

## CURRICULUM VITAE

02/05/2021

### **Julia Krushkal, PhD**

**Current position:** Computational Biologist  
Computational & Systems Biology Branch  
Biometric Research Program  
National Cancer Institute, National Institutes of Health  
9609 Medical Center Drive, Room 5W118, Rockville, MD 20850  
Tel. 240-276-5988, email [julia.krushkal@nih.gov](mailto:julia.krushkal@nih.gov)

**Research Interests:** Bioinformatic analysis of genome sequence, expression, and epigenetic data, cancer genomics, genomic analysis of drug response, molecular genetics of human disease, statistical genetics, molecular evolution, genetic epidemiology

### **Education and Training**

Ph.D. **Genetics**, 1996. Ph.D. advisor: Dr. Wen-Hsiung Li.  
The University of Texas Health Science Center at Houston

Honors Diploma **Cytology and genetics with concentration in mathematical biology**, 1990  
(equivalent of B.S./M.S. with distinction) Novosibirsk State University (Russia)

Additional Training: 1993-1994: **Courses in statistics and computer programming**, Rice University  
2006-2009: **Courses in statistics and programming**  
The University of Tennessee Health Science Center  
2012: **Scientific Review Officer training** in review and extramural funding procedures at the National Institutes of Health  
2015-2017: **Short computer programming courses** at NIH

### **Professional Experience**

10.2014-present Computational Biologist, Biometric Research Branch  
National Cancer Institute, National Institutes of Health, Rockville, MD

01.2012-10.2014 Scientific Review Officer, Population Sciences and Epidemiology IRG  
Division of AIDS, Behavioral, and Population Sciences, Center for Scientific Review  
National Institutes of Health, Bethesda, MD

07.2010-01.2012 Associate professor (*with tenure*), Department of Preventive Medicine,  
The University of Tennessee Health Science Center, Memphis, TN

09.2007-06.2010 Assistant professor (*tenure track*), Department of Preventive Medicine  
The University of Tennessee Health Science Center

07.2007-01.2012 Faculty affiliate member, Program in Bioinformatics, The University of Memphis

09.2002 - 08.2007 Assistant Professor (*non-tenure track*)  
Department of Preventive Medicine and Center of Genomics and Bioinformatics  
The University of Tennessee Health Science Center

07.2007 Research visitor: Collaborative research in bioinformatics. The University of Sydney.

01.2000 – 05.2002 Visiting Assistant Professor, Department of Biology and Biotechnology  
Worcester Polytechnic Institute, Worcester, MA

05.1997 – 12.1999 Assistant Professor (*non-tenure track/research*)  
Institute of Molecular Medicine for the Prevention of Human Disease,  
The University of Texas Health Science Center at Houston

06.1996 – 04.1997 Postdoctoral Fellow. Laboratory of Dr. Eric Boerwinkle.  
Human Genetics Center, The University of Texas Health Science Center at Houston

08.1991 – 05.1996 Graduate Student (Graduate Research Assistant).  
Graduate School of Biomedical Sciences, Program in Genetics,  
The University of Texas Health Science Center at Houston

08.1990 – 08.1991 Research Trainee, Theoretical Department, Institute of Cytology and Genetics,  
Siberian Branch of the USSR Academy of Sciences, Novosibirsk, Russia

## Past Grants, Fellowships, and Awards

- 06/10/11-01/18/12 NIH/NICHD HD-060713 R01 *Genomics and epigenomics of fetal growth regulation*. \$1,289,404 (**J. Krushkal, PI**) Principal Investigator
- 06/10/11-08/31/12 NIH/NICHD HD-055462 R01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. \$723,663 (**J. Krushkal, PI**) Principal Investigator.
- 10/01/10-08/31/12 NIH/NHLBI *Women's Health Initiative 2010-2015 extension study*. \$303,339 (Subcontract with Wake Forest University Health Sciences; K. Johnson, site PI) Co-Investigator.
- 08/15/05-08/31/11 DOE DE-FC02-02ER63446 *Genome-based models to optimize in situ bioremediation of uranium and harvesting electrical energy from waste organic matter* (D. Lovley, project PI; **J. Krushkal, UT-Memphis site PI**). Principal Investigator of the subcontract with the University of Massachusetts. \$652,519- University of Tennessee subcontract only.
- 0/01/09-06/30/11 UTHSC Clinical and Translational Science Institute *Molecular predictors of statin intolerance in patients with dyslipidemia*. \$99,289 (M. B. Elam, PI) Co-investigator
- 10/01/09-06/30/11 UTHSC Clinical and Translational Science Institute *Quantitative gene expression using a novel technology to predict chemosensitivity of breast cancer*. \$90,809 (J. Sachdev, PI) Co-investigator
- 08/01/09-06/09/11 NIH/NICHD HD-060713 R01 *Genomics and epigenomics of fetal growth regulation*. \$1,289,404 (R. Adkins, PI) Co-investigator
- 09/01/11-06/09/11 NIH/NICHD HD-055462 R01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. \$723,663 (R. Adkins, PI) Co-investigator
- 08/01/08-06/30/10 University of Tennessee Clinical and Translational Science Institute. *Genomics and epigenomics of fetal growth regulation and cognitive development*. (R. Adkins, PI) \$79,998. Co-Investigator
- 11/01/07-08/31/09 NIH/NLM R13 LM009315 *Annual UT-ORNL-KBRIN Bioinformatics Summit* (E.Rouchka, PI; **J. Krushkal, UT-Memphis site PI**). Principal Investigator of the subcontract with the University of Louisville. \$6,331 - University of Tennessee subcontract only
- 09/01/07-08/31/09 NIH/ NICHD R01 HD-055462-01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. (R. Adkins, PI). \$372,300. Co-Investigator
- 07/01/03-06/31/08 NIH/NHLBI R01 HL072375 *Genetics of cardiovascular reactivity in black youth* (B. Alpert, PI). \$2,376,320. Consultant
- 10/01/06-07/31/07 *Genetic polymorphisms in pediatric lung injury*. Contract work in genetic epidemiology for the Medical College of Wisconsin, \$6,000.
- 07/01/04-09/30/06 NIH/NICHD R21 HD4767 *Genetic polymorphisms in pediatric lung injury* (M. Quasney, PI). \$401,500. Collaborator.
- 09/01/02-08/31/05 DOE DE-FC02-02ER63446 *Analysis of the genetic potential and gene expression of microbial communities involved in the in situ bioremediation of uranium and harvesting electrical energy from organic matter* (D. Lovley, PI; **J. Krushkal, UT-Memphis site PI**). Principal Investigator of the subcontract with University of Massachusetts, \$196,460- University of Tennessee subcontract only.
- 01/01/05-12/31/05 Children's Foundation Research Center, Le Bonheur Children's Hospital. *Molecular genetic analysis of birth weight variation* (R. Adkins, PI) \$50,000. Investigator.
- 01/01/04-12/31/04 Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN *Molecular genetic analysis of birth weight variation* (R. Adkins, PI). \$50,000. Investigator.

- 01/01/03-12/31/03 Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN. *Molecular Genetic Analysis of Pre-Eclampsia* (R. Adkins, PI). \$74,000. Consultant.
- 2000 Research Development Council, Worcester Polytechnic Institute. *Computational Algorithms for Analysis of Genomic Data*. \$19,000. **Principal Investigator** (with S. Alvarez, C. Ruiz, L. Ryder, and M. Stevens).
- 1999 *Travel Award to attend the 3<sup>rd</sup> Gordon Research Conference in Molecular Evolution in Hayama, Japan*. Gordon Research Conferences and the National Science Foundation.
- 1997-1998 Minnie L. Maffett Fellowship Fund. Texas Federation of Business and Professional Women's Clubs, Inc. *Minnie L. Maffett Fellowship*.
- 1995 Graduate School of Biomedical Sciences. The University of Texas-Houston. *Student Travel Award*.
- 1988-1990 Novosibirsk State University, Russia. *Scholarship for academic excellence and scientific achievements*
- 1988 Novosibirsk State University, Russia. *Scientific Council Scholarship* (for academic excellence).

### **Grant Reviewer**

#### *Participation in study sections:*

- 2011 Ad hoc reviewer for a National Institutes of Health special emphasis panel, ZRG1 PSE-K 03M, Member Conflict: Epidemiology.
- 2002 – 2003 Appointed member, U.S. National Science Foundation Advisory Panel

#### *Mail reviewer:*

- 2019 UK Medical Research Council (Methodology Research Programme)
- 2019 Swiss National Science Foundation
- 2016 U.S.-Israel Binational Science Foundation
- 2000-2009 U.S. National Science Foundation
- 2008 Thomas F. and Kate Miller Jeffress Memorial Trust
- 1997-1999 U.S. Civilian Research and Development Foundation

### **Reviewer for Scientific Journals**

Circulation	Proceedings of the National Academy of Sciences USA
OMICS	Genetic Epidemiology
Molecular Biology and Evolution	BioSystems
Hypertension	Molecular Phylogenetics and Evolution
Bioinformatics	Journal of Molecular Evolution
Functional and Integrative Genomics	Journal of Biomolecular Structure and Dynamics
Database	Journal of Proteomics
African Journal of Biotechnology	Chemistry and Biodiversity
Current Genomics	Recent Advances in DNA & Gene Sequence
Developmental Medicine & Child Neurology	International Journal of Environmental Research and Public Health
FEMS Microbiology Letters	Nucleic Acids Research
Journal of Cancer	Journal of Clinical Oncology-Clinical Cancer Informatics (JCO-CCI)
Cancer Biology and Medicine	World Journal of Surgical Oncology
Cancer Research	Journal of the National Cancer Institute Cancer Spectrum (JNCICS)
BMC Medicine	Genomics
Cancer Informatics	

## Invited Seminar, Colloquium, and Conference Speaker

- 08/2014 *Computational analysis of genome, expression, and epigenetic information in human and model bacteria.* Biometric Research Branch, Division of Cancer Treatment and Diagnosis, National Cancer Institute, NIH, Rockville, MD
- 10/2011 *Linking genome variation to phenotypic outcomes: Genetic, epigenetic, and transcriptomic analysis of longitudinal cohort data.* Center for Scientific Review, National Institutes of Health, Bethesda, MD
- 03/2011 *Linking genome variation to phenotypic outcomes: Genetic and epigenetic analysis of a longitudinal cohort.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 03/2010 *Bioinformatics analysis of genome, sequence, and gene expression information: applications to bacterial, viral, and human data.* Department of Biology, Murray State University, Murray, KY
- 04/2009 *Phylogenetic analyses of genome sequence information from bacteria, viral pathogens, and human immune defense components.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 03/2009 *Bioinformatic analysis of genome, sequence, and expression information: an application to bacterial data. Distinguished alumna presentation.* 13<sup>th</sup> Annual Symposium, Human and Molecular Genetics Program. Graduate School of Biomedical Science, The University of Texas Health Science Center at Houston
- 12/2008 *Bioinformatics analysis of genome, sequence, and expression information.* Department of Medical Genetics, Cedars Sinai Medical Center, Los Angeles, CA
- 10/2008 *Bioinformatic analysis of bacterial gene regulation and of human and viral complement regulators.* Center for the Study of Biological Complexity, Virginia Commonwealth University. Richmond, VA
- 05/2008 IEEE 2008 International Conference on BioMedical Engineering and Informatics (BMEI 2008). Sanya, China. **Invited platform presenter: J. Krushkal, M. Puljic, B. Yan, J. F. Barbe, R. Mahadevan, B. Postier, R. A. O'Neil, G. Reguera, C. Leang, L. N. DiDonato, C. Núñez, B. A. Methé, R. M. Adkins, and D. R. Lovley.** *Genome regions involved in multiple regulatory pathways identified using GSEL, a genome-wide database of regulatory sequence elements of Geobacter sulfurreducens*  
**Session Chair:** "Applications of artificial intelligence in bioinformatics and medical informatics III"
- 11/2007 *Bioinformatic analysis of transcriptional regulation of environmentally important bacterial species.* Science Series (joint program between Departments of Biological Sciences and of Chemistry and Physics). Arkansas State University. Jonesboro, AR
- 09/2007 *Bioinformatic analysis of transcriptional regulatory sites.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 07/2007 *Bioinformatic analysis of bacterial, viral, and human genome data.* School of Biological Sciences, University of Sydney, Australia
- 10/2005 *Bioinformatics analysis of sequence, genome and expression information.* Department of Computer Science, University of Memphis, Memphis, TN
- 06/2005 *Bioinformatics analysis of genome and expression information: applications to bacterial, viral, and human data.* Department of Sciences, Holon Academic Institute of Technology, Tel Aviv, Israel
- 12/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, University of Memphis. Memphis, TN
- 05/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, Virginia State University. Colonial Heights, VA

- 05/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biological Sciences, California State University at Pomona. Pomona, CA
- 04/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biological Sciences, University of the Sciences in Philadelphia. Philadelphia, PA
- 03/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, University of Kentucky. Lexington, KY
- 02/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, St. Edward's University. Austin, TX
- 02/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, Texas A&M University. College Station, TX
- 04/2003 *Computational analysis of genetic data: bacteria, viruses, and human.* Department of Zoology, Oklahoma State University. Stillwater, OK
- 06/2001 *Computational analysis of biological information at sequence and genome level.* Department of Medicine, The University of Texas Health Science Center at San Antonio. San Antonio, TX
- 06/2001 *Computational analysis of biological information at sequence and genome level.* The University of Tennessee Health Science Center. Memphis, TN
- 03/2001 *Computational analysis of DNA and protein sequences.* Department of Biology, Amherst College. Amherst, MA. Presentation for undergraduate students.
- 01/2001 *Computational genomic analysis of human immunity and pathogenic organisms.* Department of Microbiology, University of Massachusetts. Amherst, MA.
- 11/1999 *Computational analysis of DNA data at sequence and genome level.* Program in Molecular and Cellular Biology, Department of Biochemistry and Molecular Biology, University of Massachusetts. Amherst, MA
- 02/1999 *Computational analysis of DNA data at sequence and genome level.* Department of Biology and Biotechnology. Worcester Polytechnic Institute. Worcester, MA
- 02/1998 *Multipoint gene mapping for essential hypertension. Invited Alumna Presentation.* The 5th Annual Genetics Mini-Symposium. Graduate School of Biomedical Science, The University of Texas-Houston Health Science Center.
- 11/1997 *Use of multipoint methods for gene mapping of essential hypertension.* W.M. Keck Center for Computational Biology, Rice University. Houston, TX
- 09/1997 *Molecular evolution of primate RNA viruses.* Department of Ecology and Evolutionary Biology, Rice University. Houston, TX
- 02/1997 *Computational analysis of DNA data at sequence and genome levels.* Institute of Molecular Medicine, The University of Texas Health Science Center. Houston, TX
- 10/1995 *Phylogenetic tree reconstruction for primate immunodeficiency viruses.* Colloquium. Department of Statistics, Rice University. Houston, TX
- 03/1992 *Role of CpG dinucleotides in evolution of Alu and B2 repeats in mammalian genomes.* Laboratory of Cryptobiology, Department of Polymer Research, Weizmann Institute of Science. Rehovot, Israel
- 03/1992 *Possible scheme of evolution of interspersed repeats in mammalian genomes.* Department of Mathematics and Computer Science, Bar-Ilan University. Ramat Gan, Israel

## **Seminar presentations for inter-institutional and collaborative working groups and projects**

- 2017-2020 Multiple presentations on analyses of molecular markers of sensitivity to cancer drug treatment at the NCI Pharmacodynamics (PD) and NCI Patient-Derived Models (PDM) group meetings, NCI Experimental Therapeutics (NeXT) project team meetings, and collaborative project meetings
- 12/2020 *Association of gene expression of 72 epigenetic molecular factors with DNA methylation and chemosensitivity in SCLC cell lines.* Online presentation to the NCI Small Cell Lung Cancer Consortium
- 03/2020 *Epigenome-wide DNA methylation analysis of SCLC cell lines suggests potential chemotherapy targets.* Online presentation to the NCI Small Cell Lung Cancer Consortium
- 04/2011 *GWAS and other bioinformatic analyses in CANDLE.* Nutrigenomics conference organized by the CANDLE (Conditions Affecting Neurocognitive Development and Learning in Early Childhood) Project, the Urban Child Institute, and The University of Tennessee Health Science Center. Memphis, TN.
- 04/2010 *An update on genetic and epigenetic analysis in the CANDLE Project.* Conditions Affecting Neurocognitive Development and Learning in Early Childhood (CANDLE) project meeting, Memphis, TN.
- 09/2009 *An update on computational analysis of molecular evolution and transcriptional regulation of Geobacteraceae.* 5<sup>th</sup> Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 10/2008 *Computational Analysis of Transcriptional Regulation in Geobacteraceae.* 4<sup>th</sup> Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 10/2007 *Bioinformatic Analysis of Transcriptional Regulation in Geobacteraceae.* 3<sup>rd</sup> Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 07/2007 *Bioinformatic data analysis.* Bioinformatics and Biodiversity Laboratory (Dr. Lars Jermiin, Head), University of Sydney, Australia
- 10/2006 *Computational analysis of transcriptional regulation in Geobacteraceae.* 2<sup>nd</sup> Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 06/2006 *Computational analysis of transcriptional regulation: an update.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 10/2005 *Computational prediction of operons and transcriptional regulation.* 1<sup>st</sup> Annual Genomics:GTL Geobacter Project Meeting, University of Massachusetts, Amherst, MA
- 09/2003 *Computational prediction of operons and transcription factor binding sites in Geobacteraceae: an update.* Geobacter group, University of Massachusetts, Amherst, MA
- 03/2003 *Prediction of transcription factor binding sites in Geobacteraceae.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 05/1998 *Results of the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Rio Grande City, TX
- 04/1997 *Genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Houston, TX
- 11/1997 *Update on the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Jackson, MS
- 10/1996 *Linkage mapping of hypertension-related genes.* Blood Pressure Linkage Working Meeting. Department of Human Genetics, University of Michigan. Ann Arbor, MI

### **Career Mentoring and Grant Review Outreach**

- 10.17.2019 Invited mentor participant, Trainee-Mentor Luncheon at the 2019 Annual Meeting of the American Society of Human Genetics (ASHG 2019).
- 03.20.2014 Led round table discussions of NIH grant review for early career investigators at the American Heart Association Epidemiology and Prevention, and Nutrition, Physical Activity and Metabolism 2014 Scientific Sessions, AHA EPI/NPAM 2014 (with NHLBI program staff).
- 01.08.2014 2014 New Grantee Workshop of the National Cancer Institute Division of Cancer Control and Population Genetics. Presentation: Review process and grant renewal.
- 04.20.2013 Conducted a mock study section review meeting at the Young Investigator Forum of the American Academy of Sleep Medicine (jointly with NHLBI staff).

### **Conference organizer and/or session chair**

- 03/2012 11<sup>th</sup> annual UT-ORNL-KBRIN Bioinformatics Summit. Louisville, KY.  
***Planning committee member***
- 06/2011 The 2011 Summit on Systems Biology - Molecular Networks and Disease. Richmond, VA  
***Program committee member.***
- 04/2011 CANDLE Nutrigenomics conference. Organized by The Urban Child Institute and the University of Tennessee Health Science Center. Memphis, TN.  
***Planning committee member***
- 04/2011 10<sup>th</sup> annual UT-ORNL-KBRIN Bioinformatics Summit 2011. Memphis, TN.  
***Planning committee member***
- 03/2010 UT-ORNL-KBRIN Bioinformatics Summit 2010. Lake Barkley State Park, Cadiz, KY.  
***Planning committee member***
- 06/2009 The Third Summit on Systems Biology – The Microbial World and Beyond. Richmond, VA  
***Program committee member***
- 03/2009 UT-ORNL-KBRIN Bioinformatics Summit 2009. Falls Creek Falls State Park, Pikeville, TN  
***Planning committee member. Session Chair: “Systems Biology”***
- 05/2008 IEEE 2008 International Conference on BioMedical Engineering and Informatics (BMEI 2008). Sanya, China.  
***Session Chair: “Applications of artificial intelligence in bioinformatics and medical informatics III”***
- 03/2008 UT-ORNL-KBRIN Bioinformatics Summit 2008. Lake Barkley State Park, Cadiz, KY.  
***Planning committee member.***
- 08/1990 Modeling and Computer Methods in Molecular Biology and Genetics (International Conference). Novosibirsk, Russia. ***Member of the organizing committee.***

### **Scientific Review Administration** (01.2012-10.2014)

Organized NIH Center for Scientific Review meetings to review applications in the areas of epidemiology, genetics, and epigenetics of cardiovascular outcomes, sleep, cancer, lung, blood, neuromuscular, and skeletal disorders, aging, and early child development.

## Teaching Experience

- 2015 Guest instructor in a graduate Foundation for Advanced Education in the Sciences (FAES@NIH) workshop, *Bioinformatic Analysis of Next Generation Sequencing Data (BioTech 45)*.
- 2009-2011 BIOE 824 *Genetic Epidemiology*. Department of Preventive Medicine/M.S. Program in Epidemiology, University of Tennessee Health Science Center
- 2008-2010 Guest lecturer in a graduate course, MSCI815 *Bioinformatics II* (HapMap Project module)
- 2007-2011 Guest lecturer in a graduate course, BINF 7980, *Seminar in Bioinformatics*. Graduate Program in Bioinformatics, University of Memphis
- 2003-2009 BIOE 825 *Bioinformatics for Epidemiologists*. Department of Preventive Medicine/M.S. Program in Epidemiology, University of Tennessee Health Science Center
- 2008 Educational seminars for the University of Tennessee-Memphis faculty and staff:  
*Recent advances in genomics, microarray technology, and proteomics, and their application to human health*  
*The International HapMap Project: a rich resource of genetic information*
- 2005-2008 Guest lecturer in a graduate course, BIOE 824 *Genetic Epidemiology*. Department of Preventive Medicine/Program in Epidemiology, University of Tennessee Health Science Center (lectures on microarray analysis)
- 2007 Guest lecturer in a graduate course, BIOE 840 *Special Topics: Applications from the Basic Sciences*. Department of Preventive Medicine/Program in Epidemiology, University of Tennessee Health Science Center (lectures on microarray analysis)
- 2004 Guest lecturer in a junior level course, *Cellular and Molecular Biology*. St. Edward's University, Austin, TX
- 2004 Teaching seminar in bioinformatics, *Sequence Alignments*. Virginia State University, Colonial Heights, VA
- 2002 *Bioinformatics for Epidemiologists* (seminar for faculty and staff). Department of Preventive Medicine and Center of Genomics and Bioinformatics, University of Tennessee-Memphis
- 2000-2002 BB4440 and BB544 *Bioinformatics* (for seniors and graduate students). Department of Biology and Biotechnology, Worcester Polytechnic Institute.  
BB3512 *Molecular Genetics* - a computational biology techniques course (for juniors).  
BB501 *Graduate Student Seminar and Invited Research Seminar*
- 1999 Participant in a Bioinformatics College Teachers Workshop. Boston University, Program in Bioinformatics.  
Guest lecturer in an undergraduate course:  
*Molecular Evolution*. University of Massachusetts, Amherst
- 1996-1998 Guest lecturer in graduate courses (The University of Texas-Houston Health Science Center):  
*Computational Sequence Analysis*  
*Genetics of Human Disease*  
*Biochemistry*

## **Publications**

\* undergraduate student co-authors, \*\* graduate student co-authors (at the time of work)

### **Manuscripts and Book Chapters (Peer reviewed)**

1. **J. Krushkal**, S. Negi, L. Yee, J. Evans, T. Grkovic, A. Palmisano, J. Fang, H. Sankaran, L.M. McShane, Y. Zhao, B. O'Keefe (2021) *Molecular genomic features associated with in vitro response of the NCI-60 cancer cell line panel to natural products*. Molecular Oncology 15(2):381-406. doi: 10.1002/1878-0261.12849. **Cover publication for the 02/04/2021 issue of Molecular Oncology.**
2. C. Tlemsani, L. S. Pongor, L. Girard, N. Roper, F. Elloumi, S. Varma, A. Luna, V. Rajapakse, R. Sebastian, K. Kohn, **J. Krushkal**, M. Aladjem, B. Teicher, P. Meltzer, W. Reinhold, J. Minna, A. Thomas, Y. Pommier (2020) *SCLC-CellMiner: Integrated Genomics and Therapeutics Predictors of Small Cell Lung Cancer Cell Lines Based on their Genomic Signatures*. Cell Reports, 33(3):108296
3. **J. Krushkal**, T. Silvers, W.C. Reinhold, D. Sonkin, S. Vural, J. Connelly, S. Varma, P.S. Meltzer, M. Kunkel, A. Rapisarda, D. Evans, Y. Pommier, B.A. Teicher (2020) *Epigenome-wide DNA methylation analysis of small cell lung cancer cell lines suggests potential chemotherapy targets*. Clinical Epigenetics, 12:93
4. A. Palmisano, **J. Krushkal**, M.-C. Li, J. Fang, D. Sonkin, G. Wright, L. Yee, Y. Zhao, and L. McShane (2019) *Bioinformatics tools and resources for cancer immunotherapy study*. Book chapter in: Biomarkers for the Immunotherapy of Cancer. M. Thurin, A. Cesano, Francesco M. Marincola, Eds. Humana Press, Springer Protocol, Methods and Protocol series. Pp. 649-678 (Methods Mol Biol. book series, 2020;2055:649-678) [https://doi.org/10.1007/978-1-4939-9773-2\\_29](https://doi.org/10.1007/978-1-4939-9773-2_29)
5. D.-J. Min, S. Vural, and **J. Krushkal** (2019) *Association of transcriptional levels of folate metabolism-related genes in cancer cell lines with drug treatment response*. Cancer Genetics 237:19-38
6. D.M. Evans, J. Fang, T. Silvers, R. Delosh, J. Laudeman, C. Ogle, R. Reinhart, M. Selby, J. Connelly, E. Harris, **J. Krushkal**, L. Rubinstein, J.H. Doroshow, J.M. Collins, and B.A. Teicher (2019) *Exposure time versus cytotoxicity for anticancer agents*. Cancer Chemotherapy and Pharmacology. 84:359–371. doi: 10.1007/s00280-019-03863-w.
7. Vural, R. Simon, and **J. Krushkal** (2018) *Correlation of gene expression and associated mutation profiles of APOBEC3A, APOBEC3B, REV1, UNG, and FHIT with chemosensitivity of cancer cell lines to drug treatment*. Human Genomics 12:20
8. A. Monks, Y. Zhao, C. Hose, H. Hamed, **J. Krushkal**, J. Fang, D. Sonkin, A. Palmisano, E. Polley, L. Fogli, M. Konaté, S. Miller, M. Simpson, A. Voth, M.-C. Li, E. Harris, X. Wu, J. Connelly, A. Rapisarda, B. Teicher, R. Simon, and J. Doroshow (2018) *The NCI Transcriptional Pharmacodynamics Workbench: a tool to examine dynamic expression profiling of therapeutic response in the NCI-60 cell line panel*. Cancer Research 78(24): 6807–6817
9. **J. Krushkal**, Y. Zhao, C. Hose, A. Monks, J. H. Doroshow, and R. Simon (2017) *Longitudinal transcriptional response of glycosylation related genes, regulators, and targets in cancer cell lines treated with eleven antitumor agents*. Cancer Informatics 16: 1–14
10. B.A. Teicher, T. Silvers, M. Selby, R. Delosh, J. Laudeman, C. Ogle, R. Reinhart, R. Parchment, **J. Krushkal**, D. Sonkin, L. Rubinstein, J. Morris, and D. Evans (2017) *Small cell lung carcinoma cell line screen of etoposide/carboplatin plus a third agent*. Cancer Medicine 6(8):1952-1964
11. C.M.T. Greenwood, C. Xu, S. Alam, **J. Krushkal**, R.M. Adkins, and A.K. Naumova (2017) *Genetic and epigenetic variation at the H19 imprinted region and its effect on birth weight*. Book chapter in: Epigenetics in human reproduction and development. A.K. Naumova and T.Taketo, Eds. World Scientific Publishing. Pp 185-207. doi: 10.1142/9789813144279\_0007
12. **J. Krushkal**, Y. Zhao, C. Hose, A. Monks, J. H. Doroshow, and R. Simon (2016) *Concerted changes in transcriptional regulation of genes involved in DNA methylation, demethylation, and folate-mediated one-carbon metabolism pathways in the NCI-60 cancer cell line panel in response to cancer drug treatment*. Clinical Epigenetics 8:73
13. **J. Krushkal**, L. E. Murphy, F. B. Palmer, J. C. Graff, C. A. Hovinga, K. Mozhui, F. Thomas, V. Park, T. R. Sutter, F. A. Tylavsky, and R. M. Adkins (2014) *Epigenetic analysis of neurocognitive development at 1 year of age in a community-based pregnancy cohort*. Behavior Genetics, 44(2):113-125
14. R. M. Adkins, F. A. Tylavsky, and **J. Krushkal** (2012) *Newborn umbilical cord blood DNA methylation and gene expression levels exhibit limited association with birth weight*. Chemistry and Biodiversity, 9(5):888-899.

15. **J. Krushkal**, Y. Qu, D. R. Lovley, and R. M. Adkins (2012) *Phylogenetic classification of diverse LysR-type transcriptional regulators of a model prokaryote Geobacter sulfurreducens*. Journal of Molecular Evolution. 74(3-4):187-205
16. R. M. Kelsey, B. S. Alpert, M. K. Dahmer, **J. Krushkal**, and M. W. Quasney (2011) *Alpha-adrenergic receptor polymorphisms and cardiovascular reactivity to stress in Black adolescents and young adults*. Psychopharmacology. 49(3):401-412.
17. J. W. Schroeder, K. N. Conneely, J. C. Cubells, V. Kilaru, D. J. Newport, B. T. Knight, Z. N. Stowe, P. A. Brennan, **J. Krushkal**, F. A. Tylavsky, R. N. Taylor, R. M. Adkins, A. K. Smith (2011) *Neonatal DNA methylation patterns associate with gestational age*. Epigenetics 6(12), 1498-1504.
18. R. M. Adkins, F. Thomas, F. A. Tylavsky, and **J. Krushkal** (2011) *Parental ages and levels of DNA methylation in the newborn are correlated*. BMC Medical Genetics 12:47. **Highly accessed article**.
19. **J. Krushkal**, S. Sontineni\*\*, C. Leang, Y. Qu, R. M. Adkins, D. R. Lovley (2011) *Genome diversity of the TetR family of transcriptional regulators in a metal-reducing family bacterial Geobacteraceae and other microbial species*. OMICS: A Journal of Integrative Biology, 15(7-8):495-506.
20. R. M. Adkins, **J. Krushkal**, F. A. Tylavsky, F. Thomas (2011) *Racial differences in gene-specific DNA methylation levels are present at birth*. Birth Defects Research (Part A). 91:728-736
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