BIOGRAPHICAL SKETCH

NAME Ioschikhes, Ilya P.	POSITION TITLE Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
State University of Dushanbe, USSR	MS	1978-1983	Theoretical Physics
Weizmann Institute of Science, Rehovot, Israel	PhD	1992-1997	Structural Biology
Cold Spring Harbor Laboratory, Cold Spring Harbor New York	Post-doctoral Training	1997-1999	Bioinformatics

a. Positions and Honors

Professional Experience

1983 – 1984	Senior Lab Assistant, Medical Institute, Dushanbe, USSR
1984 – 1986	Programmer (positions: engineer, senior engineer), Computer Center of the Ministry of Building, Dushanbe, USSR
1986 – 1989	Research Fellow (analyst, programmer), State University, Dushanbe, USSR
1989	Senior research fellow (analyst, programmer), "Ravshan" Scientific-Technical Center, Dushanbe, USSR
1993, 1995	Visiting Researcher, School of Biology, Georgia Institute of Technology, Atlanta, GA
1990 – 1994	Research Fellow, College of Judea and Samaria, Ariel, Israel
1999 – 2002	Instructor in the Department of Molecular Genetics, Albert Einstein College of Medicine of Yeshiva University, New York, NY
2002-Present	Assistant Professor, Department of Biomedical Informatics, The Ohio State University, College of Medicine and Public Health, Columbus, OH
2004-Present	Graduate Faculty, Biophysics Graduate Program, College of Biological Sciences, The Ohio State University, Columbus, OH

Awards, Honors and Recognitions

1983	MS degree with honors, State University, Dushanbe
1994 -1997	L. Bein scholarship for Ph.D. studies in the Weizmann Institute of Science.

b. Selected Peer-Reviewed Publications

1. **Ioshikhes I**, Bolshoy A, Trifonov EN. Preferred positions of AA and TT dinucleotides in aligned nucleosomal DNA sequences. *J. Biomol. Struct. Dyn.* 1992 Jun; **9**(6):1111-1117.
2. **Ioshikhes I**, Trifonov EN. Nucleosomal DNA sequence database. *Nucleic Acids Res.* 1993 Oct 25; **21**(21):4857-4859.
3. **Ioshikhes I**, Bolshoy A, Derenshteyn K, Borodovsky M, Trifonov EN. Nucleosome DNA sequence pattern revealed by multiple alignment of experimentally mapped sequences. *J. Mol. Biol.* 1996 Sep 20; **262**(2):129-139.
4. Bolshoy A, **Ioshikhes I**, Trifonov EN. Applicability of the multiple alignment algorithm for detection of weak patterns: periodically distributed DNA pattern as a study case. *Comput. Appl. Biosci.* 1996 Oct; **12**(5):383-389.
5. Bolshoy A, Shapiro K, Trifonov EN, **Ioshikhes I**. Enhancement of the nucleosomal pattern in sequences of lower complexity. *Nucleic Acids Res.* 1997 Aug 15; **25**(16):3248-3254.
6. Lvovsky L, **Ioshikhes I**, Raja MC, Zevin-Sonkin D, Sobolev IA, Liberzon A, Shwartzburd J, Ulanovsky LE. Interdependence between DNA template secondary structure and priming efficiencies of short primers. *Nucleic Acids Res.* 1998 Dec 1; **26**(23):5525-5532.
7. **Ioshikhes I**, Trifonov EN, Zhang MQ. Periodical distribution of transcription factor sites in promoter regions and connection with chromatin structure. *Proc. Natl. Acad. Sci. USA* 1999 Mar 16; **96**(6):2891-2895.
8. **Ioshikhes I**, Zhang MQ. Large-scale human promoter mapping using CpG islands. *Nat. Genet.* 2000 Sep; **26**(1):61-63.
9. Montgomery KT, Lee E, Miller A, Lau S, Shim C, Decker J, Chiu D, Emerling S, Sekhon M, Kim R, Lenz J, Han J, **Ioshikhes I**, Renault B, Marondel I, Yoon S-J K, Song K, Murty VVVS, Scherer S, Yonescu R, Kirsch I, Ried T, McPherson J, Gibbs R, Kucherlapati R. A high-resolution map of human chromosome 12. *Nature* 2001 Feb 15; **409**(6822):945-946.
10. Babcock M, Pavlicek A, Spiteri E, Kashork CD, **Ioshikhes I**, Shaffer LG, Jurka J, Morrow BE. Shuffling of genes with low copy repeats on 22q11 (LCR22) by Alu-mediated recombination events during evolution. *Genome Research* 2003 Dec; **12**(13):2519-2532.
11. Gershenzon NI, **Ioshikhes IP**. Synergy of human core promoter elements revealed by statistical sequence analysis. Systems Biology: Genomic Approaches to Transcriptional Regulation meeting, Poster (Abstract 47). Cold Spring Harbor NY, Mar 4-7, 2004.
12. Gershenzon NI, **Ioshikhes IP**. Development of the position-weight matrix technique for DNA/protein binding sites. Systems Biology: Genomic Approaches to Transcriptional Regulation meeting, Poster (Abstract 48). Cold Spring Harbor NY, Mar 4-7, 2004.
13. Ramaswamy A, Bahar I, **Ioshikhes I**. Structural dynamics of nucleosome core particle: Comparison with nucleosomes containing variant histones. *Proteins* 2005 Feb 15; **58**(3):683-696.

14. Gershenzon NI, **Ioshikhes IP**. Synergy of human Pol II core promoter elements revealed by statistical sequence analysis. *Bioinformatics* 2005 (in press).

15. Gershenzon NI, **Ioshikhes IP**. Promoter Classifier: software package for promoter database analysis. *Applied Bioinformatics* 2005; **4**(2) (in press).

16. Gershenzon NI, Ostrowski MC, **Ioshikhes IP**, Stormo GD. Computational technique for improvement of the position weight matrices for the DNA/protein binding sites (ETS factors as study case). *Systems Biology: Global Regulation of Gene Expression meeting*, Talk (accepted). Cold Spring Harbor NY, Mar 17-20, 2005.