RUSSIAN ACADEMY OF SCIENCES
SIBERIAN BRANCH

INSTITUTE OF CYTOLOGY AND GENETICS

PROGRAM OF THE EIGHTH INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE\SYSTEMS BIOLOGY

BGRS\SB'12
Novosibirsk, Russia
June 25–29, 2012

Novosibirsk
2012

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Alexander Ratushny Institute for Systems Biology and Seattle Biomedical Research Institute, Seattle, WA, USA
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Mikhail Voevoda Institute of Internal Medicine SB RAMS, Novosibirsk, Russia
Edgar Wingender University Medical Center Goettingen, Dept. of Bioinformatics, Goettingen, Germany
Limsoon Wong National University of Singapore, Singapore
Jaroslaw Zola Electrical & Computer Engineering, Iowa State University, Ames, IA, USA

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The Vavilov Society of Geneticists and Breeders

Department of systems biology

Chair of Information Biology NSF NSU

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THE EIGHTH INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE\SYSTEMS BIOLOGY (BGRS\SB'12)

CONFERENCE PROGRAM

SCHEDULE AT A GLANCE

The Conference Sessions will be held in the Large and Small Conference Halls of the House of Scientists, and in the Conference Halls of the Exhibition Centre and Institute of Cytology and Genetics

June 25, Monday Foyer of the Large Conference Hall

10:00-13:00 Registration of the conference participants*

*Participants who come later are welcome for registration in the Organizing Committee room (House of Scientists, room No.200) on any conference day.

House of Scientists, Large Conference Hall

13:00 **Conference Opens:**

Welcome by
Academician of the Russian Academy of Sciences **Nikolay Kolchanov**
Greetings of
Academician of the Russian Academy of Sciences **Alexander Aseev**,
Academician of the Russian Academy of Sciences **Renad Sagdeev**,
Academician of the Russian Academy of Sciences **Valentin Vlassov,**
Professor **Ralf Hofestaedt**

13:20-19:00 **PLENARY SESSION**
16:00-16:20 Coffee break
19:30-23:00 Welcome party

June 26, Tuesday *House of Scientists, Large Conference Hall*

9:30-12:50 Morning Session
MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL GENOMICS”
10:50-11:10 Coffee break
12:50-14:00 Lunch break
14:00-17:25 Evening Session
MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL GENOMICS”
15:20-15:50 Coffee break

Exhibition Centre, Conference Hall

9:00-13:00 Morning Session
MICROSYMPOSIUM: SKOLKOVO: BIOLOGY AND INNOVATIONS
10:50-11:10 Coffee break
12:30-14:00 Lunch break
14:00 -18:00 Evening Session

MICROSYMPOSIUM: SKOLKOVO: BIOLOGY AND INNOVATIONS
15:40-16:10 Coffee break

House of Scientists, Foyer of the Large (or Small) Conference Hall

18:00-20:00 **POSTER SESSION AND COMPUTER DEMOS**

June 27, Wednesday *House of Scientists, Large Conference Hall*

9:00-12:50 Morning Session
MICROSYMPOSIUM "COMPUTATIONAL AND EXPERIMENTAL GENOMICS"
10:40-11:00 Coffee break
12:50-14:00 Lunch break
14:00-18:20 Evening Session
MICROSYMPOSIUM "COMPUTATIONAL AND EXPERIMENTAL PROTEOMICS"
15:50-16:20 Coffee break

House of Scientists, Small Conference Hall

9:00-12:50 Morning Session
BIOINFORMATICS AND SYSTEMS BIOLOGY OF GENE EXPRESSION REGULATION
11:00-11:20 Coffee break
12:50 -14:00 Lunch break
14:00 -18:10 Evening Session
BIOINFORMATICS AND SYSTEMS BIOLOGY OF GENE EXPRESSION REGULATION
16:30-16:50 Coffee break

Exhibition Centre, Conference Hall

14:00-17:55 Evening Session
COMPUTATIONAL INFERENCE OF NETWORKS FROM HIGH-THROUGHPUT EXPERIMENTAL DATA
15:20-15:40 Coffee break

House of Scientists, Foyer of the Large Conference Hall

18:30-20:00 **POSTER SESSION AND COMPUTER DEMOS**

June 28, Thursday *House of Scientists, Large Conference Hall*

9:00-13:05 Morning Session
MICROSYMPOSIUM "COMPUTATIONAL AND EXPERIMENTAL PROTEOMICS"
10:50-11:10 Coffee break
13:05-14:00 Lunch break
14:00-17:30 Evening Session
MICROSYMPOSIUM "HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS"
15:50-16:10 Coffee break

House of Scientists, Small Conference Hall

9:00-12:50 Morning Session
GENE FUNCTION DISCOVERY AND SEARCH FOR NEW PHARMACEUTICAL TARGETS
10:50-11:10 Coffee break

12:30-14:00 Lunch break
14:00-17:25 Evening Session
EVOLUTIONARY BIOINFORMATICS
15:50-16:10 Coffee break

Institute of Cytology and Genetics, Conference Hall
10:00-14:10 Morning Session
GENETIC DIVERSITY OF LABORATORY ANIMALS IN ADDRESSING FUNDAMENTAL AND APPLIED PROBLEMS IN POSTGENOMIC BIOLOGY
11:30-11:50 Coffee break
14:10-15:30 Lunch break

Exhibition Centre, Conference Hall
14:00-17:05 Evening Session
COMPUTATIONAL INFERENCE OF NETWORKS FROM HIGH-THROUGHPUT EXPERIMENTAL DATA
15:20-15:50 Coffee break
Music Salon (room No. 220), House of Scientists
14:00-18:00 Evening Session
OPEN SEMINAR OF GERMAN/RUSSIAN VIRTUAL NETWORK OF BIOINFORMATICS "COMPUTATIONAL SYSTEMS BIOLOGY"
15:50-16:10 Coffee break
House of Scientists, Foyer of the Large Conference Hall
18:30-20:00 **POSTER SESSION AND COMPUTER DEMOS**

June 29, Friday *House of Scientists, Large Conference Hall*
9:30-13:10 Morning Session
MICROSYMPOSIUM "HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS"
11:15-11:40 Coffee break
13:05-14:10 Lunch break

House of Scientists, Small Conference Hall
9:00-13:30 Morning Session
MATHEMATICAL BIOLOGY AND SYSTEM MODELING
10:50-11:10 Coffee break
13:30-14:00 Lunch break

14:10-17:30 Evening Session
MICROSYMPOSIUM "HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS"
16:30-16:50 Coffee break

Institute of Cytology and Genetics, Conference Hall
14:00-17:50 Evening Session
COMPUTER BIOLOGY OF DEVELOPMENT
15:30-16:00 Coffee break
Exhibition Centre, Conference Hall

9:00-13:00	Morning Session
	SUPERCOMPUTER APPLICATIONS IN BIOINFORMATICS
11:00-11:20	Coffee break
12:40-14:00	Lunch break
14:00-17:50	Evening Session
	INTEGRATIVE BIOINFORMATICS AND INTELLIGENT KNOWLEDGE DISCOVERY/MANAGEMENT
15:30-15:50	Coffee break
	House of Scientists, Foyer of the Large Conference Hall
17:30-19:00	**POSTER SESSION AND COMPUTER DEMOS**
	House of Scientists, Small Conference Hall

19:00- 20:00 Closing Ceremony. Summaries from session chairpersons

VIII International Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology (BGRS\SB-2012)/
International Conference on Postgenomic Technology for Biomedicine (PTB-2012)

Novosibirsk, 25-29 June 2012 (Preliminary schedule)

Дата	Great Hall House of Scientists SB RAS	Small Hall House of Scientists SB RAS	Music Salon (room No. 220) of the House of Scientists SB RAS	Conference hall Inst Cytol@Genet SB RAS	Exhibition Centre SB RAS
June, 25 9-00-13-00	Registration				
14-00-19-00	Opening of the Conference plenary talks				
June, 26 9-00-13-00	MICRO SYMPOSIUM Computational and experimental genomics	Section Therapeutic proteins and nucleic acids			
14-00-19-00	MICRO SYMPOSIUM Computational and experimental genomics	Section Therapeutic proteins and nucleic acids			
June, 27 9-00-13-00	MICRO SYMPOSIUM Computational and experimental genomics	Section Bioinformatics and systems biology of gene expression regulation			Section Synthetic biology
14-00-19-00	MICRO SYMPOSIUM Computational and experimental proteomics	Section Bioinformatics and systems biology of gene expression regulation			Section Computational inference of networks from high-throughput experimental data
June, 28 9-00-13-00	MICRO SYMPOSIUM Computational and experimental proteomics	Section Gene function discovery and search for new pharmaceutical targets		MICRO SYMPOSIUM Genetic diversity of laboratory animals in addressing fundamental and applied problems in postgenomic biology	Section Bionano-technology for diagnosis and therapy
14-00-19-00	MICRO SYMPOSIUM Human genetics and personalized medicine: theoretical and experimental aspects	Section Evolutionary bioinformatics	Open seminar of German/Russian Virtual Network of Bioinformatics "Computational Systems Biology"	MICRO SYMPOSIUM Genetic diversity of laboratory animals in addressing fundamental and applied problems in postgenomic biology	Section Bionano-technology for diagnosis and therapy

June, 29 9-00-13-00	MICRO SYMPOSIUM Human genetics and personalized medicine: theoretical and experimental aspects	Section Mathematical Biology and System Modeling			Section Supercomputer applications in bioinformatics
14-00-19-00		MICRO SYMPOSIUM Human genetics and personalized medicine: theoretical and experimental aspects		Section Computer biology of development	Section Integrative Bioinformatics and Intelligent Knowledge Discovery/ Management

PLENARY SESSION

June 25, Monday *House of Scientists, Large Conference Hall* 13:20-19:00

Co-chairpersons:
Prof. Nikolay Kolchanov, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia
Prof. Valentin Vlassov, Institute of Chemical Biology and Fundamental Medicine, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia
Prof. Ralf Hofestaedt, Bielefeld University, AG Bioinformatics, Bielefeld, Germany

No.	Author(s) and Title of Talk	Timeline
1.	**Alistair Forrest** Unit Leader at RIKEN, Yokohama, Japan THE FANTOM5 PROJECT – A PROMOTER LEVEL EXPRESSION ATLAS USING SINGLE MOLECULE SEQUENCING	13:20-14:00
2.	**Egor Prokhorchouk** “Bioengineering” Center, RAS, Moscow, Russia EPIGENETICS- NEW CHALLENGES	14:00-14:40
3.	**Alexander G. Gabibov** Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia MECHANISMS OF ANTIGENS DEGRADATION	14:40-15:20
4.	**Stephan von Hörsten** Friedrich-Alexander-Universität Erlangen-Nürnberg, TRANSLATIONAL NEUROBIOLOGY OF NEURODEGENERATIVE AND NEUROPSYCHIATRIC DISORDERS: TRANSGENIC RAT AND MOUSE MODELS FOR AD, PD, SCA17, AND HD	15:20-16:00
	Coffee/tea break 16:00-16:20	
5.	**Sergei A. Nedospasov** Engelhardt Institute of Molecular Biology RAS, Lomonosov Moscow State University, Russia. German Rheumatism Research Center (DRFZ), a Leibniz Institute, Berlin, Germany. REVERSE GENETICS IN BIOLOGICAL AND IMMUNOLOGICAL STUDIES	16:20-17:00
6.	**Tatiana Nikolskaya** CEO, Founder, RosGenDiagnostics, Moscow, Russia CureMeDx, LLC, San Diego, CA ADVANCES OF SYSTEMS BIOLOGY IN TRANSLATIONAL RESEARCH AND PERSONALIZED MEDICINE	17:00-17:40
7.	**Andrey Rzhetsky** University of Chicago, USA COMPUTATIONAL ANALYSIS OF COMPLEX PHENOTYPES	17:40-18:20
8.	**Mathias Sprinzl** University of Bayreuth (Bayreuth), Germany PERSPECTIVES OF NUCLEIC ACID BIOSENSORS FOR MEDICAL APPLICATIONS ELECTRICALLY READABLE BIOCHIPS FOR RAPID RNA ANALYSIS	18:20-19:00

ORAL PRESENTATIONS

Dear speakers, please, plan your presentation time including 5 minutes for questions.

Only PowerPoint presentations made in Microsoft Office 2003, XP or earlier versions can be accepted. Use embedded pictures and animations only; picture and animation links to the Internet or to other files will not be accessible.
Slide projectors or overhead projectors are NOT available during the BGRS\SB'12 Conference.
Please, take into account that it will not be possible for you to load your presentation during the session by yourselves. Presentations are loaded on the main computer by the technician of the Organizing Committee only.

To ensure that the presentations are well prepared and compatible with the main presentation computer, we strongly advise you to bring your materials as PowerPoint files on USB device or CD disk to the Room no. 200 at the House of Scientists and check the presentation with the technician of the Organizing Committee **not later than 30 min** before the start time of the session where you are presenting. This will prevent any confusion when loading the presentations on the main computer.

You may also bring your laptop for copying your presentation to the main presentation computer. Use of your own laptop during your presentation is not recommended.

If you have any questions, please do not hesitate to contact the Organizing Committee in Room No. 200 at the House of Scientists.

June 26, Tuesday House of Scientists, Large Conference Hall

Morning Session
9:30-12:50

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL GENOMICS”

Co-chairpersons:

Dr. Victor Solovyev, Department of Computer Science, University of London, UK

Dr. Egor Prokhorchouk “Bioengineering” Center, RAS, Moscow, Russia

COMPUTATIONAL GENOMICS

No.	Author(s) and Title of Talk	Timeline
1.	**V. Solovyev[1],** I. Seledtsov[2], D. Vorobyev[2], P. Kosarev[2], V. Molodsov[2], N. Okhalin[2] [1] Department of Computer Science, Royal Holloway, University of London, UK; [2] Softberry Inc., 116 Radio Circle, Suite 400, Mount Kisco, NY, USA COMPUTATIONAL TOOLS FOR ANALYSIS NEXT GENERATION SEQUENCING DATA **KEYNOTE TALK**	9:30-10:00
2.	**I. Abnizova**, S. Leonard, T. Skelly and D. Jackson Wellcome Trust Sanger Institute, Hinxton, UK SYSTEMATIC ERRORS AND BIASES IN ILLUMINA SEQUENCING **KEYNOTE TALK**	10:00-10:30
3.	**S.M. Rastorguev**[1], A.V. Nedoluzhko[1], A.M. Mazur[1], N.M. Gruzdeva[1], S.V. Tsygankova[1], E.S. Boulygina[1], A.E. Barmintseva[2], N.S. Mugue[2], E.B. Prokhorchuk[1] [1] National Research Centre "Kurchatov Institute" (NRC "Kurchatov Institute"), Moscow, Russia [2] Russian Federal Research Institute of Fishery and Oceanography (VNIRO), Moscow, Russia POPULATION GENETIC ANALYSIS OF CASPIAN STURGEONS (*Acipencer gueldenstaedtii, Acipencer persicus*) USING NEXT GENERATION SEQUENCING AND CUSTOMIZED ILLUMINA GOLDENGATE GENOTYPING ASSAY	10:30-10:50
	Coffee/tea break 10:50-11:10	
4.	**R.Giegerich** Center of Biotechnology and Faculty of Technology, Bielefeld University SEARCHING FOR DISTANT HOMOLOGS OF SMALL, NON-CODING RNAS	11:10-11:35
5.	**A. Mazur,** A. Artemov ZAO “Genoanalytica”, Moscow, Russia NOVEL APPROACHES TO RNA SEQUENCING	11:35-12:00
6.	**A.V. Nedoluzhko**[1]**,** E.S. Pantiukh[2], S.M. Rastorguev[1], N.M. Gruzdeva[1], O.A. Shulga[3], E.B. Prokhortchouk [1,3], K.G. Skryabin[1,3] [1] National Research Centre "Kurchatov Institute" (NRC "Kurchatov Institute")**,** Moscow, Russia, [2] Lomonosov Moscow State University (MSU), Moscow, Russia, [3] Centre “Bioengineering” Russian Academy of Sciences, Moscow, Russia	12:00-12:25

	DEEP SEQUENCING CHRYSANTHEMUM microRNA ON DIFFERENT STAGES OF PLANT DEVELOPMENT	
7.	**Yu.V. Vyatkin**[1], D.N.Shtokalo[1,2,3], P.Kapranov[3], G.C.St.Laurent III[3*] [1] AcademGene LLC, Novosibirsk, Russia [2] A.P.Ershov Institute of Informatics Systems SB RAS, Novosibirsk, Russia [3] St.Laurent Institute, Providence, USA COMPUTATIONAL NEW SPLICE VARIANTS DISCOVERY USING SINGLE MOLECULE SEQUENCING TECHNOLOGY	12:25-12:50

12:50-14:00 Lunch break

Chairperson:
Dr. Igor I. Goryanin, Innovation Center "SKOLKOVO"

June 26, Tuesday House of Scientists, Large Conference Hall

Evening Session
14:00-17:25

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL GENOMICS”

Co-chairpersons:
Dr. Victor Solovyev, Department of Computer Science, University of London, UK
Dr. Egor Prokhorchouk “Bioengineering” Center, RAS, Moscow, Russia

COMPUTATIONAL GENOMICS

No.	Author(s) and Title of Talk	Timeline
1.	**E.Yu. Bragin,** V.V. Ashapkin, V.Yu. Shtratnikova, M.I. Schelkunov, D.V. Dovbnya, M.V. Donova. Innovative Technology Center “Biologically Active Compounds and Application”, Russian Academy of Sciences, Moscow. G.K.Skryabin Institute of Biochemistry & Physiology of Microorganisms, Russian Academy of Sciences, Pushchino, Moscow Region HIGH-THROUGHPUT SEQUENCING OF MYCOBACTERIUM STRAINS USED FOR STEROID COMPOUNDS BIOSYNTHESIS **KEYNOTE TALK**	14:00-14:30
2.	**E.S. Boulygina[1]**, A.V. Nedoluzko[1], S.V. Tsygankova[1], N.N.Tchekanov [2], A.M.Mazur [2], A.V. Artemov[3], E.B. Prokhortchouk[1,2], K.G. Skryabin[1,2] [1] National Research Center "Kurchatov Institute", Moscow, Russia [2] Centre “Bioengineering” of the Russian Academy of Sciences, Moscow, Russia [3] T-gene LTD, Dubna, Moscow region, Russia MASSIVE PARALLEL EXON SEQUENCING AS FUNDAMENTAL APPROACH IN STUDYING SNPS THAT CAN LEAD TO ALZHEIMER DISEASES **KEYNOTE TALK**	14:30-15:00
3.	**O.A. Mikhaylichenko[1,2],** A.Y. Goltsov[1,2,3], F.E. Gusev[1], D.A. Reshetov[1,2], T.V. Tyazhelova[1], T.A. Andreeva[1,3], N.R. Kaljina[1,3], A.P.Grigorenko[1,3,4], E.I. Rogaev[1,2,3,4] 1 Vavilov Institute of General Genetics, Moscow; [2] Lomonosov Moscow State University, [3] Research Center of Mental Health, Russian Academy of Medical Sciences, Moscow, Russia; [4] Brudnick Neuropsychiatric Research Institute, Department of Psychiatry, University of Massachusetts Medical School, 01604, MA, USA LARGE-SCALE AMPLICON TARGETING MASSIVE PARALLEL RE-SEQUENCING REVEALS NOVEL VARIANTS IN ALZHEIMER’S DISEASE GENES	15:00-15:20
	Coffee/tea break 15:20-15:50	
4.	**Kasianov A.S.**[1,2], Logacheva M.D.[3], Oparina N.J.[1], Penin A.A.[3] [1] Engelhardt Institute of Molecular Biology RAS, Moscow, Russia [2] Vavilov Institute of General Genetics RAS Moscow, Russia [3] Lomonosov Moscow State University, Moscow, Russia DE NOVO SEQUENCING, ASSEMBLY AND CHARACTERIZATION OF TRANSCRIPTOME IN TETRAPLOID PLANT CAPSELLA BURSA-PASTORIS	15:50-16:15

5.	**S.S. Pintus[1]**, M.G. Serrano[1], J.M. Alves[1,2], A. Matveyev[1], N. Sheth[1], A. Lara[1], V. Lee[1], V.N. Koparde[1], M.C. Rivera[1], L.J. Voegtly[1], T.J. Arodz[1], F. Maia da Silva[2], E. P. Camargo[2], M.M.G. Teixeira[2], G.A. Buck[1] [1]Virginia Commonwealth University, Center for the Study of Biological Complexity and the Departmnent of Microbiology and Immunology, Richmond VA, USA [2]Departamento de Parasitologia, Universidade de São Paulo, São Paulo, SP, Brazil COMPARATIVE GENOME ANNOTATION OF TRYPANOSOMATIDS	16:15-16:40
6.	**M.D.Logacheva[1,2,3],** R.A. Sutormin[2], S.A. Naumenko[2], N.V. Demidenko[2,4], D.V. Vinogradov[3], M.S. Gelfand[2,3], A.A. Penin[2,3,4] [1]A.N. Belozersky Institute of Physico-Chemical Biology, M.V. Lomonosov Moscow State University, Moscow, Russia [2]Faculty of Bioengineering and Bioinformatics, M.V. Lomonosov Moscow State University, Moscow, Russia [3]A.A. Kharkevich Institute for Information Transmission Problems, Russian Academy of Science, Moscow, Russia [4] Department of Genetics, Biological Faculty, M.V. Lomonosov Moscow State University, Moscow, Russia A DRAFT GENOME SEQUENCE OF TARTARY BUCKWHEAT, FAGOPYRUM TATARICUM**.**	16:40-17:05
7.	**M. Dyer** Ion Torrent, part of Life Technologies, San Francisco, CA, USA SEMICONDUCTOR SEQUENCING FOR LIFE (LIFE TECHNOLOGY).	17:05-17:25

June 27, Wednesday House of Scientists, Large Conference Hall

Morning Session
9:00-12:50

MICROSYMPOSIUM
“COMPUTATIONAL AND EXPERIMENTAL GENOMICS”

Co-chairpersons:
Dr. Egor Prokhorchouk “Bioengineering” Center, RAS, Moscow, Russia

Dr. Victor Solovyev, Department of Computer Science, University of London, UK

EXPERIMENTAL GENOMICS		
No.	Author(s) and Title of Talk	Timeline
1.	A.V. Mardanov, V.V. Kadnikov, V.M. Gumerov**, N.V. Ravin** Centre “Bioengineering” RAS, Moscow, Russia ADVANCES IN GENOMIC AND METAGENOMIC STUDIES OF EXTREMOPHILIC MICROORGANISMS **KEYNOTE TALK**	9:00-9:40
2.	**D. V. Semenov[1],** D. N. Baryakin[1], E. V. Brenner[1], A. M. Kurilshikov[1], V. V. Kozlov[2], Y. E. Narov[2], G. V. Vasiliev[3], L. O. Bryzgalov[3], E. D. Chikova[1], J. A. Filippova[1] E. V. Kuligina[1], V. A. Richter[1] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Novosibirsk Regional Cancer Centre, Novosibirsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia PROFILE OF THE CIRCULATING RNA IN APPARENTLY HEALTHY INDIVIDUALS AND NON-SMALL CELL LUNG CANCER PATIENTS OBTAINED WITH MASSIVELY PARALLEL SEQUENCING OF TOTAL BLOOD PLASMA RNA	9:40-10:00
3.	**E.Y. Rykova**[1], E.S. Morozkin[1], E.M. Loseva[1], K.N. Skvortsova[1], A.A. Ponomaryova[2], A.M. Kurilshikov[1], I.V. Morozov[1], O.E. Bryzgunova[1], A.A. Bondar[1], I.S. Zaporozhchenko[1], K.Y. Kapitskaya[3], T.L. Azhikina[3], N.V. Cherdyntseva[2], V.V. Vlassov[1], P.P. Laktionov[1] [1]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia [2]Cancer Research Institute, SB RAMS, Tomsk, Russia [3]Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, RAS, Moscow, Russia CIRCULATING DNA AN CANCER PATIENTS BLOOD: GENERAL CHARACTERISTICS AND WHOLE-GENOME ANALYSIS	10:00-10:20
4.	**A.N. Meshkov[1],** Z.B. Khasanova, N.V. Konovalova, T.I. Kotkina, I.V. Sergienko, Iu.A. Karpov, V.V. Kukharchuk, S.A. Boytsov[1]**.** Russian Cardiology Research Center, Moscow, Russia [1]National Research Center for Preventive Medicine Moscow, Russia GENOME-WIDE ASSOCIATION STUDY OF CARDIOVASCULAR DISEASE RISK FACTORS IN THE MOSCOW STUDY OF THE WESTERN DISTRICT	10:20-10:40

Coffee/tea break 10:40-11:00

5.	**L.O. Bryzgalov,** E.V. Antontseva, M.Yu. Matveeva, E.V. Kashina, A.G. Shilov, N.P. Bondar, T.I. Merkulova. Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia A NEW APPROACH TO IDENTIFY THE RSNPS IN THE HUMAN GENOME BASED ON CHIP-SEQ DATA	11:00-11:20
6.	**A. Baranova** Russian Center of Medical Genetics RAMS, Moscow, Russia School of Systems Biology, George Mason University, Fairfax, VA, USA BIOMARKER CHALLENGE: A CLOUD INSTEAD OF A SET OF THE VANTAGE POINTS	11:20-11:40
7.	**N. Koroban** Roche, Moscow, Russia ACTUAL APPLICATIONS AND PROSPECTS OF 454 SEQUENCING	11:40-12:00
	P. Natalin Life Technology, Moscow**,** Russia TRANSFORMING QPCR: ENABLING EXPERIMENTS NOT ACHIEVABLE IN THE PAST	12:00-12:20
8.	**N. Egorov** InterLabService, Moscow, Russia ILLUMINA - REACHING NEW HORIZONS IN NEXT GENERATION SEQUENCING	12:20-12:35
9.	**V. Zhernovkov** Helicon, Moscow, Russia REVIEW OF MODERN METHODS OF HIGH-PERFORMANCE SEQUENCING	12:35 - 12:50

13:00-14:00 Lunch break

June 27, Wednesday House of Scientists, Small Conference Hall

Morning Session
9:00-12:50

SECTION “BIOINFORMATICS AND SYSTEMS BIOLOGY OF GENE EXPRESSION REGULATION”

Co-chairpersons:
Dr. Edgar Wingender, University Medical Center Göttingen, Göttingen, Germany
Dr. Vsevolod Makeev, Vavilov Institute of General Genetics RAS, Moscow, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**Remi Houlgatte** INSERM UMR694, Centre Hospitalier Universitaire d’Angers, Angers, France META-ANALYSIS OF EXPRESSION PROFILING **KEYNOTE TALK**	9:00-9:40
2.	**H. Binder,** J. Galle, T. Rohlf, S. Prohaska, L. Hopp, L. Steiner, H. Wirth Interdisciplinary Centre for Bioinformatics, University Leipzig, Germany DISCOVERING THE EPIGENOME: GLOBAL MAPPING OF HISTONE MARKS AND MODELING TRANSCRIPTIONAL MEMORY	9:40-10:00
3.	**A. Klebanov[1,2],** T. Burdett[1], M. Kapushesky[1] [1]Functional Genomics Group, EMBL-EBI, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK [2]Research Centre for Technologies of Programming and Artificial Intelligence, National Research University of Information Technologies, Mechanics and Optics, St Petersburg, Russia DISTRIBUTED ATLAS: A RULE-BASED SYSTEM FOR QUERY FEDERATION OVER SEMANTICALLY ALIGNED GENE EXPRESSION DATA SOURCES	10:00-10:20
4.	**A.V. Klepikova**[1,3], M.D. Logacheva[2,3], A.A. Penin[1,3] [1]Department of Genetics, Biological Faculty, M.V. Lomonosov Moscow State University, Moscow, Russia, [2]A.N. Belozersky Institute of Physico-Chemical Biology, M.V. Lomonosov Moscow State University, Moscow, Russia, [3]Faculty of Bioengineering and Bioinformatics, M.V. Lomonosov Moscow State University, Moscow, Russia, THE LARGE-SCALE ANALYSIS OF ARABIDOPSIS THALIANA MUTANT LEL USING RNA-SEQ	10:20-10:40
5.	**U.Ye. Kairov**[1,2], A.Yu. Zinovyev[3], T.A. Karpenyuk[1], Ye.M. Ramanculov[2] [1]Kazakh National University after Al-Farabi, Almaty, Kazakhstan [2]National Center for Biotechnology of the Republic of Kazakhstan, Astana, Kazakhstan [3]Institute Curie, Paris, France NETWORK INTERPRETATION AND META-ANALYSIS OF INDEPENDENT COMPONENTS EXTRACTED FROM BREAST CANCER TRANSCRIPTOMES	10:40-11:00
	Coffee/tea break 11:00-11:20	
6.	Q. Li, J-Z. Zou, **I. Ernberg** Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet, Stockholm, Sweden	11:20-11:40

	INTER-CELLULAR NOISE AND TRANCRIPTIONAL CONTROL OF EPSTEIN-BARR VIRUS LATENCY PROGRAM SWITCHES IN HUMAN B CELL LINES	
7.	K.S. Shavkunov[1,2], M.N. Tutukina[1,2], I.S. Masulis[1,2], V.V.Panyukov[3], S.S. Kiselev[1,2], A.A. Deev[4], **O.N. Ozoline[1,2]** [1]Institute of Cell Biophysics RAS [2]Pushchino State Institute of Natural Sciences [3]Institute of Mathematical Problems of Biology RAS [4]Institute of Theoretical and Experimental Biophysics RAS, Pushchino, Moscow Region, Russia “PROMOTER ISLANDS” AS GENOMIC REGIONS WITH QUENCHED TRANSCRIPTION	11:40-12:00
8.	**D.N. Shtokalo[1,3],** O.V. Saik[2], G.St.Laurent III[3], A.Kel[4] [1]A.P.Ershov Institute of Informatics Systems SB RAS, Novosibirsk, Russia [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [3]St.Laurent Institute, Providence, RI, USA [4]Genexplain GmbH, Wolfenbuttel, Germany PATTERNS OF MIRNA BINDING SITES LOCATION IN 3`UTRs OF HUMAN TRANSCRIPTS	12:00-12:20
9..	**S.B. Orazova,** A.A. Bari, A.T. Ivashchenko al-Farabi Kazakh National University, Almaty, Kazakhstan PROPERTIES OF miR156a AND miR171a BINDING SITES IN PROTEIN-CODING SEQUENCE OF PLANT GENES	12:20-12:30
10.	**N.V. Demidenko[1,2],** A.A. Penin[1,2,3], M.D.Logacheva[2,3,4] [1]Department of Genetics, Biological faculty, M.V. Lomonosov Moscow State University, Moscow, Russia [2]Evolutionary Genomics Laboratory, Faculty of Bioengineering and Bioinformatics, M.V. Lomonosov Moscow State University, Moscow, Russia [3]A.A. Kharkevich Institute for Information Transmission Problems, Russian Academy of Science, Moscow, Russia [4] Department of Evolutionary Biochemistry, A.N. Belozersky Institute of Physico-Chemical Biology, M.V. Lomonosov Moscow State University, Moscow, Russia RNA-SEQ IDENTIFICATION AND ANALYSIS OF GENES CONTROLLING ABIOTIC STRESS RESPONSE IN BUCKWHEAT	12:30-12:40
11.	**V.A. Lyubetsky,** A.V. Seliverstov Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute), 19 Bolshoy Karetny per., Moscow, 127994, Russia MODELING RNA POLYMERASE INTERACTION IN PLASTIDS OF PLANTS, ALGAE AND MITOCHONDRIA OF CHORDATES: HUMAN BEARING THE MELAS MUTATION AND RAT WITH HYPOSECRETION OF THYROID HORMONE	12:40-12:50

12:50-14:00 Lunch break

June 27, Wednesday House of Scientists, Large Conference Hall

Evening Session
14:00-18:20

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL PROTEOMICS”

Co-chairpersons:
Dr. Vadim M. Govorun, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry of the RAS, Research Institute for Physico-Chemical Medicine, Moscow, Russia
Dr. Alexander G. Gabibov, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia

GENERAL AND MEDICAL PROTEOMICS		
No.	Author(s) and Title of Talk	Timeline
1.	**V.M. Govorun** Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS/Research Institute for Physico-Chemical Medicine, Moscow, Russia INTEGRATION OF –OMICS	14:00 – 14:30
2.	O.V. Tichonova, **V.G. Zgoda**, A.I. Archakov, H.V.Moskaleva Institute of Biomedical Chemistry RAMS im.V.N.Orehovicha, Moscow, Russia MASS SPECTROMETRY BASED APPROACH FOR THE CYTOCHROME P-450’S CONCENTRATION AND ACTIVITY DETERMINATION	14:30 – 14:50
3.	**D.G. Alexeev,** K.T. Momynaliev, O.V. Selezneva, I.A. Demina, O. Pobeguc, A.Tvardovsky, I.Altukhov, V.M. Govorun Research Institute for Physico-Chemical Medicine, Moscow, Russia SYSTEM BIOLOGY ANALYSIS OF HELICOBACTER PYLORI VIRULENCE AND ADAPTATION BASED ON PROTEOGENOMIC, TRANSCIPTOMIC AND METABOLOMIC ANALYSIS.	14:50 - 15:10
4.	**I.A.Demina, M.V.** Serebryakova, V. G. Ladygina, M. A. Rogova, I. G. Kondratov, A. N. Renteeva, V. M. Govorun Research Institute for Physical-Chemical Medicine of Ministry of Public Health of Russian Federation, Moscow, Russia PROTEOMIC OF MYCOPLASMAS: NANOFORMING *Mycoplasma gallisepticum*	15:10 - 15:30
5.	A.V. Tyakht, D.G. Alexeev, **A.S. Popenko**, M.S. Belenikin, I.A. Altukhov, A.V. Pavlenko, E.S. Kostryukova, O.V. Selezneva, A.K. Larin, I.Y. Karpova, V.M. Govorun Research Institute of Physico-Chemical Medicine FMBA, Moscow, Russia Moscow Institute of Physics and Technology, Dolgoprudny, Moscow Region, Russia Engelhardt Institute of Molecular Biology RAS, Moscow, Russia Institute of Bioorganic Chemistry of the RAS, Moscow, Russia RRC Kurchatov Institute, Moscow, Russia DEEP METAGENOMICS AND METAPROTEOMICS OF HUMAN GUT: DRAMAS AND DELIGHTS	15:30 - 15:50
	Coffee/tea break 15:50-16:20-	

6	**D.M.Graifer[1]**, K.N. Bulygin[1], Yu. S. Khairulina[1], D.E. Sharifulin[1], A.G. Ven'yaminova[1], L. Yu. Frolova[2], G.G. Karpova[1] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Engelhardt Institute of Molecular Biology RAS, Moscow, Russia STRUCTURAL AND FUNCTIONAL PROTEOMICS OF THE HUMAN PROTEIN SYNTHESIZING SYSTEM	16:20-16:40
7.	V.Zgoda, **O.Tikhonova**, S.Novikova, L.Kurbatov, A.Kopylov, N.Moskalyova, A.Archakov Orekhovich Institute of Biomedical Chemistry, Russian Academy of Medical Sciences SYSTEM ANALYSIS OF HUMAN CELL LINE: TRANSCRIPTOME, PROTEOME	16:40-17:00
8.	**R.H. Ziganshin,** S.I. Kovalchuk, G.P. Arapidi, I.V. Azarkin, V.M. Govorun, V.T. Ivanov Institute of Bioorganic Chemistry RAS, Moscow, Russia MASS-SPECTROMETRY-BASED IDENTIFICATION OF ENDOGENOUS PEPTIDES IN BLOOD SERUM	17:00-17:20
9.	**I.M. Larina[1]**, E.N. Nikolaev [2], L.H. Pastushkova[1], O.A. Valeeva[1], A.S. Kononihin[2], K.S. Kireev[3], E.S. Tiys[4], V.A. Ivanisenko[4], N.A. Kolchanov[4] [1]Institute of Medicobiologic Problems Russian Federation State Scientific Research Center RAS, Moscow, Russia [2]Emanuel Institute of Biochemical Physics RAS, Moscow, Russia [3]Gagarin Center of Cosmonauts Training, Star City, Russia [4]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia CHANGES IN PROTEIN COMPOSITION OF HUMAN URINE AFTER PROLONGED ORBITAL FLIGHTS	17:20-17:40
10.	**O.A. Snytnikova,[1,2],** L.V. Kopylova[1,2], I.V. Cherepanov[1,2], T.G. Duzhak[1,2], N.G. Kolosova[3], R.Z. Sagdeev[1], Y.P. Tsentalovich[1,2] [1]International Tomography Center SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia PROTEOMICS AND METABOLOMICS OF THE RAT LENS: ANALYSIS OF AGE AND CATARACT–SPECIFIC cataract-specific CHANGES	17:40-18:00
11	**I.A. Fesenko[1],** D.K. Slizhikova[1], A.V. Seredina[1], I.S. Mageyka[1] and V.M. Govorun[1,2] [1] Shemyakin-Ovchinnikov Institute of bioorganic chemistry RAS, Moscow, Russia [2] Institute of Physico-chemical medicine, Moscow, Russia MOSS PROTEOMICS AND PEPTIDOMICS. NEW INSIGHT IN THE OLD STORY. PEPTIDES IN THE STRESS ADAPTATION PROCESS	18:00 – 18:20

June 27, Wednesday House of Scientists, Small Conference Hall

Evening Session
14:00-18:10

SECTION “BIOINFORMATICS AND SYSTEMS BIOLOGY OF GENE EXPRESSION REGULATION”

Co-chairpersons:
Dr. Edgar Wingender, University Medical Center Göttingen, Göttingen, Germany
Dr. Vsevolod Makeev, Vavilov Institute of General Genetics RAS, Moscow, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**I.V. Kulakovskiy**[1,2], Y.A. Medvedeva[3], A.S. Kasianov[1,2], I.E. Vorontsov[4,1], U. Schaefer[3], V.B. Bajic[3], V.J. Makeev[1,2] [1]Vavilov Institute of General Genetics RAS, Moscow, Russia [2]Engelhardt Institute of Molecular Biology RAS, Moscow, Russia [3]King Abdullah University of Science and Technology, Thuwal, Jeddah, Saudi Arabia [4]Moscow Institute of Physics and Technology, Moscow, Russia COMPREHENSIVE COLLECTION OF HUMAN TRANSCRIPTION FACTOR BINDING SITE MODELS **KEYNOTE TALK**	14:00 – 14:40
2.	J. Keilwagen, J. Grau, I.A. Paponov, S. Posch, M. Strickert, **I. Grosse** Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany Institute of Computer Science, Martin Luther University Halle–Wittenberg, Halle, Germany Institute of Biology II, Albert–Ludwigs–University Freiburg, Freiburg, Germany DE-NOVO DISCOVERY OF DIFFERENTIALLY ABUNDANT DNA BINDING SITES INCLUDING THEIR POSITIONAL PREFERENCE **KEYNOTE TALK**	14:40 – 15:20
3.	**V.G. Levitsky**[1], D.Y. Oshchepkov[1], G.V. Vasiliev[1], N.I. Ershov[1], T.I. Merkulova[1], Kulakovskiy[2] I.V., Makeev[2] V.J. [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Genetics and Selection of Industrial Microorganisms, Moscow, Russia *IN SILICO* VERIFICATION OF CHIP-SEQ DATA	15:20-15:40
4.	**D.V. Antonets**[1], E.S. Cheryomushkin[2], Yu.V. Vyatkin[3] [1]State Research Center of Virology and Biotechnology “Vector”, Koltsovo, Russia [2]Ershov Institute of Informatics Systems, Novosibirsk, Russia [3]AcademGene LLC, Novosibirsk, Russia COMPARING HOEFFDING’S D MEASURE AND MAXIMAL INFORMATION COEFFICIENT FOR ASSOCIATION ANALYSIS	15:40-15:50

	E.A. Oshchepkova[1], E.V. Kashina [1], D.Y. Oshchepkov[1], E.V. Antontseva [1], V.A. Mordvinov[1], D.P. Furman[1,2] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia PROMOTERS OF THE GENES ENCODING THE KEY TRANSCRIPTION FACTORS IN THE INFLAMMATORY RESPONSE CONTAIN BINDING SITES FOR ARYL HYDROCARBON RECEPTOR	15:50-16:00
	I. Yevshin[1,2], Yu. Kondrakhin[1,3], R. Sharipov[1,4], T.Valeev[1,2], F. Kolpakov[1,3] [1] Institute of Systems Biology, Ltd, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia [3] Design Technological Institute of Digital Techniques, SB RAS, Novosibirsk, Russia [4] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia GTRD: ANNOTATING HUMAN GENOME WITH REGULATORY ELEMENTS USING CHIP-SEQ DATA	16:10-16:20
5.	E.A. Krutinina, G.G. Krutinin, S.G. Kamzolova, **A.A. Osypov** Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, 142290, Pushchino MR, Russia ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF TRANSCRIPTION FACTORS BINDING SITES	16:20-16:30
	Coffee/tea break 16:30-16:50	
6.	**E. Wingender**, M. Haubrock, J. Li Department of Bioinformatics, University Medical Center Göttingen, Göttingen, Germany A NEW COMPREHENSIVE CLASSIFICATION OF MAMMALIAN TRANSCRIPTION FACTORS USED FOR NETWORK CONSTRUCTION **KEYNOTE TALK**	16:50-17:20
7.	**E.V. Ignatieva** Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia TrDB: A DATABASE OF THE HUMAN, MOUSE, AND RAT TRANSCRIPTIONAL REGULATORS AND ITS POTENTIAL APPLICATIONS IN SYSTEMS BIOLOGY	17:20-17:30
8.	**A.L. Chernobrovkin**, V.G. Zgoda, A.V. Lisitsa and A.I. Archakov Institute of Biomedical Chemistry RAMS, Moscow, Russia COMPREHENSIVE ANALYSIS OF UNIDENTIFIED LC-MS FEATURES FOR INVESTIGATING PROTEINS DIVERSITY IN HIGH-THROUGHPUT PROTEOMICS EXPERIMENTS	17:30-17:40
9.	**R. te Boekhorst**[1], S. Beka[1], I. Abnizova[2] [1]School of Computer Science, University of Hertfordshire, Hatfield, UK [2]Wellcome Trust Sanger Institute, Hinxton, UK THE LOCATION OF T1 DIABETES ASSOCIATED SNPs IN REGULATORY REGIONS	17:40-17:50
10	**N.S. Khlopova**[1], T.T. Glazko[1], D. Guiatti[2], B. Stefanon[2] [1]Russian State Agrarian University – MTAA named after K.A.Timiryazev, Moscow, Russia [2]University of Udine, Italy ASSOCIATIONS BETWEEN PROMOTER POLYMORPHISMS IN KEY GENES OF LIPID METABOLISM AND MIOGENESIS AND ECONOMICALLY VALUABLE TRAITS IN PIGS	17:50-18:10

June 27, Wednesday Exhibition Centre SB RAS, Conference Hall

Evening Session
14:00-17:55

COMPUTATIONAL INFERENCE OF NETWORKS FROM HIGH-THROUGHPUT EXPERIMENTAL DATA

Co-chairpersons:
Prof. Dr. Lars Kaderali, Dresden University of Technology, Medical Faculty Carl Gustav Carus, Institute for Medical Informatics and Biometry, Dresden, Germany

Dr. Bettina Knapp, Heidelberg University, BioQuant BQ26, Heidelberg, Germany; Dresden University of Technology, Medical Faculty Carl Gustav Carus, Institute for Medical Informatics and Biometry, Dresden, Germany

No.	Author(s) and Title of Talk	Timeline
1.	**T. Beissbarth** University of Goettingen, Goettingen, Germany MODELLING DRUG RESISTANCE IN BREAST CANCER THROUGH NETWORK RECONSTRUCTION BASED ON LONGITUDINAL PROTEIN ARRAY DATA **KEYNOTE TALK**	14:00 – 14:40
2.	**B. Knapp[1,2],** J. Mazur[1,2], L. Kaderali[1,2] [1]Heidelberg University, ViroQuant Research Group Modeling, BioQuant BQ26, Heidelberg, Germany. [2]Dresden University of Technology, Medical Faculty Carl Gustav Carus, Institute for Medical Informatics and Biometry, Dresden, Germany. INFERENCE OF SIGNALING NETWORKS USING A LINEAR MODEL	14:40 – 14:55
3.	**C. Gilliam[1],** S. Balasubramanian[1], B.Q. Xie[1], D. Sulakhe[1], E. Berrocal[1], N. Maltsev[1], D. Boernigen-Nitsch [2], C. Chitturi[3], A. Paciorkowski[4], W. Dobyns[4] [1]The University of Chicago, IL, USA [2]Harvard School of Public Health, Boston, MA, USA [3]Amrita University, Amritapuri, Kerala, India [4]University of Washington, Seattle, WA, USA SYSTEMS BIOLOGY ANALYSIS OF COMPLEX DISORDERS	14:55-15:20
	Coffee/tea break 15:20-15:40	
5.	**Y.L. Orlov[1]**, G. Li[3], R. Auerbach[4], K.S. Sandhu[3], X. Ruan[3], M.J. Fullwood[3], N.L. Podkolodnyy[1], D.A. Afonnikov[1,2], E. Liu[3], C.L. Wei[3], M. Snyder[4], Y. Ruan[3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Genome Institute of Singapore, Singapore [4]Stanford University, Stanford, CA, USA 3D CHROMOSOME CONTACTS AND CHROMATIN INTERACTIONS REVEALED BY SEQUENCING	15:40-16:05
5.	V.V. Chernova[1,2], **A.A. Ermakov[1]**, A.V. Doroshkov[1], N.A. Omelyanchuk[1], V.V. Mironova[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia ANALYSIS OF TRANSCRIPTIONAL AND POSTTRANSCRIPTIONAL	16.05-16.30

	REGULATION OF AUXIN CARRIER *AtPIN1*	
6.	**I.L. Stepanenko**, O.G. Smirnova Institute of Cytology & Genetics SB RAS, Novosibirsk, Russia DYNAMICAL AND STRUCTURAL ANALYSIS OF AN APOPTOSIS NETWORK IN HEPATITIS C	16:30-16:50
7.	**M. Pyatnitskiy**[1,2]**,** I.Mazo[1,3], N.Daraselia[3], M.Shkrob[3], E. Kotelnikova[1,4] [1]Ariadne Diagnostics LLC, Rockville, USA [2]Institute of Biomedical Chemistry, RAMS, Moscow, Russia [3]Reed Elsevier, Amsterdam, Netherlands [4]Institute for Information Transmission Problems, RAS, Moscow, Russia CLUSTER ANALYSIS OF SIGNIFICANT REGULATORS AS NEW APPROACH TO PATIENTS SUBTYPING	16:50-17:15
8.	**A.L. Proskura**[1]**,** I.A. Malakhin[1, 2], T.A. Zapara[1] [1]Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia [2]The Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia MECHANISMS OF AMPA RECEPTOR TRAFFICKING AS A BASE OF CHANGING THE SYNAPTIC EFFICIENCY	17:15-17:35
	K. Schleich[1,2], U. Warnken[1], N. Fricker[1,2], M. Schnölzer[1], P.H. Krammer[1], **I.N. Lavrik**[1,2,3] [1]German Cancer Research Center (DKFZ), Heidelberg, Germany [2]Bioquant, Heidelberg, Germany [3]Institute of Experimental Internal Medicine, Otto von Guericke University, Magdeburg, Germany TOWARDS UNDERSTANDING OF APOPTOSIS REGULATION BY SYSTEMS BIOLOGY	17:35-17:55

June 28, Thursday House of Scientists, Large Conference Hall

Morning Session
9:00-13:05

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL PROTEOMICS”

Co-chairpersons:
Dr. Vladimir M. Sobolev Weizmann Institute of Science, Rehovot, Israel
Dr. Roman G. Efremov Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia

	COMPUTATIONAL PROTEOMICS	
No.	Author(s) and Title of Talk	Timeline
1.	**V.M. Sobolev** Weizmann Institute of Science, Rehovot, Israel RESIDUES FORMING FUNCTIONAL SITES IN PROTEINS ARE DISPROPORTIONALLY ASSOCIATED WITH HUMAN DISEASE-RELATED SNPS: A CASE STUDY OF METAL BINDING SITES” **KEYNOTE TALK**	9:00-9:35
2.	**V.A. Palyulin**, D.S. Karlov, E.V. Radchenko, N.S. Zefirov, V.M. Pentkovski M.V. Lomonosov Moscow State University, Moscow, Russia MOLECULAR MODELING OF NMDA RECEPTOR	9: 35-9:55
3.	**E.A. Aksianov,** A.V.Alexeevski A.N. Belozersky Institute and Faculty of Bioengineering and Bioinformatics, Moscow, Russia M.V. Lomonosov Moscow State University/Scientific-Research Institute for System Studies, Russian Academy of Sciences, Moscow, Russia ARCHIP: DETECTOR OF ARCHITECTURES IN 3D PROTEIN STRUCTURES	9:55-10:15-
4.	**M. Parsa,** Z. Pashandi, R. Mobasseri, S.S.Arab Institute for Research in Fundamental Sciences IPM / Tarbiat Modares University TMU, Tehran, Iran PUTRACER: A NOVEL METHOD FOR IDENTIFICATION OF CONTINUOUS-DOMAINS IN MULTI-DOMAIN PROTEINS	10:15 – 10:35
5.	**L. Kopylova** Bruker Daltonics, Novosibirsk, Russia NEWEST BRUKER DALTONICS DEVELOPMENTS IN MASS-SPECTROMETRY	10:35-10:50
	Coffee/tea break 10:50-11:10	
6.	**R.G. Efremov**, A.A. Polyansky, A.O. Chugunov, D.E. Nolde, V.M. Pentkovsky Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia PROTEIN-PROTEIN AND PROTEIN-MEMBRANE RECOGNITION: A COMPUTATIONAL VIEW **KEYNOTE TALK**	11:10-11:45
7.	**P.H. Nguyen** Institute de Biologie Physico-Chimique, Paris, France COMPUTER SIMULATIONS OF PROTEIN AGGREGATION	11:45-12:05
8.	**S.O. Garbuzynskiy**, D.N. Ivankov, N.S. Bogatyreva, A.V. Finkelstein Institute of Protein Research Russian Academy of Sciences, Pushino, Moscow	12:05-12:25

	region, Russia GOLDEN TRIANGLE” FOR FOLDING RATES OF GLOBULAR PROTEINS?	
9.	I. V. Kalgin, **S. F. Chekmarev**. Novosibirsk State University, Novosibirsk, Russia Kutateladze Institute of Thermophysics SB RAS, Novosibirsk, PROTEIN FOLDING TURBULENCE	12:25 – 12:45
10.	**A.P. Polyansky**, P.E. Volynsky, R.G. Efremov Max F. Perutz Laboratories, University of Vienna, Austria Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia MULTISTATE CONFIGURATION OF TRANSMEMBRANE PEPTIDE HELICAL DIMERS CONTROLLED BY THE HOST MEMBRANE	12:45 – 13:05

13:05-14:00 Lunch break

June 28, Thursday House of Scientists, Small Conference Hall

Morning Session
9:00-12:50

SECTION “GENE FUNCTION DISCOVERY AND SEARCH FOR NEW PHARMACEUTICAL TARGETS”

Co-chairpersons:
Dr.Elena I. Schwartz, Ariadne Diagnostics LLC, Rockville, USA
Dr. Frank Eisenhaber, Bioinformatics Institute (BII) Agency for Science, Technology and Research (A*STAR), Singapore

No.	Author(s) and Title of Talk	Timeline
1.	**N. Belousova** Department of Experimental Diagnostic Imaging MD Anderson Cancer Center University of Texas, USA DEVELOPMENT OF ADENOVIRUS- BASED TARGETED GENE DELIVERY TECHNOLOGY **KEYNOTE TALK**	9:00-9:35
2.	**M.Y. Pakharukova[1]**, N.I. Ershov[1], V.A. Vavilin[2], E.V. Vorontsova[1], A.V. Katokhin[1], T.G. Duzhak[3], T.I. Merkulova[1], V.A. Mordvinov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Molecular Biology and Biophysics SB RAMS, Novosibirsk, Russia [3]International Tomography Center SB RAS, Novosibirsk, Russia ORGANIZATION OF XENOBIOTIC-METABOLIZING SYSTEM PHASE 1 IN OPISTHORCHIS FELINEUS (TREMATODA, PLATYHELMINTHES).	9:35-10:00
3.	D. Simanov[1], I.Sormacheva[2], S. Mouton[1], W. Arindrarto[1], K. Van Nies[1], K. de Mulder[1], I. Mellart-Straver[1], **E. Berezikov**[1] [1]Hubrecht Institute and University Medical Center Utrecht, Utrecht, The Netherlands [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia IDENTIFICATION OF STEM CELL GENES AND DRUGS THAT AFFECT REGENERATION IN THE FLATWORM MACROSTOMUM LIGNANO	10:00-10:25
4.	S. Gastaldello, S. Callegari, G. Coppotelli, S. Hildebrand, **M.G. Masucci** Department of Cell and Molecular Biology, Karolinska Institutet, Stockholm, Sweden. CONTROL OF CULLIN-RING UBIQUITIN LIGASE ACTIVITY BY THE EPSTEIN-BARR VIRUS ENCODED DENEDDYLASE BPLF1	10:25 – 10:50
	Coffee/tea break 10:50-11:10	
5.	**P. Spitali[1]**, M. Hiller[1], V. Nadarajah[1], C. Martin[1], S. Oonk[1], Y. van der Burgt[2], J.T. den Dunnen[1], G.J. van Ommen[1], A. Aartsma-Rus[1] and P.A.C. ‘t Hoen[1] [1]Department of Human Genetics, Leiden University Medical Center, Leiden, The Netherlands; [2]Department of Parasitology, Leiden University Medical Center, Leiden, The Netherlands DISCOVERY AND VALIDATION OF SERUM BIOMARKERS FOR MONITORING OF DISEASE PROGRESSION AND THERAPEUTIC RESPONSE IN DUCHENNE MUSCULAR DYSTROPHY. **KEYNOTE TALK**	11:10-11:35
6.	**E.R. Zabarovsky**	11:35-

	Karolinska Institute and Linkoping University, Stockholm, Sweden IDENTIFICATION OF NEW METHYLATION-REGULATED GENES AS MOLECULAR TARGETS FOR PHARMACEUTICAL INTERVENTION AND DIAGNOSIS BASED ON NOTI MICROARRAYS	12:00
7.	**D.A. Afonnikov**[1,2], V.A. Ivanisenko[1], E.V. Ignatyeva[1], I.V Medvedeva[1], P.S. Demenkov[1], T.V. Ivanisenko[1], A.R. Shah[3], S. Ramachandran[3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia, [3]CSIR-Institute of Genomics and Integrative Biology, Delhi, India ANALYSIS OF SEQUENCE FEATURES SPECIFYING THE ADHESION ABILITY OF INFLUENZA A VIRUS NEURAMINIDASE AND HEMAGGLUTININ	12:00- 12:25-
8.	M. Pyatnitskiy*[1,2], E. Kotelnikova[1,3], M. Shkrob[4], A. Ferlini[5], N.Daraselia[4], I.Mazo[1,4], **E. Schwartz**[1] [1]Ariadne Diagnostics LLC, Rockville, USA [2]Institute of Biomedical Chemistry, RAMS, Moscow, Russia [3]Institute for Information Transmission Problems, RAS, Moscow, Russia [4]Reed Elsevier, Amsterdam, Netherlands [5]Department of Experimental and Diagnostic Medicine, University of Ferrara, Ferrara, Italy NOVEL APPROACH TO META-ANALYSIS OF MICROARRAY DATASETS FOR IDENTIFICATION OF NEW BIOMARKERS AND POTENTIAL DRUG TARGETS	12:25- 12:50

12:30-14:00 Lunch break

June 28, Thursday Institute of Cytology and Genetics**,** Conference Hall

Morning Session
10:00-14:10

MICROSYMPOSIUM
“GENETIC DIVERSITY OF LABORATORY ANIMALS IN ADDRESSING FUNDAMENTAL AND APPLIED PROBLEMS IN POSTGENOMIC BIOLOGY”

Chairman:

Dr. Mikhail P. Moshkin, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**J. Guillen** European Branch of AAALAC, Pamplona, Spain CURRENT STANDARDS OF LABORATORY ANIMAL CARE AND USE	10:00-10:30
2.	**J-B Prins** Leiden University Medical Center, Leiden, Holland GENETIC AND PHENOTYPIC CHARACTERISATION A MUST IN TRANSGENIC COLONY MANAGEMENT	10:30-11:00
3.	**A.N. Murashov** Institute of Bioorganic Chemistry RAS, Puschino, Russia AAALAC ACCREDITATION AND GLP PRECLINICAL TESTING (PRACTICAL ADVICES)	11:00-11:30
	Coffee/tea break 11:30-11:50	
4.	**S. von Hörsten** Friedrich-Alexander-Universität Erlangen-Nürnberg Franz-Penzoldt-Center - Experimentelle Therapie, Erlangen, Germany RODENT PHENOTYPING: "COMPREHENSIVE PHENOTYPING OF RODENTS: CLASSICAL AND AUTOMATED APPROACHES IN TRANSLATIONAL RESEARCH**”**	11:50-12:20
5.	**E. Wenzler** MBA, Deputy Sales Director Eastern Europe & Middle East, Germany INNOVATIVE METHODS FOR BEHAVIORAL ANALYSIS AND PHENOTYPING OF ANIMALS	12:20-12:40
6.	**S.A. Nedospasov** Engelhardt Institute of Molecular Biology RAS, A.N. Belozersky Institute of Physico-Chemical Biology MSU, Russia MOUSE MODELS TO STUDY PHYSIOLOGICAL FUNCTIONS OF TUMOR NECROSIS FACTOR AND LYMPHOTOXIN	12:40-13:10
7.	**M.P. Moshkin** Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia SPF-VIVARIUM IC&G SB RAS AS FACILITY FOR PRE-CLINICAL STUDIES	13:10-13:40
8.	**E. I. Fateeva** Center for Preclinical Studies “MBC Generium, Ltd”, Pokrov, Russia IMPACT OF MICROBIOLOGICAL STATUS OF LABORATORY ANIMALS ON THE EXPERIMENTAL RESULTS: WHY WE NEED HEALTH CONTROL?	13:40-14:10

14:10-15:30 Lunch break	
Round Table INTERNATIONAL STANDARDS OF BIODIVERSITY MANAGEMENT OF LABORATORY ANIMALS AND THE RUSSIAN EXPERIENCE IN THIS AREA	15:30-17:30

June 28, Thursday House of Scientists, Large Conference Hall

Evening Session
14:00-17:30

MICROSYMPOSIUM “HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS”

Co-chairpersons:
Dr. Alexander Kel, GeneXplain Inc., Germany
Dr. Yury Aulchenko, Institute of Cytology and Genetics, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**Diego Fabregat-Traver** RWTH Aachen FAST SOLUTIONS FOR STATISTICAL GENOMICS THROUGH A DOMAIN-SPECIFIC COMPILER **KEYNOTE TALK**	14:00 – 14:30
2.	**Felix Agakov** University of Edinburgh, UK APPLICATIONS OF MACHINE LEARNING TO PERSONALIZED MEDICINE **KEYNOTE TALK**	14:30 – 15:00
3.	**Nikolay Yankovsky** Vavilov Institute of General Genetics, Russia "GENETIC AND ENVIRONMENTAL FACTORS OF HEALTH OF HEALTHY PEOPLE: HOW TO FIND THEIR BY MEANS OF COMPUTATIONAL BIOLOGY METHODS?" **KEYNOTE TALK**	15:00-15:30
	Coffee/tea break 15:30-16:10	
4.	**Alexander Kel** GeneXplain Inc., Germany CLOUD PERSONALIZED DRUG DISCOVERY.	16:10-16:30
5.	**Vladimir Poroikov** Biomedical Chemistry Institute of the Russian Medical Sciences Academy, Russia COMPUTER METHODS FOR SEARCH OF DRUGS FOR PERSONALIZED THERAPY OF MULTIFACTORIAL DISEASES	16:30-16:50
6.	**Anastasia Bakulina** State Research Center of Virology and Biotechnology “Vector”, Koltsovo, Russia Software. A SIMPLE PERSONAL GENOME VIEWER	16:50-17:00
7.	**Fedor Kolpakov** Institute of Systems Biology, Ltd, Novosibirsk, Russia Software. DEVELOPMENT OF THE SOFTWARE COMPLEX “GENETICS” FOR SUPPORT INVESTIGATIONS IN MEDIC GENETICS	17:00-17:10
8.	**A. Tchourbanov** Beijing Institute of Genomics, Beijing, China PREVENTING COMMON HEREDITARY DISORDERS THROUGH TIME-SEPARATED TWINNING	17:10-17:30

June 28, Friday House of Scientists, Small Conference Hall

Evening Session
14:00-17:25

SECTION "EVOLUTIONARY BIOINFORMATICS"

Co-chairpersons:
Dr. Igor B. Rogozin, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia/NCBI/NLM/NIH, Bethesda MD, USA
Dr. Dmitri A. Afonnikov, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**A. Tchourbanov** Beijing Institute of Genomics (BIG), Beijing, P.R.China HIGH THROUGHPUT SSR CHARACTERIZATION AND LOCUS DEVELOPMENT FROM NEXT GEN SEQUENCING DATA **KEYNOTE TALK**	14:00 – 14:35
2.	**N. A. Zaytseva**[1], F. A. Kondrashov[2], P. K. Vlasov[2] [1]Siberian Federal University, Krasnoyarsk, Russia [2]Centre for Genomic Regulation, Barcelona, Spain EVOLUTION OF MITOCHONDRIAL TRNAS	14:35 – 15:00
3.	S. Yegorov, **S.V. Good** University of Winnipeg, Winnipeg, Manitoba, Canada USING PALEOGENOMICS TO STUDY THE ORIGIN AND MECHANISM OF DIVERSIFICATION IN VERTEBRATES: THE CASE OF THE RELAXIN FAMILY PEPTIDES AND THEIR RECEPTORS	15:00-15:25
4.	**K.V. Gunbin**[1]**,** D.A. Afonnikov[1], N.A. Kolchanov[1], A.P. Derevyanko[2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Archeology and Ethnography SB RAS, Novosibirsk, Russia IMPORTANT ROLE OF THE miRNA CHANGES IN THE HOMO NEANDERTHALENSIS AND HOMO DENISOVA EVOLUTION	15:25 – 15:50
	Coffee/tea break 15:50-16:10	
5.	**N. Oparina**[1,2], M. Zharkova[2], A. Speranskaya[1], A. Veselovsky[2] [1]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia [2]Orekhovich Institute of Biomedical Chemistry of the Russian Academy of Medical Sciences, Moscow, Russia CYTOCHROME P450 SUPERFAMILY IN VERTEBRATES: EVOLUTIONARY PATHS OF XENOBIOTIC CYP450 AND ENVIRONMENTAL «LIFESTYLES»	16:10-16:35
6.	**D. G. Naumoff** Winogradsky Institute of Microbiology RAS, Moscow, Russia EVOLUTION OF THE α-L-RHAMNOSIDASES: HISTORY OF THE LATERAL GENE TRANSFERS AND THE GENE DUPLICATIONS	16:35-17:00
7.	**E.V. Kiseleva**[1], J.Fiserova[2], M.W. Goldberg[2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Durham University, UK EVOLUTIONARY CONCERVATION OF NUCLEAR PORE ORGANIZATION AND COMPOSITION	17:00-17:25

June 28, Friday Music Salon (room No. 220), House of Scientists SB RAS

Evening Session
14:00-18:00

Open seminar of German/Russian Virtual Network of Bioinformatics
"COMPUTATIONAL SYSTEMS BIOLOGY"

Co-chairpersons:
Dr. Ralf Hofestaedt, Bielefeld University, AG Bioinformatics, Bielefeld, Germany
Dr. Alexey V. Kochetov, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Dr. Vladimir A. Ivanisenko, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**N.A. Kolchanov** Institute of Cytology & Genetics, Novosibirsk, Russia WELCOME SPEECH	14:00 – 14:10
2.	**R. Hofestaedt** Bielefeld University, Bielefeld, Germany INTEGRATION	14:10 – 14:20
3.	**V.A. Ivanisenko** Institute of Cytology & Genetics, Novosibirsk, Russia JOINT PROJECTS	14:20 – 14:35
4.	**H. Goetz** tdb Software Service GmbH, Schwabach, Germany METAGENE - INFORMATION SYSTEM FOR RARE METABOLIC DISEASES	14:35 – 14:55
5.	**B. Sommer** Bielefeld University, Bielefeld, Germany INTERGRATIVE CELL MODELING USING DATA INTEGRATION AND TEXT MINING APPROACHES	14:55-15:15
6.	**Yu. L. Orlov** Institute of Cytology & Genetics, Novosibirsk, Russia TRANSCRIPTION FACTOR BINDING SITES ANALYSIS FROM CHIP-SEQ DATA: MOTIFS AND CO-MOTIFS	15:15-15:30
7.	**I. Grosse** Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany DE-NOVO MOTIF DISCOVERY FROM CHIP-SEQ AND RNA-SEQ DATA.	15:30-15:50
	Coffee/tea break 15:50-16:10	
8.	**A.O. Bragin** Institute of Cytology & Genetics, Novosibirsk, Russia APPLICATION OF CONFORMATIONAL PEPTIDES FOR ANALYSIS OF ALLERGENIC PROTEINS	16:10-16:25
9.	**D. Braun** Bielefeld University, Bielefeld, Germany *to be specified*	16:25-16:40
10.	**I.V. Medvedeva** Institute of Cytology & Genetics, Novosibirsk, Russia INFLUENCES OF PROTEIN FUNCTIONAL SITES ENCODING	16:40-16:55

	FEATURES ON PROTEIN EVOLUTION IN EUKARYOTA	
11.	**T.V. Ivanisenko** Institute of Cytology & Genetics, Novosibirsk, Russia RECONSTRUCTION OF THE ASSOCIATIVE GENETIC NETWORKS BASED ON INTEGRATION OF AUTOMATED TEXT-MINING METHODS AND PROTEIN-LIGAND INTERACTIONS PREDICTION	16:55-17:10
12.	**E.S. Tiys** Institute of Cytology & Genetics, Novosibirsk, Russia STRUCTURE-FUNCTIONAL ORGANIZATION OF THE ASSOCIATIVE GENETIC NETWORKS	17:10-17:25
13.	**DISCUSSION**	17:25-18:00

June 29, Friday House of Scientists, Large Conference Hall

Morning Session
9:30-13:05

MICROSYMPOSIUM "HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS"

Co-chairpersons:
Dr. Mikhail Voevoda, Institute of Cytology and Genetics, Novosibirsk, Russia
Dr. Maxim Filipenko, Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia
Dr. Valery Puzyrev, Research Institute of Medical Genetics SB RAMS, Tomsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**Lina Zgaga** University of Zagreb, Zagreb, Croatia COMBINED GENOMICS AND GLYCOMICS APPROACH TO BIOMARKER DISCOVERY **KEYNOTE TALK**	9:30-10:00
2.	**Valery Puzyrev** Research Institute of Medical Genetics SB RAMS, Tomsk, Russia GENETIC SUSCEPTIBILITY PROFILE FOR COMORBIDITY VARIANTS OF MULTIFACTORIAL DISEASES	10:00-10:20
3.	**Mikhail Voevoda** Institute of Cytology and Genetics, Novosibirsk, Russia PERSONALIZED GENOMIC MEDICINE AND MODERN INFORMATION TECHNOLOGIES	10:20-10:40
4.	**Maxim Filipenko** Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia MY EXOME	10:40 – 11:00
5.	**Andrey Verner** BioRad, Moscow, Russia DROPLET DIGITAL PCR. HOW TO USE NEXT LEVEL OF QUANTIFICATION IN PERSONALIZED MEDICINE?	11:00 – 11:15
	Coffee/tea break 11:15-11:40	
6.	**Alexander Polyakov** Research Center for Medical Genetic, Moscow, Russia PERSONALIZED MEDICINE IN MONOGENIC PATHOLOGY	11:40-12:10
7.	**Valery Aushev** Institute of Carcinogenesis of N.N. Blokhin Russian Oncological Science Center RAMS, Russia CIRCULATING MICRORNAS AS POTENTIAL BIOMARKERS OF LUNG CANCER	12:10-12:30
8.	**Vladimir Maksimov** Institute of Therapy, Novosibirsk, Russia SELF-DESCRIPTIVENESS OF GWAS-IDENTIFIED GENETIC MARKERS OF COMMON DISEASES IN RUSSIAN POPULATION.	12:30-12:50

9.	**Ludmila Filatova** BioChimMak, Moscow, Russia Using of aCGH technology in personalized medicine	12:50 – 13:05

13:05-14:10 Lunch break

June 29, Friday House of Scientists, Small Conference Hall

Morning Session
9:00-13:30

SECTION “MATHEMATICAL BIOLOGY AND SYSTEM MODELING”

Co-chairpersons:
Dr. Vladimir P. Golubyatnikov, Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia
Dr. AlexanderV. Ratushny, Institute for Systems Biology, Seattle, WA, USA

No.	Author(s) and Title of Talk	Timeline
1.	**S.I. Bartsev** Institute for Biophysics SB RAS, Krasnoyarsk, Russia HEURISTIC NEURAL NETWORK MODELS IN THE INVESTIGATION OF COMPLEX BIOLOGICAL SYSTEMS **KEYNOTE TALK**	9:00-9:25
2.	**V.A. Likhoshvai** Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia MATHEMATICAL BIOLOGY OF GENE **KEYNOTE TALK**	9:25-9:50
3.	A.A.Akinshin[1], Yu.A.Gaidov[2], **V.P.Golubyatnikov[3],** I.V.Golubyatnikov[3] [1]Altai State Technical University, Barnaul, Russia [2] Novosibirsk State Pedagogical University, Novosibirsk, Russia [3] Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia NON-UNIQUENESS OF CYCLES IN GENE NETWORKS MODELS	9:50-10:10
4.	A.A. Evdokimov., **A.L. Perezhogin**, A.A. Semenov Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia Institute for System Dynamics and Control Theory SB RAS, Irkutsk, Russia MATHEMATICAL METHODS FOR ANALYZING THE DYNAMICS OF THE FUNCTIONING OF DISCRETE MODELS OF GENE NETWORKS.	10:10 – 10:30
5.	C.Maj[1,2], E.Mosca[1], I.Merelli[1], G.Mauri[2], **L.Milanesi[1]** [1] Institute for Biomedical Technologies CNR, Milano, Italy [2] University of Milano-Bicocca, Milano, Italy IDENTIFICATION OF THE KEY COMPONENTS TO CONTROL THE BEHAVIOUR OF A COMPLEX PATHWAY: A STUDY ON A MODEL OF MITOCHONDRIAL BIOENERGETICS	10:30 – 10:50
	Coffee/tea break 10:50-11:10	
6.	**A.V. Ratushny,** R.A. Saleem, K. Sitko, S.A. Ramsey, J.D. Aitchison Institute for Systems Biology, Seattle, WA, USA Seattle Biomedical Research Institute, Seattle, WA, USA ASYMMETRICALLY SELF-UPREGULATED (ASSURE) BIOMOLECULAR SYSTEMS	11:10-11:30
7.	J.C.J. Ray[1,2], **O.A. Igoshin[1]** [1]Department of Bioengineering, Rice University, Houston, Texas [2]Department of Systems Biology, UT MD Anderson Cancer Center, Houston, Texas INTERPLAY OF GENE EXPRESSION NOISE AND ULTRASENSITIVE DYNAMICS AFFECTS BACTERIAL OPERON ORGANIZATION	11:30-11:50
8.	**M. Zakhartsev[1],** A. Lapin[2], M. Reuss[2] [1]IPMB, University of Heidelberg, Germany; [2]Center Systems Biology (CSB), University of Stuttgart, Germany	11:50-12:10

	DYNAMIC MODEL OF ANAEROBIC ENERGY METABOLISM OF YEAST *SACCHAROMYCES CEREVISIAE*	
9.	**N.V. Ivanisenko[1,2]**, E.L. Mishchenko[1*], I.R. Akberdin[1], P.S. Demenkov[1], V.A. Likhoshvai[1,2], N.A. Kolchanov[1,2], V.A. Ivanisenko[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia, [2]Novosibirsk State University, Novosibirsk, Russia SUPPRESSION OF SUBGENOMIC HCV RNA BY NS3 PROTEASE ANTIVIRALS IN CELLS: A BASIC STOCHASTIC MATHEMATICAL MODEL	12:10 – 12:30
10.	**A. Zinovyev[1,2,3],** I. Kuperstein[1,2,3], E. Barillot [1,2,3], W.-D. Heyer[4] [1]Institute Curie, Paris, France [2]INSERM, U900, Paris, France [3]Mines ParisTech, Fontainebleau, France [4]University of California, Davis, CA SYNTHETIC LETHALITY WITHIN ONE PATHWAY AND CANCER TREATMENT	12:30 – 12:50
11.	**S.A. Lashin*,** Yu.G. Matushkin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia WHEN GENE NETWORKS MAY NOT WORK: COMPUTER MODELING WITH THE HAPLOID EVOLUTIONARY CONSTRUCTOR	12:50 – 13:10
12.	E.Ya.Frisman[1], **O.L. Zhdanova[2]*** [1]Complex Analysis of Regional Problems Institute FEB RAS, Birobidzhan, Russia [2]Institute of Automation and Control Processes FEB RAS, Vladivostok, Russia EVOLUTION TRANSITION TO COMPLEX DYNAMIC MODES IN STRUCTURED BIOLOGICAL POPULATIONS	13:10 – 13:30

13:30-14:00 Lunch break

June 29, Friday Exhibition Centre SB RAS, Conference Hall

Morning Session
9:00-13:00

SECTION "SUPERCOMPUTER APPLICATIONS IN BIOINFORMATICS"

Co-chairpersons:
Dr. Jaroslaw Zola, Iowa State University, Iowa, USA
Dr. Vyacheslav Ilyin, SINP MSU, Moscow, Russia
Dr. Yuriy Orlov, Institute of Cytology and Genetics, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**J. Zola** Department. of Electrical and Computer Engineering, Iowa State University, Ames, Iowa, USA LARGE SCALE METAGENOMIC CLUSTERING **KEYNOTE TALK**	9:00- 9:35
2.	**L. Milanesi** ITBA, Milan, Italy Perspective and challenge of Grid and HPC applications in Biomedical Science	9:35- 10:00
3.	**D. Braun** Bio-/Medical Informatics Department, Bielefeld, Germany PARALLEL NETWORK ANALYSIS ON INTEGRATED LIFE SCIENCE DATA	10:00- 10:20
4.	**S.I. Feranchuk**[1], U.V. Potapova[2], V.V.Potapov[2], D.V. Mukha[3] [1]Belarussian State University, Minsk, Belarus [2]Limnological Institute SB RAS, Irkutsk, Russia [3]Institute of Bioorganic Chemistry NAS, Minsk, Belarus BRI-SHUR.COM – A SITE FOR BIOINFORMATICS COMPUTATIONS	10:20- 10:40
5.	**A. Yudin** Hewlett-Packard, Novosibirsk, Russia HP view: modern trends in HPC	10:40 – 11:00
	Coffee/tea break 11:00-11:20	
6.	**F. Izquierdo-Carrasco**, A. Stamatakis Heidelberg Institute for Theoretical Studies, Heidelberg, Germany CHALLENGES ON LARGE-SCALE COMPUTATIONAL PHYLOGENETICS	11:20- 11:40
7.	**A.O. Chugunov**[**1**], D.V. Pyrkova[1], D.E. Nolde[1], V.M. Pentkovsky[2], R.G. Efremov[1] [1] Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia [2] Moscow Institute of Physics and Technology (State University), Dolgoprudny, Moscow region, Russia A BACTERIAL MEMBRANE "ACHILLES HEEL": HIGH-PERFORMANCE COMPUTER SIMULATION OF PEPTIDOGLYCAN CARRIER LIPID-II IN THE CHARGED LIPID BILAYER	11:40- 12:00
8.	**K.N. Kozlov**[1], A.M. Samsonov[2], M.G. Samsonova[1] [1]St.Petersburg State Polytechnical University, St.Petersburg, Russia [2]A.F. Ioffe Physico-technical Institute of the RAS, St.Petersburg, Russia IMPROVED DIFFERENTIAL EVOLUTION ENTIRELY PARALLEL METHOD	12:00- 12:20

9.	**N. L. Podkolodnyy**[1,2], P.S. Demenkov[1], K.V. Gunbin[1], Y.L. Orlov[1], E.S. Fomin[1], N.A. Alemasov[1], **F.A. Kazantsev[1]**, O.V. Vishnevsky[1], V.A.Ivanisenko[1], D.A. Afonnikov[1], N.V. Kuchin[2], B.M. Glinsky[2], N.A. Kolchanov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia HIGH PERFORMANCE COMPUTING IN BIOINFOMRANTICS: CASE STUDIES	12:20 – 12:40
10.	**Petunin D.V.** Intel Corporation, Novosibirsk, Russia Intel(r) MIC(Many Integrated Cores) architecture for highly parallel computations.	12:40-13:00

12:40-14:00 Lunch break

June 29, Friday House of Scientists, Large Conference Hall

Evening Session
14:10-17:30

MICROSYMPOSIUM "HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS"

Co-chairpersons:
Dr. Felix Agakov, University of Edinburgh, UK
Dr. Evgeny Rogaev, Vavilov Institute of General Genetics, Moscow, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**Evgeny Rogaev** Vavilov Institute of General Genetics, Russia NEUROGENOMICS FOR BRAIN DEVELOPMENT AND DISORDERS **KEYNOTE TALK**	14:10 – 14:40
2.	**Felix Agakov** University of Edinburgh, UK PREDICTING COMPLEX TRAITS USING GENOME-WIDE SNP DATA **KEYNOTE TALK**	14:40 – 15:10
3.	**Renat Garafutdinov** Institute of Biochemistry and Genetics Ufa Science Centre RAS, Ufa, Russia GENETIC BARCODE AS A PERSONAL IDENTIFIER OF EACH INDIVIDUAL	15:10-15:30
4.	**Alexander Chernonosov** Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia MOLECULAR-GENETIC AND METABOLOMICS APPROACHES FOR ANTI-COAGULANT THERAPY.	15:30-15:50
5	**Vladislav Baranov** St. Petersburg State University, St. Petersburg, Russia PERSONALIZED MEDICINE: EXPECTATIONS, DISAPPOINTMENTS AND HOPES	15:50-16:10
6	**Sergey Anashkin** "Genoanalytica" JSC, Moscow, Russia THE REVIEW OF EXISTING SERVICES IN THE FIELD OF PERSONALIZED GENETICS	16:10-16:30
	Coffee/tea break 16:30-16:50	
	Round Table "FUTURE OF PERSONALIZED GENETICS"	16:50–17:30

June 29, Friday House of Scientists, Small Conference Hall

Evening Session
14:00-17:50

SECTION “COMPUTER BIOLOGY OF DEVELOPMENT”

Co-chairpersons:
Dr. Eric Mjolsness, University of California, Irvine, USA
Dr. Maria G. Samsonova, St. Petersburg State Polytechnical University, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**E.Mjolsness** University of California, Irvine, USA MATHEMATICAL MODELING LANGUAGES FOR MORPHODYNAMICS **KEYNOTE TALK**	14:00 – 14:30
2.	**V.V. Mironova** [1], N.A. Omelyanchuk[1], E.S. Novoselova[1], A.V. Doroshkov[1], F.V. Kazantsev[1], A.V. Kochetov[1,2], E. Mjolsness[3], V.A. Likhoshvai[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Departments of Computer Science and Mathematics; Institute for Genomics and Bioinformatics, University of California, Irvine, USA COMBINED IN SILICO/IN VIVO ANALYSIS OF AUXIN MEDIATED MECHANISMS OF ROOT APICAL MERISTEM DEVELOPMENT	14:30 – 14:50
3.	**J. Szymanowska-Pułka** Department of Biophysics and Plant Morphogenesis US, Katowice, Poland DESCRIPTION OF A LATERAL ROOT DEVELOPMENT IN TERMS OF THE GROWTH TENSOR	14:50-15:10
4.	A. Urbain[1], J.-C. Palauqui[1], S.V. Nikolaev[2] ,N.A. Kolchanov[2], **A. Trubuil[1]** [1]INRA, Paris, France [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia ON 3D RECONSTRUCTION AND LINEAGE OF ARABIDOPSIS EMBRYOS FROM A COLLECTION OF OBSERVATIONS OF FIXED SAMPLES BASED ON CONFOCAL MICROSCOPY	15.10-15.30
	Coffee/tea break 15:30-16:00	
5.	**Jaap A. Kaandorp** University of Amsterdam, Netherlands MODELLING GENE REGULATION OF MORFOGENESIS IN THE SEA ANEMONE NEMATOSTELLA VECTENSIS **KEYNOTE TALK**	16:00-16:30
5.	K.N. Kozlov, S.Yu. Surkova, **M.G. Samsonova** St. Petersburg State Polytechnical University, Russia MODELING OF GAP GENE EXPRESSION IN DROSOPHILA *KRUPPEL* MUTANTS	16.30-16.50
6.	V.P. Golubyatnikov [1,3]**, T.A. Bukharina[2]**, D.P. Furman[2,3] [1] Sobolev Institute of Mathematics, SB RAS, Novosibirsk, Russia [2] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [3] Novosibirsk State University, Novosibirsk, Russia THE CENTRAL REGULATORY CIRCUIT OF THE MACROCHAETE MORPHOGENESIS GENE NETWORK: A MODEL OF FUNCTIONING	16:50-17:10
7.	**V. A. Scobeyeva**, V. G. Cherdantsev Lomonosov Moscow State University, Moscow, Russia	17:10-17:30

	ON THE FACTOR ANALYSIS OF MASS CTLL MOVEMENTS IN AMPHIBIAN GASTRULATION	
8.	**S.V. Nikolaev[1],** A. Trubuil[2], J.-C. Palauqui[2], N.A. Kolchanov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]INRA, Paris, France ON BIOMECHANICS OF ARABIDOPSIS EMBRYO AND INTERPRETATIONS FOR GEOMETRICAL FEATURES OF EMBRYO RECONSTRUCTIONS BASED ON CONFOCAL MICROSCOPY	17:30-17:50

June 29, Friday Exhibition Centre SB RAS, Conference Hall

Evening Session
14:00-17:50

SECTION “INTEGRATIVE BIOINFORMATICS AND INTELLIGENT KNOWLEDGE DISCOVERY/MANAGEMENT”

Co-chairpersons:
Dr. Andrey Rzhetsky, University of Chicago, USA
Dr. Evgeni E. Vityaev, Sobolev Institute of Mathematics, SB RAS, Novosibirsk, Russia

No.	Author(s) and Title of Talk	Timeline
1.	**Ralf Hofestädt**, Bielefeld University MODELING ASPECTS OF THE “VIRTUAL CELL” **KEYNOTE TALK**	14:00 – 14:30
2.	**O. Krebs[1]**, K. Wolstencroft[2], S. Owen[2], Q. Nguyen[1], F. du Preez[2], W Mueller[1], C. Goble[2], J.L. Snoep[2] [1]Heidelberg Institute for Theoretical Studies (HITS), Germany, [2]University of Manchester, United Kingdom SYSMO-DB: A COMMUNITY-BASED APPROACH TO DATA SHARING	14:30 – 14:50
3.	**V.A.Ivanisenko[1,2]**, P.S. Demenkov[1], T.V. Ivanisenko[1], E.S. Tiys[1] [1]Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia. [2]PBSoft Llc, Novosibirsk, Russia. ASSOCIATIVE NETWORK DISCOVERY SYSTEM (ANDSYSTEM): AUTOMATED LITERATURE MINING TOOL FOR EXTRACTING RELATIONSHIPS BETWEEN DISEASES, PATHWAYS, PROTEINS, GENES, MICRORNAS AND METABOLITES	14:50-15:10
4.	**B.V. Semisalov[1,2],** I.N. Kiselev[1,2], R.N. Sharipov[2,3], F.A. Kolpakov[1,2] [1]Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia [2] Institute of Systems Biology, Ltd, Novosibirsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia COMPUTATIONAL AND ANALYTICAL ASPECTS OF A NEW COMPLEX MODEL DESCRIBING HUMAN CARDIOVASCULAR SYSTEM	15.10-15.30
	Coffee/tea break 15:30-15:50	
5.	**Lars Jensen** University of Copenhagen - Copenhagen, Denmark (DK) NETWORK BIOLOGY: LARGE-SCALE BIOMEDICAL DATA AND TEXT MINING **KEYNOTE TALK**	15:50-16:20
6.	**D. Parkhomchuk[1]**, T. Kamphans[2], V. Heinrich[1], P. Krawitz [1]Department of Medical and Human Genetics, Charite, Universitätsmedizin Berlin, Berlin, Germany [2]GeneTalk, Berlin, Germany GENETALK: AN EXPERT EXCHANGE PLATFORM FOR ASSESSING RARE SEQUENCE VARIANTS IN PERSONAL GENOMES	16.20-16.40
7.	**K.N. Kozlov[1,2]**, P. Baumann[3,4], J. Waldmann[3], M.G. Samsonova[1,2] [1]St.Petersburg State Polytechnical University, St.Petersburg, Russia	16:40-17:00

	[2]ProStack LLC, St.Petersburg, Russia [3]Jacobs University, Bremen, Germany [4]Rasdaman GmbH, Bremen, Germany PROCESSING OF BIOMEDICAL IMAGES IN TERAPRO	
8.	**R. Henderson** National Institutes of Health, Bethesda, Maryland USA MODELING EMERGENT PROPERTIES OF BIOLOGICAL SYSTEMS WITH AN AGENT-BASED SIMULATION SUITE	17:00 - 17:20
9.	**Y.Y.Vaskin[1],** E.E. Vityaev[2], I.V. Khomicheva[3] [1]Novosibirsk State University, "UniPro" Company, Novosibirsk, Russia [2]Istitute of Mathematics SB RAS, Novosisbrsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia DATA MINING TOOL FOR ANALYSIS OF REGULATORY REGIONS OF GENES: INTEGRATION OF EXPERT DISCOVERY AND UGENE	17:20 - 17:40

House of Scientists**,** Small Conference Hall

19:00- 20:00 Closing Ceremony. Summaries from session chairpersons

POSTER SESSION AND COMPUTER DEMONSTRATION

Poster Size: The maximum size allowed for each poster
is 0.7m wide × 1.2m high.
Please note that this is a portrait (vertical) poster.

Authors must bring their posters printed and ready, as no facilities to produce posters at the Conference are available. Organizers will provide boards and push pins to display your posters. Posters should be readable from a distance of about two to three feet—for easy reading by several people at one time.

The poster session and computer demonstration will be held during the whole conference since 26 till 29 June. The poster reports are subdivided into the groups according to the scientific sessions' schedule. The posters being presented during the subject scientific session shall be posted starting from 9:00 to 20:00 in the Small (or Large) Conference Hall Foyer.

From 18:30 to 20:00 presenters are expected to remain at their individual displays to be available for questions and informal discussion of the poster content.

Material should be removed soon after the ending of the poster session. In the case the author(s) does not take away the poster, it will be removed by the BGRS\SB'12 Organizing Committee.

If you have any questions, please do not hesitate to contact the Organizing Committee
in Room No. 200 at the House of Scientists.

POSTER PRESENTATIONS AND COMPUTER DEMOSTRATION
(BY SECTIONS)

June 26, Tuesday House of Scientists, Foyer of Large Conference Hall

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL GENOMICS”

V.S. Amstislavskiy, M. Sultan, K. Kim, S. Schrinner, H. Lehrach, M.-L. Yaspo
Max Planck Institute for Molecular Genetics, Berlin, Germany
COVERAGE DEPTH ANALYSIS IN NEXT GENERATION SEQUENCING DATA

A A. Arakelyan
Institute of Molecular Biology NAS RA, Yerevan, Armenia
PATHWAY SIGNAL FLOW ANALYSIS FOR HIGH-THROUGHPUT GENE EXPRESSION DATA

E.E. Astafieva, T.V. Karpushkina, K.A. Kulikova, T.T. Glazko
Russian State Agrarian University – Moscow Agricultural Academy named after K.A. Timiryazev (RSAU–MTAA), Moscow, Russia
EVALUATION OF GENOMIC INSTABILITY IN SEVERAL SPECIES OF MAMMALS USING THE MICRONUCLEI TEST

D. N. Baryakin[1], D. V. Semenov[1], E. V. Brenner[1], A. M. Kurilshikov[1], V. V. Kozlov[2], Y. E. Narov[2], G. V. Vasiliev[3], L. A. Bryzgalov[3], E. D. Chikova[1], J. A. Filippova[1] E. V. Kuligina[1], V. A. Richter[1]
[1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
[2]Novosibirsk Regional Cancer Centre, Novosibirsk, Russia
[3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
SMALL NON-CODING RNAs OF HUMAN BLOOD PLASMA OF HEALTHY DONORS AND PATIENTS WITH NON-SMALL CELL LUNG CANCER.

E.A. Borzov[1], A.V. Marakhonov[1], A.V. Baranova[1,2], M.Yu. Skoblov[1, 3]
[1]Federal State Budgetary Institution “Research Centre for Medical Genetics” under the Russian Academy of Medical Sciences, Moscow, Russia
[2]School of Systems Biology, College of Science, George Mason University, Fairfax, VA USA
[3]State Budgetary Institution of Higher Education “Moscow State Medical and Dental University”, Moscow, Russia.
RANDTRAN: RANDOM TRANSCRIPTOME SEQUENCE GENERATOR

Eu.Yu.Bushmelev
Siberian federal university, Krasnoyarsk, Russia
POPULATION STUDY OF THE VARIATION IN TRIPLET DISTRIBUTIONS OBSERVED ALONGSIDE A CHROMOSOME, FOR YEAST SPECIES

V.N. Danilenko, E.U.Poluektova, K.M. Klimina, D.H. Kjasova, J.V.Chervinetz, D.B. Malko, V.J.Makeev, F. Gusev, T.V.Tyajelova, D.A. Reshetov, E.I.Rogaev
N.I.Vavilov Institute of General Genetics RAS, Moscow, Russia
SEQUENCE AND ANNOTATION OF THE CHROMOSOME OF PROBIOTIC STRAIN LACTOBACILLUS RHAMNOSUS 24

A.P. Dovgerd, D.O. Zharkov
SB RAS Institute Chemical Biology and Fundamental Medicine, Novosibirsk, Russia
APPLICATION OF REPAIR ENZYMES TO IMPROVE THE QUALITY OF THE DNA TEMPLATE IN PCR AMPLIFICATION OF DEGRADED DNA.

Elkina M.A., Astafjeva E.E., Glazko T.T.
Russian State Agrarian University–MTAA named after K.A.Timiryazev, Moscow, Russia
IRAP-PCR MARKERS AND MICRONUCLEI TEST IN THE CHARACTERIZATION OF GENETIC STRUCTURE OF THE KALMYK SHEEP AND TYPES OF THE EDILBAY SHEEP

A. Goodman, A. Montana, E. Neal, J. VanderKelen, M. Black, C. Kitts, A. Dekhtyar
California Polytechnic State University, San Luis Obispo, CA, USA
DEVELOPMENT OF A NOVEL PYROSEQUENCING-BASED METHOD FOR STUDYING *E. COLI* DIVERSITY AND MICROBIAL SOURCE TRACKING.

E.V. Ignatieva, V.G. Levitsky, N.S. Yudin
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
ANALYSIS OF SNP DISTRIBUTION AND INTER-SNP DISTANCE IN THE HUMAN GENOME

A. Grigorenko[1,2], Y. Moliaka[1], I. Alexandrov[1], E. Rogaev[1,2].
[1]University of Massachusetts Medical School, USA;
[2]Vavilov Institute of General Genetics, Research Center of Mental Health, Moscow**.**
SEARCH FOR FUNCTIONAL PATHWAYS FOR INTRAMEMBRANE ASPARTIC PROTEASE IMPAS1/SPP.

A.V. Katokhin,D.A. Afonnikov, V.Yu. Ovchinnikov, G.V. Vasiliev, E.V. Kashina, V.A. Mordvinov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
IDENTIFICATION OF miRNAS OF THREE OPISTHORCHID LIVER FLUKES

K.V. Krutovsky[1,2,5], E.A. Vaganov[2], I.V. Chubugina[2,3], N.V. Oreshkova[4], I. N. Tretyakova[4], T.V. Tyazhelova[5]
[1]Department of Ecosystem Science and Management, Texas A&M University, College Station, TX, USA
[2]Genome Research Center, Siberian Federal University, Krasnoyarsk, Russia
[3]Center for Forest Protection, Krasnoyarsk, Russia
[4]V.N. Sukachev Institute of Forest, SB RAS, Krasnoyarsk, Russia
[5]N.I. Vavilov Institute of General Genetics, RAS, Moscow, Russia
COMPLEX GENOME SEQUENCING: PRELIMINARY DATA OF SIBERIAN LARCH COMPLETE GENOME SEQUENCING

V.G. Levitsky[1], A.V. Vershinin[2]
[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2]Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia
THE ROLES OF THE MONOMER LENGTH AND NUCLEOTIDE CONTEXT OF PLANT TANDEM REPEATS IN NUCLEOSOME POSITIONING

M.L. Markelov, M.A. Gordukova, K.V. Kuleshov, V.G. Dedkov, M.V. A. Figueroa
FBIS Central Research Institute for Epidemiology, Moscow, Russia
DEVELOPMENT OF THE OPTIMAL ALGORITHM OF BACTERIAL WHOLE GENOME SEQUENCING ON MISEQ AND GS JUNIOR 454 SEQUENCERS/

Yu.G. Matushkin, V.G.Levitsky, Yu.L.Orlov, V.A.Likhoshvai
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Novosibirsk State University, Novosibirsk, Russia
CORRELATION BETWEEN TRANSCRIPTION EFFICIENCY INITIATION AND TRANSLATION EFFICIENCY FOR SACCHAROMYCES CEREVISIAE AND SCHIZOSACCHAROMYCES POMBE

I. A. Novikov, M. Y. Fursov, I. E. Efremov
Novosibirsk Center of Information Technologies ‘Unipro’
UGENE ASSEMBLY BROWSER: A TOOL FOR NGS DATA VISUALIZATION

A.A. Ponomaryova[1], E. Y. Rykova[2], N.V. Cherdyntseva[1], T.E. Skvortsova[2],
A.Y. Dobrodeev[1], A.A. Zav’yalov[1], S.A. Tuzikov[1], V.V. Vlassov[2], P.P. Laktionov[2]
[1]Cancer Research Institute, SB RAMS, Tomsk, Russia
[2]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia
EPIGENETIC STATUS AND QUATITATIVE CHARACTERISTICS OF CIRCULATING DNA IN LUNG CANCER

F. Pošćić[1], N. Khlopova[2]
[1]Udine University, Udine, Italy
[2]RSAU-MTAA named after K.A. Timiryazev, Moscow, Russia
NEW ALGORITHM FOR IDENTIFICATION OF INDIVIDUAL DIFFERENCES IN GENE EXPRESSION

Yu. A. Putintseva
[1]Siberian Federal University, Krasnoyarsk, Russia
3Krasnoyarsk state medical university, Krasnoyarsk, Russia
COMPARATIVE ANALYSIS OF TRIPLETS FREQUENCY IN MITOCHONDRIAL GENOMES

D.A. Reshetov[1,2], L.I. Shagam[1,2], T.V. Tyazhelova[1], A.P.Grigorenko[1,3,4], T.A. Andreeva[1,3], O.A. Mikhaylichenko[1,2], M.S. Protasova[1], A.Y. Goltsov[1,3], A.A. Zenin[5], F.E. Gusev[1], E.I. Rogaev[1,2,3,4]
[1]Vavilov Institute of General Genetics, Moscow;

[2]Lomonosov Moscow State University,
[3]Research Center of Mental Health, Russian Academy of Medical Sciences,Moscow, Russia
[4]Brudnick Neuropsychiatric Research Institute, Department of Psychiatry, University of Massachusetts Medical School, USA;
[5]Institute of Functional Nuclear Electronics NRNU MEPHI
GENOME SEQUENCES OF CENTENARIANS PRODUCE A BASIS FOR GENOME SCALE LONGEVITY STUDIES

M.G.Sadovsky, E.M.Mirkes
Institute of computational modelling of SB RAS, Krasnoyarsk, Russia
INTRIGUING STRUCTURES IN TRIPLET DISTRIBUTION ALONGSIDE A GENOME

A. Samoshkin[1], S. Dulev[2], D. Loukinov[3], J.A. Rosenfeld[4], A. V. Strunnikov*
* Guangzhou Institutes of Biomedicine and Health, Molecular Epigenetics Laboratory, 190 Kai Yuan Avenue, Science Park, Guangzhou 510530, Guandong, China
[1] NIH NCI, Genome Structure and Function Section, Bethesda, MD, USA
[2] Ludwig-Maximilians-Universität, Adolf Butenandt Institut, 80539 Munich, Germany
[3] NIH NIAID, Laboratory of Immunopathology, Rockville, MD, USA
[4] Division of High Performance and Research Computing, University of Medicine & Dentistry of New Jersey, Newark, NJ, USA
A MAP OF ANAPHASE CHROMOSOMAL BREAKS INDUCED BY CONDENSIN LOSS

E.M. Sergeeva[1], D.A. Afonnikov[1], L.L. Bildanova[1], M.K. Koltunova[1], E.M. Timonova[1], E.A. Salina[1]
[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
TOWARDS AN ANALYSIS OF THE STRUCTURE OF THE SHORT ARM OF 5B CHROMOSOME OF THE BREAD WHEAT TRITICUM AESTIVUM L.

A. Sharma[1], L. Alomair[1], K. Doyle[1], M. Sikaroodi[3], A. Cherepanova[4], P. Laktionov[4], A. Birerdinc[1,2], P. Gillevet[3], A. Baranova[1,2,3,5]
[1]School of Systems Biology, George Mason University, Fairfax VA 22030,
[2]Betty and Guy Beatty Center for Integrated Research, Inova Health System, Falls Church, VA 22042,
[3]Microbiome Analysis Center, George Mason University, Manassas, VA 20100,
[4]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia.
[5]Research Centre for Medical Genetics, Moscow, Russia
NEXTGEN SEQUENCING REVEALS EXTENSIVE RNA EDITING IN PLASMACYTOID DENDRITIC AND OTHER PRIMARY CELLS

P. Shelyakin, A. Kaznadzey
Institute for Information Transmission Problems RAS, Moscow, Russia
DIVERSION OF GENOME LOCI AND CO-LOCALIZATION PATTERNS STUDY OF THE PROTEIN FAMILIES FROM DIFFERENT FUNCTIONAL CLASSES OF THE BACTERIAL CARBOHYDRATE METABOLISM

N.N. Vtyurina[1,2], S.L. Grokhovsky[1], A.B. Vasiliev[2], I.I. Titov[3], P.M. Ponomarenko[3], M.P. Ponomarenko[3], S.E. Peltek[3], Yu.D. Nechipurenko[1,2], N.A. Kolchanov[3,4,5]
[1]Engelhardt Institute of Molecular Biology RAS, Moscow, Russia
[2]Lomonosov Moscow State University, Moscow, Russia
3Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[4]Novosibirsk State University, Russia
[5]National Research Centre "Kurchatov Institute", Moscow, Russia
CONTEXTUAL DNA FEATURES SIGNIFICANT FOR THE DNA DAMAGE BY THE 193 NM ULTRAVIOLET LASER BEAM

L.P. Zakharenko[1,2], T.P. Bak[1], O.M. Ignatenko[2]
[1]Institute of Cytology and Genetics SB RAS, [2]Novosibirsk State University, Novosibirsk, Russia
HOW LONG SEQUENCED GENOME CAN REMAIN STABLE

June 27, Wednesday House of Scientists, Foyer of Large Conference Hall

SECTION “BIOINFORMATICS AND SYSTEMS BIOLOGY OF GENE EXPRESSION REGULATION”

E.A. Ananko, V.G. Levitsky, V.M. Efimov, D.A. Afonnikov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
RECOGNITION OF NFAT5 BINDING SITES

N.V.Baginskaya, E.V. Kashina, M.Yu. Shamanina
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
EFFECT OF CHRONIC O-AMINOAZOTOLUENE TREATMENT ON XENOSENSORS CAR, PPARA, PPARG GENES AND THEIR TARGET GENES EXPRESSION IN MICE CC57BR/MV AND DD/HE.

M.S. Belenikin[1,2], A.S. Speranskaya[1,3]*, N.V. Melnikova[1], N.Y. Oparina [1], M.V. Darii[1,4], A.A. Dmitriev [1], A.A. Slavokhotova[5], T.V. Korostyleva[5], A.V. Kudryavtseva[1], T.I. Odintsova[5]
[1]Engelgardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia
[2]Research Institute of Physico-Chemical Medicine of Russian Federal Medico-Biological Agency, Moscow, Russia
[3]Lomonosov Moscow State University, Department of Biology, Moscow, Russia
[4]Lomonosov Moscow State University, Department of Chemistry, Moscow, Russia
[5]Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia
SEQUENCING AND DE NOVO TRANSCRIPTOME ASSEMBLY OF STELLARIA MEDIA (L.) VILL.

M.B. Chaley[1], V.A. Kutyrkin[2]
[1]Institute of Mathematical Problems of Biology RAS, Pushchino, Russia
[2]Moscow State Technical University n.a. N.E. Bauman, Moscow, Russia
LATENT STATISTICAL ORGANIZATION OF CODING AND NONCODING REGIONS IN HUMAN GENOME

I.A. Drachkova , P.M. Ponomarenko, L.K. Savinkova, M.P. Ponomarenko, T.V. Arshinova, N.A. Kolchanov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
EXPERIMENTAL EXAMINING OF PROGNOSES *IN SILICO* TBP BINDING TO TATA BOX WITH SNP ASSOCIATED WITH HUMAN DISEASES

E.V. Ignatieva, E.V. Kashina, M.Yu. Shamanina, V.A. Mordvinov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
IN SILICO RECONSTRUCTION OF MULTI-PROTEIN COMPLEX INTERACTING WITH THE COMMON REGULATORY REGIONS IN THE HUMAN CYP1A1/1A2 INTERGENIC SEQUENCE

A.T. Ivashchenko, A.S. Issabekova, O.A. Berillo, V.A. Khailenko
Al-Farabi Kazakh National University, Almaty, Kazakhstan
FEATURES OF hsa-miR-1279 BINDING SITES IN PROTEIN CODING SEQUENCE OF *PTPN12*, *MSH6*, *ZEB1* GENES

K. Korla
University of Hyderabad, Hyderabad, India.
LINGUISTIC ANALYSIS OF SHORT SEQUENCES IN THE INTRONS AND EXONS FOR TLR1

E.A. Krutinina, G.G. Krutinin, S.G. Kamzolova, A.A. Osypov
Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, Pushchino, Russia
NEW EVIDENCES OF THE ELECTROSTATIC NATURE OF PROMOTERS UP-ELEMENT COMBINED WITH ITS OTHER PHYSICAL PROPERTIES

E.A. Krutinina, G.G. Krutinin, S.G. Kamzolova, A.A. Osypov
Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, Pushchino, Russia
ELECTROSTATICS AND BENDING IN PROMOTER FUNCTIONING DURING THE GLOBAL METABOLIC SWITCH

V.G. Levitsky
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
DNA MOTIF SEARCH BY GENETIC ALGORITHM

A.A. Lomzov, Y.N. Vorobjev, D.V. Pyshnyi
Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
COMPUTING DNA OLIGONUCLEOTIDES HYBRIDIZATION ENTHALPY WITHIN MOLECULAR DYNAMICS MODELING

A.V. Marakhonov[1], N.S. Sadovskaya[1], A.V. Baranova[1,2], M.Yu. Skoblov[1,3]
[1]Federal State Budgetary Institution “Research Centre for Medical Genetics” under the Russian Academy of Medical Sciences, Moscow, Russia
[2]School of Systems Biology, College of Science, George Mason University, Fairfax, VA USA
[3]State Budgetary Institution of Higher Education “Moscow State Medical and Dental University”, Moscow, Russia
VALIDATION OF AFFYMETRIX PROBE SETS: NEW APPROACHES TO THE OLD PROBLEM

N.A. Omelyanchuk, P.P. Ponomarenko, M.P. Ponomarenko
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
THE ROLE OF MATURE MICRORNA NUCLEOTIDE CONTEXT IN THEIR FUNCTIONING

Y. L. Orlov[1], D. Chen[2], O. Dobrovolskaya[1], Y. Meng[2], L. Chen[2], D.A. Afonnikov[1], M. Chen[2]
[1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[2]Zhejiang University, Hangzhou, China
COMPUTER ANALYSIS AND DATABASE PRESENTATION OF ANTISENSE TRANSCRIPTION ASSOCIATED WITH MICRORNA TARGETS IN PLANT GENOMES

Y.L. Orlov[1,2], G. Li[3], D.A. Afonnikov[1,2], B. Lim[3], N. Clarke[3], M. Huss[3], K.V. Gunbin[1], Y. Ruan[3], N.L. Podkolodnyy[1,4], M. Chen[5], H.-H. Ng[3]
[1]Novosibirsk State University, Novosibirsk, Russia
[2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[3]Genome Institute of Singapore, Singapore
[4]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Russia
[5]Zhejiang University, Hangzhou, China
TRANSCRIPTION FACTOR BINDING AND CHROMATIN MODIFICATIONS ANALYSIS BY CHIP SEQUENCING DATA

A.A. Osypov, G.G. Krutinin, E.A. Krutinina, S.G. Kamzolova
Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, Pushchino, Russia
DEPPDB – A PORTAL FOR ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF NATURAL GENOMES

D.Y. Oshchepkov[1], E.V. Kashina[1], E.A. Oshchepkova[1], E.V. Antontseva[1], M.Yu. Shamanina[1], D.P. Furman[1,2], V.A. Mordvinov[1]
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ELICITING THE ROLE OF DIOXIN IN REGULATION OF THE GENES INVOLVED IN CYTOKINES SYNTHESIS BY MACROPHAGES

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INTRON LENGTH DEPENDS ON PHASES OF SURROUNDING INTRONS

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SEARCHING AND CLASSIFICATION OF BINDING SITES OF SIGMA FACTORS OF CLOSTRIDIUM DIFFICILE

V.S. Sokolov, V.A. Likhoshvai, T.M. Khlebodarova, D.Y. Oshchepkov, V.M. Efimov, I.V. Babkin
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STUDY OF PROMOTERS OF *YODA* AND *BHSA* GENES ENCODING STRESS RESPONSE PROTEINS IN *E. COLI*

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THE UNDERLYING MECHANISMS OF REPROGRAMMING OF HUMAN UMBILICAL VEIN ENDOTHELIAL CELLS (HUVEC)

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ELECTROSTATIC PROPERTIES OF T7 DNA PROMOTERS

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PHYSICAL PROPERTIES OF T7 NATIVE PROMOTERS DNA: CONTRIBUTION OF DNA ELECTROSTATICS AND DUPLEX STABILITY TO PROMOTER EFFICIENCY

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INVESTIGATION OF VOLE NANOG REGULATORY REGION

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CLUSTERING OF *E.COLI* PROMOTER ELECTROSTATIC PROFILES

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FUNCTIONAL INTERPLAY OF OVERLAPPING PROMOTERS PREDICTED WITHIN PHOR/BRNQ “PROMOTER ISLAND”

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VARIABILITY OF GENE EXPRESSION IN MOUSE BRAIN DEPENDS ON PREDICTED TBP-AFFINITY OF ITS CORE PROMOTER

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ORGANIZATION, EVOLUTION, STRUCTURE AND COMPUTATIONAL PREDICTION OF HUMAN miRNAS

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IPSscan: THE EXTENDED MATRIX METHOD FOR PREDICTION OF TRANSCRIPTION FACTOR BINDING SITES

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THE P53IPS MODEL FOR SELF-ORGANIZING META-PREDICTION OF P53-BINDING SITES AND P53-TARGET GENES

SECTION “COMPUTATIONAL INFERENCE OF NETWORKS FROM HIGH-THROUGHPUT EXPERIMENTAL DATA”

E.V. Ignatieva, V.A. Ivanisenko, E.S. Tiys, P.S. Demenkov, M.P. Moshkin, S.E. Peltek.
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APPLICATION OF THE ANDVisio COMPUTER SYSTEM TO THE INTERPRETATION OF BIOLOGICAL FUNCTIONS OF PROTEINS, DIFFERENTIALLY EXPRESSED IN BRONCHOALVEOLAR LAVAGE OF MICE AFTER A ONE-TIME INTRANASAL ADMINISTRATION OF SIO_2 NANOPARTICLES

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IN SILICO EVIDENCE OF THE NOTCH SIGNALING PLAYERS IN LEUKEMIA

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THEORETICALLY-EXPERIMENTAL RESEARCH OF VESICLE TRAFFICKING MECHANISMS IN THE SYNAPTIC PLASTICITY PROCESS

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CONSTRUCTION AND ANALYSIS OF THE PROTEIN-PROTEIN INTERACTION NETWORK FOR THE SPERMATOZOA

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A CENTRAL REGULATORY CIRCUIT OF ARABIDOPSIS CIRCADIAN CLOCK GENE NETWORK

MICROSYMPOSIUM “COMPUTATIONAL AND EXPERIMENTAL PROTEOMICS”

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THEORETICAL STUDY OF STRUCTURAL FEATURES OF VARIOLA VIRUS CRMB PROTEIN

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MOLECULAR MODELING OF CYTOSOLIC PART OF a2-SUBUNIT OF MOUSE V-ATPase

E.Barnaeva[1], R.B. Free[2], X.Hu[1], N.Southall[1], M. Bryant-Genevier[1], S. Titus[1], M.Ferrer[1], J.Marugan[1], D.R.Sibley[2]
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HIGH-THROUGHPUT SCREENING FOR THE DEVELOPMENT OF NOVEL SELECTIVE LIGANDS
OF D2 DOPAMINE RECEPTORS

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APPLICATION OF CONFORMATIONAL PEPTIDES FOR ANALYSIS OF ALLERGENIC PROTEINS

A.L. Chernobrovkin, V.G. Zgoda, A.V. Lisitsa and A.I. Archakov
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COMPREHENSIVE ANALYSIS OF UNIDENTIFIED LC-MS FEATURES FOR INVESTIGATING PROTEINS DIVERSITY IN HIGH-THROUGHPUT PROTEOMICS EXPERIMENTS

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MODELING OF PLANT KINESIN-8 MOTOR DOMAIN AND RECONSTRUCTION OF ITS L2 AND L11 LOOPS

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GP39, A NOVEL PHAGE-ENCODED INHIBITOR OF BACTERIAL RNA POLYMERASE

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THE ROLE OF CASEIN KINASES 1 IN PLANT CYTOSKELETON REGULATION

M.S. Kondratyev, A.V. Kabanov, V.I. Novoselov, A.A. Samchenko, V.M. Komarov, N.N. Khechinashvili

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ALTERNATIVE HYDROGEN BONDING IN MOLECULAR DESIGN OF THERMOSTABLE ANTIOXIDANT PROTEIN

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DIRECT COMPUTER SIMULATION OF PROTEIN-PROTEIN INTERACTION

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IN SILICO STRUCTURAL 3D MODELLING OF NOVEL *CRY1I* AND *CRY3A* GENES FROM LOCAL ISOLATES OF *BACILLUS THURINGIENSIS*

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TOWARDS AN UNDERSTANDING OF THE ROLE OF HUMAN RIBOSOMAL PROTEINS IN VARIOUS CELLULAR PROCESSES RELATED TO HEALTH AND DISEASES

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STATISTICAL ANALYSIS OF DATABASE DERIVED INTER-RESIDUE CONTACT POTENTIALS

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MOLECULAR DYNAMICS SIMULATION OF NIP7 PROTEINS FROM HYPERTHERMOPHILIC ARCHAEA AT HIGH TEMPERATURE AND PRESSURE

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PROF_PAT, THE DATABASE OF PROTEIN FAMILY PATTERNS – AN EFFECTIVE TOOL FOR SEQUENCES ANNOTATION

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COMPUTATIONAL EVALUATION OF IMPACT OF AMINO ACID SUBSTITUTION p.W172C ON STRUCTURE AND FUNCTION OF GAP-JUNCTION PROTEIN CONNEXIN 26 AND ITS ASSOCIATION WITH HEARING IMPAIRMENT

A.V. Popov, D.O. Zharkov, Yu.N. Vorobyov
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INTEGRATED APPROACH TO MOLECULAR DYNAMICS STUDY OF PROTEINS AND PROTEIN-DNA COMPLEXES

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NS2B/NS3 PROTEASE: ANALYSE OF ALLOSTERIC EFFECTS OF MUTATIONS ASSOCIATED WITH THE PATHOGENICITY OF TICK-BORNE ENCEPHALITIS VIRUS

Yu.A. Purtov, M.S. Kondratyev, O.N. Ozoline, V.M. Komarov
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STUDY OF CONFORMATIONAL FLEXIBILITY OF *E.coli* RNA POLYMERASE ALPHA SUBUNIT INTERDOMAIN LINKER

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IN SILICO STUDIES OF POTENTIAL PHOSPHORESIDUES IN THE HUMAN NUCLEOPHOSMIN/B23: ITS KINASES AND RELATED BIOLOGICAL PROCESSES

M.Skoblov, A.Marakhonov, A. Baranova
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FAMILY OF KCTD PROTEINS: STRUCTURAL AND FUNCTIONAL PECULIARITIES

L.P. Smirnova [1], V.V. Koval [2], L.V. Loginova [1], O.S. Fedorova [2], S.A. Ivanova [1]
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SEARCH OF PLASMA PROTEIN BIOMARKERS FOR SCHIZOPHRENIA

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LOOKING FOR MEANINGFUL SIGNS: THE EXPERIENCE WITH COMPARATIVE ANALYSIS OF NON-ALIGNED PROTEIN SEQUENCES

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THE VESICLE BUILDER – A PLUGIN FOR THE CELLMICROCOSMOS 2 MEMBRANEEDITOR

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NOVEL APPROACH FOR IDENTIFICATION OF DNA-BINDING PROTEINS OF BLOOD CELL SURFACE

June 28, Thursday House of Scientists, Foyer of Large Conference Hall

MICROSYMPOSIUM “HUMAN GENETICS AND PERSONALIZED MEDICINE: THEORETICAL AND EXPERIMENTAL ASPECTS”

E.V. Antontseva[1], L.O. Bryzgalov[1], M.Yu. Matveeva[1], A.A. Ponomaryova[2], A.A. Ivanova[2], E.Y. Rykova[3], N.V. Cherdyntseva[2], T.I. Merkulova[1]
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MUTATIONS IN K-RAS AND EGFR GENES AND THE SEARCH FOR SNPS, ASSOCIATED WITH THEIR OCCURRENCE

N.S. Babayan, A.L. Gevorkyan, R.M. Aroutiounian, G.G. Hovhannisyan
Yerevan State University, Yerevan, Armenia
THE COMET-FISH TECHNIQUE FOR MONITORING CANCER TREATMENT RESPONSE AT THE GENOMIC LEVEL

L.A. Belozertseva, E.N. Voronina, N.V. Koh, G.A. Cvetovskaya, G.I. Lifshic, M.L. Filipenko
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STUDY OF INTERINDIVIDUAL VARIABILITY OF WARFARIN DOSAGE AMONG POPULATION OF THE WESTERN SIBERIAN REGION OF RUSSIA

A. A. Chernonosov, V. V. Koval, N. V. Kokh, G.A. Tsvetovskaya, G. I. Lifshits, O.S. Fedorova
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CONTRIBUTION OF GENOTYPE VARIATION TO WARFARIN PHARMACOKINETICS

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BASE EXCISION REPAIR OF TRIPLET REPEAT SEQUENCES ASSOCIATED WITH NEURODEGENERATIVE DISORDERS

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VALIDATION OF THE *PPP1R12B* AS A CANDIDATE GENE FOR CHILDHOOD ASTHMA SUSCEPTIBILITY

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IDENTIFICATION OF RARE VARIANTS AND POLYMORPHISMS OF THE *IL12RB1* GENE AND ANALYSIS OF THEIR ASSOCIATIONS WITH TUBERCULOSIS.

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GENETICS AND DISEASE PROGRESSION OF FAMILIAL MULTIPLE SCLEROSIS IN NOVOSIBIRSK REGION OF RUSSIA.

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EXPERIENCE OF THE PERSONALIZED ANTIPLATELET THERAPY: THE EFFECTS OF CYP2C19 GENE

E.A. Kudryavtseva, A.S. Rozhdestvenskii, A.V. Kakulya, E.V. Khanokh, N.A. Malkova, D.S. Korobko, F.A Platonov, E.G. Aref′eva, N.N. Zagorskaya, V.M. Alifirova, M.A. Titova, I.V. Smagina, S.A. El′chaninova, A.G. Zolovkina, V.P. Puzyrev, E.Y. Tsareva, O.O. Favorova, A.N. Boiko, M.L. Filipenko
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Siberian State Medical University, Tomsk
Research Institute of Medical Genetics, SD, RAMS, Tomsk
Altai State Medical University, Barnaul
Moscow center of multiple sclerosis on the basis of hospital № 11.
IS THE ASSOCIATION BETWEEN -308G->A TNFA AND MULTIPLE SCLEROSIS INDEPENDENT OF HLA-DRB1*15?

E. V. Kulish[1], O. A. Makeeva[1,2], M. V. Golubenko[1,2], M. V. Zykov[2], V. V. Kashtalap[2].
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ASSOCIATION OF *ITGB3* AND *GNB3* VARIANTS WITH THE DEVELOPMENT OF VASCULAR COMPLICATIONS IN PATIENTS WITH ACUTE CORONARY SYNDROME

E.V. Rudikov[1], V.A. Gavrilova[1], O.Y. Fedorenko[1], E.G. Boyarko[1], A.V. Semke[1], V.A. Sorokina[2], N.V. Govorin[3], S.A. Ivanova[1].
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TARDIVE DISKINESIA AND POLYMORPHISM OF PHOSPHATIDYLINOSITOL- 4-PHOSPHATE 5-KINASE IIA GENE IN RUSSIAN SCHIZOPHRENIC PATIENTS

O.S. Shkoda, E.D.Chikova, N.V. Fomenko, P.P. Laktionov, E.Y.Rykova
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CYTOKINE PROFILE AND CIRCULATING DNA IN THE BLOOD OF PATIENTS WITH TICK-BORNE BORRELIOSIS

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DEVELOPMENT AND APPLICATION OF THE GENOMIC CONTROL METHODS FOR GENOME-WIDE ASSOCIATION ANALYSIS USING NON-ADDITIVE MODELS

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NEW CANDIDATE GENES FOR SCHIZOPHRENIA DISORDER

SECTION "GENE FUNCTION DISCOVERY AND SEARCH FOR NEW PHARMACEUTICAL TARGETS"

A.A. Arakelyan, L. Nersisyan, N. Avetisyan, G. Martirosyan.
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EXPERIMENT-BASED VALIDATION OF COMPUTATIONAL MODELS OF PYRIN - FAMILIAL MEDITERRANEAN FEVER PROTEIN

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FUNCTIONAL ANALYSIS OF PUTATIVE TUMOR SUPPRESSOR GENES KCNRG AND KCTD7

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E3 LIGASE AND THE P53 FAMILY PROTEINS INTERACTION MODELING

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IDENTIFICATION OF BIOLOGICAL TARGETS FOR VIRTUAL SCREENING OF INHIBITORS OF REPLICATION OF TICK-BORNE ENCEPHALITIS VIRUS

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A SCREENING of G-quadruplex MOTIFS AS A STRUCTURAL BASIS OF APTAMERS TO TICK-BORNE ENCEPHALITIS VIRUS GLYCOPROTEIN

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IDENTIFICATION OF NEW DERIVATIVES OF OKADAIC ACID - SELECTIVE INHIBITOR OF PROTEIN PHOSPHATASE 1 (PP1) AND 2A (PP2A)

T.O. Volkova, U.S. Bagina, N.S. Zykina, I.E. Malysheva, A.N. Poltorak
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TREATMENT OF CELLS К562/4-NQO AND К562/2-DQO WITH CHEMICAL COMPOUNDS OF MULTIDRUG RESISTANCE LEADS TO APOPTOSIS

SECTION "EVOLUTIONARY BIOINFORMATICS"

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AGROBACTERIUM-MEDIATED EVOLUTION?

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INBREEDING AND DIFFERENTLY DIRECTED DYNAMICS OF ISSR-PCR AND IRAP-PCR MARKERS POLYMORPHISM IN MUSK OXEN POPULATIONS

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GENOME SCANNING OF HORSE BREEDS BY USING OF ISSR-PCR MARKERS

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FEATURES ADAPTATION OF CHILDREN OF CHUKOTKA

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MOLECULAR EVOLUTION OF HUMAN PROTEIN-CODING GENES IN THE LIGHT OF BRAIN ORGANIZATION

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HIGHWAYS IN THE HORIZONTAL TRANSFER OF EUBACTERIAL FPG AND NEI GENES

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PEFF DB: THE WEB-AVIALABLE DATABASE OF PROTEIN EVOLUTIONAL AND FUNCTIONAL FEATURES

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COMPUTER ASSISTED STUDY OF THE GTF2I PROTEIN REPEATS EVOLUTION

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EVOLUTION OF NON-CODING MITOCHONDRIAL SEQUENCES OF THE BAIKALIAN SPONGES (LUBOMIRSKIIDAE)

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ON METRIC PROPERTIES OF EVOLUTIONARY DISTANCES

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PLACE MAKES A SEQUENCE: THE INFLUENCE OF HIGH AND LOW COPY REPEATS ON THE ORIGIN AND FATE OF MICROSATELLITES IN VERTEBRATE GENOMES

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RECOMBINATION OF MOBILE GENETIC ELEMENTS AS POSSIBLE SOURCE OF NEW ISSR-PCR MARKERS

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BIOINFORMATIC SEARCH AND PHYLOGENETIC ANALYSIS OF THE PLANT-SPECIFIC MAPS IN GENOMES OF MONOCOTS AND DICOTS

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INFORMATION STORAGE IN NON-CODING DNA PATTERNS

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SECONDARY STRUCTURE OF RNA MAY CONSTRAIN INTRON EVOLUTION

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THE RECURRENT HORIZONTAL TRANSFERS OF DIFFERENT
TRANSPOSABLE ELEMENTS BETWEEN LEPIDOPTERA SPECIES

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OSBORN LAW OF ADAPTIVE RADIATION AS A BACKGROUND OF AROMORPHOSES

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STRESS AND HOMEOMORPHY OF ADAPTATION MECHANISMS

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TENDER FOR A ECOLOGICAL NICHE AS CONDITION OF THE ARO(ALLO)MORPHOSES

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OLIGONUCLEOTIDE FREQUENCIES AND GC CONTENT OF BACTERIAL GENOMES ARE RELATED TO THE ENVIRONMENT EVOLUTION

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MOLECULAR EVOLUTION OF PROTEINS BELONGING TO AUXIN BIOSYNTHESIS GENE NETWORK IN PLANTS

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PHYLOGENETIC ANALYSIS OF ESX HOMEOBOX PROTEIN OF BUBALUS BUBALIS

June 29, Friday House of Scientists, Foyer of Small Conference Hall

SECTION “MATHEMATICAL BIOLOGY AND SYSTEM MODELING”

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KINET – A NEW WEB DATABASE ON KINETICS DATA AND PARAMETERS FOR *E.coli.*

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FOR LOOPS MODELING IN A GENOME.

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ENHANCER MODEL

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DISCRETE AUTOMATON MODEL OF GENE NETWORK WITH VARIOUS FORMS OF REGULATORY ACTIVITY OF AGENTS (BASED ON E.COLI)

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AN INVERSE PROBLEM OF IDENTIFICATION OF PARAMETERS IN ONE GENE NETWORK MODEL

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A COMPUTER SYSTEM FOR KINETIC ANALYSIS OF GENE NETWORKS

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HIGH PERFORMANCE COMPUTING WITH MGSMODELLER

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MODELING AND ANALYSIS OF DYNAMICS OF THE RIBOPYRIMIDINES DE NONO BIOSYNTHESIS IN E. COLI

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BIOUML: MODULAR MODELING OF COMPLEX BIOLOGICAL SYSTEMS

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HAPLOID EVOLUTIONARY CONSTRUCTOR: A GRAPHICAL USER INTERFACE FOR SIMULATING BACTERIAL COMMUNITIES EVOLUTION

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MODELLING KREBS CYCLE AS AN ELECTRICAL CIRCUIT

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EFFECTS OF IN- AND OUTBREEDING IN POPULATIONS OF DIPLOID ORGANISMS: COMPUTER SIMULATIONS WITH THE DIPLOID EVOLUTIONARY CONSTRUCTOR

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ABOUT SHIFT FUNCTION OF IRREGULAR POLYMERS SYNTHESIS IN MODELS OF THE MATRIX SYNTHESIS.

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SPATIALLY DISTRIBUTED MODELING OF BACTERIAL COMMUNITIES WITH HAPLOID EVOLUTIONARY CONSTRUCTOR

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A discrete dynamical system on a double circulant with an additive function of the vertices
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THE DISCRETE DINAMIC SYSTEM ON A DOUBLE CIRCULANT WITH DIFFERENT FUNCTIONS AT THE VERTICES

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MULTIPLE SOLUTIONS UNDER MODELING OF THE NITRATE UTILIZATION SYSTEM IN ESCHERICHIA COLI

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T-CELL PROLIFERATION ON IMMUNOPATHOGENIC MECHANISM OF PSORIASIS: A CONTROL BASED THEORETICAL APPROACH

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SEARCHING FOR REGULATORY CIRCUITS IN GENE NETWORKS

SECTION “COMPUTER BIOLOGY OF DEVELOPMENT”

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ROLE OF AUXIN DOSE-DEPENDENT CONTROL IN SPECIFICATION OF ROOT VASCULAR CELLS

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MATHEMATICAL MODEL OF AUXIN RESPONSIVE REPORTER DR5 ACTIVITY IN PLANT CELL

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VARIABLE PATTERNING IN DROSOPHILA EMBRYOS DUE TO BASINS OF ATTRACTION IN UNDERLYING GENE REGULATORY DYNAMICS

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ACTIVATION OF CLV3 GENE EXPRESSION IN MODEL OF THE STEM CELL NICHE STRUCTURE REGULATION IN THE SHOOT APICAL MERISTEM

SECTION “INTEGRATIVE BIOINFORMATICS AND INTELLIGENT KNOWLEDGE DISCOVERY/MANAGEMENT”

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TEpredict – SOFTWARE FOR PREDICTING T-CELL EPITOPES. AN UPDATE

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FLUORESCENCE IN SITU HYBRIDIZATION WITH CHROMOSOME-DERIVED DNA PROBES ON OPISTHORCHIS FELINEUS AND METORCHIS XANTHOSOMUS CHROMOSOMES WITHOUT SUPPRESSION OF REPETITIVE DNA SEQUENCES

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EXTRACTION OF QUANTITATIVE CHARACTERISTICS DESCRIBING WHEAT LEAF PUBESCENCE WITH A NOVEL IMAGE PROCESSING TECHNIQUE

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HETEROGENIC DATA MINING AND COMBINING

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RECONSTRUCTION OF THE ASSOCIATIVE GENETIC NETWORKS BASED ON INTEGRATION OF AUTOMATED TEXT-MINING METHODS AND PROTEIN-LIGAND INTERACTIONS PREDICTION

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TOWARDS A PUBLIC REPOSITORY FOR SYSTEMS MICROSCOPY DATA

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DEVELOPMENT OF THE SOFTWARE COMPLEX “GENETICS” FOR SUPPORT INVESTIGATIONS IN MEDIC GENETICS

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BIOINFORMATICS APPROACH TO THE STUDY OF DYSTROPIC DISEASES

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ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF NATURAL GENOMES AND THEIR ELEMENTS

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GENE-CENTRIC KNOWLEDGEBASE ON THE WEB

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UNSUPERVISED ALGORITHM BASED ON WAVELET ANALISYS FOR EXTRACTION OF INFORMATION ABOUT HIPPOCAMPAL NEURONAL ACTIVITY characteristics FROM THE EXPERIMENTAL DATA

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INFLUENCES OF PROTEIN FUNCTIONAL SITES ENCODING FEATURES ON PROTEIN EVOLUTION IN EUKARYOTA

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CLUSTERIZATION OF GENE EXPRESSION PROFILES OF HUMAN ASTROCYTIC GLIOMAS ON SELF-ORGANIZING MAPS

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DISTRIBUTED RESTFUL-WEB-SERVICES FOR THE RECONSTRUCTION AND ANALYSIS OF GENE NETWORKS

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BioUML: PLUGIN FOR STOCHASTIC MODELING OF BIOLOGICAL SYSTEMS

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INTEGRATIVE CELL MODELING USING DATA INTEGRATION AND TEXT MINING APPROACHES

SECTION “SUPERCOMPUTER APPLICATIONS IN BIOINFORMATICS”

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PROTEIN THERMAL STABILITY STUDY USING NAMD ON HIGH-PERFORMANCE CLUSTER

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HEMAEXPLORER WEBSERVER: VISUALIZATION OF GENEEXPRESSION IN THE HEMATOPOETIC SYSTEM

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COMPLEX COMPUTATIONS AND WORKFLOWS IN MOLECULAR BIOLOGY

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SOMATIC COPY-NUMBER ALTERATION CAN HELP PREDICT THE TISSUE ORIGIN OF CANCERS OF UNKNOWN PRIMARY

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HAPLOID EVOLUTIONARY CONSTRUCTOR: PARALLELIZATION AND HIGH PERFORMANCE SIMULATIONS OF PROKARYOTIC COMMUNITIES EVOLUTION

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SUPERCOMPUTER APPLICATIONS IN BIOINFORMATICS: SHARED FACILITY CENTER “BIOINFORMATICS” OF SIBERIAN BRANCH OF THE RUSSIAN ACADEMY OF SCIENCES

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THE TECHNIQUES AND TOOLS FOR THE SOLVING BIONFORMATICS TASKS IN THE DISTRIBUTED COMPUTING SYSTEMS

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CLASSIFICATION OF PURIFIED BONE MARROW POPULATIONS SORTED VIA MULTICOLOR FLOW CYTOMETRY, APPLICATIONS IN ACCUTE MYELOID LEUKEMIA

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IMPLEMENTING PERMUTATION TEST ON GPU