



Need a second opinion to help you validate the binding data you're getting from SPR, ITC or BLI?

Are your experiments stalled because you're having difficulty measuring interactions with the technology available in your lab?

If you answered yes, then you'll find success with **Monolith X**.

Get an orthogonal method that also handles your most challenging interactions when you need it to

Validate results easily

Evaluate the same target classes as other biophysical methods and more

Use same buffer composition as your primary method

Measure in crude lysates



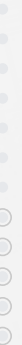
Finally tackle your challenging interactions

Measure in solution with no fear of lost activity due to immobilization required by SPR and BLI

Characterize binding events with a fraction of the volume and concentration required by ITC

Work with detergents or viscous buffers that cause issues for SPR

Measure the K_d between very different binding partners because unlike other technologies, evaluation is independent of size and mass



Characterize interactions between 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 X gives you one less thing to worry about because it has the flexibility to handle all different types of molecules and samples.

- **Proteins**
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*

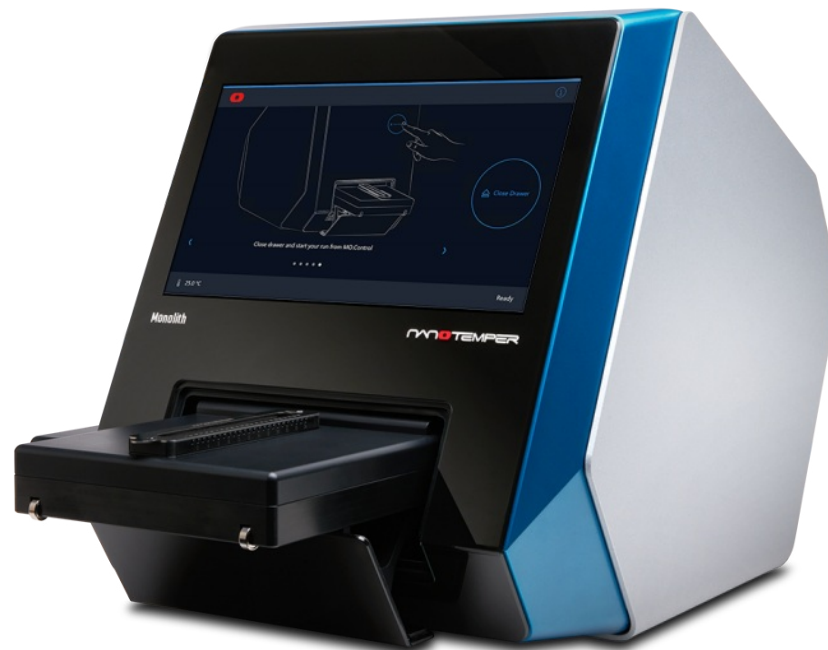
Calculate molecular ratios of binding partners

Thermodynamics*

Derive ΔG , ΔH and ΔS from calculated K_d s

*Requires offline data handling, not supported by Monolith X software

**Monolith X is blazing fast,
doesn't require experience to operate,
and is maintenance-free**



Get results in as little as 30 seconds

Yes, you read that correctly. Spectral shift measurements only take a few seconds to measure and you get the data in real-time. Talk about making quick decisions :)

Anyone in your lab can operate it

Get up and running in no time with Monolith X. The software takes you through step-by-step instructions on how to prepare and run your assay — you don't need extensive experience to run it.

Forget about a maintenance contract

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

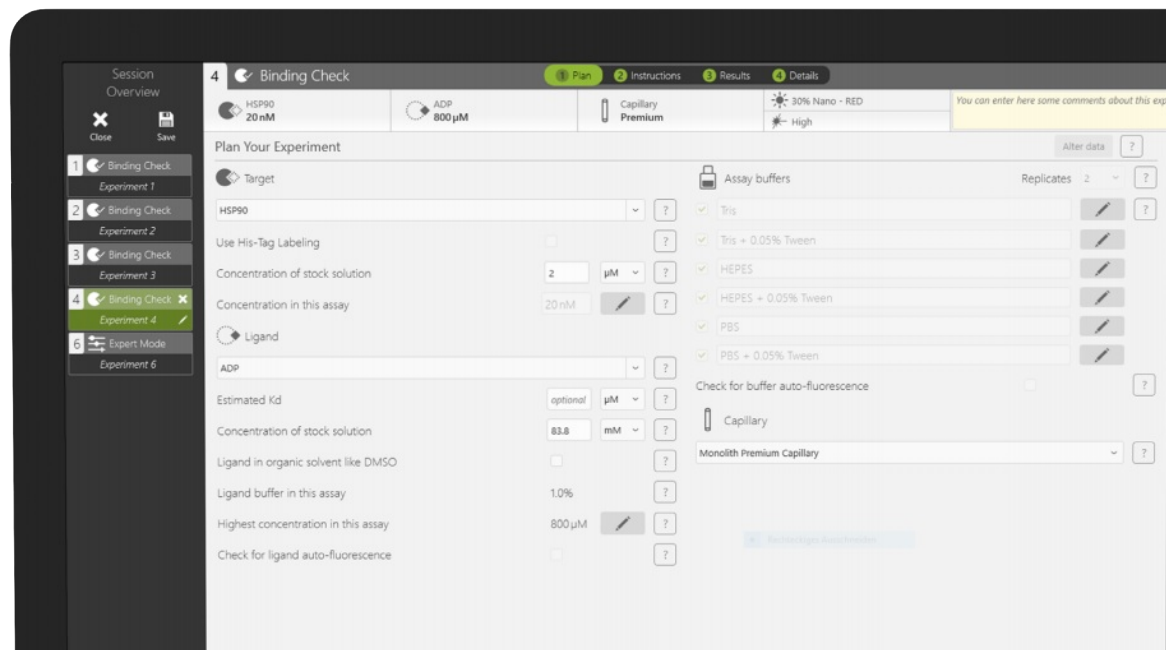
Feel confident your experiments will run smoothly with software that's smart

MO.Control 2

Most software starts once you load your samples and start your run. Monolith X'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.

Affinity Analysis - Coming September 2022

Make sure your analysis is consistent across various data sets and that you're identifying any insights across replicate measurements. Monolith X's Affinity Analysis software feature can be used to 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 and capillary chips 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 to get the highest quality data and ultimately, the best outcome.



Specifications because well, everyone asks for them



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

The logo for Nanotemper, featuring the word "NANO" in black, a red circle with a white dot inside, and the word "TEMPER" in black.

nanotempertech.com



omicspartner.com