

Annual Swiss Proteomics Meeting

19./20. April 2018, Eurotel Montreux

MEETING BOOKLET



SWISS NATIONAL SCIENCE FOUNDATION



Swiss Industry Science Fund (SISF)



SystemsX.ch
The Swiss Initiative in Systems Biology



This meeting booklet belongs to:

(please find space for your notes at the end of this booklet)



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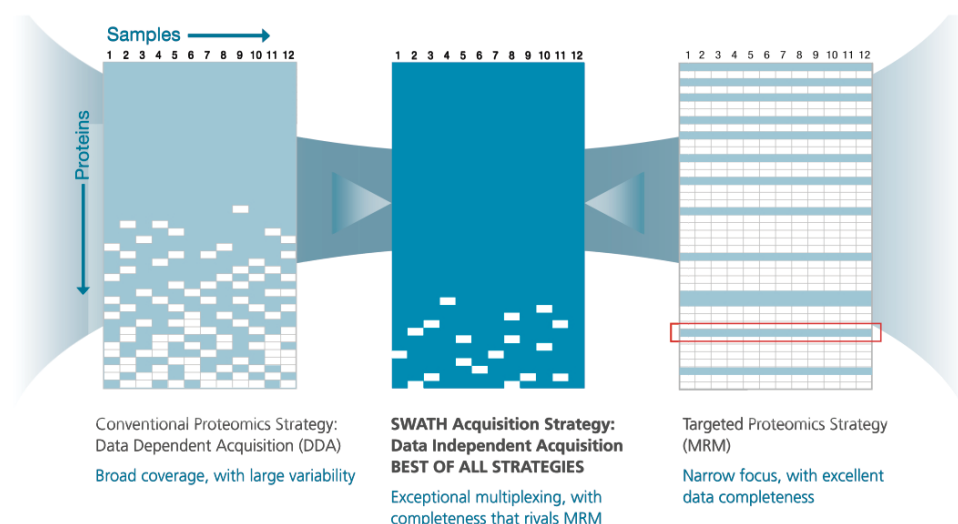
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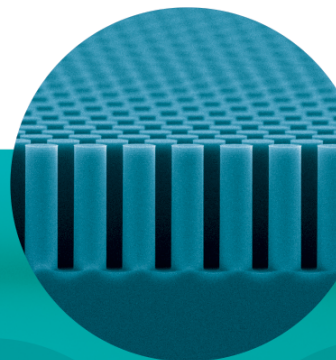
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Program Overview

Thursday, 19th April 2018

- 12:30-12:40 **Welcome: Bernd Wollscheid (ETH Zurich) & LS2 Proteomics Board**
- 12:40-16:00** **Oral Session I**
Chairs: Deborah Bonenfant (NIBR Basel) & Marc Moniatte (EPF Lausanne)
- 12:40-13:30 **Keynote 1: Jennifer Van Eyk**
(Cedars Sinai, Los Angeles, CA, USA)
"Medicine and Me: a route to individualized monitoring and intervention"
- 13:30-13:40 **Gold Sponsor Talk: Anaquant**
"A universal standard kit for label free accurate quantification in proteomics"
- 13:40 -13:55 **Flash presentations 1-3:**
Sira Echevarría Zomeño (Biognosys)
"Using resource spectral libraries in a HRM™ workflow for the discovery of lung cancer biomarkers"
Jonas Grossmann (Functional Genomics Center Zurich)
"Proteomics Bioinformatic Tools in a Core Facility"
Sabrina Casella (IRB Bellinzona)
"The APEX system: an approach for the identification of CXCR4 and ACKR3 interacting proteins"
- 13:55-14:10 **Oral presentation 1: Ilaria Piazza (ETH Zurich)**
"A systematic map of protein-metabolite interactions reveals principles of chemical communication"
- 13:55-14:25 **Flash presentations 4-6:**
Maik Müller (ETH Zurich)
"Detection of dynamic surfaceome interactions by LUX-MS"
Robin Thibault (University of Geneva)
"Large-scale reanalysis of proteomics data – An application to the HeLa cell line"
Lukas Reiter (Biognosys)
"Increasing Coverage or Throughput for Single Shot, Label Free Data Independent Acquisition (DIA)"



14:25-14:35

Gold Sponsor Talk: Biognosys

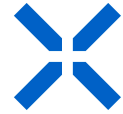
"Take a leap to quantifying the proteome – latest advancements in proteomics technologies"



14:35-14:40

"The human body: the ultimate frontier of complexity"

Documentary trailer by SystemsX.ch
The entire film can be found at
www.systemsx.ch/film



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14:40-14:50

Oral presentation 3: Sebastian Virreia Winter
(MPI Munich, DE)

"EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification"

14:50-15:05

Oral presentation 4: Ludovic Gillet (ETH Zurich)

"Proteomic analysis of minute sample amounts using Data Independent Acquisition: Application to FACS-sorted human hematopoietic stem cells"

15:05-16:00

Coffee Break

16:00-18:15

Oral Session II

Chairs: Paola Picotti (ETH Zurich) &
Alexander Schmidt (University of Basel)

16:00-16:15

Oral presentation 5: Christophe Fuerer

"Proteins in food matrices: there is a lid to every pot"

16:15-16:30

Flash presentations 7-9:

Damaris Bausch (ETH Zurich)

"Proximity Radical Tagging Strategy to study the Nanoscale Organization of the Surfaceome"

Elizaveta Solovyeva (INEPCP, RAS, Moscow, RU)

"Revealing the effect of alkylating reagents for bottom-up proteomics"

Alexander Soltermann (University of Zurich)

"Morpho-proteomics characterization of lung squamous cell carcinoma fragmentation, a histological marker of increased tumor invasiveness"

16:30-16:40

Gold Sponsor Talk: Pharmafluidics

"A novel nanoflow LCMS proteomics approach using micro pillar array columns (μ PAC™)"



- 16:40-16:55 **Flash presentations 10-12:**
- Isabell Bludau** (ETH Zurich)
"Large-scale analysis of proteoform-specific complex formation by complex-centric proteome profiling via SEC-SWATH-MS"
- Sandra Goetze** (ETH Zurich)
"MSGUIDE: A mass-spectrometry driven strategy for clinical assay development"
- Ian Lienert** (Biognosys)
"Quality Control in a Real World Setting: Implications from a Live LC-MS Facility Study"
- 16:55-17:10 **Oral presentation 6: Mathieu Brochet** (University of Geneva)
"Sub-minute Phosphoregulation of Cell Cycle Systems during Plasmodium Gamete Formation"
- 17:10-17:25 **Flash presentations 13-15:**
- Yessika De Leon Benito Revollo** (University of Zurich)
"Profiling cellular ADP-ribosylation during inflammatory signaling in immune cells by a targeted mass spectrometry approach"
- Mattheus Wildschut** (ETH Zurich)
"The Consequence of CALR Mutations on Proteostasis in Myeloproliferative Neoplasms"
- Witold Wolski** (University of Zurich)
"A Core facility solution for LFQ quantification as a service"
- 17:25-17:40 **Oral presentation 7: Marc van Oostrum** (ETH Zurich)
"Dynamics of the Neuronal Surface Proteotype"
- 17:40-17:55 **Oral presentation 8: Ulrich auf dem Keller** (Technical University of Denmark)
"Best of both: a novel hybrid PRM/DIA method on the Q Exactive HF-X"
- 17:55-18:00 **Silver Sponsor Talk: Sciex**
"New SCIEX MicroLC and wide flow range MS Ion Source - robustness and sensitivity"
- 18:00-18:15 **Oral presentation 9: Marco Faini** (ETH Zurich)
"Determining distance restraints and activation markers of native complexes with quantitative cross-linking MS"



19:00-20:00

Apéro, sponsored by Dualsystems Biotech



20:00-22:30

Dinner in the conference hotel

Friday, 20th April 2018

09:00-12:00

Oral Session III

Chairs: Loïc Dayon & Lydie Lane

09:00-09:45

Keynote 2: Matthias Selbach

(Max-Delbrück-Center for Molecular Medicine (MDC),
Berlin, DE)

"Proteome Dynamics"

09:45-10:00

Oral presentation 9: Sebastian Müller (Biognosys)

"Longitudinal Blood Protein Profiling with Stable Isotope Standards and Data-Independent Acquisition Analysis During Influenza Vaccination"

10:00-10:15

Flash presentations 16-19:

Christian Feller (ETH Zurich)

"Development of histone epi-proteomics technology and its application to identify regulatory principles of chromatin structure and function"

Kathrin Nowak (University of Zurich)

"Identification of novel ADP-ribosylated proteins using an engineered Af1521 macrodomain with enhanced ADP-ribose binding capacity"

Emanuela Milani (ETH Zurich)

"Hepatitis B Virus HBx protein hijacks host signaling networks to modulate viral replication"

10:15-10:20

Silver Sponsor Talk: Thermo Fisher Scientific

"Latest enhancements in High Throughput Proteomics"

ThermoFisher
S C I E N T I F I C

10:20-11:00

Coffee Break

11:00-11:15

Flash presentations 20-22:

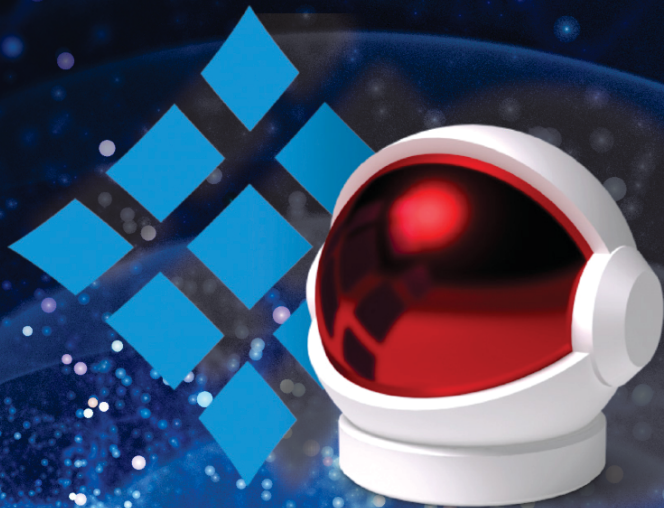
Vytautas Iesmantavicius (FMI Basel)

"Pipeline for antibody-enriched proteome-wide PTMs analysis"

Kathrin Frey (ETH Zurich)

"Associating HDL proteotype with clinical HDL particle signaling capacity"

	Fangfei Zhang (ETH Zurich) <i>"sysPTM [histone]: A proteomics tool for analyzing protein modification patterns applied to the histone sub-proteome"</i>
11:15-11:30	Oral presentation 10: Ornella Cominetti (Nestlé Institute of Health Sciences S.A.) <i>"The differential plasma proteome of obese and overweight individuals undergoing nutritional weight loss and maintenance"</i>
11:30-11:45	Flash presentations 23-25: Florian Marty (Biognosys) <i>"Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results"</i> Emma Ricart Altimiras (SIB Lausanne) <i>"Bionotator and NRPro: Bioinformatics Tools for the study of Nonribosomal Peptides"</i> Markus Müller (Vital-IT, SIB, Lausanne) <i>"Estimating the proportion of proteasomal spliced peptides in the HLA ligandome"</i>
11:45-12:00	Oral presentation 11: Peter Blattmann (ETH Zurich) <i>"Systems pharmacology dissection of cell-specific cholesterol regulation mechanisms reveals large pharmacodynamic variability"</i>
12:10-12:20	Awards and Closing remarks <i>Chairs: Manuel Tzouros (Hoffmann-La Roche Basel) & Oliver Rinner (Biognosys)</i>
12:10-12:20	Best oral presentation prize & best flash talk prize
12:20-12:30	Closing remarks – Bernd Wollscheid & LS2 Proteomics Board
12:30-14:00	Farewell Lunch
14:00-15:00	LS2 Proteomics Board Meeting



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to quantifying
the proteome**

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NEXT GENERATION PROTEOMICS

Keynote Lectures

Keynote lecture I: Thursday, 19.4.2018 12:40-13:30



Jennifer Van Eyk
(Cedars Sinai, Los Angeles, CA,
USA)

“Medicine and Me: a route to individualized monitoring and intervention”

Keynote lecture II: Friday, 20.4.2018 09:00-09:45



Matthias Selbach
(Max-Delbrück-Center for
Molecular Medicine (MDC),
Berlin, DE)

“Proteome Dynamics”

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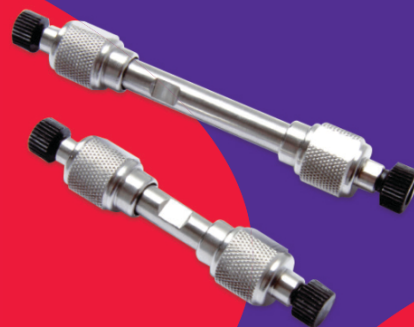
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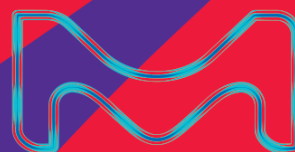
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- Stable Isotope-labeled products
- Mass Spectrometry Standards and Analytical kits
- Broad range of antibodies



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proteomics

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THE HUMAN BODY

THE ULTIMATE FRONTIER OF COMPLEXITY

The documentary film about **SystemsX.ch** reveals what it takes to understand the human system from a biological point of view. Since 2007, the Swiss research initiative in systems biology has supported around 250 interdisciplinary research projects at the interface between biology, physics, chemistry, mathematics and medicine as well as engineering and computer science. The documentary, titled “The human body: the ultimate frontier of complexity“, explains how these projects are helping decipher the mechanisms of the human body, and how systems biology is opening up new possibilities in the study, diagnosis and development of (personalized) therapies to treat serious illnesses or age-related disorders.



Watch the film at
www.systemsx.ch/film



SystemsX.ch
The Swiss Initiative in Systems Biology

Sponsor talks & abstracts

Gold sponsor talks:



ANAQUANT

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"A universal standard kit for label free accurate quantification in proteomics"

Quentin Enjalbert, Business Development Manager, Anaquant
quentin.enjalbert@anaquant.com

Shotgun proteomics analysis is mainly used for protein and peptide identification and relative quantification while targeted analysis is used for relative and absolute quant.

The advantage of Shotgun proteomics is the ability to detect and identify many proteins in unknown samples. However, quantification evaluation is relatively complicated since no calibrated standards are used.

In targeted proteomics, quantification evaluation is usually performed with isotopic labeled peptides but it is mandatory to know proteins of interest before analysis.

In order to avoid performing both shotgun and targeted analysis, we have developed a new strategy based on the TOP3 principle (Silva et al. Mol Cell Proteomics.2006 Apr; 5(4):589-607. Epub 2006 Jan 5). We have developed a 54 peptides calibration curve representing 18 different proteins, to quantify in a single MS and label-free analysis, in a range encompassing 3 orders of magnitude. All the selected peptides were chosen according to their sequence, their signal response and their specificity

This strategy consists in performing, within the sample, a titration curves with those standard proteotypic peptides based on TOP3 values of each standard protein. Once the linear calibration curve performed, quantification evaluation of all detected proteins, based on their TOP3 peptide values, can be done in a single MS and label-free analysis in a range of 3 orders of magnitude.

To help the sample preparation of such a well calibrated standard peptide mix, the READYBEADS® technology was used and allows preparing the internal calibration curve in less than 3 minutes directly in the sample of interest.

Results obtained on a therapeutic sample demonstrated the ability of the approach to evaluate the concentration of hundreds of proteins in a single MS run. The so developed kit might provide a universal stable internal standard for quantification evaluation in many different applications.



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“Take a leap to quantifying the proteome – latest advancements in proteomics technologies”

Oliver Rinner, CEO Biognosys
oliver.rinner@biognosys.ch



PharmaFluidics

“A novel nanoflow LCMS proteomics approach using micro pillar array columns (μ PAC™)”

Dr Paul Jacobs, COO PharmaFluidics, Dr Jeff Op de Beeck, Application Development Manager, and Katrien Vanhonacker, VP Business Development and Sales
katrien.vanhonacker@pharmafluidics.com

For complex biological samples—which often include analytes with a wide range in polarity and molecular weight, and many isomers—separations are often challenging, even when using ultrahigh-pressure liquid chromatography and high-resolution mass spectrometry.

For complex samples like these, it can be beneficial to use micro-chip based pillar array chromatography columns. In contrast to conventional LC columns that contain randomly packed beads as their stationary phase, micro-chip based pillar array chromatography columns have a separation bed of perfectly ordered and freestanding pillars obtained by lithographic etching of a silicon wafer. The regular mobile phase flow pattern through these micro-chip pillar array columns adds very little dispersion to the overall separation, resulting in better peak resolution, sharper elution peaks and increased sensitivity. The freestanding nature of the pillars also leads to much lower back pressure buildup, and makes it possible to operate longer columns.

PharmaFluidics develops and commercializes a unique μ PAC range of micro-Chip based chromatography columns for use in biomarker, diagnostics and drug research & development applications in the global biotech and pharma industries. During the presentation, the principles of the micro-chip based pillar array columns and related benefits in terms of robustness and longevity will be explained. High resolution data obtained for proteomic analysis using micro-chip based pillar array columns will be demonstrated.

Silver sponsor talks:

ThermoFisher S C I E N T I F I C

"Latest enhancements in High Throughput Proteomics"

Guido Sonsmann , Area Sales Manager, and Daniel Grenno, Area Sales Manager
Thermo Fisher Scientific
guido.sonsmann@thermofisher.com

The Q Exactive HFX has been the latest Addition to the Benchtop Orbitrap Family and is highly suitable for various Proteomics Workflows. Its versatility to answer today's question will be presented.

- Sensitivity, Speed for DDA experiments
- CE-MS
- AP MALDI



"New SCIEX MicroLC and wide flow range MS Ion Source - robustness and sensitivity"

Christian Baumann, AWS, SCIEX Germany
Bernd Müller, AWS, SCIEX Germany
christian.baumann@sciex.com

Modern LC-MS analytical strategies always have to find a balance between sensitivity and robustness. Whereas NanoLC approaches are very sensitive, but also known as not very robust for large studies, the more rugged Highflow LC systems often lack sensitivity for certain application areas.

Microflow LC approaches combine those two key features sensitivity and robustness in a simple and easy-to-establish way.

SCIEX introduces a new MicroLC system together with a new universal MS Ion Source for all flow rate regimes.

Space for notes

Space for notes

Space for notes



ANAQUANT

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ANAQUANT is a private Contract Research Organization (CRO) specialized in targeted protein quantification by Mass spectrometry for Biologics and Biomarkers analysis. Its main goal is to assist and support scientists in their daily work.

Founded in 2014 by Tanguy Fortin (PhD), ANAQUANT has established a strong partnership with the Institute for Analytical Sciences (ISA Lyon, FRANCE) headed by the Professor Jérôme Lemoine. Thus, the company benefits of leverages proprietary technology and more than 15 years of experience of the laboratory's team with industrial companies.

As expert and trusted partner, ANAQUANT provides customized services and standards to pharmaceutical and biotech companies from early-Nonclinical phases to last development steps for biologics, vaccines or biomarkers projects.

Our mission is to bring our partners reliable solutions which contribute to the selection of their best drug candidates and guarantee a better control of their biologic to limit failure during further clinical phase.

Our solutions are based on our customized services for analytical method development but also on our patented technology called READYBEADS[®], a new tool that helps LC-MS users by saving time and gaining in peace of mind.



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Organizers

The executive committee of the LS² section Proteomics

- Bernd Wollscheid, President (ETH Zurich)
- Lydie Lane (Swiss Institute of Bioinformatics, Lausanne)
- Paola Picotti (ETH Zurich)
- Alexander Schmidt (Biozentrum Basel)
- Loïc Dayon (Nestlé Institute of Health Sciences)
- Manuel Tzouros (Roche Pharmaceuticals, Basel)
- Oliver Rinner (Biognosys AG)
- Deborah Bonenfant (Novartis Institutes for BioMedical Research, Basel)
- Marc Moniatte (EPF Lausanne)



<https://www.ls2.ch/sections/proteomics>

Life Sciences Switzerland (LS²)

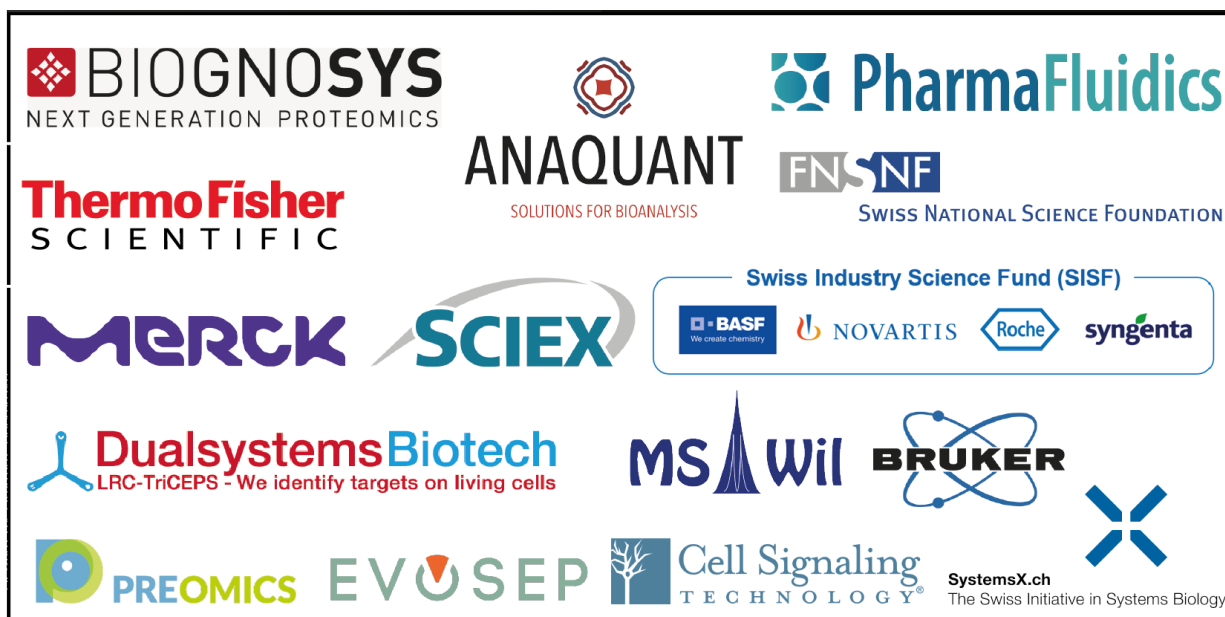
- Carolin von Schoultz (Scientific Officer)
- Jacqueline Oberholzer (Executive Secretary)
- Dagmar Bocakova (design, bocakova@gmail.com)
- Dominique Ritter (administration)
- Michael Vögeli (IT)

Upcoming Proteomics events

- **EuPA:** 16-20 June, Santiago de Compostela, Spain
- **HUPO**
 - 2018: 30 Sep 2018 - 03 Oct 2018, Orlando, US
 - 2019: 15 Sep 2019 - 19 Sep 2019, Adelaide, Australia
- **ASMS**
 - 66th ASMS Conference, June 3 - 7, 2018, San Diego, US
 - 67th ASMS Conference, June 2 - 6, 2019, Atlanta, US

Sponsors

We are extremely grateful to the sponsors of this year's meeting!



Thank you all for your participation!

Feedback to:
info@ls2.ch



Life Sciences Switzerland LS²
Design by Dagmar Bocakova
Zurich 2018

meetings.ls2.ch/proteomics-2018