

## Program of the MCCMB2017

<b>Thursday, July 27th</b>	
9:00	Registration and morning coffee
10:00	OPENING
<b>Epigenomics</b>	
10:20	Transgenerational transmission of environmental information in animals <i>Tanya Vavouri</i>
11:00	Reconstruction of regulatory pathways from methylation QTL data <i>Matthias Heinig</i>
11:40	COFFEE
<b>Chromatin Structure</b>	
12:10	Understanding genome and chromatin structure by RNA biogenesis and degradation <i>Albin Sandelin</i>
12:50	Factors shaping structural organization of chromatin <i>Ekaterina Khrameeva</i>
13:10	RNA-DNA interactions in chromatin <i>Alexandra Galitsina</i>
13:30	LUNCH
<b>Animal development</b>	
15:00	Generating robustness and precision during embryonic development <i>Eileen Furlong</i>
15:40	Widespread conservation of developmental regulation of alternative splicing in mammals <i>Pavel Mazin</i>

16:00	Single cell transcriptomics reveals sequential fate selection points and mechanism of cell fate commitment of the neural crest <i>Ruslan Soldatov</i>
16:20	Frequency and properties of mosaic somatic mutations in a normal developing brain <i>Alexej Abyzov</i>
16:40	Genes with clonal monoallelic expression contribute disproportionately to expression variation in humans <i>Svetlana Vinogradova</i>
17:00	COFFEE and <b>POSTERS</b>
19:30:00 sharp	LEAVE FOR DINNER

<b>Friday, July 28th</b>	
9:00	Morning coffee
<b>Transcriptomics</b>	
10:00	InfoSigMap: Google Maps of informative gene signatures visualizes their compositional and functional redundancies in transcriptomic studies <i>Andrei Zinovyev</i>
10:40	Global transcriptional network reveals that tocopherols rescue TREM2-driven microglial dysfunction in vivo <i>Alexander Predeus</i>
11:00	InFusion: advancing discovery of fusions genes and chimeric transcripts from RNA-sequencing data <i>Konstantin Okonechnikov</i>
11:20	Expression analysis of human miRNA - mRNA interactome <i>Olga Plotnikova</i>
11:40	COFFEE
<b>Integration and Modeling</b>	
12:10	Understanding key features of CRISPR/Cas system induction through modeling <i>Marko Djordjevic</i>
12:30	Protein synthesis: From the whole translome to individual codons and back <i>Pavel Baranov</i>
13:10	Robustness of Hunchback gene pattern formation due to dynamic equilibrium in gap gene system in an early Drosophila embryo <i>Ekaterina Myasnikova</i>
13:30	LUNCH

14:40	Biocad. Sponsored talk
<b>Comparative Genomics</b>	
15:00	Evidence of ancient extreme conservation of genomic regions in animal genomes <i>Dmitry Korkin</i>
15:40	Appearance of new splice sites on human lineage is associated with positive selection and splicing changes <i>Stepan Denisov</i>
16:00	Evolution of brain active gene promoters in human lineage towards the increased plasticity of gene regulation <i>Valentin Suslov</i>
16:20	Using historical collections to understand the evolutionary response of bees to an emergent parasite <i>Alexander Mikheyev</i>
17:00	COFFEE
<b>Cells and Mutations</b>	
17:30	Analysis of clone-specific molecular and phenotypic characteristics <i>Peter Kharchenko</i>
18:10	Error-prone bypass of pre-existing damages during the replication of the lagging strand is substantial source of mutations in cancers and germline <i>Vladimir Seplyarskiy</i>
18:30	Mutational signatures of DNA repair deficiencies and cytotoxin exposures in <i>C. elegans</i> <i>Nadezda Volkova</i>
18:50	LEAVE FOR THE BOAT TRIP

<b>Saturday, July 29th</b>	
9:00	Morning coffee
<b>Evolution</b>	
10:00	Progress and perspectives in understanding genetic control of complex human traits <i>Yurii Aulchenko</i>
10:40	Large scale fitness landscape of a protein-coding gene <i>Fyodor Kondrashov</i>
11:20	Contribution of copy number variants to phenotypic diversity of domestic dog breeds. <i>Inna Povolotskaya</i>
11:40	COFFEE
<b>Cancer</b>	
12:10	Analysis of neuroblastoma super-enhancer landscape identifies two distinct malignant cell types <i>Valentina Boeva</i>
12:50	A quantitative framework of integrating multi-modal cancer genomic data <i>Chen-Hsiang Yeang</i>
13:10	Dormant origins initiate short-scale replication forks: an evidence from cancer genomes and Okazaki fragments sequencing <i>Artem Artemov</i>
13:30	LUNCH
<b>Bacteria</b>	
15:00	The Dps nucleoid protein from <i>E. coli</i> : is DNA protection accompanied by transcriptional regulation? <i>Maria Tutukina</i>

15:20	Determinants of spacer choice during naïve and primed CRISPR adaptation by type I-E CRISPR-Cas system of <i>Escherichia coli</i> <i>Ekaterina Savitskaya</i>
15:40	Reconstruction of transcription control networks in Mollicutes by high-throughput identification of promoters <i>Gleb Fisunov</i>
16:00	Comparative genomics analysis of human gut microbiome demonstrated broad distribution of metabolic pathways for mucin glycans foraging <i>Dmitry Ravcheev</i>
16:20	Assessing and integrating the various levels of complexity in plant-microbe interactions <i>Muhammad Naseem</i>
16:40	COFFEE
<b>Botanic Garden</b>	
17:10	Phylotranscriptomic hourglass patterns of embryonic and post-embryonic plant development <i>Ivo Grosse</i>
17:50	TRANSFAC-ing the rice genome <i>Tatiana Tatarinova</i>
18:10	Nicotiana genomes: beyond tobacco <i>Nikolai Ivanov</i>
18:30	Using DNA metabarcoding to identify the composition of herbal teas: comparative analysis of Illumina and ion semiconductor high-throughput sequencing platforms <i>Kamil Khafizov</i>

<b>Sunday, July 30th</b>	
9:00	Morning coffee
<b>Protein Structure: Interactions</b>	
10:00	Spatial distribution of coding diseases-associated single-nucleotide variants in complexes <i>Olga V. Kalinina</i>
10:40	Molecular modelling and BiFC studies of protein-protein interactions in cytokinin signaling <i>Dmitriy Arkhipov</i>
11:00	Regulation of cellular networks by controlling protein structure disorder <i>Nikolay Dokholyan</i>
11:40	COFFEE
<b>Systems biology</b>	
12:10	Non-random distribution of homo-repeats in eukaryotic and bacterial proteomes and their impact on biological functions <i>Oxana Galzitskaya</i>
12:30	Approaches to building spatio-temporal models of splicing regulation that include RNA structure <i>Dmitry Pervouchine</i>
12:50	Harnessing the wealth of genomic sequence information: from the detection of novel sequence motifs to the discovery of mobile RNA molecules in plants <i>Dirk Walther</i>
13:30	LUNCH
<b>Protein Structure: Folding and Modeling</b>	

15:00	There and back again: A stereoscopic view on the protein folding puzzle <i>Alexei Finkelstein</i>
15:40	Self-consistency test reveals systematic bias in programs for prediction destabilization upon mutation <i>Dmitry Ivankov</i>
16:00	3D features of proteins and their structural changes related to phosphorylation <i>Boris Sobolev</i>
16:20	Cryo-electron microscopy-based integrative atomic-resolution modeling of the TOM GIP complex <i>Valery Veresov</i>
16:40	COFFEE
<b>Protein Structure: Function</b>	
17:10	Computational structural biology of sodium channels <i>Boris Zhorov</i>
17:50	Bioinformatic analysis of subfamily-specific positions reveals a previously unknown regulatory site in Glyceraldehyde 3-phosphate dehydrogenase family of proteins <i>Dmitry Suplatov</i>
18:10	The impact of human genetic variability on ligand-protein interactions and individual drug response <i>Peter Vlasov</i>
18:30	FAREWELL PARTY



























































































Sunday, July 30<sup>th</sup> – 15:00

## **There and back again: A stereoscopic view on the protein folding puzzle**

Alexei Finkelstein

The ability of protein chains to spontaneously form their spatial structures is a long-standing puzzle in molecular biology. Experimentally measured folding times of single-domain globular proteins range from microseconds to hours: the difference (10-11 orders of magnitude) is the same as that between the life span of a mosquito and the age of the universe. Here, we describe two physical theories of rates of overcoming the free-energy barrier separating the natively folded (N) and unfolded (U) states of protein chains, considering both directions of this transition: "U-to-N" and "N-to-U". In the theory of protein folding rates, a special role is played by the point of thermodynamic (and kinetic) equilibrium between the native and unfolded state of the chain; here, the theory obtains the simplest form. Paradoxically, a theoretical estimate of the folding time is easier to get from consideration of protein unfolding (the "N-to-U" transition) rather than folding, because it is easier to outline a good unfolding pathway of any structure than a good folding pathway that leads to the stable fold, which is yet unknown to the folding protein chain. And since the rates of direct and reverse reactions are equal at the equilibrium point (as follows from the physical "detailed balance" principle), the estimated folding time can be derived from the estimated unfolding time. Theoretical analysis of the "N-to-U" transition outlines the range of protein folding rates in a good agreement with experiment. Theoretical analysis of folding (the "U-to-N" transition), performed at the level of formation and assembly of protein secondary structures, outlines the upper limit of protein folding times (i.e., of the time of search for the most stable fold). Both theories come to essentially the same results; this is not a surprise, because they describe overcoming one and the same free-energy barrier, although the way to the top of this barrier from the side of the unfolded state is very different from the way from the side of the native state; and both theories agree with experiment. In addition, they predict the maximal size of protein domains that fold under solely thermodynamic (rather than kinetic) control and explain the observed maximal size of the "foldable" protein domains.

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## Posters

1	Bioinformatic analysis of the antibody repertoire induced in young and old donors in response to yellow fever vaccination <i>Anna Obratsova</i>
2	Distinct features of the T cell receptor repertoire in human regulatory T-cells <i>Sofya Kasatskaya</i>
3	In silico prediction of new minor histocompatibility antigens. <i>Dmitry Malko</i>
4	Comparative analysis of V-D-J rearrangement junction sequences that encode T-cell receptors recognizing similar and distinct antigens <i>Aleksey Eliseev</i>
5	Convolutional architecture for prediction of peptide-MHC binding affinities <i>Rudolph Layko</i>
6	Deep learning model for prediction of probability for thymic selection for T-cell receptor sequences <i>Sophya Tolstoukhova</i>
7	Rational design of catalytic antibody A.17 <i>Valentina Maslova</i>
8	The effect of SNPs on gene regulation and metabolic processes in autism <i>Polina Shichkova</i>
9	Validation of novel hereditary cancer genes identified upon exome sequencing: a focus on primer design <i>Ilya Bizin</i>

10	Accurate HIV-1 population diversity analysis using deep sequencing with Primer ID approach <i>Aleksandra Vasileva</i>
11	Workflow for replicable Sanger sequencing of NGS-derived mutations in clinical application <i>Marina Orlova</i>
12	Human SNP associations with genetically determined disorders <i>Polina Avdyunina</i>
13	Identification of new potential targets for treatment of coinciding asthma and hypertension <i>Olga Zolotareva</i>
14	Analysis of mutations associated with idiopathic restrictive cardiomyopathy <i>Svetlana Tarnovskaya</i>
15	Differential expression meta-analysis may help to reveal the basis of energy metabolic deficiency common to neurodegenerative diseases <i>Alexander Osypov</i>
16	The interplay between Spliceosomal Components and Cellular Stress mediated by chemo- and radiotherapy <i>Ksenia Anufrieva</i>
17	Interpreting genomes and transcriptomes of patients with rare genetic diseases <i>Sergey Naumenko</i>
18	Construction of regulatory networks by integrating gene expression, promoter methylation and copy number alteration data for prostate cancer <i>Rinat Sultanov</i>

19	IGNG1-IGNG3 locus, its possible role in the multiple sclerosis, and biases SNP allele frequencies for europeoid and non-europeoid populations <i>Marina Fridman</i>
20	FLOating Window Projective Separator (FloWPS): a method of data transfer for expression-based features from cell lines to cancer patients during SVM-based prediction of drug efficiency in personalized medicine <i>Nicolas Borisov</i>
21	Detailing the Quaternary structure of the virus using tritium planigraphy <i>Alexsey Dolgov</i>
22	Cure for primary dopaminergic midbrain neurons by GPR139 agonists using structure based virtual screening and molecular dynamics simulation <i>Aman Chandra Kaushik</i>
23	Sequence and structure features of GroE substrates orthologs in <i>Mycoplasma</i> <i>Marina Parr</i>
24	Spectrum of proline-specific peptidases in dikarya fungi <i>Nikita Alkin</i>
25	Gene Ontology terms in scoring of docked protein models <i>Anna Hadarovich</i>
26	Investigating residue coevolution in proteins from a structural perspective <i>Alexey Morgunov</i>
27	Proteoforms scouting in HepG2 cell line <i>Olga Kiseleva</i>

28	Applying deep-learning techniques to identification of pathogenic amino acid substitutions <i>Ivan Reveguk</i>
29	Model of multisite tau protein phosphorylation for prediction of sensitivity to therapeutic interventions. <i>Alexander Stepanov</i>
30	Cofactor-binding studies of the Williams Syndrome related methyltransferase WBSCR27 in solution <i>Sofia Mariasina</i>
31	Molecular modeling of catalytic and lectin domains in neuraminidase A from <i>Streptococcus pneumoniae</i> <i>Yana Sharapova</i>
32	Allosteric inhibitor Doramapimod can bind to human p38 $\alpha$ MAP Kinase even when the activation loop is in the DFG-in state <i>Dmitry Suplatov</i>
33	<i>Pseudomonas aeruginosa</i> phage EL chaperonin and a proposed model of its folding cycle. <i>Natalia V. Sernova</i>
34	QASDOM: a meta-server for scoring, analysis and ranking of protein-protein docking models <i>Anastasia Anashkina</i>
35	Identification of amino acid residues affecting on the specificity of interaction of protein kinases and small molecular inhibitors <i>Dmitry Karasev</i>
36	Poxviral chemokine-binding proteins: theoretical study of structure and function evolution <i>Denis Antonets</i>

37	Optimums of the environmental conditions affect amyloidogenic properties of prokaryotic proteomes <i>Kirill S Antonets</i>
38	Identification of amyloid-forming proteins in the <i>Escherichia coli</i> proteome <i>A.O. Kosolapova</i>
39	Descriptive analysis of <i>Arabidopsis thaliana</i> L. protein-protein interaction network: revealing of key members. <i>Sergey Pesyak</i>
40	Evolutionary genomics of antibiotic resistance <i>Semen Leyn</i>
41	Identification of bacteria transcription factor targets by machine learning <i>Irina Garanina</i>
42	Evolution of <i>Burkholderia spp</i> <i>Olga Bochkareva</i>
43	The Dps bacterial nucleoid protein is associated with sugar metabolism <i>Tatiana Bessonova</i>
44	Diversity of the HrpF/NoIX/PopF protein in plant pathogenic bacteria <i>Aleksandr Ignatov</i>
45	Lateral transfer of restriction-modification systems and their components <i>Andrei Alexeevski</i>
46	Avoidance of restriction-modification systems sites in the metagenome of Antarctic Deep Lake shows interaction of species in the metagenomic community <i>Anna Ershova</i>

47	Genomic reconstruction of metabolic pathways for the utilization of carbohydrates in the human intestinal microbiota <i>Arthur Murtazin</i>
48	Metabolic exchange by essential vitamins in the human intestinal microbiota <i>Dmitry Rodionov</i>
49	Inference of phenotypes for amino acid metabolism in human gut microbiome using subsystems approach <i>German Ashniev</i>
50	Shotgun sequencing based detection of microbial community shifts during multi-step electrogenic bacteria selection <i>Larisa Kiseleva</i>
51	H-NS nucleoid protein binds to the oppA-oppB intergenic region of the <i>E. coli</i> oppABCDF operon and controls oppB expression. <i>Nataliia Sukharicheva</i>
52	Avoidance of recognition sites of restriction-modification systems as bacteriophage anti-restriction strategy <i>Ivan Rusinov</i>
53	Antisense transcription may contribute to a fine-tuned expression of sugar regulators in <i>Escherichia coli</i> <i>Nataliya Markelova</i>
54	Comparative analysis of non-local events in strain evolution within prokaryotic species <i>Andrei Alexeevski</i>
55	<i>Brucella</i> and <i>Bartonella</i> nucleotide pangenome comparative analysis <i>Alexandra Simonova</i>

56	Machine learning approaches in metagenomic sequencing analysis related to human oral microbiota composition associated with periodontitis <i>Yaw-Ling Lin</i>
57	RNA-DNA interactions in chromatin <i>Aleksandra Galitsyna</i>
58	Alteration of the chromatin structure in response to lamin depletion <i>Sergey Starikov</i>
59	Epigenome marks interaction defines chromatin compartments <i>Elena Stavrovskaya</i>
60	Dissecting epigenetic effects of Polycomb-group proteins in epidermal self-renewal and differentiation <i>Vasily Zubov</i>
61	Integrative modelling methods for understanding nucleosome dynamics. <i>Grigoriy Armeev</i>
62	Characterization of genes encoding target enzymes related in amino acid biosynthesis and herbicide resistance <i>Jung-Sup Kim</i>
63	KrATER: K-mer Analysis Tool Easy to Run <i>Sergei Kliver</i>
64	Exon-Intron Structure Database: a tool for intron analysis <i>Irina Poverennaya</i>
65	Dual coding regions prediction <i>Kseniya Petrova</i>

66	New version of sleeping chironomid's genome assembly using Illumina and PacBio data <i>Olga Kozlova</i>
67	CAGE application for avian embryogenesis <i>Ruslan Deviatiiarov</i>
68	CpG traffic lights are markers of regulatory regions in humans <i>Anna V. Lioznova</i>
69	Long-term space flight mediated changes in promoter landscape in Zebrafish ( <i>Danio rerio</i> ) tissues. <i>Alexander Cherkasov</i>
70	Novel ChIP-Seq simulation software (isChIP) for data analysis optimization <i>Yuriy Orlov</i>
71	Changes in mutational processes and patterns of mutations during cancer development <i>Mariia Andrianova</i>
72	Features of miR-1322 binding sites in the coding area of mRNA orthologic genes <i>Dana Aisina</i>
73	Context-dependent selection of upstream start codons in Homo sapiens lineage <i>Svetlana Iarovenko</i>
74	Molecular adaptations of subterranean rodents to underground lifestyle <i>Olga Bondareva</i>
75	Negative selection in <i>Drosophila melanogaster</i> missense alleles <i>Nadezhda Potapova</i>

76	The analysis of upstream open reading frame using comparative genetics. <i>Kirill Prosvirov</i>
77	Regression analysis for automated detection of horizontal gene transfer <i>Alexander Panchin</i>
78	Exact correspondence between walks in nucleotide and protein sequence spaces <i>Dmitry Ivankov</i>
79	Finding multi-dimensional epistasis in high-throughput experimental data at the level of individual genotypes <i>Dmitry Ivankov</i>
80	SELVa: Simulator of Evolution with Landscape Variation <i>Elena Nabieva</i>
81	Evidence of balancing selection in parallel evolution of closely related gammarus species genomes <i>Valentina Burskaia</i>
82	The signatures of recombination and gene conversion in the bdelloid rotifer <i>Adineta vaga</i> <i>Olga A. Vakhrusheva</i>
83	Parallel adaptation to the freshwater in a number of independent White Sea populations of threespine sticklebacks <i>Nadezhda Terekhanova</i>
84	The Evolutionary Moulding in plant-microbial symbiosis: coevolution of signal transduction systems <i>Anna Igoikina</i>

85	Causes of single position fitness landscape changes <i>Anastasia Stolyarova</i>
86	Accumulation of mutations in experimental evolution of basidiomycete fungus <i>Schizophyllum commune</i> <i>Aleksandra Bezmenova</i>
87	Structural dynamics of Interaction between human telomeric DNA G-quadruplex 21-mer and naphthalene diimide compound MM4 <i>Christian Solis-Calero</i>
88	Comparison small nucleic acids derivatives hybridization parameters obtained by molecular dynamics and experimentally <i>Victor Golyshev</i>
89	RNA triplexes within the known RNA 3D structures <i>Eugene Baulin</i>
90	Short stems in RNA secondary structure <i>Eugene Baulin</i>
91	Detection of signal beyond secondary structure from SHAPE experiment <i>Alexandra Pogorelskaya</i>
92	Influence of nucleotide sequence on conformational flexibility of the RNA dangling ends in the complexes with DNA: molecular dynamics studies <i>Alexander Lomzov</i>
93	SMARTIV: a novel method for RNA sequence and structure motif discovery from in-vivo binding data <i>Maya Polishchuk</i>

94	DEPPDB v.3 and its use to study electrostatic and other physical properties of genome DNA and its elements relevant to their biological functions <i>Alexander Osypov</i>
95	Ribosome drop-off rate in <i>E. coli</i> depends on mRNA properties <i>Evgenia Khodzhaeva</i>
96	Role of electrostatics in transcription regulation in prokaryotes <i>Alexander Osypov</i>
97	Codons and amino acids biases around transcription factors binding sites are due to their electrostatics <i>Alexander Osypov</i>
98	Fast identification of statistically significant lncRNA-RNA interactions in a transcriptome-wide search <i>Ivan Antonov</i>
99	Approaches to building spatio-temporal models of splicing regulation that include RNA structure <i>Dmitry Pervouchine</i>
100	reaBuilding a pipeline for analysis of short-d RNA-seq data and natural transcriptomic variation in <i>Caenorhabditis elegans</i> <i>Cristian Riccio</i>
101	Developmental trajectory of liver stem/progenitor cells at single-cell resolution <i>Xianbin Su</i>
102	Discovery of novel cell-penetrating antimicrobial peptides by transcriptome deep analysis <i>Ekaterina Graftskaia</i>

103	Transcriptome analysis of pectobacteria-infected tobacco plants <i>Rim Gubaev</i>
104	Modeling of components of desiccation stress in anhydrobiotic cells <i>Alexander Nesmelov</i>
105	Tissue-specific transcriptional profile in the edible dormice is strongly affected by hibernation <i>Guzel Gazizova</i>
106	De novo transcriptome analysis of two early developmental stages of shiitake mushroom <i>Lubov Gapa</i>
107	Gene expression profiling in peripheral blood mononuclear cells reveals dependency on multiple sclerosis activity <i>Alexander Abramov</i>
108	RNAcentral: progress in the development of the non-coding RNA sequence Ddatabase <i>Boris Burkov</i>
109	Near single-cell transcriptomics analysis of differential expression in <i>Helix lucorum</i> statocysts under microgravity <i>Alexander Osypov</i>
110	Using de novo transcriptome for identification genes involved in cryotolerance in the turtle leech <i>Ozobranchus jantseanus</i> <i>Svetlana Kuznecova</i>
111	Genome under extreme desiccation: shifting transcription initiation regions in anhydrobiotic cell line <i>Elena Minkina</i>

112	Comparative analysis of PR gene expression in tomato inoculated with rhizobacterial Lipopolysaccharides against <i>Fusarium oxysporum f. sp. lycopersici</i> <i>Meenu Saraf</i>
113	Identification and characterization of HPV-host fusion transcripts in HNSCCs <i>Lada Koneva</i>
114	Associations between alternative polyadenylation and RNA secondary structure <i>Danila Bredikhin</i>
115	Differential alternative splicing by RNA-seq data in brain areas of laboratory rats with aggressive behavior <i>Yuriy Orlov</i>
116	Transcriptome profiling of primary glioma cell cultures <i>Nataly Gubanova</i>
117	Phylogenetic analyses of sugarcane cultivars for sugar content and early maturation using simple sequence repeat markers <i>Thangadurai Devarajan</i>
118	Genomic selection of superior Nili Ravi buffalo bull for increasing milk production in Pakistan <i>Saher Islam</i>
119	Advanced parser for biomedical texts <i>Anton Karazeev</i>
120	A multi-scale model of cellular morphodynamics <i>Siarhei Hladyshau</i>
121	Using machine learning approach to improve base calling in next generation sequencing data <i>Denis Antonets</i>

122	Ion channels in defecation motor program in nematode <i>Heterorhabditis megidis</i> <i>Yuri Panchin</i>
123	<i>Aurelia japonica</i> : molecular and chromosomal evidence <i>Anastasiia Kotova</i>
124	Distinguishing highly and lowly active CRISPR/Cas9 sgRNA via Inception-based Deep Convolutional Neural Network <i>Bogdan Kirillov</i>
125	Scaling of the active transport systems in oocyte: 3D agent-based simulations <i>Marat Sabirov</i>
126	DNA sequence complexity measures and analysis of short sequencing reads <i>Irina Abnizova</i>
127	A new method of evaluating genome assemblies based on kmers frequencies <i>Kirill Romanenkov</i>
128	Evolution and systematics of plastids of rhodophytic branch <i>Oleg Zverkov</i>
	Computational design and biological evaluation of novel HIV-1 entry inhibitors based on glycosphingolipids <i>Alexander Andrianov</i>
	NGS-SSR based biomarkers for diagnosis of human diseases <i>Arghavan Alisoltani</i>
	Detecting origins of interferons signalling sensitivity <i>Karol Nieniałowski</i>

	<p>ARE-mediated regulatory system in glioma <i>Alina Astakhova</i></p>
	<p>In silico discovery of novel fusion inhibitor scaffolds targeting a membrane proximal external region of HIV-1 gp41 <i>Alexander Andrianov</i></p>
	<p>De novo design of potential HIV-1 entry inhibitors based on the click chemistry concept: a computational study <i>Alexander Andrianov</i></p>
	<p>Detailing the quaternary structure of the helical virus using tritium planigraphy <i>Elena Bogacheva</i></p>
	<p>Influenza virus Nuclear Export Protein (NEP) 3D structure reconstruction probed as an example for improvement of approach to the protein 3D structures prediction <i>Anastasia Golovko</i></p>
	<p>Structural insights into TOM-mediated proapoptotic activation of Bax <i>Anna Dudko</i></p>
	<p>MutHTP: Mutations in Human Transmembrane Proteins <i>M. Michael Gromiha</i></p>
	<p>Identification of novel inhibitor of MAPKs from <i>Leishmania donovani</i>: Comparative in-silico analysis <i>Prakash Saudagar</i></p>
	<p>Isolated chromosome sequencing for evolutionary genomics <i>Alexey Makunin</i></p>

	<p>Reconstruction and analysis of the human protein-protein interaction network involved in response to tick-borne encephalitis virus infection <i>Elena Ignatieva</i></p>
	<p>Reconstruction and analysis of the protein-protein interaction network involving GWAS genes associated with elevated body mass index <i>Elena Ignatieva</i></p>
	<p>Proteomics analysis and mining of effector weaponries of <i>Cochliobolus lunatus</i> reveals CL[xxx]LHM-motif during colonization of potato leaf <i>Louis Bengyella</i></p>
	<p>Determining the spatial chromatin organization upon desiccation process in the insect cells using Hi-C technology. <i>Alina Ryabova</i></p>
	<p>Interplay between chromatin contact frequency and expression levels in <i>Drosophila melanogaster</i>, <i>Mus musculus</i> and <i>Homo sapiens</i> genomes <i>Margarita Samborskaya</i></p>
	<p>Analysis of distal gene regulation based on ChIP-seq and ChIA-PET data and biophysical models of chromosome contacts <i>Arthur Dergilev</i></p>
	<p>Molecular evolution analysis of genetic network related to plant trichome development <i>Alexey Doroshkov</i></p>
	<p>NGS application for mutational stability monitoring of viral drug targets <i>Youri Kravatsky</i></p>

	Prediction of start codons and mRNA translation efficiency using RiboSeq-based weight matrices <i>Oxana Volkova</i>
	Assessment of translation efficiency from ribosome profiling and mRNA-seq data <i>Oxana Volkova</i>
	De novo identification and taxonomic analysis of human blood peptides, not being a product of known human genes <i>Maria Osetrova</i>
	Role of DNA sequence in establishing histone modifications in humans <i>Anatoliy Zubritskiy</i>





