Mini Symposium: "Bridging the gap between two omics worlds: transcriptomics and proteomics."

Friday, November 29th, 2013
14:00-16:00

Ghent University, Rommelaere Institute - Auditorium 1.39,
A. Baertsoenkaai 3, 9000 GENT

Cancer Proteogenomics

Prof. Dr. David Fenyö (NYU Center for Health Informatics and Bioinformatics, US - www.fenyolab.org)

Abstract: Novel approaches arise in cancer prevention and early detection, based on tools for the study of tumor proteogenomics and biomarker identification. These are carried out through the creation of tumor-specific sequence collections representing somatic alterations on the tumor proteome, which are being used for protein identification and biomarker discovery.

Protein identification based on ribosome targeted mRNA fragments

Dr. Gerben Menschaert (BioBix Group, FBE-UGent, Belgium - www.biobix.be)

Abstract: The newly developed ribosomes profiling (RIBO-seq) approach provides genome-wide information about protein synthesis by monitoring mRNA that enters the translation machinery, while highly sensitive mass spectrometry provides information about the protein composition of a sample. Integrating these technologies can provide more intuitive information about the proteins being synthesized and the identification of novel translation products as well as a better understanding of the translation mechanism.

Improved MS/MS peptide identification through Machine Learning

Dr. Sven Degroeve (Compomics Group, VIB-UGent, Belgium - www.compomics.com)

Abstract: Sensitive and accurate peptide sequence identification from MS^2 spectra is critical for bridging the gap between the signals observed in the mass spectrometry machine and the biological entities (peptides) that generated them. In this presentation we show how the peak intensity information present in an MS^2 spectrum can contribute significantly to the sensitivity and accuracy of peptide identification methods. We do this by computing new PSM features from MS^2 peak intensity predictions computed by our MS2PIP tool.