

Focal Molography: From Fundamentals to DNA-Encoded Library Screening and Membrane Protein Target Characterization

SPS Meeting 11.9.2024



The people behind focal Molography - lino Biotech AG



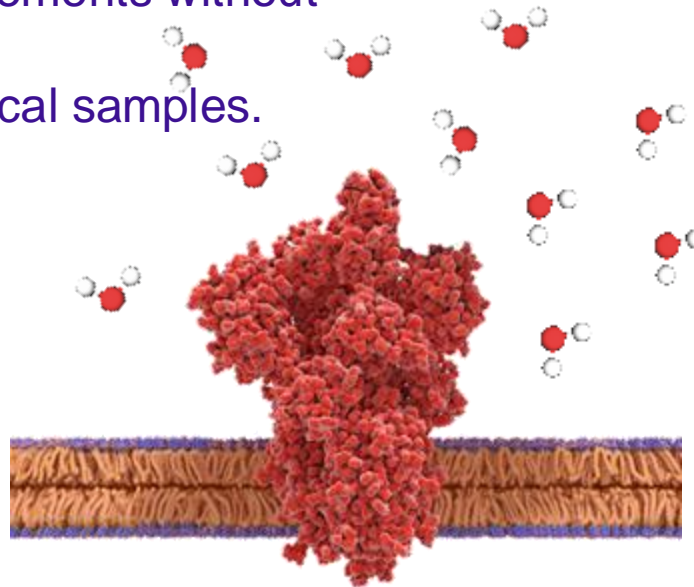
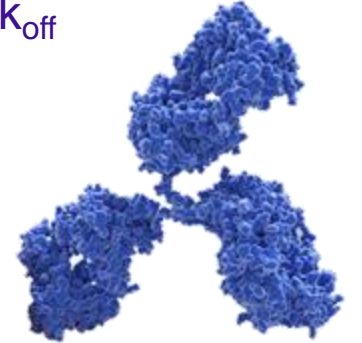
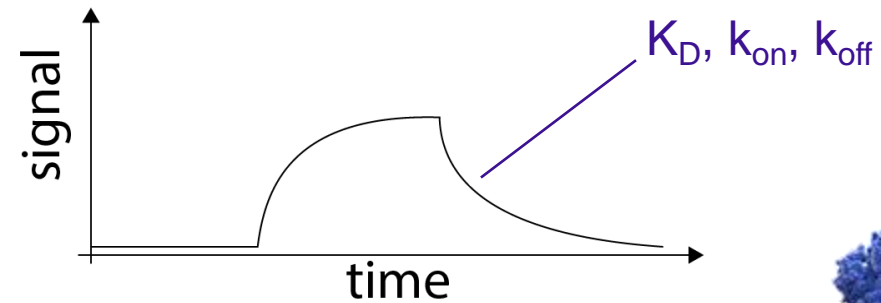
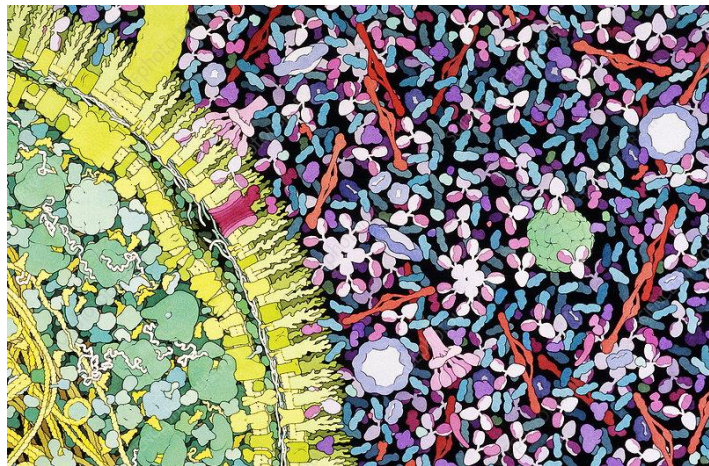
- Founded in 2020 as ETH/Roche spinoff
- Acquired by Miltenyi Biotec in Feb. 2023
- located in Adliswil

12 People (9 PhDs, 3 MA):

- 3 Physicist
- 2 Biologists
- 4 Chemists
- 2 Material scientists
- 1 Mech. Engineer

What is focal Molography?

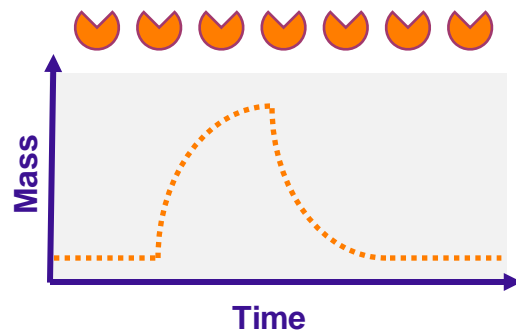
- focal Molography is a surface based real-time label-free biosensor
- This allows two measurement principles:
 - affinity and kinetic measurements
 - concentration measurements
- Key feature: It can do such measurements without any stabilization (temperature) and in nonpurified complex biological samples.



How are biomolecular Interactions measured today?

Biomolecular interaction analysis (BIA)

Detection principle in label-free detection



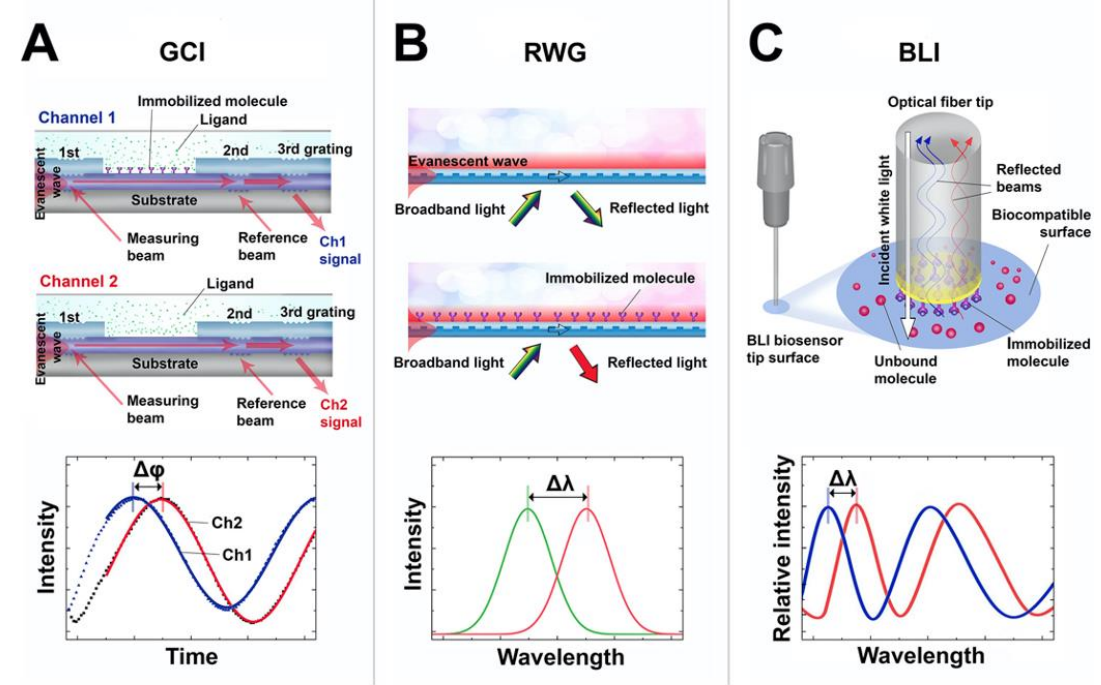
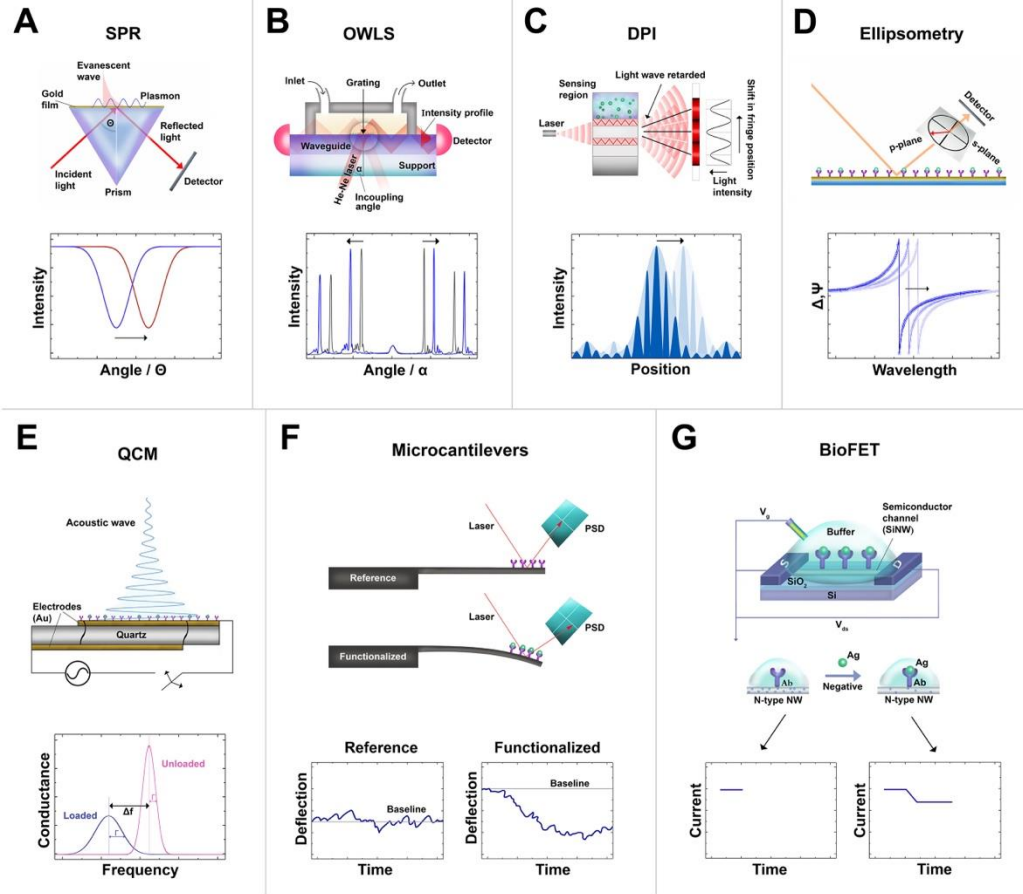
Kinetics and thermodynamic parameters in **clean media** which are important to in-detail understand biological interactions. Results: Conc., K_D , off-rate, on-rate, enthalpy (ΔH) and entropy (ΔS)



Very established field
by different technologies and companies



How do these sensors work?



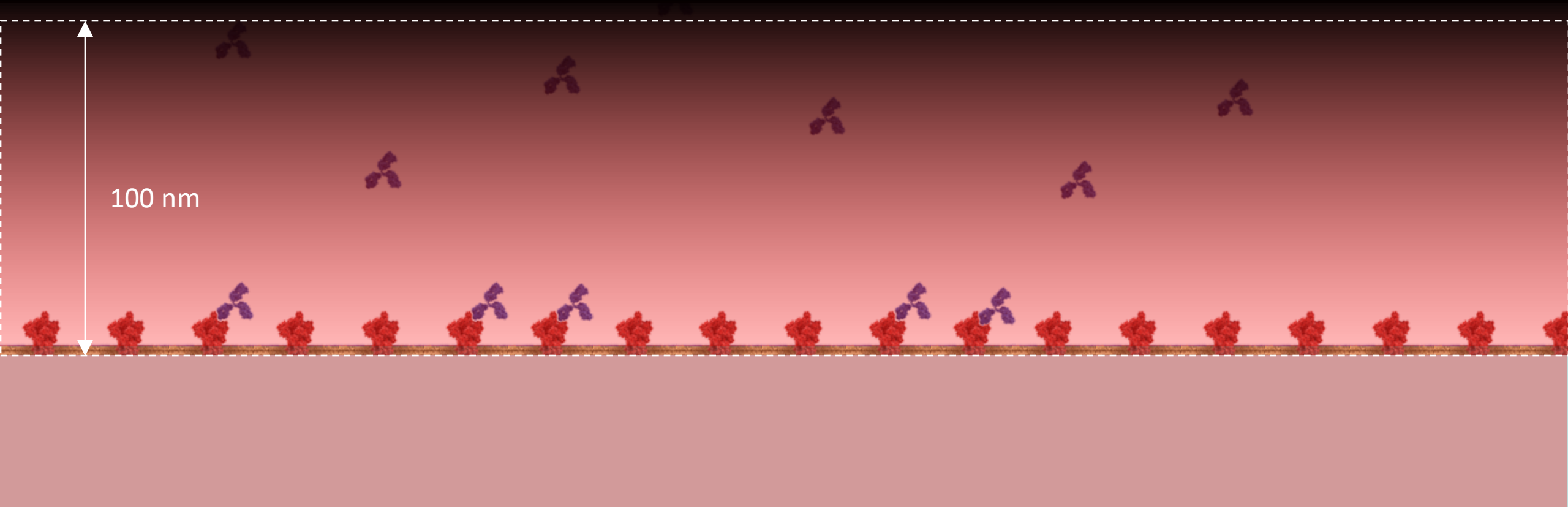
- Known as refractometric sensors
- In principle: Very sensitive techniques

A. Saftics, S. Kurunczi, B. Peter, I. Szekacs, J. J. Ramsden, and R. Horvath, *Data Evaluation for Surface-Sensitive Label-Free Methods to Obtain Real-Time Kinetic and Structural Information of Thin Films: A Practical Review with Related Software Packages*, Adv. Colloid Interface Sci. **294**, 102431 (2021).

Sensing principle: Correlation of the refractive index change within a tiny measurement volume defined by the evanescent field to a change in the number of molecules



Lets put one of these sensors in a **biological environment**



Lets put one of these sensors in a biological environment

In a biological sample, **molecules of interest** represent only a **small fraction of the biomolecular mass** in the sensing volume, despite the affinity difference.

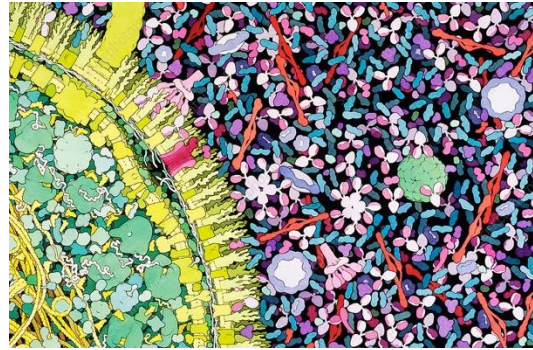
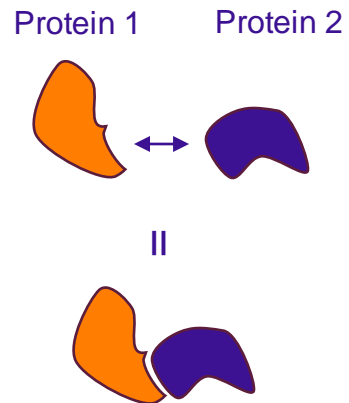
In addition, temperature, concentration and buffer changes all affect the refractive index.



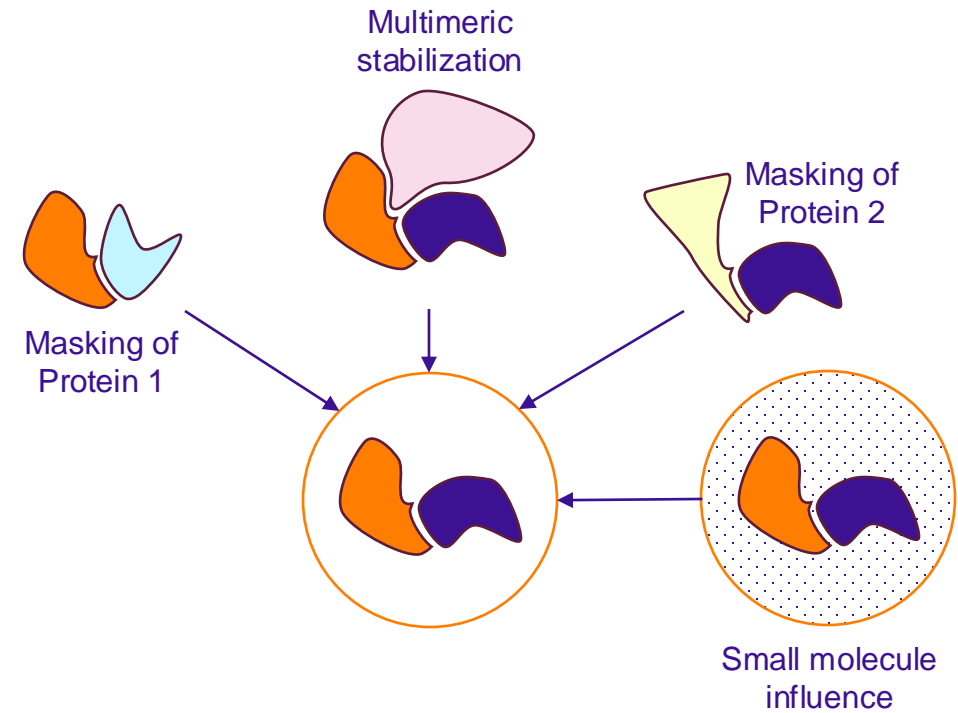
State of the art molecular sensors are cross-sensitive and can only operate in controlled conditions.

Why characterization in **complex media** (blood, living cells etc)?

Typical simplified interaction experiment



This is how the reality looks like



To measure interactions in a complex media we need

Robust and sensitive biosensors

I. PILLAR

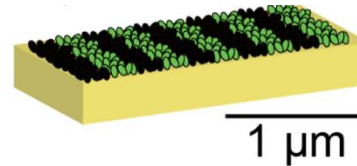
Darkfield illumination
By evanescent waves



Only illuminate where needed

II. PILLAR

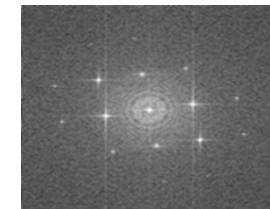
Submicron Modulation



Make the analyte bind in a pattern

III. PILLAR

Detection in Fourier space



Read the pattern by diffraction

A. Frutiger, C. Fattinger, and J. Vörös, Ultra-Stable Molecular Sensors by Sub-Micron Referencing and Why They Should Be Interrogated by Optical Diffraction—Part I. The Concept of a Spatial Affinity Lock-in Amplifier, *Sensors* 21, 469 (2021).

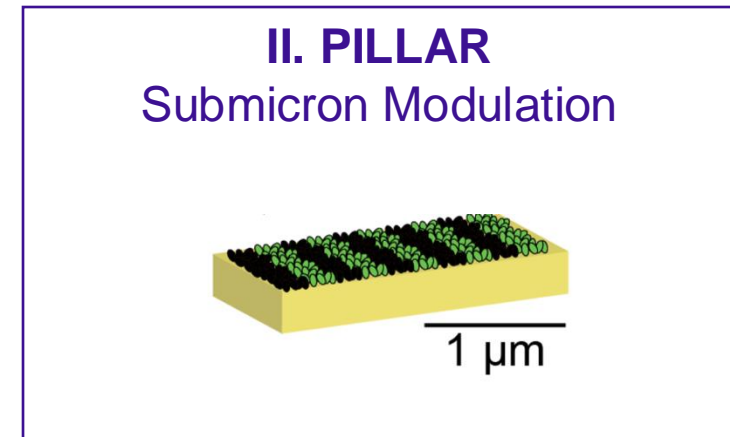
A. Frutiger, K. Gatterdam, Y. Blickenstorfer, A. M. Reichmuth, C. Fattinger, and J. Vörös, Ultra Stable Molecular Sensors by Submicron Referencing and Why They Should Be Interrogated by Optical Diffraction—Part II. Experimental Demonstration, *Sensors* 21, 9 (2020).

Why is a **macroscopic reference inferior** to a **distributed reference** on the **molecular length scale**?

Macroscopic reference:



To understand it we need to look at the **length scales of environmental noise**...



Make the analyte bind in a pattern

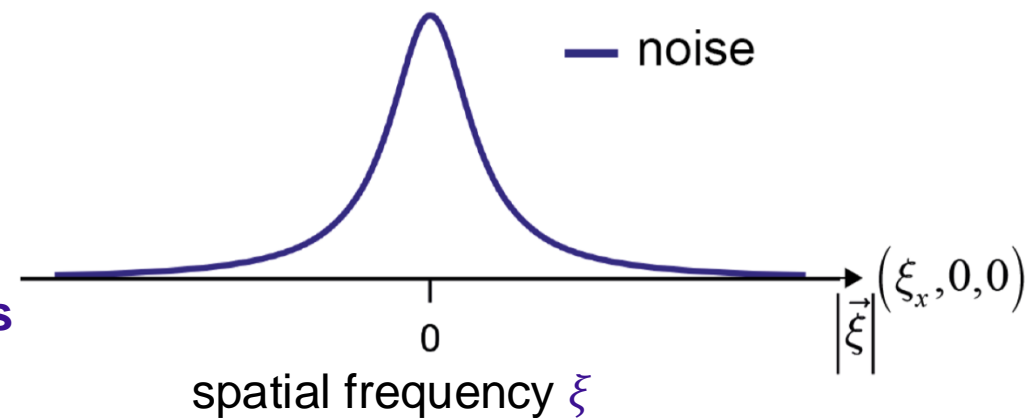
Most environmental noise is situated at low spatial frequencies (longer length scales)...

...because it is governed by the advection-diffusion equation.

$$\frac{\partial T(\vec{r}, t)}{\partial t} = -D_T \nabla^2 T(\vec{r}, t) + \frac{q(\vec{r}, t)}{\rho c_p},$$

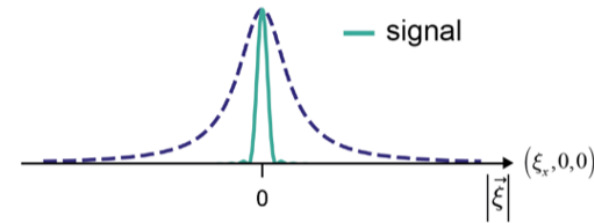
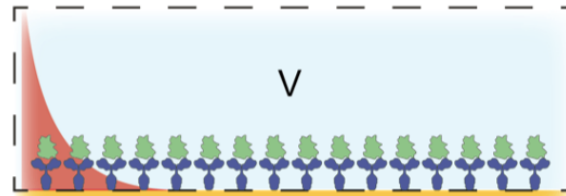
Intuitive explanation: Speed of diffusion is finite
→ **gradients in concentration,**
temperature relax faster on nm than mm scales

Power spectrum is $1/\xi$ distributed:



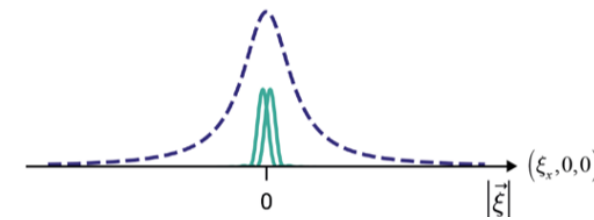
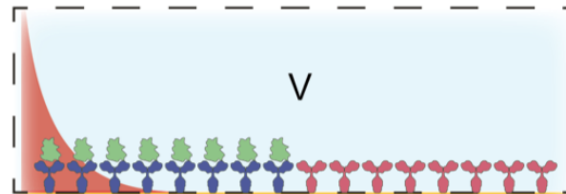
The binding signal can be shifted to a high spatial frequency and separated from the noise by modulation

Sensor signal
unreferenced



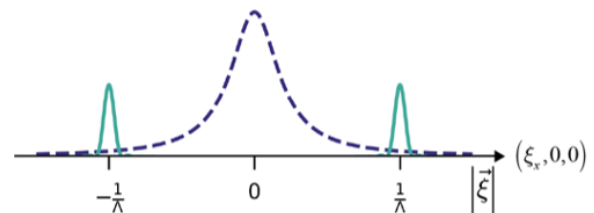
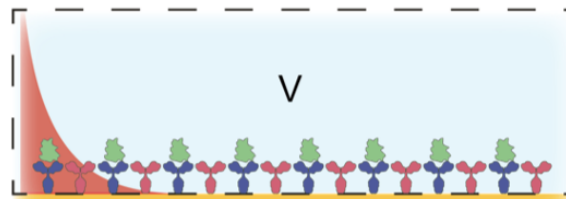
Noise and signal
overlap

Sensor signal
referenced



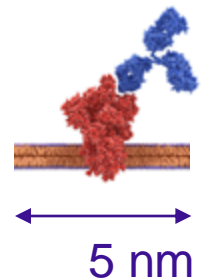
Noise and signal
still overlap

Sensor signal
sub-micron
referenced

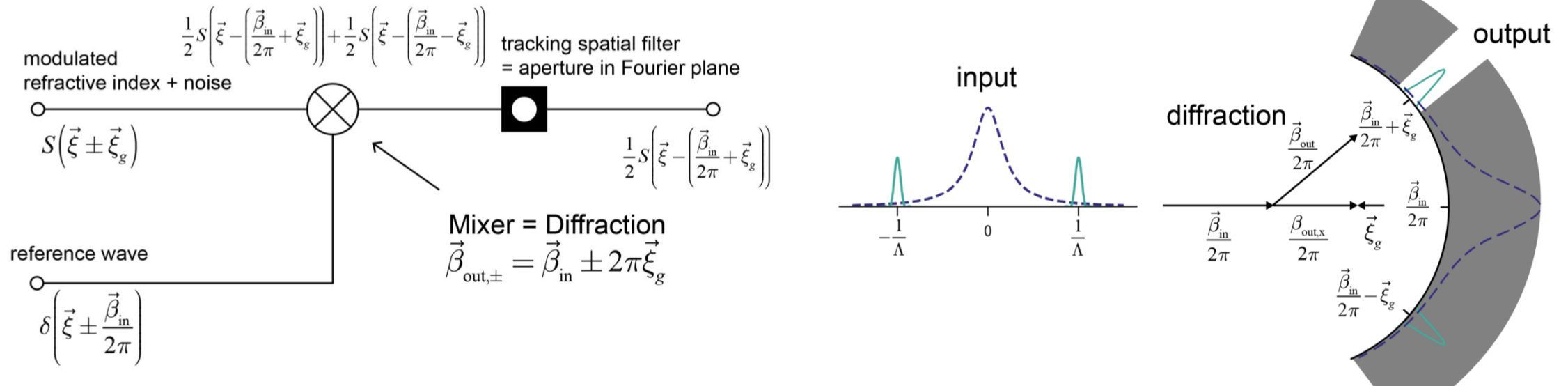


Noise and signal
separated

Modulation frequency should be as close to the inverse molecular length scale as possible.



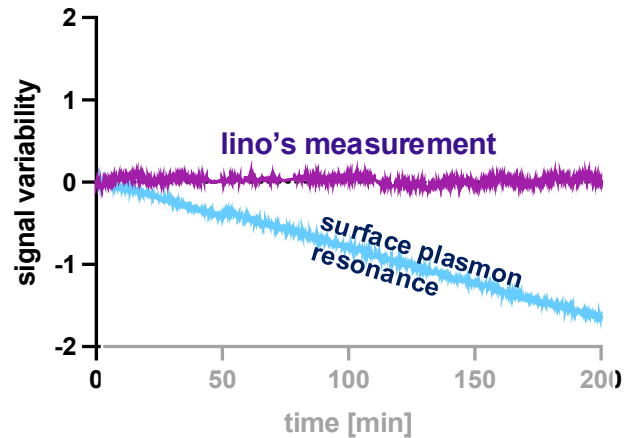
Mixing and filtering can be achieved via diffraction of waves and Fourier plane filtering



Tracking of the signal (lock-in) can be achieved by a pinhole or an array detector in a Fourier plane.

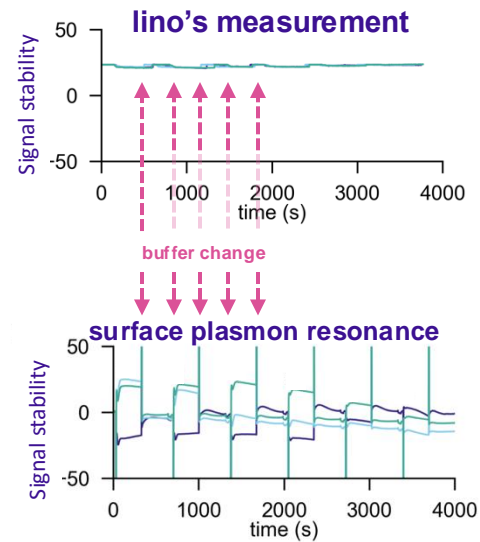
Spatially locked in sensors have unique properties

Long-term signal stability



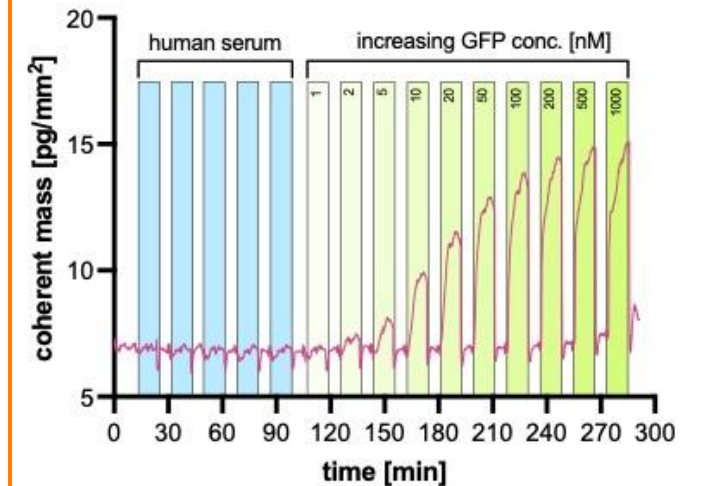
The technology is essentially drift-free. Here, the signal against the latest versions of the Biacore 8K is shown over multiple hour. [Experiment was the signal stability under running buffer flow over multiple hours; no binding signal change is expected]

Low medium influence



Molography has no artefacts from buffer changes during the measurement. Competitors (SPR) cannot tolerate buffer changes. [Experiment was the injection of different glycerol concentrations; no binding signal is expected]

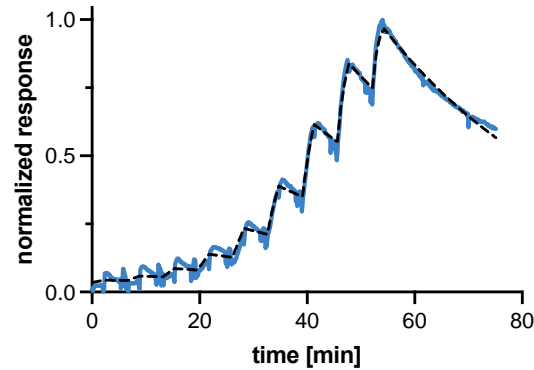
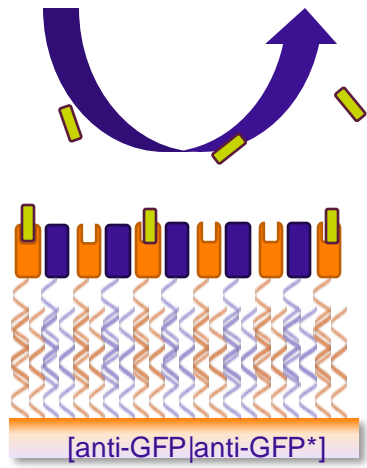
Excellent signal to noise ratio in complex media



Molography works in crude samples like competitors can only do in buffer. Non-specific binding of serum proteins hardly generates a response. [Experiment detects spiked GFP in 50% human serum down to 2 nM concentrations]

Kinetic characterization PBS-T versus human serum

Spiked PBS-T buffer

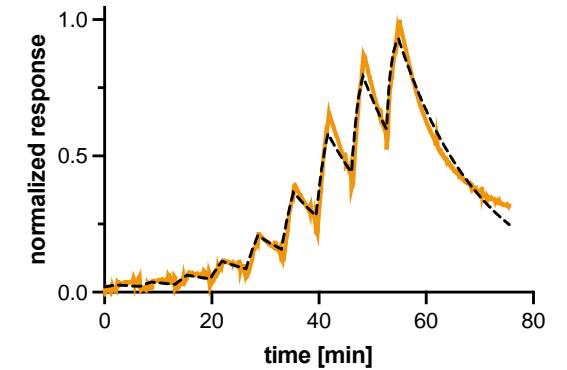
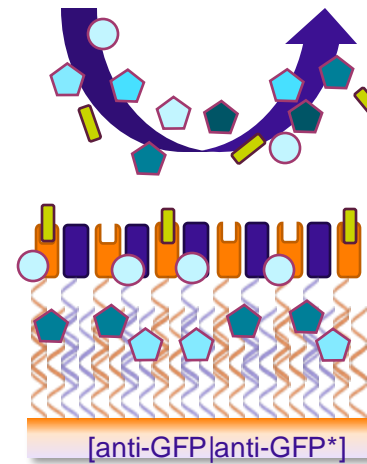


The assay format was first established in a classical PBS-T based interaction system. Therefore, increasing GFP concentrations were injected onto sensor surface and evaluated by a 1:1 Langmuir model. The median sensorgram is shown exemplary.

Mean kinetic values with SD (N=54)

k_{on}	$4.4 \pm 8.5 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$
k_{off}	$4.5 \pm 0.8 \times 10^{-4} \text{ s}^{-1}$
K_D	$1.2 \pm 1.2 \times 10^{-9} \text{ M}$

Spiked human serum



In a second step the assay was performed in 50% human serum. The medium was spiked with identical increasing concentrations of GFP followed by the identical evaluation. The median sensorgram is shown exemplary.

Mean kinetic values with SD (N=51)

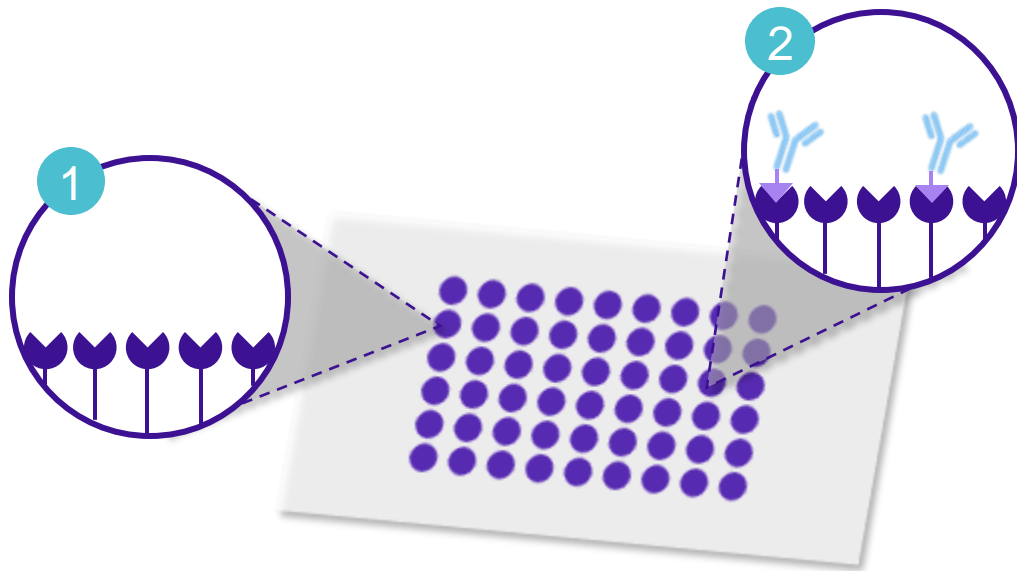
k_{on}	$6.1 \pm 3.5 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$
k_{off}	$1.3 \pm 1.0 \times 10^{-3} \text{ s}^{-1}$
K_D	$2.6 \pm 3.5 \times 10^{-9} \text{ M}$

General surface functionalities for sensor chips

Click Chemistry

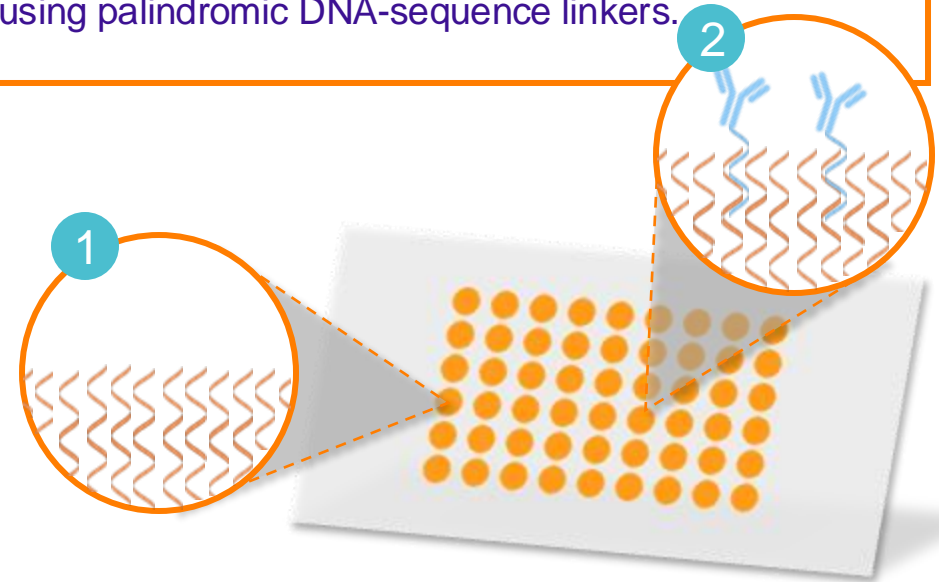
Biomolecules can be immobilized in a covalent fashion to the sensor surface via an optimized Click Chemistry strategy.

The underlying biocompatible polymer is a 2D PEG layer equipped with the molographic template structure.

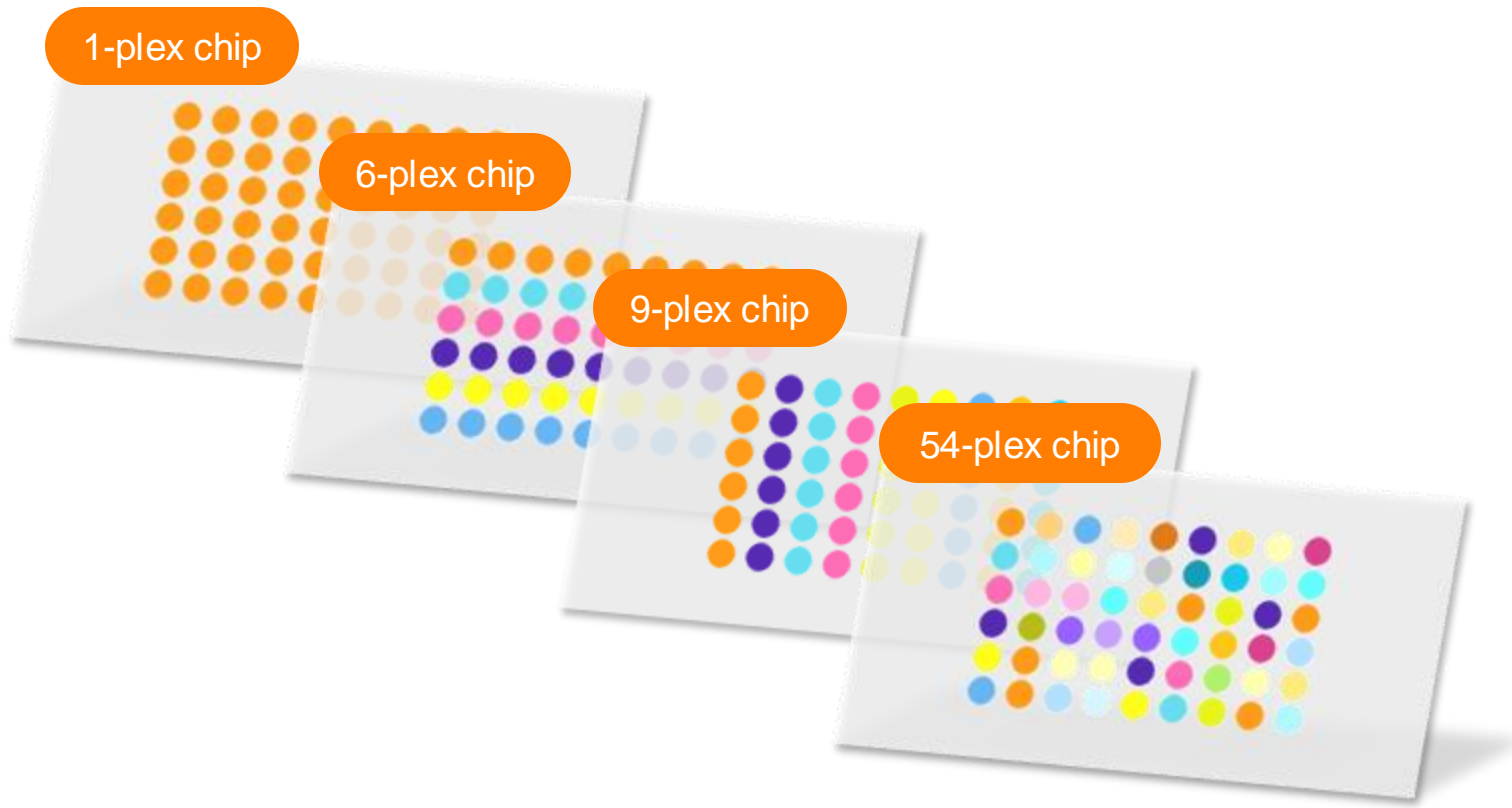


DNA directed

Sensor chips are fabricated with a well-defined DNA oligonucleotide pattern for individual Molograms. The different DNA sequences are attached to the Mologram by established micro-spotting techniques. For biological functionalization, different target-types can be linked to individual Molograms using palindromic DNA-sequence linkers.



DNA directed immobilization is the basis for multiplexed chips



Sensor Chip

Sensor chips are spotted with a pre-functionalized pattern for various multiplexed applications.

In combination with a disposable fluidic cassette a broad set of sensor chips can be easily realized

Application example

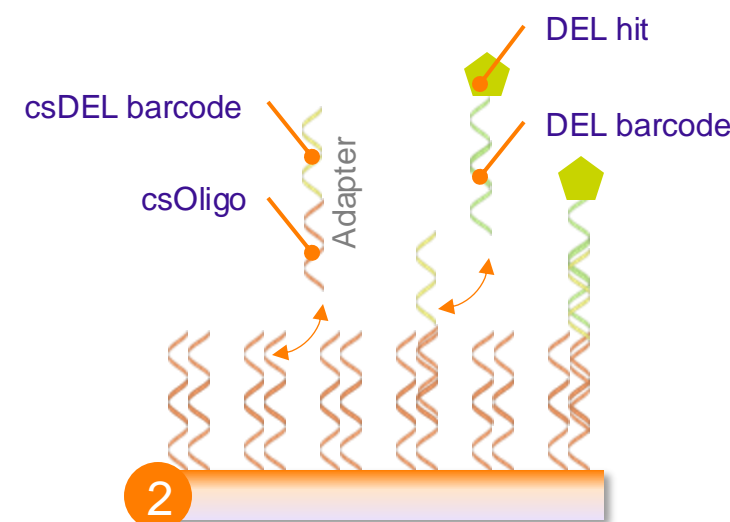
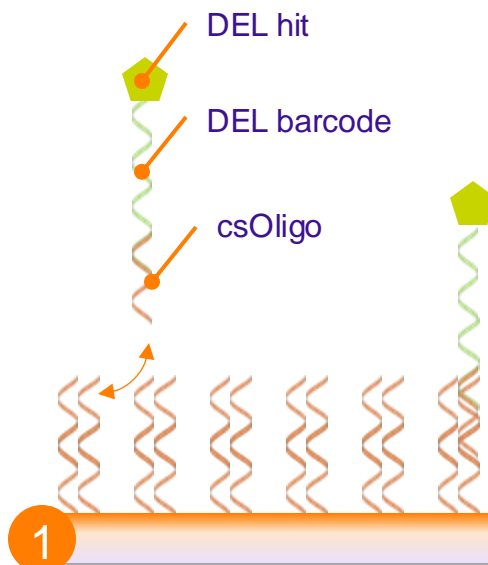
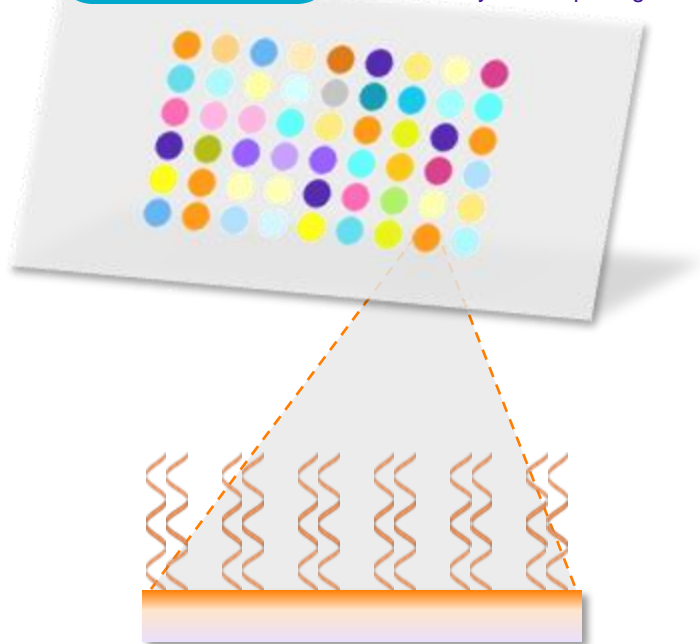
DEL (DNA encoded library) hit validation

DEL hit screening with Molography

Working principle

54-plex chip

54 orthogonal capture ssDNA (single strand) sequences fabricated by micro spotting



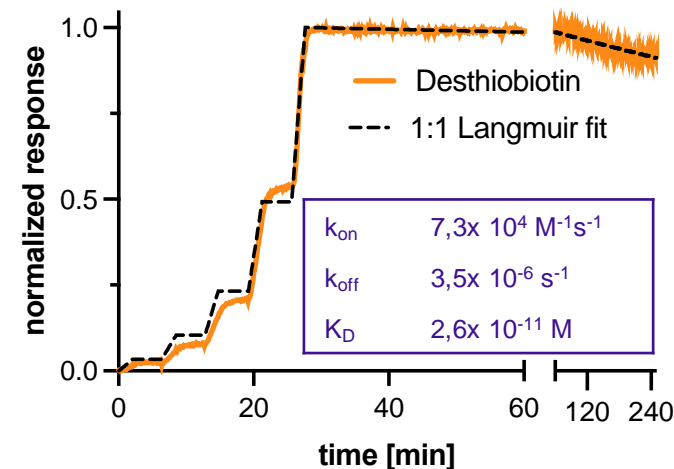
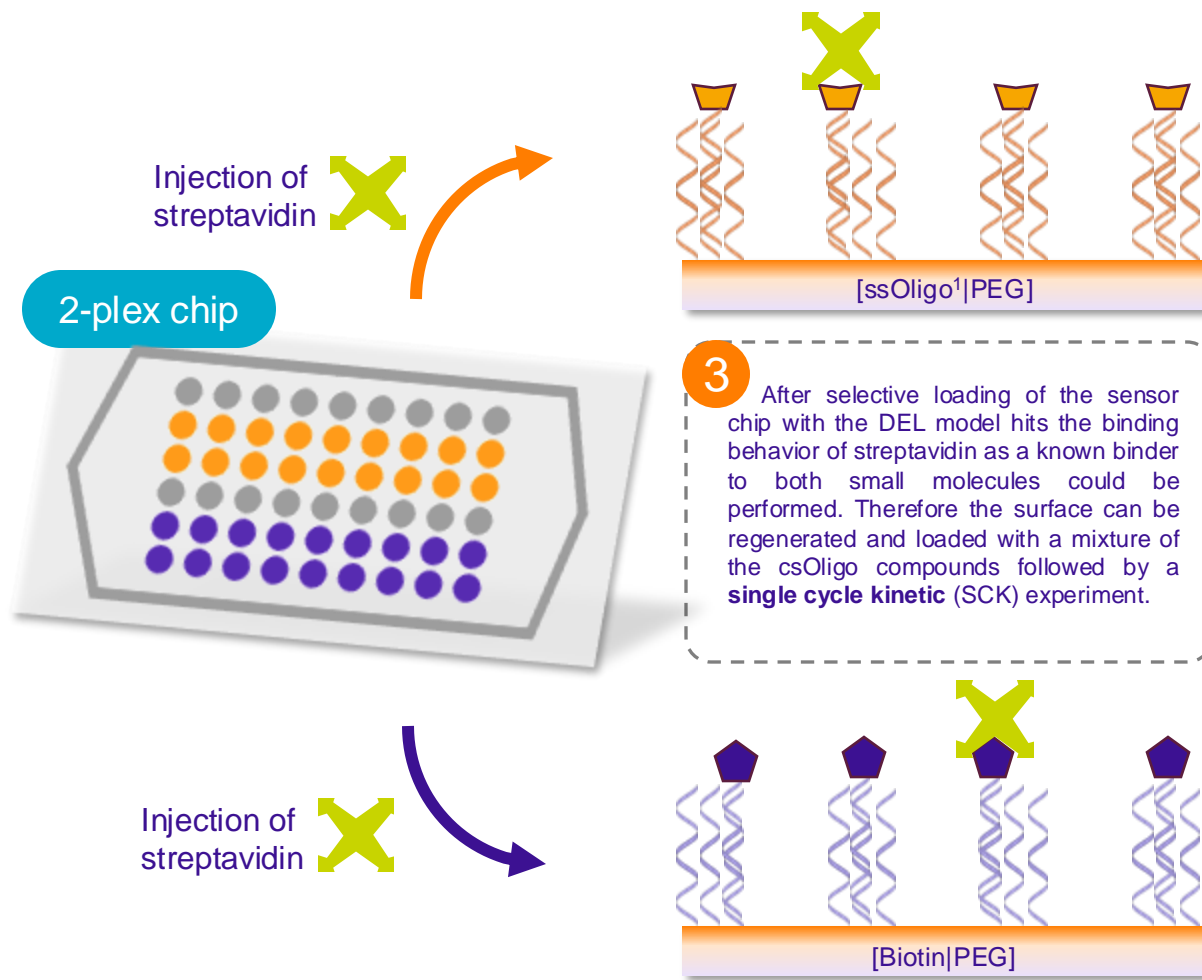
A **pre-functionalized sensor chip** with 54 molograms modified with different **ssOligos** (surface strain) is used for further kinetic characterization of DEL hits. The DNA based DEL barcode attached to the small molecule compound is used for a convenient immobilization on the ready to use multiplexed oligonucleotide chip. Currently two working modes are possible.

If the customer is able to elongate the DNA barcode of the DEL hits a **csOligo** (complementary strain) can be added accordingly to the sequences on the sensor chip. A single injection of 54 DEL hits with unique csOligo tags can be automatically injected by the autosampler resulting in **DNA directed immobilization (DDI)** of the ligands to the 54 molograms.

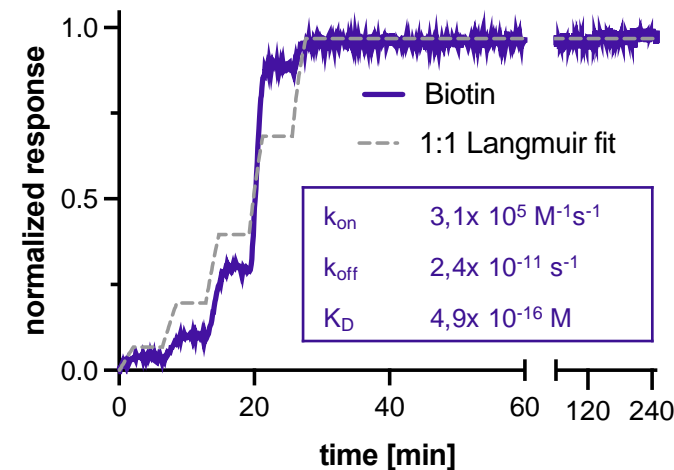
If the DEL barcode can not be modified an adapter oligonucleotide can be provided consisting of a **csOligo** and **csDEL barcode**. This bridging oligo can be used for DDI guided functionalization of the 54 molograms. The kinetic characterization of the target protein can be performed by a single cycle kinetics approach fully guided by the instruments software.

DEL hit screening with Molography

Direct kinetic characterization



It is known in literature that Biotin/streptavidin interaction is nearly covalent while the desthiobiotin/streptavidin interaction can be broken by specific condition. The weaker interaction is also visible by the existing off-rate in the long dissociation phase of the experiment.



The plotted graphs are again a single sensorgram of a representative mologram of the whole 18 mologram subarray. The used 1:1 Langmuir fit of the SCK shows small deviations for the biotin interaction. This could be due to depletion effect. In general such a high affinity interaction is also borderline to what can be measured

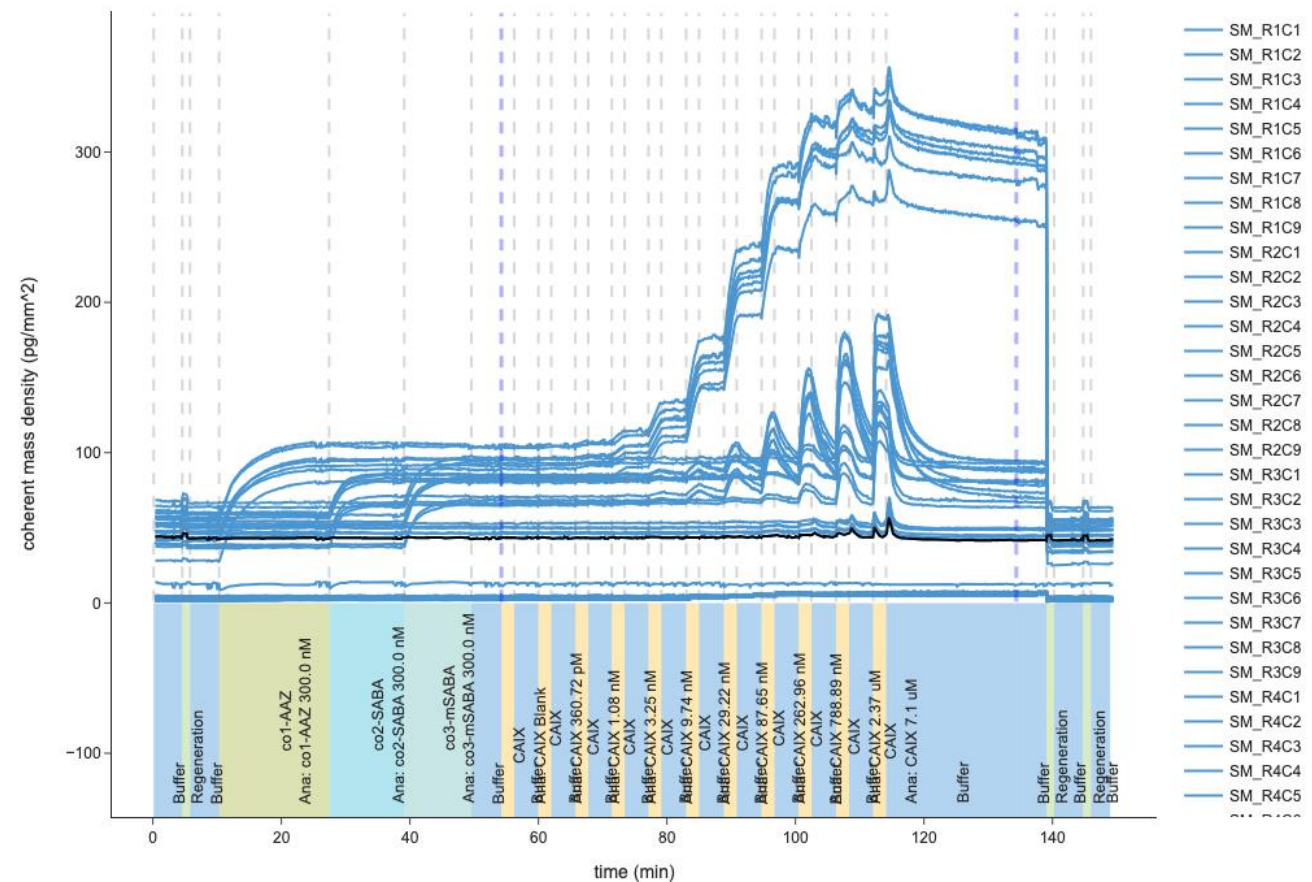
DEL screen of Carbonic Anhydrase IX on 3 plex chip

Compound Immobilization

Kinetic Screen

Compounds:

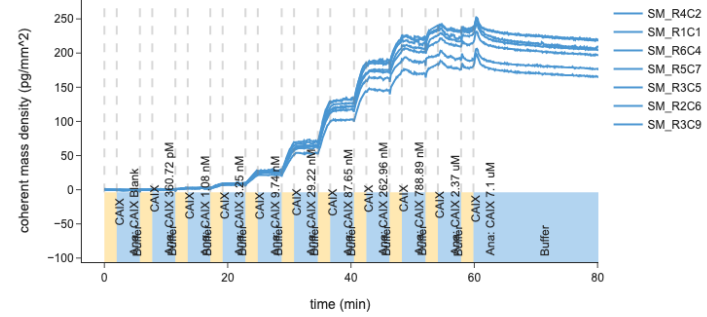
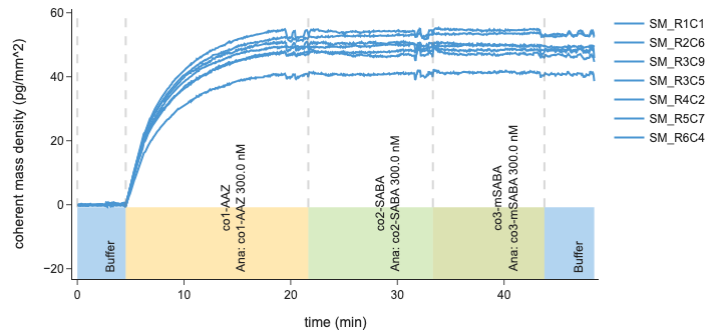
- AAZ (Acetazolamide)
- SABA (Sulfamoylbenzoic Acid)
- mSABA (meta-Sulfamoylbenzoic Acid)



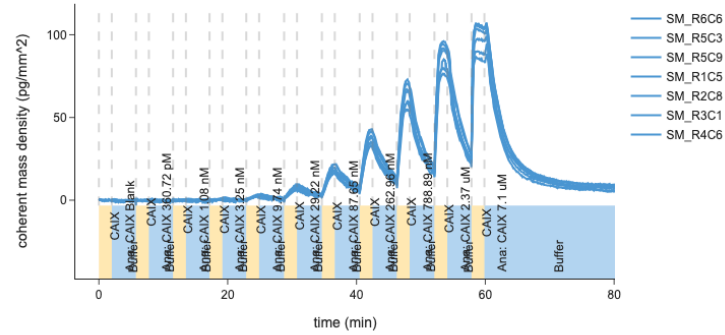
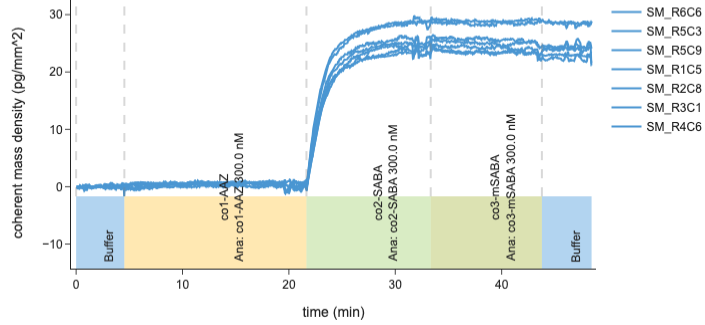
Compound Immobilization

Kinetic Screening

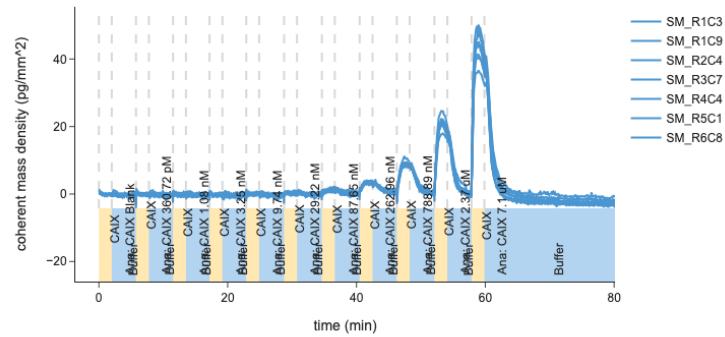
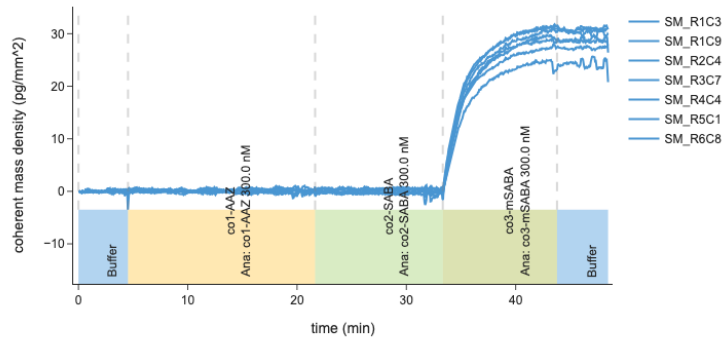
AAZ



SABA

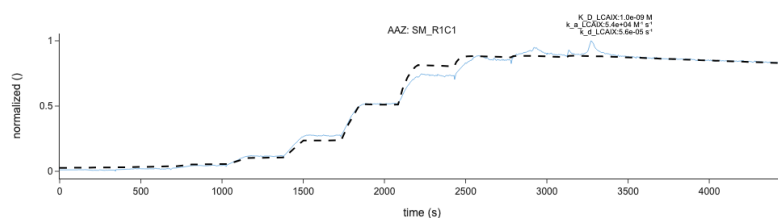


mSABA

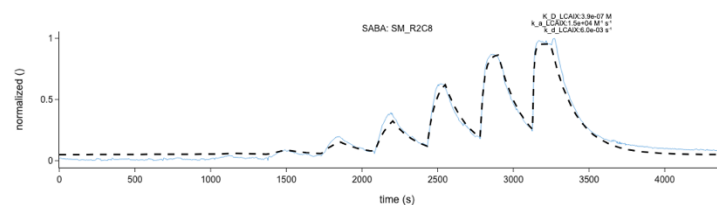


Kinetic parameters Carbonic Anhydrase IX

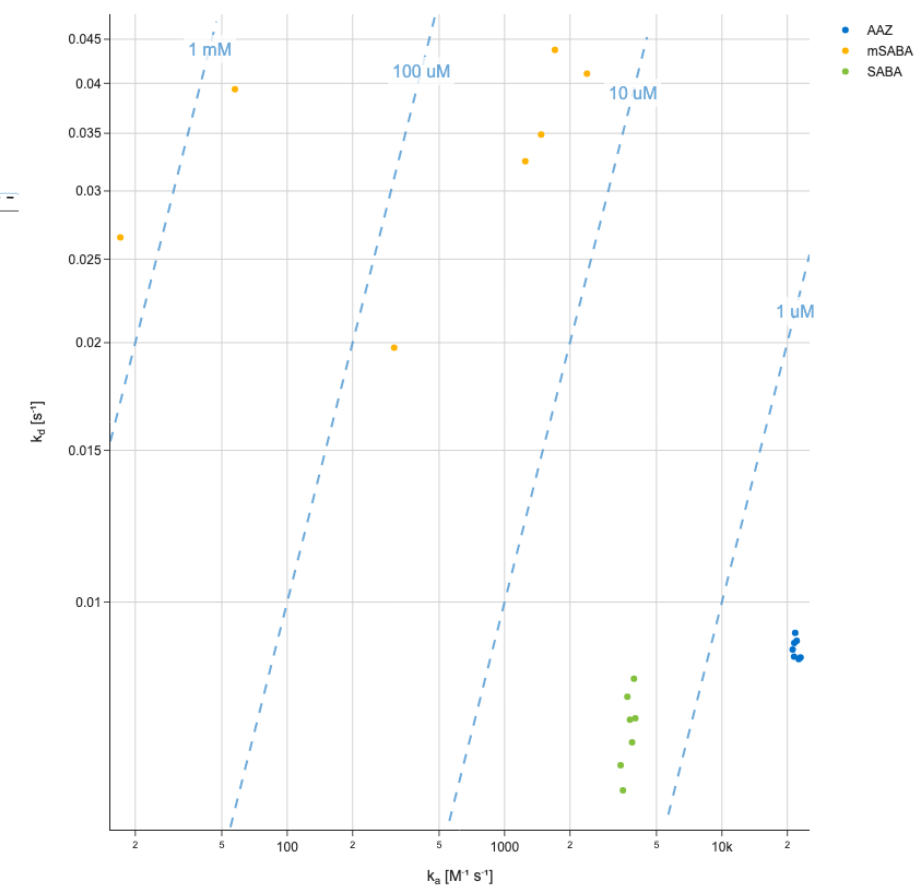
AAZ



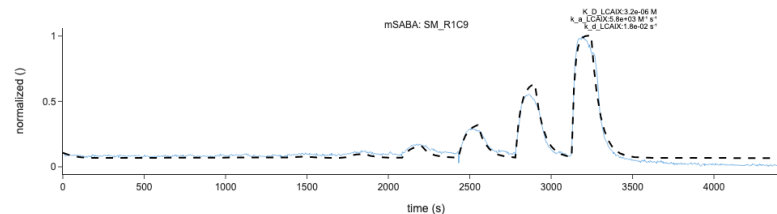
SABA



Isoaffinity map



mSABA



Compound	K_D	$k_{on} [M^{-1}s^{-1}]$	$k_{off} [s^{-1}]$
AAZ	790 pM	5.75e04	4.6e-05
SABA	326 nM	2e04	6.5e-03
mSABA	2 uM	7.5e03	1.46e-02

DEL hit validation with Molography

Customer benefits

Kinetic Information

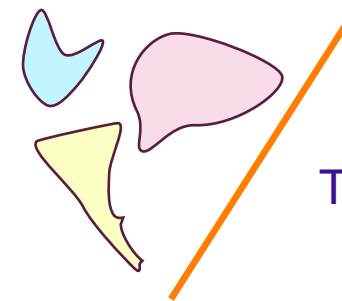
Target 1 

Target 2 

DEL Hits



Cross reactivity



Tissue Extracts

Full kinetic profile of interaction

Going crude: An additional unique benefit of focal Molography would be to test DEL hits against the biological matrix where the drug would be finally delivered. Thereby potential interfering biological interactions (drug masking) could be evaluated.

Application example

Membrane receptor Characterization

analytical
chemistry

pubs.acs.org/ac

Article

Quantification of Molecular Interactions in Living Cells in Real Time using a Membrane Protein Nanopattern

Andreas Michael Reichmuth, Mirjam Zimmermann, Florian Wilhelm, Andreas Frutiger, Yves Blickenstorfer, Christof Fattinger, Maria Waldhoer,* and János Vörös*

Cite This: <https://dx.doi.org/10.1021/acs.analchem.0c00987>

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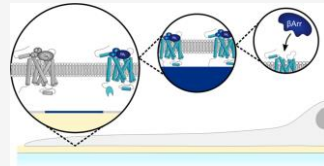
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Supporting Information

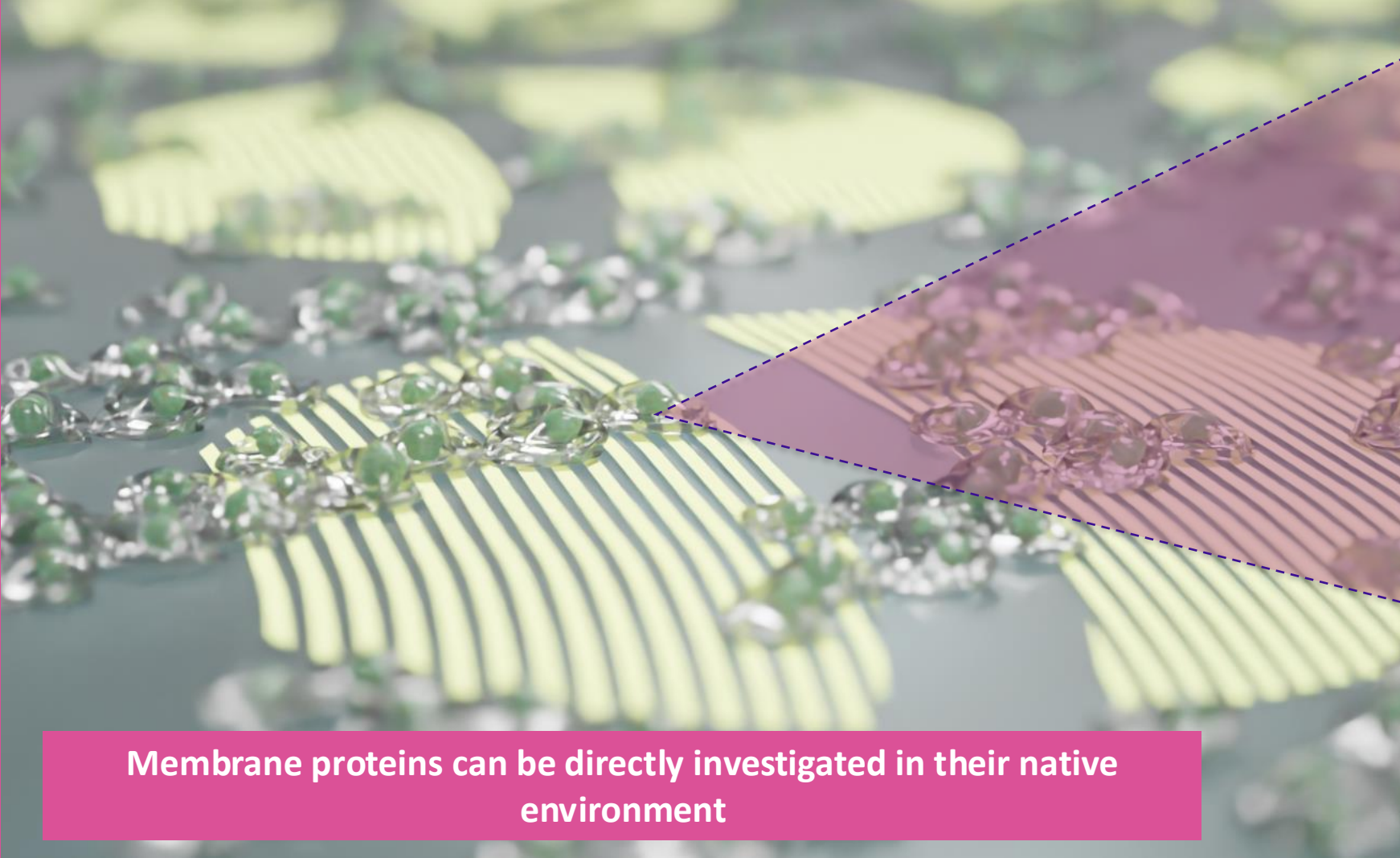
ABSTRACT: Molecular processes within cells have traditionally been studied with biochemical methods due to their high degree of specificity and ease of use. In recent years, cell-based assays have gained more and more popularity since they facilitate the extraction of mode of action, phenotypic, and toxicity information. However, to provide specificity, cellular assays rely heavily on biomolecular labels and tags while label-free cell-based assays only offer holistic information about a bulk property of the investigated cells. Here, we introduce a cell-based assay for protein–protein interaction analysis. We achieve specificity by spatially ordering a membrane protein of interest into a coherent pattern of fully functional membrane proteins on the surface of an optical sensor. Thereby, molecular interactions with the coherently ordered membrane proteins become visible in real time, while nonspecific interactions and holistic changes within the living cell remain invisible. Due to its unbiased nature, this new cell-based detection method presents itself as an invaluable tool for cell signaling research and drug discovery.



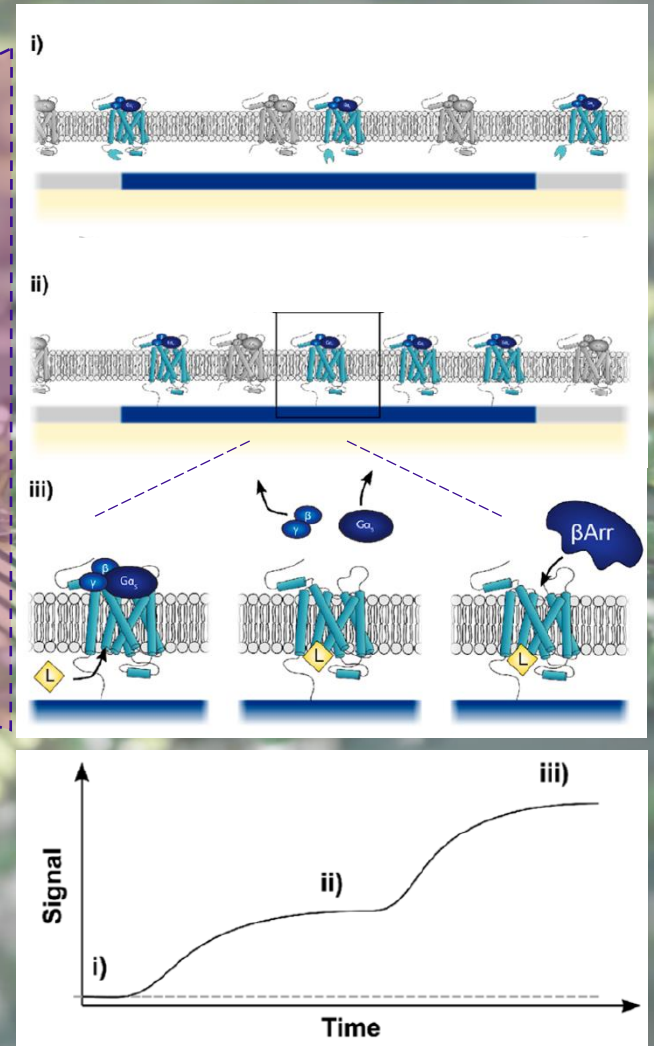
The ability to examine living cells in a physiologically relevant context is crucial to the understanding of cellular processes and emanating drug discovery efforts. While traditional biochemical assays are well-established and provide high molecular specificity, they often fail to report functional and cytological insight. Live cell assays, on the other hand, facilitate studies on stimulus-induced toxicity and phenotypic

evanescent wave into the sample defines the volume in which the sensor is sensitive to changes of the shape or the bulk refractive index of adherent cells on the sensor surface.^{1,14} Redistribution of any cellular content within this sensing volume results in an overall change in the refractive index. However, this detection process is inherently cross-sensitive, since both specific and nonspecific molecular processes as well

Drug screening: Ruling out off-target binding and accelerating drug development



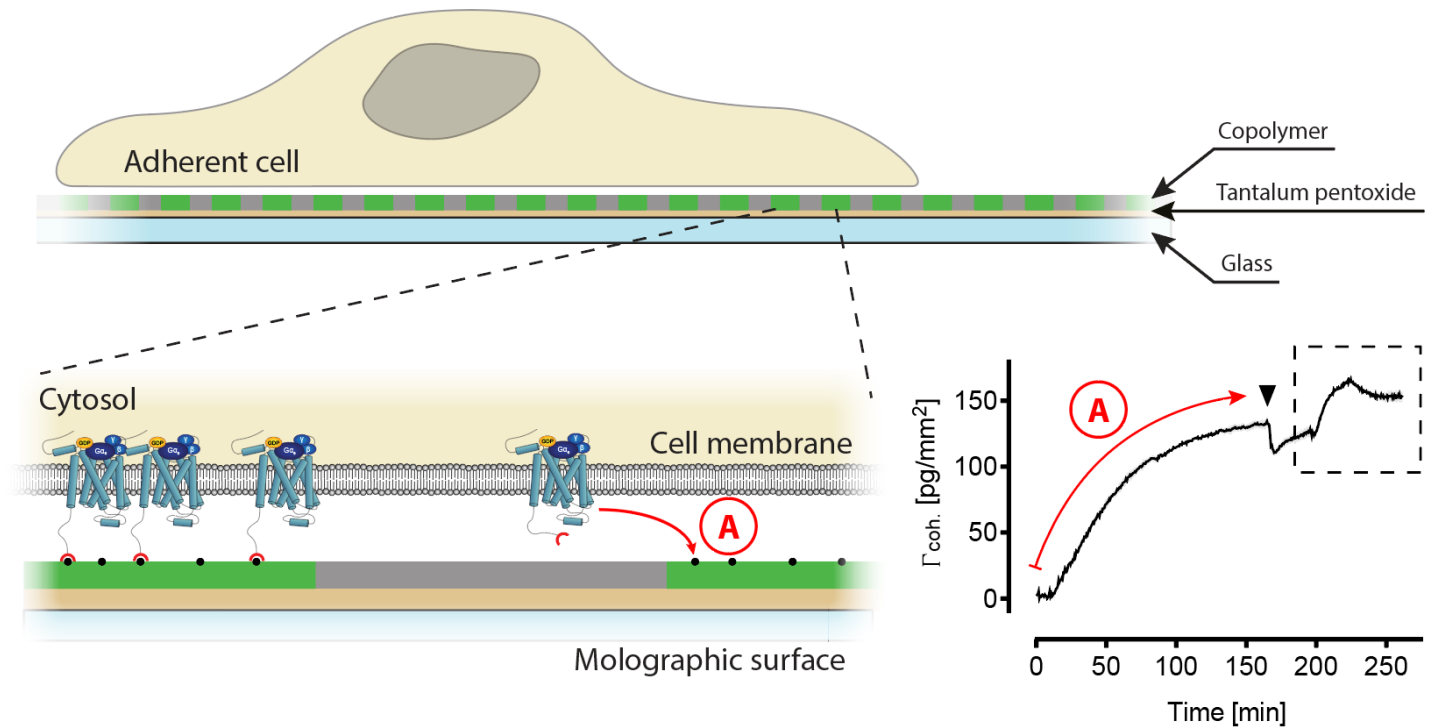
Membrane proteins can be directly investigated in their native environment



Detection of G-protein coupled receptors (β 2AR) in living cells

Formation of a functional SNAP- β 2AR transmembrane mologram in HEK293 cells.

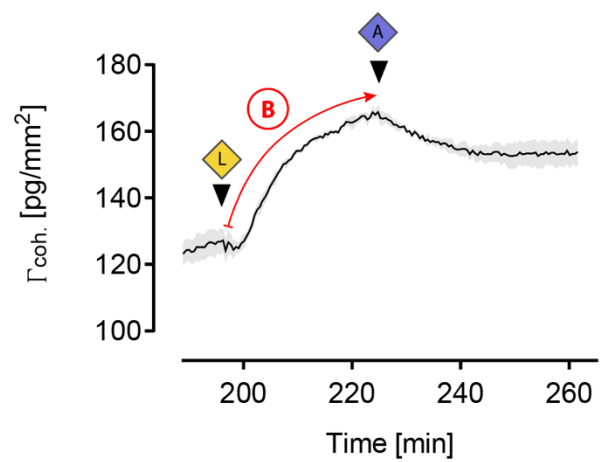
Cells are plated on a sensor chip with previously employed template molograms. The GPCRs arrange within the cell membrane over the course of about 150 min shown by the molographic signal (red arrow). Medium is exchanged for the assay (black triangle).



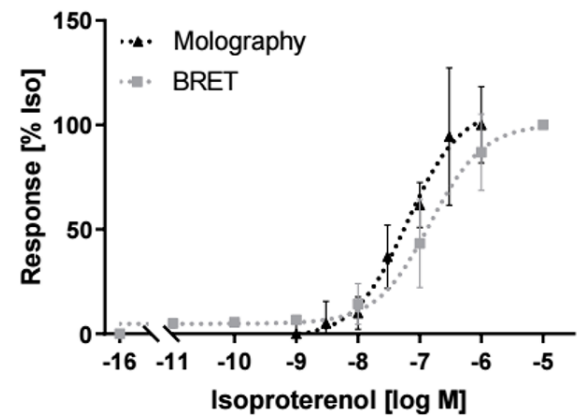
Additional Data

✓ Unmodified HEK293 cells → no signal increase

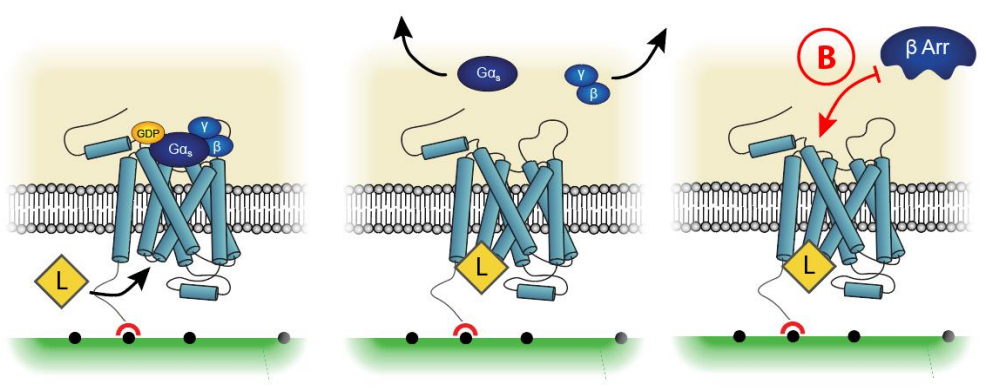
Detection of G-protein coupled receptors (β 2AR) in living cells



Stimulation of the SNAP- β 2ARs with 1 μ M isoproterenol (first triangle) shows an increase in the molographic signal, which is partially reversed by the addition of a 10 μ M amount of the competitive antagonist ICI 118,551 (second triangle).



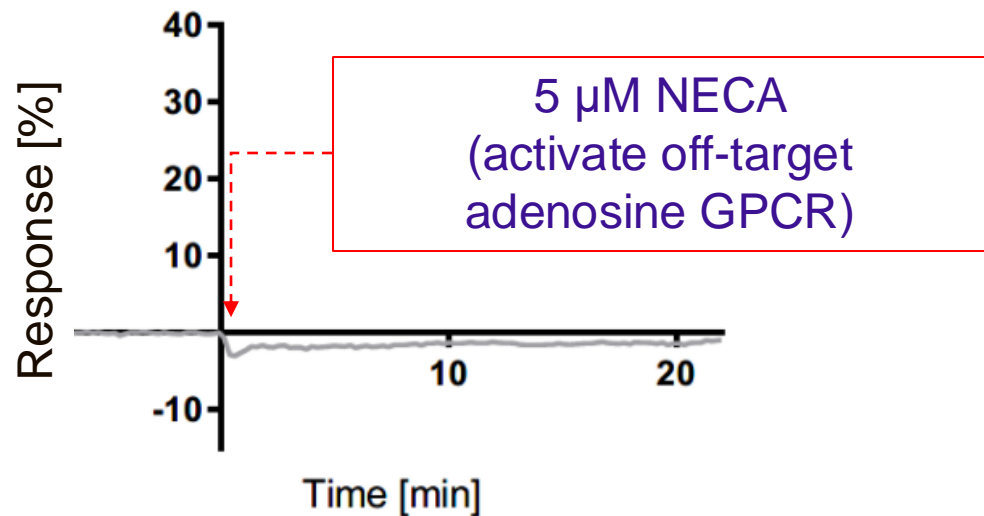
Cell-based molography compared to classical BRET arrestin recruitment assay.
For the molographic assay, cells were treated with increasing concentration of isoproterenol (left). The molographic signal was normalized to 1 μ M isoproterenol (=100%).



- ✓ Quantification and identification of binding partner
 - ✓ Determination of receptor occupancy
 - ✓ Concentration-response curves
 - ✓ Receptor deorphanization
- Compatibility of target specific characterization with living cells**

Source: Reichmuth et al. 2020. "Quantification of Molecular Interactions in Living Cells in Real Time Using a Membrane Protein Nanopattern." *Analytical Chemistry* 92 (13): 8983–91.

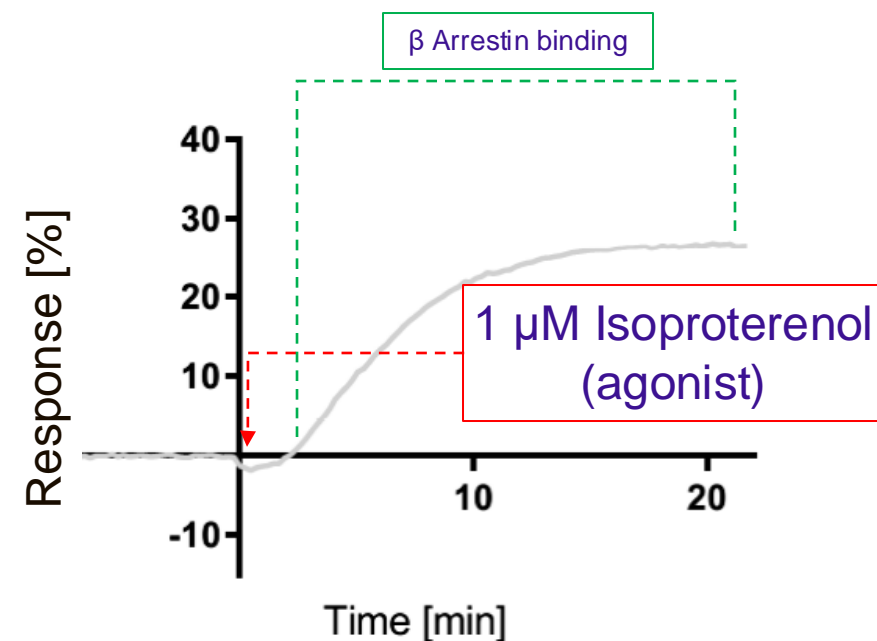
Detection of G-protein coupled receptors (β 2AR) in living cells \rightarrow *off-target controls*



- ✓ Effect of injection of dummy ligand
- ✓ Effect on off-target GPCR signaling

Additional Data

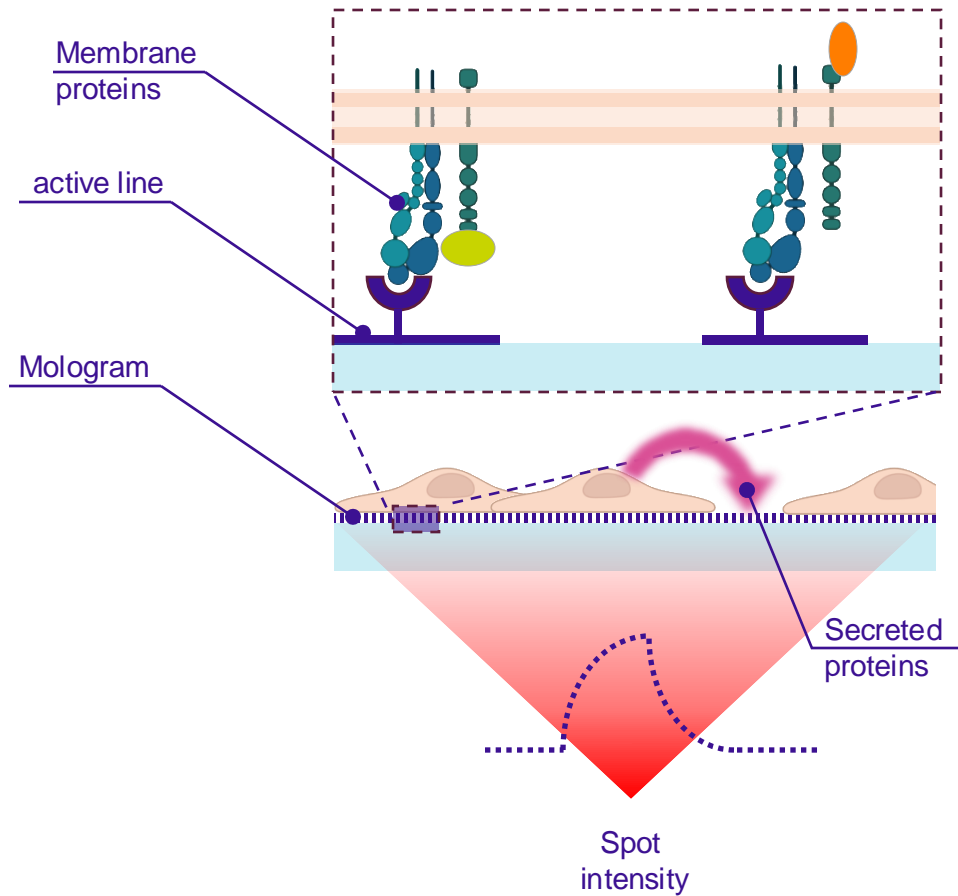
- ✓ β Arrestin knock-out \rightarrow no signal increase
- ✓ β Arrestin knock-out + β Arrestin plasmid \rightarrow signal increase



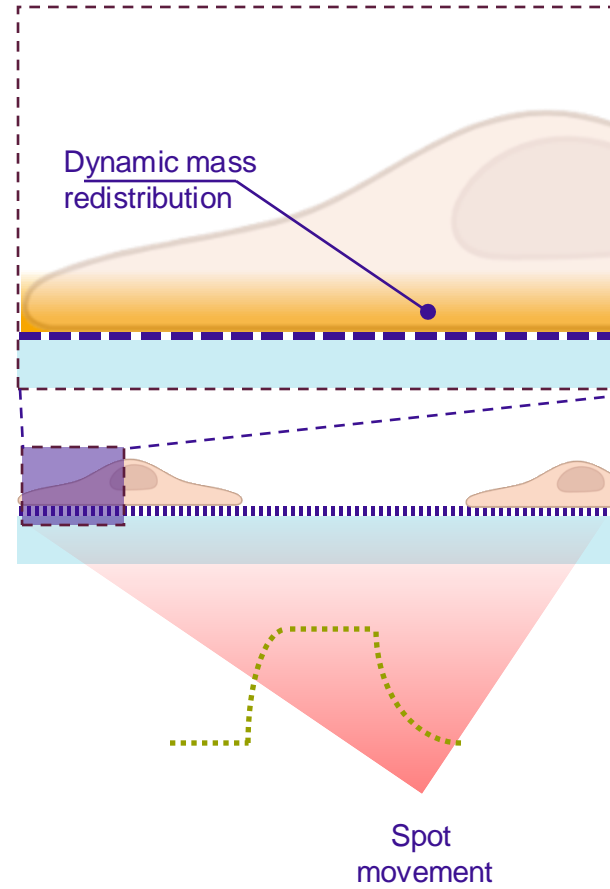
- ✓ Positive control for target GPCR

Data generation for cell mediated interaction

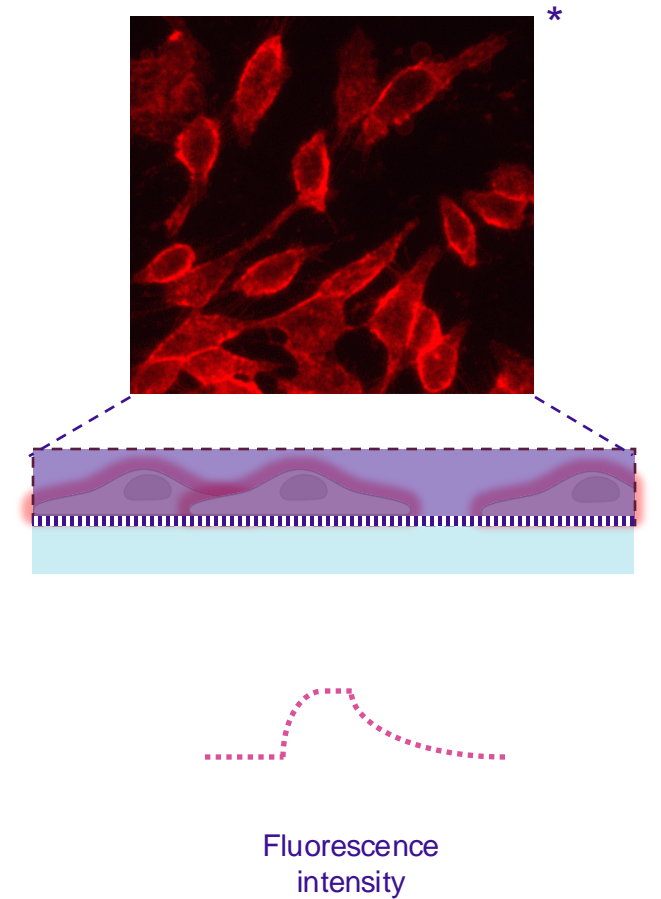
Diffractometric Data
- Focal Molography -



Refractometric Data
- SPR like -



Fluorescence Data
- Microscopy like -



* Example image from aatbio.com; recorded with third-party microscope

Data generation for cell mediated interaction

Diffractometric Data

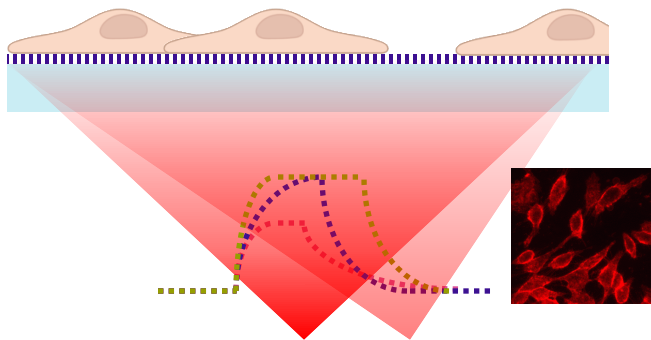
- Focal Molography -

Refractometric Data

- SPR like -

Fluorescence Data

- Microscopy like -

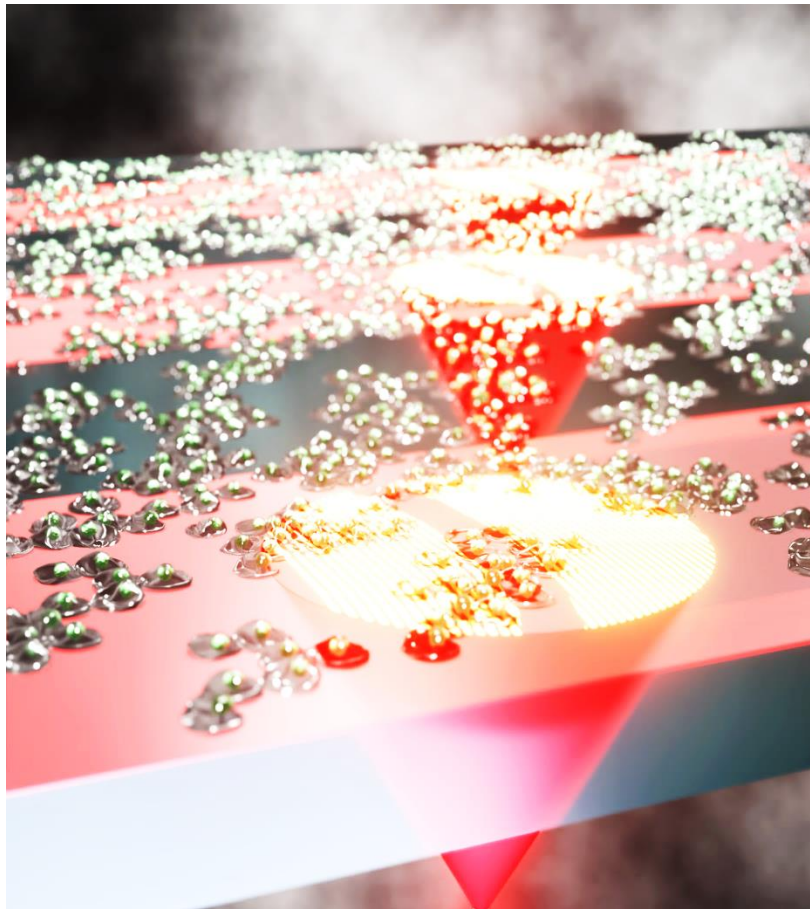


All combined in one benchtop instrument

1. Cell adhesion
2. Receptor yes/no
3. Receptor activation
4. Drug binding



Summary



Miltenyi Biotec

Thank you for your attention!



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