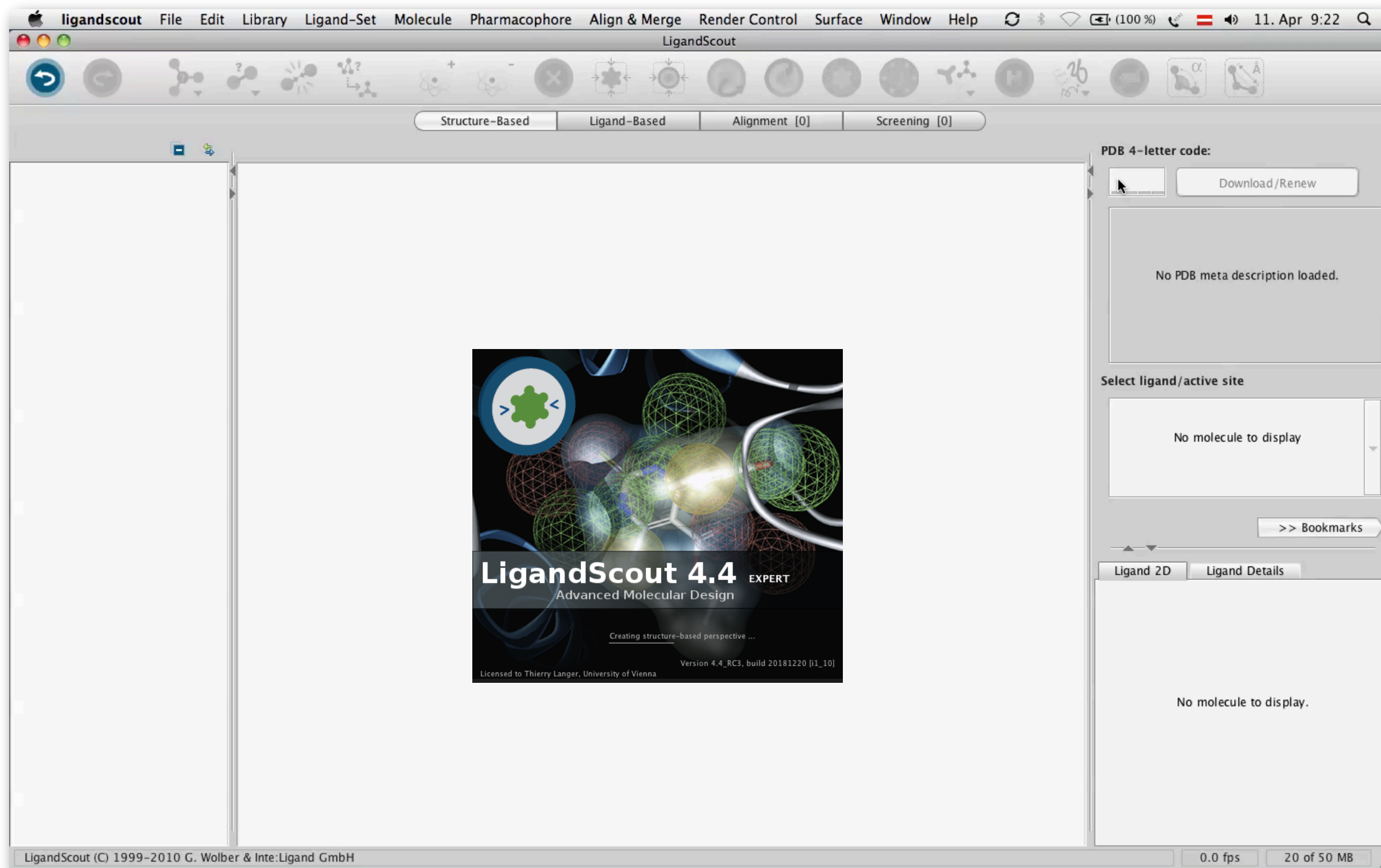
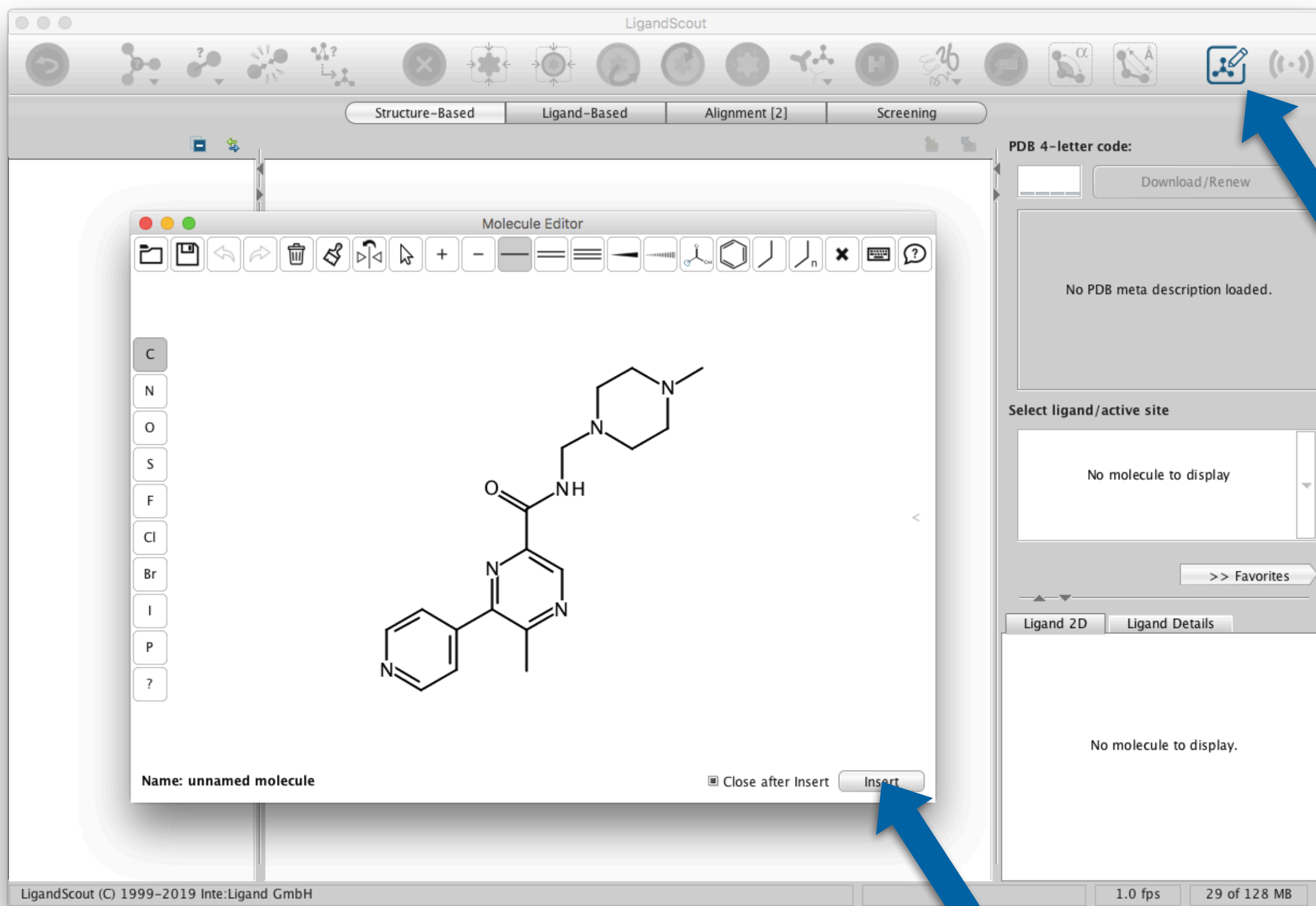


News about LigandScout and the Inte:Ligand KNIME Extensions

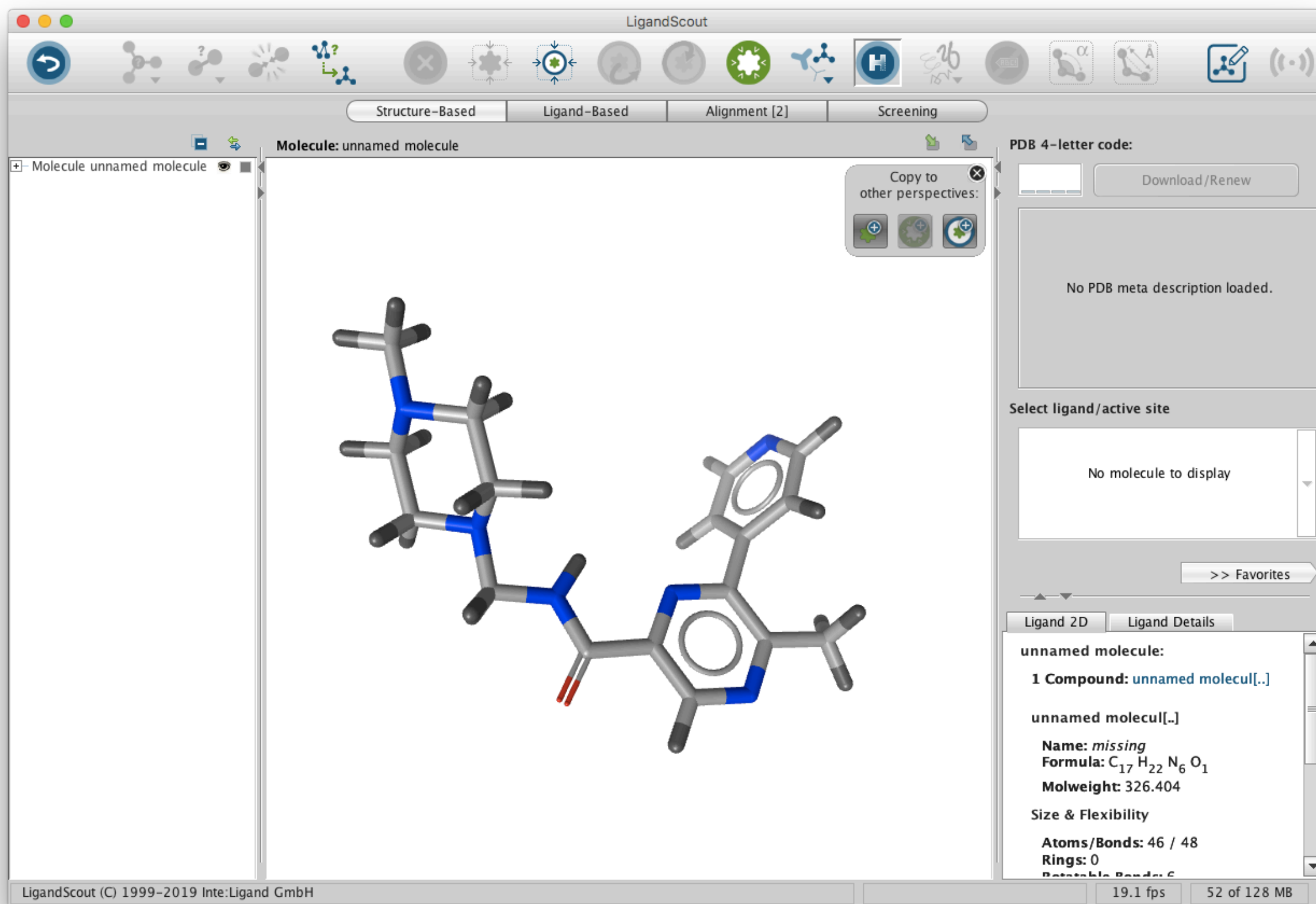
What's New in LigandScout 4.4



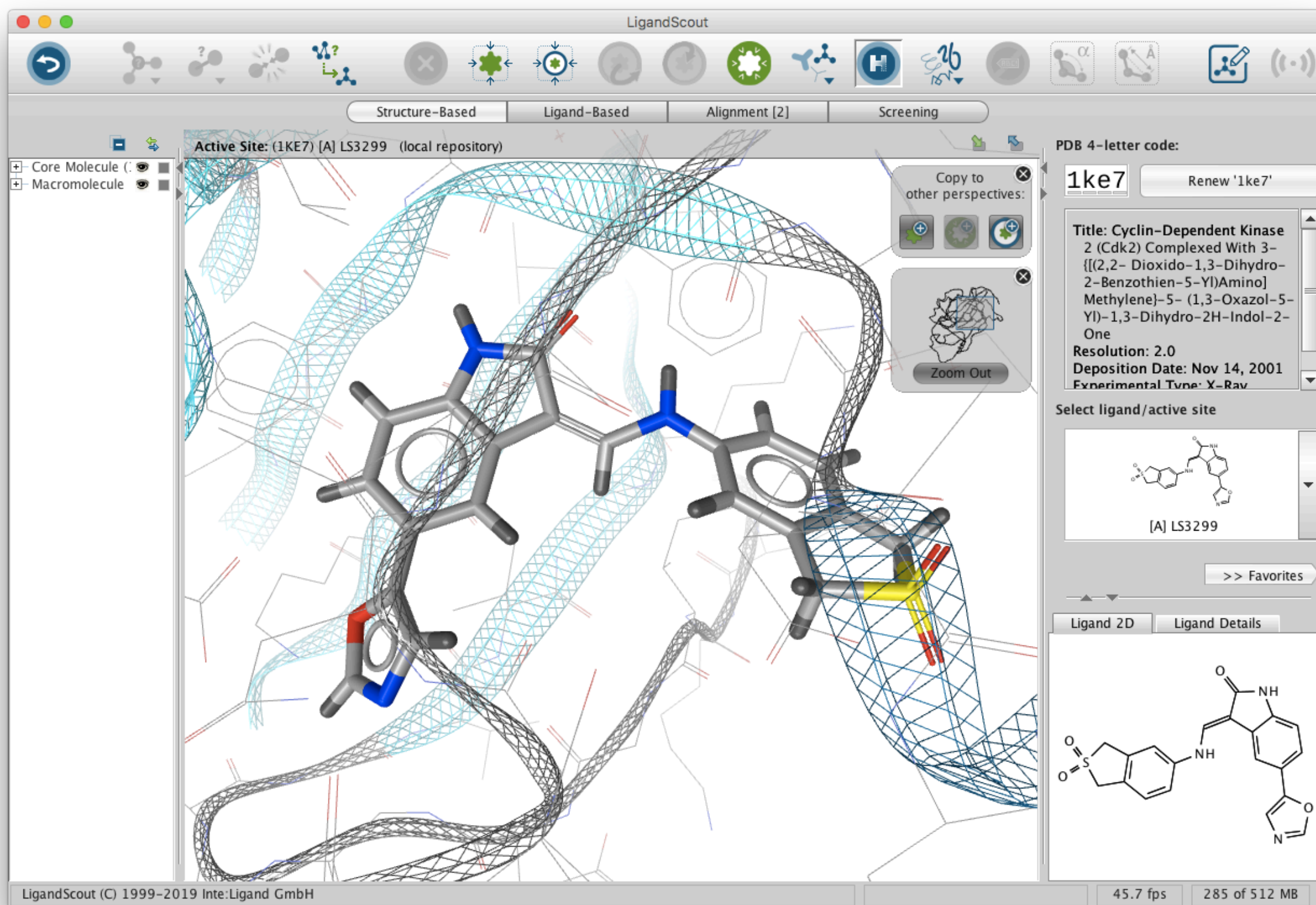
New 2D Molecule Editor



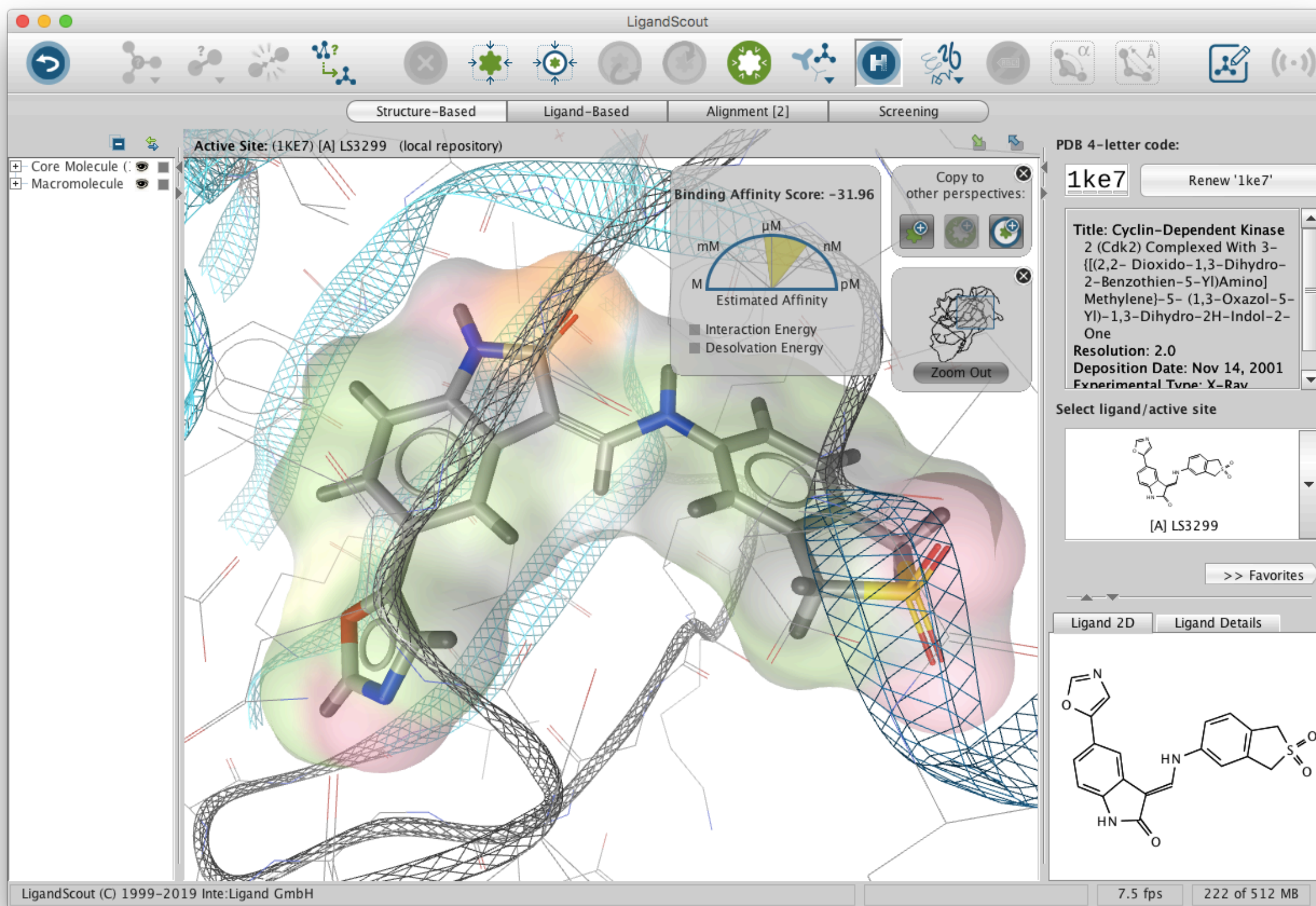
New 2D Molecule Editor



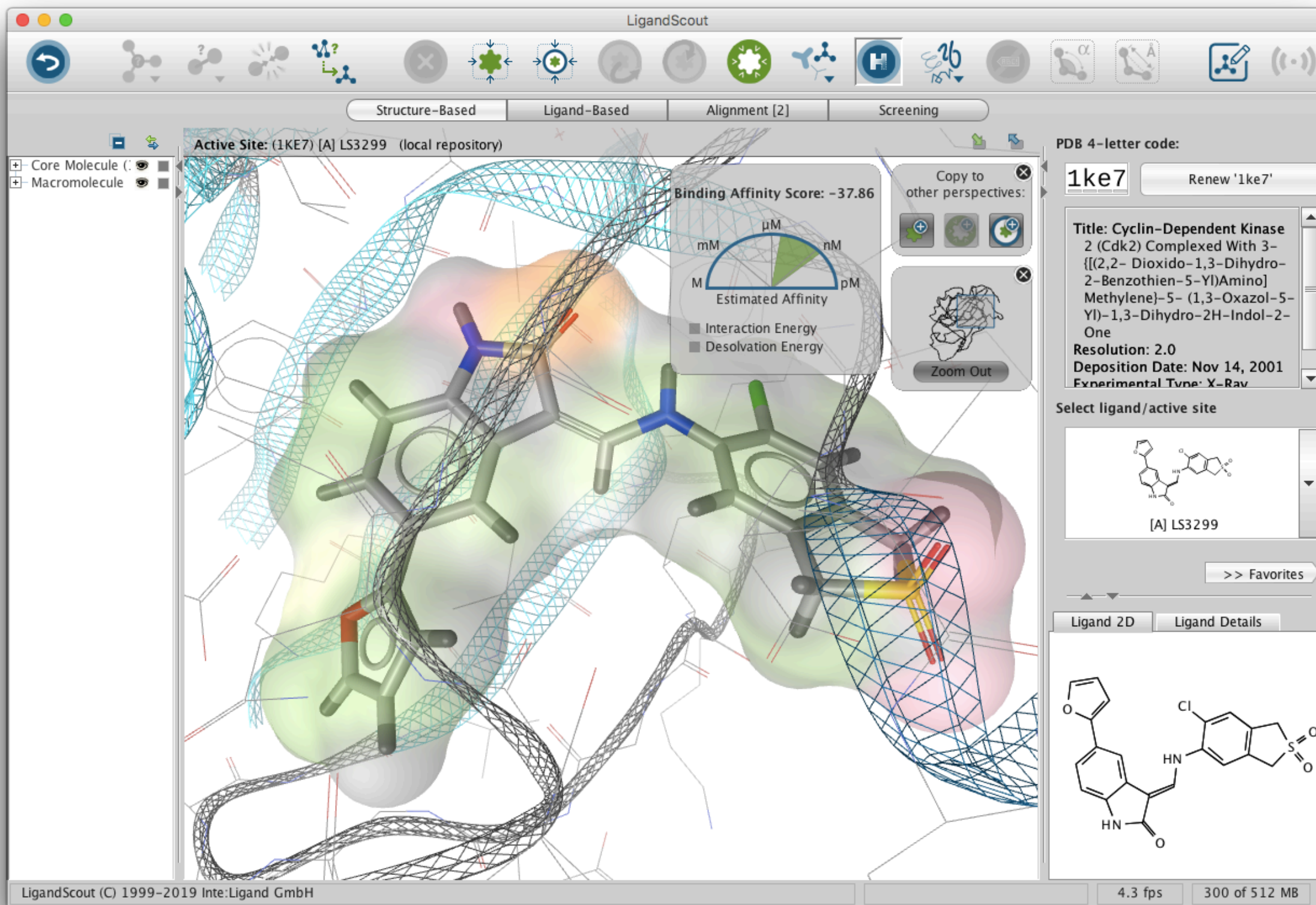
New: Interactive Binding Affinity Estimation



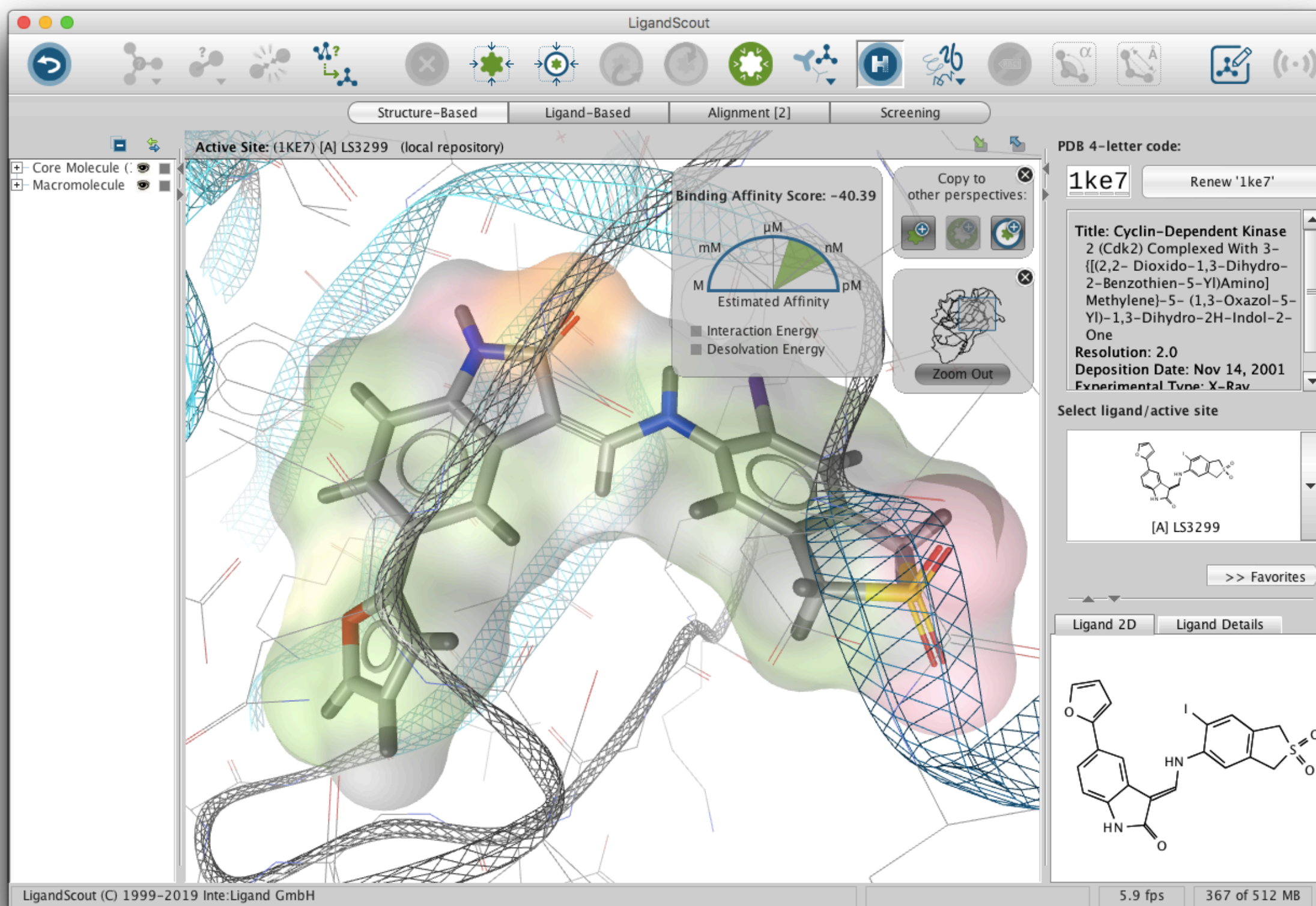
Interactive Binding Affinity Estimation



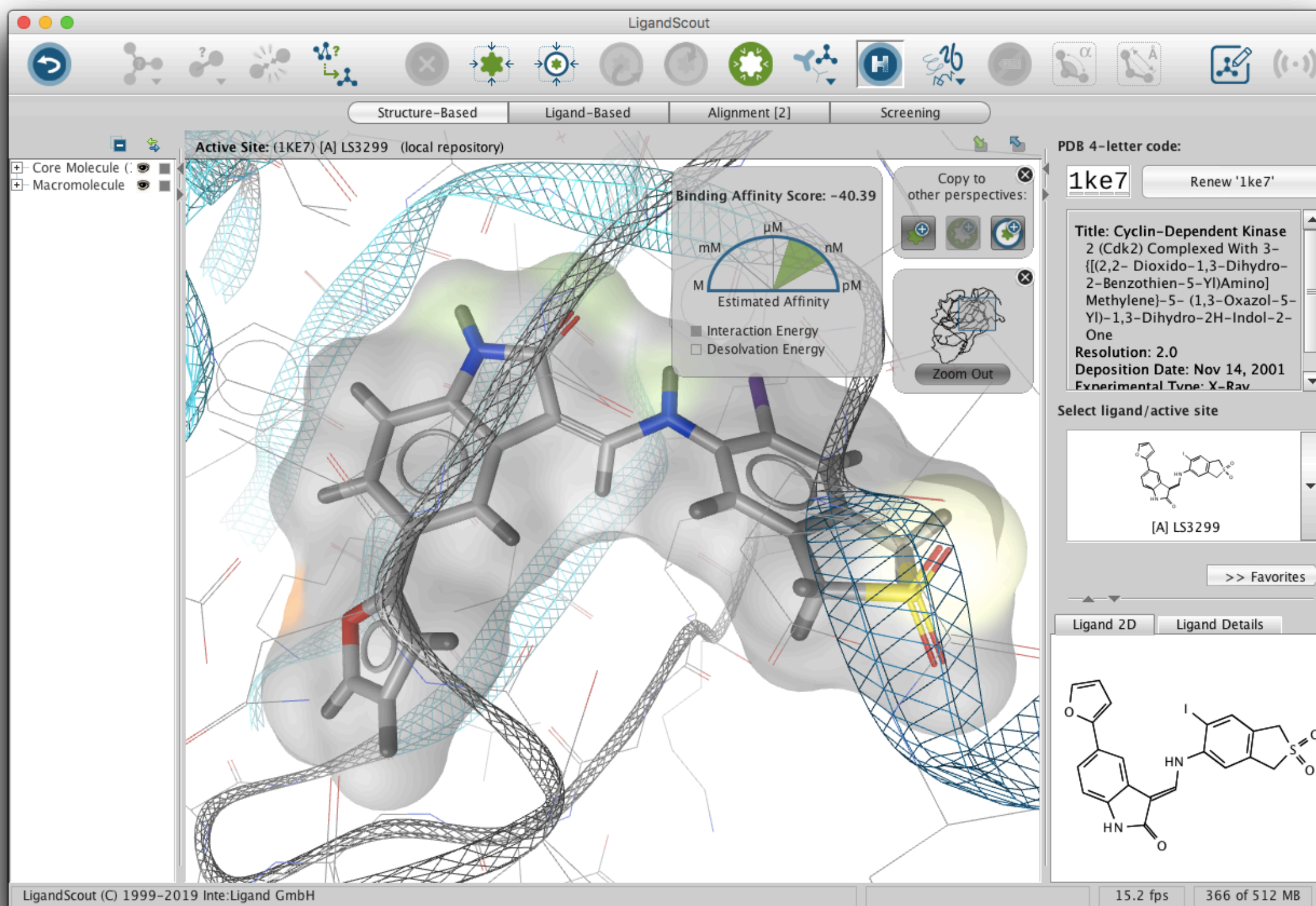
Interactive Binding Affinity Estimation



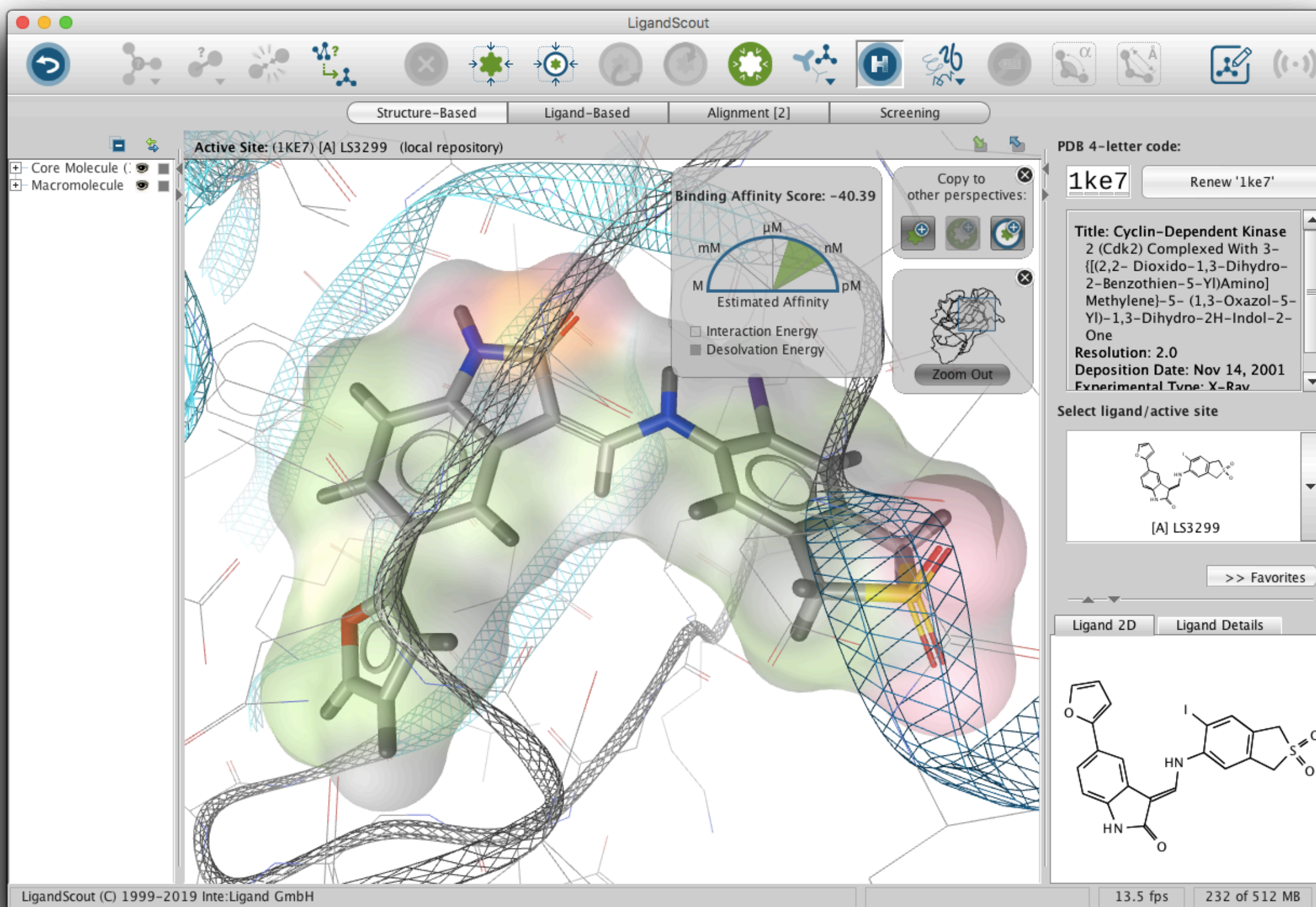
Interactive Binding Affinity Estimation



Interactive Binding Affinity Estimation



Interactive Binding Affinity Estimation



Interactive Data Analysis: Radar Plot

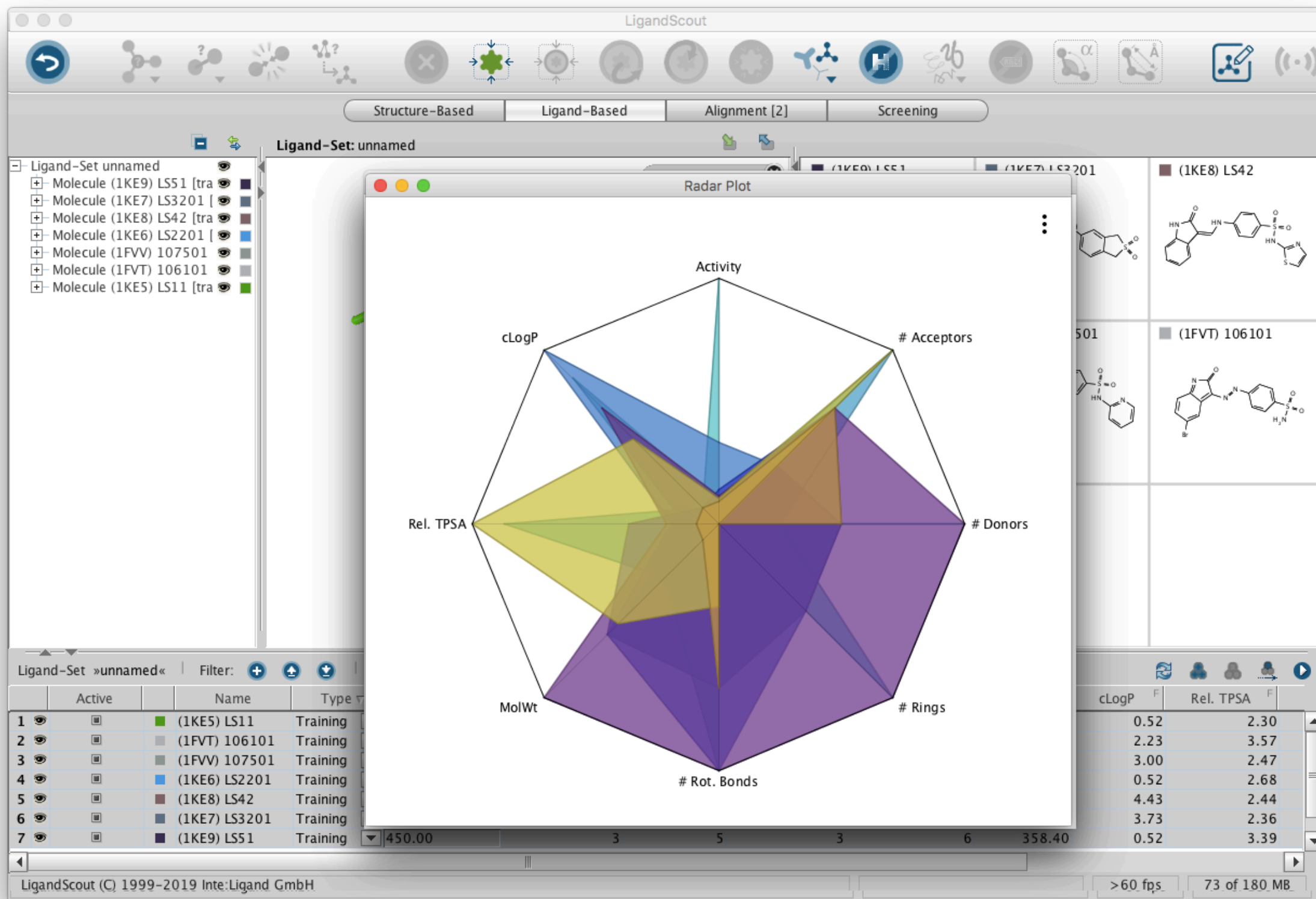
The screenshot displays the LigandScout software interface. A 'Select Properties' dialog box is open, allowing users to choose properties for a Radar Plot. The dialog has two columns: 'Exclude:' and 'Include:'. The 'Exclude:' column contains '# Confs.', '# Heavy Atoms', and 'TPSA [Ertl]'. The 'Include:' column contains 'Activity', '# Acceptors', '# Donors', '# Rings', '# Rot. Bonds', 'MolWt', 'Rel. TPSA', and 'cLogP'. There are '>>' and '<<' buttons between the columns. At the bottom of the dialog are 'Cancel' and 'Ok' buttons.

The background interface shows a 'Ligand-Set: unnamed' window with a list of molecules on the left and a table of their properties on the right. The table has columns for 'Active', 'Name', and 'Type'. The molecules listed are (1KE5) LS11, (1FVT) 106101, (1FVV) 107501, (1KE6) LS2201, (1KE8) LS42, (1KE7) LS3201, and (1KE9) LS51, all of which are 'Training' molecules.

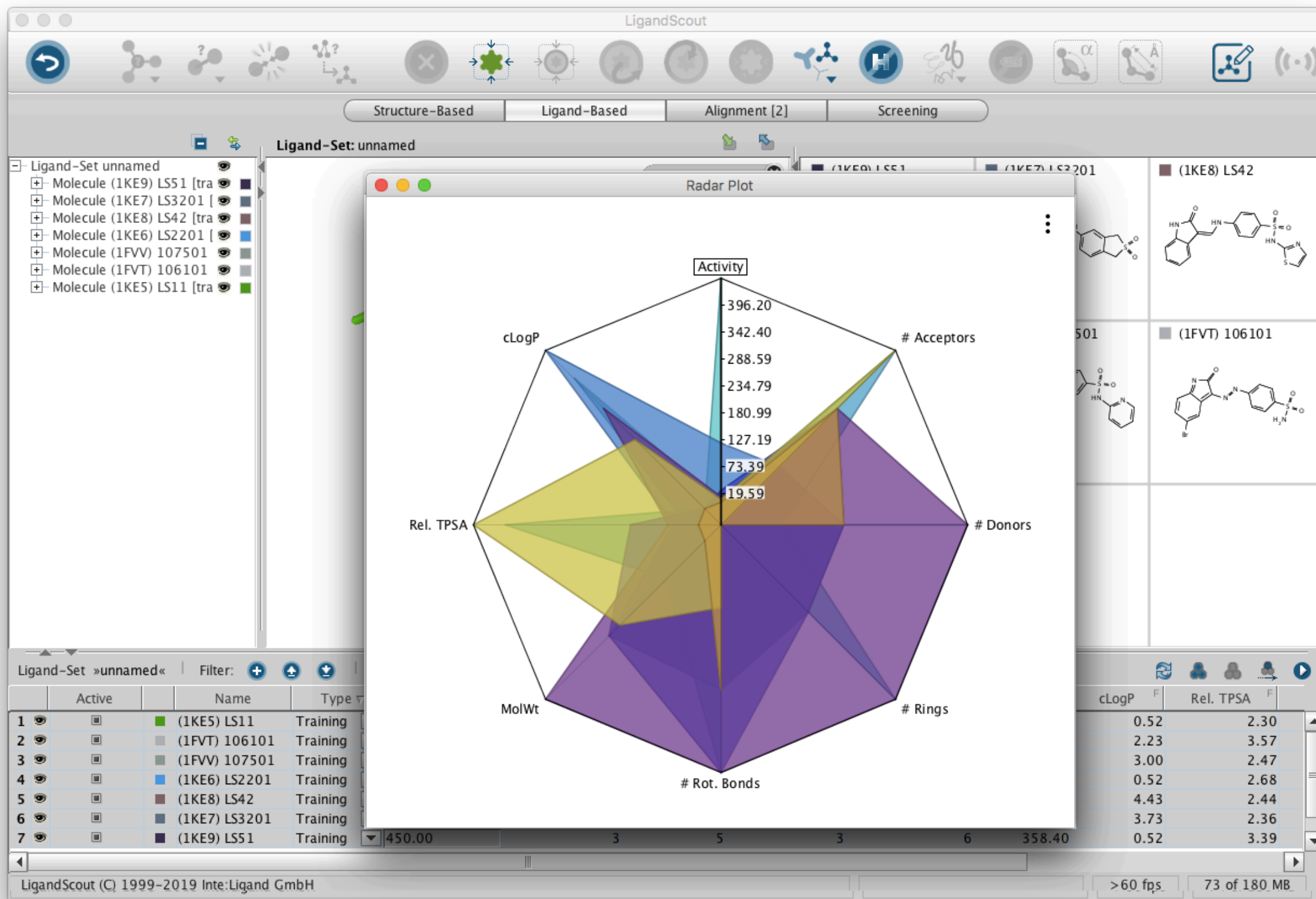
Active	Name	Type
<input checked="" type="checkbox"/>	(1KE5) LS11	Training
<input checked="" type="checkbox"/>	(1FVT) 106101	Training
<input checked="" type="checkbox"/>	(1FVV) 107501	Training
<input checked="" type="checkbox"/>	(1KE6) LS2201	Training
<input checked="" type="checkbox"/>	(1KE8) LS42	Training
<input checked="" type="checkbox"/>	(1KE7) LS3201	Training
<input checked="" type="checkbox"/>	(1KE9) LS51	Training

At the bottom of the interface, there is a status bar showing 'LigandScout (C) 1999-2019 Inte:Ligand GmbH', a progress bar, and performance metrics: '> 60 fps' and '73 of 180 MB'.

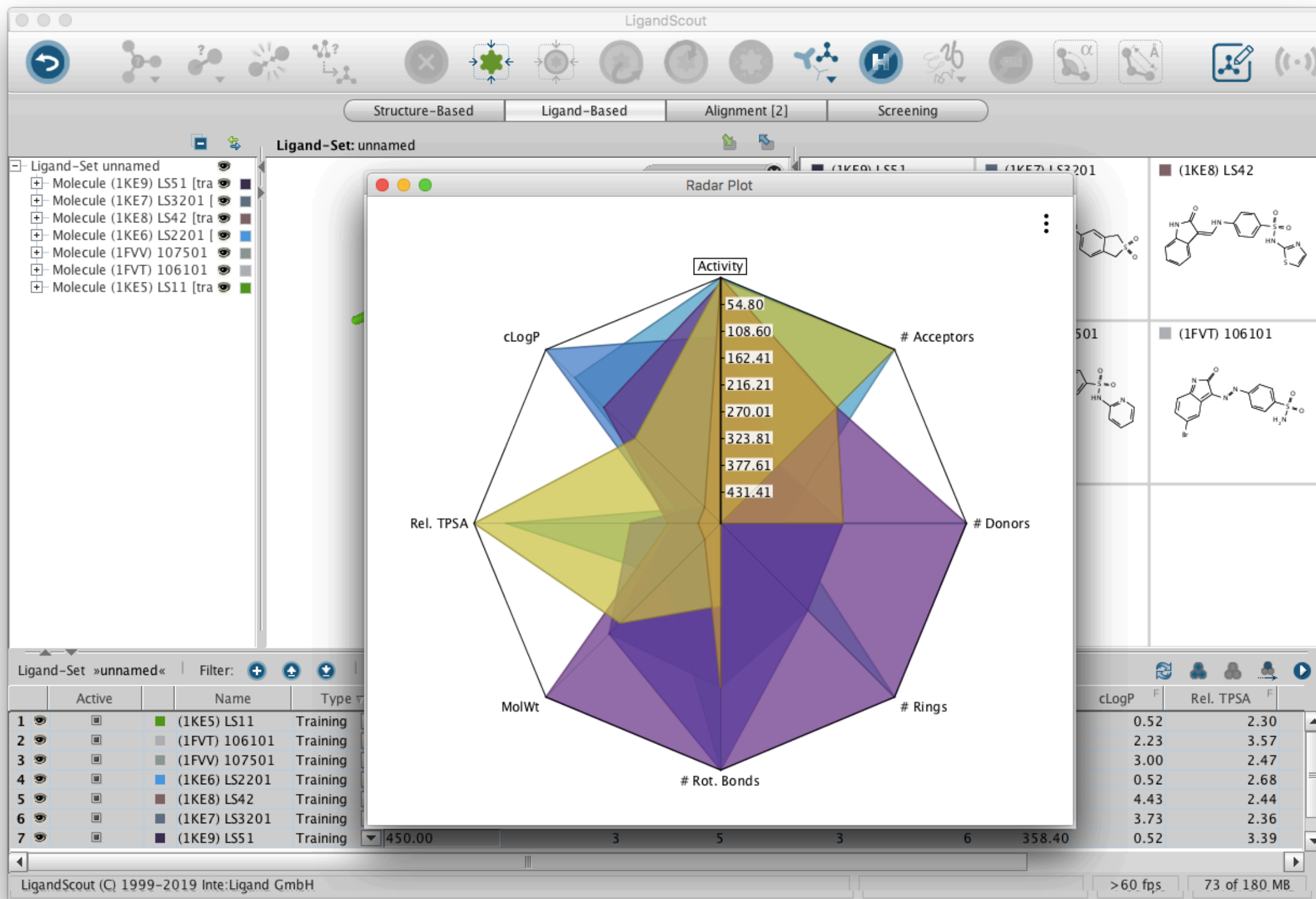
Interactive Data Analysis: Radar Plot



Interactive Data Analysis: Radar Plot

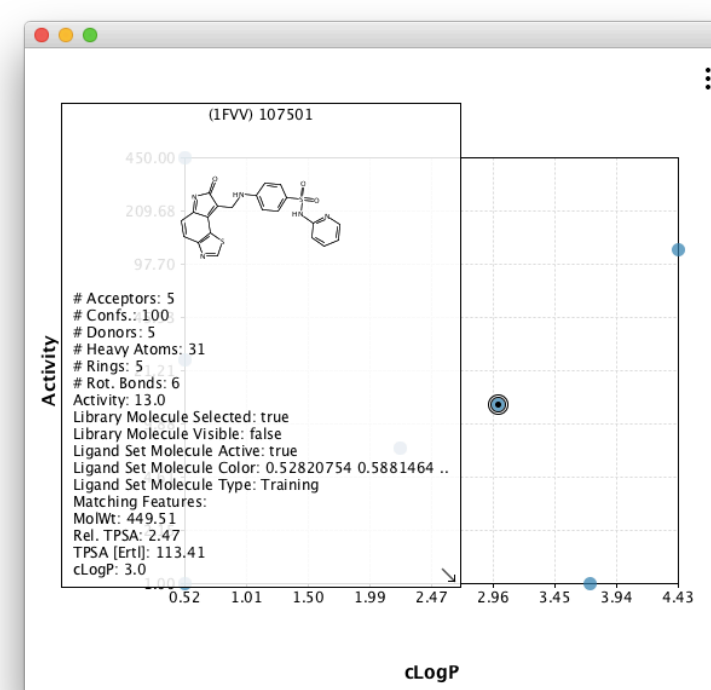
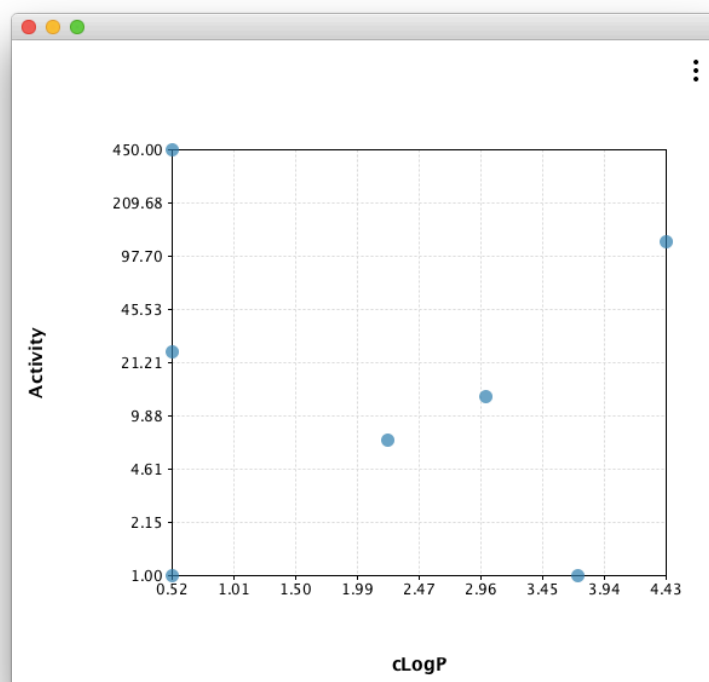
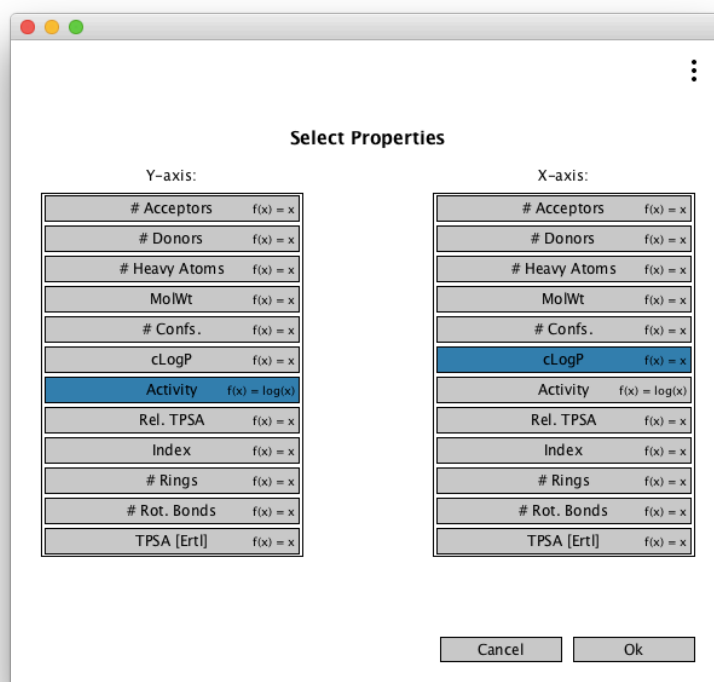


Interactive Data Analysis: Radar Plot



Interactive Data Analysis

- New features in scatter & parallel coordinate plots
 - Invert axes
 - Scale axes with pre-defined math functions and define ranges
 - Obtain molecular information interactively



What's New in LigandScout 4.3 ?

- Remote execution from the GUI:
 - iScreen on local HP clusters or on the Amazon Cloud*
 - idbgen on local HP clusters or on the Amazon Cloud*
- Halogen bond acceptor feature
- New fully searchable online help system

Remote Execution from the GUI

LigandScout Remote: A New User-Friendly Interface for HPC and Cloud Resources

Thomas Kainrad,^{*,†,‡,ID} Sascha Hunold,^{*,†,ID} Thomas Seidel,^{§,ID} and Thierry Langer^{§,‡,ID}

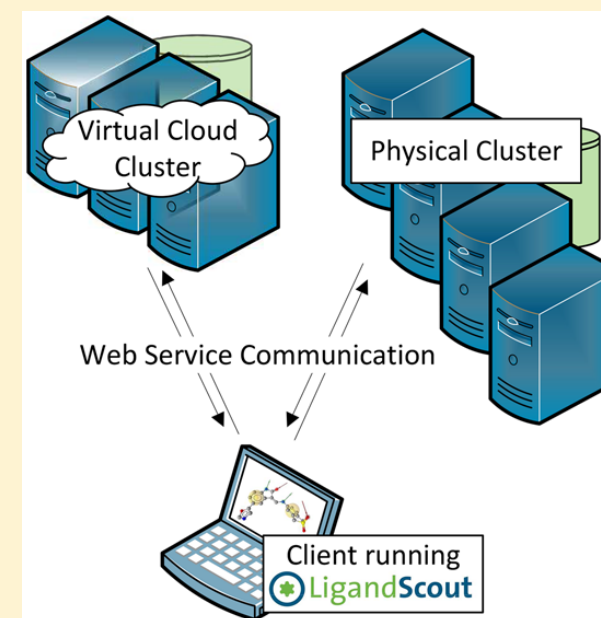
[†]Faculty of Informatics, TU Wien, A-1040 Vienna, Austria

[‡]Inte:Ligand Software Development and Consulting GmbH, A-1070 Vienna, Austria

[§]Department of Pharmaceutical Chemistry, University of Vienna, A-1090 Vienna, Austria



ABSTRACT: High-performance computing (HPC) clusters play a major role in scientific research. However, working with these clusters is often cumbersome, especially for researchers without a formal background in computer science. It requires preparation and transfer of the input data, manual gathering of results, and command-line expertise. Current approaches for improving accessibility to remote HPC clusters are focused on providing web-based graphical front-ends that allow jobs to be submitted to the distributed resource management system running on the cluster. This comes with significant usability benefits over command-line usage but does not circumvent the need for manual handling of the input and output files. With LigandScout Remote, we propose a different solution. Our software enables the seamless integration of HPC resources into the LigandScout desktop application that scientists use also in their day-to-day work. By handling necessary data conversion and network communication transparently to the user, this approach completely evades any HPC usability barriers. We show that the developed software combines the usability of local graphical desktop applications with the performance of HPC clusters.



Remote Execution from the GUI

Load Remote Screening Job

Select Remote Screening Job to load and which data to include ?

Available Slots: 282/768 Filter criteria: User: tkainrad Pharmacophore

Job Name	ID	Compounds Screened	Hit Count	Total #Compounds	Progress	Created	Finished	Duration	Error Message
job_75	75	1021001	61	1297868	78%	Wed, 5 Dec 2018 11:46			
job_72	72	1261901	151	1297868	97%	Wed, 5 Dec 2018 11:38			
job_70	70	20292	0	20292	100%	Wed, 5 Dec 2018 11:24	Wed, 5 Dec 2018 11:29	5m 11s	
job_69	69	1288869	169	1297868	99%	Wed, 5 Dec 2018 11:22			
job_68	68	753412	18	1297868	canceled (53%)	Wed, 5 Dec 2018 11:18			Job canceled on purpose.
job_61	61	1297868	0	1297868	Current Progress	Wed, 5 Dec 2018 10:59	Wed, 5 Dec 2018 11:39	39m 53s	
job_58	58	20292	0	20292	100%	Wed, 5 Dec 2018 10:53	Wed, 5 Dec 2018 10:58	5m 4s	
job_57	57	2997	0	2997	100%	Wed, 5 Dec 2018 10:49	Wed, 5 Dec 2018 10:50	1m 2s	
job_56	56	20310	0	26503	canceled (76%)	Wed, 5 Dec 2018 10:48			Job canceled on purpose.

Screening Settings

Scoring function: absolute

Max. number of omitted features: 0

Min. number of required features: 3

☐ Compound time-out (in minutes): 0

Screening mode: Match all query features

Retrieval mode: FIRST

☒ Check exclusion volumes

Job Details and Import Settings

Used screening databases:

zinc_fragments.ldb
chembl_21 - 4 Chunks

Input Compound Databases

Scheduler Sub-Job Executions:

ID	Status	Progress
805147	Running	92%
805148	Running	0%
805149	Running	5%
805150	Running	7%
805151	Running	60%
805152	Done	100%
805153	Running	84%

Sub-Job Progress

Query Pharmacophores:

(1KE6) [A] LS2299
(1KE7) [A] LS3299
(1KE8) [A] LS4299

Input Pharmacophores

Boolean expression:

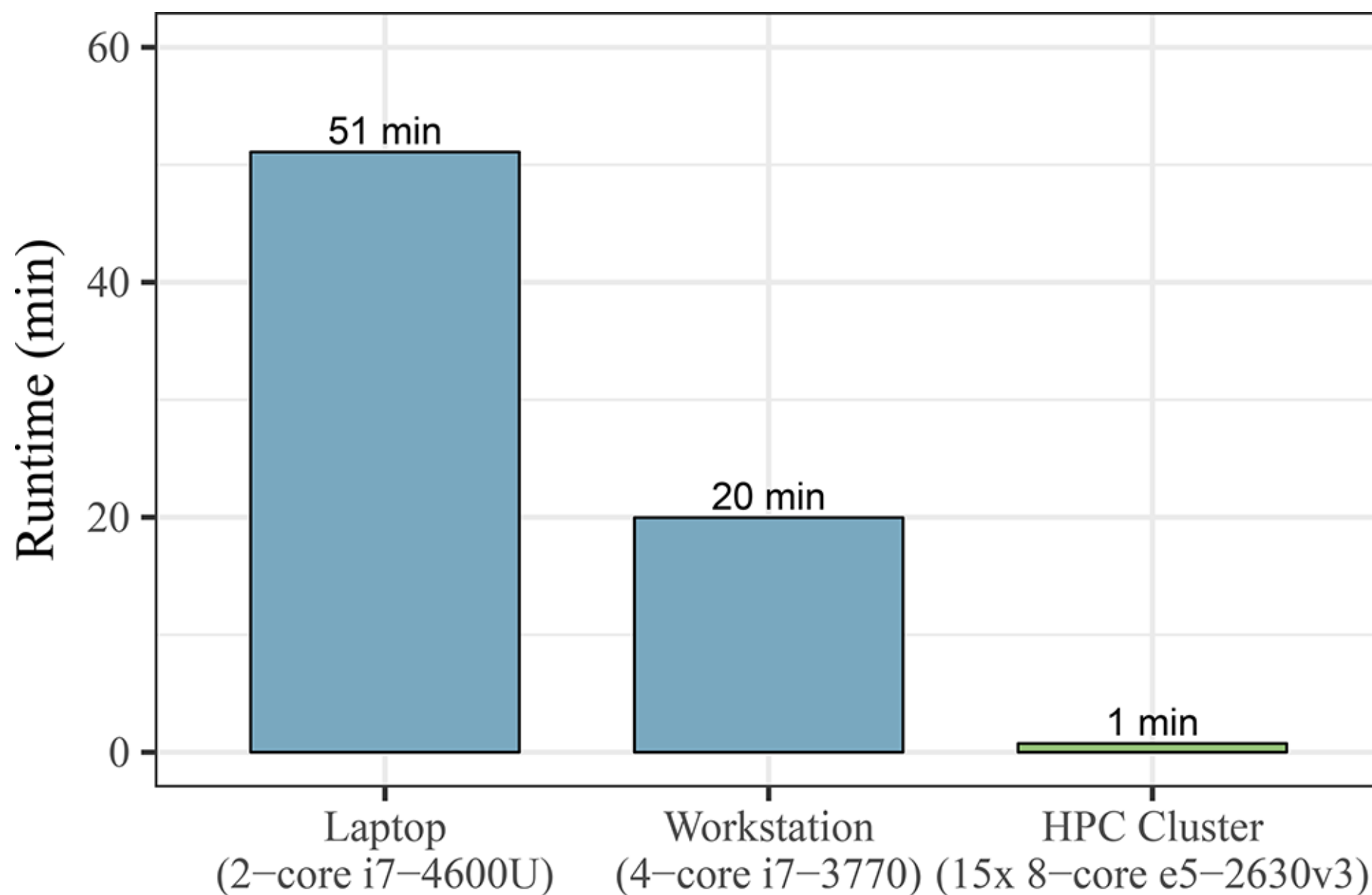
Import Data:

☒ Pharmacophores ☒ Result Hitlist
☒ Boolean Expression ☒ Input Databases
☒ All data

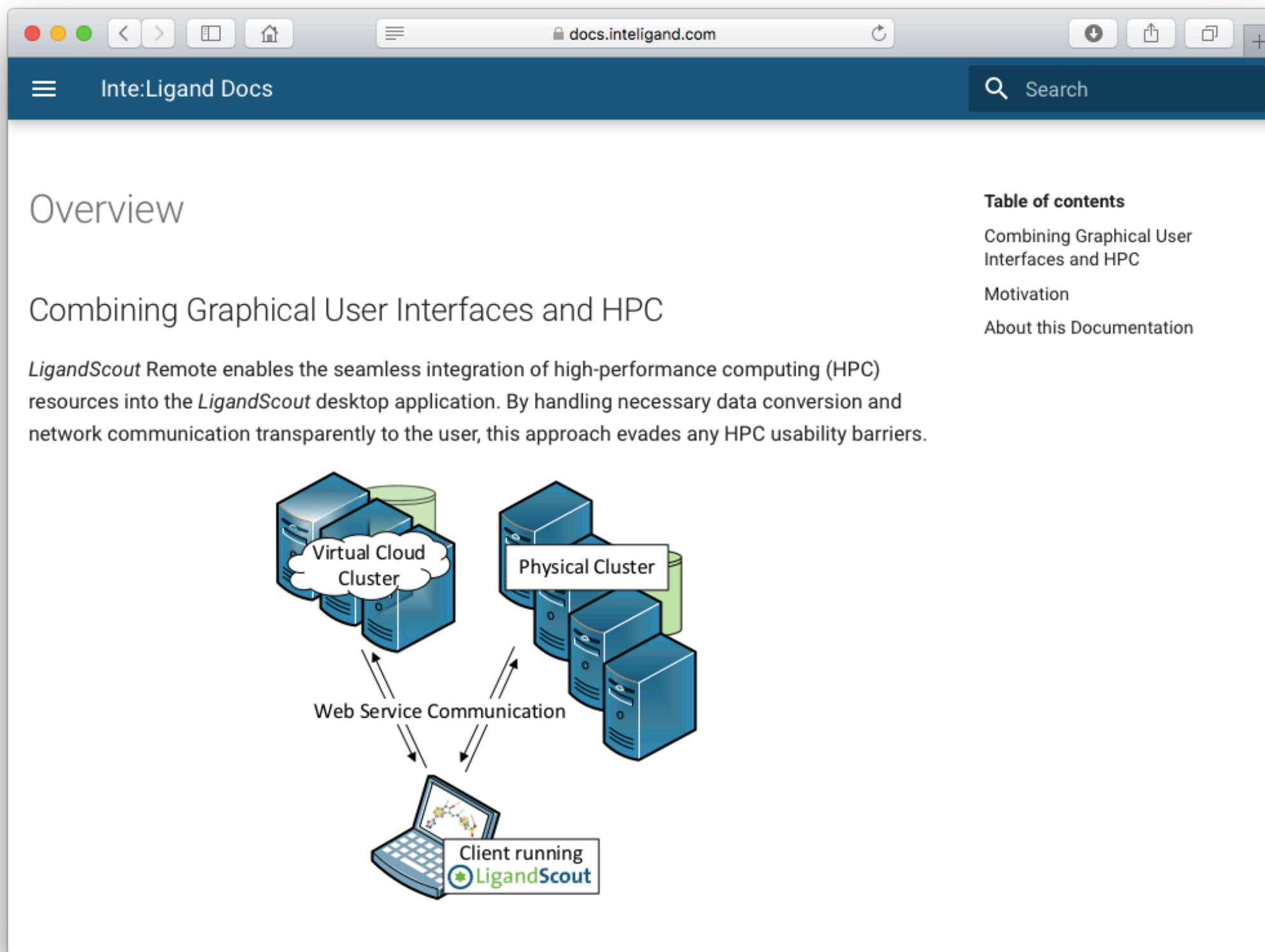
Data Selection

Manual Refresh Auto-Refresh Cancel Load

Screening Performance Comparison



<https://docs.inteligand.com/ls-remote>



The screenshot shows a web browser window with the address bar displaying `docs.inteligand.com`. The page title is "Inte:Ligand Docs". A search bar is located in the top right corner. The main content area is titled "Overview" and "Combining Graphical User Interfaces and HPC". Below this, a paragraph describes the *LigandScout* Remote integration. To the right, a "Table of contents" lists the sections: "Combining Graphical User Interfaces and HPC", "Motivation", and "About this Documentation". At the bottom, a diagram illustrates the architecture: a "Virtual Cloud Cluster" and a "Physical Cluster" are connected via "Web Service Communication" to a "Client running LigandScout".

Inte:Ligand Docs

Search

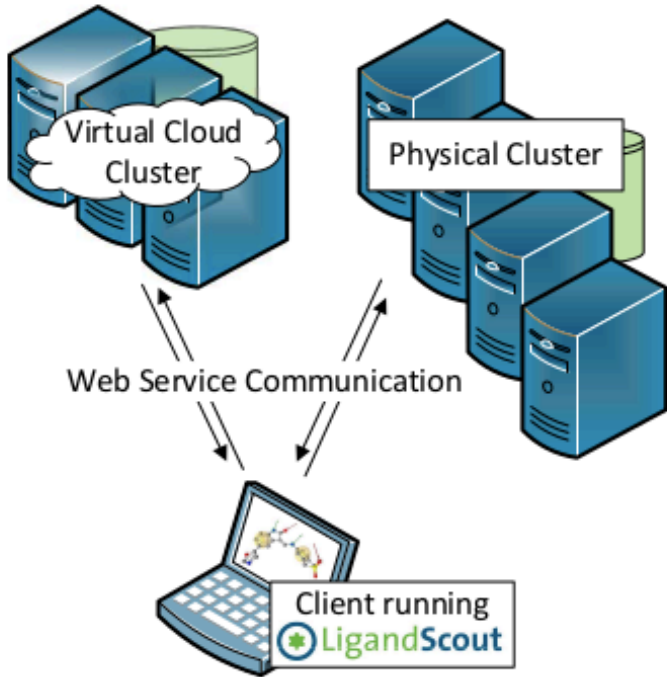
Overview

Combining Graphical User Interfaces and HPC

LigandScout Remote enables the seamless integration of high-performance computing (HPC) resources into the *LigandScout* desktop application. By handling necessary data conversion and network communication transparently to the user, this approach evades any HPC usability barriers.

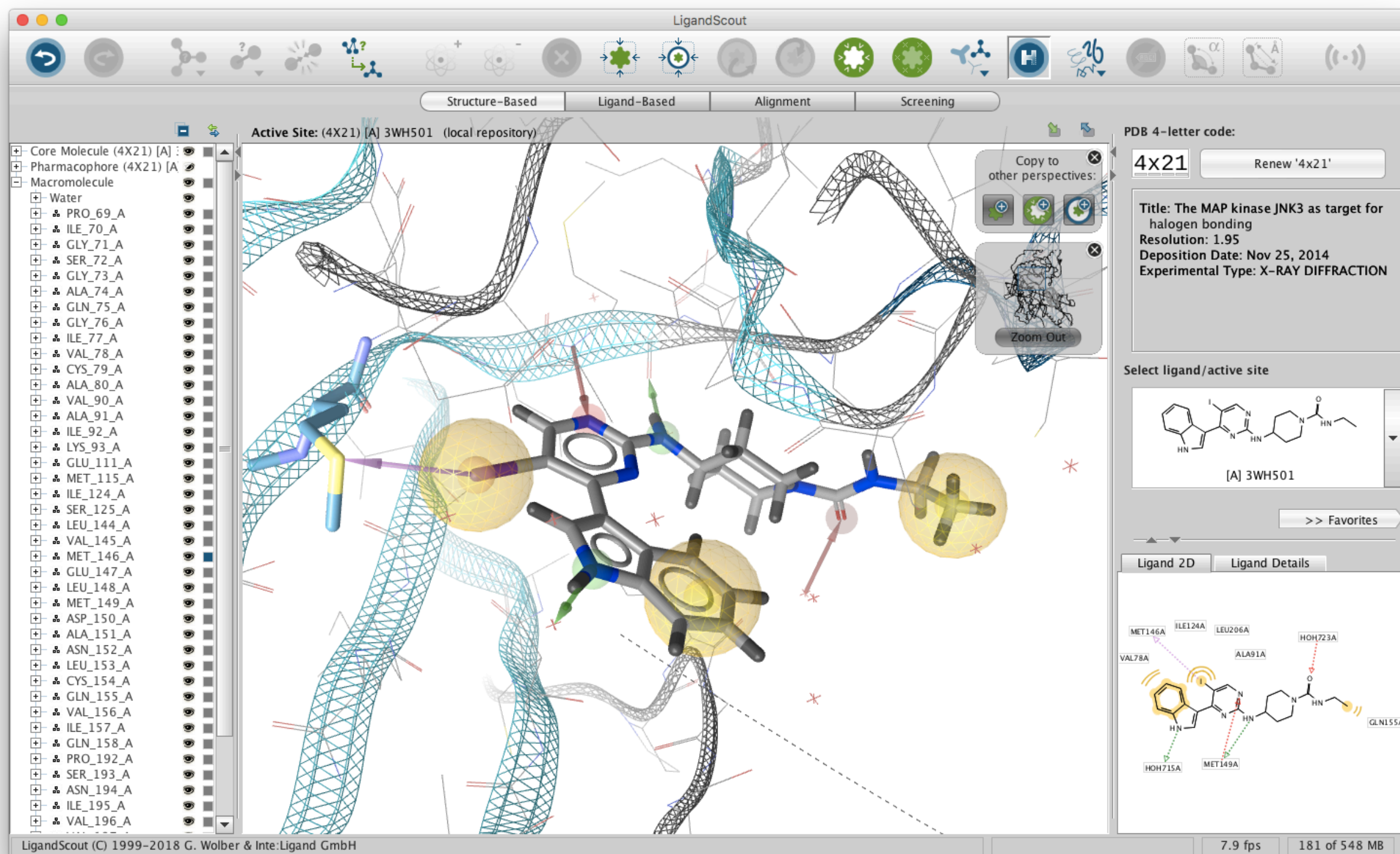
Table of contents

- Combining Graphical User Interfaces and HPC
- Motivation
- About this Documentation



```
graph TD; VCC[Virtual Cloud Cluster] <-->|Web Service Communication| PC[Physical Cluster]; VCC <-->|Web Service Communication| CL[Client running LigandScout]; PC <-->|Web Service Communication| CL;
```


New: Halogen Bond Acceptor Feature



Fully Indexed Online Help Manual

LigandScout - Help

Chapters

Search

1. Help Overview


2. Introduction

3. File Handling, Data Management and Networking

4. LigandScout Perspectives

5. Introduction to Pharmacophore Modeling

Chapter 1. Help Overview



The graphic features a green background with a molecular structure at the top left and a large circular icon on the right containing a gear-like shape with greater-than and less-than symbols. The text 'LigandScout Online Manual' is in the top right corner.

Welcome to the LigandScout interactive help system. You can start with the introduction or directly learn more about ...

- ... what's new in LigandScout 4
- ... how to align molecules and pharmacophores
- ... how to generate excluded volume coats
- ... how to create shared feature pharmacophores
- ... how to use the graphical user interface and explore a specific binding site
- ... how to use LigandScout for virtual screening

What was new in LigandScout 4.2 ?

- User interactive charts for analyzing and filtering tables
- Fully editable tables, import & export from and to Excel
- Fully editable parameter sets for library filtering
- Find ligands present in the PDB database in any table
- Remodelled workflow for ligand-based pharmacophore generation
- Visualization of multiple superimposed binding sites
- MD trajectory import from Amber & Gromacs, in addition to Charmm
- Automated creation of pharmacophores from MD trajectories
- Tools for analysis of pharmacophores derived from MD

Some Unique Features of LigandScout

Structure-based pharmacophore modeling

- Automated recognition of ligand-protein interactions
- User-friendly analysis of tautomers & side chain rotamers

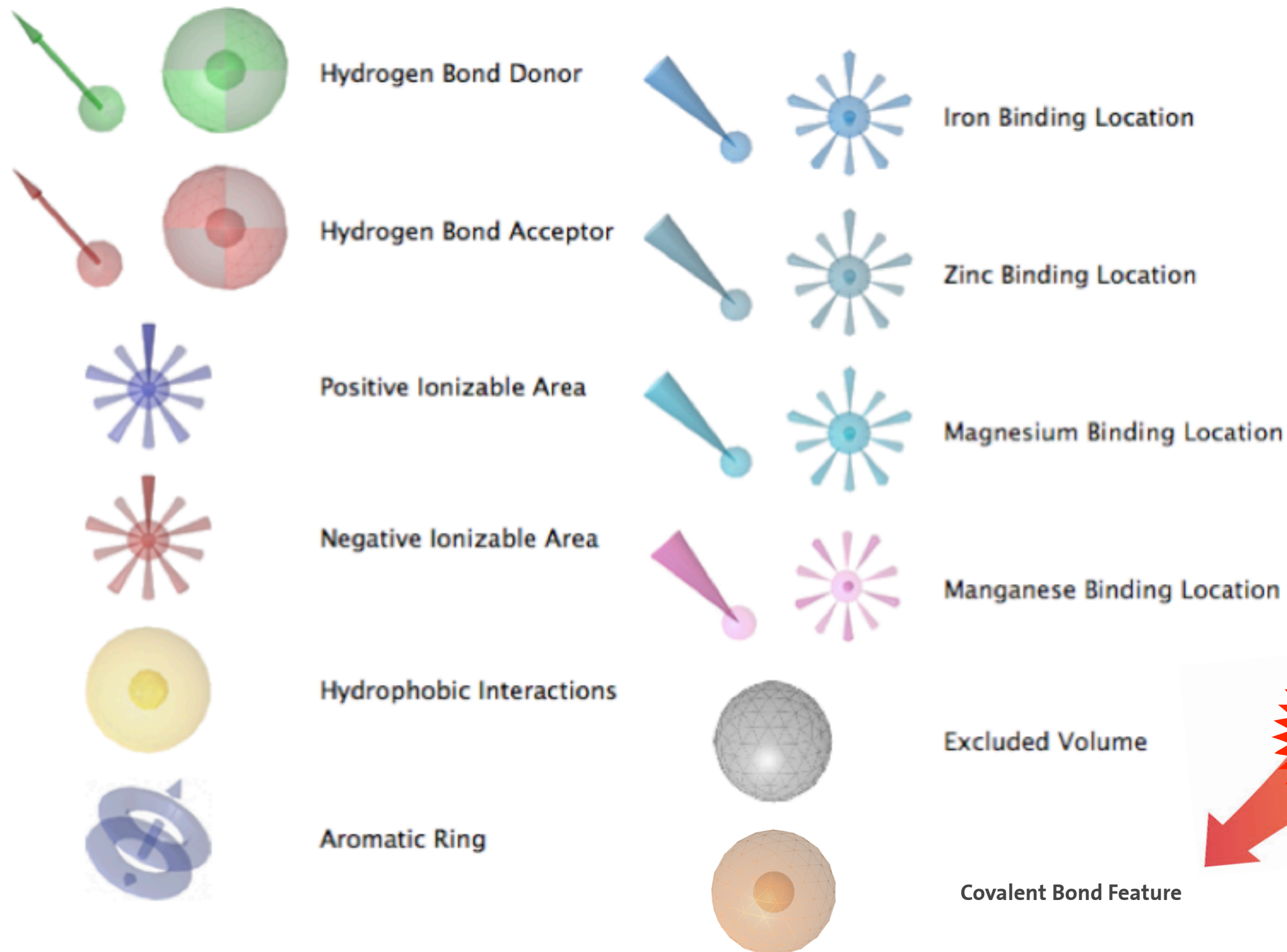
Ligand-based pharmacophore modeling

- Pharmacophore-based ligand clustering
- Automated creation of exclusion volume for ligand-based pharmacophores
- Unlimited number of features per pharmacophore

Virtual screening

- Speed & accuracy increases with the number of features

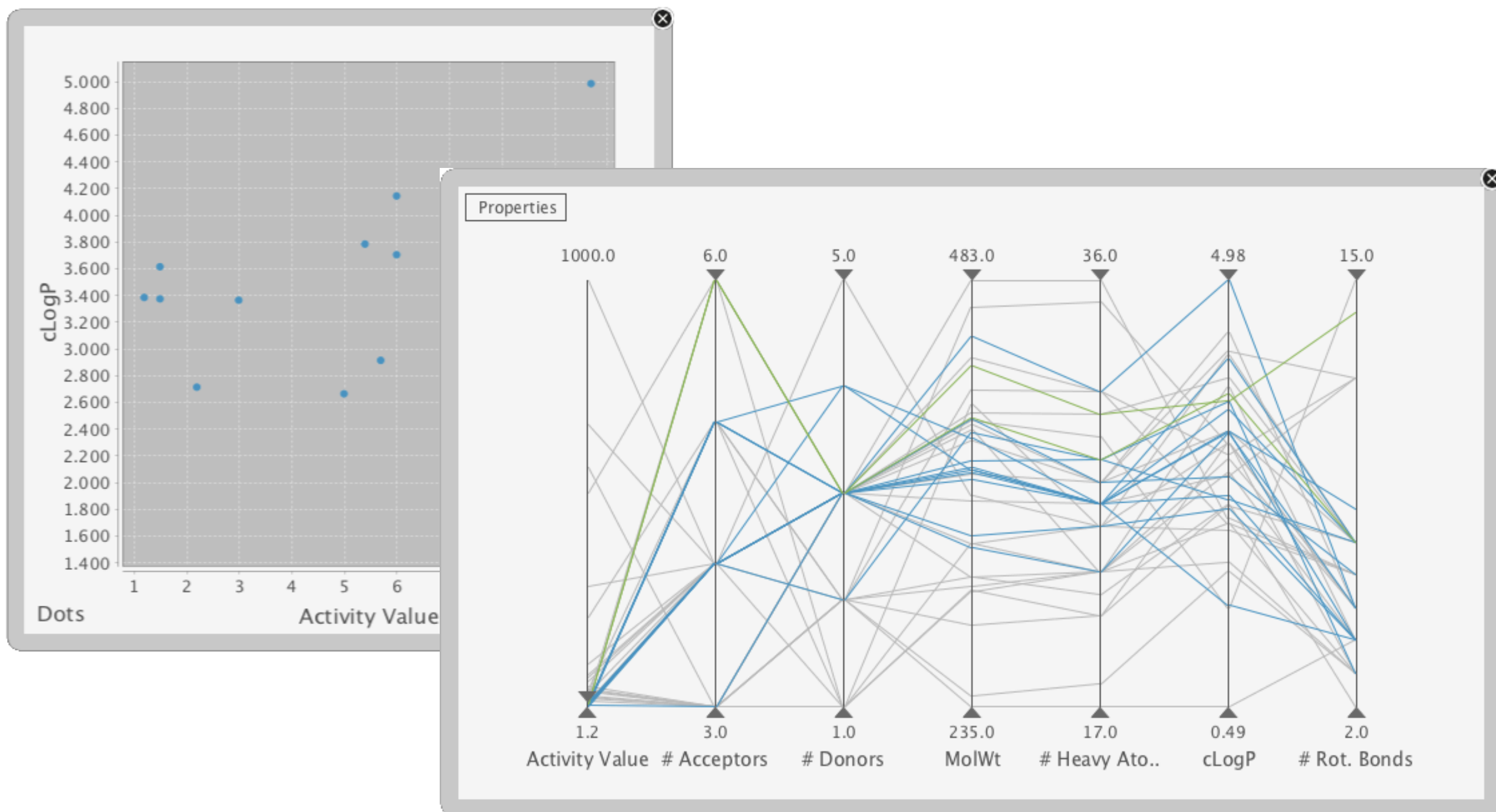
LigandScout Pharmacophore Features



NEW!

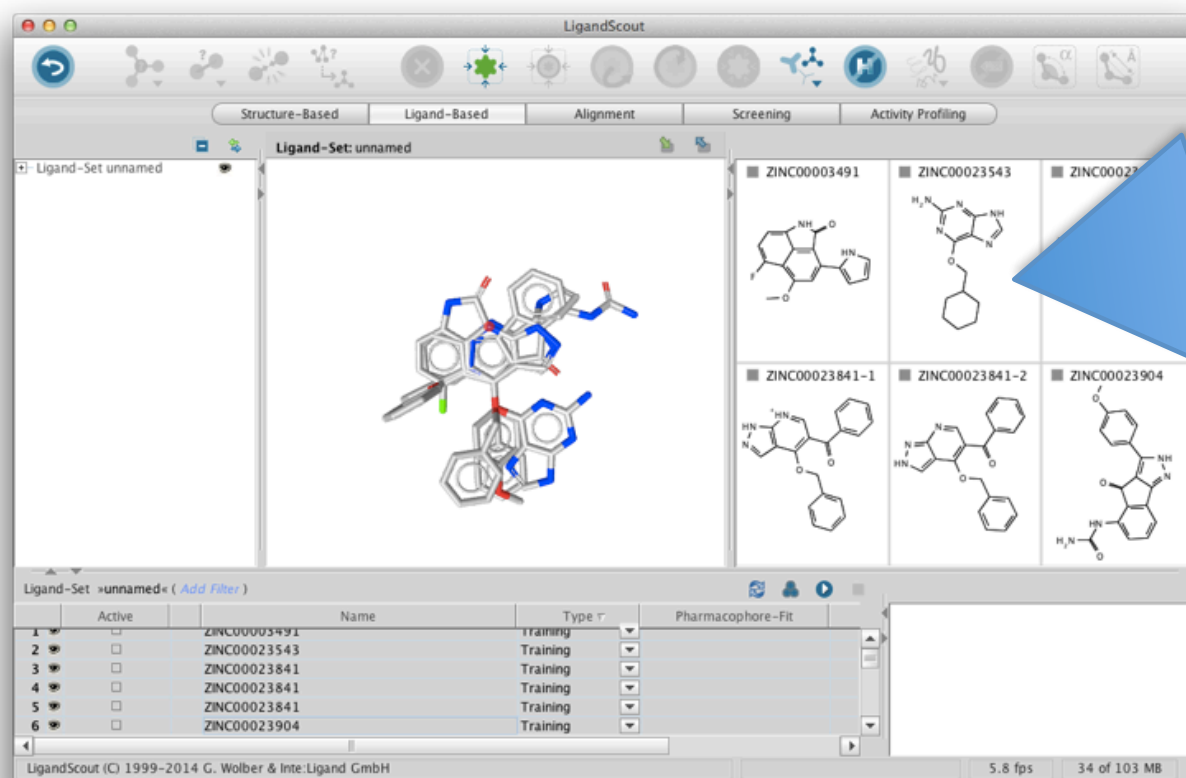
Interactive Charts

- Use interactive charts for analyzing and filtering your tables



Tables: Now Fully Editable

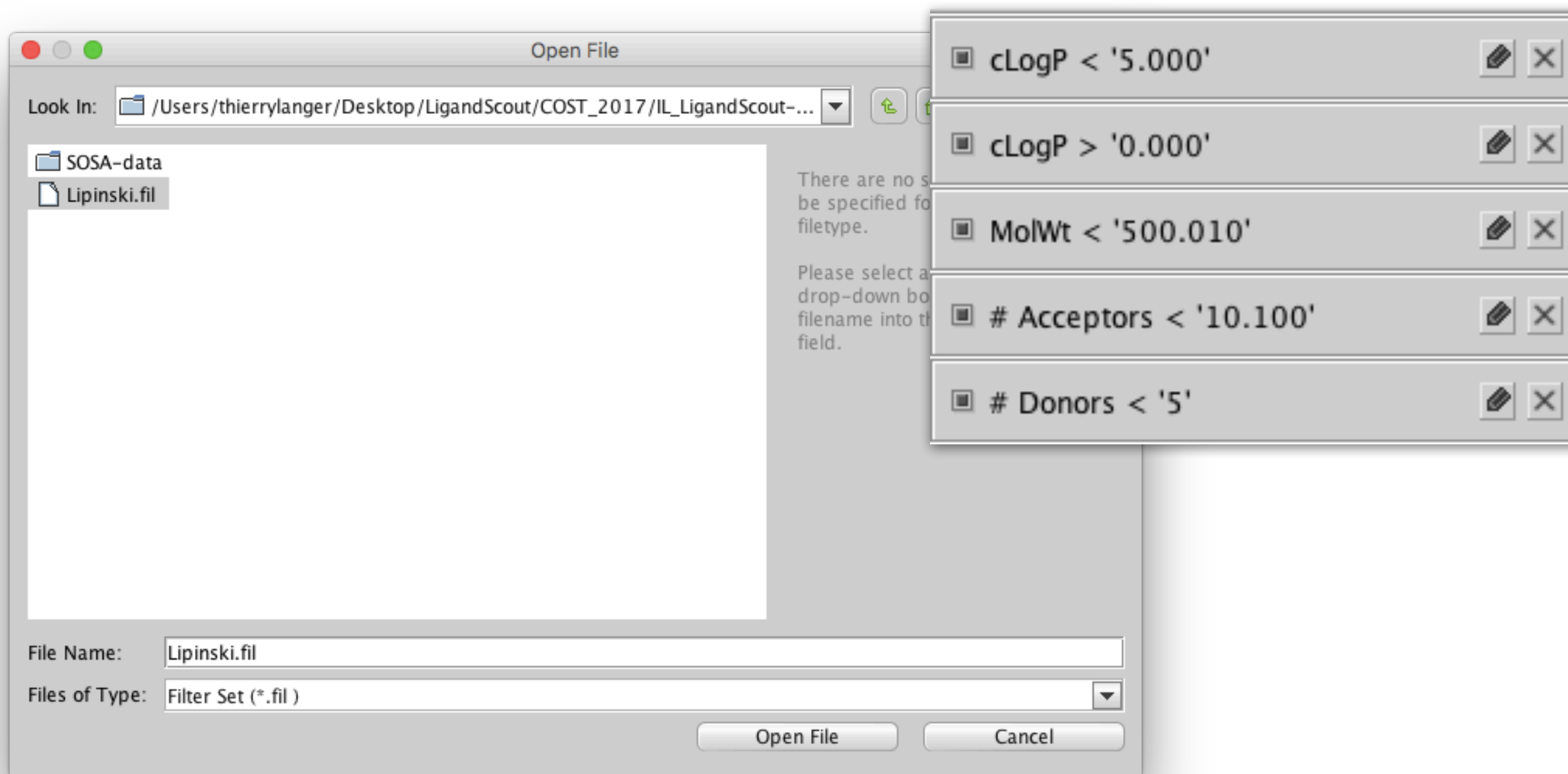
- Add and remove information, import & export from and to Excel



	A	B	C	D	E	F	G	H	I	J
	Name	Mol. Weight	# Heavy Atoms	# Acceptors	# Rot. Bonds	cLogP	# Rings	# Donors	Rel. TPSA	
1	ZINC00003491	28.0	57.88	21	3	3.26	4	2	1.81	
2	ZINC00023543	24.0	89.71	18	4	1.89	3	2	2.56	
3	ZINC00023841	329.36	67.87	25	4	3.25	4	1	1.7	
4	ZINC00023841	330.37	69.12	25	3	2.67	4	2	1.69	
5	ZINC00023841	329.36	67.87	25	4	3.25	4	1	1.7	
6	ZINC00023904	334.33	110.1	25	4	2.56	4	3	2.82	
7	ZINC00023904	334.33	110.1	25	4	2.56	4	3	2.82	
8	ZINC00023904	334.33	110.1	25	4	2.56	4	3	2.82	
9	ZINC00582575	388.9	87.89	27	4	4.23	3	3	1.69	
10	ZINC00603011	402.48	135.88	28	6	3.78	4	3	2.72	
11	ZINC01487345	400.48	108.56	29	6	1.53	3	3	1.9	
12	ZINC01641925	298.35	87.89	22	4	1.09	3	3	2.2	
13	ZINC01649340	354.46	87.89	26	4	2.92	3	3	1.69	
14	ZINC03591113	406.56	95.3	30	3	3.23	5	3	1.54	
15	ZINC03814433	431.49	130.16	30	5	1.6	4	4	2.46	
16	ZINC03814434	467.55	74.03	35	3	2.24	8	2	1.19	
17	ZINC03814435	483.55	94.26	36	4	1.44	8	3	1.5	
18	ZINC03814437	431.9	128.02	30	6	1.29	3	3	2.37	
19	ZINC03814439	370.52	95.3	27	3	2.67	5	3	1.62	
20	ZINC03814440	341.32	115.4	24	5	2.41	4	2	3.5	
21	ZINC03814441	395.24	113.65	23	4	2.95	3	3	3.34	
22	ZINC03814443	329.38	87.3	23	3	3.08	3	3	2.3	
23	ZINC03814444	401.47	112.55	27	5	2.91	4	3	2.68	
24	ZINC03814447	398.46	100.19	27	4	4.43	4	3	2.44	
25	ZINC03814449	308.34	74.33	23	3	2.5	4	2	1.91	
26	ZINC03814450	359.36	152.68	25	5	3.46	3	3	4.02	
27	ZINC03814450	359.36	152.68	25	5	3.46	3	3	4.02	
28	ZINC03814451	370.41	145.58	27	6	3.03	3	3	2.97	
29	ZINC03814452	301.35	55.11	23	3	3.84	4	1	1.45	
30	ZINC03814452	302.36	56.36	23	2	3.26	4	2	1.45	
31	ZINC03814453	373.41	110	26	5	4.14	3	3	2.62	
32	ZINC03814454	419.51	87.81	31	5	1.73	4	3	1.51	
33	ZINC03814454	420.52	89.06	31	4	1.15	4	4	1.51	
34	ZINC03814455	311.43	68.02	20	4	3.3	2	1	1.84	
35	ZINC03814457	235.25	106.78	17	5	0.54	2	2	3.56	
36	ZINC03814457	235.25	106.78	17	5	0.54	2	2	3.56	
37	ZINC03814458	245.29	89.71	18	4	1.67	3	2	2.72	

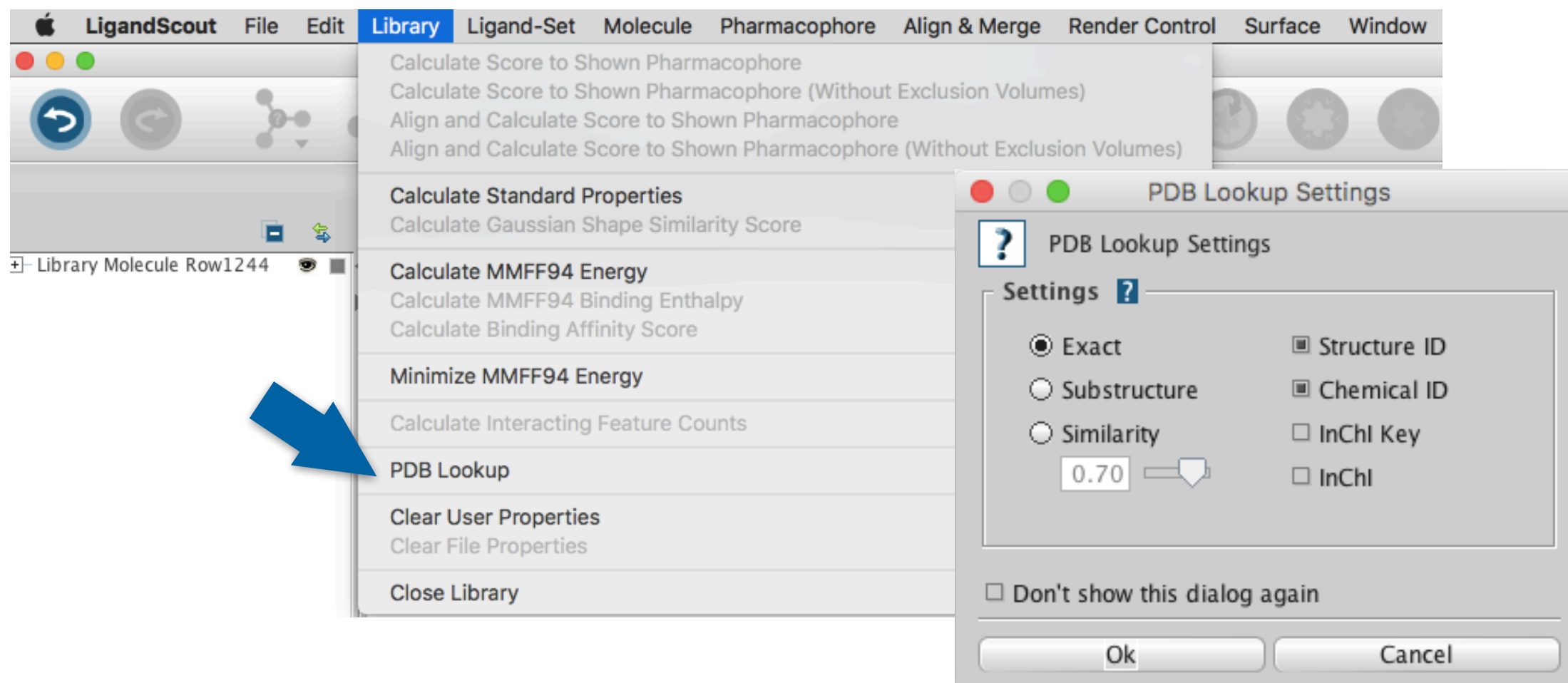
Table Filtering

- Save and import your parameter sets for table and library filtering



PDB Online LookUp

- Find out if a molecule from your table is present in the PDB database
- Check also for similar structures or search for substructures



PDB Online LookUp

- Find out if a molecule from your table is present in the PDB database
- Check also for similar structures or search for substructures

The screenshot shows the LigandScout application interface. The 'Library' menu is open, and a blue arrow points to the 'PDB Lookup' option. The 'PDB Lookup Settings' dialog box is displayed, allowing users to configure search parameters. The 'Settings' section includes radio buttons for 'Exact', 'Substructure', and 'Similarity' (set to 0.70), and checkboxes for 'Structure ID', 'Chemical ID', 'InChI Key', and 'InChI'. A 'Cancel' button is visible at the bottom right of the dialog.

Name	...	Chemical ID	Structure ID
NU-6102	12	4SP	5M57,4EOK,5LQF,4EOR,2C6O,1H1S,2W9,2W8
STAUROSPORINE	33	STU	2CLQ,2HW7,3S95,5OOR,4QFG,4CFH,5ISO,2PZY,4ERW,3A4O,4...
Row6832	11	D42	2B52
SELICICLIB	20	RRC	2A4L,1UNL,3DDQ,1YGK
PURVALANOL A	31	P01	1YOM,2IZU,2Z7S
INDIRUBIN SULFATE	30	SU9	1PF8,3PY0,3PY1
(7S)-HYDROXYL-STAUROSPORINE	5	UCN	1OKZ,1NVQ,1PKD
Row653	28	HDY	1OIR
Row3341	22	LS5	1KE9,4FKP
Row2862	23	LS4	1KE8
Row2674	24	LS3	1KE7
Row1763	25	LS2	1KE6
Row202	26	LS1	1KE5
Row8112	18	II7	1G5S

Single Click Ligand-based Model Generation

- Use new single click generation workflow

Ligand-Set: CDK2-Ligands

Copy to other perspectives:

Selected Ligands:

- CHEMBL83775
- CHEMBL23254_PURVAL
- CHEMBL14762_SELICIC
- CHEMBL23327_PURVAL

	Active	Name	Type	Matching Features	Cluster ID	Pharmacophore-Fit
1	<input type="checkbox"/>	CHEMBL294884	Ignored		14	
2	<input type="checkbox"/>	CHEMBL309925	Ignored		14	
3	<input type="checkbox"/>	CHEMBL78959	Ignored		14	
4	<input type="checkbox"/>	CHEMBL103355	Ignored		13	72.82
5	<input type="checkbox"/>	CHEMBL72461	Ignored		13	72.81
6	<input checked="" type="checkbox"/>	CHEMBL23327_PURVALANOL A	Training		12	77.85
7	<input checked="" type="checkbox"/>	CHEMBL14762_SELICICLIB	Training		12	78.56
8	<input checked="" type="checkbox"/>	CHEMBL23254_PURVALANOL B	Training		12	86.05
9	<input checked="" type="checkbox"/>	CHEMBL83775	Training		12	78.77
10	<input type="checkbox"/>	CHEMBL269882	Ignored		11	

Model-12-1 Score: 0.8182

LigandScout (C) 1999-2017 G. Wolber & Inte:Ligand GmbH | 9.0 fps | 335 of 1168 MB

Single Click Ligand-based Model Generation

- Use new single click generation workflow

Ligand-Set: CDK2-Ligands

Copy to other perspectives:

Type: [Ligand-Based] [Structure-Based] [Alignment] [Screening]

Active	Name	Type	Matching Features	Cluster ID	Pharmacophore-Fit
1	CHEMBL294884	Ignored		14	
2	CHEMBL309925	Ignored		14	
3	CHEMBL78959	Ignored		14	
4	CHEMBL103355	Ignored		13	72.82
5	CHEMBL72461	Ignored		13	72.81
6	CHEMBL23327_PURVALANOL A	Training		12	77.85
7	CHEMBL14762_SELICICLIB	Training		12	78.56
8	CHEMBL23254_PURVALANOL B	Training		12	86.05
9	CHEMBL83775	Training		12	78.77
10	CHEMBL269882	Ignored		11	

Name	Score
Model-12-1	0.8182

LigandScout (C) 1999-2017 G. Wolber & Inte:Ligand GmbH

9.0 fps 335 of 1168 MB

Single Click Ligand-based Model Generation

- Use new single click generation workflow

The screenshot displays the LigandScout software interface, which is used for ligand-based model generation. The interface is divided into several sections:

- Top Bar:** Contains icons for various functions and tabs for "Structure-Based", "Ligand-Based", "Alignment [3]", and "Screening [5]".
- Left Panel:** A tree view showing the "Ligand-Set: CDK2-Ligands" with a list of molecules: CHEMBL83775, CHEMBL23254, CHEMBL14762, CHEMBL23327, and a "Pharmacophore Solution Mod".
- Central View:** A 3D molecular model of a ligand bound to a protein, with a "Copy to other perspectives:" button.
- Right Panel:** A grid of 2D chemical structures for selected molecules: CHEMBL83775, CHEMBL23254_PURVAL, CHEMBL14762_SELICIC, and CHEMBL23327_PURVAL. Each structure shows pharmacophore features like HBA, HBD, and AR.
- Bottom Panel:** A table listing the ligands and their pharmacophore fit scores. The table has columns for "Active", "Name", "Type", "Matching Features", "Cluster ID", and "Pharmacophore-Fit".

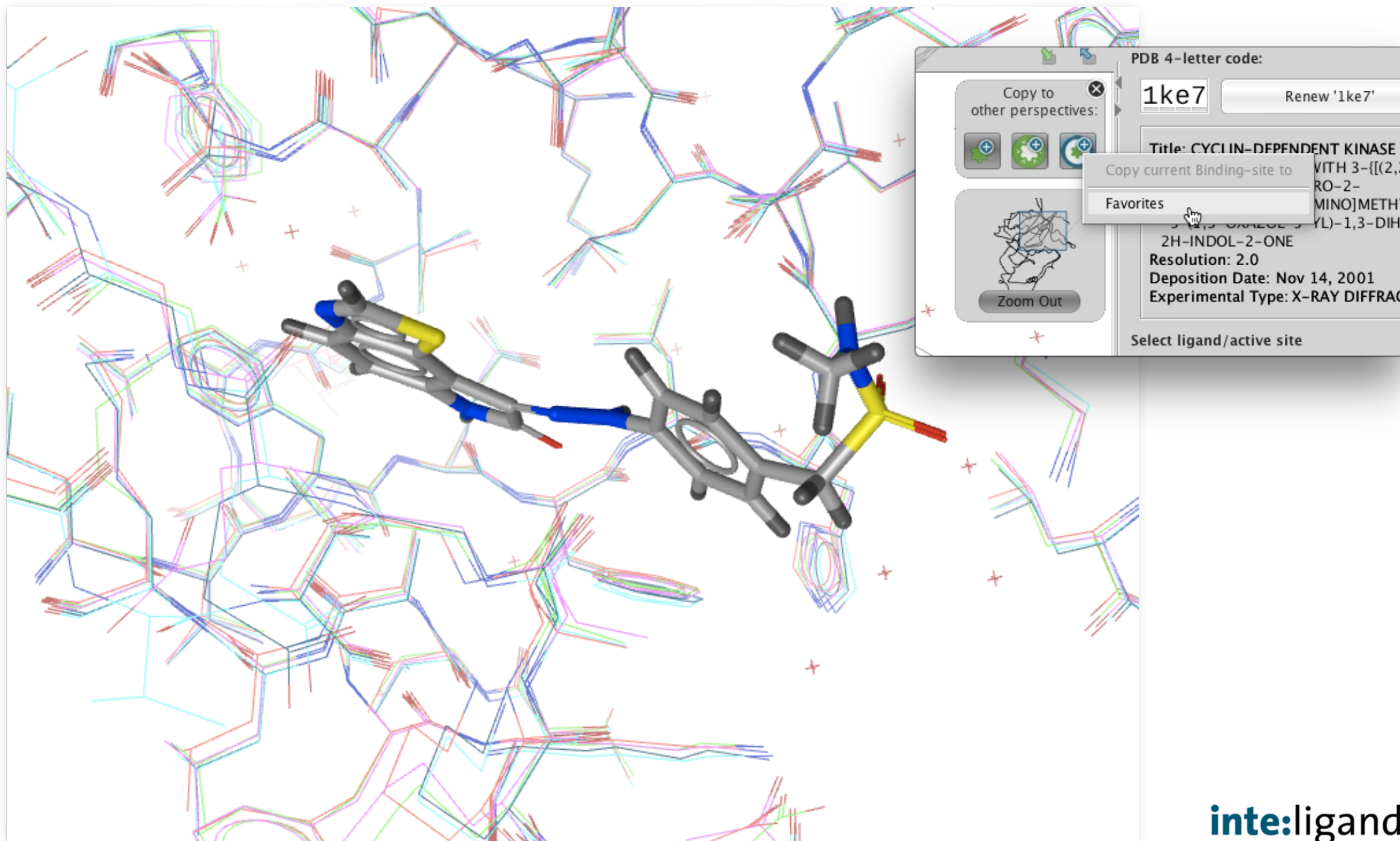
Red boxes highlight the "Type:" dropdown menu in the left panel and the "Type:" dropdown menu in the bottom panel, both showing three options: a green triangle, a blue triangle, and a grey triangle. Another red box highlights a set of icons in the bottom right, including a refresh icon, a cluster icon, a pharmacophore icon, and a play button icon.

	Active	Name	Type	Matching Features	Cluster ID	Pharmacophore-Fit
1	<input type="checkbox"/>	CHEMBL294884	Ignored		14	
2	<input type="checkbox"/>	CHEMBL309925	Ignored		14	
3	<input type="checkbox"/>	CHEMBL78959	Ignored		14	
4	<input type="checkbox"/>	CHEMBL103355	Ignored		13	72.82
5	<input type="checkbox"/>	CHEMBL72461	Ignored		13	72.81
6	<input checked="" type="checkbox"/>	CHEMBL23327_PURVALANOL A	Training		12	77.85
7	<input checked="" type="checkbox"/>	CHEMBL14762_SELICICLIB	Training		12	78.56
8	<input checked="" type="checkbox"/>	CHEMBL23254_PURVALANOL B	Training		12	86.05
9	<input checked="" type="checkbox"/>	CHEMBL83775	Training		12	78.77
10	<input type="checkbox"/>	CHEMBL269882	Ignored		11	

LigandScout (C) 1999-2017 G. Wolber & Inte:Ligand GmbH

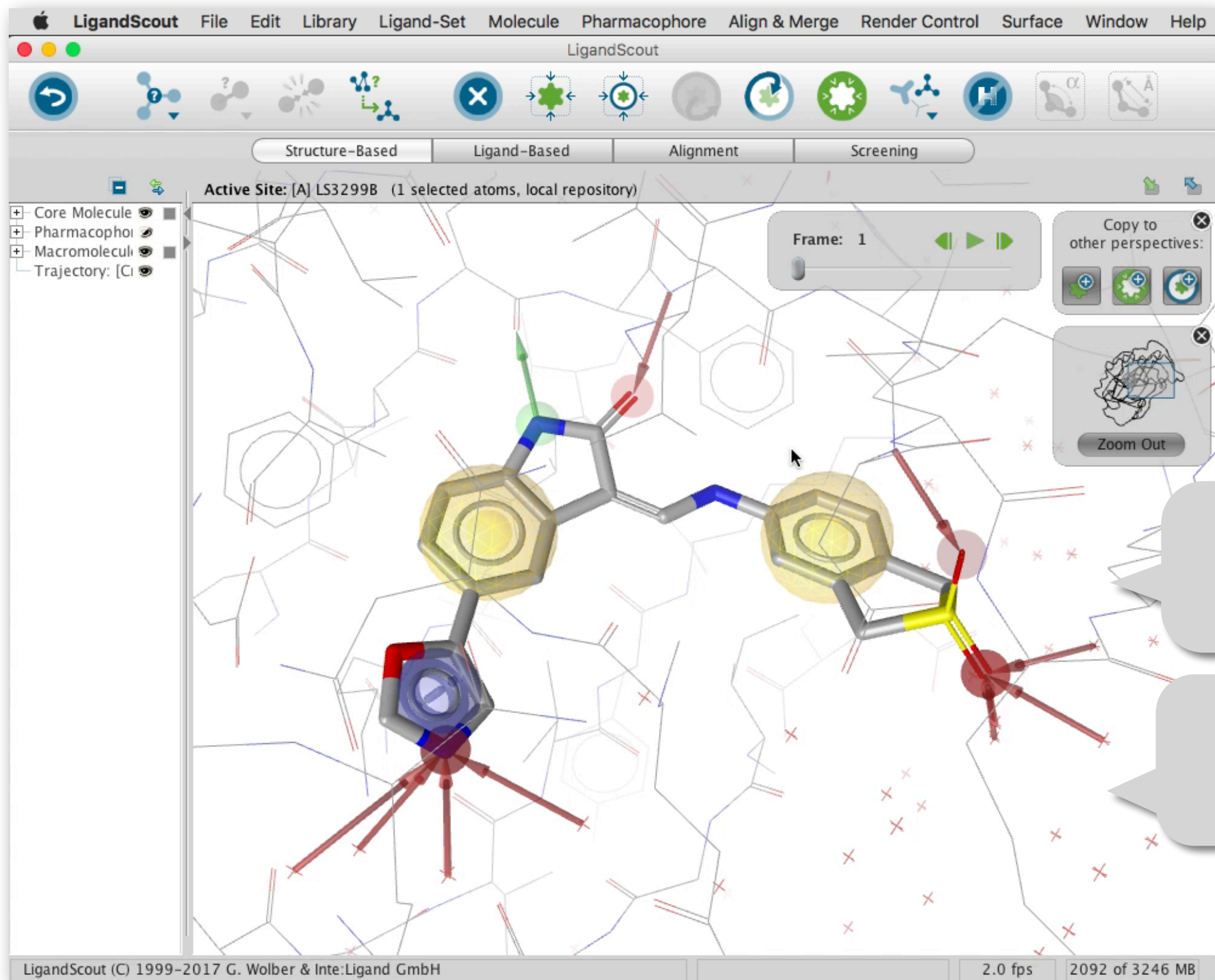
Protein Binding Site Analysis

- Visualize multiple superimposed binding sites in the favorites view



MD Trajectory Analysis

- Create automatically pharmacophores from your MD trajectories

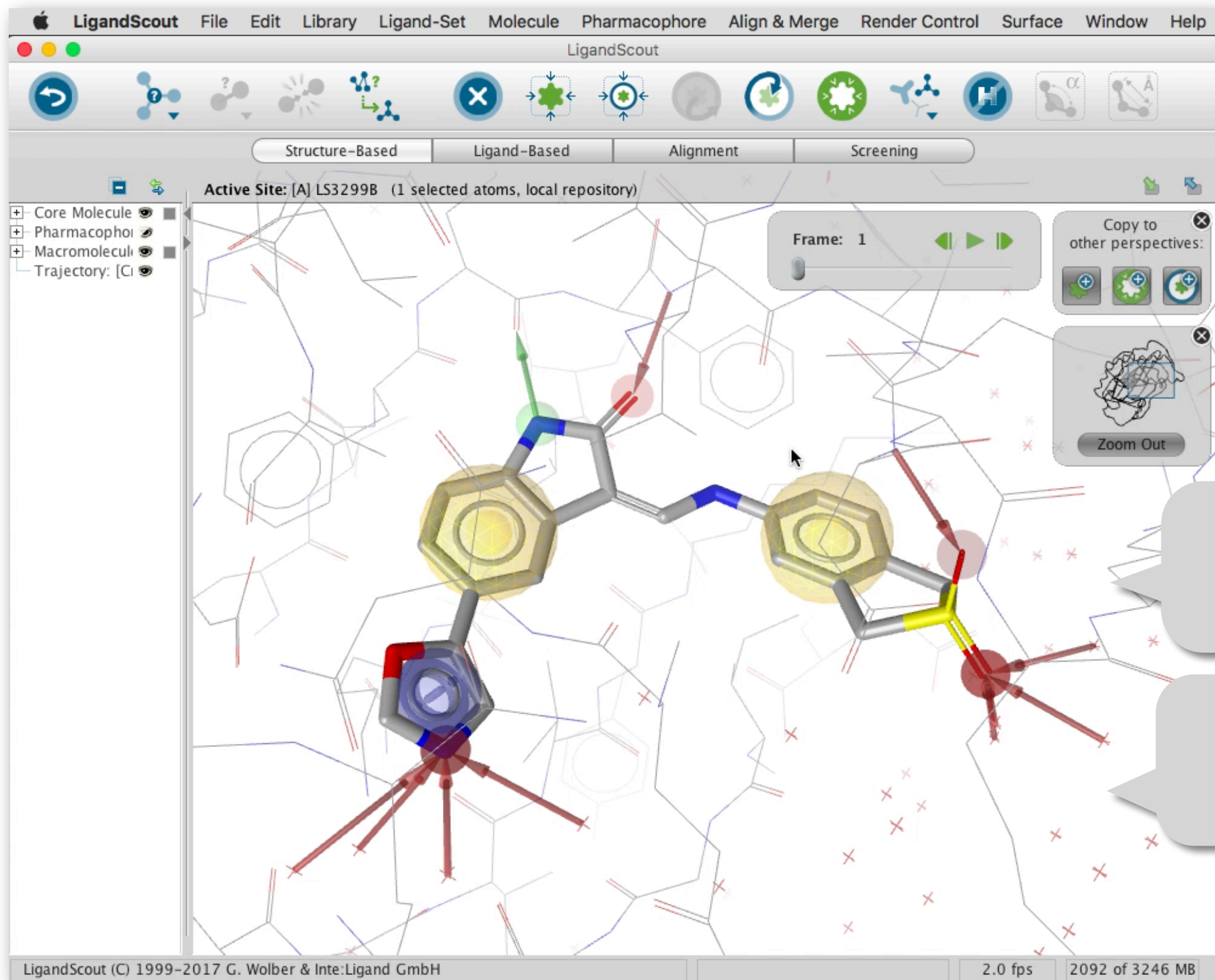


CTRL + F10
Windows & Linux

CMD + fn + F10
macOS

MD Trajectory Analysis

- Create automatically pharmacophores from your MD trajectories

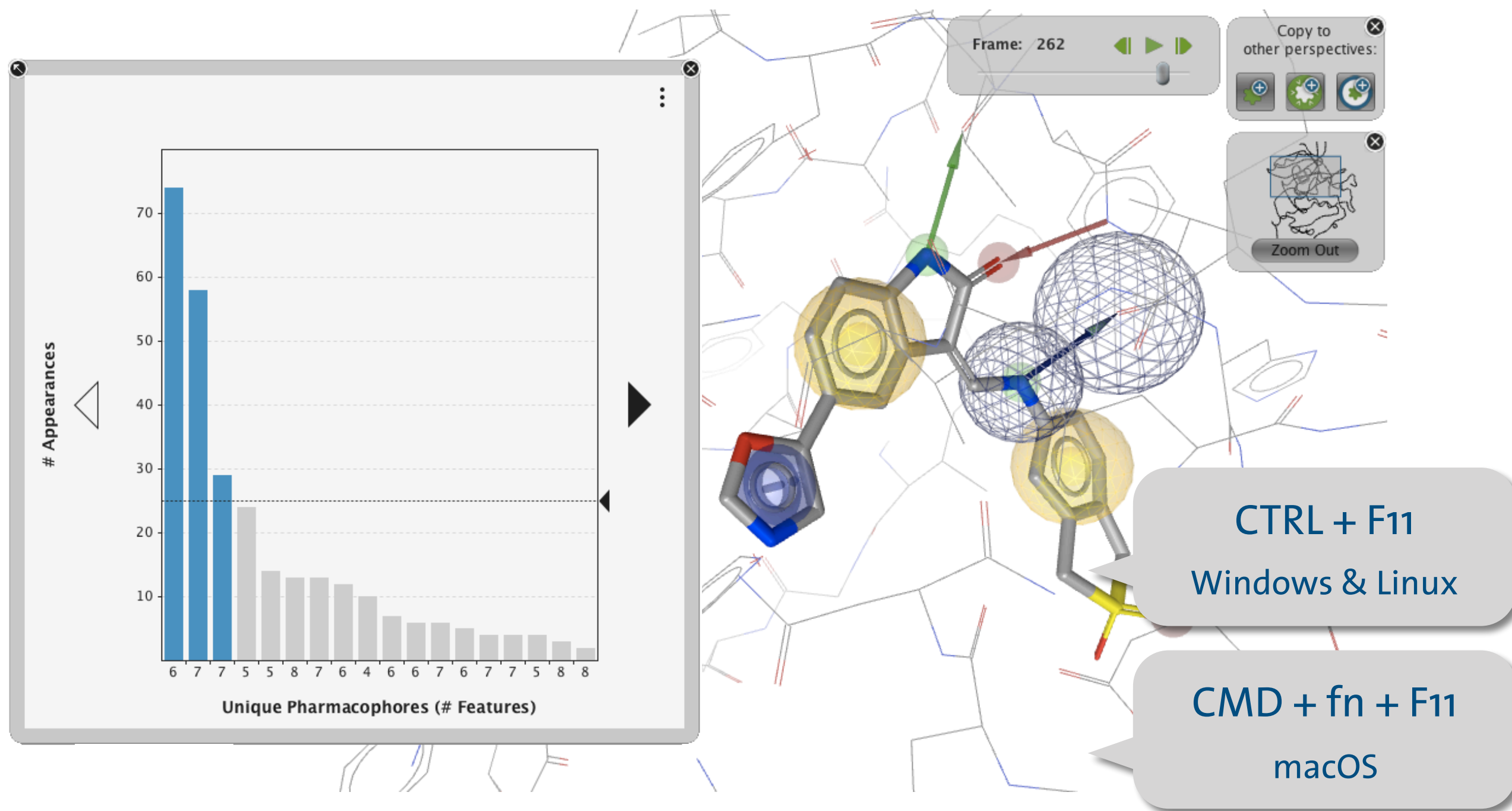


CTRL + F10
Windows & Linux

CMD + fn + F10
macOS

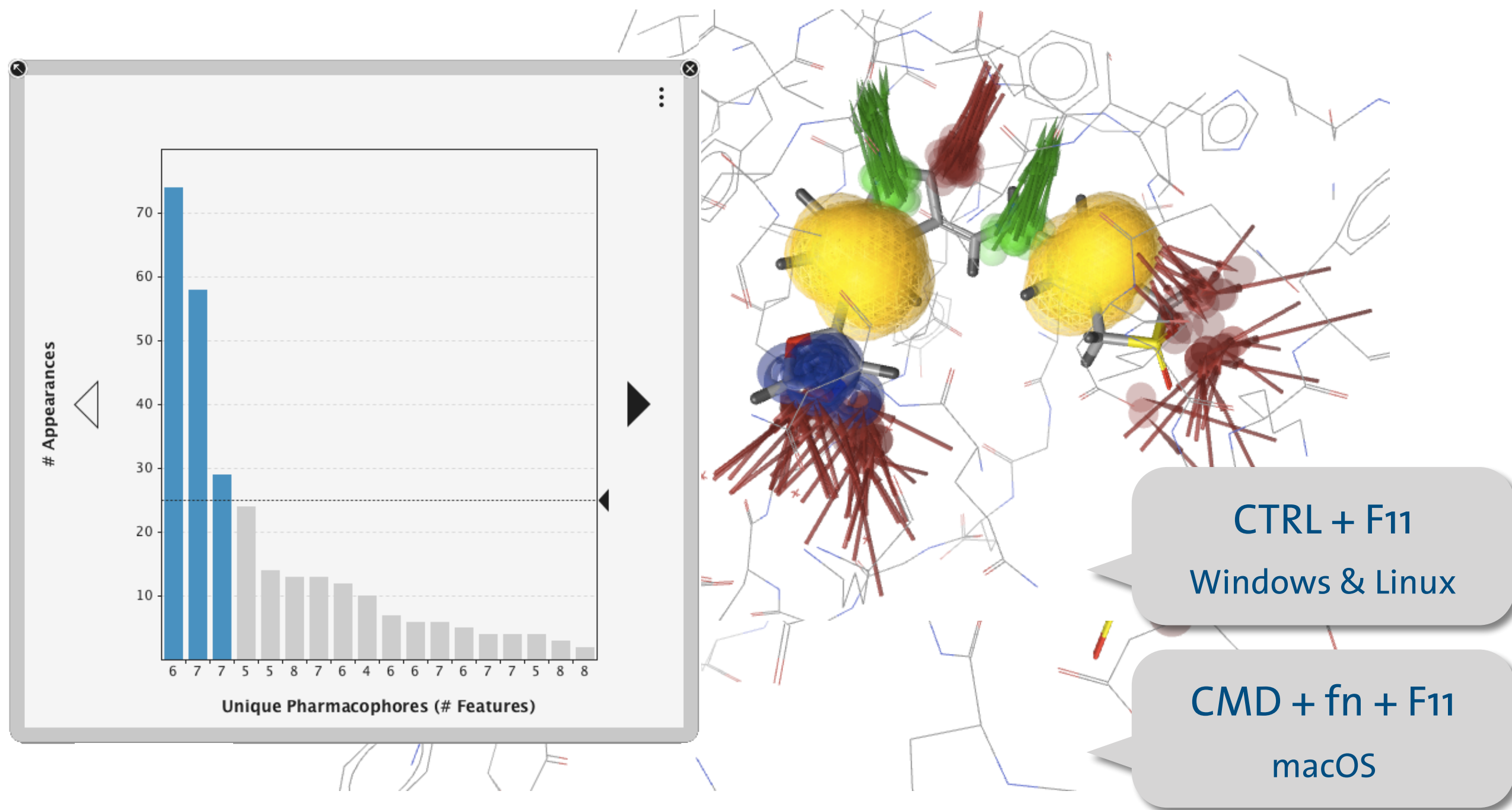
Tools for Pharmacophore-based MD Analysis

- Find all different unique pharmacophore models



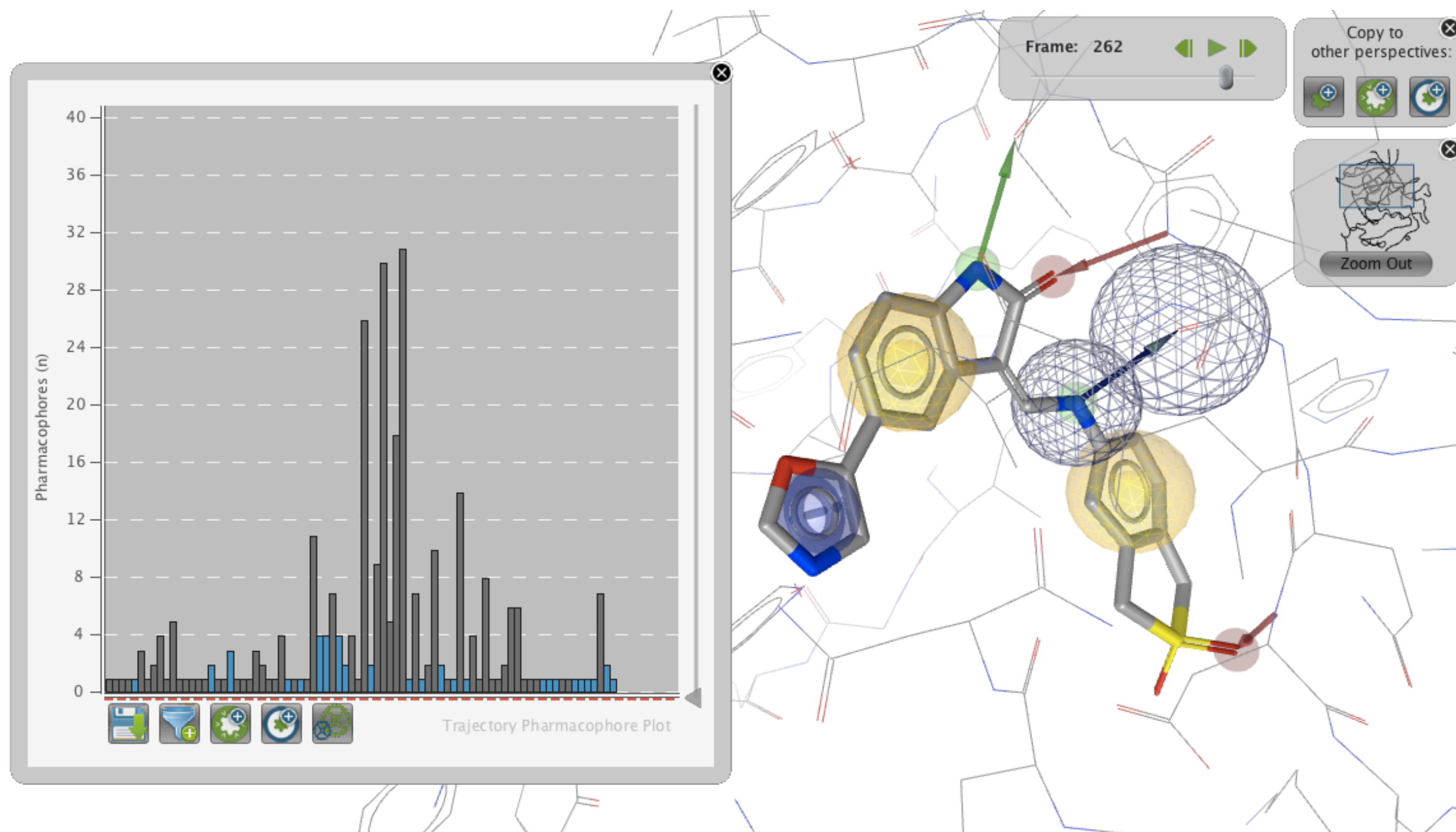
Tools for Pharmacophore-based MD Analysis

- Find all different unique pharmacophore models



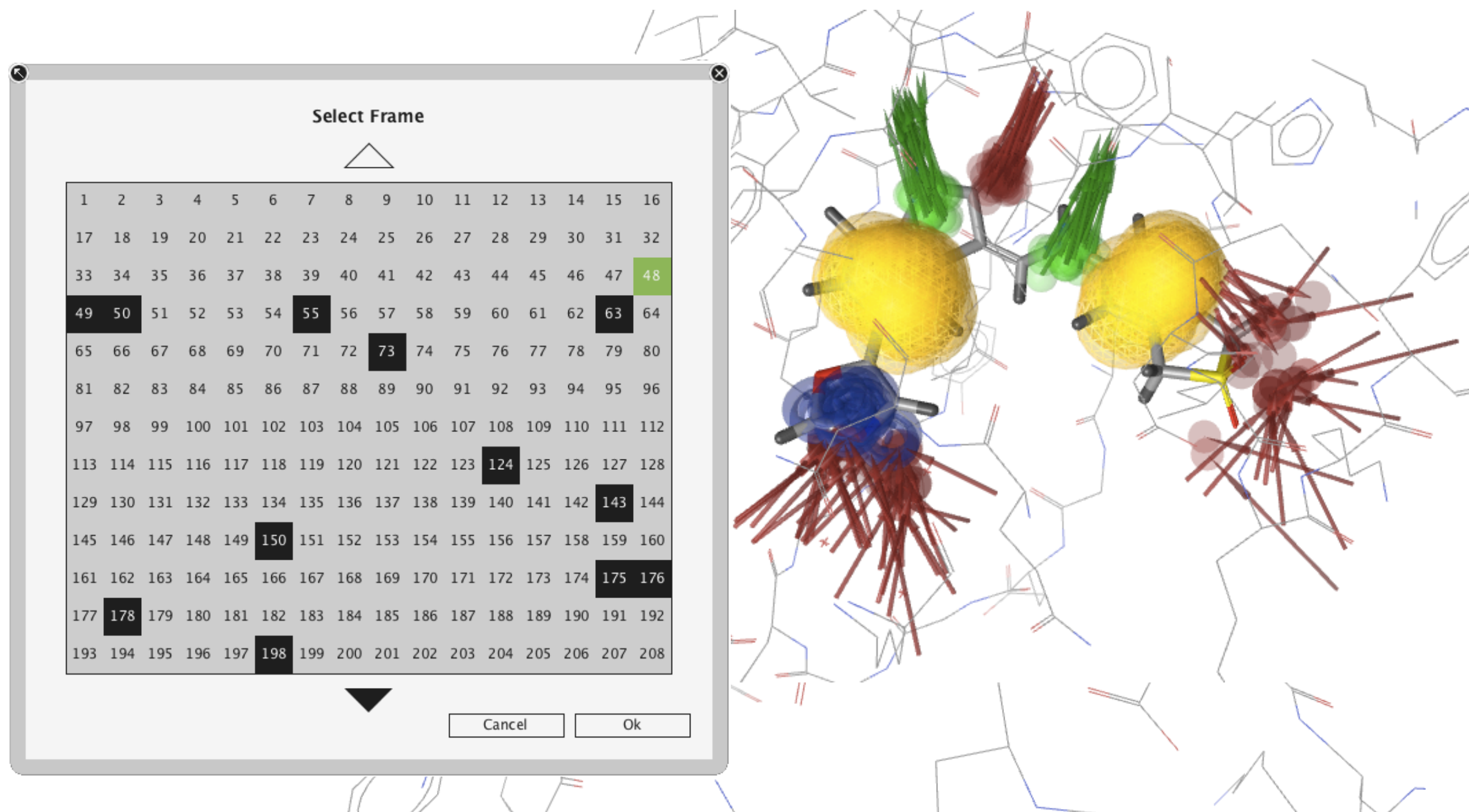
Tools for Pharmacophore-based MD Analysis

- Find all frames containing a selected pharmacophore feature



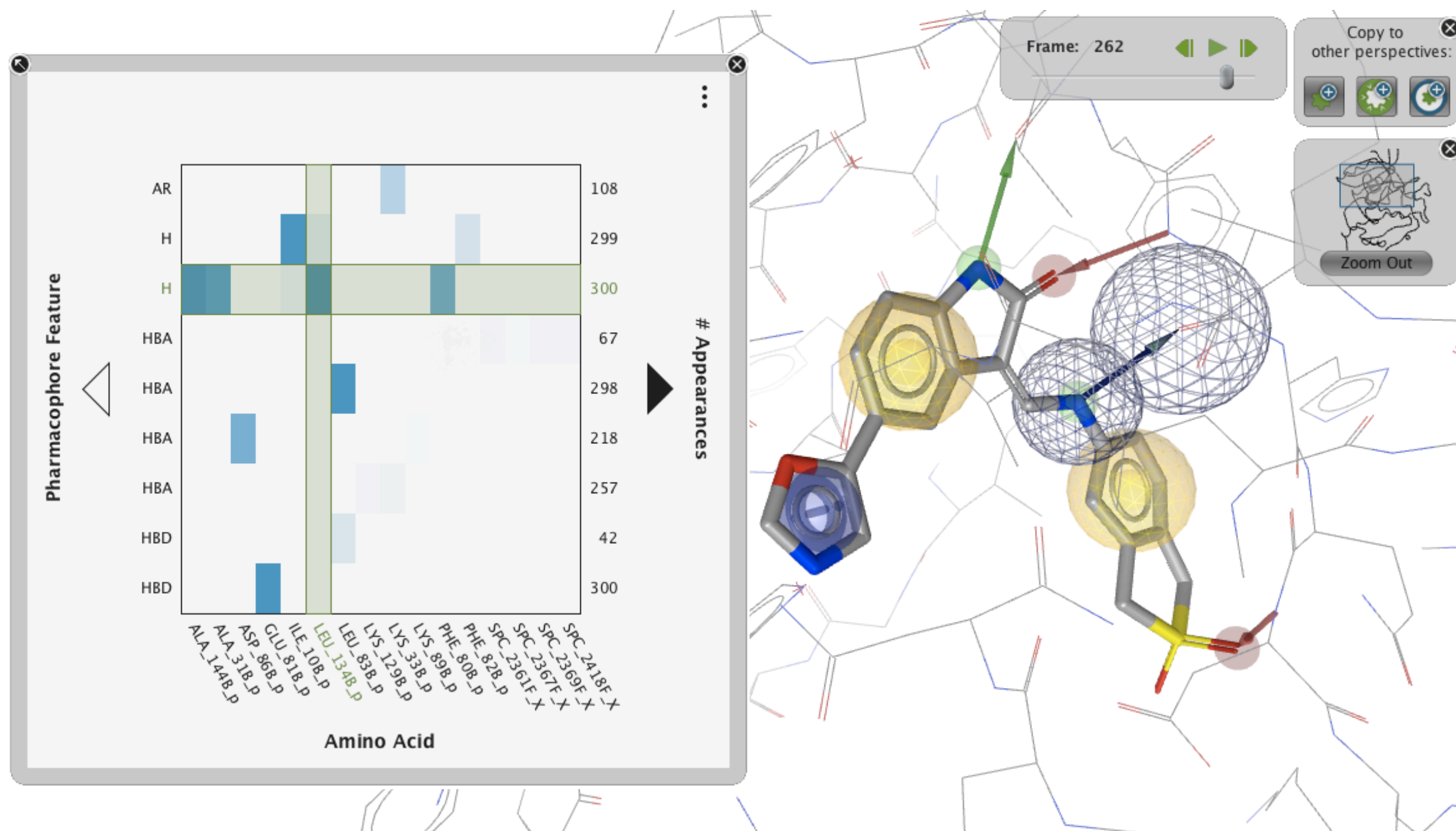
Tools for Pharmacophore-based MD Analysis

- Find all frames containing a selected pharmacophore feature



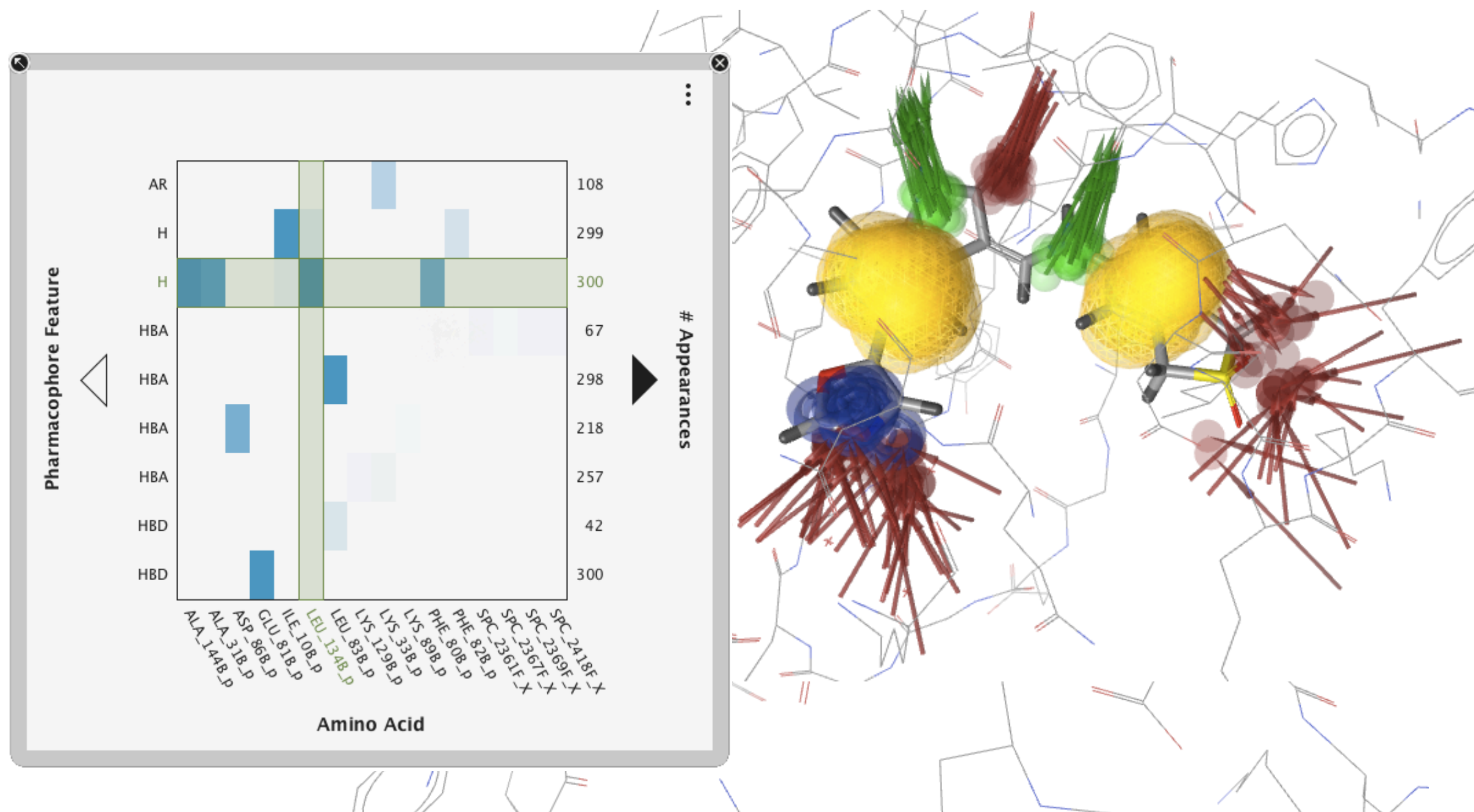
Tools for Pharmacophore-based MD Analysis

- Display pharmacophore interaction map



Tools for Pharmacophore-based MD Analysis

- Display pharmacophore interaction map



New Features in LigandScout 4.1

Usability Enhancement

- Drag & Drop
- Extended pharmacophore editing
- Extended table functionality & export
- Automatic background job queuing system

Drag & Drop Molecule Files into GUI

Press and drag

Release

LigandScout

Structure-Based Ligand-Based Alignment Screening Activity Profiling

Ligand-Set: unnamed

ZINC00003491 ZINC00023543 ZINC00023841

ZINC00023841-1 ZINC00023841-2 ZINC00023904

Ligand-Set: unnamed (Add Filter)

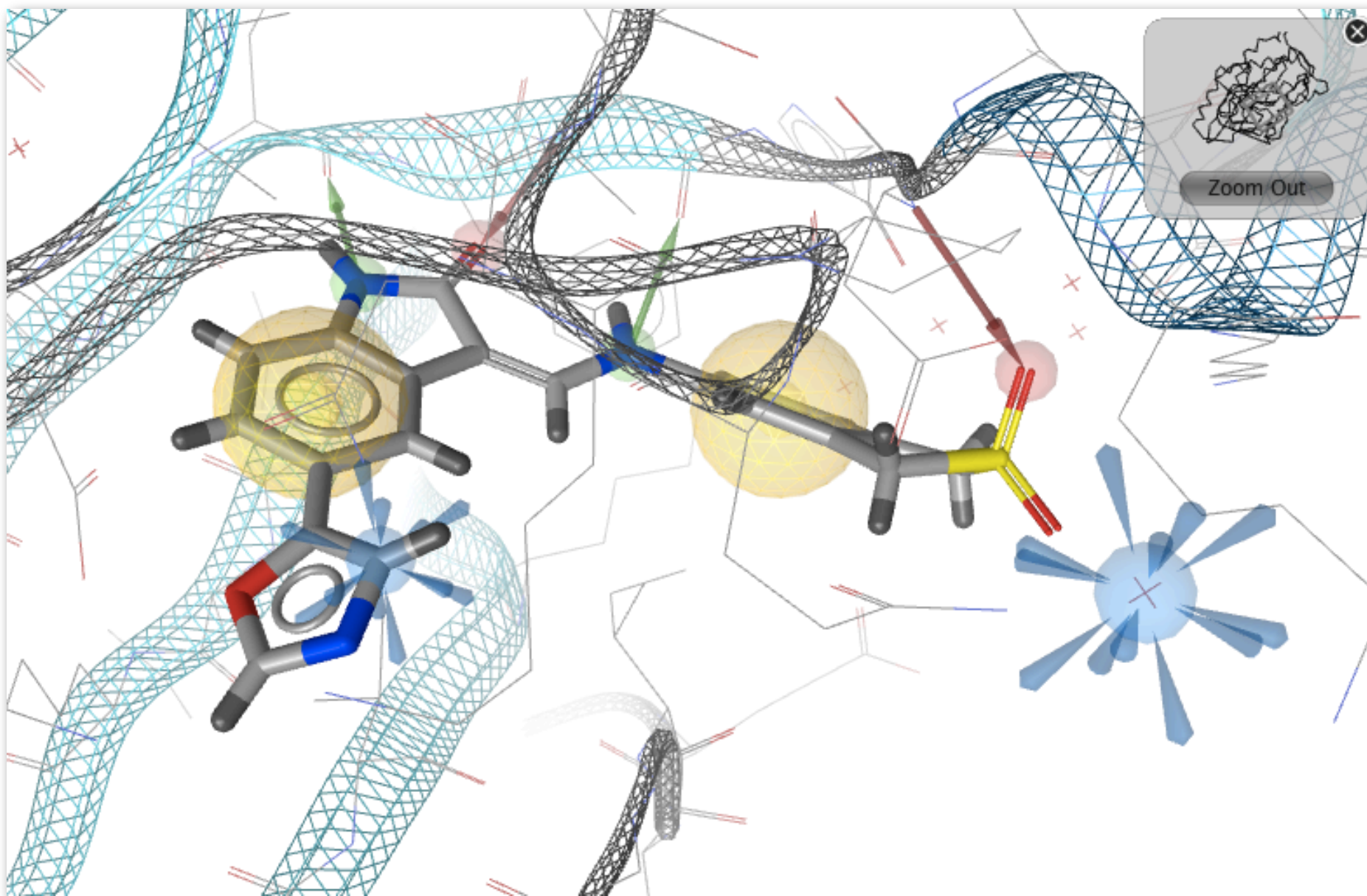
	Active	Name	Type	Pharmacophore-Fit
1	<input checked="" type="checkbox"/>	ZINC00003491	Training	
2	<input type="checkbox"/>	ZINC00023543	Training	
3	<input type="checkbox"/>	ZINC00023841	Training	
4	<input type="checkbox"/>	ZINC00023841	Training	
5	<input type="checkbox"/>	ZINC00023841	Training	
6	<input type="checkbox"/>	ZINC00023904	Training	

LigandScout (C) 1999-2014 G. Wolber & Inte:Ligand GmbH

5.8 fps 34 of 103 MB

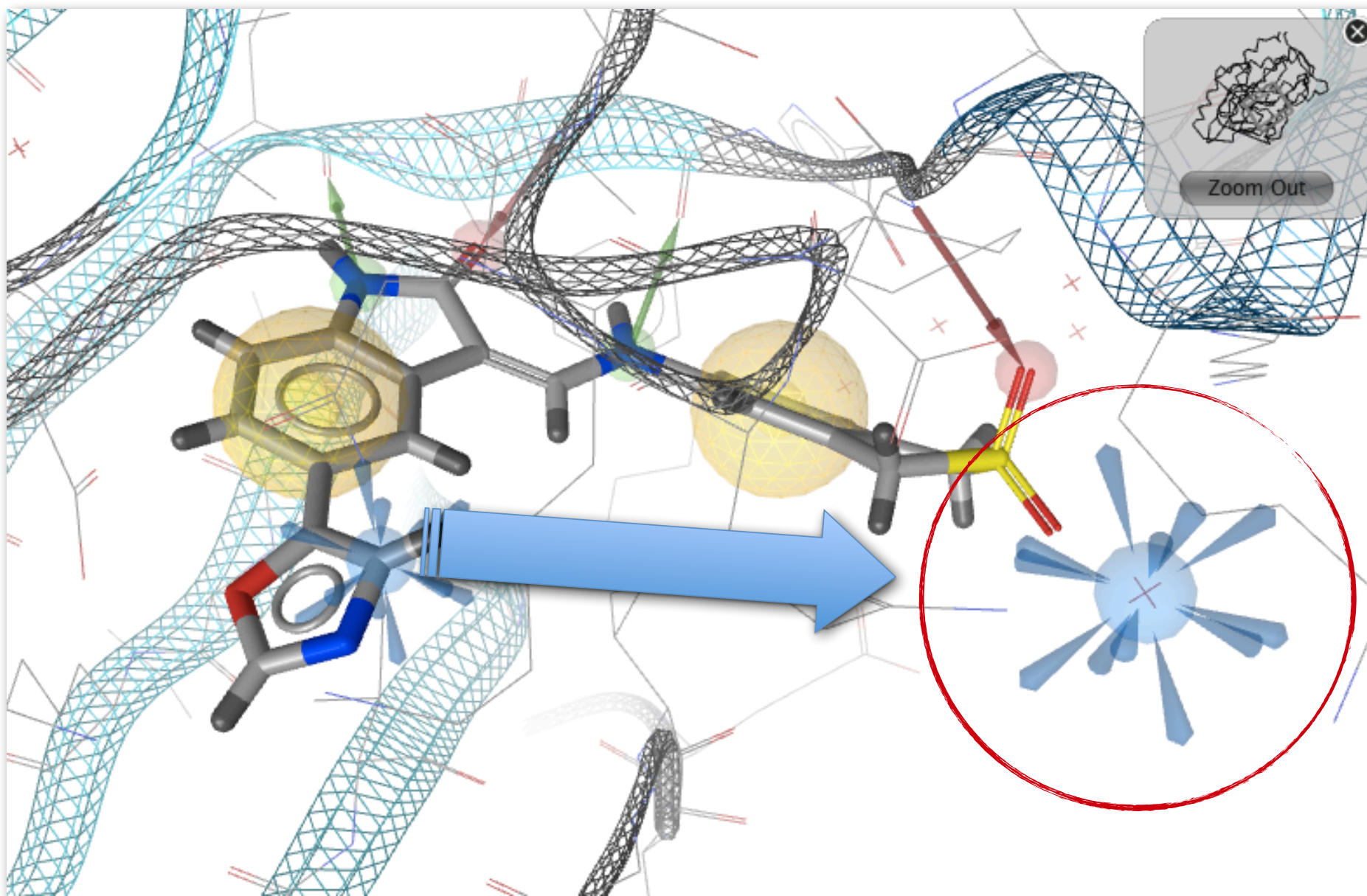
Extended Pharmacophore Editing

- Move pharmacophore features in 3D space



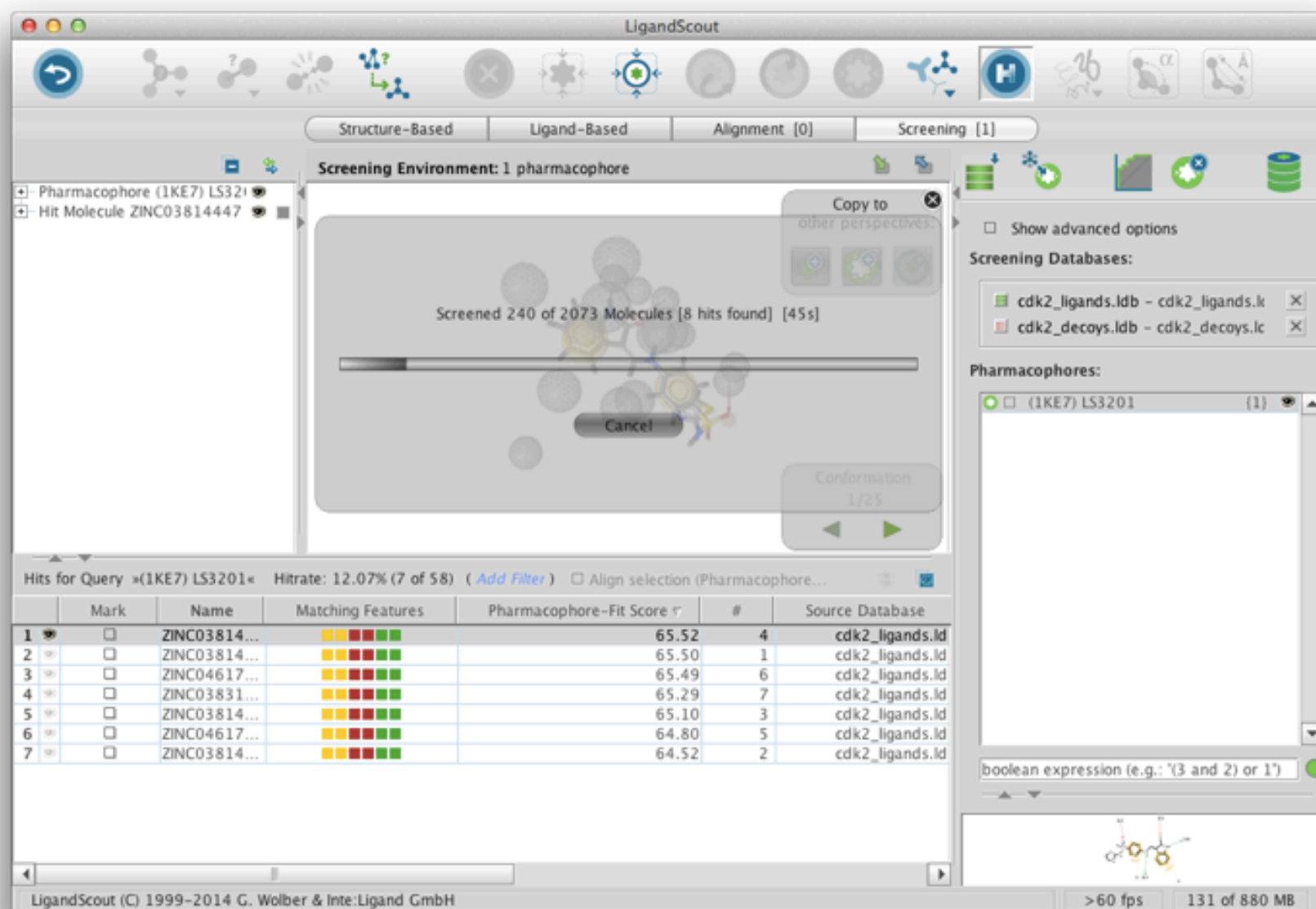
Extended Pharmacophore Editing

- Move pharmacophore features in 3D space



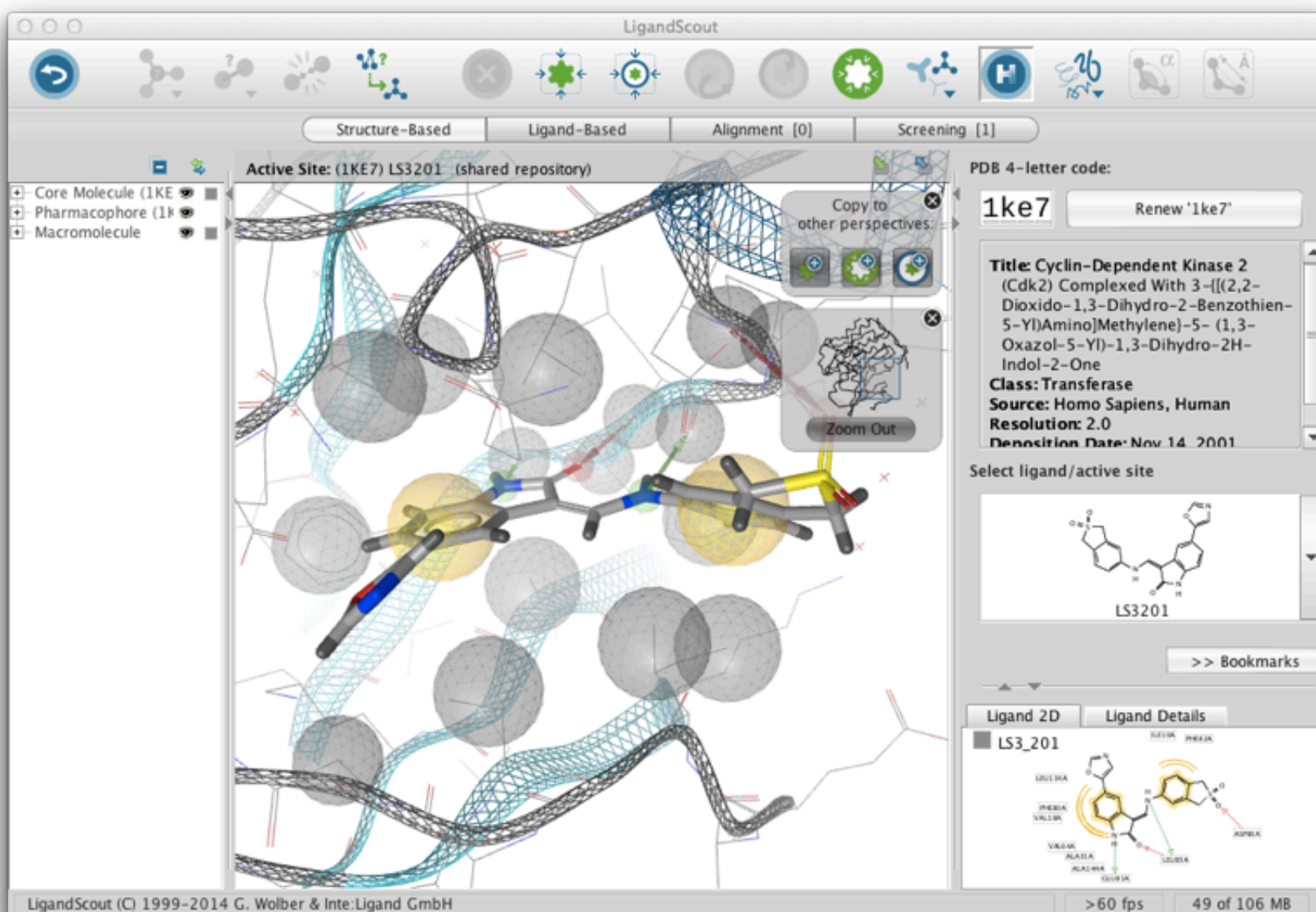
Background Job Queuing System

e.g. while screening in the GUI, continue modeling ...



Background Job Queuing System

e.g. while screening in the GUI, continue modeling ...



New Features in LigandScout 4.1

Usability Enhancement

- Drag & Drop
- Extended pharmacophore editing
- Extended table functionality & export
- Automatic background job queuing system

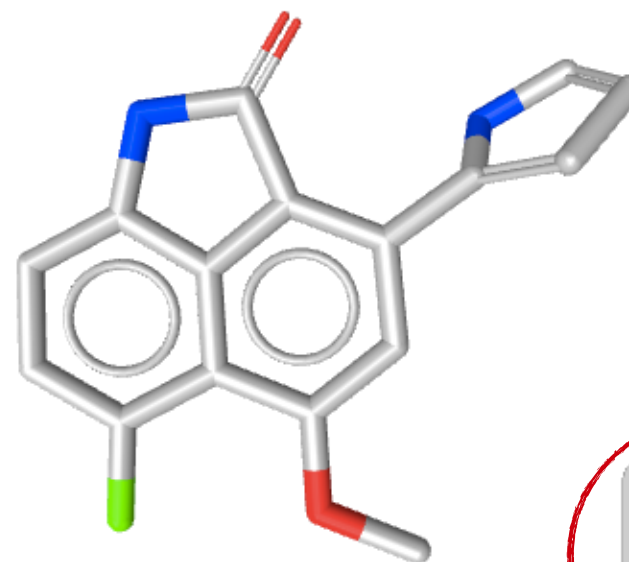
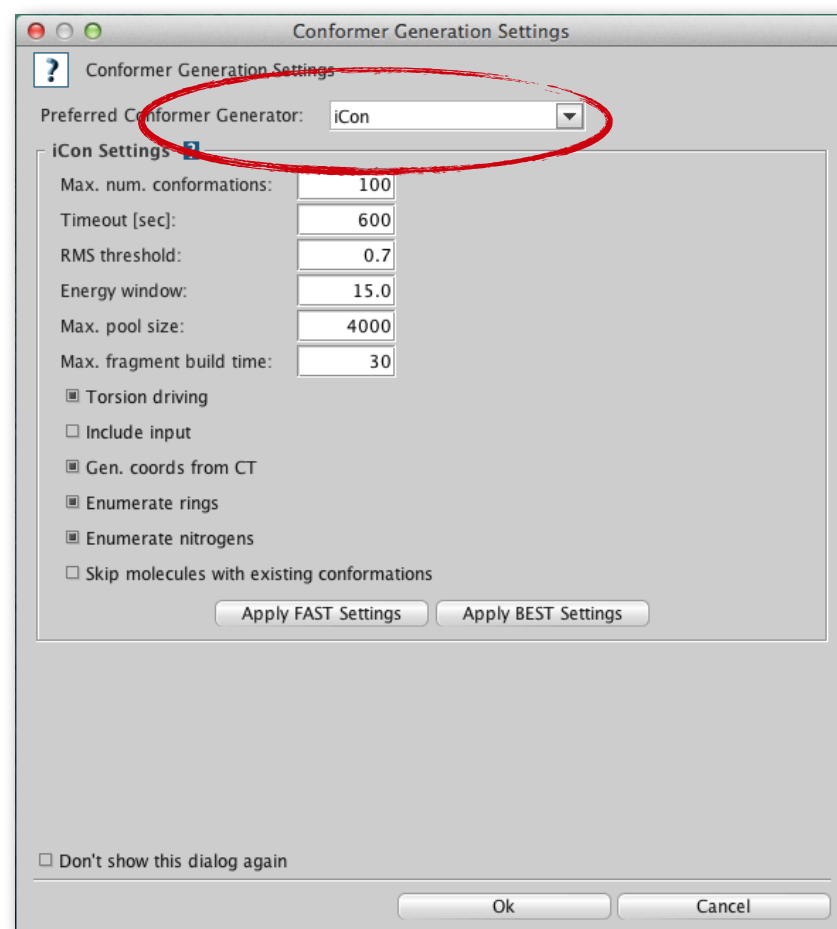
New Functionality

- New conformer generator in addition to OMEGA
- Apo protein binding site pharmacophore generation
- Integration into KNIME workflow environment
- Molecular dynamics trajectory pharmacophore analysis
- Docking with AutoDock 4.2 / AutoDock Vina

New Features in LigandScout 4.1

New conformer generator “iCon”

- Higher accuracy, better conversion rate
- Visualization of conformational energy values



Extensive Table Management

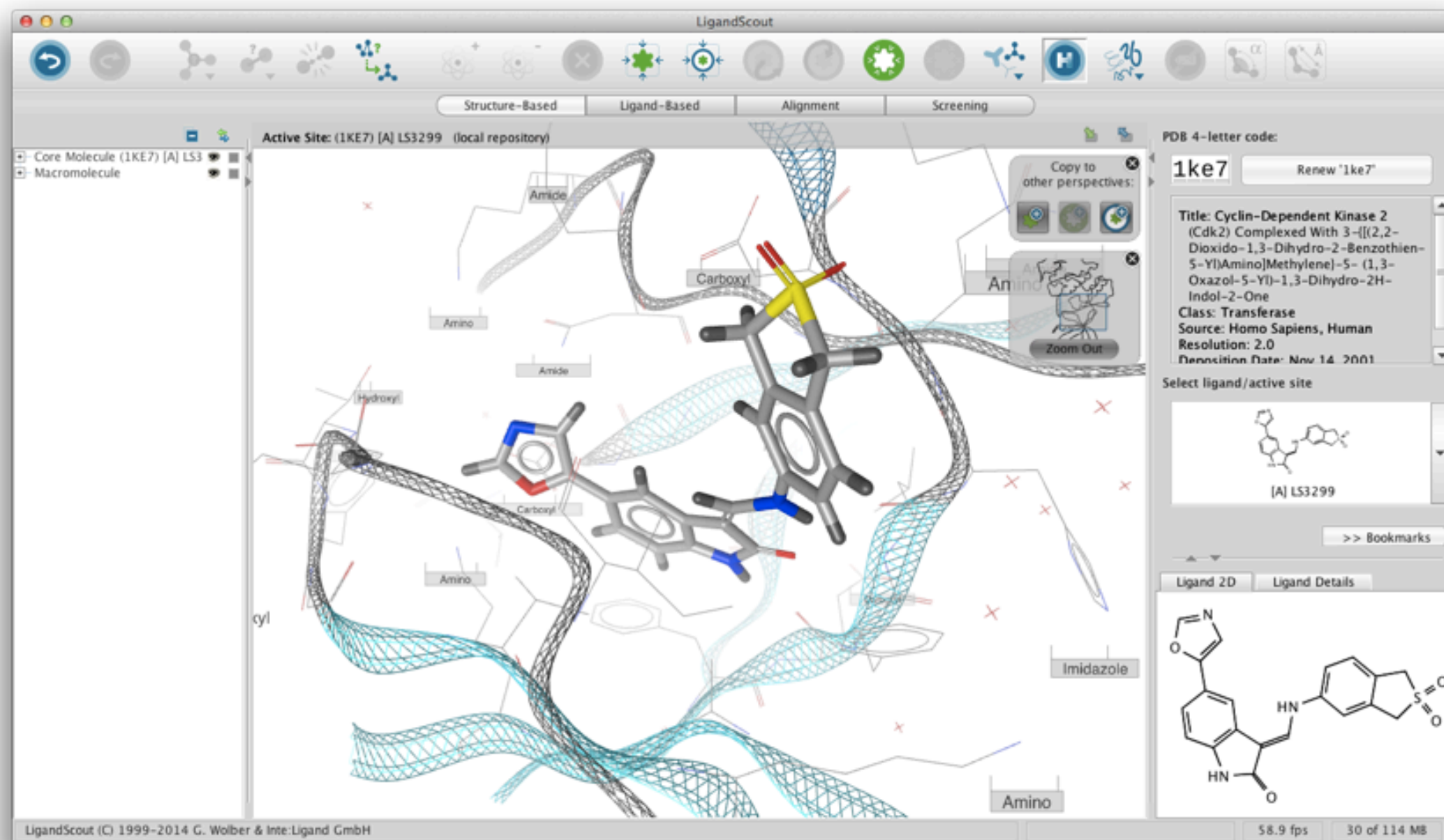
New: Relational database behind each table

- allows rapid filtering and selecting of data subsets

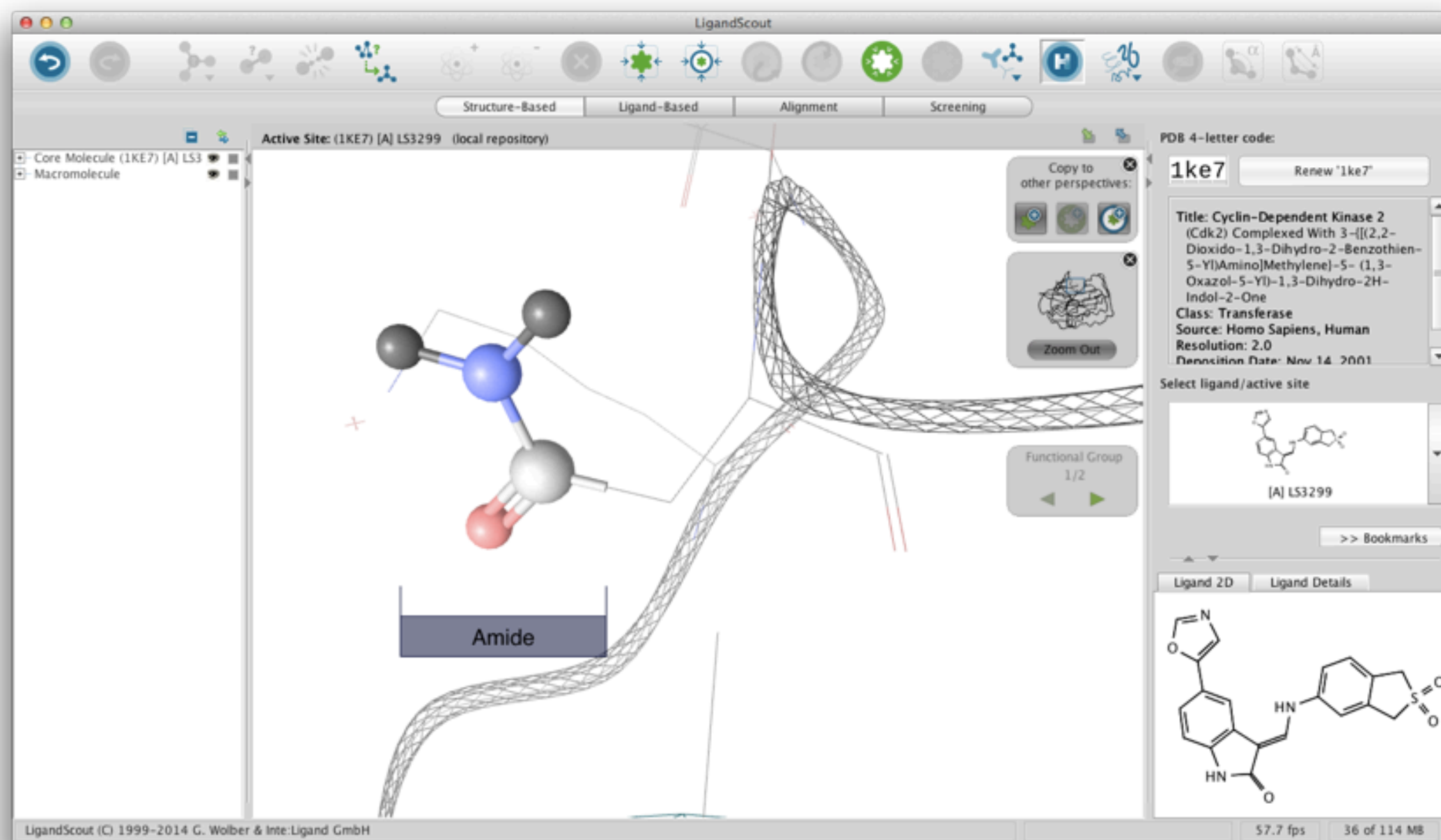
The screenshot displays the LigandScout software interface. At the top, there is a toolbar with various icons and a tabbed menu with options: Structure-Based, Ligand-Based, Alignment, Screening, and Activity Profiling. Below the tabs, the library is identified as 'dud-cdk2.sdf'. In the center, a chemical structure is shown. To the right of the structure, there is a 'Copy to other perspectives:' button with three sub-options. Below the structure, a table of results is displayed. The table has columns for Mark, Name, #, mol index, MolWt, cLogP, and TPSA [Ertl]. A red circle highlights the left sidebar, which contains a list of filters: MolWt > 200.00, MolWt < 400.00, cLogP > 2.00, and cLogP < 5.00. The table shows 12 rows of data, with the third row (ZINC00003491) highlighted. The status bar at the bottom indicates 'LigandScout (C) 1999-2014 G. Wolber & Inte:Ligand GmbH', '1.9 fps', and '25 of 103 MB'.

Mark	Name	#	mol index	MolWt	cLogP	TPSA [Ertl]
1	ZINC03814458	27	27.0	245.29	2.05	89.71
2	ZINC00023543	5	5.0	247.3	2.27	89.71
3	ZINC00003491	1	1.0	282.27	4.02	57.88
4	ZINC03814470	32	32.0	285.26	2.42	105.93
5	ZINC03814452	18	18.0	301.35	4.03	55.11
6	ZINC03814464	51	51.0	302.36	2.97	80.76
7	ZINC03814452	20	20.0	302.36	3.45	56.36
8	ZINC03814464	53	53.0	303.36	2.39	82.01
9	ZINC03814476	35	35.0	304.31	2.41	87.74
10	ZINC03814449	16	16.0	308.34	2.5	74.33
11	ZINC03814477	37	37.0	310.33	2.61	100.87
12	ZINC03814455	28	28.0	311.43	3.3	68.02

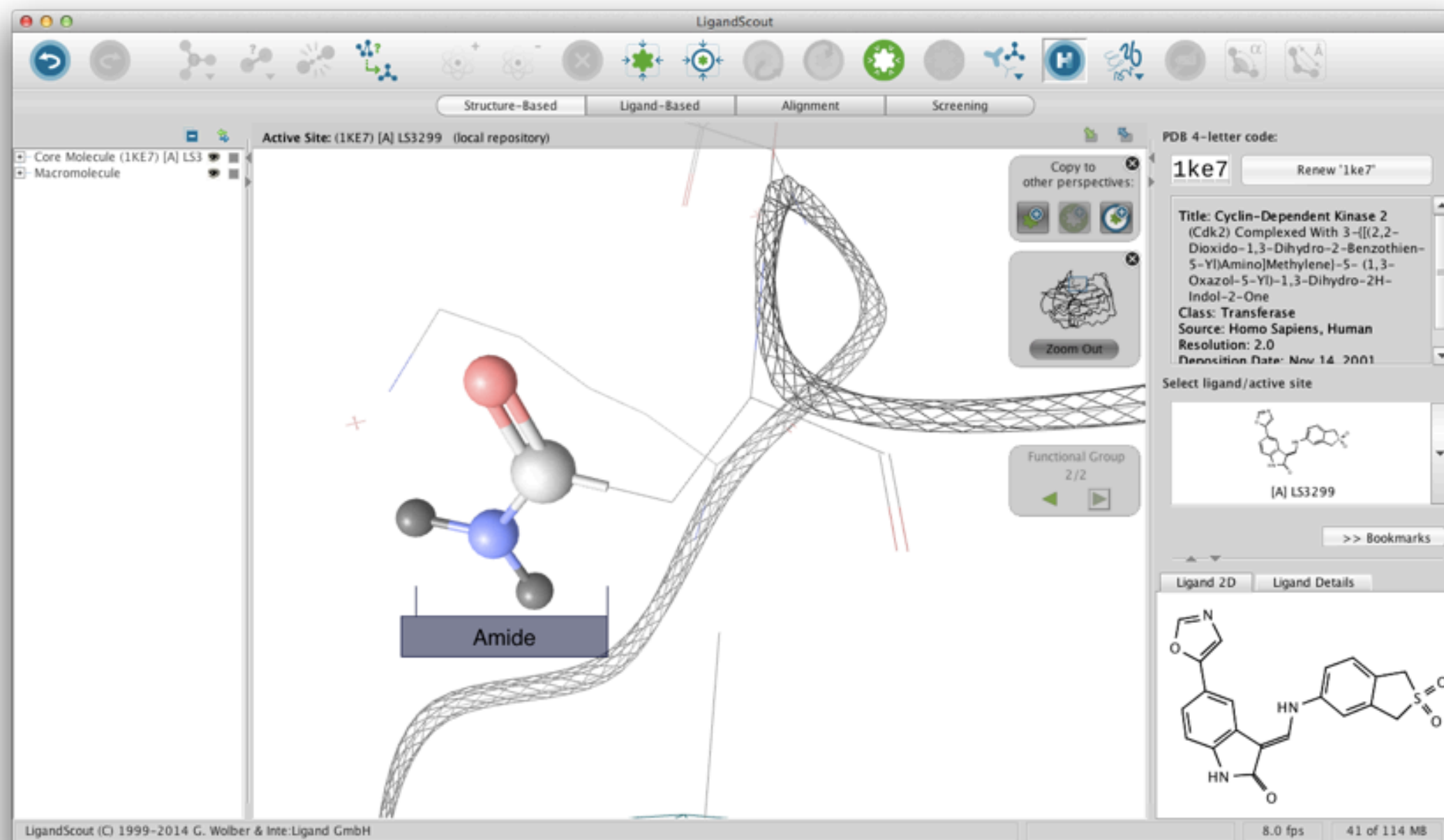
Binding Site Amino Acid Analysis & Editing



Binding Site Amino Acid Analysis & Editing



Binding Site Amino Acid Analysis & Editing



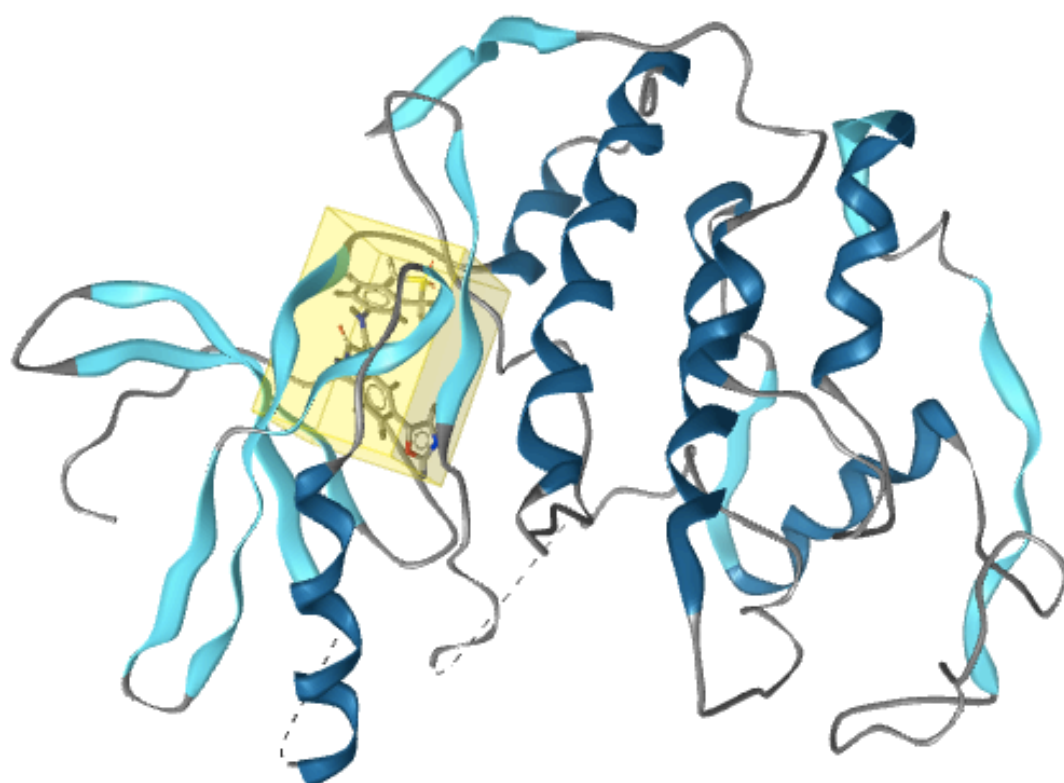
Create Pharmacophores from Apo Protein Site

**Intuitive modeling of pharmacophores in empty binding sites
(e.g in apo protein / allosteric sites)**

- Detect protein pockets using the Pocket Finder
- Calculate a grid-based ligand accessible surface
- Calculate interaction feature probabilities
- Create automatically customized apo-site model
- User can add pharmacophore features on surface points

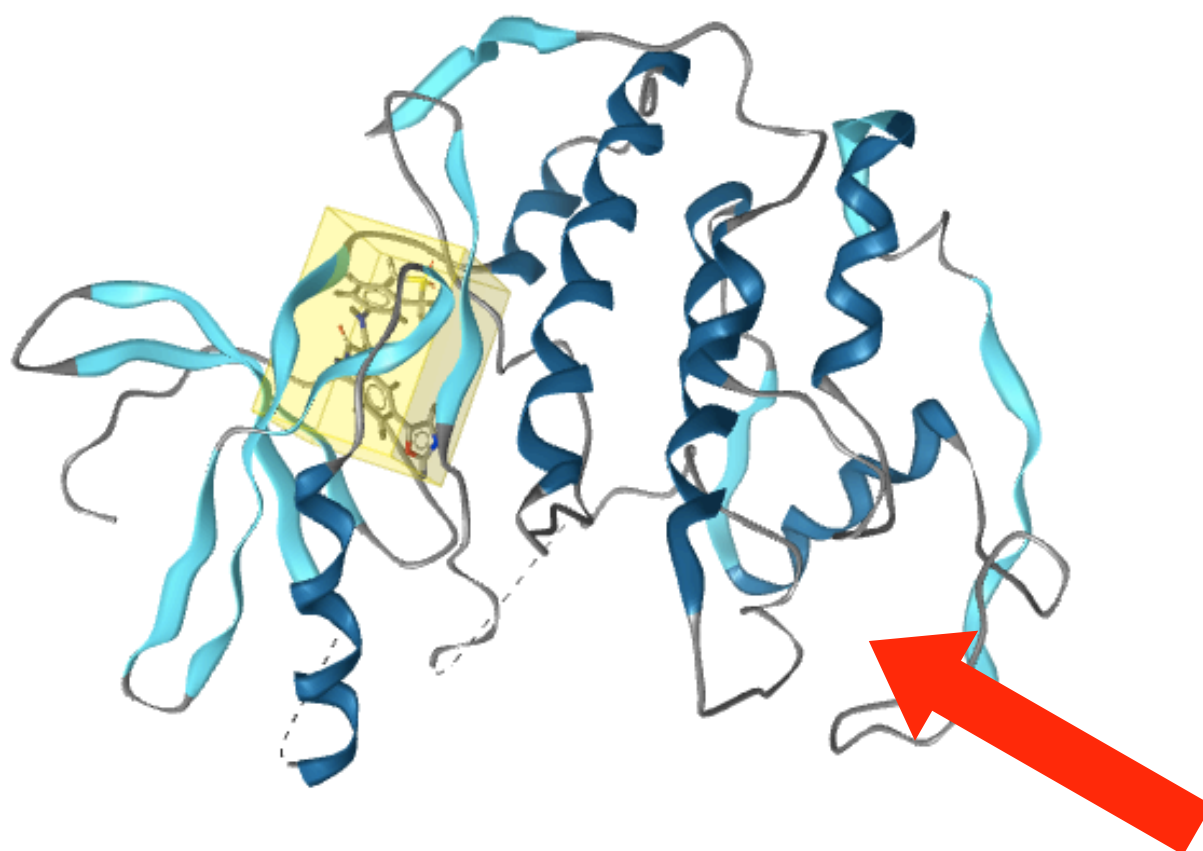
Explore Empty Protein Sites

- Create binding sites wherever you want or use the new pocket finder



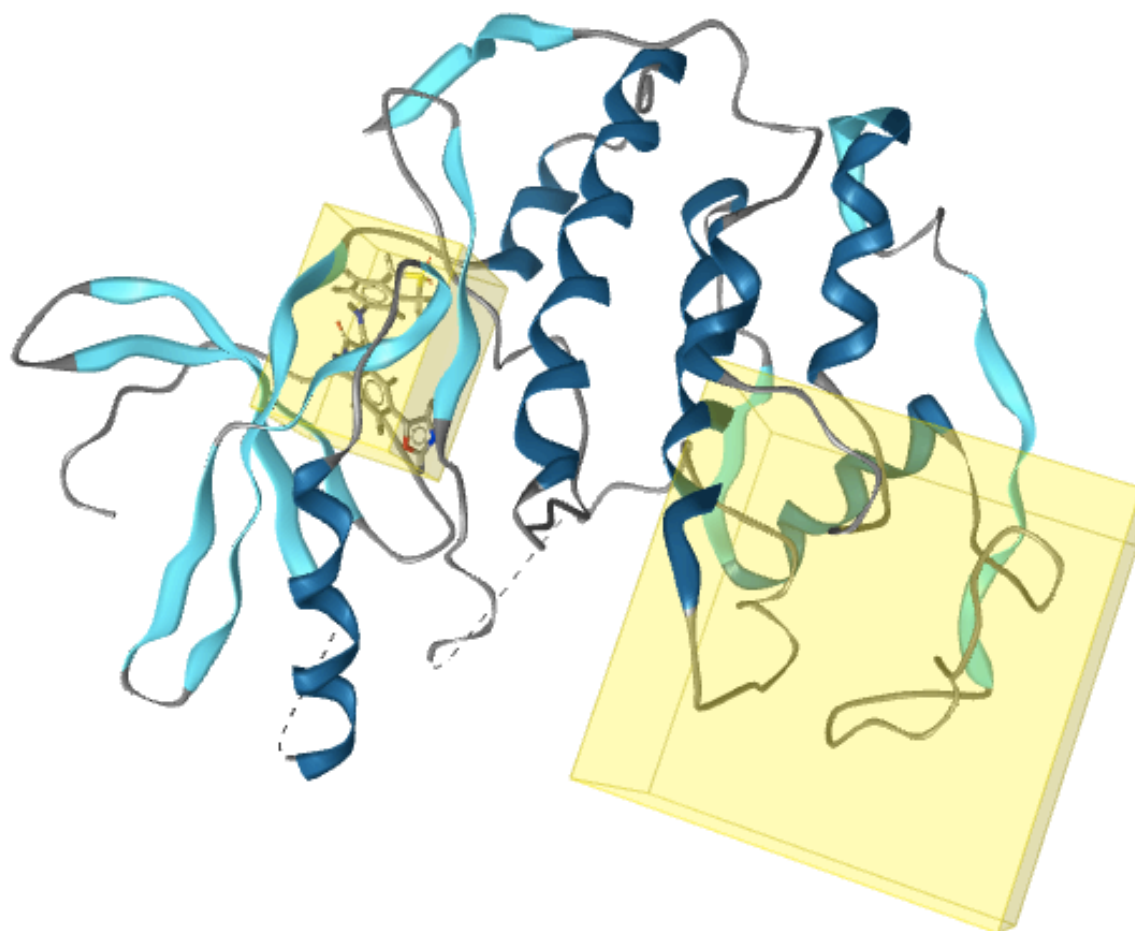
Explore Empty Protein Sites

- Create binding sites wherever you want or use the new pocket finder

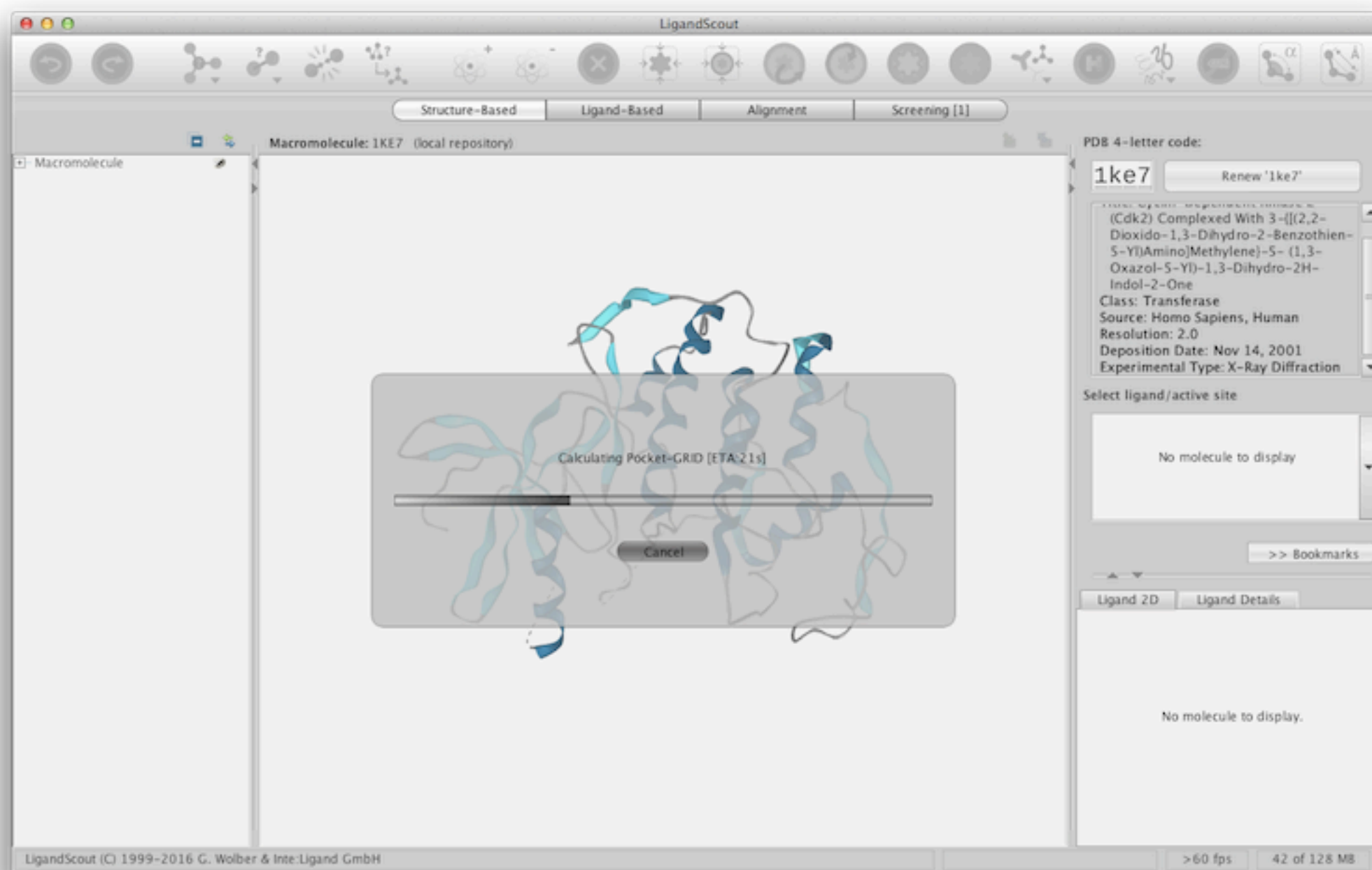


Explore Empty Protein Sites

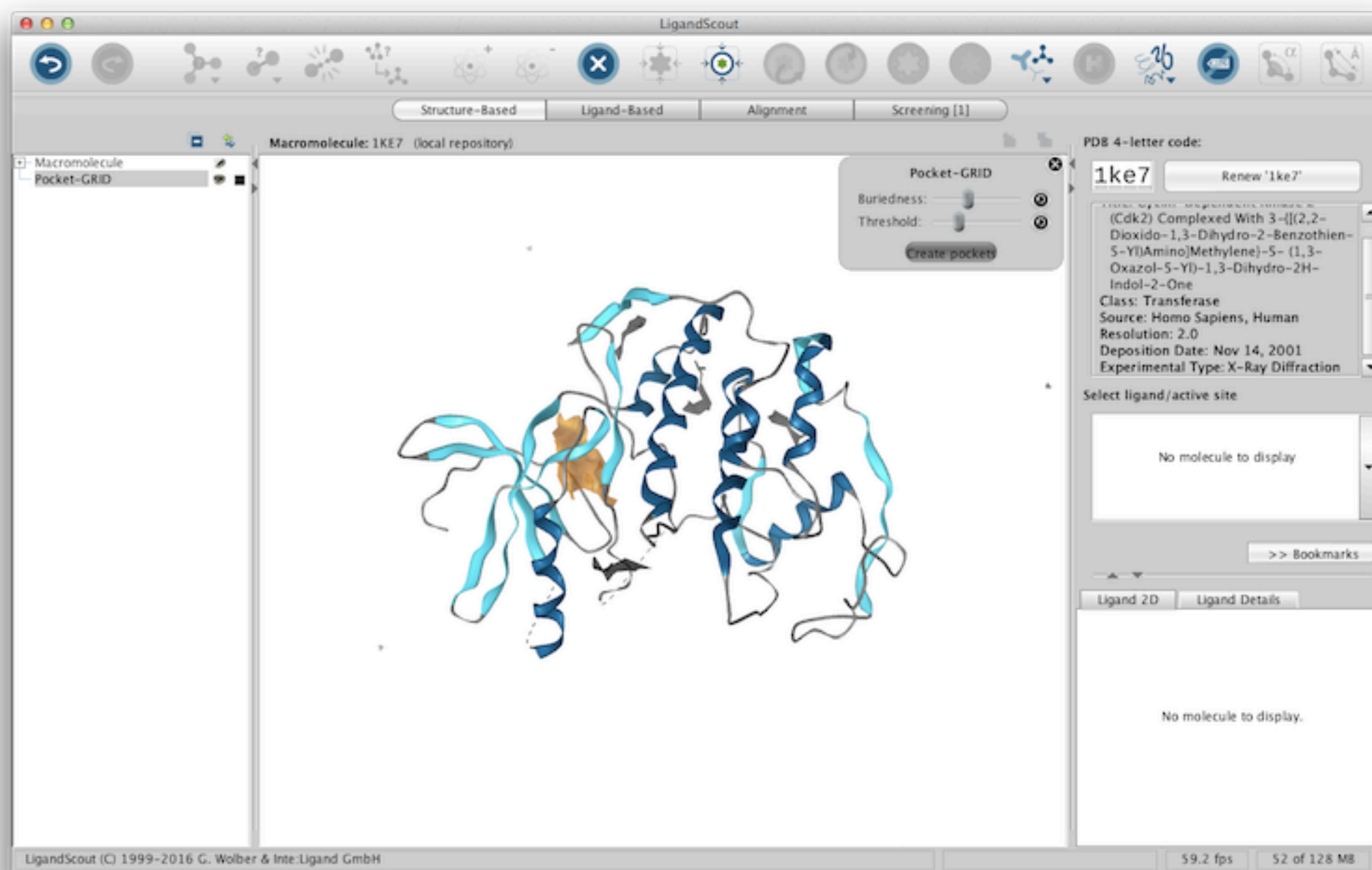
- Create binding sites wherever you want or use the new pocket finder



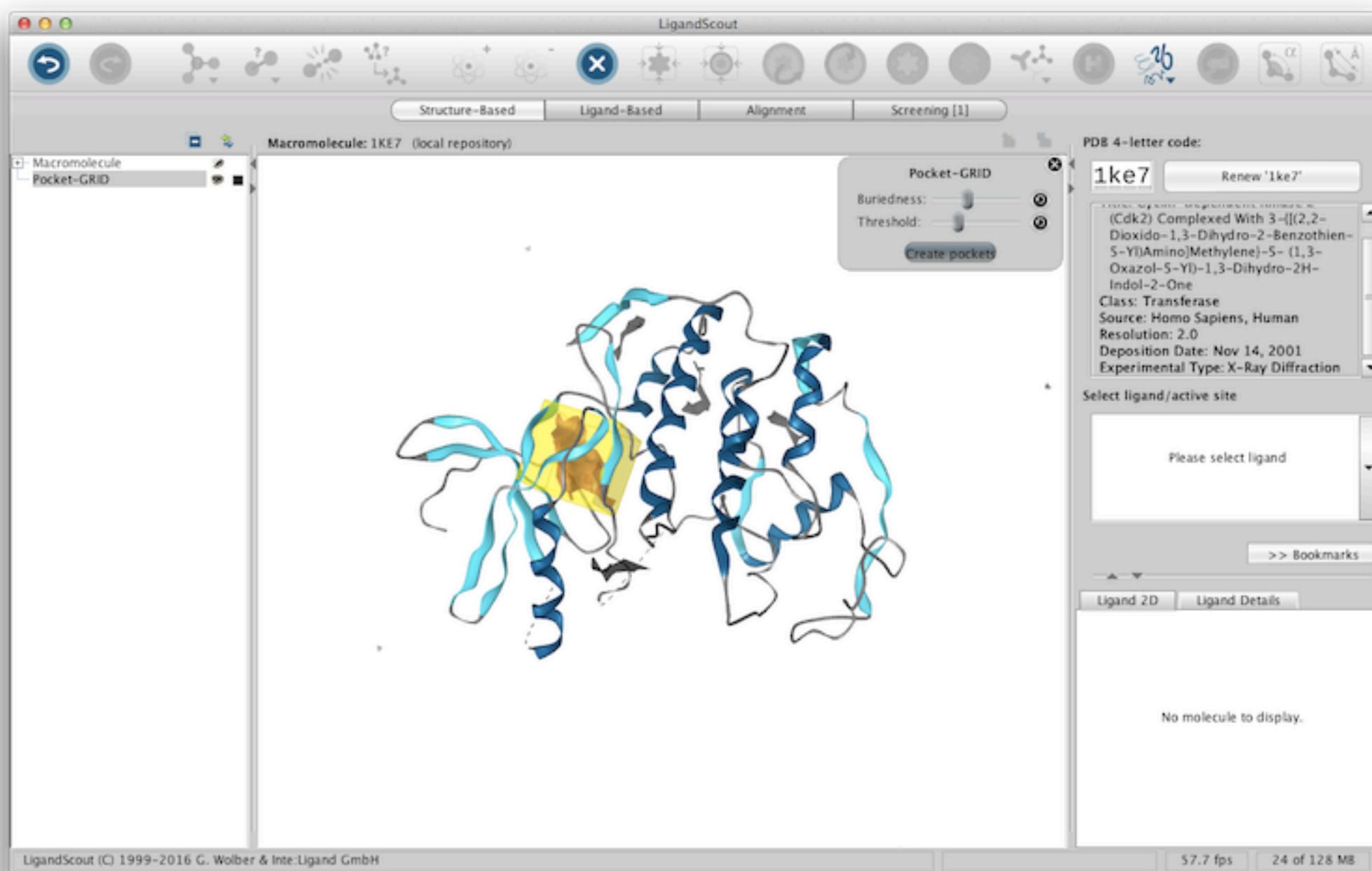
Pocket Finder



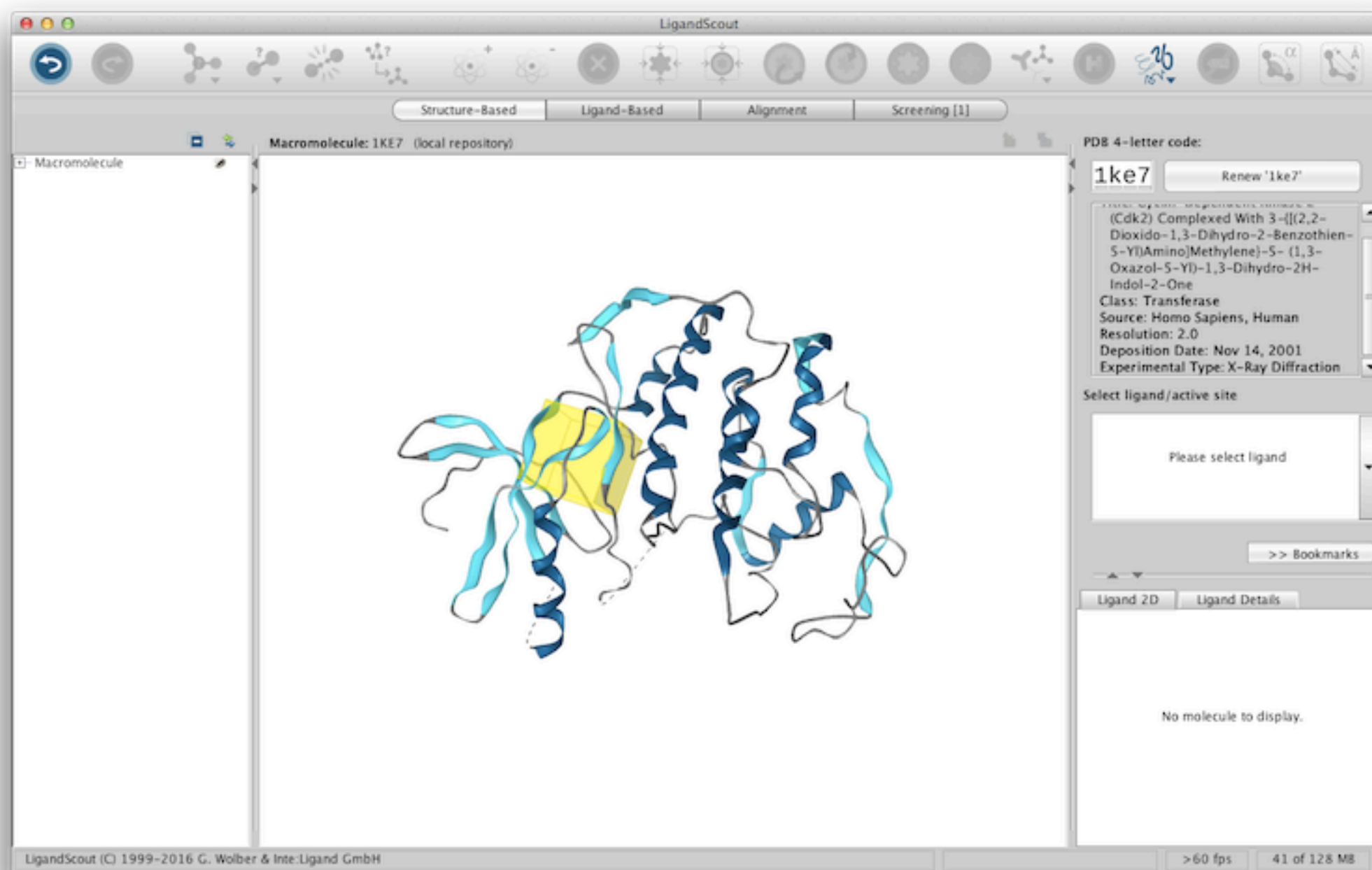
Pocket Finder



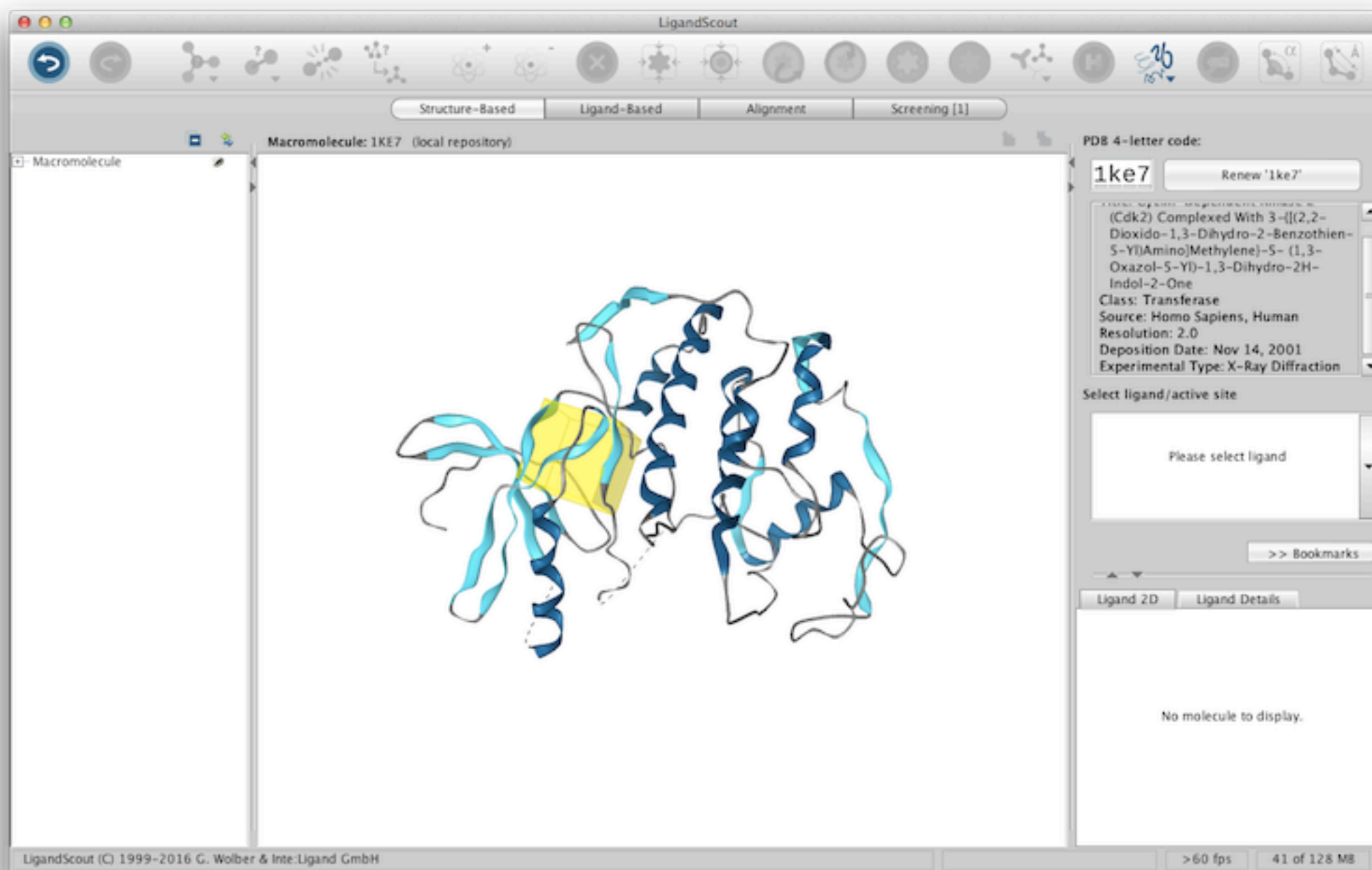
Pocket Finder



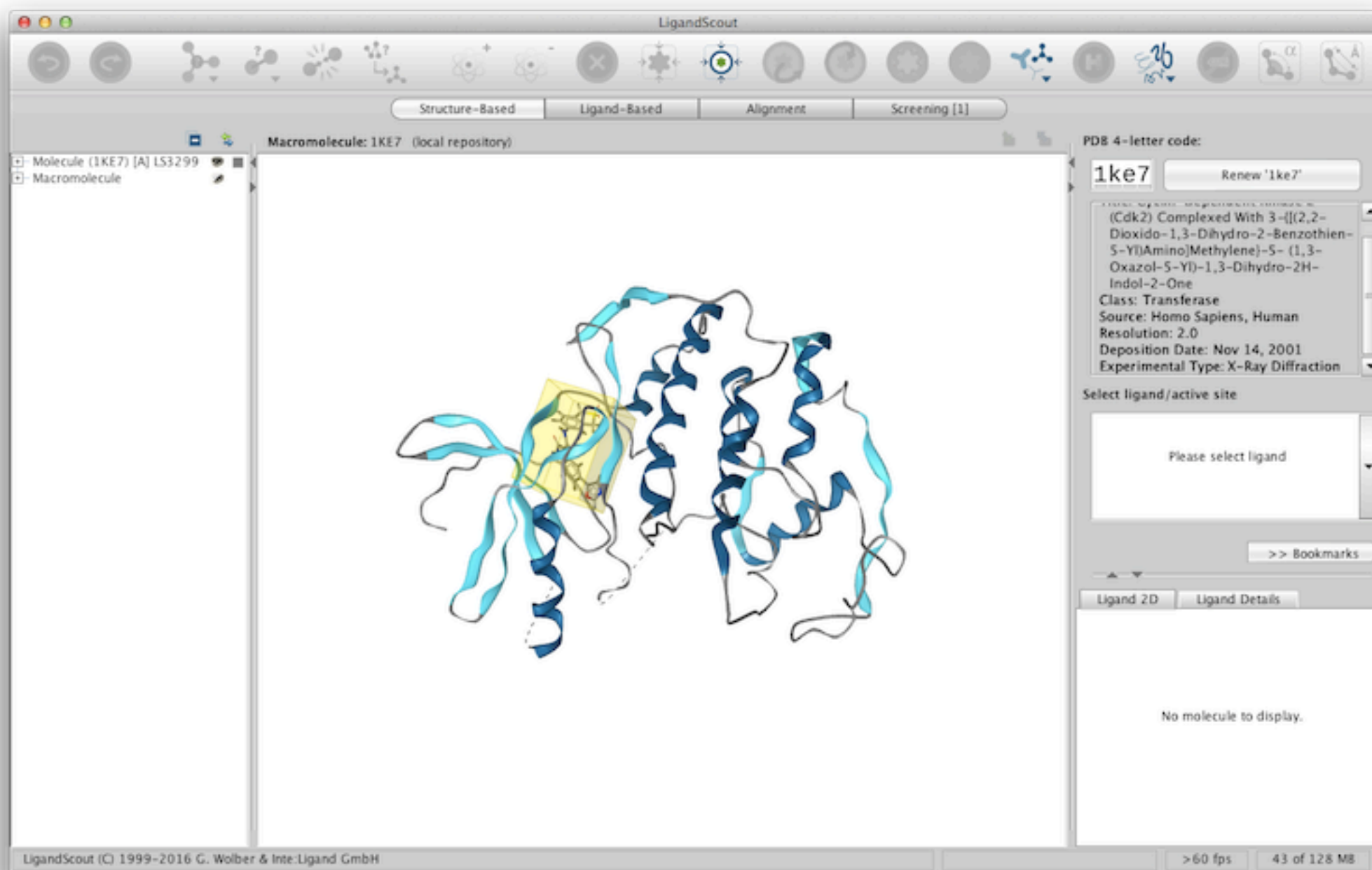
Pocket Finder



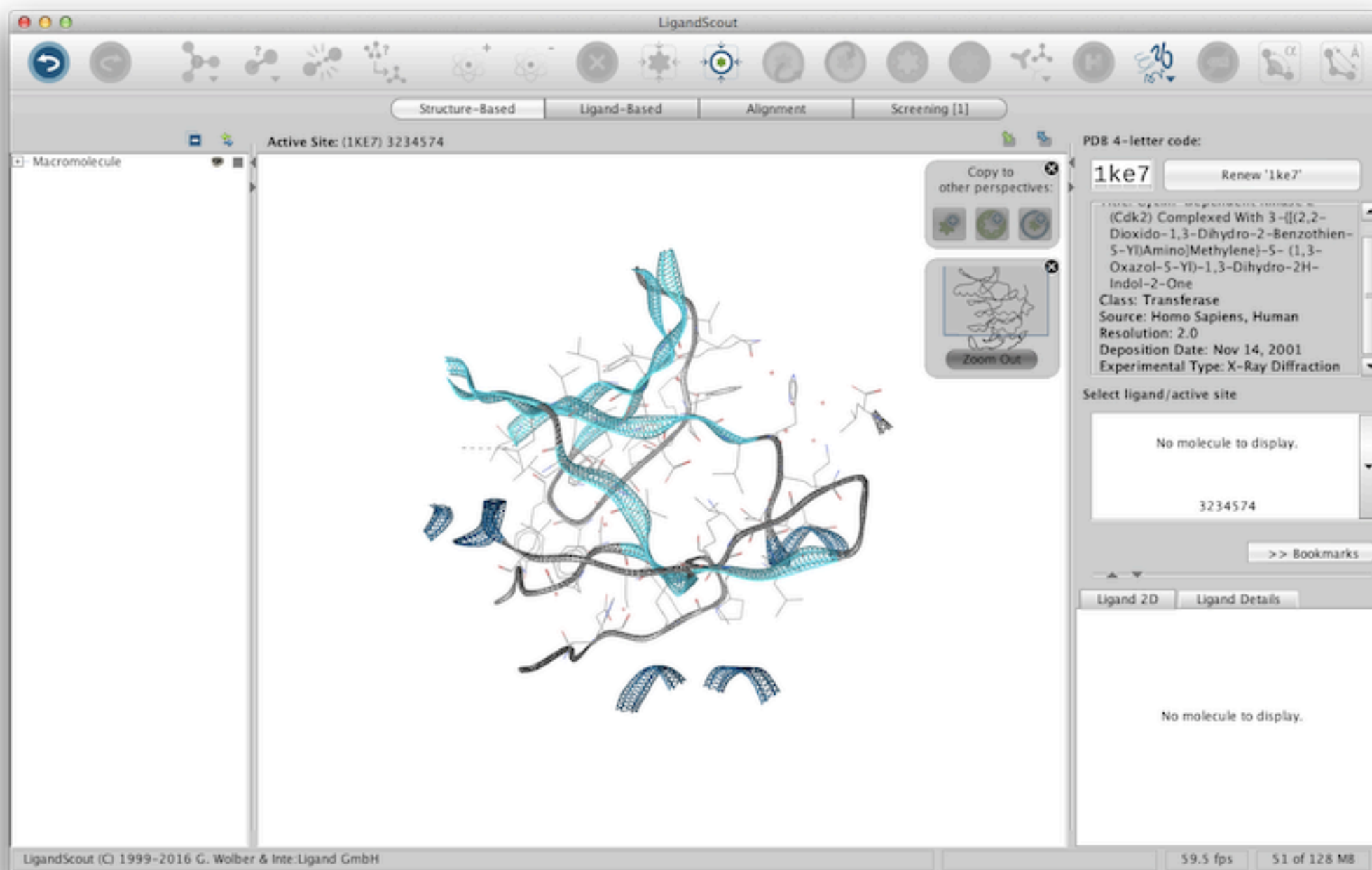
Comparison with Original Ligand Position



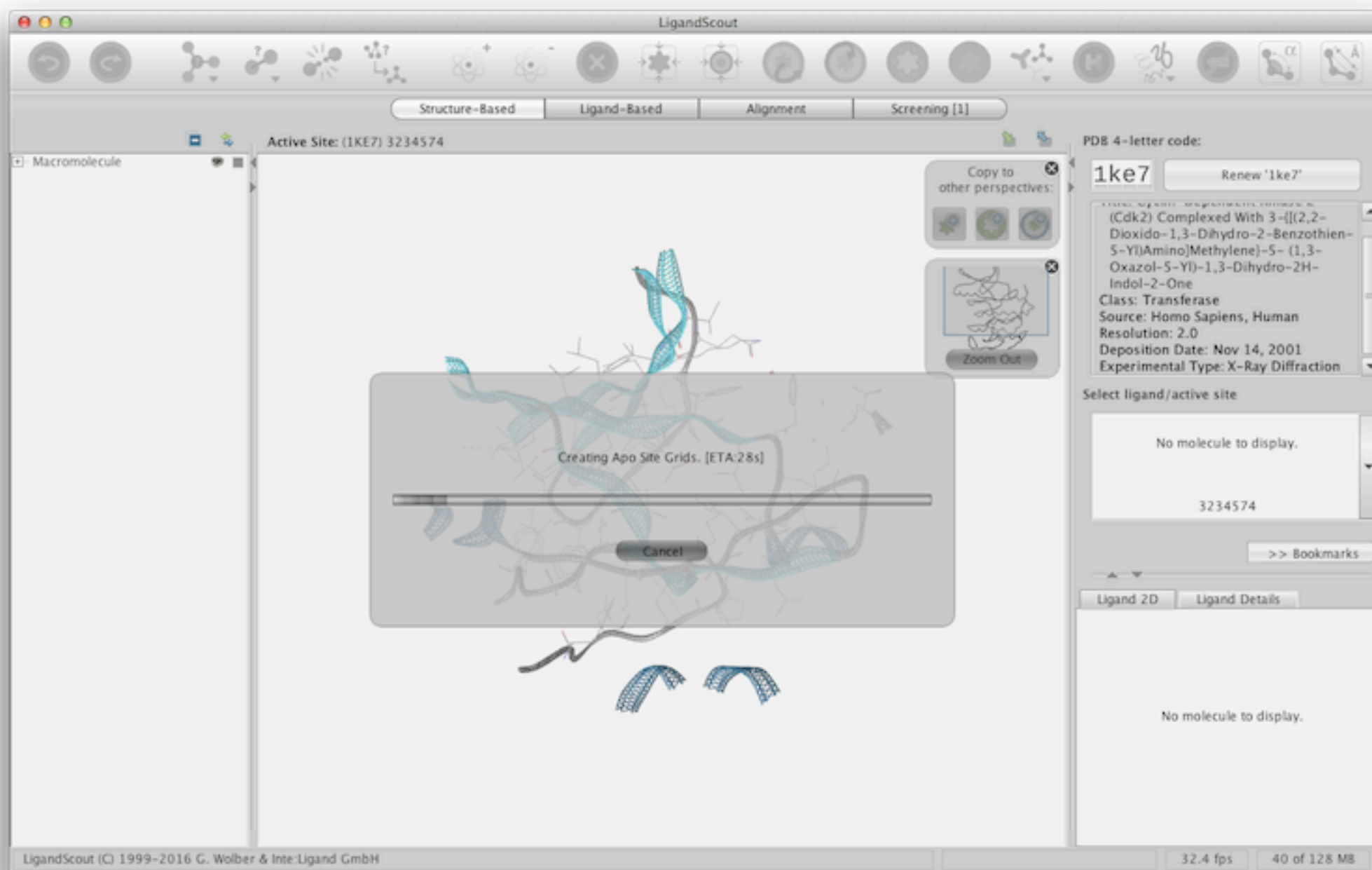
Comparison with Original Ligand Position



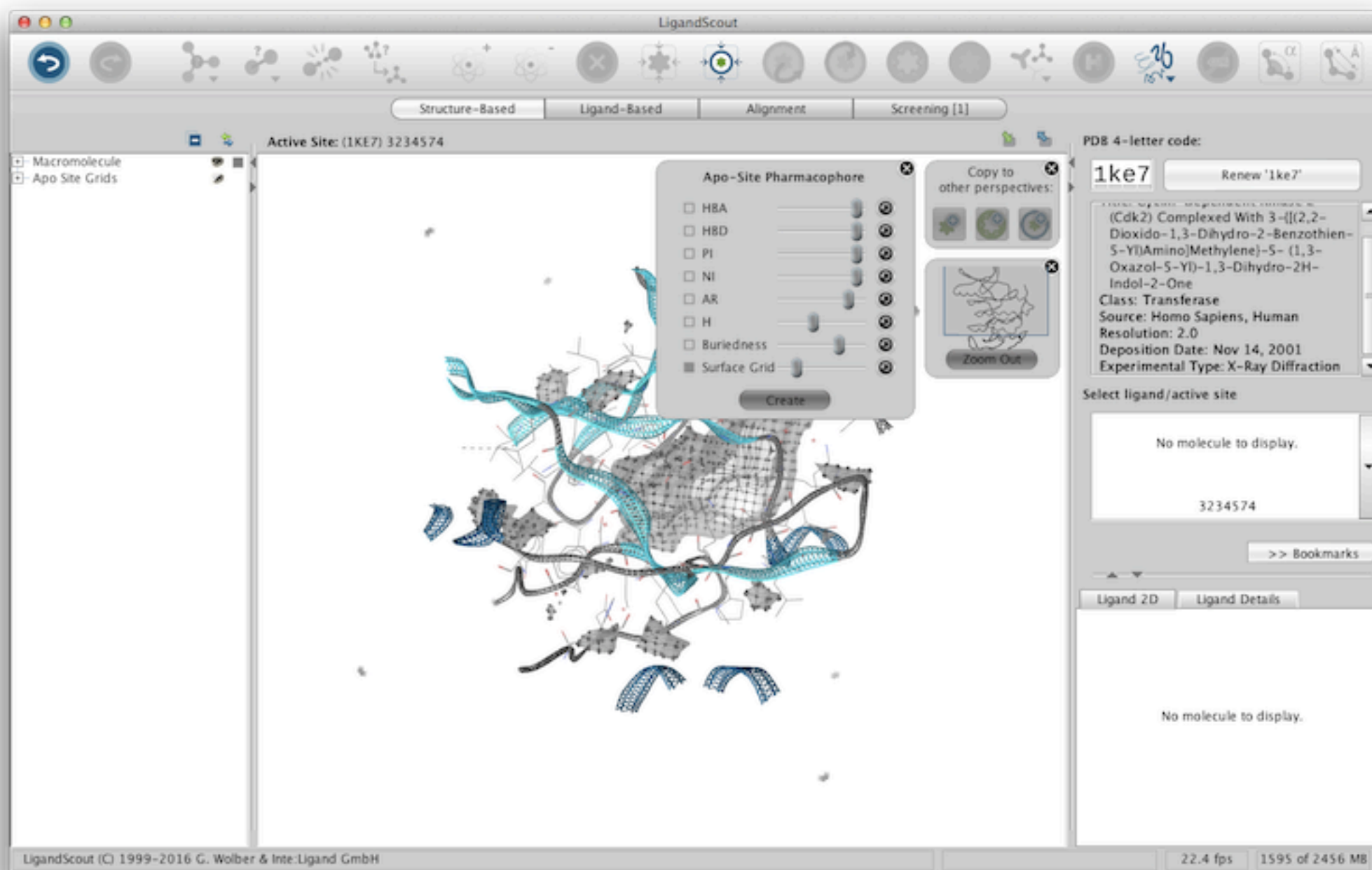
Apo Binding Site Pharmacophore Generation



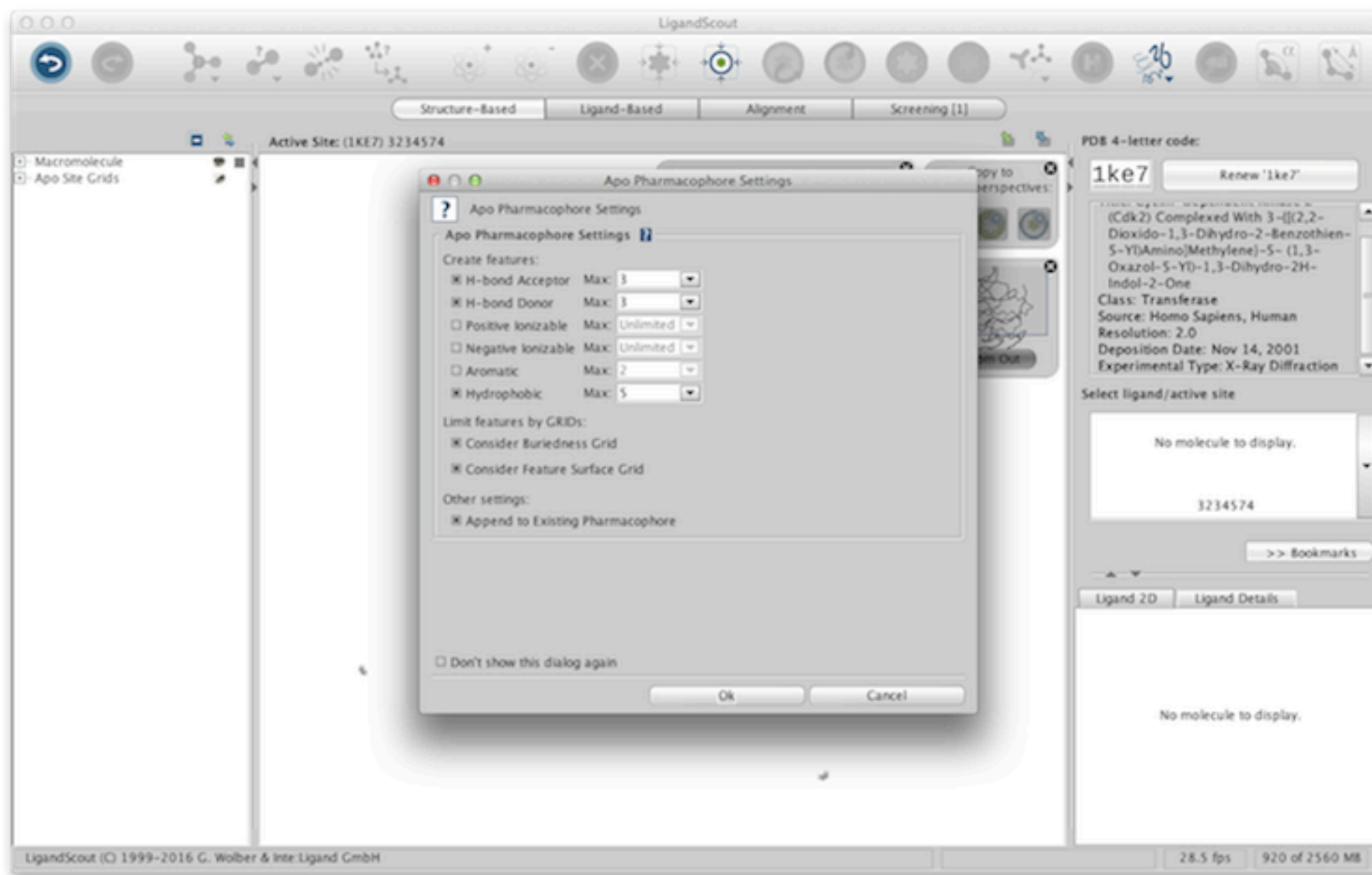
Apo Binding Site Pharmacophore Generation



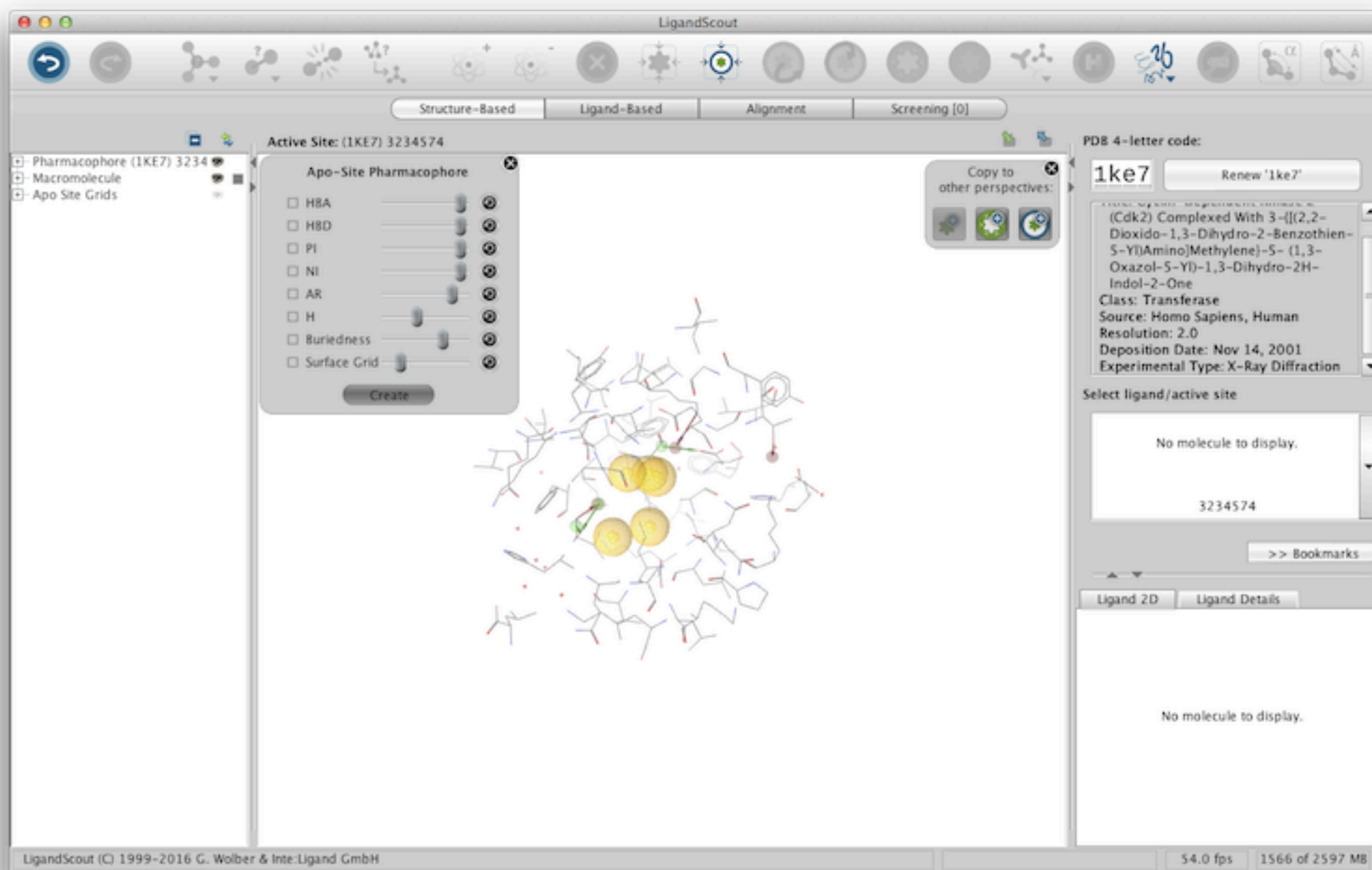
Apo Binding Site Pharmacophore Generation



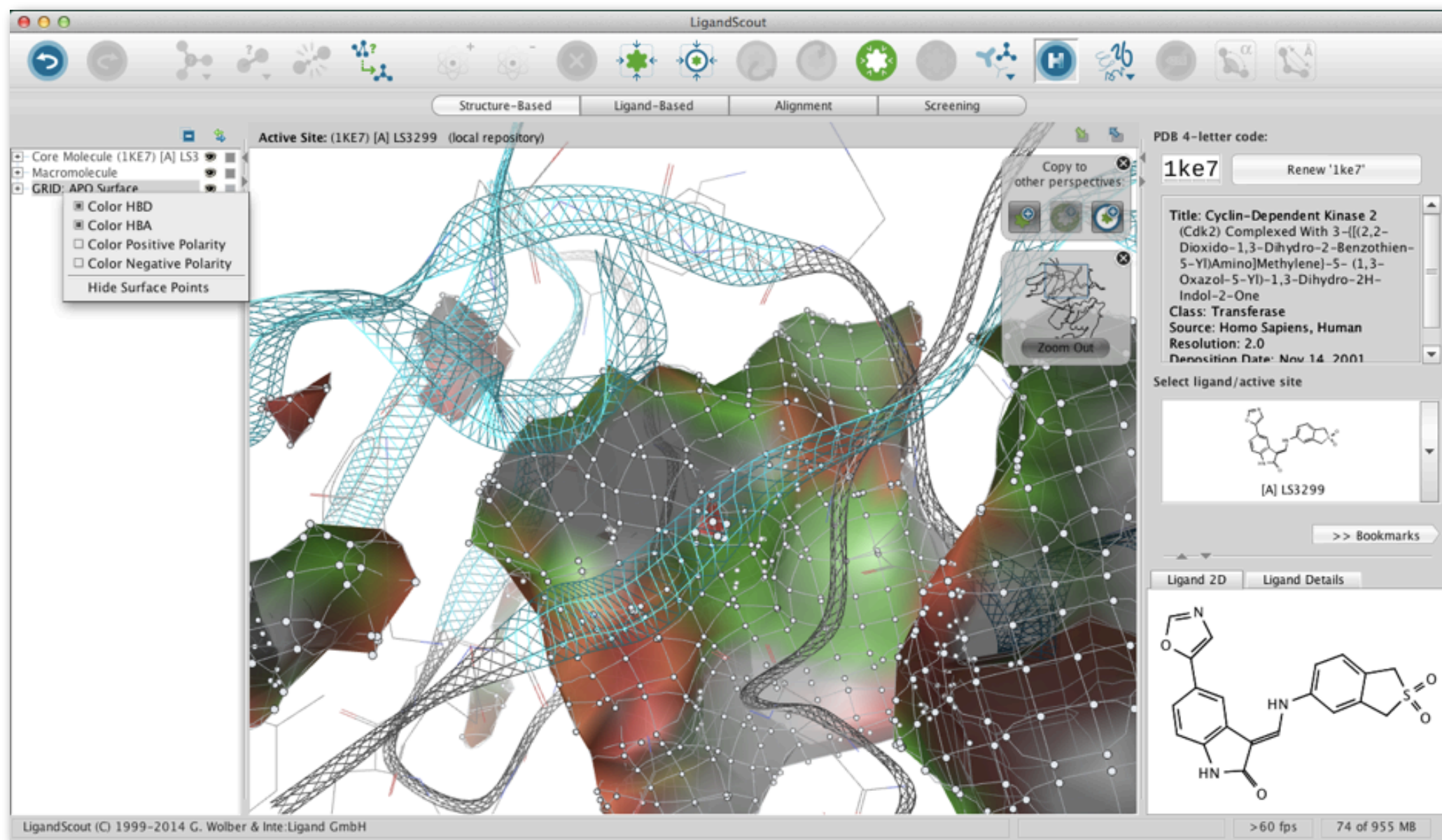
Apo Binding Site Pharmacophore Generation



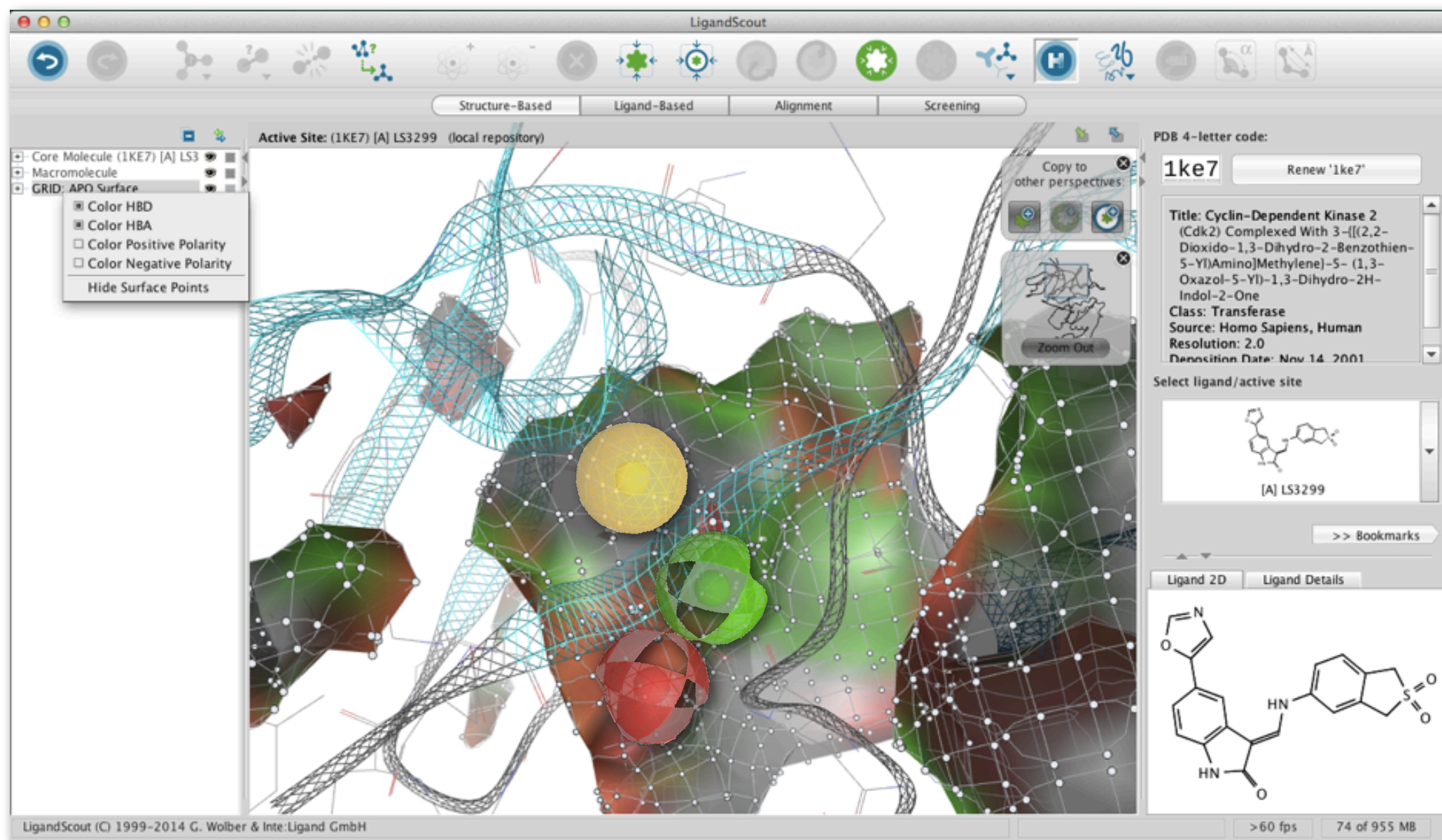
Apo Binding Site Pharmacophore Generation



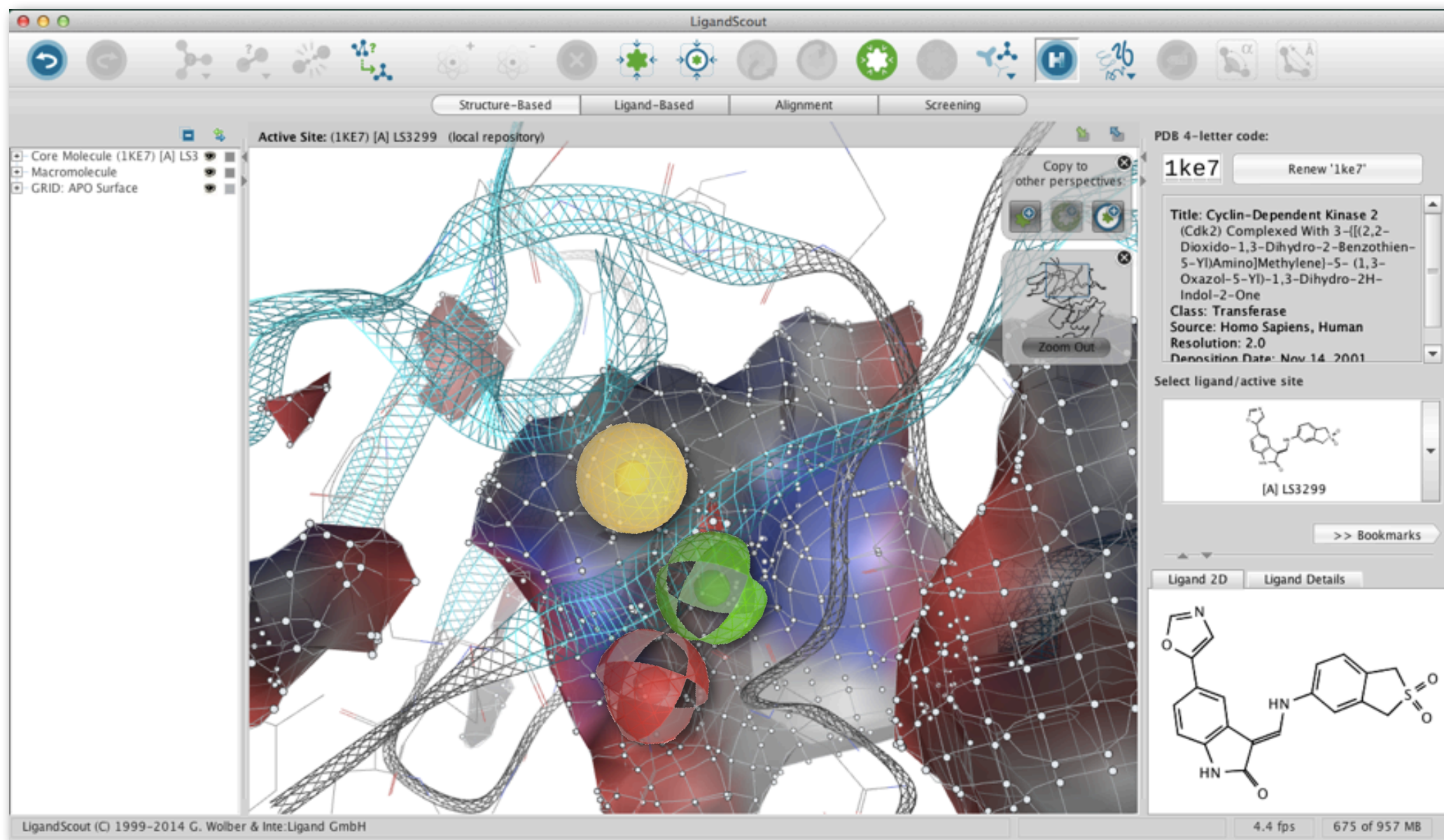
Manual Apo Site Pharmacophore Building



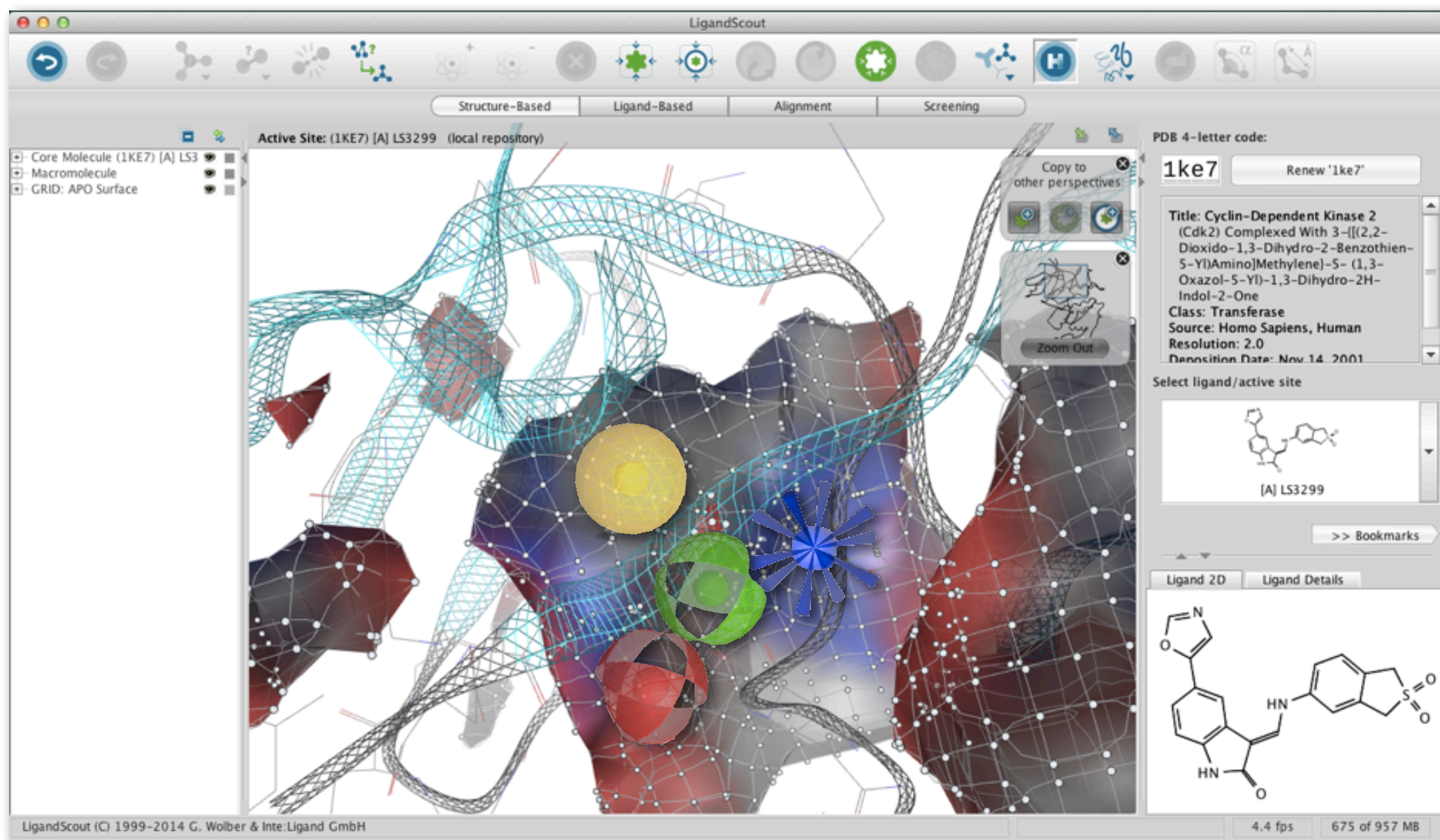
Manual Apo Site Pharmacophore Building



Manual Apo Site Pharmacophore Building



Manual Apo Site Pharmacophore Building



Docking With AutoDock 4.2 / AutoDock Vina

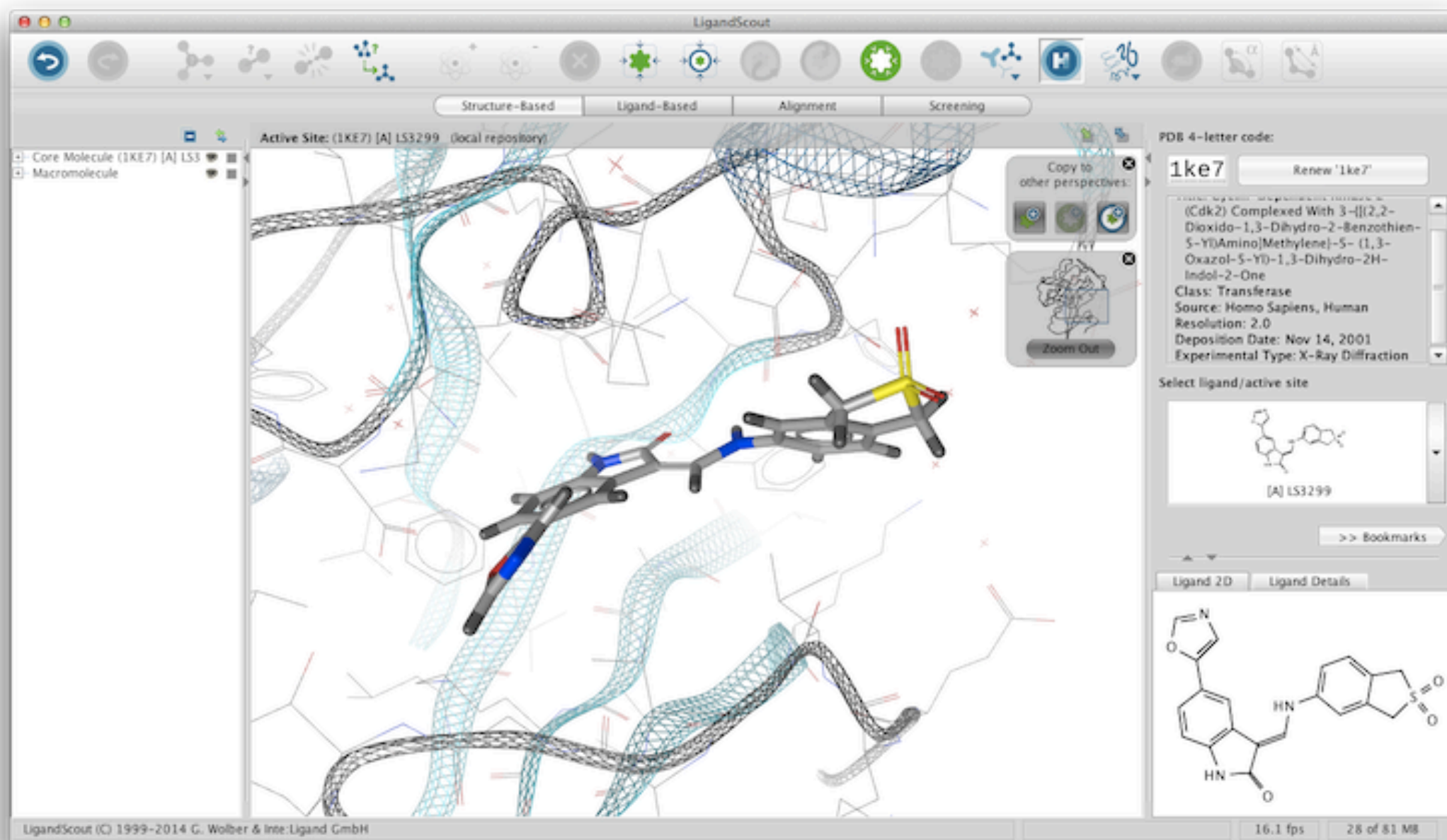
Integration: High Quality Docking & Pharmacophores

- Interactive docking in active site viewer
- Analyze and filter the results in flexible table view
- Re-score interactively using pharmacophores
- Estimate binding enthalpies using MMFF94s
- Estimate free energy of binding using new scoring function

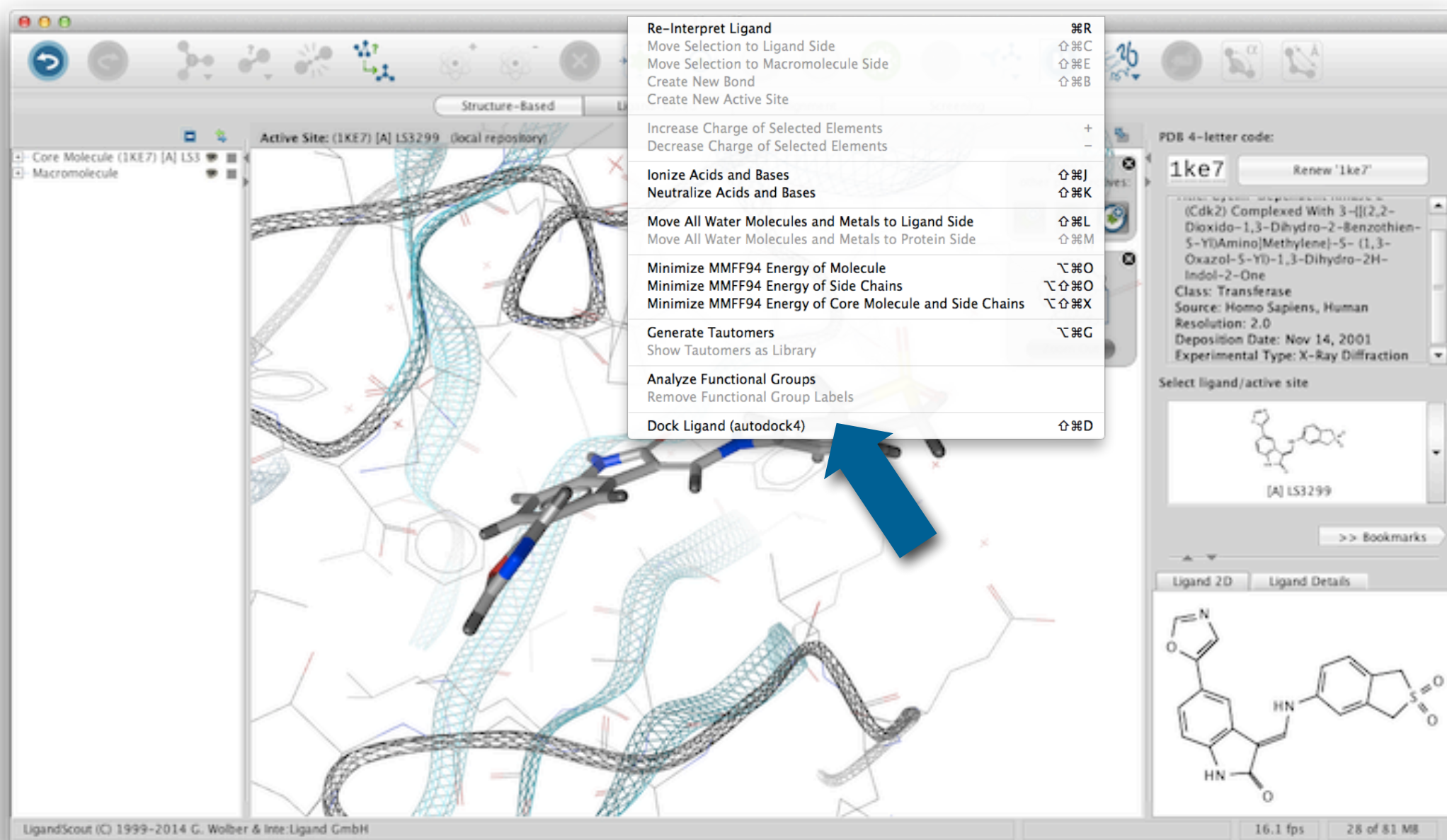
Makes docking user friendly and understandable

- Seamless workflows in most user friendly interface

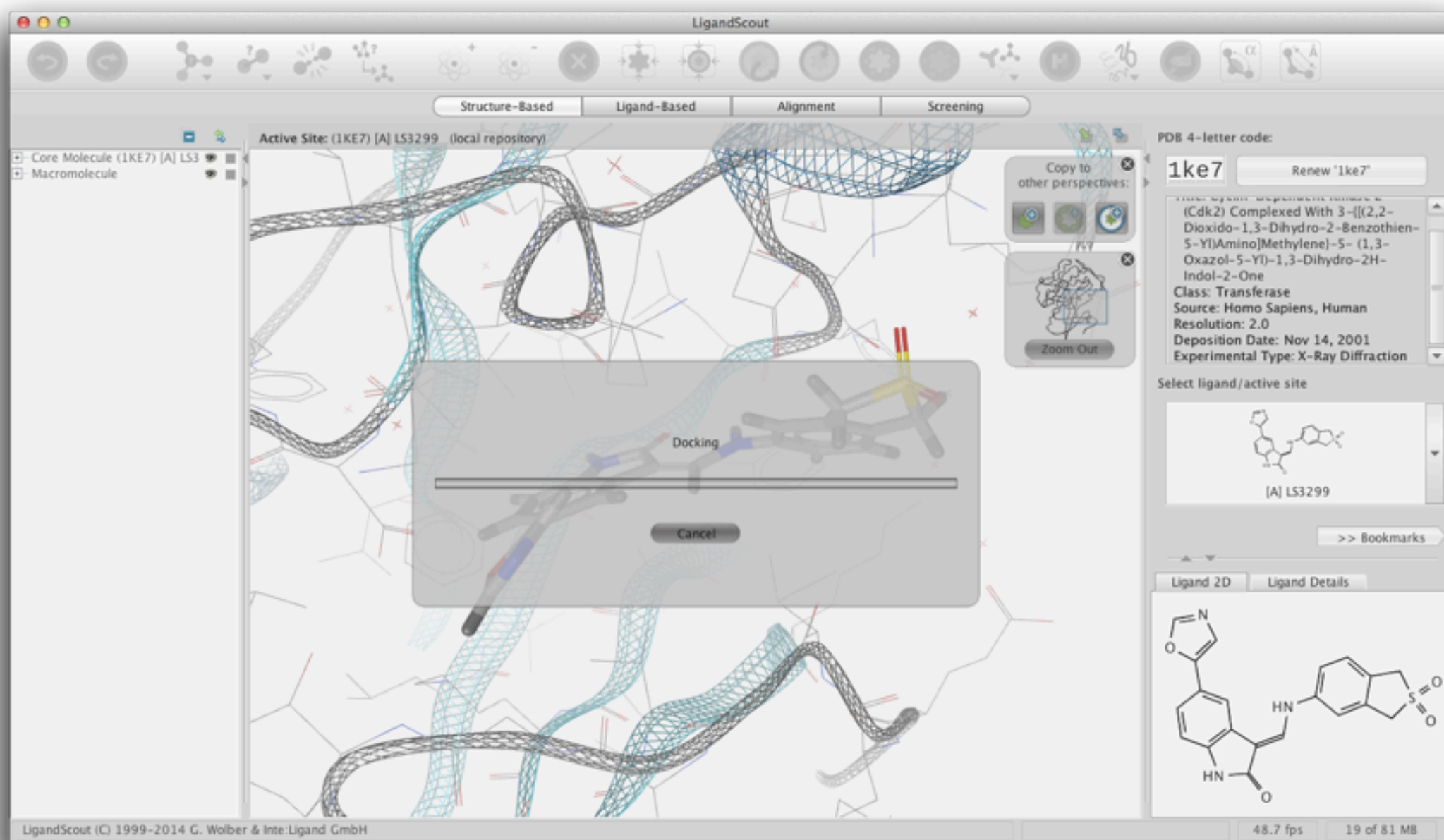
Docking With AutoDock 4.2 / AutoDock Vina



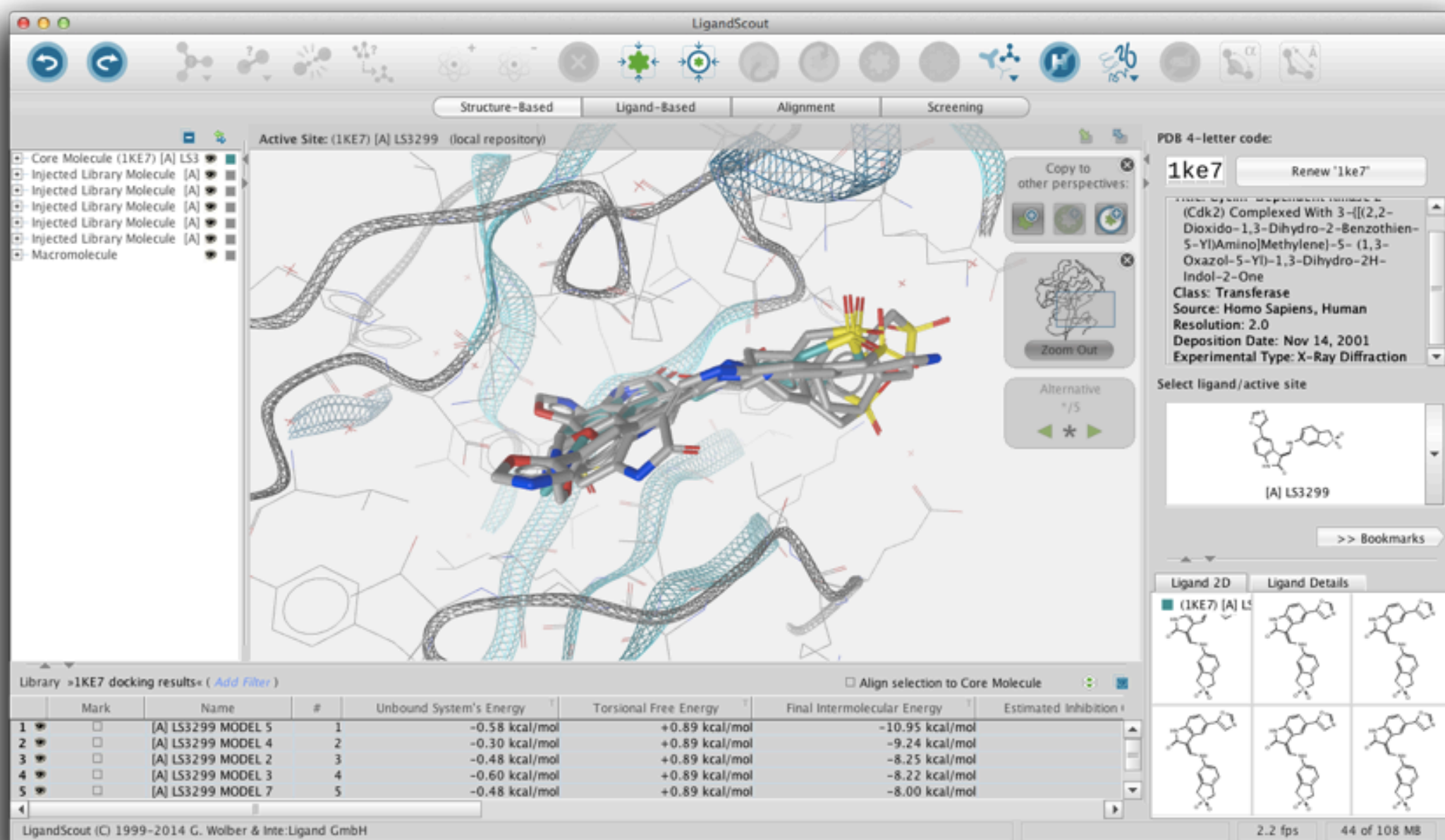
Docking With AutoDock 4.2 / AutoDock Vina



Docking With AutoDock 4.2 / AutoDock Vina



Docking With AutoDock 4.2 / AutoDock Vina



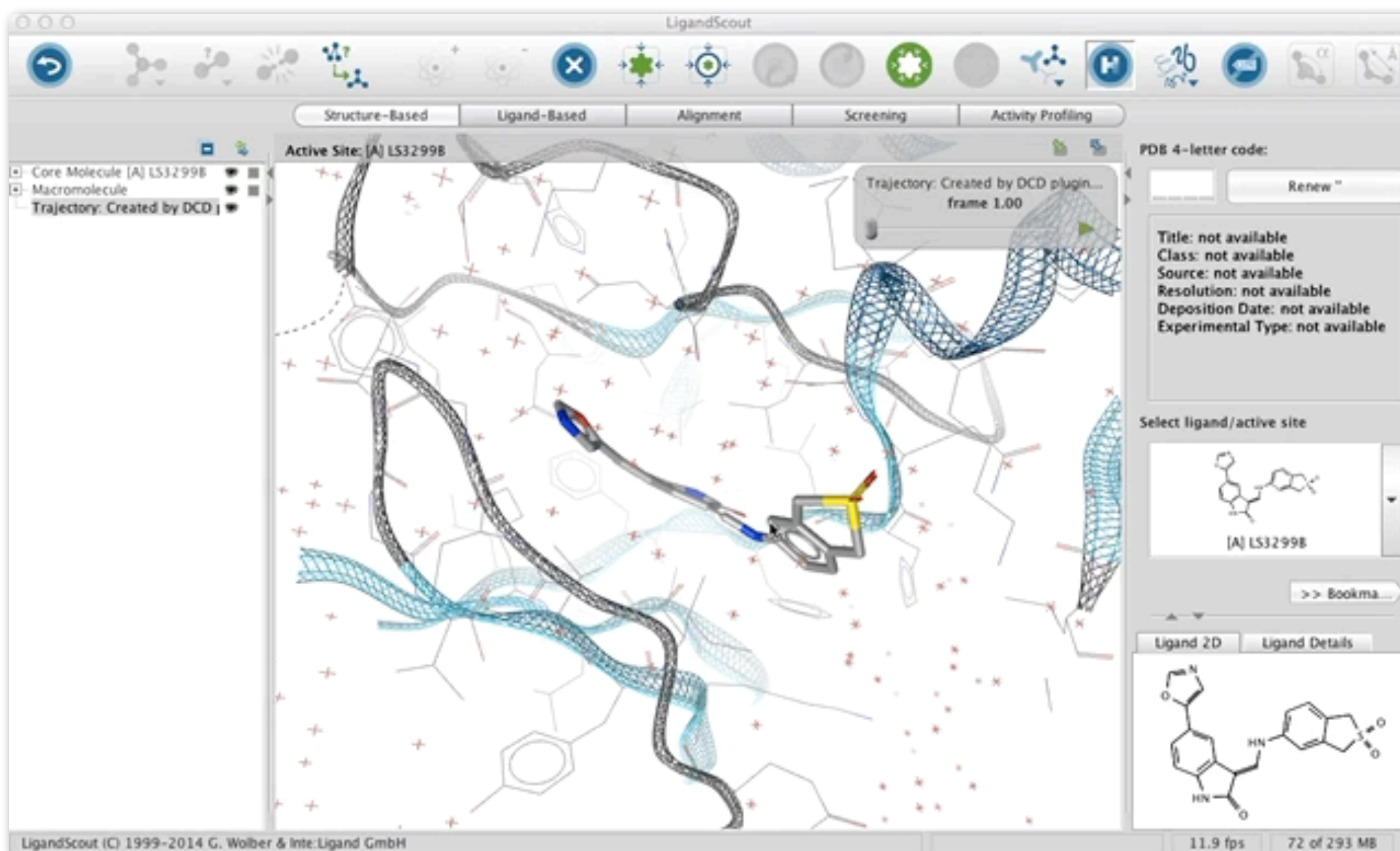
Reading Molecular Dynamics Trajectories

Integration of MD into the Pharmacophore World

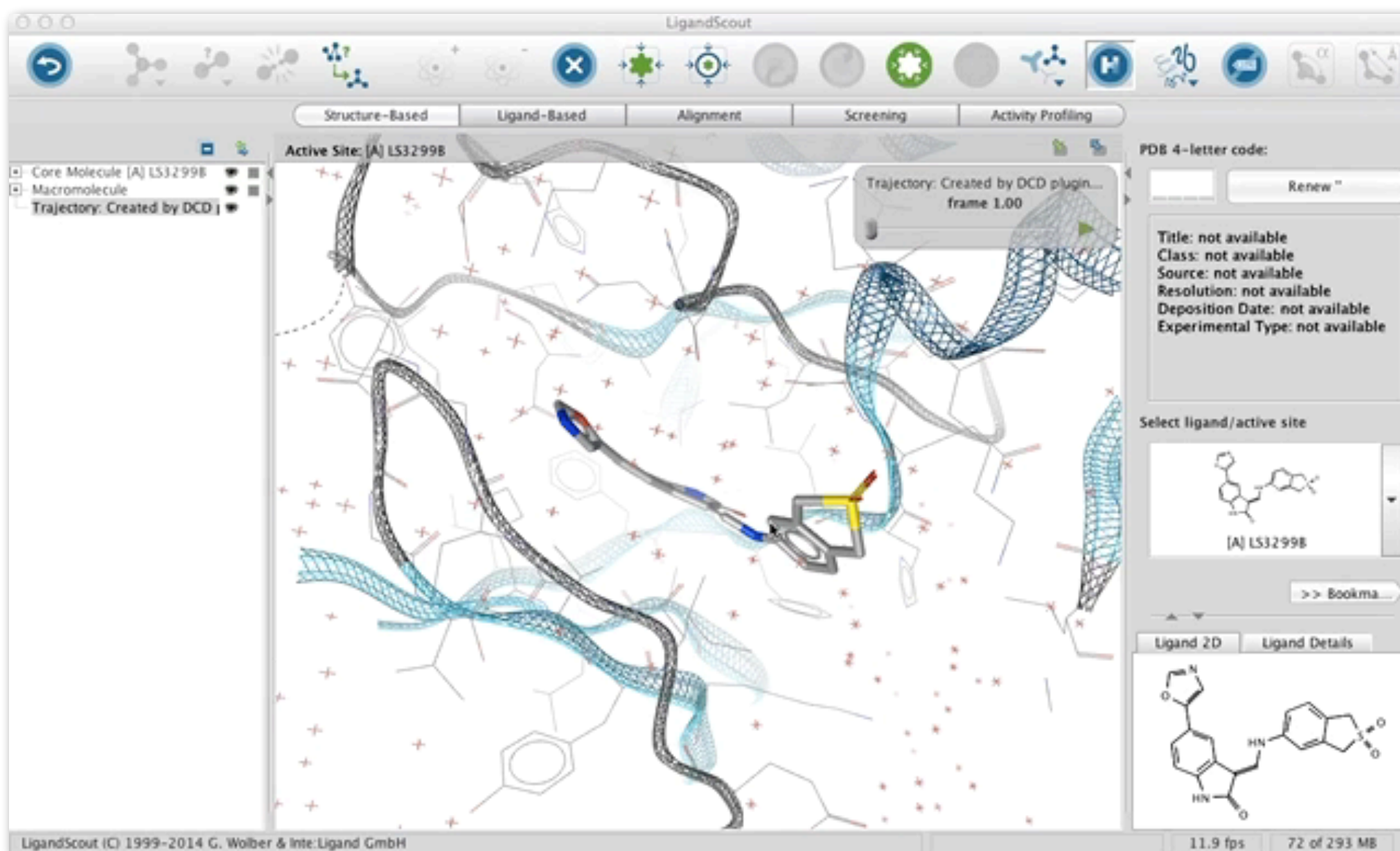
- Create multiple pharmacophore models directly from MD Analyze conformational behaviour of ligand/protein complex
- Analyze the formation of transient binding pockets
- Dock ligands into transient pockets

Makes MD trajectory analysis rapid and transparent

Analyzing MD within LigandScout



Analyzing MD within LigandScout



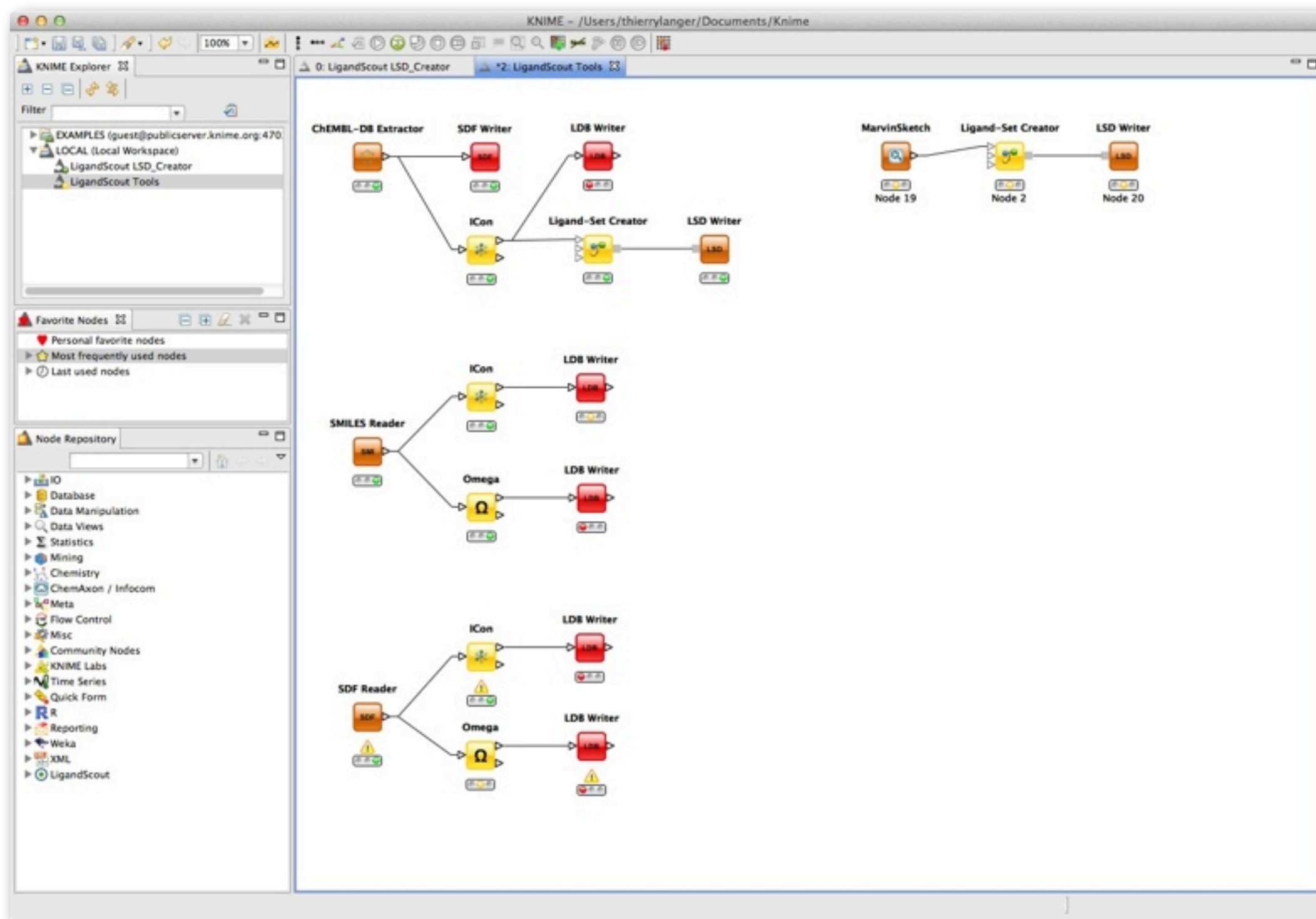
LigandScout KNIME Integration

LigandScout functionality available in KNIME workflow

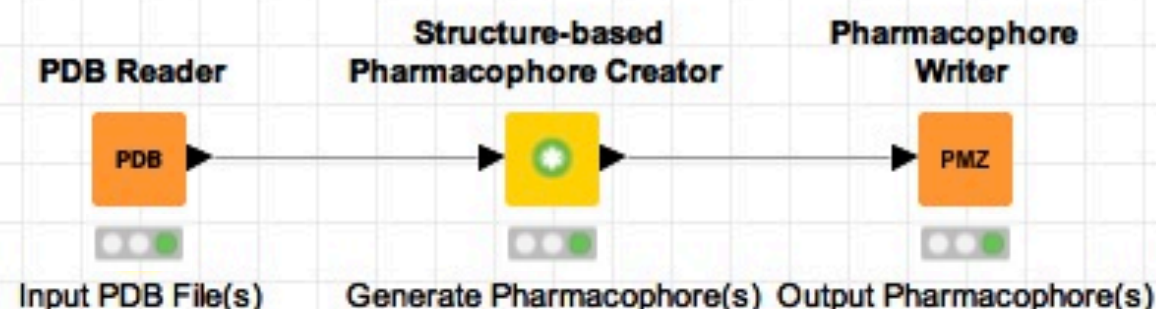
- Molecular structure data input and output
- Data set manipulation
- Conformational analysis
- LigandScout 3D database generation
- Query builder for ChEMBL online databank
- Patent searching in SureChEMBL
- Virtual screening & Activity profiling
- MD trajectory analysis using pharmacophores
- Access to Inte:Ligand's Pharmacophore Databases (license necessary)

Deploy easy-to-use workflows to co-workers

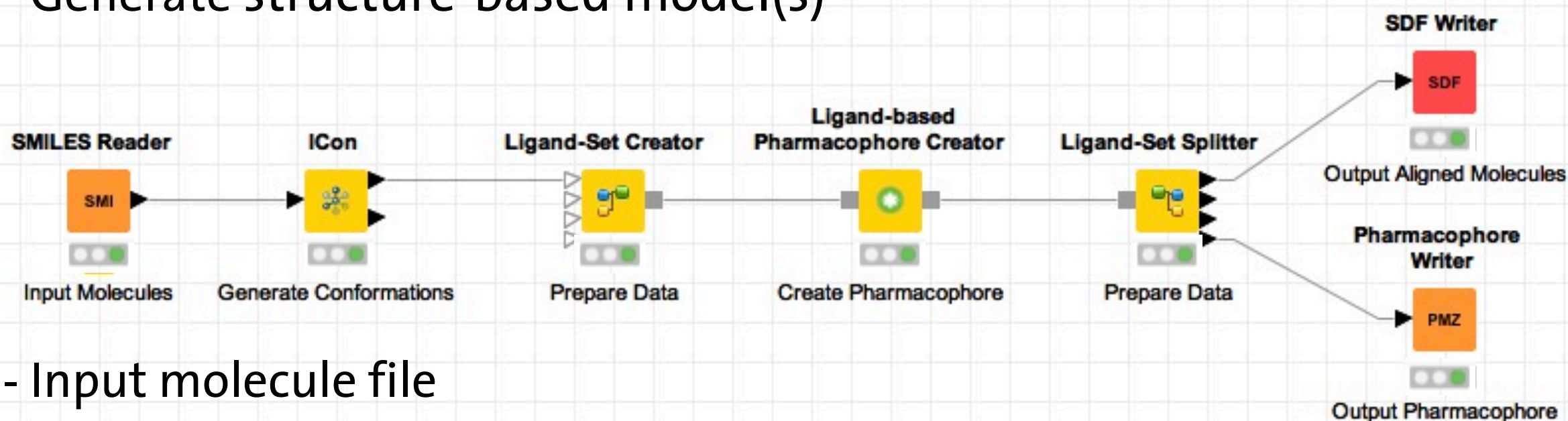
KNIME Workflows



Batch Mode Pharmacophore Generation

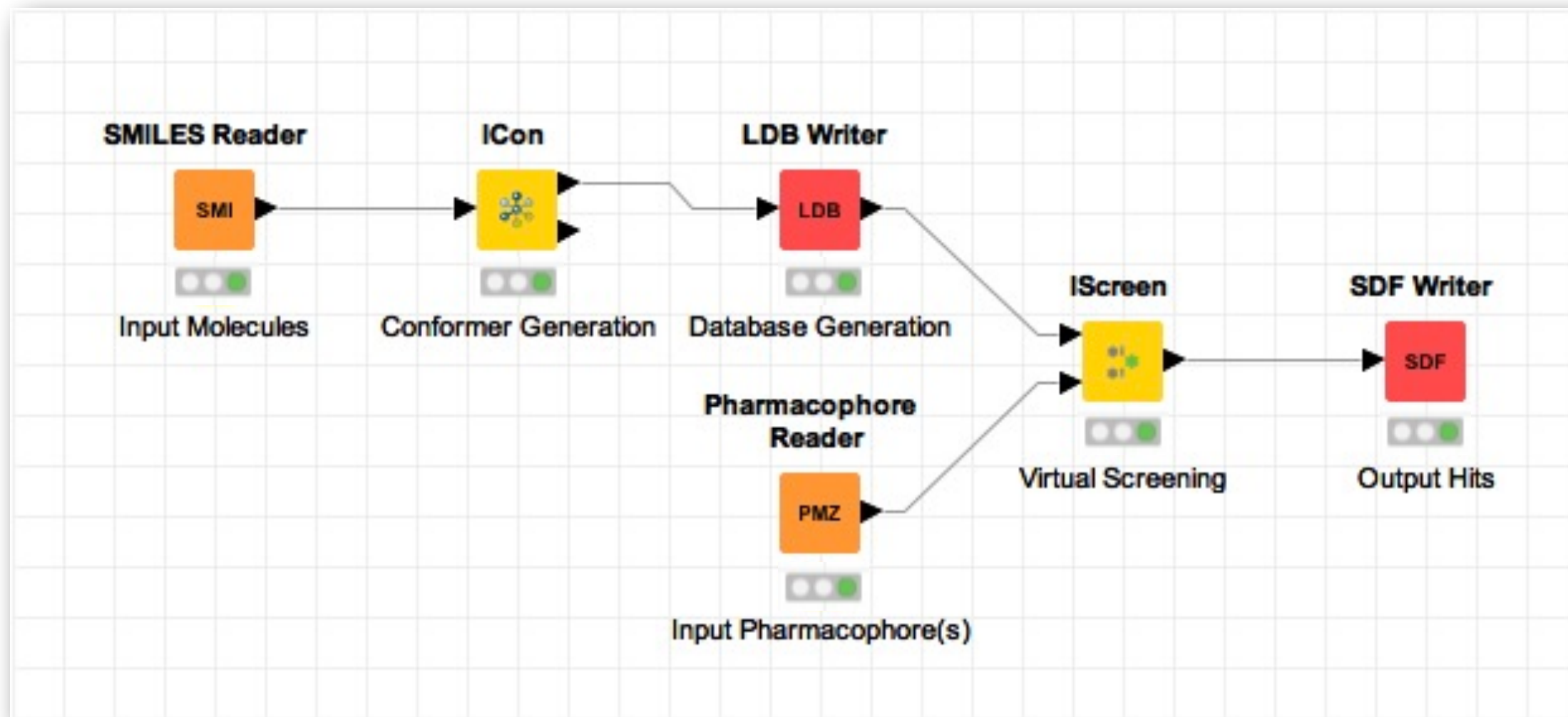


- Input pdb protein-ligand complex file(s)
- Generate structure-based model(s)



- Input molecule file
- Generate ligand-based model(s)

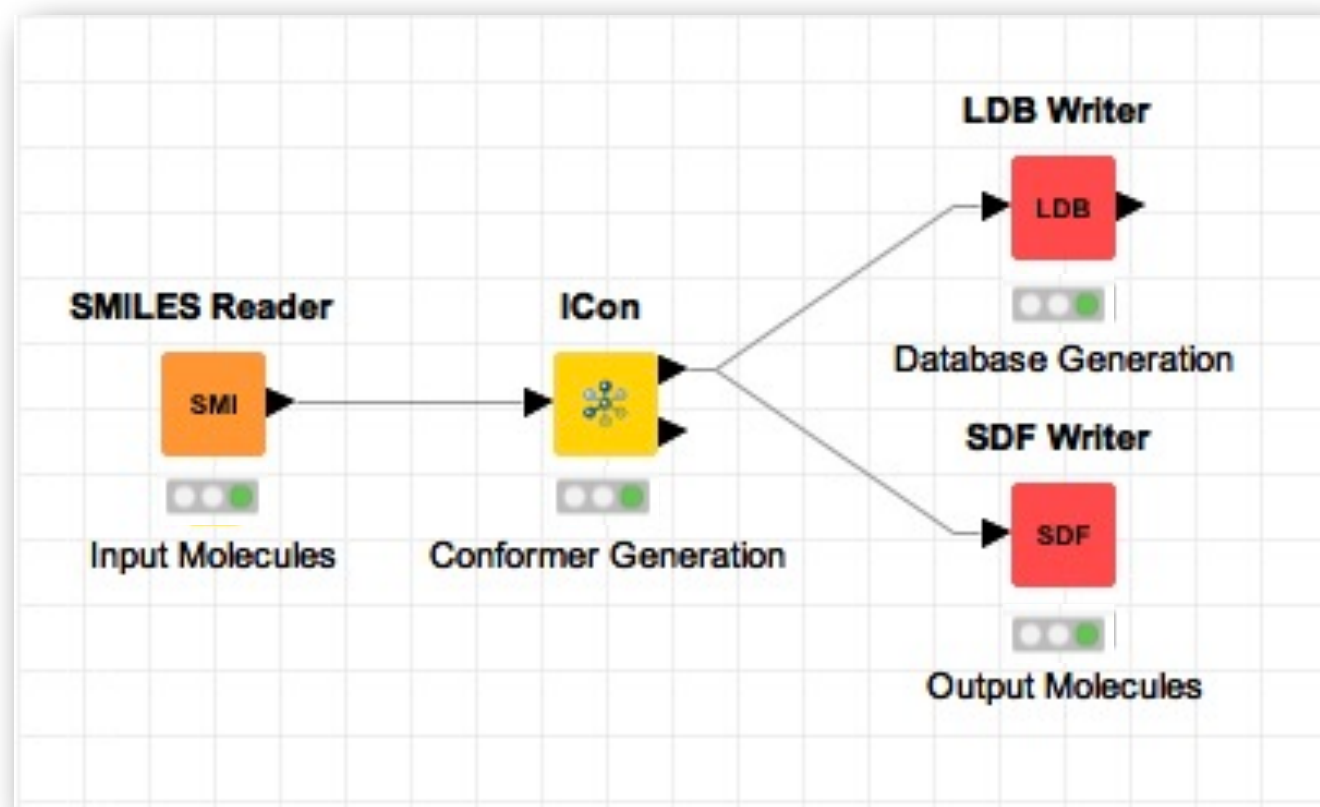
LigandScout KNIME Extensions



- Input molecule files (smiles/sdf/mol2)
- Screen with your favorite pharmacophore model(s)
- Retrieve ranked hits

Automated Conformational Analysis

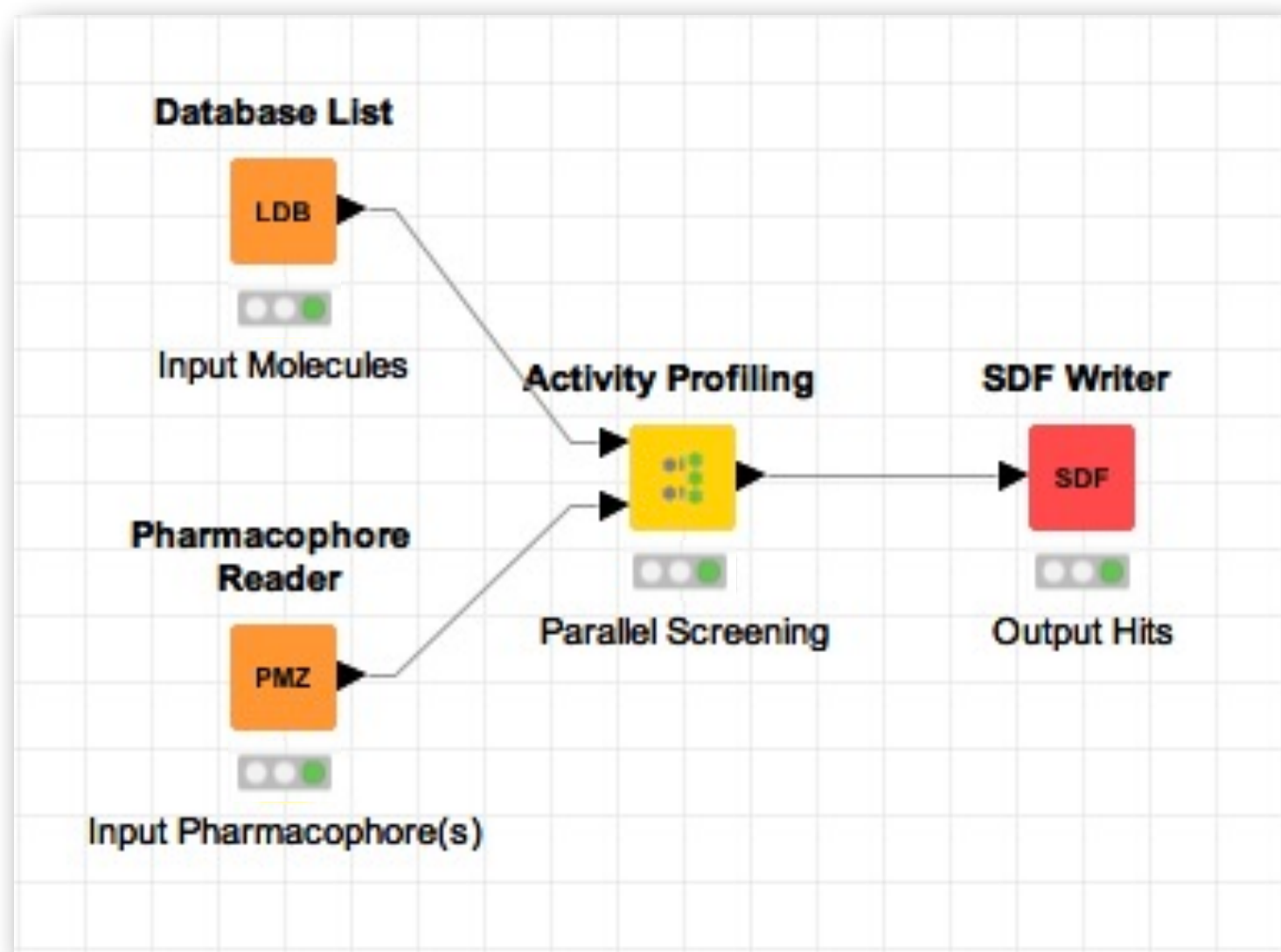
Building of a 3D multiconformational database for VS



- Input molecule files (smiles/sdf/mol2)
- Retrieve LigandScout compound database or multiconf SDF

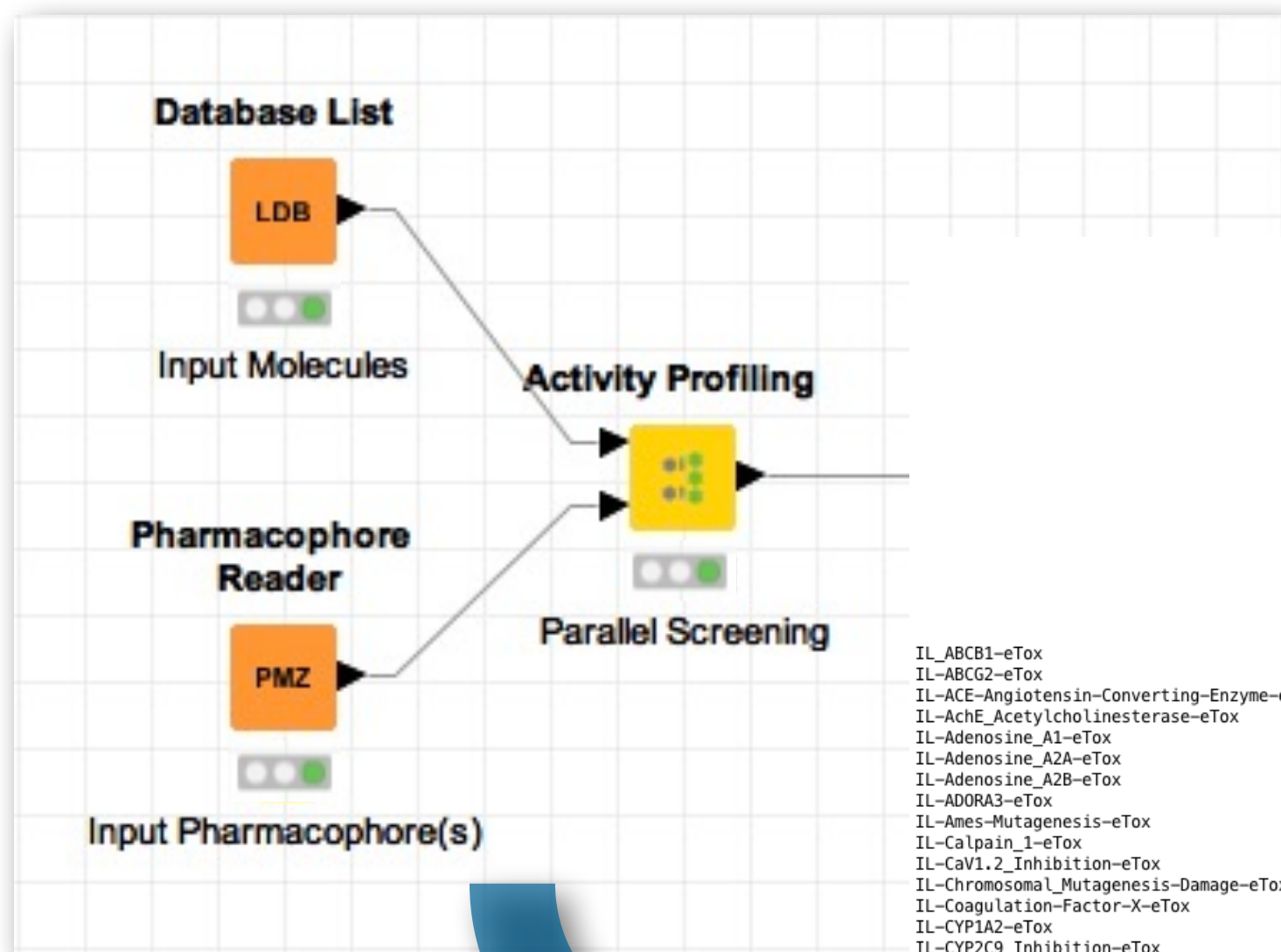
LigandScout KNIME Extensions

e. g. Automated Compound Activity Profiling



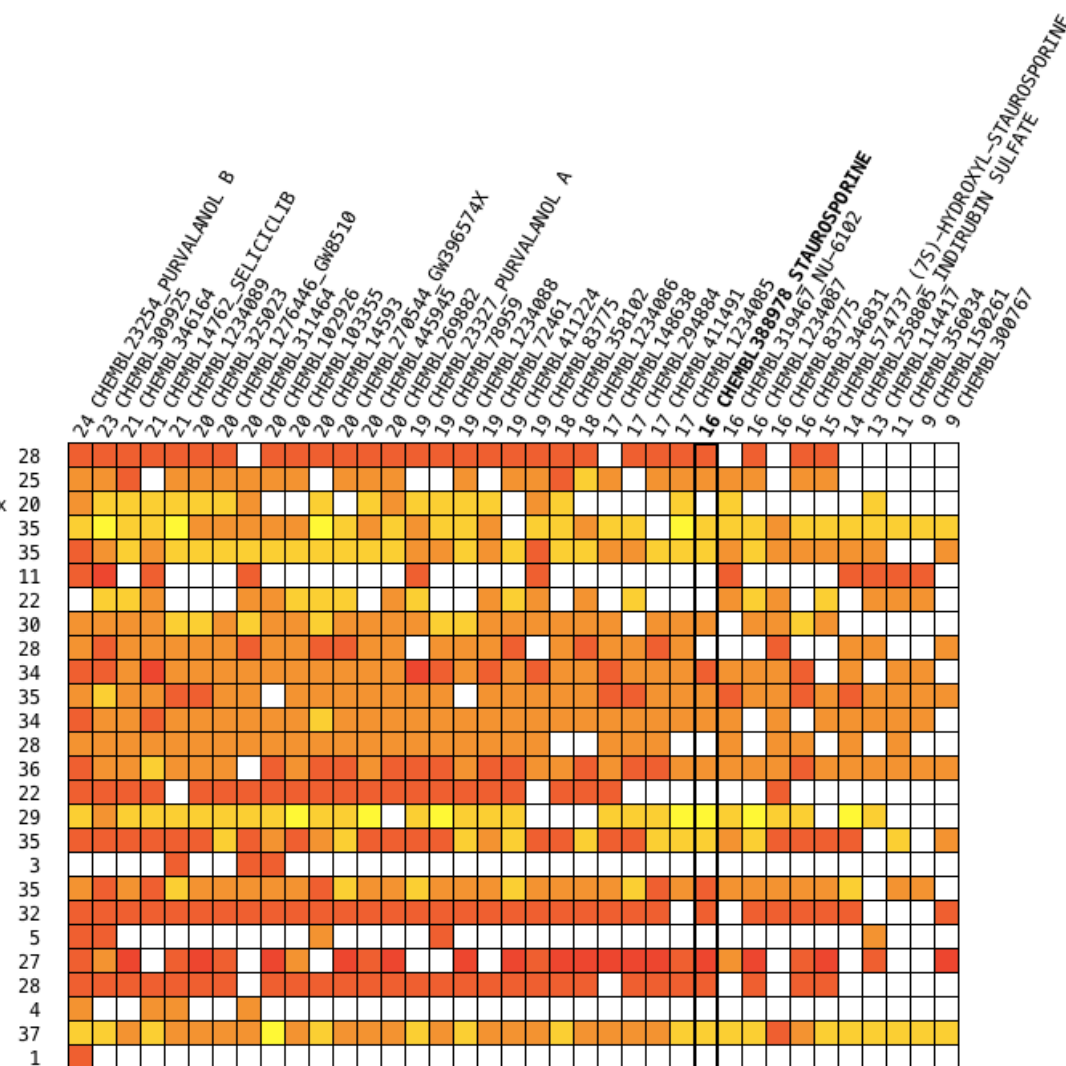
LigandScout KNIME Extensions

e. g. Automated Compound Activity Profiling



IL-ABCB1-eTox
 IL-ABCG2-eTox
 IL-ACE-Angiotensin-Converting-Enzyme-eTox
 IL-AchE_Acetylcholinesterase-eTox
 IL-Adenosine_A1-eTox
 IL-Adenosine_A2A-eTox
 IL-Adenosine_A2B-eTox
 IL-ADORA3-eTox
 IL-Ames-Mutagenesis-eTox
 IL-Calpain_1-eTox
 IL-Cav1.2_Inhibition-eTox
 IL-Chromosomal_Mutagenesis-Damage-eTox
 IL-Coagulation-Factor-X-eTox
 IL-CYP1A2-eTox
 IL-CYP2C9_Inhibition-eTox
 IL-CYP2C9-Selectivity-1R90-A-eTox
 IL-CYP2D6-Inhibition-eTox
 IL-CYP2D6-Selectivity-eTox
 IL-3CYP3A4-Inhibition-eTox
 IL-CYP3A4-Selectivity-eTox
 IL-LACTB-Inhibition-eTox
 IL-MAPK1-eTox
 IL-MDR1-eTox
 IL-Nav1.5-eTox
 IL-OAT4-eTox
 IL-RAR-alpha-eTox

Pharmacophores: 26 Molecules: 37



Inte:Ligand's Toxicity Assessment Models

7 year collaborative EC Project on Toxicity Prediction

Executive Committee



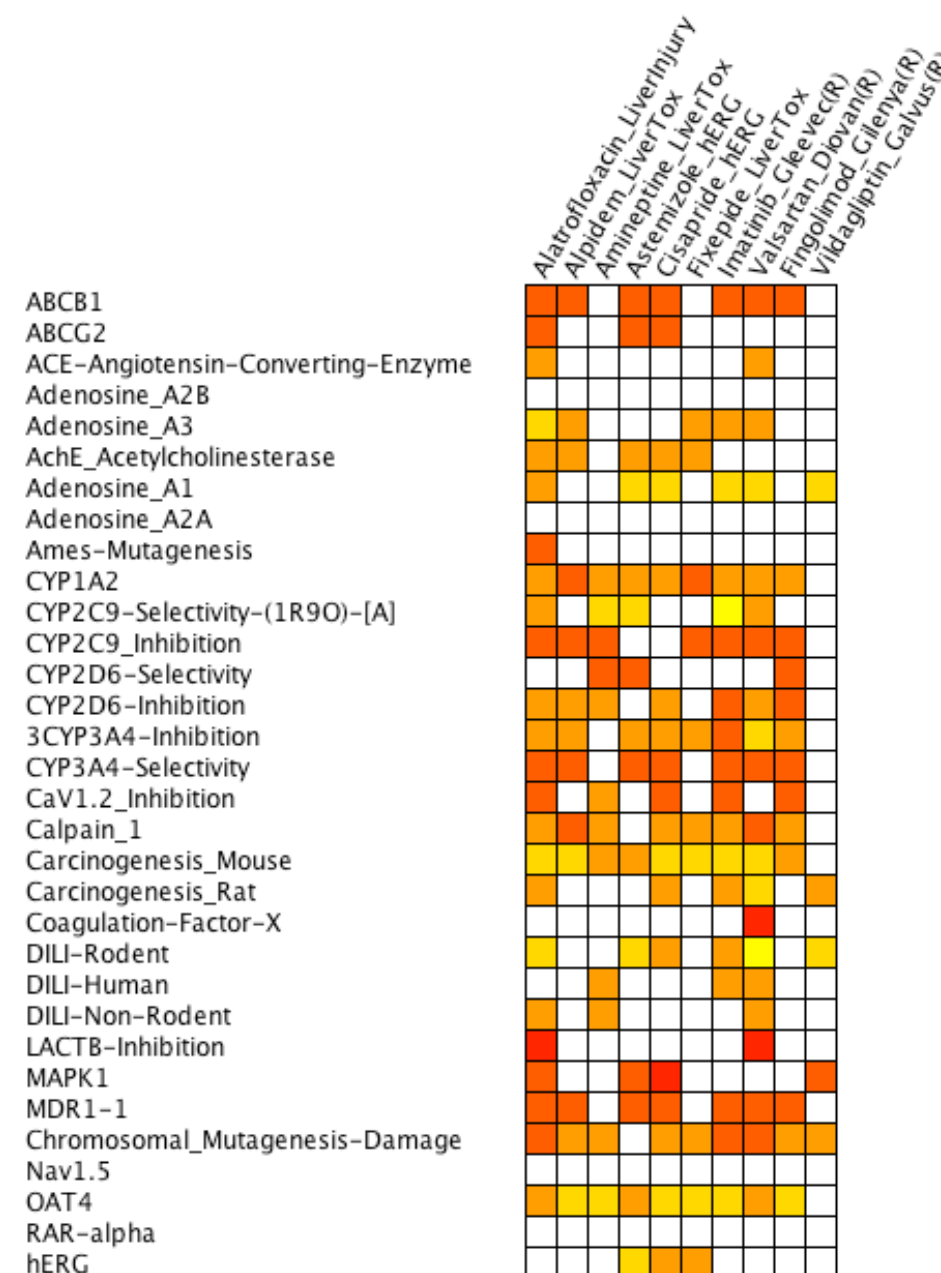
EFPIA



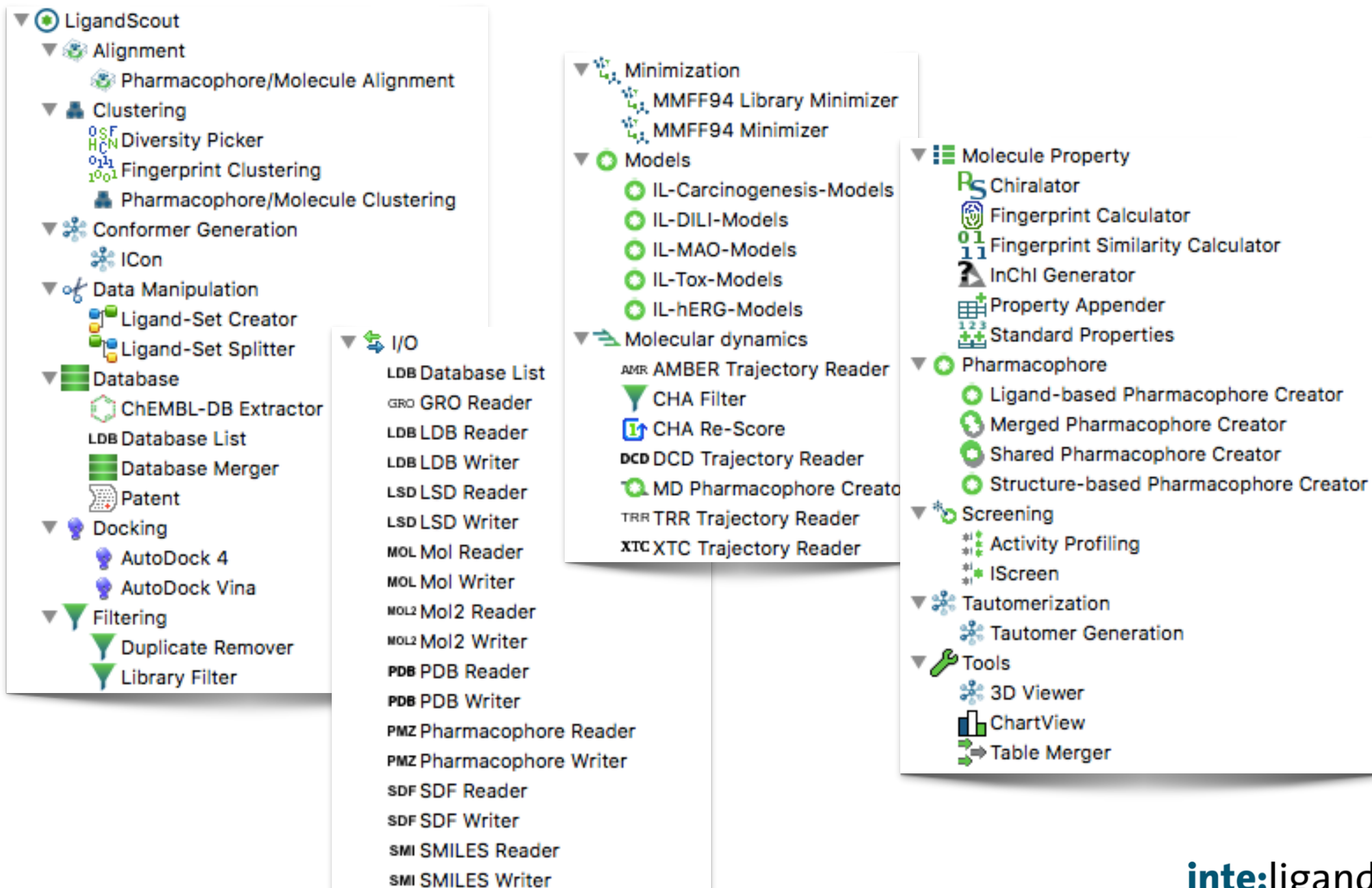
Academia



SMEs



KNIME Nodes Available for ...



KNIME Tutorial Workflows

Create Ligand Based Pharmacophore Models

Experience level: Intermediate
Time needed: 15 minutes

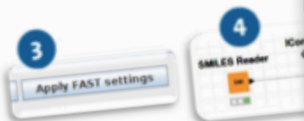
Node Repository	Sequence
<ul style="list-style-type: none"> o I/O - PDB Reader o Pharmacophore <ul style="list-style-type: none"> - Ligand-based Pharmacophore Creator 	<ul style="list-style-type: none"> o Read a SMILES file by using "SMILES" o Connect the output of "SMILES" Conformer Generator" node o Configure "Icon Conformer Generator" o Connect the first port of "Icon Conformer Generator" with the second input port of "Clustering" node and execute it o Connect the second output port of "Pharmacophore/Molecule Clustering" with the first port of "Ligand-based Pharmacophore Creator" o Configure "Ligand-based Pharmacophore Creator" by selecting the "Treat cluster input" option o Connect "Ligand-based Pharmacophore Creator" with "Pharmacophore Writer" node o Export all pharmacophores to a file o Choose the folder in which to save the file and execute the node

Description

Description
In the Node Repository panel, open the "LIG" drop do:
In the "SMILES Reader" [1] node and drag and drop it into the
F6 [2] A pop-up window for configuration will appear
the triangle light underneath the node, which was red
right click on it and press "Execute" from the pop-up
visit the Node Repository panel again and open the "
Look for the "Icon Conformer Generator" node and dr
node (black triangle) with the input port of the "Icon
node and configure it. In the pop-up window, click o
(F7). In the "Clustering" drop down menu select the "
connect the first output of the "Icon Conformer Gene
"Pharmacophore" drop down menu, drag and drop:
second output port of "Pharmacophore/Molecule Clu
configure it selecting the "Treat cluster individually
the first output port of the "Ligand-based Pharmac
pharmacophores to a single file" and choose a nam
Press OK and execute the node (F7). [4] The program
the pharmacophore model(s) you have generated.

Where to go from here:

- Screening database(s) against pharmacophore
- Use generated pharmacophores for Activity Prediction



Create Structure Based Pharmacophore Models

Experience level: basic
Time needed: 10 minutes

Node Repository	Sequence	Advanced controls (opt.)
<ul style="list-style-type: none"> o I/O <ul style="list-style-type: none"> - PDB Reader - Pharmacophore Writer o Pharmacophore <ul style="list-style-type: none"> - Structure-based Pharmacophore Creator 	<ul style="list-style-type: none"> o Read a PDB file by using "PDB Reader" node o Connect the output of "PDB Reader" node with "Structure-based Pharmacophore Creator" node o Configure "Structure-based Pharmacophore Creator" node and execute it o Connect "Structure-based Pharmacophore Creator" node with "Pharmacophore Writer" node o Configure "Pharmacophore Writer" node selecting "Export all pharmacophores to a single file" o Choose the folder in which save my_model.pmx, then execute the node 	<ul style="list-style-type: none"> o Prepare batch mode processing: <ul style="list-style-type: none"> - Configure "PDB Reader" node to read multiple PDB files at the same time o Modify pharmacophore creation parameters <ul style="list-style-type: none"> - Configure "Structure-based Pharmacophore Creator" node to add the exclusion volume coat to the model o Explore the options of the "Pharmacophore Writer" node (e.g. pharmacophore models saved as separate files)

Description

Description

In the Node Repository panel, open the "I/O" drop down menu in the LigandScout section to see all the Input/Output nodes. Look for the "PDB Reader" [1] node and drag and drop it into the workspace. Configure the "PDB Reader" node by using a left double click or by pressing F6. [2] A pop-up window for configuration will appear and you enter the path to the PDB file you want to load. Press the "Add" button. You can add multiple PDB files. After pressing OK, the traffic light underneath the node, which was red before, will turn to yellow. Press F7 to execute the node (alternatively, you can right click on it and press "Execute" from the pop-up menu). The traffic light will turn green once the node has finished the task. Now, visit the Node Repository panel again and open the "Pharmacophore" drop down menu in the LigandScout drop down menu. Look for the "Structure-based Pharmacophore Creator" node and drag and drop it into the workspace. Connect the output port of the "PDB Reader" node (black triangle) with the input port of the "Structure-based Pharmacophore Creator" node (black triangle) [3]. Select the "Structure-based Pharmacophore Creator" node and configure it. In the pop-up window, select the minimum number of features necessary or creating the model [3] and set the flag for adding an exclusion volume card. After pressing OK, execute the node as before (F7). Once the task is finished the traffic light underneath the "Structure-based Pharmacophore Creator" node will turn green. In the "I/O" drop down menu select the "Pharmacophore Writer" node and drag and drop it in the workspace, connect the output of the "Structure-based Pharmacophore Creator" node with it and start the configuration as before. In the pop-up windows select "Export all pharmacophores to a single file" and choose a name for the output (you can also browse for the folder). [4] Press OK and execute the node (F7). The program will save a file in the specified directory containing the pharmacophore model(s) you have generated.

Where to go from here:

- Screening database(s) against pharmacophore model(s)
- Cluster pharmacophores
- Use generated pharmacophores for Activity profiling



Calculate Physicochemical Properties and Filter a Database

Level: basic
Time: 5 minutes

<p>by using "SDF Reader" node</p> <p>Input of "SDF Reader" node with "Standard</p> <p>ard Properties" node and execute it</p> <p>Properties" node with "Library Filter" node</p> <p>y Filter" node and execute it</p> <p>output port of "Library Filter" node with</p> <p>id output port of "Library Filter" node with</p>	<p>Advanced controls (opt.)</p> <ul style="list-style-type: none"> Calculate physicochemical properties: <ul style="list-style-type: none"> Configure "Standard Properties" node to compute different sets of properties Modify filtering parameters: <ul style="list-style-type: none"> Add other text and/or numeric filters in "Library Filter" node Configure the "Library Filter" node adding multiple properties to your filter Explore all the filtering operators (equal, different, smaller than, greater than)
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Drop down menu in the LigandScout section to see all the input/output nodes. Look for the workspace. Configure the node as showed in previous tutorial cards (by pressing Repository panel again and open the "Molecule Properties" node (by pressing "Standard Properties" node and drag and drop it into the workspace. Connect the output chemical properties you want to compute (these properties will be used in the next step) at once by pressing the corresponding "Select all" button. After pressing OK, execute and select the "Library Filter" node and drag and drop it in the workspace, connect the node and continue with its configuration. In the pop-up windows, the "Library Filter" node is by string (pressing the "[abc]" button)[1 red circle] or numeric property (pressing the "[num]" button) will appear. Configure the row by choosing "MW[1]" in the "[num]" until "<" symbol appears. Write then in the editable text box a value to use for filtering, the node will filter out molecules with molecular weight smaller than 400. Explore the workspace respectively. The "SDF Writer" node connected to the first output port of the "Library Filter" node and drag two of them in the workspace. Connect them with the second output port of the "Library Filter" node (the one connected to the first output port of the "Library Filter" node greater than 400, while the one connected to the second output port of the "Library Filter" node failed_molecules.sdf for the second). Execute them with F7.[4]



Perform Virtual Screening

Experience level: intermediate
Time needed: 15 minutes

f controls (opt.)

controls (opt.)

band parameters:
are "SDF Reader" node to extract name
different column
"Icon Conformer Generator" settings (e.g.
ST settings)
Parameters for "iScreen" node:
the scoring function
segment screening mode
different retrieval modes
the node in order to not check the
columns
mode processing:
Pharmacophore Reader" node to read
is at the same time
can expression with "iScreen" node
not 3. Numbers are referred to the
pres ranking in the "Pharmacophore

Into the workspace. Configure the pop the "Icon Conformer Generator" part of the "SDF Reader" node. In the pop-up window, "IO" drop down menu, select the "Icon Conformer Generator" node. In the "IO" drop down menu, select the "SDF file" (3). Execute and then drop down menu. Add the "Macrophore Model" node to the second input port of the "Icon Conformer Generator" node. Name for the output file. Execute the "SDF Reader" node as a sdf file.