Group	:	Surface-bound Analytical Chemistry
Project	:	**Mass spectrometric analysis of SPR-bound anti-cancer drugs**
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Keywords
Surface Plasmon Resonance, protein-ligand interaction, mass spectrometry, analytical chemistry

Introduction
Diagnostic tests and biological pharmaceuticals rely on the specific interaction between a protein (antibody, enzyme) and a ligand. For the development of such a test it is of crucial importance to know what ligands are bound to the protein inside a biological fluid (e.g. blood, urine). A general impression of ligand binding and their kinetics can be obtained by Surface Plasmon Resonance (SPR). Although this is a powerful technique it does not give any information about the chemical nature of the ligand(s).
On the other hand, mass spectrometry (MS) is one of the most important analysis techniques for the detection of potential ligands such as lipids, vitamins, hormones, sugars, etc. because of its high selectivity, sensitivity, structure elucidation and "screening" abilities. For this reason it would be ideal if we would be able to combine SPR with MS: we would have both binding kinetics and identification of the ligands. Modern pharmaceuticals like antibody-drug conjugates suffer from partial degradation inside the body; with a combination of SPR and MS we could find out what the structures of the fragments are and whether they are still able to bind to their targets.

Goal
Up to now, MS itself is not directly compatible with SPR so in this project we will develop a method to 1) monitor selective binding of known and unknown ligands to proteins on an SPR chip, and 2) disrupt the binding in such a way that the ligand can be studied by MS while keeping the integrity of the biomolecule, such that the precious SPR chip can be reused.

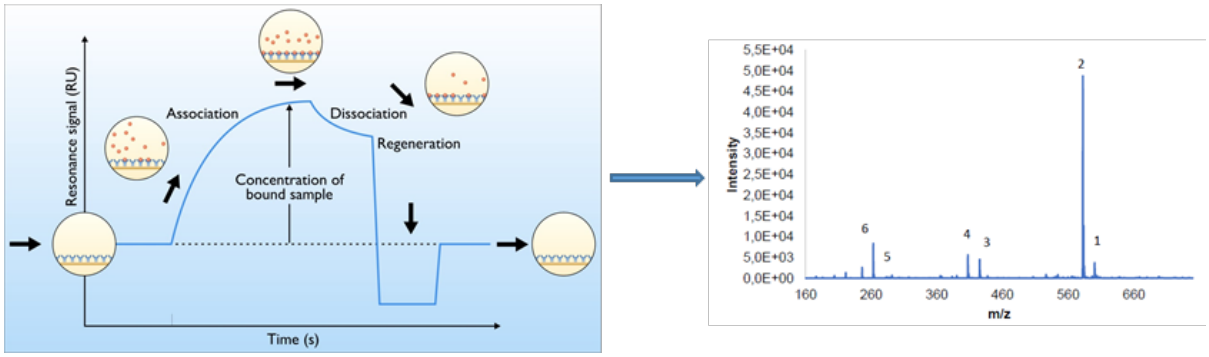

Fig. 1. Typical SPR sensorgram that displays binding kinetics of the ligand, subsequently leading to an informative mass spectrum of the ligand.

Topics to be studied
Immobilisation of a protein to an SPR chip; disrupting the ligand-protein bond by our proprietary method; detection and quantitation of ligands by high resolution MS; analysis of the integrity of the SPR chip; optimisation of the disruption technique.

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