Prática de Docking

Introdução a modelagem, docking e dinâmica molecular (Foco em Doenças Negligenciadas)

Prepare o Ligante

- Abra sua estrutura com ligante (4CYQ) no Pymol
- Selecione seu ligante de interesse
- Exporte a molécula

Encontre o centro da caixa

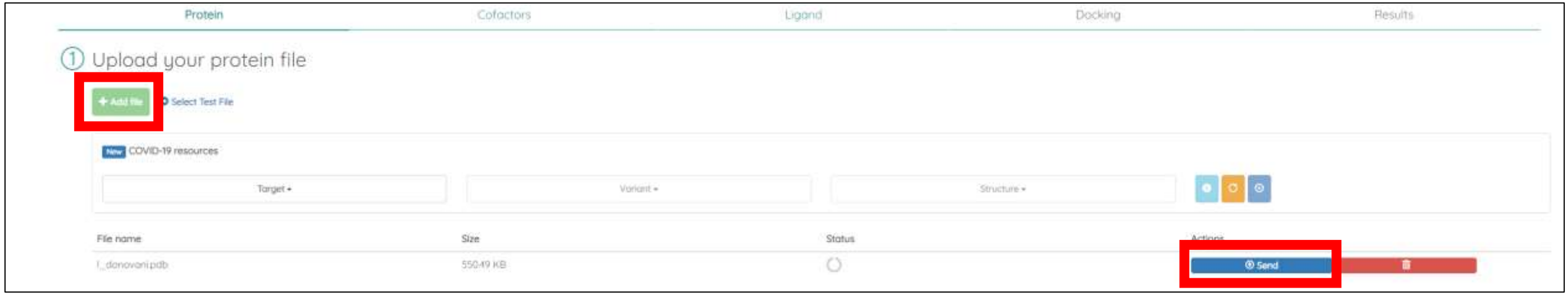
. Abra o PDB do ligante no bloco de notas
. Encontre as coordenadas XYZ de alguma das moléculas
. Guarde essa informação

Prepare a Proteína

- Ainda com a estrutura anterior aberta, abra o PDB do seu modelo
- Alinhe seu modelo à estrutura de referência
- Exporte a proteína

Selecione o Arquivo da sua Proteína

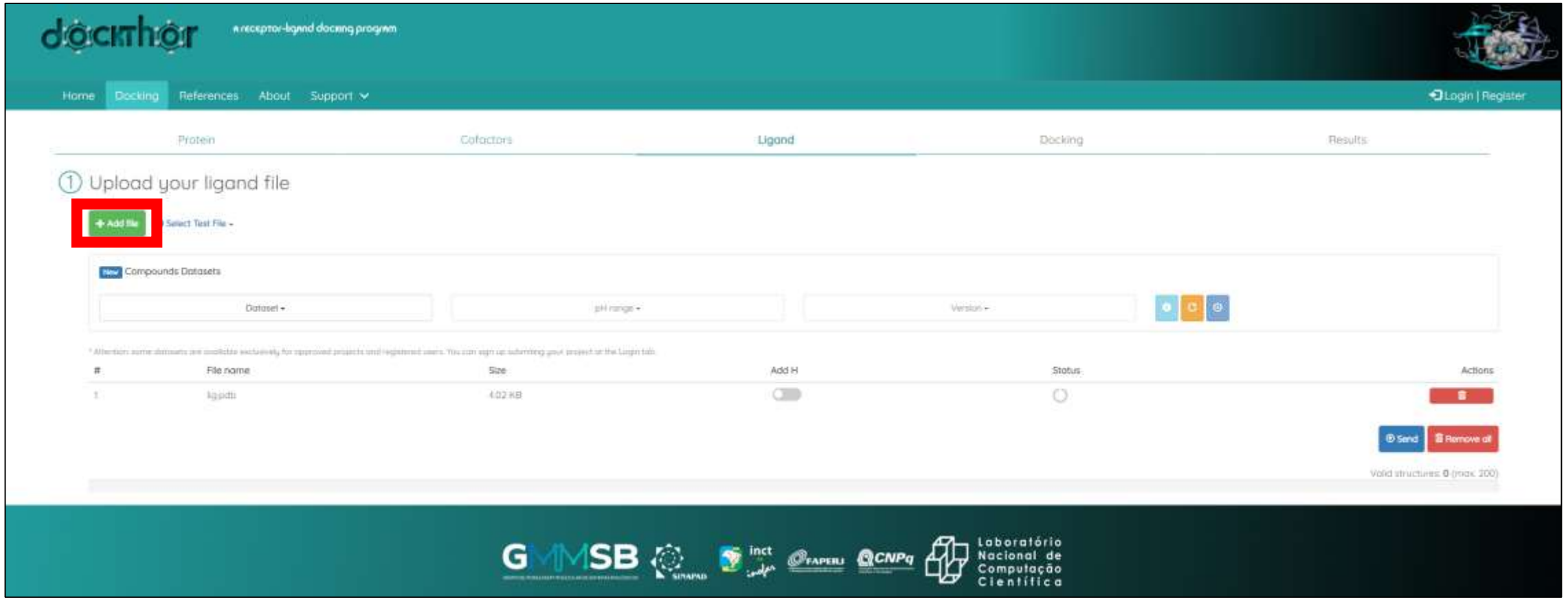
Na página https://dockthor.lncc.br/v2/index.php#



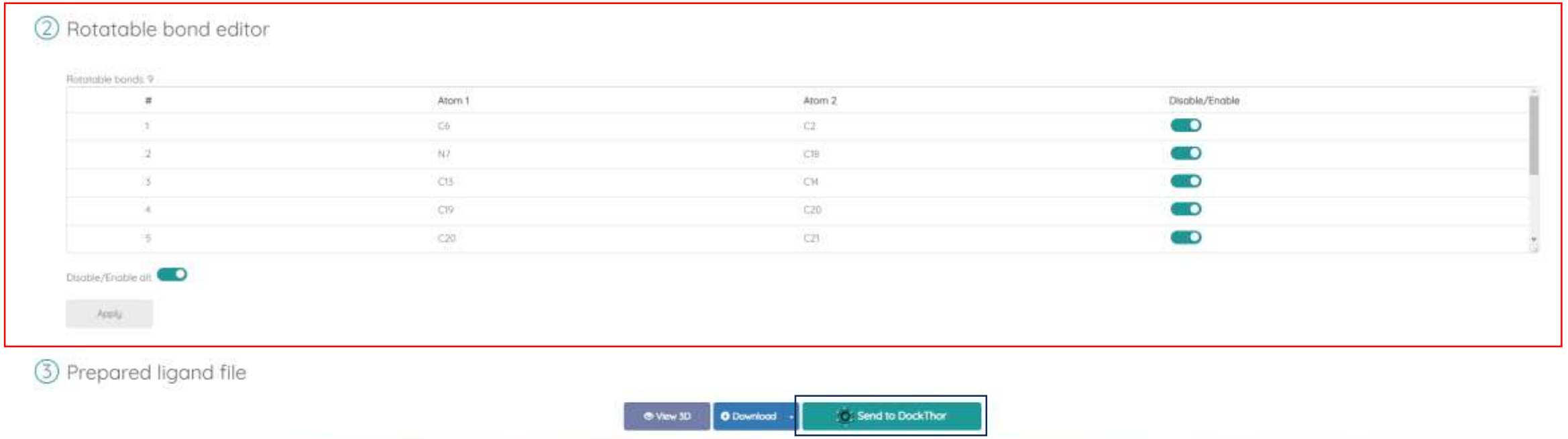
Protone e envie a Estrutura

Se Necessário, Adicione Cofatores

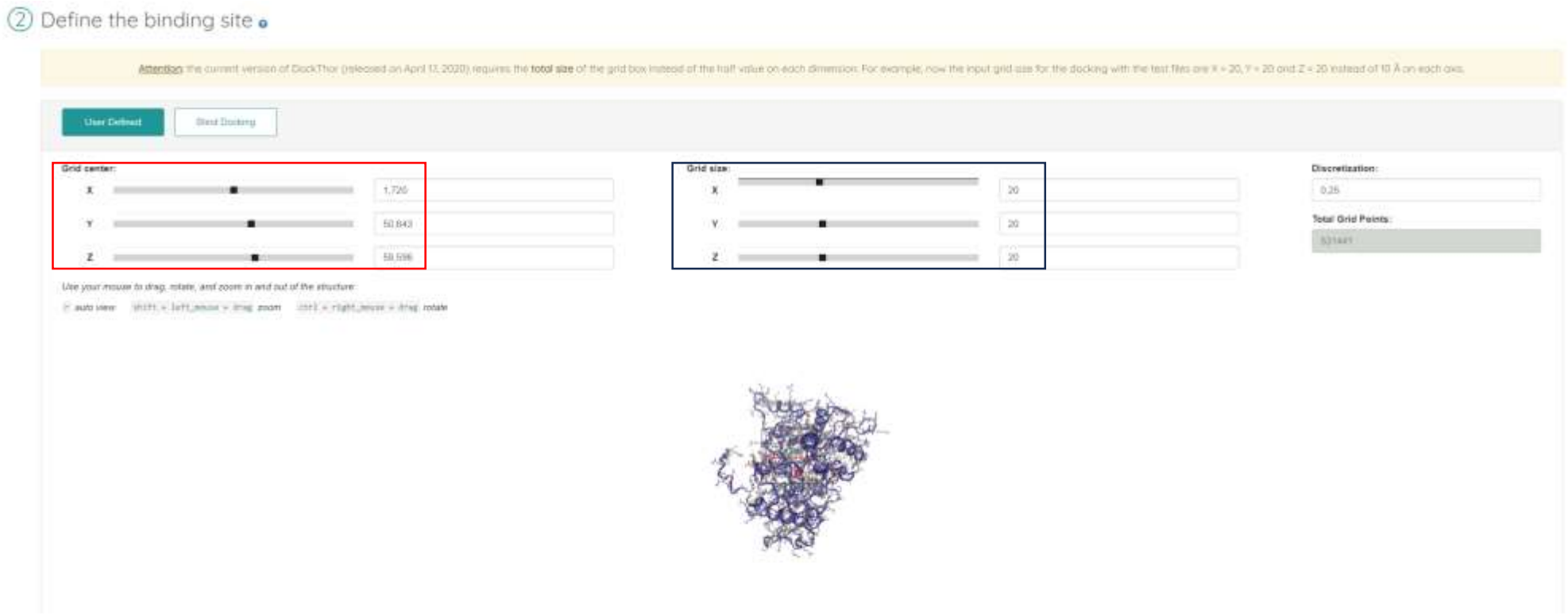
Selecione Seu Ligante



Defina Quais Ligações Devem Ser Consideradas Rotáveis

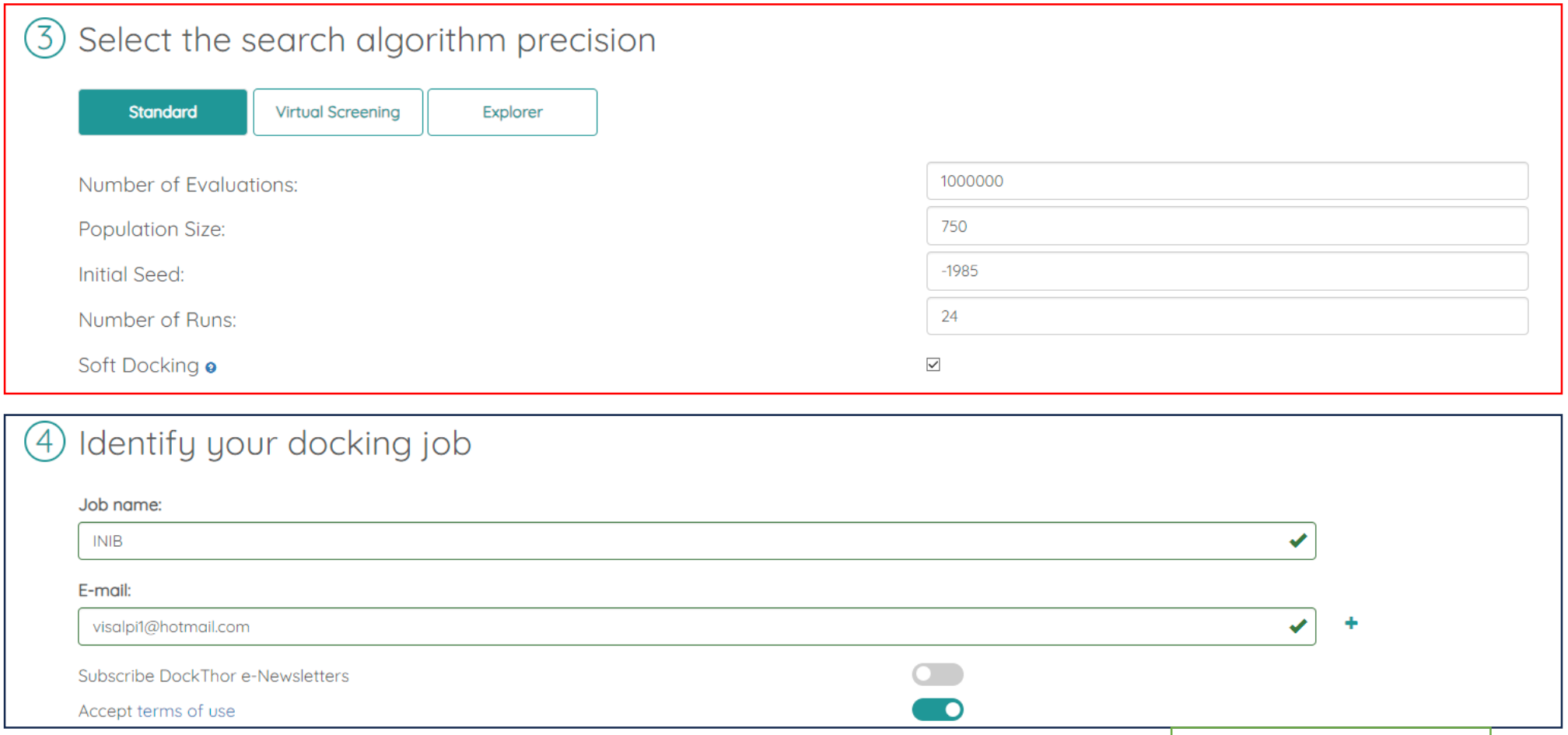


Defina As Coordenadas XYZ E Dimensões Da Caixa



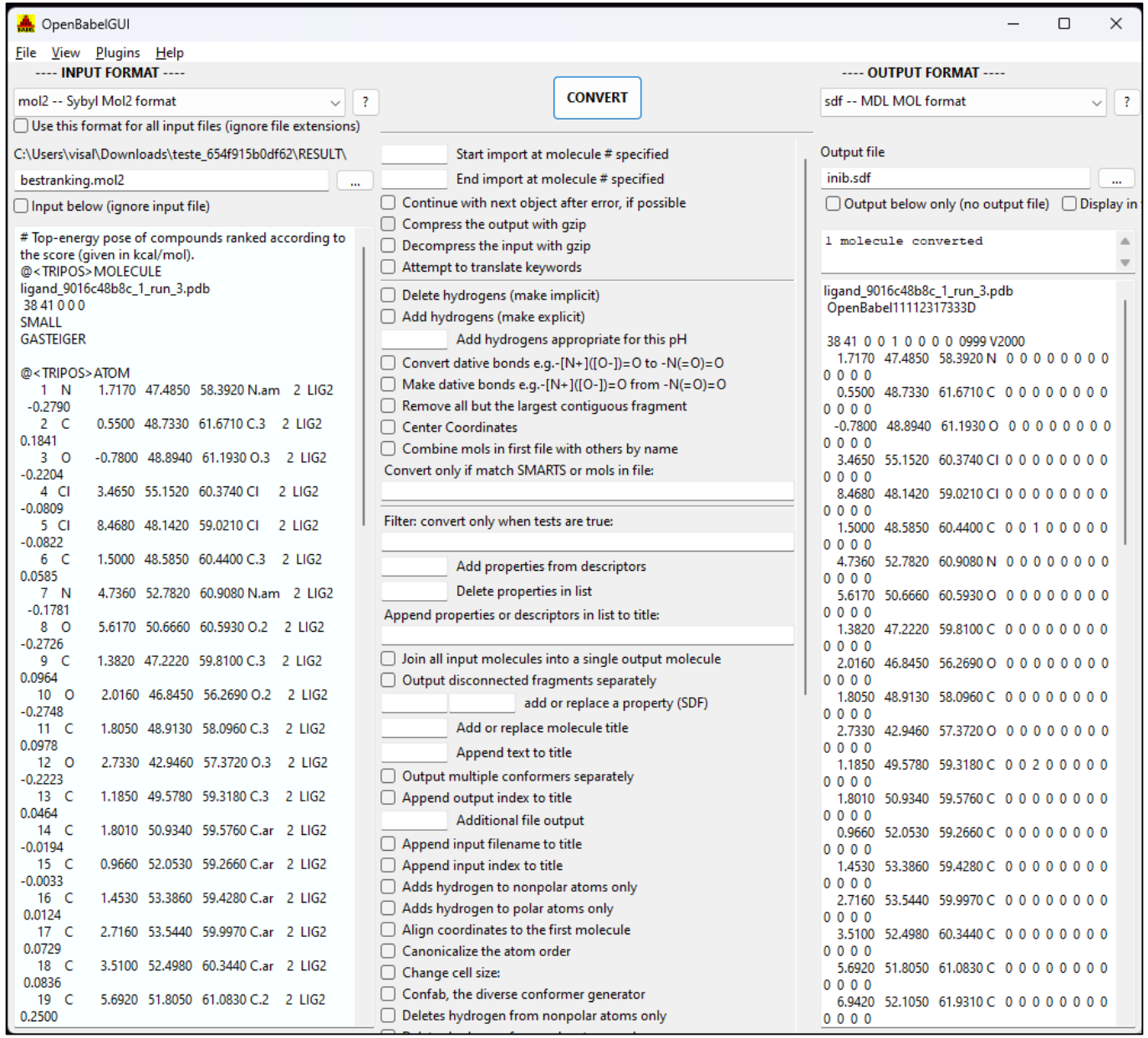
X = 1.720
Y = 50.643
Z = 59.596

Selecione Os Parâmetros De Docking E Coloque Identificadores



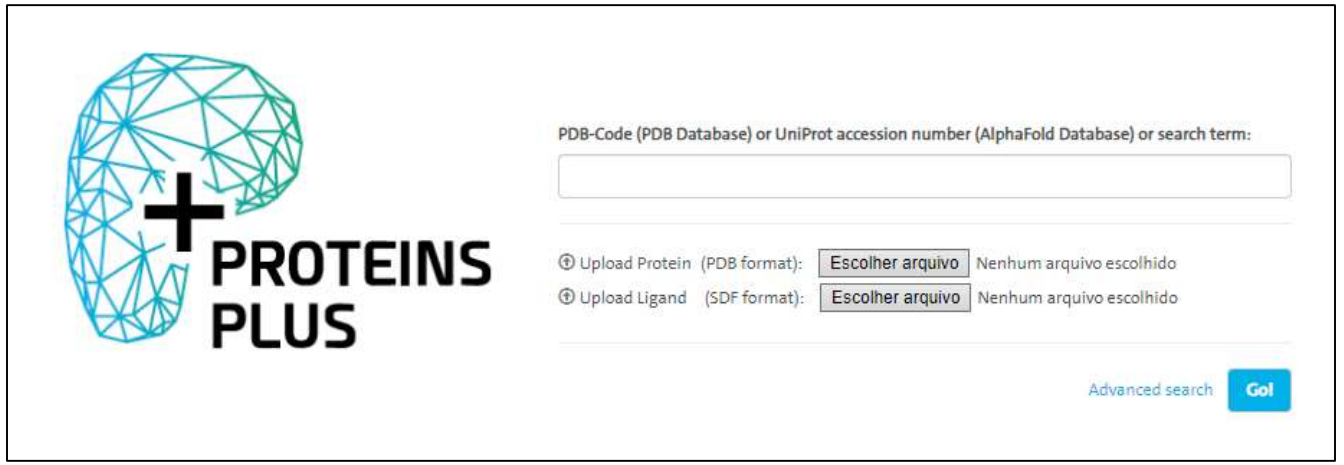
Parâmetros de Análise e download

Observe os Resultados

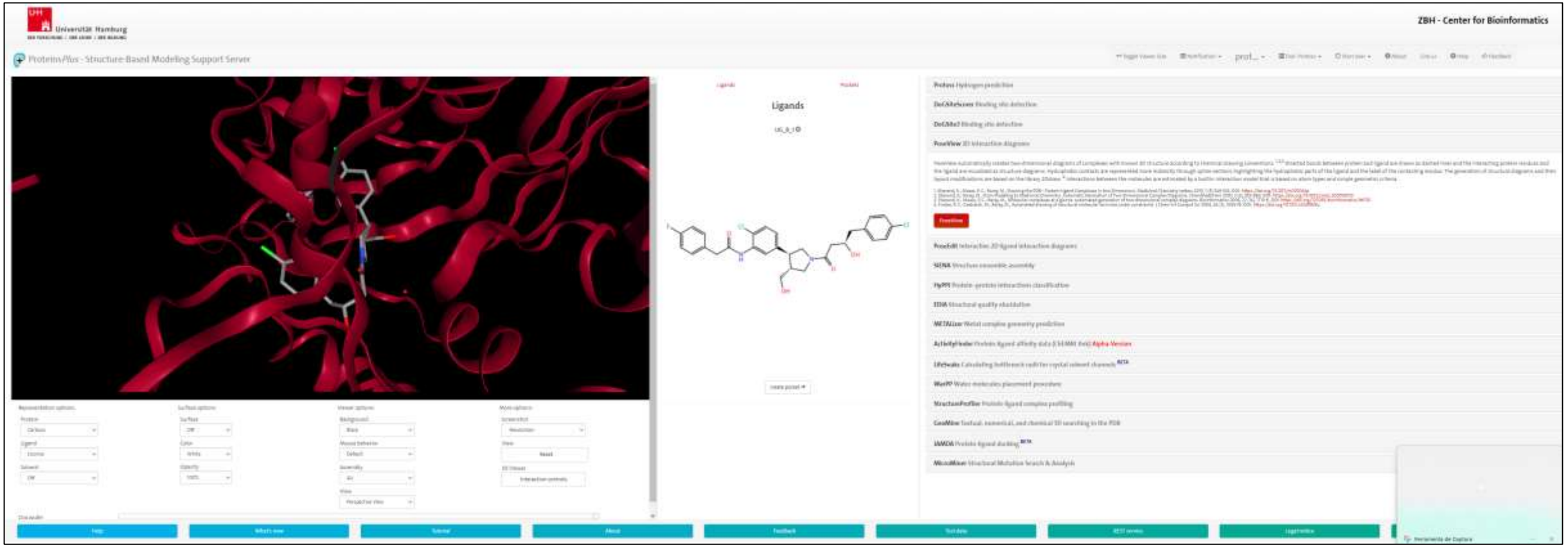

OpenBabelGUI
File View Plugins Help
---- INPUT FORMAT ----
mol2 -- Sybyl Mol2 format
Use this format for all input files (ignore file extensions)
C:\Users\visal\Downloads\teste_654f915b0df62\RESULT\
bestranking.mol2
Input below (ignore input file)
Top-energy pose of compounds ranked according to the score (given in kcal/mol).
@<TRIPOS>MOLECULE
ligand_9016c48b8c_1_run_3.pdb
38 41 0 0 0
SMALL
GASTEIGER
@<TRIPOS>ATOM
1 N 1.7170 47.4850 58.3920 N.am 2 LIG2 -0.2790
2 C 0.5500 48.7330 61.6710 C.3 2 LIG2 0.1841
3 O -0.7800 48.8940 61.1930 O.3 2 LIG2 -0.2204
4 Cl 3.4650 55.1520 60.3740 Cl 2 LIG2 -0.0809
5 Cl 8.4680 48.1420 59.0210 Cl 2 LIG2 -0.0822
6 C 1.5000 48.5850 60.4400 C.3 2 LIG2 0.0585
7 N 4.7360 52.7820 60.9080 N.am 2 LIG2 -0.1781
8 O 5.6170 50.6660 60.5930 O.2 2 LIG2 -0.2726
9 C 1.3820 47.2220 59.8100 C.3 2 LIG2 0.0964
10 O 2.0160 46.8450 56.2690 O.2 2 LIG2 -0.2748
11 C 1.8050 48.9130 58.0960 C.3 2 LIG2 0.0978
12 O 2.7330 42.9460 57.3720 O.3 2 LIG2 -0.2223
13 C 1.1850 49.5780 59.3180 C.3 2 LIG2 0.0464
14 C 1.8010 50.9340 59.5760 C.ar 2 LIG2 -0.0194
15 C 0.9660 52.0530 59.2660 C.ar 2 LIG2 -0.0033
16 C 1.4530 53.3860 59.4280 C.ar 2 LIG2 0.0124
17 C 2.7160 53.5440 59.9970 C.ar 2 LIG2 0.0729
18 C 3.5100 52.4980 60.3440 C.ar 2 LIG2 0.0836
19 C 5.6920 51.8050 61.0830 C.2 2 LIG2 0.2500
CONVERT
Start import at molecule # specified
End import at molecule # specified
Continue with next object after error, if possible
Compress the output with gzip
Decompress the input with gzip
Attempt to translate keywords
Delete hydrogens (make implicit)
Add hydrogens (make explicit)
Add hydrogens appropriate for this pH
Convert dative bonds e.g.-[N+]([O-])=O to -N(=O)=O
Make dative bonds e.g.-[N+]([O-])=O from -N(=O)=O
Remove all but the largest contiguous fragment
Center Coordinates
Combine mols in first file with others by name
Convert only if match SMARTS or mols in file:
Filter: convert only when tests are true:
Add properties from descriptors
Delete properties in list
Append properties or descriptors in list to title:
Join all input molecules into a single output molecule
Output disconnected fragments separately
add or replace a property (SDF)
Add or replace molecule title
Append text to title
Output multiple conformers separately
Append output index to title
Additional file output
Append input filename to title
Append input index to title
Adds hydrogen to nonpolar atoms only
Adds hydrogen to polar atoms only
Align coordinates to the first molecule
Canonicalize the atom order
Change cell size:
Confab, the diverse conformer generator
Deletes hydrogen from nonpolar atoms only
---- OUTPUT FORMAT ----
sdf -- MDL MOL format
Output file
inib.sdf
Output below only (no output file)
Display in
1 molecule converted
ligand_9016c48b8c_1_run_3.pdb
OpenBabel11112317333D
38 41 0 0 1 0 0 0 0 0999 V2000
1.7170 47.4850 58.3920 N 0 0 0 0 0 0 0 0 0 0 0 0
0.5500 48.7330 61.6710 C 0 0 0 0 0 0 0 0 0 0 0 0
-0.7800 48.8940 61.1930 O 0 0 0 0 0 0 0 0 0 0 0 0
3.4650 55.1520 60.3740 Cl 0 0 0 0 0 0 0 0 0 0 0 0
8.4680 48.1420 59.0210 Cl 0 0 0 0 0 0 0 0 0 0 0 0
1.5000 48.5850 60.4400 C 0 0 1 0 0 0 0 0 0 0 0 0
4.7360 52.7820 60.9080 N 0 0 0 0 0 0 0 0 0 0 0 0
5.6170 50.6660 60.5930 O 0 0 0 0 0 0 0 0 0 0 0 0
1.3820 47.2220 59.8100 C 0 0 0 0 0 0 0 0 0 0 0 0
2.0160 46.8450 56.2690 O 0 0 0 0 0 0 0 0 0 0 0 0
1.8050 48.9130 58.0960 C 0 0 0 0 0 0 0 0 0 0 0 0
2.7330 42.9460 57.3720 O 0 0 0 0 0 0 0 0 0 0 0 0
1.1850 49.5780 59.3180 C 0 0 2 0 0 0 0 0 0 0 0 0
1.8010 50.9340 59.5760 C 0 0 0 0 0 0 0 0 0 0 0 0
0.9660 52.0530 59.2660 C 0 0 0 0 0 0 0 0 0 0 0 0
1.4530 53.3860 59.4280 C 0 0 0 0 0 0 0 0 0 0 0 0
2.7160 53.5440 59.9970 C 0 0 0 0 0 0 0 0 0 0 0 0
3.5100 52.4980 60.3440 C 0 0 0 0 0 0 0 0 0 0 0 0
5.6920 51.8050 61.0830 C 0 0 0 0 0 0 0 0 0 0 0 0
6.9420 52.1050 61.9310 C 0 0 0 0 0 0 0 0 0 0 0 0

3D é muito difícil ver todas as interações

- Abra o site proteins.plus
- Coloque o arquivo .pdb da proteína e .sdf do ligante
- Envie os dados pra plataforma



Selecione o PoseView e a Molécula De Interesse



Analise o Gráfico 2D