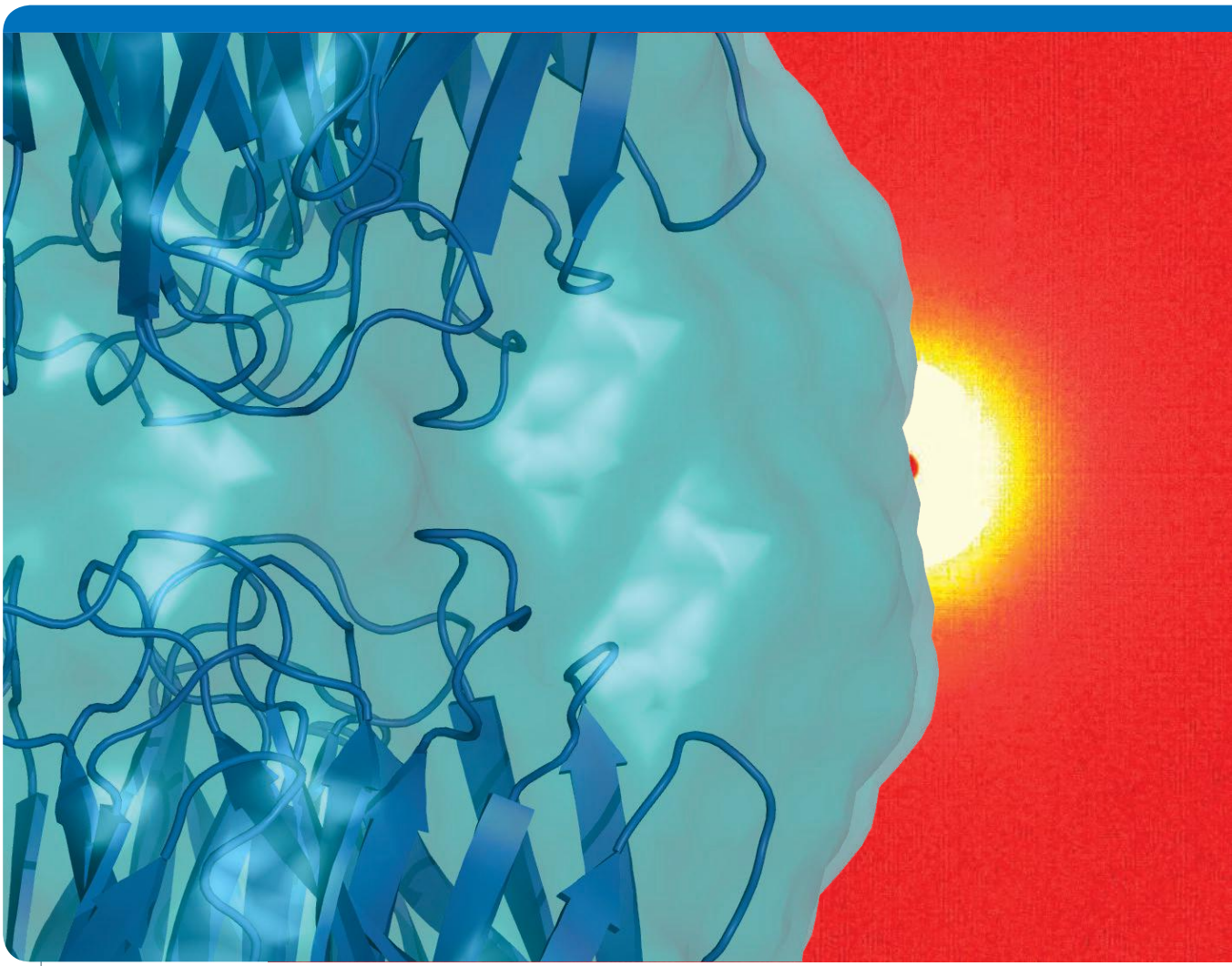


NANOSTAR

- Compact, High-performance SAXS Solution for Structural Biology

SAXS

Innovation with Integrity

SAXS – Expanding the Frontiers of Structural Biology

Biological small-angle X-ray scattering (BioSAXS) is becoming an essential technique in structural biology. For both simple and complex systems, SAXS is a great complimentary tool for elucidating the size, conformation, and flexibility of biological molecules in solution—under physiologically-relevant conditions.

Additionally, since SAXS requires minimal sample preparation, it is possible to get valuable structural information faster than almost any other technique.

A more recent development is the advance of powerful new software tools that allow SAXS data to be quantitatively combined with structural data from other techniques such as crystallography, NMR, or molecular dynamics, to solve structures that are otherwise intractable. This promises to expand further the application of this SAXS.

NANOSTAR features and benefits

- METALJET source and HELIOS-P optics for the brightest and highest-quality beam available in the home laboratory
- SCATEX scatterless pinholes for the highest flux and lowest parasitic scattering
- VÅNTEC-2000, the largest photon-counting detector available in the home laboratory, for the best signal-to-noise ratio
- SCÅTTER, the most powerful and easiest-to-use software package for macromolecular SAXS
- Best angular resolution for low Q_{min}
- Very compact system
- Dual-port configurations with seamless integration with D8 VENTURE crystallography systems

NANOSTAR – High-Performance SAXS Experiments for your Home Laboratory

Despite the dramatic growth of SAXS as a biological research tool, the method has been largely restricted to synchrotron beamlines. However, with the recent availability of stronger in-house sources such as the METALJET, even the most challenging biological SAXS experiments have become feasible in the home laboratory. The new NANOSTAR combines the most brilliant home-lab X-ray source with our unique scatterless SCATEX pinholes to create a compact system with high flux and ultra-low parasitic scattering.

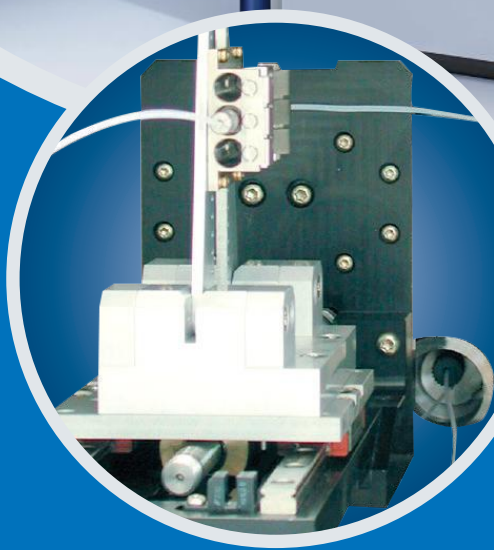
Pinhole collimation has long been preferred for high-resolution SAXS measurements, since there is no smearing of the scattered X-ray signal (as occurs in, for example, Kratky geometries). In addition, pinhole collimation allows the entire scattered X-ray pattern to be recorded, providing a much better signal-to-noise ratio for the integrated SAXS profiles. This is in contrast to Kratky systems, where only a fraction of the scattered X-ray profile can be recorded.

However, to minimize parasitic scatter, traditional pinhole systems have employed three-pinhole collimation—resulting in longer beam paths and lower flux. With two scatterless pinholes, the NANOSTAR's unique configuration gives you the best of both: the high flux of a Kratky system together with the better resolution and signal-to-noise ratio of a pinhole system.

The NANOSTAR combines the most brilliant home-lab X-ray source with a compact beampath, ultra-low parasitic scattering, and a full-field-of-view photon-counting detector for the best SAXS performance in the home laboratory.

METALJET X-ray Source and Optics

- The brightest source available in the home lab
- No external cooling water or 3-phase power required, for easy siting and installation
- Fully integrated: all source configuration, autocalibration and adjustment is automated
- Unique, patented low-figure-error optics preserve all of the METALJET's brightness
- Synchrotron-quality optics
- Parallel beam with three times the flux of conventional optics
- Divergence below 0.5 mrad
- SCATEX pinholes for reduced parasitic scatter and twice the flux

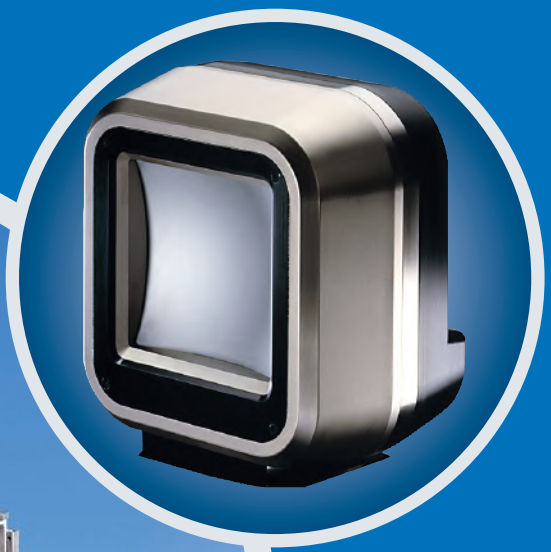


Dual-port Solution

The NANOSTAR can be configured as a stand-alone or dual-port system. Have the best of both worlds with single crystal diffraction on one port and SAXS on the other. Even if you don't need a second port right now, your future needs may change. The dual-port configuration can be implemented with a single end station, which gives you the flexibility to easily upgrade your capabilities.

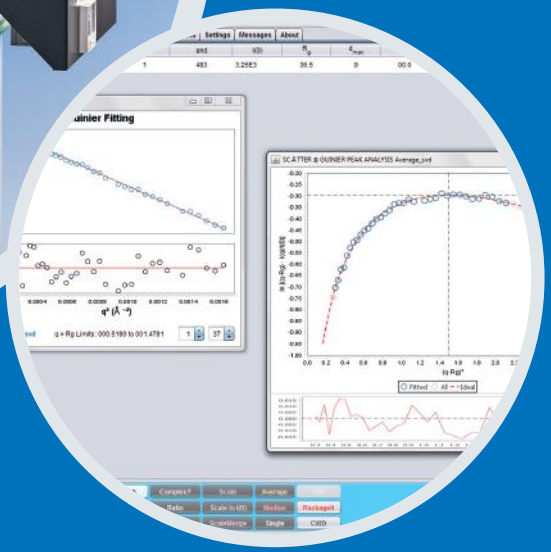
Versatile Sample Chamber

- Large sample chamber accommodates a variety of sample holders
- Temperature-controlled liquid sample stage holds up to six sample cells
- Excellent sample visibility with large, transparent, radiation-tight door
- Automated sample loader for unattended analysis of up to 96 samples (optional)
- Highest experimental flexibility thanks to flanges for additional supply connections
- Optional flow cell



VÅNTEC-2000 Photon-counting Detector

- Largest active area available in the home laboratory: 14 cm × 14 cm
- High-sensitivity, real-time photon counter
- High dynamic range
- Radiation hard
- No gaps
- No charge sharing
- Lowest noise of any detector, less than two noise counts per pixel *per year*
- High spatial resolution
- Large active area with the entire scattering range collected in one exposure



SCÅTTER Software

- Fully integrated with the state-of-the-art Guinier, Porod, and Kratky analysis for size, shape, and flexibility determination
- Automated calculation of R_g, D_{max}, and P(r) function
- Go beyond simple bead modelling with, the most mathematically-sophisticated algorithms for envelope determination
- Direct fitting of PDB models to SAXS data
- *Ab initio* structure determination via NMR or X-ray

Flow cell

- Changing the sample without breaking the vacuum in the sample chamber
- Temperature controlled and stabilized environment (243 K to 393 K)
- Manual load via syringe or
- High throughput autoloader from 96-well plates (optional)
- Improved sample quality by adding an in-line HPLC

METALJET with HELIOS MX

- The METALJET uses a liquid target consisting of a galliumrich alloy.
- Shorter-wavelength Ga-Kα radiation causes less radiation damage and facilitates highmultiplicity data sets
- The optimized HELIOS MX optics provides a beam optimized for the best signal-to-noise ratio
- Always fresh, self-healing target for high power load with long-term constant beam intensity

Revolutionary Path Planning

- Revolutionary control software using advanced algorithms for optimized goniometer performance
- Software uses a 3-D model of the current hardware configuration for real-time path planning
- Extension with custom 3-D models is possible
- Component recognition

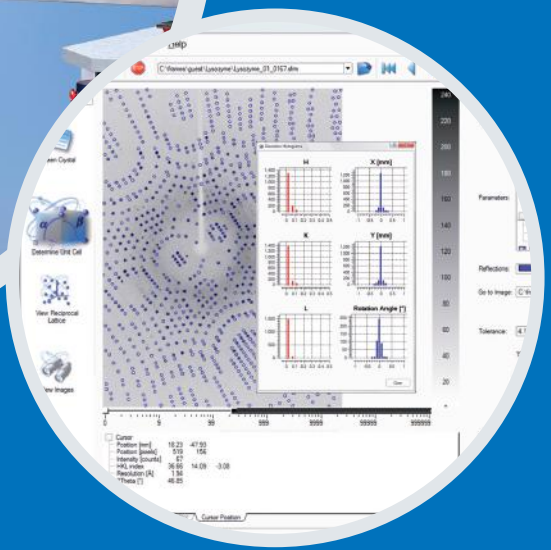
KAPPA Goniometer

The KAPPA 4-circle goniometer's open geometry offers ultimate sample positioning freedom, for unconstrained multiplicity of observations. The detector-to-sample distance is automatically optimized based on unit cell dimensions and crystal quality.

- Easy sample mounting and harvesting
- SNAP-LOCK mount for simple exchange
- Set of optimized collimators included

PHOTON II Charge-Integrating Pixel Array Detector

- Largest monolithic active area: 140 cm2
- Quantum-limited sensitivity
- High speed: up to 70 frames per second
- Zero readout dead time
- No nonlinearity at high count rates
- No charge sharing means better intensity



PROTEUM3

- Easy to use data collection and integration software
- Guides through the entire experiment with minimum input and maximum performance
- Intuitive GUI for extensive graphical feedback
- Most complete semi-automated pipeline suggesting proper defaults
- Perfect for both, quality assessment and phasing
- Easy twin handling of up to eight domains
- New phasing module for SAD, SIR and MAD data
- Easy data ex- and import to and from XDS

ISX Stage

- Versatile stage for *in situ* plate screening
- Mounts on the KAPPA sample stage
- Fully-motorized plate stage for screening and data collection form multi-well plates
- Compatible with all SBS-format multi-well plates
- Access to all wells in one setting

List of selected publications

Bothe J.R., Tonelli M., Ali I.K., Dai Z., Frederick R.O., Westler W.M., Markley J.L. (2015) *The Complex Energy Landscape of the Protein IscU.* Biophys J., **109,** 1019-25.

Tay, M. Y. F., Saw, W. G., Zhao, Y., Chan, W. K. K., Singh, D., Chong, Y., Forwood, J. K., Ooi, E. E., Grüber, G., Lescar, J., Luo, D., and Vasudevan, S. G. (2015) *The C-terminal 50 amino acid residues of Dengue NS3 protein are important for NS3-NS5 interaction and viral replication.* J. Biol. Chem., **290,** 2379-2394.

Nartey, W., Basak, S., Kamariah, N., Manimekalai, M.S.S., Robson, S., Wagner, G., Eisenhaber, B., Eisenhaber, F., and Grüber, G. (2015) *NMR studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial 2-Cys peroxiredoxin machinery.* FEBS J., **282,** 4620-4638.

Helmich, K., et al. (2016) *Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of β-Aryl Ether Bonds in Lignin.* JBC, **291,** 5234-5246

Manthei, K.A., Hill, M.C., Burke, J.E., Butcher, S.E. and Keck, J.L. (2015) *Structural mechanisms of DNA binding and unwinding in bacterial RecQ helicases.* PNAS, **112,** 4292-4297.

NANOSTAR Specifications	
X-Ray generator	METALJET
Flux at sample	> 10^9 ph/s (Ga Kα)
Collimation	2 SCATEX pinholes, variable diameter
Incident beam optics	Montel optics, parallel beam
Sample volume	≥ 2 µL
Sample Stage	6 capillaries, motorized (others available)
Detector distance	32 – 92 cm
q-range	0.005 – 0.58 $Å^{-1}$
Camera length	190 cm
Max. dimensions of the dual port solution	206 cm × 397 cm × 129 cm (h × w × d)
Detector	VÅNTEC-2000
Detector type: Active area: Sensor pixel size: Max. global counting rate: Noise: Maximum dynamic range:	photon counting 140 × 140 mm^2 68 µm 1.6 × 10^6 cps < 1.5 noise counts per pixel per year > 10^9 cps

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