nicoya

COMPLETE BIOPHYSICAL INSIGHT.

From discovery to development, Nicoya's portfolio of biophysical characterization tools enable label-free, quantitative insight across binding kinetics, protein stability, and conformational dynamics, empowering earlier, more confident decision-making.

One partner.
One connected workflow.
Real insight.

Modern biologics and peptide development demands more than a single technique. Understanding how molecules bind, change, fold, and stabilize requires orthogonal, complementary tools—delivering clarity across the full molecular story.

Nicoya's portfolio combines label-free kinetics, structural insight, fast reaction analysis, and stability profiling into intuitive, automation-ready platforms trusted by tens of thousands of scientists worldwide.

"Alto's pre-packaged consumables are a game changer for both discovery and routine work. In discovery, skipping buffer prep at different pH levels saves significant time and effort. Rapidly testing multiple conditions - binding, regeneration, and treatment - streamlines optimization. Without these ready-to-use reagents, many of these steps wouldn't happen at all."

Dr. Kerry Oliver, President & CSO, Radix BioSolutions

"SUPR-DSF has changed how we approach routine stability and formulation screening. The 384-well plate format allows us to screen hundreds of conditions in parallel using far less protein, so stability experiments are no longer a bottleneck. Sample preparation fits seamlessly into our existing workflows and automation. The low cost per experiment means consumables aren't a limiting factor, which has made it much easier to generate timely stability data for early developability decisions."

Lun Xin, Associate Director,
Analytical, Formulation and Drug Product Development,
WuXi Biologics

"The Chirascan system at the Manchester Institute of Biotechnology is used to advance biological, biochemical, and medical research. Our scientists use CD to gain an understanding of how mutations, buffer or stress conditions affect protein structure and to confirm the stereostructure of small molecules. The system is routinely used by more than 25 scientists and is typically in use 90% of the time. The system is intuitive making user training straightforward. Users return to the Chirascan because it is highly reproducible, has excellent signal:noise and delivers results quickly."

Dr. Derren Heyes, University of Manchester

"The OpenSPR is a very versatile and affordable system that has allowed us to accurately measure protein-protein and protein-peptide interactions without the need to label the interacting molecules."

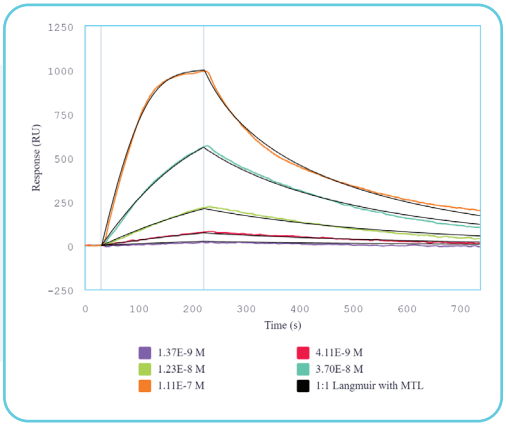
Dr. Guy Guillemette, Associate Professor of Chemistry,
University of Waterloo

REVO

Scalable Digital SPR for Accessible Kinetics and Screening

Revo delivers label-free binding kinetics and affinity data with a streamlined digital SPR workflow designed for accessibility and speed. With low sample consumption and scalable throughput, Revo enables rapid hit identification, affinity ranking, and early kinetic insight without the complexity of traditional SPR systems.

Revo supports confident decision-making early in discovery, helping teams move faster while preserving data quality.



ALTO

High-Throughput Digital SPR for Confident Kinetic Characterization

Alto is Nicoya's fully automated digital SPR platform for high-confidence kinetic and affinity analysis at scale. By combining cartridge-based workflows with automated sample handling, Alto minimizes variability while delivering reproducible, publication-quality data across large sample sets.

Alto's Automation Suite is the world's first fully automatable SPR system, and is designed to empower scientists to perform 24/7 unattended SPR analysis.

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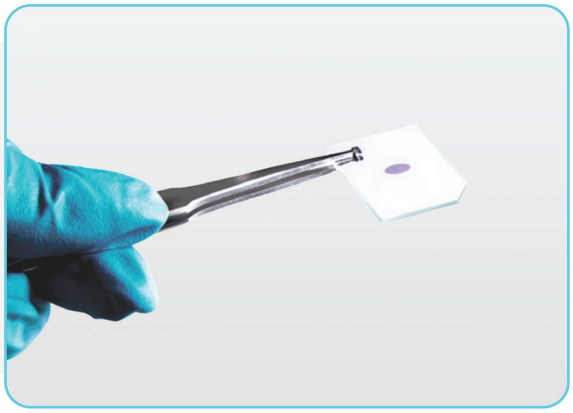
OpenSPR

Benchtop SPR for Rapid Interaction Validation

OpenSPR brings reliable, label-free SPR measurements to a compact benchtop format, enabling first-pass interaction validation and structure–function exploration. Utilizing our proprietary localized SPR (LSPR) technology, the OpenSPR platform provides accurate and robust data, all from your lab bench.

Its ease of use makes it ideal for early discovery, orthogonal confirmation, and labs new to SPR.

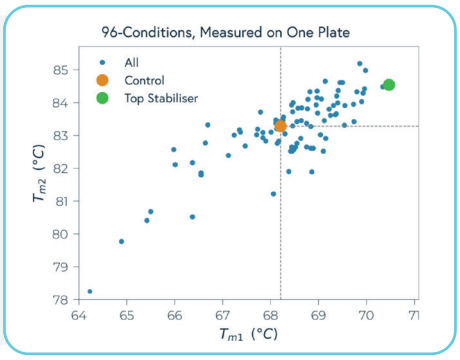


SUPR-DSF

Plate-Based Thermal Stability Screening Without Dyes

By providing precise melting temperature (T_m) and non-reversibility onset temperature (T_{nr}) measurements with minimal sample, SUPR-DSF enables rapid binder ranking, formulation screening, and stress testing.

The platform integrates seamlessly into discovery and development workflows to support stability-driven decision-making.



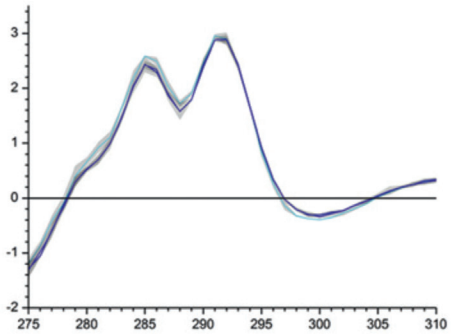
Chirascan

High-Sensitivity Circular Dichroism for Structural Insight

Chirascan circular dichroism spectroscopy enables detailed analysis of protein secondary structure, folding, and conformational changes. With high signal-to-noise performance and reproducible baselines, Chirascan supports higher-order structure analysis, comparability studies, and stability assessment.

It provides essential structural context for understanding how molecules fold, change, and respond to stress.

Determine innovator HOS characteristics. CD analysis of tertiary structure in a highly absorbing chiral formulation buffer suggested differences in tryptophan region of Fab fragments from different innovator lots.



SX20

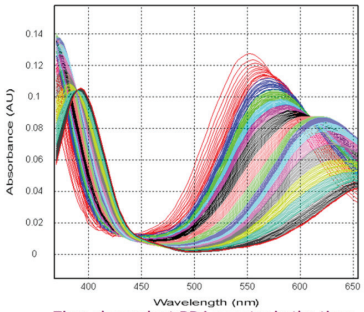
Ultra-Fast Stopped-Flow Kinetics for Reaction Mechanisms

SX20 captures rapid reaction kinetics and transient intermediates using stopped-flow spectroscopy at millisecond timescales.

By resolving fast biochemical events inaccessible to steady-state methods, SX20 enables detailed characterization of enzyme mechanisms, binding kinetics, and reaction pathways.

The platform is ideal for mechanistic studies requiring precise temporal resolution.

High-speed spectral acquisition reveals reaction intermediates in real time. SX20 captures the full evolution of complex mechanisms across the UV–Vis range, enabling global analysis and multi-step kinetic modeling.



Time-dependent PDA spectra in the time range of 1 ms to 20 s

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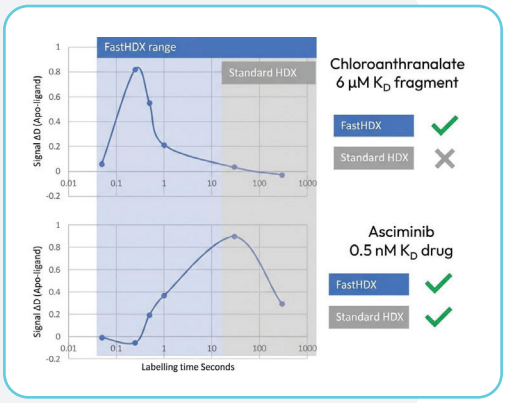
FastHDX

Millisecond HDX-MS for Transient Protein Dynamics

FastHDX extends hydrogen–deuterium exchange into the millisecond regime, revealing transient, non-equilibrium protein conformations that conventional HDX-MS workflows miss. By resolving early exchange events, FastHDX enables identification of weak allosteric binders, dynamic structural transitions, and intrinsically disordered regions.

This capability opens new development avenues by delivering mechanistic insight earlier and with greater temporal precision.

Traditional HDX Misses Key Events. Deuterium uptake in disordered proteins and peptides, rapid small molecule binding and transient conformational changes occur within milliseconds. With a minimum labeling time of 30s, traditional HDX is unable to capture these events, creating development blind spots.



DISCOVERY AND OPTIMIZATION

Explore molecular interactions, characterize emerging candidates, and deepen your scientific understanding with fast, sensitive label-free binding kinetics tools that deliver dependable, publication-quality results.

MECHANISM OF ACTION & CHARACTERIZATION

Reveal how molecules bind, fold, react, and evolve by integrating orthogonal biophysical techniques that clarify interactions, structural shifts, and mechanisms of action.

STABILITY & QUALITY

Ensure molecules remain stable, consistent, and fit for development by integrating orthogonal biophysical insights that reveal structural integrity, functional performance, and risk under stress.

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