ASSIGNMENT 5

KUSHAGRA AGARWAL 2018113012 CNS

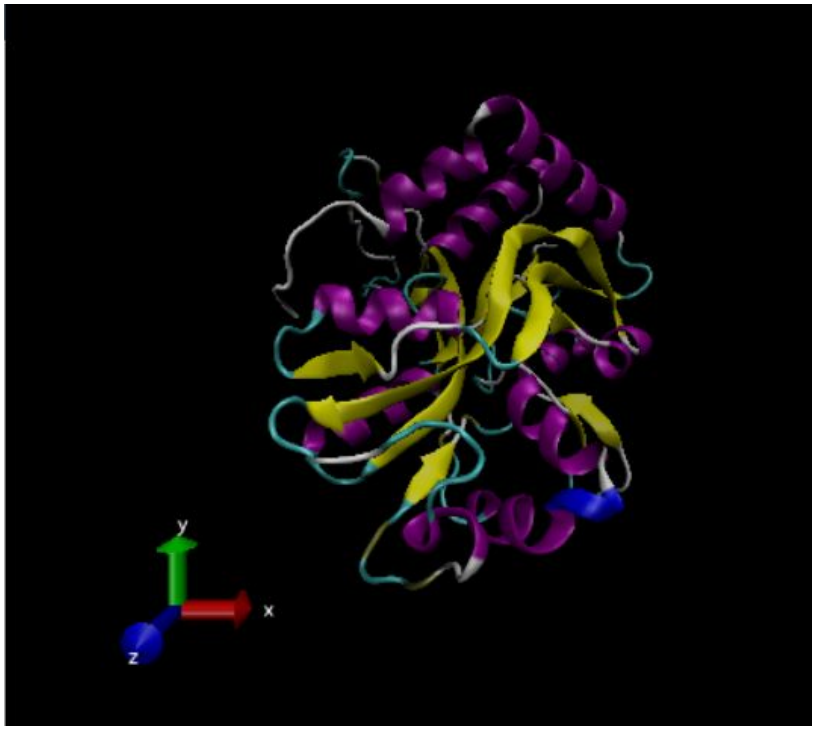
Q1) The Protein I chose:

1PB8

Organism(s): Rattus norvegicus

Expression System: Escherichia coli.

A) The molecule as viewed in VMD in the New Cartoon representation and colour coding representing the different Secondary Structures looks like this

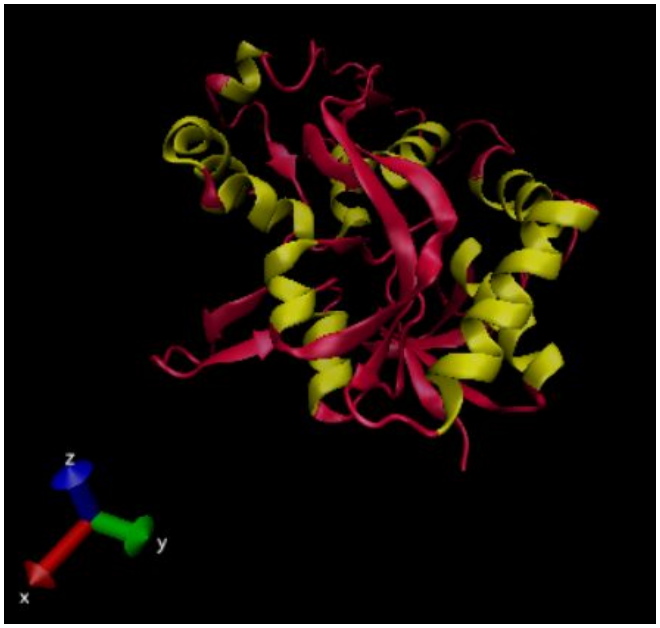


Alpha-Helix (Purple), 3-10-Helix(Blue), Extended-Beta(Yellow), Bridge-Beta(Tan), Turn(Cyan), Coil(White).

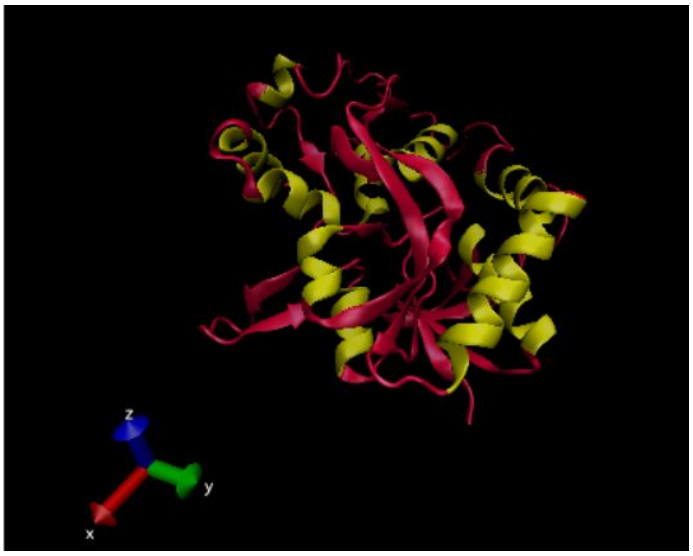
Now individually representing the different Secondary Structures:

Yellow Represents the Secondary Structure and Red the rest of the protein.

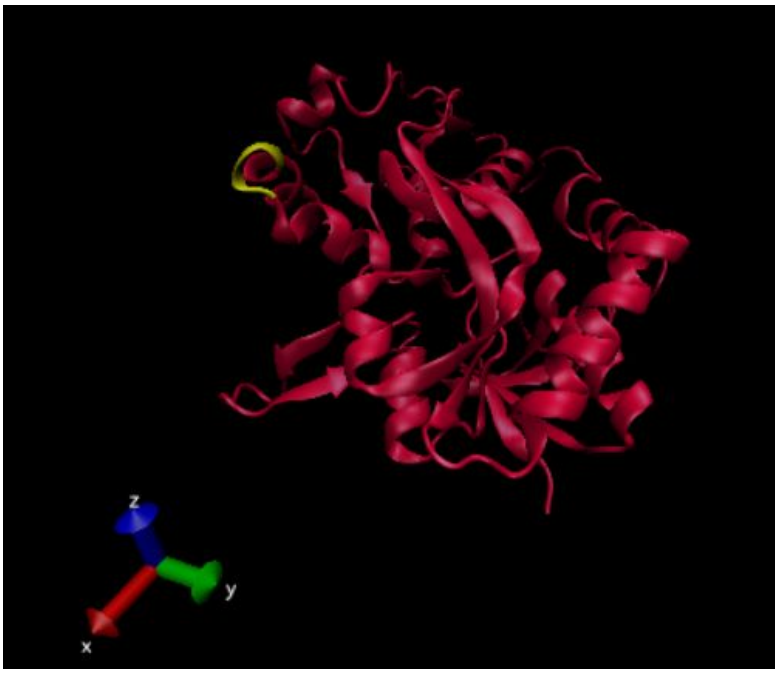
HELIX



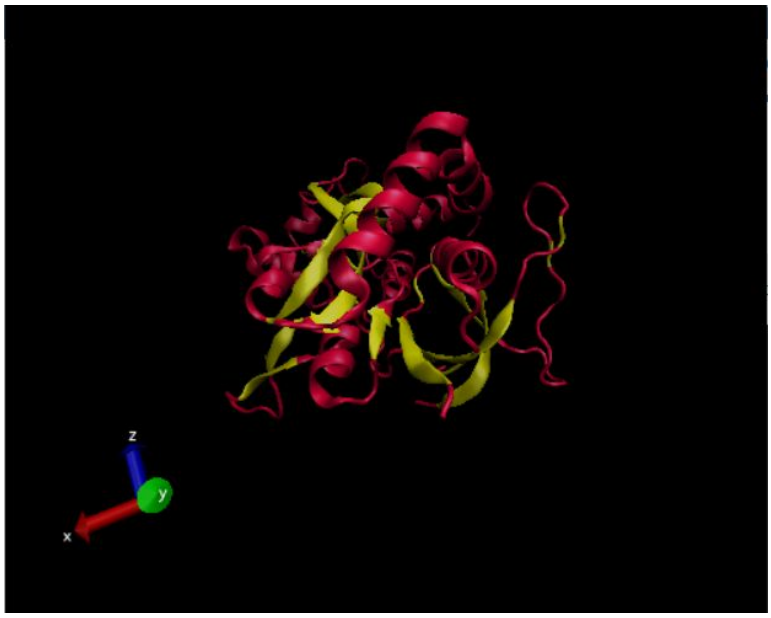
a)Alpha Helices



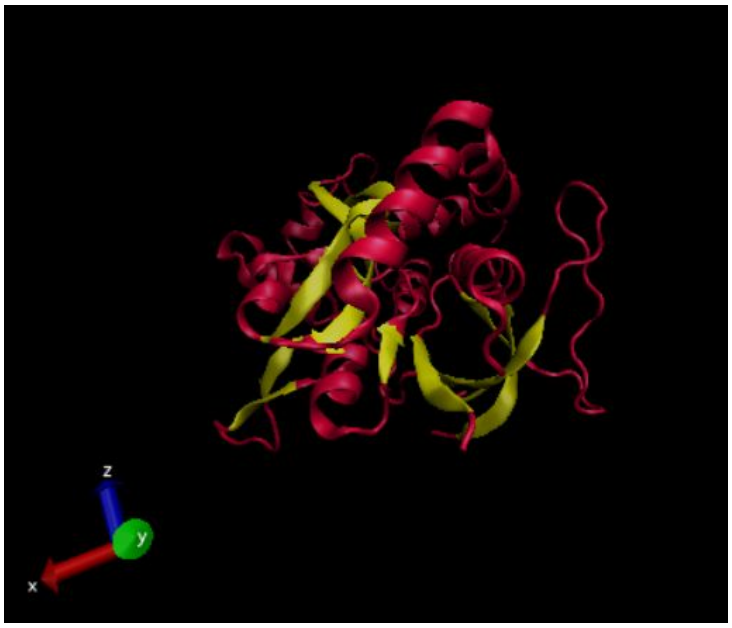
b)3-10-Helices



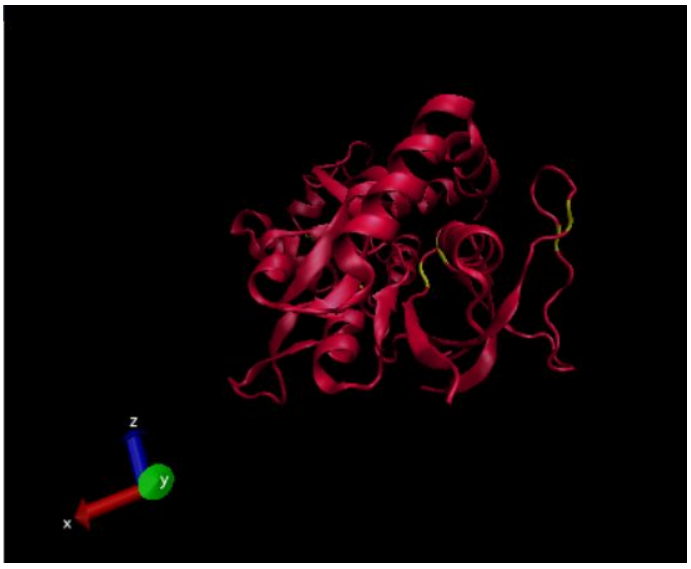
BETA SHEETS



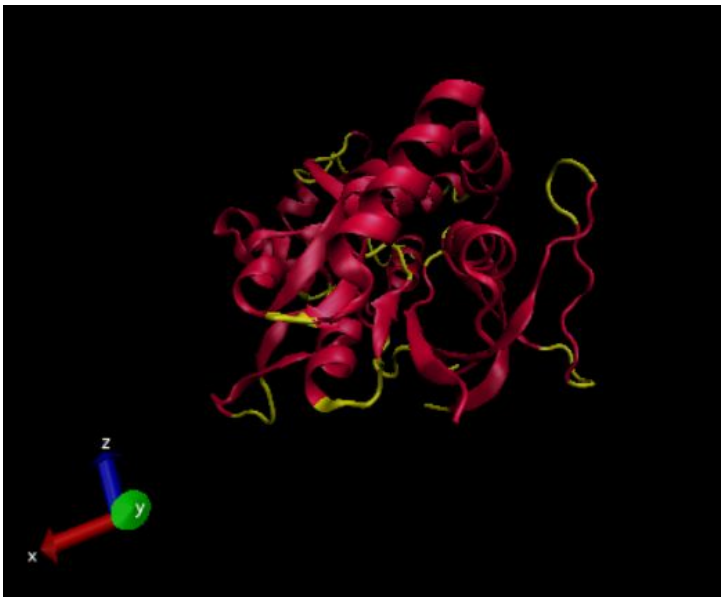
a)Extended-Beta



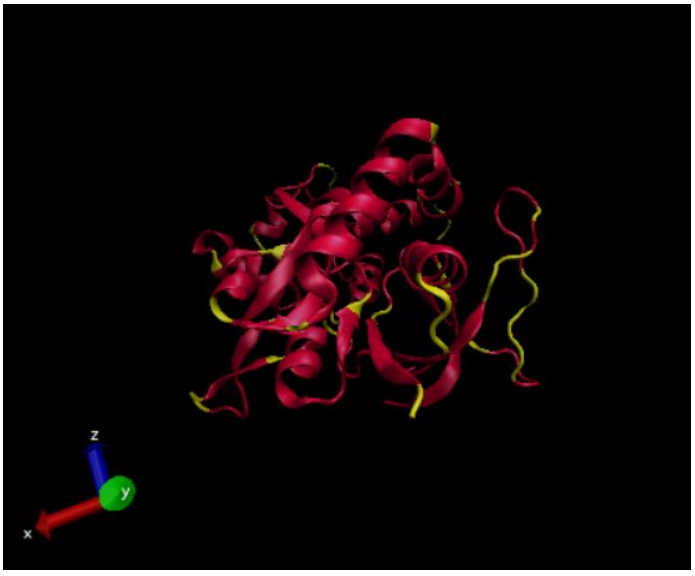
b)Beta-Bridge



TURN



COILS



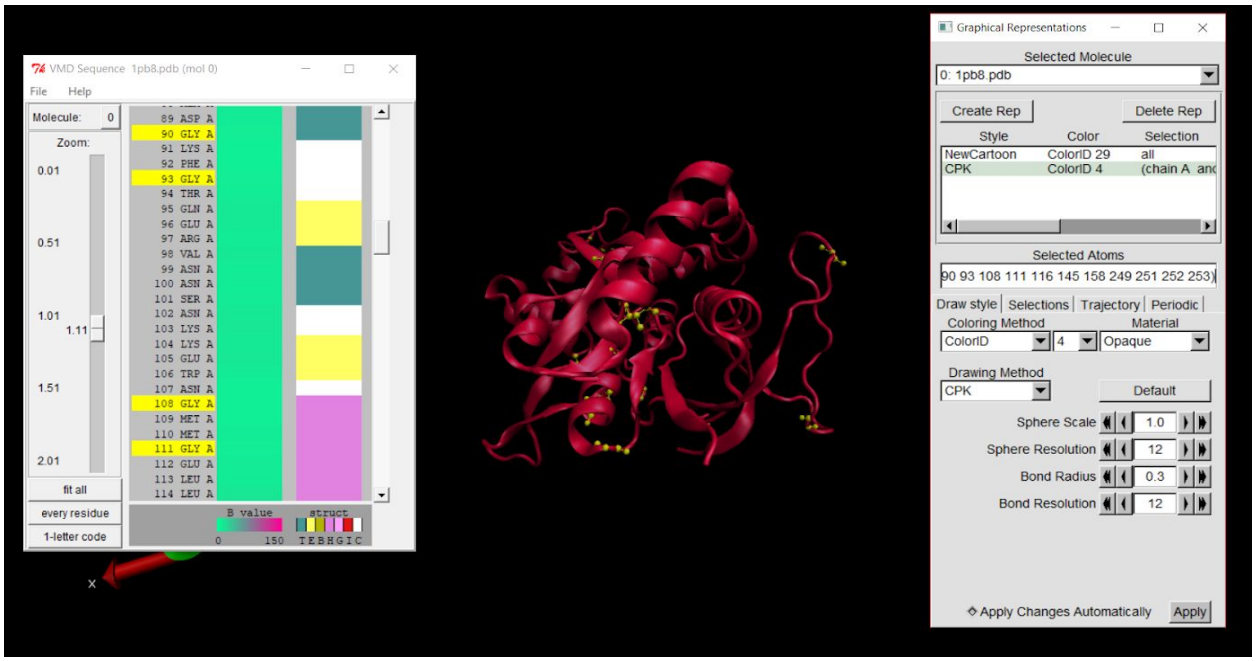
All the secondary structures present in my protein molecule have been listed above.

Pi-Helix is not present in the protein.

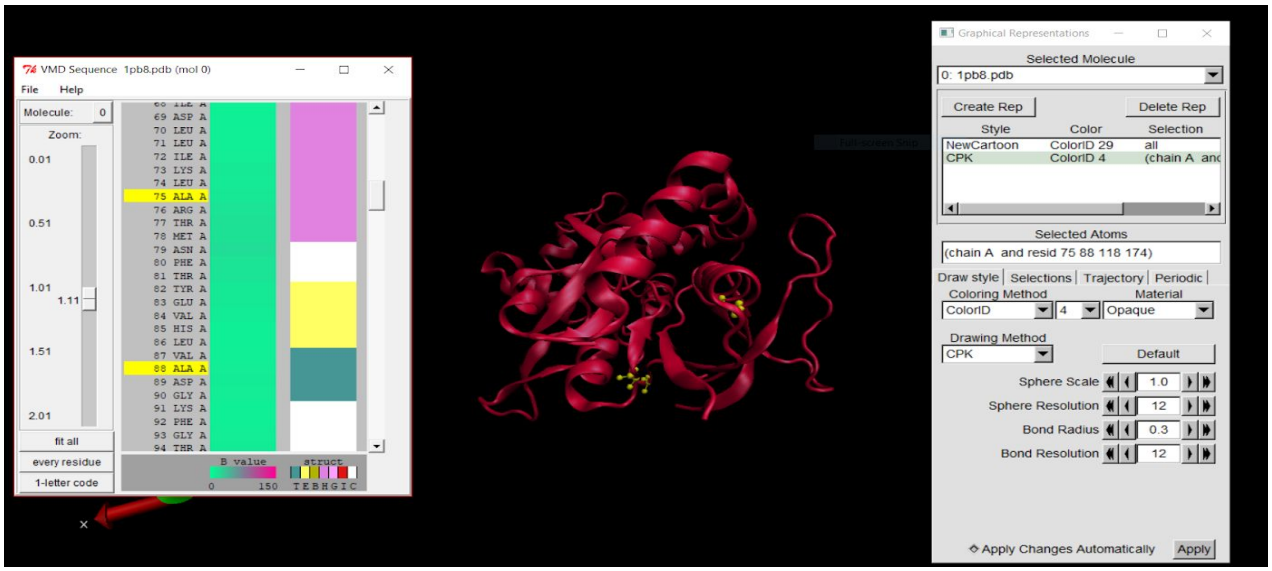
B) Residues that are actively binding the ligand.

There are 20 amino acids that occur in repetition in any protein. The following will have 20 amino acid residues one by one in their CPK format in Yellow, and the rest of the molecule in New Cartoon format in Red.

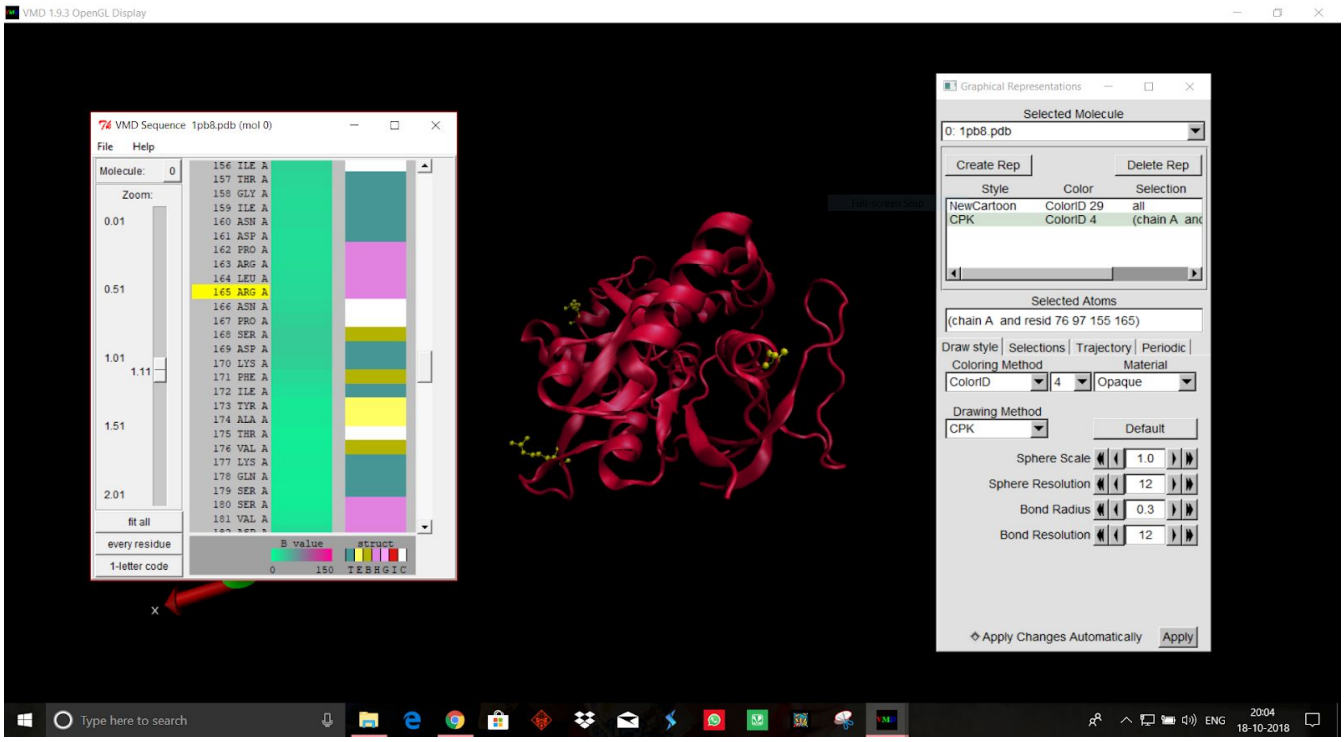
Glycine GLY



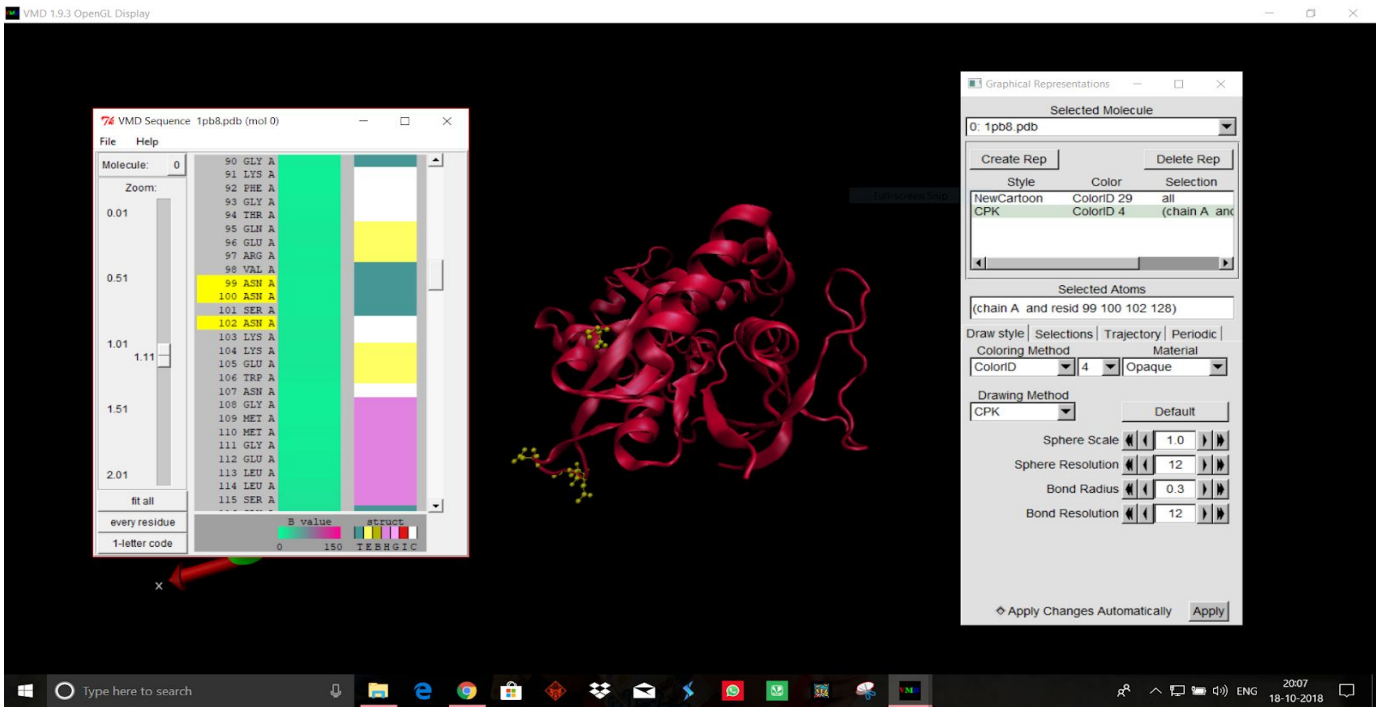
Alanine ALA



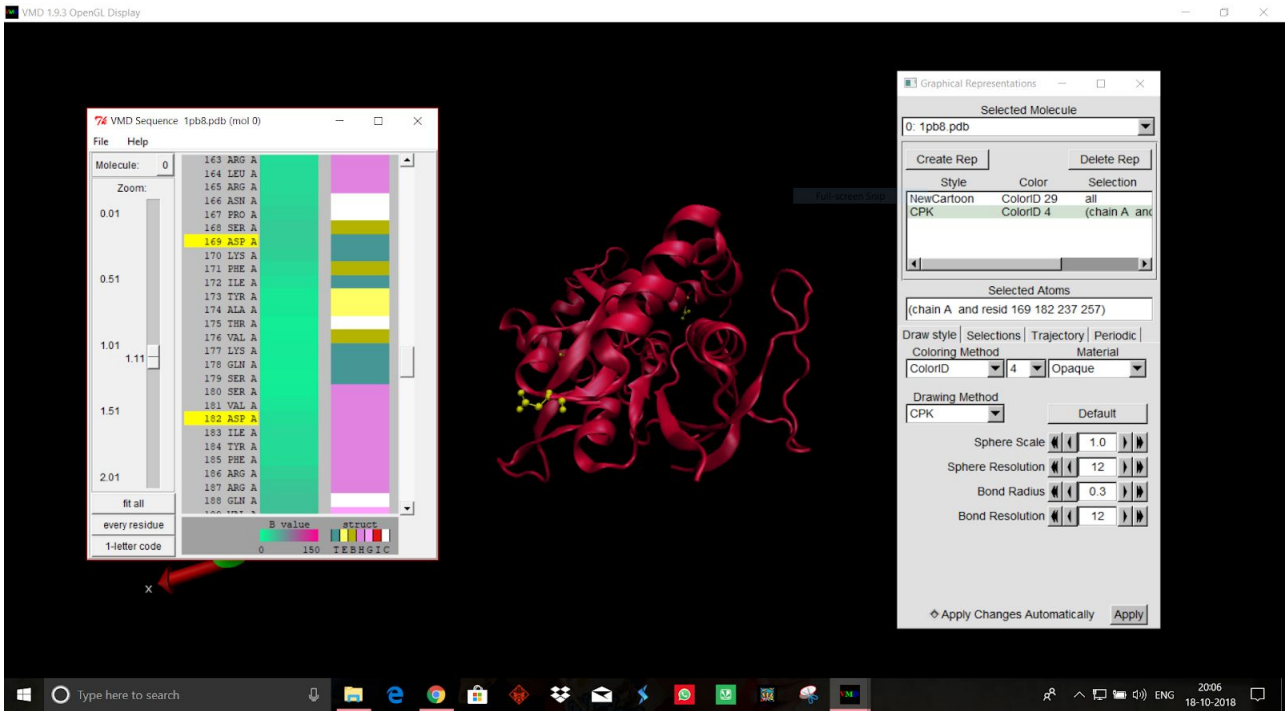
Arginine ARG



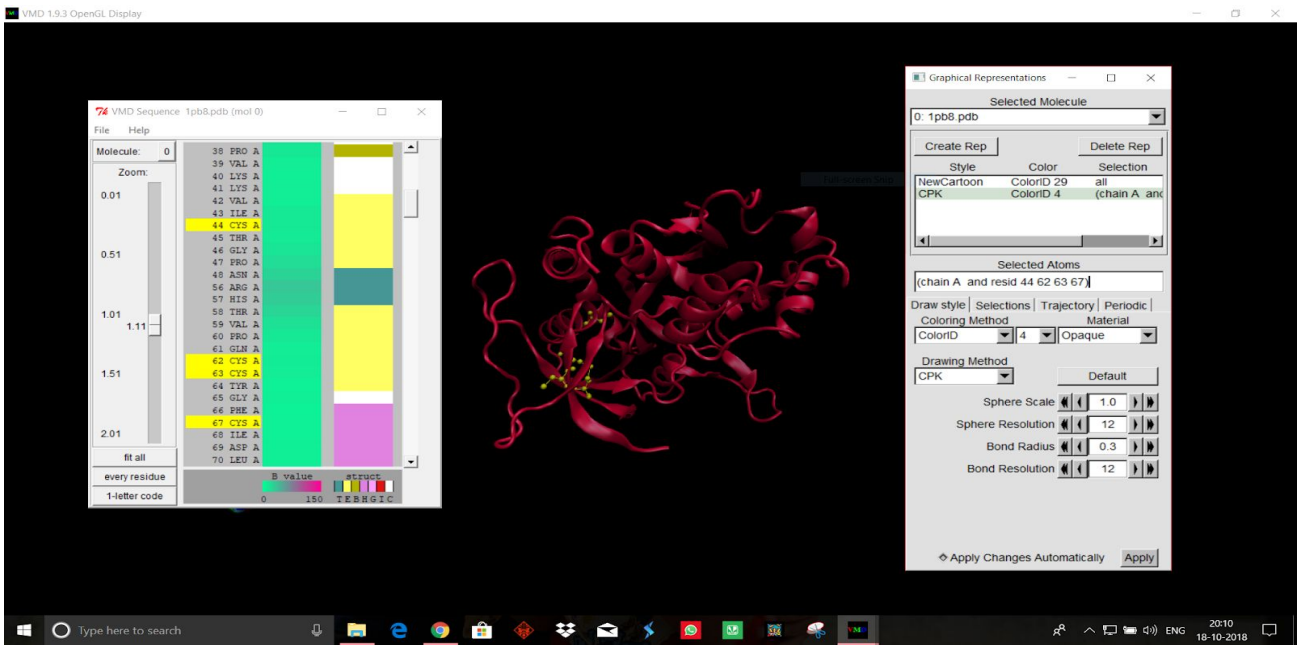
Asparagine ASN



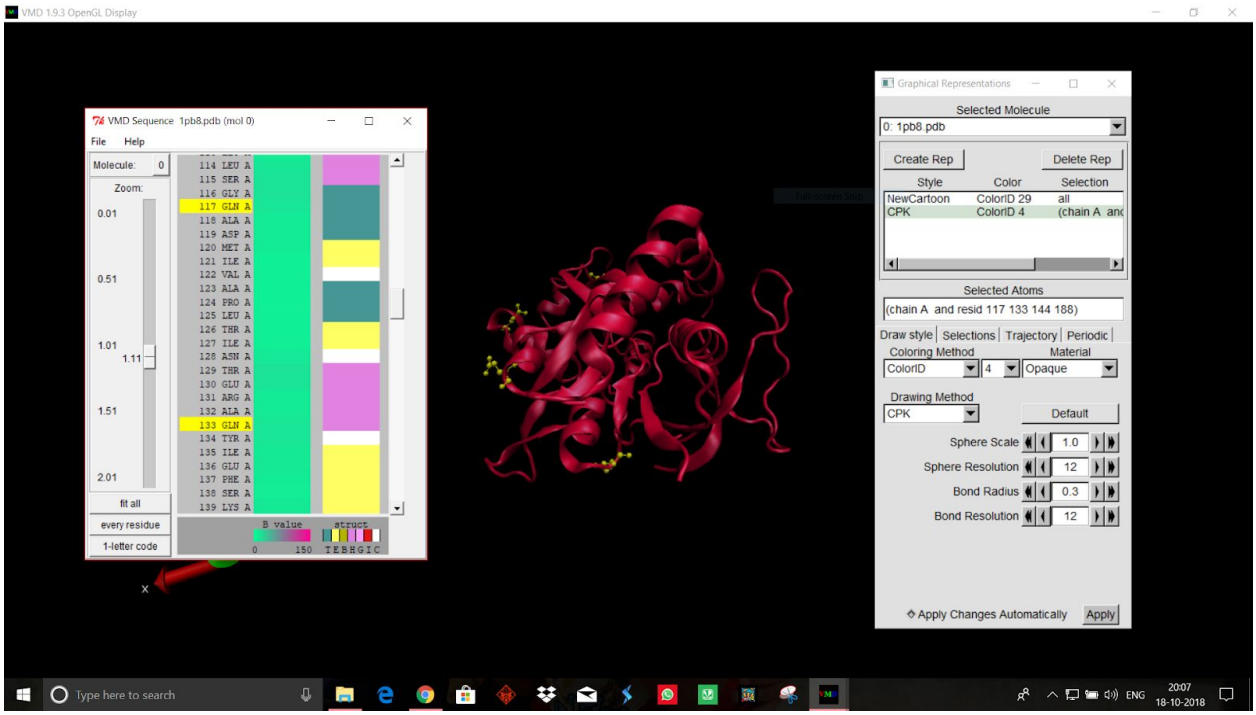
Aspartic Acid ASP



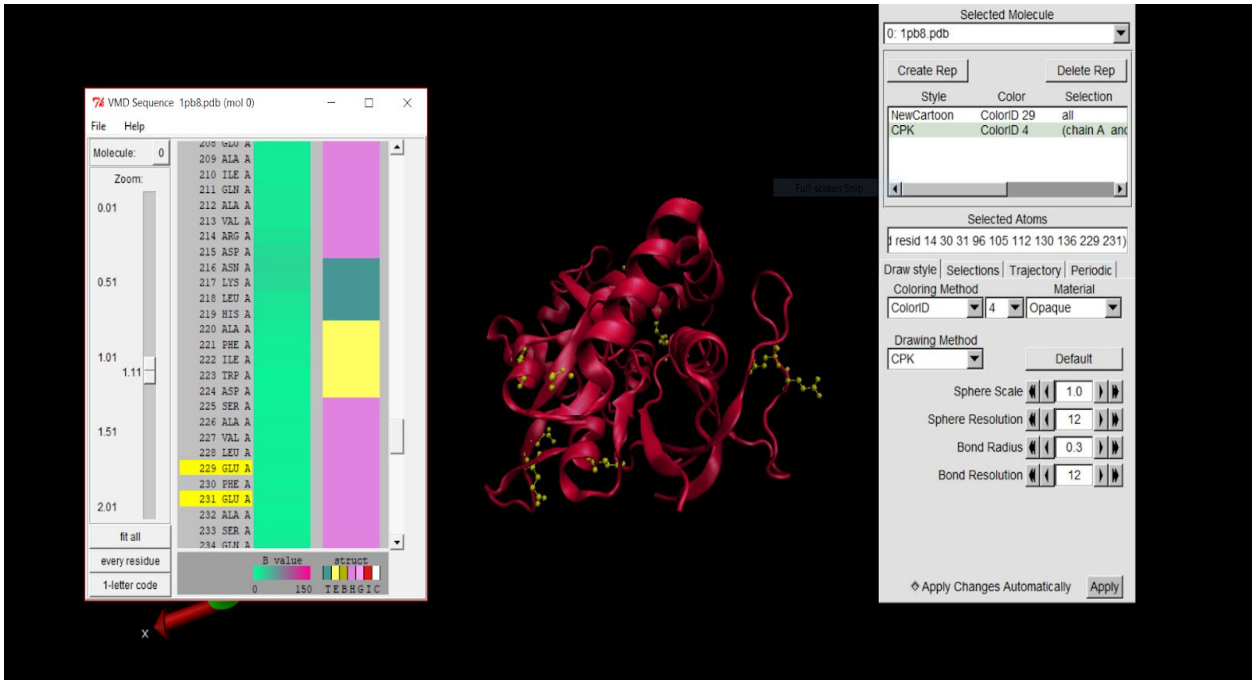
Cysteine CYS



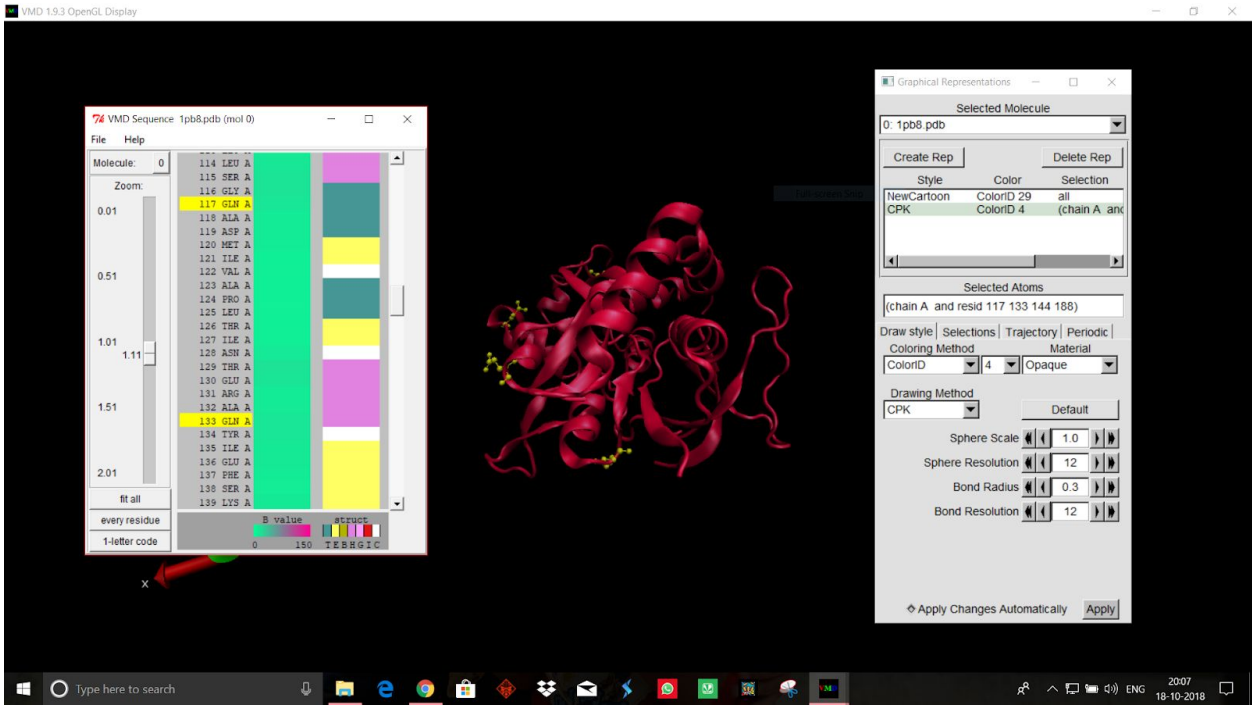
Glutamine GLN



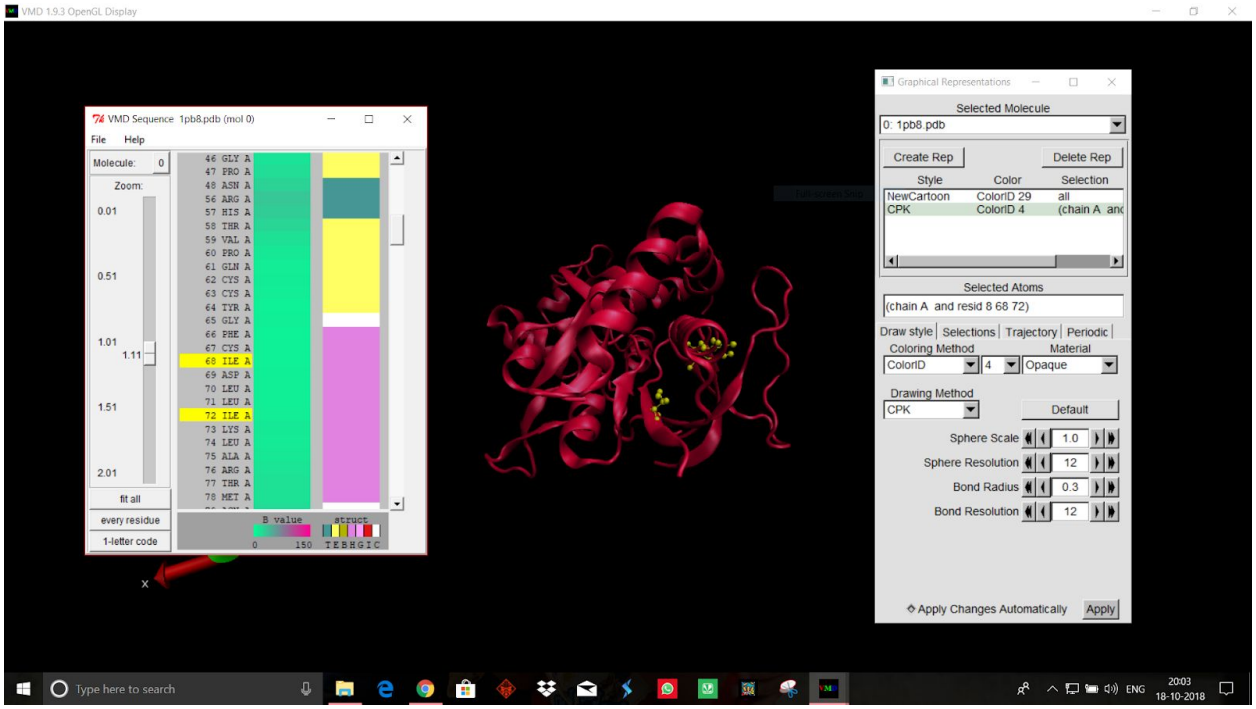
Glutamic Acid GLU



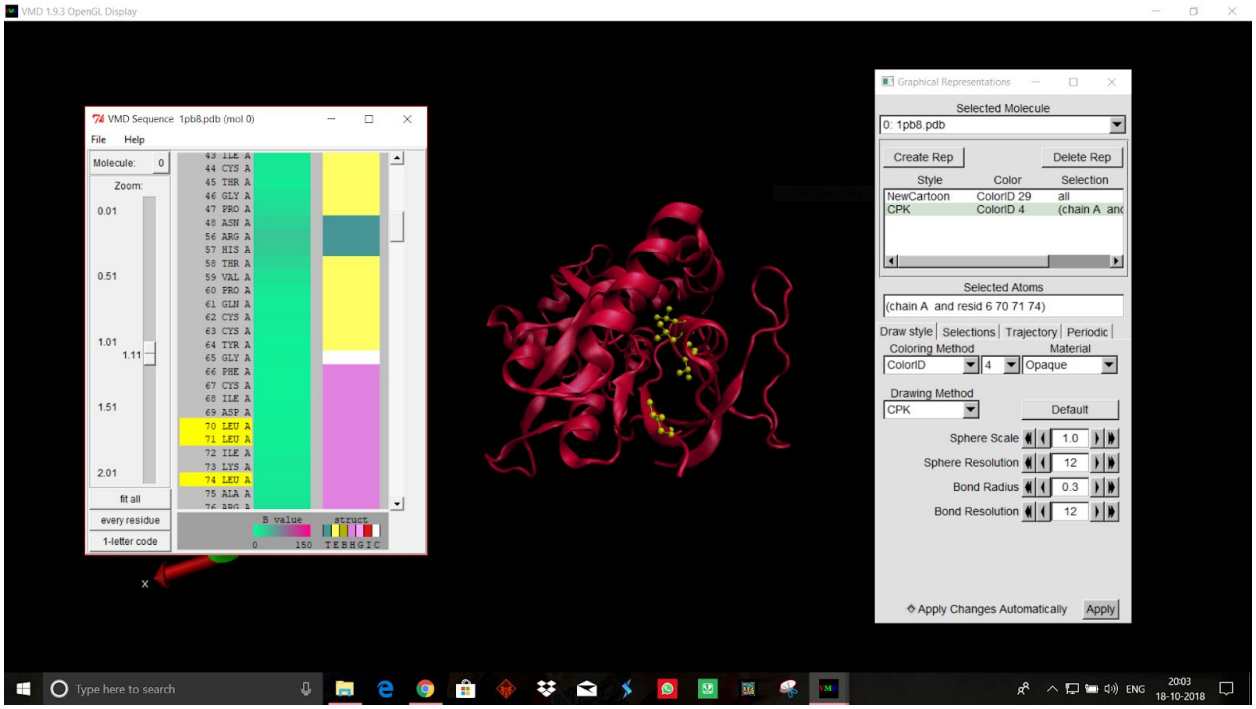
Histidine HIS



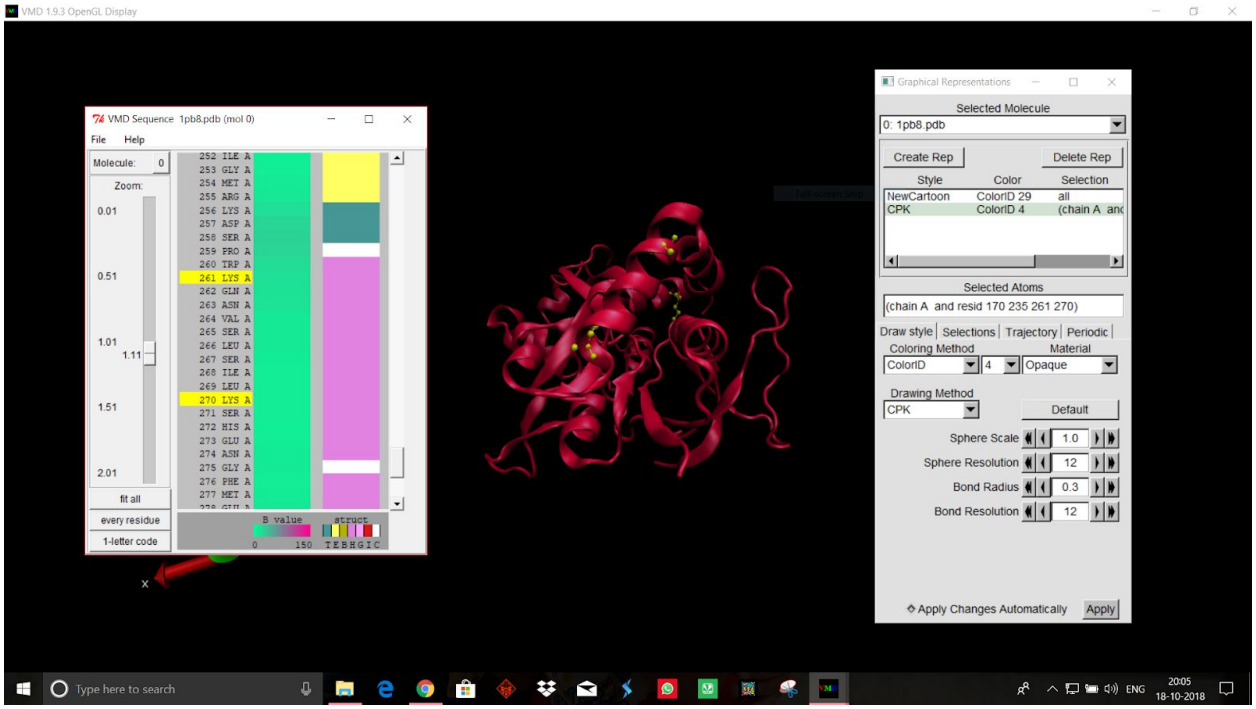
Isoleucine ILE



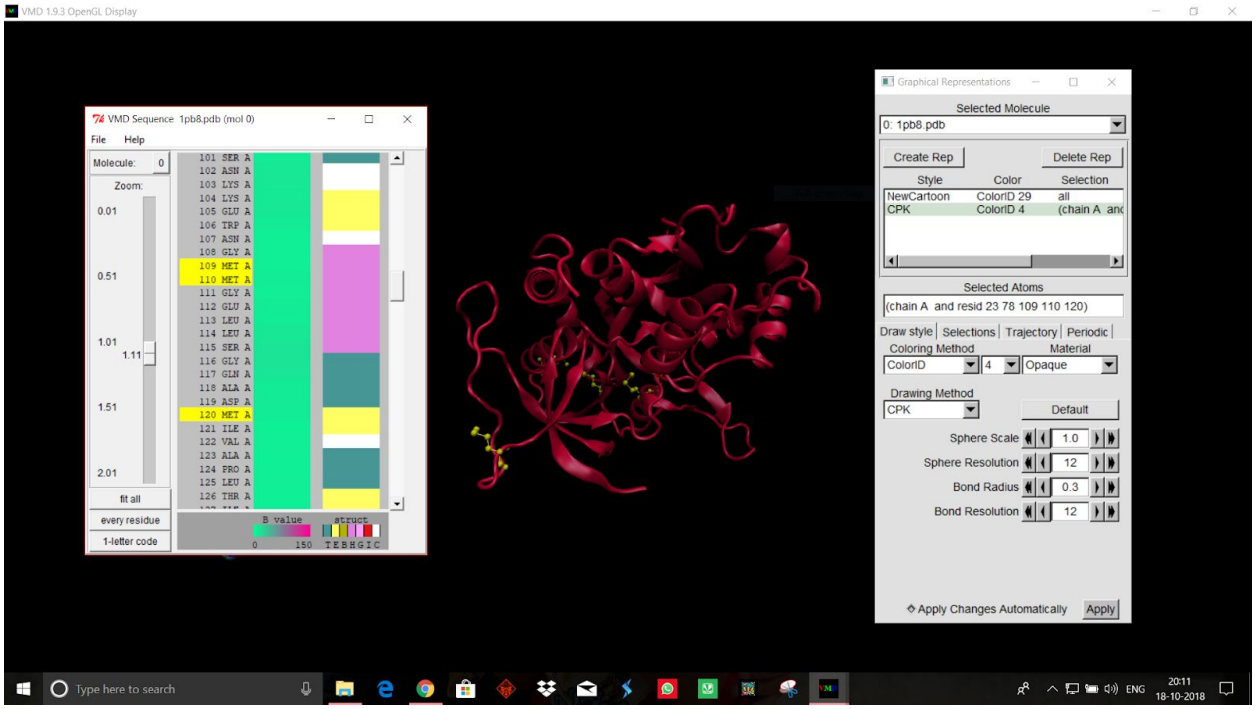
Leucine LEU



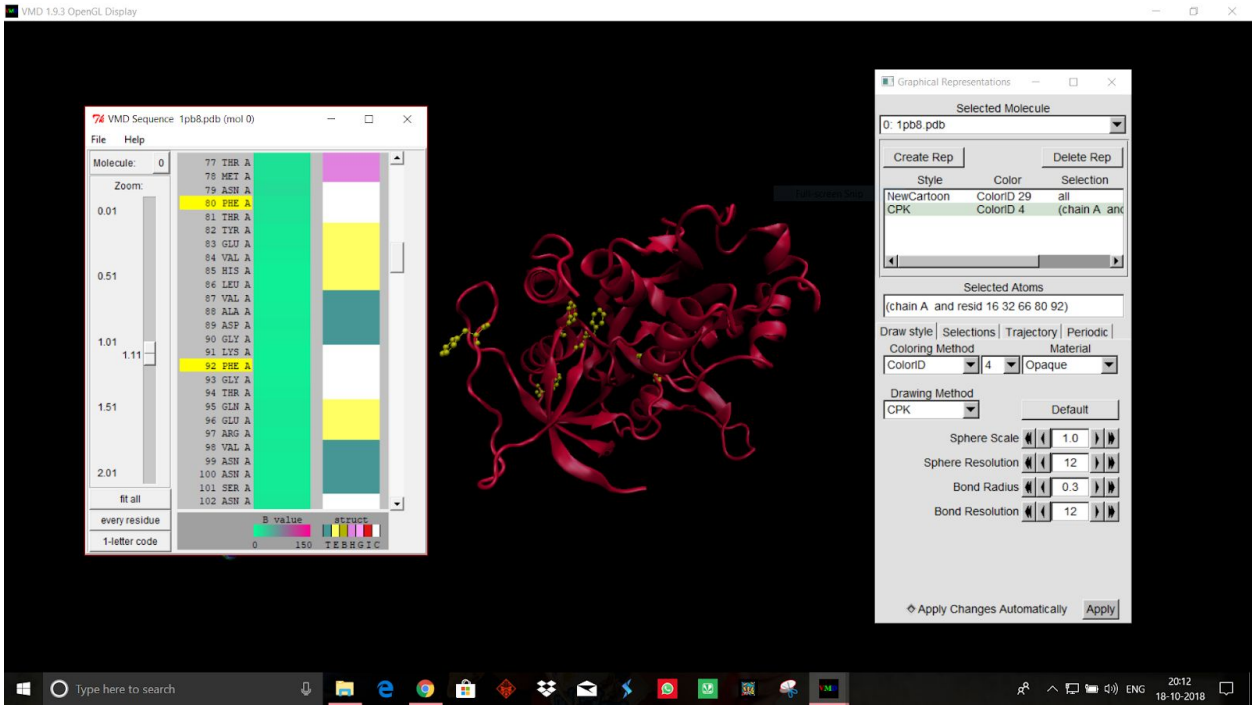
Lysine LYS



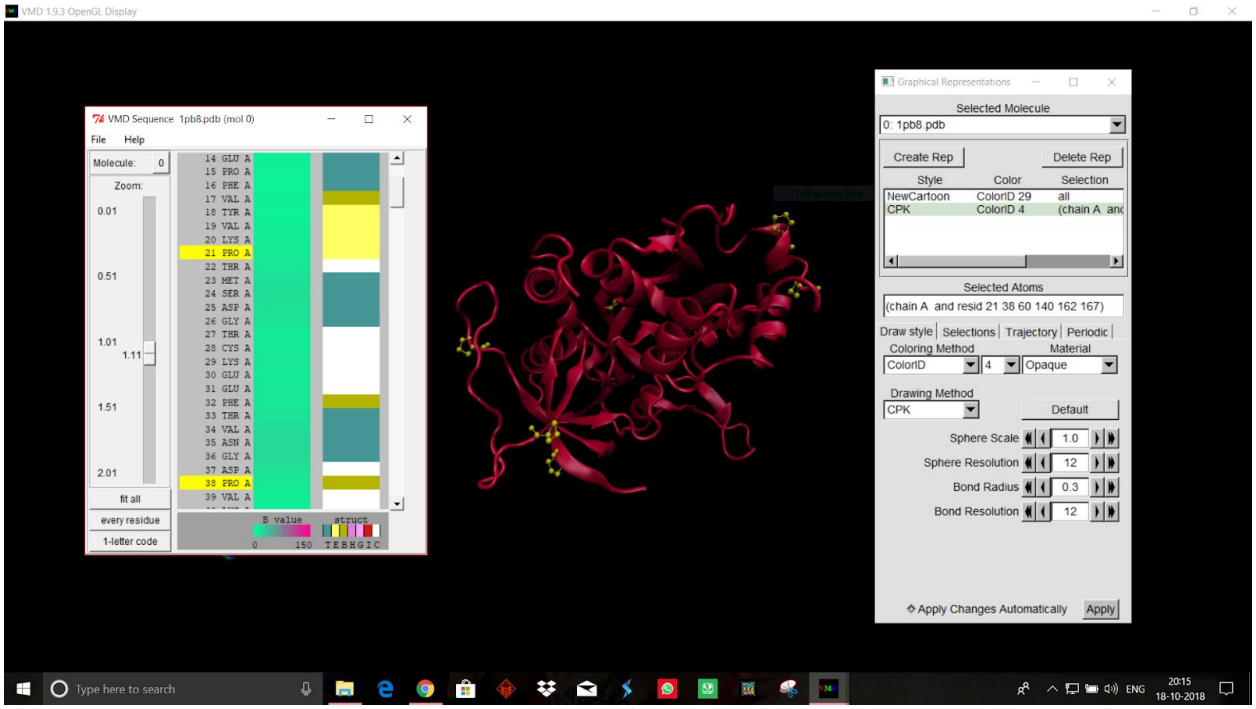
Methionine MET



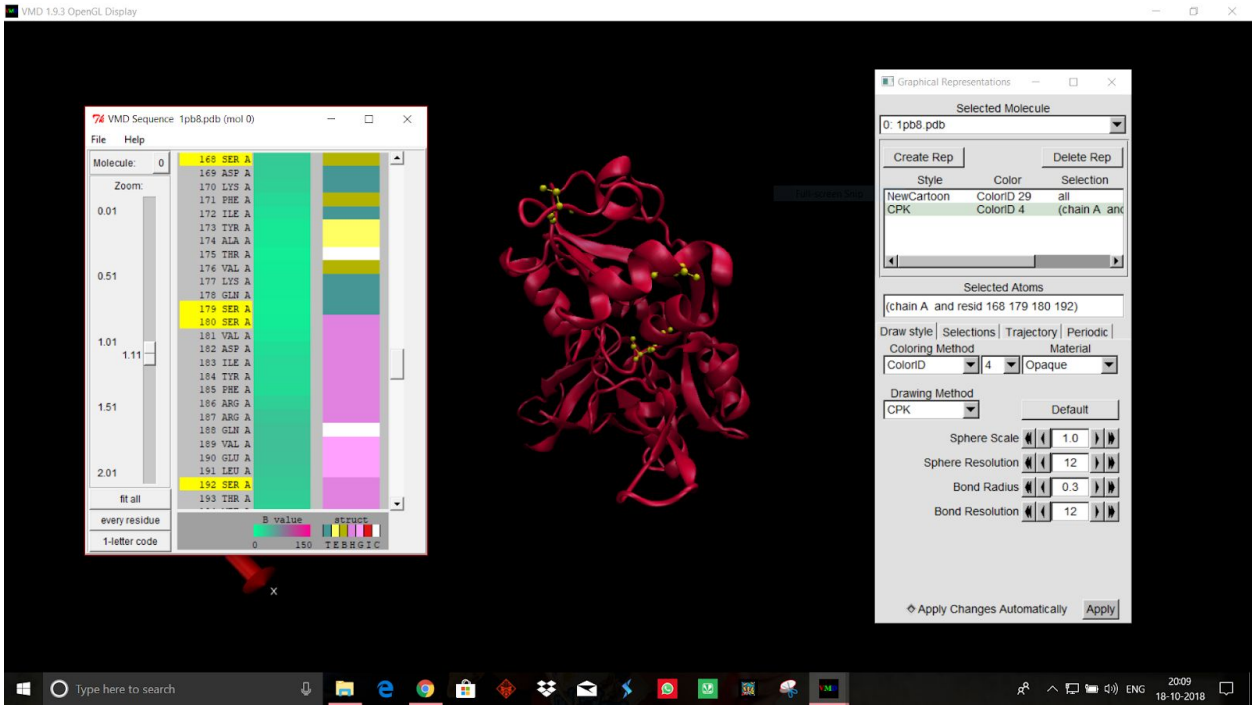
Phenylalanine PHE



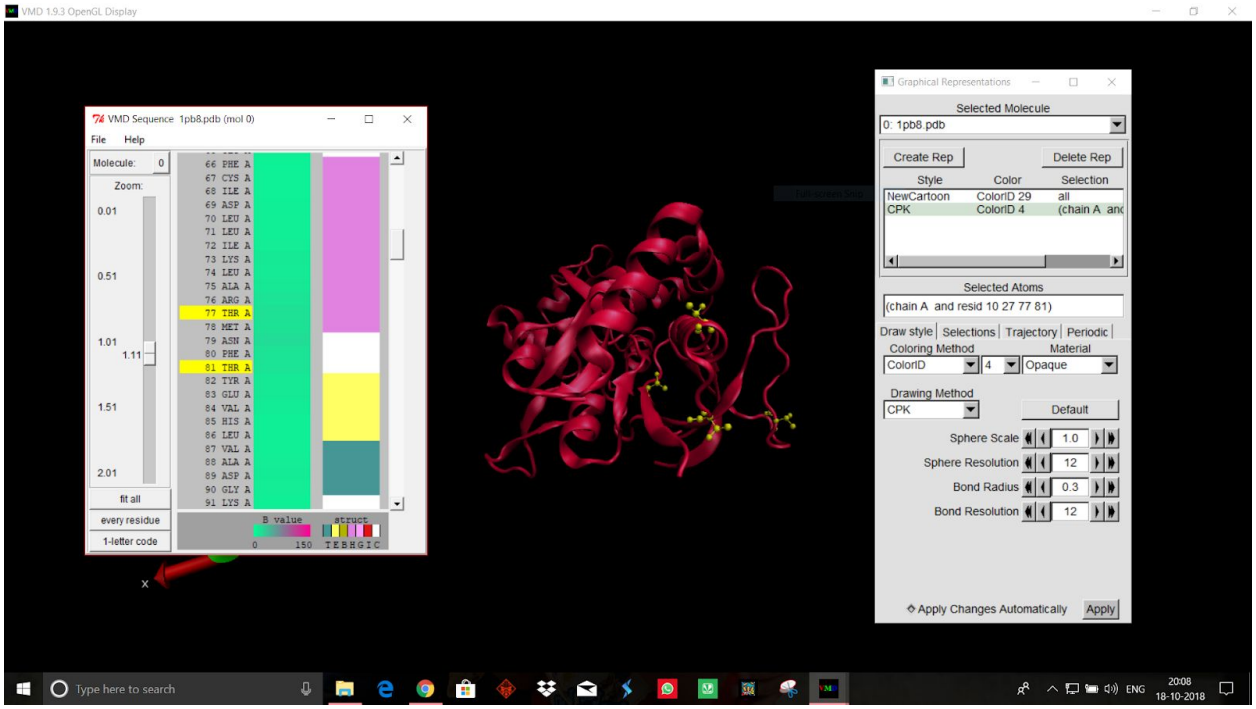
Proline PRO



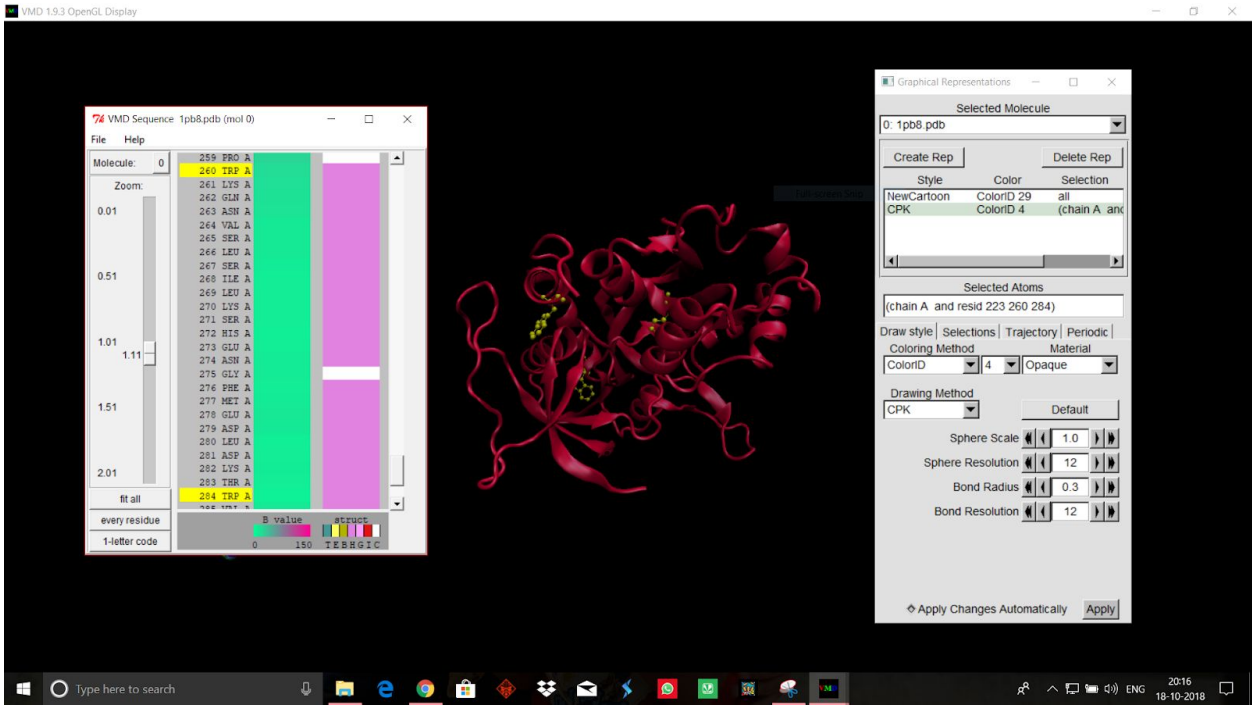
Serine SER



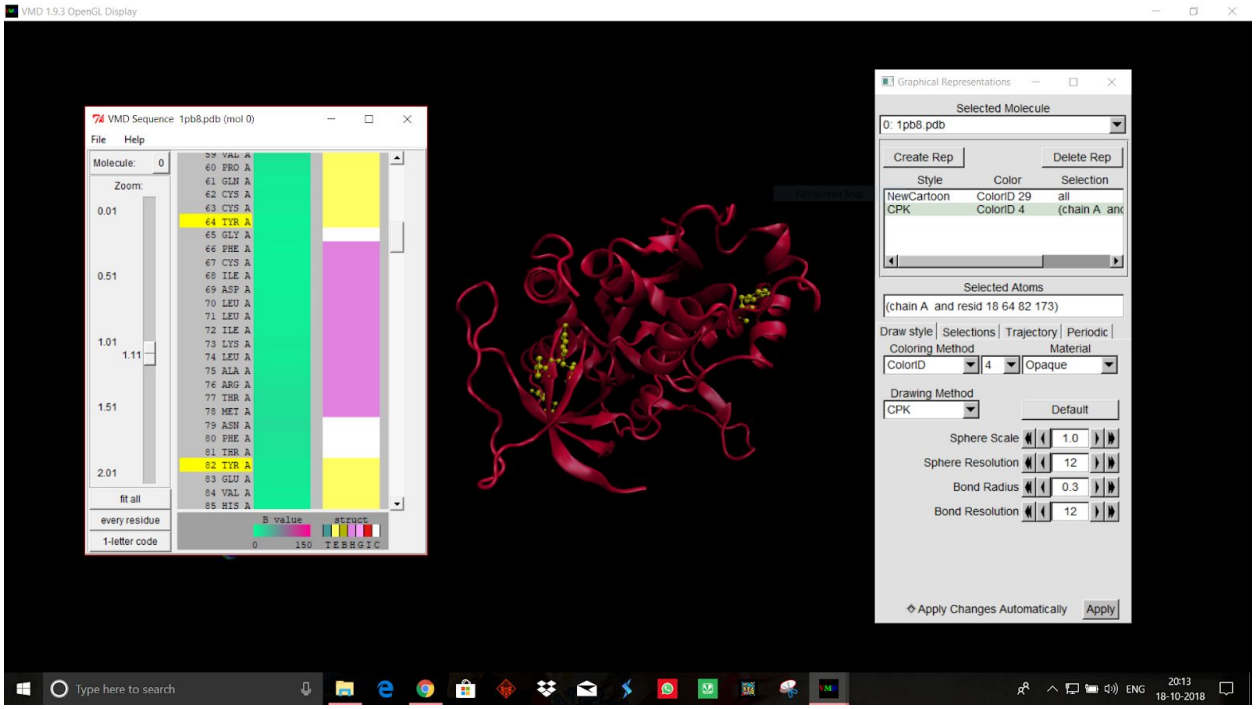
Threonine THR



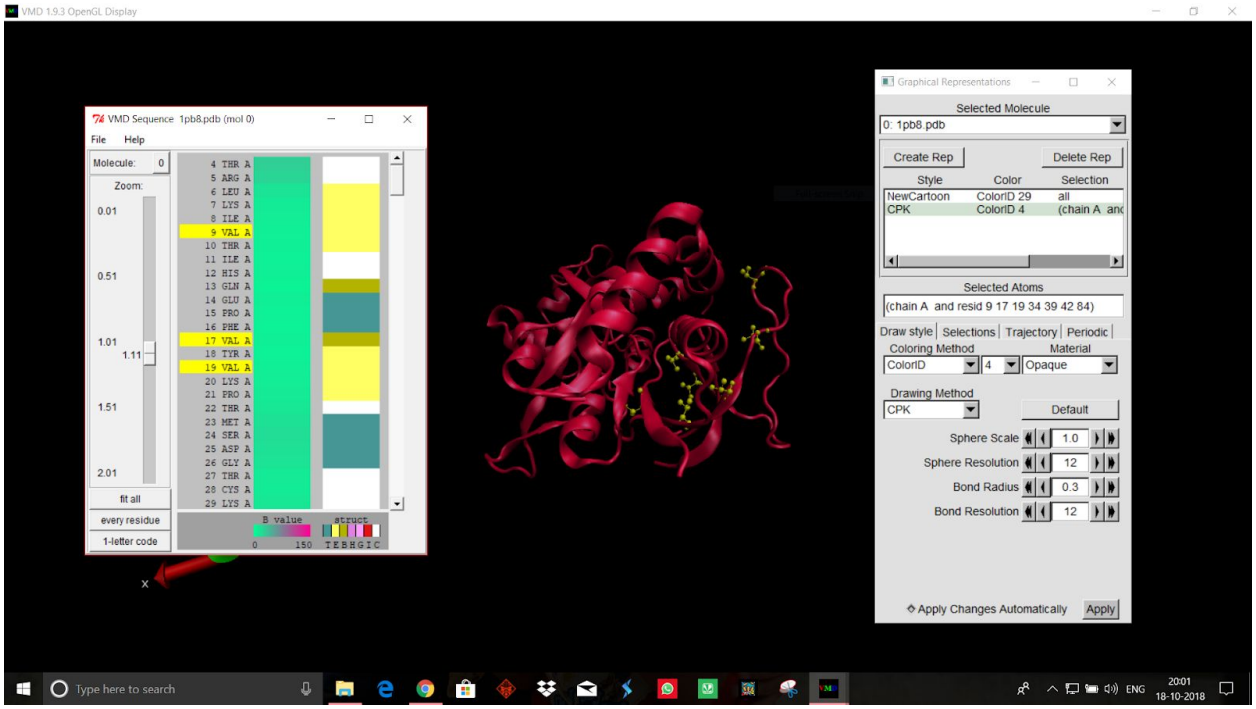
Tryptophan TRP



Tyrosine TYR

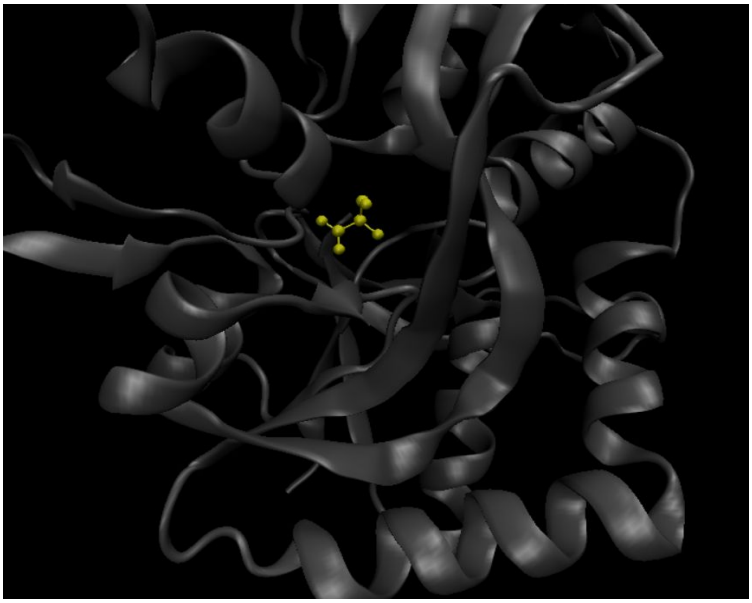


Valine VAL



Residue that is Actively Binding Ligands

DSN 901(LIGAND)



SITE 1 AC1 9 PHE A 92 PRO A 124 THR A 126 ARG A 131

SITE 2 AC1 9 SER A 179 SER A 180 VAL A 181 TRP A 223

SITE 3 AC1 9 ASP A 224

The above lines mean that there are 9 residues actively binding at the Site AC1-

PHE 92, PRO 124, THR 126, ARG 131, SER 179, SER 180, VAL 181, TRP 223, ASP 224

are the 9 residues with their respective ResIds.

HETATM 2173 N DSN A 901 21.106 41.763 40.469 1.00 10.77 N

HETATM 2174 CA DSN A 901 21.285 40.323 40.165 1.00 9.67 C

HETATM 2175 C DSN A 901 22.695 40.063 39.583 1.00 8.40 C

HETATM 2176 O DSN A 901 22.986 38.895 39.303 1.00 9.17 O

HETATM 2177 OXT DSN A 901 23.423 41.079 39.436 1.00 9.00 O

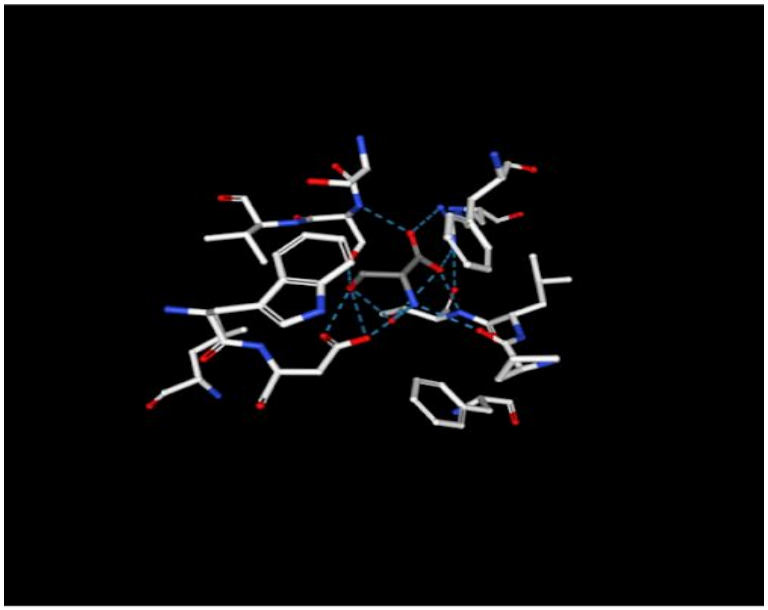
HETATM 2178 CB DSN A 901 20.986 39.472 41.385 1.00 12.98 C

HETATM 2179 OG DSN A 901 21.715 39.878 42.508 1.00 14.03 O

The above lines represent the coordinates of the various atoms present in DSN 901.

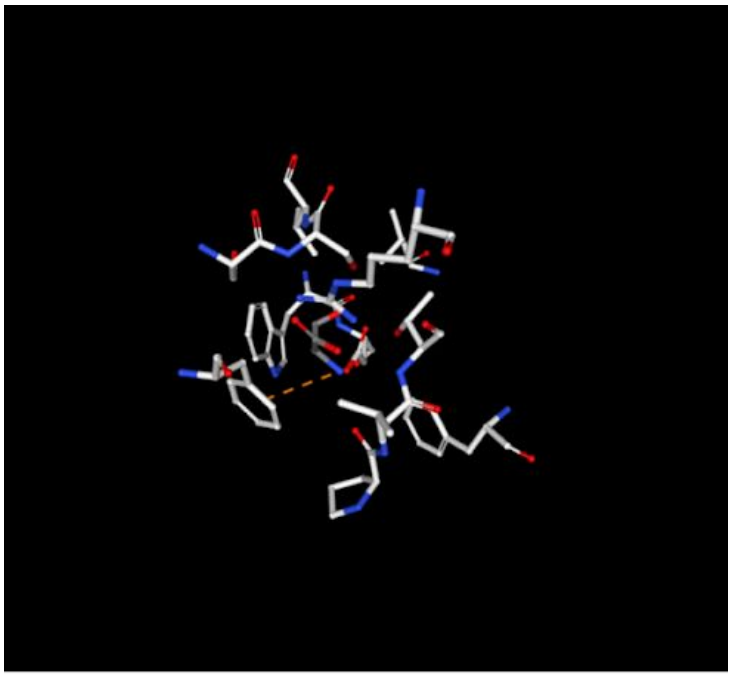
C) Non-Bonded Interactions

a)Hydrogen bonds(Blue)

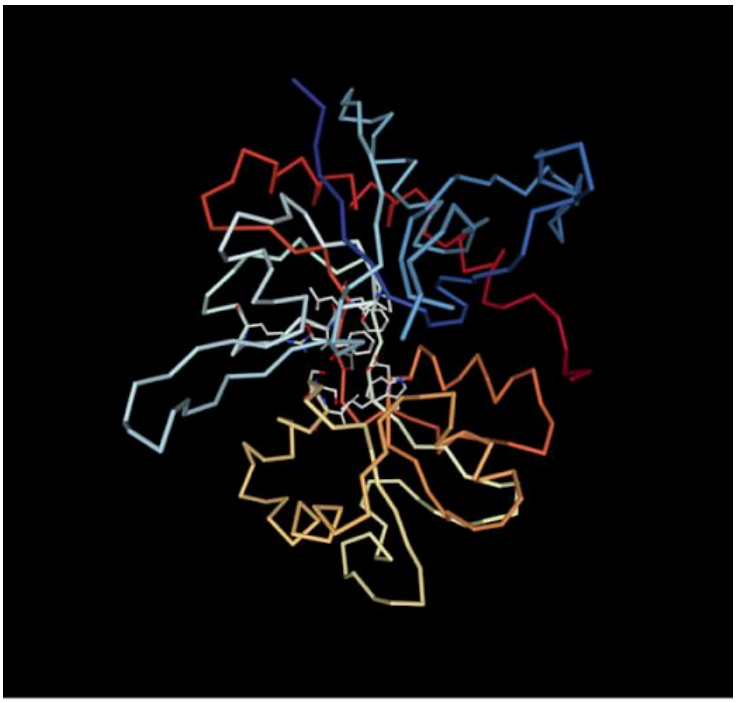


b)Hydrophobic Interaction(Grey)

c) Pi-Interactions(Orange)



d)Polymer Bonds



The molecules contains various types of non bonded interactions which are listed below along with a few examples of residues in the molecule showing these interactions.

- **Disulphide bridges**: Between sulphur atoms of cysteines within 2.2 Angstroms

Position	Residue	Chain	Position	Residue	Chain	Distance
236	CYS	A	290	CYS	A	2.02
28	CYS	A	62	CYS	A	2.04
44	CYS	A	63	CYS	A	2.04

- **Hydrophobic Interactions:** Between Water and molecule within 5 Angstroms

Position	Residue	Chain	Position	Residue	Chain
6	LEU	A	120	MET	A
6	LEU	A	260	TRP	A
6	LEU	A	8	ILE	A

- **Intra Protein Main Chain Main Chain Hydrogen Bonds**

POS	CHAIN	RES	ATOM	POS	CHAIN	RES	ATOM	Dd-a	Dh-a	A(d-H-N)	A(a-O=C)
6	A	L	N	81	A	T	O	2.85	1.91	160.53	138.19
8	A	I	N	6	A	L	O	3.46	3.09	103.65	88.58
8	A	I	N	83	A	E	O	2.82	1.85	168.63	163.08

Dd-a = Distance Between Donor and Acceptor

Dh-a = Distance Between Hydrogen and Acceptor

A(d-H-N) = Angle Between Donor-H-N

A(a-O=C) = Angle Between Acceptor-O=C

- **Intra Protein Main Chain Side Chain Hydrogen Bonds**

POS	CHAIN	RES	ATOM	POS	CHAIN	RES	ATOM	MO	Dd-a	Dh-a	A(d-H-N)	A(a-O=C)
7	A	LYS	N	119	A	ASP	OD2	-	2.86	1.93	157.13	124.98
10	A	THR	OG1	122	A	VAL	O	-	2.78	9.99	999.99	151.02
12	A	HIS	ND1	17	A	VAL	O	-	3.30	2.55	139.13	145.86

- **Side Chain Side Chain Hydrogen Bonds**

POS	CHAIN	RES	ATOM	POS	CHAIN	RES	ATOM	MO	Dd-a	Dh-a	A(d-H-N)	A(a-O=C)
27	A	THR	OG1	23	A	MET	SD	-	3.86	9.99	999.99	999.99
27	A	THR	OG1	25	A	ASP	OD1	-	2.72	9.99	999.99	999.99
27	A	THR	OG1	25	A	ASP	OD2	-	3.45	9.99	999.99	999.99

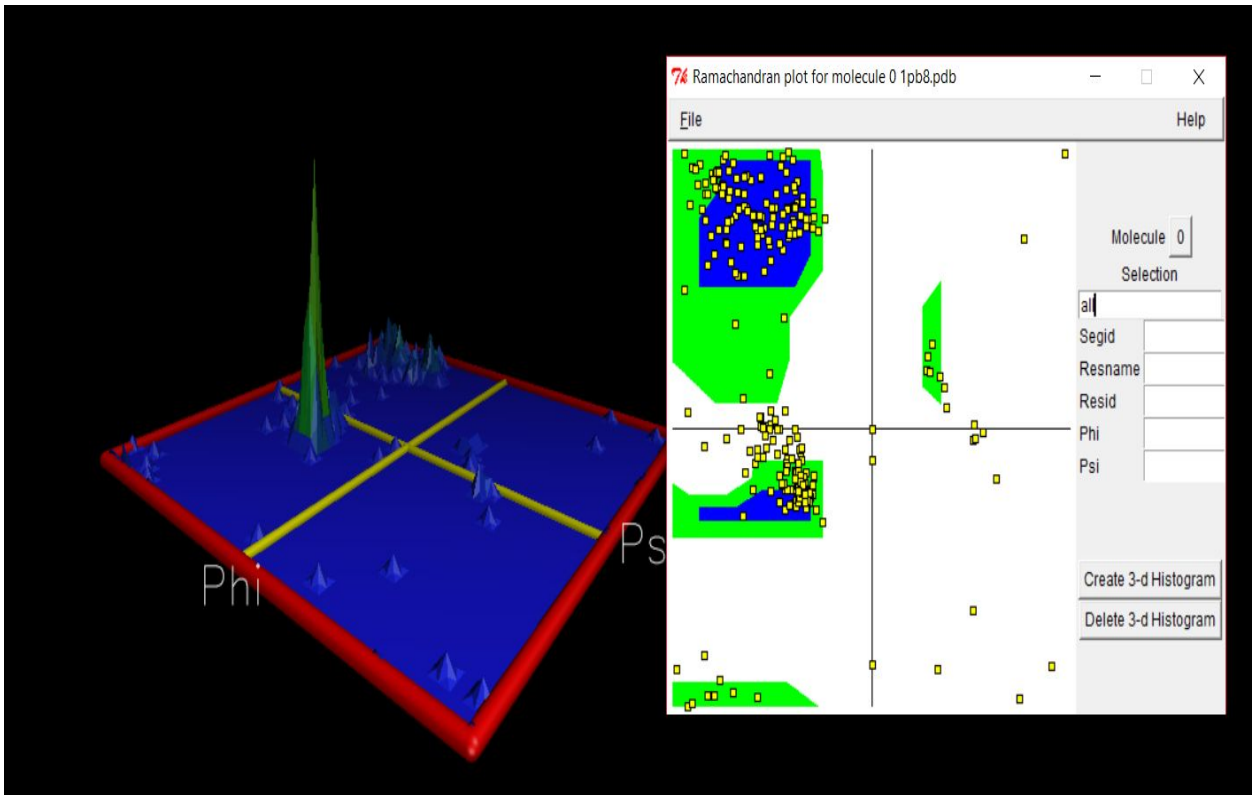
- **Ionic Interactions** within 6 Angstroms

POS	RES	CHAIN	POS	RES	CHAIN
5	ARG	A	83	GLU	A
12	HIS	A	14	GLU	A
14	GLU	A	20	LYS	A

- **Cation-Pi Interactions** within 6 Angstroms

Position	Residue	Chain	Position	Residue	Chain	D(cation-Pi)	Angle
64	TYR	A	41	LYS	A	4.79	146.45
66	PHE	A	142	LYS	A	5.03	128.97
171	PHE	A	163	ARG	A	4.41	142.86

Q2) A) RAMACHANDRAN PLOT



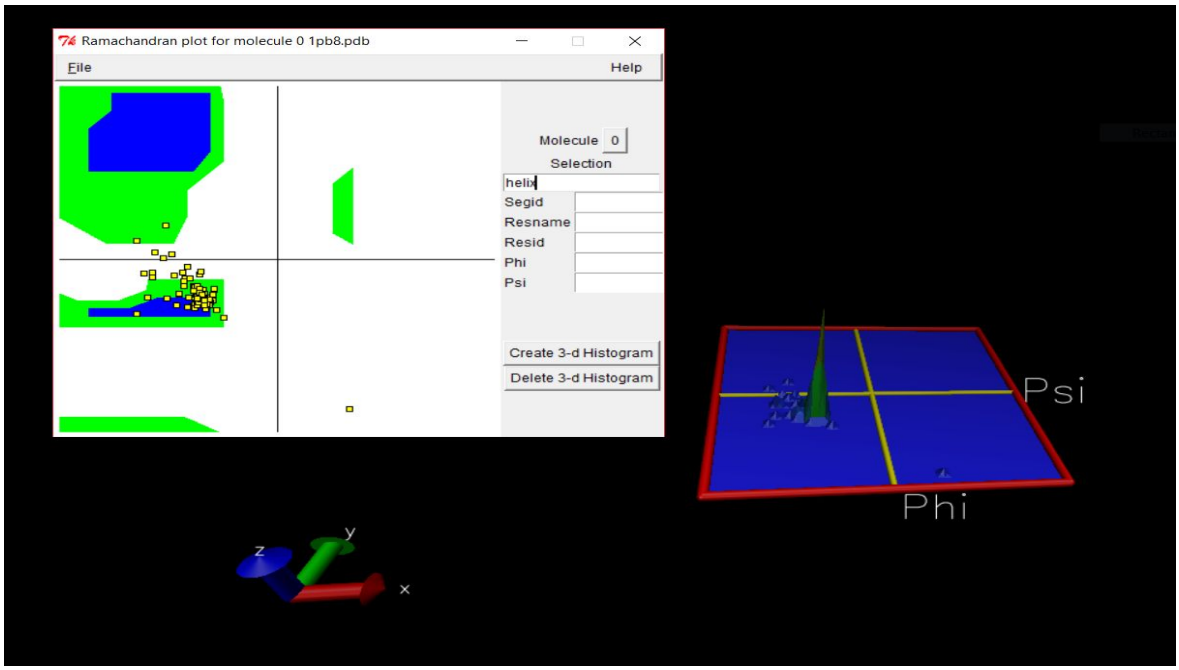
Ramachandran Plot for the whole Protein

Along with the Ramachandran plot, is a histogram representing the frequency of occurrence of different residues in the different areas represented by colours.

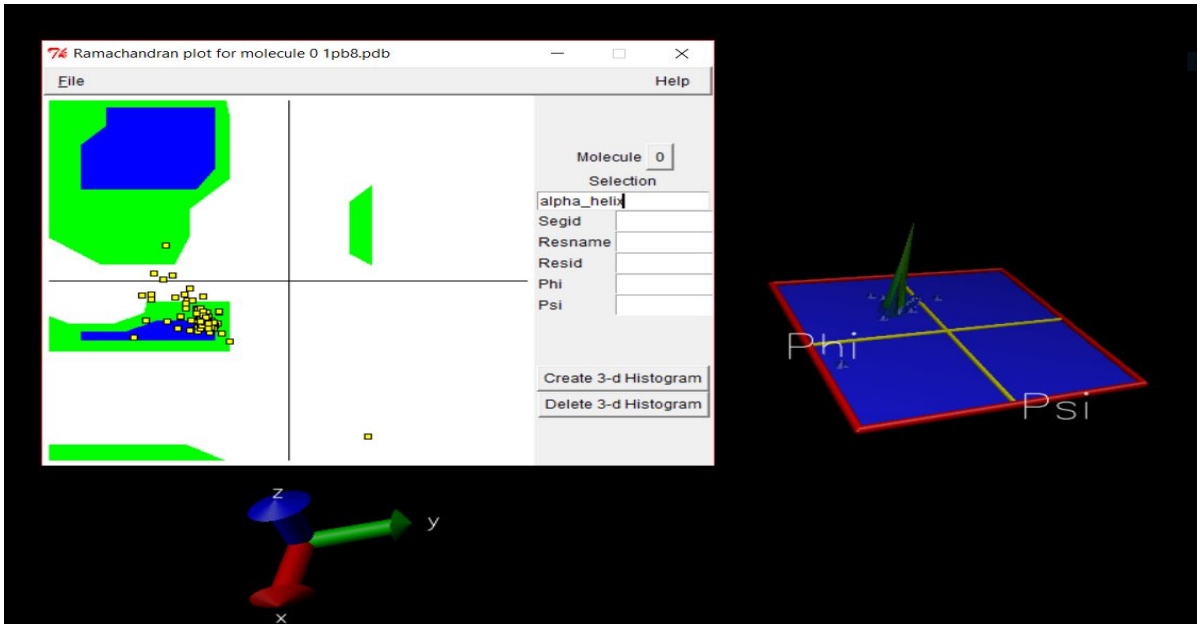
In principle, second quadrant represents beta sheets, third the helices and fourth represent most of the residues falling in the forbidden region.

Ramachandran Plots and Histograms for different Secondary Structures follow:

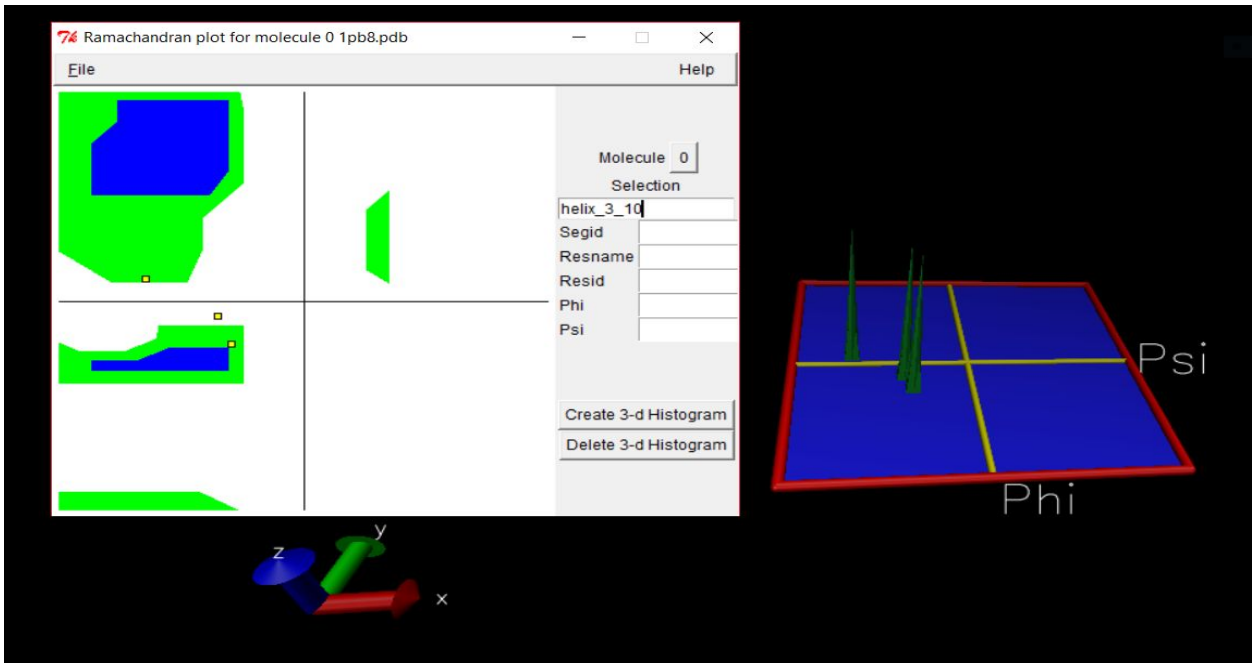
HELIX



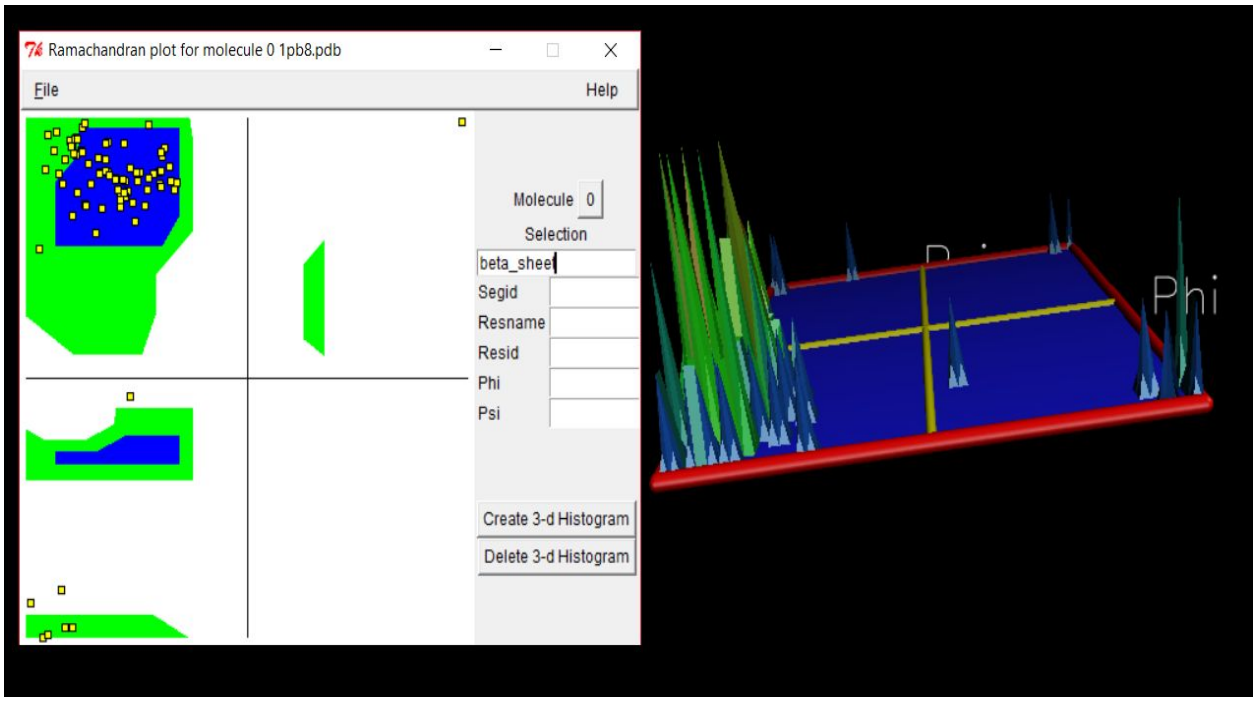
ALPHA-HELIX



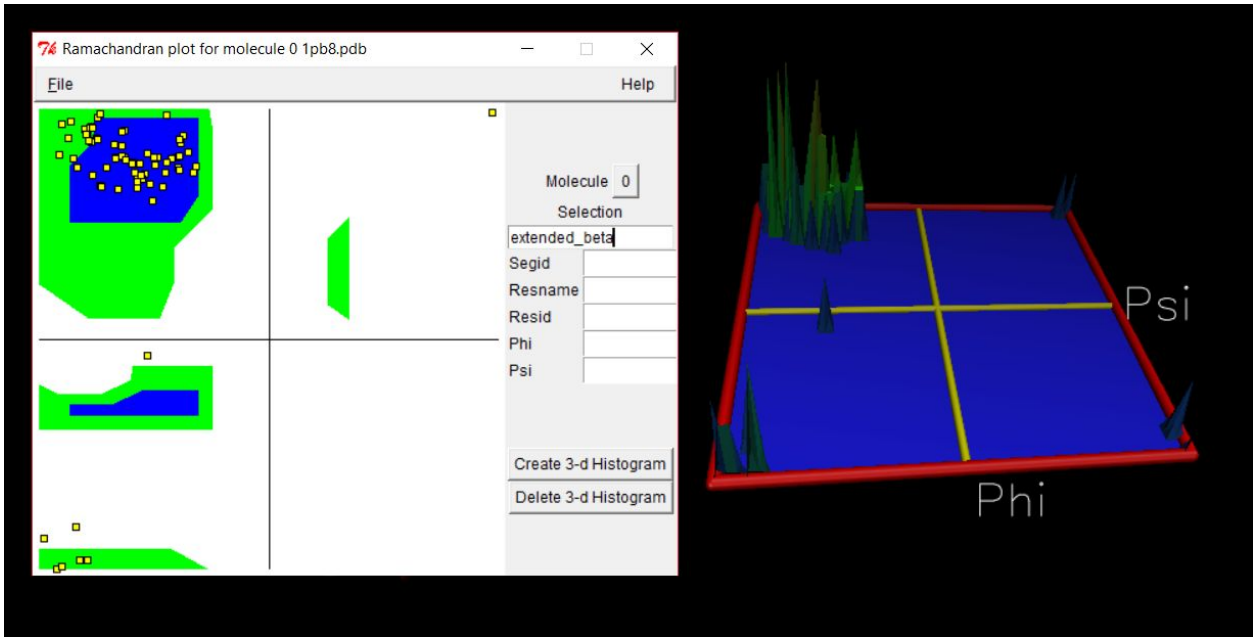
3-10-HELIX



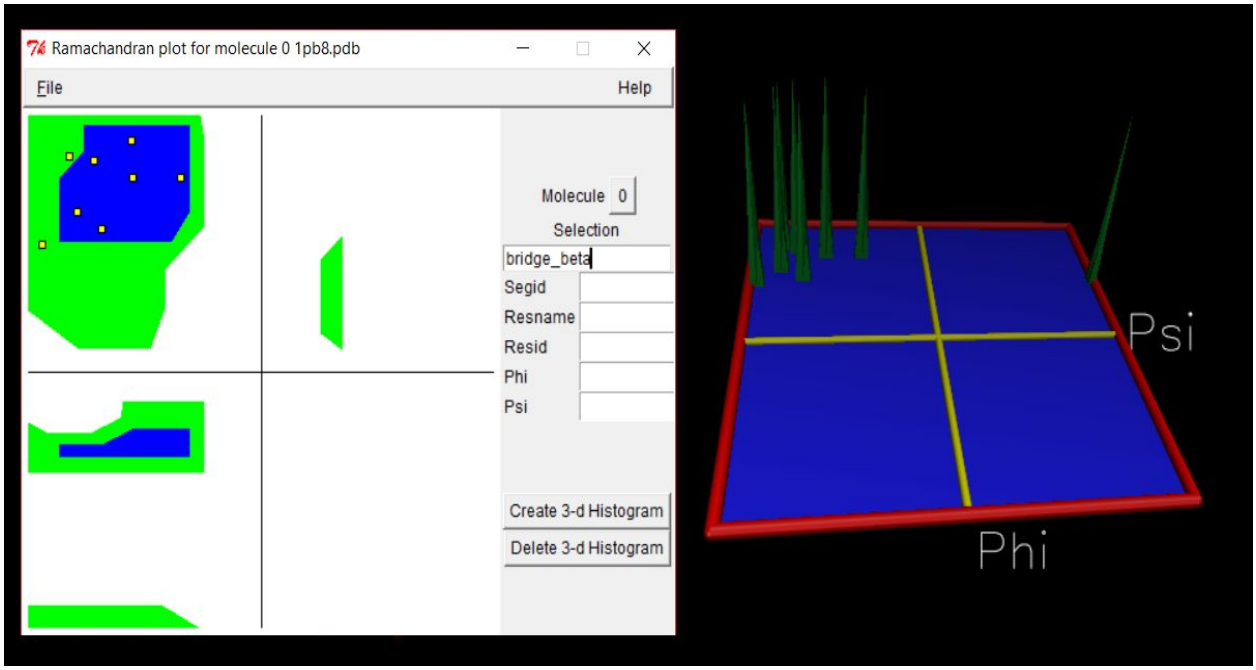
BETA-SHEETS



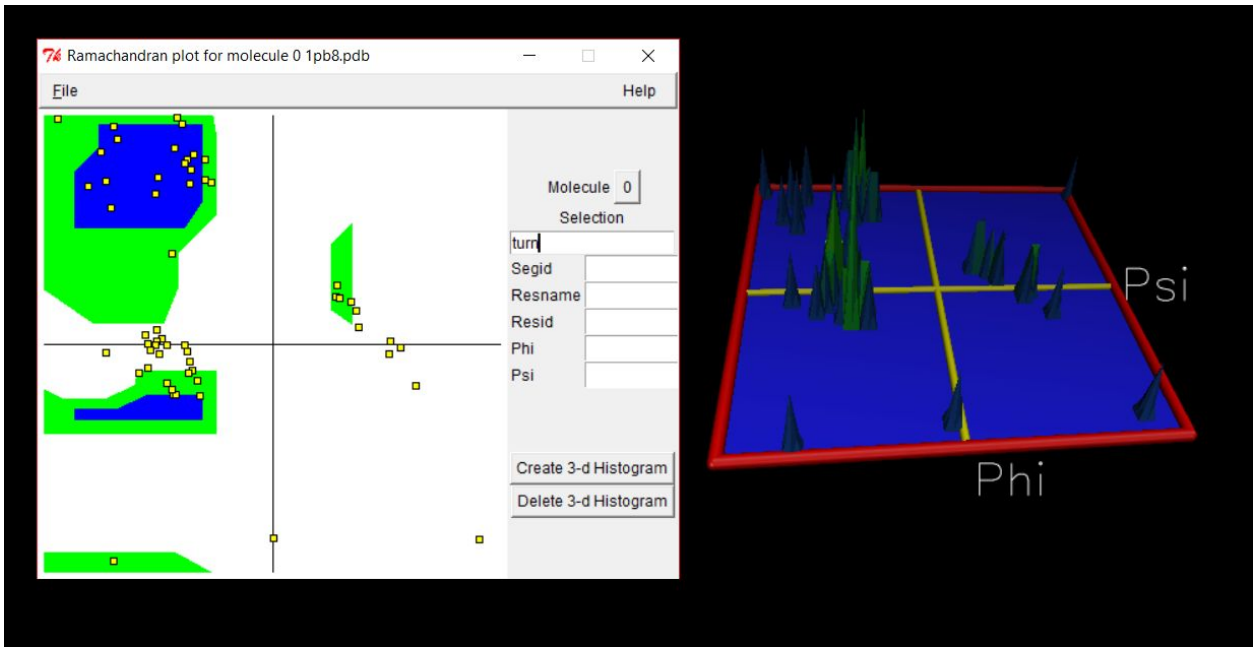
EXTENDED-BETA



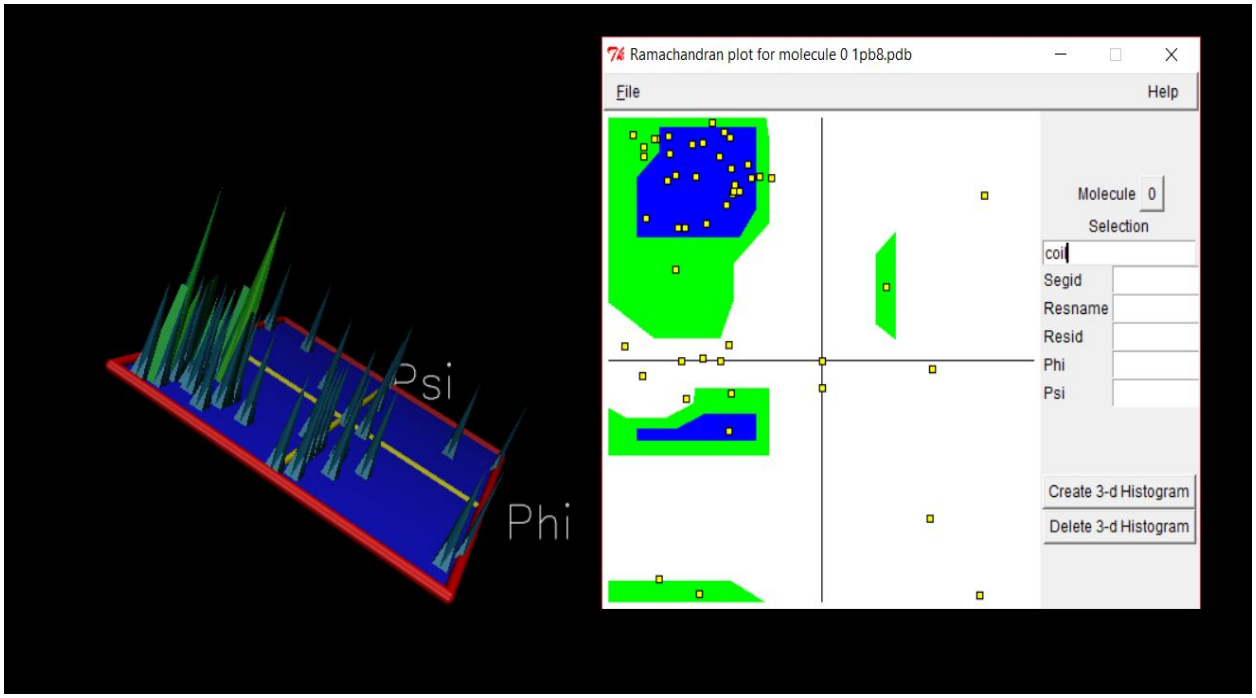
BRIDGE-BETA



TURNS


Ramachandran plot for molecule 0 1pb8.pdb
File
Help
Molecule 0
Selection
turn
Segid
Resname
Resid
Phi
Psi
Create 3-d Histogram
Delete 3-d Histogram
Psi
Phi

COILS


Psi
Phi
Ramachandran plot for molecule 0 1pb8.pdb
File
Help
Molecule 0
Selection
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Create 3-d Histogram
Delete 3-d Histogram

B) FORBIDDEN REGION RESIDUES

The residues falling in the white region are referred to as the ones in the forbidden region. Following is a list of these residues as observed from the Ramachandran Plot.

The order of angles is Phi and then Psi.

GLY 93
137.66864516057967
122.9450279909663

GLY 46
174.2728261670109
177.22145676280914

ASN 216
65.94650981979083
26.205586753248774

GLY 90
67.48752650433336
13.589141697036979

GLY 36
92.92448209841118
2.763196759001327

DSN 901
0.0
0.0

GLY 116
100.03274525115572
-2.3284614186998844

GLY 275
93.27446906339922
-6.184368505372076

GLY 26
91.69064988918595
-7.639286702087298

THR 4
0.0
-20.826283213202625

GLY 153
112.507547915122
-32.21707557278344

GLY 242
91.5751915615337
-117.58163809210707

GLY 108
59.73174118366504
-155.38399626260974

ARG 56
0.0
-152.17238061942228

GLY 65
133.3253612126908
-174.89700595654887

GLY 158
162.4583361815629
-153.73590283308755

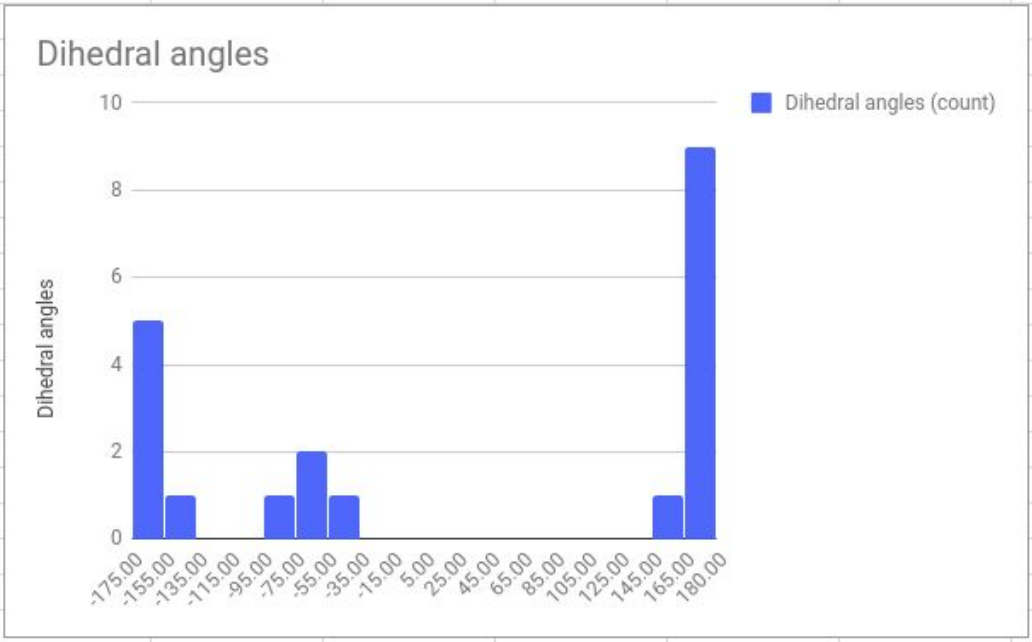
LYS 261
ASP 291
TYR 287
HIS 201
SER 292
TYR 134
TRP 284
TRP 260
ASP 119
GLN 234
LYS 217
PHE 141
SER 115
SER 233
ARG 163
ASP 169
CYS 236
GLU 190
ILE 159
LYS 282
GLY 145
GLN 144
THR 175
ASP 291
THR 241
PRO 15
ASN 274
PRO 259
ASN 48
PHE 245
LYS 200
ASP 89
ASN 102
ILE 159
GLU 190
ALA 132
PRO 167

The above listed 53 are the residues falling in the forbidden region for the protein.

3) Solvated and Unsolvated Butane

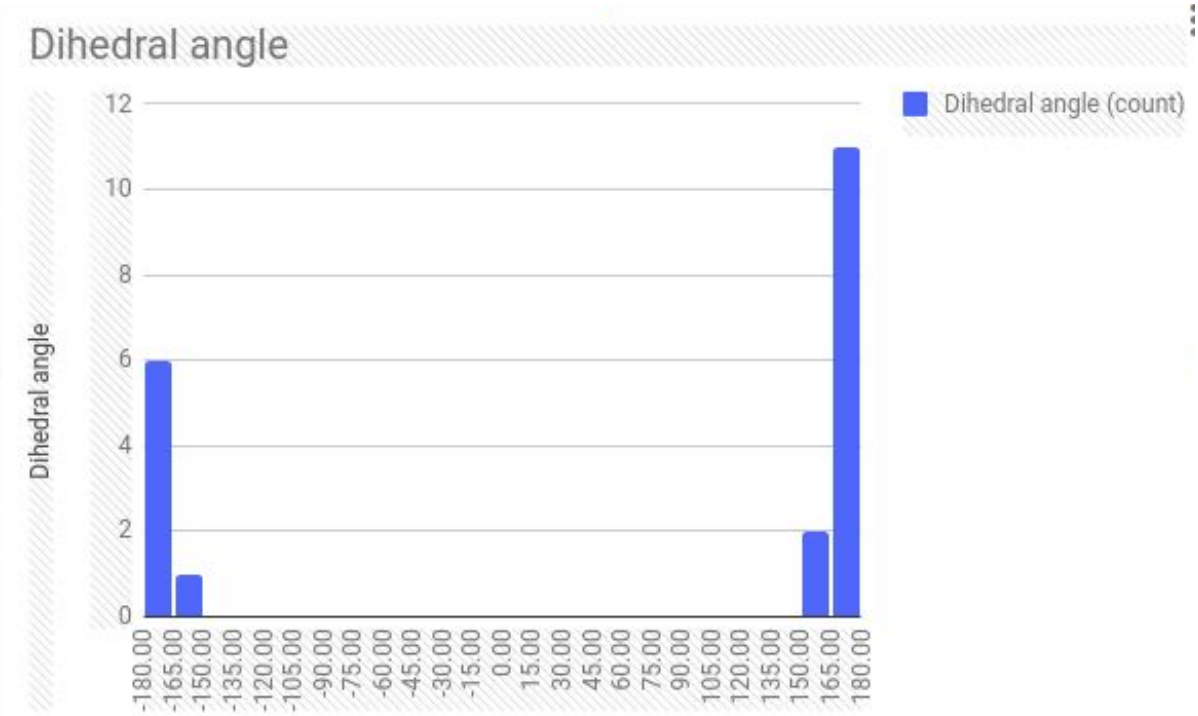
Frequency of Different Dihedral Angles for Solvated Butane

Dihedral angles
-148.3662415
170.010849
169.7238922
-172.6492462
160.8505554
179.9411163
176.7983398
-172.3665009
-85.09091187
-62.40852356
-58.24843216
-50.40098572
-159.9320221
-168.265274
-170.8392944
178.3189697
177.4645996
178.3197784
175.2298279
172.9406433



Conclusions from the Graph : The highest probability is seen for dihedral angles ranging between -155 to +165. These dihedral angles correspond to the anti form of the solvated butane. The anti form was expected to have highest stability theoretically, as there exists least steric hindrance between carbon carbon atoms. Also as the highest probability of dihedral corresponds to that range, the theoretical analogy is confirmed as the molecule would like to remain in the conformer which will correspond to the least energy which in solvated butanes case is anti form. Gauche form is also stable as is evident from a slightly good probability existing for it.

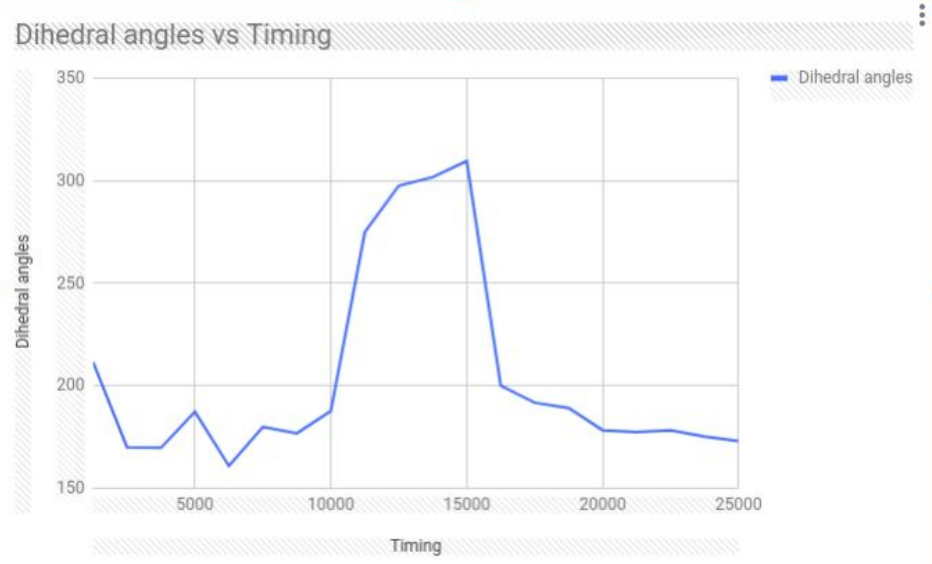
Frequency of different Dihedral Angles for Unsolvated Butane



The Unsolvated butane also shows similar results like the solvated one ashere also the anti conformer is the most stable as is evident from the graph. The highest probability of dihedral angles lie in the range -165 to +165 which correspond again to the anti form.

The histograms are plotted with the dihedral angles on the x axis and the number of occurrences as frames proceed along the y axis. With this being said it is quite evident that the most probable conformation would have the tallest bar. Therefore indirectly we can even understand the probability of existence in these conformers from the histogram.

3)B) Anti and Gauche Transitions



The above graph gives the dihedral angles with the different times corresponding to the frames in the log file.

Theoretically transition from Anti to Gauche should be a slower process than vice versa as Anti is more stable than Gauche and a system would want to continue to exist in the more stable form rather than transitioning to a comparatively less stable form.

From the graph the analogy prevails as it takes 5000 units of time for the system to convert from Anti to Gauche but only 1250 to convert from Gauche to Anti. The rate of transition of dihedral angles can also be found by finding the slope of the line graph at different times.
