

## BIOGRAPHICAL SKETCH

Provide the following information for the key personnel in the order listed for Form Page 2.  
Follow the sample format on preceding page for each person. **DO NOT EXCEED FOUR PAGES.**

NAME  Alexandre V. Morozov	POSITION TITLE  Associate Professor of Physics		
eRA Commons User Name  ALEXMOZ			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Rostov State University, Rostov-on-Don, Russia	Diploma (M. Sc.)	1995	Physics
University of Washington, Seattle	M. Sc.	1997	Physics
University of Washington, Seattle	Ph. D.	2003	Physics
University of Washington, Seattle	Postdoctoral	2003	Biophysics
Rockefeller University, New York	Postdoctoral	2003-2007	Biophysics

### A. Personal Statement

The overall goal of my research is to predict gene regulation on a whole-genome scale, including the variation that is influenced by cell type, environmental signals, developmental stage, and disease state. Broadly speaking, I seek to improve our current understanding of the "transcriptional and post-transcriptional regulatory code" that links DNA sequence with gene expression levels. To this end, I and the members of my research group are currently pursuing several projects: **(a) Studies of chromatin structure and its effect on gene regulation** (including both individual nucleosome positions and higher-order chromatin structure). We use sequence-dependent DNA mechanics models as well as techniques from statistical mechanics and polymer physics to predict nucleosome positions both *in vitro* (where they are determined by DNA sequence alone) and *in vivo*, where chromatin structure is dynamically modified via competition with other DNA-binding factors and the action of chromatin remodeling enzymes. Our computational models are guided by large-scale maps of nucleosome and DNA-binding factor positions and occupancies obtained using high-throughput sequencing and hybridization to microarrays. **(b) Biophysical models of protein evolution.** Amino acid substitutions that have accumulated in evolved proteins and protein complexes provide important clues to their stability and function. We are developing evolutionary theories and phylogenetic descriptions that explicitly take protein energetics as well as protein-protein and protein-DNA interactions into account. **(c) Protein-DNA recognition code.** We use a combination of protein-DNA structural data and high-throughput *in vitro* protein-DNA binding assays to model protein-DNA interactions on the genomic scale. These models will be combined with the models of chromatin structure to gain insight into the mechanisms of gene regulation on the dynamic chromatin template.

### B. Positions and Honors

#### Professional Positions

1993-95	<i>Diploma thesis research</i> in the Laboratory of Prof. Vedrinskii R.V., Rostov State University, Rostov-on-Don, Russia
1996-99	<i>Graduate Teaching Assistant</i> , Department of Physics, University of Washington, Seattle, WA
1999-03	<i>Predoctoral Research Assistant</i> in the Laboratory of D.Baker, HHMI, University of Washington, Seattle, WA
2003	<i>Postdoctoral Fellow</i> in the laboratory of D.Baker, HHMI, University of Washington, Seattle, WA
2003-07	<i>Postdoctoral Fellow</i> in the laboratory of E.D.Siggia, Rockefeller University, New York, NY
2007-08	<i>Visiting Professor</i> , Center for Studies in Physics & Biology, Rockefeller University, New York, NY

2007-12      *Assistant Professor*, Department of Physics & Astronomy and the BioMaPS Institute for Quantitative Biology, Rutgers University, Piscataway, NJ  
2012-present Associate Professor, Department of Physics & Astronomy and the BioMaPS Institute for Quantitative Biology, Rutgers University, Piscataway, NJ

### Awards/Honors/Synergistic activities

- J. Soros Undergraduate Student Stipend (1994-1995)
- Leukemia and Lymphoma Society Postdoctoral Fellowship (2005-2008)
- Alfred P. Sloan Research Fellowship (2009-2013)
- BioMaPS Summer School co-organizer (2008)
- Aspen Center for Physics workshop co-organizer (2012)
- Banff International Research Station workshop co-organizer (2013)
- Invited lecturer, “Networks in Biology, Social Science and Engineering” summer school, Indian Institute of Science, Bangalore, India
- Reviewer for scientific journals including *Nature Structural & Molecular Biology*, *Proceedings of the National Academy of Sciences*, *Physical Review Letters*, *Genome Research*, *Genome Biology*, *Nucleic Acids Research*, *BMC Structural Biology*, *Journal of Physical Chemistry*, *Physical Review*, *Proteins: Structure, Function and Bioinformatics*, *PLoS Computational Biology*
- Frontiers in Bioinformatics and Computational Biology, Associate Editor (2011-present)
- PLoS Computational Biology, Guest Editor (2011-present)
- Reviewer for Horizon Breakthrough grants, Netherlands Genomics Initiative (2009)
- Reviewer for Challenge grants, National Institutes of Health (2009)
- Grant reviewer for the Bankhead-Coley Cancer Research Program (Florida Department of Health) (2010)
- Grant reviewer for U.S.-Israel Bi-national Science Foundation (2010)
- Grant reviewer for the Kansas City Area Life Sciences Institute (2011)
- Grant reviewer for Israel Science Foundation (2012)

### **C. Selected Peer-reviewed Publications**

#### **Most relevant to the current application (in chronological order)**

1. **Morozov, A.V.** & Siggia, E.D. (2007). Connecting protein structure with predictions of regulatory sites. Proc.Nat.Acad.Sci. 104, 7068-7073. PMCID: PMC1855371
2. **Morozov, A.V.**, Fortney, K., Gaykalova, D.A., Studitsky, V.M., Widom, J. & Siggia, E.D. (2009). Using DNA mechanics to predict *in vitro* nucleosome positioning. Nucl. Acids Res. 37, 4707-4722. PMCID: PMC2724288
3. Locke, C., Tolkunov, D., Moqtaderi, Z., Struhl, K. & **Morozov, A.V.** (2010). High-throughput sequencing reveals a simple model of nucleosome energetics. Proc.Nat.Acad.Sci. 107, 20998-21003. PMCID: PMC3000311
4. Tolkunov, D., Zawadzki, K., Elfving, N., **Morozov, A.V.** & Broach, J.R. (2011). Chromatin remodelers clear nucleosomes from intrinsically unfavorable sites to establish nucleosome-depleted regions at promoters. Mol. Biol. Cell 22, 2106-2118. PMCID: PMC3113774
5. Chereji, R., Tolkunov, D., Locke, C. & **Morozov, A.V.** (2011). Statistical mechanics of nucleosome ordering by chromatin-structure-induced two-body interactions. Phys. Rev. E Rapid Comm. 83, 050903. PMCID: PMC3254185

## **Additional recent publications of importance to the field (in chronological order)**

1. **Morozov, A.V.**, Kortemme, T., Tsemekhman, K. & Baker, D. (2004). Close agreement between the orientation dependence of hydrogen bonds observed in protein structures and quantum mechanical calculations. Proc. Nat. Acad. Sci. 101, 6946-6951. PMID: PMC406446
2. **Morozov, A.V.**, Havranek, J.J., Baker, D. & Siggia, E.D. (2005). Protein-DNA binding specificity predictions with structural models. Nucl. Acids Res. 33, 5781-5798. PMID: PMC1270944
3. Haq, O., Levy, R.M., **Morozov, A.V.** & Andrec, M. (2009). Pairwise and higher-order correlations among drug-resistance mutations in HIV-1 subtype B protease. BMC Bioinformatics 10 Suppl. 8:S10. PMID: PMC2745583
4. Zawadzki, K.A., **Morozov, A.V.** & Broach, J.R. (2009). Chromatin-dependent transcription factor accessibility rather than nucleosome remodeling predominates during global transcriptional restructuring in *Saccharomyces cerevisiae*. Mol. Biol. Cell 20, 3503-3513. PMID: PMC2719568
5. Chereji, R. & **Morozov, A.V.** (2011). Statistical mechanics of nucleosomes constrained by higher-order chromatin structure. J. Stat. Phys. 144, 379-404. PMID: PMC3156456
6. Tsitron, J., Ault, A.D., Broach, J.R. & **Morozov, A.V.** (2011). Quantitative decoding of complex chemical mixtures with sensor arrays. PLoS Comp. Biol. 7, e1002224. PMID: PMC3202980
7. Manhart, M., Haldane, A. & **Morozov, A.V.** (2012). A universal scaling law determines time reversibility and steady state of substitutions under selection. Theor. Popul. Biol. 82, 66-76. PMC Journal - In Process
8. Tolkunov, D. & **Morozov, A.V.** (2012). Single temperature for Monte Carlo optimization on complex landscapes. Phys. Rev. Lett. 108, 250602. PMC Journal - In Process
9. Locke, G., Haberman, D., Johnson, S.M. & **Morozov, A.V.** (2012). Global chromatin states and nucleosome positioning in *C.elegans*, submitted.
10. Haq, O., Andrec, M., **Morozov, A.V.** & Levy, R.M. (2012). Correlated electrostatic mutations provide a reservoir of stability in HIV protease, submitted.

## **D. Research Support**

### **Ongoing Research Support**

1. National Institutes of Health (NIH) R01 HG004708 - A. Morozov (PI) 02.2009 - 02.2013  
"Biophysical Models for Prediction and Design of Eukaryotic Chromatin Structure"

The goal of this project is to construct computational models of nucleosome positioning and energetics and use them to predict how chromatin structure affects gene regulation and other cellular functions.

2. Alfred P. Sloan Research Fellowship 06.2009 – 06.2013

The goal of this study is to develop phylogenetic models of protein evolution that would explicitly take protein stability and function into account, and more generally merge concepts from population genetics and protein physics into a coherent phylogenetic theory.