

EUROCORES Programme European Collaborative Research

EuroDYNA - Final Report



What is EUROCORES?

The EUROCORES (European Collaborative Research) Scheme is a flexible framework that promotes excellence in collaborative research and networking. Offered by the European Science Foundation (ESF), EUROCORES tackles scientific questions in and across all disciplines by means of an integrated European or even global effort.

The Programmes encourage and foresee networking and collaboration of researchers to achieve synthesis of scientific results across the programme, to link to related programmes, and to disseminate results. EUROCORES Programmes allow national research funding organisations in Europe and beyond to support top class research in and across all scientific areas, by matching the needs articulated by the scientific community with their strategic priorities. Funding decisions on the projects and the research funding remain with the national research funding organisations, based on international peer review operated by ESF. ESF also provides support for networking the researchers and for the scientific synthesis of research results and their dissemination. Until December 2008 this is supported through a contract with the European Commission under the Sixth Framework Programme (EC Contract no. ERAS-CT-2003-980409). From January 2009 onwards this support will be provided by the national Funding Organisations participating in the Programmes. www.esf.org/eurocores

Programme Structure and Governing Bodies

A EUROCORES Programme is overseen by a *Management Committee* formed by one representative of each of the participating national funding agencies and the EUROCORES Programme Coordinator.

An international, independent *Review Panel* oversees the scientific aspects of the Programme. This includes assessment of outline proposals, selection of externally peer reviewed full proposals and the monitoring of the overall scientific progress of the Programme.

The *Scientific Committee* is formed by the Project Leaders of all funded Collaborative Research Projects (CRPs) and the EUROCORES Programme Coordinator. It is responsible for the networking and dissemination activities within the framework of the EUROCORES Programme.

Final Evaluation

Each EUROCORES Programme is subjected to a final evaluation by the Review Panel. The final evaluation concerns the overall achievements of the Programme as a whole and as such complements the evaluations of individual projects conducted at the national level. The merits of a Programme will be assessed on the basis of the scientific achievements highlighted by the Project Leaders as well as the usefulness and impact of the networking, training and dissemination activities undertaken. To this end, emphasis is placed on the activities which took place between the various CRPs with the aim to assess the added value of the Programme.

For the final evaluation of EuroDYNA, the Review Panel assessed the final reports of the CRPs and in addition attended the final EuroDYNA conference, during which the Project Leaders presented the highlights of their respective CRP. During a subsequent Review Panel meeting, the merits of the Programme and lessons to be learned were discussed.

This summary report is composed of three sections. The first one - EuroDYNA Recommendations - provides an overview of the Programme's achievements and recommendations for future research topics to scientists and funders; the second section highlights EuroDYNA's publications and in the last section, the Governing Bodies of EuroDYNA are presented.

Cover picture:

Spread of human mitotic chromosomes stained for the proteins condensin (red), cohesin (blue) and the centromere specific histone, CENPA (green). Micrograph by Peter Lenart, IMP, Vienna.



EUROCORES Programme

Dynamic Nuclear Architecture and Chromatin Function (EuroDYNA)

EuroDYNA Recommendations



Introduction

EuroDYNA¹, the European Collaborative Research (EUROCORES) Programme whose aim it was to shed light onto the functioning of the nucleus, the control centre of a cell, came to an end in 2008. Over a three-year period the Programme offered scientists the possibility of teaming up with peers and exploring new research directions in a flexible manner.

EuroDYNA accommodated nine thematic Collaborative Research Projects (CRPs), bringing together a total of 40 European research groups. Overall, the Programme combined expertise in different fields such as dynamic chromatin structure and nuclear architecture, regulation of gene expression, RNA processing and transport as well as genome surveillance. The latest technologies in molecular biology and biochemistry were employed together with advanced microscopy, structural analysis and computational approaches in order to gain a deeper insight into how the nucleus operates.

The Programme was funded by two sources: National funding agencies from eight European countries joined forces to provide a total of seven Million Euro to conduct research within the framework of EuroDYNA. This was complemented by a total of 170.000 Euro to support the networking and dissemination activities of funded scientists across CRPs, through the EU's Framework Programme 6.

The Programme's achievements

During its three-year life span, EuroDYNA offered its members a diverse array of networking opportunities, of which the annual conferences were particularly successful. This is illustrated by the fact that 17 new collaborations were formed between scientists across several thematic CRPs, a development that otherwise would not have happened. This is also where the added value of EuroDYNA kicked in as scientists with related yet slightly different research interests got together on a regular basis to present their data and have stimulating debates with the possibility of setting up new research initiatives. This interaction was further developed through short-term visits of students between the CRP labs.

EuroDYNA was also active beyond its boundaries, forging links with EU-networks and other EUROCORES Programmes within the same discipline and across scientific disciplines. For instance, in 2006 and 2007, two brain storming meetings took place involving members of EuroDYNA and SONS² (a EUROCORES Programme in the Physical Sciences) to facilitate cross-disciplinary exchange at the interface of molecular biology and material science/nanoscience. Within the Life Sciences, EuroDYNA members participated in a Mini-Symposium held by the EUROCORES RNAQuality in 2007 and the RNAQuality Training Workshop in 2008.

EuroDYNA held its last community event at The Wellcome Trust Conference Center in Hinxton, UK from 28-31 May 2008. This final conference highlighted the scientific achievements generated during the Programme's lifetime and provided a forum for discussion between EuroDYNA investigators and members of the EuroDYNA Review Panel. On the whole, EuroDYNA has produced numerous high-level publications, including articles in Nature and Cell, and the cross-CRP and cross-EUROCORES interactions have already successfully laid the foundation for joint publications and grant submissions.

Future prospects

EuroDYNA has yielded fruit and in order to build on the Programme's achievements, the EuroDYNA Review Panel and the EuroDYNA investigators discussed future opportunities in the field. Their recommendations, presented on the following pages, are meant to serve both the scientific community and funders alike; the scientific community for the development of new collaborative projects, the submission of a new EUROCORES theme proposal, etc.; the funders to raise awareness with regards to emerging topics to be supported on a national or transnational level across Europe.

Astrid Lunkes EUROCORES Programme Coordinator for EuroDYNA The Programme is composed of nine Collaborative Research Projects (CRPs), with a fairly broad array of topics, focus and size. While the achievements vary between CRPs, the Panel was impressed by the overall output of papers produced during the Programme's 3-year lifetime. The integration of different disciplines was clearly considered an added value of the Programme as was the interaction between different CRPs. Most of these interactions were unforeseen and some have already led to joint CRP publications or grant submissions.

The Panel highlighted the added value of the networking activities, in particular the annual EuroDYNA conferences; these meetings proved to be an effective means to initiate new collaborations across CRPs and to generate new insights. The Panel was also very positive about the training possibilities the Programme offered to young scientists, be it within or across CRPs. They felt that it was important to expose the younger generation to the breadth and interdisciplinary character of the field.

The Panel indicated that the Programme did very well in terms of the dissemination of results to the scientific community at large. On the other hand, they felt that investigators should in general be more implicated in science communication with the lay public through open days/guided tours, newspaper interviews and articles, radio programmes etc..

On the whole, the Review Panel considered EuroDYNA a real success with all CRPs having been very productive in terms of publications, contributions to networking and training, as well as dissemination activities. While a lot of joint publications have already come out, more are to be expected in the future, especially those originating from recently started cross-CRP interactions.

The Panel recommended that EuroDYNA investigators build on the achievements of the Programme by:

1. Continuing to "create opportunities" through the organization of workshops/small conferences which could replace the annual EuroDYNA conference.

2. Linking up with other EUROCORES Programmes where possible (i.e. RNAQuality)

3. Submitting a new EUROCORES Theme proposal. A good concept for a Call today would be to focus on structural aspects, looking at different resolution ranges and encouraging the use of the latest technologies to address longstanding questions around the functioning of the nucleus.

Recommendations for Future Research Topics

When the EuroDYNA Call was published in 2003, the domain of nuclear dynamics was more difficult to study through lack of adequate equipment and technology. New developments and technological advances have since emerged and have opened new possibilities for future research in this domain.

Members of the EuroDYNA Review Panel and EuroDYNA investigators felt that a good concept for a Call in the near future would be to focus on structural aspects, looking at different resolution ranges and encouraging the use of the latest technologies to address longstanding questions around the functioning of the nucleus. Amongst others, investigation of the following subtopics could be envisaged:

- structure of higher order organisation of the nucleus and what controls it
- dynamics of nuclear structures and how these are controlled
- structural analysis of nuclear bodies
- regulation of nuclear processes in time
- three-dimensional control of gene expression: how gene/chromatin positioning affects expression capacity
- quantitative and theoretical approaches to analyse how molecules get together (molecular crowding)
- application of the use of new technologies to the study of chromatin conformation and function
- molecular mapping of gene contacts in the three dimensional nuclear space (using eg "chromosome conformation capture" (3C))
- organization of interphasic chromosomes
- intranuclear transport
- meiosis and oocyte maturation

→ could be developed into an own Call topic since it is highly relevant for research on fertility and genetic diseases.

Networking and Dissemination Activities

Annual Meetings

3rd EuroDYNA Meeting | 28 - 31 May 2008, The Wellcome Trust Conference Centre in Hinxton, UK



EuroDYNA takes lid off the genome

European researchers have made significant progress unravelling how genes are governed and why this sometimes goes wrong in disease. The key lies in the dynamic ever-changing structure of the chromatin, which...

EuroDYNA leaves healthy genomic research ecosystem as legacy Europe's position as a major player in genome research has been boosted by the European Science Foundation's three-year EUROCORES Programme EuroDYNA. As it draws to a close, EuroDYNA is leaving behind a healthy European ecosystem of interacting...

read more at www.esf.org/eurodyna

2nd EuroDYNA Meeting | 12 - 14 October 2006, Gregor Mendel Center in Brno, CZ



EuroDYNA conference magnifies small components for big issues: finding the answer to human disease

At a recent EuroDYNA conference in Brno, Czech Republic, 60 scientists from nine European countries came together to present their research in the field of genetics and cell nucleus architecture...

Finding a cure for cancer: the holy grail of science To find a cure for cancer, the modern-day plague of our society is synonymous to finding the holy grail of science...

read more at www.esf.org/eurodyna

Kick-off meeting | 22 - 24 September 2005, Thun, CH

The EuroDYNA community met for the first time to present their projects and to discuss the needs of the field and future activities; the importance of annual conferences was highlighted on this occasion.

Training

Fourth International Summer School on DNA and Chromosomes | 19 June - 1 July 2006, Corsica, FR

The Summer School aimed to integrate the various biological and physical approaches used to study DNA and chromosomes.

Short-term visits

EuroDYNA labs from different CRPs participated in the exchange of EuroDYNA students and postdocs.

Networking and Dissemination Activities

Topical Workshops

How we can benefit from each other

Impact of stress on the chromatin dynamics and global gene transcription in yeast and mammalian cells | 3 July 2006, Vienna, AU

Two of EuroDYNA's CRPs focusing on stress-induced global changes in gene expression in yeast and mammals respectively, came together to exchange techniques and reagents and to establish collaborations.

Establishing links with other European Projects

Chromatin-associated phosphorylation and dephorsphorylation | 18 - 20 January 2007, Vienna, AU

The workshop was dedicated to combine the systems biology experience of the EU-FP6 QUASI team with the experience of EuroDYNA groups for the development of novel approaches. This contributed to the submission of a joint article and joint grant proposal.

Activities across EUROCORES Programmes

Biologists meet physicists head on in 2006 and 2007

EuroDYNA – SONS brainstorming meetings | 4 December 2007, Lisbon, PT and 27 September 2006, Brussels, BE

ESF organised brainstorming meetings for investigators of the EUROCORES Programmes EuroDYNA and SONS (Self-organised Nanostructures) interested in, and working at the interface of molecular biology and physics. With biology becoming increasingly multidisciplinary ESF works to facilitate cross-disciplinary exchange. The meetings led to the introduction of short-term visits as networking activity for the EUROCORES Scheme at large and the submission of joint proposals.

RNAQuality establishes ties with EuroDYNA

Mini-Symposium on RNA Biogenesis and Quality Control | 18 September 2007, Aarhus, DK

The symposium was initiated to provide an efficient platform for establishing collaborations across CRPs within the RNAQuality Programme, as well as links to laboratories within the EuroDYNA Programme.

Workshop on Structure and function of mRNP | 4-8 August 2008, Aarhus, DK

This training workshop continued to foster links between RNAQuality and EuroDYNA. It involved PIs of both EUROCORES Programmes as lecturers. In addition, students from both the EuroDYNA and the RNAQuality network benefited from the event.

Networking and Dissemination Activities

Dissemination Events

International conference on Telomeres and Genome Stability | 30 August - 3 September 2006, Villars-sur-Ollon, CH

EuroDYNA was highlighted as sponsor of this international event. The visibility was further increased through the talk of EuroDYNA's Chair and poster presentations by EuroDYNA members.

Session on Chromatin and Cell Cycle at the ELSO meeting | 1 September 2007, Dresden, DE

Dissemination from the event:

- At the ELSO meeting in Dresden in September 2007, members of the EuroDYNA community as well as invited speakers from the US and Canada came together for a EuroDYNA-organised session. On this occasion talks focused on the subject "Chromatin and the cell cycle" and the speakers covered everything from plant cells, via Drosophila cells to mammalian cells...
- Coling Logie, Chair of the EuroDYNA Scientific Committee, speaks about scientific achievements through the EUROCORES Programme EuroDYNA and his personal experience at the ELSO Conference, Dresden, Germany in September 2007...

more at www.esf.org/eurodyna

A moment with Colin Logie



Colin Logie

A moment with Colin Logie

In a recent interview, Colin Logie, Chair of the EuroDYNA Scientific Committee, talks about organising the EuroDYNA session at ELSO and about future challenges for the cell biology field and for EuroDYNA.

Why did you choose the topic "Chromatin and the cell cycle" for the EuroDYNA session at ELSO?

Although we know a lot about the cell, DNA and chromatin, we still lack insight into how it functions. To understand how things function you have to put them into context. One thing about life is that it is cell based and one thing about cells is that they are always the product of the cell division of a previous cell. So, to really understand chromosomes we really have to understand how the chromosomes behave in the cell cycle. I think during the session we saw an example of very disparate talks ending up with conclusions about chromosomes which fitted together because they fit the context of the cell cycle as the common denominator.

What, in your opinion, are the challenges in your field?

One of the frontiers of this field is to really see what happens inside living cells. We have done many beautiful experiments in the recent past (by we, I mean the Scientific Community) but what we really need is multi-molecular assembly dynamics data. These things are very difficult to see at the moment and we really need to be able to see them to find out which factors are playing roles of messengers and which ones are playing more structural roles. Essentially it boils down to physically describing the isomerisations that take place in the cell, the DNA and also in the membranes. We also need to find ways of estimating the energetic code of each transaction and of integrating these types of data over multiple length scales from the nanometer to the micrometer. From this we should be able to formulate a mathematical description of biological systems.

What's also a big challenge is our ability to monitor things at the right timescale. We know that molecules function on the level of millions as well as thousands of a second and this spans six maybe even seven orders of magnitude. Right now we don't have good modelling systems to integrate all the data at those different time and length scales and I think that's a major challenge. It's not so complicated to address this. We need durable funding of scientific research; we need to maintain and sometimes also improve career opportunities, support institutes where innovation and originality are encouraged and promote communication amongst scientists. The latter is very important and something that ESF has been doing very well. We need communication between disciplines but also within disciplines.

What can the Scientific Community expect from EuroDYNA as a collaboration?

One field which is moving forward at the moment is nanoscience. By looking in great detail using biophysical methods on single molecules we are actually studying nanomotors which are driven by ATP. The exciting application for this is that maybe one day such motors can be harvested to produce DNA-based machines. EuroDYNA's contribution in this field involves what we are doing in defining the forces that are deployed by these motors. At the moment the physical description of biology is lagging behind but we are getting there now by finding forces, distances and time.

The brains behind EuroDYNA



Niels Galjart



David Shore

EUROCORES is the European Science Foundation's flagship activity. It supports interdisciplinary research in non-traditional areas, thereby opening new horizons in science. With EuroDYNA, one of the EUROCORES Programmes, coming to an end, some of the Project Leaders have shared their experiences from the Programme with us.

"Thanks to EuroDYNA, nine research projects were funded that may otherwise not have been funded. Therefore, European research in the area of nuclear dynamics and architecture has been stimulated. Without EuroDYNA I would not have been able to perform the research I have carried out over the last three years. One aspect of EuroDYNA that I like a lot is the lack of bureaucratic burden compared to other research programmes. Another very important aspect is that the EUROCORES programmes are suggested by the scientists themselves (bottom-up approach). Finally, a great added value is the willingness at ESF to stimulate discussion among scientists, by organizing conferences, workshops and brainstorm meetings. As a EuroDYNA member I have benefited enormously from this valuable resource," said Niels Galjart, Department of Cell Biology and Genetics, Erasmus University, Rotterdam and the Project Leader of "Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation".

There is no doubt that EuroDYNA has achieved some great results and many of these results stem directly from the EUROCORES Programmes' focus on networking and collaboration. David Shore, University of Geneva and the Project Leader of "Environmental stress-induced dynamic modulation of chromatin structure, gene expression and nuclear architecture in yeast" commented, "My project recently entered into collaboration with a lab in Vienna. This wouldn't have happened if it weren't for EuroDYNA. The Vienna group is interested in understanding how arsenic affects cells and of course this has important global health implications. Arsenic is a pollutant in drinking water in many places in the world. Our collaboration began at a EuroDYNA meeting in Brno; we presented a gene we were working on that's involved in growth regulation in yeast cells and also in the cellular response to stress (which is what our project is aimed at understanding) when we were approached by a researcher from the Vienna group. The Vienna researcher noticed that this gene had also come up in his studies as a regulator of the cellular response to arsenic poisoning. As a result, we got together and did some more work which has now led to a manuscript ready for submission".



Pavel Kovarik



René Ketting

EuroDYNA has been successful in generating new and exciting collaborations that have been hugely beneficial to the people involved. Now the scientists are focusing on what happens next. EuroDYNA is finishing but new collaborations have been set up.

"For me personally, the rather generous funding of the networking activities within EuroDYNA turned out to be very useful. Although I still maintain close links with the original members of my Collaborative Research Project (CRP), I have now made several links with members of other CRPs which are also relevant for my future research," said Pavel Kovarik, Vienna Biocenter Institute of Microbiology and Genetics and the Project Leader of "Control of stress and interferon regulated gene expression by transcription factors, histone modification and nuclear compartmentalisation" during a recent interview.

This viewpoint is shared by René Ketting, Hubrecht Laboratory, Netherlands Institute for Developmental Biology and the Project Leader of "Nuclear actions of mRNAs". "I think scientific collaboration is essential. Many of my papers have resulted from collaborations that have been forged through meetings and exchange programmes. In my experience these collaborations are formed *de novo* on very different occasions, but a collective such as EuroDYNA is certainly a good catalyst for such interactions.

EuroDYNA is likely to have established new collaborations that will start to pay off in the future. I therefore think that the impact will not be limited to just the scientific progress that has been made during the funding period but will extend far beyond."

Find full profiles of these and other Project Leaders on the EuroDYNA website at www.esf.org/eurodyna

Cell biology of messenger RNA biogenesis

Abstract

Major events in the life cycle of a messenger RNA (mRNA) include transcription, splicing, 3' end processing, export from the nucleus to the cytoplasm, translation and degradation. These processes are intimately linked through proteins that bind to the mRNA in a specific and coordinated fashion. During the lifetime of an mRNA, the composition of associated protein complexes is under constant change. Through this Network the participating teams wish to study the dynamics of mRNA biogenesis making use of a wide range of multidisciplinary approaches. These include yeast genetics, molecular biology, structural biology, biochemical assays, proteomics, DNA microarrays, RNA interference, and live cell microscopy. The first Work Package of this proposal aims to dissect functional interactions between transcription initiation, RNA polymerase II, quality control and pre-mRNA processing events. The second Work Package is focused on the dynamics of premRNA processing machines. The third Work Package aims to investigate the functional relevance of shuttling between the nucleus and the cytoplasm of proteins involved in mRNA biogenesis.

Partners (FCT, FNU, SNF, NWO)

Prof Maria do Carmo-Fonseca (Project Leader) University of Lisbon, Portugal

Dr Torben Heick Jensen

University of Aarhus, Denmark

Prof Walter Keller University of Basel, Switzerland

Prof Jørgen Kjems University of Aarhus, Denmark

Prof Angela Krämer-Bilbe University of Geneva, Switzerland

Dr Ulrike Kutay Swiss Federal Institute of Technology (ETH), Zurich, Switzerland

Dr Marc Timmers University of Utrecht, The Netherlands

Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation

Abstract

The multi-zinc finger proteins BORIS and CTCF are unique and conserved factors with a role in transcriptional regulation, the organization of chromatin into distinct domains and imprinting. BORIS is expressed in the testis in cells that do not express CTCF. Abnormal upregulation of BORIS, on the other hand, may be linked to tumorigenesis. Thus, while binding to similar sites in the genome, these proteins could have distinct roles. We have generated inducible BORIS and CTCF knock out mice and are generating GFP- (or biotin)-tagged BORIS and CTCF knock in mice. From the inducible knock out mice cell lines have been isolated, which can be transfected with (mutant) multi-zinc finger proteins and/or DNA contructs with particular binding sites. Using these tools we will perform microscopic (live) imaging analysis (group Galjart), affinity purifications of biotin-tagged proteins (groups Galjart and Renkawitz) and structural analysis, like DNA loop formation (group Renkawitz) on the different types of mice, tissues and cells. This proposal aims at understanding the dynamic behaviour of both multi-zinc finger proteins during the cell cycle and the relevance of this behaviour and of these proteins for the maintenance of chromatin structure.

Partners (DFG, NWO)

Dr Niels Galjart (Project Leader) Erasmus University, Rotterdam, The Netherlands

Prof Rainer Renkawitz Justus-Liebig-Universität, Giessen, Germany

Spatio-temporal organisation of genome surveillance in live cells

Abstract

Surveillance of the genome, which is vital for cellular function, cancer avoidance and many aspects of development, is comprised of a series of DNA repair and damage response pathways. Defects in damage surveillance result in severe genetic disorders. The mechanisms of these pathways are understood in varying degrees of detail, and the aim of this proposal is to understand the dynamics of the protein constituents within the cell nucleus before and after different DNA damaging treatments, as well as the inter-relationships between the different pathways. Normal and characterised mutant proteins tagged with GFP and its spectral variants, are either available from the participating laboratories or will be generated as part of the proposal. Motilities of the proteins are measured using variations of fluorescence recovery after photobleaching combined with whole cell or localised irradiation with either UV light or ionising radiation. The complementarity of the partners comes from their expertise in (1) different surveillance pathways and provision of tagged proteins; (2) advanced microscopic techniques; (3) delivery of different types of localised irradiation; (4) computer simulation. Through the integration of the different expertises, unique materials and reagents, and specialised equipment from the participating groups, the proposal forms a comprehensive and multidisciplinary approach to understanding the dynamics of genome surveillance in mammalian cells.

Partners (DFG, FNU, MRC, NWO)

Dr Roland Kanaar (Project Leader) Erasmus University, Rotterdam, The Netherlands

Prof Jiri Bartek Institute of Cancer Biology, Copenhagen, Denmark

Prof Thomas Cremer Ludwig-Maximilians Universität, Munich, Germany

Prof Günther Dollinger Technische Universität Munich, Germany

Dr Anna A. Friedl Ludwig-Maximilians Universität, Munich, Germany

Prof Jan H.J. Hoeijmakers Erasmus University, Rotterdam, The Netherlands

Dr Adriaan Houtsmuller Erasmus University, Rotterdam, The Netherlands

Prof Alan Robert Lehmann University of Sussex, UK

Dr Jiri Lukas Institute of Cancer Biology, Copenhagen, Denmark

Prof Leon H.F. Mullenders University of Leiden, The Netherlands

Dr Wim Vermeulen Erasmus University, Rotterdam, The Netherlands

Nuclear action of miRNAs

Abstract

Double stranded RNA (dsRNA) is potent inducer of gene silencing. The mechanism by which these molecules induce silencing is evolutionary conserved, and represents a very powerful and specific way of gene activity control. One of the intermediates of this silencing process is a short RNA(Srna) molecule that has been named short interfering RNA (siRNA) or micro RNA (miRNA). These molecules act as guides for either an RNA degradation enzyme that is active in the cytosol or a complex that targets translation inhibition. In addition to these cytosolic events, nuclear effects of dsRNA have also been observed. In plants, dsRNA leads to methylation of homologous DNA sequences, and induces transcriptional silencing when promoter DNA is targeted. In yeast, dsRNA mediated processes have been implicated in centromere function. In animals, evidence for such nuclear effects has been obtained as well. For example, phenotypes of C. elegans mutants defective in RNAi suggest an impaired centromere function, and partially overlap with phenotypes associated with defects in the maintenance of silent chromatin states. In this research proposal we aim at a better understanding of the nuclear effects of dsRNA. We will do this by analyzing nuclear dsRNA processing, by identifying nuclear sRNA, by analyzing proteins associating with the nuclear sRNA and by analyzing the effects of nuclear sRNA on chromatin modifications and transcriptional activity.

Partners

(NWO, FWF)

Dr René F. Ketting (Project Leader)

Netherlands Institute for Developmental Biology, Utrecht, The Netherlands

Dr Majori Matzke

Austrian Academy of Sciences, Vienna, Austria

Control of stress and interferon regulated gene expression by transcription factors, histone modification and nuclear compartmentalisation

Abstract

The precise regulation of gene expression in response to extracellular stimuli plays a key role in life and biological diversity. Specific transcription factors, general transcription machinery, histone modifying enzymes, chromatin remodeling complexes, as well as nuclear architecture all have roles in gene transcription. How these individual events are coordinated in time and space, and integrated into appropriate transcriptional responses is a challenging yet unresolved question. We will address this issue using as a model the transcription of stress and interferon regulated genes. Both signalling pathways can be activated by independent stimuli and may therefore be studied separately. However, under physiological conditions, the stress and interferon signalling cascades are often activated simultaneously resulting in enhanced transcriptional responses. This synergism is essential for defense against pathogens and in tumor surveillance. Our studies on the order, location and contribution of stress and interferon-induced changes in chromatin modification and nuclear architecture will improve our understanding of the regulation of gene expression and open up new possibilities to combat diseases, such as cancer and infections. The availability of cells and animals with specific genes of the stress and interferon pathways inactivated will enable us to test the working hypotheses under physiological conditions.

Partners (FWF, GAČR)

Dr Pavel Kovarik (Project Leader) Institute of Microbiology and Genetics, Vienna, Austria

Dr Pavel Hozák

Institute of Molecular Genetics, Prague, Czech Republic

The role of linker histone variants and their phosphorylation in chromatin structure and function

Abstract

The linker histones are known to contribute to the formation and maintenance of higher order chromatin structures but their physiological functions are still largely unknown. They display a complex pattern of variants and recent data suggest that they may have specific roles in epigenetic control of gene expression. The cell cycle dependent phosphorylation of certain serine and threonine residues in the charged tails of the linker histones is most probably of major importance in determining the architecture of chromatin during cell proliferation and differentiation, but the molecular details of this process are very unclear. Aberrant chromatin structure may contribute to malignant transformation and tumour formation. This project aims at elucidating these mechanisms by combining the expertise of Herbert Lindner's laboratory in Linköping. All three research groups have many years' experience in linker histone research and the laboratories complement each other well, offering a large range of methods and techniques in analytical chemistry, structural biology, biophysics, and cytochemistry. Together, these investigations should contribute to increased understanding of epigenetic mechanisms involved in chromatin architecture, regulation of cell growth and differentiation, and in malignant transformation and tumour progression.

Partners (FWF, MRC)

Prof Herbert Lindner (Project Leader) University of Innsbruck, Austria

Prof Jean O. Thomas University of Cambridge, UK

Associated Partner: **Prof Ingemar Rundquist** University of Linköping, Sweden

Chromatin higher order dynamics: a single molecule approach

Abstract

Higher order structure of eukaryotic chromosomes is governed by protein/DNA interactions that mediate the folding of DNA into chromatin fibres. Chromatin fibre structure revolves around nucleosomes, the fundamental units of chromatin. SNF2 ATPases and histone modifying enzymes remodel nucleosomes and have been documented to play key roles in the generation, maintenance and alteration of the epigenetic code during the cell cycle and during ontogeny. We propose to study the influence of chromatin remodelling factors on the physical properties of chromatin fibres. To this end, fully recombinant model polynucleosomal arrays suited for physico-chemical characterisation will be generated. Second, defined prototypic chromatin remodelling activities will be purified in preparative quantities. Last, state-of-the-art single molecule magnetic tweezers and time-lapse Atomic Force Microscopy will be employed to rigorously investigate the physical properties and dynamics of chromatin higher order structural transitions catalysed by chromatin remodellers. With this combined multidisciplinary approach we expect to elucidate nucleosome mediated higher order chromatin structural transitions with an unsurpassed degree of resolution.

Partners

(NWO, DFG)

Dr Colin Logie (Project Leader) University of Nijmegen, The Netherlands

Dr Alexander Brehm Philipps-Universität Marburg, Germany

Dr John van Noort University of Leiden, The Netherlands

The control of chromosome structure by cohesion/ condensin complexes

Abstract

All organisms possess sophisticated mechanisms to respond to environmental stress. The robust transcriptional response to osmostress in yeast works through a conserved MAP kinase signaling pathway that leads to a major reprogramming of the cell's transcriptional state. The MAPK Hog1 acts directly at a large number of promoters to induce expression of osmostress-reponse genes, while a less well understood mechanism(s) causes coordinate down-regulation of growth-related genes, such as those encoding ribosomal proteins. Our primary aim will be to characterize and elucidate mechanisms underlying the dynamic changes in chromatin structure and modification states that accompany both the induction and down-regulation of genes following osmostress, using chromatin immunoprecipitation as our standard experimental tool. We will also employ high throughput genetic screens and advanced biochemical methods to understand how the chromatin remodeling / modification machinery interacts with global and gene-specific transcription factors and how these interactions promote dramatic changes in transcription rates. Finally, advanced cell biological methods (e.g. FRAP) will be used to characterize the dynamic nuclear trafficking and chromatin association of specific transcription factors following osmostress. These studies should yield new and important insights into mechanisms by which chromatin modification is linked to highly dynamic changes in transcription and overall nuclear architecture.

Partners (DFG, FWF, MRC)

Dr Jan-Michael Peters (Project Leader) IMP, Vienna, Austria

Prof Terence David Allen Paterson Institute for Cancer Research, Manchester, UK

Dr Roland Eils German Cancer Research Centre, Heidelberg, Germany

Dr Jan Ellenberg EMBL, Heidelberg, Germany

Dr Jan Löwe Medical Research Council, Cambridge, UK

Prof Kim Nasmyth University of Oxford, UK

Environmental stress-induced dynamic modulation of chromatin structure, gene expression and nuclear architecture in yeast

Abstract

All organisms possess sophisticated mechanisms to respond to environmental stress. The robust transcriptional response to osmostress in yeast works through a conserved MAP kinase signaling pathway that leads to a major reprogramming of the cell's transcriptional state. The MAPK Hog1 acts directly at a large number of promoters to induce expression of osmostress-reponse genes, while a less well understood mechanism(s) causes coordinate down-regulation of growth-related genes, such as those encoding ribosomal proteins. Our primary aim will be to characterize and elucidate mechanisms underlying the dynamic changes in chromatin structure and modification states that accompany both the induction and down-regulation of genes following osmostress, using chromatin immunoprecipitation as our standard experimental tool. We will also employ high throughput genetic screens and advanced biochemical methods to understand how the chromatin remodeling / modification machinery interacts with global and gene-specific transcription factors and how these interactions promote dramatic changes in transcription rates. Finally, advanced cell biological methods (e.g. FRAP) will be used to characterize the dynamic nuclear trafficking and chromatin association of specific transcription factors following osmostress. These studies should yield new and important insights into mechanisms by which chromatin modification is linked to highly dynamic changes in transcription and overall nuclear architecture.

Partners (SNF, FWF)

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2008

CRP - Cell biology of messenger RNA biogenesis

Thomsen R., Saguez C., Nasser T. and Jensen T.H.: General, rapid and transcription-dependent disassembly of the nucleolus in *S. cerevisiae* mRNA export mutants. RNA (2008), Feb 7; [Epub ahead of print].

Damgaard C.K., Kahns S., Lykke-Andersen S., Nielsen A.L., Jensen T.H. and Kjems J.: A 5' splice site enhances the recruitment of basal transcription initiation factors *in vivo*. Molecular Cell (2008) 271-278.

Jensen M.M., Christensen M.S., Bonven B. and Jensen T.H. : Requirements for chromatin reassembly during transcriptional downregulation of a heat shock gene in *S. cerevisiae*. FEBS (2008), 275(11):2956-64.

Kammler S., Lykke-Andersen S. and Jensen T.H.: The RNA exosome component hRrp6 is a target for 5-fluorouracil in human cells. Mol. Cancer Res. (2008), *accepted*

Assenholt, J., Mouaikel, J., Libri, D. and Jensen, T.H.: Exonucleolysis is required for all aspects of nuclear mRNA quality control in yeast THO mutants. RNA (2008), 14(11):2305-13

Saguez C., Schmid M., Olesen J.R., Ghazy M., Poulsen M.B., Nasser T., Moore C. and Jensen T.H.: Nuclear mRNA surveillance in THO/sub2 mutants is triggered by inefficient polyadenylation. Cell (2008), 31(1):91-103.

Rougemaille M., Kisseleva-Romanova E., Gudipati R.K., Lemoine S., Blugeon C., Boulay J., Jensen T.H., Devaux F. and Libri D.: Non-productive docking of mRNPs to the nucleopore in THO/*sub2* mutants. Cell (2008), 135(2):308-21.

Andersen K.R., Jensen T.H. and Brodersen D.E.: Take the "A" tail - quality control of ribosomal and transfer RNA. BBA (2008), 1779(9):532-7.

Schmid M. and Jensen T.H.: Quality Control of mRNP in the nucleus. Chromosoma (2008), 117(5):419-29.

Rahbek, U.L., Howard. K.A., Oupicky, D., Dong,M., Nielsen, A.F., Raarup, M-R., Besenbacher,F., Kjems, J.: Intracellular siRNA and precursor miRNA trafficking using Bioresponsive Copolypeptides. J. Gene Med.. 10:81-93. (2008).

Damgaard, C.K., Lykke-Andersen, S., Kahns, S., Nielsen, A.L., Jensen, T.H. and Kjems, J.: A proximal 5' splice site stimulates transcriptional initiation in vivo. Molecular Cell 29:271-78 (2008).

Torarinsson, E., Yao, Z., Wiklund E.D., Bramsen, J.B., Hansen, C., Kjems, J., Tommerup, N., Ruzzo, W.L.and Gorodkin, J.: Comparative genomics beyond sequence based alignments: RNA structures in the ENCODE regions. Genome Research. 2008, 18(2):242-51.

Howard, K.H., Paludan, S.R., Behlke, M.A., Besenbacher, F., Deleuran, B. and Kjems, J. : Chitosan/siRNA nanoparticle-mediated TNFα knockdown in peritoneal macrophages for anti-inflammatory treatment in a murine arthritis model. Mol.Therapy, 2008, *accepted*

CRP - Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation

Heath H, de Almeida CR, Sleutels F, Dingjan G, van de Nobelen S, Jonkers I, Ling KW, Gribnau J, Renkawitz R, Grosveld F, Hendriks RW, Galjart N. (2008). CTCF regulates cell cycle progression of alphabeta T cells in the thymus.EMBO J. 2008, 27(21):2839-50.

CRP - Spatio-temporal organisation of genome surveillance in live cells

E.A. Maltseva, N.I. Rechkunova, I.O. Petruseva, W. Vermeulen, O.D. Schärer and O.I. Lavrik. Crosslinking of nucleotide excision repair proteins with DNA containing photoreactive damages. Bioorganic Chemistry (2008) *in press.*

C. Dinant, M. van Royen, W. Vermeulen and A.B. Houtsmuller. Measuring Fluorescence Resonance Energy Transfer in Living Cells from GFP to YFP with Spectral Imaging and Quantitative Acceptor Photobleaching. J. of Microscopy (2008) *in press*.

D. Hoogstraten, S.Bergink, V. Verbiest, M. Luijsterburg, B. Geverts, A. Raams, C. Dinant, J. H. J. Hoeijmakers, W. Vermeulen (corresponding author) and A.B. Houtsmuller. DNA-damage sensing by xeroderma pigmentosum group C in living cells. J. of Cell Sci. (2008) *in press.*

Greubel C, Hable V, Drexler GA, Hauptner A, Dietzel S, Strickfaden H, Baur I, Krücken R, Cremer T, Friedl AA, Dollinger G (2008) Quantitative Analysis of DNA Damage Response Factors after Sequential Ion Microirradiation. Radiat Env Biophys, 2008, 47(4):415-22

Greubel C, Hable V, Drexler GA, Hauptner A, Dietzel S, Strickfaden H, Baur I, Krücken R, Cremer T, Dollinger G, Friedl AA (2008) Competition effect in DNA damage response. Radiat Env Biophys 2008, 47(4):423-9.

Fousteri M, Mullenders LH. Transcription-coupled nucleotide excision repair in mammalian cells: molecular mechanisms and biological effects. Cell Res, 2008 18 (1), 73-84.

CRP - Nuclear action of miRNAs

Kanno T, Bucher E, Daxinger L, Huettel B, Böhmdorfer G, Gregor W, Kreil D, Matzke M, Matzke AJM (2008) An SMC hinge domain containing protein is required for RNA-directed DNA methylation. Nature Genetics, *in press.*

CRP - Control of stress and interferon regulated gene expression by transcription factors, histone modification and nuclear compartmentalisation

Kovarik P, Sauer I, Schaljo B. 2008 Molecular mechanisms of the anti-inflammatory functions of interferons. Immunobiology. 212(9-10):895-901.

Iwona Sadzak, Melanie Schiff, Irene Gattermeier, Reingard Glinitzer, Ines Sauer, Armin Saalmüller, Edward Yang, Barbara Schaljo and Pavel Kovarik . Recruitment of Stat1 to chromatin is required for interferoninduced serine phosphorylation of Stat1 transactivation domain. PNAS 2008, *accepted*

CRP - The role of linker histone variants and their phosphorylation in chromatin structure and function

Lindner HH: Analysis of histones, histone variants, and their posttranslationally modified forms. Electrophoresis 2008, 29(12):2516-32.

Gréen A, Sarg B, Genheden U, Koutzamani E, Lindner HH & Rundquist I (2008) Histone H1 dephosphorylation is not a general feature in early apoptosis. Biochemistry 2008, 47(28):7539-47.

Sarg B., Chwatal C., Talasz H. and Lindner HH.: Testis specific linker histone H1t is multiple phosphorylated during spermatogenesis: Identification of the phosphorylation sites J Biol Chem. 2008 Nov 29. [Epub ahead of print]

Cato L., Stott K., Watson M and Thomas J.O.: The interaction of HMGB1 and linker histones occurs through their acidic and basic tails. J Mol Biol. 2008, 31;384(5):1262-72.

CRP - Chromatin higher order dynamics: a single molecule approach

Murawska M, Kunert N, van Vugt J, Längst G, Kremmer E, Logie C, Brehm A. dCHD3, a novel ATPdependent chromatin remodeler associated with sites of active transcription. Mol Cell Biol. (2008) 8:2745-57.

Kruithof M, Chien F, de Jager M, van Noort J. Subpiconewton dynamic force spectroscopy using magnetic tweezers. Biophys J. (2008) 94(6):2343-8.

CRP - The control of chromosome structure by cohesion/ condensin complexes

Wendt; K.S., Yoshida K., Itoh T., Bando M., Koch B., Schirghuber E., Tsutsumi S., Nagae G., Ishihara K., Mishiro T., Yahata K., Imamoto F., Aburatani H., Nakao M., Imamoto N., Maeshima K., Shirahige K. and Peters J.-M. (2008). Cohesin mediates transcriptional insulation by CTCF. *Nature*, 451,796-801.

Harder N, Eils R, and Rohr K (2008) Automated classification of mitotic phenotypes of human cells using fluorescent proteins, Methods Cell Biology, 85, 539-554

CRP - Environmental stress-induced dynamic modulation of chromatin structure, gene expression and nuclear architecture in yeast

Kraft, C., Deplazes, A., Sohrmann, M, and Peter, M. (2008) "Mature ribosomes are selectively degraded on starvation by an autophagy pathway requiring the Ubp3p/Bre5p ubiquitin protease". *Nature Cell Biology, in press.*

Hosiner, D., Lempiäinen, H., Reiter, W., Urban, J., Loewith, R.L., Ammerer, G., Rudolf Schweyen, R., Shore, D. and Schüller, C. (2008) Arsenic Toxicity to Saccharomyces cerevisiae Is a Consequence of Inhibition of the TORC1 Kinase Combined with a Chronic Stress Response. Mol Biol Cell. *Accepted*

2007

CRP - Cell biology of messenger RNA biogenesis

Abruzzi K., Denome S., Olesen J.R., Haaning L.L., Assenholt J., Jensen T.H. and Rosbash M.: A novel plasmid-based microarray screen identifies suppressors of $\Delta rrp6$ in *Saccharomyces cerevisiae*. Mol. Cell. Biol. (2007) 1044-1055.

Blechingberg J., Holm I.E., Nielsen K.B., Jensen T.H., Jorgensen A.L., Nielsen A.L. Identification and characterization of GFAPkappa, a novel glial fibrillary acidic protein isoform. Glia. (2007) 497-507.

Rougemaille M., Olesen J.R., Thomsen R., Seraphin B., Libri D. and Jensen T.H.: Dissecting mechanisms of mRNA surveillance in THO/sub2 complex mutants. EMBO J. (2007) 2317-2326.

Blechingberg J., Lykke-Andersen S., Jensen T.H., Jørgensen A.L. and Nielsen A.L. Regulatory Mechanisms for 3'-end Alternative Splicing and Polyadenylation of the Glial Fibrillary Acidic Protein, GFAP, Transcript. Nucleic Acid Res. (2007) 7636-7650.

Lykke-Andersen S. and Jensen T.H.: Overlapping pathways dictate termination of RNA polymerase II transcription. Biochimie. (2007) 1177-1182.

Liu, X., Howard, K.A., Dong, M., Kjems, J.: Chitosan/siRNA nanoparticles for gene silencing: formulation and characterization. Biomaterials 28:1280-8 (2007).

Nielsen K.B., Sørensen, S, Cartegni, L., Corydon, T.J., Doktor, T.K., Schroeder, L.D., Reinert, T.S.,, Elpeleg, O., Krainer, A.R., Gregersen, N., Kjems, J. and Andresen B.S.: Seemingly Neutral polymorphic variants may confer immunity to splicing inactivating mutations - a synonymous SNP in exon 5 of MCAD protects from deleterous mutations in the flanking exon splicing enhancer. Am. Jour. of Hum. Gen. 80:416-32 (2007)

Novotny, G., Sonne, S.B., Nielsen, J.E., Jonstrup, S.P., Hansen, M.A., Skakkebaek, N., Meyts, E.R., Kjems, J and Leffers, H.: Translational repression of E2F1 mRNA in carcinoma in situ and normal testis correlates with expression of the miR-17-92 cluster. Cell Death Differ. 14:879-82 (2007).

Andersen ES, Lind-Thomsen A, Knudsen B, Kristensen SE, Havgaard JH, Larsen N, Sestoft P, Kjems J, Gorodkin J. Detection and editing of structural groups in RNA families. RNA 13:1850-9. (2007)

Jakobsen, MR, Haasnoot, J, Wengel, J, Berkhout, B. and Kjems, J Efficient inhibition of HIV-1 expression by LNA modified antisense oligonucleotides and DNAzymes targeted to functionally selected binding sites" Retrovirology. 4:29 (2007).

Andersen, M.O., Howard, K.A., Paludan, S.R., Besenbacher, F., Kjems, J.: Delivery of siRNA from lyophilised polymeric surfaces. Biomaterials. 29:506-12. (2007)

Howard, K.A., Kjems, J.: Polycation-based Nanoparticle Delivery for Improved RNAi Therapeutics. Expert Opin Biol Ther. 7:1811-22 (2007)

Lykke-Andersen, S, Piñol-Roma, S. and Kjems, J.: The human ADAR1 transcripts contain an alternative retained intron within a region that functions both as a 5'UTR and an ORF. 13:1732-44. (2007)

Bramsen, J.B., Lauersen, M.B., Damgaard, C.K., Willsen, S.L., Wengel, J., and Kjems, J.: Improved silencing properties of small interfering RNAs with segmented sense strand. Nucleic Acids Res. 35:5886-97 (2007).

Klaas W. Mulder, Akiko Inagaki, E. Cameroni, Florence Mousson, Sebastiaan G. Winkler, C. De Virgilio C, Martine A. Collart, H.Th.Marc Timmers (2007) Modulation of Ubc4p/Ubc5p-mediated stress responses by the RING-finger-dependent ubiquitin-protein ligase Not4p in Saccharomyces cerevisiae. Genetics 176, 181-192.

Michiel Vermeulen, Klaas W. Mulder, Sergei Denissov, W.W.M.Pim Pijnappel, Frederik M.A. van Schaik, Radhika A. Warrier, Marijke P.A. Baltissen, Henk G. Stunnenberg, Matthias Mann and H.Th.Marc Timmers (2007) Selective anchoring of TFIID to nucleosomes by trimethylation of histone H3 lysine four. Cell 131, 58-69.

Klaas W. Mulder, Arjan B. Brenkman, Akiko Inagaki, Niels J.F. van den Broek and H.Th.Marc Timmers (2007) Regulation of histone H3K4 tri-methylation and PAF complex recruitment by the Ccr4-Not complex. Nucleic Acids Res. 35, 2428-2439.

Florence Mousson, Annemieke Kolkman, W.W.M. Pim Pijnappel, H.Th.Marc Timmers and Albert J.R. Heck (2007) Quantitative proteomics reveals regulation of dynamic components within TATA-binding protein (TBP) transcription complex. Mol. Cell Prot. - in press.

Braga, J., McNally, J.G., Carmo-Fonseca, M. (2007) A reaction-diffusion model to study RNA motion by quantitative fluorescence recovery after photobleaching. Biophys. J. 92(8):2694-703.

Carneiro, T., Carvalho, C., Braga, J., Rino, J., Milligan, L., Tollervey, D., Carmo-Fonseca, M. (2007) Depletion of the yeast nuclear exosome subunit Rrp6 results in accumulation of polyadenylated RNAs in a discrete domain within the nucleolus. Mol Cell Biol 27(11):4157-65.

Rino, J., Carvalho, T., Braga, J., Desterro, J.M., Lührmann, R., Carmo-Fonseca, M. (2007) A stochastic view of spliceosome assembly and recycling in the nucleus. PLoS Comput Biol 10: 2019-31.

Custódio, N., Vivo, M., Antoniou, M., Carmo-Fonseca, M. (2007) Splicing and cleavage independent requirement of RNA polymerase II CTD for mRNA release from the transcription site. J Cell Biol 179(2):199-207.

CRP - Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation

Mohan, M., Bartkuhn, M., Herold, M., Philippen, A., Heinl, N., Bardenhagen, I., Leers, J., White, R.A., Renkawitz-Pohl, R., Saumweber, H., and Renkawitz, R. (2007). The Drosophila insulator proteins CTCF and CP190 link enhancer blocking to body patterning. The EMBO Journal 26, 4203-4214.

Holohan, E.E., Kwong, C., Adryan, B., Bartkuhn, M., Herold, M., Renkawitz, R., Russell, S., and White, R. (2007). CTCF Genomic Binding Sites in Drosophila and the Organisation of the Bithorax Complex. PLoS genetics 3, e112.

Rathke, C., Baarends, W.M., Jayaramaiah-Raja, S., Bartkuhn, M., Renkawitz, R., and Renkawitz-Pohl, R. (2007). Transition from a nucleosome-based to a protamine-based chromatin configuration during spermiogenesis in Drosophila. Journal of cell science 120, 1689-1700.

CRP - Spatio-temporal organisation of genome surveillance in live cells

N.G. Jaspers, A. Raams, M.C. Silengo, N. Wijgers, L.J. Niedernhofer, A.R. Robinson, G. Giglia-Mari, D. Hoogstraten, W.J. Kleijer, J.H. Hoeijmakers and W. Vermeulen First case of human ERCC1 deficiency has cerebro-oculofacio-skeletal syndrome with a mild defect in nucleotide excision repair and severe developmental failure., Am J Hum Genet 80 (2007); 457-466.

S. Bergink, N.G. Jaspers and W. Vermeulen Regulation of UV-induced DNA damage response by ubiquitylation, DNA Repair 6 (2007); 1231-1242.

M.S. Luijsterburg MS, J. Goedhart, J. Moser, H. Kool, B. Geverts, A.B. Houtsmuller, L.H. Mullenders, W. Vermeulen, R. van Driel. Dynamic in vivo interaction of DDB2 E3 ubiquitin ligase with UV-damaged DNA is independent of damage-recognition protein XPC. J. Cell Sci. 120 (2007); 2706-2716.

C. Dinant, M. de Jager, J. Essers, W.A. van Cappellen, R. Kanaar, A.B. Houtsmuller, W. Vermeulen. Activation of multiple DNA repair pathways by sub-nuclear damage induction methods. J. Cell Sci. 120 (2007); 2731-2740.

F. Nicassio, N. Corrado, J.H. Vissers, L.B. Areces, S. Bergink, J.A. Marteijn, B. Geverts, A.B. Houtsmuller, W. Vermeulen, P.P. Di Fiore, E. Citterio. Human USP3 is a chromatin modifier required for S phase progression and genome stability. Curr. Biol. 17 (2007); 1972-1977.

Löffler, H., Rebacz, B., Ho, A. D., Lukas, J., Bartek, J., and Krämer A. Chk1-dependent regulation of Cdc25B activity functions to coordinate mitotic events. Cell Cycle, 5, 2543-2547 (2007).

Löffler, H., Bochtler, T., Fritz, B., Tews, B., Ho, A. D., Lukas, J., Bartek, J., and Krämer, A. DNA dmageinduced accumulation of centrosomal Chk1 contributes to its checkpoint function. Cell Cycle 6, 2541-2548 (2007).

Bartek J., and Lukas, J. DNA damage checkpoints: From initiation to recovery or adaptation. Curr. Opin. Cell Biol., 19, 238-245 (2007).

van der Wees C, Jansen J, Vrieling H, van der Laarse A, Van Zeeland A, Mullenders L. Nucleotide excision repair in differentiated cells. Mutat Res, 2007 Jan 3, 614 (1-2), 16-23.

Jill Moser, Hanneke Kool, Saskia Lagerwerf, Keith Caldecott, Leon H.F. Mullenders, Maria I. Fousteri. Gap filling in mammalian nucleotide excision repair involves DNA polymerase δ /XRCC1-DNA Ligase IIIa and an S-phase dependent utilisation of DNA polymerase ϵ /DNA ligase I. Mol Cell, 2007 6, 1642-1650.

Martijn S. Luijsterburg , Joachim Goedhart , Jill Moser, Hanneke Kool , Bart Geverts , Adriaan B. Houtsmuller, Leon H.F. Mullenders, Wim Vermeulen and Roel van Driel. DDB2 E3 ubiquitin ligase interacts with UV-damaged DNA independently of damage recognition protein XPC in living cells. J Cell Sci, 2007 120, 2706-2716.

Vrouwe MG, Elghalbzouri-Maghrani E, Meijers M, Schouten P, Godthelp BC, Bhuiyan ZA, Redeker EJ, Mannens MM, Mullenders LH, Pastink A, Darroudi F. Increased DNA damage sensitivity of Cornelia de Lange syndrome cells: evidence for impaired recombinational repair. Hum Mol Genet , 2007 16, 1478-87.

Lehmann AR, Niimi A, Ogi T, Brown S, Sabbioneda S, Wing JF, Kannouche PL, Green CM. Translesion synthesis: Y-family polymerases and the polymerase switch. DNA Repair (Amst). 2007, 6:891-9.

Mailand, N., Bekker-Jensen, S., Faustrup, H., Melander, F., Bartek, J., Lukas, C., and Lukas, J. The RNF8 ubiquitin ligase promotes assembly of repair proteins at the DNA damage-modified chromatin. Cell, 131, 887-900 (2007).

Bekker-Jensen, S., Fugger, K., Danielsen, J. R., Gromova, I., Celis, J., Bartek, J., Lukas, J., and Mailand, N. Human Xip1 (C2orf13) is a novel regulator of cellular responses to DNA strand breaks. J. Biol. Chem., 282, 19638-19643 (2007).

Melander, F., Bekker-Jensen, S., Falck, J., Bartek, J., Mailand, N., and Lukas, J. Phosphorylation of MDC1 by casein kinase 2 mediates retention of NBS1 at the DNA damage-modified chromatin. J. Cell Biol., in press (2007).

CRP - Nuclear action of miRNAs

Houwing S., Kamminga L.M., Berezikov E., Cronembold D., Girard A., van den Elst H., Filippov D.V., Blaser H., Raz E., Moens C.B., Plasterk R.H., Hannon G.J., Draper B.W., Ketting R.F. (2007) A role for Piwi and piRNAs in germ cell maintenance and transposon silencing in Zebrafish.Cell 29:69-82

Huettel B, Kanno T, Daxinger L, Bucher E, van der Winden J, Matzke AJM, Matzke M (2007) RNA-directed DNA methylation mediated by DRD1 and Pol IVb: a versatile pathway for transcriptional gene silencing in plants. Biochim Biophys Acta 1769: 358-374.

Matzke M, Kanno T, Huettel B, Daxinger L, Matzke AJM (2007a) Targets of RNA-directed DNA methylation. Curr Opin Plant Biol 10: 512-519.

Tops, B.B., Plasterk, R.H.A. and Ketting, R.F. (2007) C. elegans Argonaute proteins ALG-1 and ALG-2; almost identical yet different. Cold Spring Harb Symp Quant Biol. 71:189-94

Matzke M, Kanno T, Huettel B, Daxinger L, Matzke AJM (2007b) RNA-directed DNA methylation and Pol IVb in Arabidopsis. Cold Spring Harb Symp Quant Biol. 71: 449-459.

Ketting RF (2007): A Dead End for MicroRNAs.Cell.131(7):1226-7.

CRP - Control of stress and interferon regulated gene expression by transcription factors, histone modification and nuclear compartmentalisation

Vlasakova, J., Novakova, Z., Rossmeislova, L., Kahle, M., Hozak, P. and Hodny, Z. (2007) Histone deacetylase inhibitors suppress IFN{alpha}-induced up-regulation of promyelocytic leukemia protein. Blood, 109, 1373-1380.

Janderova-Rossmeislova, L., Novakova, Z., Vlasakova, J., Philimonenko, V., Hozak, P. and Hodny, Z. (2007) PML protein association with specific nucleolar structures differs in normal, tumor and senescent human cells. Journal of Structural Biology, 159, 56-70.

Piskacek, S., Gregor, M., Nemethova, M., Grabner, M., Kovarik, P., and Piskacek, M. (2007) Nine-amino-acid transactivation domain: Establishment and prediction utilities. Genomics, 89:756-768.

CRP - Chromatin higher order dynamics: a single molecule approach

Koopmans WJ, Brehm A, Logie C, Schmidt T, van Noort J. Single-pair FRET microscopy reveals mononucleosome dynamics. J Fluoresc. (2007) 6:785-95.

Campsteijn C, Collin-Wijnands AMJ, Logie C. Reverse Genetic Analysis of the Yeast RSC Chromatin Remodeler Reveals a Role for RSC3 and SNF5 Homolog 1 in Ploidy Maintenance. PLoS Genet. (2007) 3(6): e92

van Vugt JJ, Ranes M, Campsteijn C, Logie C. The ins and outs of ATP-dependent chromatin remodeling in budding yeast: biophysical and proteomic perspectives. Biochim Biophys Acta. (2007) 1769(3):153-71.

CRP - The control of chromosome structure by cohesion/ condensin complexes

Lipp, J.J., Hirota, T., Poser, I. and Peters, J.-M. (2007). Aurora B controls the association of condensin I but not condensin II with mitotic chromosomes. J. Cell Sci. 120, 1245-1255.

Schmitz, J. Watrin, E., Lénárt, P., Mechtler, K., and Peters, J.-M. (2007). Sororin is required for stable binding of cohesin to chromatin and for sister chromatid cohesion in interphase. Curr. Biol. 17, 630-636.

Nakajima, M., Kumada, K., Hatakeyama, K., Noda, T., Peters, J.-M. and Hirota, T. (2007). The complete removal of cohesin from chromosome arms depends on separase. J. Cell Sci. 120, 4188-4196.

Koch, B. Kueng, S., Ruckenbauer, C. and Peters, J.-M. (2007). The Suv39h-HP1 histone methylation pathway is dispensable for enrichment and mitotic protection of cohesin at centromeres in mammalian cells. Chromosoma, 117, 199-210

Schuh M, Ellenberg J. (2007). Self-organization of MTOCs replaces centrosome function during acentrosomal spindle assembly in live mouse oocytes. Cell. 130, 484-498.

Daigle N, Ellenberg J. (2007) LambdaN-GFP: an RNA reporter system for live-cell imaging. Nat Methods. 4(8):633-636.

Mora-Bermúdez F, Gerlich D, Ellenberg J. (2007) Maximal chromosome compaction occurs by axial shortening in anaphase and depends on Aurora kinase. Nat Cell Biol. 9(7):822-831.

Watrin, E. and Peters, J..M. (2007). Molecular biology. How and when the genome sticks together. Science 317, 209-210. (Review)

Mora-Bermúdez F, Ellenberg J. (2007) Measuring structural dynamics of chromosomes in living cells by fluorescence microscopy. Methods 41(2):158-167.

CRP - Environmental stress-induced dynamic modulation of chromatin structure, gene expression and nuclear architecture in yeast

Zapater M, Sohrmann M, Peter M, Posas F, de Nadal, E. (2007) "Selective requirement for SAGA in Hog1mediated gene expression depending on the severity of the external osmostress conditions". *Mol Cell Biol.* 27:3900-10.

2006

CRP - Cell biology of messenger RNA biogenesis

Kyburz, A., A. Friedlein, H. Langen, and W. Keller: Direct interactions between subunits of CPSF and the U2 snRNP contribute to the coupling of pre-mRNA 3' end processing and splicing. Mol. Cell 23, 195-205 (2006).

Mansfeld, J., Güttinger, S., Hawryluk-Gara, L.A., Mall, M., Galy, V., Haselmann, U., Mühlhäusser P., Wozniak, R.W., Mattaj, I.W.*, Kutay, U. and Antonin, W. The conserved transmembrane nucleoporin NDC1 is required for nuclear pore complex assembly in vertebrate cells. Mol. Cell (2006) 22(1): 93-103.

Midtgaard, S.F.; Assenholdt, J.; Jonstrup A.T.; Van, L.B.; Jensen, T.H. and Brodersen, D.: Structure and substrate specificity of the yeast nuclear exosome component, Rrp6p. PNAS (2006) 11898-11903.

Kanamori, N.; Madsen, L.H.; Radutoiu, S.; Frantescu, M.; Quistgaard, E.M.H.; Miwa, H.; Downie, J.A.; James, E.K.; Felle, H.H.; Haaning, L.L.; Jensen, T.H.; Sato, S.; Nakamura, Y.; Tabata, S.; Sandal, N. and Stougaard, J.: A nucleoporin is required for induction of Ca²⁺ spiking in legume nodule development and essential for rhizobial and fungal symbiosis. PNAS (2006) 359-364.

Zhelkovsky, A.; Tacahashi, Y.; Nasser, T., He, X.; Sterzer, U.; Jensen, T.H.; Domdey, H. and Moore, C.: The role of the Brr5/Ysh1 C-terminal domain and its homolog, Syc1, in mRNA 3' end processing in *Saccharomyces cerevisiae.* RNA (2006) 435-445.

Paca-Uccaralertkun S, Damgaard CK, Auewarakul P, Thitithanyanont A, Suphaphiphat P, Essex M, Kjems J, Lee TH. The Effect of a Single Nucleotide Substitution in the Splicing Silencer in the tat/rev Intron on HIV Type 1 Envelope Expression. AIDS Res Hum Retroviruses. 22:76-82 (2006).

Lützelberger, M., Simathamby, T, Das, A., Berkhout, B And Kjems, J. A novel non-coding exon in the gag-pol gene is required for HIV-1 RNA stability. 281(27):18644-51., J. Bio. Chem. (2006).

Howard, K.A. Lui, X., C.K. Damgaard, C..K., Rahbek, U.L., Andersen, M.Ø., Hovgaard, M.B., A. Schmitz, A., Zoffmann, S.,1, Nyengaard, J., F. Besenbacher, F. 1 and Kjems, J.: RNA Interference in Vitro and in Vivo Using a Novel Chitosan/siRNA Nanoparticle System. Mol Ther. Mol Ther. 14:476-84 (2006).

Jonstrup, S.P., Kock, J., Kjems, J. (2006) A miRNA detection system based on padlock probes and rolling circle amplification. RNA 12(9):1747-52(2006).

Kammler, S., Otte, M., Hauber, I., Kjems, J., Hauber, J., and Schaal, H.: The strength of the HIV-1 3' splice sites affects Rev function. Retrovirology 3:89. (2006).

G.Sebastiaan Winkler, Klaas W. Mulder, Vivian J. Bardwell, Eric Kalkhoven and H.Th.Marc Timmers (2006) Human Ccr4-Not complex is a ligand-dependent repressor of nuclear receptor-mediated transcription. EMBO J. 25, 3089-3099.

Custódio N, Antoniou M, Carmo-Fonseca M (2006) Abundance of the largest subunit of RNA polymerase II in the nucleus is regulated by nucleo-cytoplasmic shuttling. Exp Cell Res. 312: 2557-67

Kozlova N, Braga J, Lundgren J, Rino, J, Young, P, Carmo-Fonseca, M. (2006) Studies on the role of NonA in mRNA biogenesis. Exp Cell Res. 312: 2619-30.

Gama-Carvalho, M., Barbosa-Morais, N.L., Brodsky, A.S., Silver, P.A., Carmo-Fonseca, M (2006). Genome wide identification of functionally distinct subsets of cellular mRNAs associated with two nucleocytoplasmic-shuttling mammalian splicing factors. Genome Biol. 7(11):R113

CRP - Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation

Wesoly, J., Agarwal, S., Sigurdsson, S., Bussen, W., Van Komen, S., Qin, J., van Steeg, H., van Benthem, J., Wassenaar, E., Baarends, W.M., Ghazvini, M., Tafel, A.A., Heath, H., Galjart, N., Essers, J., Grootegoed, J.A., Arnheim, N., Bezzubova, O., Buerstedde, J.M., Sung, P., and Kanaar, R. (2006). Differential contributions of mammalian Rad54 paralogs to recombination, DNA damage repair, and meiosis. Molecular and Cellular Biology 26, 976-989.

Splinter, E., Heath, H., Kooren, J., Palstra, R.J., Klous, P., Grosveld, F., Galjart, N. and de Laat, W. (2006). CTCF mediates long-range chromatin looping and local histone modification in the beta-globin locus. Genes & Development 20, 2349-2354.

CRP - Spatio-temporal organisation of genome surveillance in live cells

S. Bergink, F.A. Salomons, D. Hoogstraten, T.A. Groothuis, H. de Waard, J. Wu, L. Yuan, E. Citterio, A.B. Houtsmuller, J. Neefjes, J.H. Hoeijmakers, W. Vermeulen and N.P. Dantuma. DNA damage triggers nucleotide excision repair-dependent monoubiquitylation of histone H2A, Genes Dev 20 (2006) 1343-1352.

J. Essers, W. Vermeulen and A.B. Houtsmuller. DNA damage repair: anytime, anywhere? Curr Opin Cell Biol 18 (2006) 240-246.

G. Giglia-Mari, C. Miquel, A.F. Theil, P.O. Mari, D. Hoogstraten, J.M. Ng, C. Dinant, J.H. Hoeijmakers and W. Vermeulen. Dynamic Interaction of TTDA with TFIIH Is Stabilized by Nucleotide Excision Repair in Living Cells, PLoS Biol 4 (2006) e156.

E.A. Maltseva, N.I. Rechkunova, I.O. Petruseva, V.N. Silnikov, W. Vermeulen and O.I. Lavrik. Interaction of nucleotide excision repair factors RPA and XPA with DNA containing bulky photoreactive groups imitating damages, Biochemistry (Mosc) 71 (2006) 270-278.

S. Bergink, L.A. Severijnen, N. Wijgers, K. Sugasawa, H. Yousaf, J.M. Kros, J. van Swieten, B.A. Oostra, J.H. Hoeijmakers, W. Vermeulen and R. Willemsen. The DNA repair-ubiquitin-associated HR23 proteins are constituents of neuronal inclusions in specific neurodegenerative disorders without hampering DNA repair, Neurobiol Dis 23 (2006) 708-716.

J.O. Andressoo, J.R. Mitchell, J. de Wit, D. Hoogstraten, M. Volker, W. Toussaint, E. Speksnijder, R.B. Beems, H. van Steeg, J. Jans, C.I. de Zeeuw, N.G. Jaspers, A. Raams, A.R. Lehmann, W. Vermeulen, J.H. Hoeijmakers and G.T. van der Horst. An Xpd mouse model for the combined xeroderma pigmentosum/Cockayne syndrome exhibiting both cancer predisposition and segmental progeria, Cancer Cell 10 (2006) 121-132.

L.J. Niedernhofer, G.A. Garinis, A. Raams, A.S. Lalai, A.R. Robinson, E. Appeldoorn, H. Odijk, R. Oostendorp, A. Ahmad, W. van Leeuwen, A.F. Theil, W. Vermeulen, G.T. van der Horst, P. Meinecke, W.J. Kleijer, J. Vijg, N.G. Jaspers and J.H. Hoeijmakers. A new progeroid syndrome reveals that genotoxic stress suppresses the somatotroph axis, Nature 444 (2006) 1038-1043.

A. Zotter, M.S. Luijsterburg, D.O. Warmerdam, S. Ibrahim, A. Nigg, W.A. van Cappellen, J.H. Hoeijmakers, R. van Driel, W. Vermeulen and A.B. Houtsmuller. Recruitment of the nucleotide excision repair endonuclease XPG to sites of UV-induced dna damage depends on functional TFIIH, Mol Cell Biol 26 (2006) 8868-8879.

Hauptner, A., Krücken, R., Greubel, C., Hable, V., Dollinger, G., Drexler, G.A., Deutsch, M., Löwe, R., Friedl, A.A., Dietzel, S., Strickfaden, H., Cremer, T (2006). DNA repair protein distribution along the tracks of energetic ions. Radiat Prot Dosim 122:147-149.

Hauptner, A., Friedland, W., Dietzel, S., Drexler, G.A., Greubel, C., Hable, V., Strickfaden, H., Cremer, T., Friedl, A.A., Krücken, R., Paretzke, H.G., Dollinger. G (2006). Spatial distribution of DNA double strand breaks from ion tracks. Mat Fys Medd Dan Vid Selsk 52: 59-85.

Dollinger, G., Bergmaier, A., Hauptner, A., Dietzel, S., Drexler, G.A., Greubel, C., Hable, V., Reichart, P., Krücken, R., Cremer, T., Friedl, A.A (2006). Hydrogen microscopy and analysis of DNA repair using focused high energy ion beams. Nuclear Instruments and Methods in Physics Research B 249:270-277.

Hable, V., Dollinger, G., Greubel, C., Hauptner, A., Krücken, R., Dietzel, S., Cremer, T., Drexler, G.A., Friedl, A.A., Löwe, R (2006). Methods for quantitative evaluation of dynamics of repair proteins within irradiated cells. Nuclear Instruments and Methods in Physics Research B 245:298-301.

Fousteri M, Vermeulen W, van Zeeland AA, Mullenders LH. Cockayne syndrome A and B proteins differentially regulate recruitment of chromatin remodeling and repair factors to stalled RNA polymerase II in vivo. Mol Cell, 2006 23, 71-82.

van Haaften G, Romeijn R, Pothof J, Koole W, Mullenders LH, Pastink A, Plasterk RH, Tijsterman M. Identification of conserved pathways of DNA-damage response and radiation protection by genome-wide RNAi. Curr Biol, 2006 16, 1344-50.

de Gruijl FR, Mullenders LH, Stout GJ. Elimination of keratinocytes stagnant in s-phase through epidermal turnover instead of in situ situ apoptosis. Cell Cycle, 2006 5, 565-6, 2006.

CRP - Nuclear action of miRNAs

Huettel B, Kanno T, Daxinger L, Aufsatz W, Matzke AJM, Matzke M (2006). Endogenous targets of RNAdirected DNA methylation and Pol IV in Arabidopsis. *EMBO J 25*: 2828-2836.

Ketting, R.F. (2006): Partners in Dicing. Genome Biol. 7: 210

CRP - Control of stress and interferon regulated gene expression by transcription factors, histone modification and nuclear compartmentalisation

Sauer I., Schaljo B., Vogl C., Gattermeier I., Kolbe T., Muller M., Blackshear P.J., and Kovarik P. 2006. Interferons limit inflammatory responses by induction of tristetraprolin. Blood, 107:4790-7

CRP - The role of linker histone variants and their phosphorylation in chromatin structure and function

Rundquist I. and Lindner H.H.: Analyses of linker histone – chromatin interactions in situ. Biochem. Cell Biol. 84:427-436, 2006

Sarg B, Helliger W, Talasz H, Förg B, and Lindner HH: Histone H1 phosphorylation occurs site-specifically during interphase and mitosis. Identification of a novel phosphorylation site on histone H1. J.Biol.Chem. 281,6573-6580, 2006

CRP - Chromatin higher order dynamics: a single molecule approach

Bouazoune K. and Brehm A. ATP-dependent chromatin remodeling complexes in Drosophila Chromosome Res. (2006), 14, 433-449.

Ozdemir A, Masumoto H, Fitzjohn P, Verreault A, Logie C. Histone H3 lysine 56 acetylation: a new twist in the chromosome cycle. Cell Cycle. (2006) 5(22):2602-8.

CRP - The control of chromosome structure by cohesion/ condensin complexes

Gerlich, D., Hirota, T., Koch, B. Peters, J.-M., and Ellenberg, J. (2006). Condensin I stabilizes chromosomes mechanically through a dynamic interaction in live cells. *Curr. Biol.* 16, 333-344

Watrin, E., Schleiffer, A., Tanaka, K., Eisenhaber, F., Nasmyth, K. and Peters, J.-M. (2006). Human Scc4 is required for loading of cohesin onto chromatin, sister chromatid cohesion and progression through mitosis. *Curr. Biol.* 16, 863-874.

Gerlich, D., Koch, B., Dupeux, F., Peters, J.-M., and Ellenberg, J. (2006). Live cell imaging reveals a stable cohesin-chromatin interaction after but not before DNA replication. *Curr. Biol.* 16, 1571-1578.

Kueng, S., Hegemann, B., Peters, B.H., Lipp, J.J., Schleiffer, A., Mechtler, K. and Peters, J.-M. (2006). Wapl controls the dynamic association of cohesin with chromatin. *Cell* 127, 955-967.

Neumann B, Held M, Liebel U, Erfle H, Rogers P, Pepperkok R, Ellenberg J. (2006) High-throughput RNAi screening by time-lapse imaging of live human cells. *Nat Methods*. 3(5):385-390.

Ulrich, M., Kappel, C., Beaudouin, J., Hezel, S., Ulrich, J., Eils, R. (2006) Tropical-parameter estimation and simulation of reaction-diffusion models based on spatio-temporal microscopy images. *Bioinformatics* 22, 2709-2710.

Watrin, E. and Peters, J.-M. (2006). Cohesin and DNA damage repair. Exp. Cell Res. 312, 2687-2693.

2005

CRP - Cell biology of messenger RNA biogenesis

Jensen, T.H. and Moore, C.: Reviving the Exosome. Cell (2005) 660-662

Thomsen, R.; Nielsen, P.S. and Jensen, T.H.: Increased RNA-FISH sensitivity by using short fluorescent LNA probes. RNA (2005) 1745-1748

Saguez C.; Olesen, J.R. and Jensen, T.H.: Formation of Export Competent mRNP: Escaping Nuclear Destruction. Curr. Opin. Cell Biol. (2005) 287-293.

Olesen, J.R.; Libri, D. and Jensen, T.H.: A link between transcription and mRNP quality in *Saccharomyces cerevisiae* RNA Biology (2005) 149-152.

Furnes, C, Arnesen, T, Askjaer, P., Kjems, J. and Szilvay, A.M.: HIV-1 Rev oligomerization is not obligatory in the presence of an extra basic domain. Retrovirology 2:39. (2005).

Klaas W. Mulder, G.Sebastiaan Winkler and H.Th.Marc Timmers (2005) DNA damage and replication stress induced transcription of RNR genes is dependent on the Ccr4-Not complex. Nucleic Acids Res. 33, 6384-6392.

CRP - Role of multi zinc finger proteins CTCF and BORIS in the dynamic change of the nuclear architecture and chromatin function during cell cycle and differentiation

Burke, L.J., Zhang, R., Bartkuhn, M., Tiwari, V.K., Tavoosidana, G., Kurukuti, S., Weth, C., Leers, J., Galjart, N., Ohlsson, R., and Renkawitz, R. (2005). CTCF binding and higher order chromatin structure of the H19 locus are maintained in mitotic chromatin. Embo J 24, 3291-3300.

CRP - Spatio-temporal organisation of genome surveillance in live cells

Dollinger, G., Hable, V., Hauptner, A., Krücken, R., Reichart, P., Friedl, A.A., Drexler, G., Cremer, T., Dietzel, S (2005) Microirradiation of cells with energetic heavy ions. Nuclear Instruments and Methods in Physics Research B 231:195-201.

Alekseev S, Kool H, Rebel H, Fousteri M, Moser J, Backendorf C, de Gruijl FR, Vrieling H, Mullenders LH. Enhanced DDB2 expression protects mice from carcinogenic effects of chronic UV-B irradiation. Cancer Res, 2005 65,10298-306.

Theron T, Fousteri MI, Volker M, Harries LW, Botta E, Stefanini M, Fujimoto M, Andressoo JO, Mitchell J, Jaspers NG, McDaniel LD, Mullenders LH, Lehmann AR. Transcription-associated breaks in xeroderma pigmentosum group D cells from patients with combined features of xeroderma pigmentosum and Cockayne syndrome. Mol Cell Biol, 2005 25, 8368-78.

Fousteri M, van Hoffen A, Vargova H, Mullenders LH. Repair of DNA lesions in chromosomal DNA: impact of chromatin structure and and Cockayne syndrome proteins. DNA Repair, 2005 4, 919-25. Review.

Moser J, Volker M, Kool H, Alekseev S, Vrieling H, Yasui A, van Zeeland AA, Mullenders LH. The UVdamaged DNA binding protein mediates efficient targeting of the nucleotide excision repair complex to UVinduced photo lesions. DNA Repair, 2005 2,4, 571-82.

CRP - The role of linker histone variants and their phosphorylation in chromatin structure and function

Sarg B, Green A, Soderkvist P, Helliger W, Rundquist I, and Lindner HH: Characterization of sequence variations in human histone H1.2 and H1.4 subtypes. FEBS J. 272, 3673-3683 (2005)

CRP - Chromatin higher order dynamics: a single molecule approach

Bouazoune K. and Brehm A. dMi-2 chromatin binding and remodeling activities are regulated by dCK2 phosphorylation. J. Biol. Chem. (2005), 280, 41912-41920.

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Scanning (Atomic) Force miscroscopy image of the SMClike protein complex RAD50/MRE11/NBS1, involved in the early cellular response to DNA double-strand breaks. The complex consists of a globular DNA binding domain and two protruding coiled-coil arms (50 nm in length) that are required to tether broken DNA molecules.

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