SINGLE CRYSTAL X-RAY DIFFRACTION

APEX5

Setting new standards for Crystallographic Software

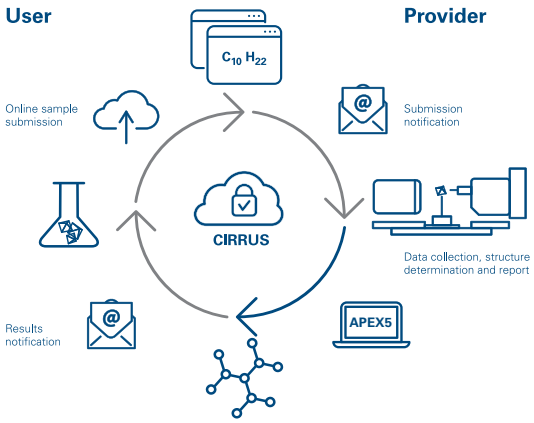
APEX offers an all-encompassing solution for crystallography, from instrument control to refined structure publication. World-class data processing engines are seamlessly integrated with a modern graphical interface providing an intuitive user experience - suitable for both novice and experienced crystallographers. The software is supported by Bruker's dedicated team of specialists, offering hands-on training and assistance when needed.

A Legacy of Experience

With almost three decades of continuous development, testing, and improvements since its initial release, APEX software exemplifies unmatched experience and expertise in the field of crystallography.

The Benefits of APEX5

The APEX5 software suite redefines the standard in single crystal X-ray diffraction, offering unparalleled data acquisition and processing speeds and capabilities, precise structure refinement, and seamless publication.



By Crystallographers, For Crystallographers

Our team of software developers has many expert crystallographers who have meticulously incorporated invaluable customer feedback. APEX5 now boasts numerous new features specially designed to meet the evolving needs of modern crystallography laboratories.

Future-Proof and Performance-Oriented

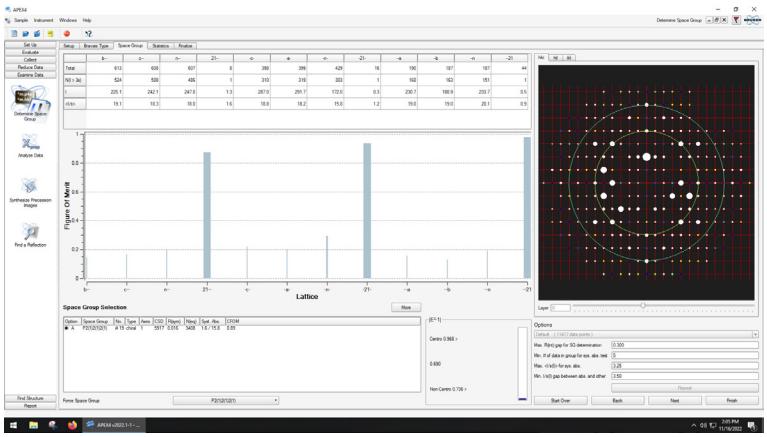
Fully 64-bit compatible, APEX5 leverages all available CPU cores for significantly faster data processing. The software efficiently handles enormous data streams from increasingly rapid data collections, making it futureproof for years to come.

Usability and Performance: A Perfect Pair

APEX5 streamlines the entire experimental process, offering reliable data collection strategy calculations, data integration, scaling, structure solution, model building, and refinement. Its unique path-planning software, based on state-of-the-art robotic trajectory algorithms, optimizes the use of flexible goniometers, maximizing data quality in minimal time.

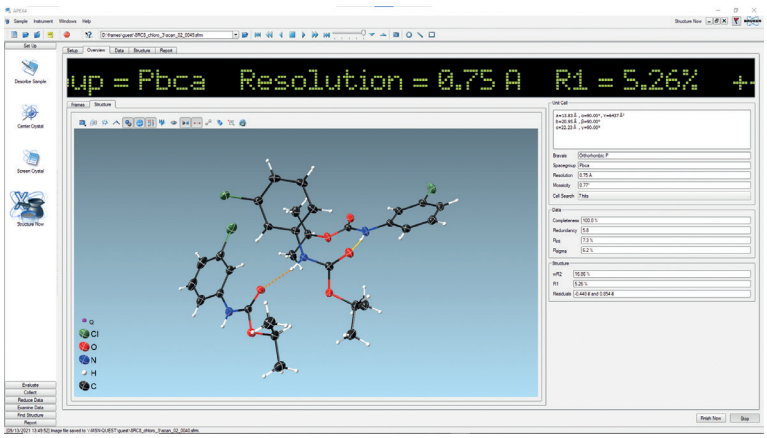
Easier Model Building

Simplify model building and completion with APEX5's outstanding graphical user interface. Whether you're a novice or an expert, building a complete model becomes a breeze. Refinement history allows easy rollback in case of unsuccessful attempts.



Space Group Determination

Rewritten from scratch, a new interface wraps around the famous XPREP engine. For many years the crystallographic community has adored XPREP when space group determination becomes a challenge, standard cases are treated on the fly.



Model Building

A modern approach to interactive model-building for structure refinement is powered by SHELXLE. A creative combination of graphical interface and text-based input with auto-completion makes structure refinement easy. Electron density maps let you look beyond the spherical model and let you capture minute details of your structure.

Integrity Check for Accurate Models

Automatic checks, based on IUCr's checkCIF, ensure the integrity of your refined crystal structure. This approach expedites model building and avoids inconsistencies during the structure determination.

Reciprocal Space Viewer - Unmatched Handling of Challenging Samples

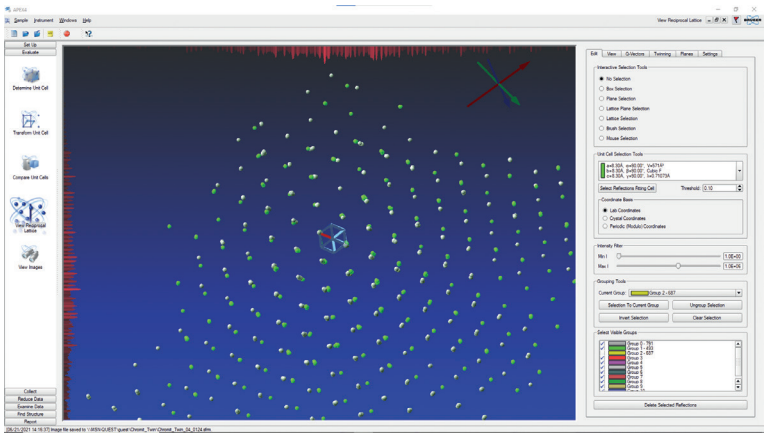
Utilize the reciprocal space viewer within APEX5 to successfully handle difficult--to-index samples. With a proven track record, this tool allows crystallographers of all experience levels to tackle even the most complex problems, including twinned and modulated samples.

STRUCTURE NOW - Automated Structure Determination

Revolutionize your routine structure determinations with STRUCTURE NOW. It offers fully automated structure determination without the need for extensive crystallographic training. Intelligent algorithms enable optimal data collection and processing. It automatically refines the structure, provides molecular graphics, and generates a comprehensive report for publication.

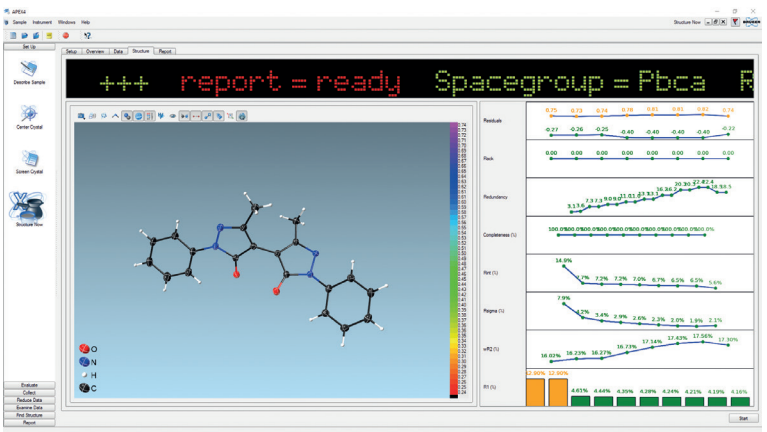
Introducing CIRRUS - Your Gateway to the Cloud

CIRRUS is a new cloud-based sample management workflow for crystallography service providers. It enables you to conveniently manage your users and their requested jobs in one place. This saves time and ensures your information is always accurate and up-to-date. CIRRUS provides your users with standardized templates for sample submission, ensuring you have all the details needed to seamlessly start the measurement in APEX5.



Reciprocal Lattice Viewer

The GPU accelerated plug-in faster and without an upper data limit helps to display and interactively modify reflection arrays. Visually separating twin components and determining q-vectors of incommensurate structures is now faster than ever with many new options. Without a doubt, the reciprocal lattice viewer is one of the most powerful tools for tackling challenging crystallographic problems. The plug-in helps to display and interactively modify reflection arrays. Removing artifacts from strong amorphous scatterers or visually separating twin components and determining q-vectors of incommensurates is easily achieved. The reciprocal lattice viewer is a powerful tool for tackling the most challenging crystallographic problems.



Automated Structure Determination

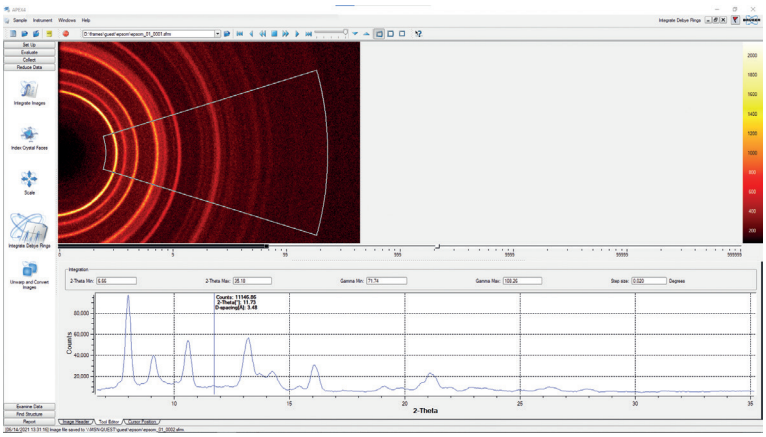
New to crystallography or pressed for time? Just specify the formula, and let STRUCTURE NOW do the rest. The module will automatically determine the quality of your sample and plan the best data collection strategy, process all data, and solve and refine the structure. The module provides molecular graphics and a complete HTML report with all tables and information necessary for publication

Empowering the Crystallographic Community

By being a part of the Bruker Users' Group, APEX5 users gain access to a vibrant global family in crystallography. Exchange insights, receive timely responses, and stay informed on the latest developments within the community.

Designed for the Future

APEX5 continues to evolve, driven by invaluable user suggestions and the collective experience of the scientific community. This forward-thinking approach ensures that APEX5 remains at the forefront of cutting-edge crystallography software.



Powder Diffraction Evaluation
It doesn't always have to be a single crystal. Your single crystal diffraction system is perfectly suited for collecting and processing high-quality powder diffraction data. The plug-in handles diffraction from polymers, fibers, and partially-oriented powders, and provides export to the full suite of Bruker XRD software.

Unlock the potential of APEX5 - Your gateway to enhanced crystallographic research and unparalleled performance.

Bruker AXS
info.baxs@bruker.com

bruker.com

Worldwide offices
bruker.com/baxs-offices

Online information
bruker.com/apex5