PROGRAMME

2nd Danube Conference on Epigenetics
5-8 October 2016, Budapest, Hungary

Organized by

Hungarian Biochemical Society

Hungarian Academy of Sciences, Research Centre for Natural Sciences

Hungarian Academy of Sciences
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Wednesday, October 5 - Hungarian Academy of Sciences

16:00   Introduction

16:30   **Keynote Lecture**  
        Chair: Laszlo Tora  
        **Eileen Furlong**  
        Functional insights into chromatin topology and gene expression during embryonic development  
        *Sponsored by EMBO*

17:30-19:00  **Single-cell epigenetics**  
              Chairs: Iannis Talianidis, Amos Tanay

17:30-18:00  ** Alexander van Oudenaarden**  
              Revealing novel cell types, cell-cell interactions, and cell lineages by single-cell sequencing

18:00-18:15  **Juliette Dabin**  
              Contribution of parental histone dynamics to epigenome stability after DNA damage

18:15-18:30  **Zichuan Liu**  
              Daxx and PRC1 control integrity and segregation of paternal chromosomes in mouse early embryos

18:30-19:00  **Mario Nicodemi**  
              Hierarchical folding of chromosomes in neuronal differentiation and its link to epigenetics

19:00-19:15  Coffee break

19:15-20:00  **Single-cell epigenetics**  
              Chairs: Iannis Talianidis, Amos Tanay

19:15-19:30  **Guillaume Filion**  
              HIV and human chromatin

19:30-20:00  **Christoph Bock**  
              Epigenetic biomarkers: Ready for clinical diagnostics  
              *Sponsored by Diagenode*

20:00   Welcome dinner
Thursday, October 6 - RCNS

9:00-10:30  Metabolism and epigenetics
Chairs: Erica Watson, Bálint L. Bálint

9:00-9:30  Iannis Talianidis
H4K20 monomethylation regulates RNA Pol-II elongation and plays an important role in the transcriptional control of hepatic metabolic pathways

9:30-9:45  Florence Cammas
Functions of the HP1 network in liver homeostasis

9:45-10:00  Tamas Arányi
Dynamic DNA methylation changes due to acute metabolic stress in mice

10:00-10:30  Ueli Schibler
Posttranscriptionally controlled ribosome assembly rhythms drive diurnal cycles in global liver mass and macromolecular content

10:30-11:00  Coffee break

11:00-12:00  Metabolism and epigenetics
Chairs: Erica Watson, Bálint L. Bálint

11:00-11:15  Sabine Fraschka
Deciphering the transcriptional regulatory network of the human malaria parasite Plasmodium falciparum

11:15-11:30  Tibor Pankotai
Transcriptional outcomes in response to DNA damage

11:30-12:00  Andrew Pospisilik
β-cell PRC2 focuses transcription of select lineage genes and thus prevents de-differentiation and Diabetes in mouse and Man

12:00-13:00  Lunch break
13:00-14:30  **Developmental epigenetics**  
Chairs: J. Andrew Pospisilik, Tibor Pankotai

13:00-13:30  **Petra Hajkova**  
Epigenetic reprogramming in vivo: How and why?

13:30-13:45  **Pierre-Antoine Defossez**  
A histone mimic within DNA Ligase 1 recruits UHRF1 to sites of DNA replication: implications for DNA remethylation

13:45-14:00  **Ivett Baksa**  
Small RNA-based regulation during temperature adaptation in Arabidopsis

14:00-14:30  **Amos Tanay**  
Single cell approaches to cellular memory

14:30-15:00  Coffee break

**Live DEMO Show on the exhibition booth of**  
- Single cell analysis with QIAGEN: sample prep, amplification, NGS library prep and targeted panels  
- Fast and cost-effective methylation studies with a fully automated QIAGEN workflow (QIAcube, Rotor-Gene Q, Pyromark Q48 Advanced)

15:00-15:45  **Developmental epigenetics**  
Chairs: J. Andrew Pospisilik, Tibor Pankotai

15:00-15:15  **Alessio Zippo**  
MYC favors the onset of tumorigenesis by inducing epigenetic reprogramming of mammary epithelial cells towards a stem cell-like state

15:15-15:45  **Ferenc Mueller**  
Developmental dynamics of epigenomic features of cis-regulatory elements in early embryo development

15:45-16:15  Coffee break

16:15-18:00  **Poster viewing**

19:30  **Beer session**  
*Optional program, costs not covered by the registration fee. Participants should get to the pubs individually – maps will be provided.*
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<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Title</th>
<th>Details</th>
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<tr>
<td>9:00-10:30</td>
<td>Chromatin architecture</td>
<td>Chairs: Gábor Szabó, Petra Hajkova</td>
<td>Ana Pombo</td>
<td>Genome Architecture Mapping: A spatial approach to map chromatin contacts</td>
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<tr>
<td>9:30-9:45</td>
<td></td>
<td>Judit Balog</td>
<td>Heterozygous mutations in DNMT3B cause derepression of the subtelomeric D4Z4 macrosatellite array and contribute to the development of muscle disease</td>
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<td>9:45-10:00</td>
<td></td>
<td>Lóránt Székvölgyi</td>
<td>A Set1C-centric view of meiotic recombination initiation</td>
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<td>10:00-10:30</td>
<td></td>
<td>Leonie Ringrose</td>
<td>Beyond memory: The secret life of Polycomb Response Elements</td>
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<tr>
<td>11:00-11:45</td>
<td>Chromatin architecture</td>
<td>Chairs: Gábor Szabó, Petra Hajkova</td>
<td>Irene Cantone</td>
<td>Cell fusion-mediated reprogramming reveals a link between variability of human X chromosome inactivation in somatic cells and pluripotency-induced gene reactivation</td>
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<td>11:15-11:45</td>
<td></td>
<td>Wouter de Laat</td>
<td>Multi-contact 4C reveals multi-way three-dimensional chromatin conformation</td>
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<td>11:45-13:45</td>
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<td>Poster session</td>
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<td>13:45</td>
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<td>Sandwiches, Free afternoon</td>
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<td>20:00</td>
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<td>Gala Dinner – Danube cruise</td>
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<tr>
<td>9:00-10:30</td>
<td>Transcriptional regulation and epigenetics</td>
<td>Imre Boros, Tamás Arányi</td>
<td>The ATAC and SAGA coactivator complexes are highly dynamic in the nuclear environment with fast and slow chromatin interacting populations</td>
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<tr>
<td>9:00-9:30</td>
<td>Laszlo Tora</td>
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<td>Epromoters define a new class of regulatory elements with dual promoter and enhancer functions in mammals</td>
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<tr>
<td>9:30-9:45</td>
<td>Salvatore Spicuglia</td>
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<td>Silencing of transposable elements by PIWI-interacting RNAs</td>
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<td>9:45-10:00</td>
<td>Chantal Vaury</td>
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<td>Epigenetic control of pervasive transcription and genomic stability</td>
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<td>10:00-10:30</td>
<td>Tamas Fischer</td>
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<td>Super-enhancers and person-to-person genetic variability in the context of the 1000 Genomes Project</td>
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<tr>
<td>10:50-11:35</td>
<td>Transcriptional regulation and epigenetics</td>
<td>Imre Boros, Tamás Arányi</td>
<td>Transgenerational Epigenetics: Lessons from Arabidopsis</td>
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<td>10:50-11:05</td>
<td>Bálint L. Bálint</td>
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<td>RNA methylation in stem cells and cancer</td>
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<td>11:05-11:35</td>
<td>Michaela Frye</td>
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<td>Drosophila gut microbiome is involved in transgenerational inheritance of acquired traits</td>
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<td>11:35-13:00</td>
<td>13:00-14:30</td>
<td>Ana Maria Pires Pombo, Lóránt Székvölgyi</td>
<td>Sponsored by Institute Français</td>
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<td>13:00-13:30</td>
<td>Vincent Colot</td>
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<td>Transgenerational inheritance</td>
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<td>13:30-13:45</td>
<td>Aman Zare</td>
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<td>How abnormal folate metabolism haunts our descendants</td>
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<td>13:45-14:00</td>
<td>Kallayanee Chawengsaksophak</td>
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<td>The epigenetic modifier Fam208a is essential for mouse gastrulation</td>
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<td>14:00-14:30</td>
<td>Erica Watson</td>
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<td>Epigenetic modifier Fam208a is essential for mouse gastrulation</td>
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<td>14:30-15:00</td>
<td>Poster prizes and concluding remarks</td>
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<td>2nd Danube Conference on Epigenetics</td>
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<td>Posters</td>
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| P-01 | **Hakan Akca**  
miR-548as could be a novel suppressor of TGFβR1 to inhibit epithelial-to-mesenchymal transition in NSCLC |
| P-02 | **Caroline Bacquet**  
Applying environmental epigenomics to assess adaptation to global change in Heliconius melpomene butterfly populations |
| P-03 | **Marine Baptissart**  
Developmental programming in response to maternal overnutrition |
| P-04 | **Raymond Blind**  
Readers, writers and erasers of nuclear PIP3 |
| P-05 | **Laszlo Bodai**  
Exploring the role of histone modifications in Huntington's disease |
| P-06 | **Dóra Bojcsuk**  
Canonical elements drive super-enhancer formation |
| P-07 | **Pedro Castelo-Branco**  
Hypermethylation of the TERT promoter predicts biochemical relapse in prostate cancer |
| P-08 | **Vin Yee Chung**  
The interplay between transcription factor GRHL2 and epigenetics in the regulation of EMT in ovarian cancer |
| P-09 | **Sébastien Coassolo**  
Role of the chromatin-remodelling complex NURF and NuRD in epigenetic regulation of melanoma gene expression |
| P-10 | **Ixchelt Cuaranta Monroy**  
Genome-wide studies during adipocyte differentiation from mouse pluripotent stem cells |
| P-11 | **Luiza Diniz Ferreira Borges**  
Epigenetic in the development: Detection of histones deacetylases in melipona scutellaris (apidae, meliponini) |
| P-12 | **Edina Erdős**  
Genome-wide mapping of COUP-TFII and ERa co-occupancy in breast cancer cells |
| P-13 | **Sercan Ergun**  
In silico analysis of potential cernas in renal cell carcinoma |
P-14 Sercan Ergun
Analysis of 3’UTR shortening of ABCB1 gene in Imatinib-resistant CML cells in terms of potential ceRNAs by a computational study

P-15 Dominique Fauvin
Next generation epigenetics – Innovative research tools for the accurate analysis of DNA modifications

P-16 Erfaneh FirouziNiaki
Histone type, modification and cell cycle phasespecific characterization of nucleosome stability in situ

P-17 Erfaneh FirouziNiaki
Measurement of interstrand DNA crosslinks generated by anticancer agents through a modified alkaline comet assay

P-18 Anna Fortuny Gonzalez
Histone dynamics in response to DNA damage in heterochromatin domains

P-19 Marybeth Francis
Inflammation differentially affects histone methylation state of promoters of inflammatory genes and structure proteins

P-20 Zsuzsanna Gaál
Expression levels of Warburg-effect related microRNAs in hematological malignancies of the adults

P-21 Kay Gully
Molecular mechanisms of elicitor-induced epigenetic changes in Apple and Arabidopsis thaliana

P-22 Anca-Sarmiza Gültekin-Tigan
The cyclin-dependent kinase CDK6 as key regulator of the cancer epigenome

P-23 Attila Horváth
Characterization and modeling of lineage-specific enhancer states and transitions in macrophages

P-24 Mette Jacobsen
Adipocyte gene expression and DNA methylation patterns differ significantly between lean and obese pigs.

P-25 Aeri Kim
Erythroid activator NF-E2, TAL1 and KLF1 play roles in forming the LCR HSs in the human adult β-globin locus

P-26 Gergő Kovács
Rybp plays essential role in neural differentiation of mouse embryonic stem cells
P-27  Janina Ličytė
Direct decarboxylation of 5-carboxylcytosine by DNA C5-methyltransferases

P-28  Cha Min Ho
Free hemoglobin change gene expression involving in cell-cell signaling through different DNA methylation in THP-1-derived macrophages

P-29  Celine Morey
The non-coding gene Ftx promotes Xist upregulation at the onset of X-chromosome inactivation

P-30  Iraia Muñoa Hoyos
The epigenetic regulator complex Polycomb/H3K27me3 plays a role in the epigenetic memory induced by morphine upon EpiLC differentiation

P-31  Gergely Nagy
IL-4 reshapes the RXR cistrome in mouse bone marrow-derived macrophages

P-32  Péter Nánási
The effect of histone modifications and DNA superhelicity on nucleosome stability

P-33  Péter Nánási
Nucleosome stability through the spectacles of quantitative imaging

P-34  Csilla Emese Németh
Epigenetic role of Vitamin C in the pathomechanism of Arterial Tortuosity Syndrome

P-35  Zsofia Nemoda
Controlling for cell composition of peripheral biological samples in candidate gene DNA methylation analyses

P-36  Dragos Nica
Association of global DNA hydroxymethylation with cadmium in gastropod hepatopancreas

P-37  Tünde Nyiko
Functional and molecular characterization of an epigenetically controlled PUMILIO-regulatory protein in Arabidopsis.

P-38  Colleen ORyan
Differential DNA methylation associated with Autism Spectrum Disorder in a South African cohort

P-39  Colleen ORyan
The serotonin transporter gene (SLC6A4) shows differential regulation between children with ASD and typically developing children in a South African population

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| P-40 | Lilla Ozgyin  
Genomic determinants of molecular phenotype differences between B-lymphobastoid cells of a CEU trio |
| P-41 | Luca Pagliaroli  
MicroRNA regulation in Tourette Syndrome candidate genes |
| P-42 | Luca Pagliaroli  
Changes in DNA methylation profiles followed by sub-chronic treatment with psychiatric drugs aripiprazole and riluzole in the rat striatum and prefrontal cortex |
| P-43 | Cristina Popescu  
Dynamic changes of epigenetic biomarkers (5mC and 5hmC) in biofluids of prostate cancer patients undergoing hormonal treatment |
| P-44 | Petra Priščáková  
Plasma DNA methylation profiles of genes associated with metastasis in breast cancer patients |
| P-45 | Vanda Repiská  
Methylation of genes associated with invasiveness of breast cancer |
| P-46 | Helene Royo  
The histone H3 lysine 36 demethylase KDM2A/FBXL11 is essential for Polycomb-mediated gene repression during germ cell development |
| P-47 | Hussein Sabit  
Epigenetic regulation of P21, RASSF1, PTEN, and P53 in human breast cancer cells using different chemotherapeutic drugs |
| P-48 | Osama Said  
Procaine induces epigenetic changes in HCT 116 colon cancer cells |
| P-49 | Kristine Salmina  
Retrotransposition caused and autophagy-aided heterochromatin release in etoposide treated senescent teratocarcinoma PA1 cells |
| P-50 | Rita Seeböck  
What happens to the Epigenome in 2D/3D cell culture? |
| P-51 | Ioan-Ovidiu Sirbu  
qRT-PCR evaluation of selected microRNAs’ expression in amniotic fluid and chorionic villus samples from Down syndrome pregnancies |
| P-52 | Ioan-Ovidiu Sirbu  
Plasma microRNA expression profiles in Parkinson's disease |
| P-53 | Gordana Supić  
miR-183 and miR-21 Expression as Biomarkers of Progression and Survival in Tongue Carcinoma Patients |
| P-54 | **Gábor Szabó**  
The effect of histone modifications and DNA superhelicity on nucleosome stability |
|------|----------------------------------------------------------------------------------------------------------------------------------|
| P-55 | **Agnes Tantos**  
Intrinsic protein disorder in histone lysine methylation |
| P-56 | **Violeta Trusca**  
Apolipoprotein E upregulation by dexamethasone in macrophages |
| P-57 | **Borbála Vető**  
Inhibition of DNA methyltransferase leads to increased genomic 5-hydroxymethylcytosine levels in lymphoid cells |
General information

Venue

October 5, 2016
Hungarian Academy of Sciences, The Academy Club
Budapest
Széchenyi tér 9.
H-1051

October 6-8, 2016
Research Centre for Natural Sciences, Hungarian Academy of Sciences
Budapest
Magyar tudósok körútja 2.
H-1117

Registration desk

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<td>Wednesday, 5 October</td>
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<td>Thursday, 6 October</td>
<td>8:00-18:00</td>
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<tr>
<td>Friday, 7 October</td>
<td>8:00-14:00</td>
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<tr>
<td>Saturday, 8 October</td>
<td>8:00-15:00</td>
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Important phone numbers

English is usually spoken at the emergency numbers listed below.
Central help number: 112

- Ambulance: 104
- Police: 107
- General enquiries: 197
- International enquiries: 199
- Hungarian Automobile Club help number: 188
- Fire brigade: 105
- Central help number: 112
- Inland enquiries: 198
Social programs

Welcome reception
Wednesday, 5 October 2016     20:00
Hungarian Academy of Sciences, The Academy Club

The organisers invite you for a dinner on the evening of your arrival. We wish to serve you with some refreshment after your travel. Our other aim is to create a familiar atmosphere where you can meet old friends, and make new relationships, too.
Included in the registration fees.

Beer session
Thursday, 6 October 2016      19:30

We arrange a "Beer session" in local pubs during the evening. This time participants will have the opportunity to assign for the program, and have a short discussion about their preferred questions with the invited speakers (5 minutes/participant). We would like to invite you to join us that night, and if you wish, present a short elevator pitch.
Optional program, costs not covered by the registration fee

Gala dinner & River cruise
Friday, 7 October 2016      20:00
Budapest by night on the board of the “Primus” Boat
Gathering is a green area next to the Petőfi bridge latest at 19:45. Please check our map below to see the meeting point.

During this event we wish to serve you an excellent feast. PLEASE NOTE! The boat cruises on the river during the banquet, so there is no possibility to arrive later or leave earlier.
Presenters’ guidelines

Invited presentations
Each presentation takes 20+10 minutes discussion.

Oral presentations
Each presentation takes 10+5 minutes discussion.

Technical instructions:
Please prepare your presentation in .ppt, .pptx (Microsoft Office PowerPoint 97-2013 format) or .pdf file. If you wish to have a video, please contact the technician in the lecture hall in a break before your presentation (or preferably earlier) to check it in advance. Please upload your presentation at latest in the break before your session.

If you wish to use your own notebook please contact the technician.

Posters
Each poster might be mounted during the whole Conference. Posters left on the boards after the removal deadline will be removed by the organisers.

Mounting: 6th October, from 8:00
Removal: 8th October, before 15:00
NOTES