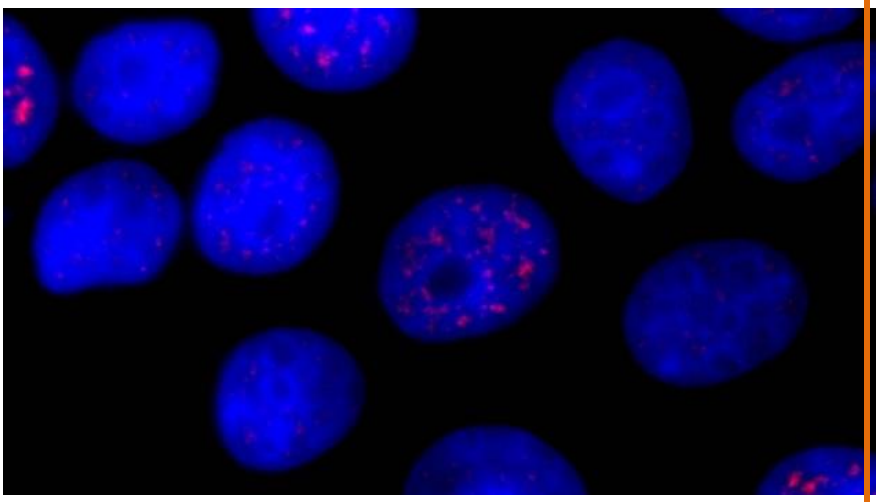
RESEARCH CONFERENCES



ESF-EMBO Conference

Long Regulatory RNAs

13 – 18 September 2014

Pultusk, Poland

Chaired by: Andreas Werner

Co-chaired by: Sven Diederichs

http://rna.esf.org/

Highlights & Scientific Report

Conference Highlights

Please provide a brief summary of the conference and its highlights in non-specialist terms (especially for highly technical subjects) for communication and publicity purposes. (ca. 400-500 words)

Long noncoding and regulatory RNAs are a new and exciting topic with emerging roles in gene regulation and potential implications in disease, development and evolution. The conference on "long regulatory RNAs" in Pultusk, Poland was attended by 68 scientists, a relatively small audience, likely being the result of an unpredictable accumulation of similarly themed meetings during late summer 2014. On the positive side, this resulted in a vibrant and productive meeting with an excellent scientific standard und unusually active interaction between all participants and speakers.

In his opening plenary lecture, Reuven Agami (The Netherlands Cancer Institute) gave a first intense glance at the fascinating versatility of regulatory RNAs and used the tumour suppressor p53 to demonstrate how noncoding RNAs transcribed in enhancer regions help to coordinate a genome wide response to stress. He introduced many of the emerging concepts and mechanisms that were expanded on in the following sessions. The first day focused on regulatory mechanisms involving long noncoding RNAs and set them into a genome-wide perspective. Maite Huarte (University of Navarra) expanded on p53 and described a p53-induced regulatory RNA (Pint) which reduces cell motility and tumour invasion. Further excellent talks given by Gunter Meister, John Rasko and Marvin Jens gave detailed insights into different regulatory mechanisms orchestrated by long and short regulatory RNAs. Their elegant and unpublished results often challenged established views and lead to heated discussions. The deleterious consequences of aberrant levels of a particular noncoding RNA, Malat1, were highlighted by three different speakers, Stephanie Dimmeler (University of Frankfurt), Mitch Guttman (California Institute of Technology) and Sven Diederichs (German Cancer Research Center). Malat1 is a very highly expressed regulatory RNA, however, its presence only seems to be essential to cope with stress. Elegant experiments were presented to suggest modes of action and biological and pathological roles for Malat1, most interestingly however, the different studies came to somewhat divergent conclusions. This stimulated lively discussions and clearly highlighted the timeliness of this meeting's focus.

The second half of the meeting featured a series of exciting presentations on regulatory noncoding RNAs in development and in germ cells. Unpublished highlights were presented explaining how germ cells cope with transposable elements, also addressing the very first steps of piRNA processing that are still very poorly understood (Donal O'Carroll, EMBL Monterotondo, Ramesh Pillai, EMBL Grenoble).

Excellent short talks complemented the invited lectures and provided fresh-from-the-bench insights into current pressing problems in the field. For example, long "noncoding" RNAs were found associated with ribosomes (Rory Johnson, CRG, Barcelona) and a comparative view of noncoding RNAs was presented by Igor Ulitsky (Weizmann Institute) providing arguments to support functionality of noncoding RNAs. Additional highlights were the lively poster sessions where practical tips were exchanged, help offered and collaborations fostered. Prizes were awarded for outstanding oral and poster contributions to Anna Vilborg, Yale; Christina Ernst, Cambridge; and Luis Arnes, New York.

To conclude, the meeting was small but outstanding in its scientific content and the interactions among all participants.

X ☐	I hereby authorise ESF – and the conference partners to use the information contained in the above section on 'Conference Highlights' in their communication on the scheme.

Scientific Report

Executive Summary

(2 pages max)

My personal impression is that all the participants enjoyed the outstanding science and the lively, informal atmosphere at the conference and that the meeting was a great success. The event ran very smoothly and without event thanks to the expert support from Marie-Laure Schneider and the warm hospitality of all members of staff at the Hotel Dom Polonii in Pultusk.

21 speakers were invited (8 women/13 men) including four speakers who are at the start of an independent research career (Maïwen Caudron-Herger, Florian Pauler, Marvin Jens and Laura Poliseno). The mix of established and young scientists was very well received and contributed essentially to the informal atmosphere and the constructive discussions. The meeting had a clear European focus with only one speaker each from the USA, South Africa and Australia and the rest from 11 different European countries. The short talks were given by 7 women and 14 men. The gender balance was exactly 50:50 for all participants. 12 participants (18%) came from overseas (India, Israel, Korea, China, Brazil, USA and Japan – in addition to aforementioned speakers) and the rest from 11 European countries with Germany contributing the largest contingent (11 participants).

The conference went extremely well, both from a scientific and a technical point of view. All the registered speakers and participants travelled to Pultusk and enjoyed an unusually warm and sunny five days at the Hotel Zamek Dom Polonii. All sessions featured interesting talks without technical glitches and plenty of time for discussion. The only changes to the programme concerned the "Look forward discussion" which was moved before dinner to allow for more informal interactions; and likewise, the last session on Wednesday (17th of September) was moved back an hour to fully profit from the glorious sunshine. (Both these changes were stipulated by participants and readily implemented by the chairs and Marie-Laure).

The Hotel Zamek Dom Polonii was a fantastic conference venue with a spacious meeting hall and impeccably functioning projection facilities. Catering and accommodation were well received and staff was very helpful and omnipresent. The remote location of the conference venue had pros and cons: On the one hand, it generated a highly productive melting pot atmosphere among participants with very little opportunities to escape. On the other hand, the place is rather difficult to reach. This may also have hampered the acquisition of meeting sponsors. These minor concerns, however, do not diminish the overwhelmingly positive impact of the meeting.

Scientific Content of the Conference

(1 page min.)

- *Summary of the conference sessions focusing on the scientific highlights*
- *Assessment of the results and their potential impact on future research or applications*

The human genome only contains about 20,000 protein coding genes, in fact not many more than much less complex organisms such as worms. This astonishing finding from the Human Genome Project suggests that our evolution (and that of multicellular animals) is driven by increasingly entangled networks in which regulatory RNAs play an essential part. Recent research suggests that non-protein coding RNA molecules (lncRNA) play important roles in a novel paradigm of gene regulation and many cellular functions beyond.

The full scale of the impact of RNA on gene regulation is only emerging, largely because investigations into the roles and mechanisms of long regulatory RNAs face some formidable experimental and conceptual challenges. Provoked by the generally very low expression level of noncoding RNAs and their poor conservation between species, for example, many findings are discussed controversially. To account for these particular circumstances, the meeting had a broad focus and aimed to be both educational and cutting edge. Retrospectively, we can say that these objectives were fully met. Without exception, the oral presentations were discussed lively and both poster sessions ran for more than two hours. The vibrant atmosphere was certainly helped by the relatively small number of participants and the structure of the programme with generous slots for discussion.

The presentations could be grouped into three particular, over-arching themes including mechanistic aspects of regulatory RNAs (sessions I, II and III), the impact of regulatory RNAs in disease (sessions IV and VII) and the role of noncoding RNAs in development and evolution (sessions V and VI). All the topics were covered by invited speakers, short talks and posters and were also discussed informally during breaks. The report follows the thematic grouping rather than the chronological order.

The meeting started with an excellent plenary lecture given by Reuven Agami focusing on the interplay between p53 and a specific type of regulatory RNAs, so-called enhancer RNAs. He explained that p53 exerts its genome-wide regulatory influence by binding to enhancer sequences and promoting the transcription of enhancer RNAs that in turn regulate distal gene expression. These steps also involve the modification of chromatin marks on histone proteins.

Mechanistic aspects of regulatory RNAs: Mitchell Guttman, Maite Huarte, Gunter Meister, Marvin Jens, John Rasko, Florian Pauler, Anton Wutz, Anders H. Lund. Short talks: Anna Vilborg, Anna Postepska-Igielska, Mario Flores, Niels Montano Frandsen, Marcel Köhn, Aleksandra Kornienko, Rory Johnson, Andrzej Dziembowski, Lovorka Stojic, Puri Fortes, Daniel Andergassen.

X chromosome inactivation and parental imprinting are paradigms of RNA- mediated gene silencing which featured prominently in a number of talks (M.G., A.W., F.P). It was reported that a number of noncoding RNAs (XIST, TSIX, AIRN, Plet1 and Plet1 antisense, to name a few) are directly involved in targeting chromatin marks that promote transcriptional silencing, but also the importance of the nuclear and chromosomal architecture was particularly highlighted. Many of the transcription- and regulatory sites co-localize and the interactions are –at least in part- orchestrated by long regulatory RNAs. The impact of Argonaute proteins and Dicer (key components of RNA interference) on the assembly and processing of RNA containing regulatory complexes were discussed in detail (G.M., M.J.). Interesting novel aspects of miRNA precursors were presented and the concept of "passive" binding (without processing) of Dicer to double-stranded RNA structures was suggested. Genome-wide regulatory impact of long nocoding RNAs was demonstrated in response to p53-activation and B-Raf (M.H., A.L.) with severe phenotypic consequences. For example, cell motility is regulated by the p53-induced lncRNA Pint, possibly via interference with chromosome segregation. Later, the focus turned to RNA mediated generation of complexity via alternative splicing and intron retention. In an engaging seminar John Rasko introduced intron retention as a common phenomenon during blood cell development and found that predominantly genes involved in morphological changes were

affected.

Particular scientific highlights were presented during the excellent short talks, some of which challenge existing paradigms. For example, Anna Vilborg detected a large number of stress induced noncoding RNAs downstream of coding genes that remain associated with chromatin. Various steps of the life of lncRNAs were highlighted (A.V., A.K, R.J., A.D.), from transcription to the association with ribosomes (is this a strategy to target ectopic lncRNAs for degradation?) and exosome-mediated degradation. Examples of lncRNAs antisense to coding genes interfering with transcription (F.P, L.S.) and intercalating with DNA double strands (A. P-I) were reported and intensely discussed. Furthermore, two interesting biological systems were presented where lncRNAs play an essential function including viral infection of human cells (P.F.) and histone transcriptional termination (M.K.). Three short talks focused on methods to investigate regulatory RNAs using computational tools (M.F., D.A.) and a strategy to knock down the expression of lncRNAs (NM.F.). The sessions were highly informative and lively. Established concepts as well as novel and provocative findings were presented.

Regulatory RNAs in disease: Sven Diederichs, Stefanie Dimmeler, Laura Poliseno, Maïwen Caudron-Herger, Wlodzimierz Krzyzosiak. Short talks: Ciro Bonetti; Doron Ginsberg, Luis Arnes, Mariangela Morlando, Francesco Ghini, Tetsuro Hirose.

Regulatory RNAs are prominently investigated in cancer and it has been shown that particular lncRNAs could be used as tumour markers or play important roles in tumorigenesis. A particularly interesting lncRNA is MALAT1, highly abundant and up-regulated in many cancers. While MALAT1 plays an important role in lung cancer metastasis and in the vascular system, Malat1 knockout mice do hardly show any abnormal phenotype. Malat1 featured prominently in three invited seminars (Sv.D., St.D., M.G.) and hypotheses were presented suggesting specific roles in splicing (based on the colocalization with nuclear speckles) or histone modification. A role of repetitive Alu sequences in the structural organization of the nucleolus was elegantly established by Maïwen Caudron-Herger. The theme of structural or "architectural" RNAs was expanded in a highly informative short talk by Tetsuro Hirose who outlined the role of NEAT1 and chromatin modifying complexes in the formation and maintenance of paraspeckles. The other two talks focused on the role of microRNAs in drug resistance in melanoma (L.P.) and the potential of using short RNAs to target trinucleotide repeat disorders (W.K.). Francesco Ghini investigated the degradation of microRNA using a 4-S-Uridine labelling technique and reported in his short talk a significant variation in half-life times that varied for specific miRNAs according to the physiological state of the cells. The fascinating diversity of regulatory RNAs became apparent in the following short presentations that focused on lncRNAs in specific diseases or development (C.B., D.G., L.A., M.M.). Differentially regulated lncRNAs were identified in B cell lymphomas (C.B.) and retinoblastoma (D.G.). Furthermore, the concept of lncRNAs acting as molecular sponges for microRNAs was presented in the context of muscle development (M.M.) and the hypothesis was extensively discussed. Beta cells secrete insulin and play an essential role in diabetes and Luis Arnes explained in his elegant presentation how two regulatory RNAs influence beta cell differentiation. These two sessions with a focus on diseases revealed the fascinating diversity of RNA-mediated gene regulation and also highlighted the difficulties and pitfalls that are often encountered when studying lncRNAs.

Noncoding RNAs in development and evolution: Sandra Duharcourt, Nicola Illing, Noora Kotaja, Donal O'Carroll, Alena Shkumatava, Petr Svoboda, Andreas Werner. Short talks: Ramesh Pillai, Igor Ulitsky, M. Aydin Akbudak, Qianwen Sun.

The first session focused on noncoding, regulatory RNAs in both the male and the female germ line. Noora Kotaja gave an overview of male germ line development and focused then on a particular RNA processing structure, the chromatoid body. This dynamic structure comprises a myriad of RNAs and proteins and the specific nature of its components suggest that the chromatoid body plays a major role in germ cell development. This hypothesis was expanded (A.W.) to suggest that the chromatoid body

plays a role in a putative control mechanism to assess the transcriptional output of the genome. Donal O'Carroll gave an elegant account of the biological roles of piRNAs during spermatogenesis. Using mouse models with conditional knock-down of various piRNA-related effector proteins, he established a comprehensive picture of piRNA function during sperm development, particularly focusing on transposon silencing and chromatin modifications. This presentation was complemented by the exciting short talk by Ramesh Pillai who gave first insights into the so far poorly understood synthesis of primary piRNA precursors. Petr Svoboda focused on the female germ cell development and introduced a specific, alternatively spliced form of Dicer. It is driven by a murine transposon, is essential for female gametogenesis and was shown to produce endogenous siRNA. The second session focused on RNA-mediated regulation of cellular processes in other organisms than mouse and human; since lncRNAs are not well conserved during evolution different paradigms may apply in distantly related species. Sandra Duharcourt introduced an interesting model system, Paramecium, to study RNA-driven elimination of DNA. The principle of RNA delivering the specificity to precisely target enzyme complexes is well established, however, in Paramecium, the RNA guide is used to identify the presence or absence of a specific sequence. Such strategy may well be applicable to other model systems to licence or count nucleic acids. Nicola Illing and Alena Shkumatava introduced bats and zebrafish as model systems to study lncRNAs during development. Zebrafish offer unique advantages (transparency of embryos, gene knock-down strategies) to study the impact lncRNAs -such as "Cyrano"- on embryonic development. The knockdown of "Cyrano" by splice-site targeting morpholinos led to a distinct phenotype particularly in the developing nose of the embryos. Bats, on the other hand, express a set of lncRNAs that show a particular pattern in fore- and hind limb development: Interestingly, the hind limbs show small, claw like digits, the fore limbs develop into the wings with elongated digits and interdigital membranes and lincRNAs may contribute to establishing these morphological differences. Phylogenetic conservation of lncRNAs was addressed by Igor Ulitsky and he presented a very useful, comprehensive overview. Finally, two short talks (M.A.A., Q.S.) gave a brief glimpse at regulatory RNAs in plants. The two sessions were highlights of the meeting and gave a fascinating account of cutting edge research into regulatory RNAs.

The field of regulatory and noncoding RNAs is very young and exciting. Anytime and everywhere these kinds of transcripts can be detected -thanks to the ever more sensitive detection methods. A much more challenging endeavour follows the detection (and probably proud baptism; see 'business meeting') with its characterization and robust confirmation of 'functionality' of the novel transcript. What 'functionality' actually entails and what kind of experimental evidence is needed to prove it, is still a matter of intense debate. This question dominated a number of after-talk and poster discussions. The informal atmosphere was particularly helpful to early career researchers to discuss particular issues of biological relevance in their own work. Other technical questions relating to sequencing depth, methods to interfere with the expression of noncoding RNA, their visualization and methods to reliably establish intermolecular interactions were intensely discussed. On a conceptual level, a number of talks focused on architectural aspects and the role of lncRNAs in establishing frameworks for cellular processes. To conclude, the meeting was lively and refreshing, full of pioneering spirit but combined with the expertise and caution of established leaders in the field –much to the profit of both early career and established scientists.

Forward Look

(1 page min.)

- *Assessment of the results*
- *Contribution to the future direction of the field – identification of issues in the 5-10 years timeframe*
- *Identification of emerging topics*

Both chairs and also Marie-Laure Schneider received overwhelmingly positive informal feedback at the end of the meeting. The excellent quality of the talks was appreciated as well as the generous time for discussions after the presentations. The relatively small size of the meeting and its duration meant that everyone interacted to foster collaborations and exchange expertise. The European focus of the meeting was also positively mentioned. In summary, the aim of organizing a scientifically outstanding, informal and broadly educational meeting was achieved in every aspect.

The application of high throughput technology in biomedical research has fundamentally reversed the logic of current experimental strategies. Whereas initially biological phenomena were described and eventually molecular components responsible for the observation were identified, we now face an almost unlimited choice of sequences, proteins, lncRNAs that require functional characterization and confirmation of biological relevance. Solving these problems requires novel analytical strategies to analyze function, to monitor interactions and to visualize components. These emerging techniques, for example to monitor direct interactions between different classes of macromolecules (RNA, DNA and proteins) were discussed in detail in a number of different sessions.

The majority of regulatory RNAs form networks that influence multiple cellular processes. Low expression of individual network components and redundancy make these regulatory systems difficult to track experimentally. The current reductionist approach is not suited to reveal a meaningful role for a particular component in a regulatory network. Accordingly, knock-out studies hardly produce significant phenotypes and even if they do, the connection between the insult and the result often remains obscure. These challenges will require meaningful generation and assessment of large data sets to demonstrate trends and subtle effects. A comparable accuracy needs to be achieved to describe specific phenotypes, for example in the development and the cognitive behavior of animals.

With the development of TALENs and CRISPR-Cas9 methodology, genetic engineering has made impressive progress, however, knock-on effects on genome architecture and transcriptionally coupled gene loci will pose a formidable challenge to these knock-out strategies. Several groups also reported that targeting lncRNAs with genome editing poses a much greater and yet mostly unsolved challenge than mRNAs.

The cellular and subcellular architecture of a cell has an essential influence on the functioning of regulatory networks and lncRNAs have emerged as organizers of these three-dimensional structures. In the future, it will become increasingly important to resolve intermolecular interactions in the context of the cellular architecture, potentially adding time resolution. In that sense, cross-discipline collaborations with cell biologists may be a way forward.

- Is there a need for a foresight-type initiative?

Considering that the field of regulatory RNAs is still in its infancy and the overwhelming potential of RNA in medicine and biomedical research, we would strongly support such an initiative.

Business Meeting Outcomes

- *Election of the Organising Committee of the next conference*
- *Identified Topics*
- *Next Steps*

There were three main points on the business meeting agenda:

- Future meetings on regulatory RNAs

- The nomenclature of noncoding RNAs

- Potential funding strategies

Meetings: It was noted that ESF will discontinue their meeting series by the end of 2015. Nevertheless, all participants expressed their interest in a follow-up meeting on regulatory, noncoding RNAs, particularly one with a European focus. Participants were encouraged to explore other European organizations (EMBO) or national societies (Royal Society, professional societies) to obtain funding for a meeting in two years' time.

Nomenclature: A number of talks at the meeting presented screens for long noncoding RNAs linked to a specific cellular process or a disease. How these novel lncRNAs should be named was discussed in the context of clarity, inter species comparison and searchability. A recent article by Mathew Wright (HUGO Gene Nomenclature Committee) should answer most of the questions. However, several of these suggestions were controversially discussed – especially the question whether lncRNAs should be named based on the closest protein-coding gene given that most lncRNAs putatively do not (only) act in cis on their immediate neighbors. It was pointed out that these names should be easy to pronounce (at conferences) and "googlable". [http://www.humgenomics.com/content/8/1/7]. A related problem was discussed with respect to a lncRNA database. It was mentioned that just very recently a site was launched [http://rnacentral.org/] that enables key word and sequence searches across ten noncoding RNA expert databases.

Funding: Funding was considered to be better discussed informally in small groups among the meeting participants.

Atmosphere and Infrastructure

- *The reaction of the participants to the location and the organisation, including networking, and any other relevant comments*

Full marks for both! A warm "thank you" to all the participants of the meeting and the staff of the Hotel Dom Polonii for making this event such a success!

Sensitive and Confidential Information

This report will be submitted to the relevant ESF Scientific Review Group for review.

In order to promote transparency, it is ESF policy to also publish the Scientific Reports on its website. Any confidential information (i.e. detailed descriptions of unpublished research, confidential discussions, private information) should therefore not be included in this report. Confidential issues can be addressed in the next page, which will not be published.

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☐	in this report

Confidential Issues

- *Any other issues, not to be included in the published report.*

N/A

Date & Author: Newcastle, 1st of October 2014

Andreas Werner and Sven Diederichs

ESF-EMBO Long Regulatory RNAs

13 – 18 September 2014, Pultusk, PL

Scientific PROGRAMME

Saturday 13 September	
17:00 onwards	Registration at the ESF desk
19:00	Welcome Drink
20:00	Dinner

Sunday 14 September	
08:45– 09:00	Conference Opening – **Andreas Werner, Sven Diederichs**
09:00– 10:00	Plenary Lecture: ***Reuven Agami,*** EnhancerRNAs at the service of p53
Session 1: The genomics of regulatory RNAs Chair: **Sven Diederichs**, German Cancer Research Center, Heidelberg, DE	
10:00 – 10:40	***Mitchell Guttman***, lncRNAs: Function and Mechanism in Controlling Cellular Identity
10:40 – 11:00	***Anna Vilborg***, Widespread Inducible Transcription Downstream of Human Genes
11:00 – 11:30	Coffee break
11:30 – 12:10	***Maite Huarte***, LncRNA components of the p53 pathway
12:10 – 12:30	***Anna Postepska-Igielska***, Genome-wide isolation and functional characterization of DNA:RNA triplex structures
12:30 – 12:50	***Mario Flores***, Perturbation of Competing Endogenous RNA networks by lncRNAs
13:00	Lunch
Session 2: Mechanistic aspects of RNA-mediated regulation Chair: **Anton Wutz**, ETH, Zurich, Switzerland	
14:30 – 15:10	***Gunter Meister***, RNA binding proteins as modulators of coding and non-coding RNA functions
15:10 – 15:50	***Marvin Jens***, Transcriptome-wide binding of human and *C.elegans* Dicer: the known and the unknown of an ancient protein
15:50 – 16:10	***Niels Montano Frandsen,*** Development of single stranded RNaseH recruiting antisense oligonucleotides for analysis of lncRNA function in cell culture/animals

16:10 – 16:30	***Marcel Köhn,*** The Y3** ncRNA promotes the 3'-end processing of canonical histone mRNAs
16:30 – 17:00	Coffee break
17:00 – 17:40	***John Rasko,*** Orchestrated intron retention regulates normal granulocyte differentiation.
17:40 – 18:00	***Aleksandra Kornienko,*** Defining the lncRNA transcriptome of human primary granulocytes
18:10 – 18:30	***Rory Johnson,*** The majority of cytoplasmic long noncoding RNAs are associated with ribosomes
Poster Session	
19:00	Dinner
20:30-22:00	Poster session

Monday 15 September	
Session 3: Paradigms of gene regulation by RNAs Chair: **Alena Shkumatava**, Institut Curie, Paris, Fr	
09:00 – 09:40	***Florian Pauler***, Macro lncRNAs as a paradigm for silencing by transcription
09:40 – 10:20	***Anton Wutz***, Induction and function of chromatin modifications by the long noncoding Xist RNA
10:20 – 10:40	***Andrzej Dziembowski,*** The human DIS3 nuclease clears the cell of pervasive transcription products and controls the level of unstable long noncoding RNAs
10:40 – 11:10	Coffee break
11:10 – 11:50	***Anders H. Lund***, LncRNA in Senescence
11:50 – 12:10	***Lovorka Stojic***, Transcriptional interference by long non-coding RNA GNG12-AS1 regulates tumour suppressor DIRAS3
12:10 – 12:30	***Puri Fortes,*** Efficient HCV replication requires cellular long non-coding RNAs
12:30 – 12:50	***Daniel Andergassen,*** A novel bioinformatic pipeline to determine the extent of tissue-specific regulation of imprinted expression
13:00	Lunch

Session 4: LncRNA and disease I Chair: **Mitchell Guttman**, California Institute of Technology, Pasadena, USA	
15:00 – 15:40	***Sven Diederichs,*** Long Noncoding RNA in Cancer
15:40 – 16:20	***Stefanie Dimmeler,*** Non-coding RNAs in cardiovascular diseases
16:20 – 16:40	***Ciro Bonetti***, Oncogenic and tumor-suppressive properties of lincRNAs in lymphomagenesis
16:40 – 17:10	Coffee break & Group Photo
17:10 – 17:50	***Laura Poliseno***, MAPK pathway-regulated microRNAs in melanoma
17:50 – 18:10	***Doron Ginsberg,*** E2F1-regulated long non-coding RNAs modulate cell proliferation and viability
18:10 – 18:30	***Luis Arnes,*** Examining the role of novel long noncoding RNAs in beta cell biology
Poster Session	
19:00	Dinner
20:30-22:00	Poster Session

Tuesday 16 September	
Session 5: Noncoding RNA in the germline Chair: **Sandra Duharcourt**, University of Diderot, Paris, FR	
09:00 – 09:40	***Noora Kotaja***, Germ granule-mediated RNA regulation in haploid male germ cells
09:40 – 10:20	***Petr Svoboda***, Fates of expressed long dsRNA in mammalian cells
10:20 – 10:40	***Ramesh Pillai,*** Mechanism of noncoding RNAs: A piRNA amplifier complex assembled on an RNA clamp
10:40 – 11:10	Coffee break
11:10 – 11:50	***Andreas Werner***, Natural antisense transcripts
11:50 – 12:30	***Donal O'Carroll***, Non-coding solutions to developmental challenges
13:00	Lunch
Afternoon	Half-day excursion
19:00	Dinner
20:00-21:00	Forward Look Plenary Discussion

Wednesday 17 September	
Session 6: RNA regulation in development and differentiation Chair: **Donal O'Carroll**, EMBL, Monterotondo, IT	
09:00 – 09:40	***Sandra Duharcourt***, RNA-mediated programmed genome rearrangements in the model organism Paramecium
09:40 – 10:20	***Nicola Illing*****,** Role of Long non-coding RNAs in Evo-Devo
10:20 – 10:40	***Igor Ulitsky***: Evolution of lincRNA genes in vertebrates
10:40 – 11:10	Coffee break
11:10 – 11:50	***Alena Shkumatava***, Conserved functions of lincRNAs in vertebrate development
11:50 – 12:10	***M. Aydin Akbudak,*** Suppression of Arabidopsis genes by terminator-less transgene constructs
12:10 – 12:30	***Qianwen Sun,*** Antisense lncRNA COOLAIR Connects Transcriptional Shut-down with Chromatin Modification at FLC during Cold-induced Epigenetic Silencing
13:00	Lunch
Session 7: LncRNA and disease II Chair: **Andreas Werner**, Newcastle University, Newcastle, UK	
15:00 – 15:40	***Wlodzimierz Krzyzosiak***, Expanded CUG and CAG repeats in transcripts may serve as sponges for natural and artificial microRNAs
15:40 – 16:00	***Mariangela Morlando***: The crosstalk between linc-MD1, miR-133 and HUR promotes skeletal muscle differentiation
16:00 – 16:20	***Francesco Ghini,*** Uncovering microRNA dynamic degradation in cancer through metabolic labeling
16:20 – 16:50	Coffee break
16:50 – 17:30	**Maïwen Caudron-Herger**, Making and breaking the nucleolus with Alu element-containing RNAs
17:30 – 17:50	***Tetsuro Hirose,*** The common mechanism underlying assembly of the nuclear granules on the architectural noncoding RNAs
17:50 – 18:30	**Plenary discussion:** Everything You Always Wanted to Know About Noncoding RNA -But Were Afraid to Ask
20:00	Get-together & Conference Dinner

Thursday 18 September
Breakfast & Departure