

# AutoSite2- A fast and accurate protein-ligand binding-site prediction method

## Overview

*AutoSite2* identifies the most suitable pockets for a ligand to bind to a macromolecule. It proceeds in two steps. First, *AutoSite2* analyzes the high affinity regions over the receptor and find pockets of varying sizes. In the second step, *AutoSite2* selects and ranks pockets according to their suitability to hold a ligand with a given volume.

This tutorial is designed to you get started with the command line execution of the program to obtain binding sites represented as fill points, for a receptor (pdb:1wbz), First go to the [Downloads](#) page to obtain the software and install it following the installation instruction.

To run this tutorial you will also need a receptor file in PDBQT format ([example](#)) and potentially a ligand ([example](#))

## Step 1: Receptor analyze.

Linux command:

```
> $WHERE_YOU_INSTALLED/MGLTools2-  
latest/bin/pythonsh $WHERE_YOU_INSTALLED/MGLTools2-  
latest/MGLToolsPcks/AutoSite/bin/AS.py -bc ratio 1.2 -sc -steps 4 -r  
1wbz_P_recFixed.pdbqt -o ./
```

MacOSX command:

```
>  
/Library/MGLTools2/latest/bin/pythonsh /Library/MGLTools2/latest/MGLToolsP  
ckgs/AutoSite/bin/AS.py -bc ratio 1.2 -sc -steps 4 -r 1wbz_P_recFixed.pdbqt -o ./
```

-bc is a command line option allowing to specify the lower bounds of affinity cutoff values used by *AutoSite2* when it scans affinity cutoff values. In this particular the lower bounds are given as a ratio of the default cutoff values used by *AutoSite*, i.e. -bc ratio 1.2 means to use 1.2 \* default cutoff values.

-sc informs *AutoSite* to scan a range of cutoff values (i.e. perform the *AutoSite* Algorithm to search for pockets with various sizes).  
-steps defines the number of steps used in *AutoSite2* algorithm.

The result of this command line is a save in a file describing a tree structure that can be queried to identify the best pockets for a given ligand volume.

## Step 2: Pocket selection and re-ranking.

With a given ligand file.

Linux command:

```
> $WHERE_YOU_INSTALLED/MGLTools2-  
latest/bin/pythonsh $WHERE_YOU_INSTALLED/MGLTools2-  
latest/MGLToolsPcks/AutoSite/bin/preparePocket.py -f 1wbz_P_pep.pdb -p True
```

MacOSX command:

```
>  
/Library/MGLTools2/latest/bin/pythonsh /Library/MGLTools2/latest/MGLToolsP  
cks/AutoSite/bin/preparePocket.py -f 1wbz_P_pep.pdb -p True
```

Or with a given volume:

Linux command:

```
> $WHERE_YOU_INSTALLED/MGLTools2-  
latest/bin/pythonsh $WHERE_YOU_INSTALLED/MGLTools2-  
latest/MGLToolsPcks/AutoSite/bin/preparePocket.py -s 900 -p True
```

MacOSX command:

```
>  
Library/MGLTools2/latest/bin/pythonsh /Library/MGLTools2/latest/MGLToolsPc  
kgs/AutoSite/bin/preparePocket.py -s 900 -p True
```

*AutoSite2* peptide scoring function is used with flag “-p True”

## Step 3: Results.

In the original folder where *AutoSite2* is executed, all the pockets in the tree structure are saved and the topology information is saved in `pockettree.txt`. Pockets that best match the ligand volume are in the folder named “pockets” with their rankings indicated in the file name.