The Schrödinger KNIME extensions

Computational Chemistry and Cheminformatics in a workflow environment

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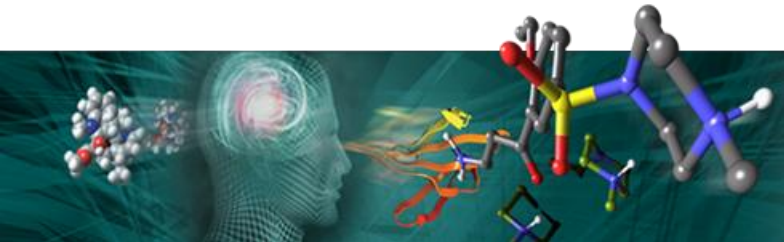

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What are the Schrödinger extensions?

- **Modelling and computational chemistry**
- **150+ nodes**
  Linux and Windows 32 and 64 bit

Molecular Mechanics – Macromodel
Molecular Dynamics – Desmond
Quantum Mechanics – Jaguar

Cheminformatics – Canvas
Pharmacophore modeling – Phase
Combinatorial Libraries – Combiglide

Docking – Glide
Protein Structure Prediction – Prime, IFD

Protein preparation
Ligand preparation – LigPrep, Epik
Property generation – Qikprop ...
Filtering

Tools for data and structure manipulation
Scripting – shell, Python
Reporting

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KNIME workflow page- http://www.schrodinger.com/knimeworkflows/

Cheminformatics
- Substructure Search
- Clustering, diversity selection, similarity search
- Database analysis , MCS

Docking and post-processing
- Protein preparation and Glide grid generation
- Docking and scoring, Virtual screening, Ensemble docking
- Loop over docking parameters
- Validate docking parameters

Pharmacophore modeling
- Phase Shape screening
- Phase hypothesis identification
- Phase database screening ◄

Molecular Mechanics
- Compare conformational search methods

Quantum mechanics
- Conformational search and QM optimization

(using the Report designer)

Library design
- Library enumeration

Homology modeling
- Model building and refinement
- Induced Fit Docking

Real World Examples
- Vendor database preparation

Metanodes
- Run Maestro 1:1
- SiteMap

General tools
- Python script node use-cases

including a Run PyMOL prototype
- Chemistry external tool node use-cases
- Run maestro command node use-cases
- Output column structure option philosophy

KNIME workbench
- Workflows in the current workspace
- GroupBy Use-cases

KNIME workbench- looper
- Group Looper, Unpivot

Simplest, **most exciting**, **new** and improved ◄ workflows

New features

- **Infrastructure**
  - **Mac** port
  - Ease of use: new **start-up script options** (including one to run stand-alone KNIME installation)

    improved console log, faster start-up

- **KNIME menu in Maestro**
  - **Connect to KNIME** mode to exchange structures with a KNIME session
  - Build, import, edit and **run workflows from Maestro** on project table data. Dynamically generated GUI to alter some parameters.

    Disconnected calculations and progress tracking in Jobcontrol.

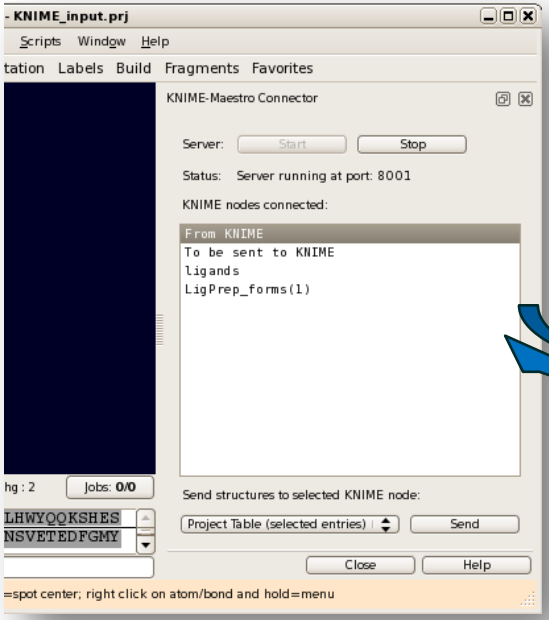
    Workflow tools and examples available on the Workflow web page:
    - Protein RMSD matrix, PDB list preparation, Align multimer chains
    - Internal similarity, Vendor database filtering
    - ...

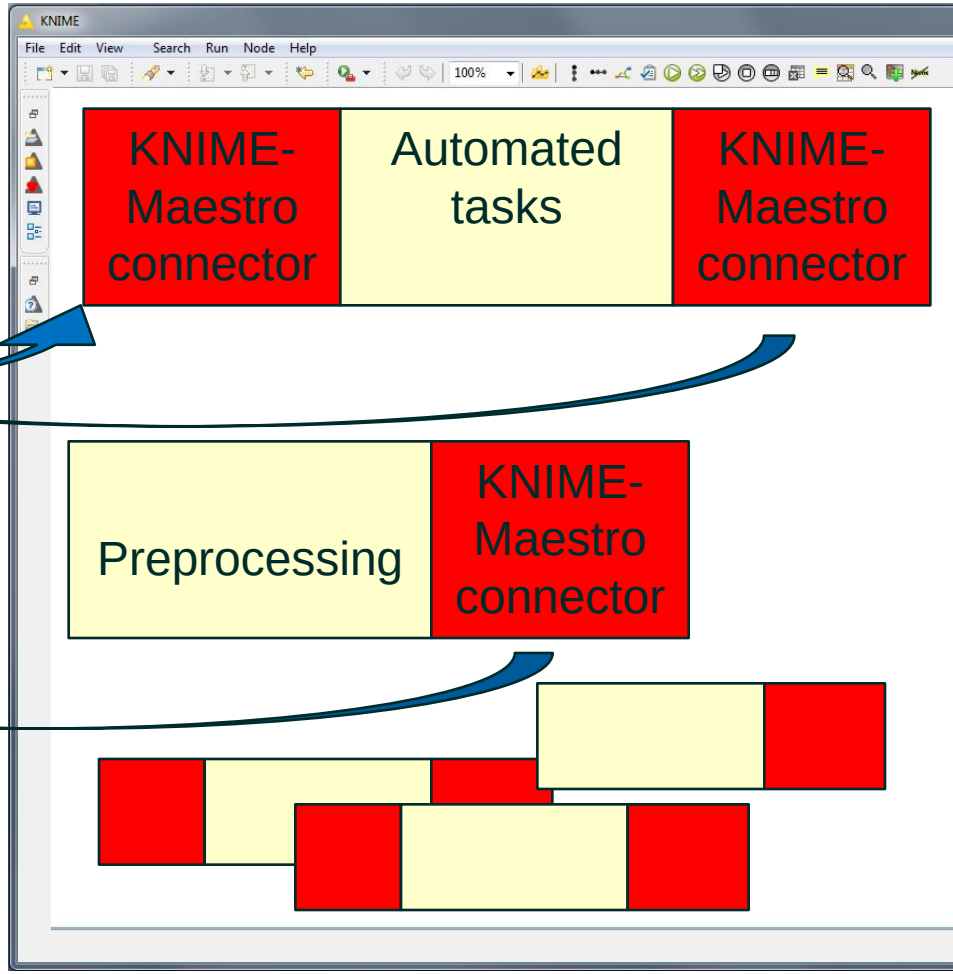
KNIME – Maestro connection

Maestro
Visual inspection, selections ...

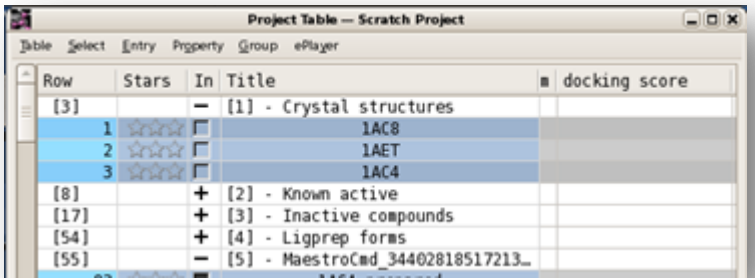
Server

KNIME
used interactively





Project table
Store the results



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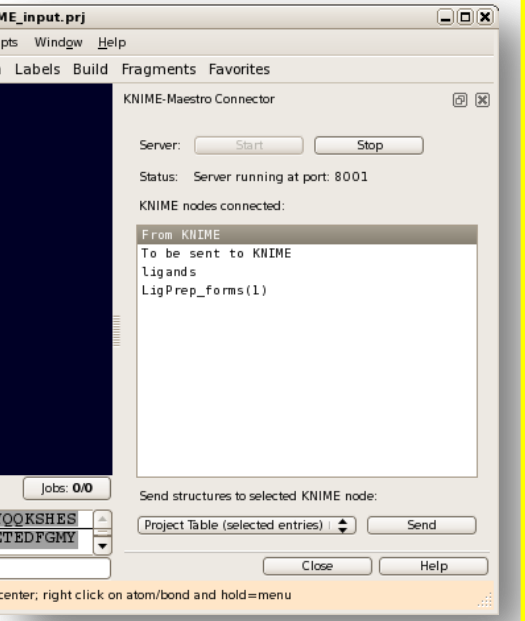
KNIME – Maestro connection

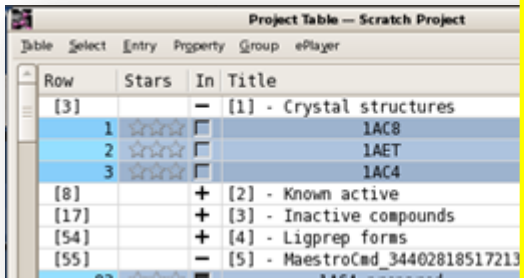
Maestro

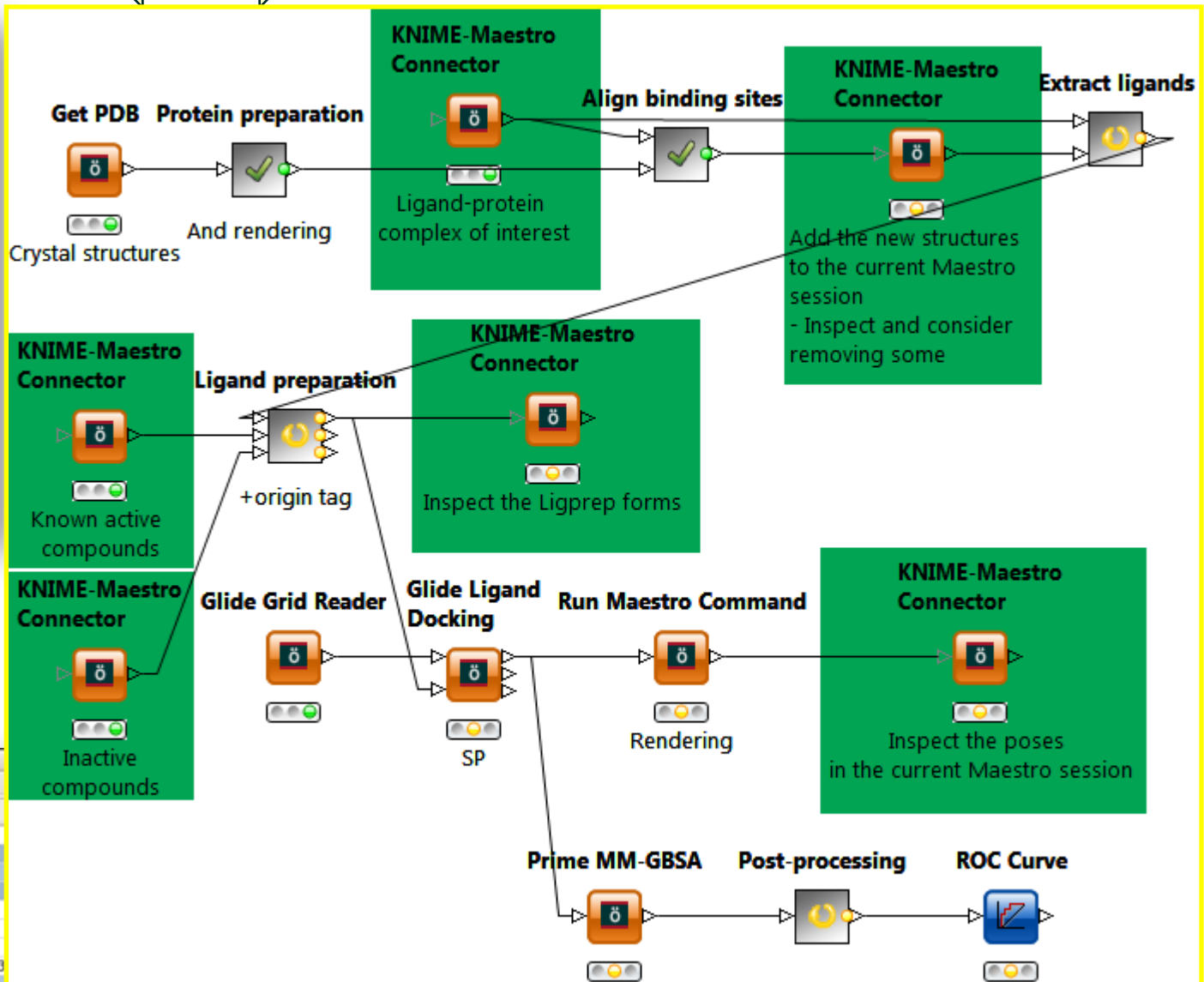
Server

KNIME

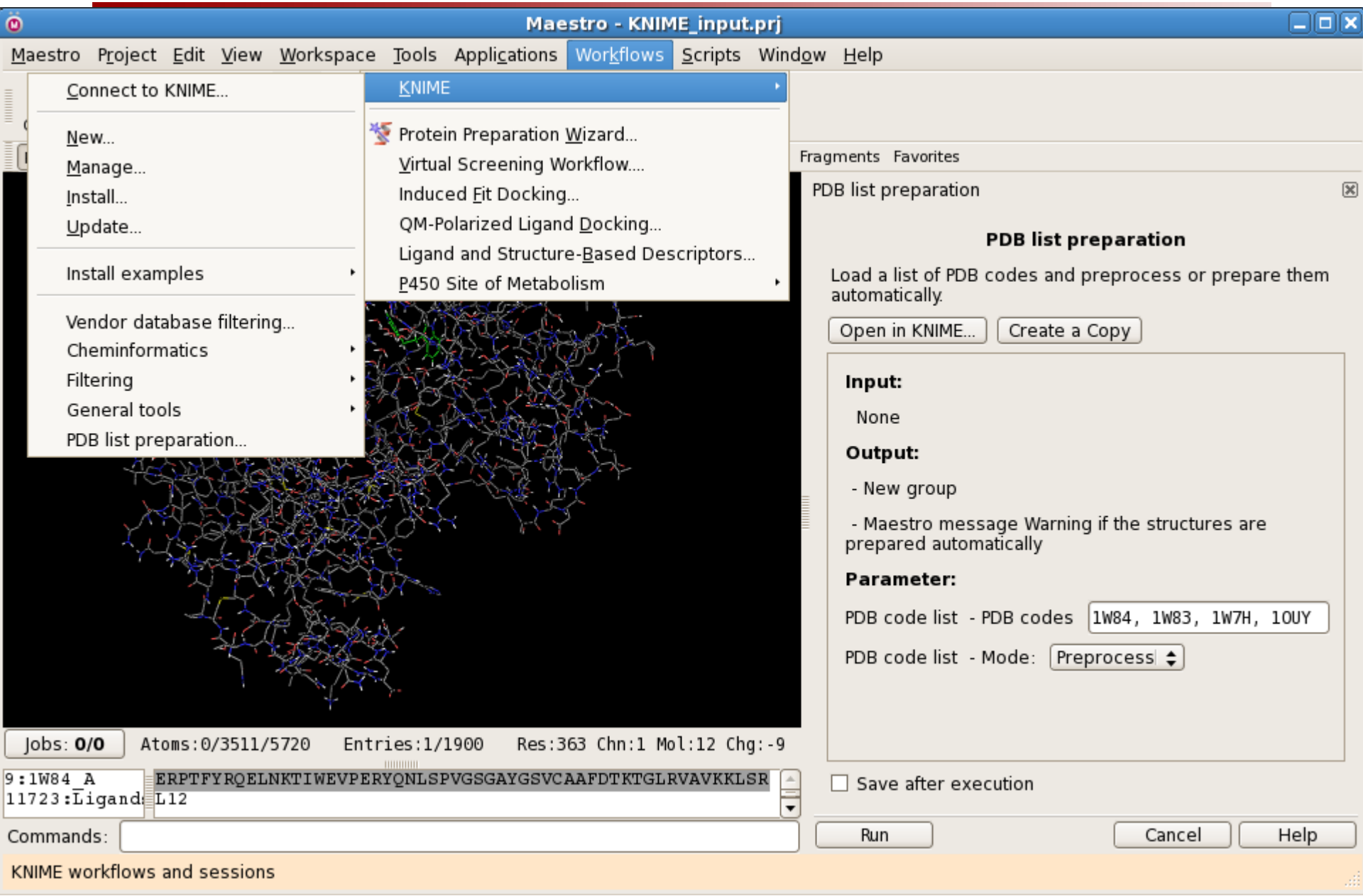


Project table





Run workflows from Maestro



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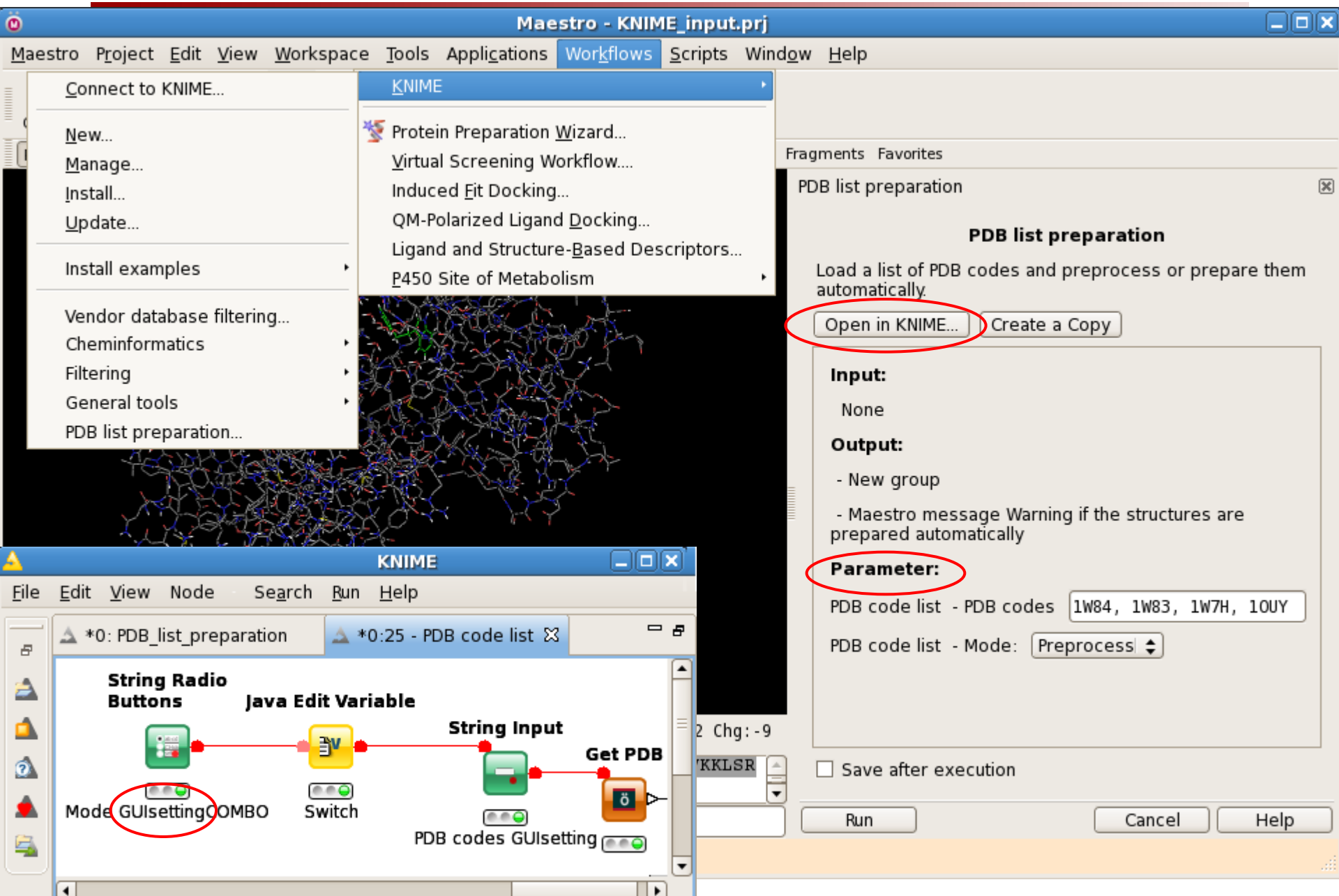

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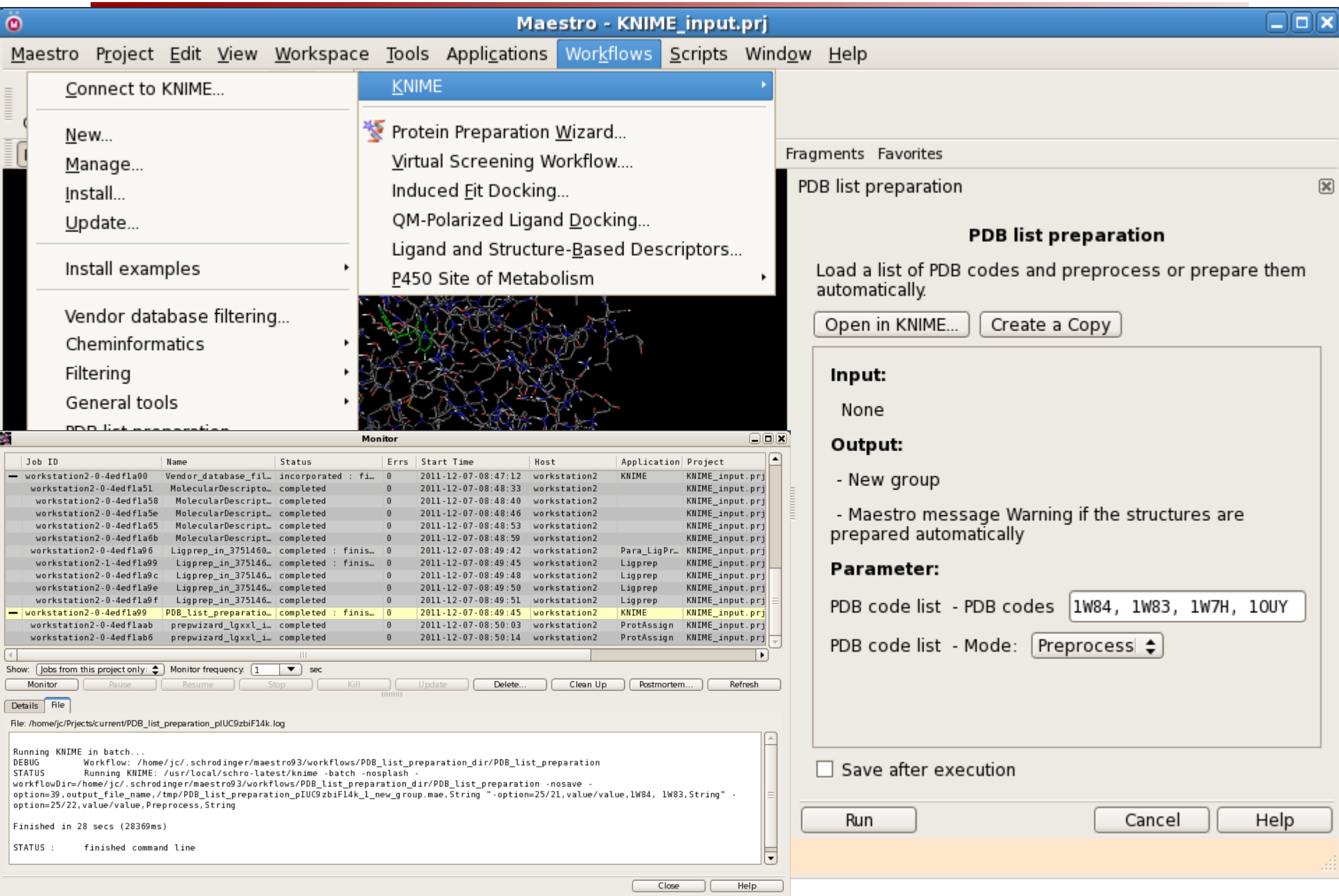


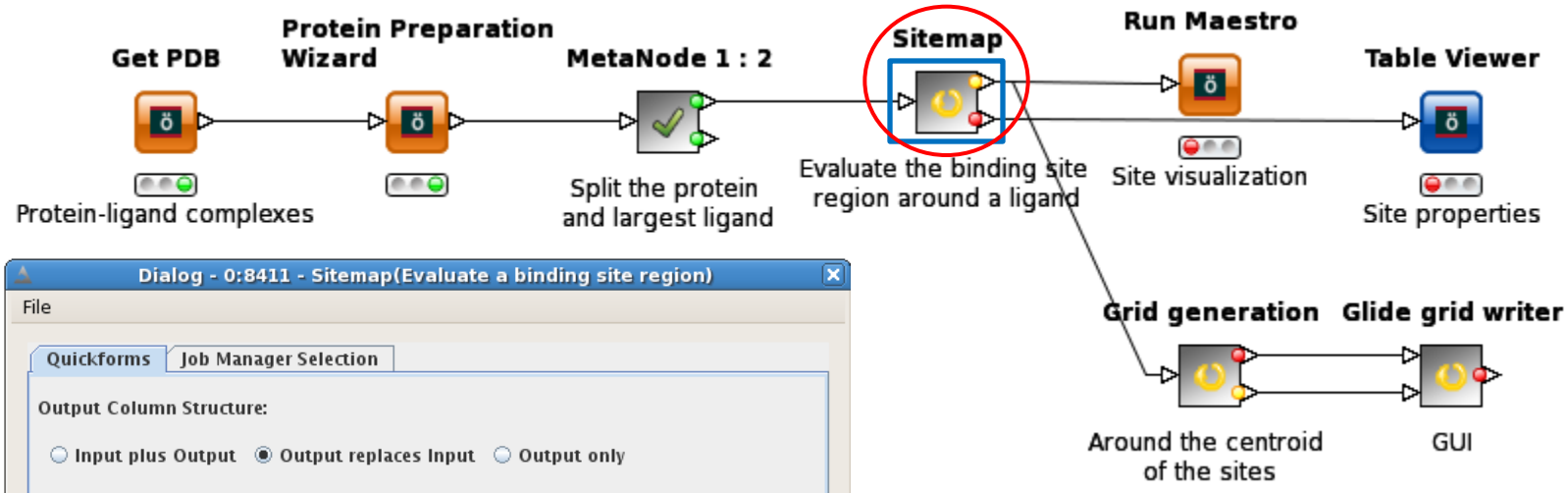
New features

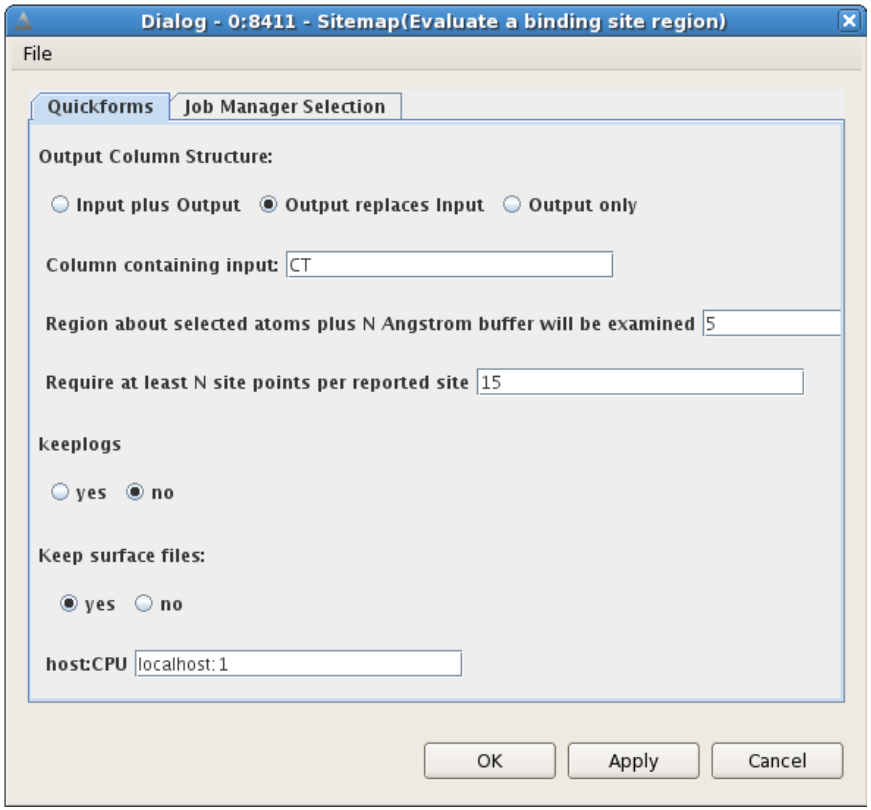
- **Node functionalities**
  - Many fixes and minor improvements
  - Column types: new **Surface type**. Phase hypothesis and Glide grid type improvement
  - **Python script node** new functions (easier metanode development), access to Flow variables

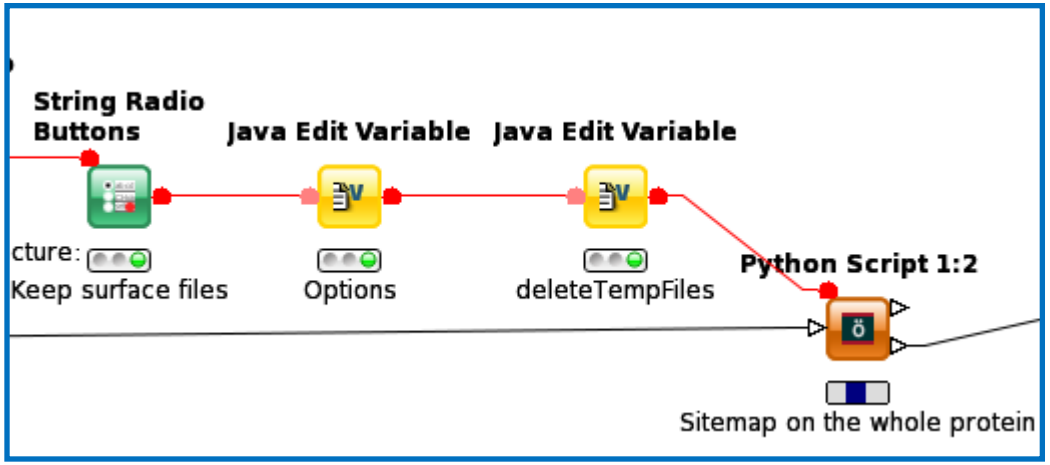
- **Nodes/metanodes**
  - Run Maestro 1:1,* Run PyMOL *
  - Jaguar pKa, Jaguar ESP surface
  - Sitemap *
  - Glide grid writer
  - Prime loop sampling, Prime energy

* first version already available on the Workflow page

Some new metanodes and surface cell type







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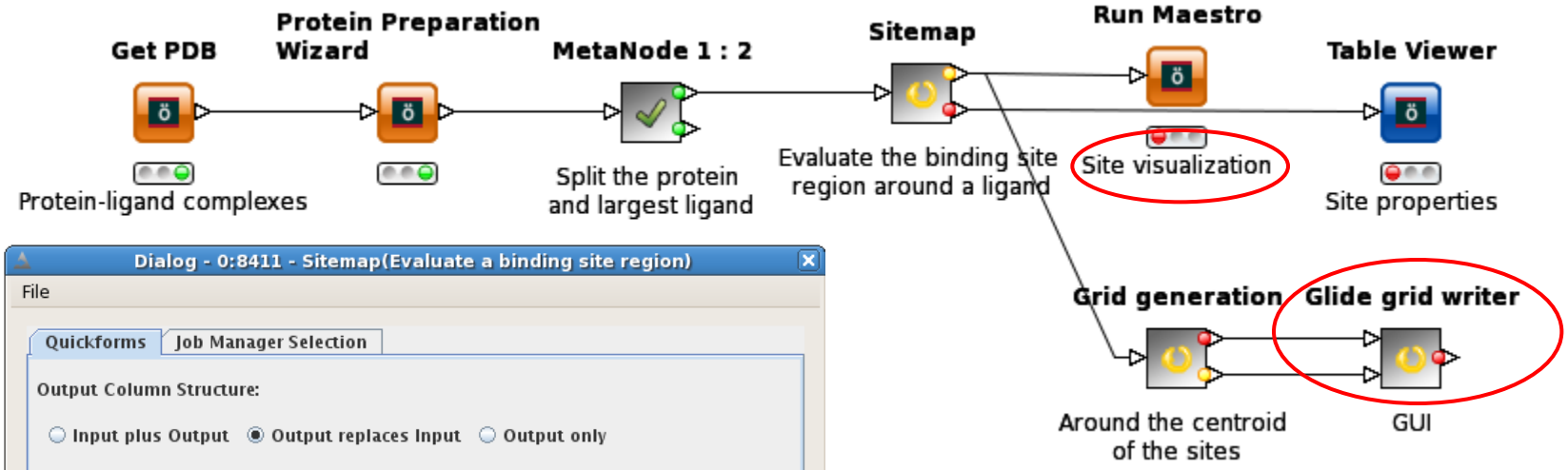
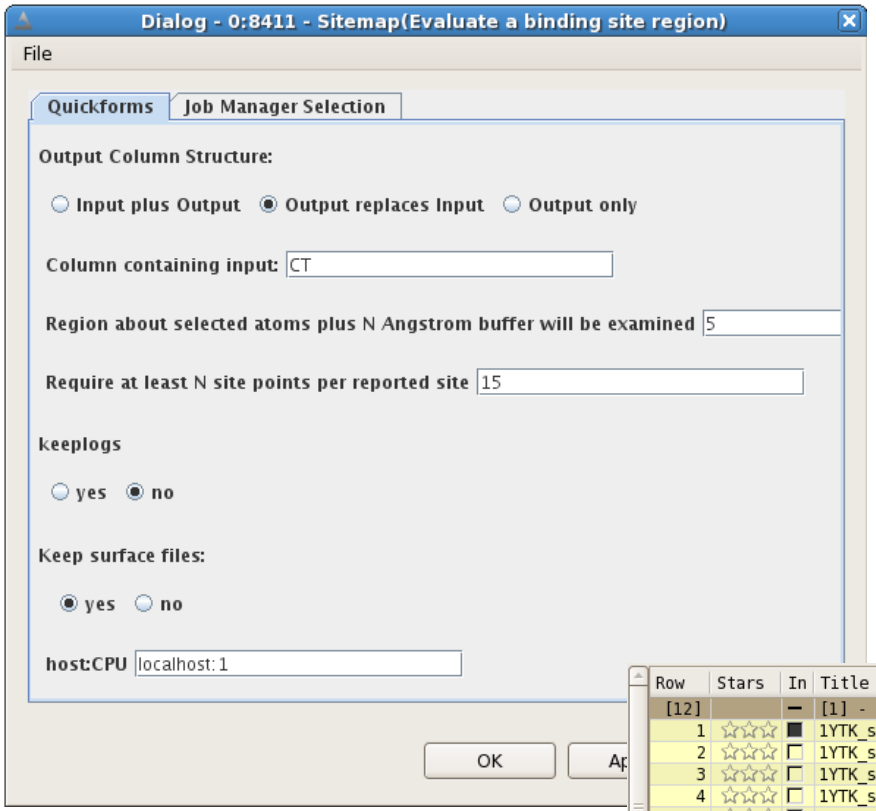
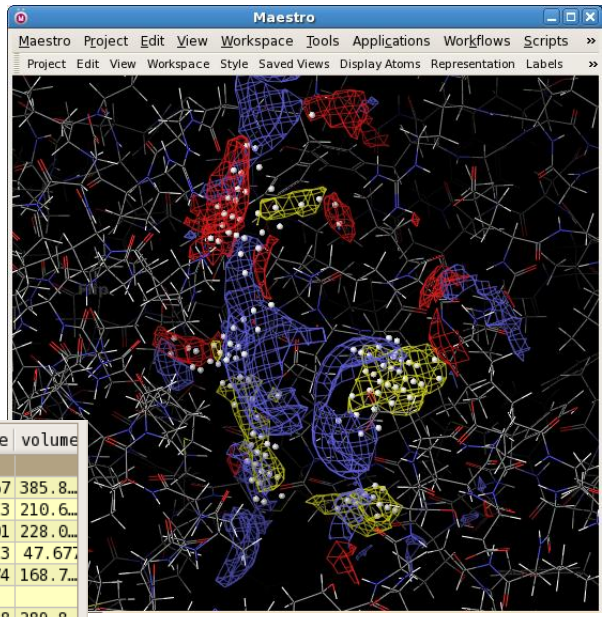
Application example







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2	☆☆☆	□	1YTK_site_2	S	2	0.966	81	0.723	210.6…
3	☆☆☆	□	1YTK_site_3	S	3	0.956	73	1.001	228.0…
4	☆☆☆	□	1YTK_site_4	S	4	0.806	21	0.723	47.677
5	☆☆☆	□	1YTK_site_5	S	5	0.772	56	0.774	168.7…
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7	☆☆☆	□	3DT1_site_1	S	7	1.169	125	1.238	289.8…
8	☆☆☆	□	3DT1_site_2	S	8	1.020	150	0.951	468.1…
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Schrodinger KNIME extensions

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Schrödinger Developers

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What are the Schrödinger extensions?

- **Modelling and computational chemistry in a workflow environment**
- **150+ nodes covering the whole Schrodinger Suite**
- **Run on Linux and Windows 32 and 64 bit versions**

Molecular Mechanics
- MacroModel Single Point Energy, Minimization, Coordinate Scan
- ConfGen
- Conformational Search
- Premin, Impref, Uffmin

Quantum Mechanics
- Jaguar Single Point Energy, Minimization
- NMR Shielding Constants
- Jaguar Charges

Molecular Dynamics
- Desmond System builder
- Desmond Molecular Dynamics
- Trajectory extract frames and manipulation
- Trajectory reader, CMS reader

Cheminformatics

Fingerprint Based Tools
- Fingerprint Generation
- Generate Pairwise Matrix, and 2 Inputs
- Similarity Matrix, Dissimilarity Selection
- Build Report and Hierarchical Clustering

Filters and Mining Tools
- MCS
- Substructure Search
- Structure, REOS Filters

Utilities and Converters
- PCA, MDS
- Combine Fingerprints, Concatenate Bitvectors, Convert Fingerprint to Bitvector, etc

Modeling
- Bayes Model Building, prediction
- PLS Model Building, Prediction

Pharmacophore Modeling
- Phase Shape
- Phase DB Query, File Query
- Phase DB Creation
- Phase Hypothesis Identification

Combinatorial Libraries
- CombiGlide Reagent Preparation and Library Enumeration
- Fragments from Molecules and joiner

Docking and Scoring
- Glide Grid Generation
- Glide Ligand Docking
- Glide Multiple Ligand Docking
- XP Visualizer

Post-processing
- Prime MM-GBSA
- Embrace Minimization
- Strain Rescore, Pose Entropy
- Pose Filter, Glide Merge, Sort Results
- Glide Ensemble Merge

Protein Structure Prediction
- BLAST
- Prime Build Homology Model
- Prime Side Chain Sampling, Minimization
- IFD and individual steps

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Schrödinger nodes

- **Generate, manipulate, analyze and visualize chemical data and structures**
- **Interactive and automated analysis. Presentation and communication of results**

Protein Preparation
- Protein Preparation Wizard
- Protein Assignment

Ligand Preparation
- LigPrep and the individual steps
- Epik

Property Generation
- QikProp, Molecular Descriptors
- Canvas descriptors

Filtering
- Ligfilter, Ligparse, Propfilter

Scripting
- Run Maestro Command
- Chemistry External nodes
- Python Script nodes

Reporting
- Run Maestro, Run Canvas
- Spreadsheet viewer
- Table viewer

Tools

Data Manipulation
- Compare Ligands
- Lookup and Add Columns
- Group and Ungroup MAE

Structure Manipulation
- Add Hydrogens
- Delete Atoms
- Split by Structure
- MAE atom/bond property Parser
- Extract, Set and Delete MAE Properties
- Set Molecule Title, MAE Index

Utilities
- Get PDB
- Align Binding Sites
- Protein Structure Alignment
- RMSD
- Assign Bond Orders
- Unique Title Check
- Check PDB Name
- SD Format Checker
- Generate Smarts, Unique Smiles
- RRHO Entropy
- Boltzmann Population
- Volume Overlap Matrix

Readers/Writers
- CSV Reader (several inputs)
- Molecule Reader and Writer
- SD, PDB, Mol2 Reader nodes
- Sequence, Alignment Readers and Writers
- Fingerprint Reader and Writer
- Hypothesis Reader and Writer
- Glide Grid and Multiple Grid Reader
- Variable Based Glide Grid Reader

Converters
- String-to-Type
- Molecule-to-MAE, MAE-to-Pdb, to-SD, to-Smiles and to-Mol2, SD-to-Smiles
- PoseViewer-to-Complexes and Complexes-to-PoseViewers
- Hartree-to-kcal/mol and kJ-to-kcal

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