

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-angiotensin 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 resources

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/pdbsitecan.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 all 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 (1999-2002)
 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-B (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 eukaryotic 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 amino acid 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., Hofstaedt 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., Hofstaedt 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., Hofstaedt 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., Hofstaedt 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., Hofstaedt 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*. Linköping, 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., Hofstaedt 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. *Proceedings 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. *Proceedings 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. *Proceedings 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. *Proceedings 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. *Proceedings 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, I.I., 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.

Kolchanov N.A., Ananko E.A., Likhoshvani V.A., Podkolodnaya O.A., Ignatieva E.V., Ratushny A.V., Matushkin Yu.G. Gene networks description and modeling in the GeneNet system, Chapter 5. In *"Gene Regulation and Metabolism"*. (Eds. Julio Collado-Vides and Ralf Hofstadt) The MIT Press, Cambridge, Massachusetts, 2002, 149-180.

Ananko E.A., Podkolodny N.L., Stepanenko I.L., Ignatieva E.V., Podkolodnaya O.A., Kolchanov N.A. GeneNet: a database on structure and functional organisation of gene networks. *Nucleic Acids Res*, 2002, 30(1):398-401.

Kolchanov N.A., Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Pozdnyakov M.A., Podkolodny N.L., Naumochkin A.N., Romashchenko A.G. Transcription Regulatory Regions Database (TRRD): its status in 2002. *Nucleic Acids Res*, 2002, 30(1):312-7.

Valuev V.P., Afonnikov D.A., Ponomarenko M.P., Milanesi L., Kolchanov N.A. ASPD (Artificially Selected Proteins/Peptides Database): a database of proteins and peptides evolved in vitro. *Nucleic Acids Res*, 2002, 30(1):200-202.

Kutsenko A.S., Gizatullin R.Z., Al-Amin A.N., Wang F., Kvasha S.M., Podowski R.M., Matushkin Y.G., Gyanchandani A., Muravenko O.V., Levitsky V.G., Kolchanov N.A., Protopopov A.I., Kashuba V.I., Kisselev L.L., Wasserman W., Wahlestedt C., Zabarovsky E.R. Not I flanking sequences: a tool for gene discovery and verification of the human genome. *Nucleic Acids Res*, 2002, 30(14):3163-70.

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 Y.G. GeneNet database: description and modeling of gene networks. *In Silico Biol*, 2002, 2(2):97-110.

Orlov Y.L., Filippov V.P., Potapov V.N., Kolchanov N.A. Construction of stochastic context trees for genetic texts. *In Silico Biol*, 2002, 2(3):233-47.

Vityaev E.E., Orlov Y.L., Vishnevsky O.V., Pozdnyakov M.A., Kolchanov N.A. Computer system "Gene Discovery" for promoter structure analysis. *In Silico Biol*, 2002, 2(3):257-62.

Hofstadt R, Kolchanov N, Reinitz J. Information and simulation systems for the analysis of gene regulation and metabolic pathways. *In Silico Biology*, 2002, 2:35-36.

Kochetov A.V., Sarai A., Vorob'ev D.G., Kolchanov N.A. The context organization of functional regions in yeast genes with high-level expression. *Mol Biol (Mosk)*, 2002, 36(6):1026-34.

Ananko E.A., Podkolodny N.L., Ignatieva E.V., Podkolodnaya O.A., Stepanenko I.L., Kolchanov N.A. GeneNet system: its status in, 2002. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:70-73.

Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Pozdnyakov M.A., Podkolodny N.L., Naumochkin A.N., Romashchenko A.G., Kolchanov N.A. Transcription Regulatory Regions Database (TRRD): its status in 2002. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 1:10-13.

Borisova I.A., Zagoruiko N.G., Likhoshvai V.A., Ratushny A.V., Kolchanov N.A. Diagnostics of mutations based on analysis of gene networks. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:163-165.

Ivanisenko V.A., Grigorovich D.A., Kolchanov N.A. PDBSITE: A database on protein active sites and their environmen. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:145-148.

Ivanisenko V.A., Debelov V.A., Pintus S.S., Matsokin A.M., Nikolaev S.V., Grigorovich D.A., Kolchanov N.A. PDBSiteScan: A tool for search for the best-matching superposition in the database PDBSite. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:149-152.

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 toolsfor complex molecular biological systems. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:140-142.

Kolchanov N.A., Podkolodny N.L., Ananko E.A., Ignatieva E.V., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Lavryushev S.V., Grigorovich D.A., Kochetov A.V., Orlova G.V., Titov I.I., Vishnevsky O.V., Orlov Yu.L., Ivanisenko V.A., Vorobiev D.G., Oschepkov D.Yu., Omel'yanchuk N.A., Pozdnyakov M.A., Afonnikov D.A., Matushkin Yu.G., Likhoshvai V.A., Ratushny A.V., Katokhin A.V., Turnaev I.I., Proskura A.L., Suslov V.V., Nedosekina E.A. GeneExpress - 2002: an integrated system on gene expression regulation. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:232-234.

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. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:195-198.

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 dinamics of gene networks. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:199-202.

Likhoshvai V.A., Kochetov A.V., Matushkin Yu.G., Kolchanov N.A. Structural features of mRNA region at the translation start site. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:55-57.

Ratushny A.V., Likhoshvai V.A., Matushkin Yu.G., Kolchanov N.A. Evolution of diploid gene network of cholesterol biosynthesis regulation in a cell. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:160-162.

Ratushny A.V., Likhoshvai V.A., Kolchanov N.A. Analysis of mutational portraits of gene networks. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:157-159.

Stepanenko I.L., Podkolodnaya O.A., Kolchanov N.A. Gene networks: principles of organization and mechanisms of operation and integration. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 2:109-113.

Matushkin Yu.G., Levitsky V.G., Likhoshvai V.A., Vishnevsky O.V., Kutsenko A.S., Protopopov A.I., Zabarovsky E.R., Kolchanov N.A. Analysis of the secondary structure and nucleosomal potential of Not I sites of the human genome. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:235-239.

Kochetov A.V., Kolchanov N.A., Sarai A. Unoptimal translation start site correlates with increased content of in-frame downstream AUG codons at the beginning of CDS of eukaryotic mRNAs. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:52-54.

Titov I.I., Kochetov A.V., Kolchanov N.A., Sarai A. Computer analysis of mRNA untranslated regions of hypoxia-induced corn genes. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:46-48.

Kochetov A.V., Sarai A., Grigorovich D.A., Kolchanov N.A. Database on mRNA-located eucariotic translational signals. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:40-42.

Pozdnyakov M.A., Vityaev E.E., Ananko E.A., Busygina T.V., Ignatieva E.V., Proskura A.L., Podkolodnaya O.A., Podkolodny N.L., Merkulova T.I., Kolchanov N.A. Detection of the core structure of transcription factor binding sites. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:251-254.

Afonnikov D.A., Ivanisenko V.A., Grigorovich D.A., Valuev V.P., Nikolaev S.V., Kolchanov N.A. Resources for the analysis of protein sequences and structures in the GeneExpress system. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:138-140.

Nikolaev S.V., Afonnikov D.A., Ivanisenko V.A., Bazhan S.I., Kolchanov N.A. Comparison of methods for predicting proteasome cleavage motifs. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:108-111.

Nikolaev S.V., Ivanisenko V.A., Afonnikov D.A., Bazhan S.I., Kolchanov N.A. An index for estimating the efficiency of antigenic epitope generation during proteasomal proteolysis. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:112-114.

Vishnevsky O.V., Avdeeva I.V., Kolchanov N.A. Study of the specific contextual features of translation initiation and termination regions in eukaryotes. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:72-76.

Vityaev E.E., Kostin V.S., Podkolodny N.L., Kolchanov N.A. Natural classification of nucleotide sequences. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:197-199.

Vityaev E.E., Pozdnyakov M.A., Orlov Yu.L., Vishnevsky O.V., Podkolodny N.L., Kolchanov N.A. Gene Discovery computer system for analysis of regulatory regions. Proceedings of the *Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3:257-259.

Zagoruiko N.G., Pichueva A.G., Kutnenko O.A., Borisova I.A., Kochetov A.V., Ivanisenko V.A.,

Nikolaev S.V., Likhochvai V.A., Ratushny A.V., Kolchanov N.A. Application of the method of intellectual data analysis to solving the problems of bioinformatics. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3;204-207.

Kolchanov N.A., Valishev A.I., Popova N.A. On specialization "BIOINFORMATICS" in the Novosibirsk State University and High College of informatics of Novosibirsk State University. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 3;220-221.

Brunk B., Crabtree J., Diskin S., Mazzarelli J., Zigouras N., Alkalaeva E., Bogdanova V., Trifonoff V., Vorobjeva N., Katokhin A., Kolchanov N., Stoeckert C. Manual annotation of the human and mouse gene index: www.allgenes.org. *Proceedings of the Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2002)*, 2002, 1:182-184.

Vityaev E.E., Orlov Yu.L., Pozdnyakov M.A., Vishnevsky O.V., Kolchanov N.A., Kovalerchuk B.K. Knowledge discovery for promoter structure analysis. *Proceedings of the International Conference on Imaging Science, Systems, and Technology*, Eds.: Hamid R. Arabnia, Youngsong Mun, Las Vegas, Nevada, USA, June 24-27, 2002, CSREA Press, v.1:122-128.

Vityaev E.E., Orlov Yu.L., Vishnevsky O.V., Kovalerchuk B.Ya., Belenok A.S., Podkolodnii N.L., Kolchanov N.A. Knowledge discovery for gene regulatory regions analysis. In: *Knowledge-Based Intelligent Information Engineering Systems and Allied Technologies*, KES, 2002. (Eds. E.Damiani, R. Howlett, L.Jain, N. Ichalkaranje) IOS Press, Amsterdam, 2002, part 1, 487-491.

Ratushny A.V., Likhoshvai V.A., Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Matushkin Y.G., Kolchanov N.A. Computer dynamic modeling of gene networks and the analysis of the action of mutations. *10th Intern. Conf. on Intelligent Systems for Molecular Biology, Conf. program*, 2002, 107.

Kolchanov N.A. Bioinformatics of genomic regulation and structure. *Mol Biol (Mosk)*. 2001,35(6): 931-3.

Kolchanov N.A., Podkolodnaia O.A., Anan'ko E.A., Ignat'eva E.V., Podkolodnyi N.L., Merkulov V.M., Stepanenko I.L., Pozdnyakov M.A., Belova O.E., Grigorovich D.A., Naumochkin A.N. Regulation of eukaryotic gene transcription: description in the TRRD database. *Mol Biol (Mosk)*, 2001, 35(6):934-42.

Kochetov A.V., Grigorovich D.A., Titov, II, Vorob'ev D.G., Syrnik O.A., Vishnevskii O.V., Sarai A., Kolchanov N.A. mRNA-FAST (mRNA-Function, Activity, SStructure) computer system. *Mol Biol (Mosk)*, 2001, 35(6):1039-47.

Pozdnyakov M.A., Vityaev E.E., Anan'ko E.A., Ignat'eva E.V., Podkolodnaia O.A., Podkolodnyi N.L., Lavriushev S.V., Kolchanov N.A. Comparative analysis of methods for recognizing potential transcription factor binding sites. *Mol Biol (Mosk)*, 2001, 35(6):961-9.

Vityaev E.E., Orlov Iu L., Vishnevskii O.V., Belenok A.S., Kolchanov N.A. Computer system "Gene Discovery" for searching for regularities in organization of eukaryotic regulatory sequences. *Mol Biol (Mosk)*, 2001, 35(6):952-960.

Afonnikov D.A., Kolchanov N.A. The conserved characteristics of DNA-binding domains belonging to the

homeodomain class that are associated with coadaptive substitutions of amino acid residues. *Dokl Biochem Biophys*, 2001, 380:352-355.

Kolchanov N.A., Hodgman C. The 2nd international conference on the Bioinformatics of Genome Regulation and Structure (BGRS-2000), Novosibirsk, August 2000. *Bioinformatics*, 2001, 17:997.

Levitsky V.G., Podkolodnaya O.A., Kolchanov N.A., Podkolodny N.L. Nucleosome formation potential of eukaryotic DNA: calculation and promoters analysis. *Bioinformatics*, 2001, 17(11):998-1010.

Afonnikov D.A., Oshchepkov D.Y., Kolchanov N.A. Detection of conserved physico-chemical characteristics of proteins by analyzing clusters of positions with co-ordinated substitutions. *Bioinformatics*, 2001, 17(11):1035-46.

Levitsky V.G., Podkolodnaya O.A., Kolchanov N.A., Podkolodny N.L. Nucleosome formation potential of exons, introns, and Alu repeats. *Bioinformatics*, 2001, 17(11):1062-4.

Valuev V.P., Afonnikov D.A., Ponomarenko M.P., Kolchanov N.A. ASPD (Artificial Selected Proteins/Peptides Database) - a tool for proteomic studies. *European Journal of Biochemistry*, 2001, 268(Suppl. 1):44.

Ponomarenko J.V., Furman D.P., Frolov A.S., Podkolodny N.L., Orlova G.V., Ponomarenko M.P., Kolchanov N.A., Sarai A. ACTIVITY: a database on DNA/RNA sites activity adapted to apply sequence-activity relationships from one system to another. *Nucleic Acids Res*, 2001, 29(1):284-7.

Ponomarenko J., Ponomarenko M., Orlova G., Kolchanov N., Sarai A. Conformational B-helix DNA properties specific to DNA free energy of protein binding to DNA with point mutation focused on SNP-analysis. *Proceedings of the Pacific Symposium on Biocomputing (PSB '2001), January 3-7, 2001, Hawaii, USA*, (Eds. Altman R.S., et al.), Singapore: World Scientific, p. 118.

Kochetov A., Grigorovich D., Sarai A., Kolchanov N. Database on mRNA-located eukaryotic expression signals influencing translation efficiency and specificity. *Proc. Int. Conf. "RNA as therapeutic and genomics target'2001"* Novosibirsk, Russia. 2001, 64.

Vityaev E.E., Orlov Yu.L., Vishnevsky O.V., Kovalerchuk B.K., Belenok A.S., Podkolodny N.L., Kolchanov N.A. Computer system "Gene Discovery" for functional annotation of DNA sequences. In: *ECML'2001 Workshop Machine Learning as Philosophy of Science*. (Eds. Korb K.B., Bensusan H.) Freiburg, Sept., 2001, 1-11.

Kel-Margoulis O.V., Romashchenko A.G., Kolchanov N.A., Wingender E., Kel A.E. COMPEL: a database on composite regulatory elements providing combinatorial transcriptional regulation. *Nucleic Acids Res*, 2000, 28(1):311-5.

Kolchanov N.A., Podkolodnaya O.A., Ananko E.A., Ignatieva E.V., Stepanenko I.L., Kel-Margoulis O.V., Kel A.E., Merkulova T.I., Goryachkovskaya T.N., Busygina T.V., Kolpakov F.A., Podkolodny N.L., Naumochkin A.N., Korostishevskaya I.M., Romashchenko A.G., Overton G.C. Transcription regulatory regions database (TRRD): its status in 2000. *Nucleic Acids Res*, 2000, 28(1):298-301.

Ponomarenko J.V., Orlova G.V., Ponomarenko M.P., Lavryushev S.V., Frolov A.S., Zybova S.V., Kolchanov N.A. SELEX_DB: an activated database on selected randomized DNA/RNA sequences addressed to genomic sequence annotation. *Nucleic Acids Res*, 2000, 28(1):205-8.

Kolchanov N.A., Anan'ko E.A., Kolpakov F.A., Podkolodnaia O.A., Ignat'eva E.V., Goriachkovskaia T.N., Stepanenko E.L. Gene networks. *Mol Biol (Mosk)*, 2000, 34(4):533-44.

Vasil'ev G.V., Merkulov V.M., Kobzev V.F., Merkulova T.I., Ponomarenko M.P., Podkolodnaia O.A., Ponomarenko Iu V., Kolchanov N.A. Point mutations in region 663-666 of intron 6 of the tryptophan oxygenase gene, connected with a series of mental disorders, disrupts the transcription factor YY1 binding site. *Mol Biol (Mosk)*, 2000, 34(2):214-22.

Ivanisenko V.A., Grigorovich D.A., Kolchanov N.A. PDBSite: a database on biologically active sites and their spatial surroundings in proteins with known tertiary structure. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS2000)*, 2000, 2:171-174.

Ananko E.A., Kolpakov F.A., Kolchanov N.A. GeneNet database: a technology for a formalized description of gene networks. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:174-177.

Titov I.I., Kolchanov N.A., Schroder H.C. Model of phosphate high-affinity transport in bacteria. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 3:62-64.

Ignatieva E.V., Podkolodny N.L., Kolchanov N.A. Informational support of ontology for transcription regulation (ISOTR). *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 3: 99-102.

Kel-Margoulis O.V., Romashchenko A.G., Deineko I.V., Kolchanov N.A., Wingender E. Kel A.E. Database on composite regulatory elements in eukaryotic genes (COMPEL). *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS2000)*, 2000, 1:45-48.

Kolchanov N.A., Podkolodny N.L., Ponomarenko M.P., Ananko E.A., Ignatieva E.V., Kolpakov F.A., Levitsky V.G., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Vorobiev D.G., Lavryushev S.V., Grigorovich D.A., Ponomarenko J.V., Kochetov A.V., Orlova G.V., Kondrakhin Y.V., Titov I.I., Vishnevsky O.V., Orlov Yu.L., Valuev V.P., Ivanisenko V.A., Oschepkov D.Yu., Omel'yanchuk N.A., Pozdnyakov M.A., Kosarev P.S., Goryachkovskaya T. N., Fokin O.N., Kalinichenko L.A., Kotlyarov Yu.V. Integrated system on gene expression regulation GeneExpress 2000. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:12-17.

Kolchanov N.A. Regulatory genomic sequences: coding, organization, and function. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:168-172.

Levitsky V.G., Kolchanov N.A. Nucleosome organization of chromatin in eukaryotic genes and structure-functional genome regions. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:90-93.

Ananko E.A., Podkolodnaya O.A., Ignatieva E.V., Kel-Margoulis O.V., Kel A.E., Merkulova T.I., Stepanenko I.L., Goryachkovskaya T. N., Podkolodny N.L., Grigorovich D.A., Naumochkin A.N., Korostishevskaya I.M., Lokhova I.V., Romashchenko A.G., Kolchanov N.A. Transcription Regulatory

Regions Database (TRRD). *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:18-21.

Kochetov A.V., Vorobiev D.G., Sirinko.A., Kisselev L.L., Kolchanov N.A. Contextual features of yeast mRNA 5'UTRs potentially important for their translational activity. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:67-70.

Kochetov A.V., Sirmik O.A., Komarova M.L., Trifonova E.A., Kolchanov N.A., Shumny V.K. Translational features of 5'UTR-located miniORFs. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:74-77.

Kondrakhin Y.V., Milanesi L., Lavryushev S.V., Schug J., Kolchanov N.A. Recognition groups: a new method for description and prediction of transcription factor binding sites. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS2000)*, 2000, 1:62-65.

Titov I.I., Vorobiev D.G., Kolchanov N.A. Mass analysis of RNA secondary structures using a genetic algorithm. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 2:138-142.

Vorobiev D.G., Titov I.I., Kochetov A.V., Kolchanov N.A. Structural features of mRNA 5'UTRs of eukaryotic genes expressed at high and low levels. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 2:135-137.

Grigorovich D.A., Ivanisenko V.A., Kolchanov N.A. Structure and format of the EnPDB database accumulating spatial structures of DNA, RNA and proteins. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 2:119-121.

Levashova Z.B., Kaledin V.I., Ponomarenko M.P., Kobzev V.F., Vasiliev G.V., Ponomarenko J.V., Podkolodnaya O.A., Merkulova T.I., Kolchanov N.A. Single nucleotide polymorphism in the region of 288-296 bp of intron 2 of the *k-ras* gene, related to lung tumor susceptibility, causes alteration in the set of proteins binding to this region. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:164-167.

Merkulova T.I., Vasiliev G.V., Ponomarenko M.P., Kobzev V.F., Podkolodnaya O.A., Ponomarenko Yu.V., Kolchanov N.A. Analysis of the region of intron 6 of the human *TDO2* gene in that point mutations associated with psychiatric disorders are located with the aid of computer and experimental approaches. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:134-137.

Vityaev E.E., Podkolodny N.L., Vishnevsky O.V., Kosarev P.S., Ananko E.A., Ignatieva E.V., Podkolodnaya O.A., Kolchanov N.A. Detecting patterns of structure-function organization of regulatory genomic sequences in a first order logic. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2000)*, 2000, 1:150-152.

Valishev A.I., Kolchanov N.A., Podkolodny N.L., Melnikov V.N., Alsynbayeva L.G., Yaroslavtseva R.G., Haans W.J.A. Bioinformatics: novel profile of vocational education. *Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure (BGRS2000)*, 2000, 2:232-234.

Levitsky V.G., Katokhin A.V., Kolchanov N.A. Inherent modular promoter structure and its application for recognition tools development. *Computational Technologies*, 2000, 5(Special Issue): 41-47.

Afonnikov D.A., Oshchepkov D.Yu., Kolchanov N.A. A method of estimation of variances and covariances of protein physico-chemical characteristics in families of homologous sequences. *Computational Technologies*, 2000, 5(Special Issue):79-86.

Kolchanov N.A., Podkolodny N.L., Ananko E.A., Podkolodnaia O.A., Ignatieva E.V., Merkulova T.I., Goryachkovsky T.N., Stepanenko I.L., Kel-Margoulis O.V., Kel A.E., Naumochkin I.M., Grigorovich D.A., Lokhova I.V., Romashchenko A.G. Transcription Regulatory Regions Database (TRRD): new possibilities. *Computational Technologies*, 2000, 5(Special Issue):32-40.

Titov I.I., Ivanisenko V.A., Kolchanov N.A. Fitness - a WWW-resource for RNA folding simulation based on genetic algorithm with local minimization. *Computational Technologies*, 2000, 5(Special Issue):48-56.

Vishnevsky O.V., Katokhin A.V., Babenko V.N., Overton G.C., Kolchanov N.A. Open reading frame reconstruction by using EST multiple alignment and dynamic programming. *Computational Technologies*, 2000, 5(Special Issue):16-25.

Anan'ko E.A., Kolpakov F.A., Kolesov G.B., Kolchanov N.A. Automatic generation of gene network schemes based on their formalized description in the GeneNet database. *Biofizika*, 1999, 44 (4):628-631.

Ponomarenko M.P., Ponomarenko Iu V., Podkolodnaia O.A., Frolov A.S., Vorob'ev D.V., Kolchanov N.A., Overton G.C. Averaging results of site recognition can increase the accuracy of annotating the human genome. *Biofizika*, 1999, 44(4):649-654.

Ponomarenko M.P., Ponomarenko Iu V., Kolchanov N.A. Contribution of signals and antisignals in the mutational spectrum of the td-intron insertion site. *Biofizika*, 1999, 44(4):655-63.

Frolov A.S., Lavriushev S.V., Grigorovich D.A., Kel A.E., Ptitsyn A.A., Kolchanov N.A., Podkolodnyi N.L., Solov'ev V.V., Milanesi L., Bourne P., et al. WWWMGs: an integrated server for molecular-genetic studies. *Biofizika*, 1999, 44(5):832-836.

Kolchanov N.A., Ponomarenko M.P., Kel A.E., Kondrakhin Iu V., Frolov A.S., Kolpakov F.A., Goriachkovskaia T.N., Kel O.V., Anan'ko E.A., Ignat'eva E.V., et al. GeneExpress: an integrator for databases and computer systems accessible by the Internet and intended for studying eukaryotic gene expression. *Biofizika*, 1999, 44(5):837-41.

Ponomarenko M.P., Shindialov I., Bourne P., Kolchanov N.A. LIKENESS: a system for rapid retrieval of similar conformation of proteins and their spatial structures. *Biofizika*, 1999, 44(5):821-31.

Kolchanov N.A., Ananko E.A., Podkolodnaya O.A., Ignatieva E.V., Stepanenko I.L., Kel-Margoulis O.V., Kel A.E., Merkulova T.I., Goryachkovskaya T.N., Busygina T.V., Kolpakov F.A., Podkolodny N.L., Naumochkin A.N., Romashchenko A.G. Transcription Regulatory Regions Database (TRRD): its status in 1999. *Nucleic Acids Res*, 1999, 27(1):303-6.

Levitsky V.G., Ponomarenko M.P., Ponomarenko J.V., Frolov A.S., Kolchanov N.A. Nucleosomal DNA property database. *Bioinformatics*, 1999, 15(7-8):582-92.

Ponomarenko M.P., Ponomarenko J.V., Frolov A.S., Podkolodnaya O.A., Vorobyev D.G.,

- Kolchanov N.A., Overton G.C. Oligonucleotide frequency matrices addressed to recognizing functional DNA sites. *Bioinformatics*, 1999, 15(7-8):631-643.
- Kochetov A.V., Ponomarenko M.P., Frolov A.S., Kisselev L.L., Kolchanov N.A. Prediction of eukaryotic mRNA translational properties. *Bioinformatics*, 1999, 15(7-8):704-12.
- Ponomarenko J.V., Ponomarenko M.P., Frolov A.S., Vorobyev D.G., Overton G.C., Kolchanov N.A. Conformational and physicochemical DNA features specific for transcription factor binding sites. *Bioinformatics*, 1999, 15(7-8):654-68.
- Kolchanov N.A., Ponomarenko M.P., Frolov A.S., Ananko E.A., Kolpakov F.A., Ignatieva E.V., Podkolodnaya O.A., Goryachkovskaya T.N., Stepanenko I.L., Merkulova T.I., Babenko V.V., Ponomarenko Y.V., Kochetov A.V., Podkolodny N.L., Vorobiev D.V., Lavryushev S.V., Grigorovich D.A., Kondrakhin Y.V., Milanese L., Wingender E., Solovyev V., Overton G.C. Integrated databases and computer systems for studying eukaryotic gene expression. *Bioinformatics*, 1999, 15(7-8):669-86.
- Ponomarenko M.P., Ponomarenko J.V., Frolov A.S., Podkolodny N.L., Savinkova L.K., Kolchanov N.A., Overton G.C. Identification of sequence-dependent DNA features correlating to activity of DNA sites interacting with proteins. *Bioinformatics*, 1999, 15(7-8):687-703.
- Vasiliev G.V., Merkulov V.M., Kobzev V.F., Merkulova T.I., Ponomarenko M.P., Kolchanov N.A. Point mutations within 663-666 bp of intron 6 of the human *TDO2* gene, associated with a number of psychiatric disorders, damage the YY-1 transcription factor binding site. *FEBS Lett*, 1999, 462(12):85-8.
- Kolchanov N.A., Frolov A.S., Lavryushev S.V., Grigorovich D.A., Kolpakov F.A., Ananko E.A., Podkolodny N.L., Overton G.C., Ptitsyn A.A. WWWMGs: an integrative server for molecular genetic studies. In: *Proceedings of the international conference "Advances in Systemics, Signals, Control and Computers, SSCC'99, Durban, South Africa"* (Ed. Bajic V.B.), IAAMSAD and SAB ANS, 1999, 2:316-320.
- Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Merkulova T.I., Podkolodny N.L., Frolov A.S., Kolchanov N.A. The genes regulated by PPARs: the presentation in the TRRD database. *E2: Keystone Symposia on Molecular and Cellular Biology. The PPARs: Transcriptional Links to Obesity, Diabetes and Cardiovascular Disease*. Keystone, Colorado, April 28 -May 2, 1999, Abstract #126, p.34.
- Ponomarenko M.P., Frolov A.S., Ponomarenko J.V., Podkolodnaya O.A., Vorobyev D.V., Kolchanov N.A., Overton G.C. Mean-recognition: a systematic approach increasing the accuracy of the functional site recognition for the genomic DNA annotation. *Proceedings of the World Multiconference on Systemics, Cybernetics and Informatics, SCI'98*, (Ed. N. Callaos, L. Holmes), Orlando, Florida, July 12-16, 1998, 4:224-230.
- Kolchanov N.A., Matushkin Yu.G., Frolov A.S. Regulation mechanisms in biological systems. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:111-114.
- Ananko E.A., Kolpakov F.A., Kolesov G.B., Kolchanov N.A. Gene networks: a database and its automated visualization through the internet in the GeneNet computing system. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:82-85.

Kel-Margoulis O.V., Kel A.E., Frisch M., Romashchenko A.G., Kolchanov N.A., Wingender E. COMPEL: a database on composite regulatory elements. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:54-57.

Kolesov G.B., Kolpakov F.A., Kolchanov N.A. New method for the study of the modular structure of transcription regulatory regions. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 2:430-433.

Kolchanov N.A., Ignatieva E.V., Kel-Margoulis O.V., Kel A.E., Ananko E.A., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Goryachkovsky T.N., Kolpakov F.A., Podkolodny N.L., Lavryushev S.V., Grigorovich D.A., Frolov A.S., Romashchenko A.G. Transcription Regulatory Regions Database (TRRD): new possibilities provided by release 4.0. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:25-28.

Kochetov A.V., Ponomarenko M.P., Vorobiev D.G., Frolov A.S., Kisselev L.L.1, Kolchanov N.A. Eukaryotic mRNAs encoding abundant and scarce proteins are dissimilar in many structural features of 5'-untranslated leaders. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:214-217.

Ponomarenko M.P., Frolov A.S., Ponomarenko J.V., Vorobiev D.G., Levitsky V.G., Podkolodnaya O.A., Overton G.C.& Kolchanov N.A. B-DNA-VIDEO:an active database for the significant BDNA features of transcription factor binding sites. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:66-70.

Kolchanov N.A., Ponomarenko M.P., Kondrakhin Y.V., Frolov A.S., Kolpakov F.A., Kel A.E., Kel-Margoulis O.V., Ananko E.A., Ignatieva E.V., Podkolodnaya O.A., Stepanenko I.L., Merkulova T.I., Babenko V.N., Vorobiev D.G., Lavryushev S.V., Grigorovich D.A., Ponomarenko J.V., Kochetov A.V., Kolesov G.B., Podkolodny N.L., Wingender E., Hainemeier T., Milanese L., Solovyev V.V., Overton G.C. GeneExpress system:description, analysis, and recognition of regulatory sequences in eukaryotic genomes. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:71-76.

Ponomarenko M.P., Frolov A.S., Ponomarenko J.V., Podkolodnaya O.A., Vorobiev D.G., Kolchanov N.A., Overton G.C. Recognition accuracy of DNA functional sites can be increased by averaging partial recognitions. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:158-162.

Ponomarenko M.P., Kolchanov N.A., Shindyalov I., Bourne P. Likeness: a system searching for and aligning similar protein conformations. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 2:370-374.

Likhacheva E., Ponomarenko M.P., Bogachev S., Kokoza E., Fisher P., Ponomarenko J.V., Vorobiev D.G., Kolesov G.B., Kolchanov N.A. The structural analysis of the DNA fragments associated with the nuclear lamins in *Drosophila melanogaster*. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 2:247-248.

Ponomarenko M.P., Kolchanov N.A., Ponomarenko J.V., Frolov A.S., Podkolodnaya O.A., Vorobiev D.G., Podkolodny N.L., Overton G.C. Revealing the conformational and physico-chemical DNA properties applicable for predicting the activity of DNA functional sites. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:186-190.

Ponomarenko M.P., Vorobiev D.G., Ponomarenko J.V., Kuzin F.E., Gruzdev A.D., Kolchanov N.A. Significant B-DNA conformational and physico-chemical properties of the DNA topoisomerase I sites. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 2:446-447.

Savinkova L.K., Sokolenko A.A., Rau V.A., Kobzev V.F., Ponomarenko M.P., Ponomarenko J.V., Kolchanov N.A. Quantitative computer-assisted analysis of the TATA-binding protein affinity for complementary duplexes of synthetic oligodeoxyribonucleotides. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 1:165-169.

Ponomarenko M.P., Ishchenko I.V., Frolov A.S., Ponomarenko J.V., Kolchanov N.A., Mikhailov Yu.I., Minina A.V., Ivashin S.A. Bioinformatics for humanitarians. *Proceedings of the First International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'98)*, 1998, 2:417-418.

Heinemeyer T., Wingender E., Reuter I., Hermjakob H., Kel A.E., Kel O.V., Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Kolpakov F.A., Podkolodny N.L., Kolchanov N.A. Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. *Nucleic Acids Res*, 1998, 26(1):362-371.

Kochetov A.V., Ischenko I.V., Vorobiev D.G., Kel A.E., Babenko V.N., Kisselev L.L., Kolchanov N.A. Eukaryotic mRNAs encoding abundant and scarce proteins are statistically dissimilar in many structural features. *FEBS Lett*, 1998, 440(3):351-355.

Kolpakov F.A., Ananko E.A., Kolesov G.B., Kolchanov N.A. GeneNet: a gene network database and its automated visualization. *Bioinformatics*, 1998, 14(6):529-37.

Kolchanov N.A., Kel A.E., Podkolodnaya O.A., Kel O.V., Romaschenko A.G., Wingender E., Overton G.C. TRRD, GERD and COMPEL: Databases on Gene-Expression Regulation as a Tool for Analysis of Functional Genomic Sequences. *DOE Human Genome Program Report*, U.S. Gov. Print. Office. 1998, 2:35-36.

Ponomarenko M.P., Frolov A.S., Ponomarenko J.V., Podkolodnaya O.A., Vorobyev D.V., Kolchanov N.A., Overton G.C. Mean-recognition: a systematic approach increasing the accuracy of the functional site recognition for the genomic DNA annotation. *Proceedings of the World Multiconference on Systemics, Cybernetics and Informatics, SCI'98, July 12-16, 1998, Orlando, Florida*. (Eds. N. Callaos, L. Holmes) 4:224-230.

Kolchanov N.A., Ponomarenko M.P., Kel A.E., Kondrakhin Yu V., Frolov A.S., Kolpakov F.A., Goryachkovsky T.N., Kel O.V., Ananko E.A., Ignatieva E.V., Podkolodnaya O.A., Babenko V.N., Stepanenko I.L., Romashchenko A.G., Merkulova T.I., Vorobiev D.G., Lavryushev S.V., Ponomarenko Yu V., Kochetov A.V., Kolesov G.B., Solovyev V.V., Milanese L., Podkolodny N.L., Wingender E., Heinemeyer T. GeneExpress: a computer system for description, analysis, and recognition of regulatory sequences in eukaryotic genome. *Proc Int Conf Intell Syst Mol Biol*, 1998, 6:95-104.

Ponomarenko, Kolchanov N., Kel A., Kondrakhin Y., Frolov A., Kolpakov F., Kel O., Ananko E., Ignatieva E., Podkolodnaya O., Stepanenko I., Merkulova T., Babenko V., Vorobiev D., Lavryushev S., Ponomarenko J., Kochetov A., Kolesov G., Podkolodny N. (Russia), L. Milanese (Italy), E. Wingender (Germany), T. Heinemeyer (Germany), and V. Solovyev (United Kingdom). GeneExpress: a computer system for investigating molecular mechanisms of gene expression. *Abstracts XVIIIth International Congress of Genetics, August 10-15, 1998, Beijing, China*, p. 62, 4S24.

Ponomarenko M.P., Ponomarenko Iu V., Titov, II, Kolchanov N.A., Mazin A.V., Kowalczykowski S.C. Preference of RecA-filament to the DNA sequences correlates with genetic code. *Dokl Akad Nauk* 1998, 363(1):122-5.

Kolchanov N.A., Ponomarenko M.P., Ponomarenko Iu V., Podkolodnyi N.L., Frolov A.S. Functional sites of pro- and eukaryotic genomes: computer modeling and predicting activity. *Mol Biol (Mosk)*, 1998, 32(2):255-67.

Wingender E., Kel A.E., Kel O.V., Karas H., Heinemeyer T., Dietze P., Knuppel R., Romaschenko A.G., Kolchanov N.A. TRANSFAC, TRRD and COMPEL: towards a federated database system on transcriptional regulation. *Nucleic Acids Res* 1997, 25(1):265-8.

Ponomarenko M.P., Savinkova L.K., Kel A.E., Kolchanov N.A. Computer modeling of TATA-box sequences of eukaryotic promoters. *Dokl Akad Nauk* 1997, 355(4):557-61.

Pozdniakov M.A., Rogozin I.B., Babenko V.N., Kolchanov N.A. Neighboring base effect on emergence of spontaneous mutations in human pseudogenes. *Dokl Akad Nauk* 1997, 356(4):566-8.

Kolpakov F.A., Kel A.E., Ponomarenko M.P., Kolchanov N.A. High heterogeneity of higher eukaryotic gene promoters, transcribed by RNA polymerase II. *Dokl Akad Nauk* 1997, 357(5):693-5.

Ponomarenko M.P., Ponomarenko J.V., Kel A.E., Kolchanov N.A. Search for DNA conformational features for functional sites. Investigation of the TATA box. *Pac Symp Biocomput* 1997:340-51.

Afonnikov D.A., Kondrakhin Yu.V., Titov I.I., Kolchanov N.A. Detecting direct correlations between positions in multiple alignment of amino acid sequences. Computer science and biology. Genome informatics: Function, structure, phylogeny. Proc. of the German Conference on Bioinformatics GCB'97, (Eds. Mewes H.W., Frishman D), Kloster Irsee, Bavaria, Sept. 22-24, 1997, 87-98.

Ponomarenko M.P., Ponomarenko Iu V., Kel A.E., Kolchanov N.A., Karas H., Wingender E., Sklenar H. Computer analysis of conformational features of the eukaryotic TATA-box DNA promoters. *Mol Biol (Mosk)* 1997, 31(4):733-40.

Ponomarenko M.P., Savinkova L.K., Ponomarenko Iu V., Kel A.E., Titov, II, Kolchanov N.A. Modeling TATA-box sequences in eukaryotic genes. *Mol Biol (Mosk)* 1997, 31(4):726-32.

Karas H., Kel E., Kel O.V., Kolchanov N.A., Wingender E. Integrating knowledge on transcriptional regulation of eukaryotic genes based on information from TRANSFAC, TRRD, and COMPEL databases. *Mol Biol (Mosk)* 1997, 31(4):637-46.

Kel A.E., Kolchanov N.A., Kel O.V., Romashchenko A.G., Anan'ko E.A., Ignat'eva E.V., Merkulova T.I., Podkolodnaia O.A., Stepanenko I.L., Kochetov A.V., Kolpakov F.A., Podkolodnyi N.L., Naumochkin A.A. TRRD: a database of transcription regulatory regions in eukaryotic genes. *Mol Biol (Mosk)* 1997, 31(4):626-36.

Kel O.V., Kel A.E., Romashchenko A.G., Wingender E., Kolchanov N.A. Composite regulatory elements: classification and description in the COMPEL database. *Mol Biol (Mosk)* 1997, 31(4):601-15.

Kolchanov N.A. Transcriptional regulation of eukaryotic genes: data bases and computer analysis. *Mol*

Biol (Mosk) 1997, 31(4):581-3.

Ponomarenko M.P., Kolchanova A.N., Kolchanov N.A. Generating programs for predicting the activity of functional sites. *J Comput Biol* 1997, 4(1):83-90.

Kolchanov N.A., Matushkin Yu.G. A Biological self-reproducing systems: principles of organization and evolution. *Russian Journal of Genetics*, 1997, 33(8):889-897.

Kolchanov N.A., Babenko V.N., Vishnevskii O.V., Kel A.E. Oligonucleotide vocabularies of isofunctional families of genes that code proteins. *Dokl Akad Nauk* 1996, 348(5):696-9.

Ponomarenko M.P., Kel A.E., Kolchanova A.N., Kolchanov N.A. Contextual signals and antisignals of the intron td-homing site. *Dokl Akad Nauk* 1996, 348(3):424-7.

Ptitsyn A.A., Rogozin I.B., Grigorovich D.A., Strelets V.B., Kel A.E., Milanezi L., Kolchanov N.A. Computer system "AutoGene" for automatic analysis of nucleotide sequences. *Mol Biol (Mosk)* 1996, 30(2):432-41.

Rogozin I.B., Milanese L., Kolchanov N.A. Gene structure prediction using information on homologous protein sequence. *Comput Appl Biosci* 1996, 12(3):161-70.

Rogozin I.B., Sredneva N.E., Kolchanov N.A. Somatic hypermutagenesis in immunoglobulin genes. III. Somatic mutations in the chicken light chain locus. *Biochim Biophys Acta* 1996, 1306(2-3):171-8.

Kolchanov N.A., Titov, II, Vlassova I.E., Vlassov V.V. Chemical and computer probing of RNA structure. *Prog Nucleic Acid Res Mol Biol* 1996, 53:131-96.

Kel O.V., Romaschenko A.G., Kel A.E., Wingender E., Kolchanov N.A. A compilation of composite regulatory elements affecting gene transcription in vertebrates. *Nucleic Acids Res* 1995, 23(20):4097-103.

Kel A.E., Kondrakhin Y.V., Kolpakov Ph A., Kel O.V., Romashenko A.G., Wingender E., Milanese L., Kolchanov N.A. Computer tool FUNSITE for analysis of eukaryotic regulatory genomic sequences. *Proc Int Conf Intell Syst Mol Biol* 1995, 3:197-205.

Kolchanov N.A., Vishnevsky O.V., Babenko V.N., Kel A.E., Shindyalov I.N. Identification of cDNA sequences by specific oligonucleotide sets. Computer tool and application. *Proc Int Conf Intell Syst Mol Biol* 1995, 3:206-14.

Ponomarenko M.P., Savinkova L.K., Kolchanova A.N., Kel A.E., Kolchanov N.A. Quantitative analysis of dissociation constant of transcription factor TFIID complex with synthetic ssDNA 15mers. Notes of Gene-Finding and Gene Structure Prediction Workshop, Penn Tower Hotel, Philadelphia, October 13-14, 1995, 1-5.

Kel O.V., Romachenko A.G., Kel A.E., Naumochkin A.N., Kolchanov N.A. Data representation in the TRRD - a database of transcription regulatory regions of the eukaryotic genomes. Proceedings of the 28th Annual Hawaii International Conference on System Sciences [HICSS]. v.5, Biotechnology Computing, IEE Computer Society Press, Los Alamitos, California, 1995, 42-51.

Kondrakhin Y.V., Kel A.E., Kolchanov N.A., Romashchenko A.G., Milanesi L. Eukaryotic promoter recognition by binding sites for transcription factors. *Comput Appl Biosci* 1995, 11(5):477-88.

Kondrakhin Yu V., Shamin V.V., Kolchanov N.A. Construction of a generalized consensus matrix for recognition of vertebrate pre-mRNA 3'-terminal processing sites. *Comput Appl Biosci* 1994, 10 (6):597-603.

Shindyalov I.N., Kolchanov N.A., Sander C. Can three-dimensional contacts in protein structures be predicted by analysis of correlated mutations? *Protein Eng* 1994, 7(3):349-58.

Ptitsyn A.A., Strelets V.B., Rogozin I.B., Kel A.E., Milanesi L., Kolchanov N.A. The AutoGene v1.0: a computer system for automatic molecular genetic analysis, Novosibirsk, 1994, 47 pp.

Milanesi L., Kolchanov N.A., Rogozin I.B., Kel A.E., Titov I.I. Sequence Functional Inference. Guide to Human Genome Computing (Eds. Martin J., Bishop.), Academic press, 1994, 249-312.
Kel A.E., Ponomarenko M.P., Likhachev E.A., Orlov Yu L., Ischenko I.V., Milanesi L., Kolchanov N.A. SITEVIDEO: a computer system for functional site analysis and recognition. Investigation of the human splice sites. *Comput Appl Biosci* 1993, 9(6):617-27.

Kolchanov N.A., Kel A.E., Ponomarenko M.P., Romachenko A.G., Likhachev J., Milanesi L., Lim H.A. Patterns of oligonucleotides distribution within DNA and RNA functional sites. Proceedings of the Second International Conference on Bioinformatic, Supercomputing and Complex Genome Analysis (Eds. C.R. Cantor & H.A. Lim), Jun 1992, St. Petersburg, Florida, USA, 1993, 445-464.

Rogozin I.B., Kolchanov N.A. Somatic hypermutagenesis in immunoglobulin genes. II. Influence of neighbouring base sequences on mutagenesis. *Biochim Biophys Acta* 1992, 1171(1):11-8.

Streletc V.B., Shindyalov I.N., Kolchanov N.A., Milanesi L. Fast, statistically based alignment of amino acid sequences on the base of diagonal fragments of DOT-matrices. *Comput Appl Biosci* 1992, 8(6):529-34.

Rogozin I.B., Solovyov V.V., Kolchanov N.A. Somatic hypermutagenesis in immunoglobulin genes. I. Correlation between somatic mutations and repeats. Somatic mutation properties and clonal selection. *Biochim Biophys Acta* 1991, 1089(2):175-82.

Beniukh D.N., Ponomarenko M.P., Kolchanov N.A. Classification of DNA- (RNA)-interacting proteins based on recognition of structure-function determinants. *Biofizika* 1991, 36(6):957-67.

Ponomarenko M.P., Beniukh D.N., Orlov Iu L., Kolchanov N.A. Precise recognition method of structure-function determinants of protein molecules. *Biofizika* 1991, 36(6):943-56.

Kel A.E., Kolchanov N.A., Solov'ev V.V. Theoretical analysis of mechanisms of occurrence of DNA deletions in prokaryotic genomes based on direct repeats. *Mol Biol (Mosk)* 1989, 23(1):184-92.

Kolchanov N.A., Rogozin I.B., Solov'ev V.V. Theoretical analysis of mechanisms of spontaneous and induced mutations in DNA based on repeated sequences. *Genetika* 1989, 25(9):1690-8.

Omell'ianchuk L.V., Kolchanov N.A., Ratner V.A. A phylogenetic analysis of genes of the influenza virus. Phylogenetic trees and fixation rates. *Genetika* 1989, 25(8):1391-401.

- Ratner V.A., Kolchanov N.A., Omel'ianchuk L.V. Phylogenetic analysis of genes of the influenza virus. Relationship between adaptability and neutrality. *Genetika* 1989, 25(8):1499-507.
- Kapitonov V.V., Shakhmuradov I.A., Kolchanov N.A. Evolution of Alu repeats: imitation model. *Genetika* 1989, 25(6):1111-8.
- Shakhmuradov I.A., Kapitonov V.V., Kolchanov N.A., Omel'ianchuk L.V. Evolution of Alu repeats: dynamics of distribution in genome. *Genetika* 1989, 25(9):1682-9.
- Kiseleva E.V., Kapitonov V.V., Ovchinnikova L.P., Khristoliubova N.B., Kolchanov N.A. Detection of paired transcription complexes in bacterial chromatin. *Dokl Akad Nauk SSSR* 1989, 305(5):1235-8.
- Kolchanov N.A., Solov'ev V.V., Kel A.E. Theoretical analysis of the DNA duplication mechanisms in the prokaryotic genomes on the basis of repeats. *Mol Biol (Mosk)* 1989, 23(2):537-44.
- Kolchanov N.A., Kel A.E., Solov'ev V.V. Statistical evidence for the correlation of DNA deletions in prokaryotic genomes with direct repeats. *Mol Biol (Mosk)* 1989, 23(1):175-83.
- Shakhmuradov I.A., Kolchanov N.A. tRNA as a possible primer for the initiation of reverse transcription of dispersed repeats Alu, B1, B2 and L1. *Mol Biol (Mosk)* 1989, 23(4):1130-7.
- Shakhmuradov I.A., Kolchanov N.A., Kapitonov V.V. Distribution of Alu repeats along the human genome: formation of clusters and features of insertion regions. *Mol Biol (Mosk)* 1989, 23(2):526-36.
- Solov'ev V.V., Rogozin I.V., Kolchanov N.A. Somatic hypermutagenesis in immunoglobulin genes. I. Connection of somatic mutations with repeats. A statistical weighting method. *Mol Biol (Mosk)* 1989, 23(3):783-94.
- Solov'ev V.V., Kel A.E., Kolchanov N.A. Convergent origin of repeats in genes coding for globular proteins. An analysis of the factors determining the presence of inverted and symmetrical repeats. *Zh Obshch Biol* 1989, 50(1):116-22.
- Kolchanov N.A., Shindyalov I.N. Single amino acid substitutions producing instability of globular proteins. Calculation of their frequencies in the entire mutational spectra of the alpha- and beta-subunits of human hemoglobin. *J Mol Evol* 1988, 27(2):154-62.
- Kapitonov V.V., Kolchanov N.A. Evolutionary significance of the presence in mobile genetic elements of regulatory sites reacting to the environment. Regulatory site as a trigger. *Genetika* 1988, 24(9):1696-703.
- Kel A.E., Kolchanov N.A., Solov'ev V.V. Convergent origin of the repetitions in genes coding for globular proteins. An analysis of the factors determining the presence of direct repetitions. *Zh Obshch Biol* 1988, 49(3):343-54.
- Kolchanov N.A., Kel A.E., Solov'ev V.V. Convergent origin of repeats in the genes coding for globular proteins. The modelling of the convergent origin of direct repeats. *Zh Obshch Biol* 1988, 49 (6):723-8.
- Kolchanov N.A., Shakhmuradov I.A., Kapitonov V.V., Omel'ianchuk L.V. Various aspects of evolution of Alu repeats in mammals. *Mol Biol (Mosk)* 1988, 22(5):1335-44.
- Potapov V.A., Sosnovtsev S.V., Solovyev V.V., Ivanov S.V., Romashenko A.G., Kolchanov V.A.

Structure of complex repeats in fox precentromere heterochromatin: regulatory elements of replication, recombination, and gene expression. *Dokl Akad Nauk SSSR* 1988, 299(5):1250-1255.

Omel'ianchuk L.V., Kolchanov N.A. Evolutionary study of genomes based on an analysis of primary tRNA structures. *Zh Obshch Biol* 1987, 48(2):156-66.

Kapitonov V.V., Kolchanov N.A., Shakhmuradov I.A., Solov'ev V.V. Presence in the mobile genetic elements of regions homologous to the heat shock regulatory site. *Genetika* 1987, 23(12): 2112-2119.

Kolchanov N.A., Solovyov V.V., Rogozin I.B. Peculiarities of immunoglobulin gene structures as a basis for somatic mutation emergence. *FEBS Lett* 1987, 214(1):87-91.

Shakhmuradov I.A., Kolchanov N.A., Solov'ev V.V., Ratner V.A. Enhancer-like structures in moderately repetitive sequences of eukaryotic genomes. *Genetika* 1986, 22(3):357-67.

Merkulova T.I., Solov'ev V.V., Kolchanov N.A., Plisov S., Salganik R.I. Identification of the nucleotide sequences specific for the 5'-flanking regions of the genes regulated by glucocorticoids by a computer analysis method. *Biull Eksp Biol Med* 1986, 101(4):466-8.

Shindyalov I.N., Kolchanov N.A. Analysis of the factors and implications of an empirical method for estimating the stability of mutant human haemoglobins. *J Theor Biol* 1985, 117(1):19-46.

Kolchanov N.A., Shindialov I.N. Estimation of the frequency of amino acid substitutions causing instability of the spatial structure in an overall mutation spectrum of alpha- and beta-subunits of human hemoglobin. *Genetika* 1985, 21(10):1740-8.

Kolchanov N.A., Solov'ev V.V., Rogozin I.B. Molecular mechanism of somatic hypermutagenesis in immunoglobulin genes. *Dokl Akad Nauk SSSR* 1985, 281(4):994-999.

Solov'ev V.V., Kolchanov N.A. Exon-intron structure of eukaryotic genes can be due to the nucleosome organization of chromatin and to its related characteristics of gene expression regulation. *Dokl Akad Nauk SSSR* 1985, 284(1):232-237.

Solov'ev V.V., Zharkikh A.A., Kolchanov N.A. Context analysis of polynucleotide sequences. Methods of detecting non-random repeats. I. Direct repeats in genes of beta-, beta'-, sigma subunits of Escherichia coli RNA-polymerase. *Mol Biol (Mosk)* 1985, 19(2):524-536.

Zharkikh A.A., Solov'ev V.V., Kolchanov N.A. The context analysis of polynucleotide sequences. II. Inverted repeats and complementary palindromes in RNA-polymerase genes. *Mol Biol (Mosk)* 1985, 19(3):597-609.

Shindialov I.N., Kolchanov N.A. Factors determining the instability of the conformation of human mutant hemoglobins. A method for evaluating the instability. *Mol Biol (Mosk)* 1985, 19(6):1501-13.

Ratner V.A., Omel'ianchuk L.V., Zharkikh A.A., Kolchanov N.A. Theoretical analysis of the structural characteristics and evolution of transfer RNAs. *Zh Obshch Biol* 1985, 46(6):732-42.

Solovyov V.V., Zharkikh A.A., Kolchanov N.A., Ratner V.A. The template RNAs of RNA polymerases can have compact secondary structure, formed by long double helices with partial violations of the complementarity. *FEBS Lett* 1984, 165(1):72-8.

Solovyov V.V., Kolchanov N.A. A simple method for the calculation of low energy packings of alpha-helices--a threshold approximation. I. The use of the method to estimate the effects of amino acid substitutions, deletions and insertions in globins. *J Theor Biol* 1984, 110(1):67-91.

Zharkikh A.A., Solovyov V.V., Kolchanov N.A. Conformational changes in the globin family during evolution. 1. Analysis of the evolutionary role of insertions and deletions. *J Mol Evol* 1984, 21(1):42-53.

Kolchanov N.A., Soloviov V.V., Zharkikh A.A. The effects of mutations, deletions and insertions of single amino acids on the three-dimensional structure of globins. *FEBS Lett* 1983, 161(1):65-70.

Kolchanov N.A., Solov'ev V.V., Zharkikh A.A. High saturation by direct copies in RNA-polymerase genes based on context analysis data. *Dokl Akad Nauk SSSR* 1983, 273(3):741-4.

Solov'ev V.V., Zharkikh A.A., Kolchanov N.A. RNA-polymerase matrix RNAs have a compact secondary structure formed by long double helices with partial mispairing. *Dokl Akad Nauk SSSR* 1983, 273(5):1256-61.

Zharkikh A.A., Solov'ev V.V., Kolchanov N.A. Evolutionary and conformational analysis of a family of globins. The evolutionary role of deletions and insertions. *Zh Obshch Biol* 1983, 44(6): 790-801.

Omell'ianchuk L.V., Kolchanov N.A. Recurrent relationship for the characteristic polynom of a system of enzymatic catalysis of nonbranched monomolecular reactions. *Biofizika* 1982, 27(3):404
9.

Solovyov V.V., Kolchanov N.A. Single amino acid substitutions can lead to the complete distortion of a normal tertiary structure of globular proteins. *Genetika* 1982, 18(10):1573-80.

Kolchanov N.A., Omelyanchuk L.V. Estimation of the tRNA and 5S RNA secondary structures based upon their polynucleotide chains. *Studia Biophysic*, 1982, 87(2/3):115-116.

Solovyov V.V., Kolchanov N.A. The method of calculation of low-energy conformations of alpha-helical pairs of globular proteins. *Mol Biol (Mosk)* 1981, 15(1):323-35.

Kolpakov M.G., Kolchanov N.A., Matveev P.A., Poliakov M.G., Protsenko M.I. Feedback mechanisms in the renin-angiotensin system. *Izv Akad Nauk SSSR Biol* 1977, 1:113-9.

Poliakov M.G., Kolchanov N.A. Mathematical modelling of the distribution and metabolism of angiotensin II. *Nauchnye Doki Vyss Shkoly Biol Nauki* 1975(8):41-6.

Zhegalina L.V., Kolchanov N.A., Poliakov M.G. Presence of a renin inhibitor in the plasma of intact dogs. *Biull Eksp Biol Med* 1975, 80(10):48-51.