Fidabio | cytiva

Smarter workflow. Earlier insight. Confident decisions.

Expand your drug discovery analytical toolbox

In early discovery, you might face the dilemma: move fast with limited insight, or go deep and risk falling behind. Balancing throughput, resolution, and sample use often means choosing between speed and certainty. With Fida™ Neo and Biacore™ 8 Series, you no longer have to choose. FIDA™ gives you rapid, in-solution characterization across multiple parameters. It confirms integrity, solubility, and affinity within minutes. Biacore then provides high-throughput kinetic and affinity precision, delivering trusted confirmation when you need it. Together, they create one connected, orthogonal workflow, giving you both early insight and confident validation.

A powerful duo in molecular characterization:

FIDA Systems

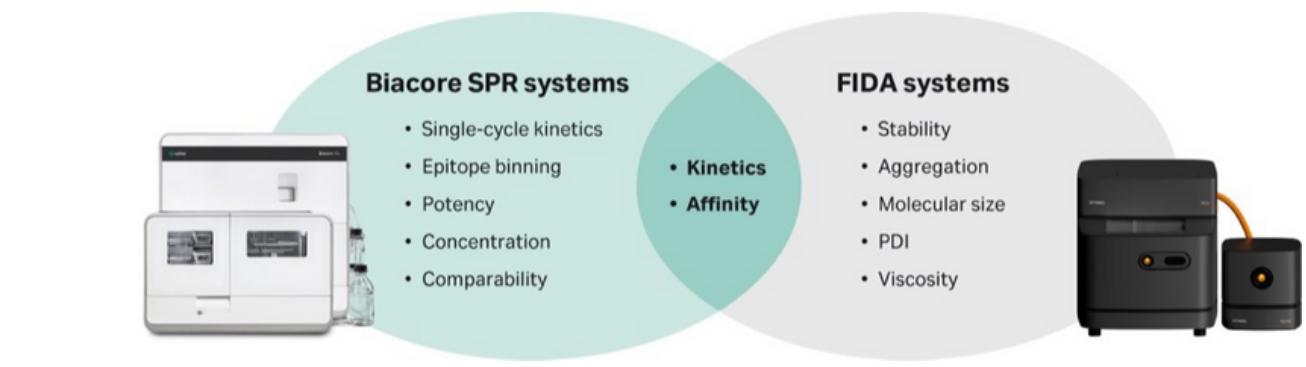
Minimal sample prep & multiple readouts

- Verify structural integrity in **5 min** using **nanoliter volumes**
- Detect solubility & **aggregation**
- Verify both in-solution **affinity (K_D) and kinetics**
- Provides **absolute** hydrodynamic radius (R_h) and polydispersity index
- 10 readouts with 1 measurement
- Combined 3 simultaneous readouts
- Suitable for challenging applications: membrane proteins, small molecules, TPD, fibrils, IDPs, weak-binding interactions

Biacore SPR Systems

High throughput & precision

- **High throughput** affinity for hit validation and lead optimization
- Quantify kinetics and gain **deeper insight** into binding mechanism
- Analyze **small to large molecules** and challenging targets
- **More information** using same platform: yes/no binding, specificity, concentration, epitope binning, potency, and parallel line analysis (PLA)



Complementary & orthogonal technologies for better informed decisions

Read our application note

Analytical Challenge	FIDA™ Systems	Biacore™ SPR Systems	Benefit of orthogonal approach
New molecular formats – multispecifics, degraders, and other complex modalities	To include structural complexity into the analytical readout	Quantifies hydrodynamic radius, polydispersity (PDI) & aggregation directly in solution	Determines kinetics and affinity under label-free, real-time conditions	Comprehensive understanding of structure–activity relationships
Membrane and intrinsically disordered proteins	Dynamic or heterogeneous conformations complicate assay design	Confirms structural integrity and solubility in native buffers	Characterizes binding mechanisms and rate constants	Greater confidence in functional relevance of kinetic data
Variable reagent quality between batches or preparations	Misfolding, oligomerization, or denaturation may alter binding behaviour	Detects size distribution and sample homogeneity within minutes	Measures interaction strength and mechanism once reagent quality is confirmed	Time savings related to the aspect of assay optimisation caused by low quality reagents
Small-molecule and fragment interactions	Solubility and aggregation can mask true binding profiles	Identifies insoluble or aggregated small molecules prior to kinetic analysis	Quantifies specific binding responses and affinity ranking	Reliable evaluation of weak or complex interactions
Complex assay development	Increasing throughput and reproducibility demands cross-validation	Orthogonal confirmation of affinity and complex formation in solution	Supplies detailed kinetic and affinity constants	Reduced rework and increased data confidence