



FEBS Workshop on Chromatin Proteomics 3-8 October 2016

Aldemar Knossos Royal Hotel
Heraklion, Crete, Greece

SCIENTIFIC PROGRAM

MONDAY OCTOBER 3	
16.00-onwards: Arrival, registration	
18.00: Opening remarks by organizers	
18.10: Keynote Lecture: Ruedi Aebersold Proteomic analyses into the Chromatin-associated subproteome	
<i>DINNER AT THE HOTEL</i>	
TUESDAY OCTOBER 4	
SESSION 1: Chromatin modifications	CHAIR: Axel Imhof
8.30: Ole N. Jensen	Deciphering PTM cross-talk in histones by mass spectrometry: Advances in middle-down protein analysis using ETD MS/MS
9.00: Robert Schneider	Novel Players in Chromatin
9.30: Short talk: Alessandro Cuomo	Combining heavy-methyl SILAC and proteomic MS-based approaches for in depth analysis of the histone protein-methylome at saturation
9.45: Short talk: Pavel Shliaha	Separation of isomeric proteoforms for full histone tails using differential ion mobility spectrometry
10.00-10.30: COFFEE BREAK	
10.30: Till Bartke	Decoding Chromatin using Chemical Biology and Proteomic Approaches
11.00: Anne-Claude Gingras	A spatio-temporal view of nuclear acetylation recognition
11.30: Short talk: Roberta Nuberini	Mass spectrometry-based mapping of histone post-translational modifications for breast

	cancer patient stratification
11.45: Short talk: Andrey Tvardovskiy	Accumulation of histone variant H3.3 is associated with profound changes in the histone methylation landscape in mouse somatic tissues with age
12.00-13.30: LUNCH BREAK	
13.30-15.00: MEET-THE-EXPERTS 1 (parallel sessions) Session 1: Quantitative Proteomics: Aebersold, Lamond, Jensen Session 2: Epigenomic maps: Vermeulen, Bartke, Bickmore	
15.00-16.30: Project discussions/Problem solving 1 (participant-speaker pairs)	
SESSION 2: Quantitative chromatin proteomics	CHAIR: Ole N. Jensen
16.30 Keynote Lecture: Angus Lamond Proteomic Analysis of Cell Cycle Variation in Gene Expression	
17.15: Falk Butter	Quantitative interactomics for histone tails, DNA and RNA
17.45: Short talk: Eva Papachristou	Immunoaffinity enrichment combined with isobaric labelling for the quantitative profiling of transcription regulation complexes
18.00: Short talk: Moritz Völker-Albert	The kinetics of chromatin assembly
18.15-18.45: COFFEE BREAK	
18.45: Jeroen Krijgsveld	Proteome meets genome: selective isolation of chromatin-associated proteins identifies novel regulators of pluripotency
19.15: Michiel Vermeulen	ZMYND8 co-localizes with NuRD on target genes and regulates poly (ADP-ribose)-dependent recruitment of GATAD2A/NuRD to sites of DNA damage
19.45: Short talk: Paul Ginno	A novel mass spectrometry method reveals chromatome dynamics during the mammalian cell cycle
20.00: Short talk: Guido van Mierlo	Dynamic PRC2 localization and distribution in multiple states of pluripotency
20.30: DINNER AT THE HOTEL	
WEDNESDAY OCTOBER 5	
SESSION 3: Functional Chromatin Proteomics	CHAIR: Michiel Vermeulen

8.30: EMBO YIP Lecture: Anja Groth Chromatin Replication and Epigenome Maintenance	
9.00: Petra Beli	Deciphering phosphorylation-dependent signaling in the cellular response to UV light
9.30: Short talk: Emilia Dimitrova	Role of the CXXC protein Fbxl19 in regulation of gene expression
9.45: Short talk: Nick Mullin	Proteomic analysis of the stem cell regulator Nanog identifies NCoR as a critical mediator of gene repression in embryonic stem cells
10.00-10.30: COFFEE BREAK	
10.30: Eric Soler	Transcription factor dynamics and long-range chromatin interactions in erythroid cells
11.00: Axel Imhof	Proteomics of chromatin boundaries-separation on a molecular and organismic level
11.30: Wendy Bickmore	Chromatin and gene regulation - using synthetic approaches to dissect cause and effect and to test mechanisms
12.00: Short talk: Joanna Lempiäinen	Hormone-dependent protein interactome of the glucocorticoid receptor
12.15: Short talk: Jofre Font Mateu	Progesterone receptor interactome in breast cancer cells
12.30-14.00: LUNCH BREAK	
14.00-16.30: POSTER SESSION 1 (Abstracts 1-18)	
17.00: EVENING OUT IN HERAKLION	
THURSDAY OCTOBER 6	
SESSION 4: Chromatin domains	CHAIR: Anja Groth
9.00: Sonia Rocha	Analysis of chromatin structure in hypoxia
9.30: Jerome Dejardin	Heterochromatin and the control of telomere maintenance
10.00: Short talk: Ines Drinnenberg	Overcoming AbCENs: Composition of CenH3-deficient kinetochores in holocentric insects
10.15: Short talk: James Hutchins	Identification and characterisation of proteins required for the recognition of metazoan DNA replication origins

10.30-11.00: COFFEE BREAK	
11.00: Robin Allshire	Epi-Proteomics: probing establishment and maintenance of specialised chromatin domains
11.30: Lothar Schermelleh	Functional chromatin organisation studied by multimodal & multidimensional super-resolution imaging
12.00: Tiziana Bonaldi	Chromatin signatures of enhancers investigated through an integrated quantitative proteomic and functional genomic approach
12.30: Short talk: Puneet Prabhakar Singh	Proteomic analysis of fission yeast CENP-A ^{Cnp1} nucleosome-associated chromatin
12.45: Short talk: Elisabeth Schmidtman	A modular approach for systematic investigation of chromatin-associated proteins under physiological conditions
13.00-14.30: LUNCH BREAK	
14.30-17.00: POSTER SESSION 2 (Abstracts 19-37)	
16.30-17.00: COFFEE BREAK	
17.00-18.30: Scientific Career Development: Advice given by selected speakers e.g. Allshire, Beli, Gingras, Schneider	
SESSION 5: Structural proteomics	CHAIR: Tiziana Bonaldi
18.30: Song Tan	Structural studies of chromatin complexes - how chromatin proteins and enzymes interact with the nucleosome
19.00: Juri Rappsilber	Protein abundance is buffered against regulatory interference by large-scale genome architecture
19.30: Short talk: Jan de Rijk	Structural and functional characterization of the interaction of chromatin reader LEDGF/p75 with its cellular and viral binding partners
19.45: Short talk: Simone Tamburri	Dissecting the role of the leukocyte specific protein Sp140 as a new epigenetic reader
20.30: DINNER AT THE HOTEL	
FRIDAY OCTOBER 7	
SESSION 5: Structural proteomics (continued)	CHAIR: Juri Rappsilber

8.30: Fan Liu	Developing structural interactomics and its application in nuclear biology
9.00: Franz Herzog	Studying the Native Kinetochore Architecture and its Role in Chromosome Segregation using Cross-Linking and Mass Spectrometry
9.30: Henning Urlaub	Analysis of UV-induced DNA–protein cross-links in a chromatin model
10.00: Short talk: John Strouboulis	Characterization of the DNMT1 protein interactome in mouse erythroid cells reveals interactions with hematopoietic transcription factors and co-repressor functions
10.15: Short talk: Grigorios Tsaknakis	Characterization of Friend of GATA-1 (FOG-1) interactions with CTCF and the cohesins in erythroid cells
10.30-11.00: COFFEE BREAK	
SESSION 6: Computational Proteomics, Data Integration	CHAIR: Wendy Bickmore
11.00: Alexey Nesvizhskii	Computational methods and tools enabling quantitative proteomics and interactomics
11.30: Alberto Paccanaro	Inference and structure discovery in protein interaction networks
12.00: Jürgen Cox	The Perseus computational platform for comprehensive analysis of (prote)omics data
12.30: Industrial Presentation: Volker Kruff, SCIEX OneOmics in the cloud: integrating multi-omics data for quantitative system biology	
13.00-14.30: LUNCH BREAK	
14.30-16.00: MEET-THE-EXPERTS 2 (parallel sessions) Session 3: Crosslinking approaches: Rappsilber, Urlaub, Liu Session 4: Chromatin domain characterization: Krijgsveld, Dejardin, Allshire	
16.00-17.30: Project discussions/Problem solving 2 (participant-speaker pairs)	
17.30-18.30: Round Table Discussion–Closing Remarks: Looking ahead in chromatin proteomics Imhof (moderator), Bickmore, Gingras, Vermeulen, Nesvizhskii, Bonaldi, Rappsilber	
20.00: DINNER AT THE HOTEL	
SATURDAY OCTOBER 8	

Breakfast and departure