ANNUAL MEETING 2011

DEPARTMENT OF MOLECULAR BIOLOGY
AARHUS UNIVERSITY
FRIDAY 10 JUNE 2011

Group posters - ”Meet a Method”

No.	Titel
1.	“Asymmetrical flow field-flow fractionation” - Going with the flow, or how gel filtration became outdated
2.	Mass Spectrometry - A method for protein identification, protein characterization, and protein quantification
3.	High throughput sequencing - small RNAs, large genomes and thousands of mutants
4.	RNA Going Green: Using fluorescence to illuminate molecular details of nucleic acid synthesis
5.	Characterization of posttranslational modifications by MALDI-TOF MS
6.	Detection of membrane phosphatidylserine by lactadherin
7.	Taming RNases
8.	2X2D with DNA
9.	Avoid moth - use Baculovirus
10.	Assaying antiviral proteins
11.	BioSAXS
12.	Investigation of vesicle traffic in cell- and mouse models
13.	Genetically Modified Mice
14.	From sequence to consequence
15.	Tools for protein interaction discovery and characterization
16.	How to work with Lipids?
17.	Prediction and validation of miRNA target sites
18.	In vivo analysis of gene and protein function in zebrafish
19.	Analysis of mRNA transport and local translation in brain cells
20.	Detection of enzyme activity at the single molecule level using rolling circle amplification signal enhancement
21.	Methods for analyzing protein-DNA complexes
22.	From moo to movie
23.	Gene expression and silencing using retroviral vectors
24.	Your way to rocket science: The comet assay
25.	Current events
26.	RIP
27.	Micropatterns: signalling the cell surface
28.	Laser capture microdissection
29.	In vivo fluorescence imaging – Where do YOUR drugs go?
30.	Nucleic acid aptamers as tools for molecular biology
31	Molecular retrovirology
32	Trangenics – Worm-Dart!

Annual Meeting 2011 - Programme

Department of Molecular Biology – Aarhus University
Friday 10 June 2011 - The Lakeside Lecture Theatres (Søauditorierne)

09:00–09:10	Introduction by Daniel Otzen
09:10–09:30	MBI goes IMBG by Erik Østergaard Jensen
09:30–10:30	**Scientific Session 1** Pontus Gourdon: Crystal structure of the copper pump suggests a three-stage copper transport pathway Thomas Kallehauge: Nuclear retention guards mRNA against premature cytoplasmic appearance Katharina Markmann: Identification and profiling of symbiosis related small RNAs in Lotus japonicus
10:30–11:00	Coffee break
11:00–12:00	**Scientific Session 2** Marianne S. Christensen: The Nuclear EXosome Targeting complex – a novel player in the nuclear RNA surveillance in human cells Jan K. Jensen: Crystal structure of the plasminogen activator inhibitor-1 in an active conformation with normal thermodynamic stability Maria Andreasen: Corneal dystrophy – linking the protein stability to the aggregation mechanism
12:00–12:15	Group photo of all staff and students
12:15–14:15	Lunch and poster session/exhibitors
14:15–14:30	**Student awards** for Lecturer of the year and Student teacher of the year
14:30–15:30	**Presentation of the new groups at IMBG** Preben Bach Holm: Research profile and expertises for the research group "Molecular Genetics and Biotechnology (MGB)", Research Centre Flakkebjerg Peter Sørensen, Research Centre Foulum: Genetic architecture of resistance to bovine mastitis Mogens Sandø Lund, Research Centre Foulum: Genomic selection
15:30-15:45	Coffee break
15:45–16:45	**Plenary lecture** Lars Peter Nielsen, Dept. of Bioscience, Aarhus University: Electronic networks connecting life
16:45–17:00	Concluding remarks
18:30–02:00	**Reception**, **dinner**, and **party** in the Maths canteen **Group poster prize award**

Crystal structure of the copper pump suggests a three-stage copper transport pathway

Pontus Gourdon[1,2*], Xiang-Yu Liu[1,2,3*], Tina Skjørringe[4], J. Preben Morth[1,2#], Lisbeth Birk Møller[4], Bjørn Panyella Pedersen[1,2†] & Poul Nissen[1,2]

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[*] These authors contributed equally to this work.

Data not published yet

Affiliation: Poul Nissen's research group

Nuclear retention guards mRNA against premature cytoplasmic appearance

Thomas Kallehauge[1,2], Edouard Bertrand[2] and Torben Heick Jensen[1]

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Data not published yet

Affiliation: Torben Heick Jensen's research group

Identification and profiling of symbiosis related small RNAs in Lotus japonicus

Katharina Markmann[1], Vikas Gupta[1,2], Jorge Quintana[1], Stig U. Andersen[1], Christian Storm Pedersen[1,2], Mikkel Schierup[1,2], and Jens Stougaard[1]

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[2]Bioinformatics Research Centre, Aarhus University, Denmark

Data not published yet

Affiliation: Jens Stougaard's research group

The Nuclear EXosome Targeting complex – a novel player in the nuclear RNA surveillance in human cells

Marianne S. Christensen[1], Michał Lubas[1,2,3], Maiken S. Kristiansen[1], Michał Domański[1], Lasse G. Falkenby[4], Søren Lykke-Andersen[1], Jens S. Andersen[4], Andrzej Dziembowski[2,3] and Torben Heick Jensen[1]

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Data not published yet

Affiliation: Torben Heick Jensen's research group

Crystal Structure of Plasminogen Activator Inhibitor-1 in an Active Conformation with Normal Thermodynamic Stability

Jan K. Jensen[1,2,*], Lawrence C. Thompson[3], Joel C. Bucci[3], Poul Nissen[1,4], Peter G. W. Gettins[5], Cynthia B. Peterson[3], Peter A. Andreasen[1,2] and J. Preben Morth[1,4,6].

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[2]Danish-Chinese Center for Proteases and Cancer, Aarhus University and
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[5]Department of Biochemistry and Molecular Genetics, University of Illinois at Chicago, Chicago, Illinois 60607, USA.
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The serpin plasminogen activator inhibitor-1 (PAI-1) is a crucial regulator in fibrinolysis and tissue remodeling. PAI-1 has been associated with several pathological conditions and is a validated prognostic marker in human cancers. However, structural information about the native inhibitory form of PAI-1 has been elusive due to its inherent conformational instability and rapid conversion to a latent, inactive structure. Here we report the crystal structure of PAI-1 W175F at 2.3 Å resolution as the first model of the metastable native molecule. Structural comparison with a quadruple mutant (14-1B) previously used as representative of the active state uncovered key differences. The most striking differences occur near the region that houses three of the four mutations in the 14-1B PAI-1 structure. Prominent changes are localized within a loop connecting -strand 3A with the F helix, in which a previously observed 310-helix is absent in the new structure. Notably these structural changes are found near the binding site for the cofactor vitronectin. Since vitronectin is the only known physiological regulator of PAI-1 that slows down the latency conversion, the structure of this region is important.

Furthermore, the previously identified chloride binding site close to the F-helix is absent from the present structure and likely to be artifactual, because of its dependence on the 14-1B mutations. Instead we found a different Cl binding site that is likely to be present in wild-type PAI-1 and that more satisfactorily accounts for the Cl stabilizing effect on PAI-1.

Affiliation: own research group

Corneal dystrophy – linking the protein stability to the aggregation mechanism

Maria Andreasen[1], Marcel Stenvang[1], Kasper Runager[1], Morten Bjerring[2], Heidi Koldsø[2], Gunna Christiansen[3], Birgit Schiøtt[2], Niels Christian Nielsen[2], Jan J. Enghild[1] and Daniel Otzen[1]

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[3]Institute of Medical Microbiology and Immunology, Aarhus University, 8000 Aarhus, Denmark

Corneal dystrophy (CD) is characterized by the abnormal accumulation of transforming growth factor β induced protein (TGFBIp) in the cornea which eventually leads to blindness. CD is inherited in an autosomally dominant way and many different mutations in TGFBIp have been linked to corneal dystrophy and can even give rise to different disease phenotypes. These different phenotypes are observed in the type of protein aggregates observed in the cornea. The majority of these mutations are located in the 4th and last fasciclin 1 domain (Fas1-4) of TGFBIp. It has been shown that changes in the stability of TGFBIp brought on by mutations in Fas1-4 can be modeled very precisely by the changes in stability of Fas1-4 domain alone. In the present study the stability of Fas1-4 is examined with biophysical tools in order to try and link the protein stability to the aggregation propensity and the type of aggregates formed. The intrinsic tryptophan fluorescence of various disease related mutants of Fas1-4 is used to monitor the chemical stability upon addition of denaturants and the kinetics of folding and unfolding through stopped-flow. Furthermore the thermal stability is monitored by circular dichroism spectroscopy. The fluorescent probe anilino naphthalene sulfonate (ANS), which detects hydrophobic patches, is used to detect the presence of possible molten globule structures of destabilized mutants. Finally the aggregation of the mutants are studied with the amyloid binding dye Thioflavin T (ThT) and the secondary structure of the resulting aggregates is examined with circular dichroism spectroscopy and Fourier-transform infra-red spectroscopy and the overall structure is determined using transmission electron microscopy. The resulting aggregation propensity and the type of aggregates formed can then be linked to the stability of the mutant.

Affiliation: Daniel Otzen's research group

Research profile and expertises for the research group "Molecular Genetics and Biotechnology (MGB)"

Preben Bach Holm, Head of Research Unit and Adjunct Professor
Research Centre Flakkebjerg

The MGB group is located at Research Centre Flakkebjerg and the staff comprises June 1, 2011 one head of research unit, eight senior scientists/associate professors, ten postdocs, fifteen PhD students and five technicians.

The research is primarily focused on the genetic and molecular mechanisms underlying the food/feed nutritional quality of Danish cereals as well as the feed quality of ryegrass. Recently these approaches have been extended to include nutrient mobilization and improvement of grass and cereal biomass quality and quantity for bioethanol production. Virtually all these studies are carried out in collaboration with Danish breeders and the agroindustry including the enzyme industry. The group undertakes counseling of the Ministry of Food, Agriculture and Fisheries and the Ministry of Foreign Affairs with regard to plant biotechnology.

The group has a general expertise in plant molecular biology and plant genetics and more specific competences in laser capture microdissection, transcriptomic analyses, heterologous expression of genes in Pichia, genetic mapping and quantitative genetics. Genetic transformation of barley and wheat is performed on a regular basis. The research efforts include the development of new transformation technologies more acceptable to the public. The MGB group is currently the only Danish research group where transformation of cereals is performed routinely.

Genetic architecture of resistance to bovine mastitis

Peter Sørensen
Department of Genetics and Biotechnology
Quantitative Genetics and Bioinformatics
Research Centre Foulum

Mastitis is the most frequent and costly disease in dairy cattle and its incidence has not declined despite improved methods of prevention and treatment. Hence, this disease is a major concern as it causes cows to suffer and is the leading cause of antibiotic use in dairy production.

Mastitis is an inflammatory reaction in the bovine mammary gland due to invasion and colonization by diverse pathogens including contagious and environmental bacteria such as Streptococcus spp., Staphylococcus spp. and coliform bacteria. We have used new genome technologies to identify genes and genetic pathways involved in the immune response of dairy cattle. Genome-wide association analysis was used to identify genomic regions affecting the resistance to clinical and subclinical mastitis. To further increase our understanding of the disease pathogenesis of mastitis we used genome-wide expression profiling to identify genes involved in the local (mammary gland) and the systemic (e.g. liver) acute phase response in dairy cows during infection. These findings have enhanced our understanding of the functional role of genes and genetic pathways in bovine mastitis. Finally, we have developed an integrative genomics approach for identifying functional modules/complexes underlying genetic resistance to bovine mastitis by using information from genome-wide expression data, genome-wide SNP data, ortholog mapping, protein interactions and biomedical text data. Our discoveries have enabled us to better understand the genetic architecture of the disease and will help us to reduce the incidence of mastitis through targeted selective breeding.

Genomic selection

Mogens Sandø Lund
Department of Genetics and Biotechnology
Quantitative Genetics and Bioinformatics
Research Centre Foulum

Genomic selection is selection based on genome-wide DNA-information. Individual animals or plants that are potential breeding candidates are DNA-tested for thousands of genetic markers covering the entire genome. These markers capture most of the genetic variation and can thus be used to predict the genetic potential or genomically enhanced breeding value of the individual candidates. Selection decisions are then made based on these breeding values.

The primary advantage of using genomic selection is that the method enables more accurate prediction of breeding values at an early stage in life. The genetic gain in the breeding scheme can thereby be accelerated. Another advantage is that the method allows new traits, and traits that are difficult to measure, to be incorporated into the breeding scheme.

In the near future genomic selection will be based on whole-genome sequences and complex trait phenotypes collected from a large number of individuals in different populations and in different environments. These massive amounts of data will provide the basis for what has been termed "bridging the genotype-phenotype gap"; i.e. understanding how variation at the sequence level gives rise to variation in observed phenotypes.

Improved understanding of the genetic architecture of complex traits can make genomic selection even more revolutionising as it will enable selection decisions to be based on detailed information on not only gene effects but also the interaction of genes with other genes as well as with specific environments.
Genomic selection is currently revolutionising cattle breeding and has a similar potential in many animal and plant breeding schemes. Even though these breeding schemes are vastly different, the basic mechanisms of genomic selection are similar.

Plenary lecture: Professor Lars Peter Nielsen

Department of Bioscience, Aarhus University

Electronic networks connecting life

The finding of electric currents coupling distant living processes in nature has stirred a host of new questions and speculations in science. How can we explain transmission of electrons from an oxidation process in one place to a reduction process centimeters away? What microbes may catalyze the electrochemical reactions and structure a common electric grid? Are bacterial nanowires the key conductors and how do they function at the molecular level? Does electric symbiosis make ecological and evolutionary sense? What are the implications for nutrient cycling and biosphere-geosphere interactions?

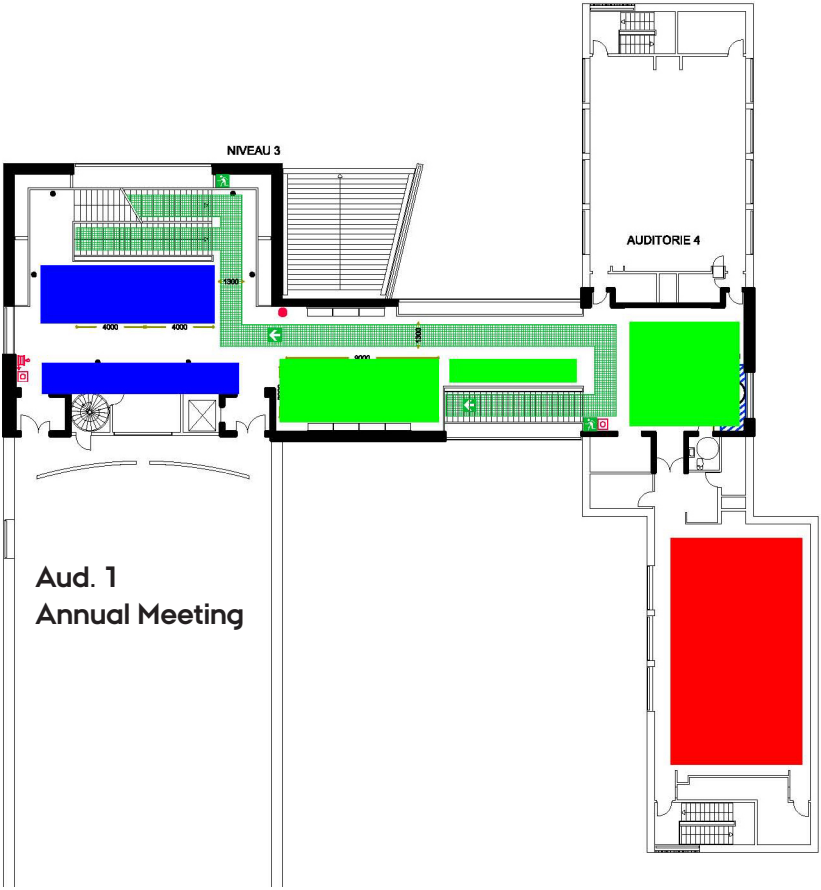
Exiting studies in the past year have provided some answers and ideas, but much is left before we can even imagine how electromicrobiogeophysiochemistry works all the way from molecular electron transfer to electric fields in the landscape.

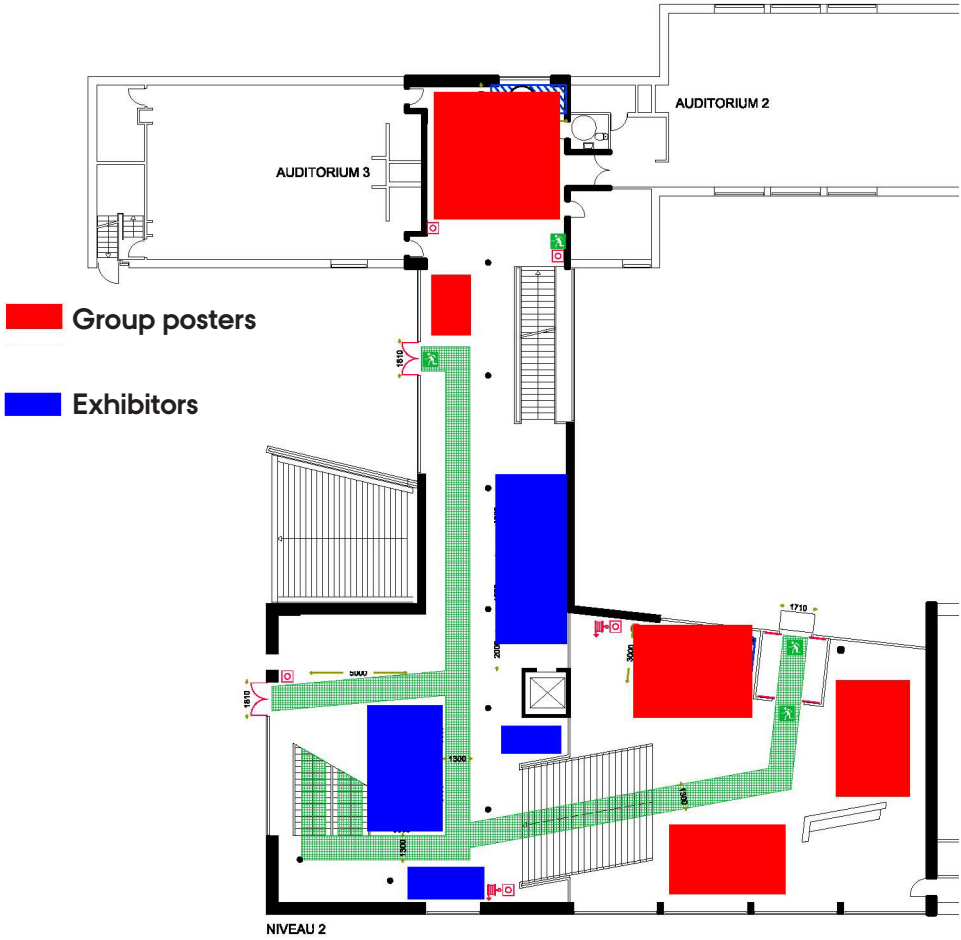
Lars Peter Nielsen is well known for his impressive ability to come up with unconventional solution models in connection with understanding nature and its processes. As early as two decades ago, his invention of the so-called isotope pairing method created at one fell swoop an oportunity to gain far greater understanding of the nitrogen compounds cycling process in nature. This method has had great significance for our knowledge about the background to algal bloom and fish mortality in the inner Danish waters.

In addition to being an expert in his field, Lars Peter Nielsen is interested in converting his research results into practical application in areas such as developing biological air purification for removing odour and ammonia emissions from pig farms.

Professor Nielsen has worked at the Department of Bioscience, Aarhus University, since 1990. He was appointed professor as of 1 January 2011.

Group posters
Food, coffee and drinks
Exhibitors





EXHIBITORS

FORSKNINGSSTØTTEENHEDEN

AU-HR

AGSOS

VWR & BIE & BERNTSEN

AH diagnostics

DANDIAG

SIGMA-ALDRICH

In Vitro as
Leverandør til de danske laboratorier

HOUNISEN

BIO LAB

KEM EN TEC

invitrogen™

Fisher Scientific
Part of Thermo Fisher Scientific

Th. Geyer

MD Scientific


Kappa