24-25 November 2021 omics-ssp.com/ssp

## 10th Symposium on Structural Proteomics

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| 24 November, 2021 - online |        |   |  |  |  |
|----------------------------|--------|---|--|--|--|
| 14:00-14:20                | Online | <ul> <li>Evgeniy Petrotchenko, PhD, Senor Scientist,<br/>Laboratory of Omics Technologies and Big Data for<br/>Personalized Medicine and Health, Skolkovo Institute of<br/>Science and Technology</li> <li>Christoph H. Borchers, Ph.D., Full Member at McGill<br/>Centre for Translational Research in Cancer, Senior<br/>Investigator at Lady Davis Institute for Medical Research<br/>Director of Segal Cancer Proteomics Centre, Professor,<br/>Department Oncology, Faculty of Medicine at McGill<br/>University; Head of Laboratory of Omics technologies and<br/>Big data for Personalized Medicine and Health, Visiting<br/>Professor at the Center for Computational and Data-<br/>Intensive Science and Engineering, Skoltech</li> <li>Evgeniy N. Nikolaev, Corresponding member of<br/>Russian Academy of Sciences, Full professor of Skolkovo<br/>Institute of Science and Technology, Head of Laboratory of<br/>Mass Spectrometry</li> </ul> | Opening Ceremony   |  |  |
| 14:20-14:40                | Online | <b>Michael O. Glocker</b> , Professor, Proteome Center<br>Rostock University of Rostock   | "From Intact Transition Epitope Mapping to<br>Seroconversion Analysis by Affinity-Mass<br>Spectrometr" |  |  |
| 14:40-15:00                | Online | <b>Petr Popov</b> , Assistant Professor, Center for<br>Computational and Data-Intensive Science and<br>Engineering, iMolecule, Skolkovo Institute of<br>Science and Technology  | "Spatiotemporal identification of binding sites with computer vision"                                  |  |  |
| 15:00-15:20<br>15:20-15:40 | Online | Anna Potapenko, Research Engineer, DeepMind   | "Highly accurate protein structure prediction with AlphaFold" Break                                    |  |  |
| 13.20-13.40                |        |   | Dicak  |  |  |

| 15:40-16:00        | Online | Albert Konijnenberg, Product Manager<br>Integrative Structural Biology, Thermo Fisher<br>Scientific  | "Mass spectrometry based screening methods for<br>quality assessment of Cryo-EM samples"   |
|--------------------|--------|--|--|
| 16:00-16:20        | Online | Henning Urlaub, Research Group Leader at the<br>Max Planck Institute, professor at the University<br>Medical Center Göttingen                                  | "UV and chemical crosslinking of proteins to RNA<br>and DNA in vitro and in vivo - LC-MS/MS and<br>database search"                      |
| 16:20-16:40        | Online | <b>Dmitry N. Ivankov,</b> Assistant Professor, Center<br>of Life Sciences, Skolkovo Institute of Science<br>and Technology                                     | "Proteome-wide AlphaFold 3D protein structure<br>prediction: perspectives for finding stabilizing<br>mutations by in silico mutagenesis" |
| <b>16:40-16:50</b> |        |  | Break  |
| 16:50-17:10        | Online | Swantje Lenz, PhD Student, Technische Universität Berlin   | "Reliable identification of protein-protein interactions by crosslinking mass spectrometry"  |
| 17:10-17:30        | Online | <b>Frank Sobott,</b> Ph.D., ProfChair in Biomolecular<br>Mass Spectrometry at University of Leeds  | "An integrated approach to defining a-synuclein structure"   |
| 17:30-17:50        | Online | John R. Yates, III, Professor Department of<br>Chemical Physiology The Scripps Research<br>Institute   | "Structural Aspects of CFTR DF508's Failure to Mature"   |
| 17:50-18:10        | Online | Jared Mohr, Graduate Student Department of<br>Genome Sciences University of Washington   | "Multidimensional distance constraints in the mitochondrial interactome"   |
| 18:10-18:30        | Online | Manuel Matzinger, PostDoc within the Protein<br>Chemistry and MassSpec facility headed by Karl<br>Mechtler, Research Institute of Molecular<br>Pathology (IMP) | "Mimicked synthetic ribosomal protein complex for<br>benchmarking cross-linking mass spectrometry<br>workflows"                          |

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| 25 November, 2021 - online   |        |   |   |  |  |
|--|--------|---|---|--|--|
| 12:00-12:10  | Online |   | Welcoming Words   |  |  |
| 12:10-12:30  | Online | Kasper Dyrberg Rand, Professor, University of Copenhagen  | "Developing HDX-MS technology to study the<br>conformational dynamics of complex protein<br>systems"  |  |  |
| 12:30-12:50  | Online | Rudolf Aebersold, Professor ETH Zurich<br>Institute of Molecular System Biology   | "Towards the modular proteotype"  |  |  |
| 12:50-13:10  | Online | Nir Kalisman, Institute of Life Sciences, The<br>Hebrew University of Jerusalem   | "In situ CLMS study of NSP2 and Nucleocapsid<br>proteins from SARS-CoV-2"   |  |  |
| 13:10-13:30  | Online | Konstantinos Thalassinos, Professor of Mass<br>Spectrometry Institute of Structural and Molecular<br>Biology at University College London               | "Probing the Structure and Dynamics of Proteins by<br>Means of Cyclic Ion Mobility Spectrometry and<br>Electron Capture Dissociation"               |  |  |
| 13:30-14:20  |        |   | Break   |  |  |
| 14:20-14:40  | Online | Natallia Strushkevich, Assistant professor at theCenter for Computational and Data-IntensiveScience and Engineering, Skoltech                           | "Family-based approach in structural proteomics:<br>case study of cytochrome P450s (CYPome)"  |  |  |
| 14:40-15:00  | Online | <b>Petr Novak</b> , Head of the Laboratory of Structural<br>Biology and Cell Signaling Institute of<br>Microbiology of the Czech Academy of Sciences    | "Utilization of Fast Photochemical Oxidation of<br>Proteins and Top-down Mass Spectrometry for<br>Structural Characterization of Protein Complexes" |  |  |
| 15:00-15:20  | Online | <b>Richard Scheltema</b> , Assistant Professor, Utrecht University  | "PhoX driven crosslinking mass spectrometry"  |  |  |
| 15:20-15:40  | Online | <b>David Schriemer</b> , Professor, Biochemistry & Molecular Biology University of Calgary  | "Unlocking the organic chemistry toolbox: towards<br>whole human proteome crosslinking with freeze-<br>substitution"                                |  |  |
| 45 40 40 00  |        | <b>Carlos Cordeiro</b> , Associate Professor Director of<br>FT-ICR and Structural Mass Spectrometry<br>Laboratory Faculty of Sciences of the University | "How reversible is irreversibility? The case of protein   |  |  |
| 15:40-16:00  | Online | of Lisbon Campo Grande  | glycation"  |  |  |
| Join Zoom-Conference<br>https://skoltech-ru.zoom.us/j/97646035511?pwd=OG0vUVVCRzBkOXo2bUhPSWFVcThhZz09 |        |   |   |  |  |
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## Organizer

Laboratory of Omics Technologies and Big Data for Personalized Medicine and Health

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