Join conference's Telegram channel
https://t.me/mccmb21

If you get lost on the campus or need help but do not see anybody to ask for, please call

+7–977–303–88–96

Friday, July 30th	
9:30–10:00	**morning coffee**
10:00–11:30	**early morning session**
10:00	Introduction
	EVOLUTION
10:15	The world of viruses, its global organization and evolution *Eugene Koonin* *NCBI*
10:45	Heterogeneity of the GFP fitness landscape and data-driven protein design *Fedor Kondrashov* *Institute of Science and Technology Austria*
11:15	A billion-year trend of amino acid substitutions in the mitochondrial genome *Alina G. Mikhailova* *IKBFU*
11.30–12:00	**coffee break**
12:00–13:30	**late morning session**
	NON-CODING RNA
12:00	Integrative genomic discovery and drugging of long noncoding RNAs in cancer *Rory Johnson* *University College Dublin*

12:30	Translational landscape of human 3' UTRs *Pavel V Baranov* *University College Cork*
13:00	Disruption of uORFs translation is an underestimated cause of Mendelian disorders *Alexandra Yu. Filatova* *Research Centre for Medical Genetics*
	SPONSORED TALK
13:15	The sbvIMPROVER Metagenomics Diagnostics for Inflammatory Bowel Disease Challenge: Results and Lessons Learned *Lusine Khachatryan* *PMI Science*
13:30–16:00	**lunch**
13:30–14:25	**SYSTEMS BIOLOGY SESSION**
13:30	Introduction
13:40	Interpretable model for chromatin interaction probability prediction *Alexandra Galitsyna* *Skolkovo Institute of Science and Technology*
13:55	Suppression of reverse transcriptase-driven chimeric cDNA synthesis *Alexandr Gordeev* *Institute of Protein Research RAS*

14:10	Bi-directional study chromatin organization into the eukaryotic nuclei cell *Pavel Kos* *Moscow State University*
14:30–16:00	**ONLINE POSTER SESSION**
	presenters: A–F
16:00–17:30	**early evening session**
	3D CHROMATIN
16:00	Loop extrusion on busy DNA *Leonid Mirny* *MIT*
16:30	Unraveling the structure of paired homologs and sister chromatids with Hi-C and polymer modeling *Anton Goloborodko* *IMBA*
17:00	preciseTAD: a machine-learning framework for predicting boundaries of 3D genomic elements *Mikhail G Dozmorov* *Virginia Commonwealth University*
17:15	Anopheles mosquitoes revealed new principles of 3D genome organization in insects *Igor V Sharakhov* *Virginia Tech*
17:30–19:30	**coffee break and OFFLINE POSTER SESSION**
19:30–…	**welcome party**

Saturday, July 31st	
9:30–10:00	**morning coffee**
10:00–11:30	**early morning session**
	MACHINE LEARNING
10:00	Federated Machine Learning *Jan Baumbach* *University of Hamburg*
10:30	Network enriched analysis of complex biological time-series data *Richard Röttger* *University of Southern Denmark*
11:00	Style transfer with variational autoencoders is a promising approach to RNA-Seq data harmonization and analysis *Denis V Antonets* *SRC VB "Vector"*
11:15	Multi-platform cross-harmonization of gene expression profiles obtained using mRNA next-generation sequencing and microarray hybridization *Nicolas M. Borisov* *Moscow Institute of Physics and Technology*
11.30–12:00	**coffee break**
12:00–13:30	**late morning session**
	SINGLE CELLS — 1

12:00	TBA *Rahul Satija* *New York Genome Center*
12:30	Unraveling transcriptional intratumoral heterogeneity at single cell level *Andrei Zinovyev* *Institut Curie*
12:45	Single nucleus RNA-sequencing data reveals intra-tumoral heterogeneity in medulloblastoma brain tumors with extensive nodularity *Konstantin Okonechnikov* *German Cancer Research Center*
13:00	Variation of mutation rate between individual cells *Maria A Andrianova* *Skolkovo Institute of Science and Technology*
13:15	Joint model of RNA velocity on transcriptional manifold *Ruslan Soldatov* *Harvard Medical School*
13:30–16:00	**lunch**
13:30–14:10	**SYSTEMS BIOLOGY SESSION**
13:30	Identification and separation of sources of transcriptional variability in single-cell RNA-seq data *Konstantin Zaitsev* *ITMO University*

13:40	Origin of helper T cell diversity in human immunity: the study of TCR repertoires *Sofya Kasatskaya* *Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry*
13:50	"Investigation of T. thermophilus Type III CRISPR-Cas mediated bacterial defense mechanisms *Daria Artamonova* *Skolkovo Institute of Science and Technology"*
14:00	Direct reprogramming of human skin fibroblasts into insulin-producing cells using CRISPR/dCas9-SunTag-VP64 effector epigenome editing systems *Alexandr Artyuhov* *Pirogov Russian National Research Medical University*
14:10	Rational design of chimeric portal proteins of viruses *Evgeny Klimuk* *Institute of Molecular Genetics RAS*
14:30–16:00	**ONLINE POSTER SESSION**
	presenters: G–Ma
16:00–17:30	**early evening session**
	POST-TRANSCRIPTION

16:00	Conserved long-range base pairings are associated with pre-mRNA processing of human genes *Dmitri Pervouchine* *Skolkovo Institute of Science and Technology*
16:15	An extended catalogue of tandem alternative splice sites in human tissue transcriptomes *Aleksei Mironov* *Skolkovo Institute of Science and Technology*
16:30	Genome-wide search for pathogenic splice variants manifested in different genetic backgrounds *Mikhail Y Skoblov* *Research Centre for Medical Genetics*
16:45	Assessing proteome diversity raised by alternative splicing in Brain RNA-Seq data *Vladimir N Babenko* *Institute of Cytology and Genetics SB RAS*
17:00	Proteome recoding by A-to-I mRNA editing *Sergei Moshkovskii* *Pirogov Russian National Research Medical University*
17:15	Fast gene set enrichment analysis with multi-level Monte-Carlo approach *Alexey A Sergushichev* *ITMO University*
17:30–18:00	**coffee break**

18:00–19:15	**late evening session**
	SINGLE CELLS — 2
18:00	Tempora: Cell trajectory inference using time-series single-cell RNA sequencing data *Gary Bader* *University of Toronto*
18:30	Cell segmentation in spatial transcriptomics *Peter Kharchenko* *Harvard Medical School*
19:00	Multimodal by default: designing the next generation of methods and tools for single-cell multi-omics *Danila Bredikhin* *EMBL*

Sunday, August 1st	
9:30–10:00	**morning coffee**
10:00–11:30	**early morning session**
	GENETICS — 1
10:00	Biological design and prediction using evolutionary information *Deborah Marks* *Harvard Medical School*
10:30	The missing link between genetic association and regulatory function *Shamil Sunyaev* *Harvard Medical School*
11:00	Peeking inside the clockworks of regulatory single-nucleotide variants with ADASTRA and ANANASTRA *Ivan V Kulakovskiy* *Institute of Protein Research*
11:15	Within-gene epistatic selection in genetically diverse populations *Anastasia V Stolyarova* *Skolkovo Institute of Science and Technology*
11.30–12:00	**coffee break**
12:00–13:30	**late morning session**
	GENETICS — 2

12:00	Estimating the timing of multiple admixture events using 3-locus Linkage Disequilibrium *Mikhail Shishkin* *HSE University*
12:15	Quantitative genetics of human protein N-glycosylation *Yurii Aulchenko* *Institute of Cytology and Genetics SD RAS*
12:30	Mapping genes involved in control of N-glycosylation of blood glycoproteins through a large genome-wide association study *Sodbo Sharapov* *Institute of Cytology and Genetics SB RAS*
12:45	Targeted sequencing of 242 clinically important genes in a sample of Russian population from Ivanovo region *Vasily Ramensky* *National Medical Research Center for Therapy and Preventive Medicine of the Ministry of Healthcare of the Russian Federation*
13:00	Mutational spectrum of the human mitochondrial genome: somatic and germline signatures differ *Kristina Ushakova* *Immanuel Kant Baltic Federal University*
13:15	Precise mutation rate estimation on an individual site level *Vladimir Seplyarskiy* *Harvard Medical School*

13:30–16:00	**lunch**
13:30–14:20	**SYSTEMS BIOLOGY SESSION**
13:30	Integration of genomics and metabolomics data for discovery of small natural products *Alexey Gurevich* *Saint-Petersburg State University*
13:40	Mechanistic model of mutation accumulation based on differential kinetics of DNA repair *Maria Andrianova* *Skolkovo Institute of Science and Technology*
13:50	Investigation of the genetic architecture of human traits on the phenome scale *Yury Barbitoff* *Saint-Petersburg State University*
14:00	Transcriptional interference by RNA-guided DNA-binding proteins *Aleksei Agapov* *Institute of Molecular Genetics*
14:10	High-throughput analysis of short DNA fragments generated in vivo in *Escherichia coli* and *Saccharomyces cerevisiae* *Anna Shiriaeva* *Skolkovo Institute of Science and Technology/ St. Petersburg Branch of Vavilov Institute of General Genetics*
14:30–16:00	**ONLINE POSTER SESSION**
	presenters: Me–Shp

16:00–17:30	**early evening session**
	STRUCTURE
16:00	Intragenic compensatory variants: does the distance matter? *Nadezhda Azbukina* *Lomonosov Moscow State University*
16:15	New algorithms for finding combinatorially complete datasets in high-throughput mutagenesis experimental data *Dmitry N Ivankov* *Skolkovo Institute of Science and Technology*
16:30	HLA binding preferences of self-peptides are biased towards proteins with specific molecular functions *Vadim Karnaukhov* *Skolkovo Institute of Science and Technology*
16:45	Co-aggregation of amyloids: from structural principles to in silico prediction *Andrey V. Kajava* *CNRS*
17:00	Functional domain annotation of protein sequences with deep metric learning *Denis V Antonets* *SRC VB "Vector"*
17:15	MolDiscovery: Learning Mass Spectrometry Fragmentation of Small Molecules *Azat Tagirdzhanov* *St. Petersburg State University*
17:30–18:00	**coffee break**

18:00–19:30	late evening session
	BOTANICAL GARDEN AND ZOO
18:00	Models for crop species diversification within and between centers of domestication *Anna Igolkina* *Peter the Great St.Petersburg Polytechnic University*
18:15	Genomic blueprints of flax diversification and improvement *Maria Duk* *Peter the Great St.Petersburg Polytechnic University*
18:30	Numerical study of the flowering time model of wild chickpeas *Andrey Y Ageev* *Peter the Great St.Petersburg Polytechnic University*
18:45	Artificial intelligence applied to population genomics and paleogenomics *Olga Dolgova* *Center for Genomic Regulation*
19:00	A systems biology approach to understanding SARS-CoV-2 transmissibility in population *Sofija Markovic* *University of Belgrade*
19:15	A single chromosome driving rapid extremotolerant adaptation in an insect *Yuki Yoshida* *University of Tokyo*

Monday, August 2nd	
9:30–10:00	**morning coffee**
10:00–11:30	**early morning session**
	CELLS AND SIGNALS
10:00	Quantifying and Manipulating the Aging Process *Vadim N Gladyshev* *Harvard Medical School*
10:30	Identification of phenotype-specific networks from paired gene expression-cell shape imaging data *Evangelia Petsalaki* *EMBL*
11:00	Which wiring of the cell cycle opens the path to mitotic and meiotic division? *Ovidiu Radulescu* *University of Monpellier*
11:15	Learning the cell states using deep neural networks for cell type-specific interpretation of disease variants *Veniamin Fishman* *Sberbank AI Lab*
11.30–12:00	**coffee break**
12:00–13:30	**late morning session**
	COMPARATIVE AND FUNCTIONAL GENOMICS

12:00	Computational methods for genome interpretation *Emidio Capriotti* *University of Bologna*
12:30	Laying foundations for very large-scale comparative genomics *Christophe Dessimoz* *Swiss Institute for Bioinformatics*
13:00	Bringing Human Population Genetics to Protein Structure *Geoff Barton* *University of Dundee*
13:30–16:00	**lunch**
13:30–14:30	**SYSTEMS BIOLOGY SESSION**
13:30	**Awards ceremony**
13:40	The investigation of Mitochondrial Genomes of Helianthus species *Maksim Makarenko* *Institute for Information Transmission Problems*
13:50	High-Throughput Splicing Efficiency Analysis System *Sofia Mariasina* *Moscow State University/Skolkovo Institute of Science and Technology*
14:00	Computational methods for unsupervised demographic inference of multiple populations from genomic data *Ekaterina Noskova* *ITMO University*

14:10	The function and structure of pseudo-nucleus in jumbo phages *Alexei Samolygo* *Skolkovo Institute of Science and Technology*
14:20	Systematic identification and validation of novel RiPP biosynthetic gene clusters encoding YcaO-domain enzymes *Dmitrii Travin* *Skolkovo Institute of Science and Technology*
14:30–16:00	**ONLINE POSTER SESSION**
	presenters: Shu–Z
16:00–17:30	**early evening session**
	DEVELOPMENT
16:00	Pluripotency factors in zebrafish embryo *Daria Onichtchouk* *Albert-Ludwigs-University of Freiburg*
16:30	Optimal decoding of cellular identities in a genetic network *Gasper Tkacik* *Institute of Science and Technology Austria*
17:00	Early developmental asymmetries in cell lineage trees in living individuals *Alexej Abyzov* *Mayo Clinic*
17:15	The digenean complex life cycle: phylostratigraphy analysis of molecular signatures *Maksim A Nesterenko* *Saint Petersburg University*

17:30–18:00	coffee break
18:00–19:30	**late evening session**
	BACTERIA
18:00	Chromosome conformation of the hyperthermophilic archaeon *Thermofilum adornatus* *Andrey Sobolev* *Institute of Gene Biology RAS*
18:15	Method for detection of parallel adaptation with genome rearrangements in bacterial populations *Alexey Zabelkin* *ITMO University*
18:30	Evolutionary benefits of bacterial genomes with chromids *Olga Bochkareva* *IST Austria*
18:45	Black holes in the regulation of biofilm formation in *Escherichia coli* *Maria Tutukina* *Skolkovo Institute of Science and Technology*
19:00	A>G is a hallmark of oxidative damage in mitochondrial and bacterial genomes *Konstantin Popadin* *Ecole Polytechnique Federale de Lausanne*
19:15	Investigating microbial diversity of spontaneous fermentation beer and cider using Hi-C metagenomics *Ignat V. Sonets* *Institute of Gene Biology RAS*

19:30–…	farewell party

Poster session

Modelling Segmental Duplications in the Human Genome
Eldar Abdullaev *(Max Planck Institute for Molecular Genetics)*

Transformer-based model for recognition of quadruplexes using information on physical and chemical DNA properties
Ivan Agafonov *(Higher School of Econimics); Maria Poptsova*

SARS-CoV-2 escapes cytotoxic T cell immune response during long-term infection of immunocompromised patient with non-Hodgkin's lymphoma
Evgeniia Alekseeva *(Skolkovo Institute of Science and Technology); K. Safina; E. Nabieva; S. Garushyants; G. Klink; G. Bazykin*

Two Cobalt Chelatase Subunits Can Be Generated from a Single chlD Gene via Programed Frameshifting
Ivan Antonov

Single cell RNAseq-based transcriptome profiling of mesenchymal stromal cells reveals subpopulations with different responses to profibrotic stimuli
M.S. Arbatsky *(Lomonosov Moscow State University), N.A. Basalova, O.A. Grigorieva, N.I. Kalinina, A.Yu. Efimenko*

Evolution of Transcriptional Regulation of Histidine Metabolism in Gram-positive Bacteria
German Ashniev *(IITP RAS); Natalia Sernova; Alexey Shevkoplias; Ivan Rodionov; Irina Rodionova; Alexey Vitreschak; Mikhail Gelfand; Dmitry A Rodionov*

Population specific enhancer affecting optic disc development timespan underlies Glaucoma predisposition.
Roman Babenko *(Institute of Cytology and Genetics, DB RAS), Vladimir Babenko*

Enhancing eukaryotic gene structures by implementing statistical changepoint analysis of expression data using FINDER - a completely automated gene annotator
Sagnik Banerjee *(Iowa State University); Priyanka Bhandary; Margaret Woodhouse; Taner Sen; Roger Wise; Carson Andorf*

Population genomics and population multi-omics of adaptation
Antonio Barbadilla *(Universitat Autònoma Barcelona); Sònia Casillas; Jesús Murga*

Origin and splicing of mutually excluding exons and pre-mRNA secondary structure in human genes of voltage-gated calcium channels
Ilya S. Belalov *(Skolkovo Institute of Science and Technology); Timofei M. Ivanov; Marina Kalinina; Dmitri D. Pervouchine*

The power law of CRISPR-Cas systems
Ilya S. Belalov *(Skolkovo Institute of Science and Technology); Yekaterina S. Pavlova; David Paez-Espino; Andrew Yu. Morozov; Ilya S. Belalov*

Dynamics of dN/dS at short evolutionary distances
Evgenia A. Belousova *(Lomonosov Moscow State University); Anastasia V. Stolyarova; Alexey S. Kondrashov; Georgii A. Bazykin*

Multiscale investigation into the active site composition of AmiN kinase

Julia Belyaeva (Lomonosov Moscow State University); Alexander Zlobin; Andrey Golovin

The dependence of homologous recombination rate on the level of heterozygosity in hypervariable fungus *Schizophyllum commune*

Aleksandra V Bezmenova (Skolkovo Institute of Science and Technology); Elena Zvyagina; Tatiana Neretina; Anna Fedotova; Georgii Bazykin; Alexey Kondrashov

The expansion of the range of microbial rhodopsins by their artificial sequences

Elizaveta Bogdanova (Lomonosov Moscow State University); Shaitan K.V.; Novoseletsky V.N.

Application of the intron sequence of the NXF1 gene in mammalian phylogeny

Dmitrii Bondaruk (St. Petersburg State University); E.V. Golubkova; L.A. Mamon

Structure-Based Identification of Small Molecule Inhibitors for Selective Targeting of SARS-CoV-2 Main Protease: An Integrative Computational Approach

Ivan P Bosko (UIIP NASB); A.M. Andrianov; Yu.V. Kornoushenko; A.D. Karpenko; A.M. Yushkevich; K.V. Furs; A.V. Tuzikov

Convergent adaptation in mitochondria of phylogenetically distant birds: does it exist?

Valentina Burskaia (Kharkevich Institute for Information Transmission Problems); Ilja Artyushin; Nadezhda Potapova; Kirill Konovalov; Georgii A. Bazykin

Calcium coordination in enzymes: the intertwining of structural and functional features **Michelle F Buyanova** *(Lomonosov Moscow State University); Arthur O. Zalevsky; Andrey V. Golovin*
HiChew: a tool update for TAD boundaries clustering in development **Nikolai S Bykov** *(Skolkovo Institute of Science and Technology); Aleksandra A Galitsyna*
The Spatial Organization of the genome of sea sponge *Halisarca dujardini* **Alexander V Cherkasov** *(Skolkovo Institute of Science and Technology); Alina Ryabova; Olga Kozlova; Alexander Finoshin, Oksana Kravchuk; Ekaterina Khrameeva*
Modular assembly of immune-event-labeled synthetic AIRR-datasets for the development and benchmarking of AIRR-based machine learning **Maria Chernigovskaya**; *Victor Greiff*
Trajectory inference methods applied to clinical and bulk transcriptomomic data **Alexander Chervov** *(Institute Curie); Andrei Zinovyev*
MSAtoGFA: a Graph Representation of Multiple Sequence Alignments **Fawaz Dabbaghie** *(University Hospital Düsseldorf); Tobias Marschall; Olga Kalinina*
DNA-Methylation for the Detection and Distinction of 19 Human Malignancies **Ludmila Danilova** *(Johns Hopkins University); John Wrangle; James G. Herman; Leslie Cope*

Tick-borne encephalitis virus phylodynamics
Andrei A Deviatkin *(Sechenov First Moscow State Medical University); Galina Karganova; Yulia Vakulenko; Ivan Kholodilov; Alexander Lukashev*

Gene expression pattern in Edward syndrome: A bioinformatic analysis on what creates significant low life expectancy
Supantha Dey *(University of Dhaka)*

A neural network approach to the QM / MM metadynamics' quantum mechanical description level
Igor D Diankin *(Lomonosov Moscow State University); A. V. Golovin;*

The Classification of *ipaH* Genes in *Shigella* and Enteroinvasive *Escherichia*
Natalia O Dranenko *(IITP RAS); Maria Tutukina; Olga Bochkareva*

The analysis of *Drosophila melanogaster* Hi-C maps with autocorrelation function and Fourier transform
Alexey I Drozhdev *(Lomonosov Moscow State University); A.A.Galitsyna; M.S.Gelfand*

Secondary structure of the SARS-CoV-2 genome affects molecular evolution
Bogdan E. Efimenko *(IKBFU); Alexandr Voronka; Sergey Oreshkov; Konstantin Popadin; Konstantin V Gunbin*

Protein-coding potential of the human repetitive elements
Artyom A. Egorov *(Lomonosov Moscow State University); Sergey Dmitriev*

Insights into the genetic components of chronic back pain
Elizaveta E Elgaeva *(Institute of Cytology and Genetics SB RAS); Maxim B. Freidin; Frances M. K. Williams; Pradeep Suri; Yurii S. Aulchenko; Yakov A. Tsepilov*

Catalytic mechanism of MnmE GTPase as a member of ion-dependent GTPases class
Evgenia Elizarova *(Lomonosov Moscow State University); A.S. Zlobin; A.V. Golovin; A.Y. Mulkidjanian*

Two sequence variants of *yjjM* gene in the *Escherichia coli* genomes
Vera Emelianenko *(IST Austria); Olga Bochkareva; Maria Tutukina; Anna Kaznadzey*

Telling the story of best friends: marker rank statistics
Alexander Favorov *(JHMI); Vasiliy Ramensky; Andrey Mironov*

Discovery of non-AUG PANTs: Proteoforms with Alternative N Termini
Alla Fedorova *(University College Cork); Stephen Kiniry; Pavel Baranov*

Predicted Spike-ORF8 Genomic RNA-RNA Interaction Unique to SARS-CoV-2 May Allosterically Impact the Rate of Nucleocapsid Sub-genomic RNA Synthesis
Mario A Flores *(UTSA); Karla Paniagua; Yufang Jin*

Allele specific transcription factor binding sites mark positive selection loci in the human genome
Marina Fridman; *P. Bykadorov*

Asymmetrical mutagenesis drives aminoacid composition of the human mitochondrial genome
Alima Galieva (Immanuel Kant Baltic Federal University); Alina A. Mikhailova; Alina G. Mikhailova; Victor Shamanskiy; Valeria Lobanova; Kristina Ushakova; Konstantin Gunbin; Konstantin Popadin

Tandem segmentation-classification approach for localization of morphological predictors of *C. elegans* lifespan and movement
Evgeniy Galimov (AILS); Yakimovich A

RedC-nf: an automatized pipeline to map RNA-DNA interactions
Aleksandra A Galitsyna (Skolkovo Institute of Science and Technology); Mikhail D. Magnitov; Aleksey A. Gavrilov; Andrey A. Mironov

Creation of new antibacterial peptides
Oxana V Galzitskaya (Institute of Protein Research RAS); S.R. Kurpe; S.Y. Grishin; A.V. Glyakina; M.V. Slizen; A.V. Panfilov; A.P. Kochetov; E.I. Deruysheva; A.V. Machulin; A.K. Surin

Pentads: a novel pile-up analysis tool for assessing the alterations of chromatin compartments using Hi-C data
Azat Garaev (Lomonosov Moscow State University); M.D. Magnitov; S.V. Ulianov; S.V. Razin

Calculation of Sublimation Entropy and Dissociation Constants from a Simple Evaluation of Movement Range of Molecules in Crystals
Sergiy O Garbuzynskiy (Institute of Protein Research RAS); A.V. Finkelstein

Whole-genome atlas of transcribed regulatory elements expression during time-course disuse and recovery in skeletal muscles of rats
Guzel Gazizova *(Kazan Federal University); Sergey Pintus; Ilya Akberdin; Ivan Yevshin; Fedor Kolpakov; Oksana Tyapkina; Leniz Nurullin; Ruslan Devyatiyarov; Elena Shagimardanova; Pavel Makhnovskii; Daniil Popov; Oleg Gusev*

Machine-learning model for prediction of new antimicrobial peptides: *Hirudo medicinalis* metagenome case study
Ekaterina Nikolaevna Grafskaia *(FRCC PCM); Maja Malakhova; Victoria Lavrenova; Ivan Latsis; Vladislav Babenko; Vassili Lazarev*

Feature extraction by neural network trained to predict RNA structure
Lisa Grigorashvili *(Skolkovo Institute of Science and Technology); Mikhail Gelfand; Zoe Chervontseva*

Dissection of Loci Underlying Flowering Time of Guar (*Cyamopsis tetragonoloba (L.) Taub.*) via Integrated Transcriptome-Metabolome Analysis
Elizaveta Grigoreva *(ITMO University); Alexander Tkachenko; Aleksandar Beatovic; Serafima Arkhimandritova; Dmitry Karzhaev; Vladimir Volkov; Cecile Ben; Laurent Gentzbittel; Elena Potokina*

QTL mapping of oleic acid content and tocopherol composition in sunflower from VNIIMK collection
Rim Gubaev *(Skolkovo Institute of Science and Technology); S.Boldyrev; E. Martynova; A. Chernova; T. Kovalenko; S. Goryunova; D. Goryunov; T. Peretyagina; Y. Demurin; P. Khaitovich*

Automatic reconstruction of species-specific mitochondrial mutational spectra based on DNA polymorphisms
Konstantin V Gunbin *(Immanuel Kant Baltic Federal University); Konstantin Popadin*

Mitochondrial mutational spectrum in birds: evidence of increased oxidative damage in species with high level of metabolism
Yury Gusarov *(Immanuel Kant Baltic Federal University); Alina G. Mikhailova; Sergey Oreshkov; Alina A. Mikhailova; Dmitry Knorre; Leonard V. Polishchuk; Alexander Kuptsov; Konstantin V. Gunbin; Valentina Burskaya; Konstantin Popadin*

Binary metabolic phenotypes and phenotype diversity metrics for functional characterization of microbial communities
Stanislav Iablokov *(IITP); Dmitry A Rodionov*

mtDNA mammalian evolution: mice evolve by many little steps while elephants with a few big ones
Dmitrii Iliushchenko *(IKBFU); Konstantin Popadin; Konstantin V Gunbin*

Evolutionary repertoire of eukaryotic chromatin-associated proteins
Ivan Ilnitskiy *(FBB MSU); A.A. Mironov; A.A. Zharikova*

Current advances and future perspectives on single-cell Hi-C bioinformatics
Alexey Ivanov *(Higher School of Economics); Aleksandra Galitsyna; Mikhail Gelfand*

Tandem exon duplications expanding splicing repertoire
Tim Ivanov *(Skolkovo Institute of Science and Technology); Dmitri Pervouchine*

Long-range RNA-RNA pairings in human pre-mRNAs and their implications in alternative splicing
Marina Kalinina (Skolkovo Institute of Science and Technology); Olga Babadei; Dmitry Skvortsov; Svetlana Kalmykova; Olga Dontsova; Dmitri Pervouchine

Viral metagenomic analysis of publicly available genomic and transcriptomic samples from Simuliidae and Ceratopogonidae insects
Ekaterina Kamanova (State Research Center of Virology and Biotechnology "Vector"); M.E. Starchevskaya; T.S. Nepomnyashchikh; Denis V. Antonets

Inversions and translocations in a highly polymorphic fungus *Schizophyllum commune*
Asia Kamyshnikova (Skolkovo Institute of Science and Technology); Anastasia V. Stolyarova; Georgii A. Bazykin; Alexey S. Kondrashov

Indexing Sequencing Data at Petabase Scale
Mikhail Karasikov (ETH Zurich); Harun Mustafa; Daniel Danciu; Gunnar Rätsch; André Kahles

Design and Bioinformatics Analysis of Novel 2-Arylaminopyrimidine-Based Compounds as Potential Bcr-Abl Tyrosine Kinase Inhibitors
*Alexander Andrianov; Yury V Karnaushanka; **Anna D Karpenka** (UIIP NASB); Ivan P Bosko; Zhanna Ignatovich; Elena Koroleva; Julia Siniutsich*

Evolution of different genotypes of hepatitis B and hepatitis delta viruses in endemic region
Anastasia Karlsen (I. Mechnikov NIIVS); O.V. Kuzmin; F.A. Asadi Mobarhan; O.V. Isaeva; S.S. Sleptsova; Victor A. Manuylov; Andrei A. Pochtovyi; Vladimir A. Gushchin; K.K. Kyuregyan; M.I. Mikhailov

Search for the genetic determinants of yeast mtDNA suppressivity
Nataliia Kashko (Lomonosov Moscow State University); Dmitry Knorre

Computational inference of metabolic phenotypes for new bacterial isolate and metagenome-assembled genomes
*Marat Kazanov; Semen Leyn; **Dmitry A Rodionov** (IITP)*

mtDNA codon usage of Chordata is primarily shaped by mutational spectra
Eldar Khaibulin (IKBFU); Alina G. Mikhailova; Victor Shamanskiy; Konstantin Popadin

In search of molecular traces of adaptations to life in high mountains in mammals
Darya Khaleneva (Saint Petersburg State University); O.V. Bondareva; S.Yu. Bodrov; T.V. Petrova; E.A. Genelt-Yanovskiy; N.I. Abramson

Composition of metabolic loci in bacterial genomes
Evgenia Khodzhaeva (Institute for information Transmission Problems RAS); Zoe Chervontseva

Multiomic view of gene regulation in Plasmacytoid Dendritic Cells
Maksim Kholmatov (EMBL); Judith B. Zaugg

Deterministic DNA embeddings with no predefined k-mer length

Bogdan Kirillov *(Skolkovo Institute of Science and Technology); Maxim Panov*

Sensitive mapping of transposon insertions using Cas9-Targeted Nanopore sequencing and a novel pipeline

Ilya Kirov *(VNIISB); Pavel Merkulov; Sofya Gvaramiya; Murad Omarov; Maxim Dudnikov; Elizaveta Kolganova; Roman Komakhin; Mikhail Divashuk; Gennady Karlov; Alexander Soloviev*

A comparative genomic study of attenuated and virulent strains of the African swine fever virus genotype I and serogroup 2

Galina Koltsova *(Federal Research Center for Virology and Microbiology); S. Namsrayn; A. Koltsov*

Generative-Adversarial Neural Networks for Quadruplex and Z-DNA prediction

Nikita Konstantinovsky *(Higher School of Economics); Nikita Kazakov; Maria Poptsova*

Precipitant ions influence on lysozyme mono- and oligomers stability investigated by molecular dynamics simulation

Yuliya Kordonskaya *(Shubnikov Institute of Crystallography of Federal Scientific Research Centre "Crystallography and Photonics" Russian Academy of Sciences); Vladimir Timofeev; Yulya Dyakova; Margarita Marchenkova; Yuriy Pisarevskiy; Michael Kovalchuk*

A comparison of computational tools for average nucleotide identity estimation

Aleksei Korzhenkov *(NRC KI)*

Evolution of mitochondrial DNA inheritance patterns *Pavel Kravchenko;* **Dmitry Knorre** *(Belozersky Institute of Physico-Chemical Biology)*
Evolutionary insights into microbial oxylipin signalling **Georgy F Kurakin** *(Tver State Medical University); Anna Samoukina; Nadezhda Potapova*
Genotype-by-environmental interactions for chronic back pain **Ivan A Kuznetsov** *(Skolkovo Institute of Science and Technology); Yakov A. Tsepilov; Yurii S. Aulchenko*
Transfer learning for whole-genome G-quadruplex annotation **Pavel Latyshev** *(Higher School of Economics); Maria Poptsova*
Dating gene cluster acquisition: The case of Form III RubisCO-mediated transaldolase variant of the Calvin cycle **Alexander V Lebedinsky** *(Federal Research Centre «Fundamentals of Biotechnology of the Russian Academy of Sciences); Ilya Kublanov; Evgenii Frolov; Elizaveta Bonch-Osmolovskaya; Nikolay Chernyh*
Bioinformatic analysis of prokaryotic rotary ATPases: revealing the correlations between coupling ion type and microorganism physiology **Anna Valeryevna Litvin** *(Lomonosov Moscow State University); Maria S. Shoshinova; Alexander S. Yakushev; Anna S. Lapashina; Boris A. Feniouk*

A billion-year trend of amino acid substitutions in the mitochondrial genome: comparative analysis of different taxa
Valeriia V Lobanova (Immanuel Kant Baltic Federal University); Konstantin Popadin; Alina G. Mikhailova; Kristina Ushakova; Victor Shamanskiy; Alina Mikhailova; Alima Galieva

Complex evolution of Fbxl21 gene in mammals
Vassily A Lyubetsky (Institute for Information Transmission Problems of the Russian Academy of Sciences (Kharkevich Institute)); G.A. Shilovsky; O.A. Zverkov; L.I. Rubanov; A.V. Seliverstov

On Selective Imputation Using Beagle v.5.
Sergey V. Malov (Saint-Petersburg State University); Alexander Kanapin; Anastasia Samsonova; Gaik Tamazian

The stochastic nature of the interaction between CRISPR interference and replication events provides the coexistence of virus and bacteria populations
Viktor Mamontov (Skolkovo Institute of Science and Technology); Yaroslav Ispolatov; Ekaterina Semenova

Sequence determinants of cross-regulatory feedback loops in RNA-binding protein interaction network
Sergey Margasyuk (FBB MSU); Dmitri Pervouchine

mtmlSEM with random effects uncovers genotype-phenotype associations through pleitropic SNPs
Georgy A Meshcheryakov (SPbPU); Anna Igolkina

Using protein-protein interaction and gene networks to improve Connectivity Map
Mariia Minaeva (Moscow Institute of Physics and Technology); Khalimat Murtazalieva; Yulia Medvedeva

The atlas of expression of cis-regulatory elements of human craniofacial embryonic tissues ***Elena Minkina*** *(Kazan Federal University); Akberova Natlia; Shagimardanova Elena; Adameyko Igor; Gusev Oleg*
Efficient detection of structural variations using capture-Hi-C data ***Evgeniy A Mozheiko*** *(Institute of Cytology and Genetics SB RAS); Maria Gridina; Emil Valeev; Veniamin Fishman; Ludmila P. Nazarenko; Maria E. Lopatkina; Igor N. Lebdev; Maria I. Yablonskaya; Viktoria Yu Voinova; Zhanna G. Markova; Nadezhda V. Shilova*
Optimization of the directed evolution experimental design by the genetic algorithm theory ***Ekaterina Myasnikova*** *(Peter the Great Saint-Petersburg Polytechnical University); Alexander Spirov*
A sensitive method for search for orthologs of de novo annotated lncRNAs ***Dmitry E Mylarshchikov*** *(FBB MSU); Andrey Mironov*
Bcbio – a set of best practices NGS data processing pipelines for bioinformatics cores and diagnostic labs ***Sergey Naumenko*** *(Harvard Chan School of Public Health)*
Analysis of Poxviridae and Coronaviridae genomes using k-mer frequency profiles and comparison with alignment-based approach ***Tatyana S Nepomnyashchikh*** *(SRC VB "Vector"); D.V. Antonets; M.E. Starchevskaya; T.V. Tregubchak; A.N. Shvalov; E.V. Gavrilova; S.N. Shchelkunov; Rinat A. Maksyutov*

Evolution scheme of the CRISPR-Cas locus in *Xanthomonas citri* can be reconstructed based on its spacers content, but the result disagrees with the strain phylogeny for the species
***M.S. Nikitin** (MIPT); N.V. Zakharevich; I.I. Artamonova*

Comparative genomics of placozoans: fast evolution of neuronal genes in nerveless animals
***Mikhail A. Nikitin** (Lomonosov Moscow State University); Simha I. Borman; Daria Yu. Romanova; Maria D. Logacheva; Leonid L. Moroz*

A Deep Learning-Based Approach for Prediction of Potential HIV-1 Entry Inhibitors Targeting CD4-Binding Site of GP120
*Alexander Andrianov; **Grigory I. Nikolaev** (United Institute of Informatics Problems of the National Academy of Sciences of Belarus); Nikita Shuldov; Ivan P Bosko; Alexander Tuzikov*

Is bacterial species pangenome structure associated with habitat diversity?
***Daria Nikolaeva** (Skolkovo Institute of Science and Technology); Sofya K. Garushyants*

vsFilt: a new tool for structural filtration and virtual screening
***Dmitry K Nilov** (Lomonosov Moscow State University); I.V. Gushchina; D.A. Suplatov; V.K. Švedas*

New features in GADMA for efficient and flexible inference of demographic history
***Ekaterina Noskova** (ITMO University); Vladimir Ulyantsev*

A potential of polygenic risk scores as a tool to inform population screening for breast cancer
***Arina Nostaeva** (Institute of Cytology and Genetics); Tatiana Shashkova; Lennart Karssen; Yurii Aulchenko*

Chromatin association of BIRC5/survivin protein genome binding in human CD4+ T cells
Nina Oparina (GU); Malin Erlandsson; Karin M.E. Adersson; Venkatagavan Chandrasekaran; Anastasios Damdimopoulos; Sofia T. Silfverswärd; Maria I. Bkarewa

Lipidome composition of the healthy adult human brain
Maria Osetrova (Skolkovo Institute of Science and Technology); Ekaterina Khrameeva; Anna Tkachev; Elena Stekolschikova; Aleksandra Mitina; Olga Efimova; Philipp Khaitovich

Pupae recapitulate the embryonic expression program in insects undergoing radical metamorphosis
Aleksandra Ozerova (Skolkovo institute of science and technology); Mikhail Gelfand

Study of influence of homology modeling on the prediction of protein stability change upon mutation
Marina A Pak (Skolkovo Institute of Science and Technology); Dmitry N. Ivankov

What can substitution biases tell us about the origin of SARS-CoV-2
Alexander Y Panchin (Institute for Information Transmission Problems, RAS)

Classification of families of DNA-recognizing protein domains based on structural features of DNA-protein complexes
Vera Panova (Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University); Eugene Baulin; Anna Karyagina; Andrey Alexeevski; Sergey A Spirin

Genomic determinants of viral host diversity **Marina Parr** *(Technical University of Munich); Dmitrij Frishman; Tamir Tuller*
Structural descriptors-based clustering for the evaluation of the patterns in 3D-structure of vitamin D receptor **Karina Pats** *(ITMO University); Ferdinand Molnar*
In-silico identification of key regulators instigating the pre-meiotic phase during respiration in *Saccharomyces cerevisiae* **Soumita Podder** *(Raiganj University)*
Identification and structural analysis of long noncoding RNAs **Artem Y Pronozin** *(institute of cytology and genetics sb ras); Afonnikov D.*
Structure-based design of monoclonal antibodies against SARS-CoV-2 **Elena Rukhlova** *(State Research Center of Virology and Biotechnology "Vector"); Anastasia Bakulina; Dmitry Shcherbakov; Iuliia Merkuleva*
Restriction-modification systems in microbiome of Antarctic Deep Lake **I. Rusinov** *(Belozersky Institute); A. Ershova; A. Alexeevski; A. Karyagina; S. Spirin*
A new database for genome-wide RNA-chromatin interactome **Grigory Ryabykh** *(Moscow State University); Anastasiya Zharikova; Andrey Sigorskikh; Yuriy Korostelev; Andrey Mironov*

Supposed properties of enhancers associated with human-specific brain genes
Marat Sabirov *(Institute of Gene Biology RAS); Ekaterina Khrameeva*

Molecular epidemiology of HIV in Oryol district, Russia
Ksenia Safina *(Skolkovo Institute of Science and Technology); Georgii Bazykin; Yulia Sidorina; Natalya Efendieva; Elena Belonosova; Dmitry Kireev*

Comparative genomics of flax pathogen *Fusarium oxysporum* f.sp. lini
A. Kanapin; A. Samsonova; **A. Logachev***; M. Bankin; T. Rozhmina; M. Samsonova*

MutAnt: Mutation annotation machine learning algorithm for pathogenicity evaluation of single nonsynonymous nucleotide substitutions in cancer cells
Aleksandr Sarachakov *(Skoltech); Viktor Svekolkin; Zoya Antysheva; Jessica Brown; Alexander Bagaev; Nathan Fowler; Mikhail Gelfand*

Xenobiotic associated CYP450 9e2 family in Formicinae: protein family evolution and population study of black garden ant *Lasius niger* CYP9E2 genes expression
Viktoria Scobeyeva *(Moscow State University); Svetlana Zhukova; N. Yu. Oparina; I. Artyushin*

Genome-wide search for positive selection in *Schizophyllum commune*
Maria Selifanova (FBB MSU)*; Galina Klink; Anastasia Stolyarova; Georgy Bazykin*

Evolution of Insertions Sequences in the Evolution of Intracellular Pathogens *B. mallei*
Ariadna Semenova *(MSU); Olga O. Bochkareva*

How to improve real-life applicability of drug-target interaction prediction?
Ilya Senatorov *(HIPS); Olga V. Kalinina*

Development of a searching algorithm for new cell-penetrating peptides using machine learning methods
Maria Y Serebrennikova *(Federal State Budgetary Institution Federal Research and Clinical Center of Physical-chemical Medicine Federal Medical Biological Agency); Ekaterina Grafskaia; Vassili Lazarev*

Genomic adaptations of chironomids to extreme environments
Nurislam Maratovich Shaikhutdinov *(Skoltech); Galina Klink; Sofya Garushyants; Olga Kozlova; Elena Shagimardanova; Guzel Gazizova; Natalia Gogoleva; Andrey Przhiboro; Oleg Gusev; Georgii Bazykin*

Somatic deletions in the human mitochondrial genome: the global secondary structure, G-quadruplexes and direct nucleotide repeats explain majority of breakpoints
Victor Shamanskiy *(Center For Mitochondrial Functional Genomics, IKBFU); Alina Mikhailova; Kristina Ushakova; Alina Mikhaylova; Sergei Oreshkov; Dmitry Knorre; Evgenii Tretiakov; Ilia Mazunin; Konstantin V Gunbin; Konstantin Khrapko; Konstantin Popadin*

Deep learning for demographic inference from whole-genome sequences
Vladimir Shchur *(HSE University); Evgeniy Khomutov; Kenenbek Arzymatov; Viktoriya Vasileva*

Using transcriptomic data for reconstruction of earthworm phylogeny on the example of the *Eisenia nordenskioldi* complex
***Sergei V Shekhovtsov** (Institute of Cytology and Genetics SB RAS); Alexandra A. Shipova; Tatiana V. Poluboyarova; Sergei E. Peltek*

Sequence analysis of human TMTC proteins reveals their enzymatic activity and ligand binding sites
***Vladimir A. Shitov** (Siberian State Medical University); B. Eisenhaber; S. Sinha; C. K. Jadalanki; Q. W. Tan; F. L. Sirota; F. Eisenhaber*

Deep learning model for Hi-C maps prediction
***Alexey Shkolikov** (Moscow State University); Aleksandra Galitsyna; Mikhail Gelfand*

A search of embryonic selection traces: transmission disequilibrium of slightly-deleterious variants from parents to the offspring with Down syndrome
***Kseniia Sholokhova** (Center for Mitochondrial Functional Genomics); Konstantin Gunbin; Victor Shamanskiy; Louis-Alexandre Ongaro; Konstantin Popadin*

SPAN and JBR - tools for semi-supervised peak calling
***Oleg Shpynov** (JetBrains Research); Roman Chernyatchik; Petr Tsurinov; Maxim Artyomov*

Regulation of splicing in Sirt6-KO mouse brain
***Artemy Shumskiy** (Skoltech); Dmitrii Smirnov; Ekaterina Khrameeva; Deborah Toiber*

New RNAs revealed by RNA-chromatin interactions
Andrey Sigorskikh *(Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University); Grigory Ryabykh; Yuri Korostelev; Anastasiya Zharikova; Andrey Mironov*

optimalTAD: a novel algorithm for Topologically Associating Domain optimal set prediction
Dmitrii Smirnov *(Skolkovo Institute of Science and Technology); Ekaterina Khrameeva*

The species-specific burden of slightly deleterious mutations in mammals
Anastasia D Sokol *(Immanuel Kant Baltic Federal University); Alina Mikhailova; Konstantin Gunbin; Konstantin Popadin*

New database and software for topology-based pathway analysis of human gene expression data: overview and application example
Maxim I Sorokin *(Sechenov University); Alexander Simonov; Victor Tkachev; Anton Buzdin*

Fast simulation of viral genealogies in global pandemic
Vladimir Shchur; ***Vadim Spirin*** *(HSE University); Victor Pokrovskii; Evgeni Burovski; Russell CorbettDetig*

Predicting quality of phylogenetic inference by machine learning
Aleksei Efremov; ***Sergey A Spirin*** *(Belozersky Institute)*

PhyloBench, a benchmark for evaluation of phylogenetic programs
Alexei Efremov; Andrey Sigorskikh; Dmitry Penzar; Anna Karyagina; ***Sergey A Spirin*** *(Belozersky Institute)*

Reverse transfer of ideas from genetic algorithms to synthetic biology
Alexander V Spirov (IEPhB RAS); Ekaterina M. Myankova

Modeling of active transport of bicoid mRNA in early Drosophila embryo development
Alexander V Spirov (IEPhB RAS); Ekaterina M. Myasnikova; Marat A. Sabirov

The rich inner world of Colorado potato beetles – a metagenomic survey of viral diversity in public data
Maria Starchevskaya (State Research Center of Virology and Biotechnology "Vector"); Denis V Antonets; Yuri Vyatkin; Tatyana Tregubchak; Tatyana Bauer; Ekaterina Kamanova; Tatyana Nepomnyaschih; Ulyana Rotskaya; Elena Kosman

Integrative approach to intermediate filament structure
Sergei V Strelkov (KU Leuven); Anastasia V. Lilina; Giel Stalmans; Pieter-Jan Vermeire; Jan Fiala; Petr Novak

Gene Set Co-regulation Analysis
Vladimir Sukhov (ITMO University); Maxim Artyomov; Alexey Sergushichev

Functional significance of structural plasticity of the loop 422-437 in the active site of Neuraminidase A from *Streptococcus pneumoniae*
Dmitry Suplatov (Lomonosov Moscow State University); Yana Sharapova; Vytas Švedas

Zebra3D: a tool for bioinformatic analysis of 3D-determinants of functional diversity in protein superfamilies using machine learning
*Daria Timonina; Yana Sharapova; Vytas Švedas; **Dmitry Suplatov** (Lomonosov Moscow State University)*

Image processing methods for analysis of cellular structure of epithelial tissue **Svetlana Surkova** *(Peter the Great St. Petersburg Polytechnic University); Maria Samsonova; Konstantin Kozlov*
On Selective Imputation Using Beagle v.5. **Gaik Tamazian** *(St. Petersburg State University); Alexander Kanapin; Anastasia Samsonova; Sergey V. Malov*
Identification of conservative patterns of G-quadruplexes and transcription binding sites **Julia Terentjeva** *(Higher School of Economics); Maria Poptsova*
Utilizing machine learning methods and cellular gene expression patterns of longevity for identification of new lifespan-extending interventions **Stanislav Tikhonov** *(Lomonosov Moscow State University); Alexander Tyshkovskiy*
Bioinformatic analysis of local 3D-structure patterns in protein superfamilies **Daria Timonina** *(Lomonosov Moscow State University, Faculty of Bioengineering and Bioinformatics); Yana Sharapova; Vytas Švedas; Dmitry Suplatov*
Heat shock protein 90 as a long-term buffer of a species-specific mutational burden **Valeria N Timonina** *(Immanuel Kant Baltic Federal University, Center for Functional Mitochondrial Genomics); Anastasia Sokol; Evgenii Tretiakov; Konstantin V Gunbin; Konstantin Popadin*

Data-driven approach for traits definition for multivariate genetic analysis of N-glycome composition
Anna Timoshchuk (MIPT); Nadezhda A. Potapova; Gordan Lauc; Tim Spector; Sodbo Sharapov; Yurii S. Aulchenko

Shared heredity: a method to model genetic basis of correlated traits
Evgeny Tiys (Institute of cytology and genetics); Gulnara R. Svishcheva; Sofia G. Feoktistova; Elizaveta E. Elgaeva; Sodbo Z. Sharapov; Yakov A. Tsepilov

Assembly and annotation of the sable (*Martes zibellina*) and pine marten (*Martes martes*) genomes
Andrey Tomarovsky (Computer Technologies Laboratory, ITMO University); Azamat A. Totikov; Violetta R. Beklemisheva; Polina L. Perelman; Natalia A. Serdyokova; Tatiana Bulyonkova; Ksenia A. Koniaeva; Alexei V. Abramov; Alexander S. Graphodatsky; Klaus-Peter Koepfli; Roger A. Powell; Sergei F. Kliver

Reconstruction of the demographic history for three populations of the least weasel *Mustela nivalis*
Azamat Totikov (Computer Technologies Laboratory, ITMO University); Andrey A. Tomarovsky; Polina Perelman; Natalia Serdyokova; Violetta R. Beklemisheva; Tatiana M. Bulyonkova; Karol Zub; Viktor V. Panov; Anna S. Mukhacheva; Alexei V. Abramov; Klaus-Peter Koepfli; Alexander S. Graphodatsky; Jose Melo-Ferreira; Sergei F. Kliver

FARM – new Association Rule Mining method using Fishbone diagrams
Petr Tsurinov (JetBrains Research); Oleg Shpynov; Maxim Artyomov; Nina Lukashina; Daria Likholetova

Prediction of inton-exon gene structure for reads by a convolution neural network
***Leonid Uroshlev** (Institute of Higher Nervous Activity and Neurophysiology RAS); A.P. Beletskiy*

Fitness landscape learning, canalization and fast evolution
***Sergey Vakulenko** (Institute for Mechanical Engineering Problems, RAS, S. Petersburg Problems); John Reinitz; Ovidiu Radulescu; Dmitry Grigoriev*

Semi-extractability of coding and non-coding RNAs
***Anna Valyaeva** (Lomonosov Moscow State University); Maria A. Tikhomirova; Anastasia A. Zharikova; Anna V. Fedotova; Andrey A. Mironov; Eugene V. Sheval*

Systematic analysis of age-dependent lipidome alterations in rat tissues
***Anastasiia Velikanova** (Skoltech); Aleksandra Mitina; Elena Stekolschikova; Olga Efimova; Ekaterina Tyulkova; Elena Rybnikova; Pavel Mazin; Philipp Khaitovich*

De novo identification of alternative polyadenylation from RNA-seq data
***Maria Vlasenok** (Skoltech); Dmitri Pervouchine*

Analysis of the mutation spectrum and selective constraints of SARS-CoV-2
***Alexandr Voronka** (Immanuel Kant Baltic Federal University); Bogdan Efimenko; Sergei Oreshkov; Konstantin Gunbin; Konstantin Popadin*

Small RNAs in *Paramecium* response to *Preeria caryophila* infection
Yulia Yakovleva *(Saint Petersburg State University); Sivarajan Karunanithi; Marcello Pirritano; Franziska Drews; Martin Simon; Alexey Potekhin*

Modelling of the evolutionary pathway from anti-restriction to anti-CRISPR function
Daria Yanovskaya *(Moscow Institute of Physics and Technology (National Research University)); M.A. Skutel; O.S. Musharova; A. B. Isaev*

Genomic analysis of skin cancers from Xeroderma Pigmentosum subgroups revealed mechanisms behind UV mutational signatures formation
Andrey A Yurchenko *(Institut Gustave Roussy); Tirzah B. P. Lajus; Hiva Fassihi; Chikako Nishigori; Konstantin Gunbin; Fatemeh Rajabi; Ismael Padioleau; Carlos F. M. Menck; Alain Sarasin; Patricia Kannouche; Sergey Nikolaev*

Let's go analytic! Two exact models of the mtDNA mutagenesis and their ramifications
Valerian A Yurov *(Immanuel Kant Baltic Federal University); Konstantin Popadin*

Single Cell Navigator allows cross-matching of public scRNA-seq data: study case of tumor immune microenvironments
Konstantin Zaitsev *(ITMO University); Maria Firulyova; Maxim N. Artyomov*

Causal relationships between human IgG N-glycosylation traits and twelve associated diseases
Olga O. Zaitseva *(Genos Ltd); Sodbo Sharapov; Gordan Lauc; Lucija Klaric; Yakov Tsepilov*

pmx.qmmm: automated protein structure and topology generation for QM/MM calculations
Arthur O Zalevsky (Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS); Alexander Zlobin; Andrey Golovin

Assembling genomes on chromosome-level leading by the example of two malaria vector genomes
Anton A Zamyatin (ITMO University); Pavel Avdeyev; Jiangtao Liang; Atashi Sharma; Chujia Chen; Varvara Lukyanchikova; Nikita Alexeev; Zhijian Tu; Max A Alekseyev; Igor V. Sharakhov

In silico design of inhibitors of cathepsin G based on β-ketophosphonate
Nikita Zernov (Peter the Great St. Petersburg Polytechnic University); L.S. Hunanyan

RNA-DNA integractome analysis
Anastasia A Zharikova (FBB MSU); Andrey I. Sigorskikh; Yuriy D. Korostelev; Andrey A. Mironov

Features of chromatin structure & gene expression during *D. discoideum* development
Irina Zhegalova (Skoltech); A. Galitsyna; A. Luzhin; S. Ulianov; E. Khrameeva

Primary sequence of the Japanese quail's nucleolar organizer region
Alina A Zhukova (The Herzen State Pedagogical University of Russia); Zakharov G.A.; Kulak M.M.; Saifitdinova A.F.

Development of method for predicting synergistic combinations of small molecules based on RNA-seq data **Dinara Ziganshina** *(Moscow Institute of Physics and Technology); Khalimat Murtazalieva; Yulia Medvedeva*
A platform for storage and analysis of results of genome-wide association studies of sheep **Alexander S Zlobin** *(Kurchatov Genomic Center of Institute of Cytology and Genetics SB RAS); Anatoliy Kirichenko; Tatyana Shashkova; Natalya Volkova; Pavel Borodin; Lennart Karssen; Yakov Tsepilov; Yurii Aulchenko*
DESMOND 2.0: Identification of differentially expressed biclusters and investigation of their network properties **Olga Zolotareva** *(Technical University of Munich); Olga I. Isaeva; Zoe Chervontseva; Alexey Savchik; Evgenia Zotova; Olga Lazareva; David B. Blumenthal; Nina K. Wenke; Martin Ester; Jan Baumbach*