

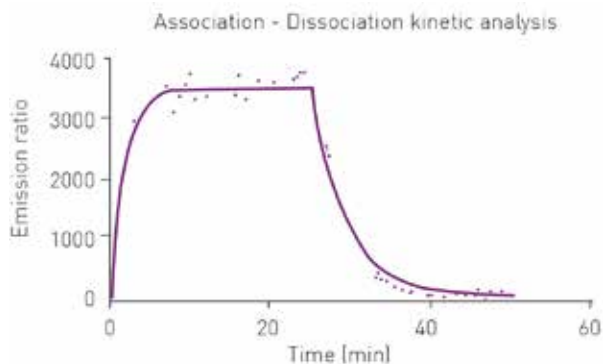
PHERAstAr[®] FSX

Easily resolve your binding events on a microplate reader

The study of binding kinetics can be efficiently performed in microplates using real-time interaction assays. This approach enables the use of kinetic assays for screening purposes and supports the study of even low-affinity compounds.

The PHERAstAr[®] FSX multi-mode microplate reader offers unique and dedicated features to efficiently monitor kinetic binding events.

- High temporal resolution ▶ For the fastest kinetics
- Injection at point of read ▶ Don't miss any data
- FRET, TR-FRET, FP & BRET kinetic detection ▶ Complete flexibility
- Dual emission in all read modes ▶ The best assay precision & speed



Example of TR-FRET-based association and dissociation kinetic curve acquired on the PHERAstAr FSX.



Dedicated PHERAstar FSX features

Simultaneously inject & read

Capture information at any time during the kinetic response. With our on-board injectors, you can simultaneously add reagents and read, making sure that no important data point is missed even in rapid equilibration kinetics.



Simultaneous Dual Emission

By detecting two separate emission wavelengths (e.g. donor/acceptor) in a single measurement, Simultaneous Dual Emission significantly reduces read times and improves data quality for FRET, TR-FRET, FP and BRET.



Dedicated detectors

Assay specific detectors are used to ensure the best assay performance. Two matched detectors with photon measurement system are used for TRF and TR-FRET detection, allowing for microsecond detection and optimal data acquisition.



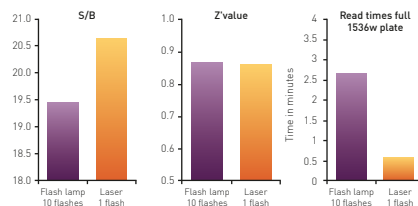
Stable temperature incubation

Temperature can significantly affect kinetic binding parameters. The PHERAstar FSX with heating plates above and below the microplate, allows precise and stable incubation from ambient + 3° to 45°C.



The highest read frequency in TR-FRET

With 60 flashes/sec, the TRF laser allows for ultra-fast data sampling. This significantly improves data quality and statistics, and makes sure that no event is missed, even in very fast binding kinetics.



Integrated binding models

The MARS data analysis software simplifies kinetic binding data reduction with calculation models for ligand association, dissociation and competitive inhibition.

