

# Biacore X100

Readily accessible protein interaction analysis – in your lab



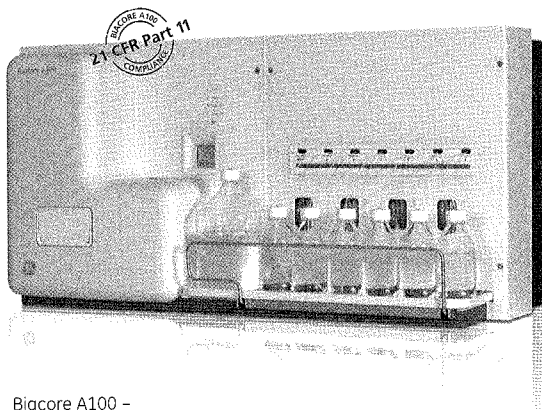
# Base your decisions on the best

Draw conclusions with confidence

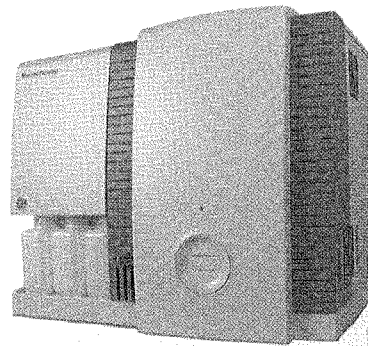
Drawing the right conclusion at the right time is key to your success, from basic research through drug discovery and development to manufacturing QC.

For more than 15 years Biacore™ systems have provided scientists with exceptional insights and superior quality, information-rich data on molecular interactions.

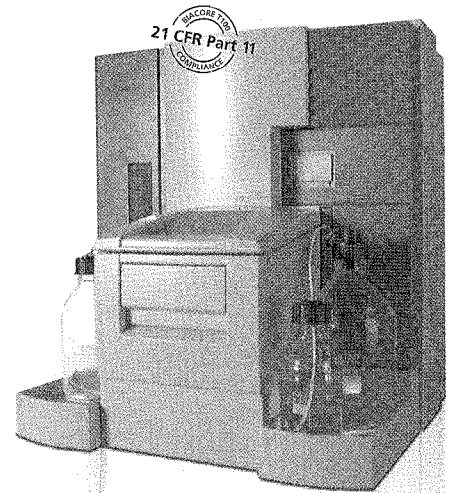
Biacore systems continue to set the benchmark for label-free interaction analysis, enabling scientists the world over to make critical decisions with confidence.



Biacore A100 – unmatched productivity



Biacore Flexchip – array-based comparative profiling



Biacore T100 – unmatched performance

## Facts

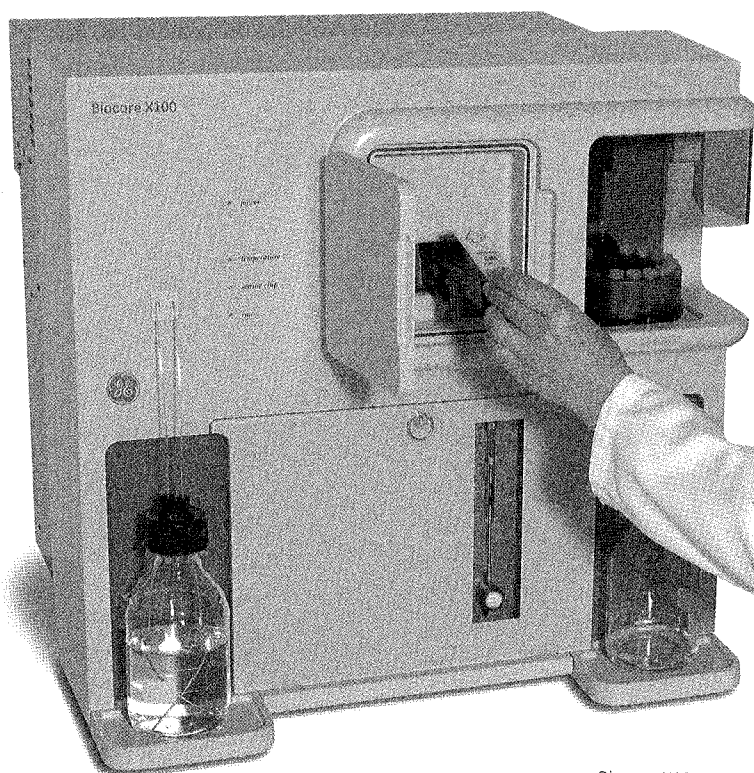
Biacore systems are cited in over 4500 peer-reviewed scientific publications and are utilized extensively in academic research institutes and universities worldwide. They are also used by the world's leading pharmaceutical and biotechnology companies

# Biacore X100

Readily accessible protein interaction analysis - in your lab

Biacore X100 is an automated, user-friendly system that brings label-free protein interaction analysis to busy, multi-project laboratories.

- Ready to run solution for comprehensive characterization of interactions
- Real insights into protein functionality and biological mechanisms
- Quality data to reach the right conclusions, whatever your area of research



Biacore X100 -  
ready to run research system

# Label-free protein interaction analysis

Biacore systems provide unique and comprehensive data on the interactions between biomolecules.

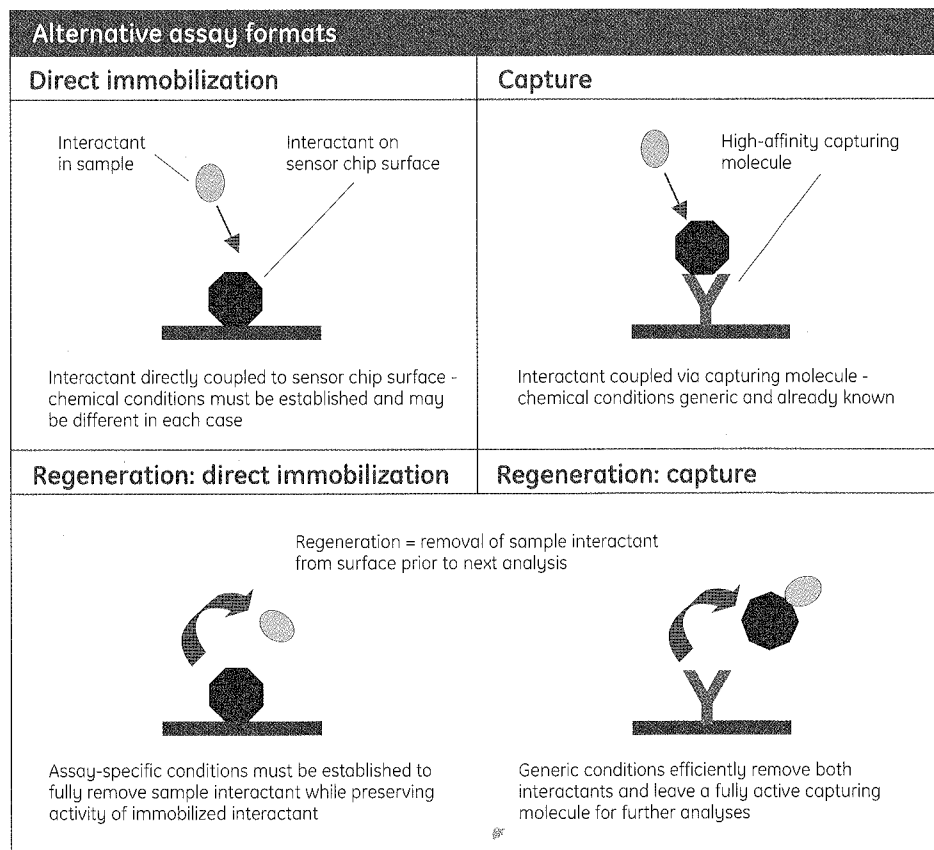
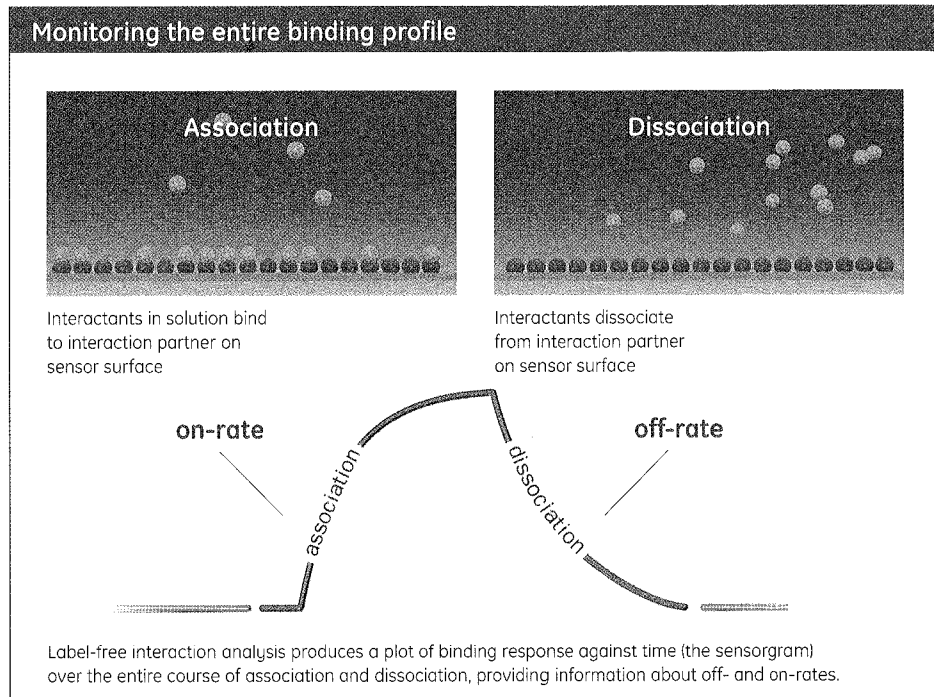
- Yes/no binding
- Binding selectivity
- Binding affinity
- Binding kinetics
- Active concentration
- Thermodynamics

Non-invasive detection enables direct analysis in complex media such as serum and cell supernatants.

Sensitive, label-free detection with real-time monitoring of binding events and a wide range of sensor chips, enable analysis of most types of molecular interactions, involving:

- Proteins
- Nucleic acids
- Carbohydrates
- Lipids
- LMW compounds
- Whole cells
- Viruses/bacteria

Detection and monitoring of the entire binding profile, without the use of labels, gives a clear understanding of the complete interaction process, unlike end-point assays which provide only a 'snapshot' of what is happening.



# From inspiration to publication

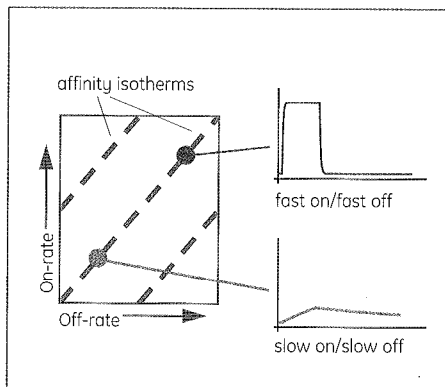
## Using the data

Real-time binding data is essential for the understanding of dynamic interactions between proteins and other molecules that drive and regulate biological processes.

- Define structure/function relationships
- Understand the dynamics of molecular pathways
- Select better research tools, diagnostics and therapeutics

## Define critical differences that determine biological, diagnostic, or therapeutic function

Overall binding strength is dependent on the ratio of on- and off-rates. Interactions of equal affinity may have significantly different kinetic properties that affect their function. Molecules with similar affinities are easily differentiated using on-/off-rate maps.



In this example, two molecules with identical affinities show kinetic profiles that differ by several orders of magnitude. These differences could not be seen using end-point analyses

## Mirror real-time dynamics of biological processes.

High-quality data on binding kinetics facilitates the understanding of interactions throughout life-science research.

### On-rate

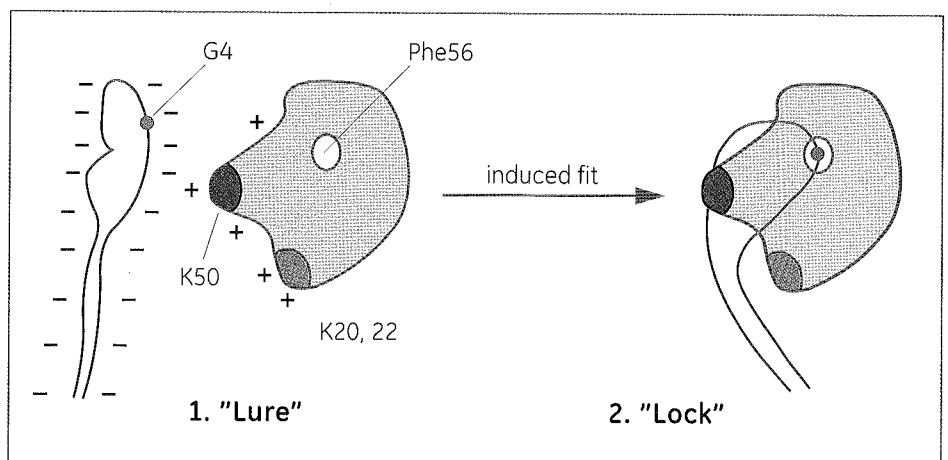
- Driven by molecular recognition
- Controls the formation of binding complexes

### Off-rate

- Driven by binding stability
- Controls the dissociation of binding complexes

## Reveal key binding mechanisms

Analysis of the on- and off-rate behavior of mutant proteins enables you to define the precise contribution of individual amino acids to protein function. Kinetic analysis is the optimum method for revealing the mechanism of binding.



mutation	affinity	on-rate	off-rate
Phe56Ala	↓ 6600 x	↓ 4.7 x	↑ 1400 x
U1hpII G4C	↓ 8700 x	↓ 3.5 x	↑ 2500 x

A two-step "lure and lock" mechanism for binding of the U1A spliceosomal protein to its RNA target defined by kinetic analysis of key U1A mutations. (Data courtesy of Dr. Ita Laird-Offringa).

# Biacore X100 – accelerating your research

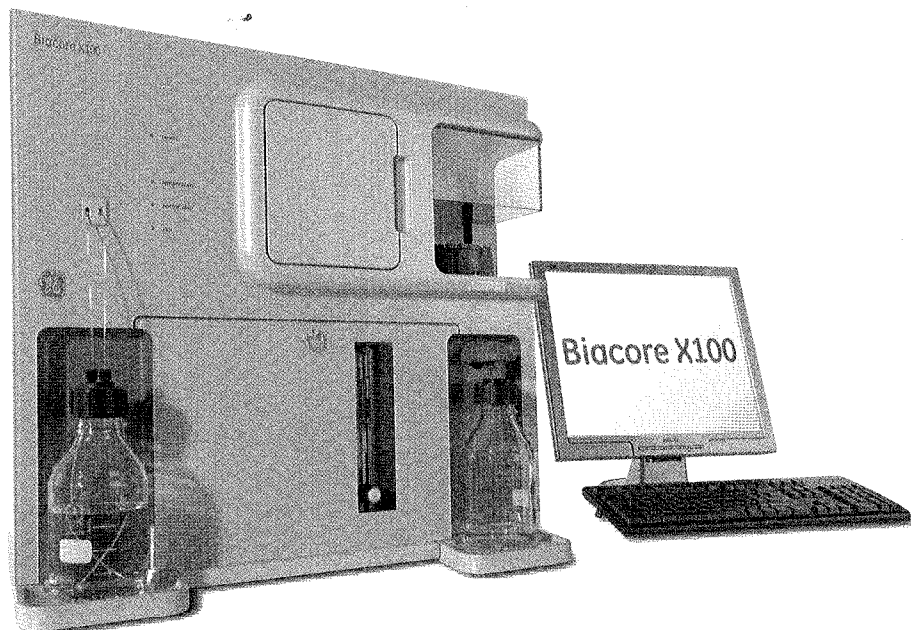
Unparalleled ease-of-use and versatility: ideal in multi-project environments

## Rapidly generate usable data

Biacore X100 makes label-free, protein interaction analysis readily accessible to every busy life science laboratory.

From day one, the straightforward system is ready to run, enabling you to gain results. High-quality data enables users to better understand interaction dynamics.

- Simple to operate
- Processes up to 15 samples automatically in a single run
- Sensor chips reusable for multiple runs
- Versatile assay formats

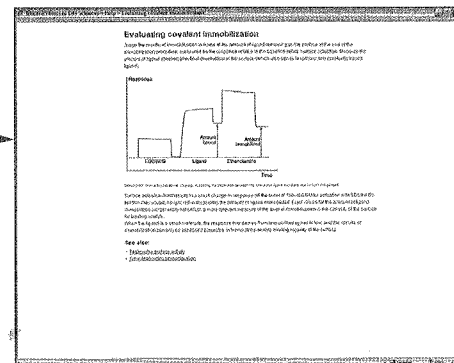
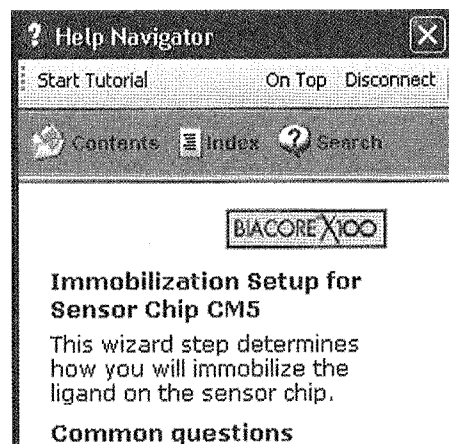
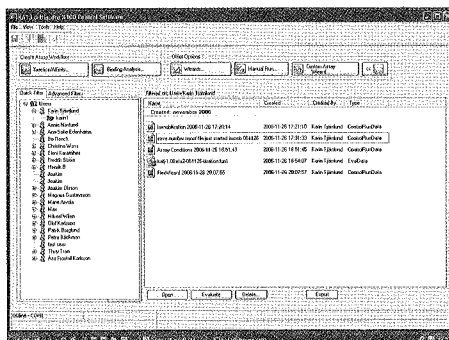


## Built-in guidance

- Short learning curve for new users
- Intuitive, wizard-based software for fast and easy set up, assay run and evaluation
- Integrated methodology support - Includes recommendations, tips and troubleshooting

## Supplementary support instantly available if required

- A wealth of additional knowledge - directly accessible on the web from the Biacore X100 software



# Run successful assays from day one

## Research goal

Compare the binding (specificity, affinity and on-/off-rates) of variant Affibody® molecules to the EGF receptor family member, HER2.

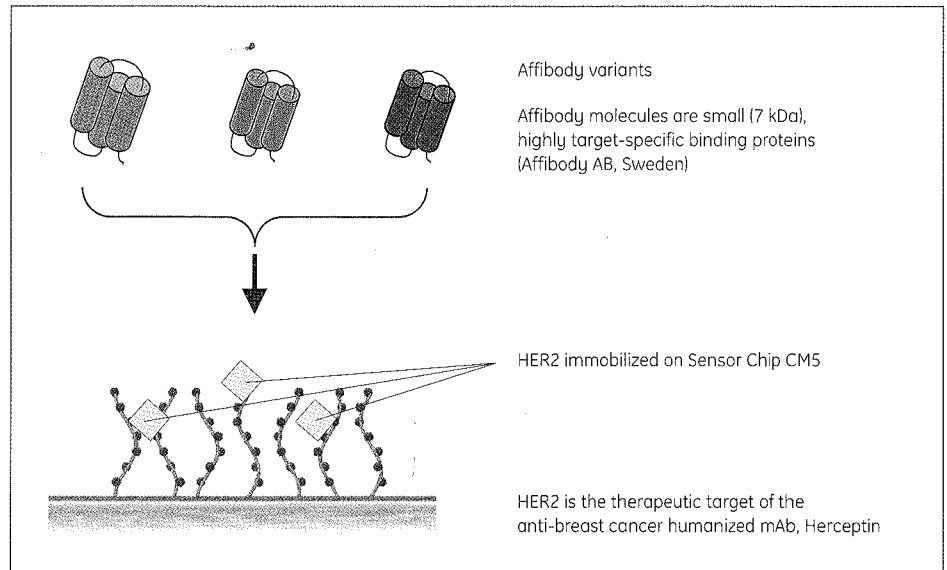
## Rapidly define specificity of Affibody variants

By comparing binding levels to immobilized HER2 and a reference protein, Thuy rapidly established specific binding to the target for all variants.

## Straightforward kinetic characterization of high-affinity interactions

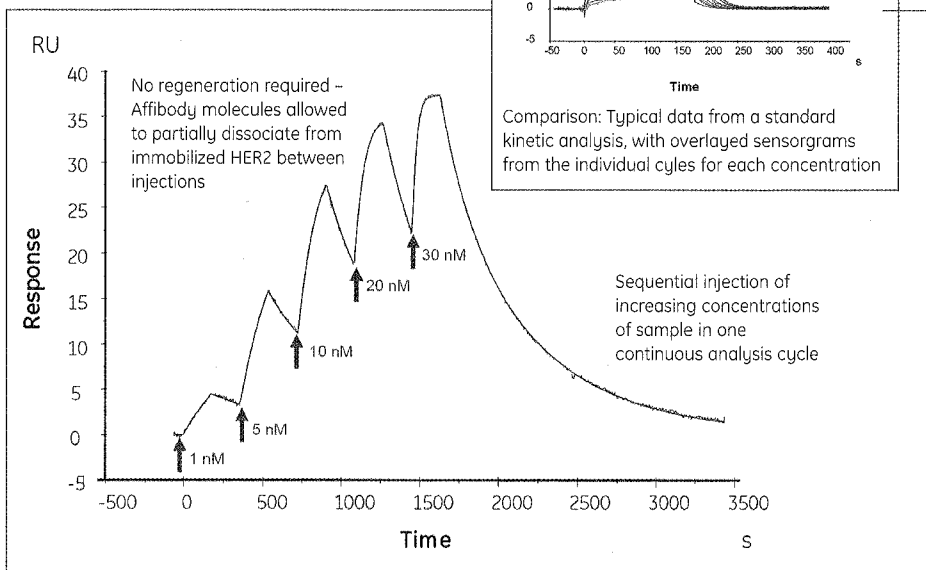
During a standard kinetic assay, a different concentration of sample is measured in each successive analysis cycle and all remaining bound sample is removed between cycles by regeneration.

The Affibody variants were, however, very difficult to regenerate. To overcome this problem Thuy used single-cycle kinetics to easily and quickly acquire the data.



“The software wizards were easy to use, and the help function was extremely useful to have. I got good at this very quickly!”

Thuy Tran, PhD student, Uppsala University, Sweden



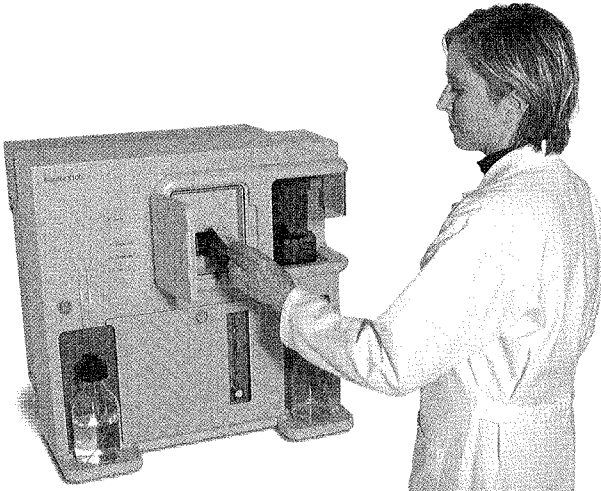
Biacore X100 Evaluation Software collates all partial association and dissociation events. On- and off-rate parameters (rate constants,  $k_a$  and  $k_d$ ) are automatically calculated.

- Affinities in 34 nM to 22 pM range
- On-rates varied from  $1.4$  to  $8.2 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$
- Off-rates varied from  $7 \times 10^{-5}$  to  $3 \times 10^{-1} \text{ s}^{-1}$

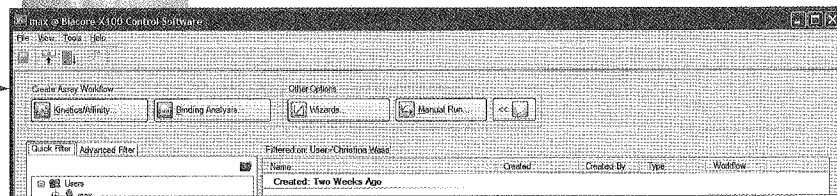
We gratefully acknowledge Thuy Tran and Professor Jörgen Carlsson, Uppsala University, Sweden for this collaboration

# Ready to run protein interaction analysis

Guidance every step of the way

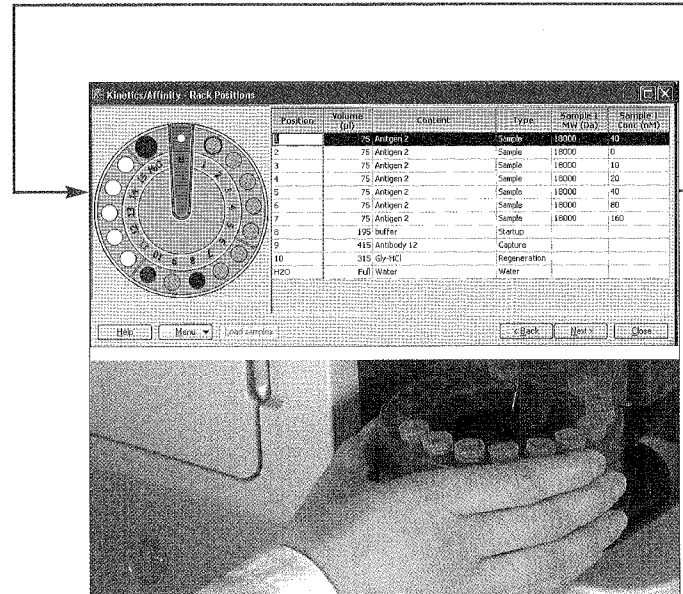


1 Select application type



Biacore X100 is an intuitive, user-friendly system. Software wizards provide guidance during the assay set-up, enabling the user to be up and running quickly. Built-in support leads users through every step of the process, from surface preparation and workflow structure, to data analysis and assessment.

The inherent sensitivity and flexibility of the system fulfils multiple analysis requirements (kinetics, affinity, specificity, concentration) using various assay formats.



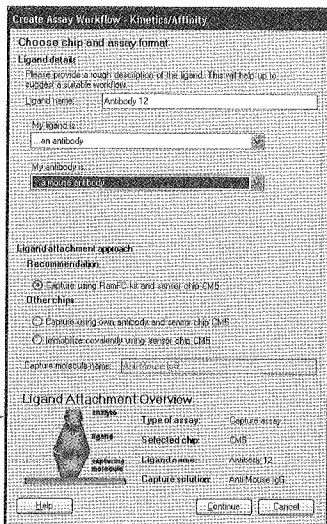
5 Let the software specify minimum volumes required - no sample wastage



**2** Specify sample properties

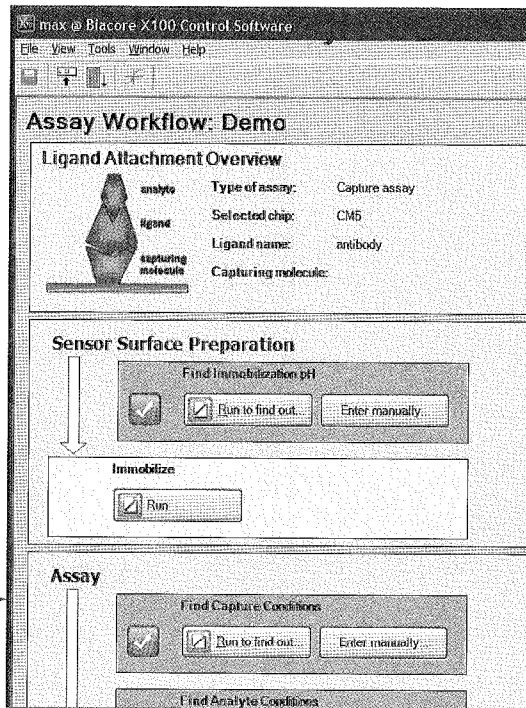
- Is a tag available?
- Is the molecule an antibody?

Software suggests optimal sensor chip and capture kit

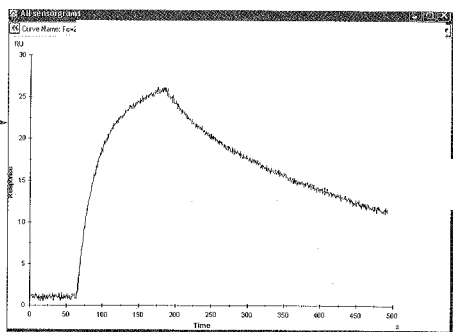
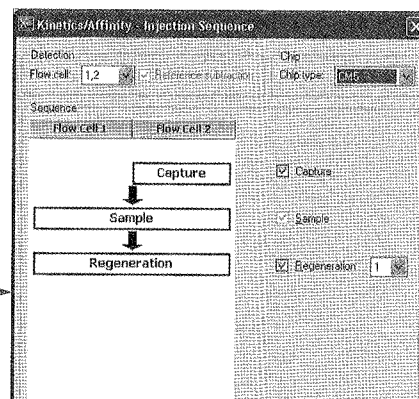


**3** The recommended workflow is outlined

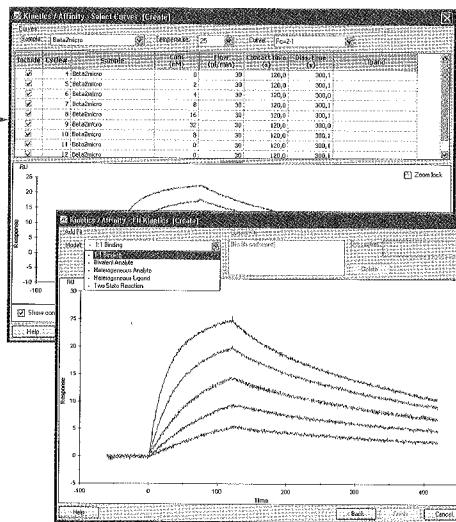
- Guidance is provided at every step, from surface preparation to data analysis



**4** Software wizards support every step during the assay

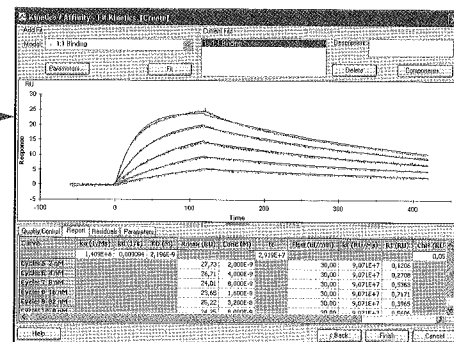


**6** See interactions as they happen



**7** Evaluate data in a few simple steps

- Identify which data to include
- Select an appropriate model



**8** View results

- Intuitive QC tools provide guidance on data quality
- Valid conclusions facilitated by quality data analysis
- Final results displayed



Set-up to results in a matter of hours

# Versatility and convenience

Rapid analysis with minimal assay development

## Solutions for every application

- A range of sensor chips  
(see selection guide page 12)
- Different assay formats:  
direct immobilization or capture

## Capture recommended as default assay format for ease of use

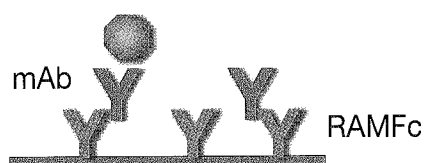
- Optimized immobilization protocols provided
- Generic regeneration step pre-defined
- Facilitates analysis if covalent coupling between an interactant and a surface is difficult
- Ensures specific orientation of the interacting molecule

## Assay flexibility

- Optional custom-assay design function with flexible, Open-assay Wizard\*
- Single-cycle kinetic analysis is available when standard kinetic assays are difficult or time-consuming\*
- Interaction analysis can be run at temperatures from 4-40° C with software support and inline degasser\*

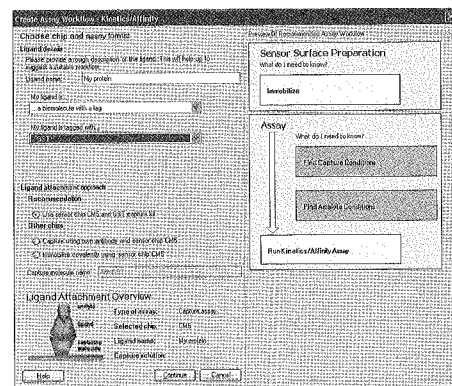
## Capture kits are available for a variety of molecules such as:

- GST-fusion proteins  
- GST Capture Kit
- Mouse and human antibodies  
- Mouse Antibody Capture Kit  
- Human Antibody Capture Kit



## Biacore X100 software is tailored for use with capture kits

- Identify tag during sample-information step
- Software recommends most appropriate kit
- Software support:
  - assay parameters pre-optimized
  - efficient use of reagents ensured



\*Available with Biacore X100 Plus Package

# Built-in Biacore expertise to fast-track your research

## Round-the-clock methodology support

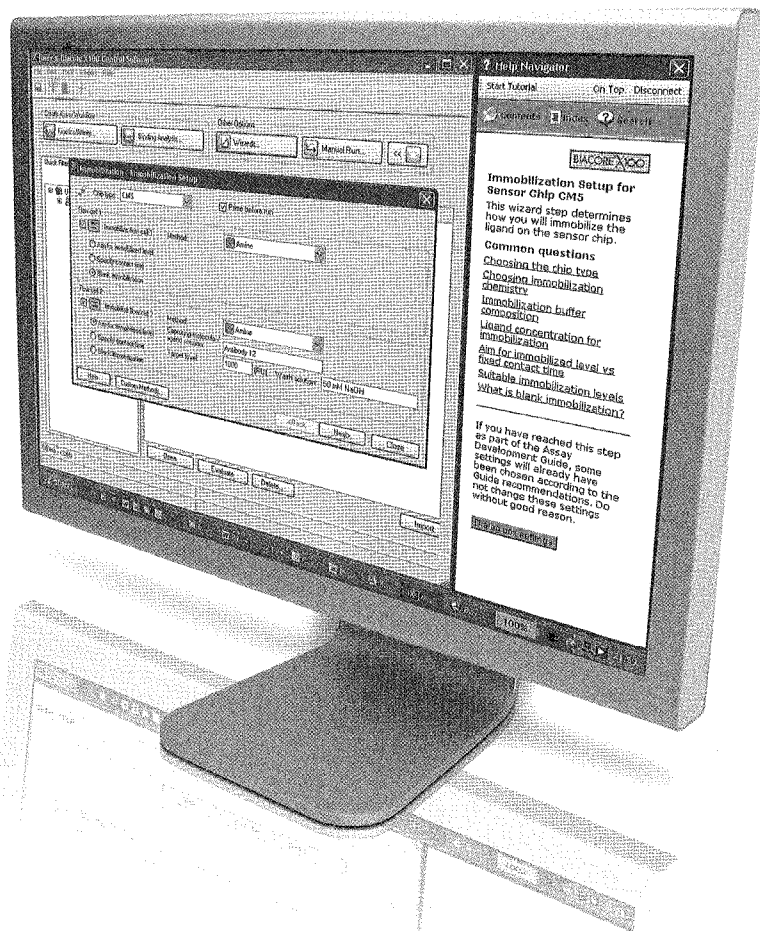
### Up and running straight away

First-time users can benefit from 'quick start' assistance to get up and running.

Integrated software support is provided for the Biacore X100 Getting Started Kit\* which includes instructions and reagents for performing a simple interaction analysis.

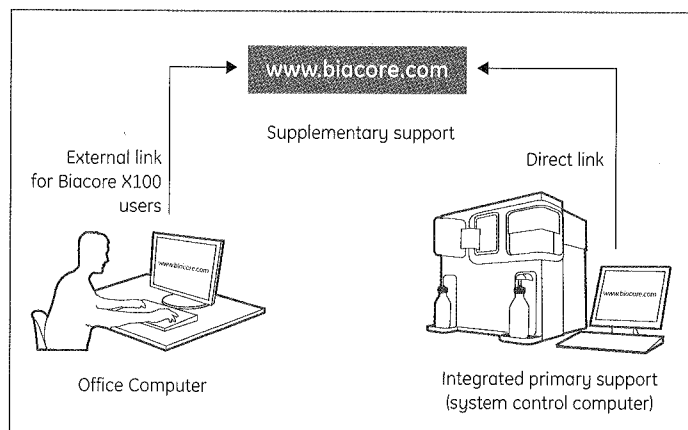
### Fully integrated primary support helps you every step of the way

- Support synchronized with software workflow
- Support includes recommendations, tips and troubleshooting



### Supplementary support available 24/7

- A wealth of in-depth, web-based supplementary support is directly available via hotlinks in the integrated primary support software/system
- Support is also accessible at [www.biacore.com](http://www.biacore.com) to system owners with a product key



\* Optional item

# Solutions for every application







## Sensor chip selection guide

A comprehensive range of sensor chips facilitates selection of the most suitable sensor chip surface, according to the nature of the molecule to be coupled, or the requirements of the analysis.

	Sensor Chip CM5	Sensor Chip CM4
Molecule to be immobilized		
Proteins	<ul style="list-style-type: none"> <li>● The first choice for immobilization of proteins via -NH<sub>2</sub>, -SH, -CHO, -OH, -COOH</li> </ul>	<ul style="list-style-type: none"> <li>● Useful if contaminants have a high positive charge</li> </ul>
Tagged proteins	<ul style="list-style-type: none"> <li>● For GST-tags (surface is derivatized with anti-GST antibody)</li> </ul>	
LMW molecules, typically <1000 Da	<ul style="list-style-type: none"> <li>●</li> </ul>	<ul style="list-style-type: none"> <li>●</li> </ul>
Membrane-associated molecules		
Nucleic acids	<ul style="list-style-type: none"> <li>● When modified with an amine group</li> </ul>	<ul style="list-style-type: none"> <li>● Useful if contaminants have a high positive charge</li> </ul>
Carbohydrates	<ul style="list-style-type: none"> <li>● When modified with an aldehyde group</li> </ul>	<ul style="list-style-type: none"> <li>● Useful if contaminants have a high positive charge</li> </ul>
Viruses or intact cells		

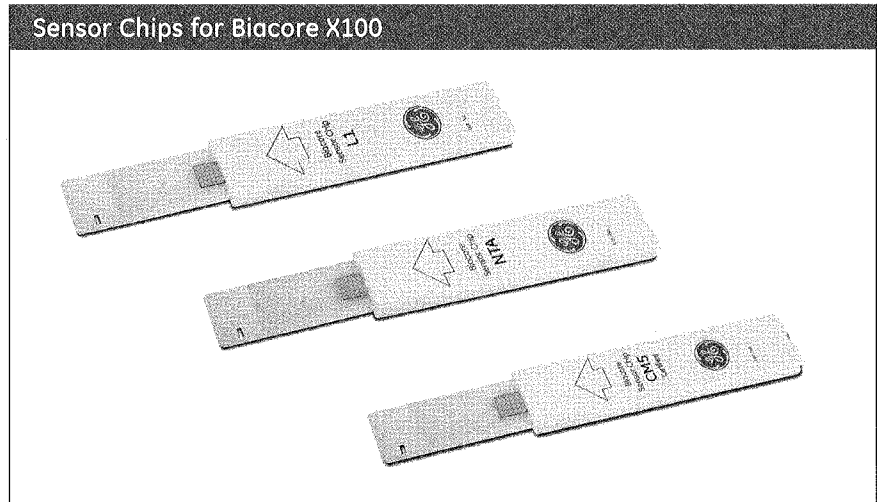
● Recommended choice    ● Good alternative



Sensor Chip CM3	Sensor Chip C1	Sensor Chip SA	Sensor Chip HPA	Sensor Chip L1	Sensor Chip NTA
					
● If partner in solution is very large e.g. a molecular complex	● If partner in solution is multivalent or very large e.g. a molecular complex	● When biotinylated			
					● For His-tags
●					
			● Incorporate molecule into a lipid monolayer	● incorporate molecule into a lipid bilayer	
● If partner in solution is very large e.g. a molecular complex	● If partner in solution is multivalent or very large e.g. a molecular complex	● When biotinylated			
● If partner in solution is very large e.g. a molecular complex	● If partner in solution is multivalent or very large e.g. a molecular complex	● When biotinylated			
● Keep large particles close to the surface to maintain sensitivity	● Keep large particles close to the surface to maintain sensitivity				

Recommendations in this table are based on the experience of scientists who have studied thousands of different protein interactions since the first Biacore system was introduced

For more information visit [www.biacore.com](http://www.biacore.com)



\*Capture Kits and Sensor Chips not to the same scale

# Product specifications and ordering information

Technical information and specifications	
Detection technology	Surface Plasmon Resonance (SPR) biosensor
Information provided	Kinetic, affinity ( $k_a$ , $k_d$ , $K_D$ ) and specificity. Concentration analysis*
Automation	Maximum 15 samples, 24 hours unattended operation
Molecular weight detection	Down to 200 Da in various sample environments
Number of flow cells	2
Required sample volume	Injection volume + 20-30 $\mu$ l (application dependent)
Flow rate range	From 1-100 $\mu$ l/min
Analysis temperature range	4-40° C (maximum 10 degrees below ambient temperature)*
Kinetics: Association rate constant ( $k_a$ ): Dissociation rate constant ( $k_d$ ):	$10^3 - 10^7 \text{ M}^{-1}\text{s}^{-1}$ (for typical protein-protein interactions) $10^{-5} - 0.1 \text{ s}^{-1}$
Detection limit	Typically 0.1 nM for >10 000 Da analytes Typically 1 nM for <10 000 Da analytes
Dimensions (W x D x H) (footprint, excluding System Controller/computer)	Instrument: 596 x 593 x 563 mm
Net weight	Total: 47 kg
Mains requirements	Processing Unit and System Controller: Aurorange 100-240 Vac, 50-60 Hz, protective earthing
Power consumption	Processing Unit: max 4 A (at 100 Vac) System Controller: max 7.2 A (at 100 Vac)
Data handling and storage	OS: Microsoft® Windows® XP (Professional), database storage
Safety and EMC standards	Complies with and applies to Europe and North America (US and Can) standards

\*functionality included in Biacore X100 Plus Package

## Biacore X100 system includes:

- Processing unit
- System controller
- Biacore X100 control and evaluation software
- Local database (Oracle Database XE)
- Windows XP operating system

## Optional Biacore X100 Plus Package includes:

- Inline degasser
- Variable assay temperature control (4-40° C)
- Custom Assay Wizard – includes user-defined methods and single-cycle kinetic analysis
- Concentration Analysis Wizard
- Custom immobilization
- User-defined fitting models for kinetics and affinity

Please contact your local representative for specific information.

®

# Service and support

## Getting the most out of label-free interaction analysis

A comprehensive range of service programs, support tools and information services is available to support the system range. Our goal is to provide you with the optimum level of support so that your Biacore system continues to make a key contribution to your research.

### Online support including:

#### Support tools:

- BIA simulation to perform dry-run experiments
- Tech tips & protocols
- Immobilization and regeneration database to quickly optimize experimental conditions

#### Software and downloads

- Download the latest software version
- Download and review software notes, handbooks and the latest news about your system and software

#### Training

- Getting started kit
- Training courses

#### Instrument service

- Service contract
- Extended warranty
- Maintenance visits

#### Publications

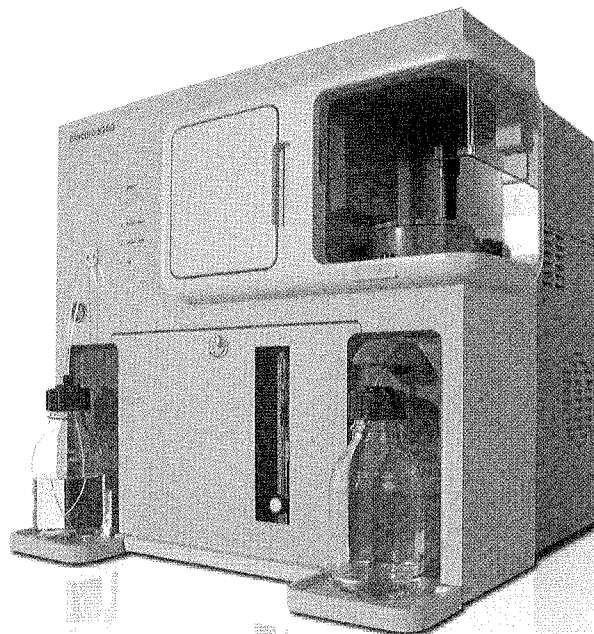
- On-line reference database

#### MSDS

- Find Material Safety Data Sheets relating to consumables

#### Online product center

- Find up-to-date prices, product descriptions and ordering information
- Generate personalized purchase lists



## Biacore, part of GE Healthcare

The integration of Biacore's world-leading protein interaction analysis systems into the product portfolio of GE Healthcare Life Sciences creates a center of excellence that offers a wide range of solutions to the life science community.

Technical and commercial resources available through GE Healthcare enable faster development of innovative products that are designed to fulfill your requirements for interaction analysis. Together we can deliver unbeatable solutions to elucidate disease mechanisms, develop and produce novel therapeutics, detect and characterize immune responses, or purify and characterize protein therapeutics.

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imagination at work

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