

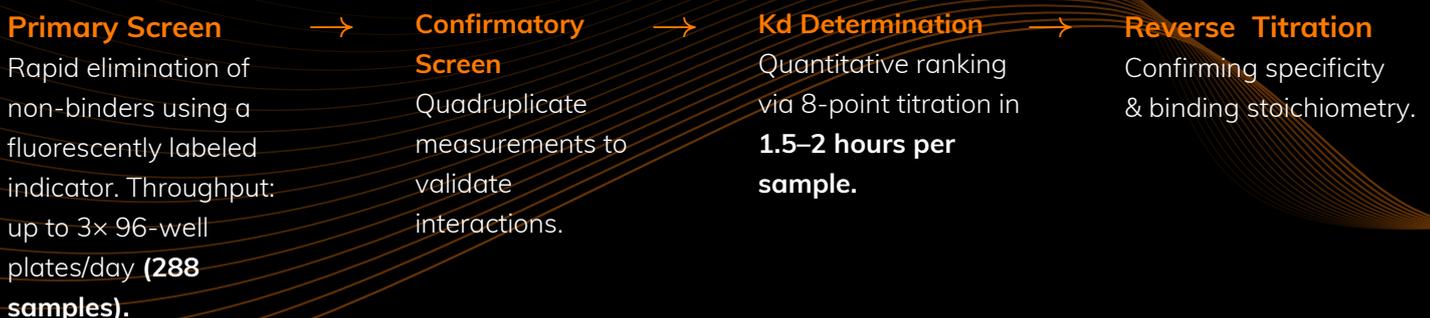
50x faster screening with FIDA

How did Tozaro boost their screening throughput from 6 to up to 288 samples daily, reducing months of work to just days?

Tozaro (Previously MIP Discovery / Diagnostics) ingeniously reimaged its affinity reagent screening workflow using FIDA, transforming interaction analysis from slow and labor-intensive to fast and precise. The benefit? They managed to achieve greater efficiency, scalability, and decision-making power in molecular interaction analysis.

The problem: Traditional techniques such as Surface Plasmon Resonance (SPR) created throughput bottlenecks, limiting the ability to evaluate large polymer libraries quickly and cost-effectively.

The solution: FIDA-Driven Workflow:



After these steps, **only selected candidates are progressed to SPR** to assess surface immobilization effects, eliminating the need for SPR in primary screening. By their innovative adaptation of FIDA, Tozaro **replaced** SPR for most polymer interaction screening analyses, streamlining research and accelerating discovery.



→ The benefits?

50x

increase in throughput: from ~6 polymers/day (SPR) to up to 288/day (FIDA).

30min - 3 hours

30 min for small molecules to 3 hours for proteins long screens for a full 96-well plate screened in with FIDA. Meanwhile, SPR could process only ~6 samples/day, requiring **16+ days to screen** the same number of samples.

Up to 10x

(Up to) reduction in sample consumption – fewer replicates and lower volumes needed due to direct in-solution measurements.

1.5–2

hours per sample to get a binding affinity data (for an 8-point titration)

By replacing SPR with FIDA for polymer interaction analysis, Tozaro streamlined research, reduced time-to-decision, and dramatically increased efficiency in polymer screening workflows.

SPR

16+ days

~6 polymers/day

FIDA

30min - 3 hours

up to 288 polymers/day



Ask yourself, what could you do with such time and sample savings?



100% Plasma binding measurements

that change big pharma's workflows

How did a large pharmaceutical company measure binding affinity and kinetics in-solution & in 100% plasma?

A big, German, pharma company had the ambition to measure K_d and binding kinetics in 100% plasma to correlate it with values from surface based technologies in buffer solutions - & they succeeded by using the right technology to do so.

The challenge: They knew that binding kinetics in buffer might not accurately represent how interactions behave in plasma. Without this insight, they risked advancing drug candidates based on misleading buffer-based kinetics, potentially leading to costly late-stage failures. Identifying these discrepancies early would allow them to prioritize the most promising compounds, reduce unnecessary follow-up experiments, ultimately improving efficiency and lowering development costs.

The solution: While traditional methods provided valuable insights, they did not reflect the complexity of physiological conditions. No available technology could provide direct, in-solution kinetic measurements in a plasma environment—until they turned to FIDA. It was the only technology that allowed them to measure in-solution binding kinetics directly in 100% plasma, giving them the data needed to make better-informed decisions. What was the process?

Measuring K_d and kinetic parameters

Directly in 100% plasma, ensuring physiological relevance.



Cross-validation with BLI

Assessing the correlation between in-solution K_d and on-/off-rates measured with FIDA and values obtained from BLI in buffer.



Comparing with buffer conditions

Measuring the same interaction in buffer to identify key differences in affinity and kinetics.



Analyzing the impact of plasma

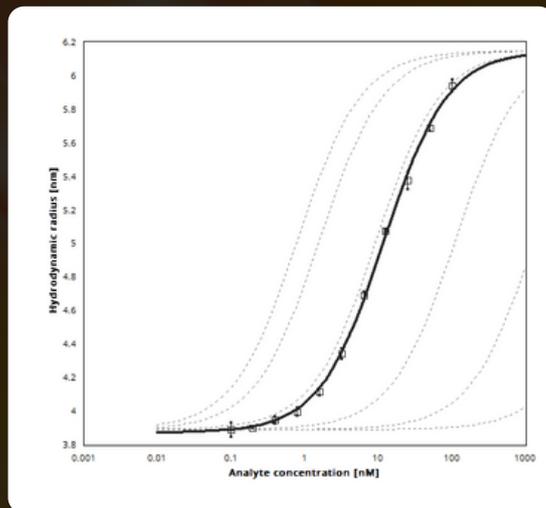
Quantifying how plasma components influence kinetic parameters and refining their decision-making.

What they discovered?

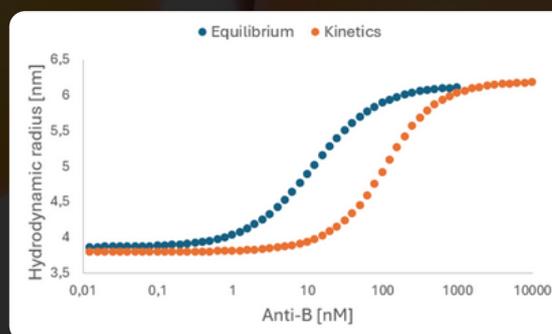
These differences highlighted why early validation of in-solution kinetics in plasma is critical to avoid investing in misleading buffer-based data.

The in-solution K_d in plasma was **8x weaker** than in buffer, revealing how plasma components affect affinity.

On-rates were **5x slower**, and off-rates were **2x faster** in plasma than in buffer. The difference between buffer and plasma is clearly distinguishable with FIDA technology.



Binding Curve in 100% plasma



Kinetics determination in 100% plasma

→ The benefits?

The gain of **physiologically relevant kinetic data** early in the drug development process.

By integrating early-stage FIDA measurements in 100% plasma, they streamlined their workflow, **improved candidate selection**, and **minimized late-stage failures**.

The insights allowed them to confidently prioritize viable drug candidates, **avoid costly setbacks**, and make more reliable, physiologically relevant decisions.

Ultimately accelerating the drug development process while reducing costs.

Screening de novo designed protein binders in unpurified lysate

The problem: Computational design produces binders at scale, but screening them efficiently is the bottleneck. Traditional validation does not provide structural data, requires purified material and multiple assays to determine whether a design binds with sufficient affinity and stability, slowing down the transition from design to decision.

The solution: By providing functional and structural data in a single measurement and directly from crude expression material, FIDA allows evaluation of binding, stability, and solution behavior at an early stage. This shifts validation from a sequential, resource-intensive process to an early, decision-driven step.

Properties of an ideal experimental binder screening pipeline:

FIDA:

- 01 Require tiny amounts of sample Operational definition of tiny: 96-well workflow
- 02 Require minimal pre-treatment Principal concern: avoid purification of binders
- 03 Provide answer or ranking from one measurement
- 04 Affinity determination with same assay
- 05 Speed & automation

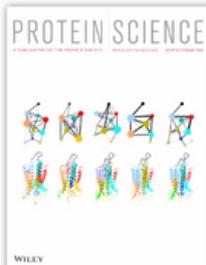
Nice to have: Additional biophysical information: stability, homogeneity, structure

Magnus Kjæregaard - Aarhus University

How to screen de novo designed protein binders in unpurified lysate using flow induced dispersion analysis?

Learn about streamlined binder development from Prof. Magnus Kjæregaard from the department of molecular biology and genetics at Aarhus University.

Watch now



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This article also appears in:
Tools for Protein Science 2025

Screening de novo designed protein binders in unpurified lysate using flow induced dispersion analysis

Learn More



If we sparked your curiosity, go ahead, **book a discovery call** to explore if FIDA could be something just right for you.



[Press here to speed up your research.](#)