Schrödinger Software Release 2015-2 Documentation

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- Induced Fit Docking
- Field-Based QSAR
- Ligand and Structure-Based Descriptors
- Physics-Based ADME/Tox
- QM-Polarized Ligand Docking
- Semiempirical NDDO Guide
- Virtual Screening Workflow

Quick Reference

- Cluster Setup for Schrödinger Jobs
- Glide Docking
- Ligand Preparation
- Job Options Supported, by Product
- Phase Command-Line Database Tasks
- Phase Command-Line Pharmacophore Modeling
- Phase Pharmacophore Modeling in Maestro
- Preparing a Library of Compounds for Glide or Phase
- Protein Preparation
- QikProp Descriptors and Properties
- Recommended Settings for Jaguar
- Running Distributed Schrödinger Jobs
- Schrödinger Product Installation on Linux
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- Schrödinger Utilities
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- Job Control Guide
- Multiple Sequence Viewer
- Protein Preparation Guide
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- Python Pipeline Manual

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- BioLuminate User Manual
- BioLuminate Quick Start Guide

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- · Canvas Python API

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- Desmond Quick Start Guide
- Desmond User's Guide (from D. E. Shaw Research)
- Desmond Tutorial (from D. E. Shaw Research)
- Desmond/GPU for Desmond 2.0 Users (from D. E. Shaw Research)

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- Maestro Elements Tutorial: Visualization
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• Materials Science Suite User Manual

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- Phase Quick Start Guide
- Phase Command Line Tutorial: Developing Pharmacophore Models
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