

CASA FRONTIERS OF SCIENCE

DATE & TIME

Wednesday, January 15th, 2020

LOCATION

Science Park 904, 1098XH Amsterdam, room C0.05

PROGRAM

14:30 Tea & coffee

Chair: Garry Corthals

15:00 Ruedi Aebersold

The modular proteome and its significance

16:00 End

On 15 January 2020, **Prof. Ruedi Aebersold** from the ETH Zurich will visit Science Park Amsterdam to give a seminar on analytical technology and applications his group has developed for proteome and systems biology based research. Aebersold's groups have pioneered several widely used techniques and generated a range of open access/open source software and statistical tools that have contributed to making proteomic research results more transparent, reproducible and accurate. Such techniques have been applied to a wide range of projects in basic and translational research world-wide.

If you wish to meet Prof. Aebersold or have enquires about the seminar please contact prof. Garry Corthals at corthals.lab@gmail.com.

The seminar is open access through support afforded by the John van Geuns Fonds and Sciex.

Abstract

Biological or clinical phenotypes and the cellular response to stimuli arise from the biochemical state of a cell or tissue which, in turn, is the result of the composition of biomolecules and their organization in the cell. At present, there is neither a comprehensive theory nor computational models that generally predict phenotypes or cellular responses to signals. Nevertheless, such predictions are frequently attempted, particularly in clinical research, exemplified by personalized/precision medicine, even though there is a large degree of variability between individuals in a population. It is therefore an important question which type(s) of molecular information, either by themselves or integrated with other data, will increase the ability to predict phenotypes from molecular measurements beyond what is possible today and how the variability of a population affects these predictions. The biochemical literature indicates that proteins is particularly rich in biological information. To date, most proteomic studies have focused on the identification and quantification of proteins. However, most proteins associate with other proteins and/or other types of bio molecules and carry out their function as protein modules and a multitude of such functional modules constitutes the biochemical state of the cell. We refer to a specific instance of proteome composition and organization as the proteotype. In this presentation we will discuss computational and mass spectrometry based experimental methods to infer or measure the modular organization of the proteotype. We will then examine how genomic variability affects the molecular landscape and phenotype.

Bio

Ruedi Aebersold is a Swiss and Canadian scientist trained at the Biocenter, University of Basel. He completed his education at Caltech. He is a Professor at ETH Zurich and the University of Zurich. He was on the faculties of the Universities of British Columbia and Washington and co-founded, with Lee Hood and Alan Aderem, the Institute for Systems Biology in Seattle. He has co-founded several companies and holds several public service appointments. He was awarded an honorary doctorate of the University of Lund, Sweden and the work of the group was recognized with numerous prizes and awards. The research focus of his group is the proteome. The group has pioneered several widely used techniques and generated a range of open access/open source software and statistical tools that have contributed to making proteomic research results more transparent, reproducible and accurate. In his group these techniques have been applied to a wide range of projects in basic and translational research.