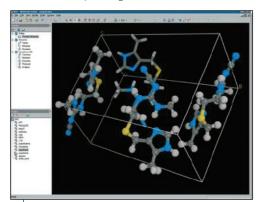# BIOVIA MATERIALS STUDIO REFLEX PLUS
DATASHEET

BIOVIA Materials Studio Reflex Plus is an advanced version of BIOVIA Materials Studio Reflex, adding the extensively validated Powder Solve[1,2] technology to the standard BIOVIA Materials Studio Reflex functionality. BIOVIA Materials Studio Reflex Plus offers a complete package for determining crystal structures from medium-to-high quality powder diffraction data.

The ideal method for solving crystal structures is single-crystal X-ray diffraction. Growing single crystals of appropriate size, however, is often difficult or even impossible, whereas powder samples are readily available for analysis by powder diffractometry.

Despite the problems associated with peak overlap, a high-quality powder diffraction pattern generally contains enough information for unambiguously determining the corresponding crystal structure. A number of techniques are available to index the pattern, which allows cell parameters to derive from the positions of diffraction peaks. Knowledge of systematic absences can help determine the most likely space groups. Taking into account the molecular connectivity and the wellknown geometry of certain molecular fragments, the atomic arrangement in the unit cell can be described by a small number of parameters. It is possible to determine these structural parameters from the intensity distribution of the powder diffraction pattern, although solving crystal structures from powder diffraction data remains a difficult computational problem for more complex crystals.

Figure 1: This structure of the drug cimetidine was determined from its experimental powder diffraction pattern (pictured inside) using the Powder Solve technology.

THE POWDER SOLVE APPROACH

BIOVIA Materials Studio Reflex Plus helps you to solve various problems:

- The BIOVIA Materials Studio Reflex Powder Indexing tools allow you to determine the cell parameters and crystal system by indexing the experimental powder diffraction pattern
- The modified Pawley procedure available in the BIOVIA Materials Studio Reflex Powder Refinement module refines the cell parameters, peak shape, and background arameters, and is a helpful tool for confirming the indexing result and narrowing down the list of possible space groups
- The Powder Solve algorithm performs a search of possible arrangements and conformations of the molecular fragments in the unit cell. It finds a structure for which the simulated powder pattern matches the experimental one as closely as possible and is also chemically viable
- A final refinement of the proposed solution is performed with the rigid-body Rietveld refinement functionality available in BIOVIA Materials Studio Reflex.

POWDER INDEXING

Indexing the experimental powder pattern is often the most challenging step in determining crystal structures from powder diffraction data. Four methods are provided for indexing powder patterns: TREOR90[3], DICVOL91[4], ITO15[5], and X-Cell[6]. It is important to use a high-quality powder pattern. Such a powder pattern typically contains narrow peaks that show little overlap with other peaks, making it easy to identify each peak's 2θ position. Once the cell parameters and lattice class have been determined, systematic absences can be used to limit the number of possible space groups.

While synchrotron sources usually provide powder patterns that are more easily indexed, high-quality laboratory powder diffraction data can also be used with success. The higher the quality of your powder pattern, the more detailed information it contains, and subsequently the greater your chance of success.

PAWLEY REFINEMENT

Once indexing is complete, a list of possible space groups must be established based on chirality, density, and consideration of systematic absences. The Pawley refinement functionality helps confirm the indexing result and explore the effect of systematic absences, aiding in the determination of the possible space groups. In Pawley refinement, various parameters are adjusted to minimize the weighted R-factor, Rwp, that describes the agreement between the experimental powder diffraction pattern and a simulated one.

Peak intensities are treated as independent parameters. In addition, a wide range of variables can be refined, such as the unit cell, the background, a choice of peak profile and asymmetry functions, crystallite size, lattice strain, and the zero point shift of the diffraction pattern. By repeating the Pawley refinement in different space groups, the effect of systematic absences on the simulated powder diffraction pattern is readily visualized. The refinement is based on a modified Pawley[1,6] procedure that consists of two steps. In step one, the integrated intensities and background coefficients are optimized while the peak shape, cell parameters, and zero-point shift are fixed. In step two, the opposite takes place, with all parameters being optimized except for the intensities and background coefficients. This two-step process is continued until convergence is achieved.

POWDER SOLVE

The next step for structure determination involves Powder Solve; an indirect method that employs a Monte Carlo simulated annealing or parallel tempering algorithms. Before starting Powder Solve, the user must define each torsional degree of freedom to be explored during the simulation. One degree of

freedom in the system, i.e., translational, rotational, or torsional, is modified by a random amount during each simulated annealing step, after which a powder pattern is calculated. This simulated pattern is then compared to the experimental powder pattern using Rwp as a measure of similarity.

Optionally, Powder Solve allows to apply a close contact penalty function during structure determination. This option is particularly useful when working with low-quality powder data, as it will ensure that Powder Solve finds chemically feasible solutions, without bad contacts between structural fragments. When a promising structure is found Powder Solve performs a rigid-body Rietveld refinement with respect to the parameter space to locate the local minimum. The iterative process of modifying one degree of freedom and comparing powder patterns continues in order to minimize Rwp. Structures with low Rwp values are automatically saved to trajectory files. Multiple cycles to determine the structure are performed in order to confirm the final solution. A wide range of compounds have been successfully examined using this methodology, including solvates, salts, and flexible molecules.
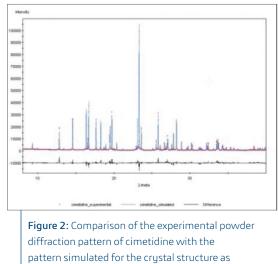
RIETVELD REFINEMENT

The final step for structure determination is Rietveld refinement[8,9] where users can refine candidate crystal structures obtained from Powder Solve against experimental powder diffraction data by minimizing the weighted R-factor, Rwp. Flexibility is provided through the wide range of refinement parameters available -unit cell, atomic, peak profile and asymmetry, crystallite size and strain broadening, preferred orientation, background, zero-point shift, intensities. Rietveld refinement with energies incorporates an accurate description of potential

energy in conjunction with Rwp during a Rietveld refinement process optimizing a combined figure of merit so that not only the simulated pattern of the resulting structure matches the experimental diffraction data, but also the potential energy of the structure is close to a global minimum. Pareto optimization10 can be used to calculate a set of possible optimal refinement solutions automatically as a sequence of Rietveld refinement with energies calculations with changing energy weights. Pareto optimization for a structure solution represents a trade-off to provide best possible Rwp(min) and energy(min) compromises.

THE BIOVIA MATERIALS STUDIO ADVANTAGE

BIOVIA Materials Studio Reflex Plus is a operated within the BIOVIA Materials Studio® environment, allowing for a high degree of interactivity with other BIOVIA Materials Studio products and Windows® applications. The molecules or molecular fragments used in the structure search can be easily constructed using BIOVIA Materials Studio sketching and molecular mechanics tools, or by being imported from other sources.

Results obtained by indexing, Pawley refinement, structure solution, and Rietveld refinement are readily passed on between the different modules involved in the structure determination procedure. A powerful rigid body Rietveld refinement program is available to carry out the final structure refinement. Crystal structures are readily visualized using BIOVIA Materials Studio Visualizer.

Figure 2: Comparison of the experimental powder diffraction pattern of cimetidine with the pattern simulated for the crystal structure as determined by BIOVIA Materials Studio Reflex Plus.

Finally, results can easily be shared with colleagues and copied and pasted to standard word processors, spreadsheets, and presentation packages.

FEATURES

General

- BIOVIA Materials Studio Reflex Plus is a complete package for structure determination from powder diffraction data, covering indexing, Pawley refinement, structure solution, and Rietveld refinement
- Reads in a variety of diffractometer file formats including Bruker, Stoe, Scintag, Jade, Philips, JCAMP, Galactic SPC, GSAS raw, ILL, PAnalytical XRDML
- Allows for different X-ray sources with multiple wavelengths and user-defined polarization
- Suitable for X-ray, neutron, and electron diffraction.

- Can handle any possible space group, both standard and nonstandard settings, accounting for systematic absences
- Benefits from straightforward interaction with other BIOVIA Materials Studio products as well as other PC applications
- Pawley refinement and Rietveld refinement jobs can be submitted to remote server machines in addition to synchronous execution on local client
- Powerful but easy to use; intuitive definition of degrees of freedom

POWDER SOLVE

- Final parameters from Pawley refinement are automatically transferred to Powder Solve
- Choice of two global search algorithms, MC simulated annealing and MC parallel tempering
- Close contact penalty function ensures chemically viable solutions
- Automated tool to estimate the appropriate number of steps for each structure solution problem
- Determination of preferred orientation correction during structure solution search
- Automatic setting of all simulation parameters.
- Multiple structure solution cycles can be performed to confirm results
- As structures produce lower Rwp values, they are saved to a trajectory file
- Automatic rigid body Rietveld refinement of promising structures during structure solution search
- Extensive analysis tools to examine results from single or multiple structure solution cycles
- Proposed solution can be further refined with the rigid body Rietveld Refinement tool
- Works with good quality lab data as well as synchroton data
- Based on full profile comparison - moderate peak overlap not a problem
- Well validated for complex compounds, including solvates, salts, and flexible molecules
- Works for organics and inorganics
- Client-server architecture allows calculations to run on powerful servers, while analysis is performed

To learn more about BIOVIA Materials Studio, go to **accelrys.com/materials-studio**

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