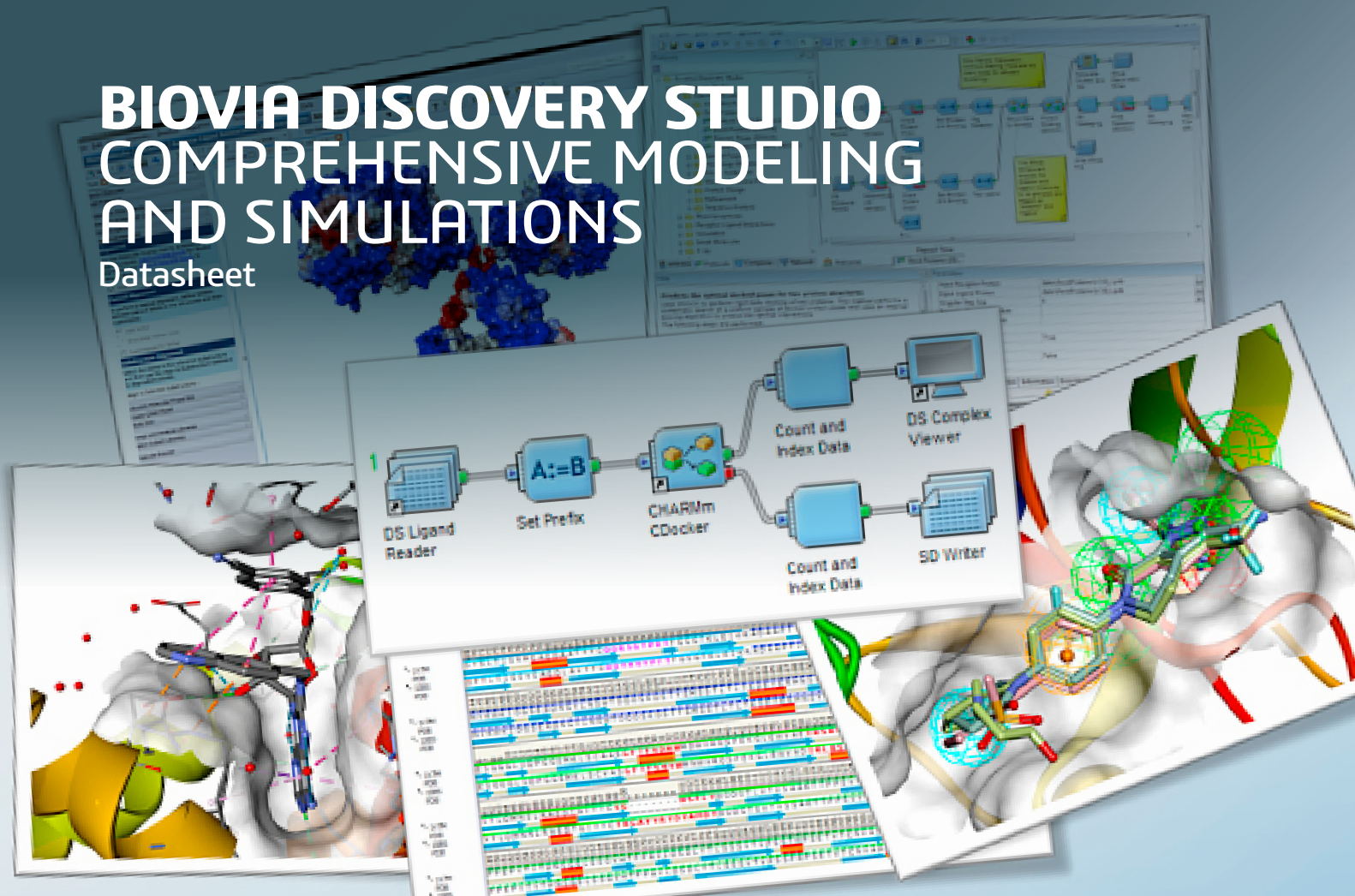


BIOVIA DISCOVERY STUDIO COMPREHENSIVE MODELING AND SIMULATIONS

Datasheet



A SUITE OF VALIDATED SCIENCE TECHNOLOGIES

Drug discovery is a multi-objective optimization. Scientists have to optimize both biochemical potency and at the same time, optimize other characteristics such as ADME and toxicity. Built on BIOVIA Pipeline Pilot and utilizing gold-standard applications backed by years of peer-reviewed research (e.g., **CHARMm**, **MODELER**, **ZDock**, **Delphi**, **Catalyst**, **DMol³**, **Vamp**, **TopKat**, **AggMap** and **Developability Index**), BIOVIA Discovery Studio® software is the most comprehensive, scalable, collaborative research environment for Life Sciences discovery research.

BIOVIA DISCOVERY STUDIO

BIOVIA Discovery Studio is a comprehensive suite of validated science applications built on **BIOVIA Pipeline Pilot**. The software delivers a unique blend of open, scalable, collaborative research tools designed for today's Life Sciences discovery research needs.

Comprehensive science portfolio

- Science solutions address research needs from early stage discovery through to preclinical and biotherapeutic formulations development

Mature science

- The core science underpinning Discovery Studio is backed by up to 30 years of peer-reviewed research

Collaborative research

- With DS Visualizer, Discovery Studio offers a genuinely free visualization and collaboration framework

Discovery Studio: A native Pipeline Pilot-based application

- Every Discovery Studio task is a Pipeline Pilot protocol ensuring a truly open modeling and simulation environment
 - Customizable, extensible science
 - Scalable architecture
 - Deployable workflows
 - Enables scientific innovation
- Out of the box integration with third party applications, including CCDC **GOLD*** and University of Illinois at Urbana-Champaign **NAMD†**
- Discovery Studio sub-licenses the following Pipeline Pilot component collections: Core, Integration, Reporting, Chemistry, Sequence Analysis, ADMET

COMPREHENSIVE PREDICTIVE SCIENCE SUITE

Simulations:

- Best-in-class simulations based on **BIOVIA CHARMM® forcefield engine**, including single point, minimization, Molecular Dynamics simulations and Free energy calculations
- Full ab initio DFT-based Quantum Mechanics with **DMol³**, semi empirical (**VAMP**) and hybrid QM/MM (**DMol³/CHARMM**)

Macromolecule Design and Analysis:

- Market leading **MODELER** homology modeling algorithm
- Best-in-class pH-based protein ionization tools
- Unique pH-based protein stability and binding affinity mutation analysis
- Reliable protein-protein binding prediction with **ZDOCK**

Antibody Development

- The first and most complete set of structure prediction and simulation tools specifically for antibody research
- Proven automated structure prediction workflows designed to deliver best in class antibody homology models
- Unique patented **AggMap** protein aggregation and **Developability Index**
- Rapidly identify sequence motifs associated with post-translational modification (PTM) sites in biotherapeutics

Structure-based design (SBD)

- Novel physics-based (**CHARMm CDOCKER**) docking engine
- Unique set of non-bond analysis monitors that include favourable, unfavourable and unsatisfied interaction types
- Novel MMP-based Activity Cliffs

Fragment-based design (FBD)

- Use classical Medicinal Chemistry reactions to enumerate *in situ*, using *ca.* 10k pre-filtered reagents from **BIOVIA ACD**
- Scaffold hop *in situ* using *ca.* 1.5M commercially available compounds from **BIOVIA SCD**
- Novel Karplus **MCSS** (Multiple Copy Simultaneous Search) fragment docking engine

Pharmacophore and Ligand-based design:

- Market leading **CATALYST** pharmacophore engine
- Includes unique receptor-ligand pharmacophore creation
- The largest validated ligand profiling database, **PharmaDB**

QSAR, ADMET and TOPKAT Predictive Toxicology

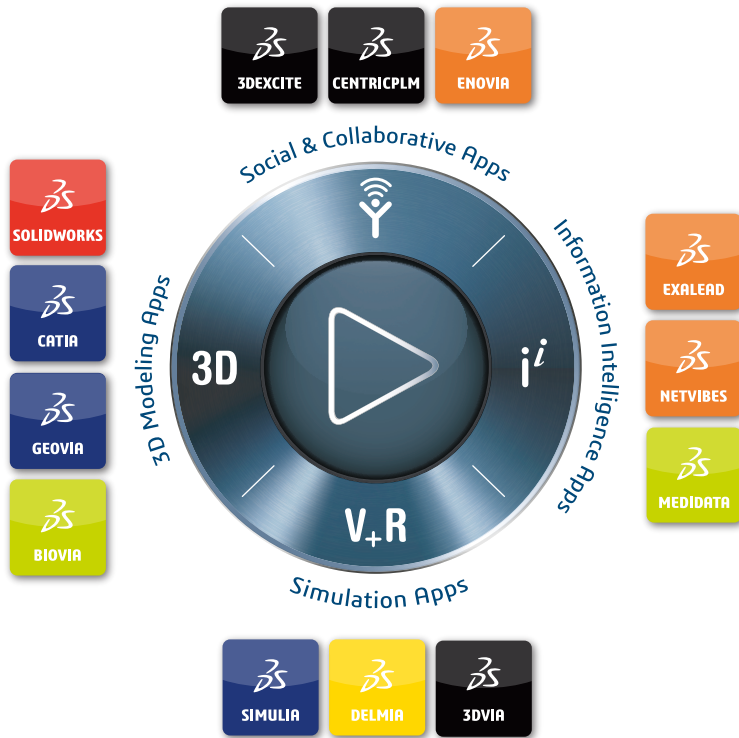
- QSAR: Calculate physicochemical, topological fingerprint properties and create PLS, GFA, MLR and more
- Most extensive set of ADMET and predictive toxicology models, including BBB penetration, Hepatotoxicity, CYP2D6, AMES, Rat Oral LD50 and many more

X-ray

- Using **CNX**, generate electron density maps, perform full refinements and use **HT-X PIPE** to run automated structure determination of protein-ligand complexes

To learn more about BIOVIA Discovery Studio, go to:

3ds.com/biovia



Our 3DEXPERIENCE® platform powers our brand applications, serving 11 industries, and provides a rich portfolio of industry solution experiences.

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