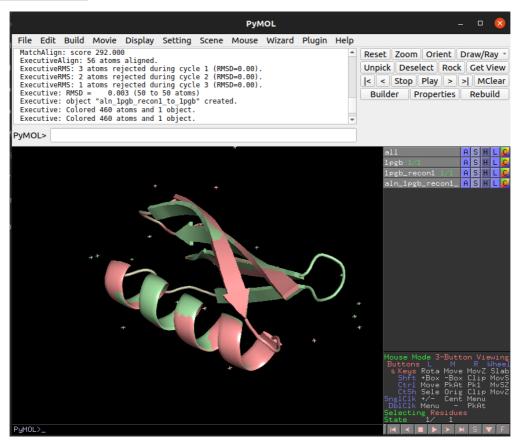
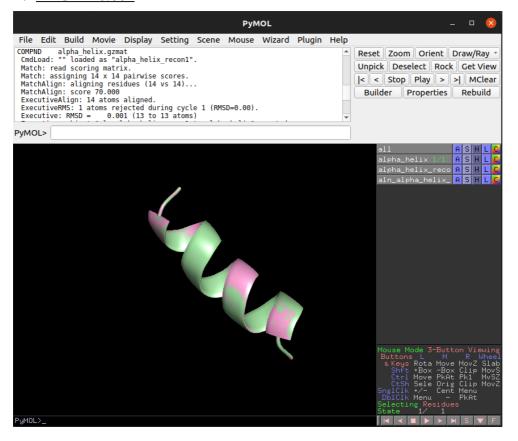
## Excercise 1:

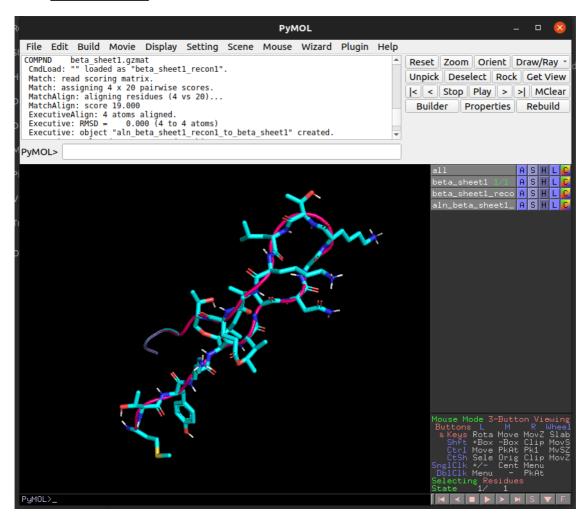
1PGB : RMSD = 0.003



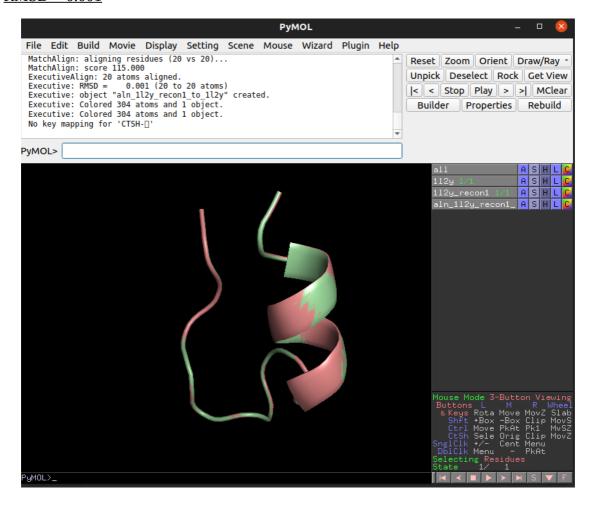
## Alpha-Helix: RMSD = 0.001



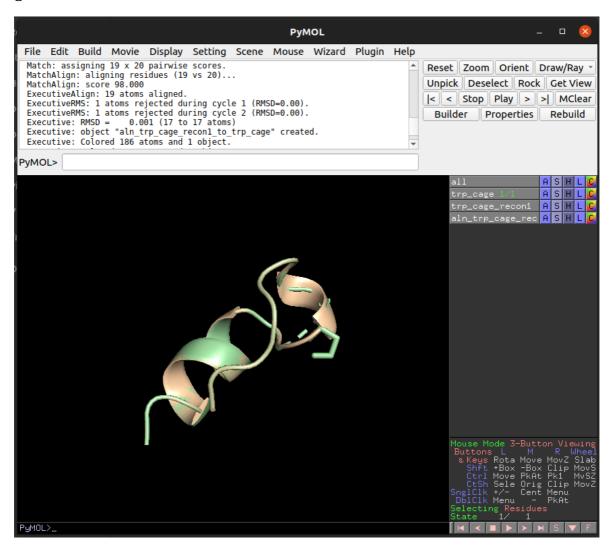
## Beta-Sheet: RMSD = 0.000



## 1L2Y : RMSD = 0.001



## TRP Cage: $\underline{RMSD} = 0.001$



# Efficacy of OpenBabel Tool:

We can observe the RMSD values of the alignment of reconstructed PDB with the original PDB. As we can see the RMSD value is very small, thus signifying that the deviation between the atoms of the two molecules is very small. Thus, we can conclude that the reconstructed molecule is very close to the original one with which we started. Thus overall we can say that efficacy of openBabel is pretty high which means that the tool is good to use.

## Excercise 2:

I used 2 other commands/features present in open babel. They are as follows --

1. <u>obprop</u> – Prints the properties of input PDB in the terminal itself. Attached screenshots of the output of all the molecules.

## 1PGB:

## Alpha-Helix:

#### Beta-Sheet-1:

beta\_sheet1.pdb C97H169N24O31S \*\*\* Open Babel Warning in InChI code

#1 :Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#2 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#3 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#3 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#4 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#4 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#5 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): N(4); Ambiguous stereo: center(s)

#6 : Accepted unusual valence(s): Accepted (alpha) (10); Ambiguous stereo: center(s): accepted (alpha) (10); Ambiguous stereo: center(s): accepted (alp num\_atoms num\_bonds 325 20 54 num\_residues num\_rotors MET-THR-TYR-LYS-LEU-ILE-LEU-ASN-GLY-LYS-THR-LEU-LYS-GLY-GLU-THR-THR-THR-GLU-ALA sequence num\_rings logP PSA 591.821

#### Beta-Sheet-2:

beta\_sheet2.pdb 1 C81H127N17O29 formula mol\_weight 1802.97

exact\_mass 1801.9

canonical\_SMILES [NH3]CCCC[C00H](C(=0)N[C0H](C(=0)N[C0H](C(=0)NCC(=

64(42(4)101)94-73(120)53(29-45-16-12-11-13-17-45)92-76(123)66(44(6)163)95-69(116)51(18-14-15-27-82)89-75(122)65(43(5)102)93-68(115)41(3)86-76(117)54(32-62(111)112)90-72(119)55(33-63(113)114)91-71(118)52(28-85)(105)28-40(2)100)30-46-19-22-50(104)23-20-46;/h11-13,16-17,19-20,22-23,36-37,40-44,47-49,51-57,64-67,83,96-97,100-104,125-126H,10,14-15,18,21,24-35,38-39H2,1-9,82H3,(H,84,121)(H,85,106)(H,86,117)+,66+,67+,79-,80+,81-;/m1./s1

num atoms num\_residues num\_rotors

sequence num\_rings GLU-TRP-THR-TYR-ASP-ASP-ALA-THR-LYS-THR-PHE-THR-VAL-THR-GLU

-0.7322 716.72

MR \$\$\$\$

## 1L2Y:

\* Open Babel Warning in PerceiveBondOrders
Failed to kekulize aromatic bonds in OBMol::PerceiveBondOrders

\*\*\*\* Open Babel Warning in InChI code
#1 :Ambiguous stereo: center(s)
InChI InChI=Is/C273H423N670955. 24H20/c1-35-129(16)210(329-254(415)173(102-124(6)7)309-235(396)162(65-47-53-96-277)303-249(410)176(106-150-70-76-154(353)77-71-150)320-266(427)213(138(25)343)332
-228(389)157(280)92-99-436-34)261(422)17-772(101-123(4)5)247(408)312-180(109-189)(282)356)230(391)287-119-192(359)296-160(63-45-51-94-275)229(400)333-214(139(26)344)267(428)318-171(100-122(2)3)246(407)30
-159(62-44-56)-93-274)229(390)286-118-193(360)298-166(82-88-197(365)366)224(806)392-235(329)350)271(432)233-221(146(33)351)272(433)339-217(142(29)347)264(422)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-217(142(29)347)264(429)347-126(40)339-117(140-142)349-126(40)329-169(40)327-276(40)319-16(40-46-52-9-5-76)224(365)306-182(111-191(284)358)25(412)316-186(115-264(379)388)252(413)313-181(110-196(283)357)23(39)289-121-195(362)325-266(125(8)9)257(418)323-183(112-261(373)374)232(39)388-126-194(361)297-136(116-196)283-136(116-1

num\_atoms 931
num\_bonds 93
num\_conds 93
num\_conds 80
num\_restdues 80
num\_rotors 262
sequence MET-THR-LYS-LEU-ILE-LEU-ASN-GLY-LYS-THR-LEU-LYS-GLY-GLU-THR-THR-THR-GLU-ALA-VAL-ASP-ALA-ALA-THR-ALA-GLU-LYS-VAL-PHE-LYS-GLN-TYR-ALA-ASN-ASP-ASN-GLY-VAL-ASP-GLY-GLU-TRP-THR-TYR-ASP-ASP
P-ALA-THR-LYS-THR-PHE-THR-VAL-THR-GLU
num\_rings 7
loop -2.2829

## TRP-Cage:

2. <u>obabel -ofpt</u> – Gives the Tanimoto coefficient between a SMILES string and all the molecules SDF Format :

Attached screenshots of the output of all the molecules.

#### 1PDB:

```
1 molecule converted
>1pgb.pdb
>1pgb.pdb    Tanimoto from 1pgb.pdb = 1
Possible superstructure of 1pgb.pdb
2 molecules converted
```

## Alpha-Helix:

#### Beta-Sheet-1:

#### 

#### Beta-Sheet-2:

```
1 molecule converted
>beta_sheet2.pdb
>beta_sheet2.pdb Tanimoto from beta_sheet2.pdb = 1
Possible superstructure of beta_sheet2.pdb
2 molecules converted
```

#### 1L2Y:

```
1 molecule converted
1 molecule converted
>1l2y.pdb
>1l2y.pdb Tanimoto from 1l2y.pdb = 1
Possible superstructure of 1l2y.pdb
2 molecules converted
```

# TRP-Cage:

We can observe from the above results that the Tanimoto Coefficient between the Original Structure and Reconstructed Structure is 1 for all the above molecules.

Thus, we can confirm that the iner-conversion efficacy of the Open Babel software is very high and it is a very powerful tool which can be used for inter-conversion of molecules.