### **System description**

This is triple configuration system, that can be reconfigured as:

- BioXolver with detector in air for solution scattering
- Materials SAXS/WAXS/GISAXS/GIWAXS in with sample in vacuum.
- Materials SAXS/WAXS/GISAXS/GIWAXS with the sample in air
  Interlocked chamber doors
- Segmented Flight Path used to change the sample-to-detector distance
- Detector in air with 2D mapping of 200mm diameter exit window.

Minimal reconfiguration will be needed when switching between the different configurations.

1) BioXolver Configuration: The Materials Sample Goniometer and imaging mirror are removed from the sample chamber to provide a clean open path for scattering from the solution in the capillary of the BioCube, attached to the front exterior face of the sample chamber. The capillary in the BioCube is oriented horizontally and aligned vertically with a stepper motor. The vertical motion is precision guided by crossed roller bearing rails and sealed under vacuum by sliding o-ring seals.

2) Materials SAXS/WAXS in Vacuum Chamber: The BioCube is lowered and the direct beam, collimated by the 2 scatterless slits, passes through an open position above the capillary and into the sample chamber. The user will mount the sample goniometer using location references to reproducibly place it in the correct, pre-aligned position.

3) Materials SAXS/WAXS in with the Sample in Air: The incident collimation path and detection flight path are covered with atmospheric caps to isolate the sample region in air. Kapton windows are used for the windows on the atmospheric caps. With the sample in air, the sample imaging must be removed, and the cone for the detection path is used only for SAXS. For WAXS with the sample in air, simply remove the cone.



# BioXolver<sup>\*</sup> Accelerate your biostructural research

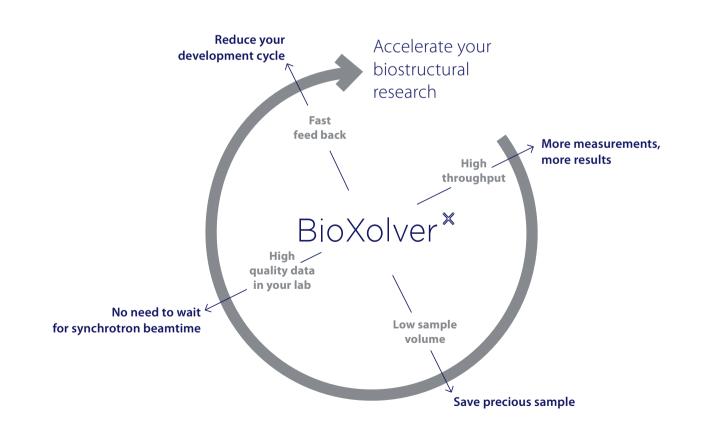


## BioXolver \* Accelerate your biostructural research

SAXS has a proven track record for reliable determination of shape, related parameters and even dynamics and interactions of macromolecules in solutions.

Until now, SAXS measurements were limited to synchrotron facilities or low throughput laboratory setups requiring large quantities of sample.

The BioXolver, with its unique features, overcomes these limitations. It offers high data quality, fast full automation of multi-sample measurements and data analysis, combined with the capability to work reliably with very small volumes of sample. Best of all, this capability is available right in your lab, allowing you to shorten your development cycle and accelerate your biostructural research.





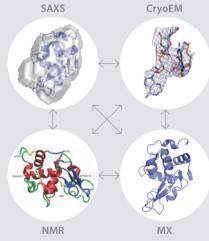
#### Macromolecular shape & dynamics With the BioXolver, get information on:

- > Radius of gyration (Rg)
- > Molecular weight
- > Maximum intra-particle distance
- > Degree of folding
- > 3D envelope



### Small Angle X-ray Scattering for structural biology

SAXS is complementary to other structural biology techniques:



- > Wide range of length scales down to 1 nm
- ightarrow Solutions studied in their natural environment
- > Adapted for proteins and large complexes

## BioXolver<sup>\*</sup> High throughput measurements & results

From sample to results on 192 samples in an automated way.



The BioXolver offers maximum throughput. Each step of the characterization process, from sample handling to measurement and data analysis is optimized to provide the biologist with fast and reliable results.

### Short sample to sample cycle time

The sample is handled automatically by the in-line pipetting robot which takes it to the beam for automatic measurement. Once the measurement is made, structure results are available in a few minutes. The sample cell is automatically cleaned & dried, ready for the next sample. Loading & cleaning cycle only takes between 1 and 2 minutes.

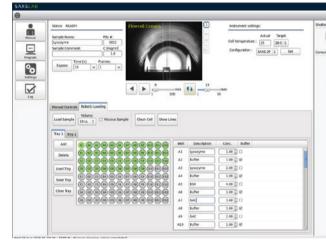
### More measurements, more results

Biostructural studies can be a very iterative process. With its fully automatic measuring process and short cycle time, the BioXolver supplies a high number of structure results per day. This reduces your development cycle, in particular when you need to investigate solutions in a large range of conditions.

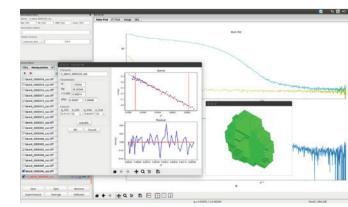
### Reproducibility of your measurements is ensured

Robotic pipetting and handling from the sample plate to the measurement cell minimize user intervention and increase the reliability of comparative measurements. Up to 192 samples can be loaded & measure & the automated software suite.









### Up to 192 samples can be loaded & measured automatically thanks to the in-line pipetting robot

Ι.

### Place the 2 x 96 well trays on the instrument.

Experiments start with placing a standard 96 well plate on the thermalized holders of the instrument. The BioXolver can hold and run two such plates simultaneously.

Decide your experiment sequence, press

The smart Graphical User Interface allows to quickly program the experiment sequence including the

start and walk away.

automated cleaning process.

3

## The in–line pipetting robot does automated handling of samples in synchronization with the X-ray measurement.

The sequence includes automated cleaning and drying of the sample cell in between each sample. The in-line pipetting robot with tubeless handling ensures a short transport and fast cycle per sample.

## 4.

The automated software package analyzes and compiles the results for you.

The instrument notifies you via e-mail upon completion. Just retrieve your results remotely.

#### 4•5

## BioXolver<sup>\*</sup> Low sample volume consumption

At the core of the BioXolver, the conjunction of an in-line pipetting robot and machine vision ensures a total consumption as low as 5 µL per protein concentration or sample condition.



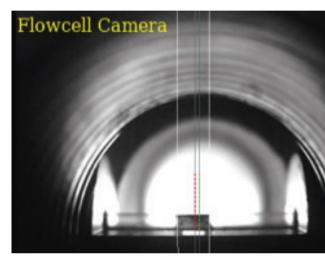
### In-line pipetting robot with tubeless handling

The sample changer is based on a pipetting robot positioned next to the X-ray beam to handle transport of the sample from the well plate directly to the measurement cell. It is thus not only fast, but also highly precise and reliable.



### Direct injection into the BioCube measurement cell

Tubeless handling of the protein prevents any sample loss and protein shearing. Low surface tension solutions such as lipid complexes or surfactants can be handled easily without the sample breaking apart.



### Automated sample positioning by machine vision

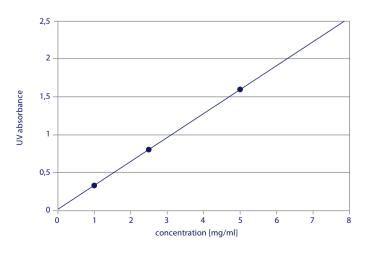
Once placed in the BioCube measurement cell, the sample is automatically positioned in the X-ray beam by means of machine vision. No manual intervention or expert eye is required and the X-ray scattering measurement is started directly by the instrument.

#### Save precious money and sample

Preparing a solution of protein is a costly process, especially for new drug candidates. With a total sample consumption per tested condition down to 5  $\mu$ L, the BioXolver reduces significantly the cost of your experiment by reducing the total volume of protein required.

#### Do more with your sample

Reducing the sample volume per measurement increases the amount of possible experiments from the same preparation volume. This is highly beneficial for screening studies covering a wide range of solution conditions.







### Sample integrity for accurate measurements

The sample is maintained at the selected temperature both in the well plate during storage and in the BioCube during measurements. The in-line pipetting robot avoids cross-contamination of samples through the use of disposable tips, tubeless handling for no sample loss, and the fully automated sample cell cleaning and drying.

## Optional in-line simultaneous UV-Vis measurement

*In situ* UV measurement directly in the measurement cell provides concentration information of the sample before and after X-ray exposure.

## BioXolver\* High quality data directly in your lab



#### With the BioXolver, data of excellent quality is available in the lab.

Data quality is extremely important for a BioSAXS system due to low contrast and weak scattering from biological samples. It is essential that every part of the instrument is optimized for maximum X-ray intensity and lowest possible noise.

Benefiting from 17 years of continuous R&D in SAXS from Xenocs, the BioXolver offers a unique combination of both the capability to study low scattering proteins and a unique level of automation.

Optimized for low signal measurements with a photon counting detector in vacuum, a high precision and static flow-cell, no interfering windows in the beam path, careful data normalization and cosmic radiation correction, the BioXolver delivers excellent sensitivity and data quality.





BioXolver. Thyroglobulin (669 kDa) solution, c = 4 mg/mL, 5 min exposure time.

#### Less dependency on synchrotrons

Due to the instrument's excellent data quality, many experiments can now just as easily be done with the BioXolver in a time frame of minutes. Without the need to travel for synchrotron beamtime, samples will always be fresh out of the lab, ensuring maximum sample and data quality.

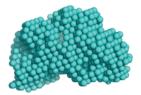
### Fast results and high quality data in your lab

The BioXolver provides good data even on weakly scattering samples.





Lysozyme solution (14.3 kDa), c = 1.5 mg/mL, 5 min exposure time.





**Synchrotron,** from SASDA98 Thyroglobulin (669 kDa) solution, c = 3.9 mg/mL, www.sasbdb.org

### Reduce your development cycle

The BioXolver provides structural information such as shape and interactions of proteins in solutions resembling *in vivo* conditions on a daily basis. This reduces the research and development cycle for biostructural investigations, protein formulation and crystallization studies.

## BioXolver\* Services & support

The BioXolver is supported by a comprehensive service offer in order to help our customers worldwide take full benefit of the instrument during its complete lifetime.

#### On-site installation and operational training

Our team of support engineers ensures a smooth installation as well as training on quick start of the system and first level of maintenance.

Operational training is provided right after the installation and includes training on good practise for biostructural SAXS measurements.

#### Advanced training

Xenocs offers a choice of comprehensive training programmes, from introduction training on the use of SAXS for biostructural research and good laboratory practises, to advanced scientific training on data analysis. With a team composed of several BioSAXS experienced application scientists, we provide continuous training, both on-site and online, to ensure the transmission of experience and knowledge to our customers worldwide.

#### Customer support

Customer support is managed by one of our central facilities - Sassenage in France, Amherst in the US, Copenhagen in Denmark, or Singapore - , in collaboration with our team of local agents for first level of support. All our local service teams are supported by Xenocs corporate service engineers, product specialists or application scientists according to our ISO 9001 support and maintenance programme.

BioXolver configurations	BioXolver	BioXolver L
Utilisation	Research on biological macro-molecules in solution	Research on biological macro-molecules, including large complexes and interactions
X-ray source	Microfocus GeniX 3D, MetalJet, add-on to RAG	
Optic	Aspheric single reflection multilayer optic	
Collimation	Motorized scatterless point collimation	
Sample cell	Xenocs thermalized BioCube flow-cell with camera and pump	
Sample handling	Pipetting robot with disposable tips	
Sample capacity	Up to 2 x 96 well plates (thermalized)	
Minimum sample volume	Down to 5 μL	
Cleaning	Automated cleaning and drying with three cleaning fluids	
Detector	Dectris in-vacuum hybrid pixel photon counting detector	
Detector configuration	Fixed detector distance	Variable detector distance
Data reduction and analysis sofware	RAW and ATSAS	
Q-range and typical protein size*	0.006 $\text{\AA}^{\text{-1}}$ / MW < 200 MDa / Rg < 135 Å	0.003 Å-1 / MW < 1.5 GDa / Rg < 270 Å
Overall Length	3.2 m (2.7 m as add-on to existing source)	4.2 m
Options	UV-Vis, separate temperature control for sample trays and BioCube	
Services	Installation, training, hot-line, maintenance contract	

\* Theoretical limit assuming globular proteins

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