

study table. It is here that your molecules are united with their properties. Descriptors provide an all-round quality set of physicochemical properties which, when interfaced with the unique genetic function approximation, give you unrivalled capabilities to calculate your QSAR. Combined with the integrated presentation and data organization and analysis capabilities, QSAR is the tool of choice for materials discovery.

The Materials Studio Advantage

QSAR is operated from within the Materials Studio® software environment. Materials Studio provides a user-friendly interface, complying with Windows® standards.

QSAR at glance

- **Study table** - provides the heart of your QSAR calculations, enabling cut/copy/paste/sorting, function definition, storing of links to structures, and flexible cell coloration
 - **Data structure import** - users can import sets of materials and associated experimental data from industry standard molecular structures and data files
 - **Molecule viewing capabilities** - users have the power of MS Modeling at their fingertips to draw, manipulate, and display their materials
 - **Descriptors** - QSAR users may select from the following sets of build-in descriptors:
 - Atomistic (charges, atoms counts etc.)
 - Spatial (molecular mass, volume, surface area etc.)
 - Other descriptors (fragments counts, crystal cell dimensions, polymorph etc.)
 - Fast descriptors provide an extensive list of topological thermodynamic, information content, e-state and structural properties, including the Jurs descriptors
 - VAMP, the semi-empirical quantum mechanics engine, provides energy, orbitals (HOMO/LUMO), multipoles etc.
- Additionally, the following descriptors can be licensed:
- Forcite, allows the use of the molecular mechanics/dynamics engine and allow access to energetics (total, non-bond, and optimized structure)

- DMol³ Descriptors allow the calculation of accurate electronic energies and atomistic properties such as susceptibility to nucleophilic attack using the DMol³ quantum mechanical module.
- **Initial Data Analysis** - this unites a series of techniques to spot patterns in your data. Methods include: univariate analysis, data standardization, data transformation, correlation matrix, graphical analysis, principal components analysis, and cluster analysis and validation
- **Model Building** - here the calculation engine builds your QSAR relation. Users can choose from standard techniques such as multiple linear regression, partial least squares, or use the unique genetic function approximation.
- **Model Validation** - here you decide whether the model you have built describes your data well. In addition to each model builder's own validation, cross-validation, ANOVA and graphical validation (predicted vs. observed) is provided.
- **Model Management** - allows users to apply, import, export (xml format), copy or delete models. This also allows user to run their model when they want. Exporting models allows you to share your models with other MS Modeling users.
- **Data Fragmentation/Subsetting** - your data table can be sorted and filtered to allow you to find groups of molecules.
- **Candidate Generation** - candidate molecules can be drawn or sets of molecules from industry standard molecular structures files can be imported.
- **Project Management** - you can save your projects at any time, allowing you to share your work with colleagues. It includes structures, models, and tables.



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