# Antigen discovery for development of personalized cancer immunotherapy

**Michal Bassani-Sternberg**

*Ludwig Institute for Cancer Research, Lausanne, Switzerland*

The precise identification and prioritization of antigenic peptides presented by class-I and -II human leukocyte antigens (HLA-I and -II) recognized by autologous T cells is essential for advancing cancer immunotherapies. Although several clinical neoantigen prediction pipelines are currently available, none support the direct integration of mass spectrometry immunopeptidomics data, which can reveal antigenic peptides from a variety of canonical and non-canonical sources. To address this gap, we have developed NeoDisc, a unique 'end-to-end' clinical proteo-genomic pipeline.NeoDisc is a rapid, modular computational pipeline that integrates state-of-the-art publicly available and in-house software for genomics, transcriptomics, immunopeptidomics, and in-silico tools to identify, predict, and prioritize tumor-specific and immunogenic antigens from multiple sources. In my presentation I will demonstrated the superiority of NeoDisc in prioritizing neoantigens compared to recent neoantigen prioritization pipelines and highlight its diverse features enabling personalized antigen discovery.