Nikolay A. Kolchanov, Dr.Sci., Prof.

Curriculum Vitae and List of Publications

- **Date of Birth:** January 9, 1947
- **Work Address:** Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Prospect Lavrenyieva 10, Novosibirsk, 630090, Russia
- **Telephone:** +7(3833) 333468
- **FAX:** +7(3833) 331278
- **E-mail:** kol@bionet.nsc.ru

Work Experience and Current Position:

1974-1983 Research associate scientist, Theoretical Department, Institute of Cytology and Genetics, Novosibirsk, Russia 1992 - Present Deputy Director, Institute of Cytology and Genetics,Novosibirsk, Russia 1983-1989. Senior research scientist, Theoretical Department, Institute of Cytology and Genetics, Novosibirsk, Russia 1989 - Present. Head of the Laboratory of Theoretical Molecular Genetics, Institute of Cytology and Genetics,Novosibirsk, Russia

Area of expertise:

- Human Genome Project: functional sites analysis; functional sites databases; development of the computer system for analysis of nucleotide sequences of human genome.
- Theoretical investigation of sequences, experience in design, development and application of computer resources for:
  o RNA molecule secondary structure prediction.
  o Molecular evolution.
  o Molecular mechanisms of mutations and recombinations appearance.
  o Computer analysis of mobile genetic elements.
  o Protein structure computer analysis: protein molecules databases

Education Background:

Full secondary school, 1955 - 1965.
Novosibirsk State University, Faculty of Natural Sciences 1965-1972.
Novosibirsk State University, Faculty of Natural Sciences, Post-graduate course in the 1972 - 1974.

Degrees

1971: B.S. Mathematical Biology, Novosibirsk State University, Novosibirsk, Russia

1974: B.S.(Honors) Mathematical Biology, Novosibirsk State University, Novosibirsk, Russia

1975: Ph. D., Institute of Cytology and Genetics, Novosibirsk, Russia

1989: Dr.Sci., Institute of Cytology and Genetics, Novosibirsk, Russia

1992: Professor, Institute of Cytology and Genetics, Novosibirsk, Russia

2003: Corresponding member, Russian Academy of Sciences

Thesis

Degree: PhD. Genetics, 1975 Title: "Investigation of renin-angeotensin system based on mathematical and experimental models". Institution: Novosibirsk Institute of Cytology and Genetics Thesis advisor: Vadim A.Ratner, Prof., Dr.Sci. Degree: Dr.Sci. in Genetics, 1988 Title: "Theoretical investigation of structural-functional organization and evolution of genetic macromolecules". Institution: Novosibirsk Institute of Cytology and Genetics.

Scientific supervisor of studies resulted in creating WWW resourses

GeneExpress 2.1 http://wwwmgs.bionet.nsc.ru/mgs/gnw/
TRRD - database of transcription regulatory regions on eukaryotic genomes (TRRD);

http://wwwmgs.bionet.nsc.ru/mgs/gnw/trrd/
The GeneNet system is designed for formalized description and automated visualization of gene networks http://wwwmgs.bionet.nsc.ru/mgs/gnw/genenet/ EnPDB database is made by reformatting PDB in a way allowing for extended search possibilities on PDB. http://wwwmgs.bionet.nsc.ru/mgs/gnw/enpdb/
GeneExpressSystem DNA level
http://wwwmgs.bionet.nsc.ru/mgs/gnw/dna.shtml
RNA level
http://wwwmgs.bionet.nsc.ru/mgs/gnw/rna.shtml
Protein level

http://wwwmgs.bionet.nsc.ru/mgs/gnw/pdbsite/,

http://wwwmgs.bionet.nsc.ru/mgs/systems/fastprot/pdbsitescan.html

Genenet works level

http://wwwmgs.bionet.nsc.ru/mgs/gnw/

Awards and Grants:

International Collaboration

1. National Institutes of Health Grant "High Throughput Annotation of Genomic DNA Sequence" No.2 R01HG-01539-04A2 (2000-2004)
2. NATO SCIENCE PROGRAMME, COLLABORATIVE LINKAGE GRANT PDD(CP)-(LST.CLG 979815) "Development of an Integrative Approach for Transcription Regularity Rule Extraction" (2003-2005)
3. US National Science Foundation FIBR PR 03-106 "Developing modeling and bioinformatics" (2003-2007)
4. NATO SCIENCE PROGRAMME, COLLABORATIVE LINKAGE GRANT PDD № LST.CLG.979816
5. "Gene Networks of Co-Expressed Genes: Modeling and 5'-UTR Sequence Analysis" (2003-2005)
6. The Department of Energy Subgrant "Information Management Infrastructure for Systemic Annotation of Vertebrate Genomes" No. 535228 CFDA 81.049 (1999-2002)
7. INTAS Project No. 21-2382 "Involvement of Epstein-Barr virus encoded proteins in signal transduction in virally transformed and in EBV-carrying malignant B cells" (2002-2004).
8. INTAS Monitoring Conference Grant, Conference Reference No. INTAS 01-MO-210 The Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS 2002, Akademgorodok, Novosibirsk, Russia, 14-20, 2002.
9. CONTRACT GRANT AGREEMENT ICA2-CT-2000-6003. PROJECT TITLE: "TWO-PHASES CONFERENCE ON BIODIVERSITY AND DYNAMICS OF ECOSYSTEMS IN NORTH EURASIA" To be held in Akademgorodok, Novosibirsk; the preliminary phase on August 21-26, 2000 and the final phase on July 9-14, 2001.
10. INTAS-International Association for the promotion of co-operation with scientists from the New Independent States of the former Soviet Union grant: Development of early markers for detection of environmental stress in aquatic organisms. INTAS-96-1787. 1997-2000
11. CRDF PROJECT NUMBER RB0-1276 Developing Cancer Immunome Database (2001-2002)

Ministry of Industry, Science and Technology of Russian Federation

1. Development of software for analysis of the structure–function properties of human genome (2002-2004)
2. State contract with the Federal Agency of Science and Innovations "Identification of Promising Targets for the Action of New Drugs Basing on Reconstruction of Gene Networks" under the priority direction "Living Systems" (2004-2005)
3. **Contract** with the Institute of Molecular Genetics RAS "Development of Mathematical Model of Cell Cycle Regulation in the Yeast Cell" within the problem "Development of Mathematical Model of the Eukaryotic Cell" under the federal target research program "Development of New Directions in Biotechnology and Provision of Biosafety" (2004-2005)
4. **State contract** "Dynamics of Gene Pools of Plants, animals, and humans" (2004-2005)
5. Contract **No. 38/2004** with the Engelhardt Institute of Molecular Biology RAS (Moscow) under the state contract No. 43.073.1.1.2508 of January 31, 2002 under the project "Detection of Specific Features of the Human Genome" under the federal target research program "Studies and Developments in Priority Directions of Science and Technologies", block 1 "Oriented Basic Research", section "Technologies of Living Systems", subsection "Biology" (2002-2004)
6. Contract **No. 37/2004** with the Institute of Zoology RAS "Informational System on Biodiversity" under the **state contract No. 43.073.1.1.2510** of January 21, 2002 under the federal target research program "Studies and Developments in Priority Directions of Science and Technologies" for 2002–2006, block 2 "Basic and applied research and development" for 2002–2006, section "Technologies of Living Systems", subsection "Biology" (2002-2004)

Russian Foundation for Basic Research and others:

1. Integrated Digital Library for 3D structures and function of DNA, RNA, Proteins and Gene nets, 01-0790376 (1999-2002).
2. RFBR 05-07-98011-r_ob'_v Development of the software and informational tools for modeling ecosystems basing on GIS technologies and data of remote sensing (2005-2007)
3. RFBR 05-07-98012-r_ob'_v Development of computer portal on bioinformatics basing on GRID technologies (2005-2007)
4. RFBR 03-07-96837 Development of the geoinformational system "The Space–Time Dynamics of Biodiversity of Western Siberia and Northern Ural" (2003-2005)
5. RFBR 03-07-96833 Supercomputer calculations in molecular biology and genetics (2003-2005)
6. RFBR 03-04-48829 Computer study of the efficiency of expression of genes depending on their nucleotide composition

(2003-2005)

7. RFBR 02-07-90355 Development of the software package Gene Discovery for creating knowledge bases at al levels of analysis and modeling of genomic DNA (2002-2004)
8. RFBR 02-04-48802-a Development of theoretical and experimental approaches to design of genetic engineering systems for control of dynamic behavior of gene networks (2002-2004)
9. Interdisciplinary integration project of basic research of SB RAS "Self-organization, Catalysis, and Processes of Chemical Evolution in Gravitationally and thermodynamically Unstable Systems Modeling Early Stages of the Earth's Formation" No. 148 (2003-2005)
10. The project "Description and Analysis of Biodiversity of Dynamics of Siberian Ecosystems Using Informational Technologies" with the RAS Program on biodiversity (12.4) (2003-2005)
11. The project "Computer Modeling and Experimental Construction of Gene Networks" of the Program of the RAS Presidium on molecular–physicochemical biology (10.4) (2003-2005)
12. Grant under the RAS Presidium subprogram 2 of program 25 for basic research "Origin and Evolution of the Biosphere" (2004-2005)
13. Computer analysis of regulatory sequences controlling expressions of eukaryotic genes, 00-04-49229 (19992002)
14. Software-informational support of studying complicated molecular-genetical systems (GeneNet system), 0207-90359 (2002-2004).
15. Research of structural-functional organization and evolution of gene networks: computer analysis and modeling, 03-04-48506 (2003-2005).
16. System of computer-assisted support of experimental and theoretical research of transcription regulation mechanisms 03-07-90181-в (2003-2005).
17. Investigation of transcription factor binding sites by experimental and theoretical approaches, 03-04-48469a (2003-2005).
18. The integrated database of arrangement and characteristic of nucleosome formation sites of genome DNA sequences, 03-04-48555-a (2003-2005).
19. Interdisciplinary Integration Project on basic research No. 65 SB RAS "The simulation of basic genetic processes and systems" (2000-2002)
20. Interdisciplinary Integration Project on basic research No. 66 SB RAS "Basic Problem in Biodiversity and Dynamics of Ecosystem" (2000-2002).
21. Interdisciplinary Integration Project on basic research No. 119 SB RAS "Gene networks: theoretical analysis, computer simulation, and experimental construction" (2003-2005)

22. Interdisciplinary Integration Project on basic research No. 145 SB RAS "Biodiversity and ecosystem dynamics: informational technologies and simulation" (2003-2005)
23. Russian State Committee of High Schools Development of theory of structural-functional organization of biopolymers,O-57-96, (1996-2000)

Ph.D. supervised:

Supervised about 20 PhD since 1985, including:

1. **Orlov Yu.L.** Analysis of regulatory genomic sequences by computer methods of genetic text complexity estimations, Novosibirsk, 2004.
2. **Vishnevsky O.V.** Computer analysis of the context organization of regulatory and coding regions on the basis of oligonucleotide motifs, Novosibirsk, 2004.
3. **Afonnikov D.A.** Computer analysis of the coordinated amino acid substitutions in the families of homologous protein sequences, , Novosibirsk, 2003.
4. **Ponomarenko Yu.V.** Computer analysis of conformational and physicochemical properties of eukariotic transcription factor binding sites, Novosibirsk, 2002.
5. **Kondrakhin Y.V.** <Computer analyzing and recognizing the transcription regulatory regions in eukaryotic genomes>, Institute Cytology and Genetics, Novosibirsk, 1996.
6. **Ponomarenko M.P.** <Investigating the genetic texts by using the computer technology SITEVIDEO>, Institute Cytology and Genetics, Novosibirsk, 1994.
7. **Streletz V.V.** <Databanks and algorithms for aligning and classifying the nucleotide and aminoacid sequences>, Institute Cytology and Genetics, Novosibirsk, 1992.
8. **Kel' A.E.** <Theoretical analyses of the structure, function and evolution of the short genomic repeats>, Institute Cytology and Genetics, Novosibirsk, 1991.

9. **Salamov A.A.** "Computer system for investigation of globular protein secondary structure", Institute Cytology and Genetics, Novosibirsk, 1991.
10. **Rogozin I.B.** " Theoretical analysis of the mechanisms of spontaneous and induced mutations" Institute Cytology and Genetics, Novosibirsk, 1990.

Memberships

- Member of the Scientific Council of Russian Foundation for Basic Research
- HUGO member
- Member of the Scientific Council of the Russian National Human Genome Project.
- Member of the Scientific Council on Molecular Biology of the Russian Academy of Sciences.
- Member of editorial board Russian journal <Molecular Biology>
- Member of editorial board of www journal <In Silico Biology>

Bibliography:

Author of more than 400 scientific publications, including 6 monographs, **3** educational books for university students and the following main publications:

Monographs:

Bioinformatics of Genome Regulation and Structure II. (Eds. N.Kolchanov ,R. Hofestaedt , L.Milanesi), Springer Science+Business Media, Inc., New York, 2006,556 pp.
Bioinformatics of genome regulation and structure. (Eds. N.Kolchanov and R. Hofestaedt), Kluwer Academic Publishers, Boston/Dordrecht/London, 2004,373 pp.
Ratner V.A., Zharkikh A.A., Kolchanov N.A., Rodin S.N., Solovyov V.V., Antonov A.S. Molecular Evolution (Biomathematics: v. 24), Springer-Verlag, Berlin Heidelberg New York ,1996, 433 pp.
Computer Analysis of Genetic Macromolecules: Structure, Function and Evolution, (Eds. N.A. Kolchanov, H.A. Lim), World Scientific Pub. co., Singapore, New Jersey, London, Hong Kong, 1994, 556 pp. Author (co-editor with H.A. Lim)
Modelling and computer methods in molecular biology and genetics. (Novosibirsk, August 28 September,1990). (Eds V.A. Ratner and N.A. Kolchanov), Nova science Publishers, Inc., 1992,508 pp.
Ratner V.A.,Zharkikh A.A,Kolchanov N.A.,Rodin S.N.,Solovyev V.V. Shamin V.V. Problems of the theory of molecular evolution. (Ed.R.I. Salganik) "Science",Siberian Branch of the USSR Academy of Science, Novosibirsk, (Russ) 1985,259 pp.

Educational books for university students:

Educational books for university students: Solovyev V.V., Kell A.E., Rogozin I.B., Kolchanov N.A. The application of computers in Molecular Biology. The theory of genetic texts. Novosibirsk State University (Russ), 1987, 90pp. Kolchanov N.A.,Solovyev V.V.,Shindyalov I.N.,Strelets V.B. The application of computers in Molecular Biology. The structural organization of globular proteins. Novosibirsk State University (Russ),1986, 90 pp. Kell A.E., Kolchanov N.A.,Solovyev V.V.The mathematical modeling in the molecular biology and genetics. The theory of the mutational process: deletions and duplications. Novosibirsk State University ,1989,86 pp.

Selected Articles:

Omelyanchuk N., Mironova V., Poplavsky A., Podkoldny N., Kolchanov N., Mjolsness E., Meyerowitz E. AGNS, a database on expression of *Arabidopsis* genes. In: *Bioinformatics of Genome Regulation and Structure II*. (Eds. Kolchanov N., Hofestaedt R., Milanesi L.) Springer Science+Business Media, Inc., New York, 2006, 433-442.

Ananko E., Oshchepkov D., Nedosekina E., Levitsky V., Lokhova I., Smirnova O., Likhoshvai V., Kolchanov N. Study of the interactions between viral and human genomes during transformation of B cells with Epstein-Barr virus. In: *Bioinformatics of Genome Regulation and Structure II*. (Eds. Kolchanov N., Hofestaedt R., Milanesi L.) Springer Science+Business Media, Inc., New York, 2006, 443-450.

Kolchanov N., Ignatieva E., Podkolodnaya O., Ananko E., Stepanenko I., Merkulova T., Khlebodarova T., Merkulov V., Podkolodny N., Grigorovich D., Poplavsky A., Romashchenko A. Transcription Regulatory Regions Database (TRRD): a source of experimentally confirmed data on transcription regulatory regions of eukaryotic genes. In: *Bioinformatics of Genome Regulation and Structure II*. (Eds. Kolchanov N., Hofestaedt R., Milanesi L.) Springer Science+Business Media, Inc., New York, 2006, 43-53.

Levitsky V., Ignatieva E., Vasiliev G., Limova N., Busygina T., Merkulova T., Kolchanov N. The SiteGA tool for recognition and context analysis of transcription factor binding sites: significant dinucleotide features besides the canonical consensus exemplified by SF-1 binding site. In: *Bioinformatics of Genome Regulation and Structure II*. (Eds. Kolchanov N., Hofestaedt R., Milanesi L.) Springer Science+Business Media, Inc., New York, 2006, 31-41.

Orlov Yu.L., Levitsky V.G., Smirnova O.G., Podkolodnaya O.A., Khlebodarova T.M., Kolchanov N.A. VMM: a variable memory Markov model prediction of nucleosome formation sites. In: *Bioinformatics of Genome Regulation and Structure II*. (Eds. Kolchanov N., Hofestaedt R., Milanesi L.) Springer Science+Business Media, Inc., New York, 2006, 85-95.

Levitsky V.G., Katokhin A.V., Podkolodnaya O.A., Furman D.P., Kolchanov N.A. NPRD: Nucleosome Positioning Region Database. *Nucleic Acids Res,* 2005, 33(Database issue):D67-70.

Ananko E.A., Podkolodny N.L., Stepanenko I.L., Podkolodnaya O.A., Rasskazov D.A., Miginsky D.S., Likhoshvai V.A., Ratushny A.V., Podkolodnaya N.N., Kolchanov N.A. GeneNet in 2005. *Nucleic Acids Res,* 2005, 33(Database issue):D425-7.

Vishnevsky O.V., Kolchanov N.A. ARGO: a web system for the detection of degenerate motifs and large-scale recognition of eukaryotic promoters. *Nucleic Acids Res,* 2005, 33(Web Server issue): W417-22.
Ivanisenko V.A., Eroshkin A.M., Kolchanov N.A. WebProAnalyst: an interactive tool for analysis of quantitative structure-activity relationships in protein families. *Nucleic Acids Res,* 2005, 33(Web Server issue):W99-104.

Ivanisenko V.A., Pintus S.S., Grigorovich D.A., Kolchanov N.A. PDBSite: a database of the 3D structure of protein functional sites. *Nucleic Acids Res,* 2005, 33(Database issue):D183-7.

Kochetov A.V., Sarai A., Rogozin I.B., Shumny V.K., Kolchanov N.A. The role of alternative translation start sites in the generation of human protein diversity. *Mol Genet Genomics,* 2005, 273 (6):491-6.

Oshchepkov D.Yu., Bugreev D.V., Kolchanov N.A., Nevinsky G.A. Computer analysis of the

conformational and physico-chemical properties of DNA Topoisomerase I cleavage sites. *Mol. Biol (Mosk)*, 2005, 39(3):488-496.

Orlov Yu.L., Levitsky V.G., Podkolodnaya O.A., Khlebodarova T.M., Kolchanov N.A. Prediction of nucleosome formation sites in gene regulatory regions. *Proceedings of the International Moscow Conference on Computational Molecular Biology (MCCMB'05)*, Moscow State University, 2005, 270-271.

Kochetov A.V., Kolchanov N.A., Sarai A. The role of alternative translation start sites in generation of human protein diversity. *Proceedings of the International Moscow Conference on Computational Molecular Biology (MCCMB'05)*, Moscow State University, 2005, 177-178.

Pintus S., Ivanisenko V.A., Kolchanov N.A. Computer analysis of structure and evolution of functional sites of the DNA-binding domain of human P53 protein. *Proceedings of the International Moscow Conference on Computational Molecular Biology (MCCMB'05)*, Moscow State University, 2005, 297-298.

Nedosekina E.A., Ananko E.A., Likhoshvai V.A., Oshchepkov D.Yu., Kolchanov N.A. Modelling of signal transduction and gene expression regulation in immune system cells. In: *Proceedings of the Conference on Modeling and Simulation in Biology, Medicine and Biomedical Engineering*. Linkoping, Sweden, 2005, May 26-27, 125-128.

Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Stepanenko I.L., Khlebodarova T.M., Merkulova T.I., Pozdnyakov M.A., Proscura A.L., Grigorovich D.A., Podkolodny N.L., Naumochkin A.N., Romashchenko A.G., Kolchanov N.A. Transcription Regulatory Regions Database (TRRD): description of transcription regulation and the main capabilities of the database. In: *Bioinformatics of Genome Regulation and Structure.* (Eds. Kolchanov N., Hofestaedt R.) Kluwer Academic Publishers, Boston/Dordrecht/London, 2004, 81-92.

Oshchepkov D.Yu., Turnaev I.I., Pozdnyakov M.A., Milanesi L., Vityaev E.E., Kolchanov N.A. Sitecon - a tool for analysis of DNA physicochemical and conformational properties: E2F/DP transcription factor binding site analysis and recognition. In: *Bioinformatics of Genome Regulation and Structure.* (Eds. Kolchanov N., Hofestaedt R.) Kluwer Academic Publishers, Boston/Dordrecht/London, 2004, 93-102.

Pichueva A.G., Kochetov A.V., Milanesi L., Kondrakhin Yu.V., Kolchanov N.A. Correlations between sequence features of yeast genes functional regions and the level of expression. In: *Bioinformatics of Genome Regulation and Structure.* (Eds. Kolchanov N., Hofestaedt R.) Kluwer Academic Publishers, Boston/Dordrecht/London, 2004, 125-132.

Kondrakhin Yu.V., Podkolodnaya O.A., Kochetov A.V., Erokhin G.N., Kolchanov N.A. Statistical analysis of microarray data: identification and classification of yeast cell cycle genes. In: *Bioinformatics of Genome Regulation and Structure.* (Eds. Kolchanov N., Hofestaedt R.) Kluwer Academic Publishers, Boston/Dordrecht/London, 2004, 331-342.

Nedosekina E.A., Ananko E.A., Milanesi L., Likhoshvai V.A., Kolchanov N.A. Mathematical simulation of dynamics of macrophage gene network activated by lipopolysaccharides and/or interferon-gamma. In: *Bioinformatics of Genome Regulation and Structure.* (Eds. Kolchanov N., Hofestaedt R.) Kluwer Academic Publishers, Boston/Dordrecht/London, 2004, 283-292.

Ivanisenko V.A., Pintus S.S., Grigorovich D.A., Kolchanov N.A. PDBSiteScan: a program for searching for active, binding and posttranslational modification sites in the 3D structures of proteins. *Nucleic Acids*

Res, 2004, 32(Web Server issue):W549-54.

Afonnikov D.A., Kolchanov N.A. CRASP: a program for analysis of coordinated substitutions in multiple alignments of protein sequences. *Nucleic Acids Res,* 2004, 32(Web Server issue):W64-8.

Kolchanov N.A., Podkolodnaia O.A., Anan'ko E.A., Afonnikov D.A., Vishnevskii O.V., Vorob'ev D.G., Ignat'eva E.V., Levitskii V.G., Likhoshvai V.A., Omel'ianchuk N.A. Integrated computer system for regulating eukaryotic gene expression. *Mol Biol (Mosk),* 2004, 38(1):69-81.

Kolchanov N.A., Latypov A.F., Likhoshvai V.A., Matushkin Yu.G., Nikulichev Yu.V., Ratushny A.V. Problems of optimal control in gene network dynamics and methods for their solving. *Izvestiya RAS. Theory and systems of control (Rus).* 2004, 6:36-45.

Suslov V.V., Gunbin K.V., Kolchanov N.A., Omelyanchuk N.A. Genetic mechanisms of morphological evolution, part 1. Siberian Journal of Ecology *(Rus)* 2004, 11(5):599-610.

Suslov V.V., Gunbin K.V., Kolchanov N.A., Omelyanchuk N.A. Genetic mechanisms of morphological evolution, part 2. Siberian Journal of Ecology *(Rus)* 2004, 11(5):611-621.

Suslov V.V., Gunbin K.V., Kolchanov N.A. Genetic mechanisms of biological complexity encoding. Ecological genetics *(Rus).* 2004, 2(1):13-26.

Likhoshvai V.A., Fadeev S.I., Matushkin Yu.G., Demidenko G.V, Kolchanov N.A. Mathematical modeling of regulatory circuits of gene networks. *J Computational Mathematics and Mathematical Physics (Rus).* 2004, 44(10):1921-1940.

Omelianchuk N.A., Mironova V.V., Poplavsky A.S., Kukeeva Yu.A., Podkolodny N.L., Kolchanov N.A. AGNS: Arabidopsis GeneNet Supplementary Database. *Proceedings of the Fourth International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2004)*, 2004, 2:121-124.

Kochetov A.V., Sarai A., Kolchanov N.A. Translational polymorphism as a potential source of eukaryotic proteins variety. *Proceedings of the Fourth International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2004)*, 2004, 1:107-109.

Ratushny A.V., Likhoshvai V.A., Ignatieva E.V., Kolchanov N.A. Robustness of key components of homeostatic gene networks to a wide range of mutations. *The 12th International Conference on Intelligent Systems for Molecular Biology (ISMB 2004) and 3rd the European Conference on Computational Biology (ECCB 2004), Conference programme*, 2004, p. 219.

Ratushny A.V., Likhoshvai V.A., Ignatieva E.V., Kolchanov N.A. Robustness of homeostatic gene networks target products to a wide range of mutations and perturbations in the cell. *ISMB 2004 and ECCB 2004 Satellite Meeting, Special Interest Group in Simulations and Modelling, Book of abstracts*, 2004, p. 29.

Kolchanov N.A., Pozdnyakov M.A., Orlov Y.L., Vishnevsky O.V., Podkolodny N.L., Vityaev E.E., Kovalerchuk B. Computer system "Gene Discovery" for promoter structure analysis. In:*Artificial Intelligence and Heuristic Methods in Bioinformatics*. (Eds.: Frasconi and R. Shamir) IOS Press, 2003, 173-192.

Stepanenko I., Kolchanov N. Apoptosis gene network: description in the GeneNet and TRRD

databases. *Ann N Y Acad Sci,* 2003, 1010:16-8.

Kochetov A.V., Kolchanov N.A., Sarai A. Interrelations between the efficiency of translation start sites and other sequence features of yeast mRNAs. *Mol Genet Genomics,* 2003, 270(5):442-7.

Ratushny A.V., Likhoshvai V.A., Ignatieva E.V., Kolchanov N.A. Resilience of cholesterol concentration to a wide range of mutations in the cell. *Complexus*, 2003, 1:142-148.

Zagoruiko N.G., Kolchanov N.A., Pichueva A.G., Kutnenko O.A., Borisova I.A., Kochetov A.V., Ivanisenko V.A., Nikolaev S.V., Likhoshvai V.A., Ratushnyi A.V. Data mining techniques in bioinformatics. *Pattern Recognition and Image Analysis,* 2003. 13(4):550-555.

Kolchanov N.A., Hofestaedt R. The 3rd International conference on bioinformatics of genome regulation and structure (BGRS'2002). Preface. *In Silico Biology* 2003, 3(1-2):1-2.

Kolchanov N.A., Likhoshvai V.A., Ananko E.A., Stepanenko I.L.,Podkolodnaya O.A., Ignatieva E.V., Ratushny A.V., Nedosekina E.A., Podkolodny N.L. GeneNet Discovery: gene networks reconstruction,analysis and modeling. *Proceedeings of the First International Moscow Conference on Computational Molecular Biology (MCCMB'03)*, Moscow, Russia, 2003, 109-111.

Pichueva A.G., Kochetov A.V., Kondrakhin Yu.V., Kolchanov N.A Relationship between the contextual features of yeast core promoter and the level of gene expression. *Proceedeings of the First International Moscow Conference on Computational Molecular Biology (MCCMB'03)*, Moscow, Russia, 2003, 187.

Proscura A.L., Levitsky V.G., Oshchepkov D.Yu., Pozdnyakov M.A., Ignatieva E.V., Kolchanov N.A. Expression of lipid metabolism genes: description in TRRD database and computer-assisted analysis. *Proceedeings of the First International Moscow Conference on Computational Molecular Biology (MCCMB'03)*, Moscow, Russia, 2003, 194-195.

Afonnikov,D.A., Nikolaev,S.V., Ivanisenko,V.A., Kolchanov,N.A. Classification of local spatial environment of amino acid residues by physicochemical characteristics in transcription factor DNA-binding domains. *Proceedeings of the First International Moscow Conference on Computational Molecular Biology (MCCMB'03)*, Moscow, Russia, 2003, 17-18.

Ratushny A.V., Likhoshvai V.A., Matushkin Y.G., Kolchanov N.A., Borisova I.A., Zagoruiko N.G. Computer analysis of mutations and evolution of gene networks. *Proceedeings of the First International Moscow Conference on Computational Molecular Biology (MCCMB'03)*, Moscow, Russia, 2003, 198-199.

Ratushnyi A.V., Likhoshvai V.A., Ignat'eva E.V., Matushkin Y.G., Goryanin, II, Kolchanov N.A. 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, 389:90-93.

Kochetov A.V., Pichueva A.G., Kondrakhin Yu.V., Titov S.E., Kolchanov N.A. The contextual features of higher plant mRNA 5'-untranslated regions as related to the translation initiation mechanisms. *Biofizika.* 2003, 48(1):76-80.

Kolchanov N.A., Suslov V.V., Shumnyi V.K. Molecular evolution of genetic systems
Paleontological Journal, 2003, N6:58-71.

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