

# Getting Started with SIR



**Download** SIR software from:

<https://www.ba.ic.cnr.it/softwareic/sir/sir-download/>



**Windows:** 64-bit: Windows 10, 11

**File:** sir-xx.yy.zz-win64.exe



**Mac OS X:** macOS 12 (Monterey) and later, Apple Silicon (arm64)

**File:** sir-xx.yy.zz-arm64.dmg



**GNU/Linux:** Ubuntu 26.04 LTS, Ubuntu 24.04 LTS, other Debian-based distributions, Red Hat-based distributions (e.g., RHEL, Fedora)

**File:** sir-xx.yy.zz-codename\_amd64.deb, expo2-xx.yy.zz-Source.tar.gz



**Docker** image. **File:** sir-2.0.6-docker.tar.gz

# Getting Started with Expo



## Installation notes:

<https://www.ba.ic.cnr.it/softwareic/sir/installing-the-program-2/>



**The documentation** is available at the link:

<https://www.ba.ic.cnr.it/softwareic/sir/>



## Tutorials:

<https://www.ba.ic.cnr.it/softwareic/sir/tutorial-and-lectures/>

# Technical Details

- Program written in Fortran and C++



- Program is built using OpenGL and Qt 6 libraries



- Licensed under terms of GNU General Public License



# SIR: A Program for Structure Solution

SIR is designed for the automatic *ab initio* and non *ab initio* **crystal structure solution** of small, medium and macromolecules according to the following scheme:

## *Ab initio* phasing approaches:

- Modern Direct Methods (MDM)
- Standard Direct Methods (SDM) ✓
- Vive la Difference (VLD)
- Patterson techniques

## *Non ab initio* phasing approaches:

- Simulated Annealing ✓
- Molecular Replacement
- SAD/MAD

**Ab initio methods**



**No starting structural model**  
(no coordinates)

**Non-ab initio methods**



**A model is supplied**  
(known fragment,  
homologous structure,  
known molecular  
geometry)

But in both cases, you still need:

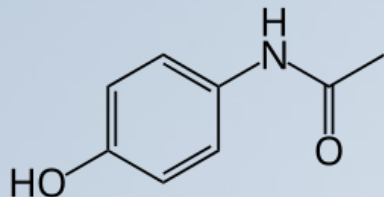
- Experimental diffraction data
- Crystallographic symmetry
- Basic chemical information



# Structure of the SIR Input File

The input consists of a sequence of **comments**, **commands** and **directives**. The commands start with a '%' character and directives must follow the related command. Sir2024 input file can be created using a text editor or by means of the GUI provided by the program.

## Crystal structure solution of paracetamol



Space group:  $P 2_1/c$

Cell:  $a=7.08$   $b=9.37$   $c=11.68$   $\beta=97.47$

Chemical formula:  $C_8H_9NO_2$

Cell Formula Units: 4

Reflection file name: [paracetamol.hkl](#)

Format file: (3i4, 2f8.2)

Reflection type:  $F^2$

Electrons

*paracetamol.sir*

```
!TEST on Paracetamol
%structure paracetamol
%job paracetamol
%data
  cell 7.08 9.37 11.68 90 97.47 90
  space P 21/n
  content (C8H9NO2)4
  reflections paracetamol.hkl
  electrons
%continue
```

# Main SIR Commands

## **%STRUCTURE** *string*

This command is used to specify the project name and to define the names of the output files generated by the program (e.g. *loganin*, *paracetamol\_form2*, *sample01*).

## **%JOB**

This is a brief description of the project (e.g. *my beautiful structure, data provided by Mauro Gemmi, sample no. 3*).

## **%DATA**

Specifies the experimental diffraction data and the basic information required for structure solution.

## **%PHASE**

Phasing routine and Direct Space Refinement routines.

## **%FRAGMENT** *file*

Used to import a structural model (for Simulated Annealing).

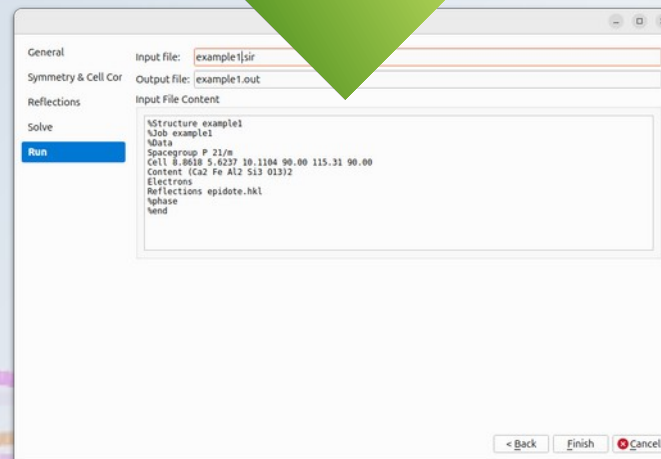
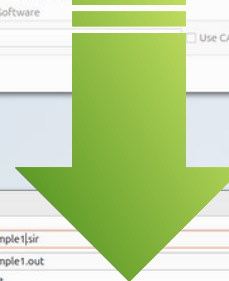
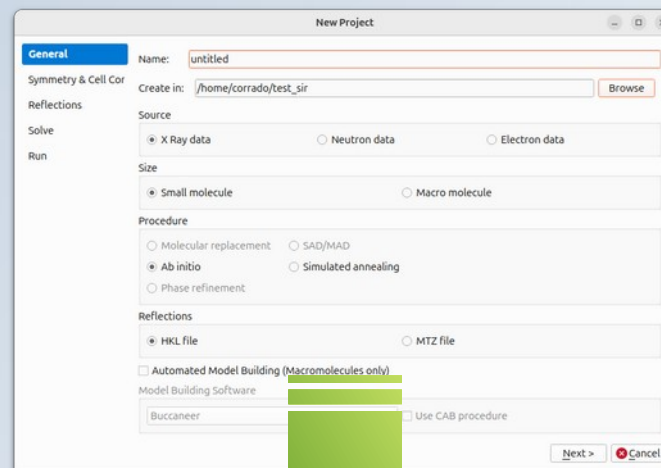
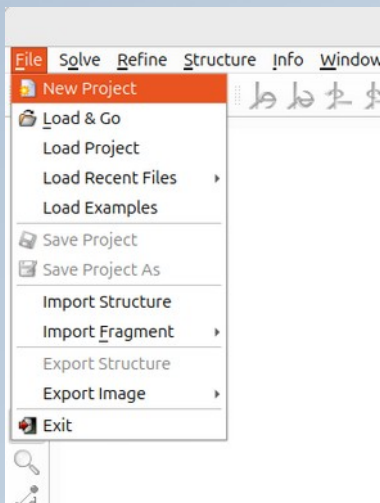
## **%SANNEAL**

Simulated Annealing routine.

## **%END**

End of the input file

# How to Make a SIR Input File with the GUI



# Example 1: Direct-Methods Structure Solution of $\text{Ca}_2\text{FeAl}_2\text{Si}_3\text{O}_{13}$

```
%Structure epidote
```

```
%Job Test on Epidote
```

```
%Data
```

```
Cell      8.8618 5.6237 10.1104 90 115.313 90
```

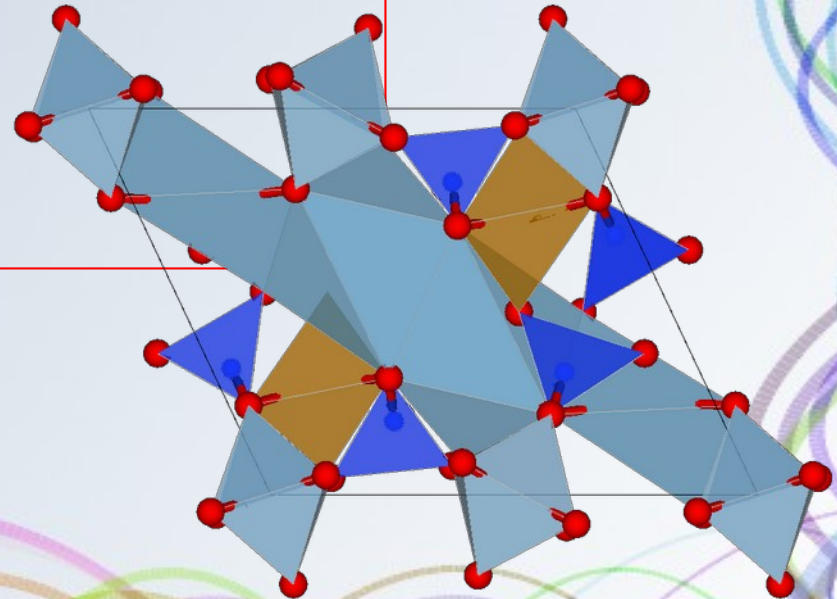
```
Content (Ca2 Fe Al2 Si3 O13)2
```

```
Space P 21/m
```

```
Reflections epidote.hkl
```

```
Electrons
```

```
%continue
```



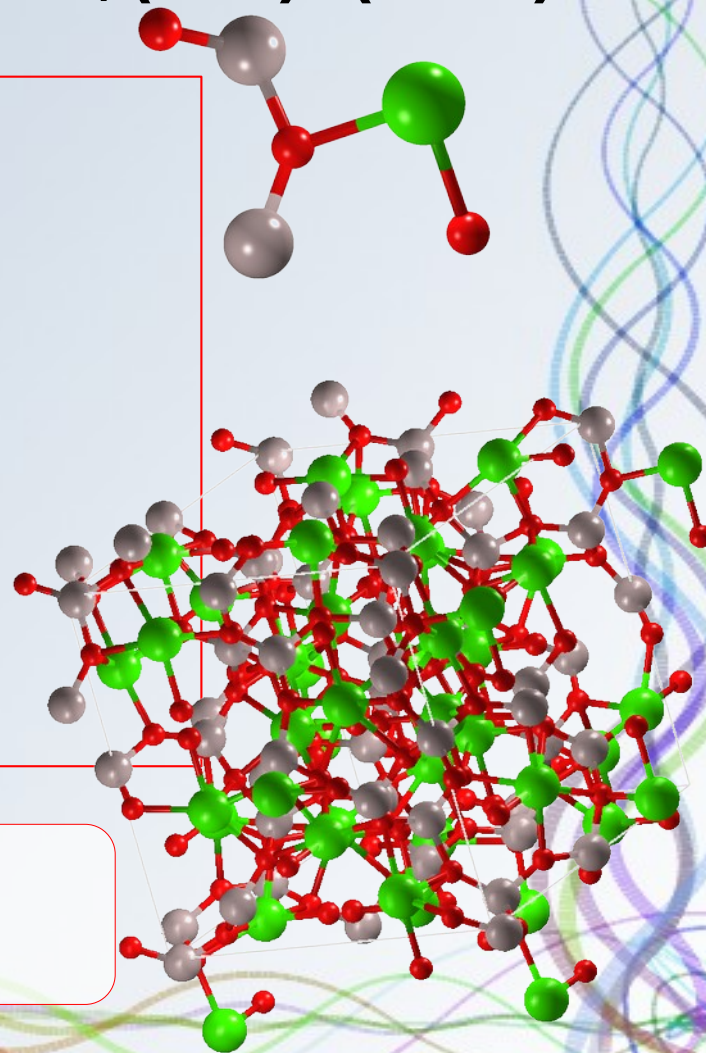


## Example 2: Structure Solution of Mayenite, $(\text{CaO})_{12}(\text{Al}_2\text{O}_3)_7$

```
%structure mayenite
%job Mayenite - Calcium Oxide - Aluminium Oxide
%data
  cell 11.989 11.989 11.989 90.000 90.000 90.000
  space I -4 3 d
  cont [(CaO)12(Al2 O3)7]2
  refl mayenite.hkl
  fobs
  electrons
%continue
```

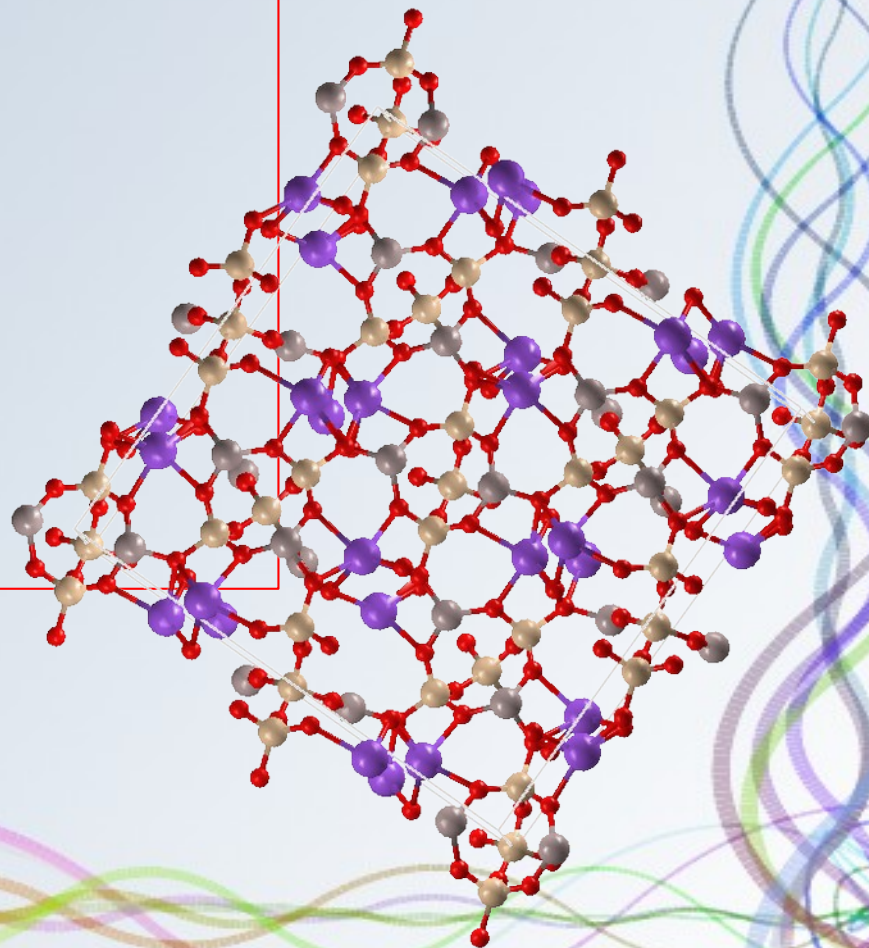
SIR can also be launched from the command line as:

```
sir input_file [output_file] [--nogui][--auto]
```



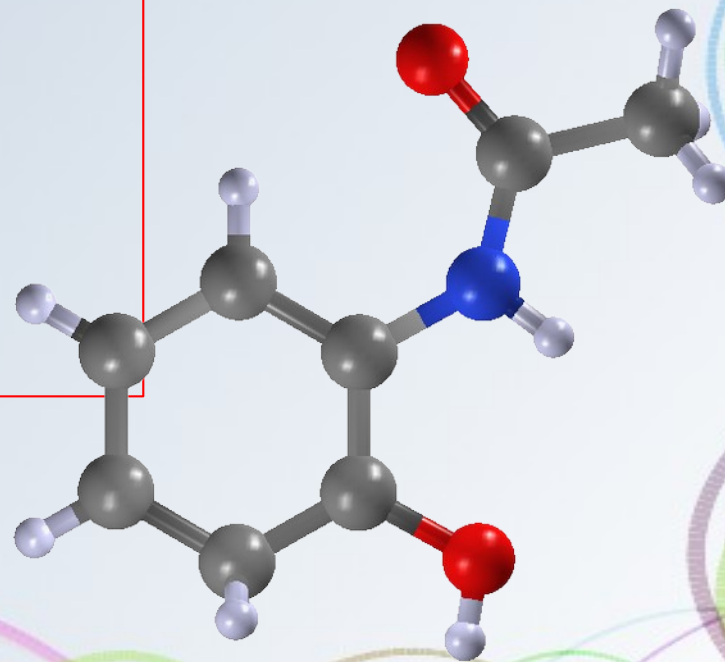
# Example 3: Structure Solution of Natrolite, $\text{Na}_2\text{Al}_2\text{Si}_3\text{O}_{10}\cdot 2\text{H}_2\text{O}$

```
%Structure natro
%Job Test on Natrolite
%Data
  Cell      18.8278 18.667 6.6414 90  90  90
  Content   [Na2 Al2 Si3 O10 (H2O)2]8
  Space F d d 2
  Reflections natrolite.hkl
  Electrons
%continue
```



## Example 4: Structure Solution of Orthacetamol

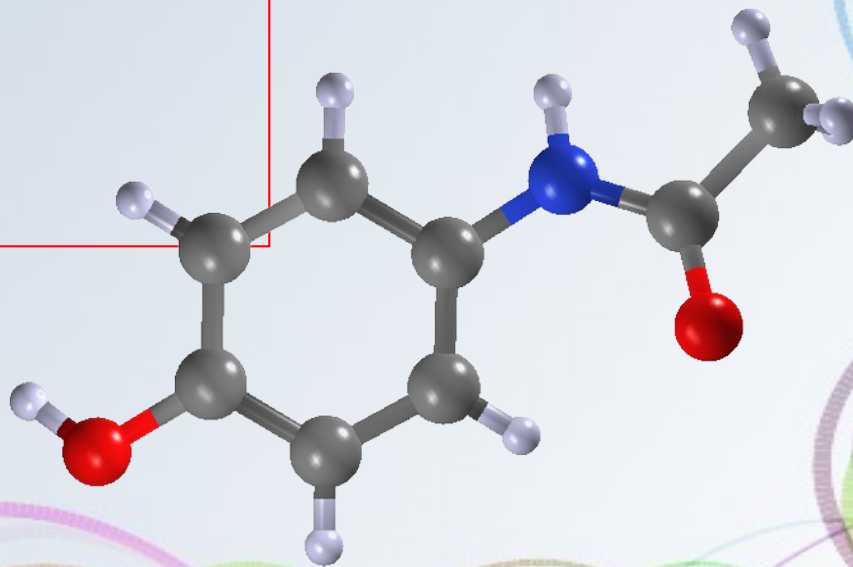
```
%Structure orthacetamol
%Job Test Structure: Orthacetamol
%Data
  Cell    10.3  10.3  13.9  90  90  90
  Content (C8 H9 N O2)8
  Space C 2/c
  Reflections orthacetamol.hkl
  Electrons
  resm 0.9
%continue
```



\*Andrusenko et al., Angew. Chem. Int. Ed. 2019, 58, 10919–10922

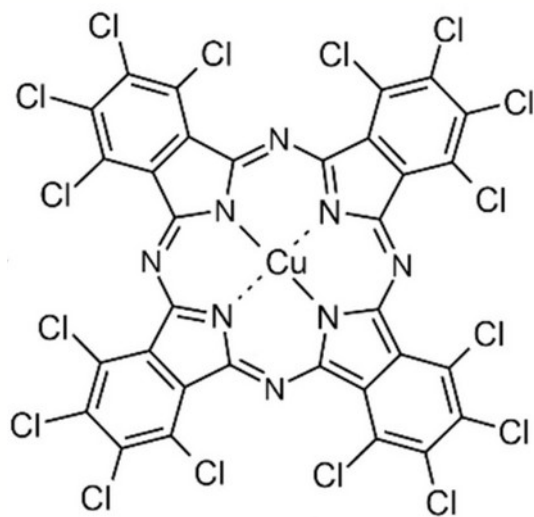
## Example 5: Structure Solution of Paracetamol

```
%structure paracetamol  
%job paracetamol  
%data  
  cell 7.08 9.37 11.68 90 97.47 90  
  space P21/n  
  content (C8H9NO2) 4  
  reflections paracetamol.hkl  
  electrons  
%continue
```





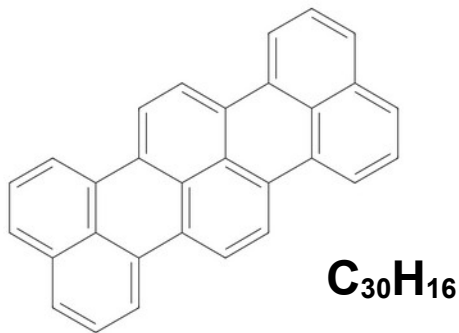
## Example 6: Structure Solution of Copper Perchlorophthalocyanine



**CuPcCl<sub>16</sub>**  
**CuC<sub>32</sub>N<sub>8</sub>Cl<sub>16</sub>**  
**Pigment Green 7**

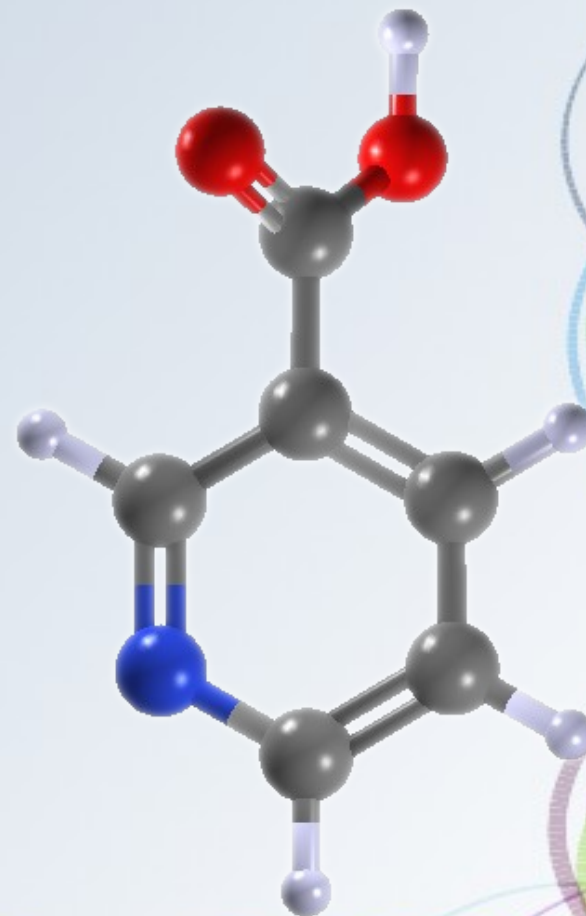
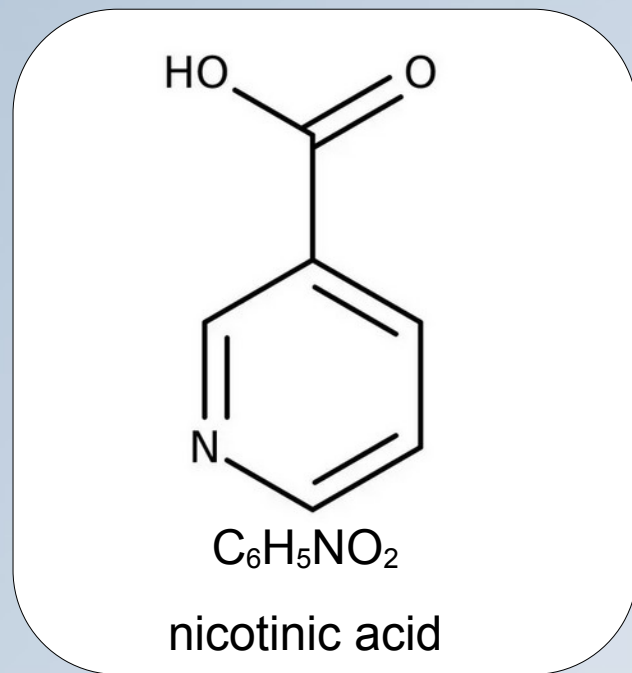
```
%Structure pigmentg7
%job copper perchlorophthalocyanine
%Data
Cell 17.685 25.918 3.8330 90 95.05 90
Content (C32 N8 Cl16 Cu)2
Spacegroup C 2/m
Reflections pigmentg7.hkl
electrons
%Continue
```

## Example 7: Structure Solution of Terrylene



```
%Structure terrylene
%Job Test on Terrylene
%Data
    Cell 11.4 10.4 14.4 90 95.6 90
    Content  C 120 H 64
    Space P 21/a
    Reflections terrylene.hkl
    Electrons
%Continue
```

## Example 8: crystal structure determination of nicotinic acid \*

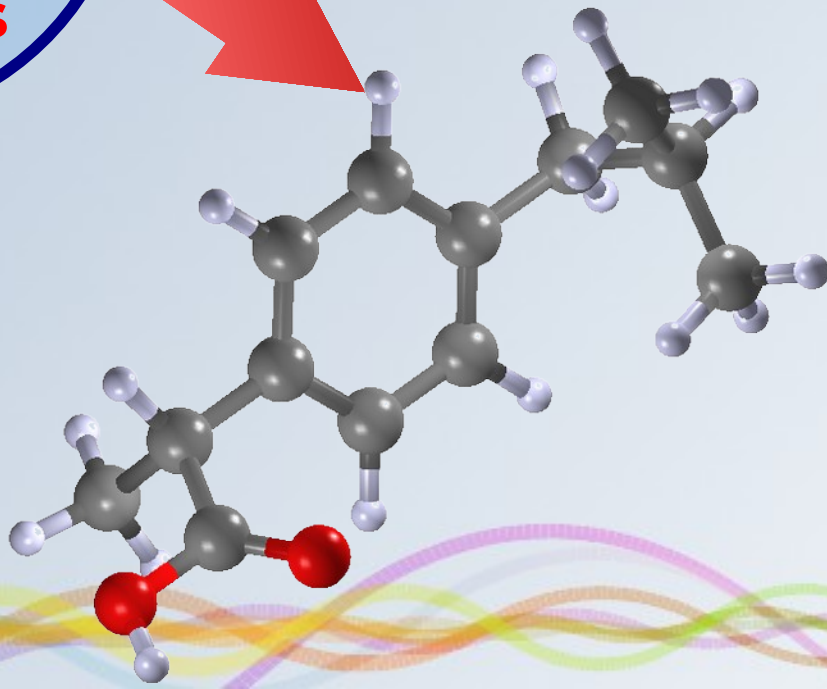


nicotin\_acid.mol

(\*) Acta Cryst. (2016). A72, 236–242

**Check for  
similar  
molecules in  
databases**

**Building starting  
model**





# Crystal Structure Databases\*

*Non-commercial databases are in red*

- **CSD** (Cambridge Structural Database) (organics & organometallics):  
<http://www.ccdc.cam.ac.uk/>
- **ICSD** (Inorganic Crystal Structure Database)  
(inorganics, elements, minerals & intermetallics): <http://icsd.ill.fr/>
- **COD** (Crystallography Open Database) (general database):  
<http://www.crystallography.net/>

**Other databases:** ICDD PDF-4+, American Mineralogist Crystal Structure Database, MINCRYST, Zeolite Structures Database, ...

**File format:** CIF (Crystallographic Information File)

\*Joint special issue: [Acta Cryst. B58, 317-422 \(2002\)](#)

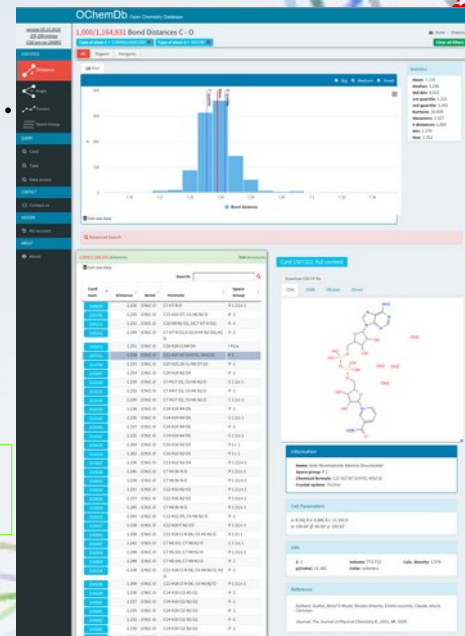
# Free Chemistry Databases

- PubChem: <https://pubchem.ncbi.nlm.nih.gov/>
- NIST Chemistry WebBook: <http://webbook.nist.gov/chemistry/>
- Drugbank: <http://www.drugbank.ca/>

**Other databases:** ZINC, eMolecules, ChEBI, NMRShiftDB, ...

**Chemical file formats:** *sdf*, *mol*, *mol2*, *cml*, *SMILES*, ...

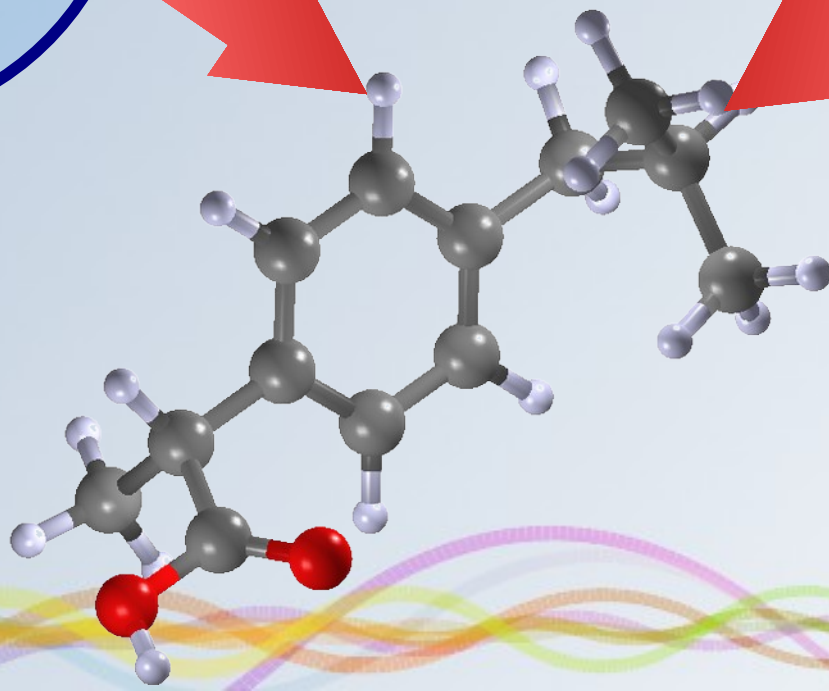
<http://www.ba.ic.cnr.it/ochemdb/>



# Building starting model

**Check for  
similar  
molecules in  
databases**

**Optimize  
Molecular  
geometry by  
computational  
chemistry**



# Geometry optimization

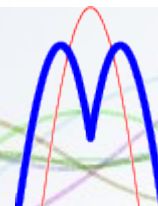
## Three levels of theory

- Molecular-mechanics force fields (**MM**)
- Semi-empirical methods (**SE**)  **MOPAC**
- *Ab initio* methods: Hartree–Fock methods, density functional theory (**DFT**)

Strategy: **MM** → **SE** → **DFT**



**NWCHEM**  
HIGH-PERFORMANCE COMPUTATIONAL  
CHEMISTRY SOFTWARE





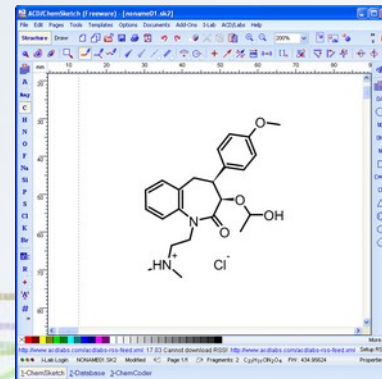
# Molecule editor

## *A molecule editor allows*

- Sketch molecules in 2D or 3D format
- Optimize the geometry by force field method
- Create input file for the quantum-chemistry calculations
- Read output files of the most common computational packages

## *Some free available software*

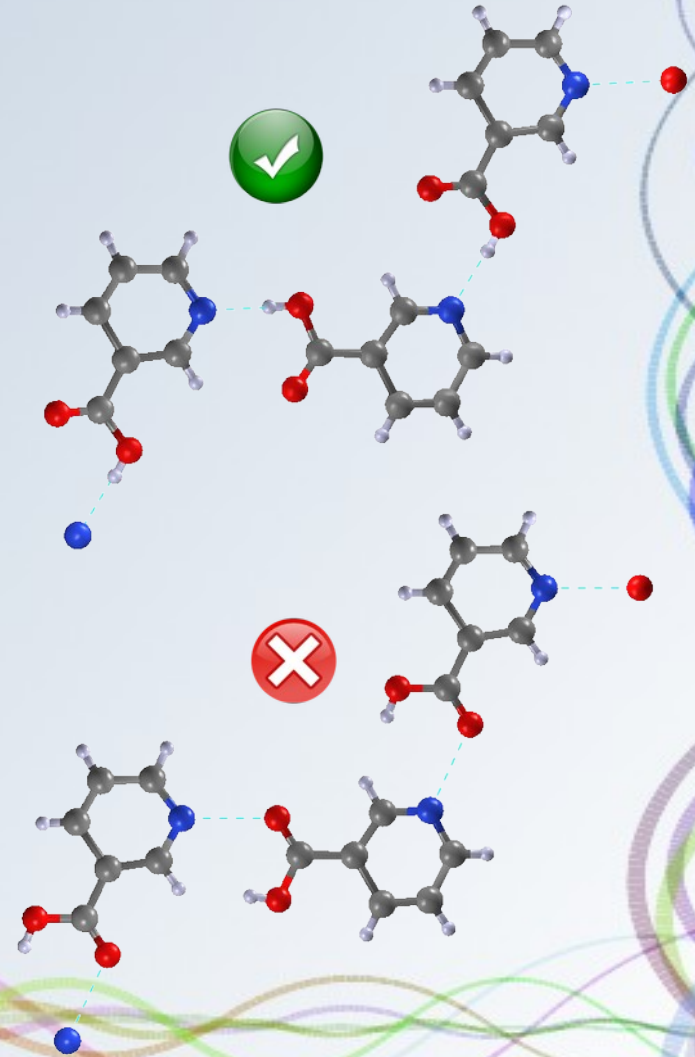
- ChemSketch <https://www.acdlabs.com/resources/free-chemistry-software-apps/chemsketch-freeware/>
- Avogadro [http://avogadro.openmolecules.net/wiki/Main\\_Page](http://avogadro.openmolecules.net/wiki/Main_Page)
- MarvinSketch <http://www.chemaxon.com/products/marvin/>
- Gabedit <http://gabedit.sourceforge.net/>



# Example 8: crystal structure determination of nicotinic acid

Example 8/ nicotin\_acid.sir

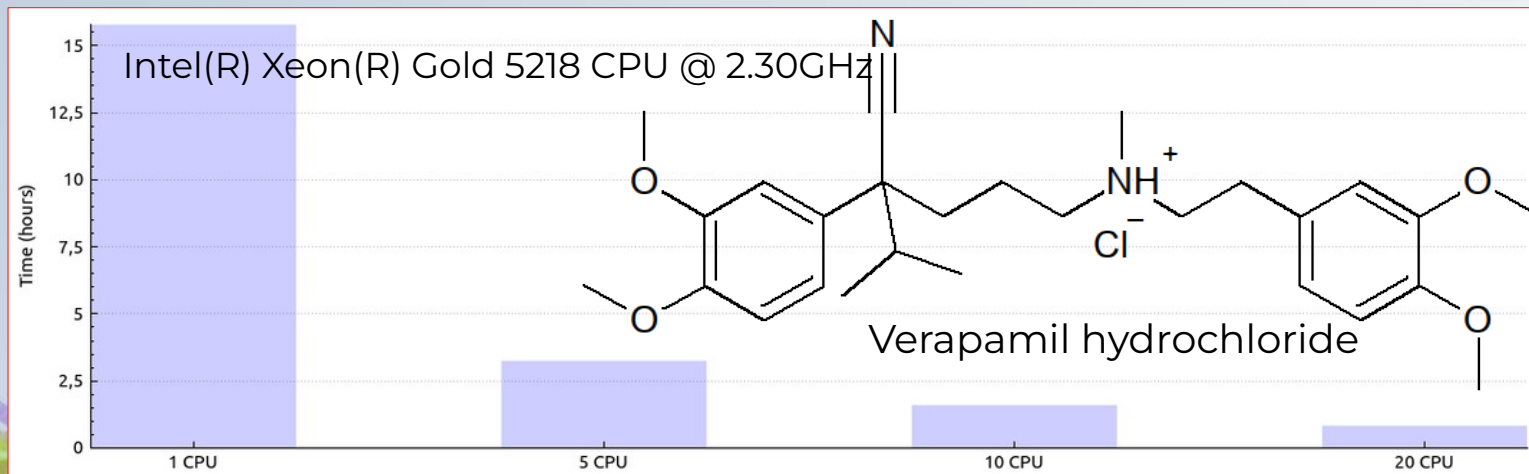
```
%window
%structure nicotin_acid
%job Acta Cryst. (2016). A72, 236–242
%data
cell 7.303 11.693 7.33 90 113.68 90
space P21/c
formula (C6 H5 N O2)4
refl nicotin_acid.hkl
format (3I4,2F8.2)
electrons
!wave 0.02508
%fragment nicotin_acid.mol
%anneal
%end
```



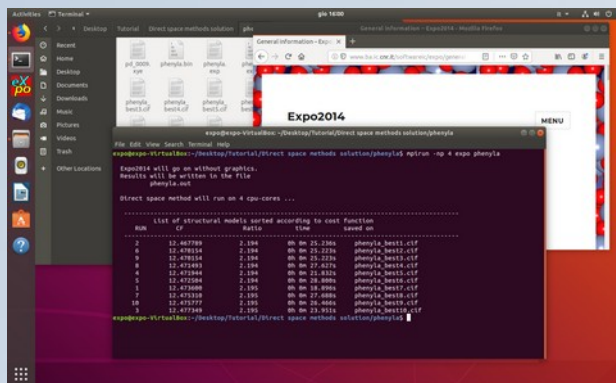
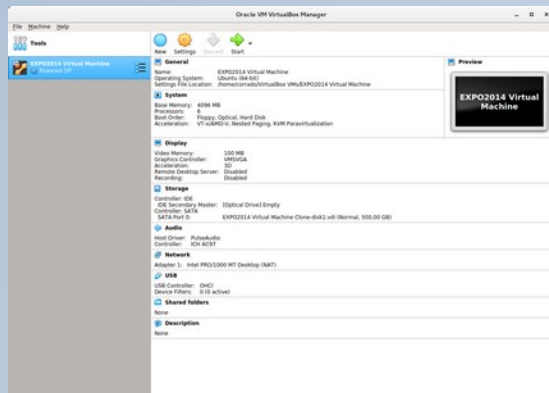
# Running the Parallel Version of SIR

- Computer with multi-core CPUs and Linux environment.
- MPI installed.
- Compiling SIR from source and linking with MPI libraries
- Run SIR by using the launcher **mpirun** with the appropriate options

```
mpirun -np 20 sir2024 input_file.exp
```



# Running parallel version of SIR



## Windows Subsystem for Linux (WSL)

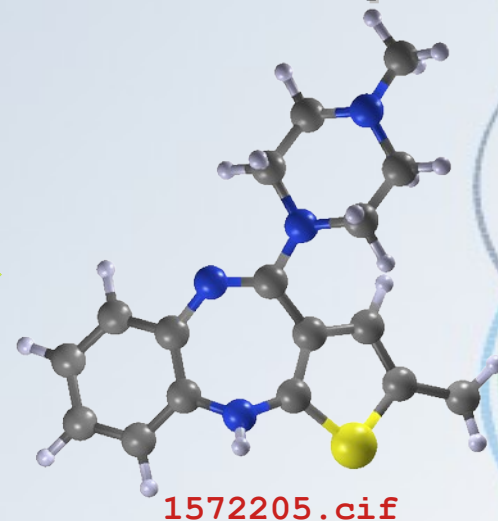
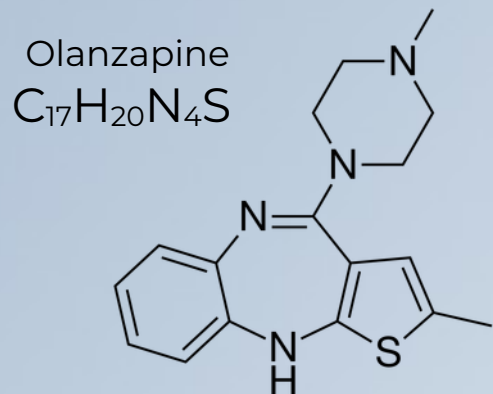
<https://learn.microsoft.com/en-us/windows/wsl/install>



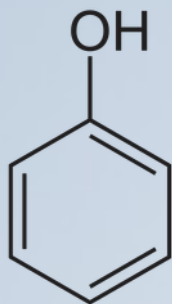
```
docker run --rm \
-e PUID="$(id -u)" -e PGID="$(id -g)" \
-v "$PWD:/work" \
sir:<version> mpirun -np <NUM_TASK> sir <FILE.exp>
```



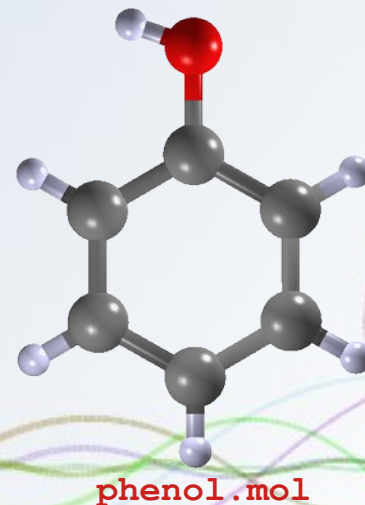
# Example 9: crystal structure determination of olanzapine cocrystal \*



Phenol  
 $C_6H_6O$



PubChem



\* Acta Cryst. (2020). B76, 1036–1044

# Load crystal structures from COD

“File” menu → “Import Fragment” menu → “From COD”

The screenshot displays the slr-2.0.6 software interface. On the left, a 3D ball-and-stick model of a complex organic molecule (olanzapine) is shown. On the right, the 'Import Fragment from COD' dialog box is open, showing search results for the formula C<sub>17</sub>H<sub>20</sub>N<sub>4</sub>S.

**Import Fragment from COD**

Basic Search: Cell, Space Group, Bibliography, Filters

Text:

Formula:

Elements:

NOT these elements:

No. of elements min and max:

COD id:

Downloads: **6 results found** Search

| <input type="checkbox"/>            | COD number | Spacegroup | Formula      | Cell Volume | Cell Parameters                         |
|-------------------------------------|------------|------------|--------------|-------------|-----------------------------------------|
| <input checked="" type="checkbox"/> | 1572205    | P 1 21/c 1 | C17 H20 N4 S | 1664        | 10.708 16.476 10.065 90 110.43 90       |
| <input type="checkbox"/>            | 2018274    | P 1 21/c 1 | C17 H20 N4 S | 1622.7      | 9.913 16.5329 9.9992 90 98.023 90       |
| <input type="checkbox"/>            | 2203128    | P 1 21/c 1 | C17 H20 N4 S | 1600.9      | 10.388 14.839 10.567 90 100.64 90       |
| <input type="checkbox"/>            | 2237783    | P -1       | C17 H20 N4 S | 1640.2      | 9.172 12.224 15.563 86.933 86.99 70.382 |
| <input type="checkbox"/>            | 4507586    | P 1 21/c 1 | C17 H20 N4 S | 1556        | 10.3411 14.521 10.5314 90 100.291 90    |
| <input type="checkbox"/>            | 4507587    | P 1 21/c 1 | C17 H20 N4 S | 1586.9      | 9.8544 16.314 9.9754 90 98.304 90       |

Details

**Chemical Names:** olanzapine

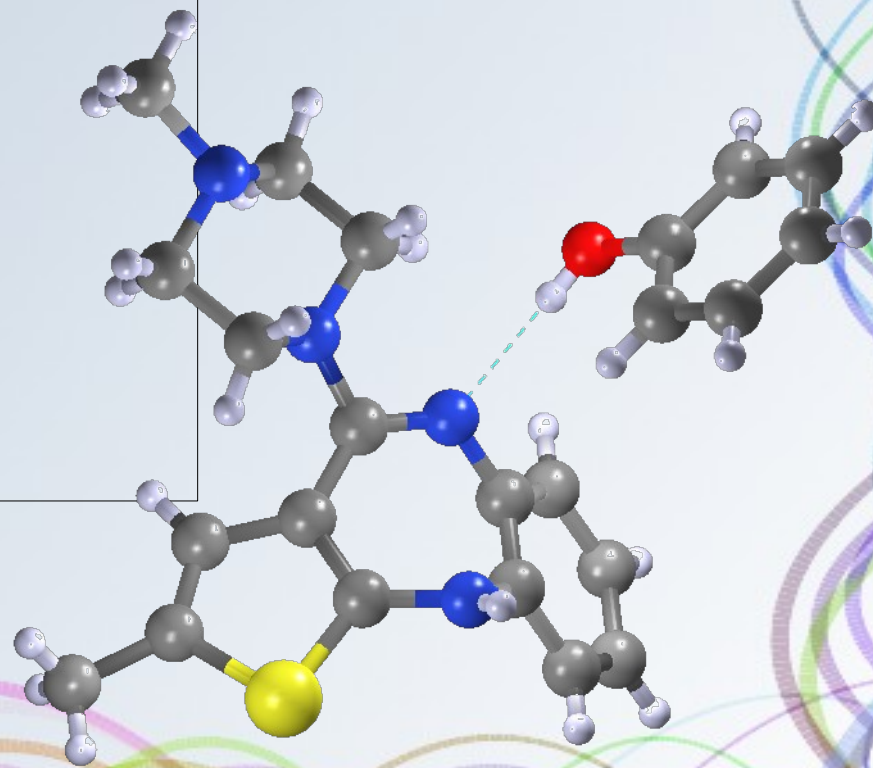
**Bibliography:** Anyfanti, Goulielmina; Husanu, Elena; Andrusenko, Iryna; Marchetti, Danilo; Gemmi, Mauro  
The crystal structure of olanzapine form III.  
IUCr, 2024, 11  
<https://doi.org/10.1107/S2052252524007383>

Import Close

# Example 2: crystal structure determination of olanzapine cocrystal

Example 2/test 1/olanphen.sir

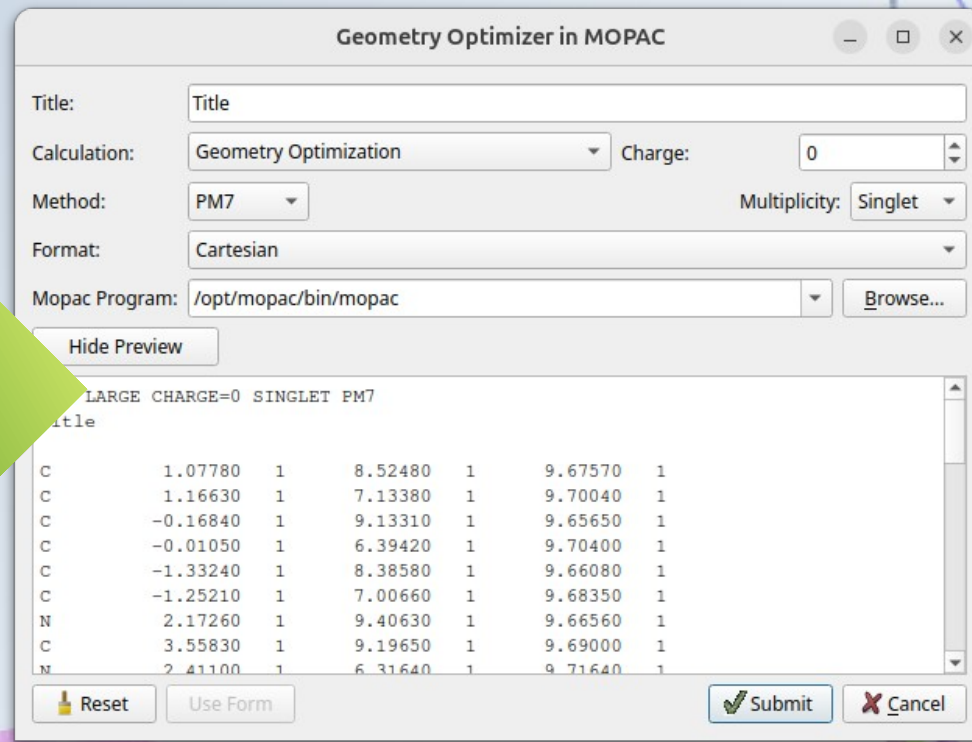
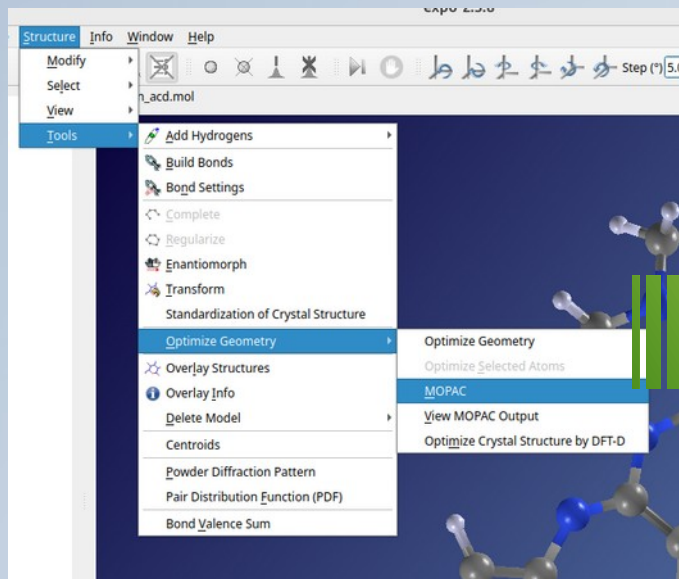
```
%window
%structure olanphen
%job olanzapine+phenol
%data
  cell  9.00 10.6 12.0 92.0 97.0 103.0
  formula ((C17 H20 N4 S) (C6 H5 O H))2
  space P -1
  reflections olanphen.hkl
  format (3i4,2f10.2)
  electrons
!   wave 0.035
!   known olanphen.cif
%fragment 1572205.cif
%fragment phenol.mol
%anneal
%end
```





# Geometry optimization by MOPAC

MOPAC is a semiempirical quantum chemistry software package available FREE. Download link: <http://openmopac.net/downloads.html>



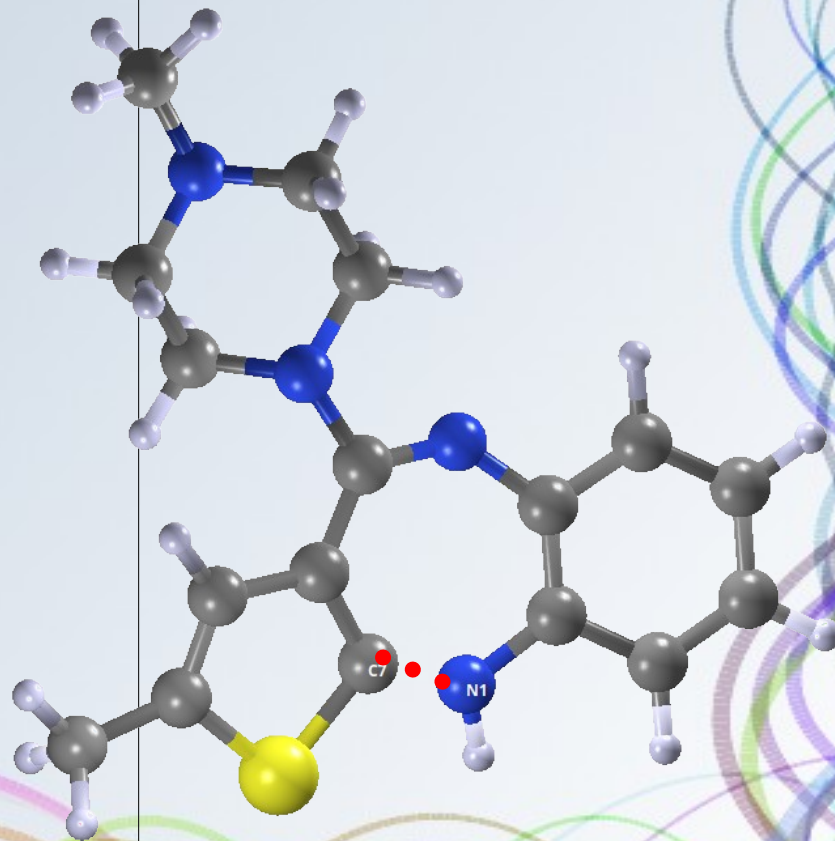
Graphical User Interface for MOPAC



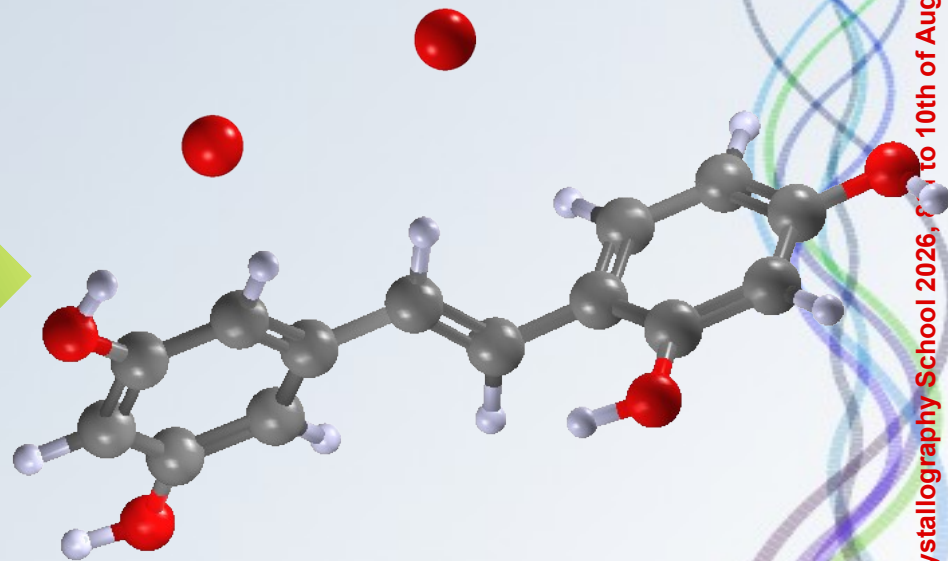
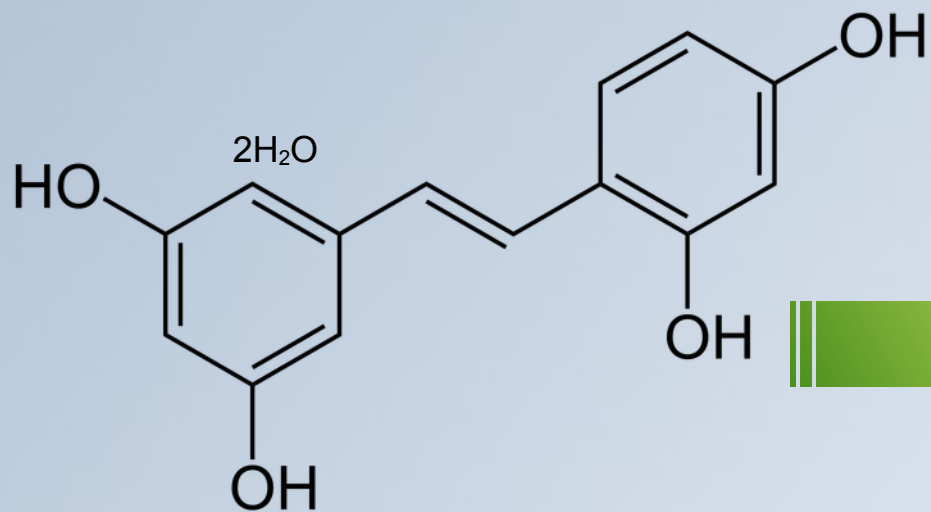
# Example 2: crystal structure determination of olanzapine cocrystal

*Example 2/test 2/olanphen.sir*

```
%window
%structure olanphen
%job olanzapine+phenol
%data
  cell  9.00 10.6 12.0 92.0 97.0 103.0
  formula ((C17 H20 N4 S) (C6 H5 O H))2
  space P -1
  reflections olanphen.hkl
  format (3i4,2f10.2)
  electrons
!   wave 0.035
!   known olanphen.cif
%fragment olanzapine_mopac.mol
cut N1 C7
%fragment phenol.mol
%sanneal
rest N1 C7 1.36 0.01
niter 1000
nrun 20
%end
```



## Example 10: crystal structure determination of oxyresveratrol dihydrate\*



Oxyresveratrol.mol

\*ACS Omega 2024, 9, 41555–41564

# Imposing anti-bumping restraints

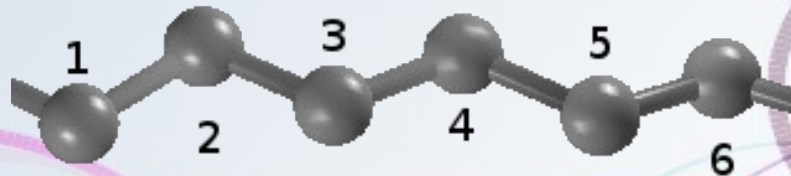
$$CF_{bump} = \sum_{ij}^n w_{ij} (d_{ij}^{min} - d_{ij}^{model})^{2k}$$

$$k = 2$$

$$d_{ij}^{model} < d_{ij}^{min}$$

$$d_{ij}^{min} = \epsilon(R_i^{vdW} + R_j^{vdW})$$

All nonbonded interactions between atoms that are separated by a path of bonds containing 4 rotatable bonds or less are excluded



Only 1-5 interactions are considered

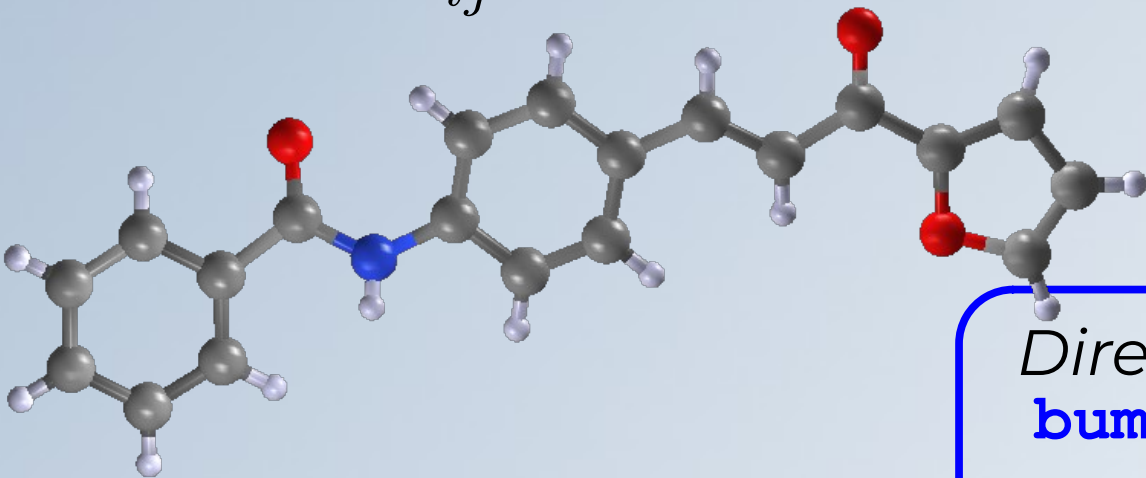
# Imposing anti-bumping restraints

$$CF_{bump} = \sum_{ij}^n w_{ij} (d_{ij}^{min} - d_{ij}^{model})^{2k}$$

$$k = 2$$

$$d_{ij}^{model} < d_{ij}^{min}$$

$$d_{ij}^{min} \equiv \epsilon(R_i^{vdW} \mp R_j^{vdW})$$



```
%sannel  
bscale 0.8  
bump
```

Directive:

**bump**

or

**bump atoms1 atoms2 [dist]**

**Warning: time-consuming procedure, use only  
if the diffraction data are not of sufficient quality**



# Example 10: crystal structure determination of oxyresveratrol dihydrate\*

Example 10/Dihydrate\_Oxyresveratrol.sir

```
%window
%structure Dihydrate_Oxyresveratrol
%job Dihydrate Oxyresveratrol
%data
  cell 8.872 8.112 9.292 90 90.929 90
  space Pc
  formula (C14 H12 O4 (H2O)2)4
  refl Dihydrate_Oxyresveratrol.hkl
  format (3i4,2f10.2)
  electrons
  !known Dihydrate_Oxyresveratrol.cif
  !wave 0.0335
%fragment Oxyresveratrol.mol
%fragment atoms O2
!deletehydro
%sanneal
intdof C3 C4 0
bump
%end
```

