



Hands-on tutorials of AutoDock 4 and AutoDock Vina

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AutoDock

<http://autodock.scripps.edu>

AutoDock is a suite of automated docking tools. It is designed to predict how small molecules, such as substrates or drug candidates, bind to a receptor of known 3D structure.

AutoDock 4.2

Morris, G. M., Huey, R., Lindstrom, W., Sanner, M. F., Belew, R. K., Goodsell, D. S. and Olson, A. J. (2009) [Autodock4 and AutoDockTools4: automated docking with selective receptor flexibility](#). *J. Computational Chemistry* 2009, **16**: 2785-91.

AutoDock 3 & 4

Morris, G. M., Goodsell, D. S., Halliday, R.S., Huey, R., Hart, W. E., Belew, R. K. and Olson, A. J. (1998), [Automated Docking Using a Lamarckian Genetic Algorithm and an Empirical Binding Free Energy Function](#) *J. Computational Chemistry*, **19**: 1639-1662.

AutoDock 4 Scoring Function

Huey, R., Morris, G. M., Olson, A. J. and Goodsell, D. S. (2007), [A Semiempirical Free Energy Force Field with Charge-Based Desolvation](#) *J. Computational Chemistry*, **28**: 1145-1152.

AutoDock 2.4

Morris, G. M., Goodsell, D. S., Huey, R. and Olson, A. J. (1996), [Distributed automated docking of flexible ligands to proteins: Parallel applications of AutoDock 2.4](#) *J. Computer-Aided Molecular Design*, **10**: 293-304.

AutoDock 1

Goodsell, D. S. and Olson, A. J. (1990), [Automated Docking of Substrates to Proteins by Simulated Annealing](#) *Proteins: Structure, Function and Genetics.*, **8**: 195-202.

AutoDock 4 is free and is available under the GNU General Public License. 2

AutoDock Vina

<http://vina.scripps.edu/>

AutoDock Vina: Improving the Speed and Accuracy of Docking with a New Scoring Function, Efficient Optimization, and Multithreading

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Department of Molecular Biology, The Scripps Research Institute, La Jolla, California

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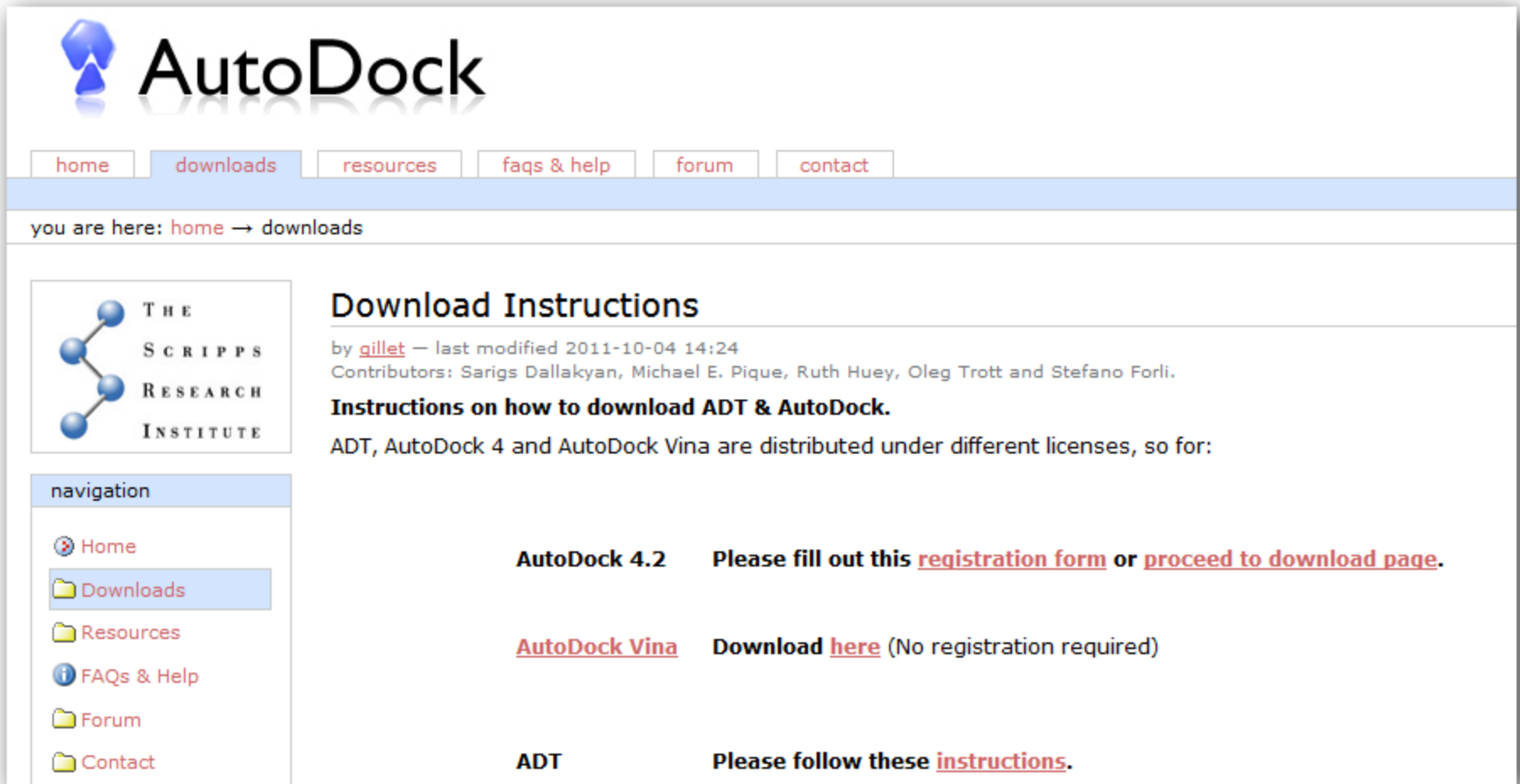
Abstract: AutoDock Vina, a new program for molecular docking and virtual screening, is presented. AutoDock Vina achieves an approximately two orders of magnitude speed-up compared with the molecular docking software previously developed in our lab (AutoDock 4), while also significantly improving the accuracy of the binding mode predictions, judging by our tests on the training set used in AutoDock 4 development. Further speed-up is achieved from parallelism, by using multithreading on multicore machines. AutoDock Vina automatically calculates the grid maps and clusters the results in a way transparent to the user.

© 2009 Wiley Periodicals, Inc. J Comput Chem 31: 455–461, 2010

Because the scoring functions used by AutoDock 4 and AutoDock Vina are different and inexact, on any given problem, either program may provide a better result.

AutoDock Vina is available under the Apache license, allowing commercial and non-commercial use and redistribution.

<http://autodock.scripps.edu/downloads>



The screenshot shows the AutoDock website interface. At the top left is the AutoDock logo, a blue stylized 'A' with a reflection. To its right is the text 'AutoDock' in a large, bold, black font. Below the logo and text is a horizontal navigation bar with buttons for 'home', 'downloads', 'resources', 'faqs & help', 'forum', and 'contact'. The 'downloads' button is highlighted. Below the navigation bar is a breadcrumb trail: 'you are here: home → downloads'. On the left side, there is a sidebar with a logo for 'THE SCRIPPS RESEARCH INSTITUTE' (a blue molecular structure) and a 'navigation' menu with links for Home, Downloads (highlighted), Resources, FAQs & Help, Forum, and Contact. The main content area is titled 'Download Instructions' and includes the following text: 'by gillet — last modified 2011-10-04 14:24', 'Contributors: Sarigs Dallakyan, Michael E. Pique, Ruth Huey, Oleg Trott and Stefano Forli.', and 'Instructions on how to download ADT & AutoDock.' Below this, it states 'ADT, AutoDock 4 and AutoDock Vina are distributed under different licenses, so for:' and lists three options: 'AutoDock 4.2' with instructions to fill out a registration form or proceed to a download page; 'AutoDock Vina' with a download link and note that no registration is required; and 'ADT' with instructions to follow specific instructions.

AutoDock

home downloads resources faqs & help forum contact

you are here: home → downloads

THE SCRIPPS RESEARCH INSTITUTE

Download Instructions

by [gillet](#) — last modified 2011-10-04 14:24
Contributors: Sarigs Dallakyan, Michael E. Pique, Ruth Huey, Oleg Trott and Stefano Forli.

Instructions on how to download ADT & AutoDock.

ADT, AutoDock 4 and AutoDock Vina are distributed under different licenses, so for:

AutoDock 4.2	Please fill out this registration form or proceed to download page .
AutoDock Vina	Download here (No registration required)
ADT	Please follow these instructions .

These programs were installed on VM.



The screenshot shows the MGLTools website interface. At the top, the logo "MGLTools" is displayed in a large, white, serif font against a blue background featuring a molecular model. Below the logo is a navigation bar with links for Home, Downloads, Screenshots, Documentation, Packages, ePMV, Support, and Forum. The main content area is titled "Downloads" and includes a byline for Sargis Dallakyan, contributors' names, and a link to license agreements. A section for "MGLTools 1.5.6 Release Notes" contains a table of download links for various operating systems and architectures. A sidebar on the left provides a "Navigation" menu with icons for Home, Downloads, Updates, Latest Builds, Screenshots, Documentation, Packages, ePMV, Support, and Forum. At the bottom of the page, there is a link to "What are PMV, ADT and Vision?".

MGLTools

Home | Downloads | Screenshots | Documentation | Packages | ePMV | Support | Forum

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Downloads

by [Sargis Dallakyan](#) — last modified 2015-07-16 13:41
Contributors: Anna Omelchenko, Michel Sanner, Sowjanya Karnati

[License Agreements.](#)

[MGLTools 1.5.6 Release Notes](#)

	<ul style="list-style-type: none">■ mgltools_win32_1.5.6_Setup.exe	<ul style="list-style-type: none">■ mgltools_win32_1.5.6.zip
	<ul style="list-style-type: none">■ mgltools_Linux-x86_1.5.6_Install GUI installer (GLIBC_2.3, libstdc++.5.X).■ mgltools_Linux-x86_64_1.5.6_Install GUI installer (GLIBC_2.4, libstdc++.6.X).	<ul style="list-style-type: none">■ mgltools_i86Linux2_1.5.6.tar.gz Tarball installer (GLIBC_2.3, libstdc++.5.X).■ mgltools_x86_64Linux2_1.5.6.tar.gz Tarball installer (GLIBC_2.4, libstdc++.6.X).
	<ul style="list-style-type: none">■ (Snow) Leopard - Mac OS X 10.5 and 10.6 - Intel■ (Snow) Leopard - Mac OS X 10.5 and 10.6 - PPC	<ul style="list-style-type: none">■ mgltools_i86Darwin9_1.5.6.tar.gz■ mgltools_ppcDarwin9_1.5.6.tar.gz
	<ul style="list-style-type: none">■ Source All Platforms	

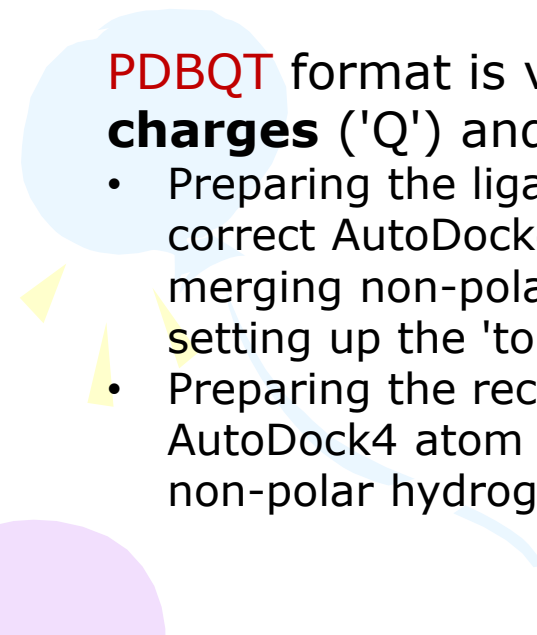
■ [What are PMV, ADT and Vision?](#)

AutoDockTools (ADT) is developed to help set up the docking. ADT is included in **MGLTools** packages.



In general, each docking (AutoDock 4 and/or AutoDock Vina) requires:

1. structure of the receptor (protein), in pdbqt format
2. structure of the ligand (small molecule, drug, etc.) in pdbqt format
3. docking and grid parameters (search space)



PDBQT format is very similar to PDB format but it includes **partial charges** ('Q') and AutoDock 4 (AD4) **atom types** ('T').

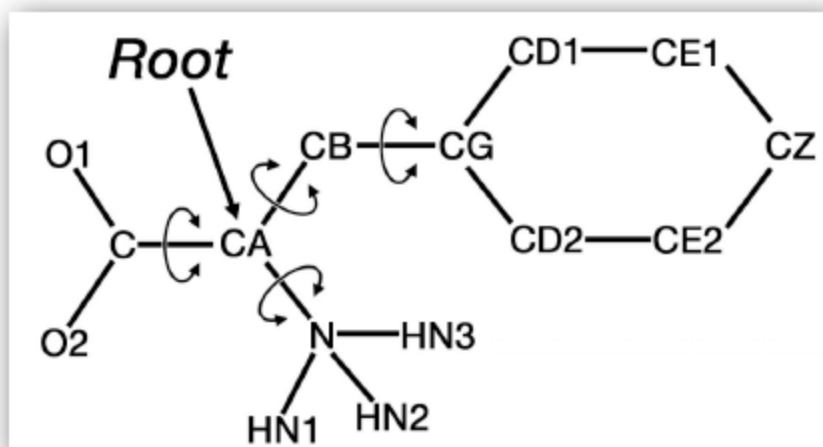
- Preparing the ligand involves ensuring that its atoms are assigned the correct AutoDock4 atom types, adding Gasteiger charges if necessary, merging non-polar hydrogens, detecting aromatic carbons if any, and setting up the 'torsion tree'.
- Preparing the receptor involves ensuring that its atoms conform to the AutoDock4 atom types by adding Gasteiger charges if necessary, merging non-polar hydrogens and detecting aromatic carbons.

Sample PDBQT file

```

REMARK 4 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 1 A between atoms: N_1 and CA_5
REMARK 2 A between atoms: CA_5 and CB_6
REMARK 3 A between atoms: CA_5 and C_13
REMARK 4 A between atoms: CB_6 and CG_7
ROOT
ATOM 1 CA PHE A 1 25.412 19.595 12.578 1.00 12.96 0.287 C
ENDROOT
BRANCH 1 2
ATOM 2 N PHE A 1 25.225 18.394 13.381 1.00 13.04 -0.065 N
ATOM 3 HN3 PHE A 1 25.856 17.643 13.100 1.00 0.00 0.275 HD
ATOM 4 HN2 PHE A 1 25.558 18.517 14.337 1.00 0.00 0.275 HD
ATOM 5 HN1 PHE A 1 24.247 18.105 13.350 1.00 0.00 0.275 HD
ENDBRANCH 1 2
BRANCH 1 6
ATOM 6 CB PHE A 1 26.873 20.027 12.625 1.00 12.45 0.082 C
BRANCH 6 7
ATOM 7 CG PHE A 1 27.286 20.629 13.923 1.00 12.96 -0.056 A
ATOM 8 CD2 PHE A 1 27.470 22.001 14.050 1.00 12.47 0.007 A
ATOM 9 CE2 PHE A 1 27.877 22.571 15.265 1.00 13.98 0.001 A
ATOM 10 CZ PHE A 1 28.108 21.754 16.360 1.00 13.84 0.000 A
ATOM 11 CE1 PHE A 1 27.919 20.380 16.242 1.00 13.77 0.001 A
ATOM 12 CD1 PHE A 1 27.525 19.821 15.027 1.00 11.32 0.007 A
ENDBRANCH 6 7
ENDBRANCH 1 6
BRANCH 1 13
ATOM 13 C PHE A 1 25.015 19.417 11.141 1.00 13.31 0.204 C
ATOM 14 O2 PHE A 1 24.659 20.534 10.507 1.00 12.12 -0.646 OA
ATOM 15 O1 PHE A 1 25.024 18.283 10.608 1.00 13.49 -0.646 OA
ENDBRANCH 1 13
TORSDOF 4

```



<http://autodock.scripps.edu/faqs-help/faq/what-is-the-format-of-a-pdbqt-file>

Both ligand and receptor PDBQT files used for the standard AutoDock 4 force field have additional requirements:

- Gasteiger PEOE **partial charges**.
- A united-atom representation (i.e. only polar hydrogens). A united atom representation can be obtained by first computing the partial charges for an **all-hydrogen** model of the molecule. Then, for each non-polar heavy atom that has any hydrogens bonded to it, the partial charge of the hydrogen should be added to that of the bonded heavy atom, then this hydrogen atom can be deleted.

Ideally, the structure of protein and ligand should already have all hydrogens added.

Most structures were solved by X-ray so the protons are missing in the PDB file.

Add hydrogens and/or charges to the structure

- **UCSF Chimera**

- **Open Babel**

Open Babel is a chemical toolbox, which can be used for converting files, molecular searching, hydrogen addition and deleting, Gasteiger-Marsili partial charge calculation, etc.

<http://openbabel.org>

- **pdb2pqr**

pdb2pqr prepares structures for further calculations by reconstructing missing atoms, adding hydrogens, assigning atomic charges and radii from specified force fields, and generating PQR files. PQR files are PDB files where the occupancy and B-factor columns have been replaced by per-atom charge and radius.

<http://www.poissonboltzmann.org>

http://nbc-222.ucsd.edu/pdb2pqr_2.1.1 (web server)



Return to [the PDB2PQR homepage](#).

This server enables a user to convert **PDB** files into PQR files. PQR files are PDB files where the oc B-factor columns have been replaced by per-atom charge and radius.

pKa calculations are performed by **PROPKA**.

For more information on PDB2PQR please see the:

- [Home Page](#)
- [Register \(and help support PDB2PQR & APBS\)](#)
- [User Guide](#)
- [Examples](#)
- [Release Notes](#)

If you use the PDB2PQR service in a publication, please cite:

Dolinsky TJ, Nielsen JE, McCammon JA, Baker NA. PDB2PQR: an automated pipeline for the execution, and analysis of Poisson-Boltzmann electrostatics calculations. Nucleic Acids Research W665-W667 (2004). [\[Link\]](#)

Note: In order to distribute server load, the PDB2PQR server currently is limited to a maximum size atoms per protein. If you are interested in using PDB2PQR for larger proteins, you are encouraged command line version of PDB2PQR from the [PDB2PQR download page](#). For additional limitations [PDB2PQR user guide](#)

Note: This server uses automatic refreshing to update the status of your PDB2PQR submission. D back button on your browser while the server is running.

Please enter either:

- a PDB ID:
- upload a PDB file: No file selected.

Pick a forcefield to use:

- AMBER
- CHARMM
- PARSE
- PEOEPB
- SWANSON
- TYLO6
- User-defined forcefield ([help](#)): No file selected.

User-defined names ([help](#)): No file selected.

* If you select user-defined forcefield, you also need to specify a user-defined .names file.

Pick an output naming scheme to use ([help](#)):

- Internal naming scheme ([What's this?](#))
- AMBER
- CHARMM
- PARSE
- PEOEPB
- SWANSON
- TYLO6

Available options:

- Ensure that new atoms are not rebuilt too close to existing atoms
- Optimize the hydrogen bonding network
- Assign charges to the ligand specified in a MOL2 file: No file selected.
- Create an **APBS** input file (this also enables the option to run APBS and visualize your results through the web interface, if it has been installed)
- Add/keep chain IDs in the PQR file
- Insert whitespaces between atom name and residue name, between x and y, and between y and z
- Create Typemap output
- Make the protein's N-terminus neutral (requires PARSE forcefield)
- Make the protein's C-terminus neutral (requires PARSE forcefield)

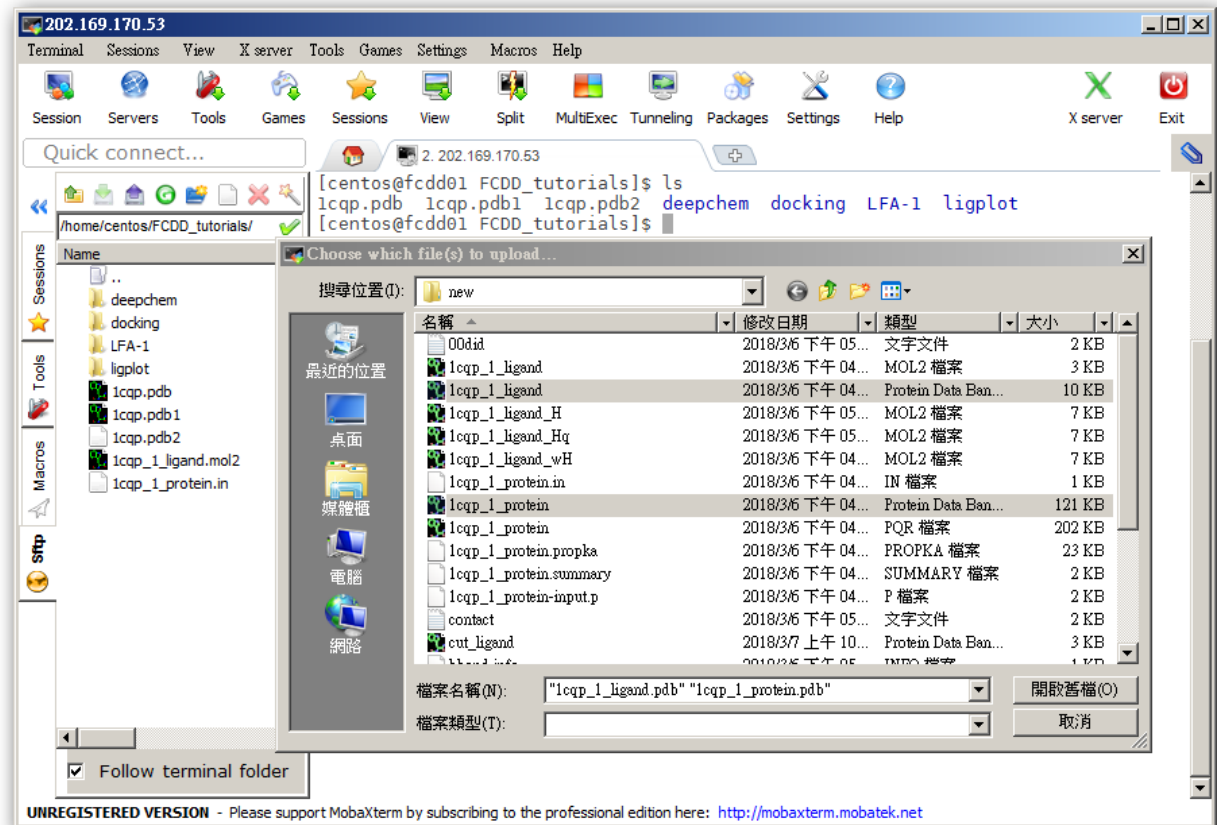
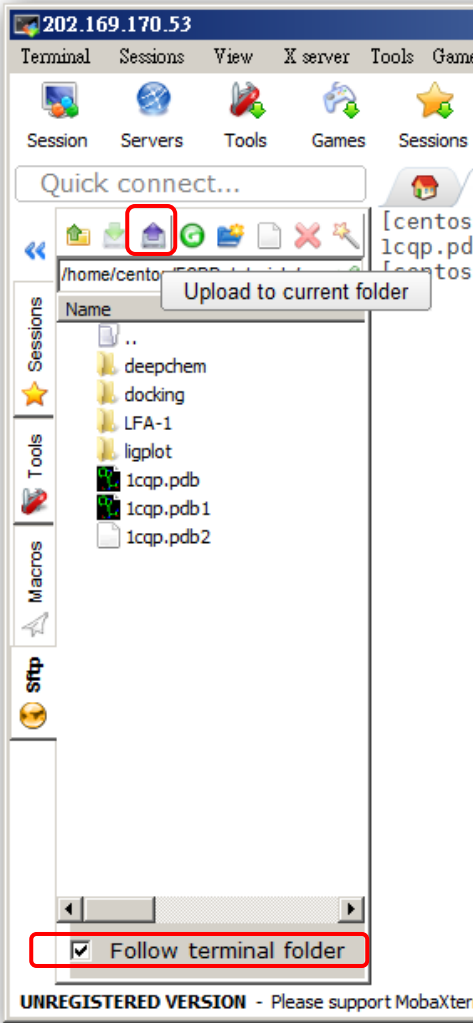
pKa Options*:

- Use pH
- No pKa calculation
- Use **PROPKA** to assign protonation states at provided pH
- Use PDB2PKA to parametrize ligands and assign pKa values (requires PARSE forcefield) at provided pH

* Warning: PDB2PKA is currently experimental and the process can take a very long time. The webserver will kill any jobs that last longer than one week. See the [Release Notes](#) for changes since the last version.

\$ cd ~/FCDD_tutorials
\$ ls

Upload the ligand and protein PDB to VM server.



Prepare structure files

```
$cd ~/FCDD_tutorials/docking  
$mkdir 1_preparation  
$cp 1cqp_1_protein.pdb 1cqp_1_ligand.pdb ./1_preparation  
$cd 1_preparation  
  
$obabel -ipdb 1cqp_1_ligand.pdb \  
-omol2 -O 1cqp_1_ligand_wH.mol2 -p 7.4  
  
$/opt/pdb2pqr/pdb2pqr --with-ph=7.4 \  
--ph-calc-method=propka --apbs-input \  
--ff=amber --ffout=amber --verbose --summary \  
1cqp_1_protein.pdb 1cqp_1_protein.pqr  
  
## use scripts from ADTools to prepare pdbqt file  
$prepare_ligand4.py -l 1cqp_1_ligand_wH.mol2 -v -o ligand.pdbqt  
$prepare_receptor4.py -r 1cqp_1_protein.pqr -v -o receptor.pdbqt
```

<http://autodock.scripps.edu/faqs-help/how-to/how-to-prepare-a-ligand-file-for-autodock4>

<http://autodock.scripps.edu/faqs-help/how-to/how-to-prepare-a-receptor-file-for-autodock4>

```
prepare_ligand4.py -l filename
```

Description of command...

```
-l ligand_filename
```

Optional parameters:

```
[-v] verbose output
[-o pdbqt_filename] (output filename)
[-d] dictionary to write types list and number of active torsions
[-A] type(s) of repairs to make:
      bonds_hydrogens, bonds, hydrogens
[-C] do not add charges
[-p] preserve input charges on atom type, eg -p Zn
[-U] cleanup type:
      nphs_lps, nphs, lps, ''
[-B] type(s) of bonds to allow to rotate
[-R] index for root
[-F] check for and use largest non-bonded fragment (False)
[-M] interactive (default is automatic)
[-I] string of bonds to inactivate composed of
      of zero-based atom indices eg 5_13_2_10
      will inactivate atoms[5]-atoms[13] bond
      and atoms[2]-atoms[10] bond
      (default is '')
[-Z] inactivate all active torsions
      (default is leave active)
```

```
prepare_receptor4.py -r filename
```

Description of command...

```
-r receptor_filename
```

Optional parameters:

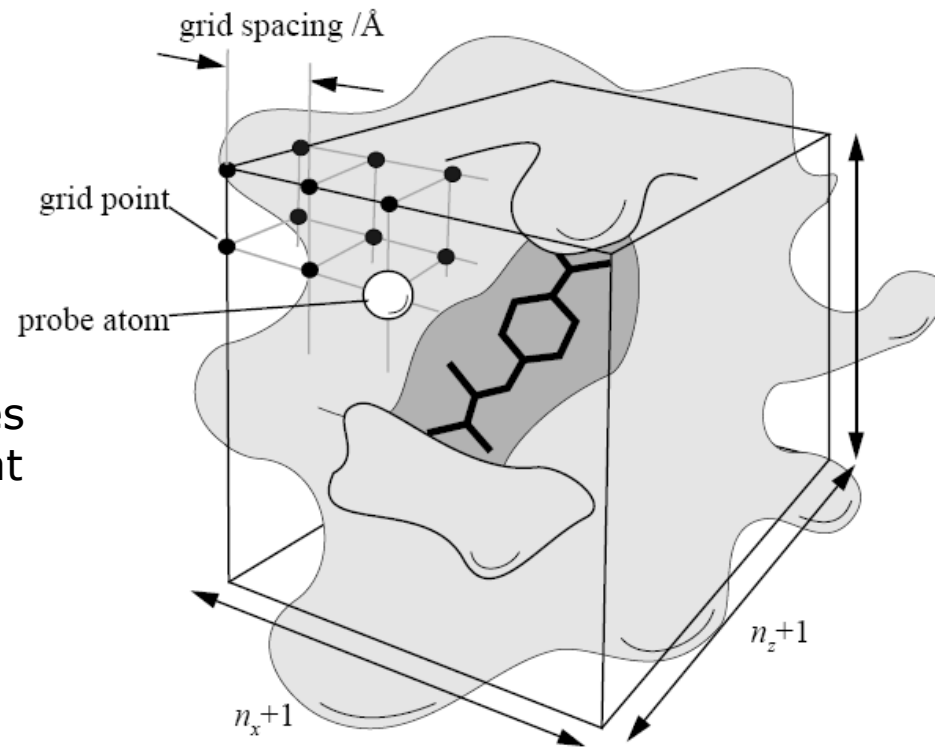
```
[-v] verbose output (default is minimal output)
[-o pdbqt_filename] (default is 'molecule_name.pdbqt')
[-A] type(s) of repairs to make:
      'bonds_hydrogens': build bonds and add hydrogens
      'bonds': build a single bond from each atom with no bonds to its closest neighbor
      'hydrogens': add hydrogens
      'checkhydrogens': add hydrogens only if there are none already
      'None': do not make any repairs
      (default is 'None': do not to make any repairs)
[-C] preserve all input charges ie do not add new charges
      (default is addition of gasteiger charges)
[-p] preserve input charges on specific atom types, eg -p Zn -p Fe
[-U] cleanup type:
      'nphs': merge charges and remove non-polar hydrogens
      'lps': merge charges and remove lone pairs
      'waters': remove water residues
      'nonstdres': remove chains composed entirely of residues of
                  types other than the standard 20 amino acids
      'deleteAltB': remove XX@B atoms and rename XX@A atoms->XX
      (default is 'nphs_lps_waters_nonstdres')
[-e] delete every nonstd residue from any chain
      'True': any residue whose name is not in this list:
              ['CYS', 'ILE', 'SER', 'VAL', 'GLN', 'LYS', 'ASN',
               'PRO', 'THR', 'PHE', 'ALA', 'HIS', 'GLY', 'ASP',
               'LEU', 'ARG', 'TRP', 'GLU', 'TYR', 'MET']
              will be deleted from any chain. NB: there are no
              nucleic acid residue names at all in the list.
      (default is False which means not to do this)
[-M] interactive
      (default is 'automatic': outputfile is written with no further user input)
```

Search Space

- center (X, Y, Z coordinate of the center)
- dimension (size in the X, Y, Z dimension)

AutoDock 4 performs the docking of the ligand to a set of grid maps describing the target protein. These grids are pre-calculated by autogrid4. The search space is defined by these grids in terms of grid points, grid spacing, and grid center.

AutoDock Vina does not require pre-calculating grid maps. Instead, it calculates the grids internally, for the atom types that are needed, and it does this virtually instantly. The search space is defined by the dimension in Angstrom and the center coordinates.



$$\text{dimension (\AA)} = \text{grid spacing} \times (\text{number of grid points} - 1)$$



The screenshot shows the MGLTools website interface. At the top, there is a navigation bar with links for Home, Downloads, Screenshots, Documentation, Packages, ePMV, Support, and Forum. The main content area is titled "Downloads" and includes a sub-header "MGLTools 1.5.6 Release Notes". Below this, there is a table listing download links for various operating systems and architectures. A sidebar on the left contains a navigation menu with links to Home, Downloads, Updates, Latest Builds, Screenshots, Documentation, Packages, ePMV, Support, and Forum. The Scripps Research Institute logo is also visible in the top left corner.

MGLTools

Home Downloads Screenshots Documentation Packages ePMV Support Forum

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Downloads

by [Sargis Dallakyan](#) — last modified 2015-07-16 13:41
Contributors: Anna Omelchenko, Michel Sanner, Sowjanya Karnati

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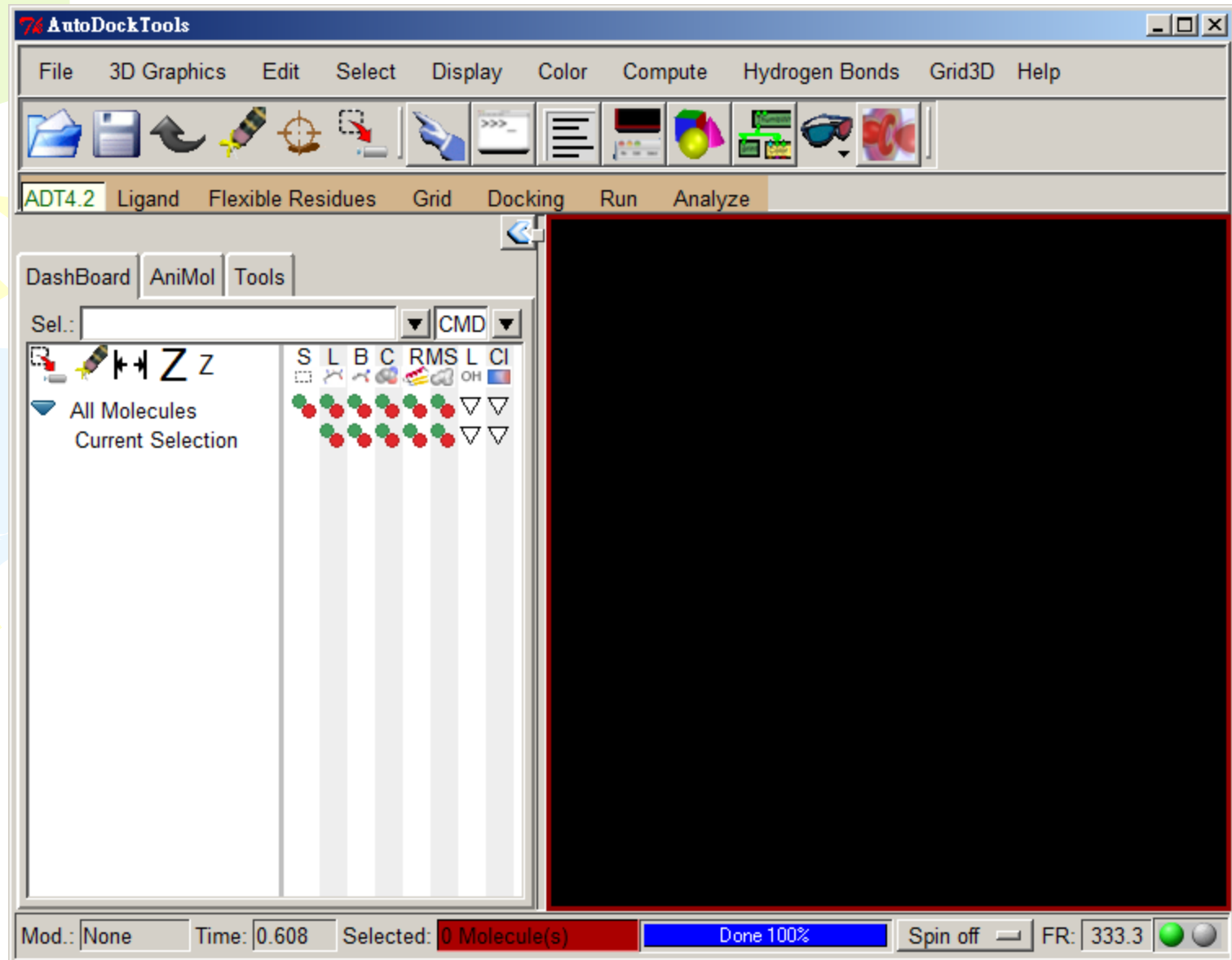
[MGLTools 1.5.6 Release Notes](#)

	<ul style="list-style-type: none">■ mgltools_win32_1.5.6_Setup.exe	<ul style="list-style-type: none">■ mgltools_win32_1.5.6.zip
	<ul style="list-style-type: none">■ mgltools_Linux-x86_1.5.6_Install GUI installer (GLIBC_2.3, libstdc++.5.X).■ mgltools_Linux-x86_64_1.5.6_Install GUI installer (GLIBC_2.4, libstdc++.6.X).	<ul style="list-style-type: none">■ mgltools_i86Linux2_1.5.6.tar.gz Tarball installer (GLIBC_2.3, libstdc++.5.X).■ mgltools_x86_64Linux2_1.5.6.tar.gz Tarball installer (GLIBC_2.4, libstdc++.6.X).
	<ul style="list-style-type: none">■ (Snow) Leopard - Mac OS X 10.5 and 10.6 - Intel■ (Snow) Leopard - Mac OS X 10.5 and 10.6 - PPC	<ul style="list-style-type: none">■ mgltools_i86Darwin9_1.5.6.tar.gz■ mgltools_ppcDarwin9_1.5.6.tar.gz
	<ul style="list-style-type: none">■ Source All Platforms	

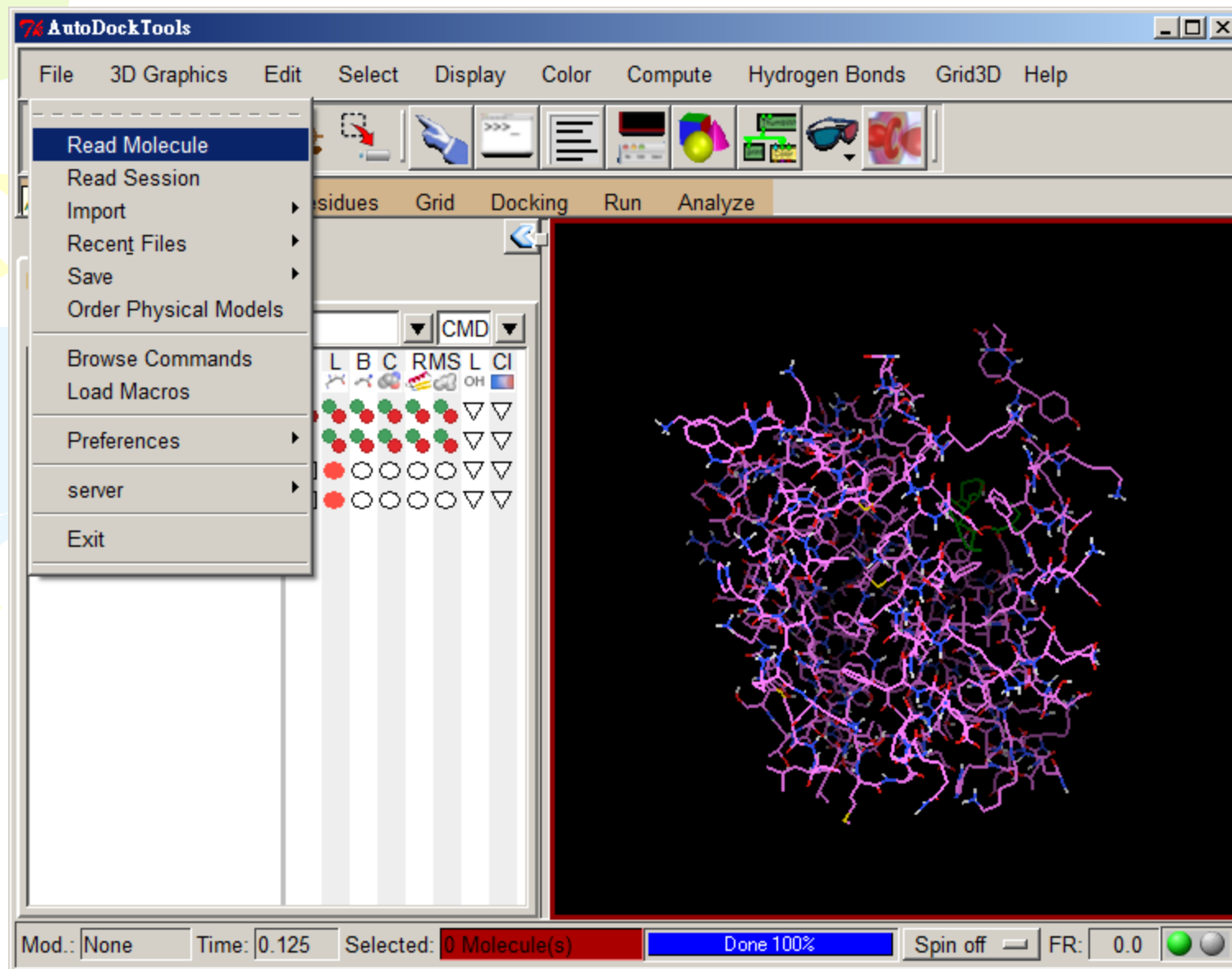
■ [What are PMV, ADT and Vision?](#)

AutoDockTools (ADT) is developed to help set up the docking. ADT is included in **MGLTools** packages.

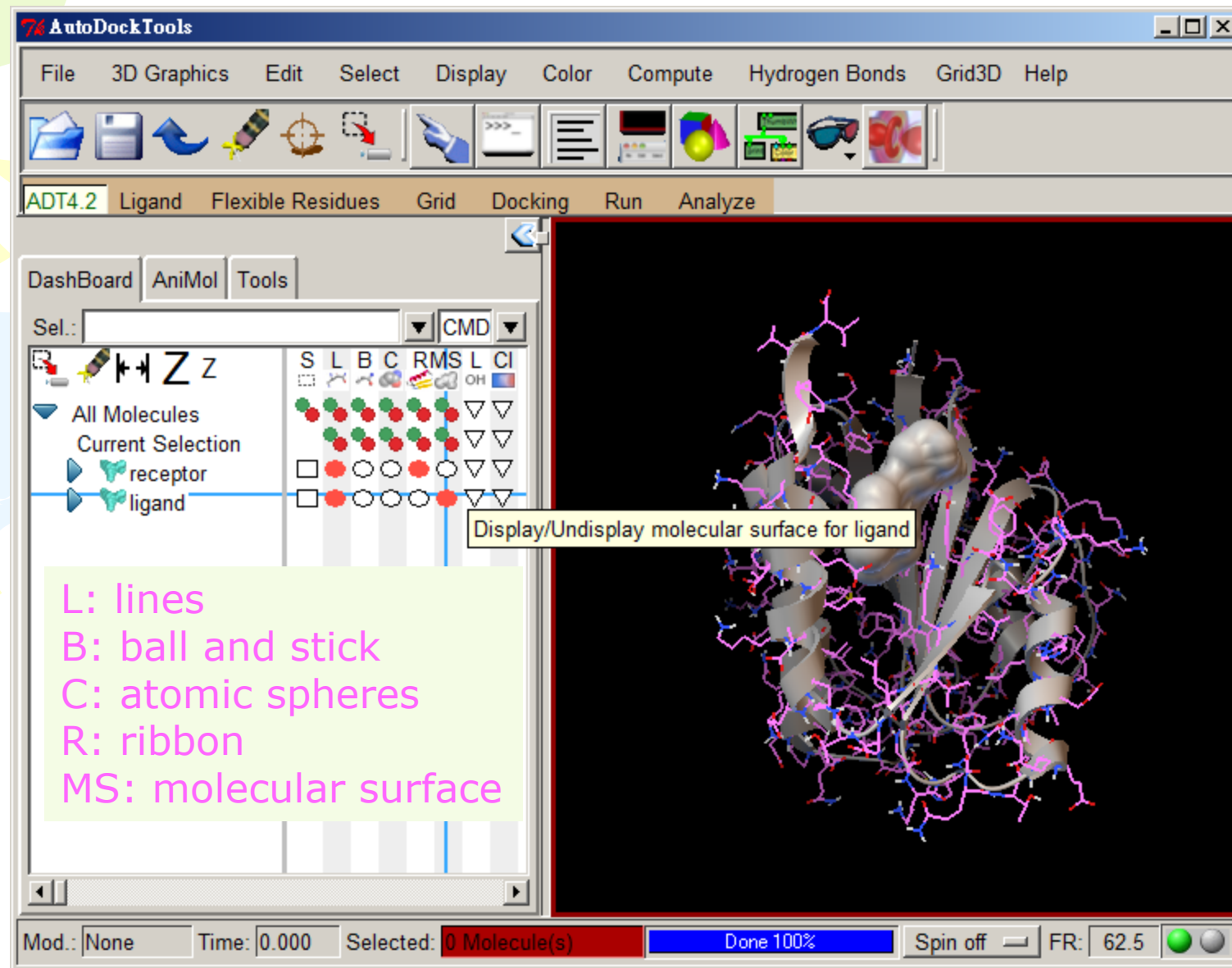
Launching AutoDockTools



read in receptor.pdbqt and ligand.pdbqt



change the presentation of molecules



AutoDockTools

File 3D Graphics Edit Select Display Color Compute Hydrogen Bonds Grid3D Help

ADT4.2 Ligand Flexible Residues Grid Docking Run Analyze

DashBoard AniMol Tools

Sel.: [] CMD []

All Molecules
Current Selection
receptor
ligand

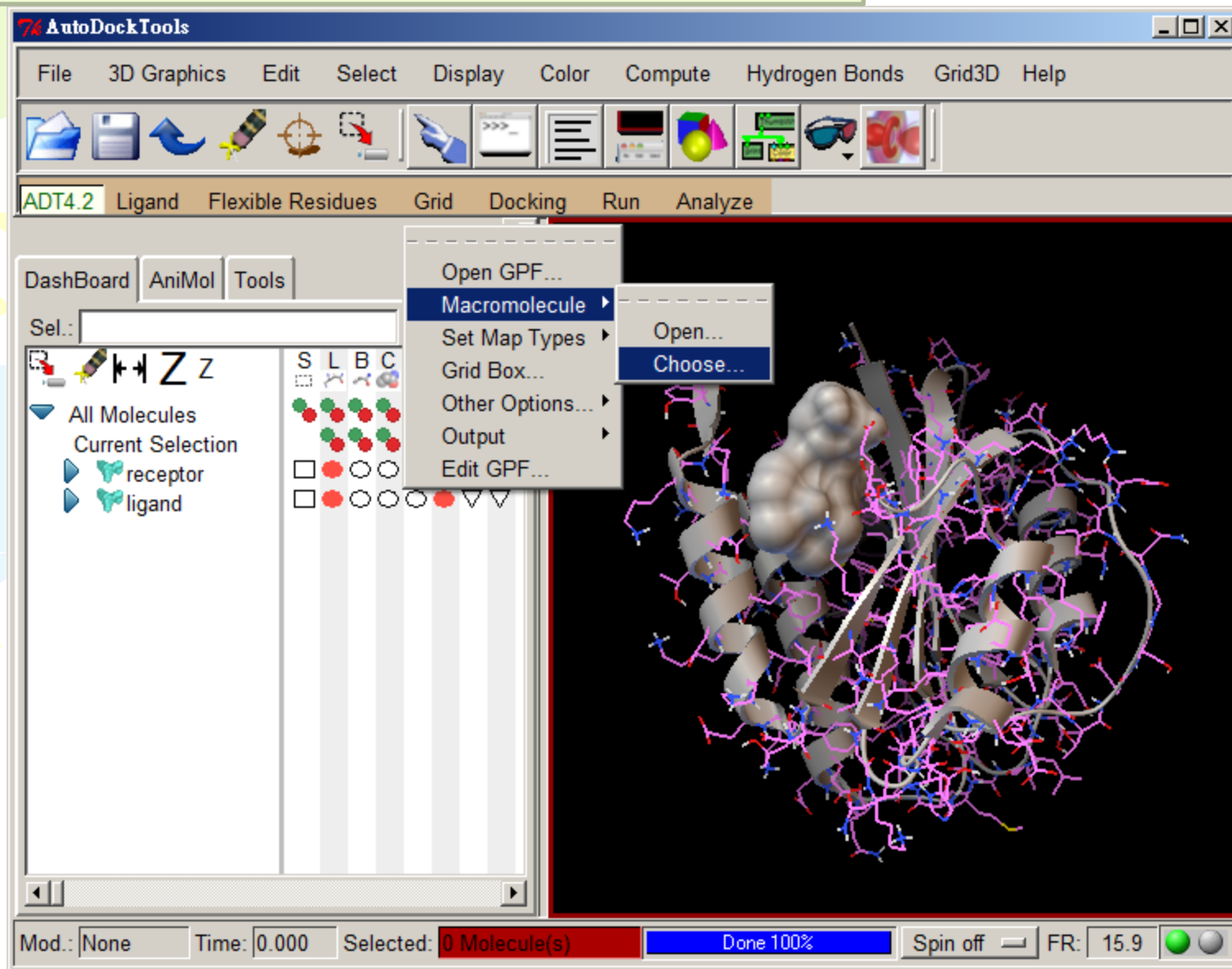
S	L	B	C	RMS	L	CI
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Display/Undisplay molecular surface for ligand

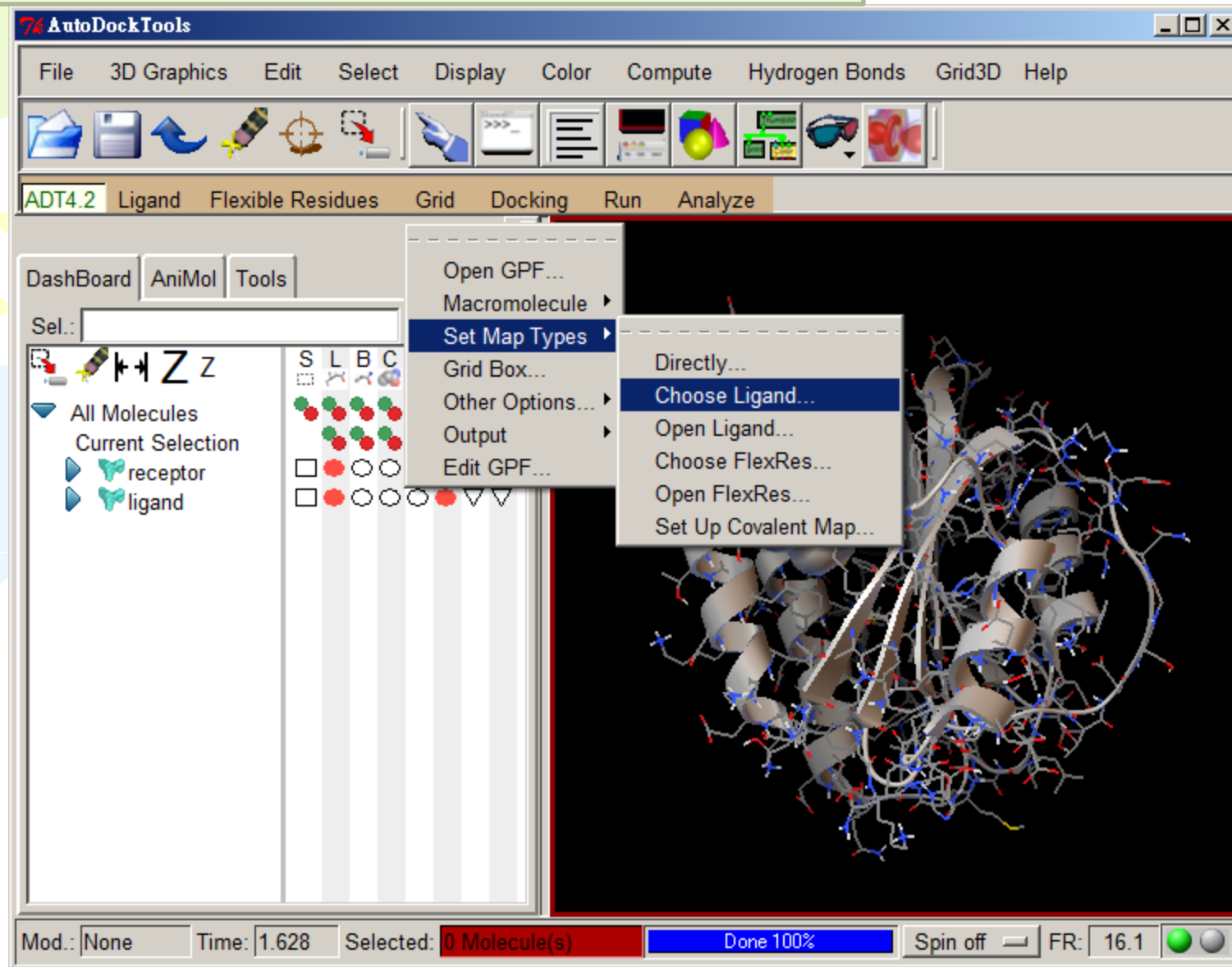
L: lines
B: ball and stick
C: atomic spheres
R: ribbon
MS: molecular surface

Mod.: None Time: 0.000 Selected: 0 Molecule(s) Done 100% Spin off FR: 62.5

Choose **Grid** → **Macromolecules** → **Choose**



Choose **Grid** → **Set Map Types** → **Choose Ligand**



Choose **Grid** → **Grid Box**

AutoDockTools

File 3D Graphics Edit Select Display Color Compute Hydrogen Bonds Grid3D Help

ADT4.2 Ligand Flexible Residues Grid Docking Run Analyze

DashBoard AniMol Tools

Grid Box...

Mod.: None Time: 0.015 Selected: 0 Molecule(s) Done 100% Spin off FR: 62.5

Grid Options

File Center View Help

Current Total Grid Pts per map: 64000

number of points in x-dimension: 40

number of points in y-dimension: 40

number of points in z-dimension: 40

Spacing (angstrom): 0.375

Center Grid Box: <offset>

x center: 45.936

y center: 11.84

z center: 25.188

Adjust grid parameters to make sure the grid box can cover the entire ligand and the binding pocket.

The screenshot displays the AutoDockTools interface. The main window shows a 3D model of a protein (red ribbon) with a ligand (green and red spheres) docked in its binding pocket. A red grid box is overlaid on the protein and ligand. The 'Grid Options' dialog box is open, showing the following parameters:

Parameter	Value
Current Total Grid Pts per map	83205
number of points in x-dimension	42
number of points in y-dimension	44
number of points in z-dimension	42
Spacing (angstrom)	0.375
Center Grid Box:	<offset>
x center	51.672
y center	13.764
z center	25.188

The status bar at the bottom indicates: Mod.: None, Time: 0.031, Selected: 0 Molecule(s), Done 100%, Spin off, FR: 62.5.

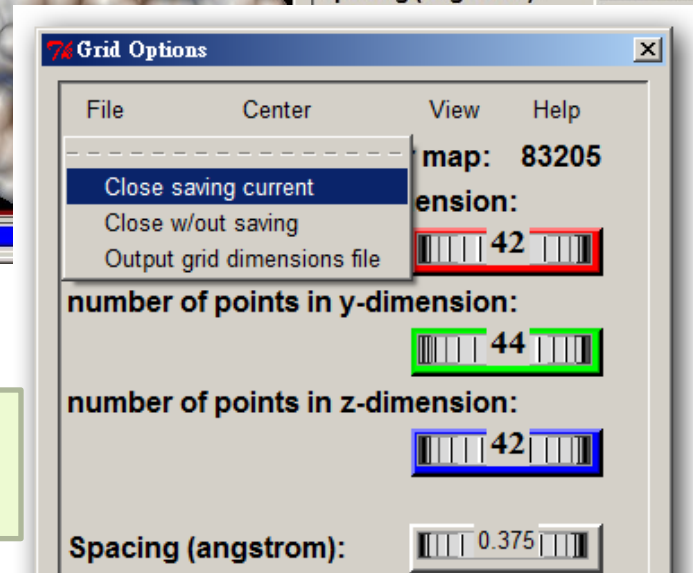
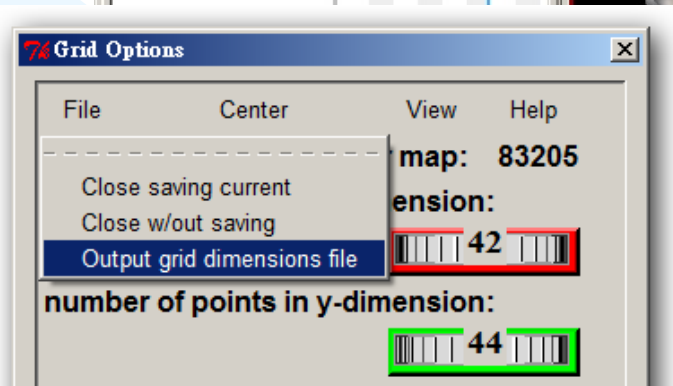
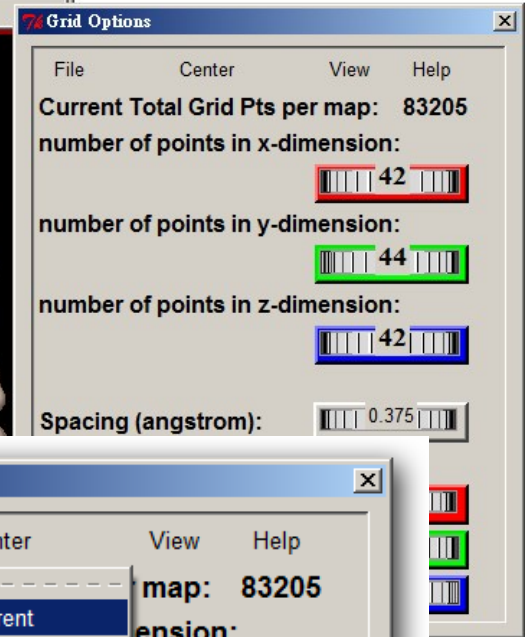
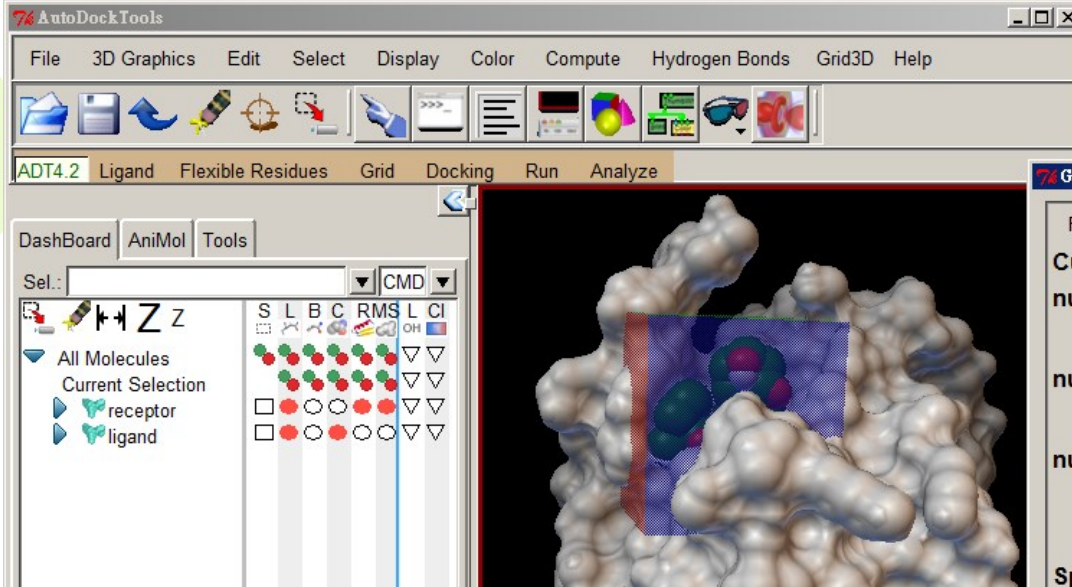
Grid Options

Choose **Center** → **Center on ligand**

The screenshot shows the AutoDockTools interface. The main window displays a 3D molecular model of a protein-ligand complex. The Grid Options dialog box is open, showing the following settings:

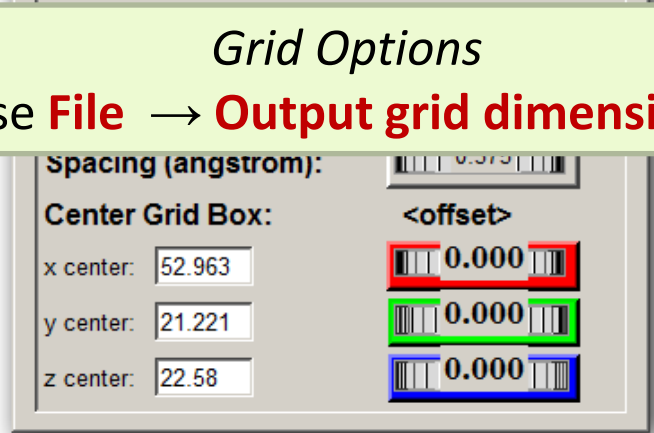
- File: Center View Help
- Current number of points in x-dimension: 83205
- number of points in y-dimension: 42
- number of points in z-dimension: 44
- Spacing (angstrom): 0.375
- Center Grid Box: <offset>
- x center: 47.241
- y center: 19.304
- z center: 22.58

The status bar at the bottom shows: Mod.: None, Time: 0.031, Selected: 0 Molecule(s), Done 100%, Spin off, FR: 62.5



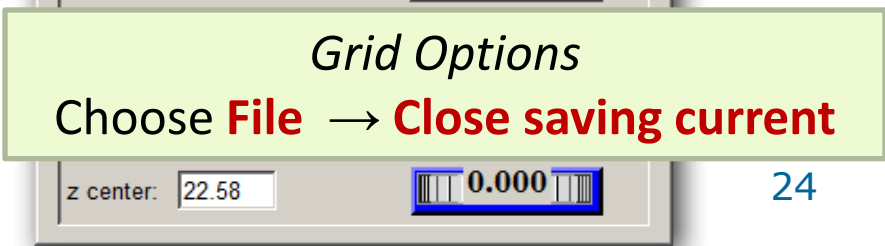
Grid Options

Choose **File** → **Output grid dimensions file**



Grid Options

Choose **File** → **Close saving current**



Search Space

AutoDock 4

spacing 0.375
npts 42 44 42
center 52.963 21.221 22.580

AutoDock Vina

$0.375 \times 41 = 15.375$
 $0.375 \times 43 = 16.125$
dimensions 15.375 16.125 15.375
center 52.963 21.221 22.580

Docking with Autodock4

```
$pwd  
$cd ..  
$mkdir 2_docking  
$cd 2_docking  
$mkdir autodock4 autodock_vina  
$cd autodock4  
$cp ../../1_preparation/*.pdbqt ./
```

AutoDock 4

```
spacing 0.375  
npts 42 44 42  
center 52.963 21.221 22.580
```

```
##prepare grid parameter and docking parameter files  
$prepare_gpf4.py -l ligand.pdbqt -r receptor.pdbqt  
$prepare_dpf4.py -l ligand.pdbqt -r receptor.pdbqt  
##edit grid parameter file (receptor.gpf)  
$vi receptor.gpf  
##edit docking parameter file (ligand_receptor.dpf)  
$vi ligand_receptor.dpf  
  
## generate grid maps  
$autogrid4 -p receptor.gpf -l receptor.glg  
## perform docking  
$autodock4 -p ligand_receptor.dpf -l ligand_receptor.dlg
```

AutoDock4 Grid Parameter File: GPF

The grid parameter file specifies an AutoGrid calculation, including the size and location of the grid, the atom types that will be used, the coordinate file for the rigid receptor, and other parameters for calculation of the grids.

Sample Grid Parameter File (from tutorial)

```
npts 60 60 60 # num.grid points in xyz
gridfile 1hsg.maps.fld # grid_data_file
spacing 0.375 # spacing(A)
receptor_types A C HD N OA SA # receptor atom types
ligand_types A C NA OA N HD # ligand atom types
receptor 1hsg.pdbqt # macromolecule
gridcenter 2.5 6.5 -7.5 # xyz-coordinates or auto
smooth 0.5 # store minimum energy w/in rad(A)
map 1hsg.A.map # atom-specific affinity map
map 1hsg.C.map # atom-specific affinity map
map 1hsg.NA.map # atom-specific affinity map
map 1hsg.OA.map # atom-specific affinity map
map 1hsg.N.map # atom-specific affinity map
map 1hsg.HD.map # atom-specific affinity map
elecmap 1hsg.e.map # electrostatic potential map
dsolvmap 1hsg.d.map # desolvation potential map
dielectric -0.1465 # <0, AD4 distance-dep.diel;>0,
constant
```

AutoDock4 Docking Parameter File: DPF

```
autodock_parameter_version 4.2      # used by autodock to validate parameter set
outlev ADT                          # diagnostic output level
seed pid time                        # seeds for random generator
unbound_model bound                 # state of unbound ligand

ligand_types A C NA OA N HD        # atoms types in ligand
fld lhsg.maps.fld                   # grid_data_file
map lhsg.A.map                      # atom-specific affinity map
map lhsg.C.map                      # atom-specific affinity map
map lhsg.NA.map                     # atom-specific affinity map
map lhsg.OA.map                     # atom-specific affinity map
map lhsg.N.map                      # atom-specific affinity map
map lhsg.HD.map                     # atom-specific affinity map
elecmap lhsg.e.map                  # electrostatics map
desolvmap lhsg.d.map                # desolvation map
move ind.pdbqt                      # small molecule
about 0.3689 -0.2148 -4.9865        # small molecule root center

tran0 random                        # initial coordinates/A or random
quaternion0 random                  # initial orientation
dihe0 random                        # initial dihedrals (relative) or random

ga_pop_size 150                     # number of individuals in population
ga_num_evals 2500000                 # maximum number of energy evaluations
ga_num_generations 27000             # maximum number of generations
ga_elitism 1                         # top individuals to survive to next generation
ga_mutation_rate 0.02               # rate of gene mutation
ga_crossover_rate 0.8                # rate of crossover
set_ga                               # set the above parameters for GA or LGA

sw_max_its 300                      # iterations of Solis & Wets local search
sw_max_succ 4                       # consecutive successes before changing rho
sw_max_fail 4                       # consecutive failures before changing rho
sw_rho 1.0                          # size of local search space to sample
sw_lb_rho 0.01                      # lower bound on rho
ls_search_freq 0.06                 # probability of performing local search
set_pswl                             # set the above pseudo-Solis & Wets parameters

ga_run 10                           # do this many hybrid GA-LS runs

rmstol 2.0                          # cluster_tolerance/A
analysis                             # perform a ranked cluster analysis
```

The docking parameter file specifies the files and parameters for an AutoDock calculation, including the map files that will be used for the docking, the ligand coordinate files, and parameters for the search.



<http://autodock.scripps.edu/faqs-help/manual>

[AutoDock 4.2 User Guide](#)

<http://autodock.scripps.edu/faqs-help/how-to>

[How to prepare a grid parameter file for AutoGrid 4](#)

[How to prepare a docking parameter file for AutoDock4](#)

[How to prepare a flexible residue file for AutoDock4](#)

<http://autodock.scripps.edu/faqs-help/tutorial>

[Using AutoDock 4 with AutoDockTools](#)

[Using AutoDock 4 for Virtual Screening](#)

Water, metal ion, covalent bond involved?

- [Hydrated ligand docking](#)
- [AutoDock force field for ZN metalloproteins](#)
- [AutoDock4 covalent docking](#)

```
##results
```

```
$vi ligand_receptor.dlg
```

```
Number of distinct conformational clusters found = 3, out of 10 runs,  
Using an rmsd-tolerance of 2.0 A
```

```
CLUSTERING HISTOGRAM
```

Cluster Rank	Lowest Binding Energy	Run	Mean Binding Energy	Num in Cluster	Histogram							
					5	10	15	20	25	30	35	
1	-9.28	3	-9.05	6	#####							
2	-8.84	7	-8.71	3	###							
3	-8.29	5	-8.29	1	#							

Rank	Sub-Rank	Run	Binding Energy	Cluster RMSD	Reference RMSD	Grep Pattern
1	1	3	-9.28	0.00	2.22	RANKING
1	2	4	-9.13	1.10	2.02	RANKING
1	3	2	-9.03	1.83	2.72	RANKING
1	4	10	-9.01	1.95	2.82	RANKING
1	5	9	-8.96	1.99	2.93	RANKING
1	6	6	-8.87	0.65	2.22	RANKING

```
$grep "RANKING" ligand_receptor.dlg > ranking.txt
```

```
3 1 5 -8.29 0.00 2.62 RANKING
```

Estimated Free Energy of Binding in kcal/mol
Estimated Inhibition Constant(Ki)

```
MODEL 3  
USER Run = 3  
USER Cluster Rank = 1  
USER Number of conformations in this cluster = 6  
USER  
USER RMSD from reference structure = 2.224 A  
USER  
USER Estimated Free Energy of Binding = -9.28 kcal/mol [= (1)]  
USER Estimated Inhibition Constant, Ki = 158.19 nM (nanomolar)
```

```
## get conformation of the lowest energy ligand
$write_lowest_energy_ligand.py -f ligand_receptor.dlg

## convert pdbqt to pdb
$pdbqt_to_pdb.py -f ligand_BE.pdbqt

## get conformations from docking result (dlg) file
$write_conformations_from_dlg.py -d ligand_receptor.dlg
$mkdir poses
$mv ligand_*.pdbqt poses

## make complexes structure
$write_all_complexes.py -d ligand_receptor.dlg -r receptor.pdbqt
$mkdir complexes
$mv receptor_ligand_*.pdbqt complexes
```

Docking with Autodock Vina

```
$cd ../autodock_vina  
$cp ../../1_preparation/*.pdbqt ./
```

```
##perform docking
```

```
$vina --receptor receptor.pdbqt --ligand ligand.pdbqt \  
  --center_x 52.963 --center_y 21.221 --center_z 22.58 \  
  --size_x 15.375 --size_y 16.125 --size_z 15.375 \  
  --out vina_out.pdbqt --log vina.log
```

```
##put some parameters in the config.txt file
```

```
$vi config.txt
```

```
$vina --config config.txt --log vina.log
```


AutoDock Vina

```
dimensions 15.375 16.125 15.375  
center    52.963 21.221 22.580
```

```
receptor = receptor.pdbqt  
ligand = ligand.pdbqt  
center_x = 52.963  
center_y = 21.221  
center_z = 22.58  
size_x = 15.375  
size_y = 16.125  
size_z = 15.375  
out = out.pdbqt
```

```
$vina --config configB.txt --ligand ligandB.pdbqt \  
  --out outB.pdbqt -log vinaB.log
```

```
receptor = receptor.pdbqt  
center_x = 52.963  
center_y = 21.221  
center_z = 22.58  
size_x = 15.375  
size_y = 16.125  
size_z = 15.375
```

<http://vina.scripps.edu/tutorial.html>
<https://youtu.be/-GVZP0X0Tg8>

<http://vina.scripps.edu/download.html>

Download:

The current version is 1.1.2 (May 11, 2011).

Windows	autodock vina 1 1 2 win32.msi	(0.5 MB)	Compatibility, installation and usage notes
Linux	autodock vina 1 1 2 linux x86.tgz	(1.2 MB)	Compatibility, installation and usage notes
MacOSX	autodock vina 1 1 2 mac.tgz	(0.9 MB)	Compatibility, installation and usage notes
Source	autodock vina 1 1 2.tgz (browse)	(0.1 MB)	Building from source

See also: [GUIs, web interfaces, etc.](#) | [Old versions](#) | [History of changes](#)

```
##results
```

```
$vi out.pdbqt
```

```
$grep "REMARK VINA RESULT" out.pdbqt
```

```
## get conformations from outout.pdbqt
```

```
$/opt/autodock_vina/bin/vina_split --input out.pdbqt \  
--ligand vinaDock_
```

```
$pdbqt_to_pdb.py -f vinaDock_1.pdbqt
```

```
$mkdir poses
```

```
$mv vinaDock_*.pdbqt poses
```

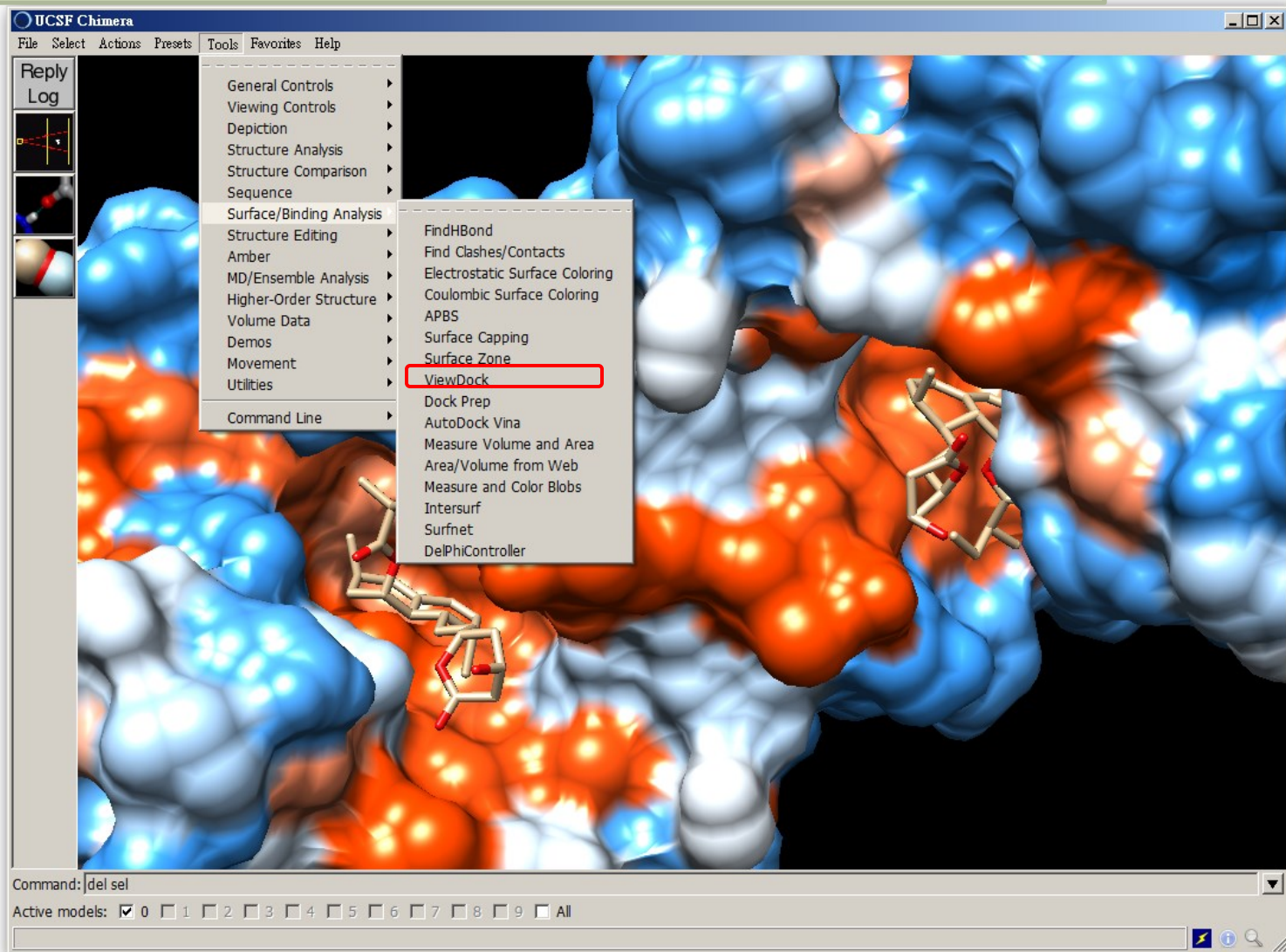
REMARK VINA RESULT:	-8.1	0.000	0.000
REMARK VINA RESULT:	-6.8	1.671	3.283
REMARK VINA RESULT:	-6.7	1.866	7.035
REMARK VINA RESULT:	-6.6	1.858	6.818
REMARK VINA RESULT:	-6.6	2.237	5.650
REMARK VINA RESULT:	-6.6	1.969	4.588
REMARK VINA RESULT:	-6.5	1.464	4.336
REMARK VINA RESULT:	-6.4	1.946	3.985
REMARK VINA RESULT:	-6.4	2.037	4.066

The predicted binding affinity is in kcal/mol.

```
vinaDock_1.pdb    vinaDock_3.pdbqt  vinaDock_6.pdbqt  vinaDock_9.pdbqt  
vinaDock_1.pdbqt  vinaDock_4.pdbqt  vinaDock_7.pdbqt  
vinaDock_2.pdbqt  vinaDock_5.pdbqt  vinaDock_8.pdbqt
```

Download docked poses (AutoDock4 and AutoDock Vina)
Use chimera to view the protein structure and the docked poses

Choose **Tools** → **Surface/Binding Analysis** → **ViewDock**



UCSF Chimera

File Select Actions Presets Tools Favorites Help

Reply Log

ViewDock - C:\Users\elfin\Downloads\FDCC2018\test\test2\out.pdbqt

S	Score	RMSD l.b.	RMSD u.b.
V	-8.1	0.0	0.0
V	-6.8	1.671	3.283
V	-6.7	1.866	7.035
V	-6.6	1.858	6.818
V	-6.6	2.237	5.65
V	-6.6	1.969	4.588
V	-6.5	1.464	4.336
V	-6.4	1.946	3.985
V	-6.4	2.037	4.066

REMARK VINA
REMARK 8 a
REMARK sta
REMARK 1
REMARK 2
REMARK 3
REMARK 4
REMARK 5

Command: del sel

Active models: 0 1 2 3 4 5 6 7 8 9 All

UCSF Chimera

File Select Actions Presets Tools Favorites Help

Reply Log

ViewDock - C:\Users\elfin\Downloads\FDCC2018\test\test2\out.pdbqt

S	Score	RMSD l.b.	RMSD u.b.
V	-8.1	0.0	0.0
V	-6.8	1.671	3.283
V	-6.7	1.866	7.035
V	-6.6	1.858	6.818
V	-6.6	2.237	5.65
V	-6.6	1.969	4.588
V	-6.5	1.464	4.336
V	-6.4	1.946	3.985
V	-6.4	2.037	4.066

Chimera Model #1.6

REMARK VINA RESULT: -6.6 1.969 4.588
REMARK 8 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 1 A between atoms: C1_1 and O4_23
REMARK 2 A between atoms: C8_11 and C10_13
REMARK 3 A between atoms: C10_13 and C11_14
REMARK 4 A between atoms: C11_14 and C12_15
REMARK 5 A between atoms: C14_17 and O3_18

Virtual Screening with Autodock Vina

One receptor and a set of search space
Many small molecules

```
## prepare small molecules
## download dbfda-interesting.sdf from ZINC15
$mkdir mol2 pdbqt
$cd mol2
$obabel -isdf ../dbfda-interesting.sdf -omol2 -Ofda_.mol2 \
      -p 7.4 --append zinc_id -m
$cd ../
$obabel -isdf dbfda-interesting.sdf -osmi -O dbfda.smi \
      --append zinc_id --addoutindex
$sh prepare_ligand.sh
```

```
#!/bin/bash
cd mol2
for f in fda_*.mol2; do
    b=`basename $f .mol2`
    echo Processing ligand $f $b.pdbqt
    prepare_ligand4.py -l $f -o $b.pdbqt
    mv $b.pdbqt ../pdbqt
done
```

```
## perform docking for each small molecules
```

```
$vi configB.txt
```

```
$sh vina_screen.sh
```

```
receptor = receptor.pdbqt  
center_x = 52.963  
center_y = 21.221  
center_z = 22.58  
size_x = 15.375  
size_y = 16.125  
size_z = 15.375
```

```
#!/bin/bash
```

```
mkdir dock
```

```
cd pdbqt
```

```
for f in fda_*.pdbqt; do
```

```
  b=`basename $f .pdbqt`
```

```
  echo Processing ligand $b
```

```
  mkdir -p ../dock/$b
```

```
  /opt/autodock_vina/bin/vina --config ../configB.txt --ligand $f \  
    --out ../dock/${b}/${b}_docked.pdbqt \  
    --log ../dock/${b}/log.txt
```

```
  /opt/autodock_vina/bin/vina_split \  
    --input ../dock/${b}/${b}_docked.pdbqt \  
    --ligand ../dock/${b}/${b}_vd
```

```
done
```

perform docking for each small molecules

\$cd dock

\$grep "VINA RESULT" */fda_*vd*.pdbqt | sort -k4 -r | sed -e 's/:REMARK VINA RESULT://g' > sum.txt

```
[centos@fcdd01 dock]$ cat sum.txt
fda_998/fda_998_vd1.pdbqt      -7.1      0.000      0.000
fda_998/fda_998_vd2.pdbqt      -7.0      1.735      2.548
fda_998/fda_998_vd3.pdbqt      -6.9      1.446      1.973
fda_998/fda_998_vd5.pdbqt      -6.8      2.981      5.422
fda_998/fda_998_vd4.pdbqt      -6.8      2.652      4.736
fda_998/fda_998_vd7.pdbqt      -6.6      2.564      5.110
fda_998/fda_998_vd6.pdbqt      -6.6      2.526      4.902
fda_998/fda_998_vd8.pdbqt      -6.5      2.273      4.856
fda_996/fda_996_vd1.pdbqt      -6.5      0.000      0.000
fda_998/fda_998_vd9.pdbqt      -6.4      3.529      6.321
fda_996/fda_996_vd2.pdbqt      -6.4      2.380      6.550
fda_999/fda_999_vd1.pdbqt      -6.4      0.000      0.000
fda_997/fda_997_vd1.pdbqt      -6.4      0.000      0.000
```

Databases for virtual Screening

- ZINC

A free database of commercially-available compounds for virtual screening. ZINC contains over 230 million purchasable compounds in ready-to-dock, 3D formats. ZINC also contains over 750 million purchasable compounds you can search.

<http://zinc15.docking.org/>

<http://zinc.docking.org/pdbqt/>

- NCI Diversity Set

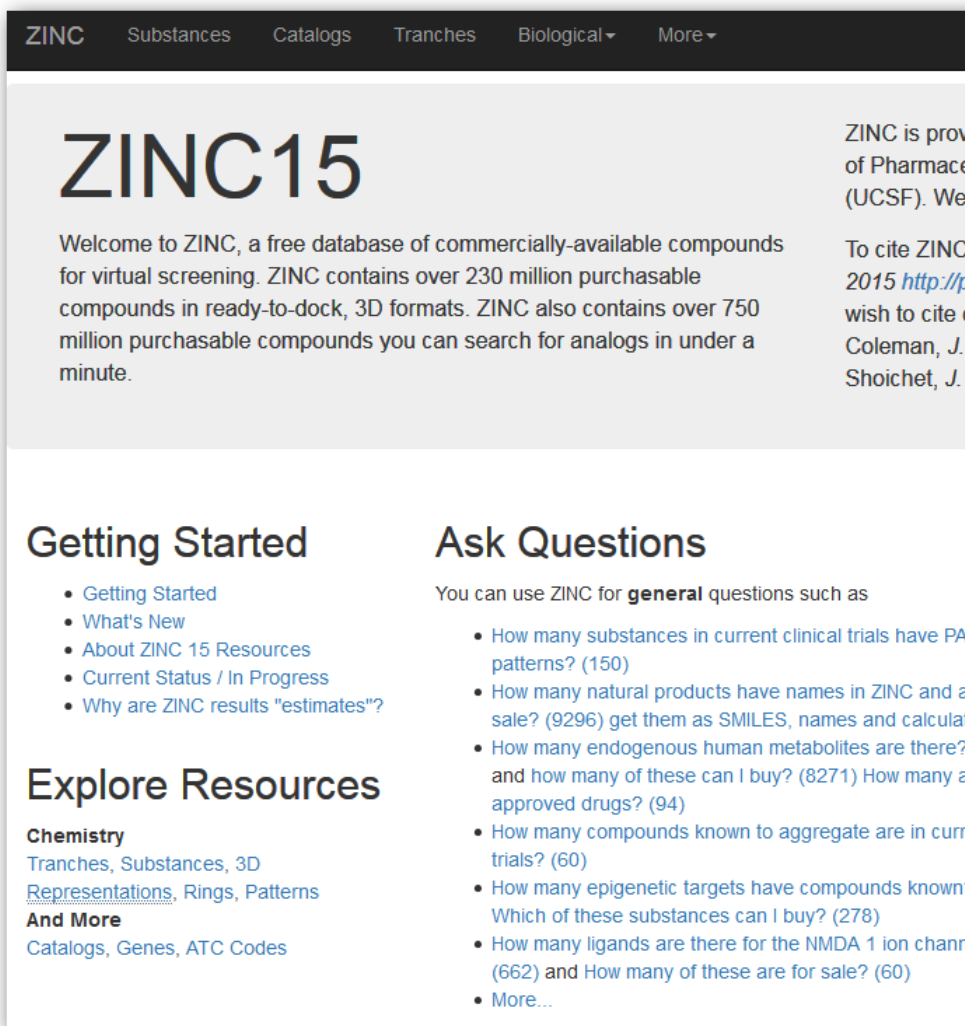
<https://wiki.nci.nih.gov/display/NCIDTPdata/Compound+Sets>

- PDBbind

<http://www.pdbbind.org>

<http://www.pdbbind.org.cn/>

<http://zinc15.docking.org/>



The screenshot shows the ZINC15 website homepage. At the top is a navigation bar with links for ZINC, Substances, Catalogs, Tranches, Biological, and More. The main heading is "ZINC15". Below it is a welcome message: "Welcome to ZINC, a free database of commercially-available compounds for virtual screening. ZINC contains over 230 million purchasable compounds in ready-to-dock, 3D formats. ZINC also contains over 750 million purchasable compounds you can search for analogs in under a minute." To the right of this message is a short paragraph: "ZINC is provided by the Center for Pharmaceutical Research (UCSF). We wish to cite Coleman, J. and Shoichet, J." Below the welcome message are three sections: "Getting Started" with a list of links, "Ask Questions" with a list of questions you can ask, and "Explore Resources" with links for Chemistry and And More.

ZINC

Substances Catalogs Tranches Biological More

ZINC15

Welcome to ZINC, a free database of commercially-available compounds for virtual screening. ZINC contains over 230 million purchasable compounds in ready-to-dock, 3D formats. ZINC also contains over 750 million purchasable compounds you can search for analogs in under a minute.

ZINC is provided by the Center for Pharmaceutical Research (UCSF). We wish to cite Coleman, J. and Shoichet, J.

Getting Started

- Getting Started
- What's New
- About ZINC 15 Resources
- Current Status / In Progress
- Why are ZINC results "estimates"?

Ask Questions

You can use ZINC for **general** questions such as

- How many substances in current clinical trials have PA patterns? (150)
- How many natural products have names in ZINC and a sale? (9296) get them as SMILES, names and calculated
- How many endogenous human metabolites are there? and how many of these can I buy? (8271) How many approved drugs? (94)
- How many compounds known to aggregate are in current trials? (60)
- How many epigenetic targets have compounds known? Which of these substances can I buy? (278)
- How many ligands are there for the NMDA 1 ion channel (662) and How many of these are for sale? (60)
- More...

Explore Resources

Chemistry
Tranches, Substances, 3D Representations, Rings, Patterns

And More
Catalogs, Genes, ATC Codes

zinc.docking.org/pdbqt/

<http://zinc.docking.org/pdbqt/>

- Parent Directory
- [ChemBridge FullLibrary2011.tar.gz](#)
- [ChemBridge FullLibrary2011/](#)
- [NCI DiversitySet2.tar.gz](#)
- [NCI DiversitySet2/](#)
- [README](#)
- [VitasMLabs Feb2012.tar.gz](#)
- [VitasMLabs Feb2012/](#)
- [asinex.tar.gz](#)
- [asinex/](#)
- [asinex_newMay2011_fixedForVinaInDec.tar.gz](#)
- [asinex_newMay2011_fixedForVinaInDec/](#)
- [chembridge buildingblocks pdbqt 1000split.tar.gz](#)
- [chembridge buildingblocks pdbqt 1000split/](#)
- [drugbank nutraceuticals.tar.gz](#)
- [drugbank nutraceuticals/](#)
- [drugbank smallmol.tar.gz](#)
- [drugbank smallmol/](#)
- [enamine 052011 pdbqt.tar.gz](#)
- [enamine 052011 pdbqt/](#)
- [fda approved.tar.gz](#)
- [fda approved/](#)
- [fda approved full Tautomers 2011 8 2.tar.gz](#)
- [fda approved full Tautomers 2011 8 2/](#)
- [full nci ALL TAUTOMERS 2011.tar.gz](#)
- [full nci ALL TAUTOMERS 2011/](#)
- [human metabolome pdbqt 1000split.tar.gz](#)
- [human metabolome pdbqt 1000split/](#)
- [otava.tar.gz](#)
- [otava/](#)
- [zinc natural products.tar.gz](#)
- [zinc natural products/](#)