

Fluidity One-M

Quantify binding affinity, size,
concentration and stoichiometry
in solution, all at once.



A new class of in-solution measurement

Proteins play critical roles in the human body, maintaining and regulating the structure and function of tissues and organs. To deliver this task, more than 75% of proteins interact with at least one other.

Understanding these interactions on a quantitative level is therefore essential to understand cellular functions and subsequently help develop and optimize successful vaccines, drugs and treatments.

Microfluidic Diffusional Sizing (MDS) technology implemented in the Fluidity One-M system brings a new tool to your analytical characterization toolbox enabling robust and comprehensive analysis of protein interactions in solution.

MDS measures protein molecular size (hydrodynamic radius – R_h). This simple and direct property can be used to determine protein interaction affinity and calibration-free concentration or binding stoichiometry, all at once.

By using fluorescence detection, MDS enables binding analysis of proteins in their native environment, such as serum and cell lysate, with high specificity.

MDS requires a very small volume of sample and works with traditional targets like proteins, peptides, DNA, RNA, and lipids, as well as unconventional systems like PROTACs, membrane protein nanodiscs, and amyloid aggregates.

Fluidity One-M is flexible, robust and easy-to-use. A powerful tool to help you tackle your most challenging targets with confidence.



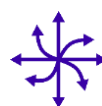
Direct

In-solution measurement



Multi-attribute

Size, affinity, stoichiometry and ligand concentration all at once



Versatile

Wide range of affinity, traditional to complex samples, even in serum or cell lysate



Simple

Mix & measure, no immobilization



Quick turnaround

Output results within 25 min for 24 data points

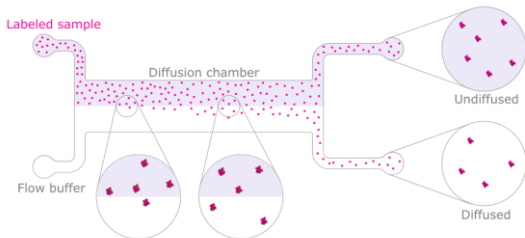


Unbiased

No calibration, no prior biophysical knowledge required

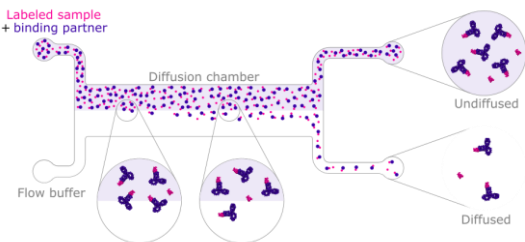
How does it work?

Microfluidic Diffusional Sizing (MDS) measures molecular size (hydrodynamic radius) of a sample by evaluating its diffusion in a microfluidic chamber.



Fluorescently labelled proteins enter the microfluidic diffusion chamber together with an auxiliary fluid, in two parallel laminar streams. The rate of diffusion of proteins from one stream to the other depends on the protein molecular size (top)

The rate of diffusion and hydrodynamic radius (R_h) of the protein can be calculated based on the ratio of fluorescence signal detected in the two streams at the end of the chamber.



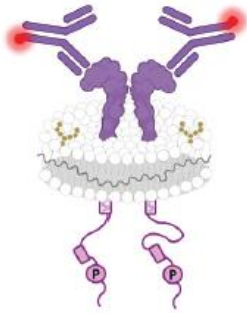
When the labelled protein is mixed with a binding partner (bottom), if binding occurs, the measured size of the complex increases according to the bound fraction. This change in size can easily be used to interrogate their interactions.

With MDS, you can see how proteins truly interact

- ✓ Directly measure size changes – quantitative, easy to interpret, built-in QC
- ✓ Calculate binding affinity (K_D) from measurement of protein in free form and against a titration of binding partner
- ✓ Determine concentration of binding partners without calibration or standards
- ✓ Study binding stoichiometry to understand the protein mechanism of action
- ✓ Unique capability to distinguish between high affinity-low concentration and low affinity-high concentration systems

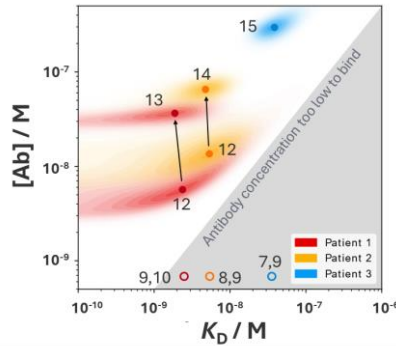
MDS answers your questions

Membrane-Protein Affinity and Concentration Assay



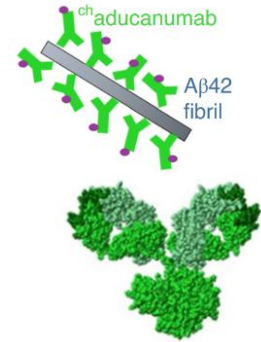
MDS measures trastuzumab interaction with membrane-embedded full-length HER2

Seroaffinity and Concentration Assay



Increased antibody concentration measured in patient polyclonal serum samples over time (days)

Neuroaffinity and Stoichiometry Assay



MDS constructs interaction fingerprint between Aducanumab and amyloid-β (mAb:AB42 = 1:4.5)

... and expands access to biology

From basic research to drug development, MDS can help you tackle your most challenging targets (i.e., membrane proteins, multi-protein complexes or intrinsically disordered proteins) even in complex mixtures like crude cell lysate, undiluted serum or plasma.

Basic Research

Drug Discovery

Process

Development

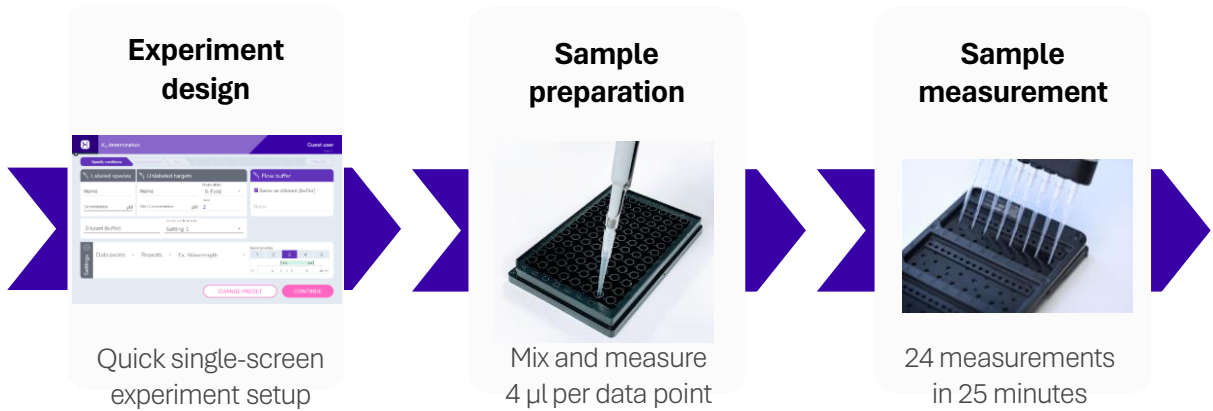
Quality Control

Translational &

Clinical Research

- Use innovative targets. Validate and characterize hits without having to purify
- Optimize leads & understand interaction stoichiometry
- Unlock competition experiments and study ternary complexes
- Measure antibody expression and affinity in cell lines
- Follow changes in protein activity during process optimization, purification, and formulation development
- Monitor protein viscosity and aggregation
- Simultaneously obtain concentration and affinity of serum antibodies to overcome limitations of ELISA titers
- Study PK and serum stability

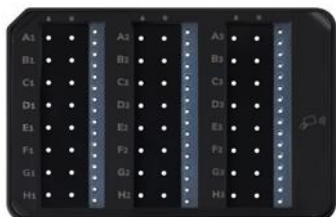
Complex research in a simple workflow



Fluidity One-M

Robust protein interaction analysis made easy

Fluidity One-M brings you the flexibility and confidence to analyze any binding events thanks to the proprietary MDS technology. It is very easy to use even for first time users. Integrated, simple workflows and data analysis enable instant readout of size and affinity values after your measurement.



Multi-attribute results

Binding affinity, stoichiometry, size, and concentration, all at once



Maintenance-free design

Fluidic-free benchtop device ensures minimal maintenance, intuitive touchscreen control



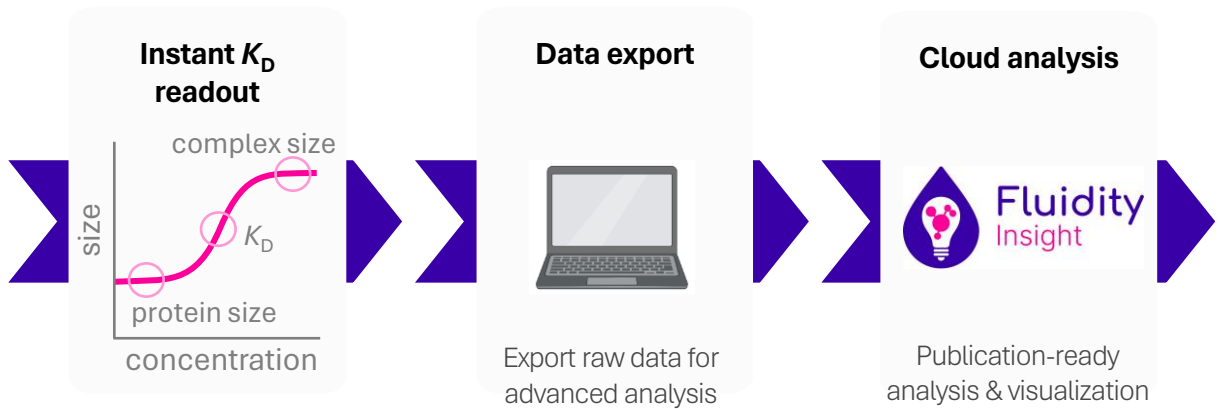
Plate-based consumables

Disposable 24-well plate prevents cross-contamination, rapid loading using multichannel pipette



Ready-to-run workflows

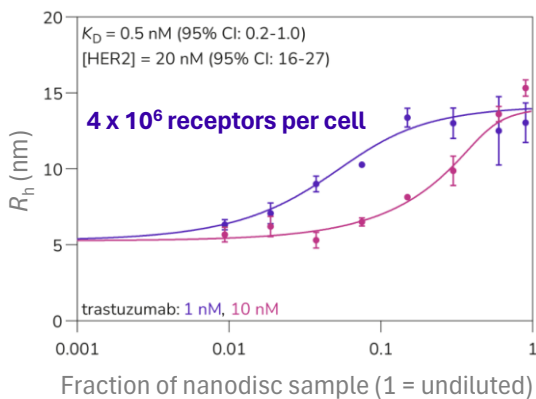
Integrates with workflows for lead optimization, cell-line development, or serological immunoassays




Fluidity Insight is available on the cloud to help you optimize your experiment setup, access advanced algorithms for analyzing concentration and stoichiometry, and combine measurements from multiple runs to develop insightful data sets.

Measure what really matters

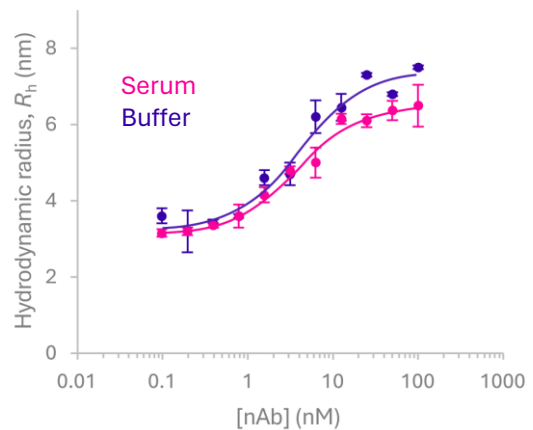
Every interaction is unique, so we make the Fluidity One-M and Fluidity Insight flexible to tailor the analysis to your need.




 K_D , receptor expression level

Membrane protein structure & activity might change after purification, so Fluidity One-M directly measures embedded receptor proteins.

More importantly, Fluidity Insight will provide you the protein concentration, or expression level of the receptor in the cell sample.

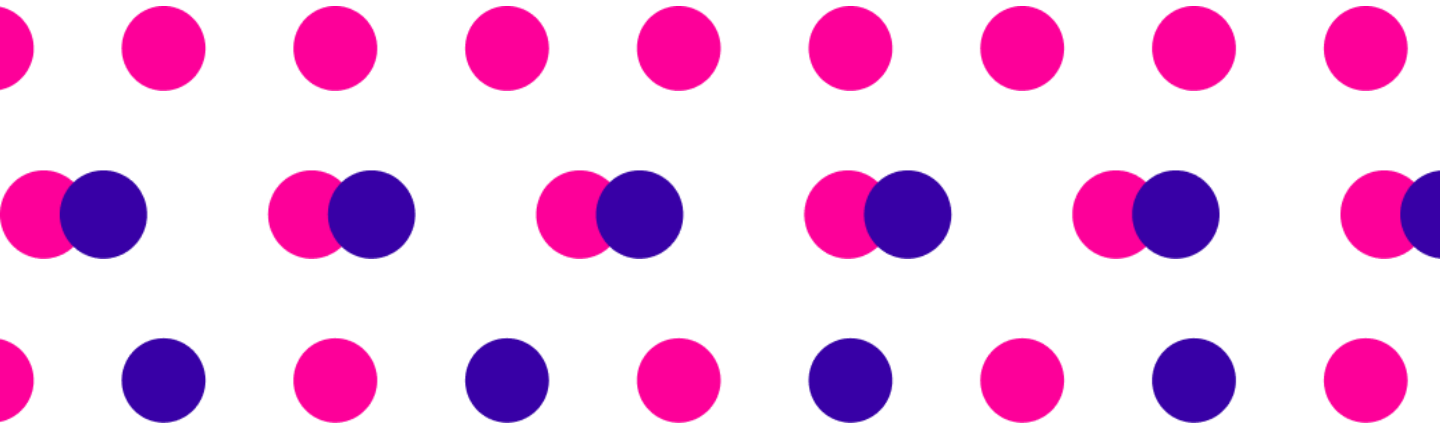


 K_D in serum, K_D in buffer

Biological interactions can be highly sensitive to matrixes, and affinity also changes in different biofluids. Fluidity One-M measures affinity in buffers and in crude serum, providing transferability from discovery to late-stage research in a single platform.

Specifications

Parameter	Specification
Throughput	24 measurements in 25 minutes to determine K_D
Size range - Hydrodynamic radius, R_h	1 – 20 nm
Molecular weight range	1.4 kDa – 14 MDa
Sensitivity range (labeled HSA in PBS)	1 nM – 3 μ M Alexa Fluor™ 488 100 pM – 3 μ M Alexa Fluor™ 647
Sample volume per data point	4 μ L
Typical sample consumption to determine one K_D	50 – 80 μ L
Compatibility	Compatible with crude samples such as undiluted serum or plasma Compatible with aqueous and biological buffers including components such as TRIS, HEPES, PBS, NaCl, KCl, TWEEN, DMSO and DMF
Fluorescent labels	Alexa Fluor™ 647 and equivalents, RFP/Cy5, Alexa Fluor™ 488 and equivalents, GFP/FITC
Weight - Dimensions	35 kg - 666 x 432 x 489 mm (D x W x H), drawer out
Temperature control	25 °C (actively controlled)
Operating environment	15 °C to 30 °C
Power requirements	100 – 240 V AC, 50 – 60 Hz
Safety and EMC standards	Designed to comply with all relevant safety and EMC standards



About us



It's not just the proteins that make life, it's the interactions among them. Here at Fluidic Sciences, we make protein interaction analysis easy and robust by developing transformative in-solution technologies and accessible instruments that help scientists quickly and accurately understand how proteins truly interact.

For more information about us, please visit our website fluidic.com.