

# PROGRAM | THURSDAY 8 MARCH

08:45 - 09:15 Registration & coffee

09:15 - 09:20 Welcome by Alexander Botzki

Plenary session 1

Hall: Auditorium

## INTEGRATIVE OMICS

Chair: Diether Lambrechts

09:20 - 09:55 Insights from methylome analysis  
**Stephan Beck, UCL, UK**

09:55 - 10:30 Computational approaches for understanding single-cell variation  
**Oliver Stegle, EMBL-EBI, UK**

10:30 - 11:00 Coffee break

11:00 - 11:35 Epigenome profiling to unveil (dye)regulated pathways in health and disease  
**Henk Stunnenberg, Radboud Institute for Molecular Life Science, NL**

11:35 - 12:10 Network-guided integrative analysis for genotype-phenotype mapping in clonal systems  
**Kathleen Marchal, Ghent University, BE**

12:10 - 12:45 Modularity, classification and networks in analysis of big biomedical data  
**Ron Shamir, Tel Aviv University, IL**

12:45 - 13:30 Lunch

13:30 - 14:30 Poster session

Plenary session 2

Hall: Auditorium

## STRUCTURAL BIOINFORMATICS

Chair: Joost Schymkowitz

14:30 - 15:15 Drug repurposing for ageing research  
**Janet Thornton, EMBL-EBI, UK**  
*keynote*

15:15 - 15:50 Protein homeostasis of a metastable subproteome associated with Alzheimer's disease  
**Michele Vendruscolo, University of Cambridge, UK**

15:50 - 16:05 SNPMuSiC - towards the prediction and interpretation of deleterious coding variants in terms of protein structural stability changes  
**François Ancien, ULB, BE**

16:05 - 16:35 Coffee break

16:35 - 17:10 Intrinsically disordered proteins mutated in cancer  
**Zsuzsanna Dosztanyi, Eötvös Loránd University, HU**

17:10 - 17:45 Designing synthetic amyloid peptides as a tool for protein functional knockdown  
**Frederic Rousseau, VIB-KU Leuven Center for Brain & Disease Research, BE**

17:45 - 18:20 Functional families in the CATH classification give insights on protein evolution and the impacts of splicing  
**Christine Orengo, University College London, UK**

18:20 - 19:15 Reception

20:00 Conference dinner

08:45 - 09:20 Coffee

Plenary session 3

Hall: Auditorium

## PROTEOMICS/METABOLOMICS

Chair: Lennart Martens

09:20 - 09:55 Having your cake and eating it too: Can proteomics be both comprehensive and quantitative?

**Michael MacCoss**, *University of Washington, Department of Genome Sciences, US*

09:55 - 10:30 The Virtual Metabolic Human: Recon 3D, AGORA, and more

**Ines Thiele**, *-Luxembourg Centre for Systems Biomedicine, University of Luxembourg, LU*

10:30 - 11:00 Coffee break

11:00 - 11:35 Native MS in structural biology: surface collisions of protein complexes

**Vicki Wysocki**, *Ohio State University, US*

11:35 - 12:10 From its origins to the modern metabolic network

**Markus Ralser**, *The Francis Crick Institute, UK*

12:10 - 12:25 Systems proteomics of gene expression

**Georg Kustatscher**, *University of Edinburgh, UK*

12:25 - 13:15 Lunch

13:15 - 14:15 Poster session

Plenary session 4

Hall: Auditorium

## SYSTEMS BIOLOGY

Chair: Brigida Gallone

14:15 - 15:00 **keynote** Hybrid mass spectrometry approaches targeting cellular signaling  
**Albert Heck**, *Utrecht University, NL*

15:00 - 15:35 Single-Cell Gene Regulatory Networks  
**Stein Aerts**, *VIB-KU Leuven Center for Brain & Disease Research, BE*

15:35 - 15:50 Genetic and transcriptome analysis of ABCA7 in Alzheimer's disease  
**Arne De Roeck**, *VIB - University of Antwerp, BE*

15:50 - 16:20 Coffee break

16:20 - 16:55 Profiling individual field-grown plants to reverse engineer plant molecular systems and their impact on yield phenotypes  
**Steven Maere**, *VIB-UGent Center for Plant Systems biology, BE*

16:55 - 17:10 Network Dynamics of ER- $\alpha$  activation in response to estradiol reveals the ER mediated reprogramming of GRHL2  
**Andrew Holding**, *University of Cambridge, UK*

17:10 - 17:45 Deeper understanding of microbiomes as a benefit of forgetting microbial names  
**Yana Bromberg**, *Rutgers University, US*

17:45 - 18:00 Closing remarks by Alexander Botzki