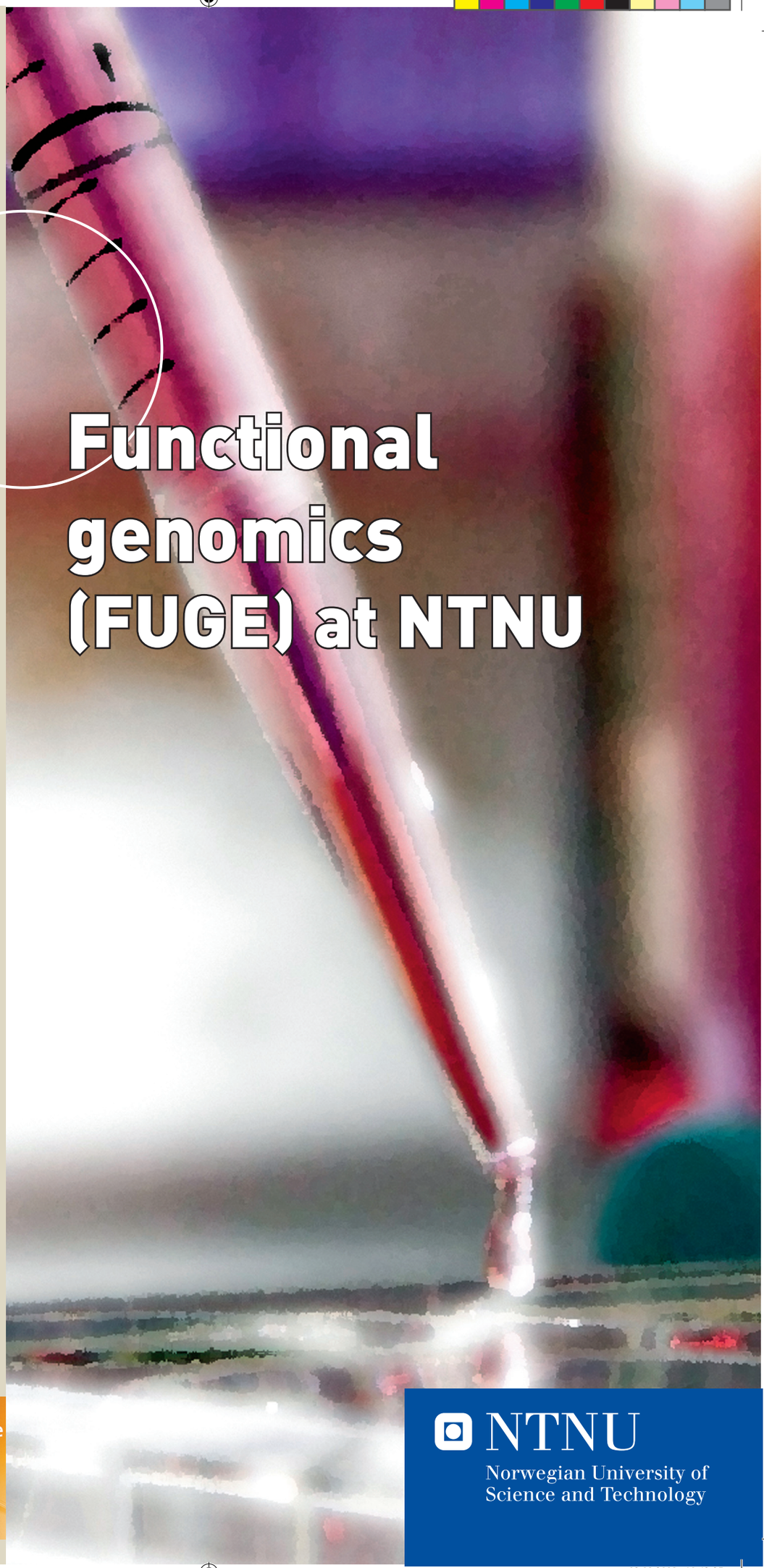
Functional genomics (FUGE) at NTNU

Annual Report 2008



FUGE

Large-scale Programme
The Research Council of Norway

NTNU
Norwegian University of Science and Technology

FUGE Mid-Norway

Faculty of Natural Sciences and Technology
Natural Science Building
Norwegian University of Science and Technology (NTNU)
N-7491 Trondheim
Norway

Phone: (+47) 735 96 064
E-mail: postmottak@nt.ntnu.no

2008 FUGE Mid-Norway Board:

Head:	Associate Professor Åse Krøkje, Faculty of Natural Sciences and Technology, NTNU
Deputy head:	Vice-Dean Helge Klungland, Faculty of Medicine, NTNU
Members:	Professor Kjell Bratbergsengen, Faculty of Information Technology, Mathematics and Electrical Engineering, NTNU Associate Professor Berge Solberg, Faculty of Social Sciences and Technology Management, NTNU Head of Research Hans Kotlar, StatoilHydro Head of Research Trond Ellingsen, SINTEF Director Gudmund Marhaug, Helse Midt-Norge
Observers:	Adjunct Professor Magne Børset, Faculty of Medicine, NTNU Professor Marit Otterlei, Faculty of Medicine, NTNU
Secretary:	Dr. Scient. Janne Østvang, Faculty of Natural Sciences and Technology, NTNU

2008 FUGE Mid-Norway committee:

Head:	Adjunct Professor Magne Børset, Faculty of Medicine, NTNU
Members:	Professor Finn Drabløs, Faculty of Medicine, NTNU Professor Svein Valla, Faculty of Natural Sciences and Technology, NTNU Professor Atle Bones, Faculty of Natural Sciences and Technology, NTNU Associate Professor Pauline Haddow/Wacek Kusnierczyk, Faculty of Information Technology, Mathematics and Electrical Engineering, NTNU Associate Professor Rune Nydal, Faculty of Arts, NTNU Senior Researcher Kjetil Hindar, Norwegian Institute for Nature Research Professor Frank Skorpen, Faculty of Medicine, NTNU Professor Marit Otterlei, Faculty of Medicine, NTNU
Observer:	Researcher Trond Størseth, SINTEF
Secretary:	Dr. Scient Janne Østvang, Faculty of Natural Sciences and Technology, NTNU
FUGE coordinator in Mid-Norway:	Janne Østvang (Adviser at the Faculty of Natural Sciences and Technology)

COVER PAGE : Photo: Wacek Kusnierczyk

Contents Page

Introduction – Another good FUGE year

By Magne Børset
Head of FUGE committee in mid-Norway

Again we can celebrate a successful year for activities related to functional genomics (FUGE) in Mid-Norway. All the FUGE platform nodes located in our region are up and going, and offer services to scientists who need cutting edge technology in their research.

The platform nodes are all briefly presented in this annual report. Many of the research papers from these platforms and from research groups within this field have appeared in highly ranked journals and some have even been awarded prestigious prizes. The 2008 Cozzarelli Prize, an award for the paper of the year in biological sciences in PNAS, a prestigious American journal, was recently given to a joint paper from two departments at NTNU, the Trondheim-based bioinformatics company Interagon and a research group from Duarte, California.

Furthermore, research groups from our region have again succeeded in attracting substantial external funding. Six projects from NTNU were granted funding in 2008 from the Research Council of Norway under the open research programme FRIBIO/-BIOMED, despite a total funding rate in this programme of merely 10 %. Regrettably, funding for independent scientist-initiated research in Norway is very scarce. It is therefore extremely important that groups from our region have the standing and quality to be able to compete successfully for such grants. This is only possible thanks to substantial support from NTNU and other local sources.

Success creates success; and we need to build our activity around groups that have already proved their excellence. New groups will then emerge budding from these excellent groups.

To attract competent people is an important challenge in our region. Viewed from more densely populated areas of the world, our corner seems exotic but maybe more suitable for exciting tourism than for career building. For a couple of our FUGE nodes, lack of competent applicants to positions has reduced the possibility to exploit their resources. This emphasizes the importance of excellent FUGE-related graduate programmes at NTNU and at the colleges in our region. We know that Trondheim and NTNU are very popular among students. Each year many of NTNU's graduate programmes recruit a proportionally higher number of excellent students than similar programmes at other universities in our country. We should more actively present the opportunities in FUGE-related activities to students and incorporate functional genomics in educational programmes. Also we need to convince bright students that Mid-Norway is attractive also as a permanent place of residence.

2008 was the first full year of the FUGE II period. However, we already need to focus on the future beyond FUGE II. In the Research Council of Norway, the planning for the period after 2012 is already well under way. "Biotechnology" might be the keyword for the next period. What will then become of the FUGE platforms? Only those platforms that are dynamic, creative and able to provide indispensible service will survive. Given the performance and merits of our local nodes so far, I think many of them will be able to meet this challenge.

About FUGE in Mid-Norway

The successful mapping of the genomes of humans and selected animals, plants and micro-organisms has opened new doors for scientists who study biological processes in the field of functional genomics. FUGE is a national plan designed to enhance the quality and activity of functional genomics research in Norway, funded by the Research Council of Norway.

FUGE's backbone is the technology platforms that offer service and research related to specific technologies that are useful for functional genomics. There are seven nodes connected to different technology platforms in mid-Norway.

While a portion of the region's functional genomic projects have received funding from the Research Council of Norway, many research groups at NTNU conduct functional genomics research. These groups are found at the Faculty of Medicine, the Faculty of Natural Sciences and Technology, the Faculty of Information Technology, Mathematics and Electrical Engineering, as well as the Faculty of Arts.

FUGE's mid-Norway group is governed by a board and a committee, and has an adviser who coordinates FUGE activities.

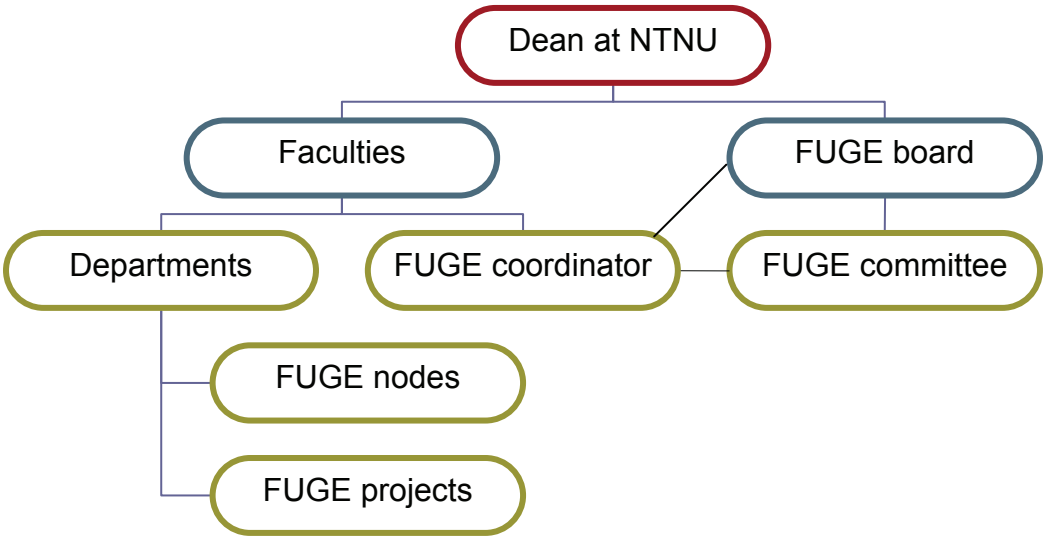


Figure 1. Organization of the FUGE activity in Mid-Norway.
FUGE Mid-Norway is governed by a board and a steering committee. In addition, there is an adviser who coordinates the FUGE activity in Mid-Norway. The technology nodes and the FUGE projects are administrated by different departments at NTNU.

Visit us at http://www.ntnu.no/fuge **(Norwegian)**
http://www.ntnu.no/research/fuge **(English)**

The FUGE nodes in Mid-Norway

Nationwide there are ten different FUGE Technology Platforms with nodes distributed all over Norway. In the region of Mid-Norway, there are seven nodes. The activity of these nodes will briefly be presented here:

The Norwegian Proteomics Consortium -NorProteomics

In 2008, the proteomics laboratory was appointed a node within the Norwegian Proteomics Consortium, NorProteomics with service responsibility for research groups in Mid-Norway and NTNU. Services offered are protein identification, de-novo sequencing and analysis of post-translational modifications.

Through 2008 the node has performed proteomics service analyses within several projects at NTNU/SINTEF as follows:

Service:
Marit W. Anthonsen, NTNU: Analysis of phosphorylation status of IRF3 and potential implication in signalling of viral infection. This has been a large project that will continue in 2009. It includes a large number of MS and MS/MS scans subsequent to TiO4-purification of phosphopeptides, and manual interpretation of spectra.

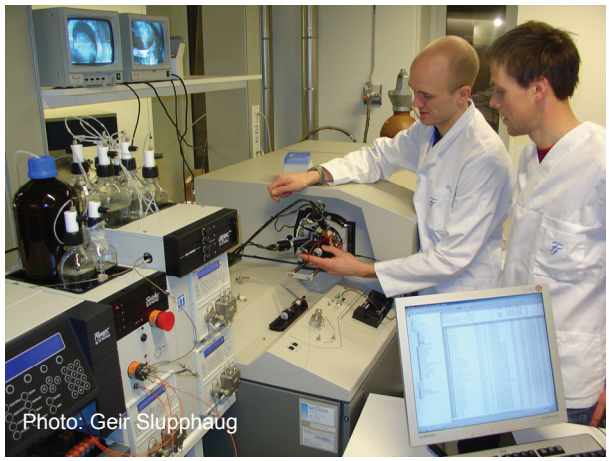
Iciar Martinez, Sintef: De novo sequencing of proteolytic activities isolated from pelagic fish subject to belly bursting.

Hans Krokan, NTNU: Analysis of post-translational modification in the active site of oxidative demethylases of the AlkB-family.

Marit Otterlei, NTNU: Analysis of post-translational modifications in PCNA and its function in protein:protein interactions.

Kurt I. Draget, NTNU: Analysis of Insulin oligomerisation.

Augustin Arukwe, NTNU: Quantitative analysis and identification of fish proteins by 2D-PAGE.



Researchers in activity by the MALDI TOF-TOF in the proteomics lab.

Other research activities:
Ole-Jan Iversen NTNU: Analysis of psoriasis-associated proteins.

Geir Slupphaug, NTNU:
i) The interactomics of DNA repair (Channel 3, FUGE 2)
ii) Proteomic profiling to identify biomarkers associated with treatment with the cytostatic drugs melphalan and 5-FU (2D-DIGE, and SILAC)
iii) Regulation of mammalian DNA base-excision repair by phosphorylation and ubiquitinylation

Courses:
MOL3007. Laboratory course in proteomics
Tutoring and teaching of researchers in 2D- and MS-based proteomics.

Other:
Implementation of new equipment and software in 2008: Robotic spotpicker, DeCyder Software for 2D-DIGE quantification, MASCOT Distiller 2.2
Finally, the laboratory has undergone rebuilding (DMF financing) to make more room for benchwork, as well as streamlining 2D-gel analysis.

The Norwegian Bioinformatics Platform

The FUGE Bioinformatics technology platform is organized as a national network with nodes in Bergen, Oslo and Trondheim and they have a close collaboration with Tromsø. The platform is responsible for a helpdesk service providing bioinformatics support to projects and research groups, and also contributes bioinformatics competence as an active partner in research projects. At NTNU the platform is associated with the research group for Bioinformatics & Gene Regulation, which provides a strong research basis for the technology services provided by the platform.

The technology platform is based on a close collaboration between the network nodes, where each node will contribute its specialized bioinformatics competence towards research projects, coordinated through the national helpdesk. The NTNU node has particular responsibility for services associated with gene regulation, including both transcription factor (TF) based regulation and regulation through non-coding RNA molecules (ncRNA / microRNA). We have developed improved tools for identifying regulatory TF modules (Compo) and for benchmarking such tools. Benchmarking is a standardized approach for comparing the performance of different tools, and is essential for identifying optimal methods. Our benchmarking tools are available on the web, and have been used by other groups for benchmarking. We are now using these tools for developing methods for improved mapping of gene regulation, both through research collaborations and as master's projects. MicroRNAs regulate genes by interaction with messenger RNA (mRNA) thereby blocking translation. We are developing improved methods for identifying target genes of microRNAs. Through international collaboration we have also shown that microRNAs may regulate gene transcription by affecting the gene promoter, rather than the mRNA. This knowledge is important for understanding the regulatory potential of microRNAs.

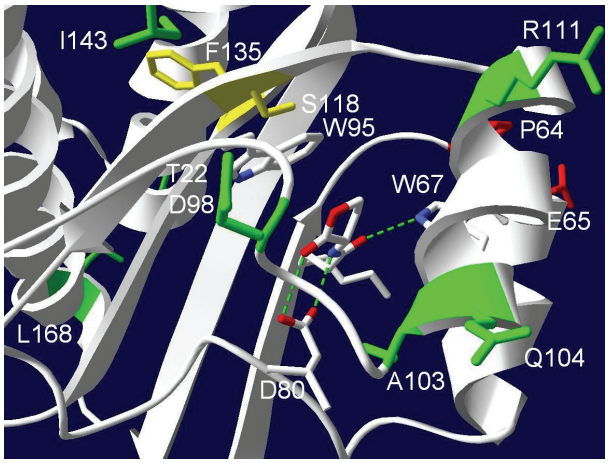
The NTNU node also has a close collaboration with the FUGE Proteomics technology platform through a shared position. As part of this collaboration the platform is developing improved tools for large scale analysis of proteomics data from mass spectrometry.

Through the helpdesk as well as direct collaboration the NTNU node has contributed to several research projects. Relevant examples are mapping and analysis of transcription factor binding sites in genes involved in immune response (Marit W. Anthonsen, NTNU) and proliferative response (Katarina Jørgensen, NTNU), structure prediction of bacterial gene regulators (Svein Valla, NTNU) and viral proteins

(Siri Mjaaland, Norwegian School of Veterinary Science) and analysis of bacterial quorum signalling components (Live Nesse, National Veterinary Institute)

The NTNU node is responsible for the course MTEK3001 Applied Bioinformatics and Systems Biology, which is part of the specialization in bioinformatics in the International Master in Medical Technology. It is also involved in BT8102 Molecular and Cellular Bioinformatics, TDT4287 Algorithms for Bioinformatics and other courses. It has been responsible for the Programme for Bioinformatics guest lectures in 2008. In 2009 the NTNU node will be responsible for several courses, seminars and meetings, including the national bioinformatics meeting for PhD candidates and postdocs (BFYS 2009).

http://www.bioinfo.no/
http://tare.medisin.ntnu.no/



Ligand binding in bacterial cell-cell communication.

BIOINFORMATICS

is the application of information technology to the field of molecular biology.

Bioinformatics nowadays entails the creation and advancement of databases, algorithms, computational and statistical techniques, and theory to solve formal and practical problems arising from the management and analysis of biological data. (*Wikipedia*)

Biobanks for Health – BioHealth Norway

The FUGE technology platform Biobanks for Health (BioHealth Norway) is a joint collaborative project between NIPH (Mother and Child), UiB, UiO, UiTø and NTNU together forming a large population based cohort established for genetic epidemiologic research. The cohort consists of biological samples and standardized health and exposure data from ~ 500 000 Norwegian individuals of all ages, corresponding to approximately 1/10 of the Norwegian population. BioHealth comprise of CONOR (Cohort of Norway – Tromsø, HUNT 2, HUSK, HUBRO, OPPHED, TROFINN, HUNT 3 and Tromsø 6) and MoBa (Mother Child Cohort) of which samples from CONOR are stored at the National Norwegian Biobank (HUNT Biobank).

The biobank is specially designed for this purpose and is offering state-of-the art infrastructure for sample handling and processing. In addition, a completely automated sample storage and retrieval facility for DNA samples operating at -20°C (installed by REMP AG, Switzerland) will be operational within the first half of 2009.

The Biobank is using the Nautilus LIMS (Laboratory Information Management System) developed by Thermo Electron Corporation for cold chain logistics and management and as sample inventory system. The LIMS is integrated with a fully automated sample fractionation and aliquotting system operating at 4°C developed and implemented by RTS® (Robotic Technology Systems, UK). This unit was initially used for processing the HUNT3 samples.

DNA has been extracted from 120 000 samples from the CONOR biobank. Standard protocols for DNA extraction and quality control has been developed on and implemented. The Biobank has manual as well as automated DNA isolation facilities with a throughput of 200-300 samples per day. A robotic system (Biomek NX from Beckman Coulter) for assessment of DNA quality and yield with the same throughput is used. DNA concentration is determined by pico green / standard curve measurements and concentrations normalized to either 5, 25 or 50 ng/µl. In addition, every 8th sample is measured spectrophotometrically to determine the OD260/280 ratio for quality assessment and for an independent concentration determination. On every 8th sample SNP analyses for quality control are also performed with either Roche's Light Cycler System or with a high-throughput 7900HT FAST real time PCR System from Applied Biosystems.

For the other regional cohorts, the same procedures are followed regarding processing, quality control and storage of samples. However, the final step involving DNA measurements and concentration normalization of each sample are done on a project basis before delivery.

The Biobank has established standard protocols for the selection, quality control and delivery of samples for internal and external projects. In 2008 the Biobank was occupied with 16 projects involving the delivery of ~ 26 000 samples of which ~ 2000 were serum samples and the rest DNA-samples from HUNT 2 and Tromsø 4.

The 7900HT system located in the Biobank is suitable for analysing few SNPs on a large number of samples. At the present set-up the throughput in the Biobank is approximately 5000 genotypes a day. In addition to quality testing of DNA, this system is used for SNP genotyping on a project related basis. In addition to internal projects the systems was used in 3 external projects in 2008 involving from 1- 4 SNPs on ~ 7000 samples.

FUGE II nodes in Mid-Norway:

- The Norwegian Bioinformatics Platform
  - Node leader Mid-Norway: Finn Drabløs
- Biobanker for Helse – BioHealth Norway
  - Node leader Mid-Norway: Kristian Hveem
- The Norwegian Microarray Consortium – NMC
  - Node leader Mid-Norway: Arne Sandvik
  - Node leader Mid-Norway (plants): Atle Bones
- The Norwegian Molecular Imaging Centre – NorMIC
  - Node leader Mid-Norway (sub cellular imaging): Catharina De Lange Davies
  - Node leader Mid-Norway (whole animal imaging): Olav Haraldseth
- The Norwegian Proteomics Consortium – NorProteomics
  - Node leader Mid-Norway: Geir Slupphaug

The Norwegian Microarray Consortium - NMC

Microarray is a powerful technology that allows simultaneous measurement of expression levels for up to tens of thousands of genes. With the technology of today you can measure the expression genes in almost any kind of species on earth.

Service provided by NMC at NTNU in 2008:

RNA inn Data out service. For gene expression analysis service, three platforms have been offered (spotted arrays, Affymtrix and Illumina). The general service includes RNA quantity and quality control, labelling, hybridization and scanning of the arrays. Initial data analysis includes image analysis, quality control and generation of list of differentially expressed genes. About 40 different groups/people have used this lab service and about **1150 RNA samples** have gone through our service (Illumina app. 900, Affymetrix app. 20 and spotted arrays app.230 samples). Thirty of these projects are related to different departments at NTNU, three projects related to St. Olavs Hospital, one project from HiST, one from Sintef, three projects from the University of Bergen (including Haukeland University Hospital, Institute of Marine Research in Bergen and NIFES), one project from the Norwegian Institute of Public Health in Oslo, and one project from the University of Tromsø.

In 2008 we also have established a new microRNA (Illumina) service and about **464 samples** have been run through this system. This is related to three projects, two at NTNU and one at the Norwegian Institute of Public Health in Oslo.

DNA in Data out service. New this year is also that we have set up an Illumina whole genome SNP service. About **500 DNA samples** have been run through this pipeline with excellent results. The project was related to NTNU and HUNT.

Illumina CSPro certification:
During 2008 our lab has been working to certify our RNA and DNA service, and in March 2009 we successfully completed the Illumina CSPro™ certification for Gene Expression and SNP genotyping, gaining entry to an elite group of Illumina genomics service providers globally. Illumina CSPro is a collaborative service provider partnership dedicated to ensure the delivery of the highest-quality data available for genetic analysis applications.

Microarray printing service:
During 2008, the NTNU node of the NMC FUGE platform, has take over the national responsibility for microarray printing. We have printed about 400 Arabidopsis arrays and 20 cod arrays for groups at NTNU, and been involved in two projects, printing two microbe genomes (200 arrays), for a group at the University of Oslo and one project printing 200 cod arrays for NIFES in Bergen.

Bioinformatics data analysis service:
Our group offers an extended bioinformatics data analysis service. Most of the service has been aimed towards practical analysis, summary and presentation of gene expression microarray data for researchers present at NTNU, according to the project described in section RNA/DNA in Data out lab service. Establishing microRNA microarray technology as a part of our service has been a major goal during this period and development of analysis methods for quality assurance, pre-processing and statistical analysis of microRNA data has been undertaken. In-house software for quality assurance and pre-processing of microRNA data was developed in order to deliver microRNA analysis to customers.

Courses:
In 2008 our personnel have been responsible for organizing lectures and lab training at the NTNU PhD courses Mol8003 and Mol8004 (Microarray technology and data analysis). About 35 students participated on these courses. We also participated with lectures at other master's and PhD courses at NTNU (e.g. Mol3011 and Mol3006). In addition, two of us have also participated at platform related courses in Oslo and Tromsø in 2008.

National FUGE II Platforms:

- The Norwegian Bioinformatics Platform
- Biobanker for Helse – BioHealth Norway
- The Norwegian centre for integrative genetics – CIGENE
- The Norwegian Microarray Consortium – NMC
- The Norwegian Structural Biology Centre – NORSTRUCT
- The Norwegian Molecular Imaging Centre – NorMIC
- The Norwegian Proteomics Consortium – NorProteomics
- The Norwegian Zebrafish Platform – ZEBRAFISH
- Ultra-High Throughput Sequencing Platform - UTSP

The Norwegian Microarray Consortium - NARC

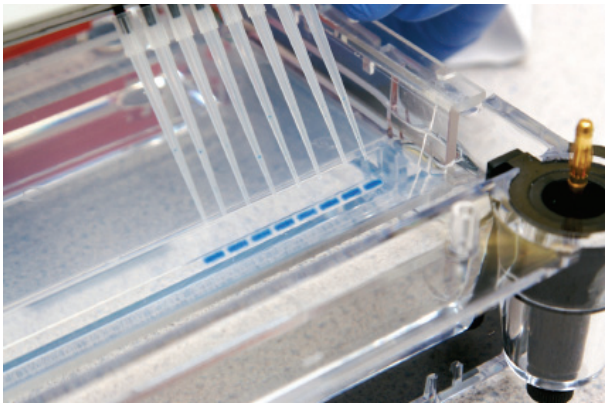
The NTNU Cell and Molecular Biology (CMB) group is host to the Norwegian Arabidopsis Research Centre (NARC). The NARC lab at NTNU is equipped with state of the art equipment for microarray analysis. We have to our disposal a semi-automatic hybridization station (Advalytix ArrayBooster TM) and an Agilent microarray scanner.

The Microarray node has in 2008 conducted transcript analysis for a number of research groups both at NTNU and nationally. Most of the analyses have been done on the model plant Arabidopsis thaliana, but we have also been running analyses on other plants, Lemna minor, Fragaria vesca, Brassica napus and Phaeodactylum tricornutum.

Services at the NARC node for 2008:

Researchers at IBI/NT:
Ishita Ahuja
Ole Petter Thangstad
Anna Kusnierczyk
Jens Rohloff
Per Winge
Ralph Kissen
Marianne Nymark
Tore Brembu
Ann-Iren Kitang
Brita Kvaløy
Margrethe Jørstad

National researchers:
Melinka Butenko, UiO
Anna Levandowska Sabat, UMB
Paul Grini, UIO
Rolf Selset, Calcus AS
Muath Alsheikh, Graminor.
Ralf Westling (Germany)



The
Norwegian Molecular Imaging Consortium
- NorMIC
- Subcellular Interactions and Imaging

The unique aspect of the "Subcellular Intractions and Imaging" node is that it provides a broad assembly of experimental methods for imaging and for studies of inter- and intramolecular interactions.

The node is a collaboration between the Faculty of Medicine: Dept. of Cancer Research and Molecular Medicine, and the Faculty of Natural Sciences and Technology, Dept. of Biology and Dept of Physics.

The instrumentation includes: 2 confocal laser scanning microscopes (CLSM) and 2 CLSM for fast image acquisition used in dynamic studies, two-photon microscope, fluorescence correlation spectroscopy (FCS), as well as atomic force microscopy (AFM). In 2008 a new setup with combined AFM and total internal reflection optical microscope was installed.

In 2008 the following projects have benefitted from the service and instrumentation of the node:

Delivery of nanomedicine in tumour tissue
CLSM has been used to localize nanomedicine extra- and intracellular. FCS and fluorescence recovery after photobleaching (FRAP) have been used to study diffusion of macromolecules. FCS has also been used to study interactions between DNA and chitosan which is a potential carrier in DNA delivery.

Clinical applications of multiphoton microscopy
Multiphoton microscopy and the second harmonic signal are used for 3D imaging of atherosclerosis and valvular fibrosis without exogenous staining. Mechanical properties of the tissues are characterized.

Angiogenesis
CLSM was used to study formation of vessels in scaffolds implanted in dorsal window chambers in athymic mice.

Signalling mechanism of Toll-like receptors
A variant (TAG) of the adaptor molecule TRAM has been identified.

CLSM imaging of TAG has revealed that the molecule is expressed in endoplasmic reticulum in resting cells. Lipo-polysaccharide stimulates translocation of TAG to late endosomes and inhibits IFN-β production. Also expression and intacellular trafficking of Toll-like receptor 2 have been performed in close collaboration with the NorMIC platform in Oslo.

Selective photobleaching as a tool for studies of intracellular transport
High-speed confocal microscopy has been used for selective photobleaching of ER exports sites in *Arabidopsis thaliana* to study intracellular transport through ER-Golgi. A quantitative method has been established and used to study the role of the regulatory protein AtSAR1. ATSAR1 has been shown to be a marker for ER-export sites at the interface between ER and the Golgi apparatus.

The role of AtRAC7 in auxin signalling and root development
CLSM in combination with yeast two-hybrid interaction analysis has been used in functional studies and to localize AtRAC7 and other components involved in auxin signalling during root development. Various constructs have been made, plants transformed and analysed.

Polyelectrolyte complex formation in developing gene-delivery vectors and excipients
The AFM instrumentation has been employed for characterization of structure of polyelectrolyte complexes related to gene delivery, material formulations for drug delivery, polynucleotide-polysaccharide characterization, and structure formation of CpG DNA.

Target strategy of DNA repair proteins
The AFM instrumentation has been applied for ultrastructural determination of DNA fragments and selected DNA repair proteins as the initial phase of project aiming at elucidating the target search strategy.

The logic of olfaction
Small neural networks in invertebrates are perfectly suited for studying basic principles concerning brain processes in general. By performing intracellular recordings and staining combined with CLSM from the primary olfactory centre of the moth brain, the logic of olfactory coding mechanisms is studied

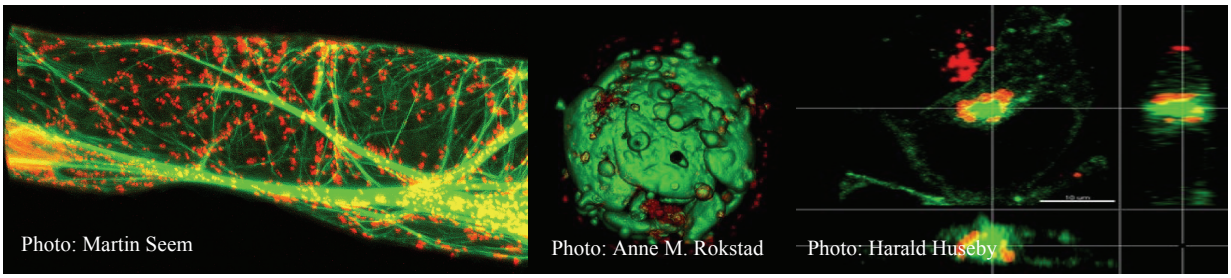


Photo: Martin Seem

Photo: Anne M. Rokstad

Photo: Harald Huseby

The Norwegian Molecular Imaging Centre - NorMIC – Whole animal imaging

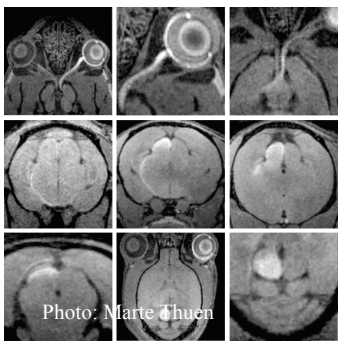
FUGE Molecular Imaging Centre Trondheim offers collaborating projects with national and international research groups that are interested in *in vivo* MR imaging and spectroscopy (MRI and MRS) of small animals. We facilitate in areas such as experimental planning, optimizing of MR protocols, running of MR experiments, post processing of MR data and writing of scientific papers.

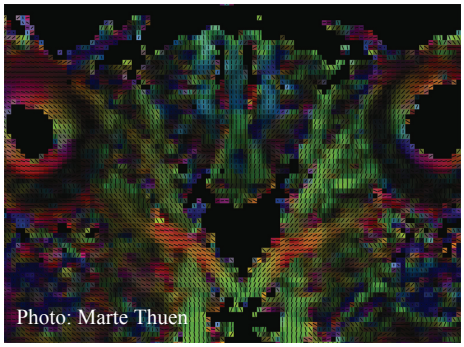
Today's research activity is mainly concentrated around preclinical studies of animal models of diseases and transgenic mice in order to survey *in-vivo* effects of gene modifications, as well as monitoring the effect of new treatments. The future goal is to be able to transfer the best ideas into clinical use, thereby opening up substantial industrial opportunities.

Activities in 2008:

- MRI monitoring of stem cells and cellular therapeutics. Project leader: Post doc Marte Thuen. Collaborator: Prof. Joel Glover, University of Oslo
- Water transport in Aquaporin deficient mice. Project leader: Post doc Tina Pavlin. Collaborator: Prof. Ole Petter Ottersen, University of Oslo.
- CNS injury caused by decompression. Project leader: PhD student Marius Widerøe/ Post doc Marte Thuen. Collaborators: Prof. Alf Brubakk, Dept. of Circulation and Medical Imaging, NTNU and Senior researcher Arvid Hope, NUI, Bergen.
- Manganese-alginate gels for controlled-release of manganese. Project leader: Researcher Christian Brekken. Collaborators: Prof Gudmund Skjåk-Bræk and Post doc Yrr Mørch, Dept. of Biotechnology, NTNU.
- High-resolution MRI of cardiac infarction. Project leader: Post doc Marte Thuen. Collaborator, Prof. Godfrey Smith, University of Glasgow and Post doc Brage Amundsen, Dept. of Circulation and Medical Imaging, NTNU.
- MR imaging of stem cells in transplant-mediated CNS repair. PhD project of Ioanna Sandvig. Supervisors: Post doc Marte Thuen, Associated Prof. Asta Håberg and Prof. Olav Haraldseth. Collaborators: Prof. Martin Berry, University of Birmingham. and MD PhD Axel Sandvig, St Olavs Hospital.
- Characterization of myocardial alternations in dysfunctional hears using complementary MR techniques. PhD project of Kristine Skårdal. Supervisors: Post doc Marte Thuen, Prof. Olav Haraldseth and Physicist Pål Erik Goa (St. Olavs Hospital). Collaborators: Prof. Ulrik Wisløf, Dept. of Circulation and Medical Imaging, NTNU.
- Molecular and functional imaging of therapeutic macromolecules in tissue. PhD-project of Nina Reitan, Dept. of Physics, NTNU. Supervisors: Prof. Catharina Davies, Dept. of Physics, NTNU.
- Manganese-enhanced and diffusion tensor imaging of the normal, injured and regenerating rat visual pathway. PhD project of Marte Thuen. Supervisors: Prof. Olav Haraldseth and Researcher Christian Brekken. Collaborators: Prof. Martin Berry, University of Birmingham. and MD PhD Axel Sandvig, St Olavs Hospital. PhD defended in Aug 2008.

If not otherwise stated, the people involved in the projects are associated with Fuge Molecular Imaging Center and employed at Dept. of Circulation and Medical Imaging, NTNU.





Meetings and Seminar

Functional genomics researchers were invited to suggest speakers for the 2008 FUGE seminar series. The seminar series was intended to develop existing functional genomics contacts and establish new ones both nationally and internationally, and featured both guest lectures and seminars.

Guest lectures 2008

- **Professor Ole Christian Lingjærde,** University of Oslo, Oslo, Norway**,** "PLS Cox regression for genome-wide".
- **Dr. Thomas M. Halder**, TOPLAB Gesellschaft für angewandte Biotechnologie mbH in Martinsried, Germany , "New Developments in Quantitative Proteomics"

Seminars 2008

- **Seminar i MR Metabolomics** – arranged by Ingrid Gribbestad.
- **Symposium in microbial biotechnology** – arranged by Sven Even Borgos and Magnus Steigedal. On the occasion of Professor Svein Vallas' 60-anniversary a symposium was held in microbial biotechnology.
- **First national user meeting for NorMIC** – arranged by Catharina de Lange Davies.
- **Conference on Systems Biology and disease** – arranged by Hans Krokan and Nils Baas.

"Oppdalsmøtet"

In addition, FUGE Mid-Norway and The Norwegian Biochemical Society (Division Trøndelag) arranged a seminar at Quality Hotel Røros. The overall goal of the seminar was to present FUGE II projects funded by the Research Council of Norway. Sixty-five researchers from Mid-Norway attended the seminar.

Information meetings 2008

The FUGE II-period had a kick-off early in 2008. In order to inform about the services provided for the FUGE II period. ,FUGE Mid-Norway arranged information meetings together with the nodes in mid-Norway throughout the spring. Altogether, we had five information meetings: Biobanks, Molecular Imaging, Proteomics, Bioinformatics and Microarray.

FUGE Mid-Norway Award 2008

To celebrate the funds received for the FUGE II period, FUGE Mid-Norway arranged a mini-seminar followed by a Christmas lunch. Thirty researchers attended the seminar, which featured a great presentation by Professor Hans Krokan on "Forskning i Norge - Utsikt fra elfenbenstårnet". After the presentation the winner of the FUGE Mid-Norway Award 2008 was presented. The first FUGE Mid-Norway award was given to PhD candidate Ingvill Bjellmo Johnsen and Prof. Marit Anthonsen (IKMM/DMF/NTNU). In addition to a diploma and a work of art the award winners got NOK 30 000 to be used for their research. After the presentation of the award winners, a Christmas lunch was served.

The FUGE Mid-Norway award winners 2008:
PhD candidate Ingvill Bjellmo Johnsen and Prof. Marit Anthonsen

Action Plan

A new action plan for the FUGE committee and board was processed for 2009. The plan can be found on our website: http://www.ntnu.no/fuge/organisasjon

Seed Funding

As a strategic action for developing and strengthening functional genomics research in Mid-Norway, FUGE Mid-Norway announced a variety of grants in 2008.

Three post doc positions

FUGE Mid-Norway was given three post doctoral positions from the NTNU SO-funds. The post doctoral positions were announced and made available for all functional genomics researchers at NTNU. An international review panel was set up to review the applications. The positions were given to:

- Trond M. Kortner, "Molecular ontogeny of digestive capability in Atlantic cod larvae", project leader: Augustine Arukwe.
- Steven Vercruysse, "Fact finding in systems biology", project leader: Martin Kuiper.
- Anna Kusnierczyk, "A system biology approach to understand plant adaptive innate immunity", project leader: Atle Bones

Engineer

In order to enhance functional genomics research areas outside the technology platforms, FUGE Mid-Norway announced SO-funds for an engineer (four years). All research groups at NTNU could apply for the funds. The engineer position was given to the system biology research group headed by Martin Kuiper.

Adjunct Professors

Three Adjunct Professors were employed with the funds given to us by the Research Council of Norway:

- Ole Nørregaard Jensen
- Eicke Latz
- Jens Nielsen

Travel grants

Funding from the Research Council of Norway made it possible to announce travel grants in order to support international networking. The grants were awarded to:

- Kirsti Kvaløy
- Carl-Jørgen Arum
- Maria Tunset Grinde
- Martin Seem
- Åsa Alexandra Borg
- Toril Holien
- Marit Sletmoen

Funds to use the technology platforms

The FUGE technology platforms offer researchers various services within specific technologies that are important to functional genomics research. To facilitate interaction between researchers and the technology platforms, FUGE Mid-Norway allocated money to researchers who planned to collaborate with and use the technology platforms. To that end, the following research grants were awarded:

- Kirsti Kvaløy
- Berit Johansen
- Frank Skorpen
- Gaute Brede
- Ralph Kissen
- Per Bruheim
- Marit Anthonsen
- Hans Krokan
- Turid Rustad
- Jens Rohloff
- Anja Bye

WEB pages

Today's technology has made it important to have updated web pages. The funds given to FUGE Mid-Norway from the Research Council of Norway supported updating or establishing of web pages – and for 2008 financial support was given to the Microarray node in Mid-Norway (Prof. Arne Sandvik).

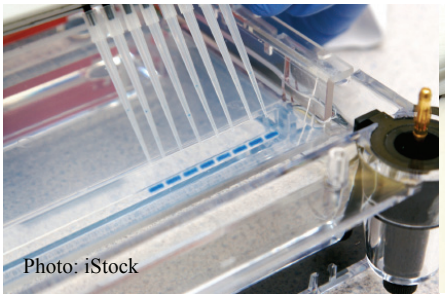


Photo: iStock

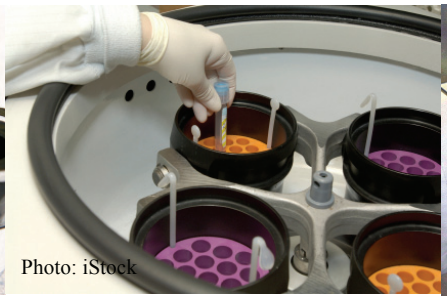


Photo: iStock


Photo: W. Kusnierczyk

Innovation

Innovation is important in functional genomics, as the discipline and its associated technologies are developing rapidly. Many of the FUGE technologies can be used for industrial and commercial development. Two focused business projects were supported by FUGE Mid-Norway in 2008:

- Vectron Biosolutions by Trond E. V. Aune
- Micronax AS by Jarle Kotsbak

Disputations

The following candidates have successfully defended their theses for a PhD degree at NTNU in 2008 within functional genomics:

- Ottar Sundheim, PhD,
  "Structure-function analysis of human enzymes initiating nucleobase repair in DNA and RNA"
- Lars Hagen, PhD,
  "Regulation of DNA Base excision repair by protein interactions and post-translational modifications".
- Nadra Jesmine Nilsen, PhD,
  "Toll-like Receptor 2, Expression, regulation and signaling".
- Marte Thuen ,PhD,
  "Manganese-enhanced and diffusion tensor MR imaging of the normal, injured and regenerating rat visual pathway".
- Line Elisabeth Sundt-Hansen, PhD,
  "Cost of Rapid Growth in Salmonid Fishes"
- Lena Neregård, PhD,
  "Growth Physiology and Behaviour in Salmonids: Focus on Growth Hormone-Induced Effects"
- Tommy Jørstad, PhD,
  "Statistical modelling of gene expression data"
- Kristin Spilker, PhD,
  "Assistert slektskap: Biopolitikk i reproduksjonsteknologienes tidsalder".
- Torun Melø, PhD,
  "Neuronal Glial Interactions in Epilepsy"
- Irina P. Eide, PhD,
  "Fetal growth restriction and pre-eclampsia: some characteristics of fetomaternal interactions".

Publications

- **Abul, Osman, Sandve, Geir Kjetil, Drabløs, Finn.** TScan: A two-step de novo motif discovery method. *Series on Advances in Bioinformatics and Computational Biology* 2008, 8:19
- **Bratlie, Marit Skyrud, Johansen, Jostein, Drabløs, Finn.** Why do bacterial genes form operons? Computational Methods in Systems Biology, Rostock, Germany, October 12-15, 2008
- **Klepper, Kjetil, Sandve, Geir Kjetil, Abul, Osman, Johansen, Jostein, Drabløs, Finn.** Assessment of composite motif discovery methods. *BMC Bioinformatics* 2008, 9:123
- **Sandve, Geir Kjetil, Abul, Osman, Drabløs, Finn.** Compo: composite motif discovery using discrete models. *BMC Bioinformatics* 2008, 9:527
- **Kim, D.H., Saetrom, P., Snove, O.J., Rossi, J.J.** MicroRNA-directed transcriptional gene silencing in mammalian cells. *PNAS* 2008, 105(42):16230-16235
- **Soifer, H.S., Sano, M., Sakurai, K., Chomchan, P., Saetrom, P., Sherman, M.A., Collingwood, M.A., Behlke, M.A., Rossi, J.J.** A role for the Dicer helicase domain in the processing of thermodynamically unstable hairpin RNAs. *Nucleic Acids Res.* 2008, 36(20):6511-6522
- **Aagaard, L., Zhang, J., von Eije, K.J., Li, H, Saetrom, P., Amarzguioui, M, Rossi, J.J.** Engineering and optimization of the miR-106b cluster for ectopic expression of multiplexed anti-HIV RNAs. *Gene Therapy* 2008, 15(23):1536-1549
- **Lee, N.S., Kim, J.S., Cho, W.J., Lee, M.R., Steiner, R., Gompers, A., Ling, D., Zhang, J., Strom, P., Behlke, M., Moon, S.-H., Salvaterra, P.M., Jove, R., Kim, K.-S.** miR-302b maintains "stemness" of human embryonal carcinoma cells by post-transcriptional regulation of Cyclin D2 expression. *Biochem. Biophys. Res. Com.* 2008, 377(2):434-440
- **Smith, D.D.; Saetrom, P.; Snove, O.J.; Lundberg, C.; Rivas, G.E.;Glackin, C.; Larson, G.P.** "Meta-analysis of breast cancer microarray studies inconjunction with conserved cis-elements suggest patterns for coordinate regulation" BMC bioinformatics 2008,9():63
- **Hung RJ, Mckay JD, Gaborieau V, Boffetta P, Hashibe M, Zaridze D, Mukeria A, Szeszenia-Dabrowska N, Lissowska J, Rudnai P, Fabianova E, Mates D, Bencko V, Foretova L, Janout V, Chen C, Goodman G, Field JK, Liloglou T, Xinarianos G, Cassidy A, McLaughlin J, Liu G, Narod S, Krokan H E, Skorpen F, Elvestad M B, Hveem K, Vatten L J, Linseisen J, Clavel-Chapelon F, Vineis P, Bueno-De-Mesquita HB, Lund E, Martinez C, Bingham S, Rasmuson T, Hainaut P, Riboli E, Ahrens**

W, Benhamou S, Lagiou P, Trichopoulos D, Holcatova I, Merletti F, Kjaerheim K, Agudo A, Macfarlane G, Talamini R, Simonato L, Lowry R, Conway DI, Znaor A, Healy C, Zelenika D, Boland A, Delepine M, Foglio M, Lechner D, Matsuda F, Blanche H, Gut I, Heath S, Lathrop M, Brennan P. A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25. *Nature* 2008 ;Volume 452: 633-637

- **Asberg, A, Hveem, Kristian,** Screening fro haemochromatosis. *Blood* 2008 ;Volume 111.(7)
- **Jansson C , Nordenstedt H , Wallander MA , Johansson S , Johnsen R , Hveem K , Lagergren J.** Severe symptoms of gastro-oesophageal reflux disease are associated with cardovascular disease and other gastrointestinal symptoms, but not diabetes: a population-based study. *Alimentary Pharmacology and Therapeutics* 2008 ;Volume 27.(1):. 58-65
- **Sjodahl K , Jia CQ , Vatten L J , Nilsen TIL , Hveem K , Lagergren J.** Body mass and physical activity and risk of gastric cancer in a population-based cohort study in Norway. *Cancer Epidemiology, Biomarkers and Prevention* 2008;Volume 17: 135-140
- **Sjödahl K, Jia C, Vatten L Johan, Nilsen T I L, Hveem K, Lagergren J.** Salt and Gastric Adenocarcinoma: A Population-Based Cohort Study in Norway. *Cancer Epidemiology, Biomarkers and Prevention* 2008 ;Volume 17.(8): 1997-2001
- **Zeggini E, Scott LJ, Saxena R, Voight BF, Marchini JL, Hu T, de Bakker PIW, Abecasis GR, Almgren P, Andersen G, Ardlie K, Bostroem KB, Bergman RN, Bonnycastle LL, Borch-Johnsen K, Burtt NP, Chen H, Chines PS, Daly MJ, Deodhar P, Ding CJ, Doney ASF, Duren WL, Elliott KS, Erdos MR, Frayling TM, Freathy RM, Gianniny L, Grallert H, Grarup N, Groves CJ, Guiducci C, Hansen T, Herder C, Hitman GA, Hughes TE, Isomaa B, Jackson AU, Jorgensen T, Kong A, Kubalanza K, Kuruvilla FG, Kuusisto J, Langenberg C, Lango H, Lauritzen T, Li Y, Lindgren CM, Lyssenko V, Marvelle AF, Meisinger C, Midthjell Kristian, Mohlke KL, Morken MA, Morris AD, Narisu N, Nilsson P, Owen KR, Palmer CNA, Payne F, Perry JRB, Pettersen E, Platou CGP, Prokopenko I, Qi L, Qin L, Rayner NW, Rees M, Roix JJ, Sandbaek A, Shields B, Sjogren M, Steinthorsdottir V, Stringham HM, Swift AJ, Thorleifsson G, Thorsteinsdottir U, Timpson NJ, Tuomi T, Tuomilehto J, Walker M, Watanabe RM, Weedon MN, Willer CJ, Illig T, Hveem K, Hu FB, Laakso M, Stefansson K, Pedersen O, Wareham NJ, Barroso I, Hattersley AT, Collins FS, Groop L, McCarthy MI, Boehnke M, Altshuler D.** Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics* 2008 ;Volume 40.(5) s. 638-645
- **Hagen L, Kavli BM, Sousa M, Torseth K, Liabakk N-B, Sundheim O, Diaz JP, Otterlei M, Hørning O, Jensen ON, Krokan HE, Slupphaug G.** Cell cycle-specific UNG2 phosphorylations regulate protein turnover, activity and association with RPA. *EMBO Journal* 2008 ;Volume 27.(1): 51-61
- **Sundheim O, Talstad VA, Vågbø CB, Slupphaug G, Krokan HE.** AlkB demethylases flip out in different ways. *DNA Repair* 2008 ;Volume 7.(11): 1916-1923
- **Visnes T, Akbari M, Hagen L, Slupphaug G, Krokan HE.** The rate of base excision repair of uracil is controlled by the initiating glycosylase. *DNA Repair* 2008 ;Volume 7.(11): 1869-1881
- **Visnes T, Doseth B, Pettersen HS, Hagen L, Sousa M, Akbari M, Otterlei M, Kavli BM, Slupphaug G, Krokan HE.** Uracil in DNA and its processing by different DNA glycosylases. *Philos Trans R Soc Lond B Biol Sci* 2008 ;Volume Nov13
- **Westbye M, Feyzi E, Aas PA, Vågbø CB, Talstad VA, Kavli BM, Hagen L, Sundheim O, Akbari M, Liabakk N-B, Slupphaug G, Otterlei M, Krokan HE.** Human AlkB homolog 1 is a mitochondrial protein that demethylates 3-methylcytosine in DNA and RNA. *Journal of Biological Chemistry* 2008 ;Volume 238.(36): 25046-25056
- **Sletmoen, M., Maurstad, G. and Stokke, B. T.** Potentials of bionanotechnology in the study and manufacturing of self-assembled biopolymer complexes and gels. *Food Hydrocolloids* **22**(1) (2008): 2-11.
- **Sæther, H.V., Holme, H., Maurstad, G., Smidsrød, O., and Stokke, B.T.** Polyelectrolyte complex formation using alginate and chitosan *Carbohydrate Polymers* **74** (2008) 813-821.
- **Marken, E. Maurstad, G. and Stokke, B.T.** Quantitative analysis of atomic force microscopy topographs of biopolymer multilayers: Surface structure and polymer assembly modes *Thin Solid Films* **516** (2008) 7770-7776.
- **Sletmoen, M. and Stokke, B.T.** Higher order structure of (1,3)-β-D-glucans and its

influence on their biological activities and complexation abilities. *Biopolymers* **89** (2008) 310-321.

- **Erikson, A., Andersen, H. N., Næss, S. N. and Davies, C. de L.** Physical and chemical modifications of collagen gels: Impact on diffusion. *Biopolymers* **89**(2) (2008):135-143.
- **Fagerli, U.-M., Holt, R. U., Holien, T., Vaatsveen, T. K., Zahn, F., Egeberg, K. W., Barlogie, B., Waage, A., Aarset, H., Dai, H. Y., Shaughnessy Jr, J. D., Sundan, A. and Børset, M.** Overexpression and involvement in migration by the metastasis-associated phosphatase PRL-3 in human myeloma cells. *Blood* **111**(2) (2008): 806-815.
- **Erikson, A., Tufto, I., Bjønnum, AB., Bruland, Ø., Davies, C De Lange.** The impact of enzymatic degradation on the uptake of differently sized therapeutic molecules. *Anticancer Research* 2008 ;Volume 28: 3557-3566
- **Hompland, T., Erikson, A., Lindgren, M., Lindmo, T., Davies, C de Lange.** Second-harmonic generation in collagen as a potential cancer diagnostic parameter. *Journal of Biomedical Optics* 2008 ;Volume 13.(05): 054050-
- **Reitan, NK., Juthajan, A., Lindmo, T., Davies, C de Lange.** Macromolecular diffusion in the extracellular matrix measured by fluorescence correlation spectroscopy. *Journal of Biomedical Optics* 2008 ;Volume 13.(5): 054040-
- **Schnell, EA., Eikenes, L., Tufto, I., Erikson, A., Juthajan, A., Lindgren, M., Davies, C de Lange.** Diffusion measured by fluorescence recovery after photobleaching based on multiphoton excitation laser scanning microscopy. *Journal of Biomedical Optics* 2008 ;Volume 13.(6): 064037-
- **Nilsen NJ, Deininger S, Nonstad U, Skjeldal F, Husebye H, Rodionov D, von, Aulock S, Hartung T, Lien E, Bakke O, Espevik T.** Cellular trafficking of lipoteichoic acid and Toll-like receptor 2 in relation to signaling: role of CD14 and CD36. J Leukoc Biol. 2008 Jul;84(1):280-91.
- **Kissen R, Rossiter JT and Bones AM, 2008.** The “mustard oil bomb”: not so easy to assemble?! Localization, expression and distribution of components of the myrosinase enzyme system. *Phytochemistry Reviews* 8: 69-86. DOI 10.1007/s11101-008-9109-1 (online 9-11-2008)
- **Ahuja I, Winge P, Kusnierczyk A, Jørstad TS, Bones AM.** Analysing and elucidating the role of Arabidopsis thioglucosidase glucohydrolase 1 (myrosinase) towards dehydration and methyl jasmonate. *Physiologia Plantarum : An International Journal for Plant Biology* 2008 ;Volume 133.(3)
- **Brembu T, Ween O, Ripel L, Winge P, Bones AM.** A possible role for the small GTPase AtRAC7 in auxin signaling in Arabidopsis. *Physiologia Plantarum : An International Journal for Plant Biology* 2008 ;Volume 133.(3)
- **Butenko M, Stenvik GE., Shi SL, Vie AK, Guo Y, Clark SE, Bones AM., Aalen, RB.** The control of floral organ abscission by inflorescence deficient in abscission (IDA) is dependent on the receptor-like kinase HAESA and HAESA-LIKE 2. *Physiologia Plantarum : An International Journal for Plant Biology* 2008 ,Volume 133.(3)
- **Thuen M, Goa PE, Bugge Pedersen T, Berry M, Summerfield MR, Sandvig A, Haraldseth O, Brekken C.** Manganese-enhanced MRI of the rat visual pathway: acute neural toxicity, contrast enhancement, axon resolution, axonal transport and clearance of Mn^{2+}. *J Magn Reson Imag* 28 (4): 855-865, 2008.
- **Widerøe M, Olsen O, Pedersen TB, Goa PE, Kavelaars A, Heijnen C, Skranes J, Brubakk AM, Brekken C.** Manganese-enhanced magnetic resonance imaging of hypoxic-ischemic brain injury in the neonatal rat. *Neuroimage* 2008 (Epub ahead of print).
- **Olsen Ø, Thuen M, Berry M, Kovalev V, Petrou M, Goa PE, Sandvig A, Haraldseth O, Brekken C.** Axon tracing in the adult rat optic nerve and tract after intravitreal injection of MnDPDP using a semi-automatic segmentation technique. *J Magn Reson Imag* 27 (1): 34-42, 2008.
- **Widerøe M, Brekken C, Kavelaars A, Skranes J, van Bel F, Heijnen C, Brubakk AM.** Manganese-enhanced MRI (MEMRI) of ongoing inflammation and delayed neuronal death six weeks after hypoxia-ischemia (HI) in the neonatal rat brain. *Archives of Disease in Childhood* 93, Suppl. II: A207-A209, 2008.
- **Berntsen EM, Samuelsen P, Lagopoulos J, Rasmussen jr. I-A, Håberg A, Haraldseth O.** Mapping the primary motor cortex in healthy subjects and patients with peri-rolandic brain lesions before neurosurgery.. *Neurological Research* 2008 ,Volume 30.(9): 968-973
- **Chappell MH, Kristoffersen A, Goa PE, Lehn H, Haraldseth O, Håberg A**. High resolution fMRI of the medial temporal lobe: is balanced SSFP a viable option? *Human Brain Mapping* 2008, 2008-06-15 - 2008-06-19

- **Larsson H, Hansen AE, Berg HK, Rostrup E, Haraldseth, O.** Dynamic contrast-enhanced quantitative perfusion measurement of the brain using T-1-weighted MRI at 3T. *Journal of Magnetic Resonance Imaging* 2008 ,Volume 27: 754-762
- **Lindqvist S, Vangberg TR, Haraldseth O, Brubakk A-M, Vik T, Skranes J.** Visual acuity in very low birth weight adolescents correlates with fractional anisotropy values in corpus callosum.. *Archives of Disease in Childhood* 2008 ,Volume 93. Suppl. 2
- **Martinussen M, Skranes J, Løhauge G, Christensen C, Haraldseth O, Fischl B, Dale A, Brubakk A-M.** Low IQ is associated with entorhinal cortical thinning in very low birth weight adolescents. *Archives of Disease in Childhood* 2008 ,Volume 93. Suppl. 2
- **Skranes J, Løhaugen G, Christensen C, Martinussen M, Vangberg TR, Haraldseth O, Fischl B, Dale A, Brubakk A-M.** Interaction between thalamic and cerebral cortical changes during development in very low birth weight adolescents. *Archives of Disease in Childhood* 2008 ,Volume 93. Suppl. 2
- **Thuen M, Haraldseth O.** Manganese-enhanced and diffusion tensor MR imaging of the normal, injured and regenerating rat visual pathway. Trondheim: NTNU 2008 (ISBN 978-82-471-7782-2) 160 s. NTNU
- **Sitter B, Bathen TF, Tessem MB, Gribbestad IS,** High-resolution magic angle spinning (HR MAS) MR spectroscopy in metabolic characterization of human cancer, *Progress in Nuclear Magnetic Resonance Spectroscopy* 54 (2009): 239–254
- **Bye A, Langaas A, Høydal MA, Kemi OJ, Heinrich G, Koch LG, Britton SL,Najja SM, Ellingsen Ø, Wisløff U.** Aerobic capacity-dependent differences in cardiac gene expression. *Physiol Genomics*. 2008 Mar 14,33(1):100-9.
- **Olsvik PA, Lie KK, Mykkeltvedt E, Samuelsen OB, Petersen K, Stavrum AK, Lunestad BT.** Pharmacokinetics and transcriptional effects of the anti-salmon lice drug emamectin benzoate in Atlantic salmon (Salmo salar L.). *MC Pharmacology* 2008, 8:16
- **Jakobsen CH, Størvold GL, Bremseth H, Follestad F, Sand K, Mack M, Olsen KS, Lundemo AG, Iversen JG, Krokan HE, Schønberg SA.** DHA induces ER stress and growth arrest in human colon cancer cells: associations with cholesterol and calcium homeostasis.*Journal of Lipid Research* Volume 49, 2008
- **Fjeldbo CS, Misund K, Günther CC, Langaas M, Steigedal TS, Thommesen L, Lægreid A, Bruland T.** Functional studies on transfected cell microarray analysed by linear regression modeling. *Nucleic Acids Research*, 2008, 1–15
- **Rye MB, Færgestad, Martens H, Wold JP , Alsberg BK.** An improved pixel-based approach for analysing images in two-dimensional gel electrophoresis. *Electrophoresis*. Volume 29 Issue 6, No. 6 March 2008:1382–1393.
- **Rye MB, Færgestad, Alsberg BK**. A new method for assigning common spot boundaries for multiple gels in two-dimensional gel electrophoresis. *Electrophoresis*. Volume 29, Issue 6: No. 6 March 2008, Pages:1359-1368.
- **Rye MB, Alsberg BK.** A multivariate spot filtering model for two-dimensional gel electrophoresis. *Electrophoresis*. Volume 29, Issue 6, Date: No. 6 March 2008, Pages: 1369
- **Kissen R, Rossiter JT, Bones AM (2008)** The 'mustard oil bomb': not so easy to assemble?! Localization, expression and distribution of the components of the myrosinase enzyme system *Phytochem Rev* (2009) 8:69–86
- **Einset J, Winge P, Bones AM and Connolly EL (2008)** The FRO2 ferric reductase is required for glycine betaine's effect on chilling tolerance in *Arabidopsis* root. *Physiologia Plantarum. An International Journal for Plant Biology* 2008; Volume134: 334–341.
- **Brembu, Tore; Ween, Ola; Ripel, Linda; Winge, Per; Bones, Atle M.** A possible role for the small GTPase AtRAC7 in auxin signaling in Arabidopsis. *Physiologia Plantarum: An International Journal for Plant Biology* 2008 ;Volume 133.(3)
- **Einset, John; Winge, Per; Bones, Atle M.; Conolly, EL.** The FRO2 Ferric reductase is required for glycine betaine's effect on chilling tolerance in Arabidopsis roots.. *Physiologia Plantarum: An International Journal for Plant Biology* 2008 ;Volume 134: 334-341
- **Jørstad, Tommy Stokmo; Midelfart, Herman; Bones, Atle M.** A mixture model approach to sample size estimation in two- sample comparative microarray experiments. *BMC Bioinformatics* 2008 ;Volume 9: 117-
- **Kissen, Ralph; Bones, Atle M.** Characterization of novel nitrile specifier proteins (NSPs) involved in glucosinolate hydrolysis in Arabidopsis thaliana. *Physiologia Plantarum : An International Journal for Plant Biology* 2008 ;Volume 133.(3)

- **Kusnierczyk, Anna; Winge, Per; Jørstad, Tommy Stokmo; Troczynska, J.; Rossiter, JT; Bones, Atle M.** Towards global understanding of plant defence against aphids - timing and dynamics of early Arabidopsis defence responses to cabbage aphid (Brevicoryne brassicae) attack. *Plant, Cell and Environment* 2008 ;Volume 31.(8): 1097-1115
- **Kusnierczyk, Anna; Winge, Per; Jørstad, Tommy Stokmo; Troczynska, Joanna; Rossiter, John T.; Bones, Atle M.** Temporal progress of Arabidopsis defence responses during the early phase of infestation with aphids. *Physiologia Plantarum : An International Journal for Plant Biology* 2008 ;Volume 133.(3)
- **Neregård, L., L. Sundt-Hansen, K. Hindar, S. Einum, J. I. Johnsson, R. H. Devlin, I. A. Fleming & B. Th. Björnsson.** 2008. Wild Atlantic salmon *Salmo salar* L. strains have greater growth potential than a domesticated strain selected for fast growth. *J. Fish Biol.* 73: 79-95.
- **Kortner T, Rocha E, Silva P, Castro LFC, Arukwe A,** Genomic approach in evaluating the role of androgens on the growth of Atlantic cod (Gadus morhua) previtellogenic oocytes, *Comparative Biochemistry and Physiology*, Part D 3 (2008) 205–218
- "Eggcellens representasjoner: Vitenskap og kultur"/ i "Vitenskap som dialog, kunnskap i bevegelse. Tverrfaglighet og kunnskapskulturer i endring," **Knut H. Sørensen, Eva Amdahhl, Helen Jøsok Gansmo og Vivian A. Lagesen** (red). Tapir akademisk forlag, Trondheim 2008
- **Alvestad S, Hammer J, Eyjolfsson E, Qu H, Ottersen OP, Sonnewald U.** Limbic structures show altered glial-neuronal metabolism in the chronic phase of kainate induced epilepsy *Neurochem Res* 33:257-66 (2008)
- **Torill E. Sjøbakk, Roar Johansen, Tone F. Bathen, Ursula Sonnewald, Roar Juul, Sverre H. Torp, Steinar Lundgren and Ingrid S. Gribbestad.** Characterization of brain metastases using high-resolution magic angle spinning MRS. *NMR in Biomedicine* 21(2):175-85 (2008).
- **Hammer J, Alvestad S, Osen K, Skar Ø, Sonnewald U, Ottersen OP**. Expression of glutamine synthetase and glutamate dehydrogenase in the latent phase andchronic phase in the kainate model of temporal lobe epilepsy. *Glia* 56(8):856-68 (2008)
- **Kondziella D, Sonnewald U, Tullberg M, Wikkelso C.** Brain metabolism in adult chronic hydrocephalus.*J Neurochem.* 106(4):1515-24 (2008)
- **I. L. Bogen, Ø. Risa, K. H. Haug, U. Sonnewal, F. Fonnum, S. I. Walaas.** Distinct changes in neuronal and astrocytic amino acid neurotransmitter metabolism in mice with reduced numbers of synaptic vesicles *J. Neurochem.* 105: 2524-2534 (2008)
- **Austgulen, Rigmor; Nguyen, Olav Toai Duc; Tommerdal, LF; Eide, Irina Poliakova; Landsem, Veslemøy Malm; Acar, Nuray; Myhre, Ronny; Klungland, Helge; Iversen, Ann-Charlotte.** The HLA-G 14 bp Gene Polymorphism and Decidual HLA-G 14 bp Gene Expression in Pre-Eclamptic and Normal Pregnancies. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 689-689
- **Iversen, Ann-Charlotte; Nguyen, Olav Toai Duc; Roten, Linda Tømmerdal; Eide, Irina Poliakova; Landsem, Veslemøy Malm; Acar, Nuray; Myhre, Ronny; Klungland, Helge; Austgulen, Rigmor.** The HLA-G 14 bp gene polymorphism and decidual HLA-G 14 bp gene expression in pre-eclamptic and normal pregnancies. *Placenta* 2008 ;Volume 29.(8): A.48-
- **Iversen, Ann-Charlotte; Nguyen, Olav Toai Duc; Tømmerdal, Linda Føll; Eide, Irina Poliakova; Landsem, Veslemøy Malm; Acar, Nuray; Myhre, Ronny; Klungland, Helge; Austgulen, Rigmor.** The HLA-G 14bp gene polymorphism and decidual HLA-G 14bp gene expression in pre-eclamptic and normal pregnancies. *Journal of Reproductive Immunology* 2008 ;Volume 78.(2): 158-165
- **Johnson, M; Dyer, T; Tommerdal, L; East, C; Austgulen, Rigmor; Blangero, J; Brennecke, S; Moses, E.** Putative Genetic Association of two Aminopeptidase Genes Under the Australian 5q Preeclampsia Susceptibility QTL. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 486-486
- **Loset, M; Mundal, S; Johnson, M; Eide, I; Moses, E; Austgulen, Rigmor.** Genome-Wide Transcriptional Profiling in Decidual Tissues from Preeclamptic Women Identifies Differentially Expressed Genes Involved in Trophoblast Invasion. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 488-488
- **Moses, Eric; Johnson, Matthew; Tømmerdal, Linda Føll; Forsmo, Siri; Curran, JE; Abraham, LJ; Charlesworth, J; Brennecke, Sean; Blangero, John; Austgulen, Rigmor.** Genetic association of preeclampsia to the inflammatory response gene SEPS1. *American Journal of Obstetrics and Gynecology* 2008 ;Volume 198.(3): 336.e1-336.e5

- **Mundal, S; Loset, M; Johnson, M; Eide, I; Moses, E; Austgulen, Rigmor.** Genome Wide Expression Profiling in Decidua Identifies Novel Angiogenesis Regulating Genes Involved in Preeclampsia. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 455-455
- **Tommerdal, L; Johnson, M; Forsmo, S; Dyer, T; Brennecke, S; Blangero, J; Moses, E; Austgulen, Rigmor.** A Norwegian Population-Based Case-Control Study Confirms Preeclampsia Susceptibility Regions on Chromosomes 5q and 13q. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 698-698
- **Tømmerdal, Linda; Johnson, M; Forsmo, Siri; Dyer, T; Brennecke, S; Blangero, J; Moses, E; Austgulen, Rigmor.** An African Origin for the PP13 Truncation Mutation 221delT. *Hypertension in Pregnancy* 2008 ;Volume 27.(4): 698-698
- **Bathen, Tone Frost; Holmgren, Kristin; Lundemo, Anne Gøril; Hjelstuen, Mari H; Krokan, Hans Einar; Gribbestad, Ingrid S; Schønberg, Svanhild Margrethe Arentz**. * Omega-3 Fatty Acids Supress Growth of SW620 Human Colon Cancer Xenografts in Nude Mice. */Anticancer Research/* 2008 ;Volume 28.(6A): 3717-3723
- **Eide, Irina Poliakova; Isaksen, Christina Vogt; Salvesen, Kjell Å; Langaas, Mette; Schønberg, Svanhild Margrethe Arentz; Austgulen, Rigmor.** Decidual expression and maternal serum levels of heme oxygenase 1 are increased in pre-eclampsia. /*Acta Obstetricia et Gynecologica Scandinavica*/ 2008 ;Volume 87.(3): 272-279
- **Pettersen, Caroline Hild; Størvold, Gro Leite; Bremseth, Hilde; Follestad, Turid; Sand, Kristin; Mack, Merete; Olsen, Karina Standahl; Lundemo, Anne Gøril; Iversen, Jens Gustav; Krokan, Hans Einar; Schønberg, Svanhild Margrethe Arentz.** DHA induces ER stress and growth arrest in human colon cancer cells: association with cholesterol and calcium homeostasis. /*Journal of Lipid Research*/ 2008 ;Volume 49: 2089-2100
- **Slagsvold, Jens Erik; Pettersen, Caroline Hild; Follestad, Turid; Krokan, Hans Einar; Schønberg, Svanhild Margrethe Arentz**. The antiproliferative effect of EPA in HL60 cells is mediated by alterations in calcium homeostasis. */Lipids/* 2008
- **Hale, M., Jensen, H., Birkhead, T. R., Burke, T. & Slate, J**. 2008. A comparison of synteny and gene order on the homologue of chicken chromosome7 between two passerine species and between passerines and chicken. *Cytogenetic and Genome Research* 121: 120-129.
- **Akbari, M. and Krokan, H.E.** Cytotoxicity and mutagenicity of endogenous DNA base lesions as potential cause of human aging. *Mech Ageing Dev.* 2008; 129:353-65.
- **Akbari, M., Visnes, T., Krokan, H.E. and Otterlei, M.** Base excision repair by human mitochondrial extracts involves both single-nucleotide insertion and long-patch DNA synthesis. *DNA Repair* 2008; 7:605-616.
- **Baekken PM, Skorpen F, Stordal E, Zwart JA, Hagen K.** Depression and anxiety in relation to catechol-O-methyltransferase Val158Met genotype in the general population: the Nord-Trøndelag Health Study (HUNT). *BMC Psychiatry*. 2008 Jun 25;8:48.
- **Bernsand M, Zhao CM, Håkanson R, Stenström B, Chen D, Norlén P.** Ischemia mobilizes histamine but not pancreastatin from ECL cells of rat stomach: evidence for a cytosolic histamine compartment. *Cell Tissue Res* 2008; 333:405-415
- **Bye A, Høydal MA, Catalucci D, Langaas M, Kemi OJ, Beisvag V, Koch LG, Britton SL, Ellingsen Ø, Wisløff U.** Gene expression profiling of skeletal muscle in exercise-trained and sedentary rats with inborn high and low VO2max. *Physiol Genomics*. 2008;35(3):213-21.
- **Egecioglu E, Stenström B, Pinnock SB, Tung LY, Dornonville de la Cour C, Lindqvist A, Håkanson R, Syversen U, Chen D, Dickson SL.** Hypothalamic gene expression following ghrelin therapy to gastrectomized rodents. *Regul Pept.* 2008;146(1-3):176-82.
- **Heath, S.C., Gut, I.G., Brennan, P., McKay, J.D., Bencko, V., Fabianova, E., Foretova, L., Georges, M., Janout, V., Kabesch, M., Krokan, H.E., Elvestad, M.B., Lissowska, J., Mates, D., Rudnai, P., Skorpen, F., Schreiber, S., Soria, J.M., Syvänen, A.C., Meneton, P., Herçberg, S., Galan, P., Szeszenia-Dabrowska, N., Zaridze, D., Génin, E., Cardon, L.R. and Lathrop, M.** Investigation of the fine structure of European populations with applications to disease association studies. *Eur. J Hum. Genet.* 2008; 16:1413-1429.
- **Gellein K, Lierhagen S, Brevik PS, Teigen M, Kaur P, Singh T, Flaten TP, Syversen T.**Trace element profiles in single strands of human hair determined by HR-ICP-MS. *Biol Trace Elem Res.* 2008;123(1-3):250-60.
- **McKay, J.D., Hung, R.J. , Gaborieau, V., Boffetta, P., Chabrier, A., ZaridzeD., Mukeria, A., Szeszenia-Dabrowska, N., Lissowska, J., Rudnai, P., Fabianova, E., Mates, D., Bencko, V., Foretova, L., Janout, V., McLaughlin, J., Shepherd, F., Montpetit, A., Narod, S., Krokan, H.E., Skorpen, F., Elvestad, M.B., Vatten, L., Njølstad, I. Axelsson, T., Lubiński, J., Matyjasik, J., Lener, M., Oszutowska, D., Chen, C., Goodman, G., Field, J.,**

Liloglou, T., Xinarianos, G., Cassidy, A., EPIC study, Zelenika, D., Boland, A. Delepine, M., Foglio, M., Lechner, D., Matsuda, F., Blanche, H., Gut, I., Heath, S., Lathrop, M., Brennan, P. Identification of gene region 5p15.33, comprising the telomerase reverse transcriptase gene, as a novel lung cancer susceptibility locus among 6,000 lung cancer cases and 9,500 controls. *Nature Genetics* 2008; 40:1404-1406

- **Myhre R, Steinkjer S, Stormyr A, Nilsen GL, Abu Zayyad H, Horany K, Nusier MK, Klungland H.** Significance of the parkin and PINK1 gene in Jordanian families with incidences of young-onset and juvenile parkinsonism. *BMC Neurol*. 2008;8:47.
- **Myhre R, Toft M, Kachergus J, Hulihan MM, Aasly JO, Klungland H, Farrer MJ.** Multiple alpha-synuclein gene polymorphisms are associated with Parkinson's disease in a Norwegian population. *Acta Neurol Scand.* 2008;118(5):320-7.
- **Myhre R, Klungland H, Farrer MJ, Aasly JO**. Genetic association study of synphilin-1 in idiopathic Parkinson's disease. *BMC Med Genet*. 2008;9:19.
- **Nørsett KG, Laegreid A, Kusnierczyk W, Langaas M, Ylving S, Fossmark R, Myhre S, Falkmer S, Waldum HL, Sandvik AK.** Changes in gene expression of gastric mucosa during therapeutic acid inhibition. *Eur J Gastroenterol Hepatol.* 2008;20(7):613-23.
- **Rakvåg TT, Ross JR, Sato H, Skorpen F, Kaasa S, Klepstad P.** Genetic variation in the catechol-O-methyltransferase (COMT) gene and morphine requirements in cancer patients with pain. *Mol Pain.* 2008;18;4:64.
- **Tessem MB, Swanson MG, Keshari KR, Albers MJ, Joun D, Tabatabai ZL, Simko JP, Shinohara K, Nelson SJ, Vigneron DB, Gribbestad IS, Kurhanewicz J.** Evaluation of lactate and alanine as metabolic biomarkers of prostate cancer using 1H HR-MAS spectroscopy of biopsy tissues. *Magn Reson Med.* 2008;60(3):510-6.
- **Toft JH, Lian IA, Tarca AL, Erez O, Espinoza J, Eide IP, Bjørge L, Draghici S, Romero R, Austgulen R.** Whole-genome microarray and targeted analysis of angiogenesis-regulating gene expression (ENG, FLT1, VEGF, PIGF) in placentas from pre-eclamptic and small-for-gestational-age pregnancies. *J Matern Fetal Neonatal Med.* 2008;21(4):267-73.
- **Larsen E, Kleppa L, Meza TJ, Meza-Zepeda LA, Rada C, Castellanos CG, Lien GF, Nesse GJ, Neuberger MS, Laerdahl JK, William Doughty R, Klungland A**. Early-onset lymphoma and extensive embryonic apoptosis in two domain-specific Fen1 mice mutants. *Cancer Res.* 2008 Jun 15;68(12):4571-9.
- **Gidskehaug, L; Anderssen, E; Alsberg, BK.** Cross model validation and optimisation of bilinear regression models, *Chemometrics and Intelligent Laboratory Systems* Volume: 93 Issue: 1 Pages: 1-10 Published: 2008.
- **Afset, JE; Anderssen, E; Bruant, G, et al.** Phylogenetic backgrounds and virulence profiles of atypical enteropathogenic Escherichia coli strains from a case-control study using multilocus sequence typing and DNA microarray analysis *Journal of Clinical Microbiology* Volume: 46 Issue: 7 Pages: 2280-2290 Published: 2008
- **Juel, Ingebjørg s.; Solligård, Erik; Tvedt, Kåre E; Skogvoll, Eirik; Jynge, Per; Beisvåg, Vidar; Erlandsen, Sten Even; Sandvik, Arne Kristian; Aadahl, Petter; Grønbech, Jon Erik.** Post-ischaemic restituted intestinal mucosa is more resistant to further ischaemia than normal mucosa in the pig. *Scandinavian Journal of Clinical and Laboratory Investigation* 2008 ;Volume 68:106-116
- **Nilsen AJ, Landin MA, Haug KH, Fonnum F, Berger U, Osmundsen H.** Comparative hepatic gene expression profiling of rats treated with 1H,1H,2H,2H-heptadecafluorodecan-1-ol or with pentadecafluorooctanoic acid. *Physiol Genomics.* 2008 Aug 15;34(3):285-303. Epub 2008 Jun 10.

Presentations within the area of popular science:

- **Berntsen EM, Haraldseth O, Håberg A.** Kirurger skjærer etter Jeopardy-spørsmål. *Dagbladet, Magasinet* [Avis] 2008-04-21 NTNU
- NRK1, Newton, ”Forelskelse og feromoner.” **Bente G. Berg**, Dept. of Psych. NTNU, [television] April 27th 2008.
- Senioruniversitetet, Trondheim, ”Luktesansens særegenenheter.” Oral presentation, **Bente G. Berg**, Dept. of Psych. NTNU, Jan 15th 2008.
- ”Norsk blod åpner døra til kreftgåten”, *Dagbladet*, April 2008
- **Kjetil Hindar,** Presentations at FUGE I’s “Sluttrapportering gjennom seminar”, Research Council of Norway Oslo 21.5.2008
- **Rigmor Austgulen**: Intervju om etablering av biobank basert på materiale fra familier med økt forekomst av preeklampsi. *Adresseavisen* 13.12.2008
- **Rigmor Austgulen**: Innslag og intervju om genetikk/svangerskapsforgiftning på lørdagsrevyen Norwegian Broadcasting Corporation (National TV). 6.12.2008

Annual Report for FUGE Mid-Norway 2008

NTNU
Innovation and Creativity

NTNU – Innovation and Creativity

The Norwegian University of Science and Technology (NTNU) in Trondheim represents academic eminence in technology and the natural sciences as well as in other academic disciplines ranging from the social sciences, the arts, medicine, architecture to fine arts. Cross-disciplinary cooperation results in ideas no one else has thought of, and creative solutions that change our daily lives.

Address, contact information

FUGE Mid-Norway
Faculty of Natural Sciences and Technology, NTNU
Realfagbygget
N-7491 Trondheim,
Norway

E-mail: postmottak@nt.ntnu.no

www.ntnu.no/forskning/fuge