CURRICULUM VITAE

12/16/2022

Julia Krushkal, PhD

Current position:
Computational Biologist
Computational & Systems Biology Branch
Biometric Research Program
National Cancer Institute, National Institutes of Health
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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 (equivalent of B.S./M.S. with distinction)	**Cytology and genetics with concentration in mathematical biology,** 1990 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 (joint graduate program with MD Anderson Cancer Center)
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 3rd 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
OMICS
Molecular Biology and Evolution
Hypertension
Bioinformatics
Functional and Integrative Genomics
Database
African Journal of Biotechnology
Current Genomics
Developmental Medicine & Child Neurology
FEMS Microbiology Letters
Journal of Cancer
Cancer Biology and Medicine
Journal of the National Cancer Institute
BMC Medicine
Cancer Informatics
Frontiers in Oncology
Seminars in Cancer Biology
Cancer Research
Proceedings of the National Academy of Sciences USA
Genetic Epidemiology
BioSystems
Molecular Phylogenetics and Evolution
Journal of Molecular Evolution
Journal of Biomolecular Structure and Dynamics
Journal of Proteomics
Chemistry and Biodiversity
Recent Advances in DNA & Gene Sequence
International Journal of Environmental Research and Public Health
Nucleic Acids Research
Journal of Clinical Oncology-Clinical Cancer Informatics (JCO-CCI)
World Journal of Surgical Oncology
Journal of the National Cancer Institute Cancer Spectrum (JNCICS)
Genomics
Clinical and Translational Medicine
British Journal of Cancer
Computational and Structural Biotechnology Journal
Journal of Molecular Endocrinology

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.** 13th 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

01/19-11/22 Project presentations on bioinformatic analysis of genetic markers of drug sensitivity at the NCI DCTD drug combination meetings, project team meetings, and meetings with NCI Experimental Therapeutics (NeXT) drug inhibitor teams, NCI Natural Products Branch, and NCI Molecular Characterization Laboratory

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.* 5th Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA

10/2008 *Computational Analysis of Transcriptional Regulation in Geobacteraceae.* 4th Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA

10/2007 *Bioinformatic Analysis of Transcriptional Regulation in Geobacteraceae.* 3rd 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.* 2nd 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.* 1st 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	11th 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	10th 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. Vural, T. L. Jensen, G. Wright, Y. Zhao (2022) *Increased copy number of imprinted genes in the chromosomal region 20q11-q13.32 is associated with resistance to antitumor agents in cancer cell lines.* Clinical Epigenetics 14:161.
2. H. Sankaran, S. Negi, L. M. McShane, Y. Zhao, **J. Krushkal** (2022). *Pharmacogenomics of In Vitro Response of the NCI-60 Cancer Cell Line Panel to Indian Natural Products.* BMC Cancer 22:512
3. **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.**
4. S. Vural, A. Palmisano, W. C. Reinhold, Y. Pommier, B. A. Teicher, **J. Krushkal** (2021) *Association of transcriptional levels of epigenetic molecular factors with DNA methylation target levels and with sensitivity to chemotherapeutic agents in cancer cell lines.* Clinical Epigenetics 13:49. https://doi.org/10.1186/s13148-021-01026-4
5. W. Zhang, Z. Zhang, **J. Krushkal,** A. Liu (2021) *Group testing can improve the cost-efficiency of prospective-retrospective biomarker studies.* BMC Medical Research Methodology 21:55
6. 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
7. **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
8. 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
9. 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
10. 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.
11. 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
12. 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
13. **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
14. 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
15. 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

16. **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
17. **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
18. 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.
19. **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
20. 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.
21. 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.
22. 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.**
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