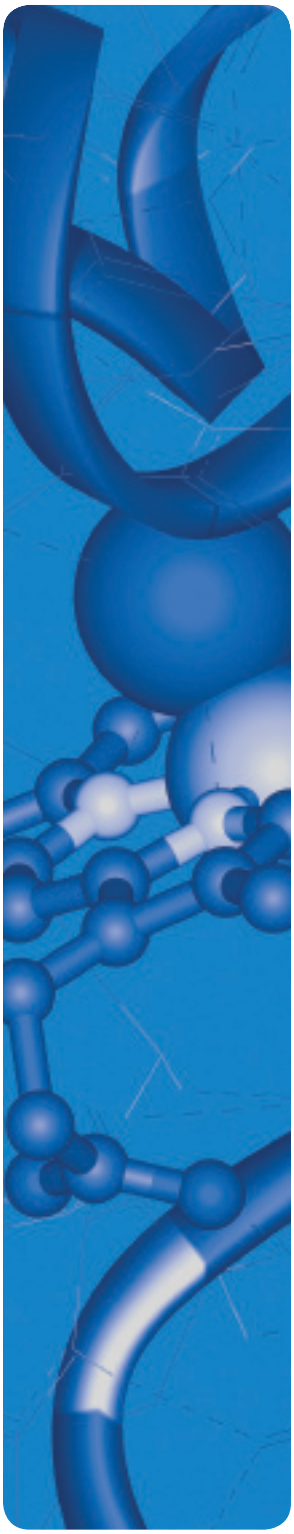
accelrys®

# Discovery Studio

## Life Science Modeling and Simulations



Discovery Studio® is a Linux®- and Windows®-based modeling and simulation environment for protein modeling and computational chemistry. From project conception to lead optimization, you'll enjoy access to best-of-breed software from a single, easy-to-use interface. Streamline your workflow by tailoring the Discovery Studio environment to your unique needs. Customize the interface to a preferred layout and modify default settings (e.g., define PDB download location) and your unique setup will persist for each session.

Discovery Studio simplifies team communication by providing functionality for customizing and sharing protocols and enabling the use of different data formats. If you or your colleagues rely on software from in-house developers or other vendors, Accelrys can integrate it into the environment because Discovery Studio is built upon the open SciTegic® Enterprise Server platform.

Functionality in Discovery Studio can be loosely grouped into the following categories: Visualization, Protein Modeling, Simulations, Analysis, and Receptor-Ligand Interactions.

### *Visualization*

| Product | Description |
|---|---|
| Discovery Studio (DS) Visualizer Pro | Visualize, analyze and share biological and chemical data via this single interface to software within the Discovery Studio environment. DS Visualizer Pro itself also provides functionality for sketching 3D molecules, visualizing dynamic changes, exploring how changes in amino acid sequence impact 3D structure, and predicting how ligands interact with a protein target. Plot molecular data information and access several data views (sequence, hierarchy, X-ray reflection, data table and table browser for MDL sd files), as well as several explorer views for jobs, files, protocols, and parameter help. |
| DS Visualizer *(free)* | View and share protein and modeling data in a clear and consistent way, and in a wide variety of industry-standard formats. This *free*, easy-to-use visualization tool is an ideal solution for managers and researchers (e.g. experimentalists) who need to collaborate with modelers, but do not need access to the expert-level analysis tools in Discovery Studio. With DS Visualizer, you can access several data views (3D model, sequence, tabular, hierarchy, electron density), as well as functionality for sketching molecules and catalyst pharmacophores and performing simple calculations, such as RMSD determination, solvent accessible surface prediction, and secondary structure prediction. |

### *Protein Modeling*

| Product | Description |
|---|---|
| MODELER | Automatically and rapidly generate a refined homology model of a protein, given only the sequence alignment to a known 3D protein structure, with this industry-standard for fast homology modeling. MODELER is the ideal solution for target discovery and for studying the structure and function of proteins across families. With MODELER, you can build protein mutants, perform loop modeling and structure-based alignments, and build models with ligands bound. Gain even further insight into protein structure and function by using MODELER in combination with Discovery Studio software for simulations and structure-based design. |

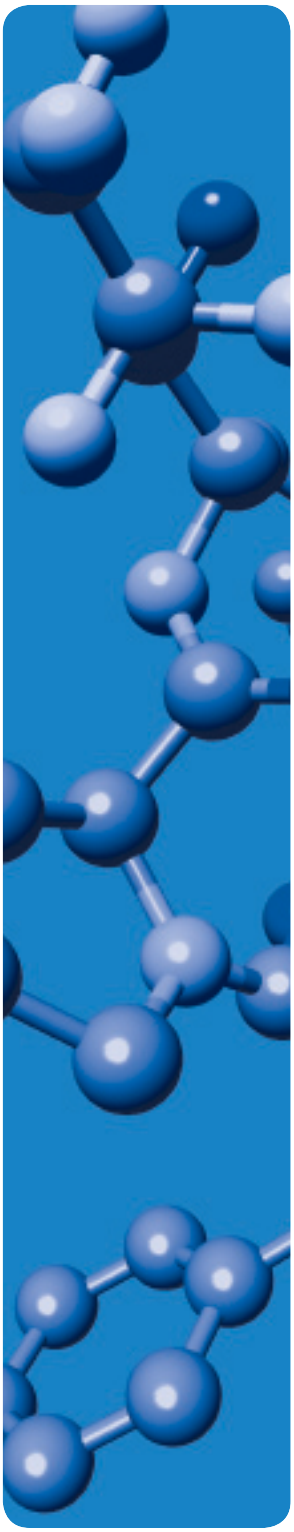
DISCOVERY STUDIO

## *Protein Modeling (Continued)*

| Product | Description |
|---|---|
| Protein Families | Gain a better understanding of the mechanism of protein function at the molecular level by analyzing the sequence conservation patterns within a family of protein sequences, as well as the position of those conserved residues on the 3D structure. Get started with your analysis quickly by taking advantage of Protein Families' easy-to-use protocols that step you through aligning a family of proteins based on sequence or structure, as well its tools for performing Evolutionary Trace analysis, which involves creation of a protein family dendrogram using the hierarchical clustering method and mapping of the information onto your 3D structure. |
| Protein Similarity Search | Take the first steps toward identifying a protein's biological function by comparing its sequence to the sequences of other known proteins. Protein Similarity Search allows you to use the popular BLAST and PSI-BLAST algorithms to identify homologs for your protein sequences by searching databases that are either installed locally or available over the internet at NCBI. Results are presented in an interactive report format that facilitates further analysis and manipulation with other Discovery Studio software. |

## *Simulations*

| Product | Description |
|---|---|
| CHARMm® | Study the energetics and motion of molecules—from small ligands to multi-component physiological complexes—with this industry-standard program for molecular mechanics and dynamics. Based on the Chemistry at Harvard Macromolecular Mechanics simulation engine, CHARMm is regularly updated to include the latest functionality developed within the scientific community. Additionally, because CHARMm is available from the same interface as Discovery Studio structure-based design tools, it is easy to perform protein-ligand calculations and analyses. You can also access the CHARMm scripting language for a greater degree of flexibility. CHARMm comes with a stand-alone typing tool that you can use in batch mode to type a library of compounds using the CHARMm forcefield and automatic parameter estimation.<br><br>Grid-based ligand docking with soft-core potentials (CDOCKER) is now available in the Discovery Studio environment. |
| CHARMm Lite | Obtain more accurate scoring and prioritization of ligands based on predicted receptor affinities using CHARMm Lite. CHARMm Lite performs *in situ* ligand minimization using the well-validated CHARMm and CFF forcefields and several minimization algorithms. It is scalable for high throughput analysis of large numbers of ligands; all jobs can be run in parallel and in background mode. |
| CFF Advanced Class II Forcefield | Optimize DNA, RNA, carbohydrates, lipids, proteins, peptides, and small-molecule models, and get a high confidence level for calculations. The forcefield parameters in CFF (Consistent Forcefield) were developed by computing the properties of 1,768 different molecules spanning 19,432 molecular structures, resulting in a robust and diverse collection of parameters applicable to most biomolecules and small molecules. |



## *Analysis*

| Product | Description |
|---|---|
| Biopolymer | Simplify model building and electrostatics analysis with Biopolymer. Biopolymer provides access to easy-to-use tools for building and modifying proteins and peptides, cleaning and splitting proteins into separate components, quickly generating property analysis reports for peptides and proteins, and calculating electrostatic potentials and solvation energies of both large and small molecules using Poisson-Boltzmann electrostatics (formerly available in DelPhi). Models of small molecules and macromolecules created with Biopolymer can subsequently be used in other Discovery Studio programs for additional analysis. With Biopolymer, you can now also build protein models (with X-BUILD technology) and fit ligands (with X-LIGAND technology) into X-ray electron density maps. |
| Analysis | Gain new insight into molecular processes by using Analysis to animate, graph, and tabulate molecular dynamics trajectories of proteins and protein-ligand complexes. Analysis is the ideal solution for helping you better understand the interplay between molecular conformation and energies in enzyme mechanisms, receptor activation, cell signaling, and signal transduction. |
| Protein Health | Access the validity of a protein structure (or part of the structure) derived from modeling studies or experimental data. Protein Health uses a method called Profiles-3D Verify to evaluate the protein structure by comparing its structural environments with the preferred environments of amino acids. Misfolded protein segments within a protein structure can be identified by this method, indicating where additional consideration should be given to structural packing. |

## *Receptor-Ligand Interactions*

In addition to the following products, an interface to GOLD—a genetic algorithm-based docking program from the Cambridge Crystallographic Data Centre—is now available from the Discovery Studio environment. A separate license for GOLD is required.

| Product | Description |
|---|---|
| LigandFit | Gain direct insight into the complementary features of ligands and their potential as lead candidates. LigandFit lets you easily dock ligands into a binding site of a macromolecular target receptor using protocols that are based on the SciTegic Enterprise Server platform. Parameters are customizable, and your settings can be saved and shared with other users. LigandFit can also be parallelized using job clustering for virtual high-throughput screening. |
| LigandFit/CAP | Avoid the frustration of having 2D compound data from commercial libraries, but needing 3D data for your ligand docking experiments. With LigandFit/CAP, you have access to a comprehensive library of ligands in 3D representation that have been prepared from the Chemicals Available for Purchase (CAP) and CAPScreening databases. |

## *Receptor-Ligand Interactions (Continued)*

| Product | Description |
|---|---|
| LigandScore | Evaluate ligand-protein interactions with well-validated and trained scoring functions and their individual descriptors. Insight gained with LigandFit will help you identify potential problems in a binding mode hypothesis, discriminate between correct and incorrect poses from docking, and prioritize posed ligands for downstream efforts such as screening or synthesis. Parameters are customizable and your settings can be saved and shared with other users. LigandScore can also be parallelized using job clustering for virtual high-throughput screening. |
| Ludi | Save time in your search for new and potentially-improved ligands with Ludi, a *de novo* ligand design program that provides a starting point for your next experiment. Ludi's robust set of design tools allows you to simulate screening before performing experimental assays, explore libraries of commercially-available ligand scaffolds, and change existing ligands by scoring candidate derivatives in the receptor binding site. Ludi is easy to use, while still providing the ability to customize parameters and save preferred settings for sharing with other users. It contains a library of drug-like fragments, but also gives the ability to add custom fragments. |
| Ludi/CAP | Accelerate your search for drug candidates with quick access to commercially-available structures that can be acquired immediately for further development. Ludi/CAP provides access to Chemicals Available for Purchase (CAP), a structural database of commercially available compounds, and CAPScreening, a database of compounds available from suppliers of screening libraries. Focus results by filtering out redundant hits and restricting searches. Known compounds retrieved from Ludi/CAP can be used as bases for generating ideas for the synthesis of novel compounds. |

For more information on Discovery Studio, visit **www.accelrys.com/products/dstudio** or contact your local sales representative.

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