# HELPING RESOLVE THE INTERACTOME BY MEANS OF LABEL FREE INTERACTION ANALYSIS

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Biacore offers a versatile, label-free technology for detailed studies of biomolecular interactions, from early research to drug discovery and development and on to QC.

Biacore delivers high quality kinetic, affinity, concentration, specificity, selectivity, and thermodynamic interaction data – in real time with exceptional sensitivity. It is possible to obtain high quality kinetics from the fastest on-rates to the slowest off-rates, analyze interactions involving the smallest low molecular weight (LMW) compounds, process up to 384 samples in unattended runs, get to the final result faster using guided workflows with built-in data quality assessments and tools, such as single cycle kinetics and calibration-free concentration analysis. Moreover dedicated tools for confident immunogenicity test or recover samples for identification by mass spectrometry can be applied thus widening the field of application for label-free technology. For this last application, Biacore T200 in combination with mass spectrometry provides the possibility to identify proteins on the basis of functional binding criteria. Sample recovery and digestion are supported by the software. Among the possible applications, we will show some examples of how Biacore technology coupled to mass spectrometry can help to resolve some bottlenecks in proteomics.

As conclusion, with this technology we increase understanding of molecular mechanisms and structure-function relationships, define potential drug targets and diagnostic markers, select and characterize biotherapeutic candidates, select and optimize lead compounds during drug discovery, detect and characterize anti-drug antibodies (ADA) in immunogenicity studies or perform time- and cost-efficient concentration analysis in vaccine development.