



6th Advanced
***in silico* Drug Design**
KFC/ADD
Tutorial:
Molecular docking intro

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UP Olomouc, 30.1.-3.2. 2023

Tutorial preparation

Programs installation:

- Pymol

<https://www.lfd.uci.edu/~gohlke/pythonlibs/#pymol-open-source>

<https://anaconda.org/conda-forge/pymol-open-source>

Autodock Tools

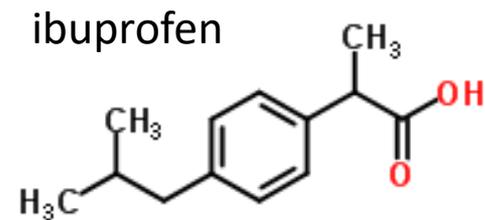
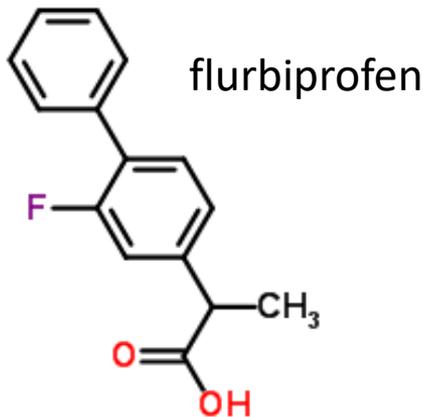
<http://mgltools.scripps.edu/>

- Autodock Vina

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

Task:

- Predict **site-of-metabolism** of some NSAID drugs (flurbiprofen, ibuprofen) which are metabolized by Cytochrome P450 2C9 (CYP2C9) (i) by **docking** into the active site of CYP2C9 or (ii) by **ligand-based SMARTCYP** web service

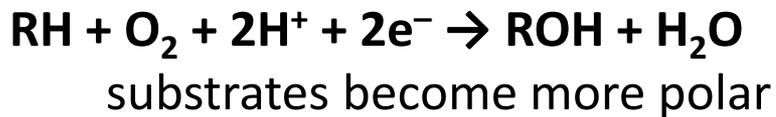


Background: Cytochrome P450 (CYP)

Diverse superfamily of hemoproteins

=> **Drug metabolism**

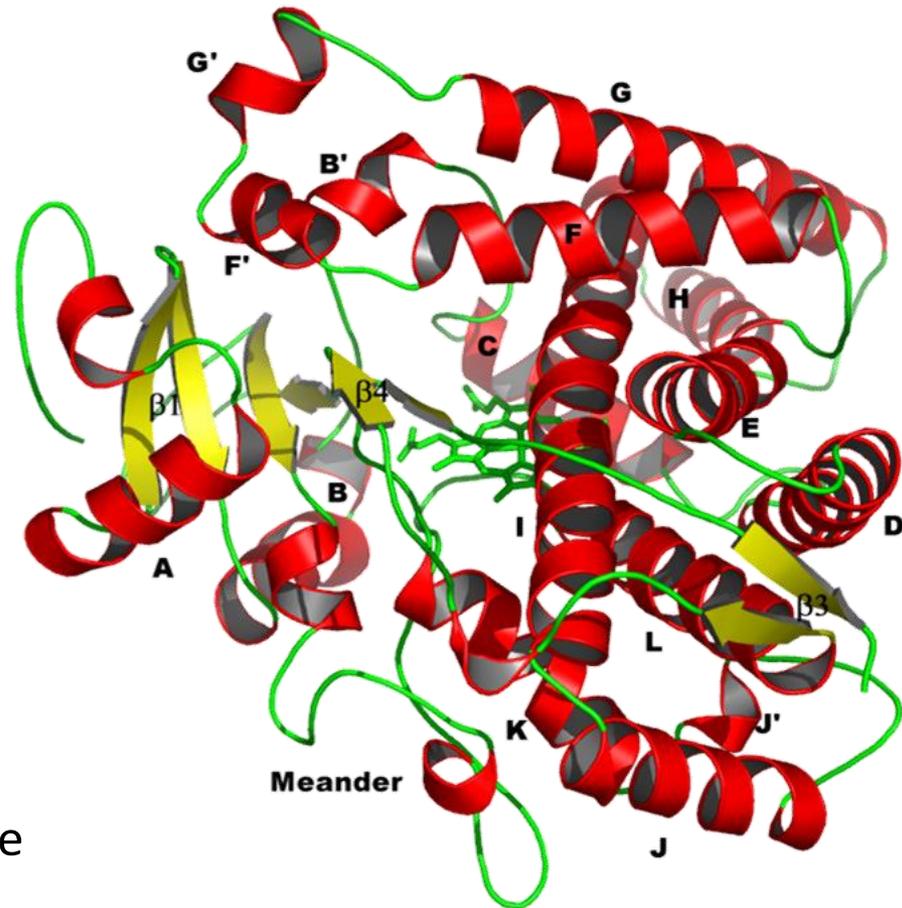
Most common reaction is a monooxygenase reaction
on heme iron



Features

Highly promiscuous (metabolize multiple substrates)

Highly regio and stereospecific



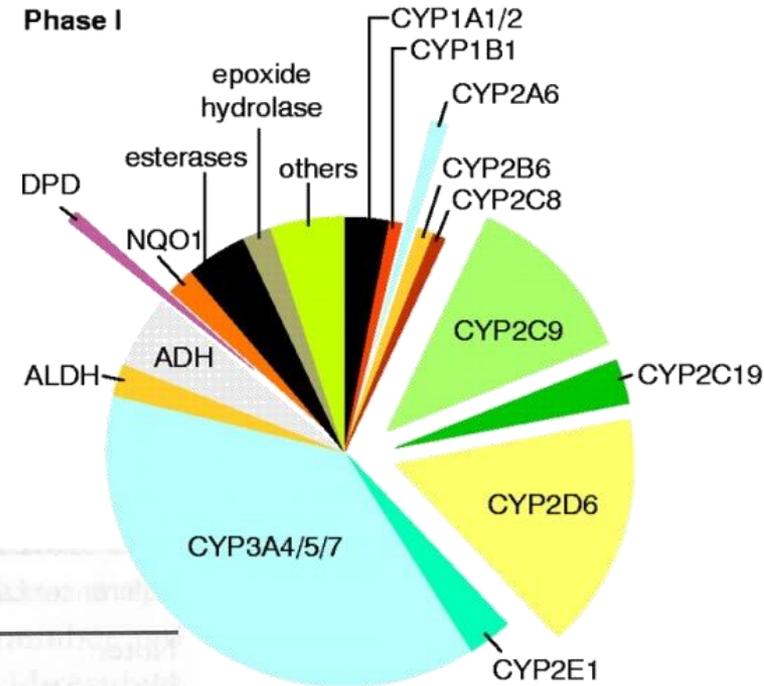
CYP2C9 (10G2)

Williams et al., Nature 424, 464, 2003

CYP Substrate Specificity

CYP family

- 75% of phase I metabolism
- One of the main reasons for failures of clinical testing => Predictions of possible metabolism needed ASAP
- Drug-Drug Interactions (grapefruit)



Evans, Relling
Science 286, 487,1999

Table 4.18 Characteristics of human P450 substrates

| CYP | General structural and physicochemical characteristics |
|------|--|
| 1A2 | Planar (poly)aromatic/heterocyclic amines and amides with 2 or 3 hydrogen bond acceptors |
| 2A6 | Compounds usually contain ketonic or nitroso groups, generally polar |
| 2B6 | Non-planar (often V-shaped) molecules, usually lipophilic with hydrogen bond donor/acceptors |
| 2C9 | Generally weakly acidic compounds with hydrogen bond donor/acceptors |
| 2C19 | Generally neutral or basic compounds with hydrogen bond donor/acceptors |
| 2D6 | Nitrogenous bases with sites of metabolism 4–7 Å from basic nitrogen |
| 2E1 | Structurally diverse generally neutral compounds of low molecular weight |
| 3A4 | Structurally diverse compounds of relatively high molecular weight |

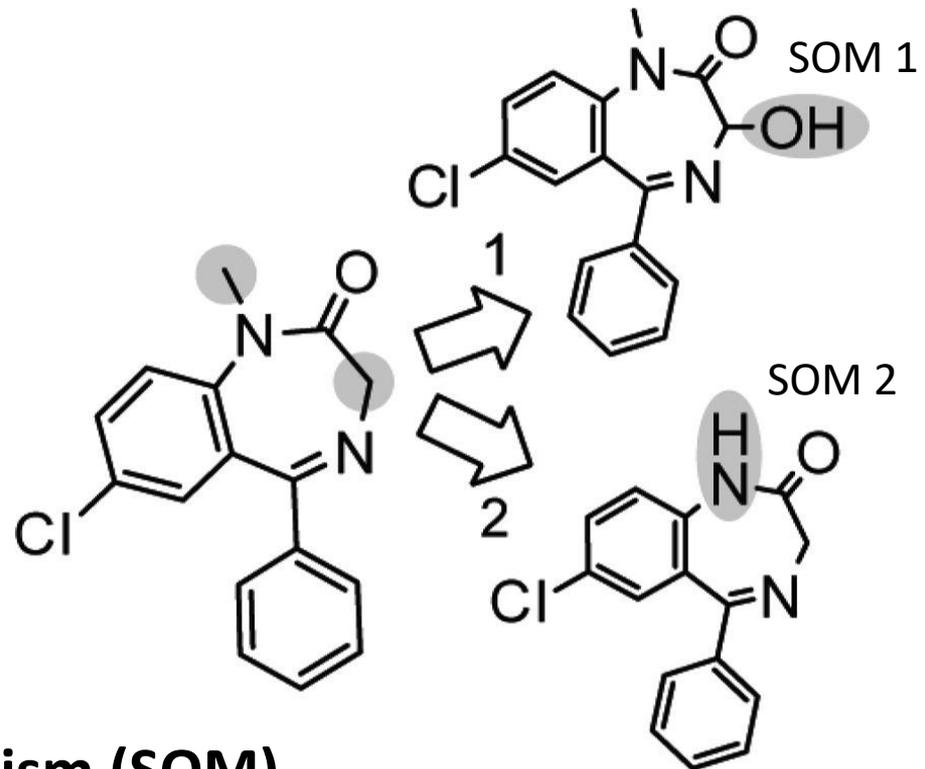
What Governs CYP Specificity?

Hard question:

- Active site
 - Size or shape => Docking
 - Flexibility
- Reactivity => SMARTCyp
- Accessibility
 - Channels
 - Membrane attachment
- Interactions with partners

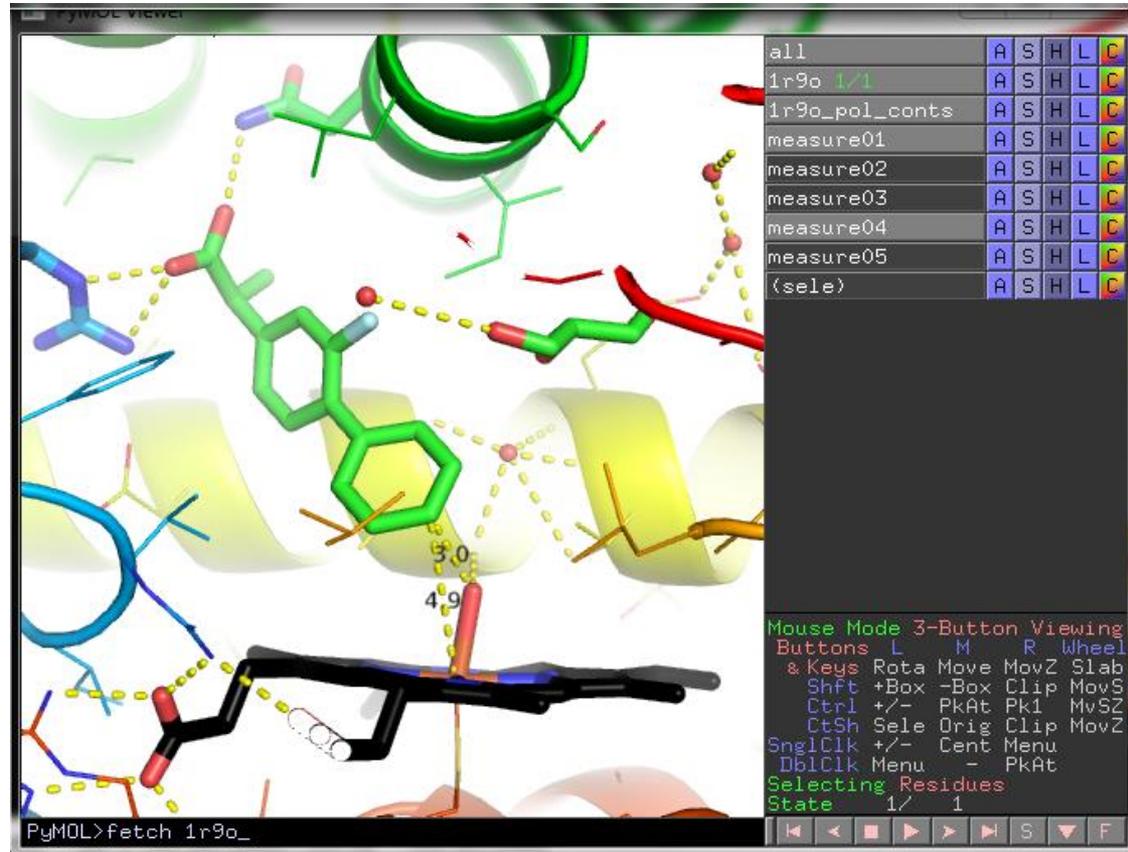
⇒ Identification of **Site-of-Metabolism (SOM)**

(weak point of drug - crucial in drug development)



CYP active site

- Contain **heme b** bound to Cys from one side and (sometimes) ligand from the other
 - **Iron** atom in heme is catalytically active
- ⇒ **SOM** is the atom closest to heme iron



Flurbiprofen in active site of CYP2C9 – PDBID: **1r9o**

PyMol vizualization by all A>preset>ligand sites>cartoon

DOCKING

Protein Selection

- Find human cytochrome P450 2C9 at PDB database: www.rcsb.org
- Select those structures with some similar molecule in active site and with good resolution ($<2.5\text{\AA}$)
- Open selected structure in Pymol

Filter: Check All View: Detailed Download Results Reports: Select one

10G2 STRUCTURE OF HUMAN CYTOCHROME P450 CYP2C9
Authors: Williams, P.A., Cosme, J., Ward, A., Angove, H.C., Matak Vinkovic, D., Jhoti, H.
Release: 2003-07-17
Experiment: X-RAY DIFFRACTION with resolution of 2.60 Å Residue Count 950
Compound: 1 Polymer [Display Full Polymer Details | Display for All Results]
1 Ligand [Display Full Ligand Details | Display for All Results]
Citation: Crystal Structure of Human Cytochrome P450 2C9 with Bound Warfarin (2003) Nature 424: 464 [Display Full Abstract | Display for All Results]
Molecule of the Month: Vitamin D Receptor

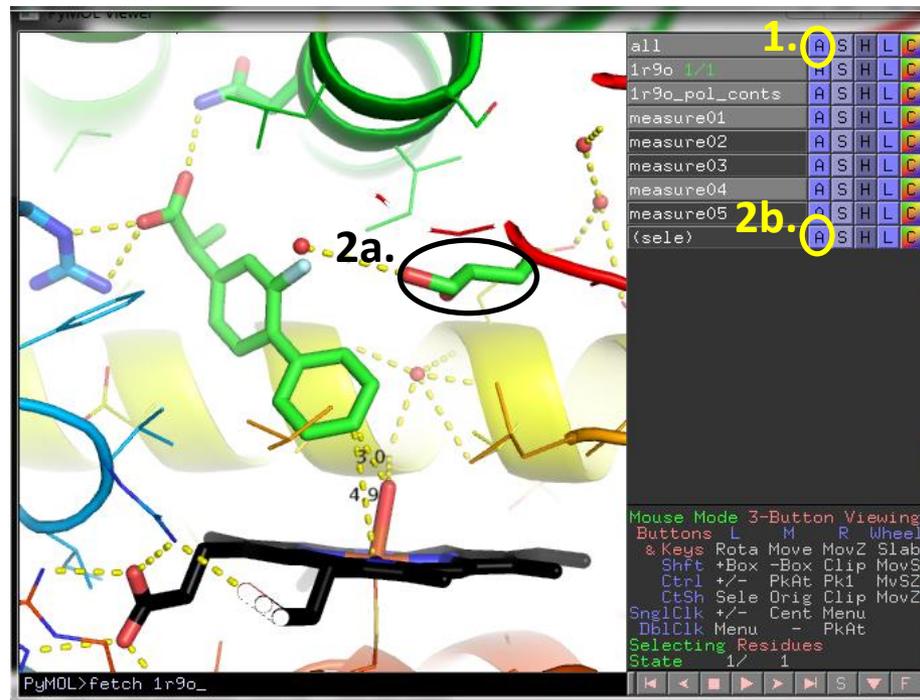
10G5 STRUCTURE OF HUMAN CYTOCHROME P450 CYP2C9
Authors: Williams, P.A., Cosme, J., Ward, A., Angove, H.C., Matak Vinkovic, D., Jhoti, H.
Release: 2003-07-17
Experiment: X-RAY DIFFRACTION with resolution of 2.55 Å Residue Count 950
Compound: 1 Polymer [Display Full Polymer Details | Display for All Results]
2 Ligands [Display Full Ligand Details | Display for All Results]
Citation: Crystal Structure of Human Cytochrome P450 2C9 with Bound Warfarin (2003) Nature 424: 464 [Display Full Abstract | Display for All Results]
Molecule of the Month: Vitamin D Receptor

1R90 Crystal Structure of P4502C9 with Flurbiprofen bound
Authors: Wester, H.J., Yano, J.K., Schoch, G.A., Griffin, K.J., Stout, C.D., Johnson, E.F.
Release: 2004-06-15
Experiment: X-RAY DIFFRACTION with resolution of 2.00 Å Residue Count 477
Compound: 1 Polymer [Display Full Polymer Details | Display for All Results]
3 Ligands [Display Full Ligand Details | Display for All Results]
Citation: The Structure of Human Cytochrome P450 2C9 Complexed with Flurbiprofen at 2.0 Å Resolution (2004) J.Biol.Chem. 279: 35630-35637 [Display Full Abstract | Display for All Results]
Molecule of the Month: Vitamin D Receptor

4NZ2 Crystal structure of CYP2C9 in complex with an inhibitor
Authors: Branden, G., Sjogren, T., Xue, Y.
Release: 2014-08-13
Experiment: X-RAY DIFFRACTION with resolution of 2.45 Å Residue Count 950
Compound: 1 Polymer [Display Full Polymer Details | Display for All Results]
4 Ligands [Display Full Ligand Details | Display for All Results]
Citation: Structure-based ligand design to overcome CYP inhibition in drug discovery projects. (2014) Drug Discov Today 19: 905-911 [Display Full Abstract | Display for All Results]
Molecule of the Month: Vitamin D Receptor

Protein and Ligand Preparation in Pymol

1. Pymol vizualization at line
all>A>preset>ligand sites>cartoon
2. Delete glycol (crystalization agent)
Select by mouse>(sele)>A>remove atoms
3. Delete waters
A>remove waters
4. Extract ligand
select by mouse>(sele)>A>extract object
5. Add hydrogens on ligand
obj01>A>hydrogens>add
6. Save ligand
File>Save Molecule>obj01>obj01.pdb
7. Add hydrogens on protein
1r9o>A>hydrogens>add
8. Save protein
File>Save Molecule>1r9o>1r9oH.pdb



Flurbiprofen in active site of CYP2C9 –
PDBID: 1r9o
Heme was colored black

Ligand Preparation – Autodock Tools

1. Start ADT or PMV program

Line starting with ADT appears

2. Select ligand

Ligand>Input>Open> *.pdb

ligand will be prepared for docking

3. Check of aromatic atoms

Ligand>Aromatic carbons>Set Names>

(Shift+left mouse over cycle)

aromatic atoms are shown in green

4. Check of rotatable torsions

Ligand>Torsion Tree> Choose Torsions...

rotatable bonds are shown in green, unrotatable

in red, shift picking can select bond to be non-

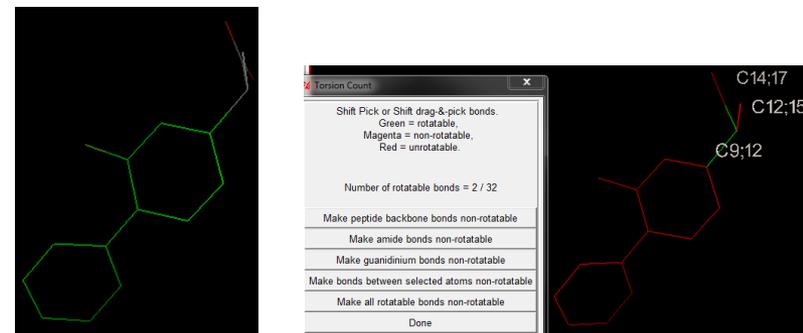
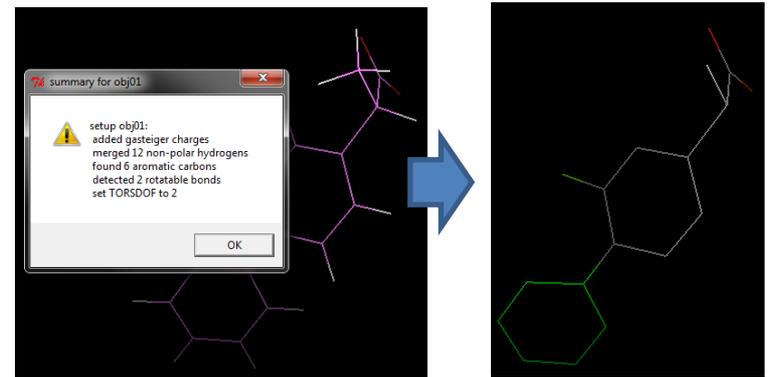
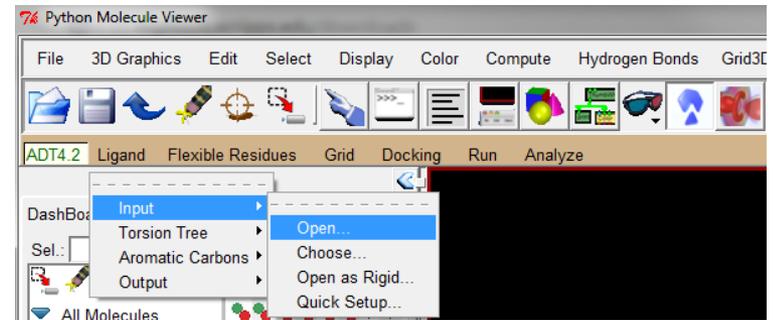
rotatable and vice versa.

Flurbiprofen have 2 rotatable bond, bond

between aromatics

5. Save pdbqt file

Ligand>Output>Save as> *.pdbqt



Ligand PDBQT file

```

REMARK 2 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 1 A between atoms: C9_10 and C12_14
REMARK 2 A between atoms: C12_14 and C14_16
ROOT atom description x [A] y [A] z [A] occ.+Bfactor+charge+ atomic type
HETATM 1 C FLP A 501 7.165 28.800 -3.419 1.00 45.59 0.001 A
HETATM 2 C1 FLP A 501 7.996 29.908 -2.978 1.00 46.26 0.012 A
HETATM 3 C2 FLP A 501 7.405 31.131 -2.409 1.00 46.93 -0.023 A
HETATM 4 C3 FLP A 501 5.918 31.186 -2.355 1.00 46.14 0.012 A
HETATM 5 C4 FLP A 501 5.110 30.094 -2.794 1.00 43.88 0.001 A
HETATM 6 C5 FLP A 501 5.733 28.920 -3.347 1.00 44.98 0.000 A
HETATM 7 C6 FLP A 501 8.208 32.219 -1.923 1.00 49.58 0.013 A
HETATM 8 C7 FLP A 501 9.477 31.935 -1.184 1.00 49.56 0.016 A
HETATM 9 C8 FLP A 501 10.293 32.997 -0.670 1.00 50.29 0.009 A
HETATM 10 C9 FLP A 501 9.984 34.388 -0.968 1.00 50.23 -0.041 A
HETATM 11 C10 FLP A 501 8.772 34.689 -1.677 1.00 51.61 0.051 A
HETATM 12 C11 FLP A 501 7.940 33.653 -2.226 1.00 51.99 0.128 A
HETATM 13 F FLP A 501 6.813 34.090 -2.912 1.00 55.17 -0.205 F
ENDROOT
BRANCH 10 14 Torsion definition> branching out of rigid ROOT part
HETATM 14 C12 FLP A 501 10.854 35.588 -0.436 1.00 50.59 0.115 C
HETATM 15 C13 FLP A 501 10.210 36.301 0.807 1.00 48.83 0.026 C
BRANCH 14 16
HETATM 16 C14 FLP A 501 11.120 36.626 -1.611 1.00 50.40 0.181 C
HETATM 17 O FLP A 501 10.588 37.740 -1.596 1.00 51.19 -0.647 OA
HETATM 18 O1 FLP A 501 11.869 36.290 -2.555 1.00 50.57 -0.647 OA
ENDBRANCH 14 16
ENDBRANCH 10 14
TORSDOF 2

```

Number of active torsions

Atom lines with charges

Atomic types:

A – aromatic carbon

C – aliphatic carbon

F – fluorine

OA – hydrogen-
bond acceptor
oxygen

Protein Preparation – Autodock Tools

1. Select Protein Grid>Macromolecule>Open>*.pdb
protein will be prepared for docking (nonpolar hydrogens merged with carbon, charges assigned) and saved as *.pdbqt (iron will have charge 0)

2. Analysis of necessary grid size

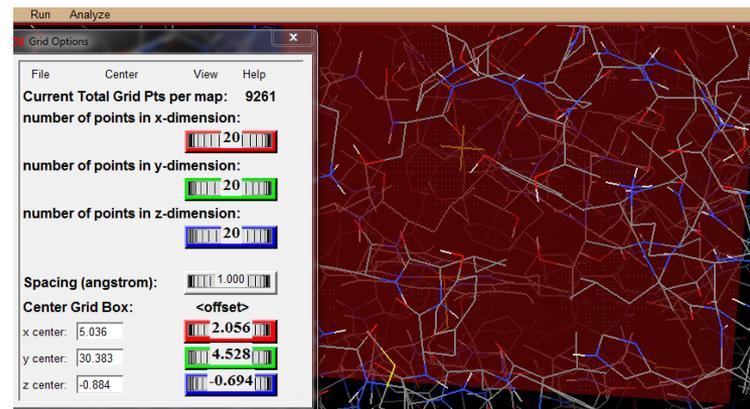
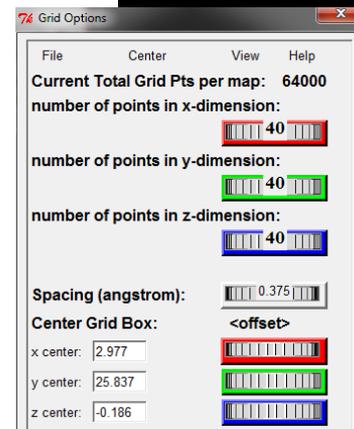
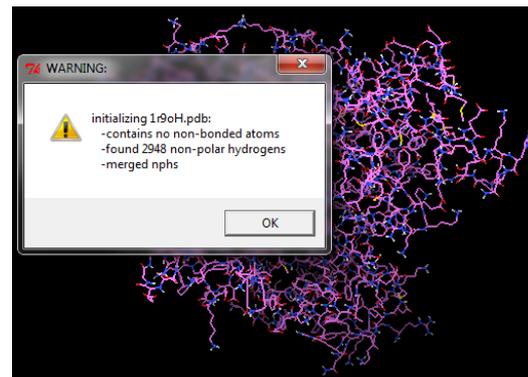
Grid>Grid Box...

cube with size will appear aromatic atoms are shown in red-green-blue sizes with yellow cross in its center

- move yellow cross over the heme iron and then above the ring using <offset> settings
- change spacing to 1 A (Vina use this settings)
- adjust size of cube so it will cover active site, but not much more
- note cube parameters

3. Edit protein PDBQT to charge iron(+2)

HETATM 4482 FE HEM A 500 5.890 24.568 -1.058 1.00 18.80 2.000 Fe



Docking Setup – Vina

- Copy **vina.exe** into the same directory as both pdbqt (i.e. Desktop)
- Open **cmd** program (type cmd into the search field in Windows start panel)
- Go to directory with files see example on right
- Type **vina.exe** to see help (Tab key will fill up name of file)
- Either it is possible to fill in all parameters in one long line or within config file (next slide)



```
C:\windows\system32\cmd.exe
C:\Users\berka>cd Desktop (cd Desktop ) change directory
C:\Users\berka\Desktop>dir (cd ..) change directory up
Svazek v jednotce C je 11312407000. (dir) list entries in directory
Sériové číslo svazku je 70CD-275A.

Úypis adresáře C:\Users\berka\Desktop
28.11.2014 00:47 <DIR> .
28.11.2014 00:47 <DIR> ..
27.11.2014 23:27 616 284 1r9o.pdb
27.11.2014 23:28 616 284 1r9oH.pdb
28.11.2014 00:17 363 926 1r9oH.pdbqt
27.11.2014 23:28 5 015 obj01.pdb
28.11.2014 00:06 28.11.2014 11:14 <DIR> Unused
08.11.2014 11:37 781 824 vina.exe
11.05.2011 11:37
Souborů: 6, Bajtů: 2 385 076
Adresářů: 3, Volných bajtů: 22 923 960 320

C:\Users\berka\Desktop>vina.exe
Missing receptor.

Correct usage:

Input:
--receptor arg rigid part of the receptor <PDBQT>
--flex arg flexible side chains, if any <PDBQT>
--ligand arg ligand <PDBQT>

Search space <required>:
--center_x arg X coordinate of the center
--center_y arg Y coordinate of the center
--center_z arg Z coordinate of the center
--size_x arg size in the X dimension <Angstroms>
--size_y arg size in the Y dimension <Angstroms>
--size_z arg size in the Z dimension <Angstroms>

Output <optional>:
--out arg output models <PDBQT>, the default is chosen based on
the ligand file name
--log arg optionally, write log file

Misc <optional>:
--cpu arg the number of CPUs to use <the default is to try to
detect the number of CPUs or, failing that, use 1>
explicit random seed
--exhaustiveness arg <=8> exhaustiveness of the global search <roughly
proportional to time>; 1+
--num_modes arg <=9> maximum number of binding modes to generate
--energy_range arg <=3> maximum energy difference between the best binding
mode and the worst one displayed <kcal/mol>

Configuration file <optional>:
--config arg the above options can be put here

Information <optional>:
```

Docking parameters file - config.txt

Protein

Ligand

Output

Box center

Box size

Search exhaustiveness

Number of reported poses

```
receptor = 1r9oH.pdbqt
```

```
ligand   = obj01.pdbqt
```

```
out      = test_out.pdbqt
```

```
log      = test_out.log
```

```
center_x = 5
```

```
center_y = 30
```

```
center_z = -1
```

```
size_x   = 20
```

```
size_y   = 20
```

```
size_z   = 20
```

```
exhaustiveness = 8
```

```
num_modes      = 9
```

Docking Run - Vina

- Run

```
vina.exe --config config.txt
```

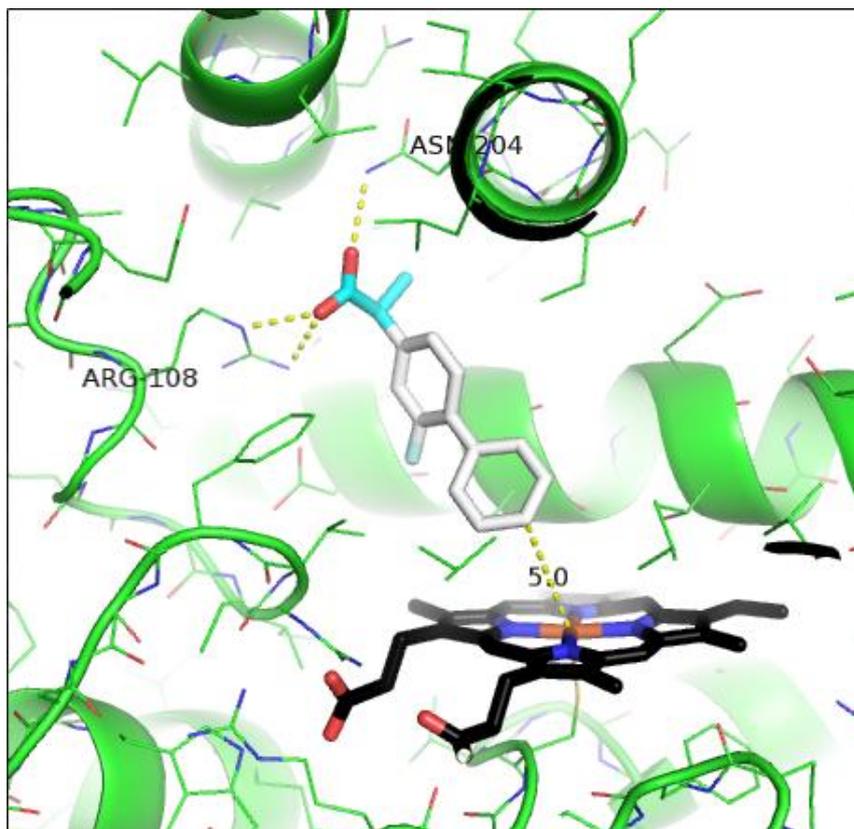
- Vina detects available number of CPUs
- docking should take about 10 s
- progress is shown with stars
- Results is shown with predicted affinity in kcal/mol, and RMSD to the first predicted pose (same info is in log file)

```
C:\Users\berka\Desktop>vina.exe --config config.txt
#####
# If you used AutoDock Vina in your work, please cite:          #
#                                                                 #
# O. Trott, A. J. Olson,                                        #
# AutoDock Vina: improving the speed and accuracy of docking   #
# with a new scoring function, efficient optimization and      #
# multithreading, Journal of Computational Chemistry 31 (2010) #
# 455-461                                                       #
#                                                                 #
# DOI 10.1002/jcc.21334                                         #
#                                                                 #
# Please see http://vina.scripps.edu for more information. #
#####
Detected 4 CPUs
Reading input ... done.
Setting up the scoring function ... done.
Analyzing the binding site ... done.
Using random seed: 863478692
Performing search ...
0%  10  20  30  40  50  60  70  80  90 100%
|-----|-----|-----|-----|-----|-----|-----|-----|
*****
done.
Refining results ... done.

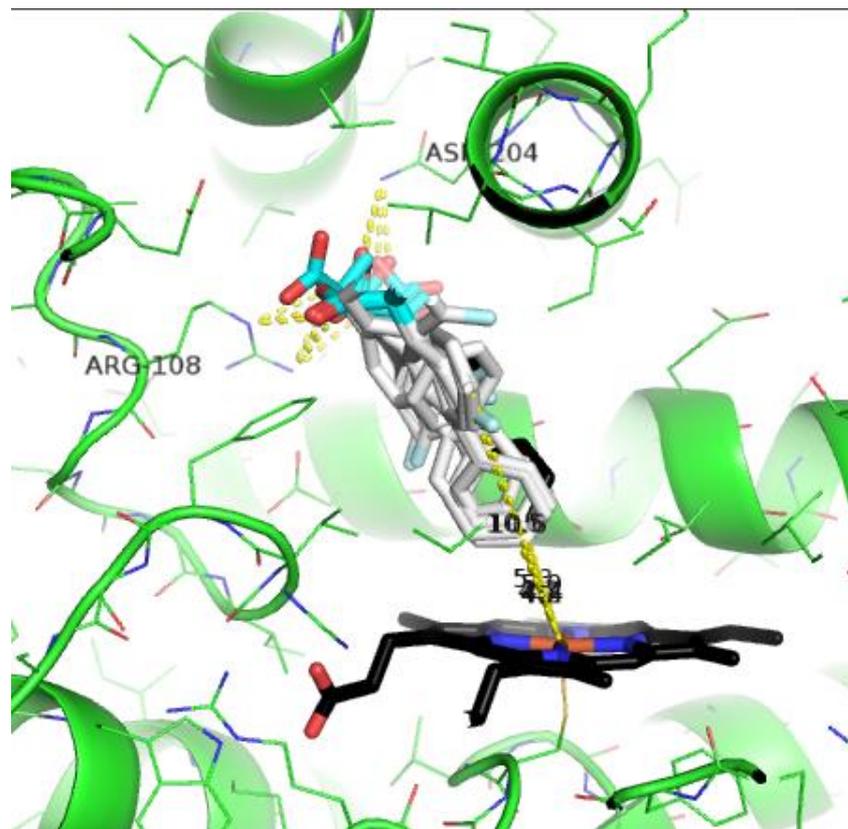
mode |   affinity | dist from best mode
     | (kcal/mol) | rmsd l.b. | rmsd u.b.
-----+-----+-----+-----
  1  |    -9.4    |    0.000  |    0.000
  2  |    -9.3    |    1.214  |    2.065
  3  |    -8.5    |    3.379  |    6.863
  4  |    -8.3    |    3.419  |    6.868
  5  |    -8.2    |    3.305  |    6.892
  6  |    -8.2    |    3.343  |    6.941
  7  |    -7.8    |    3.930  |    4.646
  8  |    -7.5    |    2.660  |    3.349
  9  |    -7.1    |    4.351  |    5.263
Writing output ... done.
```

Docking analysis – Pymol

First pose – almost same as xray



All poses overlaid over xray



Redocking was succesful

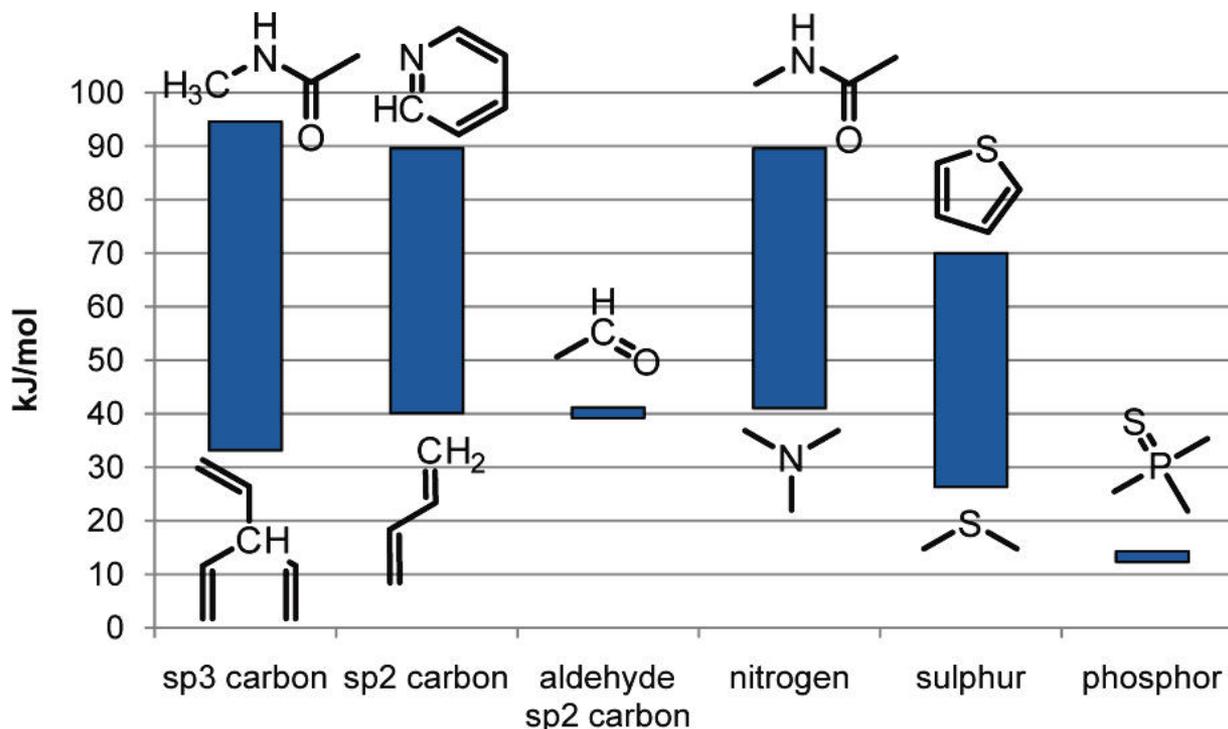
Docking – Further Exercises

- Play a little with docking parameters
 - Starting position of ligand – shift it in Pymol outside of protein
 - Exhaustiveness – as small as 1 and as large as 20
 - Charge on iron (0, 2, 3 or left there oxygen atom on iron (reactive intermediate compound I has configuration Fe=O)
 - Add free rotation between both phenyl rings
- Prepare and dock ibuprofen – will it bind similarly as flurbiprofen?
 - Build modul in Pymol
 - download sdf with major microspecies from PubChem,
 - download structure from www.rcsb.org

SMARTCYP

SMARTCyp

- Predictions of SOM (sites-of-metabolism) based on DFT calculations and cheminformatics
- Activation energies for individual CYP reactions on individual sites DFT (B3LYP/6-311++G(2d,2p))
- Comparison of HAT energies in individual fragments:

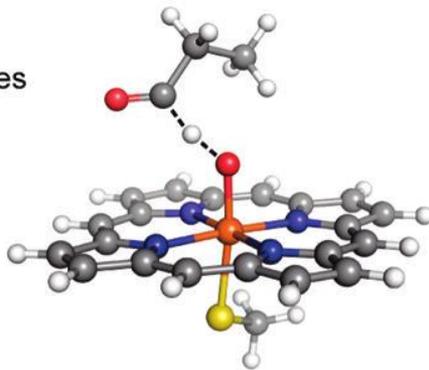


SMARTCyp – principle II

Atom Reactivity Library

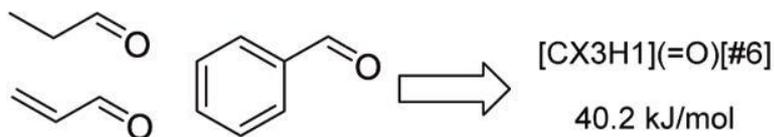
A. Calculate Quantum Chemical Reference Energies

Calculate transition state energies using density functional theory



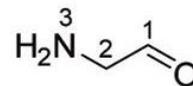
B. Define SMARTS Rules

Group calculations by fragments and calculate average energies



SMARTCyp

1. Assign Energies By SMARTS matching



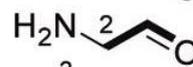
| Atom | SMARTS | Energy |
|------|-----------------|--------|
| 1 | [CX3H1](=O)[#6] | 40.2 |
| 2 | [CX4][N] | 39.8 |
| 3 | [N^3][H1,H2] | 54.1 |

2. Compute Accessibility Descriptor

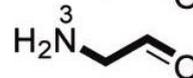
$$A_i = \text{Maxbonds}_i / \text{Maxbonds}_{\text{all}}$$



$$A_1 = 2 / 3 = 0.67$$



$$A_2 = 2 / 3 = 0.67$$



$$A_3 = 3 / 3 = 1.00$$

3. Compute Score and Rank Atoms

Score, $S = E - 8A$

Lowest score gets rank 1

$$S_1 = 40.2 - 8 \cdot 0.67 = 34.84$$

Atom 1 - Rank 2

$$S_2 = 39.8 - 8 \cdot 0.67 = 34.44$$

Atom 2 - Rank 1

$$S_3 = 54.1 - 8 \cdot 1.00 = 46.10$$

Atom 3 - Rank 3



SMARTCyp - input

- <https://smartcyp.sund.ku.dk/>

Current SMARTCyp version is 2.4.2

SMARTCyp predicts the sites in molecules that are most liable to cytochrome P450 mediated metabolism.

You have three options for submitting molecules:

Draw a molecule



Draw according to
wikipedia/ pubchem/
chemspider/ chemicalize/...

ChemDoodle®

Start SMARTCyp

Upload a file ?

Vybrat soubor Soubor nevybrán

Start SMARTCyp

Enter SMILES strings

... or more quickly just
copy here a **SMILES**

Start SMARTCyp

SMARTCyp - results

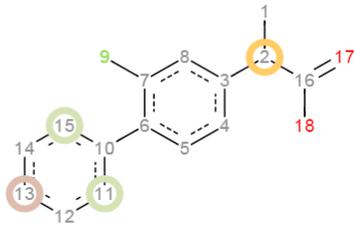
Flurbiprofen

CC(c1ccc(c(c1)F)c2ccccc2)C(=O)O

Results from SMARTCyp version 2.4.2

These results were produced: 2014-11-26_22-54-52. The infiles were: [smiles.smi].

To alternate between heteroatoms and atom numbers, move the mouse cursor over the figure.



Generic –
good for CYP3A4

| | Standard | CYP2C | CYP2D6 | | | |
|----------------|----------|--------|--------|---------------|--------|--|
| 1: null | | | | | | |
| Rank | Atom | Score | Energy | Accessibility | 2DSASA | |
| 1 | C.2 | 59.69 | 66.4 | 0.8 | 7.86 | |
| 2 | C.13 | 71.35 | 80.8 | 1 | 36.24 | |
| 3 | C.11 | 73.28 | 80.8 | 0.8 | 27.97 | |
| 4 | C.5 | 75.87 | 80.8 | 0.5 | 23.31 | |
| 5 | C.12 | 77.76 | 86.3 | 0.9 | 33.5 | |
| 6 | C.4 | 78.38 | 84.1 | 0.6 | 23.07 | |
| 7 | C.8 | 78.44 | 84.1 | 0.6 | 21.5 | |
| 8 | C.1 | 80.27 | 89.6 | 0.9 | 53.32 | |
| 9 | C.16 | 991.53 | 999 | 0.9 | 6.8 | |
| 10 | C.10 | 993.24 | 999 | 0.7 | 3.88 | |
| 11 | C.3 | 993.28 | 999 | 0.7 | 3.01 | |
| 12 | C.6 | 994.08 | 999 | 0.6 | 3.06 | |
| 13 | C.7 | 994.76 | 999 | 0.5 | 6.02 | |

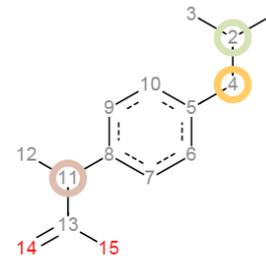
Ibuprofen

CC(C)Cc1ccc(cc1)C(C)C(=O)O

Results from SMARTCyp version 2.4.2

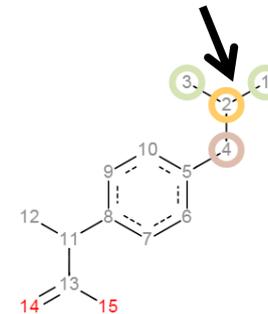
These results were produced: 2014-11-26_23-06-32. The infiles were: [smiles.smi].

To alternate between heteroatoms and atom numbers, move the mouse cursor over the figure.



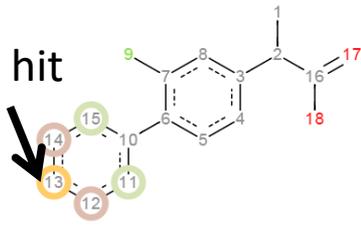
Best hit

| | Standard | CYP2C | CYP2D6 | | | |
|----------------|----------|--------|--------|---------------|--------|--|
| 1: null | | | | | | |
| Rank | Atom | Score | Energy | Accessibility | 2DSASA | |
| 1 | C.4 | 59.21 | 66.4 | 0.78 | 24.31 | |
| 2 | C.11 | 59.85 | 66.4 | 0.78 | 8.16 | |
| 3 | C.2 | 68.42 | 75.9 | 0.89 | 9.15 | |
| 4 | C.1 | 79.21 | 89.6 | 1 | 59.79 | |
| 5 | C.12 | 80.36 | 89.6 | 0.89 | 53.32 | |
| 6 | C.6 | 80.82 | 86.3 | 0.56 | 25.81 | |
| 7 | C.7 | 80.87 | 86.3 | 0.56 | 24.72 | |
| 8 | C.13 | 991.62 | 999 | 0.89 | 6.8 | |
| 9 | C.5 | 993.49 | 999 | 0.67 | 4.3 | |
| 10 | C.8 | 993.53 | 999 | 0.67 | 3.33 | |



| | Standard | CYP2C | CYP2D6 | | | |
|----------------|----------|----------|--------|-------|---------|--------|
| 1: null | | | | | | |
| Rank | Atom | Score | Energy | S2End | COODist | 2DSASA |
| 1 | C.2 | 81.43 | 75.9 | 1 | 8 | 9.15 |
| 2 | C.4 | 83.13 | 66.4 | 2 | 7 | 24.31 |
| 3 | C.1 | 87.21 | 89.6 | 0 | 9 | 59.79 |
| 4 | C.11 | 113.27 | 66.4 | 2 | 2 | 8.16 |
| 5 | C.12 | 122.87 | 89.6 | 1 | 3 | 53.32 |
| 6 | C.6 | 126.61 | 86.3 | 4 | 5 | 25.81 |
| 7 | C.7 | 132.55 | 86.3 | 4 | 4 | 24.72 |
| 8 | C.5 | 1,028.33 | 999 | 3 | 6 | 4.3 |
| 9 | C.13 | 1,045.93 | 999 | 1 | 1 | 6.8 |
| 10 | C.8 | 1,046.07 | 999 | 3 | 3 | 3.33 |

Best hit

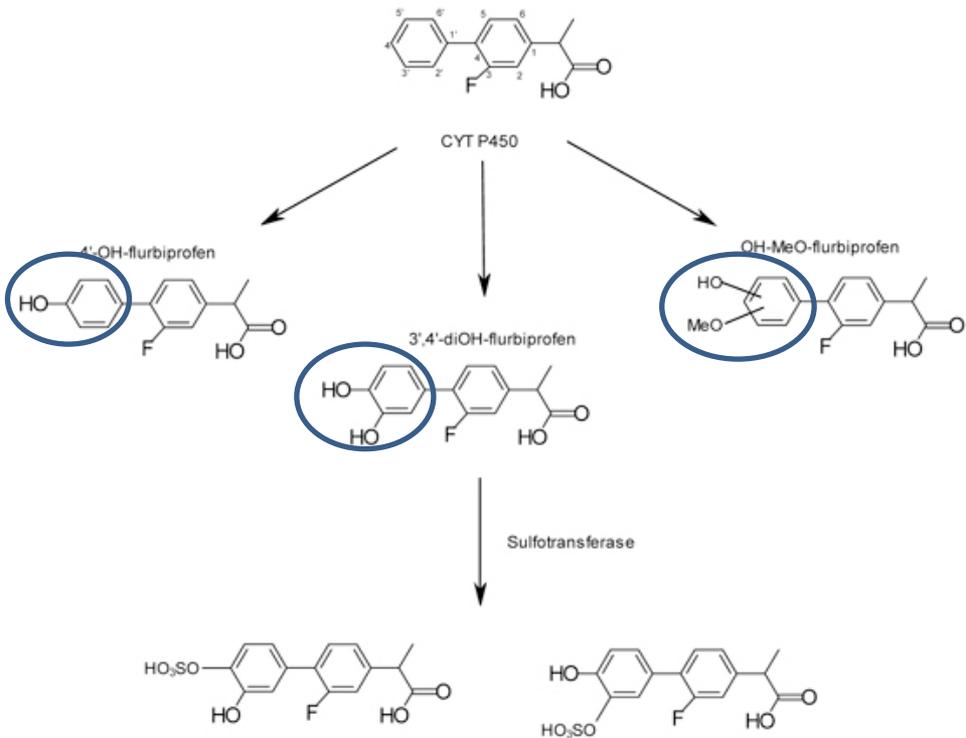


With pharmacophore
for CYP2C9

| | Standard | CYP2C | CYP2D6 | | | |
|----------------|----------|----------|--------|-------|---------|--------|
| 1: null | | | | | | |
| Rank | Atom | Score | Energy | S2End | COODist | 2DSASA |
| 1 | C.13 | 79.35 | 80.8 | 0 | 10 | 36.24 |
| 2 | C.12 | 90.86 | 86.3 | 1 | 9 | 33.5 |
| 3 | C.11 | 91.48 | 80.8 | 2 | 8 | 27.97 |
| 4 | C.2 | 113.29 | 66.4 | 2 | 2 | 7.86 |
| 5 | C.5 | 121.22 | 80.8 | 5 | 5 | 23.31 |
| 6 | C.1 | 122.87 | 89.6 | 1 | 3 | 53.32 |
| 7 | C.4 | 130.42 | 84.1 | 4 | 4 | 23.07 |
| 8 | C.8 | 130.48 | 84.1 | 4 | 4 | 21.5 |
| 9 | C.10 | 1,022.44 | 999 | 3 | 7 | 3.88 |
| 10 | C.6 | 1,034.32 | 999 | 4 | 6 | 3.06 |
| 11 | C.7 | 1,040.11 | 999 | 5 | 5 | 6.02 |
| 12 | C.16 | 1,045.93 | 999 | 1 | 1 | 6.8 |
| 13 | C.3 | 1,046.08 | 999 | 3 | 3 | 3.01 |

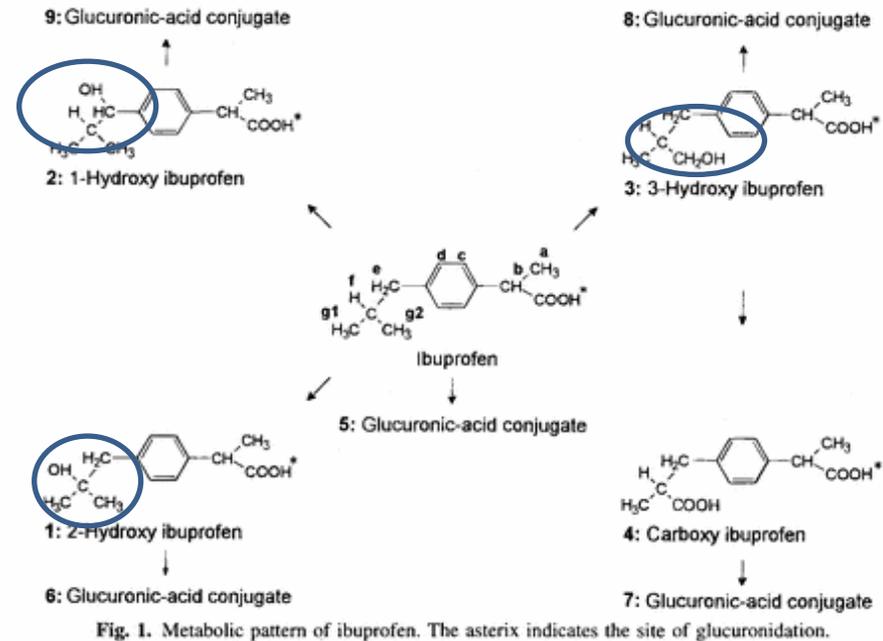
Reality check

Flurbiprofen



Ibuprofen

Major Metabolites of Ibuprofen



Reality check 2 – use experimental SOM db in SmartCyp

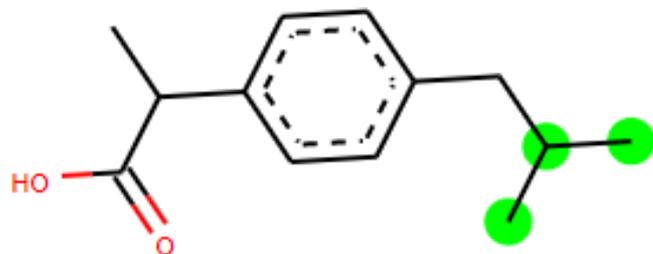
- https://smartcyp.sund.ku.dk/mol_to_som?prediction=Search

Primary SOM

Secondary SOM

Tertiary SOM

Quaternary SOMs not implemented



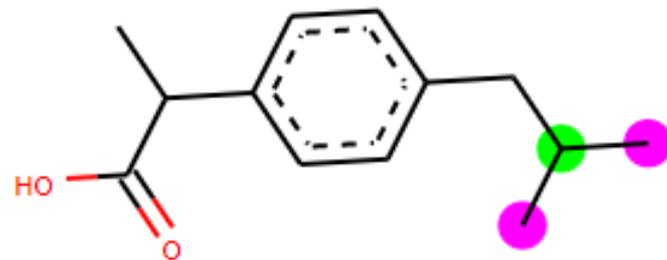
ibuprofen
CYP2C9

Primary SOM

Secondary SOM

Tertiary SOM

Quaternary SOMs not implemented



ibuprofen
CYP2C8

PyRx



PyRx - Python Prescription 0.8

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The Scripps Research Institute.

- Wrapper around Vina, Autodock Tools

<https://pyrx.sourceforge.io/> - old version 0.8 free of charge