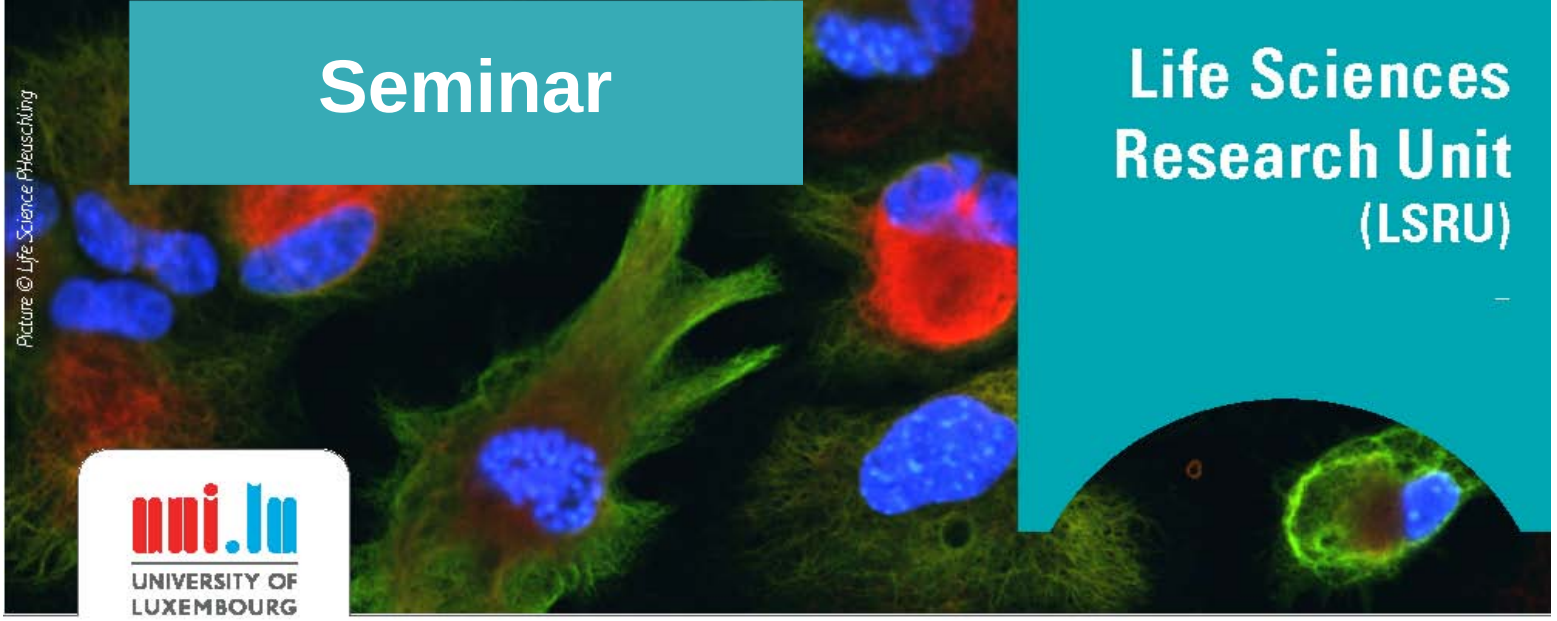

FACULTY OF SCIENCE, TECHNOLOGY AND COMMUNICATION

Blood peptides, proteins and their cellular receptors by mass spectrometry

Abstract:

Professor John G Marshall, Department of Chemistry and Biology, Ryerson University, Toronto, Canada: on sabbatical at CRP Santé and IBBL in Luxembourg.

Blood carries peptide and protein ligands which act as important regulatory signals in the body. Blood peptides and proteins activate cells by virtue of binding to cell surface receptors. The blood peptides or proteins, and their cell surface receptor complexes, have been examined and elucidated by analytical biochemistry approaches. Selective organic extraction of precipitated blood polypeptides, and preparative micro-chromatography of blood proteins, resulted in the sensitive and reproducible detection from the blood. Protein ligands bound to micro-chromatography beads captured the activated receptor complex from the surface of live cells by Live-cell Affinity Receptor Chromatography (LARC) with subsequent mass spectral elucidation. The large amounts of data from the mass spectrometry of blood peptides, proteins or their cellular receptor complexes can be stored in a relational data base. A relational database of mass spectra supports the analysis of peptide and protein identity and intensity values by classical statistical methods that provide a high degree of confidence in the results. Thus mass spectrometry data may be completely analysed using the Statistical Analysis System (SAS) common to all areas of clinical and biomedical sciences. These new laboratory, database and statistical methods have successfully detected blood peptides and proteins or their cell surface receptor complexes. The analysis of blood by organic extraction or micro-chromatography, and cell surface receptors by LARC, will be described and explained.

Where: Campus Limpertsberg – BS 1.04

When: Wednesday, 7th December 2011 - from 2:00 pm

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