

MD Simulations – day 2

Analysis



Toni Giorgino

National Research Council of Italy

toni.giorgino@cnr.it

www.giorginolab.it

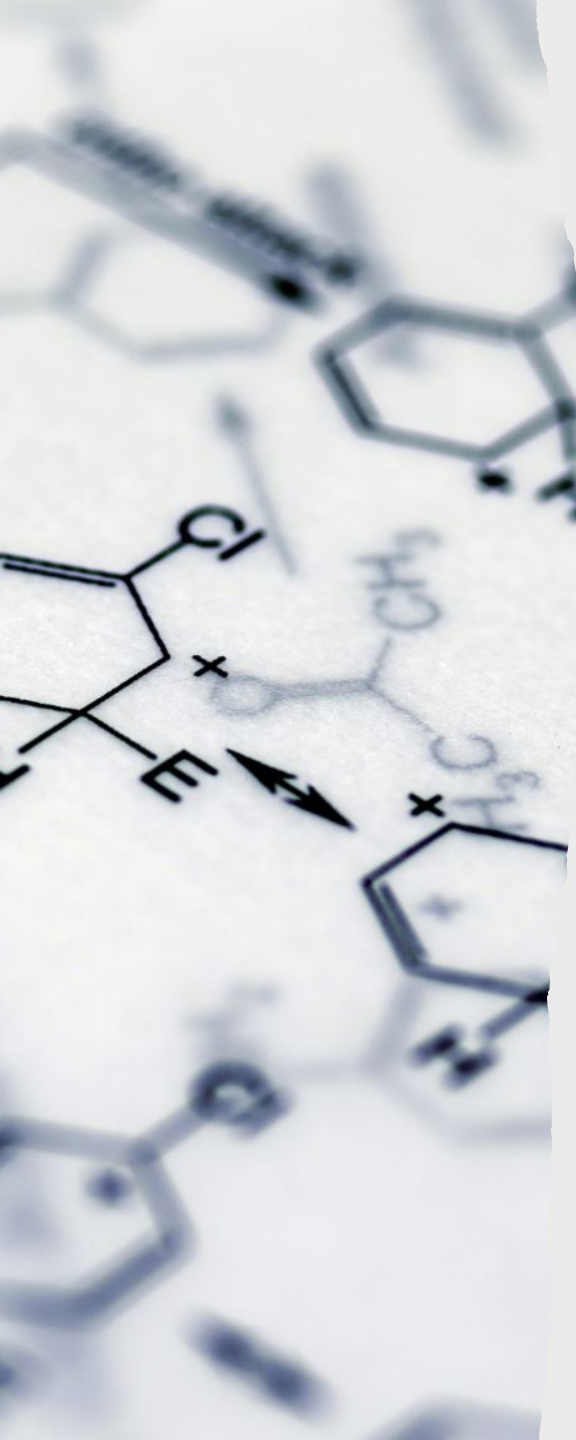


@giorginolab

for Prof. Fuxreiter's course @ University of Padova

May 2024

<https://github.com/giorginolab/MD-Tutorial-Data>



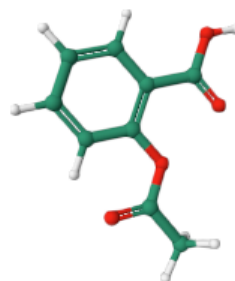
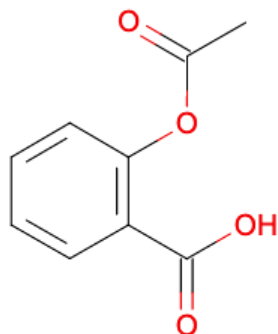
PTGS1* and **PTGS2** are the targets of nonsteroidal anti-inflammatory drugs (NSAIDs) including aspirin and ibuprofen.

Aspirin is able to produce an irreversible inactivation of the enzyme through a serine acetylation.

Inhibition of the PGHSs with NSAIDs acutely reduces inflammation, pain, and fever, and long-term use of these drugs reduces fatal thrombotic events, as well as the development of colon cancer and Alzheimer's disease.

PTGS2 is the principal isozyme responsible for production of inflammatory prostaglandins. New generation PTGSs inhibitors strive to be selective for PTGS2, to avoid side effects such as gastrointestinal complications and ulceration.

* COX1 = Prostaglandin G/H synthase 1
= PGH1_HUMAN = P23219



Toggle Hydrogen

Toggle Labels

Display Files ▾

Download Files ▾

Data API

AIN

2-(ACETYLOXY)BENZOIC ACID

Find entries where: AIN

☒ is present as a standalone ligand in **8 entries**

search

Find related ligands:

[Similar Ligands \(Stereospecific\)](#)

[Similar Ligands \(including Stereoisomers\)](#)

[Similar Ligands \(Quick Screen\)](#)

[Similar Ligands \(Substructure Stereospecific\)](#)

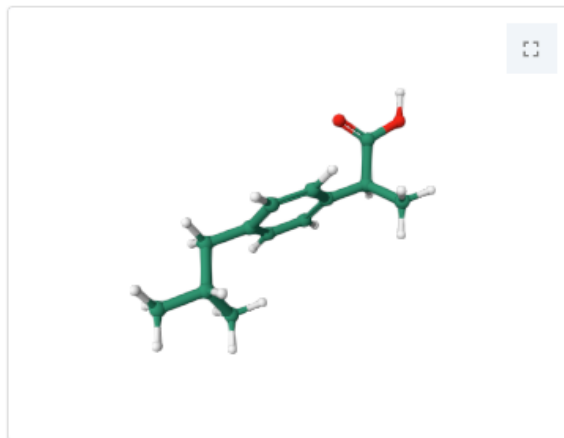
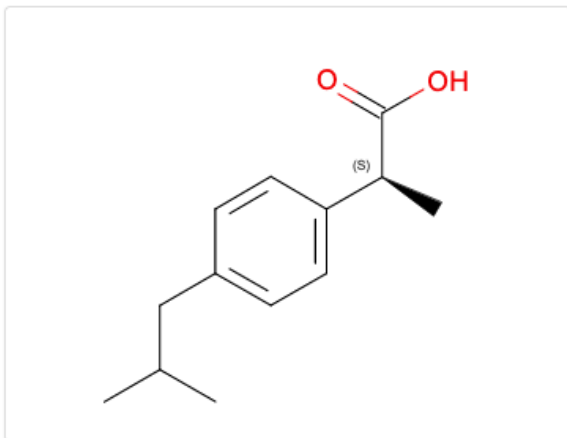
[Similar Ligands \(Substructure including Stereoisomers\)](#)

Chemical Component Summary

Name	2-(ACETYLOXY)BENZOIC ACID
Synonyms	ACETYLSALICYLIC ACID; ASPIRIN
Identifiers	2-acetyloxybenzoic acid
Formula	C ₉ H ₈ O ₄
Molecular Weight	180.157
Type	NON-POLYMER
Isomeric SMILES	CC(=O)Oc1ccccc1C(=O)O
InChI	InChI=1S/C9H8O4/c1-6(10)13-8-5-3-2-4-7(8)9(11)12/h2-5H,1H3,(H,11,12)
InChIKey	BSYNRYMUTXBXSQ-UHFFFAOYSA-N

Chemical Details

Formal Charge	0
Atom Count	21
Chiral Atom Count	0
Bond Count	21
Aromatic Bond Count	6



Toggle Hydrogen

Toggle Labels

Display Files ▾

Download Files ▾

Data API

IBP

IBUPROFEN

Find entries where: IBP

☒ is present as a standalone ligand in [14 entries](#)

search

Find related ligands:

[Similar Ligands \(Stereospecific\)](#)

[Similar Ligands \(including Stereoisomers\)](#)

[Similar Ligands \(Quick Screen\)](#)

[Similar Ligands \(Substructure Stereospecific\)](#)

[Similar Ligands \(Substructure including Stereoisomers\)](#)

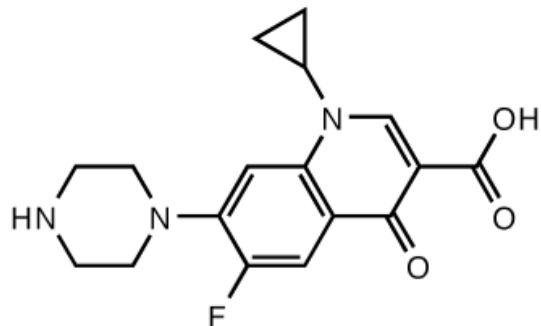
Chemical Component Summary

Name	IBUPROFEN
Synonyms	2-(4-ISOBUTYLPHENYL)PROPIONIC ACID
Identifiers	(2S)-2-[4-(2-methylpropyl)phenyl]propanoic acid
Formula	C ₁₃ H ₁₈ O ₂
Molecular Weight	206.281
Type	NON-POLYMER
Isomeric SMILES	<chem>CC(C)Cc1ccc(cc1)[C@H](C)C(=O)O</chem>
InChI	InChI=1S/C13H18O2/ c1-9(2)8-11-4-6-12(7-5-11)10(3)13(14)15/h4-7,9-10H, 8H2,1-3H3,(H,14,15)/t10-/m0/s1

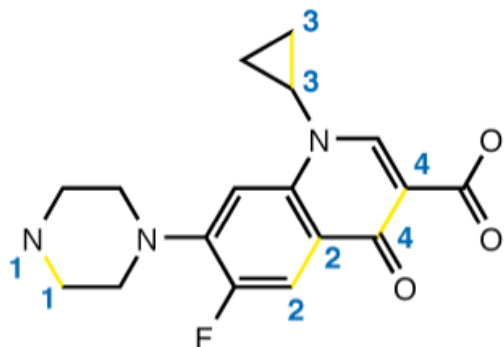
Chemical Details

Formal Charge	0
Atom Count	33
Chiral Atom Count	1
Bond Count	33
Aromatic Bond Count	6

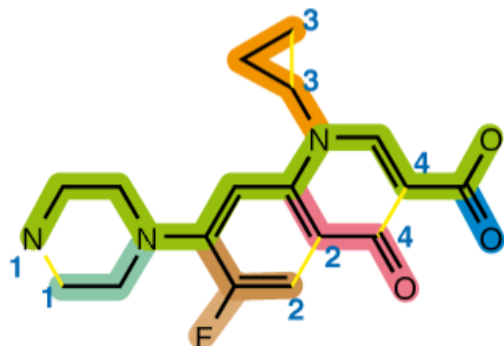
A



B



C



D

N1CCN(CC1)C(C(F)=C2)=CC(=C2C4=O)N(C3CC3)C=C4C(=O)O

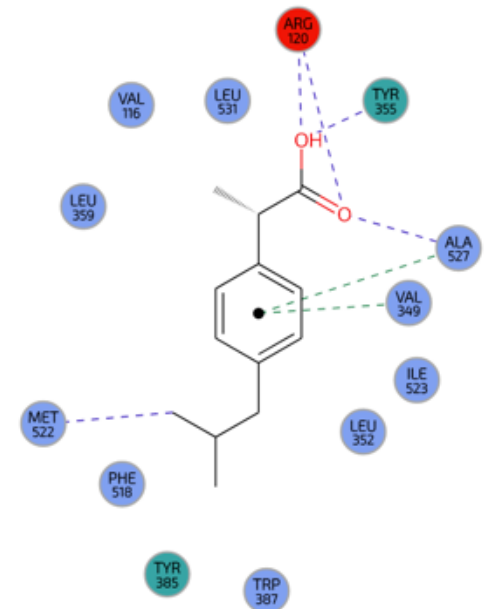
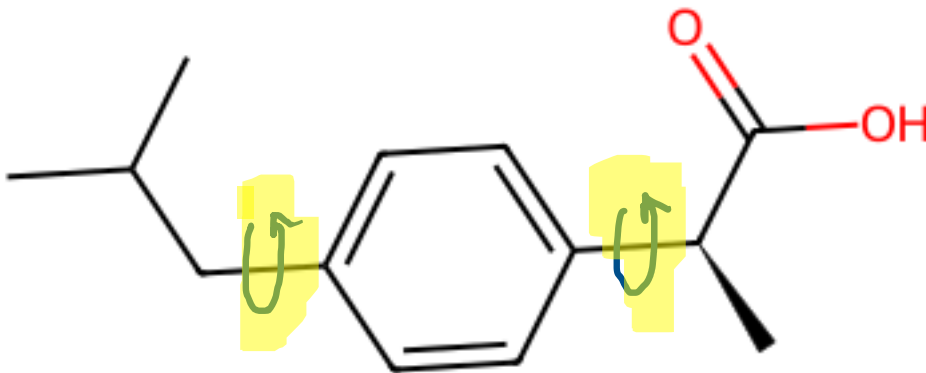
- SMILES is a “ID” representation of the molecular graph.
- However, it **can** encode stereochemistry and cis/trans isomerism.
- It does **not** encode precise 2D or 3D coordinates, which must be generated.
- It is very compact and often molecular databases are distributed as such.

General principle

- Search a $\mathbb{R}^3 \times \mathbb{R}^3 \times \mathbb{R}^m$ space to max. score

translations
rigid rotations

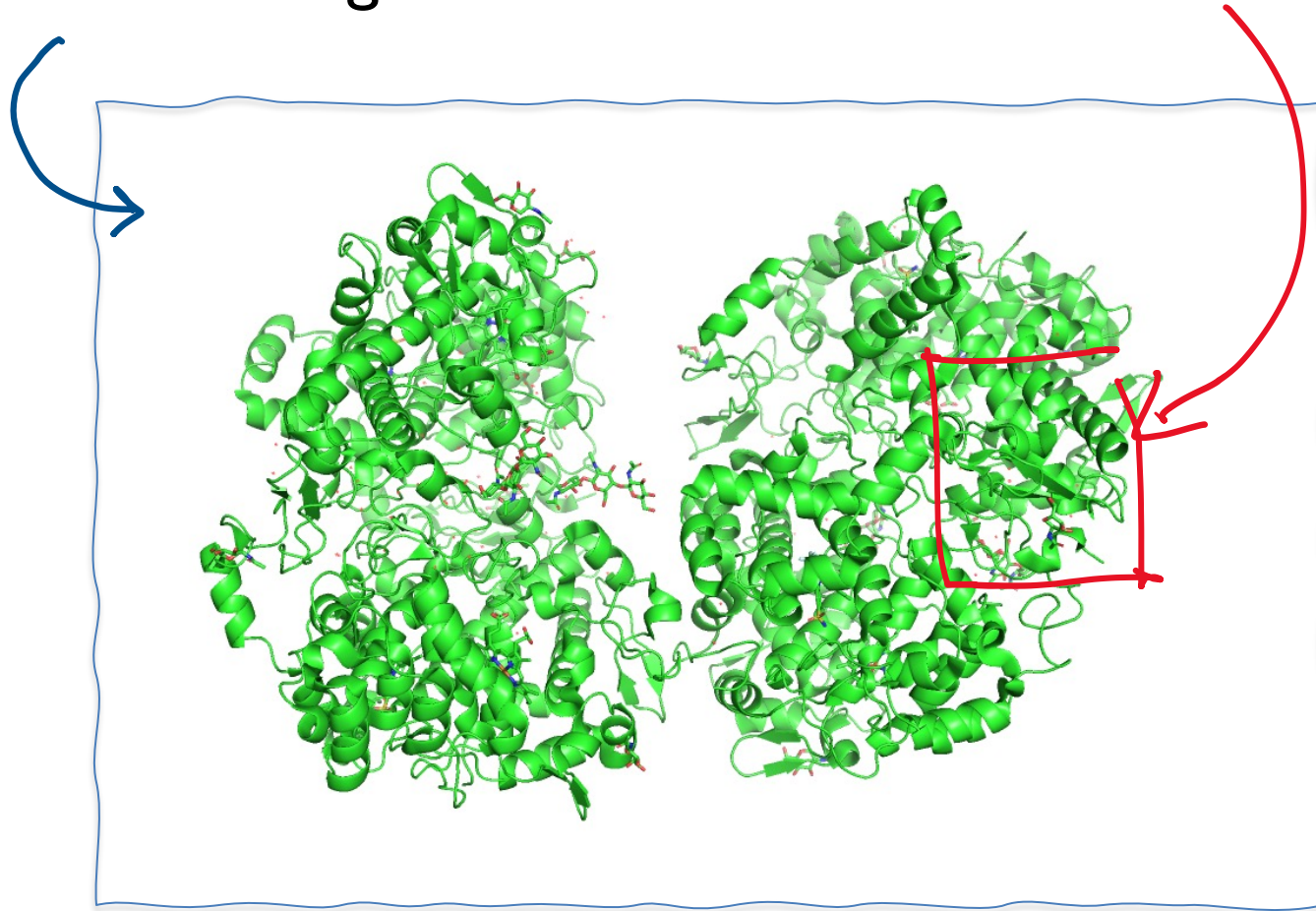
torsions



Docking types

- Blind docking

- Known-site



Pitfalls

- Protonation states
- Stereoisomerism
- Redocking optimism
- Receptor flexibility
- Receptor protonation states
- Thoroughness of the search
- Non-determinism

Advanced topics

- ML-based docking: diffusion models
 - DiffDock [1]
- Combine MD with docking
 - Ensemble docking [2]
- Enumeration of states
 - gypsum_dl [3]



giorginolab / 2024-MolSim-UniPD

<> **Code** Issues Pull requests Actions Projects Wiki Security

Files

main

Go to file

> amber-build-run-with-ligand

▼ docking

Docking_2024.ipynb

> etc

2024-MolSim-UniPD / docking /



tonigi Creato con Colab

Name

..

Docking_2024.ipynb

References

- Corso G, Stärk H, Jing B, Barzilay R, Jaakkola T. DiffDock: Diffusion Steps, Twists, and Turns for Molecular Docking: <http://arxiv.org/abs/2210.01776>
- Bender BJ, Gahbauer S, Lutten A, Lyu J, Webb CM, Stein RM, et al. A practical guide to large-scale docking. Nat Protoc. 2021 Sep 24;1–34.
- Basciu A, Mallocci G, Pietrucci F, Bonvin AMJJ, Vargiu AV. Holo-like and Druggable Protein Conformations from Enhanced Sampling of Binding Pocket Volume and Shape. J Chem Inf Model. 2019 Apr 22;59(4):1515–28.
- McNutt AT, Francoeur P, Aggarwal R, Masuda T, Meli R, Ragoza M, et al. GNINA 1.0: molecular docking with deep learning. Journal of Cheminformatics. 2021 Jun 9;13(1):43.

End