdman, A Banks, J Lieman, J Menninger, PB Ward, P Nadkarni, J Weissenbach, I Chumakov, D Cohen, P Miller, D Ward, and R Kucherlapati. "A Second Generation Physical Map of Human Chromosome 12", *Nature* 377:321-334 1995.
  - d. Nadkarni, P, A Banks, K Montgomery, J LeBlanc-Stracewski, P Miller, **KS Krauter**. "CONTIG EXPLORER: Interactive Marker-Content Map Assembly." *Genomics* 31:301-310 1996. PMID: 8838311
  - e. Weiss, A, D McDounough, B Wertman, L Acakpo-Satchivi, K Montgomery, R Kucherlapati, L Leinwand, and **KS Krauter**. "Organization of human and mouse skeletal myosin heavy chain gene clusters is highly conserved." *Proc. Natl. Acad. of Sci., USA.* 96:2958-2963, 1999. PMID: 10077619
  - f. Dennehey BK, Leinwand LA, **Krauter KS**. Diversity in transcriptional start site selection and alternative splicing affects the 5'-UTR of mouse striated muscle myosin transcripts. *J Muscle Res Cell Motil.* 2006;27(8):559-575. PMID: 16819597
3. After moving from Albert Einstein College of Medicine in New York, to the University of Colorado in Boulder, my research interests shifted again to the study of the genetics of complex traits in humans. I became a co-Investigator responsible for all genotyping and sample analyses for a nearly 15 year long center program focused on determining genetic contribution to human drug dependence.
  - a. Melroy WE, Stephens SH, Sakai JT, Kamens HM, McQueen MB, Corley RP, Stallings MC, Hopfer CJ, **Krauter KS**, Brown SA, Hewitt JK, Ehringer MA. Examination of genetic variation in GABRA2 with conduct disorder and alcohol abuse and dependence in a longitudinal study. *Behav Genet.* 2014 Jul;44(4):356-6. Epub 2014 Apr 1. PMID: 24687270
  - g. Schwantes-An T-H, Zhang J, Chen L-S, Hartz SM, et al. Association of the OPRM1 Variant rs1799971 (A118G) with Non-Specific Liability to Substance Dependence in a Collaborative de novo Meta-Analysis of European-Ancestry Cohorts. *Behav Genet.* 2016 Mar 46:151-169; PMID: 26392368
  - h. Derringer J, Corley RP, Haberstick BC, Young SE, Demmitt BA, Howrigan DP, Kirkpatrick RM, Iacono WG, McGue M, Keller MC, Brown S, Tapert S, Hopfer CJ, Stallings MC, Crowley TJ, Rhee SH, **Krauter K**, Hewitt JK, McQueen MB. *Behav Genet.* 2015 Jul;45(4):375-81. doi: 10.1007/s10519-015-9705-y. Epub 2015 Jan 31. PMID: 25637581
  - i. Stringer, S., Minică, C.C., Verweij, K.J.H., Mbarek, H., Bernard, M., Derringer, J., van Eijk, K.R., Isen, J.D., Loukola, A., Maciejewski, D.F., et al. Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32 330 subjects from the International Cannabis Consortium. *Transl Psychiatry* 2016 6, e769.

- j. Minică CC, *et al.*. Genome-wide association meta-analysis of age at first cannabis use. *Addiction*. **2018** Nov;113(11):2073–2086. PMID: 30003630.
  - k. Jiang Y, Chen S, McGuire D, Chen F, Liu M, Iacono WG, Hewitt JK, Hokanson JE, Krauter K, Laakso M, Li KW, Lutz SM, McGue M, Pandit A, Zajac GJM, Boehnke M, Abecasis GR, Vrieze SI, Zhan X, Jiang B, Liu DJ. Proper conditional analysis in the presence of missing data: Application to large scale meta-analysis of tobacco use phenotypes. *PLoS Genet*. **2018**;14(7):e1007452. PMCID: PMC6063450
  - l. Walters RK, *et al.*. Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nat Neurosci*. **2018** Dec;21(12):1656–1669. PMID: 30482948
  - m. Liu M, *et al.*. Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. *Nat Genet*. 2019 Feb;51(2):237–244. PMCID: PMC6358542
4. In the past few years the focus of my lab has shifted to the study of the influence of human genes on the oral and gut microbiomes in the context of a variety of environmental exposures including drug use, alcohol, and diet. While this is a slightly new direction for our research, we have already produce one high-impact twin study and two others are in preparation. It is clear from our work and that of our collaborators that genes have clear affects on the composition of the microbes in a variety of human niches.
- a. Stahringer SS, Clemente JC, Corley RP, Hewitt J, Knights D, Walters WA, Knight R, Krauter KS. Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. *Genome Research*. 2012 Oct 12;22(11):2146–2152.
  - b. Hemmings SMJ., Malan-Muller S., van den Heuvel LL, Demmitt BA, Stanislawski MA, Smith DG, Bohr AD, Stamper CE, Hyde ER, Morton JT, Marotz CA, Siebler PH, Braspenning M, Van Criekinge W, Hoisington AJ, Brenner LA, Postolache TT, McQueen MB, Krauter KS, Knight R, Seedat S, and Lowry CA. 2017 “The Microbiome in Posttraumatic Stress Disorder and Trauma-Exposed Controls: An Exploratory Study.” *Psychosomatic Medicine*, July 2017. 79: 936-946. PMID; 28700459
  - c. Demmitt BA., Corley RP., Huibregtse BM., Keller MC., Hewitt JK., McQueen MB., Knight, R., McDermott, I., and Krauter KS. (2017). Genetic Influences on the Human Oral Microbiome. *BMC Genomics*. 2017. 18:659-672. PMID: 28836939
  - d. Lin D, Hutchison KE, Portillo S, Vegara V, Ellingson JM, Liu J, Krauter KS, Carroll-Portillo A, Calhoun VD. (2019) Association between the oral microbiome and brain resting state connectivity in smokers. *Neuroimage*. 200:121-131. PMID: 31201984
  - e. Border R, Smolen A, Corley RP, Stallings MC, Brown SA, Conger RD, Derringer J, Donnellan MB, Haberstick BC, Hewitt JK, Hopfer C, Krauter K, McQueen MB, Wall TL, Keller MC, Evans LM. (2019) Imputation of behavioral candidate gene repeat variants in 486,551 publicly-available UK Biobank individuals. *Eur J Hum Genet*. 27:963-969. PMID: 30723318
  - f. Walters RK, Polimanti R, et al. (2018) Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. *Nat Neurosci*. 21:1656-1669. PMID: 30482948
- g.

#### D. Research support

##### Current

NIH “Population Distribution of Microbes in Add Health: Pilot Data Analyses”. (McQueen) Role on project co-I.

NIH [1R01AG066498-01](#) The Microbiome and Biological Aging in the Add Health Study (MPI Krauter) Role on project PI