CRYSTALLOGRAPHY

D8 VENTURE METALJET

Beamline Capabilities In-House

Innovation with Integrity

All about the
PHOTON IV

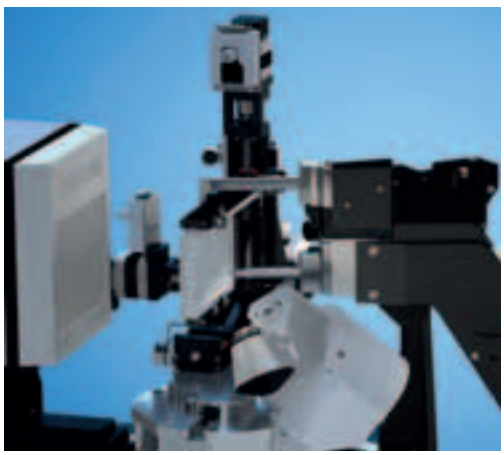
D8 VENTURE METALJET Key features

METALJET MC ultra-bright X-ray source
KAPPA multi-axis goniometer
PHOTON IV 16 detector
APEX and PROTEUM software
Automation options

All about the
METALJET MC

Unattended automated data collection—enhance productivity

The SCOUT automated sample changer screens, evaluates, and acquires data from up to 96 crystals per batch. Its software simplifies measurement management and result tracking. With nonstop operation, SCOUT boosts throughput and reduces wait times.

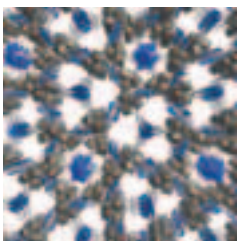


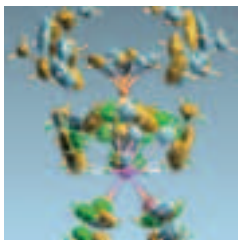
In situ crystallography—rapid crystal screening and data collection directly in plates

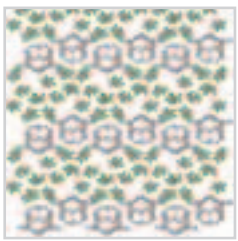
Modern chemistry and structural biology investigate targets which can be difficult to crystallize or are highly fragile. Performing crystallography directly in plates is often the solution.

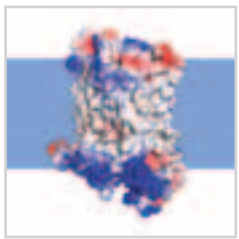
D8 VENTURE METALJET — Beamline Capabilities meet In-house Advantages

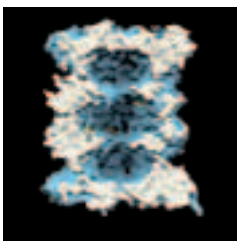
Microcrystals

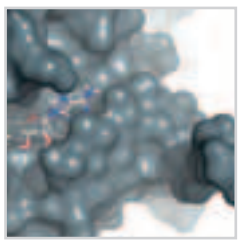

MOFs, porous materials

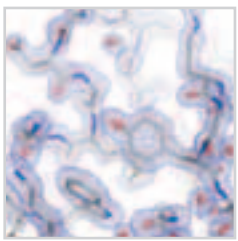

Disorder Modelling


Low crystallinity materials


Membrane proteins


Protein complex


Drug discovery


In situ structures

The unique advantages of an in-house beamline:

- Flexible access enables rapid scientific progress
- No sample shipping
- Fast turnaround accelerates crystal growth
- Immediate structure analysis from unstable crystals
- Reduced radiation damage

The D8 VENTURE METALJET enables crystal structure analysis previously only possible with synchrotron beamlines. It delivers synchrotron-level data quality in an in-house setup.The system facilitates on-site analysis of sensitive crystals, streamlining workflow and boosting productivity.

Your chemical crystallography beamline

In advanced chemistry research, crystallographers investigate complex structures such as molecular compounds as well as covalent organic and metal-organic frameworks (COFs, MOFs). The D8 VENTURE METALJET enables reliable structure determination from challenging crystals, including samples with high disorder or weak diffraction. Data of this quality was previously achievable only at synchrotron facilities and typically exceeds the quality obtained with current electron diffraction methods.

Your MX beamline—adding flexibility to MX experiments

The D8 VENTURE METALJET provides shorter exposure times and improved signal-to-noise ratios compared to standard in-house systems, making it effective for collecting data from small or weakly diffracting crystals. It is ideal for facilities focusing on membrane protein crystals, complexes, and protein-ligand studies in drug discovery. Fast measurement times and automation speed up protein-ligand research, while its ease of use improves control of crystallization projects and generates higher-quality crystals faster.

Your *in situ* beamline

In situ crystallography is straightforward with the ISX STAGE mounted on the goniometer, allowing for direct evaluation of crystals from proteins, small molecules, and molecular frameworks. Plate-based crystal experiments provide immediate data on diffraction, quality, unit-cell parameters, and space group, simplifying optimization. It avoids handling individual crystals and maintaining sample integrity. Merging datasets from multiple crystals produces complete data and reliable room-temperature structures.

Home sources vs. synchrotron beamlines

The METALJET MC delivers in-house X-ray intensities comparable to those achieved with bending magnet and superbend synchrotron beamlines.

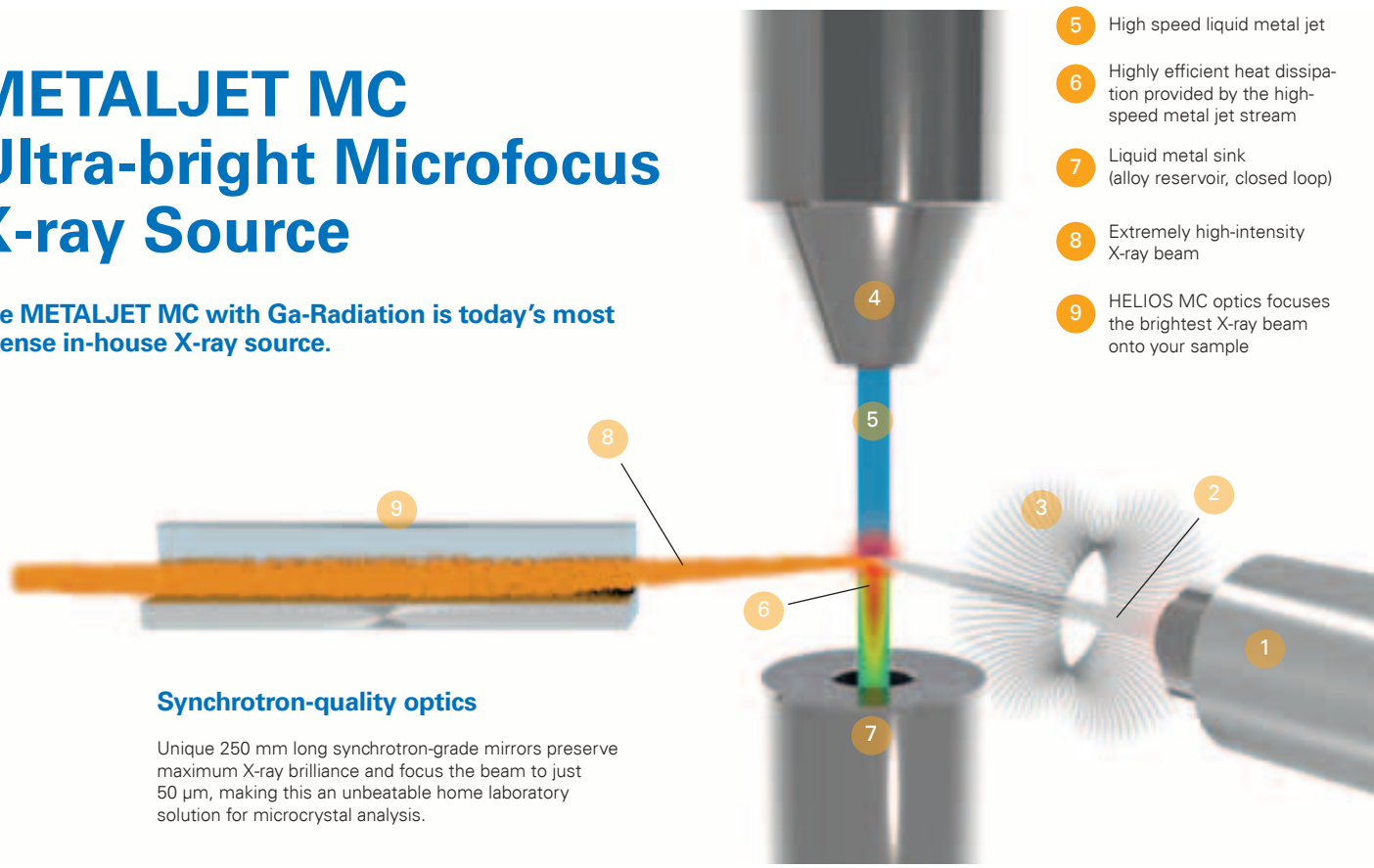
Ultra-high intensity: With X-ray intensity exceeding 2×10^{12} X-rays·mm^{-2}·sec^{-1}, the METALJET MC is more than ten times brighter than other home-sources. This results in stronger diffraction, better $I/\sigma(I)$, higher resolution, and shorter measurement times, making it the most productive home-source available.

Microfocus X-ray beam: Advanced multilayer optics produce a 50 µm diameter (FWHM) circular beam at the crystal ensuring more photons are diffracted from the smallest of crystals while minimizing background scatter. A key reason why the METALJET MC can solve structures other home sources cannot.

Ga target with K_α emission of 9.2 keV (1.341 Å): The wavelength is optimal for analyzing crystals of proteins, chemical macromolecules like COFs, MOFs, and small molecules. It provides excellent resolution, a strong anomalous signal, and reduces radiation damage, enabling detailed structure analysis and reliable absolute structure determination or protein structure solution using S-SAD.

METALJET MC Ultra-bright Microfocus X-ray Source

The METALJET MC with Ga-Radiation is today's most intense in-house X-ray source.



1. Fully stabilized, high brilliance cathode
2. High flux electron beam, focused onto the liquid metal target
3. Electron lenses for beam positioning and focusing
4. Nozzle dispensing a continuous stream of fresh liquid metal
5. High speed liquid metal jet
6. Highly efficient heat dissipation provided by the high-speed metal jet stream
7. Liquid metal sink (alloy reservoir, closed loop)
8. Extremely high-intensity X-ray beam
9. HELIOS MC optics focuses the brightest X-ray beam onto your sample

Synchrotron-quality optics

Unique 250 mm long synchrotron-grade mirrors preserve maximum X-ray brilliance and focus the beam to just 50 µm, making this an unbeatable home laboratory solution for microcrystal analysis.

PHOTON IV 16 Detector

State-of-the art photon counting CPAD taking full advantage of your in-house beamline

The PHOTON IV detector is engineered to perfectly record diffraction signal generated by the METALJET MC X-ray source, ensuring high-quality data collection even in the most demanding experimental conditions.

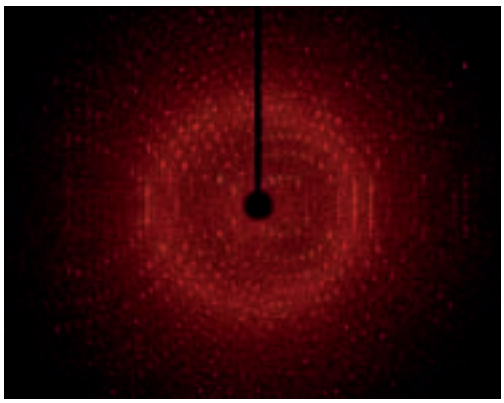
Superb reciprocal space coverage: A sensor format of 1.6 million pixels provides a large active area of 16,000 mm^2. With 100 µm pixels and a point spread smaller than a single pixel, the detector can be positioned very close to the sample. This results in capturing a larger number of reflections per frame and leads to significantly reduced measurement times.

Photon counting with Interpixel Logic: Single photon sensitivity and high-speed pixel sampling means that photons are counted in real time. The PHOTON IV's unique combination of mixed-mode detection and interpixel logic means that no photon events are missed due to pulse pileup or charge sharing. The result is more accurate data and better-quality structures.

High linear count rate and dynamic range: The PHOTON IV achieves a linear count rate of over 10^6 X-rays·mm^{-2}·sec^{-1} resulting in an excellent dynamic range. This means that the PHOTON IV records accurate intensities from strong and weak reflections on the same frame.

Point spread of less than one pixel, parallax-free: Indirect detection using a proprietary rare earth scintillator transmits each photon signal to the readout pixel with a point spread of less than one pixel. The ultra-thin scintillator ensures that signals will not spread over multiple pixels, even at high incident angles. This produces cleanly separated reflections from large unit cells, twins, or modulated crystals.

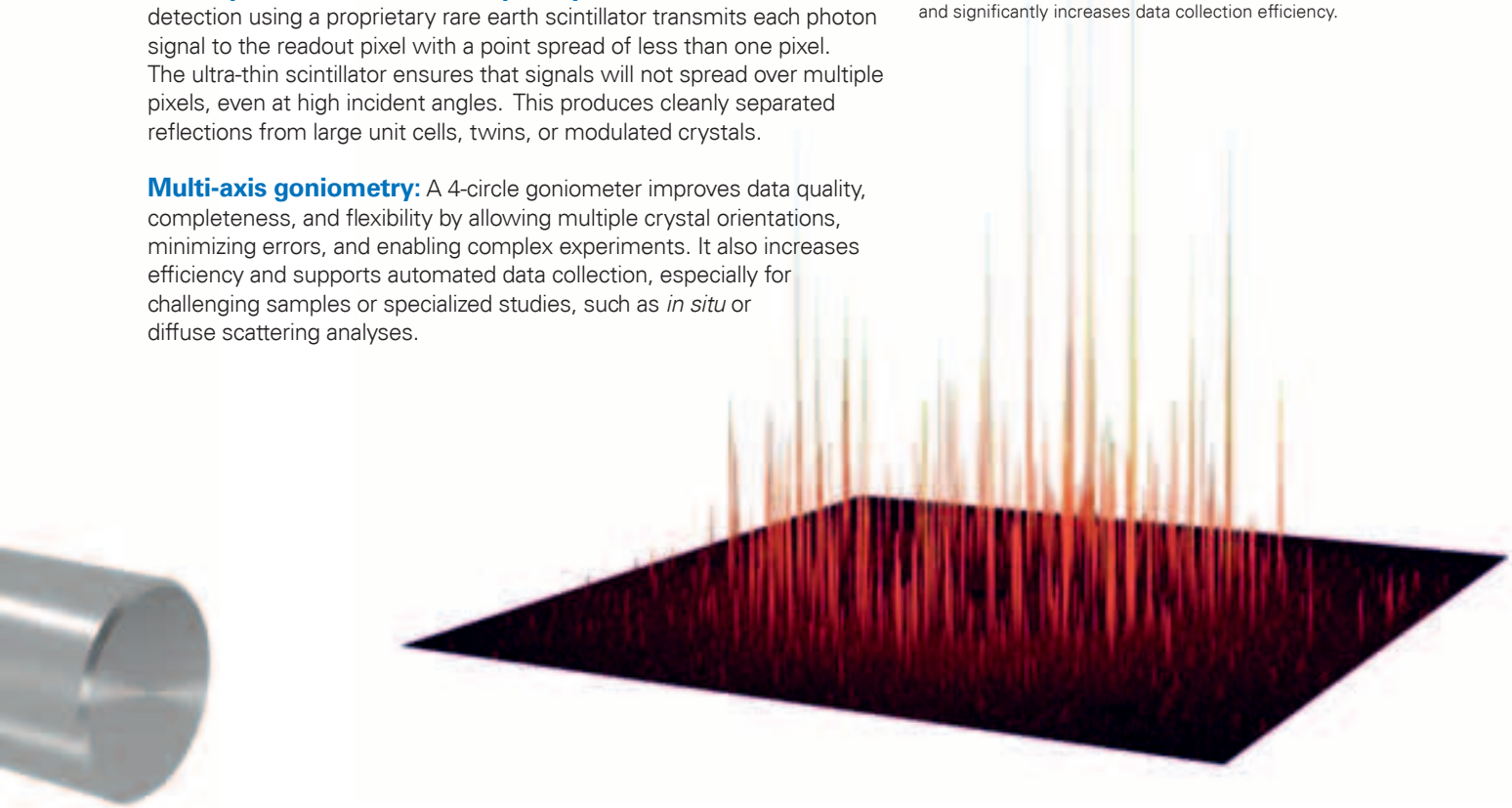
Multi-axis goniometry: A 4-circle goniometer improves data quality, completeness, and flexibility by allowing multiple crystal orientations, minimizing errors, and enabling complex experiments. It also increases efficiency and supports automated data collection, especially for challenging samples or specialized studies, such as *in situ* or diffuse scattering analyses.



Sensitivity and dynamic range

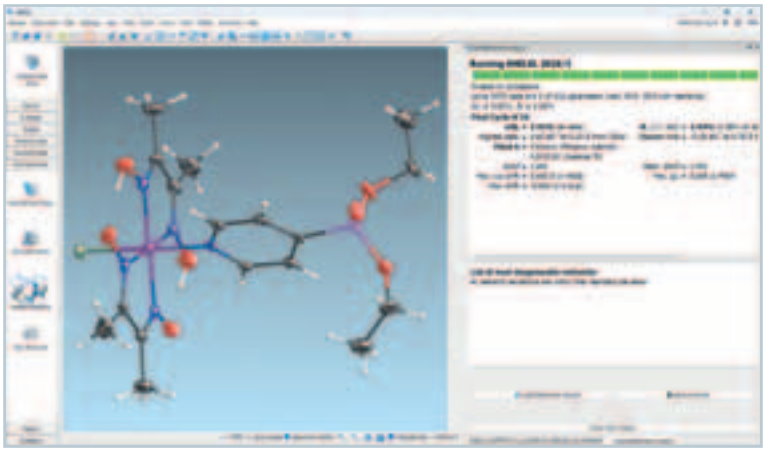
The maximum count rate and dynamic range in CPADs are defined by the image bit depth and the readout rate. The PHOTON IV combines 32 bit image depth with ultra-fast frame rates to achieve count rates more than three times higher than previous generations.

This expanded dynamic range allows for the simultaneous measurement of strong and weak reflections in the same image, eliminating the need for repetitive measurements, and significantly increases data collection efficiency.



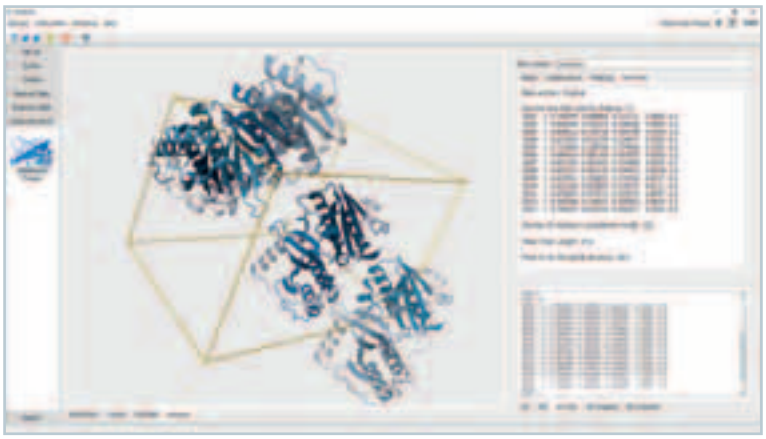
APEX software for advanced crystal structure determination

The APEX software streamlines crystal structure determination. Its modern architecture and multi-core optimization ensure fast processing of complex datasets, including twins and modulated structures. APEX interfaces seamlessly with third-party software, ensuring data integrity and streamlining workflows. Trusted by leading labs, APEX delivers reliable, publication-ready results for the most demanding research environments.



PROTEUM software for macromolecular crystallography

PROTEUM is a user-friendly software suite for protein structure determination, automating processes from crystal screening to structure validation. It features strategy optimization, molecular replacement, and robust data processing using SAINT, DIALS, and XDS. Compatible with CCP4 and Phenix, PROTEUM suits crystallographers at all levels in academia and industry.

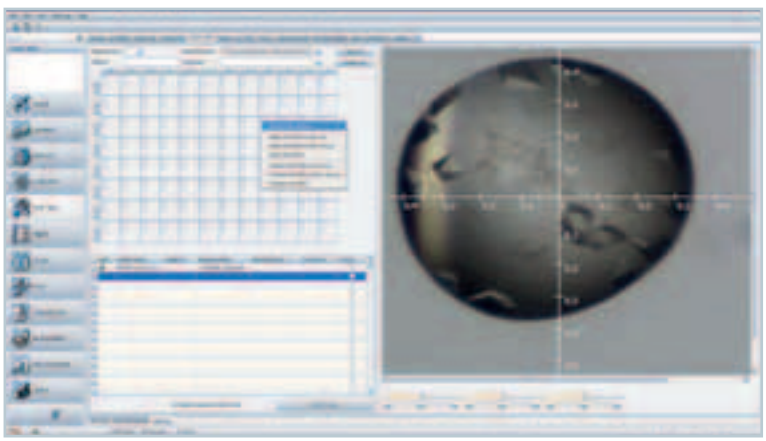


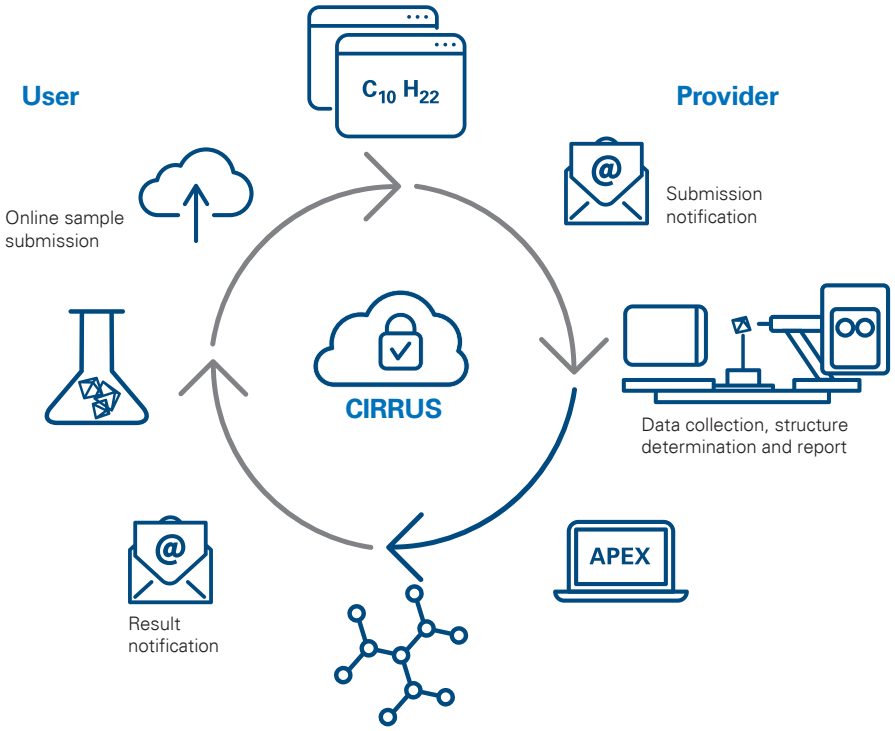
SCOUT software: streamlining SC-XRD sample management

The SCOUT user interface facilitates automated cryogenic sample handling for SC-XRD applications. It integrates robotic control, sample centering, and diffraction-based crystal screening. Users can configure workflows, monitor system status, and export structured reports. SCOUT interfaces with PROTEUM and features access-level customization, enabling reproducible, high-throughput crystallographic data acquisition.

ISX software for *in situ* crystallography

The ISX software enables automated *in situ* crystal screening directly in crystallization plates, preserving crystal integrity by eliminating harvesting and cryo-protection. It integrates optical sample selection, job queuing and automated measurement to streamline crystal identification and characterization. It is ideal for fragment screening, solvent tolerance testing, and room-temperature structure determination.





Crystallographic Software for SC-XRD and Beyond

Focused on users' needs: Developed by world-leading crystallographers, our software offers a robust multi-user environment with site licenses and individual accounts, ensuring flexibility and clarity for diverse laboratory teams. Real-time graphical feedback and progress monitoring provide users with immediate, actionable insights and confidence throughout structure determination.

Integrated data resources and interoperability: Users benefit from instant access to multiple databases covering small molecule, solid-state, and protein crystallography, supporting rapid confirmation and decision-making. Seamless interoperability guarantees accurate data exchange and integration with third-party tools, expanding research possibilities across platforms.

Enhanced safety and sample analysis: Smart Motion Protection continuously monitors the instrument to ensure all-time operational security. Automated twin handling indexes up to eight domains, facilitating deeper insights into complex sample types such as modulated, twinned, or intergrown crystals.

Continuous innovation: Our software undergoes regular updates with multiple annual releases, introducing new features and improvements to keep users at the forefront of crystallographic science and technology.

Empower your crystallography workflow with CIRRUS

CIRRUS revolutionizes crystallography service by streamlining sample management and enhancing user satisfaction. With intuitive digital submission forms and seamless APEX integration, users can submit complete, standardized data effortlessly, minimizing errors and delays. Real-time notifications keep users informed throughout the process, whether they are down the hall or across the globe. CIRRUS ensures secure, GDPR-compliant data handling and provides users with instant access to their submission history and results. By eliminating paperwork and centralizing communication, CIRRUS reduces administrative burden and accelerates turnaround times. The result? A more efficient, transparent, and user-centric experience that fosters trust, boosts productivity, and drives scientific success.

Features and Benefits

	Main characteristics		
D8 VENTURE METALJET System	The D8 VENTURE METALJET delivers synchrotron-level quality structure data from the most demanding crystals directly in your lab, whether they are large chemical frameworks or biological macromolecules. The D8 VENTURE METALJET is your own personal beamline featuring the unsurpassed intensity and small beam of the METALJET MC X-ray source combined with the large area PHOTON IV detector. The D8 VENTURE METALJET offers automated options for *in situ* crystallography and sample handling and pushes the boundaries of research, unlocking new possibilities and expanding research capabilities beyond current limits.		
	Feature		Benefit
METALJET MC Source	Ultra-high intensity beam, radiation [X-ray·s^{-1}·mm^{-2}]	2×10^{12} (Ga K_α)	Fast and reliable in-house source for data even from poor quality, weakly diffracting samples previously accessible only at synchrotrons.
	X-ray energy (wavelength) radiation [keV (Å)]	Ga K_α 9.2 (1341)	
	Beam diameter at crystal [µm]	50 (FWHM)	
	Power [W]	250	
	Cooling	Closed water circuit	
	Multilayer Optics	HELIOS MC, 250 mm confocal, graded, low figure error	
	Maintenance requirements	One scheduled visit per year	Highest intensity combined with low service needs.
PHOTON IV Detector	Photon-counting pixel-array detector	4th generation pixel-array detector technology	Higher speed and sensitivity, best data quality
	Small pixel size [µm^2]	100 × 100	Higher resolution
	Large active area [mm^2]	111 × 145, ~16,000	Faster data collection
	Readout frequency [Hz]	112	
	Count rate [counts·pixel^{-1}·sec^{-1}]	Up to 4×10^6	
	Dead time [sec]	0	
	No dead areas	Single, monolithic silicon sensor	Improved data quality
	No charge-sharing noise	0 electrons charge-sharing noise	
	Parallax [pixel]	< 1	
	Count-rate nonlinearity, before correction [%]	< 1	
	Detector absorption efficiency	Ga > 99%	High Detective Quantum Efficiency (DQE)
	No operating gas or cooling water	Completely sealed design, air cooled	No maintenance, high uptime
	High reliability	3-year warranty	
D8 Goniometer	Sphere of confusion [µm]	< 7	Best data quality
	High speed [deg/min]	Up to 3,000	Faster data collection
	Kappa geometry [deg]	-183 … +183	Highest experimental flexibility
Software	**APEX** for chemical single X-ray diffraction, **PROTEUM** for protein structure determination, **SCOUT** for automated cryogenic sample handling, **ISX** for automated *in situ* crystal screening		

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