



High throughput Virtual Screening with AutoDOCK vina program Asst.Prof Sefer BADAY İTÜ Faculty of Computer and Informatics Engineering

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Lesson 2: Preparing a library of ligands for docking

ZINC database offers a huge library of molecules that can be used in docking calculations.

https://zinc.docking.org/

ZINC Substances Catalogs Tranches Biological - More -

ZINC20

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 Irwin and Shoichet Laboratories in the Department of Pharmaceutical Chemistry at the University of California, San Francisco (UCSF). We thank NIGMS for financial support (GM71896).

To cite ZINC, please reference: Irwin, Tang, Young, Dandarchuluun, Wong, Khurelbaatar, Moroz, Mayfield, Sayle, *J. Chem. Inf. Model 2020*, in press. https://pubs.acs.org/doi/10.1021/acs.jcim.0c00675. You may also wish to cite our previous papers: Sterling and Irwin, *J. Chem. Inf. Model, 2015* http://pubs.acs.org/doi/abs/10.1021/acs.jcim.5b00559. Irwin, Sterling, Mysinger, Bolstad and Coleman, *J. Chem. Inf. Model, 2012* DOI: 10.1021/ci3001277 or Irwin and Shoichet, *J. Chem. Inf. Model.* 2005;45(1):177-82 PDF, DOI.

About -



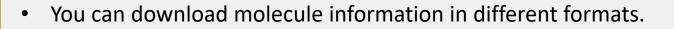
Ligand pdbqt files can be downloaded from ZINC



- Molecule information can be downloaded as the PDBQT file on ZINC
- You can filter molecule based on various criteria like drug-like, lead-like, in-Stock, clean etc.

		E	Rep. 2D :	BD React.	Standard -	Purch.	n-Stock 🕶	pH N/A 🔻	Charge N	/A • III •	Ł		
					Мо	lecular Weig	ht (up to, Da	ltons)					
		200	250	300	325	350	375	400	425	450	500	>500	Totals, by LogP
	-1												0
	0		20,326	35,387									20,326
	1		81,653	163,888									81,653
	2		182,568	404,153									182,568
LogP (up to)	2.5		102,897	268,486									102,897
	3		83,987	250,050									83,987
	3.5		52,471	184,966									52,471
	4		25,449	111,741									25,449
	4.5		9,399	55,607									9,399
	5		2,709	21,635									2,709
	>5		912	9,907									912
													562K Substances

Ligand pdbqt files can be downloaded from ZINC



		Re	Download Tr	Download Tranches										
			80 (Non-Empty) Tran	80 (Non-Empty) Tranches Selected (562,371 Substances)										
		200	250 BCCA BCCB BCEA	BBAA BBAB BBBA BBBB BBCA BBCB BBEA BBEB BCAA BCAB BCBA BCBB BCCA BCCB BCEA BCEB BDAA BDAB BDBA BDBB BDCA BDCB BDEA BDEB BEAA BEAB BEBB BECA BECB BEEA BEEB BFAA BFAB BFBA BFBB BFCA							>500	Totals, by LogP		
	-1		BFCB BFEA BFEB	BFCB BFEA BFEB BGAA BGAB BGBA BGBB BGCA BGCA BGCB BGEB BHAA BHAB BHBA BHBB BHCA BHCB BHEA BHEA BHEA BIAB BIBA BIBB BICA BICB BIEA BIEB BJAA BJAB BJBA BJBB BJCA BJCB BJEA BJEB BKAA BKAB BKBA BKBB BKCA BKCB BKEA BKEB								0		
LogP (up to)	0		2									20,326		
	1		8 Only If Modified Sinc									81,653		
	2		gg . aa . yyyy									182,568		
	2.5		10						_			102,897		
	3	21,867	Tab-Delimited (*.txt) -	Raw UR	Ls 🕶			🛓 Down	load			83,987		
Ľ	3.5	9.604	Download Format	99,778	314.985	258,411	223,888	157,406	124,425			52,471		
	4	2.005	SMILES (*.smi)	00.000								25,449		
	4	2,550	2D Only	120,000								25,449		
	4.5	626	Tab-Delimited (*.txt)√	72,796								9,399		
	5	116	3D Only DOCK37 (*.db2.gz)	34,101								2,709		
	>5	34	AutoDock (*.pdbqt.gz)	18,224								912		
Totals, by Weight			Mol2 (*.mol2.gz)	0	0	0	0	0		0		562K Substance		
		0	SDF (*.sdf.gz)						0		0	80 Tranches		

uhem

Εl

Creating pdbqt files using openbabel program



- PDBQT file format is not a common file format among the molecule databases.
- Another database might not return PDBQT files.
- In this case you can use openbabel program to create pdbqt files
- https://www.cheminfo.org/Chemistry/Cheminformatics/FormatConverter/index.html

HOME UTILITY - SPECTRA - CHEMISTRY - TUTORIAL -	DEMO - IMAGE - ML - PROTEIN - R	EFERENCES V OPENBABEL - Chemical file f V Fork Copy url
OpenBabel allows to convert nearly all the chemical formats and it very practical to quickly		
On this page we have setup a webservice allowing you to use OpenBabel without having to	install it.	
	Options	OUTPUT
Dren er norte here verr innut file	Input format*	1 REMARK Name =
Drop or paste here your input file	smi SMILES format v	2 REMARK 4 active torsions: 3 REMARK status: ('A' for Active; 'I' for Inactive)
	Output format*	4 REMARK 1 A between atoms: C_2 and C_3
	pdbqt AutoDock PDBQT format	5 REMARK 2 A between atoms: C_3 and C_4 6 REMARK 3 A between atoms: C_4 and O_5
INPUT	Generate coordinates v	7 REMARK 4 A between atoms: 0_5 and C_6
1 CCCCOclccccc1	Allows to generate 2D or 3D coordinates	8 REMARK x y z vdW Elec
	Add / Delete hydrogens No change ~	9 REMARK
	pH to add hydrogens	11 ATOM 1 C UNL 1 0.000 0.000 0.000 0.00 0.00
	Specify a pH at which the molecule should be protonated	12 ATOM 2 C UNL 1 0.000 0.000 0.000 0.00 0.00 13 ATOM 3 C UNL 1 0.000 0.000 0.000 0.00 0.00
		14 ATOM 4 C UNL 1 0.000 0.000 0.000 0.00 0.00
		15 ATOM 5 C UNL 1 0.000 0.000 0.000 0.00 0.00 16 ATOM 6 C UNL 1 0.000 0.000 0.000 0.00 0.00
		16 ATOM 6 C UNL 1 0.000 0.000 0.000 0.00 0.00 17 ENDROOT
		18 BRANCH 1 7
		19 ATOM 7 0 UNL 1 0.000 0.000 0.000 0.00 0.00 20 BRANCH 7 8
		21 ATOM 8 C UNL 1 0.000 0.000 0.000 0.00 0.00
	Convert	22 BRANCH 8 9 23 ATOM 9 C UNL 1 0.000 0.000 0.000 0.00 0.00
		24 BRANCH 9 11
🚽 🗷 🗰 🛍 ?	Use open babel to convert most of the chemical formats.	25 ATOM 10 C UNL 1 0.000 0.000 0.000 0.00 0.00 26 ATOM 11 C UNL 1 0.000 0.000 0.000 0.00 0.00
	How to proceed ?	26 ATOM 11 C UNL 1 0.000 0.000 0.000 0.00 0.00
* 2		28 ENDBRANCH 8 9
19	 Enter an input value, for example a SMILES like "CCCC" 	29 ENDBRANCH 7 8 30 ENDBRANCH 1 7
	2. Select the "Input format", for example "smi"	31 TORSDOF 4
8 Text	3. Select an output format, for example "mol"	32
$\mathbb{N}\mathcal{N}$	4. Click on "Convert"	Log
		1 molecule converted
N P		

Converting a large library of molecules into pdbqt

- If you want to create pdbqts for a large library of molecules you should run openbabel on your local computer or a HPC
- A script in bash environment can be used:
- This assumes you downloaded molecule as mol2.gz files.

```
for file in *.mol2.gz;
do
b=`basename $file .mol2.gz`;
echo $b; mkdir ${b}_pdbqt ;
cd ${b}_pdbqt;
obabel -i mol2 ../$file -h --DelNonPolarH -O new.pdbqt ---errorlevel 1 -m ;
cd ./../ ;
done
```





- <u>https://zinc.docking.org/</u>
- <u>https://open-babel.readthedocs.io/en/latest/Installation/install.html</u>

Copyright



None



Thanks.



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