

CURRICULUM VITAE

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Julia Krushkal

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Biographical Data **Married** to Ronald Adkins, Ph.D. **2 children**

Research Interests 18 years of experience in **bioinformatics and computational biology**:

Analysis of DNA and protein sequences,	Population genetics,
Gene mapping and association,	Genomics,
Expression analysis	Molecular evolution

Professional Experience

09.2002 - present	Assistant Professor Department of Preventive Medicine and Center of Genomics and Bioinformatics The University of Tennessee Health Science Center
01.2000 – 05.2002	Visiting Assistant Professor Worcester Polytechnic Institute
05.1997 – 12.1999	Assistant Professor Institute of Molecular Medicine for the Prevention of Human Diseases, The University of Texas-Houston Health Science Center
06.1996 – 04.1997	Postdoctoral Fellow Human Genetics Center, The University of Texas-Houston Health Science Center
08.1991 – 05.1996	Graduate Student Graduate School of Biomedical Sciences, Program in Genetics, The University of Texas-Houston Health Science Center
08.1990 – 08.1991	Research Trainee Theoretical Department, Institute of Cytology and Genetics, Siberian Branch of the USSR Academy of Sciences, Novosibirsk, Russia
08.1988 – 06.1990	Research for the M.Sc. degree Theoretical Department, Institute of Cytology and Genetics, Siberian Branch of the USSR Academy of Sciences, Novosibirsk, Russia
09.1985 – 06.1990	Student. Department of Natural Sciences, Program in Cytology and Genetics with Concentration in Mathematical Biology. Novosibirsk State University, Novosibirsk, Russia

Education

- Ph.D. Genetics. The University of Texas - Houston Health Science Center. May 1996
Ph.D. advisor: Dr. Wen-Hsiung Li.
 Ph.D. dissertation title: *Molecular Evolution of Primate Immunodeficiency Viruses and Hepatitis Delta Virus*
- Additional courses: Statistics and computer programming
 Departments of Statistics and Computational and Applied Mathematics
 Rice University (Houston, TX). August 1993-December 1994
- M.Sc. with distinction Cytology and genetics with concentration in mathematical biology
 (Honors Diploma) Novosibirsk State University (Novosibirsk, Russia). June 1990
 M.Sc. thesis title: *Theoretical analysis of divergence of primate Alu repeat promoters*

U.S. Federal Government Appointments

10.2002 – 09.2003 National Science Foundation Advisory Panel

Grants, Fellowships, and Awards**Active**

- 08/15/05-08/14/10 DOE *Genome-based models to optimize in situ bioremediation of uranium and harvesting electrical energy from waste organic matter.*(D. Lovley, PI)
Principal Investigator of the subcontract with University of Massachusetts. \$652,519
 (University of Tennessee subcontract only).
- 07/01/04-06/30/06 NIH/NICHD R21 *Genetic polymorphisms in pediatric lung injury* (M. Quasney, PI).
Collaborator.
- 07/01/03-06/31/2008 NIH/NHLBI R01 HL072375 *Genetics of cardiovascular reactivity in black youth* (B. Alpert, PI). Consultant.
- 01/01/01-12/31/05 Children's Foundation Research Center, Le Bonheur Children's Hospital. (R. Adkins, PI).
Molecular genetic analysis of birth weight variation. \$50,000. Investigator.

Past

- 09/01/02-08/31/05 DOE PN 02-13 *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). Principal Investigator of the subcontract with University of Massachusetts, \$196,460 (Univ. of Tennessee subcontract only).
- 01/01/04-12/31/04 Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN. (R. Adkins, PI). *Molecular genetic analysis of birth weight variation.* \$52,620.
Investigator.
- 01/01/03-12/31/03 Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN. (R. Adkins, PI). *Molecular Genetic Analysis of Pre-Eclampsia.* Consultant.
- 2000 *Computational Algorithms for Analysis of Genomic Data.* \$19,000. Principal Investigator (with S. Alvarez, C. Ruiz, L. Ryder, and M. Stevens, PIs). Research Development Council, Worcester Polytechnic Institute.
- 1999 *Travel Award to attend the 3rd Gordon Research Conference in Molecular Evolution in Hayama, Japan.* \$800. Gordon Research Conferences and the National Science Foundation.
- 1997-1998 *Minnie L. Maffett Fellowship.* \$1,500.
 Agency: Minnie L. Maffett Fellowship Fund. Texas Federation of Business and Professional Women's Clubs, Inc. Arlington, TX
- 1995 *Student Travel Award.* \$100.
 Graduate School of Biomedical Sciences, The University of Texas - Houston
- 1988-1990 *Scholarship for academic excellence and scientific achievements*
 Novosibirsk State University, Novosibirsk, Russia
- 1988 *Scientific Council Scholarship* (for academic excellence)
 Novosibirsk State University, Novosibirsk, Russia

Invited Seminar Presentations

- 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
- 09/2003 *Computational prediction of operons and transcription factor binding sites in Geobacteraceae: an update.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 04/2003 *Computational analysis of genetic data: bacteria, viruses, and human.* Department of Zoology, Oklahoma State University. Stillwater, OK
- 03/2003 *Prediction of transcription factor binding sites in Geobacteraceae.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 06/2001 *Computational analysis of biological information at sequence and genome level.* Department of Medicine, Medical School, 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
- 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
- 05/1998 *Results of the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Rio Grande City, TX
- 11/1997 *Update on the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Jackson, MS

- 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
- 04/1997 *Genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. 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
- 10/1996 *Linkage mapping of hypertension-related genes.* Blood Pressure Linkage Working Meeting. Department of Human Genetics, University of Michigan. Ann Arbor, MI
- 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

Conference and workshop presentations (in collaboration with other investigators; full list of co-authors is available upon request)

- 06/2005 105th General Meeting of American Society of Microbiology. Atlanta, GA. *Posters:*
- (1) *Genome-wide similarity search for transcription factors and their binding sites in species of Geobacter.*
 - (2) *Analysis of gene regulation in a rel_{GSU} mutant of Geobacter sulfurreducens.*
 - (3) *Complete genome sequence of Pelobacter carbinolicus: insights into mechanisms of Fe(III) reduction and evolution of the family Geobacteraceae.*
 - (4) *Reconstruction of the regulatory network of Geobacter sulfurreducens from gene expression data and sequence analysis.*
- 04/2005 UT-ORNL-KBRIN Bioinformatics Summit 2005. Lake Barkley State Park, KY. *Posters:*
- (1) *Evaluation of the Role of the Transition to Transversion Ratio on the Estimate of the Linkage Disequilibrium Coefficient.*
 - (2) *Prediction of operons and transcription regulatory sites in Geobacteraceae using comparative genomics and microarray clustering.*
- 02/2005 Genomics:GTL Contractor-Grantee Workshop III. Washington, DC. *Two posters:*
- (1) *Novel regulatory systems and adaptation of some well-known systems controlling respiration, growth, and chemotaxis of Geobacter species.*
 - (2) *Reconstruction of the regulatory network of Geobacter sulfurreducens from gene expression data and sequence analysis.*
- 10/2004 Annual meeting, American Society of Human Genetics. Toronto, Canada. *Poster presentation: Evaluation of the role of the transition to transversion ratio on the estimate of the linkage disequilibrium coefficient*
- 10/2004 7th Annual Conference on Computational Genomics organized by the Jackson Laboratory and the Institute for Genomic Research. Reston, VA. *Genome sequence of Pelobacter carbinolicus, the cytochrome-poor cousin of the Geobacteraceae.*

- 05/2004 104th General Meeting of American Society of Microbiology. New Orleans, LA. *Two posters:*
- (1) *Prediction of operons and transcription regulatory sites in Geobacteraceae using comparative genomics and microarray clustering.*
 - (2) *Investigation of the Fur regulon of Geobacter sulfurreducens*
- 03/2004 3rd UT-ORNL Bioinformatics Summit. Fall Creeks Fall, TN. *Posters:*
- (1) *Identification of similar domains in orthopoxvirus and human complement regulators.*
 - (2) *Accuracy and efficiency of Bayesian and EM inference of haplotypes in the presence of gene conversion.*
- 03/2004 2004 Genomes to Life Program Workshop. *Poster: In silico elucidation of transcription regulons and prediction of transcription factor binding sites in Geobacter species using comparative genomics and microarray clustering*
- 11/2003 Annual meeting, American Society of Human Genetics. Los Angeles, CA. *Posters:*
- (1) *Identification of similar domains in orthopoxvirus and human complement regulators.*
 - (2) *Accuracy and efficiency of Bayesian and EM inference of haplotypes in the presence of gene conversion.*
- 11/2003 Annual meeting, International Genetic Epidemiology Society. Los Angeles, CA. *Posters:*
- (1) *Computational sequence comparison of orthopoxvirus and human complement regulators.*
 - (2) *Association of polymorphisms upstream of pituitary growth hormone with term birth weight.*
- 10/2003 Annual meeting, American Association for the Study of Liver Diseases. Boston, MA. *Poster: Combination therapy for hepatitis C: Positive selection pressure at baseline is associated with virologic response.*
- 05/2003 103rd General Meeting of American Society of Microbiology. Washington, DC. *Poster: Computational prediction of transcription regulatory elements in Geobacteraceae*
- 03/2003 2nd UT-ORNL Bioinformatics Summit. Fall Creeks Fall, TN. *Poster and oral presentations: Computational prediction of transcription regulatory elements in Geobacteraceae*
- 02/2003 2003 Genomes to Life Program Workshop. *Poster: 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*
- 07/2002 Gordon Research Conference in Bioinformatics and Structural/Evolutionary Genomics. Mt. Holyoke College, So. Hadley, MA. *Poster: Computational analysis of viral proteins similar to human complement regulators.*
- 11/2001 11th Annual Meeting of the New England Molecular Evolutionary Biologists (NEMEB2000). Simth College, Northampton, MA. *Oral presentation: Computational analysis of viral sequences similar to complement regulators.*
- 06/2001 13th Biennial International C.elegans Conference, Los Angeles, CA. *Poster: Identifying promoter motifs and predicting gene expression patterns in C. elegans using data mining tools.*
- 05/2001 From Genome to Physiology. Spring 2001 Meeting of the North East Section of the American Society of Plant Physiology. *Poster: Computational analysis of a plastid-localized sequence in plants*
- 10/2000 Genetic Analysis Workshop 12. Southwest Foundation for Biomedical Research, San Antonio, TX. *Two poster presentations:*

(1) *Comparison of population-based techniques in identifying genetic variants associated with simulated complex disorder in a general population*

(2) *Genotype-specific approach to association analysis of genetic polymorphisms in a general population*

- 10/2000 11th Annual Meeting of the New England Molecular Evolutionary Biologists (NEMEB2000). Harvard University, Cambridge, MA. *Poster: Evolution of short consensus repeats.*
- 06/2000 2000 Annual Meeting: Society for Molecular Biology and Evolution and American Genetic Association. Yale University, New Haven, CT. *Oral presentation: Molecular evolution of structure and function of regulators of complement activation.*
- 11/1999 10th Annual Meeting of the New England Molecular Evolutionary Biologists (NEMEB99), State University of New York, Albany, NY. *Poster: Molecular evolution of regulators of complement activation and their homologues*
- 10/1998 48th Annual Meeting: The American Society for Human Genetics. Denver, CO. *Poster: ACT: a computer package for analysis of complex traits.*
- 10/1998 17th International Complement Workshop. Rhodes, Greece. *Poster: Evolutionary relationships among SCR containing proteins*
- 06/1998 Bioinformatics and Genome Research. Cambridge Healthtech Institute's 7th Annual International Conference. Boston, MA. *Poster: Use of phylogenetic Inference to test a viral transmission hypothesis*
- 02/1998 *Invited alumna presentation.* The 5th Annual Genetics Mini-Symposium. Graduate School of Biomedical Science, The University of Texas-Houston Health Science Center. *Oral presentation: Multipoint gene mapping for essential hypertension*
- 10/1996 Genetic Analysis Workshop 10. Watsonville, CA. *Abstract: Multipoint sib pair linkage analysis of chromosome 5 using nuclear families*
- 05/1995 Fourth International Conference on Mathematical Population Dynamics. Rice University, Houston, TX. *Oral presentation: Phylogenetic tree reconstruction for human and simian immunodeficiency viruses*
- 01/1995 Program in Genetics 2nd Annual Mini-Symposium. Graduate School of Biomedical Sciences, The University of Texas-Houston Health Science Center. *Oral presentation: Evolution of primate immunodeficiency viruses and problems of phylogenetic analysis*
- 08/1990 Modeling and Computer Methods in Molecular Biology and Genetics (International Conference). Novosibirsk, Russia. *Abstract: CpG-rich promoters of Alu-like repeats in the mammalian genome: some evolutionary characteristics*

Grant Reviewer

National Science Foundation

Reviewer for Scientific Journals

Circulation	Proceedings of the National Academy of Sciences USA
Genetic Epidemiology	Molecular Biology and Evolution
Hypertension	Molecular Phylogenetics and Evolution
Journal of Molecular Evolution	Journal of Biomolecular Structure and Dynamics
Biosystems	

Membership in Professional Organizations

American Association for the Advancement of Science

Teaching Experience

- 2003-present 825BIOE *Bioinformatics for Epidemiologists* (for graduate students). Department of Preventive Medicine and Center of Genomics and Bioinformatics, University of Tennessee Health Science Center
- 2004 Guest lecturer in a junior level course, *Cellular and Molecular Biology*. St. Edward's University, Austin, TX
- 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 Health Science Center
- 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:
Computational Sequence Analysis,
Genetics of Human Disease,
Biochemistry
The University of Texas Health Science Center
- 1998 Invited lecturer in genetics for science teachers in Brownsville, TX, area
The University of Texas-Houston program of long distance teachers' education
- 1988-1990 Supervisor and Instructor
Correspondence School in Biology for High School Students
Novosibirsk State University (Russia)
- 1985-1988 Coordinator, Program of Cooperation of the Department of Natural Sciences with High Schools. Novosibirsk State University (Russia)

Postdoctoral fellows trained Bin Yan, Ph.D. (2002-2005)
Dr. Marko Puljic (05.2005-present).

Graduate Students Trained Manish Punglyia (M.Sc., 2001)

Undergraduate Students Trained

- 2000-2001 Research project advisor and co-advisor for 14 undergraduate students on Major Qualifying Projects (1 academic year) in bioinformatics at WPI:
Frederick Tan (biotechnology/computer science major), David Phu (biotechnology/computer science), Kathryn Ferrell (biology), Maxwell Pistilli (biotechnology), Aaron Vandenstein (biotechnology), Dina Carreiro (biotechnology), Emily Gilbreath (biotechnology), Andrea Emery (biotechnology), Bryan Pardovano (biology), Ian Pushtee (computer science), Brian Murphy (computer science), James Lund (computer science), Jared Judecki (computer science), Daniel Doyle (computer science).

Publications

Peer reviewed

- E. Ciulla, A. Emery, D. Konz, and **J. Krushkal** (2005) *Computational sequence analysis of orthopoxvirus proteins similar to human complement regulators*. Gene: 355:40-47
- B. Yan, B. A. Methé, D. R. Lovley, and **J. Krushkal** (2004) *Computational prediction of conserved operons and phylogenetic footprinting of transcription regulatory elements in metal reducing bacterial family Geobacteraceae*. J. Theor. Biol. 230:133-144
- S. L. Kardia, L. S. Rozek, **J. Krushkal**, R. E. Ferrell, S.T. Turner, R. Hutchinson, A. Brown, C. F. Sing, and E. Boerwinkle (2003) *Genome-wide linkage analyses for hypertension genes in two ethnically and geographically diverse populations*. Am. J. Hypertension 16:154-157
- J. Krushkal**, M. Pistilli, K. M. Ferrell, F. Souret, and P. Weathers (2003) *Computational analysis of the evolution of the structure and function of 1-deoxy-D-xylulose-5-phosphate synthase, a key regulator of the mevalonate-independent pathway in plants*. Gene 313:127-138
- C. Shoemaker, M. Pungliya, M. Sao Pedro, C. Ruiz, S. Alvarez, M. Ward, E. Ryder, and **J. Krushkal** (2001) *Computational methods for single point and multipoint analysis of a simulated complex disorder in a general population*. In: Wijsman E.M., Almasy L., Amos C.I., Borecki I., Falk C.T., King T.M., Martinez M.M., Meyers D., Neuman R., Olson J.M., Rich S., Spence M.A., Thomas D.C., Vieland V.J., Witte J.S., MacCluer J.W., Eds. *Analysis of complex genetic traits: Applications to asthma and simulated data*. Genetic Epidemiology, Vol. 21 (Suppl. 1), Pp. S738-S745
- J. Krushkal**, O. Bat and I. Gigli (2000) *Evolutionary relationships among proteins encoded by regulators of complement activation gene cluster*. Molecular Biology and Evolution 17: 1718-1730
- Bray, M. S., **J. Krushkal**, L. Li, R. Ferrell, S. Kardia, C. F. Sing, S. T. Turner, and E. Boerwinkle (2000) *Positional genomic analysis identifies the β 2-adrenergic receptor gene as a susceptibility locus for human hypertension*. Circulation 101: 2877-2882
- J. Krushkal**, R. Ferrell, S. Mockrin, S. T. Turner, C. F. Sing, and E. Boerwinkle (1999) *Genome-wide linkage analyses of systolic blood pressure*. Circulation. 99:1407-1410
- J. Krushkal** and W-H. Li (1999) *Use of phylogenetic inference to test an HIV transmission hypothesis*. In: The Evolution of HIV. Pp. 208-232. K. A. Crandall, Ed. John Hopkins University Press, Baltimore, MD
- M. Xiong, **J. Krushkal**, and E. Boerwinkle (1998) *TDT statistics for mapping quantitative trait loci*. Annals of Human Genetics. 62: 419-429
- J. Krushkal**, C. Kemper, and I. Gigli (1998) *Ancient origin of human complement factor H*. Journal of Molecular Evolution. 47: 625-630
- J. Krushkal**, M. Xiong, R. Ferrell, C. F. Sing, S. T. Turner, and E. Boerwinkle (1998) *Linkage and association of adrenergic and dopamine receptor genes in the distal portion of the long arm of chromosome 5 with systolic blood pressure variation*. Human Molecular Genetics 7: 1379-1383
- C. I. Amos, **J. Krushkal**, T. Thiel, A. Young, D. K. Zhu, E. Boerwinkle, and M. de Andrade (1997) *Comparison of model-free linkage mapping strategies for the study of a complex trait*. In: L. R. Goldin, J. E. Bailey-Wilson, I. B. Borecki, C. T. Falk, A. M. Goldstein, B. K. Suarez, J. W. MacCluer, Eds. *Genetic Analysis Workshop 10: Detection of Genes for Complex Traits*. Genetic Epidemiology 14: 732-742
- H. Mannen, S. C.-M. Tsoi, **J. S. Krushkal**, W.-H. Li, and S. S.-L. Li (1997) *The cDNA cloning and molecular evolution of reptile and pigeon lactate dehydrogenase isozymes*. Molecular Biology and Evolution 14: 1081-1087
- J. Krushkal** and W.-H. Li. (1997) *Evolution of primate immunodeficiency viruses*. In: Advances in Mathematical Population Dynamics: Molecules, Cells and Man. Part I, Chapter 1. P. Auger and R. Jean, eds. World Scientific. Biological Systems Series
- W.-H. Li, D. L. Ellsworth, **J. Krushkal**, B. H.-J. Chang, and D. Hewett-Emmett (1996) *Rates of nucleotide substitution in primates and rodents and the generation-time effect hypothesis*. Molecular Phylogenetics and Evolution 5: 182-187

- J. Krushkal** and W.-H. Li (1995) *Substitution rates in hepatitis delta virus*. Journal of Molecular Evolution 41: 721-726
- M. Nakamuta, K. Oka, **J. Krushkal**, K. Kobayashi, M. Yamamoto, W.-H. Li, and L. Chan (1995) *Alternative mRNA splicing and differential promoter utilization determine tissue-specific expression of the apolipoprotein B mRNA-editing protein (Apobec1) gene in mice: structure and evolution of Apobec1 and related nucleoside/ nucleotide deaminases*. Journal of Biological Chemistry 270: 13042-13056
- K. Oka, K. Ishimura-Oka, M.-j. Chu, M. Sullivan, **J. Krushkal**, W.-H. Li, and L. Chan (1994) *Mouse very low density lipoprotein receptor (VLDLR) cDNA cloning, tissue-specific expression and evolutionary relationship with the low density lipoprotein receptor*. European Journal of Biochemistry. 224: 975-982
- S. N. Rodin and **J. S. Krushkal** (1992) *"Parasitic" DNA and genome: some evolutionary and coevolutionary aspects*. In: Modelling and Computer Methods in Molecular Biology and Genetics. V. A. Ratner and N.A. Kolchanov, Eds. Nova Science Publishers, New York. 351-355
- S. N. Rodin, Y. G. Matushkin, and **J. S. Krushkal** (1992). *Repeated intragenome "parasites" as a factor in molecular coevolution*. In: Modern Trends in Human Leukemia IX. Haematology and Blood Transfusion Vol. 35. Neth, Frolova, Gallo, Greaves, Afanasiev, and Elstner, Eds. Springer-Verlag, Berlin, Heidelberg. 323-328.
- A. A. Zharkikh, A. Yu. Rzhetsky, P. S. Morosov, T. L. Sitnikova, and **J. S. Krushkal** (1991) *VOSTORG: a package of microcomputer programs for sequence analysis and construction of phylogenetic trees*. Gene 101: 251-254

Published conference abstracts

- J. Krushkal**, M. Punliya, and E. F. Ryder (2004) *Evaluation of the Role of the Transition to Transversion Ratio on the Estimate of the Linkage Disequilibrium Coefficient*. The American Journal of Human Genetics 75 (Suppl.): 231.
- J. Krushkal**, A. Emery, E. Ciulla, D. Konz, R. Adkins, and I. Gigli (2003) *Identification of similar domains in orthopoxvirus and human complement regulators*. The American Journal of Human Genetics 73 (Suppl.):340
- J. Krushkal**, D. Konz, A. Emery, E. Ciulla, R. Adkins, and I. Gigli (2003) *Computational Sequence Comparison of Orthopoxvirus and Human Complement Regulators*. Genetic Epidemiology 25: 256
- R. Adkins, C. Campese, R. Vaiya, **J. Krushkal**, and T. Boyd (2003) *Accuracy and efficiency of Bayesian and EM inference of haplotypes in presence of gene conversion*. The American Journal of Human Genetics 73 (Suppl.):382
- R. M. Adkins, C. Campese, R. Vaidya, **J. Krushkal**, and T. K. Boyd (2003) *Association between polymorphisms upstream of pituitary growth hormone and term birth weight*. Genetic Epidemiology 25: 236
- J. Krushkal**, O. Bat, and I. Gigli (1998) *Evolutionary relationships among SCR containing proteins*. Molecular Immunology. 35: 350
- M. de Andrade, **J. Krushkal**, L. Yu, D. Zhu, and C. I. Amos (1998) *ACT: a computer package for analysis of complex traits*. The American Journal of Human Genetics. 63 (Suppl.): A287