Permanent residence:	USA (USA citizen naturalization is in process)
Home address:	104 Vinyard Avenue, Blacksburg, VA 24060
Office address:	Center for Molecular Medicine and Infectious Diseases, Virginia-Maryland Regional College of Veterinary Medicine, Virginia Polytechnic Institute and State University, 1800 Kraft Drive, Suite 200, Blacksburg, VA 24061
Phone numbers:	540-951-5651 (home), 540-231-9496 (office), 540-239-7806 (cell)
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Education

Ph.D. Biochemistry and Molecular Biology, Wayne State University School of Medicine, Detroit, MI, 9/93-10/98. Toxicogenomics and biochemical toxicology of xenobiotics resistance genes.

M.E. Electronics and Computer Control Systems, Wayne State University College of Engineering, Detroit, MI, 9/97-8/99. Parallel processing and supercomputing in genomics.

M.S. Microbiology, Chinese Academy of Agricultural Sciences, Beijing, China, 9/87-1/90. Transgenic plants transferred with *Bacillus thuringenesis* endotoxin gene.

B.S. Genetics, Beijing (now China) Agricultural University, Beijing, China, 9/83-7/87. Yield-correlated quantitative genetic traits of wheat.

Certificates

Mid-Atlantic Regional Centers of Excellence Biosafety Lab-3 (MARCE BSL-3) Training, University of Maryland School of Medicine, Baltimore, February 2005

Infectious & Diagnostic Materials Training, University of Maryland Department of Environmental Health and Safety, Baltimore, February 2005

Human Genetics, University of Michigan Medical School, Ann Arbor, August 1999 – August 2000

Principles and Techniques of Biochemistry and Immunology, Peking University Department of Biology, Beijing, China, May-August 1987

Skills in Life Science

Principles and techniques in bioinformatics, systems biology, computational and mathematical modeling, biostatistics and biometry, computer science, toxicology, genomics, toxicogenomics, pharmacology, pharmacogenomics, pharmacokinetics, pharmacodynamics, biochemistry, molecular biology, genetics, microbiology, infectious diseases, immunology and vaccine development, mammalian cell biology, and plant science.

Skills in Genomics, Bioinformatics and Computer Science

Languages and tools: Perl, Python, Java, C/C++, PL/SQL, BASIC, FORTRAN, JavaScript, HTML, XML, IIS, ASP, Apache, PHP, CGI

Statistics and mathematics packages: SAS, SPSS, MatLab, Mathematica

Relational database management systems: MySQL, Oracle, MS Access

Systems: Unix (Sun Solaris, Linux), Beowulf Linux multi-process parallel computing cluster, Windows 95/98/Me/NT4.0/00/XP, MS-DOS, OS/2, Mac OS

Other popular software: MS Office (Word, PowerPoint, Access, Excel, Outlook, Internet Explorer), MS Visio, ERwin, TOAD, Lotus, Sigmaplot, Photoshop, UML, Origin

Bioinformatics tools: BLAST, FASTA, SwissProt, Unigene, LALIGN, ClustalW, InterPro (Pfam, Prosite, PRINTS, SMART, ProDom), PAUP, Phylip, ESTScan, GenScan, estwisedb, DCS, TMPRED, HMMTOP, Paircoil, iPSORT, SAPS, tacg-3.5-src, EstWise, GeneWise, Entrez, GCG, Genepro, DNAsis, MacVector, PDB, 3D JigSaw, rasmol, BioEdit, DnaSP, databases and tools of NCBI/EBI /TIGR

Professional Experience

Research Scientist
Center for Molecular Medicine and Infectious Diseases, Virginia-Maryland Regional College of
Veterinary Medicine, Virginia Tech, Blacksburg, VA   10/04-

Bioinformatics, genomics, immunology, vaccine development, and molecular genetics of pathogenesis factors (capsules, lipopolysaccharides and toxins) from bacteria (*Francisella tularensis* and *Burkholderia mallei*).

Subtractive hybridization of genomic DNA samples between related species. High-throughout genomic sequencing and assembling of putative pathogenesis gene clusters.

Molecular evolution based on synonymous substitution rates (K_S) and non-synonymous substitution rates (K_A) of pathogenesis genes in different subspecies of *F. tularensis* and *B. mallei*.

Toxicology Trainee
Pharmacokinetics Branch, Experimental Toxicology Division, National Health and Environmental Effects Research Laboratory, US Environmental Protection Agency and University of North Carolina, NC
          09/04-10/04

Computational toxicogenomics and evolution of xonobiotics metabolic genes.
Comparative and structural pharmacogenomics, pharmacokinetics and pharmacodynamics of environmental xenobiotics on different eukaryotic species, especially animals.
2-D and 3-D structure predictions of toxicology and pharmacology related enzymes by bioinformatics and computational approaches.

Project Manager
Automation Creations, Inc., Blacksburg, VA   05/04-08/04

Management of a team project of "Operation and maintenance of the biological data processing system" for depositing AIDS and cancer research results.

Council Advisor
Energy Sector, Gerson Lehrman Group, Inc.   7/03-

Consultation to investment clients with knowledge, insights, and strategies in public health care and agriculture, especially, in the high-tech fields of biotechnology and bioinformatics.

Bioinformatics Scientist / Computational Biologist and Medical Modeler
Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA   08/01-08/04

Computational models of biochemical and pharmacokinetic networks of anti-HIV nucleoside analogue drugs (AZT, d4T, ABV, 3TC, ddC and ddI) along with the four natural nucleosides (A, C, G and T) in sequential phosphorylation / dephosphorylation in cytosol and mitochondrial matrix and

the corresponding transporter and exchanger across mitochondrial membrane of dividing, resting and post-mitotic cells.

Bacteria and viruses genome data mining, acquisition, vetting, consolidation, curation, annotation, and visualization for the biodefense and emerging infectious diseases pathogen projects.

Mining of protein domains from genomic and proteomic data of multiple animal and plant species in a Beowulf Linux supercomputing cluster.

Comparative, functional and structural (2-D and 3-D) genomics of animals, plants, bacteria and viruses and analysis of genome duplications of higher organisms.

Development of a seven-fold speedup pipeline for analyzing protein domains from massive amount of EST data with improved reliability.

Implementation of an integrated pipeline to directly translate, predict and store translated peptide secondary and tertiary structure information from massive EST sequences of multiple species into relational database.

Modeling the relational databases of *Arabidopsis thaliana* based SeedGenes and general EST raw sequence analysis pipeline (ESTAP) and wrote visualization interfaces for SeedGenes database.

Assistant Professor
PhD Program in Molecular Genetics and Cell Biology, University of Maine   1/01-6/06

Organizing and offering bioinformatics and toxicogenomics courses for students.
Supervising visiting students at home institute.

Staff Scientist and Director
Bioinformatics Center, Mount Desert Island Biological Laboratory, Bar Harbor, ME, and
Marine and Freshwater Biomedical Science Center,
National Institute of Environmental Health Sciences, Bar Harbor, ME   8/00-8/01

Initiated the bioinformatics program in toxicogenomics of aquatic organisms in the newly established center, including quoting and purchasing necessary start-up hardware and software.

Designed and implemented the entity relationship model and visualization web interfaces for the annotated Comparative Toxicogenomics Database.

Recruited and supervised professional staff for the Bioinformatics Center.

Postdoctoral Fellow
Dept of Human Genetics, University of Michigan Medical School, Ann Arbor, MI   8/99-8/00
(Supervisor: Thomas D. Gelehrter, M.D., Professor and Chairman)

Comparative and functional genomics and evolution of signal transduction factors.

Compared differential gene expressions from tissues (such as joints) of patients with lupus and arthritis.

Discovered that physical and functional interaction of liganded glucocorticoid receptor with C-terminal domain of Smad3 facilitates the decay of each other with coimmunoprecipitation.

Mapped the minimal domain of glucocorticoid receptor required to repress transforming growth factor β pathway with deletion, insertion and substitution mutants utilizing mammalian two hybrid systems.

Spent two months to prepare an NIH grant application (Glucocorticoid Inhibition of Transactivation by TGFβ) with the supervisor.

Research Associate
Dept of Biochemistry and Molecular Biology, Wayne State University, Detroit, MI   11/98-8/99
(Supervisor: Barry P. Rosen, Ph.D., Professor and Chairman)

Structure-function relationship of a bacterial drug transporter ATPase of an infectious *E. coli* isolate from a clinical patient by sequential amino acid deletion, insertion and substitution and published the relevant results.

Interaction between cytosol ATPase subunit and intrinsic membrane protein by gene fusion, cross-linking, *etc.*

Genomic and protein database mining for antimicrobial drug resistance determinants for evolutionary study.

M.E. Candidate
Dept of Electrical and Computer Engineering, Wayne State University, Detroit, MI   9/97-8/99

Studied and used parallel processing and supercomputing to analyze large genomic datasets.

Ph.D. Candidate
Dept of Biochemistry and Molecular Biology, Wayne State University, Detroit, MI   9/93-10/98
(Supervisor: Barry P. Rosen, Ph.D., Professor and Chairman)

Performed toxicogenomics research of multiple drug resistance operons in infectious *E. coli* strains and constructed phylogenetic trees of drug transporters with bioinformatics tools.

Compared the synteny (gene compositions and orders) of those operons and performed phylogenetic studies of relevant protein products.

Detected the expression of each of the proteins encoded by the arsenic resistance operon and purified each protein for biochemical study.

Purified wild type ArsA ATPase and over 60 mutated ArsA proteins by ion exchange, gel filtration, affinity chromatography and HPLC for intensive biochemical research.

Measured the enzymatic parameters of these enzymes in the absence/presence of effectors/substrates by UV-Vis and fluorescence spectroscopy.

Visiting Scholar
Biomedical Research Institute, University of Wisconsin   3/92-8/93

Pharmacokinetics of carrot benzylpenicillin binding protein.
Identified benzylpenicillin and vancomycin binding activities in carrot tissue.
Purified benzylpenicillin binding protein from carrot plasma membrane.
Separated CNBr-digested benzylpenicillin binding protein fragments by HPLC.
Detected the expression of *de novo* mRNAs triggered by benzylpenicillin with quantitative PCR and differential display.

Presented results at the Annual Meeting of Plant Physiology.

Research Scientist and Laboratory Manager
Biotechnology Research Institute, Chinese Academy of Agricultural Sciences   1/90-3/92

Optimized binary expression vector in plant genetic engineering.
Purified proteinase inhibitor II protein (PI II) from tomato leaves.
Transferred tomato PI II gene into rice protoplasts and regenerated transgenic plants.
Identified transgenic rice plants by Dot and Southern blots, RFLP, PCR and DNA sequencing.
Detected the chromosome number of each transgenic plant by Giemsa staining.
Managed the order of enzymes, chemicals and equipments for the lab.

Graduate Research Assistant
Laboratory of Molecular Biology, Chinese Academy of Agricultural Sciences   8/87-1/90

First transferred *Bacillus thuringenesis* insecticidal gene into rice protoplasts and obtained transgenic plants for insect-control in the world. This achievement was reported in several Chinese major media and I was awarded a national prize.
Detected the expression of insecticidal gene in transgenic rice plants with Western blots.
Cultured cell/tissue of rice, maize, wheat, cotton, tobacco and potato.
Presented accomplishments in national/international conferences and published several papers.

Student Assistant
Department of Plant Genetics and Breeding,
Beijing (now China) Agricultural University   3/86-7/87

Spent 16 months in the wheat field and lab to do breeding and collect approximately 100,000 raw data. Statistically analyzed these data and screened out yield-correlated quantitative genetic traits of wheat.

Student Assistant
Departments of Biochemistry and Microbiology,
Beijing (now China) Agricultural University   7/85-2/86

Measured the contents of proteins, saccharides and vitamins in different varieties of maize and potato for nutrition quality breeding.
Constructed genomic library of wild pea for plant genetic engineering.

Academic Memberships

American Association for the Advancement of Science
New York Academy of Sciences
American Society for Biochemistry and Molecular Biology
Mitochondria Interest Group, NIH

Review Members

Journal of Biological Chemistry
Bioinformatics
Genomics

Grant Application and Administration Experience

"Operation and Maintenance of the Biological Data Processing System", NIH. (2004) As PI.

"Simulating Mitochondrial Toxicity of Nucleoside Analogs", NIH. (2004) As Participating Investigator.

"Comparative Toxicogenomics Database", NIH, funded with $3,789,045 starting July 2001. As Co-Investigator / Staff Scientist and Bioinformatics Core Director.

"Comparative Genomics" for Maine Biomedical Research Infrastructure Network, NIH, funded with about $4,900,000 starting October 2001. As Co-Investigator / Staff Scientist and Bioinformatics Core Director.

"Pilot Grant for Comparative Toxicogenomics Database", NIH, funded with $100,000 starting August 2000. As Project PI.

"Glucocorticoid Inhibition of Transactivation by TGFβ", NIH. (2000) As Participating Postdoctoral Fellow.

Supervising and Teaching Experience

Project Manager
Automation Creations, Inc., Blacksburg, VA   05/04-
Oversee and manage a team of five for the project of "Operation and maintenance of the biological data processing system".

Director
Bioinformatics Center, Mount Desert Island Bio Lab, Bar Harbor, ME   8/00-8/01
Recruited new staff and directed four members for the newly established center.

Adjunct Assistant Professor
PhD Program in Molecular Genetics and Cell Biology, University of Maine   1/01-8/01
Gave lectures of genomics and bioinformatics

Teaching Assistant
Department of Biochemistry and Molecular Biology, Wayne State University   9/94-8/97
Gave numerous general biochemistry and molecular genetics lectures and led question-answering classes to both undergraduate and graduate students.

Assigned Duties by PIs   1/90-8/00
Supervised over twenty high school summer students, undergraduate assistants, rotation graduate students (both M.S. and Ph.D.) and lab technicians in several labs.

Honors/awards

US EPA/UNC Toxicology Trainee Award, 09/04-10/04
Sigma Xi, 1999
International Who's Who Professional, 1999
President Service Award, Wayne State University, 1999
Graduate Teaching and Research Assistantships, Wayne State University, 1994-1998
Thomas C. Rumble Fellowship, Wayne State University, 1993-1994
National Prize, Ministry of Agriculture of China, August 1990
Graduate Research Assistantships, Chinese Academy of Agricultural Sciences, 1987-1990
Undergraduate Fellowships and Assistantships, Beijing Agricultural University, 1983-1987

Peer-Reviewed Publications

1. **Li J.**, Ahmed, F., and Inzana, T. (2005) Identification of virulent genes in live vaccine strain of *Francisella tularensis* by suppression-subtractive hybridization. Manuscript is in preparation.
2. **Li J.**, Waters, S.B. and Thomas, D.J. (2005) Computational and experimental characterization of AS3MT in inorganic arsenic methylation. Manuscript is in preparation.
3. **Li, J.** (2005) A hypothetical mechanism for genome sequence divergences. Submitted.
4. **Li, J.***, Dickerman, A., and Sobral, B. (2005) *In silico* assessment of TIGR gene indices. *Nucleic Acids Res.* Manuscript is under review. (* communicating author)
5. **Li, J.** (2005) Exhausting computing condition and minimum CPU cost. *Bioinformatics.* Manuscript is under review.
6. **Li, J.**, (2005) The toxicity mechanisms of an anti-HIV regimen. Manuscript is in preparation.
7. Bradshaw, P., **Li, J.**, and Samuels, D. (2005) A computational model of mitochondrial AZT metabolism. *Biochemical J.* doi:10.1042/BJ20050749. Accepted and in press.
8. **Li J.**, Waters, S.B., Drobna, Z., Devesa, V., Styblo, M. and Thomas, D.J. (2005) Arsenic (+3 oxidation state) methyltransferase and the inorganic arsenic methylation phenotype. *Toxicol Appl Pharmacol.* 204, 164-169.
9. Zhou, T., Bhattacharjee, H., **Li, J.**, Gatti, D.L., Walmsley, A.R., and Rosen, B.P. (2000) Structure-function relationships in a novel anion-translocating ATPase, in Biochemical Society Transactions 28, 520-526, Portland Press.
10. **Li, J.**, and Rosen, B.P. (2000) The linker peptide of the ArsA ATPase. *Molecular Microbiology* 35, 361-367.
11. **Li, J.**, and Rosen, B.P. (1998) Steric limitations in the interactin of the two ATP binding domains of the ArsA ATPase. *J. Biol. Chem.* 273, 6796-6800.
12. Mukhopadhyay, R., **Li, J.**, Bhattacharjee, H., and Rosen, B.P. (1998) Metalloid resistance mechanisms, pp159-181, in Advances in Experimental Medicine and Biology 456: Resolving the antibiotic paradox, Rosen, B.P., and Mobashery, S., eds. Kluwer Academic/Plenum Publishers.
13. **Li, J.**, Bruhn, D.F., Silver, S., Roberto, F., and Rosen, B.P. (1996) The arsenical resistance operon of IncN plasmid R46. *FEMS Microbiol. Lett.* 139, 149-153.
14. **Li, J.**, Liu, S., and Rosen, B.P. (1996) Interaction of the ATP-binding sites in the ArsA ATPase, the catalytic subunit of the Ars pump. *J. Biol. Chem.* 271, 25247-25252.
15. Bhattacharjee, H., **Li, J.**, Ksenzenko, M.K., and Rosen, B.P. (1995) Role of cysteinyl residues in metalloactivation of the oxyanion-translocating ArsA ATPase. *J. Biol. Chem.* 270, 11245-11250.
16. **Li, J.**, Yang, H., and Fan, Y. (1990) Rice (*Oryza sativa* L.) plant regeneration from protoplasts of a super Chinese rice cultivar-Zhonghua No. 8. *Chin J. Biotechnol.* 6, 119-123.
17. **Li, J.** (1990) Mature plants derived from rice protoplasts. *Newsletter of Agricultural Sciences* (16), 1-2.
18. **Li, J.**, Yang, H., and Fan, Y. (1990) Rice plant regeneration from protoplasts of a Chinese cultivar. *Genetic Manipulation in Plants* 6(2), 15-20.
19. Yang, H., Guo, S., **Li, J.**, Chen, X., and Fan, Y. (1990) Direct uptake of δ-endotoxin protein gene from *Bacillus thuringenesis* into rice protoplasts and regeneration of transgenic rice. *Genetic Manipulation in Plants* 6(1), 13-21.
20. Yang, H., **Li, J.**, Guo, S., Chen, X., and Fan, Y. (1989) Transgenic rice plants produced by uptake of δ-endotoxin protein gene from *Bacillus thuringenesis* into rice protoplasts. *Scientia Agricultura Sinica* 22(6), 1-5.
21. **Li, J.** (1989) Plantlet regeneration from the protoplasts of a novel rice cultivar. *Newsletter of Agricultural Sciences* (46), 1-2.
22. Yang, H., Guo, S., **Li, J.**, Chen, X., Zhang, H., and Fan, Y. (1988) Transformation of rice protoplasts by direct uptake of a "reportable chimaeric B.t. δ-endotoxin protein gene". *Rice Genetics Newsletter* 5, 141-142.
23. Guo, S., Yang, H., Chen, X., **Li, J.**, and Fan, Y. (1988) Transient expression of insecticidal

protein-GUS fusion gene in rape protoplasts. *Collection Papers for the Annual Meeting of 863 Project on Biotechnology of China*, pp10-11.

Selected Abstracts/posters (out of about 40)

1. Ahmed, F., **Li, J.**, Azadi, P., Ryder, C., and Inzana, T. Identification of a Carbohydrate Biosynthetic Gene Cluster in *Francisella tularensis* LVS by Subtractive Hybridization and Creation of an Allelic Exchange Mutant in LVS. June 5-9, 2005, 105th American Society for Microbiology Conference, Atlanta, Georgia.
2. Dickerman, A., **Li, J.**, and Sobral, B. Plant phylogenomics: looking at genomes as products of tree-like gene evolution. Plant, Animal and Microbe Genomes X Conference. January 12 - 16, 2002, San Diego, California.
3. Zhou, T., Bhattacharjee, H., **Li, J.**, Gatti, D.L., Walmsley, A.R., and Rosen, B.P. Structure-function relationships in an anion-translocating ATPase, Biochemical Society Leeds Meeting, April 11-13, 2000.
4. **Li, J.**, and Rosen, B.P. Interaction and communication among domains of the ArsA ATPase. Graduate Student Poster Day, September 20, 1998, Detroit, Michigan.
5. Rosen, B.P., Bhattacharjee, H., Zhou, T., **Li, J.**, and Liu, S. Catalytic mechanism of a resistance ATPase. FEBS Advanced Lecture Course "ATP Binding Cassette (ABC) Transporters: from Multidrug Resistance to Genetic Disease", February 22-March 1, 1997, Vienna, Austria.
6. **Li, J.**, and Rosen, B.P. An arsenite resistance pump in *E. coli* and human cancer cells and implications for cancer cell drug resistance. Wayne State University-Michigan Biotechnology Association Expo, May 14, 1997, Detroit, Michigan.
7. **Li, J.**, and Rosen, B.P. Spatial constraints in the interaction of the ATP-binding domains of the ArsA ATPase. *FASEB J.* 11(9), pA1143, presented at 17th International Congress of Biochemistry and Molecular Biology and 1997 Annual Meeting of ASBMB, August 24-29, 1997, San Francisco.
8. **Li, J.**, and Rosen, B.P. Interaction of the ATP-binding sites in the ArsA ATPase. *FASEB J.* 10(6), pA1504, presented at ASBMB Meeting, June 2-6, 1996, New Orleans, Louisiana.
9. Bhattacharjee, H., **Li, J.**, and Rosen, B.P. Structure of ATP and metal binding sites in the oxyanion-translocating ArsA ATPase. Comparative Aspects of translocating ATPases, Satellite Symposium of the 7th FAOBMB Congress, September 29 - October 2, 1995, Australia.
10. **Li, J.**, and Chang, C.-C. (1993) Specific binding of benzylpenicillin to the microsomal membrane of carrot callus tissues. *Plant Physiol.* 102, 66.

Selected Presentations (out of about 50)

1. Pharmacokinetic modeling and simulation of biochemical metabolism of anti-HIV drug AZT in AIDS patients' mitochondria. July 23, 2004, Center for Bio/Molecular Science and Engineering, Naval Research Laboratory, Washington DC.
2. Protein Domains Mined from Genome-Wide Functional Genes. July 23, 2004, Center for Bio/Molecular Science and Engineering, Naval Research Laboratory, Washington DC.
3. Modeling and simulation of zidovudine metabolism and toxicity in mitochondria of AIDS patients. April 23, 2004, Department of Biomedical Informatics, College of Physicians and Surgeons, Columbia University, New York.
4. Comparative genomics of protein domains mined from genome-wide EST datasets. April 23, 2004, Department of Biomedical Informatics, College of Physicians and Surgeons, Columbia University, New York.
5. Mining peptide information from complete genome surrogates – large EST datasets. September 18, 2003, Departments of Biology and Computer Science, University of Nebraska - Omaha.
6. Using bioinformatics power to interpret expressed eukaryotic genes. March 27, 2003, School of Natural and Mathematical Science, The Richard Stockton College of New Jersey, Pomona, New Jersey.
7. Comparative analysis of protein domains from eukaryotic transcriptomes and proteomes.

December 16, 2002, Great Lakes WATER Institute, University of Wisconsin-Milwaukee.

8. Application of bioinformatics in crop research. August 2, 2002, Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.

9. An integrated pipeline to directly predict and store secondary structure information of peptides from large datasets of EST data. February 4, 2002, Virginia Bioinformatics Institute, Blacksburg, Virginia.

10. Progress of the comparative toxicogenomics database. July 12, 2001, The Mount Desert Island Biological Laboratory, Salisbury Cove, Maine.

11. The inhibitory mechanism of mammalian transforming growth factor β pathway by glucocorticoid receptor. June 16, 2000, Packard Bioscience Company, Meriden, Connecticut.

12. The inhibition of trans-activation of transforming growth factor β pathway by glucocorticoid receptor. June 23, 2000, CuraGen Corporation, New Haven, Connecticut.

13. Biochemical characterization of the bacterial arsenic resistance ATPase. August 2, 1999, Archer-Daniels-Midland Company, Decatur, Illinois.

14. Structural and functional characterization of the ArsA ATPase, the catalytic subunit of bacterial arsenic transport pump. July 26, 1999, Department of Molecular Biology, Princeton University, Princeton, New Jersey.

15. Molecular characterization of the ArsA ATPase, the catalytic subunit of bacterial arsenic transport pump. July 22, 1999, National Institute on Deafness and Other Communication Disorders, National Institutes of Health, Rockville, Maryland.

16. Biochemistry and molecular genetics of the bacterial arsenic transport pump. July 9, 1999, Karmanos Cancer Institute, Detroit, Michigan.

17. Biochemistry and molecular genetics of the bacterial arsenic transport pump. June 29, 1999, Department of Human Genetics, University of Michigan Medical School, Ann Arbor, Michigan.

References

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