Surface Plasmon Resonance (SPR) · Biacore T200

Cytiva · Real-time kinetics · Affinity · Epitope binning

The Biacore T200 is the industry-standard SPR system for measuring biomolecular binding kinetics and affinity in real time without labels. One binding partner (ligand) is immobilised on a sensor chip; the other (analyte) flows over the surface. The instrument detects changes in refractive index as binding occurs, producing sensorgrams that directly yield ka, kd, and KD. Suitable for protein–protein, protein–small molecule, protein–nucleic acid, antibody–antigen, and fragment interactions.

SPECIFICATIONS

Affinity range: fM to mM

ka range: 10^{3} – 3×10^{9} $M^{-1}s^{-1}$

kd range: 10^{-6} – 0.5 s^{-1}

Temperature: 4°C – 45°C

Detection limit: <0.03 RU noise

Flow channels: 4 independent

Throughput: Up to 384 samples/run

Analyte size: >100 Da to viruses

CAPABILITIES

Full kinetic characterisation: ka, kd, KD

Equilibrium affinity and steady-state analysis

Epitope binning and competition experiments

Thermodynamic analysis via temperature variation

Active concentration measurement — no standard needed (CFCA)

Amine coupling and capture-based immobilisation (His, Fc, GST tags)

pH scouting and ligand density optimisation

Single-cycle and multi-cycle kinetics modes

Sample requirements: Ligand: ~100 µL at 0.05–1 mg/mL. Analyte: ~400 µL per concentration point. Buffer: HBST (10mM Hepes pH 7.4 with 150mM NaCl and 0.05% tween -20) filtered 0.22 µm and degassed. Sample purity ≥90% recommended. Sensor chips (CM5) available, purchased separately by users.

Ideal for: Drug Discovery · Antibody Development · Fragment Screening · Biosimilars ·

Biolayer Interferometry (BLI) · Gator Prime

Gator Bio · High-throughput screening · Kinetics · Epitope binning · Quantitation

The Gator Prime is an 8-channel BLI system that measures biomolecular interactions in real time using fibre-optic biosensors in a microplate format. With no fluidics to maintain, the system is robust and low maintenance. It is particularly suited to high-throughput screening campaigns and works with crude supernatants, serum, and plasma without prior purification. Like SPR, one binding partner (ligand) is immobilised on a sensor chip.

SPECIFICATIONS

Channels: 8 simultaneous, independent spectrometers

Throughput: 1–168 samples per run

Plate format: 96-well and 384-well microplate compatible

Affinity range: pM to µM (KD)

Analytes: Proteins, antibodies, nanobodies, nucleic acids, small molecules, AAV, lipid nanoparticles

Sample types: Compatible with crude supernatants, serum, plasma

Temperature: Ambient (room temperature)

CAPABILITIES

Binding kinetics: kon, koff, KD

Concentration quantitation

Epitope binning and competition mapping

Yes/no binding screening of large compound libraries

Off-rate screening for lead selection

Antibody titre measurement

AAV capsid characterisation

Works with crude extracts — no purification required for initial screening

Sample requirements: Samples loaded into standard 96-well microplate format. Ligand immobilised on biosensor tip typically to 1nm shift on y-axis. Analyte concentration typically 0.1–10x of KD or as required for screening. Compatible with crude supernatants, serum, and plasma. Probes and plates (consumables) available, purchased separately.

Ideal for: High-Throughput Screening · Antibody Development · Drug Discovery · QC / Titre Measurement

Isothermal Titration Calorimetry (ITC) · Malvern iTC200

Malvern Panalytical · Full thermodynamic profile · Solution-phase · Label-free

Access note: This instrument is not available via standard facility booking. Please contact Dr. Devanshu Mehta (devanshu.mehta@ntu.edu.sg), for an introduction to the relevant SBS group for collaborative access.

The Malvern iTC200 directly measures the heat released or absorbed during binding events in solution. A single experiment delivers a complete thermodynamic characterisation — KD, ΔH, ΔS, ΔG, and stoichiometry (n) — without any labelling or immobilisation. This makes ITC the only technique that measures binding enthalpy directly, providing mechanistic insight into whether interactions are enthalpy- or entropy-driven.

SPECIFICATIONS

Cell volume: 200 µL (coin-shaped, Hastelloy)

Syringe volume: 40 µL

Affinity range: mM to nM (direct); nM to pM via competitive displacement

Temperature range: 2°C – 80°C

Temperature stability: ±0.00012°C

Baseline noise: 0.15 ncal/s

Cell material: Hastelloy (chemical resistance, bio-compatible)

CAPABILITIES

Complete thermodynamics in a single experiment: KD, ΔH, ΔS, ΔG, stoichiometry (n)

No labelling, modification, or immobilisation required

Picomolar affinity accessible via competitive displacement titrations

Enzyme kinetics measurements

Protein–protein, protein–drug, protein–nucleic acid, protein–lipid interactions

Structure-activity relationship (SAR) studies

Compatible with non-aqueous solvents

Ideal for: Thermodynamics · Drug Discovery · Fragment Optimisation · Structural Biology

Mass Photometry · Refeyn TwoMP

Refeyn · Single-molecule mass measurement · Native solution · Label-free

The Refeyn TwoMP measures the mass of individual molecules as they land on a glass surface, using interferometric scattering microscopy (iSCAT). This provides direct molecular mass in solution without separation, labelling, or immobilisation. It is ideal for characterising oligomeric state, complex stoichiometry, and sample heterogeneity, including large assemblies and viral vectors.

SPECIFICATIONS

Mass range: 30 kDa – 5 MDa

Mass resolution: ~25 kDa at 66 kDa; ~60 kDa at 660 kDa (FWHM)

Mass precision: ±2%

Mass accuracy: ±5% (single measurement)

Concentration range: 100 pM – 100 nM

Sensitivity: <<1 ng of protein

Sample volume: 10–20 µL per measurement

Temperature: Room temperature (measurements temperature-sensitive)

CAPABILITIES

Absolute molecular mass of individual molecules in solution

Oligomeric state determination (monomer/dimer/tetramer etc.)

Complex stoichiometry and assembly characterisation

Assembly/disassembly dynamics in real time

Sample quality control — detection of aggregates and degradation

AAV, virus-like particle, and nanoparticle characterisation

Proteins, DNA, RNA, and macromolecular complexes

No calibration standards required for relative comparisons

Sample requirements: 10–20 µL per well at 5–20 nM optimal (upto 100 nM acceptable). Stock solution ≥1 µM recommended for accurate dilution. Buffer must be filtered (0.22 µm) to remove dust and particulates. Avoid detergents above CMC and carrier proteins (e.g. BSA/casein). Measurements at room temperature — equilibrate all samples and buffers before use. Calibration standard (BSA/TG mix or MassFerence P1) required for absolute mass determination.

Ideal for: Oligomeric State · Complex Stoichiometry · Sample QC · AAV Characterisation

Mass Photometry Accessory · Refeyn MassFluidix HC

Refeyn · High-concentration mass photometry · Low-affinity interactions · Microfluidic dilution

Requires TwoMP: This is an accessory to the Refeyn TwoMP mass photometer (see entry above). Both instruments are available at the BMI Facility.

The MassFluidix HC is a microfluidics add-on accessory for the Refeyn TwoMP mass photometer. The standard TwoMP measures samples in the 100 pM–100 nM range; however, many biologically relevant complexes — particularly weak or low-affinity interactions — only form at micromolar concentrations. The MassFluidix HC raises the upper concentration limit into the micromolar range by performing a rapid on-chip dilution (<37 ms) immediately before measurement, capturing the complex in its assembled state before it has time to dissociate. This makes it uniquely suited to studying complexes that are only stable at high concentrations.

SPECIFICATIONS

Instrument type: Accessory / add-on for Refeyn TwoMP (requires TwoMP)

Concentration range: µM samples diluted on-chip to measurable nM range

Dilution time: <37 ms from sample inlet to observation area

Chip type: Microfluidic chip with reverse Tesla valve mixer

Consumable: MassFluidix HC chip (single-use; 5 measurements per chip)

Mass range: 30 kDa – 5 MDa (inherited from TwoMP)

Mass precision: ±2% (inherited from TwoMP)

CAPABILITIES

Mass photometry of samples at micromolar concentrations

Characterisation of low-affinity interactions (weak binders, transient complexes)

Detection of complexes that only assemble at high concentration

Rapid dilution preserves complex assembly state at time of measurement

Oligomeric state analysis of concentration-dependent assemblies

Same mass range, precision, and label-free nature as standard TwoMP

Sample requirements: Stock sample at µM concentration (exact optimal range depends on affinity of interaction). Dilution buffer: 5 mL of matched buffer required for on-chip dilution. Buffer must be filtered (0.22 µm) and free of particulates. Avoid detergents above CMC. Calibration performed on standard TwoMP coverslip using MassFerence P1 standard. Consumable MassFluidix HC chips required — contact facility before booking.

Ideal for: Low-Affinity Interactions · Concentration-Dependent Assembly · Weak Complex Characterisation

Dynamic Light Scattering (DLS) · Malvern Zetasizer Nano ZS

Malvern Panalytical · Hydrodynamic size · Polydispersity · Zeta potential

The Zetasizer Nano ZS measures hydrodynamic diameter and size distribution of particles and macromolecules in solution by analysing fluctuations in scattered laser light (NIBS technology). It also measures zeta potential for colloidal stability assessment. One of the fastest and most accessible instruments in the facility — ideal for routine sample quality checks before any biophysical experiment.

SPECIFICATIONS

Size range (DLS): 0.3 nm – 10 µm (hydrodynamic diameter)

Zeta potential range: 3.8 nm – 100 µm; ±500 mV

Temperature range: 0°C – 90°C (±0.1°C)

Laser: 4 mW, 633 nm He-Ne

Detection angles: 13° (forward) + 173° (backscatter, NIBS)

Min. sample volume: 12 µL (size); 20 µL (zeta potential, diffusion barrier)

Min. protein conc.: ~0.1 mg/mL for 15 kDa protein

Measurement time: First result in ~15 seconds

CAPABILITIES

Hydrodynamic radius (Rh) and size distribution

Polydispersity index (PDI) — sample homogeneity assessment

Zeta potential — colloidal stability in aqueous and non-aqueous dispersions

Molecular weight estimation (SLS/Debye plot)

Aggregation detection and monitoring

Thermal stability — melting and aggregation onset temperature (Tagg)

pH and concentration-dependent size/stability profiling

Batch and flow-mode measurements

Sample requirements: Size: 12–500 µL in standard or low-volume disposable cuvette. Minimum protein concentration ~0.1 mg/mL (15 kDa protein). Zeta potential: 750 µL in folded capillary cell. Samples should be filtered or centrifuged to remove dust. Buffer should not strongly absorb at 633 nm.

Ideal for: Sample QC · Formulation Development · Nanoparticle Characterisation · Colloidal Stability

Circular Dichroism (CD) · Applied Photophysics Chirascan

Applied Photophysics · Secondary structure · Thermal stability · Conformational changes

The Chirascan measures differential absorption of left- and right-circularly polarised light to characterise the secondary and tertiary structure of chiral molecules, primarily proteins and nucleic acids. Far-UV CD reports on backbone secondary structure (α-helix, β-sheet, random coil); near-UV CD reports on aromatic side-chain environment (tertiary structure). Peltier temperature control enables thermal melt experiments to determine Tm and thermodynamic stability.

SPECIFICATIONS

Wavelength range: 163 – 950 nm (far-UV to visible)

Temperature control: 5°C – 95°C (Peltier, ±0.1°C); manual

Detector: Photomultiplier tube (PMT); extended range with APD

Light source: 150 W Xe lamp; nitrogen purge required for far-UV (<200 nm)

Cuvette path lengths: 0.1 mm, 1 mm, 2 mm, 10 mm (user-selectable). Facility provides only 1mm cuvettes for common use.

Sample volume: ~200–300 µL (1 mm cell); ~1 mL (10 mm cell)

CAPABILITIES

Secondary structure quantification: % α-helix, β-sheet, random coil

Tertiary structure assessment (near-UV, 250–320 nm)

Thermal melt (Tm) and thermodynamic stability (ΔG, ΔH, ΔS of unfolding)

Conformational change detection upon ligand binding

Kinetics of folding/unfolding

Biosimilarity and comparability studies

Quality control for recombinant protein production

Chiral small molecule characterisation

Sample requirements: Typical protein concentration: 0.1–0.2 mg/mL in 1 mm pathlength cuvette (far-UV). Sample OD should be 0.4–1.6; never exceed OD 2. Volume: ~200–300 µL (1 mm cell) or ~1 mL (10 mm cell). Buffer: 10 mM phosphate or acetate preferred. PBS acceptable but may limit wavelength below 200 nm. Avoid: imidazole, MOPS, PIPES, high chloride (use NaF or Na_2SO_4 instead of NaCl if possible). DTT and EDTA only at sub-mM concentrations. Nitrogen purge gas required — arrange in advance.

Ideal for: Protein Folding · Biosimilarity Assessment · Formulation Development · Structural Biology

Fluorescence Spectrometry · Agilent Cary Eclipse

Agilent Technologies · Intrinsic fluorescence · Protein stability · Binding · Kinetics

The Cary Eclipse is a high-sensitivity fluorescence spectrophotometer using a pulsed Xenon flash lamp for superior signal-to-noise and inherent protection from photodegradation (sample only illuminated during acquisition). It supports four measurement modes — fluorescence, phosphorescence, chemiluminescence, and bioluminescence — and captures fast kinetic events with a data point every 12.5 ms. Room-light immunity enables flexible operation.

SPECIFICATIONS

Excitation wavelength range: 200 – 900 nm

Emission wavelength range: 200 – 900 nm

Scan rate: Up to 24,000 nm/min

Data acquisition rate: 80 data points/sec (fluorescence mode); one point per 12.5 ms

Light source: Pulsed Xe flash lamp, 80 Hz, peak power ~75 kW equivalent

Detector: R928 PMT; optional R3896 PMT for >700 nm

Temperature control: Peltier accessory available

Measurement modes: Fluorescence, phosphorescence, chemiluminescence, bioluminescence

CAPABILITIES

Intrinsic protein fluorescence (Trp/Tyr emission at ~330/305 nm)

Thermal unfolding assays — Tm via Trp fluorescence shift

Ligand binding via fluorescence quenching or enhancement

Extrinsic dye fluorescence (SYPRO Orange, ANS, ThT etc.)

Aggregation detection via light scattering or dye-based assays

Fast kinetics — binding, folding, enzymatic reactions

Phosphorescence and time-resolved measurements

Anisotropy / polarisation measurements (with accessory)

Sample requirements: Standard cuvette: 0.5–3 mL. Low-volume cuvette: 50–100 µL. Sample concentration: picomolar detection possible; typical range 10 nM–1 µM depending on fluorophore. Buffer should have low autofluorescence (avoid riboflavin, tryptophan-containing additives). Avoid highly absorbing additives at excitation wavelength (inner filter effect). Temperature-sensitive samples: use Peltier accessory.

Ideal for: Protein Stability · Ligand Binding · Aggregation Monitoring · Drug Discovery · Enzyme Kinetics

Analytical Ultracentrifugation (AUC) · Beckman ProteomeLab XL-1

Beckman Coulter · Size · Shape · Stoichiometry · Association constants — in free solution

Access note: This instrument is not available via standard facility booking. Please contact Dr. Devanshu Mehta (devanshu.mehta@ntu.edu.sg), for an introduction to the relevant SBS group for collaborative access.

The ProteomeLab XL-1 is the gold-standard instrument for characterising macromolecular size, shape, and interactions in free solution. It uses two optical systems — absorbance (UV/Vis) and Rayleigh interference — to monitor sedimentation in real time. Because measurements are based on first principles of thermodynamics and hydrodynamics, no calibration standards are required. Up to 7 samples can be run in parallel.

SPECIFICATIONS

Optical systems: Absorbance (190–800 nm) + Rayleigh interference

Max rotor speed: ~60,000 rpm

Parallel samples: Up to 7 (An-50Ti rotor)

Radial resolution: 30 µm

Abs. data acquisition: 90 sec/cell

Interference scans: 5 sec/scan

Wavelength precision: ±3 nm

Temperature: Controlled; equilibration at 20°C recommended

CAPABILITIES

Sedimentation velocity (SV): molecular weight, sedimentation coefficient (S), frictional ratio (f/f0), shape, heterogeneity

Sedimentation equilibrium (SE): association/dissociation constants (Ka), stoichiometry, oligomerisation

Absolute molecular weight — no standards or calibration required

Detection of multiple co-existing species and aggregates

Self-association and hetero-association analysis

Characterisation of particles, nanoparticles, nucleic acids, polysaccharides

Density gradient equilibrium — analyte density determination

Ideal for: Molecular Weight · Oligomerisation · Protein–Protein Interactions · Biophysical Characterisation