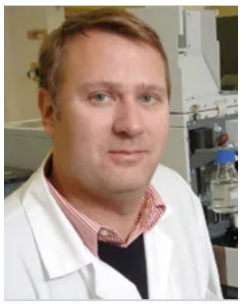
BMC-GPMLS distinguished lecture series:



Dr. Christoph Borchers

Professor and director at University of Victoria – Genome BC Proteomics Centre, Victoria, British Columbia, Canada

”Multiplex targeted protein assays for clinical research and diagnostics”

ABSTRACT:
While the majority of targeted, clinical protein analysis is still performed with immunoassays such as enzyme-linked immunosorbent assay (ELISA) or immunohistochemistry (IHC), these techniques suffer from certain drawbacks such as potential non-specificity and difficulty to multiplex. These problems can be overcome by powerful mass spectrometry-based approaches due to their non-paralleled specificity, in particular bottom-up methodologies such as multiple reaction monitoring (MRM) and immuno-matrix-assisted laser desorption/ionization (iMALDI). The use of stable isotope-labelled standard (SIS) peptides allows for very precise and accurate protein quantitation on the peptide level. MRM is highly multiplexable and allows the targeting of hundreds of proteins, whereas iMALDI achieves high sensitivity due to affinity-enrichment of target peptides from low sample amounts on simple, robust instrumentation. These techniques are in particular useful for biomarker validation and clinical use in diagnostic applications, as well as for companion diagnostics during and after drug development.
Testing for activating KRAS mutations is used to select colorectal cancer (CRC) patients who are eligible for anti-EGFR treatment. In one of our recent proteogenomic studies, phenotyping of 8 metastatic CRC (mCRC) tumors and 6 paired healthy tissues, was performed by parallel reaction monitoring (the equivalent of MRM on an Orbitrap), and mutation rates were determined on the protein level. In KRASG12V-mCRC, G12V-mutation levels were 42-100%, but one patient had only 10% KRASG12V and 90% KRASwildtype. Based on hotspot sequencing, this patient had been excluded from anti-EGFR treatment and instead received chemotherapy, but PRM-based tumor-phenotyping indicated that the patient might have benefited from anti-EGFR therapy.

BIOSKETCH: Dr. Borchers received his PhD from the University of Konstanz, Germany in 1996. From 2001 to 2006, he was the director of the University of North Carolina-Duke Proteomics Facility, Chapel Hill, NC, holding a faculty position at the UNC Medical School. From 2006 to 2019, he was a Professor in the Department of Biochemistry and Microbiology, and Director of the University-Genome British Columbia Proteomics Centre at the University of Victoria, British Columbia, Canada, where he held the Rix BC Leadership Chair in Biomedical and Environmental Proteomics. Dr. Borchers is currently a Professor in the Department of Oncology at McGill University, Montreal, Quebec, Canada, and holds the Segal Chair in Molecular Oncology. He is also the founder and Director of the Segal Cancer Proteomics Centre at the Lady Davis Institute, Jewish General Hospital, McGill University. His research involves proteomics and metabolomics technologies for clinical diagnostics and structural proteomics

Time: **Monday, December 2nd, 11.00-12.00**

Location: **Fróði auditorium, Sturlugata 8**