BGRS\SB-2016

10th anniversary International Multiconference
«Bioinformatics of Genome Regulation and Structure\ Systems Biology»

Novosibirsk, Russia, 29 August – 2 September, 2016

	29 August, Monday
8:30-10:00	Registration (*House of Scientists SB RAS, main entrance)*
10.20–16.20	**Plenary session** *(House of Scientists SB RAS, Large hall)* *Chairpersons: Prof. Nikolay Kolchanov, Prof. Ralf Hofestädt*
10:20-11.00	Opening *(House of Scientists SB RAS, Great hall)* Nikolay Kolchanov Institute of Cytology and Genetics, Novosibirsk, Russia
11.00–11.40	**Aging and cancer: stateofart and prospects for prevention** Vladimir Anisimov Department of Carcinogenesis and Oncogerontology, N.N. Petrov Research Institute of Oncology, Saint Petersburg, Russia
11.40–12.20	**Postgenome medicine as n-of-one science** Andrey Lisitsa, E.V. Kolker, H. Huan-Wen Chen, V.E. Frankevich Institute of Biomedical Chemistry, Moscow, Russia
12.20–13.00	**Active maintenance of phylotranscriptomic hourglass patterns in plant and animal embryogenesis** H.G. Drost[1], A. Gabel[1], I. Ivo Grosse[1,2], M. Quint[3,4] [1]Institute of Computer Science, Martin Luther University Halle-Wittenberg, Halle, Germany [2]German Centre for Integrative Biodiversity Research Halle-Jena-Leipzig, Leipzig, Germany [3]Department of Molecular Signal Processing, Leibniz Institute of Plant Biochemistry, Halle, Germany [4]Institute of Agricultural and Nutritional Sciences, Martin Luther University Halle-Wittenberg, Halle, Germany
13.00–14.00	Lunch
14.00–14.40	**Genetics of Aging and Dementia** Evgeny Rogaev University of Massachusetts, USA
14.40–15.20	**Regulation of RIPKs in cell survival and cell death by apoptosis and necroptosis, insights and therapeutic potential** Peter Vandenabeele VIB Inflammation Research Center, Zwijnaarde-Ghent, Belgium Department of Biomedical Molecular Biology, Ghent University, Ghent, Belgium
15.20–16.00	**Macroevolutionary and experimental assays of fitness landscapes** Fyodor Kondrashov Centre for Genomic Regulation, Barcelona, Spain
16.20–17.00	Coffee break with Thomson Reuters. **Coffee with Thomson Reuters. Integrity - essential knowledge to empower your drug discovery and development** Sergey Paramonov, Vladimir Poroikov Thomson Reuters, Moscow, Russia

29 August					
Time	*Small hall*	*Time*	*Library*	*Time*	*223*
16.40–19.40	**Section "Systems Computational Biology"** *Chairperson:* Alexander Ratushny, Celgene, Seattle, USA and Institute for Systems Biology, Seattle, USA				
16.40–17.10	**Evolution of phenotypic control by new genes through integrating and rewiring of ancestral expression networks** Manyuan Long Department of Ecology and Evolution, The University of Chicago, Chicago, USA				
17.10–17.40	**KATIS: integrative information system for complementary medicine** Ralf Hofestädt, V. Ogultarhan and A. Shoshi University Bielefeld, Bielefeld, Germany				
17.40–18.10	**FAIRDOM: Data and Model Management for Systems Biology Projects** Olga Krebs[1], R. Kuzyakiv[5], M. Golebiewski[1], S. Owen[2], Q. Nguyen[1], N. Stanford[2], K. Wolstencroft[4], J.L. Snoep[2,3], B. Rinn[5], W. Mueller[1], C. Goble[2] [1]Heidelberg Institute for Theoretical Studies, Germany [2]School of Computer Science, University of Manchester, UK [3]Department of Biochemistry, University of Stellenbosch, South Africa [4]Leiden Institute of Advanced Computer Science, Leiden University, NL [5]ETH Zurich, Swiss				
18.10–18.40	**Two models of the drosophila gap gene network with variation of maternal input** Konstantin Kozlov[1], A.V. Svichkarev[1], V.V. Gursky[1,2], I.V. Kulakovskiy[3], S.Y. Surkova[1], and M.G. Samsonova[1] [1]Peter the Great St. Petersburg Polytechnic University, St. Petersburg, Russia [2]Ioffe Institute, St. Petersburg, Russia [3]Engelhardt Institute of Molecular Biology, RAS, Moscow, Russia				
18.40–19.10	**Differential analysis of three-dimensional (d) genomics data** Guoliang Li Huazhong Agricultural University, Wuhan, China				

19.10–19.40	**Elemental metabolomics–linking environmental, food, nutrition and health sciences** P. Zhang[1], I. Giannenas[2], C.A. Georgiou[3], Vladimir Brusic[1,4] [1]Menzies Health Institute Queensland, Griffith University, Australia [2]Aristotle University of Thessaloniki, Thessaloníki, Greece [3]Department of Food Science and Nutrition, Agricultural University of Athens, Greece [4]School of Medicine and Bioinformatics Center, Nazarbayev University, Kazakhstan				
19.40–22.00	Buffet				
30 August					
9.00–13.10	**Section "Genomics, Transcriptomics and Bioinformatics"** *(House of Scientists SB RAS, Small hall)* *Chairpersons: Ivo Grosse, Halle-Wittenberg University, Halle, Germany; Vsevolod Makeev, VIGG RAS, MIPT, Moscow, Russia*				
9.00–9.30	**Transcription by alternative sigma factors: revising the rigidness paradigm** Jelena Guzina, M. Djordjevic Faculty of Biology, University of Belgrade, Studentski trg 16, 11000 Belgrade, Serbia				
9.30–10.00	**Reconstruction of transcription control network in genome-reduced bacteria by high-throughput promoters identification** Irina Garanina, G.U. Fisunov., D.V. Evsutina, V.M. Govorun Scientific Research Institute of Physical-Chemical Medicine SRI PCM, Moscow, Russia				
10.00–10.30	**Single cell expression profiling of neural crest-derived cells** Tatiana Subkhankulova[1], G. Aquino[2], A. Rocco[2], H. Schwetlick[1], R.N. Kelsh[1] [1]Department of Biology and Biochemistry, University of Bath, Bath, UK [2]Department of Microbial and Cellular Sciences, University of Surrey, Guildford, UK				
10.30–10.45	**Using Dolomite Microfluidics for sequencing the transcriptome of individual cells** Dmitry Brittal LLC "Dia M", Moscow, Russia				

10.55– 11.10	Coffee break				
11.10– 11.40	**Dissecting variance heterogeneity in human serum metabolome** Sodbo Sharapov[1,2], Tsepilov Y.A.[1,2], Ried J.S.[3], Strauch K.[3,4], Gieger C.[3], Aulchenko Y.S.[1,2] [1]Institute of Cytology and Genetics SD RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Institute of Genetic Epidemiology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany [4]Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany	**11.00-16.00**	**Section "Bioinformatics and Systems Biology of Cell Death"** *(House of Scientists SB RAS, Library)* *Chairpersons: Inna Lavrik, Otto von Guericke University, Magdeburg, Germany*		
11.40– 12.10	**HOCOMOCO COmprehensive MOdel COllection as a practical gateway to regulatory motif-ome of human and mouse transcription factors** I.E. Vorontsov, Y.A. Medvedeva, V.J. Makeev, Ivan Kulakovskiy Vavilov Institute of General Genetics, Moscow, Russia Engelhardt Institute of Molecular Biology, Moscow, Russia	11.00– 11.40	**The p53 family in cancer biology** I. Amelio[1], F. Bernassola[2], T.W. Mak[2], Gerry Melino[1,3] [1]MRC Toxicology Unit, LeicesterLE1 9HN, United Kingdom [2]The Campbell Family Cancer Research Institute, Toronto, Ontario M5G 2M9, Canada [3]University of Rome Tor Vergata, Rome, Italy		
12.10– 12.25	**Regulatory role of single CpG methylation** A. Khamis[1], A.V. Artemov[2], A.V. Lioznova[2], V.B. Bajic[1], Yulija Medvedeva[2] [1]King Abdullah University of Science and Technology [2]Research Center of Biotechnology RAS	11.40– 12.10	**Chemoresistance of lung adenocarcinoma is regulated by Tudor staphylococcal nuclease** Boris Zhivotovsky[1,2] [1]Lomonosov Moscow State University, Moscow, Russia [2]Karolinska Institutet, Stockholm, Sweden		
12.25– 12.40	**Ampliseq ™: amplification and sequencing** Ilya Volkov Department of scientific and methodological support of "Khimexpert Agency", Moscow, Russia	12.10– 12.40	**The role of kinetochore-driven microtubule formation in *Drosophila* spindle assembly** G. Pavlova[1,2,*], J. Popova[1,3,*], A. Munzarova[1,4,*], J. Galimova[1,*], A. Razuvaeva[1,4], F. Renda[5], P. Somma[5], A. Pindyurin[1,4], Maurizio Gatti[5] [1]Institute of Molecular and Cellular Biology, Novosibirsk, Russia [2]Kazan Federal University, Kazan, Russia [3]Institute of Cytology and Genetics, Novosibirsk, Russia [4]Novosibirsk State University, Novosibirsk, Russia [5]Department of Biology and Biotechnology, Sapienza, University of Rome, Rome, Italy		

12.40–12.45	**Target enrichment technologies for applied research** Dmitry Kwon Agilent Technologies Russia, Moscow, Russia	12.40–13.00	**Involvement of various cell death modalities in cytotoxic activity of lactaptin analog** Olga Koval[1,2], G.V. Kochneva[1,3], A.V. Tkachenko[1], O.S. Troitskaya[1,2], G.F. Sivolobova[1,3], E.V. Kuligina[1], A.Y. Yunusova[1], V.A. Richter[1] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Novosibirsk State University [3]State Research Center of Virology and Biotechnology "Vector", Koltsovo, Russia		
13.00–14.00	Lunch	13.00–14.00	Lunch		
14.00–19.40	**Section "Systems Computational Biology"** *(House of Scientists SB RAS, Small hall)* *Chairperson:* Alexander Ratushny, Celgene, Seattle, USA and Institute for Systems Biology, Seattle, USA	14.00–14.40	**Towards understanding the dynamics of death receptor networks** Inna Lavrik Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Otto-von Guericke-University, Magdeburg, Germany		
14.00–14.30	**Virtual biology — the foundation** Fyodor Kolpakov Institute of Systems Biology Ltd., Novosibirsk, Russia Design Technological Institute of Digital Techniques SB RAS Novosibirsk, Russia	14.40–15.10	**Delineating single cell life/death decisions in the CD95/FAS network** Jörn Buchbinder[1], D. Pischel[2], K. Sundmacher[2], R.J. Flassig[2], I.N. Lavrik[1] [1]Department of Translational Inflammation Research, Otto-von-Guericke University Magdeburg, Germany [2]Max-Planck-Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany		
14.30–14.45	**A mathematical model for predicting of IgD–CD27+B lymphocytes levels in donors' blood** Sergei Kuznetsov1*, I.V. Kudryavtsev[2], A.V. Orekhov[1], A.V. Polevshchikov[2], M.K. Serebriakova[2], V.I. Shishkin[1] [1]St. Petersburg State University, St. Petersburg, Russia [2]Institute of Experimental Medicine, St. Petersburg, Russia	15.10–15.30	**Novel approach for computational design of small molecule inhibitors of protein/protein interactions in CD95/FAS pathway** Nikita Ivanisenko[1,2], A.S. Ishchenko[1,2], I.N. Lavrik[1,3], V.A. Ivanisenko[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Otto-von Guericke-University, Magdeburg, Germany		
14.45–15.00	**Altered catecholaminergic, serotonergic, gabaergics, and glutamatergic genes**	15.30–15.50	**Associative networks of glaucoma and apoptosis**		

	expression in the ventral tegmental area of male mice under chronic social defeat stress: RNA-*SEQ* data Anna Galyamina, I.L. Kovalenko, D.A. Smagin, N.N. Kudryavtseva Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia		Olga Saik[1], P.S. Demenkov[1], O.S. Konovalova[2], M.N. Ponomareva[2], N.A. Konovalova[2], N.A. Kolchanov[1], I.N. Lavrik[3], V.A. Ivanisenko[1]. [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Tyumen State Medical Academy, Ministry of Health of the Russian Federation, Tyumen, Russia [3]Otto von Guericke University Magdeburg, Magdeburg, Germany		
15.00–15.15	**Modeling of two phases in *Drosophila* sensory organ precursor cell determination** T.A.Bukharina[*1*], D.P.Furman[*1,2*], Vladimir Golubyatnikov[*2,3*], M.V.Kazantsev [*4*] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [4]Polzunov Altai State Technical University, Barnaul, Russia				
15.15–15.30	**Generalising better: applying deep-learning to integrate deleteriousness prediction scores for whole-exome SNV studies** Ilia Korvigo, A.A. Afanasyev Moscow Institute of Physics and Technology				
15.30–15.45	**Does thyroid divergence serve as a driver of speciation in cyprinid fishes of the genus *Ballerus* (teleostei)?** Boris Levin[1]*, A.A. Bolotovskiy[1], M.A. Levina[1], A.V. Nedoluzhko[2], K.G. Skryabin[2,3,4], S.M. Rastorguev[2], E.B. Prokhortchouk[3,4] [1]Institute of Biology of Inland Waters RAS, Borok, Russia [2]National Research Center Kurchatov Institute, Moscow, Russia [3]Institute of Bioengineering, Federal Research Center "Fundamentals of Biotechnology" RAS, Moscow, Russia [4]Lomonosov Moscow State University, Faculty of Biology, Moscow, Russia				
15.45–16.00	**Parameter fitting infrastructure for rule-based modelling** O.S. Sorokina[1], Anatoly Sorokin[2,3] [1]Edinburgh University, Edinburgh, UK [2]Institute of Cell Biophysics RAS, Pushchino, Russia [3]Moscow Institute of Physics and Technology, Dolgoprudny, Russia				

16.00–16.15	Coffee break				
16.15–16.30	**Solutions for analysis of NGS-data from the company Illumina** Dania Gazizova ООО “Альбиоген”				
16.30–16.45	**Using the techniques of stochastic modelling and inhomogeneous sequential pattern recognition procedure for the prediction of the development of polygenic diseases** V.F. Prokof'ev, A.V. Shevchenko, Maksim Korolev, V.I. Konenkov Scientific Institute of clinical and experimental lymphology SB RAS, Novosibirsk, Russia				
16.45–17.00	**The bioinfornational comparison of CRISPR/Cas system structure of *Yyersinia pseudotuberculosis* strains isolated from different regions** Nadezhda Peretolchina[1], Y.P. Dzhioev[1,2], A.Y. Borisenko[1], E.A. Voskresenskaya[3], A.I. Paramonov[2], L.A. Stepanenko[1], V.I. Zlobin[1] [1]Irkutsk State Medical University, Irkutsk, Russia [2]Scientific Center of family health problems and human reproduction, Irkutsk, Russia [3]Institut Pasteur, Saint Petersburg, Russia				
17.00–17.15	**Theoretical model of mitotic spindle microtubule growth for FRAP curve interpretation** Leonid Omelyanchuk[1,2], A.F. Munzarova[1,2], T.Y. Mikhailova[2] [1]Institute of Molecular and Cellular Biology, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia				
17.15–17.30	**Computer analysis of biological networks of mammalian circadian oscillator** Nikolay Podkolodnyy[1,2,3], N.N. Tverdokhleb[1,3], E.O. Sambilova[3], S.A. Lobynya[3], Z.D.Yakubova[3], O.A. Podkolodnaya[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk [3]Novosibirsk State University, Novosibirsk				
17.30–17.45	**Principal organization of physiological regulator** Vyacheslav Fedorov				

	Institute of Laser Physics SB RAS, Novosibirsk, Russia				
17.45–17.55	**Phage infection slows down speciation caused by gene loss and horizontal gene transfer of metabolic genes in models of spatially distributed bacterial communities** Aleksandra Klimenko, Yu.G. Matushkin, N.A. Kolchanov, S.A. Lashin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia				
17.55–18.05	**Crossing valleys and reaching peak on the fitness landscapes in microbial communities under various ecological conditions: a simulation study** Zakhar Mustafin[1], D.A. Afonnikov[1,2], Yu.G. Matushkin[1,2], S.A. Lashin[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia				
18.05–18.15	**Role of membrane potential in nitrite utilization by *Escherichia Coli* cells under low substrate concentrations: the mathematical model** Natalya Ree, Likhoshvai V.A., T.M. Khlebodarova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia				
18.15–18.25	**Modeling restriction-modification systems: expressing toxic molecules within a cell** Andjela Rodic, M. Djordjevic University of Belgrade, Belgrade, Serbia				
18.25–18.35	**Differential expression in *Helix lucorum* statocysts under microgravity conditions** Alexander Osypov[1,2], P. Kolosov[1], N. Aceyev[1], E. Chesnokova[1], M. Roshchin[1], N. Bal[1], P. Balaban[1] [1]Institute of Higher Nervous Activity and Neurophysiology of RAS, Moscow, Russia, [2]Institute of Cell Biophysics of RAS, Pushchino, Russia				
18.35–18.45	**Tumor-specific cell free DNA as a biomarker of metastasis** Tatiana Gorbacheva[1], S.A. Solodskikh[1], V.yu. Bashmakov[1], V.Yu. Panevina[1], A.Y. Maslov[2], V.N. Popov[1] [1]Voronezh State University, Voronezh, Russia [2]Albert Einstein College of Medicine of Yeshiva, USA				

31 August					
9.00–13.10	Section "Evolutionary Bioinformatics" *(House of Scientists SB RAS, Small hall)* *Chairpersons:* Fyodor Kondrashov, Evolutionary Genomics laboratory and ICREA, Barcelona, Spain	**9.00–12.50**	**Section "Animal Genetics"** *(House of Scientists SB RAS, Library)* *Chairperson:* Mikhail Moshkin, ICG SB RAS, Novosibirsk, Russia		
9.00–9.35	**Patterns and mechanisms of chromosomal evolution inferred from physically mapped genome assemblies** Igor Sharakhov[1,3,4], G.N.Artemov[4], A. Peery[1], X. Jiang[3], A.B. Hall[3], Z.Tu[2,3], A.N. Naumenko[1], V.N. Stegniy[4], M.V. Sharakhova[3] [1]Department of Entomology, Virginia Polytechnic Institute and State University, Blacksburg, USA. [2]Department of Biochemistry, Virginia Polytechnic Institute and State University, Blacksburg, USA. [3]The PhD Program in Genomics Bioinformatics and Computational Biology, Virginia Polytechnic Institute and State University, Blacksburg, USA. [4]Laboratory of Evolutionary Cytogenetics, Tomsk State University, Tomsk, Russia.	9.00–9.35	**The role of functional domains of *Drosophila* septin Pnut** K.A.Akhmetova[1,2,3], N.V.Dorogova[1], M.L.Balasov[3], Svetlana Fedorova[1,2], I.N.Chesnokov[3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]University of Alabama at Birmingham, Birmingham, USA		
9.35–10.00	**Evolution of restriction-modification systems in large scale** Olga Bezsudnova[1], I.S. Rusinov,[1,2] A.S. Ershova,[2,3,4] A.S. Karyagina,[2,3,4] S.A. Spirin,[1,2,5] A.V. Alexeevski[1,2,5] [1]Faculty of Bioengineering and Bioinformatics, Moscow State University, Russia [2]Belozersky Institute of Physico-Chemical Biology, Moscow State University, Russia [3]Gamaleya Center of Epidemiology and Microbiology, Moscow, Russia [4]Institute of Agricultural Biotechnology RAS, Moscow, Russia [5]Scientific Research Institute for System Studies, RAS, Moscow, Russia	9.35–10.00	**Virome analysis for identification of viruses in bat species from Moscow region** Anna Speranskaya[1], Pimkina E.V.[1], Artyushin I.V.[2], Safonova M.V.[1], Deviatkin A.A.[1], Kuleshov K.V.[1], Dedkov V.G.[1], Shipulin G.A.[1] [1]Central Research Institute for Epidemiology, Russian Inspectorate for Protection of Consumer Right and Human Welfare, Moscow, Russia [2]Biological Faculty, Moscow State University, Moscow, Russia		
10.00–10.25	**RNA-Seq data analysis of rats with aggressive behavior in three brain areas** Anatoly Bragin, Markel A.L., Babenko V.N., Chadaeva I.V., Tiys E.S., Orlov Y.L. Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia	10.00–10.25	**Identification of breed-specific SNP-markers for *Sus scrofa domesticus* using SRA-data of NGS projects** Iosif Tsybovsky, V.N. Kipen, S.A. Kotova Scientific and Practical Centre of the State Committee of Forensic Expertises, Minsk, Belarus		

10.25–10.50	**Long-term spaceflight mediated changes in promoter landscape in Zebrafish tissues** Alexander Cherkasov[1], K.V. Arshavsky[1], V.N. Sychev[2], M.A. Levinskikh[2], O.A. Gusev[1,3,4] [1]Institute of Fundamental Biology and Medicine, Kazan Federal University, Kazan, Russia; [2]Institute for Biomedical Problems, Russian Academy of Sciences, Moscow, Russia; [3]Division of Genomic Technologies, CLST, RIKEN, Yokohama, Japan; [4]Preventive Medicine & Diagnosis Innovation Program, CLST, RIKEN, Yokohama, Japan	10.25–10.50	**Identification of the taxa of the order *Artiodactyla* for criminal investigation cases of illegal hunting** Iosif Tsybovsky, S.A. Kotova, V.I. Rybakova, A.A. Rabcava, E.A. Spivak Scientific and Practical Centre of the State Committee of Forensic Expertises, Minsk, Belarus		
10.50–11.10	Coffee break,	10.50-11.10	Coffee break,		
11.10–11.35	**Darwinian genetic drift** Dmitri Parkhomchuk, A.C.McHardy Helmholtz Center for Infection Research, Braunschweig, Germany	11.10–11.35	**The density of *Wolbachia* strain *w*MelPop in *Drosophila melanogaster* brain is inversely related to the level of *hsp67bc* gene expression** Dina Malkeyeva[1, 2], E.V. Kiseleva[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia		
11.35–12.00	**Sex chromosome evolution in Pamphagidae grasshoppers** Ilyas Jetybayev[1,2], A.G. Bugrov [2,3], O.G. Buleu ,[2,3], A.G. Bogomolov[1], N.B. Rubtsov[1,3] [1]Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2]Institute of Systematics and Ecology of Animals, SB RAS, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia	11.35-12.00	**Targeted spatial genome modification in topologically associating domains structure in mouse embryonic stem cells** Varvara Lukyanchikova, N.R. Battulin, O.L. Serov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia		
12.00–12.25	**Genetic diversity in native Siberian populations: correlation with climatic and geographical parameter** Vladimir Kharkov[1,2], A.V. Markov[1,2], I.Yu. Khitrinskaya[1], V.A. Stepanov[1,2] [1]Research Institute for Medical Genetics, Tomsk, Russia [2]Tomsk State University, Tomsk, Russia	12.00–12.25	**The spatial map of avian genome** Veniamin Fishman[1,2], N. Battulin[1,2], A. Maslova[3], O. Serov[1,2], A. Krasikova[3] [1]Institute of Cytology and Genetics SB RAS, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Saint-Petersburg State University, St. Petersburg, Russia		
12.25–12.50	**Elucidation of molecular signal of transcription response to desiccation stress in chironomid *P. vanderplanki*** Elena Shagimardanova[1], R.M. Deviatiyarov[1], T Kikawada[2], O.A. Gusev[1,3]	12.25–12.50	**Ageing of multicellular organisms as a stage of ontogenesis** Igor Erokhin National Biotechnological Company LLC, Moscow, Russia		

	Kazan Federal University, Kazan, Russia National Institute of Agrobiological Sciences, Tsukuba, Japan RIKEN, Yokohama, Japan				
	Lunch		**Lunch**		**Lunch**
14.00–18.10	**Section "Computational Pharmacology"** *(House of Scientists SB RAS, Small Hall)* *Chairpersons:* Vladimir Poroikov, Institute of Biomedical Chemistry, Moscow, Russia; Elena Schwartz, Elena Schwartz Ami-Go-Science LLC, Rockville, MD United States	**14.00–18.10**	**Section "Systems Biology of Aging"** *(House of Scientists SB RAS, Library)* *Chairpersons:* Vladimir Anisimov, President of Gerontological society of the Russian Academy of Sciences, N.N. Petrov Research Institute of Oncology, Saint-Petersburg, Russia; Alexey Moskalev, Institute of Biology, Komi Science Centre; Natalya Kolosova, Institute of Cytology and Genetics of SB RAS	**14.00–18.45**	**Section "Bioinformatics and Molecular Biology of DNA Damage Response"** *(House of Scientists SB RAS, Room 223)* *Chairpersons:* Grigory Dianov, University of Oxford, United Kindom & Institute of Cytology & Genetics, Novosibirsk, Russia
14.00–14.35	**Infant nasopharyngeal microbiome in respiratory syncytial virus cohort–a case study in developing and applying "Do It Yourself analysis tools" for the bench scientists** Andrey Tovchigrechko Research Bioinformatics, Medimmune LLC, Gaithersburg, MD United States	14:00-14:25	**Systemic role of allelic variants in a 2q22 region in major age-related diseases and lifespan** Alexander Kulminski, L. He, I. Culminskaya, Y. Loika, Y. Kernogitski, K.G. Arbeev, E. Loiko, L. Arbeeva, O. Bagley, M. Duan, A. Yashkin, F. Fang, M. Kovtun, S.V. Ukraintseva, D. Wu, A.I. Yashin Duke University, Durham, USA	14:00-14:15	**Base excison repair mechanisms. Introduction**. Grigory Dianov University of Oxford, United Kindom; Institute of Cytology and Genetics, Novosibirsk, Russia
14.35–15.00	**Disease models for cancer to select candidate biomarkers and drug target** Elena Schwartz[1], Anton Yuryev[2], Che Ross[3], Irene Riz[4] and Alexandra McPherron[1]. [1]Ami-Go-Science, 5917 Barbados Place, Rockville MD, USA [2]Elsevier, Rockville, MD, USA; [3]Johns Hopkins University, Baltimore, MD, USA [4]George Washington University, Washington DC, USA	14:25-14:50	**Neuronal transcriptional regulation of *Drosophila* life span** O. Y. Rybina[1,2], A. V. Symonenko[1], N. V. Roshina[1], A. V. Krementsova[1,3], E. R. Veselkina[1], M.I. Schelkunov[4], S. V. Sarantseva[5], Elena Pasyukova[1] [1] Institute of Molecular Genetics of RAS, Moscow, Russia [2] Moscow State Pedagogical University, Institute of Biology and Chemistry, Russia [3] N. M. Emmanuel Institute of Biochemical Physics of RAS, Moscow, Russia [4] M. V. Lomonosov Moscow State University, Russia [5] B. P. Konstantinov Petersburg Nuclear Physics Institute, Russia	14:15-14:45	**Regulation of base excision repair-canonical and non-canonical processing of genomic uracil** Hans Krokan, H.S. Pettersen, R. Mjelle, S.A. Hegre, P. Sætrom, F. Drabløs, A. Sarno, A. Galashevskaya, P.A. Aas, N.B. Liabakk, B. Doseth, G. Slupphaug, B. Kavli Norwegian University of Science and Technology, Trondheim, Norway
15.00–15.25	***In silico* screening for sulfonate-based inhibitors against promising anticancer targets** Dmitry Nilov[1]*, I.V. Gushchina[2], V.K. Švedas[1,2]	14:50–15.15	**Comparative expression landscapes in replicative and stress induced premature senescence**	14:45-15:15	**Poly(ADP-ribose) polymerase 1 and regulation of DNA repair** Olga Lavrik

	[1]Belozersky Institute of Physicochemical Biology, Lomonosov Moscow State University, Moscow, Russia [2]Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, Russia		K.C. Kural[1], N. Tandon[2], O.V. Kel-Margoulis[2], Anna Baranova[1,3,4] [1]School of Systems Biology, George Mason University, Fairfax, VA USA [2]geneXplain, Wolfenbüttel Germany [3]Federal State Budgetary Institution "Research Centre for Medical Genetics," Moscow, Russia [4]ATLAS Biomed Group, Moscow, Russia		Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia
15.25–15.50	**Identification of proteins associated with drug-induced liver injury using in silico prediction of drug-target interactions** Sergey Ivanov[1,2]*, M.I. Semin[1,2], A.A. Lagunin[1,2], D.A. Filimonov[1], V.V. Poroikov[1,2] [1]Institute of Biomedical Chemistry, Moscow, Russia [2]Pirogov Russian National Research Medical University, Medico-Biological Faculty, Moscow, Russia	15.15–15.35	**Changes in the brain transcriptome of OXYS rats as the signs of Alzheimer's disease develop and effects of SkQ1** Natalia Stefanova, N.I. Ershov, N.A. Muraleva, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia	15:15-15:45	**Speed reading at the molecular scale: how enzymes find typos in a DNA text** Dmitrij Zharkov, Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
15.50–16.10	Coffee break	15.35–15:50	**The mitochondria-targeted plastoquinone SkQ1 affects *Drosophila melanogaster* lifespan in various environment** Anna Krementsova[1], N. V. Roshina[2], E. A. Tsybulko[2], O. Y. Rybina[2], A. V. Symonenko[2], E. G. Pasyukova[2] [1]Emmanuel Institute of Biochemical Physics of RAS, Moscow, Russia [2]Institute of Molecular Genetics of RAS, Moscow, Russia	15:45-16:10	Coffee break
16.10–16.35	**Computer-aided drug repurposing: new uses for old drugs or filling gaps in biomedical knowledge?** Vladimir Poroikov, D.A. Filimonov, A.A. Lagunin, T.A. Gloriozova Institute of Biomedical Chemistry, Moscow, Russia	15.50-16.10	Coffee break	16:10-16:30	**Ku antigen displays the apurinic/apyrimidinic (AP) lyase activity on a certain types of duplex DNA** Anastasiya Kosova, S.N. Khodyreva, O.I. Lavrik Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
16.35–17.00	***In silico* design of aptamers containing g-quadruplexes** Arthur Zalevsky[1,2], A.O. Demkiv[2], A.V. Golovin[1,2] [1]Apto-Pharm LLC, Moscow, Russia [2]Faculty of bioengineering and bioinformatics, Lomonosov Moscow State University, Moscow, Russia	16:10–16.35	**Geroprotector and criteria for its evaluation** Alexey Moskalev[1-4], M. Shaposhnikov[1,2], E. Proshkina[1,2], V. Tsvetkov[4], A. Fedintsev[4], E. Chernyagina[4], A. Zhavironkov[4] [1]Institute of Biology of Komi Science Center of Ural Branch of RAS, Syktyvkar, Russia [2]Syktyvkar State University, Syktyvkar, Russia [3]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia	16:30-17:00	**Structural bioinformatics of Fpg glycosylase: search for substrate specificity in the sequence space** Anna Yudkina Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia

			[4]Moscow Institute of Physics and Technology, Dolgoprudny, Russia		
17.00–17.25	**Molecular modeling of influenza virus H1N1 hemagglutinin inhibition by camphor imines** Dmitry Baev, A.S. Sokolova, O.I. Yarovaya, T.G. Tolstikova, V.V. Zarubaev N.N. Vorozhtsov Novosibirsk Institute of Organic Chemistry SB RAS, Novosibirsk, Russia	16.35–17.00	**Perspectives for the prevention of accelerated aging** Vladimir Anisimov Department of Carcinogenesis and Oncogerontology, N.N. Petrov Research Institute of Oncology, Saint Petersburg, Russia	17:00-17:30	**DNA repair and death signalling targeted by alkylating anticancer drugs** Bernd Kaina Department of Toxicology, University Medical Center, Mainz, Germany
17.25–17.50	**Small molecule agonists of relaxin receptor** Alexander Agoulnik[1], I.U. Agoulnik[1], X. Hu[2], C. Myhr [1], Z. Huang[1], B.A. Ho[1], E. Barnaeva[2], J. Xiao[2], M. Ferrer[2], N.T. Southall[2], J.J. Marugan[2] [1]Herbert Wertheim College of Medicine, Florida International University, Miami, FL, USA; [2]NIH Chemical Genomics Center, National Center for Advancing Translational Sciences, National Institutes of Health, Rockville, MD, USA	17.00–17.25	**Systems biology, control theory and origin of aging** Alexander Khalyavkin, V.N. Krut'ko Institute of Biochemical Physics of RAS and FRC CSC RAS, Moscow, Russia	17:30-18:00	**Modulation of cognitive function by oxidative DNA base lesion repair** K. Scheffler[2], V. Rolseth[1], M.D. Bjørge[1], G. Hildrestrand[1], W. Wang[2], R. Suganthan[2], A. Kusnierczyk[2], Ch. Neurauter[1], H. Korvald[1], C. Vågbø[2], L. Luna[1], G. Slupphaug[2], L. Eide[2], Magnar Bjørås[1,2] [1]Department of Microbiology, University of Oslo and Oslo University Hospital, Oslo, Norway. [2]Department Cancer Research and Molecular Medicine, Norwegian University of Technology and Natural Sciences, Trondheim, Norway.
17.50–18.10	**The impact of human genetic variability on ligand-protein interactions and individual drug response** Peter Vlasov, O. Pich i Rosello, A.V. Vlasova, F.A. Kondrashov Centre for Genomic Regulation; Universitat Pompeu Fabra; Institució Catalana de Recerca i Estudis Avançats, Barcelona, Spain	17.25–17.50	**The role of the mechanisms of resistance to ionizing radiation in *Drosophila melanogaster* aging and longevity** Mikhail Shaposhnikov[1,2], E.N. Proshkina[1,2], L.A. Shilova[1], D.O. Peregudova[1], S.O. Zhikrivetskaya[3], A.A. Moskalev[1-4] [1]Institute of Biology of Komi Science Center of Ural Branch of RAS, Syktyvkar, Russia [2]Syktyvkar State University, Syktyvkar, Russia [3]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia [4]Moscow Institute of Physics and Technology, Dolgoprudny, Russia	18:00-18:20	**DNA damage initiating demethylation: a repair-epigenetic connection** Inga Grin[1,2], A.A. Ishchenko[3] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]CNRS UMR 8200, Gustave Roussy Cancer Campus, Villejuif, France
				18:20-18:30	**Systemic response to genetic and chemical modulation of DDR regulating wild type p53 induced phosphatase in skin, intestine and hematopoietic system** A.R. Goloudina[2], B.B. Grigorash[1], E.Y. Kochetkova[1], E. Appella[3], V.A. Pospelov[1], Oleg Demidov[1,2]

					[1]Institute of Cytology RAS, St. Petersburg, Russia [2]University of Burgundy, France [3]NCI, NIH, Bethesda, USA
				18:30-18:45	The functional interactions of pleiotropic protein yb-1 with key base excision repair factorsa Elizaveta Alemasova[1], N.A. Moor[1], K.N. Naumenko[1,2], P.E. Pestryakov[1], O.I. Lavrik[1,2] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Russia [2]Novosibirsk State University, Novosibirsk, 630090, Russia
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9.00–13.10	**Section "Bioinformatics and Systems Biology of Plants"** *(House of Scientists SB RAS, Small hall)* *Chairpersons:* Elena Salina, Institute of Cytology and Genetics of SB RAS; Ivan Paponov, Norwegian Research Institute for Agriculture and the Environment, Norway	**9:00–11.00**	**Section "Evolutionary Bioinformatics"** *(House of Scientists SB RAS, Small hall)* *Chairpersons:* Fyodor Kondrashov, Evolutionary Genomics laboratory and ICREA, Barcelona, Spain		
9.00–9.20	**Dynamic metabolic regulation by a chromosome segment from a wild species during fruit development in a tomato introgression line** Yoshinori Kanayama School of Agricultural Science, Tohoku University, Sendai, Japan	9.00–9.25	**Can long antiparallel open reading frames be encoding essential genes in prokaryotic genomes?** Denis Moshenskij, A.V. Alexeevski A.N. Belozersky Institute of Physico-Chemical Biology MSU, Moscow, Russia		
9.20–9.40	**New insights into the regulation of reactive oxygen species by auxin through gene expression analysis** Ivan Paponov[1,2*], V. Budnyk[1], T. Khodus[1], M. Paponov[1], K. Palme[1] [1]Institute of Biology II/Molecular Plant Physiology, Faculty of Biology, Albert-Ludwigs-University of Freiburg, Germany [2]NIBIO, Norwegian Institute of Bioeconomy Research, Postvegen, Norway	9.25–9.50	**Intron evolution: sliding and variability of length** Irina Poverennaya[1], D.D. Gorev[2], T.V. Astakhova[3], M.A. Roytberg[2,3]. [1] Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, Russia; [2] Moscow Institute of Physics and Technology, Moscow, Russia; [3] Institute of Mathematical Problems of Biology RAS, Pushchino, Russia		

9.40–10.00	**Genetics and physiology of wheat inflorescence development** Oxana Dobrovolskaya[1,5], P. Martinek[2], Yu.L. Orlov[1], A.A. Krasnikov[3], E.D. Badaeva[4], K.I. Popova[5], Salse J.[6], Watanabe.N.[7] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Agrotest Fyto, Ltd, Kroměříž, Czech Republic [3]Central Siberian Botanical Garden SB RAS, Novosibirsk, Russia [4]Vavilov Institute of General Genetics , RAS, Moscow, Russia [5]Novosibirsk State Agrarian University, Novosibirsk, Russia [6]INRA-UBP UMR-1095, Clermont –Ferrand, France [7]College of Agriculture, Ibaraki University, Ibaraki, Japan	9.50–10.15	**Phylogenetic analysis of DAHPS II type amino acid sequences** Anastasia Semashko, E.G. Veremeenko, N.P. Maksimova Belarusian State University, Minsk, Belarus		
10.00–10.20	***Nicotiana* genomics: from plants to genomes** N. Sierro, J.N.D. Battey, S. Ouadi, N. Bakaher, L. Bovet, A. Willig, S. Goepfert, M.C. Peitsch, Nikolai Ivanov Philip Morris International R&D, Philip Morris Products S.A., Switzerland	10.15–10.40	**The evolution of language-readiness in the hominin lineage: an analysis of open chromatin regions implicated in gene regulation** Konstantin Gunbin[1], A. Benítez-Burraco[2], F. Gusev[1], E. Rogaev[1,3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Department of Philology, University of Huelva, Huelva, Spain [3] University of Massachusetts Medical School, Worcester, USA		
10.20–10.35	**A spatial model of plant interactome and long non-coding RNA** Hongjun Chen, Jitong Xue, Ming Chen Zhejiang University, Hangzhou, China				
10.35–10.50	**Computer simulation of trichome patterning on growing wheat leaf taking into account the biomechanics of cells** Ulyana Zubairova[1], S.V. Nikolaev[1], A.V. Penenko[2], N.L. Podkolodnyy[1], S.K. Golushko[3], D.A. Afonnikov[1], and 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 [3]Design and Technology Institute of Digital Techniques SB RAS, Novosibirsk, Russia				
10.50–11.10	Coffee break				

11.10–11.30	**Nucleotide diversity analysis highlights functionally important genomic regions** Tatiana Tatarinova[1,2], E. Chekalin[3], Y. Nikolsky[3,4,5], S. Bruskin[3], D. Chebotarov[6], K.L. McNally[6], N. Alexandrov[6] [1]Center for Personalized Medicine and Spatial Sciences Institute, University of Southern California, Los Angeles, CA, USA [2]Kharkevich Institute for Information Transmission Problems, Russian Academy of Sciences, Moscow, Russian Federation [3]Vavilov Institute of General Genetics, Moscow, Russia [4]F1 Genomics, San Diego, CA, USA [5]School of Systems Biology, George Mason University, VA, USA [6]International Rice Research Institute, Los Baños, Philippines				
11.30–11.50	**Sleep of reason in the analysis of the results of research on materials «Proteomic information ofspring wheat varieties differing in resistance to infection after *Puccinia recondita* inoculation»** Kanat Sarsenbayev, A. Sarsenbayeva L.N. Gumilyov Eurasian National University, Astana, Kazakhstan				
11.50–12.10	**Study of *Armillaria borealis* pathogenicity by the comparative whole genome sequencing** Yuliya Putintseva[1,2], I.N. Pavlov[1,2], N.V. Oreshkova[1,2], V.V. Sharov[1], D.A. Kuzmin[1], S.V. Makolov[1], K.V. Krutovsky[1,3,4,5] [1]Siberian Federal University, Krasnoyarsk, Russia [2]V.N. Sukachev Institute of Forest SB RAS, Krasnoyarsk, Russia [3]Georg-August University of Göttingen, Göttingen, Germany [4]N.I. Vavilov Institute of General Genetics, RAS, Moscow, Russia [5]Texas A&M University, College Station, USA				
12.10–12.30	**Transcriptomic analysis of wheat root in response to essential nutrient deficiency: a gemome-wide comparative study** Saurabh Gupta[1], B.S. Yadav[2], S. Freilich[3], V.P. Kumar[1] [1]Department of Bioinformatics, Indian Institute of Information Technology-Allahabad, India [2]Deparment of Molecular Biology and Ecology of Plants, Tel Aviv University, Israel				

	[3] Systems Biology and Ecology ARO- Volcani Center-Bet-Dagan, Israel				
12.30–12.50	***Monotropa hypopitys* whole genome and transcriptome sequencing data** Elena Kochieva, E.V. Gruzdev, A.V. Beletsky, A.M. Mazur, A.V. Shchennikova, O.V. Shulga, M.A. Filyushin, V.V. Kadnikov, A.V. Mardanov, N.V. Ravin, K.G. Skryabin Institute of Bioengineering, Research Center of Biotechnology RAS, Moscow, Russia				
12.50–13.10	**3D map of proliferation activity in *Arabidopsis thaliana* root tips: transition domain boundaries and its bilateral symmetry** Viktoriya Lavrekha[1,2], T. Pasternak [3], N.A. Omelyanchuk[1,2], V.B. Ivanov[4], V.V. Mironova[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk,, Russia [2]LCTEB, Novosibirsk State University, Novosibirsk, Russia [3]Institute of Biology II/Molecular Plant Physiology, Centre for BioSystems Analysis, BIOSS Centre for Biological Signalling Studies University of Freiburg, Germany [4]Timiryazev Institute of Plant Physiology, Russian Academy of Sciences Moscow, Russia				
	Lunch				
14.00–18.35	**Section Section "Proteomics"** *(House of Scientists SB RAS, Small hall)* *Chairpersons:* Andrey Lisitsa, IBMC, Moscow, Russia; Sergey Peltek, ICG SB RAS, Novosibirsk, Russia		2nd IC&G SB RAS – Tohoku University Open Joint Seminar on Education and Research in High-Tech for Plant Production **Opening** Alexey Kochetov, Yoshinori Kanayama		
14.00–14.35	Nonthermal impact terahertz radiation on the living systems I.A. Mescheryakova[1], E.V. Demidova[1], T.N. Goryachkovskaya[1], E.A. Demidov[1], A.V. Bryanskaya[1], S.V. Sergeeva[1], S.L. Kiselev3, M.A. Lagarkova[3], G.N. Kulipanov[2], A.I. Semenov[2], N.A. Vinokurov[2], N.A. Kolchanov[1], V.M. Popik[2], Sergey Peltek[1] [1]The Institute of Cytology and Genetics The Siberian Branch of the Russian Academy of Sciences [2]Budker Institute of Nuclear Physics the Siberian Branch of the Russian Academy of Sciences [3]Vavilov Institute of General Genetics, RAS, Moscow		**Technological progress in Japanese horticultural production and Its academic aspects** Yoshinori Kanayama		

14.35–15.00	**Impact of 105-day isolation conditions on proteins expressed in endothelial cells, in the framework of the «Mars-500» project** L.H. Pastushkova[1], D.N. Kashirina[1], A.S. Kononikhin[1,3], Alexander Brzhozovsky[1] A.G., [1]Dobrokhotov I.V., [2]Tiys E.S., [2]Ivanisenko V.A., [3]Nikolaev E.N., [1]Larina I.M. [1]State scientific center of Russian Federation – Institute for biomedical problems RAS, Moscow, Russia [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [3]Emanuel Institute of Biochemical Physics RAS, Moscow, Russia		**Transgenic plants as genetic models** Alexey Kochetov		
15.00–15.25	**Kynurenic acid-sensitized photolysis of lens proteins under anaerobic conditions** Ekaterina Sormacheva[1], P.S. Sherin[1,2], E.A. Zelentsova[1,2], T.G. Duzhak[1,2], Yu.P. Tsentalovich[1,2], R.Z. Sagdeev[1,2] [1]International Tomography Center SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia		**Roles of pathogenesis related-10 proteins in biotic and abiotic stresses in comparison with heterologous ribonucleases** Ekaterina Trifonova		
15.25–15.50	**Looking for proteomic markers of breast cancer in blood exosomes** Oleg Tutanov[1], S.N. Tamkovich[1], Y.S. Bakakina[2], L.V. Dubovskaya[2], Y.P. Tsentalovich[3], I.D. Volotovskiy[2], P.P. Laktionov[1] [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Institute of biophysics and cellular engineers NASB, Minsk, Byelorussia [3]Institute "International Tomografic Center" SB RAS, Novosibirsk, Russia		**Towards the reference sequence of chromosome 5B of common wheat** Elena Salina **Inflorescence architecture in wheat** Oxana Dobrovolskaya		
15.50–16.10	Coffee break				
16.10–16.35	**Microbial community of the oil site of the Uzon Caldera (Kamchatka)** S.E. Peltek[1], Alla Bryanskaya[1], Y.E. Uvarova[1], A.S. Rozanov[1], T.V. Ivanisenko[1], T.K. Malup[1], V.A. Ivanisenko[1], E.V. Lazareva[2], O.V. Saik[1], S.M. Zhmodik[2], O.P. Taran[3], N.M. Slynko[1], S.V. Shekhovtsov[1], V.N. Parmon[3], N.L. Dobretsov[2], N.A. Kolchanov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]V S Sobolev Institute of Geology and Mineralogy SB RAS, Novosibirsk, Russia		**Synthesis and accumulation of a novel functional food component in tomato** Ayaka Ito		

	[3]Boreskov Institute of Catalysis SB RAS, Novosibirsk, Russia				
16.35–17.00	**Proteomic screening for amyloid-forming proteins in bacteria *Escherichia coli*** Anton Nizhnikov[1,2,3*], K.S. Antonets[1,2], K.V. Volkov [1], A.L. Maltseva [1], A.P. Galkin[1,2] [1]St. Petersburg State University, Universitetskaya nab., 7-9, St. Petersburg 199034, Russian Federation [2]Vavilov Institute of General Genetics (St. Petersburg Branch), Universitetskaya nab., 7-9, St. Petersburg 199034, Russian Federation [3]All-Russian Research Institute for Agricultural Microbiology, Podbelskogo sh., 3, Pushkin, St. Petersburg 196608, Russian Federation		**Physiological and transcriptional changes in a blossom-end rot resistant tomato introgression line IL8-3 fruit** **Tomoki Shibuya**		
17.00–17.15	**Actual approaches for qualification and quantification of proteome changes** Eugeny Vrzheschch Bio-Rad, Moscow, Russia		**Study on the regulation of cell division during early fruit development in tomato** Hideki Nariyama		
17.15–17.40	**Prediction of structural properties of uncharacterized proteins from their post-cleavage mass spectra by a multivariate statistical model** Oleg Markelov[1], A.R. Kayumov[2], M.I. Bogachev[1] [1]St. Petersburg Electrotechnical University, St. Petersburg, Russia [2]Kazan (Volga region) Federal University, Kazan, Russia		**VIGS-mediated resistance to crown gall disease** Pavel Nikulin		
17.40–18.05	**Coupled molecular dynamic and continuum electrostatic method to compute ionization of proteins as a function of pH** Yury Vorobjev Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia		**Membrane-associated kinase regulators of MAKR family genes in *Arabidopsis thaliana* L.** Daria Novikova		
			Plant delta-OAT gene expression in ontogenesis and stress response. Anastasiya Egorova		
			Functional and structural characterisation of PPD-B1 photoperiod insensitive allele Antonina Kiseleva		
			Phage-producing plants as models for expression of heterologous replicons Anna Nazarenko		

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9:00–17.00	**Section "Genomics, Transcriptomics and Bioinformatics"** *(House of Scientists SB RAS, Small hall)* *Chairpersons:* Ivo Grosse, Halle-Wittenberg University, Halle, Germany; Vsevolod Makeev, VIGG RAS, MIPT, Moscow, Russia				
9:00–9.15	**Sequencing from Roche: what the future will bring for you?** Irina Karpova LCC "Roche Diagnostics Rus", Moscow, Russia				
9.15–9.30	**Whole genome of the wooly mammoth: evolution through millenia** Artem Nedoluzhko[1,*], A.S. Sokolov[2], F.S. Sharko[2], E.S. Boulygina[1], S.V. Tsygankova[1], A.N. Tikhonov[3], K.G. Skryabin[1,2,4], E.B. Prokhortchouk[2,4] [1]National Research Center "Kurchatov Institute", Kurchatov sq. 1, 123182 Moscow, Russia. [2]Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, 60-letiya Oktyabrya av. 7-1, 117312 Moscow, Russia. [3]Zoological Institute, Russian Academy of Sciences, Universitetskaya Naberezhnaya 1, 199034 Saint Petersburg, Russia [4]Lomonosov Moscow State University, Faculty of Biology 1-12 Leninskie Gory, 119991 Moscow, Russia				
9.30–9.45	**Opisthorchiidae triad: comparative genomics of the carcinogenic liver flukes using a draft genome of *Opisthorchis felineus*** N. Ershov[1*], G. Fan[2,3], E. Prokhortchouk[4], V. Solovyev[5], Dmitry Afonnikov[1,6], H. Yang[2], V. Mordvinov[1], X. Liu[2], K. Skryabin[4,7] and The Opisthorchis Genome Consortium [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]BGI-Shenzhen, Shenzhen, China. [3]State Key Laboratory of Quality Research in Chinese Medicine, Institute of Chinese Medical Sciences, University of Macau, Macao, China. [4]Russian Federal Research Center for Biotechnology, Moscow, Russia [5]Softberry Inc., Mount Kisco, NY, US [6]Novosibirsk State University, Novosibirsk, Russia				

	[7]National Research Centre, Kurchatov Institute, Moscow, Russia				
9.45–10:00	**Genome of black garden ant: defense against virus invasion?** E.A. Konorov, Victoria Scobeyeva, M.A. Nikitin, S.N. Lysenkov, S. Nuzhdin Moscow State University, Moscow, Russia				
10:00–10:15	**In silico mouse chromocenters content** Dmitrii Ostromyshenskii, A.S. Komissarov, I.S. Kuznetsova, O.I. Podgornaya Institute of Cytology RAS, St. Petersburg, Russia				
10:15–10:30	**Transcriptome wide prediction of lncRNA-RNA interactions by a thermodynamics algorithm** Ivan Antonov, M.A. Zamkova, A.V. Marakhonov, M.Y. Skoblov, Y.A. Medvedeva Research Center of Biotechnology RAS, Moscow, Russia				
10:30–11:00	**Energy metabolic dysfunction in tumor cells, molecular mechanisms and clinical significance** Anna Kudryavtseva[1,2], A.A. Dmitriev[1], O.L. Kardymon[1], A.S. Zasedatelev[1], G.S. Krasnov[1], A.V. Snezhkina[1] [1]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia. [2]Herzen Moscow Cancer Research Institute, Ministry of Health of the Russian Federation, Moscow, Russia.				
11.00–11.20	Coffee break				
11.20–11.50	**GeneQuery: globally connected networks of GEO transcriptional profiles show hypothesis generation potential and reveal that tocopherols rescue TREM2-associated microglial dysfunction** Aleksandr Predeus[1,2*], T. Ulland[1], Y. Wang[1], V. Lampropoulou[1], W. Song[1], I. Arbuzov[3], F. Towfic[4], S. Gilfilan[1], E. Loginicheva[1], B.T. Edelson[1], B. Zeskind[4], M. Colonna[1], M.N. Artyomov[1] [1]Washington University School of Medicine, St. Louis, MO, USA [2]Bioinformatics institute, Saint Petersburg, Russia [3]ITMO University, Saint Petersburg, Russia. [4]Immuneering Corporation, Cambridge, MA, USA				
11.50–12.05	**Genome-wide transcriptomics as a platform for understanding the unusual resistance to muscle atrophy in hibernating dormice**				

	Guzel Gazizova[1]*, O.V. Tyapkina[2], O.S. Kozlova[1], M.D. Logacheva[1,3], L.F. Nurullin[2], I.M. Vikhlyantsev[4], O.A. Gusev[1,5] [1]Kazan Federal University, Kazan, Russia; [2]Kazan Institute of Biochemistry and Biophysics KSC RAS, Kazan, Russia; [3]Lomonosov Moscow State University, Moscow, Russia; [4]Institute of Theoretical and Experimental Biophysics RAS, Puschino, Russia; [5]RIKEN, Yokohama, Japan				
12.05–12.35	**The first edition of mutagenesis by CRISPR/Cas in the extreme desiccation tolerant cultured cell.** Takahiro Kikawada[1,2], Y. Miyata[1,3], Y. Sogame[1,4], T. Furusawa[1], S. Kikuta[5], R. Cornette[1], O. Gusev[6,7] [1]Institute of Agrobiological Sciences, NARO, Japan [2]Department of Integrated Biosciences, Graduate School of Frontier Sciences, The University of Tokyo, Japan [3]Center for Biological Resources and Informatics, Tokyo Institute of Technology, 4. JSPS Research Fellow, 5. Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, Tokyo, Japan, 6. Institute of Fundamental Medicine and Biology, Kazan Federal University , Russia, 7. Preventive Medicine & Diagnosis Innovation Program (PMI), RIKEN, Japan				
12.35–13.05	**miRNA binding sites in the mRNA of human titin gene** Ilya Pinsky[1], A.T. Ivashchenko[1], S.B. Labeit[2] [1]Al-Farabi Kazakh National University, Almaty, Kazakhstan [2]Institute of Integrative Pathophysiplogy, Mannheim, Germany				
13.05-14:00	Lunch				
14:00-16:00	**Expert-analytical evaluation of promising research directions in bioinformatics and systems biology**				
16:00-16:30	Closing				

Poster

«Animal Genetics»	**Denovo assembly of nuclear genome of the smallest insect *Megaphragma amalphitanum* (hymenoptera: *Trichogrammatidae*)** A.S. Sokolov[1*], A.V. Nedoluzhko[2], F.S. Sharko[1], E.S. Boulygina[2], S.V. Tsygankova[2], A.M. Mazur[1], A.A. Polilov[3], E.B. Prokhortchouk[1,2], K.G. Skryabin[1,2,3] [1]Federal Research Centre «Fundamentals of Biotechnology» of the RAS [2]National Research Centre "Kurchatov Institute" [3]Faculty of Biology, Lomonosov Moscow State University
	Genetic and molecular mechanisms crucial for hypertension development in the ISIAH rats O.E. Redina[1], L.O. Klimov[1], M.A. Ryazanova[1], L.A. Fedoseeva[1], T.O. Abramova[1], Yu.V. Alexandrovich[1], S.E. Smolenskaya[1], Ye.V. Antonov[1], N.I. Ershov[1], V.M. Efimov[1,2], A.L. Markel[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Divergence of paralogous growth hormone genes in salmonids D.N. Kamenskaya[1], M.V. Pankova[2], D.M. Atopkin[2, 3], V.A. Brykov[1 2] [1]A.V. Z hirmunsky Institute of Marine Biology, FEB RAS, Vladivostok, Russia [2]Far Eastern Federal University, School of Natural Sciences, Vladivostok, Russia [3]Institute of Biology and Soil Science, FEB RAS, Vladivostok, Russia
	Incongruent nuclear and mitochondrial genetic structure in baikalian amphipods *Gmelinoides fasciatus* M.V. Kovalenkova, Zh.V. Petunina, D.Yu. Sherbakov Limnological Institute SB RAS, Irkutsk, Russia
	A functional analysis of septin proteins in *Drosophila melanogaster* S2 cells A.L. Alekseeva[1,2]*, E.N. Andreyeva[1], L.A. Yarinich[1], A.V. Pindyurin[1,3], S.A. Fedorova[3] [1]Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia [2]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Identification of sturgeon species with mtDNA and microsatellite markers in Belarus A.Yu. Nosova The Institute of Genetics and Cytology of the NAS of Belarus, Minsk
«Evolution»	**Poxviral chemokine-binding proteins: theoretical study of structure and function evolution** D.V. Antonets[1], K.V. Gunbin[2], Nepomnyashchikh T.S.[1] [1]State Research Center of Virology and Biotechnology "Vector", Novosibirsk, Russia [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	A software system for simulating social and genetic aspects of deafness in human populations I.S. Dyachenko[1,2], O.L. Posukh[1,2], M.S. Bady-Khoo[1], M.V. Zytsar[1,2], V.Yu. Mikhalskaia[1,2], G.P. Romanov[3], N.A. Barashkov[3,4], Yu.G. Matushkin[1,2], S.A. Lashin[1,2] [1]Federal Research Center Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Institute of Natural Sciences, North-Eastern Federal University, Yakutsk, Russia [4]Yakut Scientific Center of Complex Medical Problems, Yakutsk, Russia
	Adaptation and biological time V.V. Suslov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

	Vavilov's homologous series as evolutionary force V.V. Suslov, M.P. Ponomarenko, D.A. Rasskazov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	The interaction between anaerobic respiratory complex ii and the flagellar motor A. Koganitsky[1], T. Dadosh[2], V. Kiss[1], M. Eisenbach[1] [1]Biomolecular Sciences, Weizmann Institute of Science, Rehovot, Israel [2]Chemical Research Support, Weizmann Institute of Science, Rehovot, Israel
	Ribosomal genes as phylogenetic markers for studing evolution of blue-flowered flaxes N. L. Bolsheva[1], N. V. Melnikova[1], A. A. Dmitriev[1], M. S. Belenikin[1,2], A. S. Speranskay[2], A. A. Krinitsina[2], G. S. Krasnov[1], V. A. Lakunina[1], A. V. Snezhkina[1], A. F. Sadritdinova[1], T. A. Rozhmina[3], A. V. Amosova[1], T. E. Samatadze[1], O. Yu. Yurkevich[1], N. G. Shostak[1], S. A. Zoshchuk[1], A. V. Kudryavtseva[1], O. V. Muravenko[1] [1]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia [2]Department of Higher Plants, Lomonosov Moscow State University, Moscow, Russia [3]All-Russian Research Institute for Flax, Torzhok, Russia
	Stochastic model of speciation, which describes the evolutionary branching process within the species flock in a closed ecosystem Yu.S. Bukin[1, 2], D.Yu. Sherbakov[1,3] [1]Limnological Institute SB RAS, Irkutsk, Russia [2]Irkutsk State Technical University, Irkutsk, Russia [3]Irkutsk State University, Irkutsk, Russia
	Evolution of mitochondrial genomes in Baikalian amphipods E.V. Romanova[1], V.V. Aleoshin[2], K.V. Mikhailov[2], R. M. Kamaltynov[1], M. D. Logacheva[2], E.A. Sirotinina[1], D.Yu. Sherbakov[1,3] [1]Limnological Institute SB RAS, Irkutsk, 664033, Russia [2]A.N. Belozersky Institute of Physicochemical Biology MSU, Moscow, 119991, Russia [3]Irkutsk State University, Irkutsk, 664003, Russia
	Evolution features of the three codon positions in gene of envelop protein e for different genotypes of the tick-borne encephalitis virus Yu.S. Bukin[1, 2], Yu.P. Dzhioev[3,4], I.V. Kozlova[4], S.E. Tkachev[6], D.O. Kiselev[3], A.I. Paramonov[3], O.N. Reva[3], V.I. Zlobin[3] [1]Limnological Institute SB RAS, Irkutsk, Russia [2]Irkutsk State Technical University, Irkutsk, Russia [3]Irkutsk State Medical University, Irkutsk, Russia [4]Scientific Center of Family Health Problems and Human Reproduction, SB RAS, Irkutsk, Russia [3]University of Pretoria, Pretoria, South Africa [6]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia
	Antioxidant response element controls lysosomal biogenesis master-regulator genes A.V.Chechushkov, N.K. Zenkov, E.B. Menshchikova Research Institute of Experimental and Clinical Medicine, Novosibirsk, Russia
	Some aspects of molecular evolution and recombinational variability of the Zika virus Y.P. Dzhioev[1,2], A.I. Paramonov[2], Y.S. Bukin[3,4], I.V. Kozlova[2], V.I. Zlobin[1] [1]Irkutsk State Medical University, Institute of Biomedical Technology, Irkutsk, Russia; [2]Scientific Center of family health and human reproduction problems, Irkutsk, Russia; [3]Limnological institute of the Siberian Branch of the Russian Academy of Sciences, Irkutsk, Russia; [4]Irkutsk National Research Technical University, Irkutsk, Russia.
	The distance matrix bootstrapping in the case of quantitative traits V.M. Efimov[1–4], K.V. Efimov[5], V.Y. Kovaleva[2] [1]Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2]Institute of Systematics and Ecology of Animals, SB RAS, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia

	[4]Tomsk State University, Tomsk, Russia [5]Moscow Institute of Physics and Technology (State University), Moscow, Russia
	Conservation level of the key meiotic proteins reflects their function and independent evolution in different lineages of eukaryotes T.M. Grishaeva, Yu.F. Bogdanov Vavilov Institute of General Genetics RAS, Moscow, Russia
	A computation system for randomization-based enrichment analysis using GPU: performance investigation M. Grishenko[1], A. Yakimenko[1, 2], M. Khairetdinov[1, 2], K. Gunbin[3] [1]Novosibirsk State Technical University, Novosibirsk, Russia [2]Institute Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [3]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Searching for cytolytic genetic markers of newcastle disease virus using computer assisted analysis K.V. Gunbin[1,4], M.R. Kabilov[2], K.S. Yurchenko[3], A.V. Glushchenko[3], A.M. Shestopalov[3], N.V. Gubanova[1,4] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [3]Research Center of Clinical and Experimental Medicine, SB RAMS, Novosibirsk, Russia [4]Novosibirsk State University Novosibirsk, Russia
	Punctuated evolution: the relationship between rare mutations and cladogenesis of vertebrates K. Popadin[1], K. Gunbin[2, 3] [1]Center for Integrative Genomics, University of Lausanne, Switzerland [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [3]Novosibirsk State University Novosibirsk, Russia
	Genetic diversity among eight *Dendrolimus* species in Eurasia (lepidoptera: lasiocampidae) inferred from mitochondrial COI and COII, and nuclear ITS2 markers A. Kononov[1], K. Ustyantsev[1], B. Wang[2], V. Mastro[2], V. Fet[3], A. Blinov[1], Y. Baranchikov[4] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]USDA-APHIS-PPQ CPHST, Otis Laboratory, Otis Air National Guard Base, MA, USA [3]Department of Biological Sciences, Marshall University, Huntington, USA [4]V.N.Sukachev Institute of Forest, SB RAS, Krasnoyarsk, Russia
	Comparative analysis of expression of anhydrobiosis-related genes in response to different types of ionizing radiation in the sleeping chironomid (*Polypedilum vanderplanki*) A.V. Ryabova[1], A.V. Cherkasov[1*], K. Mukae[2], T. Kikawada[3], T. Okuda[3], T. Sakashita[4], O. Gusev[1,5,6] [1]Institute of Fundamental Biology and Medicine, KFU, Kazan, Russia [2]Department of Regulatory Biology, Saitama University, Saitama, Japan [3]Anhydrobiosis Research Group, NIAS, Tsukuba, Japan [4]Takasaki Advanced Radiation Research Institute, Takasaki, Japan [5]Division of Genomic Technologies, CLST, RIKEN, Yokohama, Japan [6]Preventive Medicine & Diagnosis Innovation Program, CLST, RIKEN, Yokohama, Japan
	Invasive entomo-mycological association of *P. proximys* and its phytopatogenic symbiont in Siberia and European part of Russia A. Kononov[1], A. Blinov[1], N. Pashenova[2], N. Percova[2], Y. Baranchikov[2]. [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]V.N.Sukachev Institute of Forest, SB RAS, Krasnoyarsk, Russia
	Comparative transcriptomics provides new insights into origin of extraordinary resistance to desiccation in Australian midge *Paraborniella tonnoiri* (*Chironomidae*) O.S. Kozlova[1], E.I. Shagimardanova[1], L.Kh. Shigapova[1], R.M. Devyatiarov[1], M.D.Logacheva[2,1], R. Cornette[3], T. Kikawada[3] and O.A. Gusev[4,1] [1]Extreme Biology Laboratory, Institute of Fundamental Medicine and Biology, Kazan Federal University, Kazan, Russia [2] Laboratory of evolutionary genomics, Faculty of bioengineering and bioinformatics, Moscow State University, Moscow, Russia [3]National Institute of Agrobiological Sciences, Tsukuba, Japan

	[4] Preventive Medicine & Diagnosis Innovation Program (PMI), Division of Genomic Technologies, RIKEN, Yokohama, Japan
	Comparative genomics and transcriptomics of *Chironomidae* midges under extreme conditions O.S. Kozlova[1], A.V. Cherkasov[1], R.M. Devyatiarov[1], M.D.Logacheva[2,1], R. Cornette[3], T. Kikawada[3], A.A. Przhiboro[4] and O.A. Gusev[5,1] [1]Institute of Fundamental Medicine and Biology, Kazan Federal University, Kazan, Russia [2] Faculty of bioengineering and bioinformatics, Moscow State University, Moscow, Russia [3]National Institute of Agrobiological Sciences, Tsukuba, Japan [4]Zoological Institute, Russian Academy of Sciences, Moscow, Russia [5]Preventive Medicine & Diagnosis Innovation Program (PMI), RIKEN, Yokohama, Japan
	Project: «One hundred pedigrees of the Tuvans» D.A. Lopsan, U.N. Kavai-ool Laboratory of Genetics, Tuvan State University, Kyzyl, Russia.
	SitEx 2.0: functional sites projection on alternative spliced isoforms and homologous genes I.V. Medvedeva, P.S. Demenkov, V.A. Ivanisenko Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Molecular evolution analysis of RNA-binding Nip7 protein from deep- and shallow-water archaea K.E. Medvedev, D.A. Afonnikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Molecular evolution and systematics of flat leeches (*Hirudinea*: *Glossiphoniidae*) N.B. Mandzyak1, I.A. Kaygorodova1,2 [1]Limnological Institute SB RAS, Irkutsk, Russia [2]Irkutsk State University, Irkutsk, Russia
	Distribution of 2541-2542delCA *kdpd* frameshift mutation in genomes of *Mycobacterium tuberculosis* from Irkutsk Oblast and Yakutia O. Ogarkov[1,2,3], V. Sinkov[1,] , I. Mokrousov[4], S. Zhdanova[1], P. Khromova[1], E. Orlova[1,3] [1]Scientific Centre of the Family Health and Human Reproduction Problems, Irkutsk, Russia [2]Irkutsk State Medical Academy of Continuing Education, Irkutsk, Russia [3]Irkutsk State University, Irkutsk, Russia [4]St. Petersburg Pasteur Institute, St. Petersburg, Russia
	Electrostatics: a new old genome selection factor A.A. Osypov Institute of Higher Nervous Activity and Neurophysiology RAS, Moscow, Russia, Institute of Cell Biophysics of RAS, Pushchino, Russia
	Identification of recombination sites in the genomes of the european subtype of tick borne encephalitis virus A.I. Paramonov[1], Yu.P. Dzhioev[1,2], I.V. Kozlova[1] [1]FGBNU Scientific Center of family health and human reproduction problems, Irkutsk, Russia [2]Irkutsk State Medical University, Institute of Biomedical Technology, Irkutsk, Russia
	RNA seq analysis of marine and freshwater forms of three-spined stickleback (*Gasterosteus aculeatus*). Evolutionary and physiological mechanisms of adaptation S.M. Rastorguev[1], A.V. Nedoluzhko[1], A.M. Mazur[2], E.B. Prockhorchouk[2] [1]National Research Center “Kurchatov Institute”, Moscow, Russia. [2]Institute of Bioengineering, Research Center of Biotechnology SB RAS, Moscow, Russia.
	PQ: a new program for phylogenetic reconstruction D.Penzar[1], M.S.Krivozubov[2], S.A.Spirin[3] [1]Faculty of Bioengineering and Bioinformatics, Moscow State University, Moscow, Russia [2]Gamaleya Center of Epidemiology and Microbiology, Moscow, Russia [3]Belozersky Institute of Physico-Chemical Biology of Moscow State University and Institute of System Studies, Moscow, Russia

	Phylogenetic reconstruction within *Mycobacterium tuberculosis* Beijing genotype in northeastern Russia S. Zhdanova[1], O. Ogarkov[1,2,3], G. Alexeeva[4], M. Vinikurova[4], E. Savilov[1,4], V. Sinkov[1] [1]Scientific Centre of the Family Health and Human Reproduction Problems, Irkutsk, Russia [2]Irkutsk State Medical Academy of Continuing Education, Irkutsk, Russia [3] Irkutsk State University, Irkutsk, Russia [4]Research Practice Center for Phthisiatry, Yakutsk, Russia
	Genome and chromosome evolution of mosquitoes–vectors of human diseases M.V. Sharakhova[1,2], V.A. Timoshevskiy, A.N. Naumenko[1], A. Peery[1], G.N. Artemov[2], V.N. Stegniy[2], I.V. Sharakhov[1,2] [1]Virginia Polytechnic and State University and Fralin Life Science Institute, VA, USA. [2]Tomsk State University, Tomsk, Russia
	The mitochondrial gene order and CYTB evolution in Hymenoptera and other insects F.S. Sharko[1], A.V. Nedoluzhko[1,2], S.M. Rastorguev[2], A.A.Polilov[3], K.G. Skryabin[1,2,3], E.B. Prokhortchouk[1,3]. [1]Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, Russia [2]National Research Center "Kurchatov Institute", Moscow, Russia. [3]Lomonosov Moscow State University, Faculty of Biology ,Moscow, Russia
	Molecular phylogenetic analysis of the grasshoppers of family acrididae based on several mitochondrial and nuclear markers I.S. Sukhikh[1], A.G. Blinov[1], A.G. Bugrov[2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia
	TATA-box and gene expression norm of reaction V.V. Suslov, M.P. Ponomarenko, D.A. Rasskazov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	The *Ile462Val* polymorphism of the cytochrome *P450 CYP1A1* gene among eastern buryats compared with Russians in Trans Baikal area L.E. Tabikhanova[1], L.P. Osipova[1,2], T.V. Churkina[1], E.N. Voronina[2,3], M.L. Filipenko[2,3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia
	Genetic polymorphism of glutathione S-transferase p1 (*GSTP1*) among Buryats, Teleuts and Russians L.E. Tabikhanova[1], L.P. Osipova[1,2], T.V. Churkina[1], H. Bai,[3] E.N. Voronina[2,4], M.L. Filipenko[2,4] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Inner Mongolia University for the Nationalities, Tongliao, China. [4]Institute of Chemical Biology and Fundamental Medicine, SB RAS, Novosibirsk, Russia
	Phylogenetic analyses of *Mycobacterium tuberculosis* Ural family by WGS data from Eurasia V. Sinkov[1], O. Ogarkov[1, 2, 3], y. Bukin[4, 5], I. Mokrousov[6], S. Zhdanova[1] [1]Scientific Centre of the Family Health and Human Reproduction Problems, Irkutsk, Russia [2]Irkutsk State Medical Academy of Continuing Education, Irkutsk, Russia [3]Irkutsk State University, Irkutsk, Russia [4]Limnological Institute SB RAS, Irkutsk, Russia [5]Irkutsk National Research Technical University, Irkutsk, Russia [6]Laboratory of Molecular Epidemiology and Evolutionary Genetics, St. Petersburg Pasteur Institute, St. Petersburg, Russia
	Parasites of the genera *Nosema*, *Apicistis*, *Crithidia* and *Lotmaria* in the natural honeybee and bumblebee populations: a case study in India V. Vavilova[1], I. Konopatskaia[1, 2], M. Woyciechowski[3], S. Luzianin[4], A. Blinov[1] [1]The Federal Research Center Institute of Cytology and Genetics SB RAS, Novosibirsk, Russian Federation [2]Novosibirsk State University, Novosibirsk, Russian Federation

	[3]Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland [4]Biological Faculty, Kemerovo State University, Russian Federation
	Problem of phylogenetic position of *Dicyemids* O. Zverkov, L. Rusin, V. Lyubetsky, V. Aleoshin Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute), Moscow, Russia
	Phylogeny developed over the triplet composition of mitochondrial genomes: high synchrony in the evolution of two genetic systems V.S. Fedotova[1], M.G. Sadovsky[2], Yu.A. Putintseva[1,3] 1. Siberian Federal University, Krasnoyarsk, Russia 2. Institute of Computational Modeling, Krasnoyarsk, Russia 3. Forest Institute, Krasnoyarsk, Russia
	The significance of dissociative nucleotide changes accumulation rate in the genotype variability of tick-borne encephalitis virus for gene E D. O. Kiselev[1], S. Ju. Bukin[2], A. I. Paramonov[3], Ju. P. Dzhioev[1], V. I. Zlobin[1] [1]Irkutsk State Medical University, Irkutsk, Russia [2]Limnological Institute, Irkutsk, Russia [3]Scientific Centre for Human Reproduction and family health problems, Irkutsk, Russia
	Molecular evolution of YUCCA protein family I.I. Turnaev, V.V. Suslov, K.V. Gunbin, D.A. Afonnikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
«Computer Systems biology»	**The role of huntingtin protein-protein interactions in the processes of changing and maintenance of neurotransmission in hippocampus.** A.L. Proskura, S.O. Vechkapova, T.A. Zapara, A.S. Ratushniak. Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia
	How to accomplish a rapid defense against foreign DNA — restriction-modification systems and implications for synthetic gene circuits B. Blagojevic[1], M. Djordjevic[1], M. Djordjevic[2] [1]Institute of Physics Belgrade, University of Belgrade, Belgrade, Serbia [2]Institute of Physiology and Biochemistry, Faculty of Biology, University of Belgrade, Belgrade, Serbia
	Identification of new candidate genes for elevated body mass index near GWAS SNPs using transcript annotations from ENSEMBL and HAVANA projects. E.V. Ignatieva, V.G. Levitsky Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	The compendium of human genes controlling feeding behavior or body weight, reconstruction of networks and analysis of their properties E.V. Ignatieva, O.V. Saik, D.A. Afonnikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Biomolecular systems models semi-automatic reconstruction based on structural and quantitative information F.V. Kazantsev[1,2], I.R. Akberdin[1,5], S.A. Lashin [1,2], Natalia Ree[1], Vladimir Timonov[2], A.V. Ratushny[3,4], T.M. Khlebodarova[1], V.A. Likhoshvai [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia, [2]Novosibirsk State University, Novosibirsk, Russia, [3]Center for Infectious Disease Research, Seattle, USA, [4]Institute for Systems Biology, Seattle, USA, [5]San Diego State University, San Diego, USA
	The use of disciminant analysis and artificial neuronal network in breast cancer detection U.S Bagina, L.V. Shchegoleva, T.O. Volkova Petrozavodsk State University, Petrozavodsk, Russia
	UGENE: a toolkit for teaching students I.V. Bykova[1], O.I. Golosova[1], A.Y. Bakulina[2,3], D.A. Afonnikov[2,4], D.Y. Kandrov[1], A.Y. Palyanov[2,5], G.A. Grekhov,[1] Y.E. Danilova[1] [1]Unipro Center of Information Technologies, Novosibirsk, Russia

	[2]Novosibirsk State University, Novosibirsk, Russia [3]State Research Center of Virology and Biotechnology VECTOR, Koltsovo, Novosibirsk region, Russia [4]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [5]Institute of Informatics Systems SB RAS, Novosibirsk 630090
	Graph database for human microbiome A.A. Ryasik, E.A. Temlyakova, M.A. Orlov, A.A. Sorokin Institute of Cell Biophysics RAS, Pushchino, Russia
	Simulation of enhancer evolution in a computational model of the *Drosophila* gap gene network A.A. Chertkova[1], J. Schiffman[2], K.N. Kozlov[1], M.G. Samsonova[1], S.V. Nuzhdin[1,2], V.V. Gursky[1,3] [1]Peter the Great St. Petersburg Polytechnic University, St. Petersburg 195251, Russia [2]University of Southern California, Los Angeles, CA 90089, U.S.A. [3]Ioffe Institute, St. Petersburg, 194021, Russia
	Cluster analysis of stress-induced duplex destabilization (SIDD) profiles for *E. coli* promoters M.A. Orlov, A.A. Ryasik, E.A. Temlyakova, A.A. Sorokin Institute of Cell Biophysics RAS, Pushchino, Russia
	Orthoscape: a Cytoscape plugin for evolutionary analysis of gene networks Z.S. Mustafin[1], D.A. Afonnikov[1,2], K.V. Gunbin[1], Yu.G. Matushkin[1,2], S.A. Lashin[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Dioxin-mediated upregulation of oncostatin m in u937 macrophages D.Y. Oshchepkov[1], E.V. Kashina[1], V.A. Mordvinov[1], D.P. Furman[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	BioStore: a cloud-compatible hub for bioinformatics related tools and platforms S. Pintus[1], T. Valeev[1,2], I. Yevshin[1,2], F. Kolpakov[1,2] [1]Institute of Systems Biology Ltd., Novosibirsk, Russia [2]Design Technological Institute of Digital Techniques, The Siberian Branch of The Russian Academy of Sciences, Novosibirsk, Russia
	Sanger data processing in UniPro UGENE A.V. Tiunov, E.A. Pushkova, y.A. Algaer, G.A. Grekhov and the UGENE team Unipro Center of Information Technologies, Novosibirsk, Russia
	An ImageJ plugin for detection of wheat leaf epidermis cellular structure from confocal laser scanning microscopy U.S. Zubairova[1], P.Yu. Verman[2]and A.V. Doroshkov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Assessment of translational importance of mammalian mRNA sequence features based on ribo- and mRNA-seq data Yu.V. Kondrakhin[1,2], R.N. Sharipov[1,2], O.A. Volkova[3] [1]Design Technological Institute of Digital Techniques, SB RAS, Novosibirsk, Russia [2]BIOSOFT.RU, Ltd, Novosibirsk, Russia [3]The Federal Research Center Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
	Ultrastructural analysis of mitotic division in *Drosophila* S2 cells A.A. Strunov[1,2*], L.V. Boldyreva[2], A.V. Pindyurin[2], M. Gatti[2,3], E. Kiseleva[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Molecular and Cellular Biology, Novosibirsk, Russia [3]Sapienza University of Rome, Rome, Italy
	Ultrastructural analysis of spindle and kinetochores in augmin-depleted *Drosophila* S2 cells

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	Comparative analysis of gastrointestinal microbiome in wild and domestic quails M.N. Siniagina[1], M.I. Markelova[1], E.R. Kirillova[1], E.A. Boulygina[1], A.V. Lichoman[2] V.V. Radchenko [3] [1]Kazan Federal University, Kazan, Russia [2]Kuban State Agrarian University, Krasnodar, Russia [3]M.M. Shemyakin and Yu.A. Ovchinnikov Institute of Bioorganic Chemistry of the Russian Academy of Sciences, Moscow, Russia
	Computational model for mammalian circadian oscillator interacting with NAD+ / SIRT1 pathway O.A. Podkolodnaya[1], N.N. Tverdokhleb[1,3], N.L. Podkolodnyy[1,2,3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk [3]Novosibirsk State University, Novosibirsk
«Computational pharmacology»	**A congestion game model for virtual drug screening in a desktop grid** N.N. Nikitina, E.E. Ivashko Institute of Applied Mathematical Research, Karelian Research Center of the Russian Academy of Sciences, Petrozavodsk, Russia
	Based on the local sequence similarity method for prediction of amino acid positions related to the protein-ligand specificity D.A. Karasev[1,2], A.V. Veselovsky[1], N.Yu. Oparina [3,4], A.V. Rudik[1], D.A. Filimonov[1], B.N. Sobolev[1] [1]Institute of Biomedical Chemistry, Moscow, Russia [2]Russian National Research Medical University, Moscow, Russia [3]Engelhardt Institute of Molecular Biology, Moscow, Russia [4]Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden
	DNA duplex structure and thermodynamics by molecular dynamics simulation A.A. Lomzov, D.V. Pyshnyi Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
	Fighting with HIV-1 resistance to reverse transcriptase inhibitors by computer-aided approach O.A. Tarasova, D.A. Karasev, D.A. Filimonov, V.V. Poroikov Institute of Biomedical Chemistry, Moscow, Russia
	Molecular modeling of the interaction between indole lupane derivatives and c-Myc/Max heterodimer T. S. Frolova[1,2,3], D. S. Baev[2], A. V. Petrova[4], E. F. Khusnutdinova[4], O. I. Sinitsyna[1,3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk Institute of Organic Chemistry SB RAS, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia [4]Bashkir State University, Ufa, Russia
	Predicting of thermodynamic data of morpholino analogous of NA by computer approach and comparing with experiments V.M. Golyshev, A.A. Lomzov Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
	Computer modelling of inhibitors of protease of human hepatitis C virus based on knottin scaffold A.V. Talanova, D.S. Shcherbinin, E.F. Kolesanova, A.V. Veselovsky V.N. Orekhovich Institute of Biomedical Chemistry, Moscow, Russia
«Systems biology of plants»	**Comprehensive analysis of draft genomes of two closely related pseudomonas syringae phylogroup 2b strains infecting mono- and dicotyledon host plants** R.I. Sultanov[1,2], G.P. Arapidi[1,2], S.V. Vinogradova[3], V.M. Govorun[1,2,4], D.G. Luster[5] and A.N. Ignatov[6] [1]Moscow Institute of Physics and Technology (State University), Moscow, Russia

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	De novo sequencing and comparative analysis of chloroplast genomes for four ferns of *Dryopteris* and *Adiantum* genera M.S. Belenikin[1, 2], A.A. Krinitsina[1], S.V. Kuptsov[1], M.D. Logacheva[1], A.S. Speranskaya[1] [1]Lomonosov Moscow State University, Moscow, Russia [2]Pirogov Russian National Research Medical University, Moscow, Russia
	Development of microsatellite markers according to BAC sequencing data and their physical mapping to the bread wheat 5B chromosome M.A. Nesterov[1*], D.A. Afonnikov[1], E.M. Sergeeva[1], L.A. Miroshnichenko[2], M.K. Bragina[1], A.O. Bragin[1], G.V. Vasiliev[1], E.A. Salina[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Sobolev institute of Mathematics SB RAS, Novosibirsk, Russia
	Distinct types of EIN3-DNA interactions in various functional regions of *A. thaliana L.* genome E.V. Zemlyanskaya[1,2], D.Yu. Oshchepkov[1], V.G. Levitsky[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Heat shock proteins of potato in vitro under heat and biotic stress A.I. Perfileva, E.G. Rikhvanov Siberian Institute of Plant Physiology and Biochemistry, S. B. RAS, Irkutsk, Russia
	Identification of nuclear genes controlling chlorophyll synthesis in barley by RNA-seq N.A. Shmakov[1,2], G. V. Vasiliev[1], N. V. Shatskaya[1], A. V. Doroshkov[1], D.A. Afonnikov[1,2], E. K. Khlestkina[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; [2]Novosibirsk State University, Novosibirsk, Russia
	Mathematical modeling a reciprocal interactions between auxin and its PIN transporters in the root tip of *A. thalina L.* V. V. Kovriznykh[1,2], F.V. Kazantsev [1], N.A. Omelyanchuk[1,2], V.V. Mironova[1,2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Mechanics of plant cell unidirectional growth S.V. Nikolaev[1,2], S.K. Golushko[2], U.S. Zubairova[1], D.A. Afonnikov[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Design and Technology Institute of Digital Techniques SB RAS, Novosibirsk, Russia
	Membrane-associated kinase regulators of MAKR family genes in *Arabidopsis thaliana L.* D.D. Novikova, N.A. Omelyanchuk and V.V. Mironova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia
	Metabolite profiling of the moss *Physcomitrella patens* inoculated with pseudomonas E.D. Egorova, N.A. Baraeva, S.V. Vinogradova Research Center of Biotechnology RAS, Moscow, Russia
	Molecular evolution analysis of genes related to plant root hair and trichome development D.Yu. Konstantinov[1] and A.V. Doroshkov[2*] [1]Novosibirsk State University, Novosibirsk, Russia [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Multidimensional patterns of metabolic response in abiotic stress-induced growth of *Arabidopsis thaliana*

	B.S. Yadav[1], S. Freilich[2], E. Katz[1], A. Finkelshtein[1], D.A. Chamovitz[1] [1]Department of Molecular Biology and Ecology of Plants, Tel Aviv University, Israel [2]Newe Ya'ar Research Center, Agricultural Research Organization, Ramat Yishay, Israel
	MYC gene family in cereals: transformation in the cource of the *Triticum* and *Aegilops* genera evolution K.V. Strygina[1], E.K. Khlestkina[1,2] [1]Federal Research Center nstitute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Phsyological and transcriptional changes in a blossam-end rot resistant tomato introgression line IL8-3 fruit S. Tomoki, H. Ikeda, Y. Kanayama School of Agricultural Science, Tohoku University, Sendai, Japan
	Polymorphism of the *VRN-A1* exon-4 and exon-7 in polyploid wheat A.F. Muterko, E.A. Salina Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Sequencing of conifer genomes using ngs N.V. Oreshkova[1, 2], Yu.A. Putintseva[1, 2], D.A. Kuzmin[1], V.V. Sharov[1], V.V. Biryukov[1], S.V. Makolov[1], K.V. Krutovsky[1, 3, 4, 5] [1]Siberian Federal University, Krasnoyarsk, Russia [2]V.N. Sukachev Institute of Forest SB RAS, Krasnoyarsk, Russia [3]Georg-August University of Göttingen, Göttingen, Germany [4]N.I. Vavilov Institute of General Genetics, RAS, Moscow, Russia [5]Texas A&M University, College Station, USA
	Study on the regulation of cell division during early fruit development in tomato H. Nariyama, T. Shibuya, Y. Kanayama School of Agricultural Science, Tohoku University, Sendai, Japan
	Synthesis and accumulation of a novel functional food component in tomato A. Ito, S. Hano, N. Imoto, T. Shibuya, Y. Kanayama* *School of Agricultural Science, Tohoku University, Sendai, Japan*
	The manifestation and phytohormone responce of leaf pubescence genes in bread wheat A.V. Doroshkov, A.V. Simonov, D.A. Afonnikov, T.A. Pshenichnikova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	The occurrence of spring forms in tetraploid timopheevi wheats is associated with variation in the first intron of VRN-A1 gene A.B. Shcherban[1], A.A. Schischkina[2], E.A. Salina[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of General Genetics RAS, Moscow, Russia
	***VRN1* genes variability in tetraploid wheat species with a spring growth habit** I. Konopatskaia[1, 2], V. Vavilova[1], E.Ya. Kondratenko[1], A. Blinov[1], N.P. Goncharov[1, 3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Novosibirsk State Agrarian University, Novosibirsk, Russia
	Wheatdb2: plant trait database and information system based on Crop Ontology terms E.G. Komyshev[1], M.A. Genaev[1], A.V. Akushkina[2], D.A. Afonnikov[1, 3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State Agrarian University, Novosibirsk, Russia [3]Novosibirsk National Research State University, Novosibirsk, Russia
«Proteomics»	**Approach to predicting the solubility/insolubility of *E. coli* proteins based on their primary structure using sequence normalization and machine learning techniques**

	N.A. Alemasov[1], N.V. Ivanisenko[1], K.S. Antonets[2,3], A.A. Nizhnikov[2,3], V.A. Ivanisenko[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]St. Petersburg State University, St. Petersburg, Russia [3]Vavilov Institute of General Genetics SPB RAS, St. Petersburg, Russia
	GeneOntology biological processes sensitive to salt diet changes in an expreiment with 105-day isolation: statistical analysis of urine proteome E. Tiys[1,2], E.D. Petrovskiy[1], L.Kh. Pastushkova[3],D.N. Kashirina[3], I.M. Larina[3], V.A. Ivanisenko[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk state university, Novosibirsk, Russia [3]Institute for Biomedical Problems RAS, Moscow, Russia
	Human blood bispecific antibodies – new biochemical markers of autoimmune diseases S.E. Sedykh, V.V. Printz, V.N. Buneva, G.A. Nevinsky [1]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Identification of bacillus pumilus group strains by maldi tof ms using geometric approach K.V. Starostin, E.A. Demidov, A.V. Bryanskaya, V.M. Efimov, A.S. Rozanov, S.E. Peltek Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	***K-mer* frequency distribution of eukaryotic proteomes** A.A. Morozov Limnological Institute SB RAS, Irkutsk, Russia
	Proteomic analysis of horse milk exosomes S.E. Sedykh, L.W. Purvinsch, V.N. Buneva, G.A. Nevinsky [1]Novosibirsk State University, Novosibirsk, Russia [2]Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
	Scoring of protein docking by Gene Ontology A. Hadarovich[1, 2], I. Anishchenko[1], A.V. Tuzikov[2], P.J. Kundrotas[1], I.A. Vakser[1] [1]Center for Computational Biology and Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas, USA [2]United Institute of Informatics Problems, National Academy of Sciences, Minsk, Belarus
	Structural patterns among the diversity of flavin-dependent oxidoreductases from luminous bacteria and *e. Coli* A.A. Deeva, E.A. Temlyakova, A.A. Sorokin, E.V. Nemtseva, V.A. Kratasyuk Siberian Federal University, Krasnoyarsk, Russia Institute of Cell Biophysics RAS, Pushchino, Russia
	The role of Q/T-rich regions in the induction of amyloidogenesis K.S. Antonets[1,2*], A.A. Nizhnikov[1,2], A.P. Galkin[1,2] [1]Dept. of Genetics and Biotechnology, St. Petersburg State University, Universitetskaya nab, 7-9, St. Petersburg, 199034 Russia [2]St. Petersburg Branch, Vavilov Institute of General Genetics, Russian Academy of Sciences, Universitetskaya nab, 7-9, St. Petersburg 199034, Russia
	Proteomic of TCA – extracted compounds, isolated from human blood serum revealed new potential biomarkers, associated with autoimmune and hematooncological diseases S. Myronovkij[1], M. Starykovych[1], Y. Bobak[1], N. Negrych[2], T. Nehrych[2], M. Shorobura[2], O. Shalay[3], S. Souchelnytskyi[4], R. Stoika[1], Y. Kit[1] [1]Institute of Cell Biology, National Academy of Sciences of Ukraine, Lviv Ukraine [2]Danylo Halytsky Lviv National Medical University, Lviv, Ukraine [3]Institute of Blood Transfusion Medicine, National Academy of Medical Science of Ukraine, Lviv, Ukraine [4]Center for Translational Molecular Medicine, College of Medicine, Qatar University, Doha, Qatar
	Gene ontology analysis and network reconstruction for genes related to aging deceases and behavior

	I.V. Chadaeva, O.V. Saik, V.N. Babenko [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
«Systems biology of aging»	**Two congenic strains prove effects on cataract and retinopathy but not on brain neurodegeneration in senescence-accelerated OXYS rats** E.E. Korbolina, A.O. Vitovtov, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	The mitochondria-targeted plastoquinone SkQ1 affects *Drosophila melanogaster* lifespan in various environments A.V. Krementsova[1], N.V. Roshina[2], E.A. Tsybul'ko[2], O.Y. Rybina[2], A.V. Symonenko[2], E.G. Pasyukova[2] [1]Emmanuel Institute of Biochemical Physics RAS, Moscow, Russia [2]Institute of Molecular Genetics RAS, Moscow, Russia
	On the possible impact of exogenous 8-oxo-2'-deoxyguanosine on DNA synthesis, damage and repair in aging cell cultures and organism N.V. Marmiy[1], G.V. Morgunova[2], D.S. Esipov[1], A.N. Khokhlov[2] [1]Division of Bioorganic Chemistry, Biology Department, Moscow State University, Moscow, Russia [2]Evolutionary Cytogerontology Sector, Biology Department, Moscow State University, Moscow, Russia
	Biomarkers of age in the «stationary phase aging» model G.V. Morgunova, D.S. Esipov, M.V. Marmiy, A.N. Khokhlov Evolutionary Cytogerontology Sector, School of Biology, Lomonosov Moscow State University, Moscow, Russia
	Phosphorylation of αB-crystallin: effects of aging and cardiomyopathy N.A. Muraleva[1], V.A. Devyatkin[1, 2], N.A. Kolosova[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Neurothrophin signaling pathway in development of Alzheimer's disease-like pathology E.A. Rudnitskaya, N.A. Muraleva, N.A. Stefanova, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Development of cataract as the basic selection trait in the ontogeny of senescence-accelerated *OXYS* rats Yu.V. Rumyantseva, A.Z. Fursova, E.E. Korbolina, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Genetic control of circadian rhythms: an impact of molecular clock expression profile changes in longevity I.A. Solovev[1, 2], E.V. Dobrovolskaya[1], A.A. Moskalev[1, 2, 3] [1]Institute of Biology of Komi Scientifice Center of Ural Branch of RAS, Syktyvkar [2]Syktyvkar State University, Syktyvkar [3]Moscow Institute of Physics and Technology (State University), Russia
	Identification of pathways associated with cell death in the cortex of OXYS rats as the signs of Alzheimer's disease develop G.K. Suvorov, D.V. Telegina, E.A. Rudnitskaya, N.A. Stefanova, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Relationship of cell death in retina of rats during aging with the development of retinopathy D.V. Telegina, O.S. Kozhevnikova, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Differential expression of *shaggy*, a *Drosophila melanogaster* gene encoding GSK-3 beta, affects lifespan M.V. Trostnikov, N.V. Roshina, E.G. Pasyukova Institute of Molecular Genetics, RAS, Russia
	Mitochondrial dysfunction in sporadic Alzheimer's disease-like pathology in OXYS rat M.A. Tyumentsev[1], E.V. Kiseleva[1], V.A. Vavilin[2], N.G. Kolosova[1], N.A. Stefanova[1] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Institute of Molecular Biology and Biophysics SB RAMS, Novosibirsk, Russia
	Structural basis for the recognition and processing of DNA containing bulky lesions by the mammalian nucleotide excision repair system

	A. Evdokimov[1], A. Popov[1], I. Petruseva[1], O. Lavrik[1, 2] [1]Institute of chemical biology and fundamental medicine, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
«Bioinformatics and molecular biology synergism in DNA damage response studies»	**The frequency, spectrum and functional significance of mutations in coding sequence of TP53 gene in Russian patients with DLBCL** E.N. Voropaeva[1], T.I. Pospelova[2], M.I. Voevoda[1], V.N. Maximov[1, 2] [1]Institute of Therapy and Preventive Medicine, Novosibirsk, Russia [2]State Medical University, Novosibirsk, Russia
	DNA damage and generation of reactive oxygen species by platinum drugs: experiments on bacteria E.V. Prazdnova*, V.A. Chistyakov, M.S. Mazanko, M.N. Churilov, V.K. Chmyhalo Academy of Biology and Biotechnologies of Southern Federal University, Rostov-on-Don, Russia
	Dynamic recognition of 8-Oxoguanine by different protein folds A.V. Endutkin[1,2], C. Simmerling[3], D.O. Zharkov[1,2] [1]SB RAS Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Stony Brook University, Stony Brook, NY, USA
	TASSE: a new approach to solvent treatment in molecular dynamics A.V. Popov, Yu.N. Vorobjev, D.O. Zharkov Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia
	Additivity and non-additivity of genetic control of human metabolome Tsepilov Y.A.[1,2], Shin S.[3,4], Soranzo N.[3], Spector TD.[5], Adamski J.[6,7,8], Kastenmüller G.[9], Strauch K.[10,11], Wang-Sattler R.[12],Gieger C.[10], Aulchenko Y.S.[1,2], Ried J.S.[10] [1]Institute of Cytology and Genetics SD RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, United Kingdom [4]MRC Integrative Epidemiology Unit (IEU), University of Bristol Integrative Epidemiology, Bristol, United Kingdom [5]Department of Twin Research and Genetic Epidemiology, King's College London , London, United Kingdom [6]Institute of Experimental Genetics, Genome Analysis Center, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany [7]Institute of Experimental Genetics, Life and Food Science Center Weihenstephan, Technische Universität München, Freising-Weihenstephan, Germany [8]German Center for Diabetes Research, Neuherberg, Germany [9]Institute of Bioinformatics and Systems Biology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany [10]Institute of Genetic Epidemiology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany [11]Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany [12]Research Unit of Molecular Epidemiology, Helmholtz Zentrum München – German Research Center for Environmental Health, Neuherberg, Germany
«Genomics, transcriptomics and bioinformatics»	**Metagenomic analysis of viral communities in lake Baikal** T.V. Butina[1], Y.S. Bukin[1], A.E. Tupikin[2], M.R. Kabilov[2], O.I. Belykh[1] [1]Limnological Institute SB RAS, Irkutsk, Russia [2]Genomics Core Facility, Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia.
	Inmethyl: a tool for design of specific primers for methylation profiling of complete CPG islands G.S. Krasnov, A.V. Kudryavtseva, N.V. Melnikova, A.A. Dmitriev Engelhardt Institute of Molecular Biology RAS, Moscow, Russia
	Analysis of a powerful constitutive promoter in cultured cells of Polypedilum vanderplanki Sogame, Y.[1,2], Miyata, Y.[1,3], Deviatiiarov, R.[4], Kikuta, S.[5], Cornette, R.[1],Gusev, O.[4,6], Furusawa, T.[1], Kikawada, T.[1,7]

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	miR-619-5p binding sites in protein coding region of ortholog genes mRNA A.T. Ivashchenko, S.A. Atambayeva, R.E. Niyazova, A.Y. Pyrkova Al-Farabi Kazakh National University, Almaty, Kazakhstan
	Anhydrobiosis related promoters in Pv11 cell line R.M. Deviatiiarov[1], T. Kikawada[2], R. Cornette[2], O.A. Gusev[1,2,3] [1]Institute of Fundamental Medicine and Biology KFU, Kazan, Russia [2]National Institute of Agrobiological Sciences NIAS, Tsukuba, Japan [3]Center of Life Science Technologies RIKEN, Yokohama, Japan
	Anhydro-preservation of exogenously-expressed desiccation-sensitive enzyme luciferase using insect cells S. Kikuta[1], S. Watanabe[1], O. Gusev[2,3], Y. Sogame[4], R. Cornette[5], T. Kikawada[5] [1]Tokyo University of Agriculture and Technology, Japan [2]Kazan Federal University, Russia [3]Riken Division of Genomic Technologies, Japan [4]National Agriculture and Food Research Organization, Japan
	Association of matrix metalloproteinases gene polymorphism with the risk of developing extra-articular symptoms of rheumatoid arthritis M.A. Korolev*, Y.B. Ubshaeva, E.A. Letyagina, A.V. Shevchenko, V.F. Prokof'yev, V.I. Konenkov Scientific Institute of clinical and experimental lymphology SB RAS, Novosibirsk, Russia
	Change of the scenario of the Trp-cage miniprotein folding with temperature V.A. Andryushchenko, S.F. Chekmarev Institute of Themophysics SB RAS and Novosibirsk State University, Novosibirsk, Russia
	Characteristics of *acdS*-gene of bacteria *Pseudomonas putida* b- 37 responsible for ACC-deaminase synthesis D.S. Volkava*, S.I. Leanovich, A.A. Melnikava, E.A. Khramtsova Belarusian State University, Minsk, Republic of Belarus
	Characterization of novel alkane-degrading and biosurfactant-producing strain *Tsukamurella tyrosinosolvens PS2* A.V. Laikov, E.A. Boulygina, V.A. Romanova, T.V. Grigorieva 1 Kazan Federal University, Kazan, Russia
	Cmsearch: a tool for searching tfbs composite modules in DNA sequences S.I. Nikitin, E.S. Cheryomushkin A.P. Ershov Institute of Informatics Systems SB RAS, Novosibirsk, Russia Novel Computing Systems in Biology LLC, Novosibirsk, Russia
	Computer analysis of distal gene regulation using chromosome contacts data Y.L. Orlov[1], E.V. Kulakova[2], A.G.Bogomolov[1], V.N. Babenko[1], G. Li[3] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia [3]Huazhong Agricultural University, Wuhan, China
	Computer software for statistical analysis of genes location relative to chromosome contacts revealed by ChIA-PET E.V. Kulakova, A.M. Spitsina Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia
	Differential alternative splicing in rats brain tissues selected by aggressive behavior

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	Differential expression of glycolysis-related genes in *Hilar cholangiocarcinoma* A.V. Snezhkina[1], D.V. Kalinin[3], M.S. Fedorova[1], O.L. Kardymon[1], I.Y. Karpova[1], A.F. Sadritdinova[1,2], N.V. Melnikova[1], A.A. Belova[1,2], M.M. Belyakov[2], O.S. Sudalenko[2], N.N. Volchenko[2], A.Y. Popov[2], K.M. Nyushko[2], A.D. Kaprin[2], B.Y. Alekseev[2], A.A. Dmitriev[1], G.S. Krasnov[1], A.V. Kudryavtseva[1,2] [1]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia [2]Herzen Moscow Cancer Research Institute, Ministry of Health of the Russian Federation, Moscow, Russia [3]A.V. Vishnevsky Institute of Surgery, Moscow, Russia
	Draft genome sequence of *Streptomyces sp. IB2014 011-1* isolated from Lake Baikal macroinvertebrates I.V. Voytsekhovskaya[1], D.V. Axenov-Gribanov[1], B.T. Tokovenko[2], Y.V. Rebets[2], E.S. Protasov[1], A.N. Luzhetskyy [2], M.A. Timofeyev[1] [1]Irkutsk State University, Institute of Biology, Irkutsk, Russia [2]Helmholtz Center for Infectious Research (HZI), Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Saarbrücken, Germany
	Effects of lambertianic acid amide on epileptiform activity in hippocampal slices induced by picrotoxin or magnesium-free medium S.O. Vechkapova, A.L. Proskura*, T.A. Zapara, E.D. Sorokoumov, A.S. Ratushnyak Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia
	Features of miRNA interaction with mRNA genes in coronary heart disease A.T. Ivashchenko, R.E. Niyazova, S.A. Atambayeva, A.Y. Pyrkova Al-Farabi Kazakh National University, Almaty, Kazakhstan
	Functional analyses on the mechanism of induction of anhydrobiosis in the midge *Polypedilum vanderplanki* R. Cornette, K-I. Iwata, S. Kikuta, Y. Sogame, T. Okuda, T. Kikawada Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Functional analysis of RNA-seq transcriptomes from oesophageal cancer specimens of Kazakhstani patients U.Kairov[1]*, A.Molkenov[1], S.Rakhimova[1], A.Abilmazhinova[1], M.Zhalbinova[1], D.Yerezhepov[1], A.Akhmetova[1], Y.Zhukov[2], M.Omarov[2], M.Popova[3], A.Zinovyev[4], A.Akilzhanova[1] and Zh.Zhumadilov[1] [1]Center for Life Sciences, NLA, Nazarbayev University, Astana, Kazakhstan. [2]Oncology Center, Astana, Kazakhstan. [3]Department of Pathology, Astana Medical University, Astana, Kazakhstan. [4]Institute Curie, Paris, France.
	Genetic basis of aggression: clusterization of expression profiles E.S. Tiys[1,2], A.O. Bragin[1,2], I.V. Medvedeva[1,2], I.V. Chadaeva[1], A.L. Markel[1], Y.L. Orlov[1,2] [1] Institute of Cytology of Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
	Genetic diversity and metabolism of the Garga hot spring microbial mat A.S. Rozanov, A.V. Bryanskaya, T.K. Malup, T.V. Ivanisenko, Yu.E. Uvarova, S.E. Peltek Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Genotype distribution in patients with chronic hepatitis C analysis using multifactor dimensionality reduction method A.D. Liaudanski[1], M.S. Rodzkin[1], V.S. Pankratov[1], D.E. Danilau[2], I.A. Karpov[2], O.G. Davydenko[1] [1] Institute of Genetics and Cytology of the National Academy of Sciences of Belarus [2] Belarusian State Medical University
	GTRD–gene transcription regulation database I.S. Yevshin[1,2], R.N. Sharipov[1,2,3], Yu.V. Kondrakhin[1,2], F.A. Kolpakov*[1,2] 1Institute of Systems Biology Ltd., Novosibirsk, Russia 2Design Technological Institute of Digital Techniques, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia 3Novosibirsk National Research State University, Novosibirsk, Russia

	Gut microbiota in case of Parkinson's disease and other neurological pathologies: comparative study V.A. Petrov[1], V.M. Alifirova[1], I.V. Saltykova[1], Y.B. Dorofeyeva[1], A.V. Tyakht[2], E.S. Kostryukova[2], A.E. Sazonov[1,3] [1]Siberian State Medical University, Tomsk, Russia [2]Scientific Research Institute for Physical-Chemical Medicine, Moscow, Russia [3]Lomonosov Moscow State University, Moskow, Russia
	How sequence and structure affect the miRNA maturation P.S.Vorozheykin[1], I.I.Titov[1,2] [1]Novosibirsk State University, Novosibirsk, Russia [2]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	***In silico* modelling of experimental ChIP-seq process** T. Subkhankulova[1], F.M. Naumenko[2], Y.L. Orlov [1]Department of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK [2]Novosibirsk State University, Novosibirsk Rissia
	Interspersed repetitive sequences distribution in human chromosomes analyzed by in situ hybridization and in silico analysis A.G. Bogomolov[1,2], T.V. Karamysheva[1], N.B. Rubtsov[1,2] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
	Methods to calculate p-value of RNA of a definite shape D.G. Vorobyev, V.V. Solovyev Softberry Inc., Novosibirsk, Russia
	Online Scripting Tool for retrieving 3D human genome data A. Butyaev, J. Waldispühl McGill University, Montreal, Québec, Canada
	Predicting small RNAs from bacterial genome T. Stankovic, J. Guzina, M. Nikolic, M. Djordjevic Faculty of Biology, University of Belgrade, Serbia
	Program complex ICGenomics for analysis of high-throughput sequencing experiments I.V. Medvedeva[1], A.O. Bragin[1], K.V. Gunbin[1], P.S. Demenkov[1], O.V. Vishnevsky[1], A.M. Spitsina[2], F.M. Naumenko[2], V.N. Babenko[1], N.L. Podkolodnyy[1], Y.L. Orlov[1]* [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
	Regulation of thioredoxin genes expression in desiccation-tolerant insect *Polypedilum vanderplanki* A.A. Nesmelov[1]*, E.I. Shagimardanova[1], M.D. Logacheva[2], R. Cornette[3], T. Kikawada[3], O.A. Gusev[1,3,4,5] [1]Institute of Fundamental Biology and Medicine, Kazan Federal University, Kazan, Russia [2] Department of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, Russia [3]National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan [4]PMI Riken, Yokohama Campus, Yokohama, Japan
	RTrans: analysis of RNA-Seq differential expression using GLM approach and uncovering its biological background G.S. Krasnov, A.V. Snezhkina, N.V. Melnikova, A.A. Dmitriev, A.V. Kudryavtseva Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia
	Search for gene mutations that can potentially affect the susceptibility to tuberculosis. O.V. Saik[1], P.S. Demenkov[1], E.U. Bragina[2], M. Freidin[2], A. El-Seedy[3], R. Hofestaedt[4], V.A. Ivanisenko[1]. [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Research Institute of Medical Genetics SB RAMS, Tomsk, Russia [3] Alexandria University, Alexandria, Egypt

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	Siberian larch chloroplast genome analysis over triplet frequency distribution E.I. Bondar[1], Y.A. Putintseva[1,2], K. V. Krutovsky[2,3,4] [1]Siberian Federal university, Krasnoyarsk, Russia [2]Institute of forest of SD RAS, Krasnoyarsk, Russia [3]University of Göttingen, Göttingen, Germany [4]Texas A&M University, College Station, Texas, USA
	Statistics of intervals between similar monomers: a complementary way to assess the structural properties of biological polymers M.I. Bogachev[1], A.R. Kayumov[2], O.A. Markelov[1] [1]St. Petersburg Electrotechnical University, St. Petersburg, Russia [2]Kazan (Volga region) Federal University, Kazan, Russia
	Targeted high-throughput sequencing for MODY genes in West Siberia E.V. Shakhtshneider*, E.N. Voropaeva, D.E. Ivanoshchuk, A.K. Ovsyannikova, O.D. Rymar, Y.I. Ragino, M.I. Voevoda Institute of Internal and Preventive Medicine, Novosibirsk, Russia
	The genome wide analysis of the large tandem repeats in the closely related genomes D.I. Ostromyshenskii, O.I. Podgornaya Institute of Cytology RAS, St. Petersburg, Russia
	The influence of rare mutations in the APOB gene to the level of oxidized LDL E.Yu. Khlebus, N.V. Shcherbakova, I.S. Zhanin, A.A. Zharikova, A.I. Ershova, A.V. Kiseleva, S.A. Boytsov, A.N. Meshkov National Research Center for Preventive Medicine, Moscow, Russia
	The influence of SNP rs201381696 of a TATA box in the human *LEP* gene on expression of reporter gene *LUC* E.B. Sharypova[1], E.V. Kashina[1], O.V. Arkova[1,2], N.P. Bondar[1], T.V. Arshinova[1], P.M. Ponomarenko[3], M.P. Ponomarenko [1], and L.K. Savinkova [1] [1]Federal research center Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia; [2]Vector-Best Inc., Koltsovo, Novosibirsk Region, Russia; [3]Children's Hospital Los Angeles, Los Angeles, USA.
	The role of miR-9 and miR-98 in the regulation of HK2 gene expression in colorectal cancer A.V. Snezhkina[1], I.Y. Karpova[1], O.L. Kardymon[1], A.F. Sadritdinova[1,2], M.S. Fedorova[1], N.V. Melnikova[1], O.A. Stepanov, K.M. Klimina[4], E.N. Slavnova, K.M. Nyushko[2], N.N. Volchenko[2], M.A. Chernichenko[2], D.V. Sidorov[2], D.V. Kalinin[3], A.Y. Popov[2], G.S. Krasnov[1], A.V. Kudryavtseva[1,2]* [1]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia. [2]Herzen Moscow Cancer Research Institute, Ministry of Health of the Russian Federation, Moscow, Russia. [3]A.V. Vishnevsky Institute of Surgery, Moscow, Russia [4]Vavilov Institute of General Genetics, Russian Academy of Sciences Moscow, Russia
	The software for estimation of telomere length on individual chromosome arms in immunopathology A.G. Bogomolov[1,3], M.S. Barkovskaya[2], N.B. Rubtsov[1,3], V.A. Kozlov[2] [1]Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2]Research Institute of Fundamental and Clinical Immunology, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia
	The structure of genetic predisposition to type 1 and type 2 diabetes N.V. Tarasenko[1,2], I.A. Goncharova[1,3], A.V. Markov[1], V.P. Puzyrev[1,2] [1] Research Institute of Medical Genetics, Tomsk, Russian Federation [2] Siberian State Medical University, Tomsk, Russian Federation [3] Institute for complex issues of cardiovascular diseases, Kemerovo, Russian Federation
	Transcriptomics of the cryobiotic leech *Ozobranchus jantseanus* S.V. Kuznecova [1], D. Suzuki [2], M.D. Logacheva [3], O.S. Kozlova [1], T. Kikawada [4], R.M. Sabirov[1], O.A. Gusev[1] [1] Kazan Federal University, Kazan, Russia

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	Using the bioinformatic software technicues to search CRISPR / Cas systems in the genome of *Escherichia coli* strain O157:H7 E.I. Ivanova[1], Yu.P. Dzhioev[1,2], A.Yu. Borisenko[2], A.I. Paramonov[1], V.I. Zlobin[2], N.L. Belkova[1,3] [1]«Scientific Center of the Family Health and Human Reproduction Problems», Irkutsk, Russia [2]Irkutsk State Medical University, Irkutsk, Russia [3]Limnological Institute SB RAS, Irkutsk, Russia
	Vascular endothelial growth factor polymorphisms are associated with the earlier onset of rheumatoid arthritis V.O. Omelchenko[1]*, M. A. Korolev[1], E. A. Letyagina [1], A.V. Shevchenko[1], V.F. Prokof'yev [1], T.I. Pospelova [2], V.I. Konenkov [1] [1]Federal State Budgetary Scientific Institution «Scientific Institute of clinical and experimental lymphology» SB RAS, Novosibirsk, Russia [2]The Novosibirsk State Medical University, Novosibirsk, Russia
	Workflow for exome sequencing in identification of de novo mutation in the *NCL6* gene D.A. Petukhova, N.R. Maksimova, P.I. Guryeva, V.S. Kaymonov, M.T. Savvina Laboratory of Genome Medicine, Clinics of Medical Institute, North-Eastern Federal University