CREATE Health

Newsletter

CREATE Health - a Strategic Centre for Clinical Cancer Research at Lund University Issue 1-2007

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CREATE Health is a Strategic Centre for Clinical Cancer research located at the Biomedical Centre in Lund. The Centre is funded by the Swedish Foundation for Strategic Research. By integrating clinicians and researchers from Lund University Hospital with researchers from the Faculties of Medicine, Natural Sciences and Engineering at a superbly equipped and integrated "omics" platform, concentrated in a single area, a centre unique in its kind has been created.

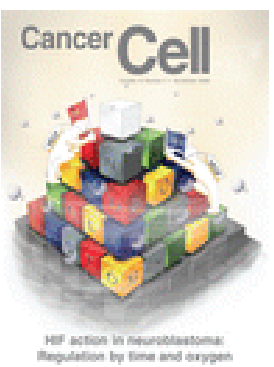
The vision of CREATE Health is to use an integrative approach to develop novel diagnostics and therapeutics, based on identified markers and molecular signatures and to create a substantial social impact for the patient, through direct application of research for selection of an optimal, individually-based, cancer treatment.

The centre is built up by the research groups of

- Carl Borrebaeck
- Åke Borg
- Sven Påhlman
- Carsten Peterson
- Carsten Rose
- Peter James
- Thomas Laurell

Latest News from Cancer Cell: HIF-2 in in Neuroblastoma

Generally, tumor hypoxia and presence of the hypoxia inducible transcription factor HIF-1α protein correlates with poor prognosis. CREATE Health's Sven Påhlman and co-workers have recently found that also the presence of endogenous HIF-2α in well-vascularized neuroblastomas, correlates with VEGF expression and unfavorable patient outcome. In addition, HIF-2α regulates classical hypoxia-driven genes at end capillary oxygen levels which indicate that HIF-2α can act oncogenically, independently of a hypoxic environment. The present data also suggests



differential utilization of HIF proteins in neuroblastoma cells at acute versus prolonged hypoxia, which could have significant implications for the design of anti-HIF-therapy in tumor disease.

Sven Påhlmsn's findings were published in the well renowned journal Cancer Cell. The paper can be downloaded from Cancer Cell's website http://www.cancercell.org/

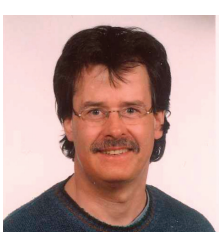
Most Cited article 2006

The article by Ingvarsson J, Lindstedt M, Borrebaeck C and Wingren C, One-Step Fractionation of Complex Proteomes Enables Detection of Low Abundant Analytes Using Antibody-Based Microarrays published in Journal of Proteome Research is being featured on the ACS Publications website as a 2006 Most-Cited Article based on citation data obtained from Thomson ISI.

2006 Most-Cited Articles are articles published in 2006 receiving the most citations in the same year. ACS Publications recognizes these articles as research of immediate interest.
The article can be downloaded at http://pubs.acs.org/cgi-bin/article.cgi/jprobs/2006/5/i01/pdf/pr050301d.pdf

Peter James: Head of the tutorials

Peter James was one of the 10 founding members of the Human Proteome Organisation (HUPO) and was the Chairman of the Education Committee for three years and then rotated off. Recently the European Proteomics Association EuPA founded an Education Committee with the aim to create a European Masters level education programme Peter is now managing the fusion of the two education committees. A series of tutorial articles is being commissioned and a set of basic and advanced proteomics are being developed that will be first tested out in Lund soon.



New employees at CREATE Health

Kristofer Wårell, PhD Student, Protein Technology

I work with method development for protein analysis by mass spectrometry. We are developing a method to make automated, targeted analysis of pre-selected proteins in complex biological samples. The idea is to identify and quantify proteins in selected cellular pathways, in contrast to current methods that are usually analysing as many proteins as possible in a sample. Our biological focus is on pathways whose protein product(s) are reported to be regulated between different samples (healthy vs disease, treatment A vs B, etc). The new method is addressing the next step in differential analysis, which is to provide more detailed characterisation of cellular pathways.

Niclas Olsson, PhD Student, Immunotechnology

The aim of my project is to develop a novel array technology, the SPCapture technology, for high-throughout (disease) proteomics. The platform is based on a peptide epitope specific scFv antibody array interfaced with a mass spectrometry read-out system. A focus will be placed on addressing the human serum and plasma proteomes where signature peptide motifs will be defined. Clinical samples will be digested, and peptides captured by immobilized scFv antibodies will be analyzed and identified by MS. The possibility of targeting non-digested proteomes will also be explored.

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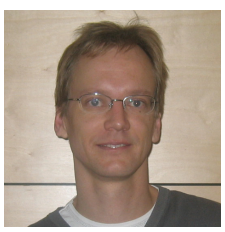
Marie Ovenberger, Erik Fredlund and Alexander Pietras, PhD Students, Molecular Medicine

The short-term goal of our project is to identify plasma membrane proteins that are differentially expressed in hypoxic versus normoxic neuroblastoma cells. We use two-phase partioning to get plasma membrane protein-enriched fractions and mass spectrometry to identify proteins. Our long-term goal is to raise antibodies against candidate proteins that have a higher expression at hypoxic conditions and by this mean we hope to specifically target tumor cells.



Markus Ringnér, PhD, Oncology

I develop computational methods for analysis of data from microarray experiments of gene expression and DNA copy number. Current research projects include developing methods to identify signaling pathways whose deregulation underlie observed gene expression signatures of tumors and to use gene expression data to investigate connections between drugs and subgroups of breast cancer.

Fredrik Levander, PhD, Protein Technology

I develop methods and software for high-throughput mass spectrometry-based proteomics. The major aim is to perform comprehensible comparisons of protein expression levels in multiple samples. Peptide and protein quantification and identification from mass spectra are the basis of the approach, and I'm working on improvements for existing computational methods as well as the integration of the methods into an easy-to use common software platform.

Elin Gustavsson, PhD Student, Immunotechnology

The aim of my project is to acquire human recombinant antibody fragments against different cancer-associated antigens through phage display selections. The selected fragments will specifically bind to their target and thereby distinguish between cancerous and healthy tissue. This characteristic makes them very useful in diagnostic, prognostic and therapeutic applications of various types of cancer.

Morten Krogh, PhD, Bioinformatics

I develop algorithms for analyzing proteomics and microarray experiments. This includes methods to correct for missing values and dye bias in 2D gel experiments, for protein identification from mass spectrometry data, and for finding activated signal transduction pathways using microarray data. Furthermore, I develop and implement statistical methods for diagnosis, prognosis, and biomarker discovery in cancer and other diseases in collaboration with research groups working with 2D gels, mass spectrometers, DNA microarrays, and antibody microarrays.

Simon Eskström, PhD, Nanotechnology

Identification of proteins and studies of protein expression, interaction, post-translational modifications are imperative for understanding biological systems. This has lead to an increased interest in the development of microanalysis systems that allows proteins to be subjected to mass screening. The aim of my research is to develop novel microfluidic sample preparation techniques in the field of proteomics, with a special focus on applications using matrix-assisted laser desorption ionization mass spectrometry (MALDI MS) for the analysis read-out. In the initial phase a microfluidic array based platform will be adapted for SPCapture.

Cecilia Ritz, PhD Student, Bioinformatics

Currently used imputation models for missing values in cDNA microarray data are based on correlations between all available measurements in the data matrix, but no information as to why a measurement is missing is included. I divide missing values in different categories based on the type of missing value, and develop a new model to improve imputation of these spots. The performance is evaluated in five different datasets.

Coming events

March 15-16

International Symposium on New Frontiers in Cancer Research and Therapy at the Nanna Svartz Auditorium, Karolinska University Hospital, Stockholm

CREATE Health's Sven Påhlman is found among the speakers.

The program can be found at http://www.createhealth.lth.se/fileadmin/create_health/pdf/OPS_program_20070206.pdf

March 21-23

Svensk Onkologisk Förening is arranging ONKOLOGIDAGARNA at Hilton Hotel in Malmö

CREATE Health is represented by Åke Borg and Sven Påhlman

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