Monolith

Because you need to characterize
the most challenging interactions

Knowing the **strength of the interactions** between key players will give you the **insights** you need to **understand the details** behind how biological processes work.

If you're having difficulty studying **challenging interactions** that include membrane proteins, PROTACs, intrinsically disordered proteins (IDPs), or RNA-based therapeutics, you'll need Monolith to characterize them.

Monolith measures the broadest range of binding affinities in-solution, using very little sample

Measure high and low affinities in the same system

Different projects have different demands. It's inevitable that you'll need to look at both weak and strong molecular interactions. With a broad sensitivity range, Monolith measures K_ds from pM to mM, so you can tackle as many projects as you want.

Measure in solution, in close-to-native conditions

Immobilizing molecules in SPR assays often causes them to lose activity, and you're left without results. Because Monolith measures in solution in most buffers, both binding partners are free to interact in their native conformation, you'll finally get results.

Characterize binding events with very little sample

It's not easy to prepare the large volumes of highly concentrated target and ligand required by ITC. With Monolith, you get a K_d in a fraction of the volume and concentration, leaving you with more sample for additional experiments.

Characterize interactions with many different types of molecules or samples

You know what types of interactions you need to characterize now, but it's always difficult to predict what you'll need to look at in the future. Monolith gives you one less thing to worry about because it has the flexibility to handle all different types of molecules and samples.

- **Protein**
  Membrane proteins, intrinsically disordered proteins (IDPs), receptors, enzymes, antibodies, and nanobodies
- **Small molecules**
  Fragments, PROTACs, ions, nanoparticles, peptides, and carbohydrates
- **Nucleic acids**
  DNA, RNA, and aptamers
- **Vesicles**
  Exosomes and liposomes
- **Platelets and whole cells**
- **Virus particles and empty capsids**

Evaluate more than a binary interaction

Competition assays
Assess relative affinities of two or more molecules for the same target

Ternary binding events
Characterize interactions that involve three or more binding partners

Derive additional information from your affinity assays

Oligomerization and aggregation
Monitor these events to understand protein functionality

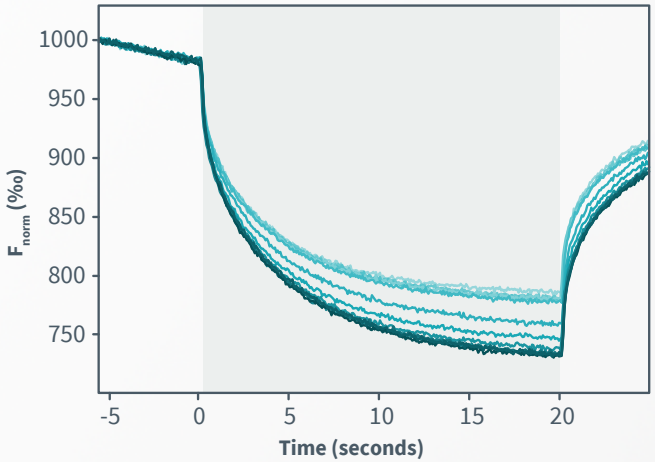
Stoichiometry*
Calculate molecular ratios of binding partners

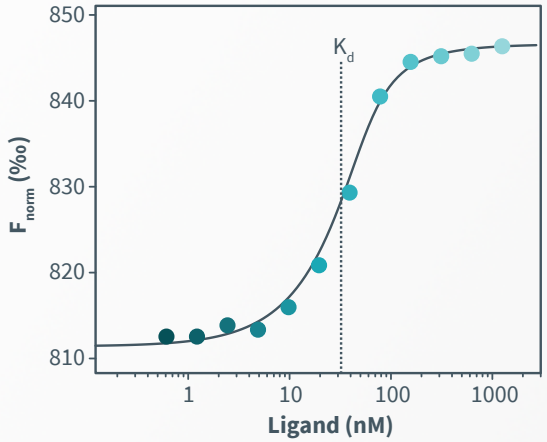
Thermodynamics*
Derive ΔG, ΔH and ΔS from calculated K_ds

*Requires offline data handling, not supported by Monolith software

Use MST technology to measure interactions

Monolith uses MST technology to quantify molecular interactions between a target and ligand by detecting changes in fluorescence intensity while a temperature gradient is applied over time (grey box, top figure). The fluorescent signal comes from the target that is either fluorescently labeled or has intrinsic fluorescence and becomes an extremely sensitive reporter for the interaction. The binding affinity is automatically determined at the end of each run without additional and lengthy data analysis. The affinity constant (K_d) is calculated from a fitted curve that plots normalized fluorescence against concentration of ligand (bottom figure).





Monolith has no fluidics — that means there's really no regular maintenance

Life is so much easier when fluidics aren't involved. Monolith doesn't require cleaning or flushing in between runs, or a maintenance contract. So, it's ready whenever you're ready.

Monolith Pico

The best choice for studying interactions spanning a broad range of affinities. Turn pico mode on to measure very strong interactions, or off for weak ones.

Monolith

Choose this if you want the most flexibility when it comes to labeling strategies. Pick the two fluorescent channels you need the most.

Monolith LabelFree

When you want to measure interactions by detecting the intrinsic fluorescence of your target protein, choose this.

Monolith specifications because well, everyone asks for them

	Monolith Pico	Monolith	Monolith LabelFree
Time it takes to get a K_d	10 minutes or less (standard mode for binding affinity)		
Dynamic range	1 pM to mM	1 nM to mM	10 nM to mM
Detected molecule range	10^1-10^7 Daltons		
Minimum sample volume measured	4 µL		
Samples per run	Up to 24		
Temperature control	20-40 °C +/- 0.5 °C (actively controlled)		
Fluorescent channels	1 (red) or 2 (red pico and blue)	2 (blue, green or red)	1 (UV)
Dimensions	36 cm W x 40 cm H x 58 cm D (71 cm D with drawer open)		
Weight	27 kg		

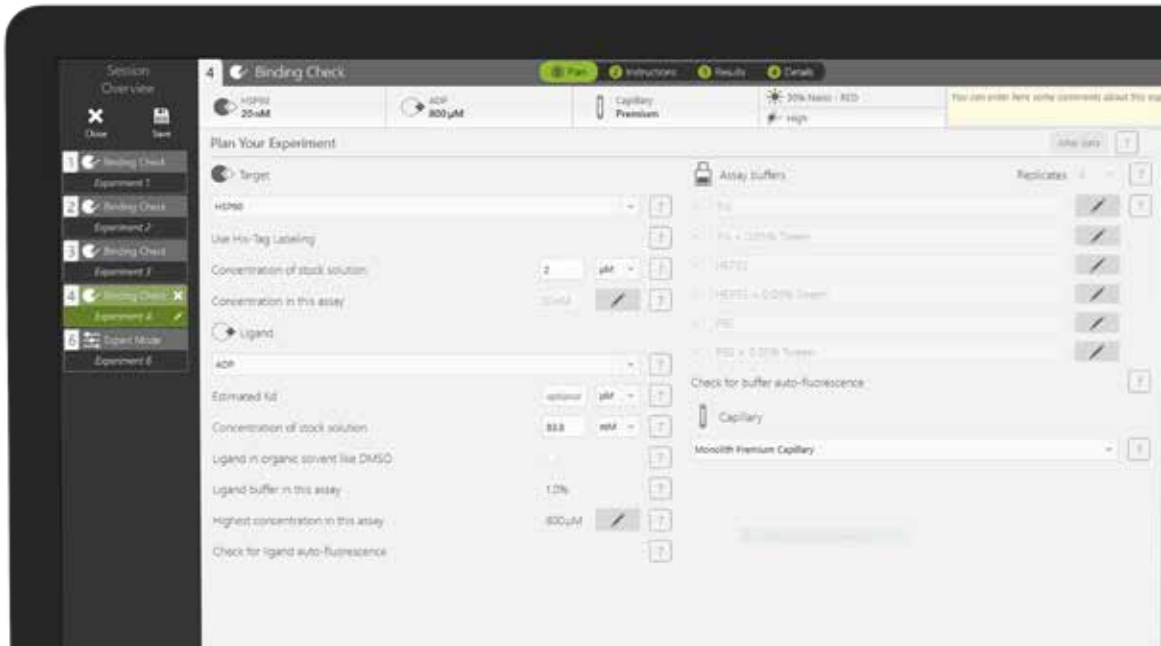
Feel confident your experiments will run smoothly with software that's smart

MO.Control 2

Most software starts once you load your samples and start your run. Monolith's MO.Control is built differently — not only do you get help with guided step-by-step experimental planning and assay setup before you start your run, but you also get immediate feedback on assay optimization based on your results after the run is over. MO.Control 2 adds the ability to optimize buffer conditions more efficiently so you can get to generating results faster.

MO.Affinity Analysis 3

Make sure your analysis is consistent across various data sets and that you're identifying any insights across replicate measurements. MO.Affinity Analysis 3 is the ideal complement to MO.Control 2 — merge and group your data sets for comparison purposes and then easily report results with presentation-worthy data and publication-ready figures.



Get great results with tailor-made consumables

Monolith capillaries are made with care — they're manufactured in a state-of-the-art facility and are rigorously tested. Pair the capillaries with one of the Monolith Protein Labeling Kits and any of the Monolith systems to get the highest quality data and ultimately, the best outcome.

nanotempertech.com/monolith

BR-MO-092020