Tuesday, July 5

- 1.2 Regulatory genomics
- 2.1 Reconstruction, computational analysis and modeling of biological systems
- 3.2 Structural biology of proteins and membranes
- 7.1 Animal Models of Pathologies
- 7.3 Neurogenomics and genetics of Behavior
- 8.1 Cellular and Molecular Biology in Human Health and Diseas
- 8.2 Experimental Pharmacology
- 8.3 Innovative Technologies in Digital and Clinical Medicine

Wednesday, July 6

- 1.1 Genomics and transcriptomics of plants and animals
- 1.3 Functional and applied 3D genomics
- 2.2 Modeling of population and ecological systems and processes
- 3.1 The role of synchrotron radiation and advanced instrumental techniques for macromolecular crystallography and pharmacology
- 3.3 Chemoinformatics and chemical biology
- 7.2 Population and evolutionary genomics of wild and domestic animals
- 8.4 Genotyping, Personalized Medicine and Bioinformatics
- 8.5 Experimental Modeling in Biomedicine
- 9.1 Mathematical immunology
- 9.2 Mathematical epidemiology
- 12.0 Systems biology of aging: experimental and computational approaches

Thursday, July 7

- 4.1 Human medical/population genomics and genetics
- 5.2 Microbial communities of natural and anthropogenic habitats
- 5.3 Industrial biotechnologies: creation of producer strains
- 5.4 Modeling and computer analysis of microbiological systems and processes
- 6.1 Genomics, genetics and system biology of plants
- 6.2 Developmental biology of plants: computational and experimental approaches
- 9.1 Mathematical immunology
- 9.2 Mathematical epidemiology
- 11.0 Symposium "Systems biology and bioinformatics of DNA repair processes and programmed cell death"

Friday, July 8

- 1.4 Evolutionary genomics, bioinformatics, and molecular phylogeny
- 4.1 Human medical/population genomics and genetics
- 4.2 Genome-wide association studies
- 5.2 Microbial communities of natural and anthropogenic habitats
- 5.3 Industrial biotechnologies: creation of producer strains
- 6.1 Genomics, genetics and system biology of plants
- 10.0 Symposium "Cognitive sciences, neurogenetics, neuroinformatics and systems computational biology"
- 12.0 Systems biology of aging: experimental and computational approaches
- 13.0 Symposium "Big genetic Data Analysis, deep learning, mathematical modeling and supercomputing"

Tuesday, July 5

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| Author | Title | Section |
| | BacRegDB: a database of bacterial regulatory elements with structural evidence | |
| Ekaterina Shitik | Capsid modifications of adeno-associated virus serotype 2 | |
| Guzel Gazizova | Dormice functional genome annotation project: the first insights on regulation of h | |
| | Evolutionary role of genomic DNA physical properties in the realization of its eleme | |
| Victoria Dikaya | Grass frog (Rana temporaria) tandem repeats in the genome and oocytes' transcrip | |
| Ruslan Sharipov I | Heterogeneity of transcription factor binding sites within ChIP-Seq datasets | 1.2 Regulatory genomics |
| Vladimir Raditsa [| Massive comparison of the 'genomic' and 'shuffled' background set generation app | |
| Elena Voropaeva | Methylation of p53-responsive microRNA genes in tumor tissue of lymphoma | |
| Pavel Vorozheykin | mitomiRs as the common regulators of gene silencing | |
| Nadezhda Sorokina I | Potential bacteriophage recombination sites inside genes containing cysteine repea | |
| Shilpa Harshan | Tocilizumab partially reverses the altered transcriptional regulation of glycolysis in c | |
| Semyon Kolmykov | Transcription factor binding sites: data integration, stable identifiers and increment | |
| Dmitry Konanov | Applicability of the Oxford Nanopore sequencing technology to DNA modifications | |
| | Computer analysis of genes associated with Kaposi's sarcoma | |
| | Development of an algorithm for facts extraction from the texts of biomedical artic | |
| Elena Ignatieva | Functional and evolutionary characteristics of the gene network controlling appetit | |
| | Gene network reconstruction and functional association studies for oncological dise | |
| | Impact of negative feedbacks on de novo pyrimidines biosynthesis in E.coli | |
| | MiRNA-dependent regulation of ERBB signaling pathway genes in patients with NAS | 2.1 Reconstruction, computational analysis and modeling of biological systems |
| <u> </u> | Modeling of contractile activity-induced fatigue in human skeletal muscle | , |
| | Morphogenesis of Drosophila melanogaster Mechanoreceptors: System Regulation | |
| | Reconstruction and analysis of the gene network of hepatocellular carcinoma unde | |
| | Reconstruction and analysis of the gene network of the external pathway of apopto | |
| | Reconstruction of mathematical frame models of bacterial transcription regulation | |
| | Variability and Robustness of the Functioning of Gene Regula-tory Networks: Role in | |
| | A model of SARS-CoV-2 spike transmembrane domain linked to the HR2 region: stru | |
| | Activation of a Trk receptor is mediated by a disordered extracellular juxtamembrar | |
| | All-D-enantiomeric peptide designed for Alzheimer's disease treatment dynamically | |
| | Analysis of binding properties of influenza hemagglutinins and human receptor ana | |
| , , , | Application of X-Ray, SAXS and essential dynamics simulations to study conformation | |
| | Bending compliance of lipid bilayer regulates the curvature threshold and pathway | |
| | Can Ca2+-regulated photoproteins perform different functions than bioluminescen | |
| | Changes in the structure and dynamics of the intracellular domain of Toll-like recep | |
| | Classification of families of DNA-recognizing protein domains based on structural fe | |
| | Comparison of Hemoglobin Sequences of Normoxic Species to Hypoxia-Resistant H | |
| | | |
| | Comparison of nucleosome unfolding by yeast and human FACT: electron microsco | |
| | Diversity of structural-dynamic properties of transmembrane domains among the in | 3.2 Structural biology of proteins and membranes |
| | Evaluation of the effect of site-directed mutagenesis on the affinity of anti-PD1 nan | |
| | In silico engineering towards enhancement of Anti-CD20 nanobody binding affinity Interaction of D-cycloserine with a D-amino acid transaminase from Haliscomenoba | |
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| Lev Sukovatyi 1 | Molecular modeling of osmolytes' effect on bacterial luciferase | |
| Lev Sukovatyi I Erik Kot I | Molecular modeling of osmolytes' effect on bacterial luciferase NMR study of lipid/protein interactions in trifluoroethanol-water mixtures propose | |
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| Olga Krasnova | Autophagy activation in 3D-spheroid leads to the mesenchymal stem cells rejuvena | |
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| | | . 5, 5, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, |
| | TCOMprehensive piomarkers of accelerated aging and morrality risk in end-crape reni | |
| Elena Kondakova | Comprehensive biomarkers of accelerated aging and mortality risk in end-stage ren MEK1/2-ERK 1/2-dependent alphaB-crystallin phosphorylation in retina: a focus on | |
| Elena Kondakova Natalia Myraleva | MEK1/2-ERK 1/2-dependent alphaB-crystallin phosphorylation in retina: a focus on | |
| Elena Kondakova Natalia Myraleva Tatiana Kozlova | MEK1/2-ERK 1/2-dependent alphaB-crystallin phosphorylation in retina: a focus on Morphological feature of the postnatal blood-brain barrier formation as one of pred | |
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| | Alternative splicing of human FMR1 gene in peripheral blood: making a single-gene Application of a novel k-mer primer design algorithm for detecting antibiotic resista | | | | |
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| | Functional enrichment analysis of cytochrome P450 genes differential expression in | | | | |
| | Genes for aryl hydrocarbon receptor signaling are associated with uterine fibroids s | A A House and distribution and associated and associated | | | |
| - 0 | Genes, encoding heat-resistant obscure (Hero) proteins: new players in ischemic str Mutation c.396dupT in the CLN6 gene - the main cause of neuronal ceroid lipofucin | 4.1 Human medical/population genomics and genetics | | | |
| | Pluripotent stem cell lines from two patients with COH1 gene mutations as the valu | | | | |
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| | Polymorphism rs1800795 of the IL6 gene in samples of Siberian indigenous ethnic g | | | | |
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| | Screening of the pathogenic variant c.3751dupA of the BRCA2 gene in women from The spectrum of mutations in the EXT1 gene among patients with Multiple Heredit; | | | | |
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| - ge ere re re re | Bioleaching of sulfide copper-nickel ores | 5.2 Microbial communities of natural and anthropogenic habitats | | | |
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| Serger Buitin | Producers and oxidizers of methane in the bottom sediments of Lake Baikal and the | | | | |
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| 7.5ya vasiicva | Software package for retrosynthesis-based prediction of metabolic pathways | 5.5 industrial biotechnologies, creation of producer strains | | | |
| | Study of the scaling possibility of the process of obtaining feed protein from natura | | | | |
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| Bogdan Kirillov | Finite element modeling of physical processes in multilayer spheroids based on Fun | 5.4 Modeling and computer analysis of microbiological systems and processes | | | |
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| , | Reconstruction of a genome-scale metabolic model for chicken whole embryo cons | | | | |
| 0-, -, | Analysis of the size and color characteristics of wheat grains and their relationship t | | | | |
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| | Natural variation of E1-E4, E9, GmFT5a genes in 180 soybean accessions adapted to | | | | |
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| Svetlana Senchurov | The pre-steady state analysis of human terminal deoxynucleotidyltransferase confo The role of active-site amino acids in template-independent DNA synthesis by hum | | | | |
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| Anna Shvaikovskaya | Concordance between the in vivo concentrations of neurospecific proteins (BDNF, N | |
| Ekaterina Semina | Identification of a novel small RNA encoded in the mouse urokinase receptor uPAR | |
| Renata Enikeeva | Impact of P2RX7 and TNF/LTA gene polymorphisms in non-verbal intelligence in me | 10.0 Cognitive sciences, neurogenetics, neuroinformatics and systems |
| Alexey Zakluta | Influence of sulfur metabolism genes on processes related to learning and memory | computational biology |
| Maryana Morozova | ation of influence of the gut microbial composition associated with colitis on mice b | |
| Ekaterina Zalomaeva | Memory formation in Drosophila with neurospecific suppression limk1 gene expres | |
| Alena Burnyasheva | Alterations of glutamatergic/GABAergic systems during healthy aging and Alzheime | |
| Daniil Peunov | Analysis of changes in microglia and cerebral endothelium in hippocampus of OXYS | |
| Daniil Yukhtanov | Analysis of mitochondrial supply of neuronal processes during the postnatal brain n | |
| Oyuna Kozhevnikova | Aqueous humor complement factor I concentration is associated with SNP of CFI ge | |
| Olga Krasnova | Autophagy activation in 3D-spheroid leads to the mesenchymal stem cells rejuvenal | 12.0 Systems highery of aging congrimental and assembly assembly assembly as a second as a seco |
| Darya Telegina | Both melatonin and mitochondrial antioxidant SkQ1 had different effect on the reti | 12.0 Systems biology of aging: experimental and computational approaches |
| Elena Kondakova | Comprehensive biomarkers of accelerated aging and mortality risk in end-stage ren | |
| Natalia Myraleva | MEK1/2-ERK 1/2-dependent alphaB-crystallin phosphorylation in retina: a focus on | |
| Tatiana Kozlova | Morphological feature of the postnatal blood-brain barrier formation as one of pred | |
| Anna Antonenko | The daily cycle of glutamate in the retina of OXYS rats during aging and the develop | |
| Dmitrii Smirnov | The emerging role of SIRT6 in the mitochondrial regulation | |
| Yuriy Orlov | Artificial Intelligence implementation in pharmaceutical products lifecycle | |
| Nikita Artemenko | Glume pubescence prediction of spikelets using computer vision techniques | 13.0 Big genetic Data Analysis, deep learning, mathematical modeling and |
| Shaburova Elizaveta | Improved MHC peptide class I interaction prediction with pretrained transformer | supercomputing |
| Gaik Tamazian | Pygenomics: Python package for processing genomic intervals and bioinformatic da | |
| Igor Busov | The system of computer vision for extracting quantitative characteristics of wheat s | |