Discover the Label-Free Platform From HORIBA Scientific

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XelPleX

Multiplex Label-Free Interaction Analysis

One System for Molecule Screening & Crude Sample Analysis

JOBIN YVON Technology

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XelPleX

Multiplex Label-Free Molecular Interaction Platform

Accelerate your research and maximize your workflow with XelPleX

XelPleX combines the power of multiplexing (measuring multiple interactions simultaneously) and the sensitivity of Surface Plasmon Resonance, resulting high-resolution kinetic profiles.

The revolutionary fluidics system and the integrated autosampler are compatible with a broad range of applications, such as ligand fishing in complex fluids, cell studies, small molecule detection, protein screening and DNA analysis.

Driven by the EzSuite software platform, XelPleX is simple to operate and is designed to maximize your workflow for large scale applications.

Information-rich technology to characterize molecular interactions

XelPleX uses Surface Plasmon Resonance imaging (SPRi) to follow **label-free binding** events in real time. Molecular interactions can be fully characterized in terms of:

- Kinetics: association (k_a) and dissociation (k_d) rates
- Affinity (K_D)
- Specificity
- Concentration
- Relative binding

Multiplexing opens the door to more than 400 interactions in less than 10 minutes

The imaging configuration of XelPleX dramatically enhances the throughput of conventional SPR. Ligand molecules are immobilized in an array format onto the sensor chip surface and are screened against the interacting partner in the sample solution.

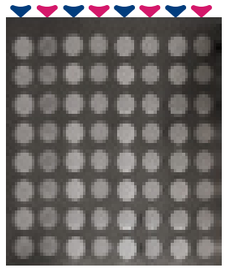
Up to several hundred molecular interactions can be analyzed simultaneously, saving you time and money.

Instant information from real time display of images

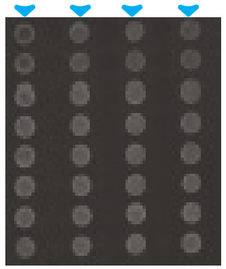
Binding events are followed in real time on the kinetic curves and also on the SPRi difference image. White spots on this image correspond to areas where binding has occurred – giving you a clear **Yes/No answer to molecule detection and recognition.**

Ligand of interest
Negative control

Target analyte



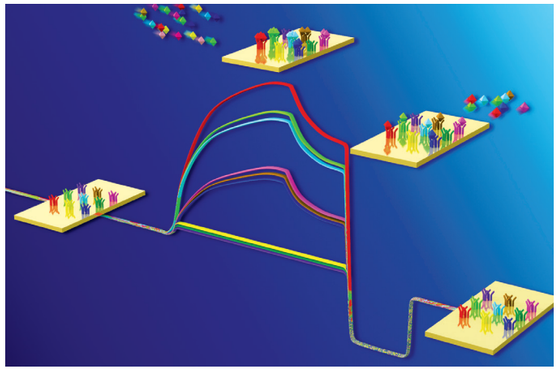
SPRi Biochip direct image before interaction



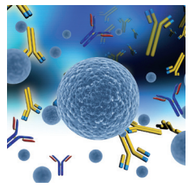
SPRi Biochip difference image after interaction. White spots show molecular interactions.

Optimized fluidics system

Working with complex samples like serum, plasma or cell lysates, in diagnostic research or drug discovery, is not an issue. The revolutionary, yet robust fluidics system is compatible with various sample solutions (concentrated, acidic or basic), and is designed for hands-off operation.

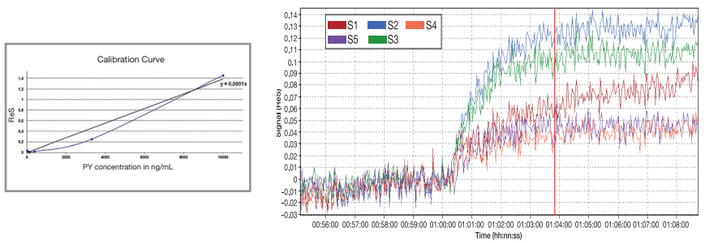


From Molecule Screening to Crude Sample Analysis

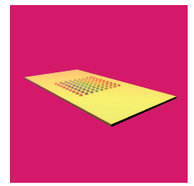


Unique label-free screening and crude sample analysis

To fully understand the details of a biological mechanism at the molecular level, it is important to characterize the biomolecular interaction in a biological relevant environment without modifying the samples or using purification procedures.
By using the XelPleX platform, analyzing crude samples at high concentrations has thus become much more realisable.

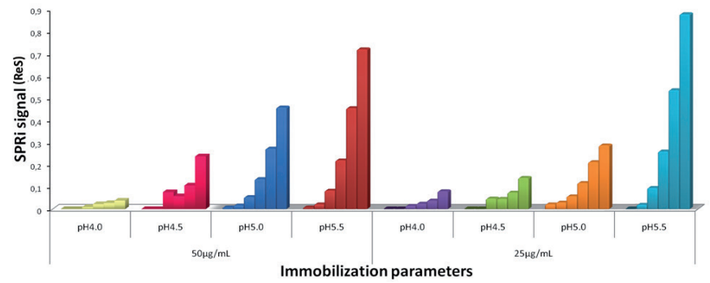


Calibration curve (left) and kinetic curves corresponding to the 5 supernatants (S) after injection of the analyte (right), generated from a single biochip



Optimize and compare for the best parameters using only one sensor chip

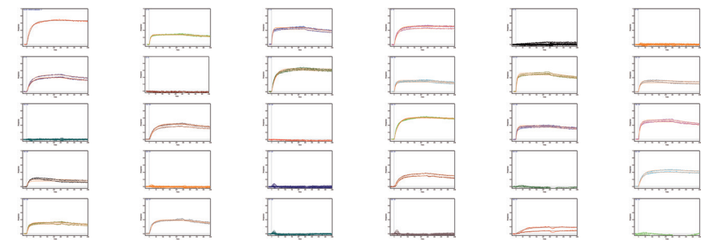
Test for different immobilization concentrations, buffers or pH on the same sensor chip, and optimize the experimental conditions of your interaction models. Use as many replicate spots as you wish to be more confident in the results.



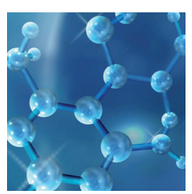
Optimization of immobilization concentration and pH on the binding response of a small molecule – protein interaction

Rank and screen your molecules during selection processes

Multiplexing helps you to rank and screen molecules such as antibodies or aptamers according to affinity or kinetic rates easily and rapidly. Thanks to the SPRi-CFM printer, molecules can be immobilized from crude media to be compatible with your bioprocessing workflow.

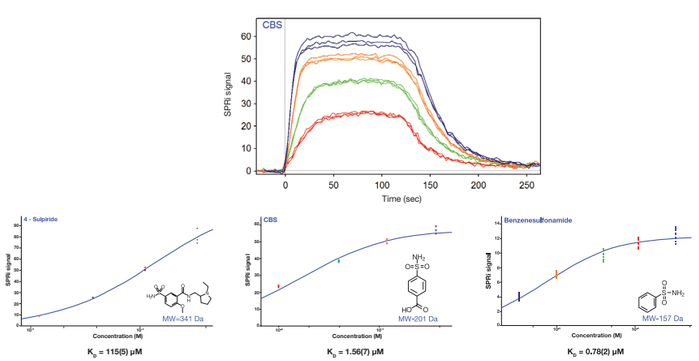


Direct kinetics comparison of 30 candidate molecules directed against the same protein

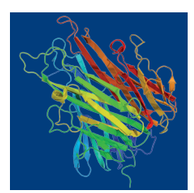


Small molecules detection made easy

The revolutionary optical and fluidics units obtain unsurpassed performance for high-sensitivity measurements. The instrument is compatible with the use of solvents, such as DMSO.

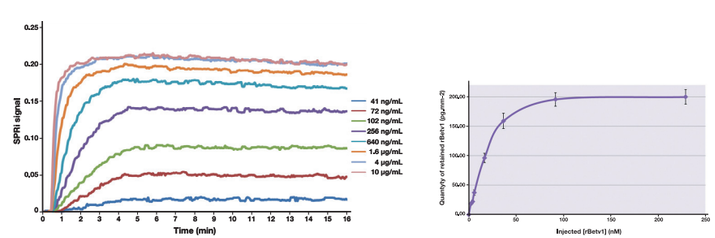


Affinity determination of small molecules (341 Da, 201 Da and 157 Da) binding to CAII

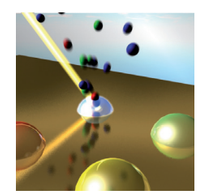


Quick and precise concentration measurements

Avoid the tedious and time-consuming steps from ELISA and determine the concentration of unknown samples in complex matrices, without labels.

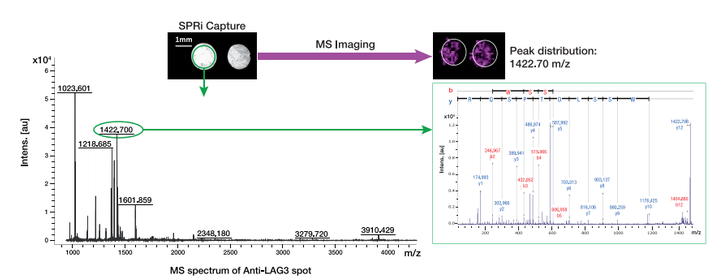


Determination of the calibration curve for the quantification of birch pollen allergen (in collaboration with RNSA, France and Stallergenes, France)



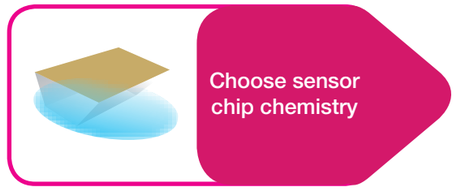
Direct MALDI-MS characterization

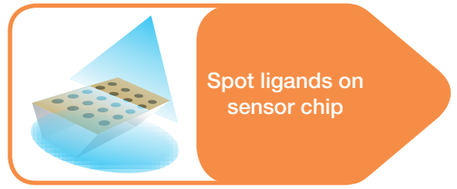
The open format of the sensor chip allows the direct combination of SPRi and MALDI-MS analysis on the same sensor chip. SPRi allows the multiplexed capture of analytes in complex solution and direct MALDI-MS can be used to characterize and identify the captured analytes from the sensor chip – no need to elute the samples.

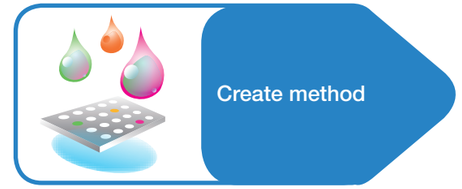


Direct capture of LAG3 protein in human plasma by SPRi and subsequent MALDI-MS identification (in collaboration with CLIPP Proteomic platform, France)

Simple Workflow for Confident Interaction Analysis

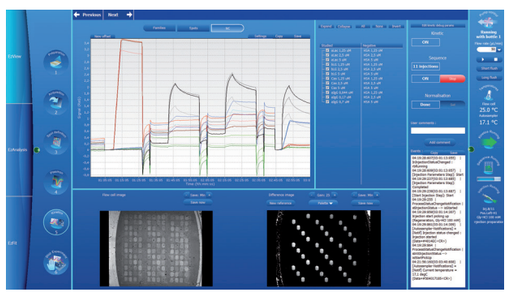




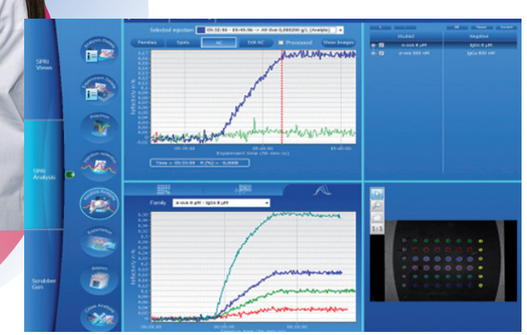


Make decisions faster with instant information display

- EzView software retrieves real time information through flow cell, SPRi difference images, and kinetics status.
- Several hundred ligands can be monitored simultaneously.
- Select as many negative controls as you wish. Accurate real time referencing brings more confidence to your results.



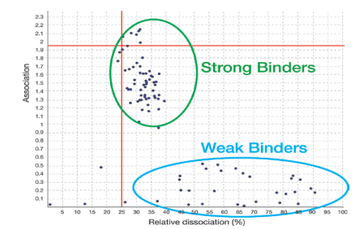
EzView control software



Quantitative analysis with EzAnalysis

Collect and report data in a flash with EzAnalysis

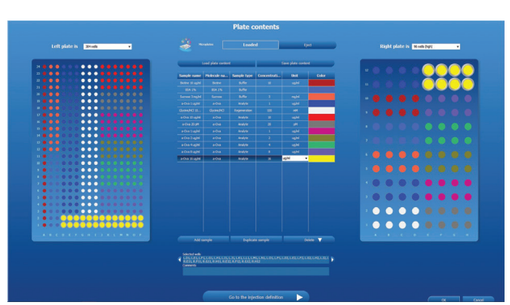
- Simply load your experiment data from the database, and perform your analysis in a few clicks.
- EzAnalysis retrieves quantitative information and performs data quality control automatically.
- Instant reporting of the experimental details (buffer, flow rate, temperature…), and of the analysis, to keep records of all your experiments.



Data clouding of a 300 peptides array for epitope mapping

Save time and money thanks to hands-off operation

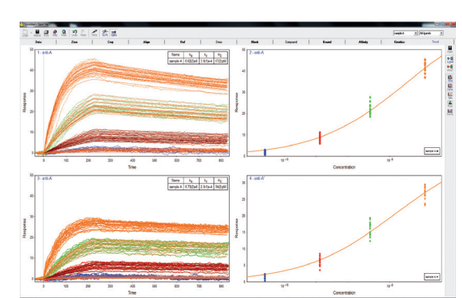
- Injection sequences can be programmed in the EzView software to automatically control the integrated autosampler.
- Enter injection parameters, save your method, and run it.
- At any time, recycle and recover your sample for more demanding applications.



Autosampler settings in EzView

Publication-ready kinetics

- EzFit (based on Scrubber) cleans and fits kinetics data to a 1:1 interaction model to calculate affinity and kinetic rates.
- Methods can be saved and applied to new data to save time.
- Each graph can be saved and exported for publication.



Data fitting in EzFit to extract kinetic rates and affinity