








PROGRAM AT A GLANCE

DAY 1: OCTOBER 30, 2017 (Monday)

8:00-9:00	Registration+Coffee		
Hall	Pirogov		
9:00-9:15	Opening <i>A. Urbani, A. Archakov, A. Svistunov, V. Chekhonin, F. Corrales</i>		
9:15-9:45	PL1 Molecular Genetics of the Rare Tumors <i>Anna Kudryavtseva, Engelhardt Institute of Molecular Biology, Russia</i> 		
9:45-10:00	Break		
Hall	Pirogov	Abrikosov	Room 265
10:00-12:00	S1 Clinical Applications Co-chairs: <i>David Goodlett, University of Maryland, USA</i> <i>Fernando Corrales, National Biotechnology Center, CSIC, Spain</i>	S2 Genomics and Beyond Co-chairs: <i>David Tabb, Stellenbosch University, South Africa</i> <i>Sergey Moshkovskii, Pirogov Russian National Research Medical University, Russia</i>	WP1 Proteoinformatics Moderators: <i>Veit Schwammle, and Julian Uszkoreit, EuBIC</i>
	12:00-13:30		
Lunch Break			
Hall	Pirogov		
13:30-14:00	PL2 Longitudinal Sampling in Proteomic Biomarker Discovery <i>David Goodlett, University of Maryland, USA</i> 		
14:00-14:30	PL3 How Sustainable Biobanking Can Drive Your Proteomics Research <i>Erik Steinfelder, BBMRI-ERIC Assembly, Austria</i> 		
14:30-15:30	Coffee Break and Poster Session		
Hall	Pirogov	Abrikosov	Room 265
15:30-17:30	S1.2 Expression and Quantitation Co-chairs: <i>Lev Levitskii, Institute for Energy Problems of Chemical Physics, Russia</i> <i>Veit Schwammle, University of Southern Denmark, Denmark</i>	S3 Precision Medicine Co-chairs: <i>Garry Corthals, University of Amsterdam, Netherlands</i> <i>Aleksandr Tanas, Research Centre for Medical Genetics, Russia</i>	WP2 How to Work with Human Genome? <i>Andrey Afanasiev, IBinom, Russia</i>
	17:30-19:30		
Welcome Event and Poster Session			



PL – Plenary Lecture, S – Session, WP – Workshop Package

DAY 2: OCTOBER 31, 2017 (Tuesday)

8:00-9:00	Registration+Coffee		
Hall	Pirogov		
9:00-9:30	<p>PL4 Can We Predict RNA from Protein? <i>Nikolaus Fortenly, Research Center for Molecular Medicine, Austria</i></p>		
9:30-10:00	<p>PL5 How Many Proteins are There? The Width and Depth of Human Proteome <i>Elena Ponomarenko, Institute of Biomedical Chemistry, Russia</i></p>		
10:00-10:15	Break		
Hall	Pirogov	Abrikosov	
10:15-12:15	<p>S4 Infections and Resistance</p> <p>Co-chairs: <i>Thierry Naas, Hopital Bicetre, France</i> <i>Olga Tarasova, Institute of Biomedical Chemistry, Russia</i></p>	<p>S5 Immunomics</p> <p>Co-chairs: <i>Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry, Germany</i> <i>Sergei Larin, Dmitry Rogachev National Research Center, Russia</i></p>	
	Lunch Break		
Hall	Pirogov		
13:30-14:00	<p>PL6 The Human Protein Atlas - Implications for Human Biology and Precision Medicine <i>Cecilia Lindskog, Uppsala University, Sweden</i></p>		
14:00-14:30	<p>PL7 Post-Genome Techno-logies as a Toolbox for Pro-Active Monitoring of Health <i>Ancha Baranova, George Mason University, USA</i></p>		
14:30-15:30	Coffee Break and Poster Session		
Hall	Pirogov	Room 265	Room 274
15:30-17:30	<p>S6 Cells and Embryos</p> <p>Co-chairs: <i>Cecilia Lindskog, Uppsala University, Sweden</i> <i>Andrey Zamyatnin, Sechenov First Medical University, Russia</i></p>	<p>WP3 Drug Development Classroom</p> <p>Moderator: <i>Andrey Khudoshin, Elsevier, Russia</i></p>	<p>WP4 Progenesis Q1 Software</p> <p>Moderator: <i>Paul Goulding, Nonlinear Dynamics, UK</i></p>

PL – Plenary Lecture, S – Session, WP – Workshop Package

DAY 3: NOVEMBER 1, 2017 (Wednesday)

8:00-9:00	Registration+Coffee		
Hall	Pirogov		
9:00-9:30	PL8 Personalised Nutrition: New Perspectives in Proteomics <i>Paola Roncada, Istituto Sperimentale Italiano L. Spallanzani, Italy</i>		
9:30-10:00	PL9 Multiplex Quantitation of Protein Expression and Phosphorylation Level in Clinical Specimen <i>Christoph Borchers, University of Victoria, Canada</i>		
10:00-10:15	Break		
Hall	Pirogov	Abrikosov	
10:15-12:15	S7 Food, Nutrition and Microbiome Co-chairs: <i>Paola Roncada, Istituto Sperimentale Italiano L. Spallanzani, Italy</i> <i>Svetlana Murzina, Institute of Biology Karelian Research Centre RAS, Russia</i>	S8 Brain and Neurodegeneration Co-chairs: <i>Evgeniy Petrotchenko, University of Victoria, Canada</i> <i>Ekaterina Khrameeva, Skolkovo Institute of Science and Technology, Russia</i>	
	Lunch Break		
Hall	Pirogov		
13:30-14:30	Young Investigators Session <i>Andrey Lisitsa, Christoph Borchers</i>		
14:30-15:00	Coffee Break and Poster Session		
Hall	Pirogov	Room 265	Room 274
15:00-17:00	S9 Health - Age - Sport Co-chairs: <i>Igor Vykhodets, Ministry of Health, Russia</i> <i>Arthur Kopylov, Institute of Biomedical Chemistry, Russia</i>	WP5 Food Intolerance Moderator: <i>Arkady Rosenstein and Marina Rosenstein, ImmunoHealth Clinic, USA</i>	WP6 Quality Control Assessment from Multi-Month Data Sets Moderator: <i>David Tabb, Stellenbosch University, South Africa</i>
	17:00-17:30 Closing Lecture (PL10) Biomarkers of Aging <i>Alexey Moskalev, Institute of Biology of Komi Science Center, Russia</i>		
17:30-17:45	Closing Ceremony <i>A. Lisitsa, F. Corrales., A. Svistunov</i>		

PL – Plenary Lecture, S – Session, WP – Workshop Package

DAILY PROGRAM

DAY 1: OCTOBER 30, 2017 (Monday)

S1 10:00-12:00 Pirogov Hall

CLINICAL APPLICATIONS

Co-chairs: *David Goodlett, Fernando Corrales*

10:00-10:20	S1.1: THE PROTEOME QUEST TO UNDERSTAND BIOLOGY AND DISEASE <i>Fernando Corrales, National Biotechnology Center, CSIC, Spain</i>
10:20-10:40	S1.2: TARGETED SCREEN OF NORMAL PROTEOME OF CANDIDATES TO AUSTROUNAUTS <i>Victor Zgoda, Institute of Biomedical Chemistry, Russia</i>
10:40-11:00	S1.3: VALIDATION OF VARIANT PEPTIDES IN CANCER CELL LINES VIA DE NOVO SEQUENCING <i>Kira Vyatkina, Saint Petersburg State University, Russia</i>
11:00-11:15	S1.4: A NEW LC CONCEPT FOR THE CLINICAL PROTEOMICS <i>Alexandre Podtelejnikov, EVOSEP, Denmark</i>
11:15-11:30	S1.5: NEXT GENERATION PROTEOMICS TECHNOLOGY FOR REPRODUCIBLE AND PRECISE PROTEIN QUANTIFICATION <i>Hongqian Yang, Thermo Scientific, Sweden</i>
11:30-11:45	S1.6: timsTOF Pro - THE NEW STANDARD FOR SHOTGUN PROTEOMICS <i>Dmitry Burmykin, Bruker Ltd., Russia</i>
11:45-12:00	Q&D

DAILY PROGRAM

DAY 1: OCTOBER 30, 2017 (Monday)

S1.2 15:30-17:30 Pirogov Hall

EXPRESSION AND QUANTITATION

Co-chairs: *Lev Levitsky, Veit Schwämmle*

15:30-15:50	S1.2.1: IdentiPy: AN OPEN-SOURCE PYTHON-BASED SEARCH ENGINE PLATFORM FOR PROTEIN IDENTIFICATION AND QUANTIFICATION IN PROTEOMICS <i>Lev Levitsky, Institute for Energy Problems of Chemical Physics, Russia</i>
15:50-16:10	S1.2.2: DNA DAMAGE AS EPIGENETIC SIGNAL <i>Dmitry Zharkov, Institute of Chemical Biology and Fundamental Medicine, Russia</i>
16:10-16:30	S1.2.3: TOOLS AND WORKFLOWS FOR REPRODUCIBLE DATA ANALYSIS <i>Julian Uszkoreit, Ruhr-Universität Bochum, Germany</i>
16:30-16:45	S1.2.4: AGE AND TISSUE DEPENDENT CHANGES IN THE EPIGENOME MEASURED BY MIDDLE-DOWN MS <i>Veit Schwämmle, University of Southern Denmark, Denmark</i>
16:45-17:00	S1.2.5: AN ENHANCED DISCOVERY 'OMICS WORKFLOW IN COMPLEX BIOLOGICAL MATRICES <i>Paul Goulding, Nonlinear Dynamics, UK</i>
17:00-17:15	S1.2.6: SWATH™: MASS SPECTROMETRY WORKFLOW TO COLLECT COMPREHENSIVE PATIENT DATA FOR METABOLOMICS AND PROTEOMICS <i>Volker Kruff, SCIEX, Germany</i>
17:15-17:30	Q&D

DAILY PROGRAM

DAY 1: OCTOBER 30, 2017 (Monday)

S2 10:00-12:00 Abrikosov Hall

GENOMICS AND BEYOND

Co-chairs: *David Tabb, Sergey Moshkovskii*

10:00-10:20	S2.1: PROTEOGENOMICS OF CLINICAL ISOLATES OF MYCOBACTERIUM TUBERCULOSIS <i>David Tabb, Stellenbosch University, South Africa</i>
10:20-10:40	S2.2: PROTEOGENOMICS OF ADENOSINE-TO-INOSINE RNA EDITING IN MODEL ORGANISMS <i>Sergei Moshkovskii, Pirogov Russian National Research Medical University, Russia</i>
10:40-11:00	S2.3: PHARMACOGENOMICS – UPDATE AND FUTURE DIRECTIONS <i>Matthias Schwab, Institute of Clinical Pharmacology, Germany</i>
11:00-11:15	S2.4: BREAST CANCER MOLECULAR CLASSIFICATION BASED ON AN NGS GENOME-WIDE DNA METHYLATION ANALYSIS BY REDUCED REPRESENTATION BISULFITE SEQUENCING <i>Vladimir Strelnikov, Research Centre for Medical Genetics, Russia</i>
11:15-11:30	S2.5: SELECTIVE AFFINITY PRECIPITATION WITH APTAMERS GREATLY IMPROVES SENSITIVITY OF PROTEIN DETECTION BY SRM <i>Sergey Radko, Institute of Biomedical Chemistry, Russia</i>
11:30-11:45	S2.6: BIOBANKING AS BASIC INSTRUMENT FOR BIOMEDICAL RESEARCH <i>Artem Muravev, Qvados-Bio, Russia</i>
11:45-12:00	Q&D

DAILY PROGRAM

DAY 1: OCTOBER 30, 2017 (Monday)

S3 15:30-17:30 Pirogov Hall

PRECISION MEDICINE

Co-chairs: *Garry Corthals, Aleksandr Tanas*

15:30-15:50	S3.1: ENGAGING RESEARCH COMMUNITIES WITH CLINICS: TOWARDS INTERPERTING AND APPLYING PROTEOME INFORMATION <i>Garry Corthals, University of Amsterdam, Netherlands</i>
15:50-16:10	S3.2: GENOME-WIDE BISULFITE DNA SEQUENCING TECHNOLOGY FOR BIOMEDICAL RESEARCH <i>Aleksandr Tanas, Research Centre for Medical Genetics, Russia</i>
16:10-16:30	S3.3: IMPACT OF PROTEOMICS IN LABORATORY MEDICINE: FROM TOTAL LAB AUTOMATION TO THE MARS MISSIONS <i>Andrea Urbani, Institute of Biochemistry and Clinical Biochemistry, Catholic University of the "Sacred Heart", Italy</i>
16:30-16:45	S3.4: GETTING PRECISION WITH METABOLOMICS-BASED DIAGNOSTICS <i>Petr Likhov, Institute of Biomedical Chemistry, Russia</i>
16:45-17:00	S3.5: CASES OF APPLYING EXOME SEQUENCING FOR DIAGNOSTICS OF ORPHAN GENETIC DISEASES <i>Elena Okuneva, Genotek, Russia</i>
17:00-17:15	S3.6: GENOTYPING AND PHENOTYPING OF ISOZYMES OF CYTOCHROME P-450 IN PATIENTS WITH ALCOHOL USE DISORDER: CORRELATION WITH HALOPERIDOL PLASMA CONCENTRATION <i>Mikhail Zastroshin, Russian Medical Academy of Continuous Professional Education, Russia</i>
17:15-17:30	Q&D

DAILY PROGRAM

DAY 2: OCTOBER 31, 2017 (Tuesday)

S4 10:15-12:15 Pirogov Hall

INFECTIONS AND RESISTANCE

Co-chairs: *Thierry Naas, Olga Tarasova*

10:15-10:35	S4.1: NGS TO DETERMINE SUSCEPTIBILITY TO ANTIBIOTICS: CHANCES AND PERSPECTIVES <i>Thierry Naas, Hospital Bicetre, France</i>
10:35-10:55	S4.2: DEVELOPMENT OF NEW ANALYTICAL WEB PLATFORM FOR ANTIMICROBIAL RESISTANCE SURVEILLANCE <i>Mikhail Edelstein, Institute of Antimicrobial Chemotherapy, Smolensk State Medical University, Russia</i>
10:55-11:15	S4.3: DECODING THE SEROLOGIC RESPONSE TO THE CANDIDA ALBICANS PROTEOME IN PATIENTS WITH INVASIVE CANDIDIASIS: FROM BIOMARKER DISCOVERY TO ASSAY VALIDATION <i>Concha Gil, Complutense University of Madrid, Spain</i>
11:15-11:30	S4.4: GENOMIC CHARACTERISTIC OF INVASIVE STREPTOCOCCUS PNEUMONIAE CIRCULATED IN THE REPUBLIC OF BELARUS <i>Anna Kharkhal, The Republican Research and Practical Center for Epidemiology and Microbiology, Republic of Belarus</i>
11:30-11:45	S4.5: ALTERNATIVE TYPING METHODS IN THE ERA OF NGS: HIGH-THROUGHPUT SNP-TYPING FOR STUDYING EPIDEMIOLOGY OF ANTIBIOTIC RESISTANCE <i>Eugene Shek, Smolensk State Medical University, Russia</i>
11:45-12:00	S4.6: COMPUTER-AIDED HIV RESISTANCE PREDICTION <i>Olga Tarasova, Institute of Biomedical Chemistry, Russia</i>
12:00-12:15	S4.7: HIGH PARAMETERS MASS CYTOMETRY FOR DISCOVERY AND DEEP PROFILING OF RARE CELL POPULATIONS <i>Alexander Kolobov, Helicon, Russia</i>

DAILY PROGRAM

DAY 2: OCTOBER 31, 2017 (Tuesday)

S5 10:15-12:15 Abrikosov Hall

IMMUNOMICS

Co-chairs: *Jiri Petrak, Sergei Larin*

10:15-10:35	S5.1: MEMBRANE PROTEOME OF RARE NEUROENDOCRINE TUMORS. COMBINED FORCES OF HPTC AND GLYCO-CAPTURE <i>Jiri Petrak, BIOCEV, Charles University, Czech Republic</i>
10:35-10:55	S5.2: RAPID DETERMINATION OF BREAST CANCER BOUNDARIES USING TISSUE SPRAY IONIZATION MASS SPECTROMETRY <i>Vitaliy Chagovets, Kulakov Research Center for Obstetrics, Gynecology and Perinatology, Russia</i>
10:55-11:15	S5.3: HOW TUMOR ESCAPES THE ATTENTION OF THE IMMUNE SYSTEM? MECHANISMS AND POSSIBLE WAYS OF THERAPEUTICAL NEGOTIATION <i>Sergei Larin, Dmitry Rogachev National Research Center, Russia</i>
11:15-11:30	S5.4: PROTEOME PROFILING OF ANTI-CANCER DRUGS <i>Alexey Chernobrovkin, Karolinska Institutet, Sweden</i>
11:30-11:45	S5.5: THE GENERATION AND USE OF RECOMBINANT SINGLE-DOMAIN ANTIBODIES TO FIGHT INFECTIOUS DISEASES <i>Sergey Tillib, Institute of Gene Biology, Russia</i>
11:45-12:00	S5.6: COMPARATIVE PROTEOMICS STUDY ON INTERFERON RESPONSE IN HUMAN GLIOBLASTOMA CELL LINES <i>Irina Tarasova, Institute for Energy Problems of Chemical Physics, Russia</i>
12:00-12:15	Q&D

DAILY PROGRAM

DAY 2: OCTOBER 31, 2017 (Tuesday)

S6 15:30-17:30 Pirogov Hall

CELLS AND EMBRYOS

Co-chairs: *Cecilia Lindskog, Andrey Zamyatnin*

15:30-15:50	S6.1: SECRETOM OF HUMAN EMBRYOS IN IVF MEDIA - CAN IT BE USED FOR IMPROVED IMPLANTATION SUCCESS RATES? <i>Goran Mitulović, Medical University of Vienna, Austria</i>
15:50-16:10	S6.2: EXPRESSION OF NATURAL ANTISENSE TRANSCRIPTS IN HUMAN GENOME <i>Yuriy Orlov, Institute of Cytology and Genetics SB RAS, Novosibirsk State University and Institute of Marine Biology Researches of RAS, Russia</i>
16:10-16:30	S6.3: CRYOBANK AS AN ATTRIBUTE OF OMICS <i>Alexei Sazanov, Saint-Petersburg State Technological Institute, Russia</i>
16:30-16:45	S6.4: REGENERATION OF BONE TISSUE IS DETERMINED BY THE PARTICIPATION OF IMMUNOCOMPETENT CELLS <i>Olga Berdugina, Ural Research Institute Phthisiopulmonology, Russia</i>
16:45-17:00	S6.5: METABOLITES PROFILING IN CULTURE MEDIUMS OF HUMAN EMBRYOS <i>Mikhail Bobrov, Kulakov Research Center for Obstetrics, Gynecology and Perinatology, Russia</i>
17:00-17:15	S6.6: 3D BUCCAL EPITHELIUM CELL CULTURE FOR THE DEVELOPMENT OF EPITHELIAL TISSUES BIOEQUIVALENT <i>Nastasya Kosheleva, Institute of General Pathology and Pathophysiology; Lomonosov Moscow State University, Russia</i>
17:15-17:30	S6.7: FLOWING VISUALIZING CYTOMETRY AMNIS: FEATURES OF THE USE IN CLINICAL DIAGNOSIS <i>Sergey Irikhin, Dia-M, Russia</i>

DAILY PROGRAM

DAY 3: NOVEMBER 1, 2017 (Wednesday)

S7 10:15-12:15 Pirogov Hall

FOOD, NUTRITION AND MICROBIOME

Co-chairs: *Paola Roncada, Svetlana Murzina*

10:15-10:35	S7.1: PROTEOMICS AND ITS APPLICATION TO IMPROVE DIAGNOSIS AND MANAGEMENT OF THE FOOD ALLERGIC PATIENT <i>Karin Hoffmann-Sommergruber, Medical University of Vienna, Austria</i>
10:35-10:55	S7.2: DEVELOPMENT OF ENZYMATIC TOOLS FOR EFFECTIVE GLUTEN DETOXIFICATION <i>Andrey Zamyatnin, Sechenov First Medical University, Russia</i>
10:55-11:15	S7.3: MARINE NATURAL RESOURCES – EXAMPLES OF HEALTH BENEFICIAL ACTIVE COMPONENTS <i>Klara Stensvåg, UiT The Arctic University of Norway, Norway</i>
11:15-11:30	S7.4: OH, MY GUT! CROWDSOURCING IN MICROBIOMICS <i>Dmitry Alexeev, Knomics, Russia</i>
11:30-11:45	S7.5: STATISTICAL PROPERTIES OF SPECIFIC HUMAN IGG. MATHEMATICAL MODELS IN IMMUNE DIETETICS <i>Arkady Rosenstein, ImmunoHealth, USA</i>
11:45-12:00	S7.6: THE HUMAN INTESTINAL MICROBIOTA IS A RESERVOIR OF RESISTANCE TO ANTIBIOTICS <i>Evgenii Olekhovich, Federal Research and Clinical Center of Physical-Chemical Medicine, Russia</i>
12:00-12:15	Q&D

DAILY PROGRAM

DAY 3: NOVEMBER 1, 2017 (Wednesday)

S8 10:15-12:15 Abrikosov Hall

BRAIN AND NEURODEGENERATION

Co-chairs: *Evgeniy Petrotchenko, Ekaterina Khrameeva*

10:15-10:35	S8.1: STRUCTURAL PROTEOMICS OF NEURODEGENERATIVE DISEASES <i>Evgeniy Petrotchenko, University of Victoria, Canada</i>
10:35-10:55	S8.2: PROTEOMIC STUDY OF THE EFFECTS OF STEM CELLS IN A T-CELL DEFICIENT BALLOON COMPRESSED SPINAL CORD INJURY RAT MODEL <i>Johannes de Munter, Maastricht University, Netherlands</i>
10:55-11:15	S8.3: METABOLIC CHANGES IN AUTISM AND THEIR EVOLUTION <i>Ekaterina Khrameeva, Skolkovo Institute of Science and Technology, Russia</i>
11:15-11:30	S8.4: OMIC SEQUENCING IN DIAGNOSTICS OF INTELLECTUAL DISABILITY: WES/WGS/TRIO <i>Alexander Lavrov, Research Centre for Medical Genetics, Russia</i>
11:30-11:45	S8.5: COMPARATIVE PROTEOMIC ANALYSIS OF SERUM FROM PATIENTS WITH BIPOLAR DISORDER AND PARANOID SCHIZOPHRENIA <i>Liudmila Smirnova, Tomsk National Research Medical Center of the Russian Academy of Sciences, Russia</i>
11:45-12:00	S8.6: MOLECULAR ASYMMETRY OF THE BRAIN: DIFFERENTIAL GENE EXPRESSION IN THE HUMAN FRONTOPOLAR CORTEX <i>Irina Dolina, National Research Center «Kurchatov Institute», Russia</i>
12:00-12:15	Q&D

DAILY PROGRAM

DAY 3: NOVEMBER 1, 2017 (Wednesday)

S9 15:30-17:30 Pirogov Hall

HEALTH - AGE - SPORT

Co-chairs: *Igor Vykhodets, Arthur Kopylov*

15:30-15:50	S9.1: PROTEIN EXPRESSION CHANGES CAUSED BY MICROGRAVITY IN SPACE <i>Eugene Nikolaev, Skolkovo Institute of Science and Technology, Russia</i>
15:50-16:10	S9.2: DIGITAL HEALTHCARE REVOLVES THE POSTGENOME ERA <i>Segal Eddie, Mobile TeleSystems PJSC ("MTS"), Russia</i>
16:10-16:30	S9.3: COMBATING DOPING IN SPORTS: PROBLEMS AND PERSPECTIVES <i>Igor Vykhodets, Ministry of Health, Russia</i>
16:30-16:45	S9.4: "CORTICOID-16" PROJECT: SIMPLE ANSWERS FOR THE COMPLEX ATHLETES <i>Dmitry Korotaev, Nasonova Institute of Rheumatology, Russia</i>
16:45-17:00	S9.5: NEXT-GEN SEQ FOR BETTER CARDIO-DIAGNOSTICS OF PROFESSIONAL ATHLETES <i>Olga Chumakova, Federal Scientific Clinical Centre, Russia</i>
17:00-17:15	S9.6: LECO PEGASUS WITH HIGH-RESOLUTION TIME-OF-FLIGHT MASS ANALYZER FOR GC/MS METHOD IN CLINICAL APPLICATION <i>Gulnara Shaidullina, LECO Corporation, Russia</i>
17:15-17:30	Q&D

DAILY PROGRAM

DAY 3: NOVEMBER 1, 2017 (Wednesday)

13:30-14:30 Pirogov Hall

YOUNG INVESTIGATORS SESSION

Co-chairs: *Andrey Lisitsa, Christoph Borchers*

13:30-13:40	YIS1: CLINICAL AND GENETIC DATABASES OF THE PATIENTS WITH ORPHAN DISEASES AS A WAY OF USING OF OMIC'S TECHNOLOGIES FOR PERSONALIZED MEDICINE <i>Maria Balashova, Sechenov First Medical University, Russia</i>
13:40-13:50	YIS2: METHOD FOR SCREENING OF INHIBITORS OF POLY (ADP-RIBOSE) POLYMERASE1 <i>Tatyana Kurgina, Institute of chemical biology and fundamental medicine SB RAS, Russia</i>
13:50-14:00	YIS3: NOVEL MECHANISM OF COFILIN REGULATION MEDIATED BY DEUBIQUITYLATING ENZYMES <i>Tatiana Sergeeva, Nizhny Novgorod State Medical Academy, Russia</i>
14:00-14:10	YIS4: UPS2 CALIBRATION SET AS A MODEL OBJECT FOR PROTEOME RESEARCH <i>Ekaterina Ilgisonis, Institute of Biomedical Chemistry, Russia</i>
14:10-14:20	YIS5: IDENTIFICATION OF PROTEINS THAT MEDIATE THE TRANSPORT OF EXTRACELLULAR DNA IN BLOOD <i>Oleg Tutanov, Institute of Chemical Biology and Fundamental Medicine SB RAS, Russia</i>
14:20-14:30	YIS6: CRISPR/CAS9-MEDIATED GENERATION OF A CELL LINE WITH PSORIASIS-ASSOCIATED POLYMORPHISM IN CARD14 GENE <i>Anna Prelovskaya, Vavilov Institute of General Genetics RAS, Russia</i>
17:15-17:30	Q&D

WORKSHOPS

Young scientists and students are invited to the Conference Workshop to discover the role of postgenome data and the importance of communication for the modern life science, healthcare and quality of life.

The number of attendees is limited to 30 persons.

We suggest that attendees bring their own laptops. Besides a web browser (Firefox, Safari or Chrome) and a running internet connection, nothing is required (an external mouse will add to your comfort).

October,	30	10:00-12:00	WP1 – Proteoinformatics
October,	30	15:30-17:30	WP2 – How to Work with Human Genome?
October,	31	15:30-17:30	WP3 – Drug Development
October,	31	15:30-17:30	WP4 – Progenesis QI Software
November,	1	15:00-17:00	WP5 – Food Intolerance
November,	1	15:00-17:00	WP6 – Quality control assessment from multi-month data sets

DAY 1: OCTOBER 30, 2017 (Monday)

WP1 10:00-12:00 Room 265

PROTEOINFORMATICS

Speakers: *Veit Schwämmle*, Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark;

Julian Uszkoreit, Medizinisches Proteom-Center, Ruhr-University Bochum, Germany

The topics of the workshop are reusable workflows for reproducible analyses of LC-MS proteomics data and the statistical analysis of quantitative LC-MS data.

Reusable workflows for reproducible analyses: We will highlight the importance of not only describing each detail of the wet lab analyses, but also the subsequent data analysis. This can be facilitated by using workflow environments like KNIME and the deposition of the workflows, together with the data, into repositories like PRIDE. In the interest of the time, the hands-on experience will be limited, but we will provide the data and tutorial material online.

Advanced statistical and multi-variate data analysis: We will give an introduction into the basic concepts of the statistical assessment of proteomics data starting with the quantitative protein/peptide measurements. Furthermore, we will show how to apply statistical testing and carry out clustering of protein expression profiles. The novel tool VSClust will be presented which combines statistics and clustering to yield better enrichment of significant features, improved cluster validation and higher output from subsequent data interpretation.

DAY 1: OCTOBER 30, 2017 (Monday)

WP2 15:30-17:30 Room 265

HOW TO WORK WITH HUMAN GENOME?

Speaker: *Andrey Afanasiev, IBinom, Russia*

Main topics:

- Genome structure and genetic variability
- Data processing and the construction of the basic analysis pipeline
- Practical application of the gene panels using iBinom – alignment, calling, annotation, and quality control
- Interpretation of the data and bioinformatics predictions

DAY 2: OCTOBER 31, 2017 (Tuesday)

WP3 15:30-17:30 Room 265

DRUG DEVELOPMENT CLASSROOM

Speaker: *Andrey Khudoshin, PhD, MBA, Direction of chemical and biological solutions of Elsevier Company in Russia, Iran and CIS countries*

The workshop is targeted at the scientists with basic training in system biology, organic chemistry and pharmacology.

To participate in the workshop, you need to have a laptop with Internet access and a CPU, RAM, video, sufficient for fast work with any Internet sites. Windows 7 and higher, last version of Google Chrome are preferred.

To prepare for the workshop, we also recommend to get acquainted with the instructions and articles on the website of the conference.

The participants of the workshop will conduct an bioinformatic analysis of a large array of experimental data (NGS or microchips) via Pathway Studio platform to identify the biological features of the disease of the patient, including the search for activated cascades of signaling pathways and targets for personalized therapy. With the help of Pathway Studio and Reaxys Medicinal Chemistry, a personalized selection of the drugs acting on the detected targets will be carried out.

DAY 2: OCTOBER 31, 2017 (Tuesday)
WP4 15:30-17:30 Room 274

PROGENESIS QI SOFTWARE

Speaker: **Paul Goulding**, *Nonlinear Dynamics, UK*

Progenesis® QI for proteomics enables researchers to quantify and identify proteins in complex discovery proteomics experiments using the advantages of label-free analysis. With support for all common vendor data formats and a guided workflow, Progenesis QI Software helps to overcome data analysis challenges, enabling rapid, objective and reliable discovery of proteins of interest from single or fractionated samples.

The workshop will consist of analysis of a simple LC-MS discovery proteomics experiment using Progenesis QI for proteomics software, in order to extract and identify biomarkers for three experimental conditions. This will include automatic data processing (alignment, peak picking and peptide identification) followed by review of the quantitative and statistical results to extract the best candidate biomarkers for each condition. There will be explanation of each analysis step and of the procedures for extracting the biomarkers. Participants who have previously downloaded and installed the software and data set will be able to follow and perform some steps of the analysis on their own laptops.

For more efficient and productive workshop please make yourself familiar with the software <http://www.nonlinear.com/progenesis/qi-for-proteomics/>

DAY 3: NOVEMBER 1, 2017 (Wednesday)
WP5 15:00-17:00 Room 265

FOOD INTOLERANCE

Speakers: **Arkady Rosensteyn**, *ImmunoHealth Int., New York, U.S.A.*;
Sergey Kondakov, *M.V. Lomonosov Moscow State University, Moscow, Russia*;
Andrey Tarasevich, *Professorial clinic of the Krasnoyarsk state medical university, Krasnoyarsk, Russia*;
Natalia Cherevko, *Siberian State Medical University, Tomsk, Russia*

Demonstration of options of the computer program «ImmunoHealth™ IT»
Marina Rosensteyn, *ImmunoHealth Int., New York, U.S.A.*

The seminar is dedicated to one of the most disputed areas of medicine – food intolerance. The new concept of dietology - interaction of food antigens with the immune system of the person or “immunodietology” is introduced.

The latest achievements in the field of determining the impact of food and the food environment on modern man and, in particular:

- various aspects of interaction of food antigens with immune system;
- determination of criterion norm pathology in immunodietology on the basis of statistically established criteria (program ImmunoHealth);
- features of laboratory diagnostics of IgG using technology of dry spots of blood (DBS) allowing to receive and keep biomaterial long time without cold chain;
- results, showing that immunological approach to creation of personal programs of food allows to customize immune system for non-drug correction of pathological states and in particular to correct mitochondrial dysfunctions.

DAY 3: NOVEMBER 1, 2017 (Wednesday)

WP6 15:00-17:00 Room 274

QUALITY CONTROL ASSESSMENT FROM MULTI-MONTH DATA SETS

Speaker: *David Tabb, Stellenbosch University, South Africa*

Large-scale experiments in proteomics may require weeks or even months of instrument time. Analysis of such sets must extend beyond simple assessment of protein identifications to include more comprehensive quality control data. In this workshop, the group will examine tables of quality control metrics from the ProteoWizard QuaMeter tool in assessing the performance of an Orbitrap over eight months of data collection for the CPTAC colon cancer project. The workshop will examine the generation of metrics, multivariate assessment via robust PCA, the recognition of outliers, and the assessment of batch effects.

POSTER SESSION

DAY 1: OCTOBER 30, 2017 (Monday)

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