Product Information Biacore T100

Biacore T100 Software version 2.0

Taking protein characterization and quantification to a new level



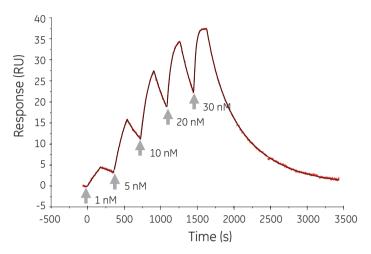
- Save assay development time with single-cycle kinetics
- Generate high quality data kinetics data for interactions that previously have been difficult to determine
- Easy assessment of data quality with simple kinetic QC tools facilitating valid interpretation
- Make concentration measurements with confidence without the need for a standard
- Validate the specified concentration of standards

Biacore™ T100 Software version 2.0 provides high quality data for protein characterization and quantification in ways that have not been possible before. Protein concentration measurements are now possible without the need for a standard. Single-cycle kinetics enables analyses that were previously difficult or impossible to determine. Improved data evaluation enables multiple samples to be analysed together with a few simple clicks, supported by inbuilt QC tools.



Faster and simpler kinetic analysis

Single-cycle kinetics enables the analysis of molecular interactions which have previously been difficult to determine, and reduces time spent on development of kinetic analysis assays.



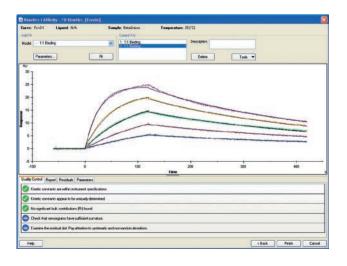
Samples are injected one after the other in the same cycle with no regeneration between injections.

Data evaluation enables multiple samples to be analysed simultaneously, simplifying the data analysis process and saving time.

Simple QC-tools for easy assessment of kinetic data

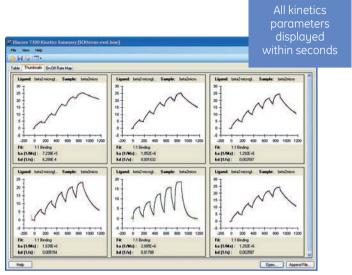
Simple QC-tools help assess data quality and facilitate valid data interpretation.

The quality of the fitting is assessed in areas such as magnitude of kinetic constants, parameter uniqueness, bulk refractive index and residuals.

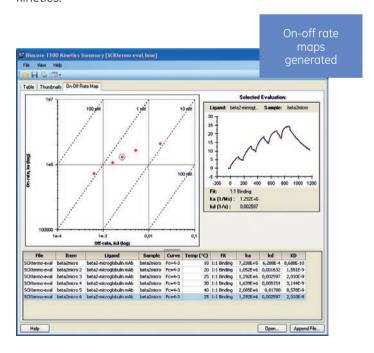


Facilitated data presentation, comparison and selection

A new Kinetic Summary tool provides an overview of sensorgrams and data, including on-off rate maps to facilitate data presentation, comparison and selection.



On-off rate maps (also called k_a/k_a plots) provide an overview of kinetic and affinity properties via a logarithmic-scale plot of association rate constants (k_a) against dissociation rate constants (k_a). Points that lie separated on the same diagonal represent interactions with the same affinity but different kinetics.



Concentration analysis without the need for standard

Knowing the accurate concentration that relates to the specific binding activity of a protein is key for many applications. Calibration-free concentration analysis (CFCA) does not require a standard curve for measuring concentration. Instead the concentration determination relies on changes in binding rate with varying flow rates, when the transport of molecules to the sensor surface is limited by diffusion.

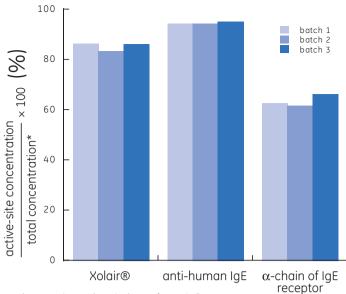
CFCA can bring great value to the discovery and development of therapeutic proteins for example by enabling:

- Concentration analysis where no satisfactory calibration standard is available.
- Checks on the validity of specified concentrations in standards.

As an example, Resistentia Pharmaceuticals AB¹ observed some variations in activity of a therapeutic protein and differences between batches.

Since no standard was available for assessing the binding activity, CFCA was used to assess protein activity.

Resistentia Pharmaceuticals AB is developing immunotherapeutic products for allergic asthma and inflammatory disorders.



* Total concentration was determined spectrofotometrically

Specific binding activity constitued 62–95 % of the total concentration (as determined by spectrophotometry). There was good consistency between batches when tested against three different binding partners molecules.

"Knowing the accurate concentration of a drug in early development and being able to relate this to specific binding activity is invaluable information in the design and conduct of pre-clinical and clinical studies. Measurements of specific binding activity raises the possibility of optimizing the production process of most biologicals and thereby increasing the proportion of active drug resulting in reduced COGS. In addition, the safety of a biological drug product may be improved by reducing the amount of inactive substance"

Stefan Persson, VP Toxicology, Resistentia AB

Additional features

Biacore T100 Software version 2.0 includes improvements in every aspect of assay set up and data analysis.

Main new functionality:

- Estimated assay time and consumption of buffer.
 Ensures minimum waste of buffer and better planning of work.
- Ligand data filtration in kinetic/affinity and thermodynamic analysis. Simplifies analysis of captureformat assays by enabling easy data filtration.
- Evaluation methods in non-GxP software. Enable the creation of user-defined plots and evaluations, saved as templates, which can be applied to other data sets.
- **Bar charts.** In addition to displaying results as plots, tables or performing curve fittings, bar charts can now be used.
- Adjustment for controls in plots. Enables adjustment of responses according to control samples in plots.
- Average calibration curve for concentration analysis.
 Enables the use of averaged calibration curve when performing concentration analysis.
- User-defined models for concentration analysis. Enables
 the use of custom models in concentration analysis in
 addition to the available linear and 4-parameter fits.
 (note: not weighted)
- Support for Windows Vista. The software has in addition to Microsoft Windows XP been tested and verified to run on Microsoft Windows Vista Business.

Biacore T100 Software version 2.0 can be purchased by ordering Biacore T100 System Operation Kit.

Product	Quantity	Code no.
Biacore T100 System Operation Kit	1	BR-1006-45
Kit includes:		
Biacore T100 software Set version 2.0		
License Agreement with product key		
Biacore T100 Software Handbook		
Biacore T100 Instrument Handbook		
Concentration Analysis Handbook		
Sensor Surface Handbook		
Biacore Advisor tutorial		
Biacore Advisor kinetics		

GE Healthcare Bio-Sciences AB Rapsgatan 23 751 84 Uppsala Sweden

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