NCiweb
NCiplot web interface

**NCIweb**

**We will analyze interactions in biosystems using nciweb**

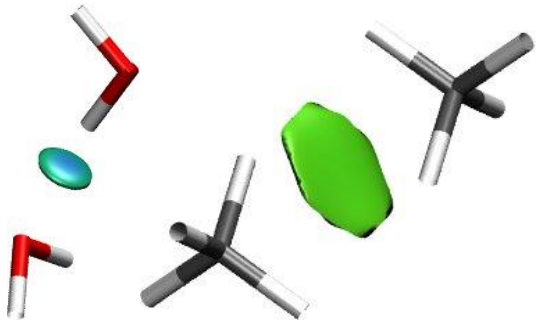
https://nciweb.dsi.upmc.fr/index.php

**http://www.lct.jussieu.fr/pagesperso/contrera/examples/xyz-files**

**Exercise 1. Looking at small molecules**

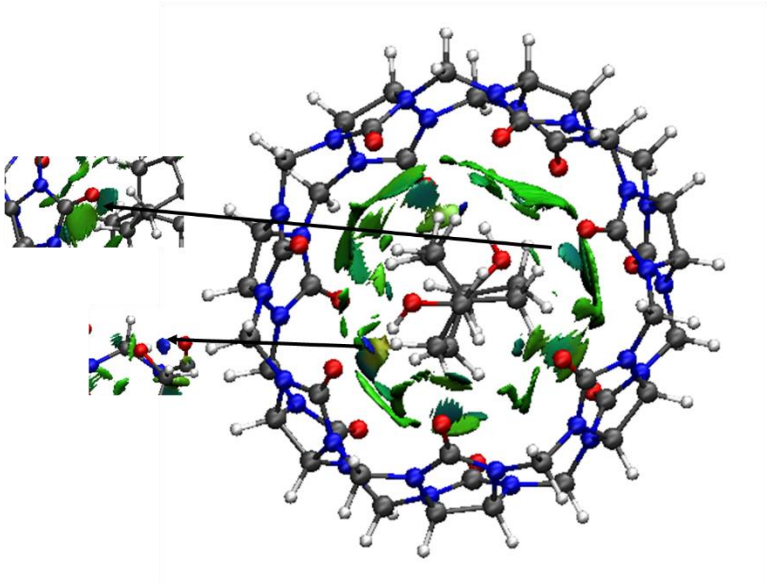
S22 is a typical database of non-covalent interactions. You can download the xyz files (geometry) of this database and look at some of the examples of the s22 set (e.g. Water dimer, Formic acid dimer, Benzene Dimer, Adenyn-Thymine - AT) with intramolecular (all) interactions.

Try to identify localized interactions (e.g. hydrogen bonds) and delocalized interactions (e.g. π stacking)



**Exercise 2. Host-guest interactions**

Host-guest and protein-ligand binding depend upon the same net sum of favourable and unfavourable non-covalent interactions and are governed by the same laws of statistical mechanics. Thus, they are great examples for understanding non-covalent interactions in more complex biomolecular systems. For a long time, there have been outstanding questions as to their magnitude: are host-guest systems capable of attaining binding affinities as strong as in protein-ligand complexes? The seven-unit cucurbitural host (CB[7]) binds cationic adamantyl, ferrocene derivatives } and bicyclo[2,2,2]octane derivatives with binding constants of $10^{9}$ to $10^{13}$ $M^{-1}$.



NCI constitutes a great tool to asses such complementarity and the extent to which weak interactions stabilize the complex.

The position of the guest is further ensured by the two hydroxyl anchorages. The lateral chains establish strong hydrogen bonds with each of the two CB7 portals. Download the bcb-cb7 file. Can you see these interactions?

**Exercise 3. Biomolecules**
**In this case we will work with pdb files from X-Ray structures, so hydrogen atoms need to be added !**

### a) BIOTIN BINDING TO STREPTAVIDIN

The binding of streptavidin and biotin (vitamine H) is one of the strongest non-covalent interactions in Nature ($K=10^{13}$ $M^{-1}$) and a paradigm for protein-ligand interactions.

**Analyze pdb 1STP. The ligand option will enable you to see the interactions leading to such high affinity. What kind of interactions are them?**

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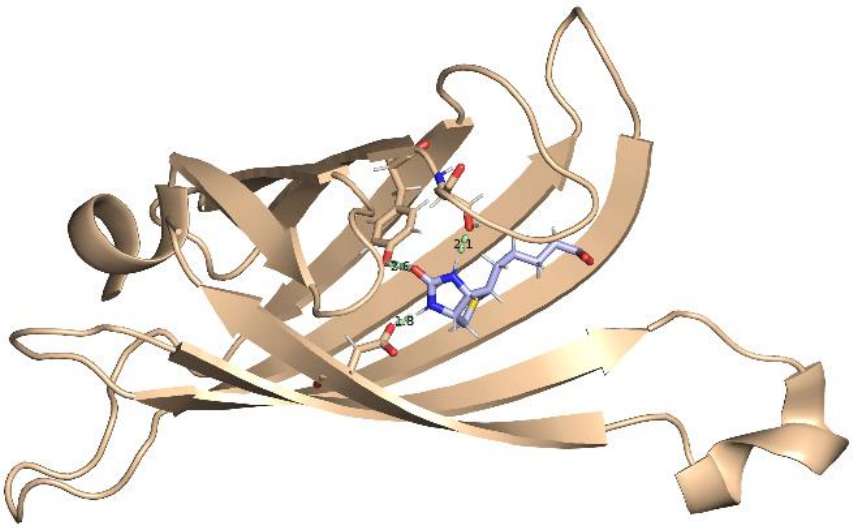

**How many hydrogen bonds do you find? Only some of them have been highlighted from the geometry in the picture…try to find all of them!**

## a) RIBONUCLEASE INHIBITOR COMPLEXED WITH RIBONUCLEASE A

Leucine-rich repeats are structural motifs largely used in molecular recognition processes as diverse as signal transduction, cell adhesion, cell development, DNA repair and RNA processing. This is the case ribonuclease inhibitor, a protein built entirely of leucine-rich repeats.

**Use pdb 1DFJ to analyse the intermolecular interactions between ribonuclease inhibitor and ribonuclease A.** Show that the symmetric, solvent-exposed parallel beta-sheets in the inhibitor (in brown) are responsible for the tight interaction.