

Program 2019

Sunday, 15.09.2019	
16:00	Registration
18:00	Welcome & Introduction
18:15	Johannes Kirchmair – University of Bergen In silico prediction of drug metabolism
19:00	Get-together Party

Monday, 16.09.2019	
09:00	Thierry Langer – University of Vienna / Inte:Ligand Adventures in Computer-Assisted Molecular Design
09:30	Claire Colas – University of Vienna Structure, Function and Ligand Discovery for Solute Carrier Transporters
10:00	David Machalz – Freie Universität Berlin (Europin) Targeting Cytochrome P450 4Z1 as Novel Cancer Target
10:15	Jennifer Hemmerich – University of Vienna (Europin) Cover: Conformational OVERsampling of toxicological datasets for deep learning
10:30	Coffee break
11:00	Dužanka Janežič – University of Primorska Protein interaction atlas for prediction of genetic variations involved in drug interactions and disease development
11:30	Matt Segall – Optibrium Multi-parameter Optimisation in Drug Discovery: Targeting compounds with a high chance of success
12:00	Gunther Stahl – OpenEye Virtual Screening – do I REAL-ly need large scale?
12:30	Lunch
14:00	Stephan Ehrlich – Schrödinger Hydrogens Matter - Considering Tautomers and Protomers in Drug Discovery
14:30	Coffee break
15:00	Workshops: OpenEye, Optibrium, Schrödinger
17:00	Poster session 1 Beer and Pretzel

Tuesday, 17.09.2019	
09:00	Gerhard Ecker – University of Vienna Computational Toxicology - from models to workflows
09:30	Doris Schütz – University of Montreal Integrating Interaction Hotspots of the Ras/SOS Complex to Rationalize Small Molecule Design
10:00	Floriane Montanari – Bayer AG Deep learning for computational chemistry: compound representation, ADMET profiles and automatic optimization
10:30	Coffee break
11:00	Martyna Pawletta - KNIME Cheminformatics in the open-source KNIME Analytics Platform
11:30	Daniela Digles – University of Vienna Accessing public databases with KNIME
12:00	Daniela Dolciami – University of Perugia (Europin) Virtual Screening Campaigns for the Identification of New Immunomodulatory Drugs Targeting AhR
12:15	Szymon Pach – Freie Universität Berlin (Europin) Design of novel NS2B-NS3 flaviviral protease inhibitors
12:30	Lunch
14:00	Andrea Cavalli – University of Bologna / BiKi Technologies Thermodynamics and Kinetics of Drug-Target Binding via Molecular Simulations
14:30	Coffee break
15:00	Workshops: BiKi Technologies, KNIME, Schrödinger
17:00	Zoe Cournia - Biomedical Research Foundation Athens Women at the Interface of Computational Chemistry and Drug Discovery

Wednesday, 18.09.2019	
09:00	Margot Ernst – Medical University of Vienna Ligand bound proteins – the underestimated skill of template choice and analysis in homology based approaches
09:30	Wolfgang Sippl – Martin Luther University of Halle-Wittenberg Design of selective histone deacetylase inhibitors - lessons learned from X-ray crystallography and molecular modelling
10:00	Gerhard Wolber – Freie Universität Berlin Exploring dynamic 3D interaction patterns for mechanistic understanding of protein-ligand binding
10:30	Coffee break
11:00	Zoe Cournia - Biomedical Research Foundation Athens Lessons learned from protein-ligand complex prediction and lead optimization with FEP in the D3R Challenge
11:30	Barbara Zdrzil – University of Vienna Intertwining Data Science and Computational Molecular Design – Recent Examples from Modeling Hepatic Uptake Transporters
12:00	Stefanie Kickinger – University of Vienna (Europin) Structural and molecular aspects of GABA transporter subtype selectivity
12:15	Nguyen Trung Ngoc – Freie Universität Berlin (Europin) Dihedral angle dynamics of GPCR activation hotspots
12:30	Lunch
14:00	Sharon Bryant – Inte:Ligand Advanced 3D-Pharmacophores and Their Use In Drug Discovery Research
14:30	Coffee break
15:00	Workshops: BioSolveIT, KNIME, LigandScout
18:00	Poster session 2 Beer and Pretzel

Thursday, 19.09.2019	
09:00	Stefan Boresch – University of Vienna Setting up MD Simulations of Biomolecules
09:30	Chris Oostenbrink - BOKU Vienna Applications of free energy calculations from molecular dynamics simulations
10:00	Eva Hellsberg – University of Vienna (Europin) Computational studies of molecular interactions in the human serotonin transporter
10:15	Chiara Luise – Martin-Luther University of Halle-Wittenberg (Europin) Computer-based approaches for the search of new Spindlin1 inhibitors
10:30	Coffee break
11:00	Anna Weinzingner – University of Vienna Computational studies on ion channels
11:30	Alexander Hillisch – Bayer AG Bayer's "Next Generation Library Initiative": Selected Examples of Computational Compound Design
12:00	Alžběta Türková – University of Vienna (Europin) Multiscale Computer-based Studies to Identify Ligand Interactions and Selectivity Among Hepatic Organic Anion Transporting Polypeptides
12:15	Florentina Troger – University of Vienna Combining structure- and ligand-based methods for toxicity prediction linked to human mitochondrial respiratory complex I inhibition and <i>in vitro</i> validation
12:30	Lunch
14:00	Marcus Gastreich – BioSolveIT Chemical Space Navigation – A Journey to 10 ²⁰ Possibilities
14:30	Coffee break
15:00	Workshops: BioSolveIT, LigandScout, ProBiS
17:00	Hugo Kubinyi Reflections on Discovery in Science
19:00	Congress Dinner at Heuriger

Friday, 20.09.2019	
09:00	Peter Etmayer – Boehringer-Ingelheim PROTACs - a New Therapeutic Modality
09:30	Arthur Garon – University of Vienna Novel Graph Representation of 3-D Pharmacophore Models Extracted from Molecular Dynamics Simulation
10:00	Klaus-Jürgen Schleifer – BASF Computational Chemistry @ BASF
10:30	Coffee break
11:00	Eva-Maria Plessl – University of Vienna Structure-activity relationship of the hERG activator ICA-105574
11:30	Philipp Schmalhorst – Boehringer-Ingelheim Extracting hidden design opportunities from protein structure ensembles
12:00	Gerhard Hessler – Sanofi Efficient Mining of Chemical Space
12:30	Lunch
14:00	Europin application talks