

CURRICULUM VITAE

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EDUCATION

- 2000-2006 **Ph.D. in Bioinformatics**, Institute of Cytology and Genetics, Novosibirsk, Russia.
Thesis: *Mathematical modeling of gene network dynamics*
- 1998-2000 **M.Sc. in Chemistry**, Novosibirsk State University, Novosibirsk, Russia.
Thesis: *Modeling of structural and functional organization and evolution of the molecular genetic systems under changing environmental conditions*
- 1994-1998 **B.Sc. in Chemical Ecology and Nature Management**, Novosibirsk State University, Novosibirsk, Russia
- 1992-1994 Specialized Educational Scientific Center of Physics and Mathematics of Novosibirsk State University, Novosibirsk, Russia

RESEARCH EXPERIENCE

- 2012-present **Senior Scientist**, Seattle BioMed, Seattle, WA 98109
- 2011-present **Affiliated Scientist**, Institute for Systems Biology, Seattle, WA 98109
- 2011-2012 **Staff Scientist**, Seattle BioMed, Seattle, WA 98109
- 2010-2011 **Research Scientist**, Institute for Systems Biology, Seattle, WA 98103
- 2006-2010 **Postdoctoral Fellow**, Institute for Systems Biology, Seattle, WA 98103
- 2006 **Research Scientist**, Institute of Cytology and Genetics, Novosibirsk, Russia
- 2003 **Visiting Scientist**, CNR Institute of Biomedical Technology (CNR-ITB), Milan, Italy
- 2000-2006 **Junior Research Scientist**, Institute of Cytology and Genetics, Novosibirsk, Russia
- 1999-2000 **Research Assistant**, Institute of Cytology and Genetics, Novosibirsk, Russia
- 1998-1999 **Research Assistant**, Institute of Chemical Kinetics and Combustion, Novosibirsk, Russia

RESEARCH INTERESTS

Computational systems biology and bioinformatics; genomics, proteomics and metabolomics; kinetic modeling of dynamical molecular systems; structural and parametric inverse problem for dynamical systems; optimal control theory; approximation theory for dynamical system models; machine learning; signal and image processing and analysis.

AWARDS/HONORS

- 2012 Dynasty Foundation Lectureship Award (series of lectures at the Institute of Cytology and Genetics, Novosibirsk, Russia)

- 2005 ISCB Travel Award (the European Conference on Computational Biology).
- 2004 ISCB Travel Award (the International Conference on Intelligent Systems for Molecular Biology and the European Conference on Computational Biology).
- 2004 FEBS Travel Award (the FEBS Special Meeting, International Conference on the Bioscience of Lipids).
- 2003 ECCB Travel Award (the European Conference on Computational Biology).
- 2002 Austrian Ministry of Science Travel Award (the International Conference on the Bioscience of Lipids).
- 2002 ISCB Travel Award (the International Conference on Intelligent Systems for Molecular Biology).
- 2001 GRC Travel Award (Gordon Research Conference on "Bioinformatics: From Inference to Predictive Models").
- 2001 Travel Award from Schloss Dagstuhl (Dagstuhl Seminar "Functional Genomics" Information and Simulation Systems for the Analysis of Gene Regulation and Metabolic Pathways).

INVITED TALKS

- 2014 Keynote at [BGRS\SB'2014](#), "Multiscale modeling as a framework for exploring molecular mechanisms of biological systems"
- 2013 "Kinetic modeling to inform mechanisms underlying complex bimolecular systems", Fred Hutchinson Cancer Research Center, Seattle, WA, USA
- 2013 "Mathematical modeling of dynamical biological systems", Department of Genomes Sciences, University of Washington, Seattle, WA, USA
- 2013 "Mathematical modeling of dynamical biological systems", Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense, Denmark
- 2013 "Mathematical modeling of dynamical biological systems", Department of Informatics, Technical University Munich, Munich, Germany
- 2012 "Identification and mathematical modeling of novel regulatory circuits that balance antiviral and inflammatory responses", Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
- 2012 "Regulation of Cu homeostasis in *H. salinarum*: computational modeling and experimental analysis", Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
- 2012 "Generalized time-frequency analysis of dynamical biomolecular systems", Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
- 2012 "ASymmetrically Self-UpREgulated (ASSURE) biomolecular systems", Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
- 2011 "Mathematical Modeling of Biomolecular Network Dynamics", Institute of Physiology, University of Zurich, Zurich, Switzerland

PATENTS AND CERTIFICATES

- 2012 "Automated Quantification of Microorganism Growth Parameters Through Temporally Resolved Microscopic Imaging" was filed with the U.S. Patent and Trademark Office (USPTO) on October 11, 2012 Authors: David Dilworth, **Alexander Ratushny**, John Aitchison
- 2012 Certificate of database registration No. 2012620064 (Russian Federation) Database "Elementary subsystems: E.coli metabolism", January 2012. Rightholder: Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences (RU). Authors: Likhoshvai V.A., Akberdin I.R., Kazantsev F.V., Ri M.T., Ri N.A., Khlebodarova T.M., Lashin S.A., Oschepkova E.A., **Ratushny A.V.**
- 2008 Certificate of software registration No. 2008612820 (Russian Federation) "A computer system for reconstruction, calculation and analysis of mathematical models of molecular genetic system (MGSmodeller)", June 2008. Rightholder: Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences (RU). Authors: Likhoshvai V.A., Kazantsev F.V., Akberdin I.R.,

Bezmaternikh K.D., Lashin S.A., Podkolodnaya N.N., **Ratushny A.V.**

- 2006 Certificate of databases registration No. 2006620196 (Russian Federation) “Database of mathematical models of molecular genetic processes (ModelER)”. Rightholder: Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences (RU). Authors: **Alexander Ratushny**, Eugenia Nedosekina, Sergei Lashin, Igor Turnaev, Nikita Vladimirov, Nikolai Podkolodny, Vitali Likhoshvai (RU).

TEACHING EXPERIENCE

Courses Taught

- 2014 Lecturer, [Summer Course: Systems Biology of Disease](#), Institute for Systems Biology, Seattle, WA.
- 2012 Lecturer, [Introduction to Systems Biology Course](#), Institute for Systems Biology, Seattle, WA.
- 2012 Lecturer, series of lectures on systems biology and mathematical modeling of dynamical biomolecular systems. Institute of Cytology and Genetics, Novosibirsk, Russia
- 2007 Lecturer, the 2nd Virtual Training Workshop on Bioinformatics organized by Asian Bioinformatics Research and Education Network ([ABREN](#)).
- 2006 Lecturer, the 1st Virtual Training Workshop on Bioinformatics organized by Asian Bioinformatics Research and Education Network ([ABREN](#)).
- 2006 Lecturer, “Actual problems of science, economics and business. (Systems biology, fundamental and applied problems. Possible commercialization of the results.)” course at the Faculty of Molecular and Biological Physics, Moscow Institute of Physics and Technology, Russia.
- 2003-2006 Lecturer and instructor, “Systems computational biology: mathematical modeling, optimization and inverse problems” special course at the Department of Information Biology, Faculty of Natural Sciences, Novosibirsk State University, Russia.
- 2001-2002 Lecturer and instructor, “Computer and mathematical modeling of molecular genetic systems” course at High College of Informatics affiliated with Novosibirsk State University, Russia.
- 1996 Lecturer and instructor, the chemistry course at the Summer School of the Specialized Educational Scientific Center of Physics and Mathematics of Novosibirsk State University, Novosibirsk, Russia.

Trainees

- 2009 John Sexton, undergraduate, Carnegie Mellon University, Pittsburgh, PA. Internship program at Institute for Systems Biology. Project: “Gene Expression Clustering and Regulatory Network Inference”.
- 2003-2007 Fedor Kazantsev, M.Sc. in Computer Sciences, Novosibirsk State University. Thesis: “Development of the environment for the molecular-genetic system dynamic modeling”.
- 2004-2006 Supervision of the team (7 people) which was working on the systems biological computer platform for investigation of *E. coli* core metabolism and its regulation. Project with Ajinomoto Co., Inc.
- 2004-2005 Natalia Apasyeva, M.Sc. in Genetics, Novosibirsk State University. Thesis: “Molecular-genetic mechanisms of regulation of *E. coli* respiration: gene network reconstruction and mathematical modeling”
- 2001-2002 Fedor Kazantsev, undergraduate, High College of Informatics affiliated with Novosibirsk State University, Russia. Annual project.
- 2001-2002 Egor Gladkikh, undergraduate, High College of Informatics affiliated with Novosibirsk State University, Russia. Annual project.
- 2001-2002 Andrei Beregov, undergraduate, High College of Informatics affiliated with Novosibirsk State University, Russia. Annual project.

EDITORIAL RESPONSIBILITIES

- 2013-present Member of the Editorial Board of the [IET Systems Biology](#) Journal

2011-present Review Editor of [Frontiers in Bioinformatics and Computational Biology](#)
2011-present Ad-Hoc reviewer for [Bioinformatics](#)
2011-present Ad-Hoc reviewer for the [EURASIP Journal on Bioinformatics and Systems Biology](#)

PROFESSIONAL ORGANIZATIONS

2011-2013 Full Member of Sigma Xi, the Scientific Research Society

OTHER PROFESSIONAL ACTIVITIES

Conference Program Committees

2014 Program committees and Co-chair of “Systems computational biology” section, [BGRS/SB’2014](#)
2012 Program committees and Co-chair of “Mathematical biology and system modeling” section, [BGRS/SB’2012](#)

RESEARCH SUPPORT

2006-2017 2P50 GM076547 NIH Quantitative Systems Biology (PI: JD Aitchison).
2011-2016 P01 AI094419 NIH Optimizing HIV immunogen-BCR interactions for vaccine development (PI: L Stamatatos).
2010-2015 U54 GM103511 NIH New Tools for Exploring the Dynamic Interactome (PI: MP Rout).
2008-2012 NIH R01 5R01GM075152-02 “Oleate-responsive gene regulatory networks governing peroxisome proliferation” (PI: JD Aitchison).

PUBLICATIONS

Peer-Reviewed Articles

1. Mast FD, **Ratushny AV**, Aitchison JD. Systems cell biology. [J Cell Biol](#), 2014, 206(6):695-706.
2. Holden JM, Koreny L, Obado S, **Ratushny AV**, Chen WM, Chiang JH, Kelly S, Chait BT, Aitchison JD, Rout MP, Field MC. Nuclear pore complex evolution: A trypanosome Mlp analog functions in chromosomal segregation but lacks transcriptional barrier activity. [Mol Biol Cell](#). 2014 Mar 5. [Epub ahead of print]
3. Wurtmann EJ, **Ratushny AV**, Pan M, Beer KD, Aitchison JD, Baliga NS. An evolutionarily conserved RNase-based mechanism for repression of transcriptional positive autoregulation. [Mol Microbiology](#). 2014 Feb 24. doi: 10.1111/mmi.12564. [Epub ahead of print]
4. Danziger SA, **Ratushny AV**, Smith JJ, Saleem RA, Wan Y, Arens CE, Armstrong AM, Sitko K, Chen WM, Chiang JH, Reiss DJ, Baliga NS, Aitchison JD. Molecular mechanisms of system responses to novel stimuli are predictable from public data. [Nucleic Acids Res](#). 2014 Feb;42(3):1442-60.
5. Schoggins JW, MacDuff DA, Imanaka N, Gainey MD, Shrestha B, Eitson JL, Mar KB, Richardson RB, **Ratushny AV**, Litvak V, Dabelic R, Manicassamy B, Aitchison JD, Aderem A, Elliott RM, Garcia-Sastre A, Racaniello V, Snijder EJ, Yokoyama WM, Diamond MS, Virgin HW, Rice CM. Pan-viral specificity of IFN-induced genes reveals new roles for cGAS in innate immunity. [Nature](#). 2014 Jan 30;505(7485):691-5.
6. Pang WL, Kaur A, **Ratushny AV**, Cvetkovic A, Kumar A, Pan M, Arkin AP, Aitchison JD, Adams MWW, and Baliga NS. Metallochaperones regulate intracellular Copper levels. [PLoS Comput Biol](#). 2013;9(1):e1002880. doi:10.1371/journal.pcbi.1002880.
7. Litvak V, **Ratushny AV**, Lampano AE, Schmitz F, Huang AC, Raman A, Rust AG, Bergthaler A, Aitchison JD, Aderem A. A FOXO3-IRF7 gene regulatory circuit limits inflammatory sequelae of antiviral responses. [Nature](#). 2012 Oct 18;490(7420):421-5.
8. **Ratushny A.V.**, Saleem R.A., Sitko K., Ramsey S.A., Aitchison J.D. Asymmetric positive feedback loops reliably control biological responses. [Mol Syst Biol](#). 2012 Apr 24; 8:577.

9. DuBois K.N., Alsford S., Holden J.M., Buisson J., Swiderski M., Bart J., **Ratushny A.V.**, Wan Y., Bastin P., Barry J.D., Navarro M., Horn D., Aitchison J.D., Rout M.P. and Field M.C. NUP-1 is a large coiled-coil nucleoskeletal protein in trypanosomes with lamina-like functions. [PLoS Biol.](#) 2012 Mar;10(3):e1001287.
10. **Ratushny A.V.**, Ramsey S.A., Aitchison JD. Mathematical modeling of biomolecular network dynamics. *Methods Mol Biol.* 2011;781:415-33.
11. **Ratushny A.V.**, Shmulevich I., Aitchison J.D. Trade-off between responsiveness and noise suppression in biomolecular system responses to environmental cues. [PLoS Comput Biol.](#) 2011;7(6): e1002091. doi:10.1371/journal.pcbi.1002091. Featured in PLoS Comp Bio June issue.
12. Saleem RA, Rogers RS, **Ratushny AV**, Dilworth DJ, Shannon PT, Shteynberg D, Moritz RL, Nesvizhskii AI, Rachubinski RA, Aitchison JD. Integrated phosphoproteomic analysis of a signaling network governing nutrient response and peroxisome induction. [Mol Cell Proteomics.](#) 2010 Sep;9(9):2076-88. Epub 2010 Apr 15.
13. Wan Y., Saleem R.A., **Ratushny A.V.**, Roda O., Smith J.J., Lin C.H., Chiang J.H., Aitchison J.D. Role of the histone variant H2A.Z/Htz1p in TBP recruitment, chromatin dynamics, and regulated expression of oleate-responsive genes. [Mol Cell Biol.](#) 2009 May;29(9):2346-58.
14. **Ratushny A.V.**, Ramsey S.A., Roda O., Wan Y., Smith J.J., Aitchison J.D. Control of transcriptional variability by overlapping feed-forward regulatory motifs. [Biophys J.](#) 2008 Oct;95(8):3715-23.
15. Likhoshvai V.A., **Ratushny A.V.** Generalized Hill function method for modeling molecular processes. *J Bioinform Comput Biol.* 2007 Apr;5(2b):521-31.
16. Mishchenko E.L., Bezmaternikh K.D., Likhoshvai V.A., **Ratushny A.V.**, Khlebodarova N.M., Ivanisenko V.A., Kolchanov N.A. Mathematical model for suppression of subgenomic hepatitis C virus RNA replication in cell culture. *J Bioinform Comput Biol.* 2007 Apr;5(2b):593-609.
17. Bezmaternykh K.D., Mishchenko E.L., **Ratushny A.V.**, Likhoshvai V.A., Khlebodarova T.M., Ivanisenko V.A. Mathematical Modeling of the Reproduction of the Hepatitis C Virus Replicon in Cell Culture. Simulation of the Action of Potential Therapeutics. *Biophysics*, 2006, Vol. 51, Suppl. 1, p. 70-74.
18. **Ratushny A.V.** and Likhoshvai V.A. Mathematical Modeling of Intracellular Membrane Transport: Receptor-Mediated Endocytosis and Degradation of Low-Density Lipoproteins. *Biophysics*, 2006, Vol. 51, Suppl. 1, p. 95-99.
19. Ananko EA, Podkolodny NL, Stepanenko IL, Podkolodnaya OA, Rasskazov DA, Miginsky DS, Likhoshvai VA, **Ratushny AV**, Podkolodnaya NN, Kolchanov NA. GeneNet in 2005. *Nucleic Acids Res.* 2005 Jan 1;33 Database Issue:D425-7.
20. **A.V. Ratushny**, V.A. Likhoshvai, E.A. Anan'ko, N.V. Vladimirov, K.V. Gunbin, S.A. Lashin, E.A. Nedosekina, S.V. Nikolaev, L.V. Omel'yanchuk, Yu.G. Matushkin, N.A. Kolchanov. Novosibirsk school of computational systems biology: history and future trends. *Informatsionnyi vestnik VOGiS*, 2005, 9(2), pp. 232-261.
21. Kolchanov NA, Podkolodnaia OA, Anan'ko EA, Afonnikov DA, Vishnevskii OV, Vorob'ev DG, Ignat'eva EV, Levitskii VG, Likhoshvai VA, Omel'ianchuk NA, Podkolodny NL, **Ratushny AV**, Suslov VV. Integrated computer system for regulating eukaryotic gene expression. *Mol Biol (Mosk).* 2004 Jan-Feb;38(1):69-81.
22. Kolchanov N.A., Latypov A.F., Lihoshvaj V.A., Matushkin Yu.G., Nikulichev Yu.V., **Ratushnyi A.V.** (2004) Optimal Control Problems in Gene Network Dynamics and the Methods for Solving Them. *Journal of Computer and System Sciences International*, Vol. 43, No. 6, pp. 862-72.
23. Golubyatnikov V., Likhoshvai V., **Ratushny A.** Existence of Closed Trajectories in 3-D Gene Networks: The journal of three dimensional images 3D forum. Vol. 18, N. 4, 2004.12, p. 96-101.
24. **Ratushny AV**, Likhoshvai VA, Ignatieva EV, Goryanin II, Kolchanov NA. Resilience of Cholesterol Concentration to a Wide Range of Mutations in the Cell. *Complexus*, 2003;1:142-148.
25. **Ratushnyi AV**, Likhoshvai VA, Ignat'eva EV, Matushkin YG, Goryanin II, Kolchanov NA. A computer model of the gene network of the cholesterol biosynthesis regulation in the cell: analysis of the effect of mutations. *Dokl Biochem Biophys.* 2003 Mar-Apr;389:90-3.

26. N.G. Zagoruiko, N.A. Kolchanov, A.G. Pichueva, O.A. Kutnenko, I.A. Borisova, A.V. Kochetov, V.A. Ivanisenko, S.V. Nikolaev, V.A. Likhoshvai, and **A.V. Ratushnyi**. Data Mining Techniques in Bioinformatics. Pattern Recognition and Image Analysis, Vol. 13, No. 4, 2003, pp. 550–555.
27. Kolchanov N.A. Nedosekina E.A., Ananko E.A., Likhoshvai V.A., Podkolodny N.L., **Ratushny A.V.**, Stepanenko I.L., Podkolodnaya O.A., Ignatieva E.V., Matushkin Yu.G. GeneNet Database: Description and modeling of Gene Networks. In Silico Biol. 2002;2(2):97-110.
28. Likhoshvai V.A., Matushkin Iu.G., **Ratushnyi A.V.**, Anan'ko E.A., Ignat'eva E.V., Podkolodnaia O.A. A generalized chemical-kinetic method for modeling gene networks. Mol. Biol. (Mosk), 2001, Nov-Dec;35(6): 1072-9.

Book Chapters

1. **A. V. Ratushny**, S. A. Ramsey, J. D. Aitchison. Mathematical modeling of biomolecular network dynamics. Gerard Cagney and Andrew Emili (eds.), [Network Biology: Methods and Applications](#), Methods in Molecular Biology, Springer Science+Business Media, LLC, 2011, vol. 781, p. 415-433.
2. Likhoshvai V.A., **Ratushny A.V.**, Bazhan S.I., Fadeev S.I., Kolchanov N.A. Modeling methods of dynamics of molecular genetic systems. "Computational systems biology", in eds. N.A. Kolchanov, S.S. Goncharov, V.A. Likhoshvai and V.A. Ivanisenko. SB RAS Press, Novosibirsk, 2008, p. 333-393.
3. **Ratushny A.V.**, Ignatieva E.V., Likhoshvai V.A. Computer Dynamic Modeling of the Gene Network Controlling Intracellular Cholesterol Homeostasis In: [Bioinformatics of genome regulation and structure](#). Ed. by N. Kolchanov and R. Hofestaedt, Kluwer Academic Publishers, Boston/Dordrecht/ London, 2004, pp. 293-300.
4. Nikolay A. Kolchanov, Elena A. Ananko, Vitali A. Likhoshvani, Olga A. Podkolodnaya, Elena V. Ignatieva, **Alexander V. Ratushny**, and Yuri G. Matushkin. Gene Networks Description and Modeling in the GeneNet System, in eds. Julio Collado-Vides and Ralf Hofestadt, "[Gene Regulation and Metabolism](#)", The MIT Press, Cambridge, Massachusetts, 2002.
5. **Ratushny A.V.**, Lihoshvai V.A., Ignatieva E.V., Matushkin U.G., Kolchanov N.A. Computer Modeling of Gene Network: the Action of Mutations. In: Molecular Genetics, Biophysics, and Medicine Today (Bresler Memorial Lectures)/ ed. V.A. Lanzov, PNPI Press, ST.Petersburg / Gatchina, 2002, pp.169-184.

Peer-Reviewed Conference Publications

1. Likhoshvai V.A., **Ratushny A.V.** *In silico* cell I. Hierarchical approach and generalized Hill functions in modeling enzymatic reactions and gene expression regulation. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, Vol. 2, pp. 13-18.
2. **Ratushny A.V.**, Usuda Y., Matsui K., Podkolodnaya O.A. Mathematical modeling of elementary processes of the gene network controlling histidine biosynthesis in *Escherichia coli*. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 25-29.
3. **Ratushny A.V.**, Nedosekina E.A. Regulation of pyrimidine biosynthesis in *Escherichia coli*: gene network reconstruction and mathematical modeling. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 35-39.
4. **Ratushny A.V.**, Smirnova O.G., Usuda Y., Matsui K. Regulation of the pentose phosphate pathway in *Escherichia coli*: gene network reconstruction and mathematical modeling of metabolic reactions. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 40-44.
5. Ananko E.A., **Ratushny A.V.**, Usuda Y., Matsui K. Aromatic amino acid biosynthesis in *Escherichia coli*: generalized Hill function model of the tryptophan-sensitive 3-deoxy-d-arabinoheptulosonate-7-phosphate synthase reaction demonstrate complicated mechanism. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 45-48.

6. **Ratushny A.V.**, Khlebodarova T.M. Mathematical modeling of regulation of *cyoABCDE* operon expression in *Escherichia coli*. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 49-54.
7. Smirnova O.G., **Ratushny A.V.** Gene network reconstruction and mathematical modeling of salvage pathways: regulation of adenine phosphoribosyltransferase activity by structurally similar substrates. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 73-77.
8. **Ratushny A.V.** Mathematical modeling of receptor mediated endocytosis of low-density lipoproteins and their degradation in lysosomes. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 151-155.
9. **Ratushny A.V.**, Bezmaternikh K.D. Conserved properties of enzymatic systems: prenyltransferase kinetics. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 156-159.
10. **Ratushny A.V.** Mathematical modeling of the gene network controlling homeostasis of intracellular cholesterol. Proc. of the 5th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2006, Vol. 2, pp. 160-164.
11. Fadeev S.I., Gainova I.A., Berezin A.Yu., **Ratushny A.V.**, Matushkin Yu.G., Likhoshvai V.A. Determination of Stationary Solutions in Gene Network Models by Homotopy Method. Proc. of the 4th Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2004, Vol. 2, pp. 29-34.
12. Golubyatnikov V.P., Likhoshvai V.A., **Ratushny A.V.** Oscillatory gene networks modeling and Hopf bifurcation. Proceedings of the 7-th International Conference Human and Computer (HC-2004), University of Aizu, Japan, September 1-3, 2004, pp.72-77.
13. Golubyatnikov V.P., Likhoshvai V.A., Fadeev S.I., Matushkin Yu.G., **Ratushny A.V.**, Kolchanov N.A. Mathematical and Computer modeling of genetic networks. Proceedings of the 6-th International Conference Human and Computer (HC-2003), University of Aizu, Japan, August 28-30, 2003, pp.200-205
14. Latypov A.F., Nikulichev Yu.V., Likhoshvai V.A., **Ratushny A.V.**, Matushkin Yu.G., Kolchanov N.A. Problems of Control of Gene Networks in a Space of Stable States. Proc. IFAC Workshop "Modelling and Analysis of Logic Controlled Dynamic Systems ", Irkutsk, Russia, 2003, pp.251-266
15. **Ratushny A.V.**, Likhoshvai V.A. Computer analysis of the effects of mutations in LDL receptor gene on the regulation of cholesterol biosynthesis in the cell. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 150-153.
16. **Ratushny A.V.**, Likhoshvai V.A., Kolchanov N.A. Analysis of mutational portraits of gene networks. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 157-159.
17. **Ratushny A.V.**, Likhoshvai V.A., Matushkin Yu.G., Kolchanov N.A. Evolution of diploid gene network of cholesterol biosynthesis regulation in the cell. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 160-162.
18. Borisova I.A., Zagoruiko N.G., Kolchanov N.A., Likhoshvai V.A., **Ratushny A.V.**, Likhoshvai V.A., Matushkin Yu.G., Kolchanov N.A. Diagnostic of mutations based on analysis of gene networks. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 163-165.
19. Latypov A.F., Nikulichev Yu.V., Likhoshvai V.A., **Ratushny A.V.**, Matushkin Yu.G., Kolchanov N.A. Problems of control of gene networks in space of stable states. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 195-198.
20. Latypov A.F., Nikulichev Yu.V., Likhoshvai V.A., **Ratushny A.V.**, Matushkin Yu.G., Kolchanov N.A. A method of solving problems of optimal control in dynamics of gene networks. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 199-202.

21. Kolchanov N.A., Podkolodny N.L., Likhoshvai V.A., Loktev K.A., Ananko E.A., Ignatieva E.V., Podkolodnaya O.A., Stepanenko I.L., Nedosekina E.A., Matushkin Yu.G., **Ratushny A.V.**, Tkachev Yu.A., Borisova I.A., Zagoruiko N.G., Dobrynin A.A., Makarov L.I., Fadeev S.I., Gainova I.A., Latypov A. F., Nikulichev Yu.V. Computer systemic biology: informational and software tools for complex molecular biological systems. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 140-142.
22. Likhoshvai V.A., Latypov A.F., Nedosekina E.A., **Ratushny A.V.**, Podkolodny N.L. Technology of using experimental data for verification of models of gene network operation dynamics. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 146-149.
23. Fadeev S.I., Berezin A.Yu., Gainova I.A., Kogai V.V., **Ratushny A.V.**, Likhoshvai V.A. Development of the program software for mathematic modeling of the gene network dynamics. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 2, pp. 173-175.
24. Zagoruiko N.G., Pichueva A.G., Kutnenko O.A., Borisova I.A., Kochetov A.V., Ivanenko V.A., Nikolaev S.V., Likhoshvai V.A., **Ratushny A.V.**, Kolchanov N.A. Application of the methods of intellectual data analysis to solving the problems of bioinformatics. Proc. of the 3rd Intern. Conference on Bioinformatics of Genome Regulation and Structure, Novosibirsk, Russia, 2002, Vol. 3, pp. 204-207.
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