DRUG DESIGN PROJECT: WINTER 2017

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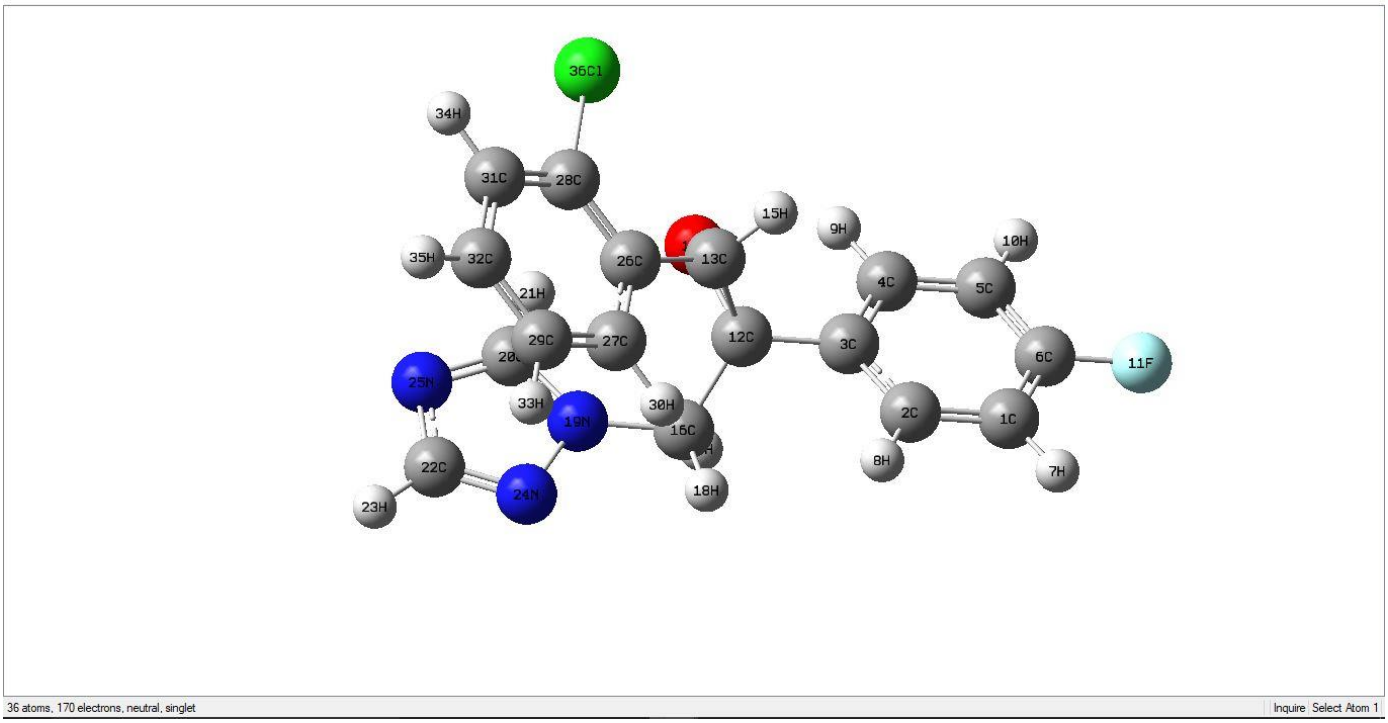
Drug: *Epoxiconazole*

Quantum computation of the drug ***Epoxiconazole*** and molecular docking with *Oxidoreductase* [PDB id: 3ibd].

Quantum Computation:

Epoxiconazole drug was drawn in Gaussian software and optimization, frequency, and molecular orbital calculations in gas phase using HF/3-21G level of theory was done. The following is the image of the drug Epoxiconazole after optimization and frequency calculation:

Image: Epoxiconzole after optimization and frequency calculation with labels and symbols



***The result of frequency calculation was examined and no imaginary frequency was found.**

Table of selective bond distance [3 distances] of Epoxiconazole in gas phase:

Label	Distance
(28C)-(36Cl)	1.815
(14O)-(12C)	1.466
(24N)-(19N)	1.398

Table of selective bond angle [3 angles] of Epoxiconazole in gas phase:

Label	Angle
(3C)-(4C)-(5C)	29.9
(23H)-(22C)-(25N)	123.1
(34H)-(31C)-(28C)	34.3

Table for HOMO, HOMO-1, HOMO-2, LUMO, LUMO+1 and LUMO+2, homo-lumo gap of Epoxiconazole

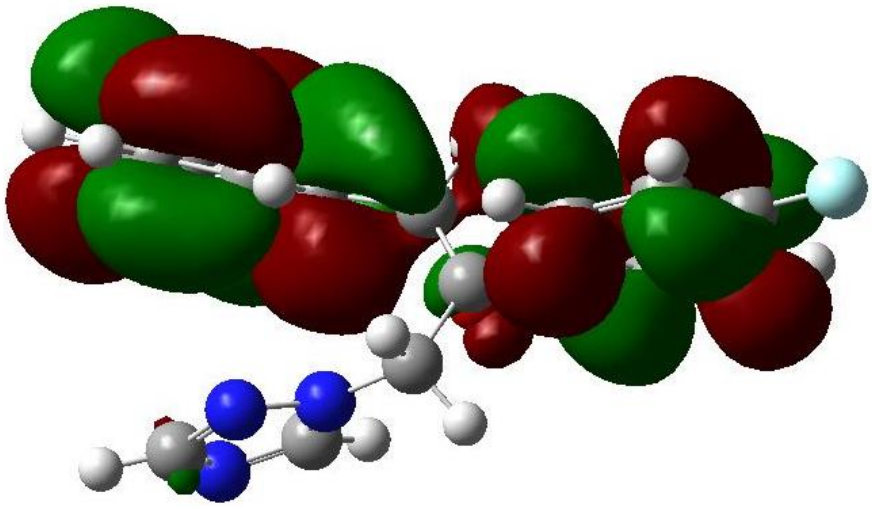
LUMO+2	**0.12335**
LUMO+1	**0.11647**
LUMO	**0.11250**
HOMO	**-0.35192**
HOMO-1	**-0.35573**
HOMO-2	**-0.36223**

***Humo-lumo gap: 0.11250 - (-0.35192) = 0.46442**

Table for the electronic energy (E), enthalpy (H), Gibbs free energy (G) and dipole moment (Debye) of Epoxiconazole

Electronic energy (E)	-1440.369012
Enthalpy (H)	-1440.368068
Gibbs free energy (G)	-1440.434870
Dipole moment (Debye)	3.8028 Debye

Image for HOMO and LUMO orbital of Epoxiconazole:



Molecular Docking:

Molecular docking between *Epoxiconazole* and the receptor protein oxidoreductase by *Autodock Vina*

Grid box size

center_x = 20.2575 center_y = 11.0403 center_z = 24.3481	size_x = 60.1667110634 size_y = 65.2751292419 size_z = 66.7326102257

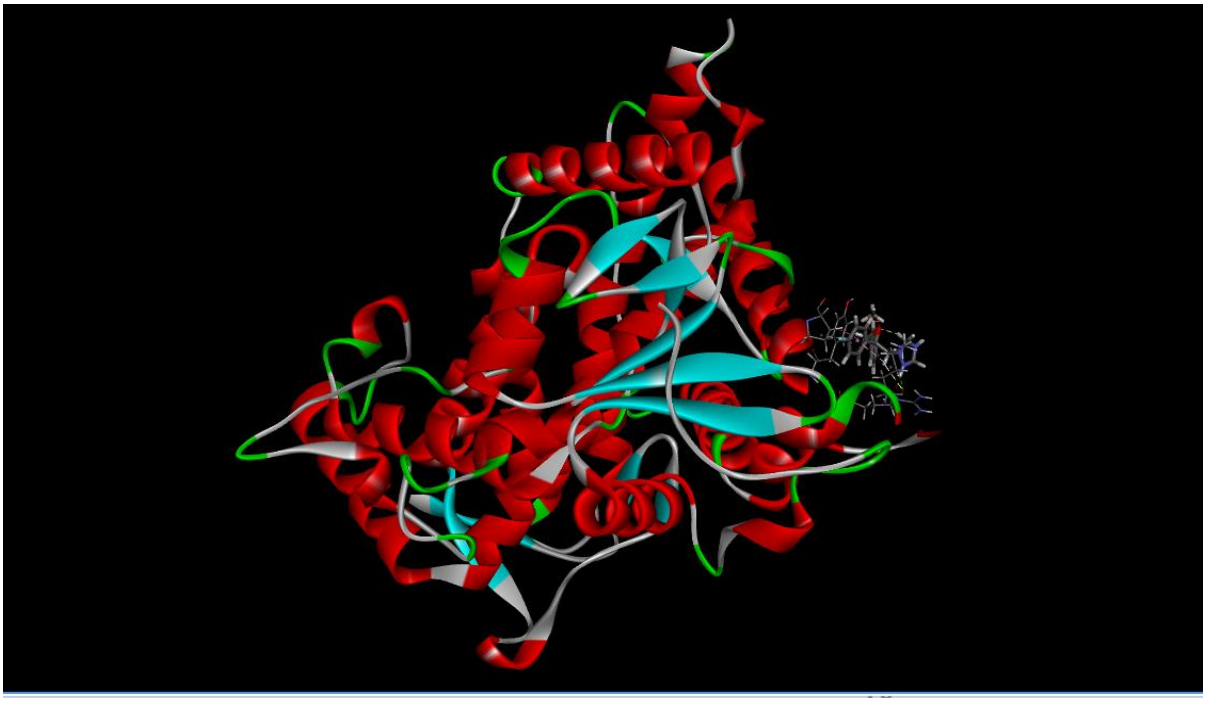
Binding energies

Ligand	Binding Affinity	rmsd/ub	rmsd/lb
3ibdoptimized_EPOXYCONAZOLEPDB	-7	0	0
3ibdoptimized_EPOXYCONAZOLEPDB	-6.5	15.577	14.468
3ibdoptimized_EPOXYCONAZOLEPDB	-6.4	36.729	35.199
3ibdoptimized_EPOXYCONAZOLEPDB	-6.4	36.811	33.799
3ibdoptimized_EPOXYCONAZOLEPDB	-6.4	40.395	38.183
3ibdoptimized_EPOXYCONAZOLEPDB	-6.4	15.687	14.19
3ibdoptimized_EPOXYCONAZOLEPDB	-6.3	4.055	2.636
3ibdoptimized_EPOXYCONAZOLEPDB	-6.3	3.939	2.553
3ibdoptimized_EPOXYCONAZOLEPDB	-6.1	33.776	32.399

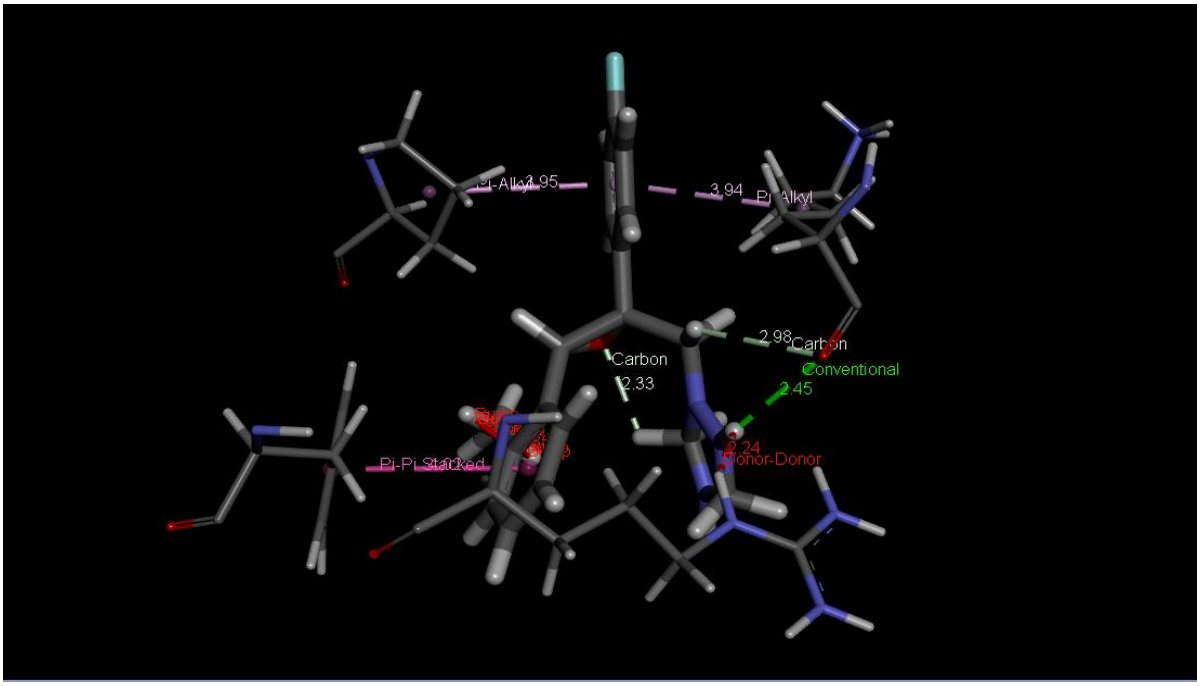
5 non-bonding interactions of drug with amino acids

Name	Parent	Distance	Category	Types	From	From Chemistry	To	To Chemistry	Angle DHA	Angle HAY	Theta	Theta 2	Gamma	Closest distance	
:UNK0:HN - A:LYS225:O	Ligand Non-bond Monitor	2.45307	Hydrogen Bond	Conventional Hydrogen Bond	:UNK0:HN	H-Donor	A:LYS225:O	H-Acceptor	130.345	160.635					
:UNK0:H17 - A:LYS225:O	Ligand Non-bond Monitor	2.97961	Hydrogen Bond	Carbon Hydrogen Bond	:UNK0:H17	H-Donor	A:LYS225:O	H-Acceptor	124.758	109.88					
:UNK0:H21 - :UNK0:O	Ligand Non-bond Monitor	2.3282	Hydrogen Bond	Carbon Hydrogen Bond	:UNK0:H21	H-Donor	:UNK0:O	H-Acceptor	110.777	93.826					
:UNK0 - A:TYR235	Ligand Non-bond Monitor	4.02348	Hydrophobic	Pi-Pi Stacked	:UNK0	Pi-Orbitals	A:TYR235	Pi-Orbitals			33.468	15.371	18.112	3.618	
:UNK0 - A:PRO106	Ligand Non-bond Monitor	3.95435	Hydrophobic	Pi-Alkyl	:UNK0	Pi-Orbitals	A:PRO106	Alkyl							
:UNK0 - A:LYS225	Ligand Non-bond Monitor	3.93833	Hydrophobic	Pi-Alkyl	:UNK0	Pi-Orbitals	A:LYS225	Alkyl							

Picture of non bonding interaction with protein visibility



Picture of non bonding interaction without protein visibility



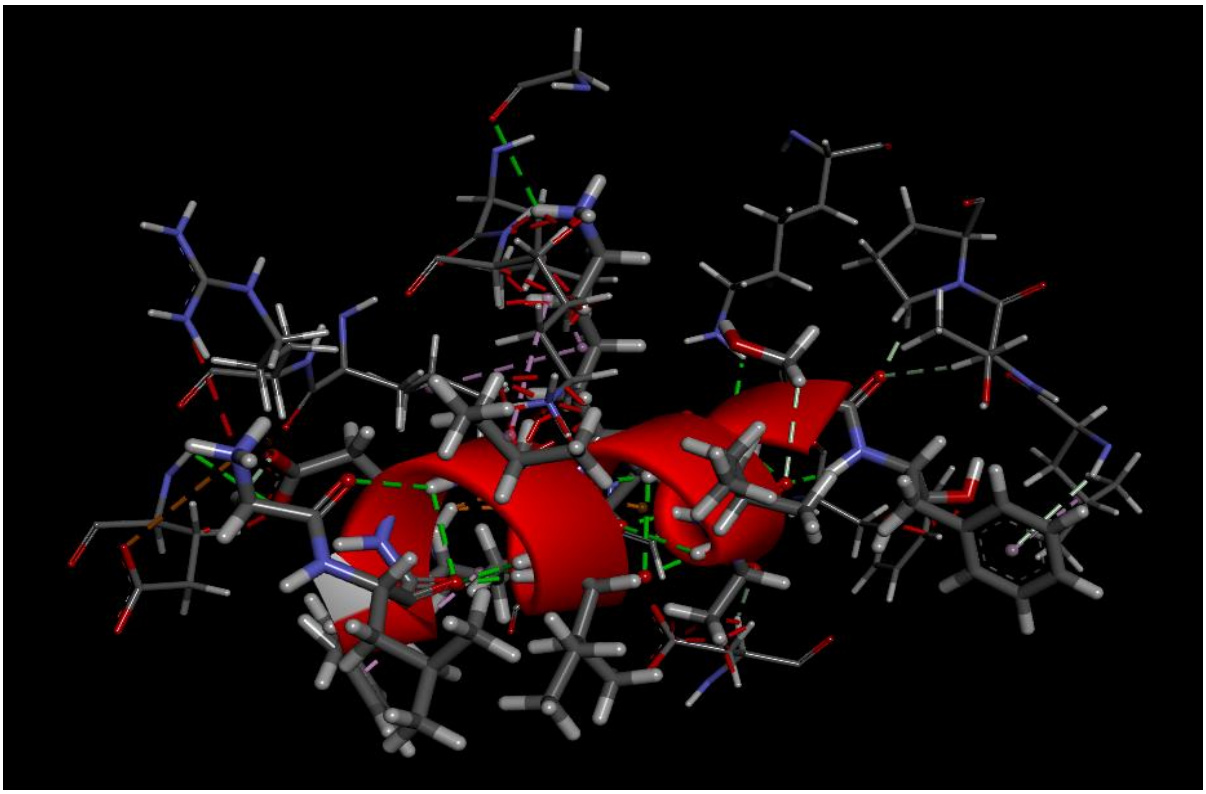
Aurein 1.2 peptide (Sequence: GLFDIIKKIAESF) is an antifungal peptide. Five structure of this peptide has been designed by PEP-FOLD3.5 then docked against 3IBD protein in patchdock.

Comparison of the Score, Area and ACE of five model peptides

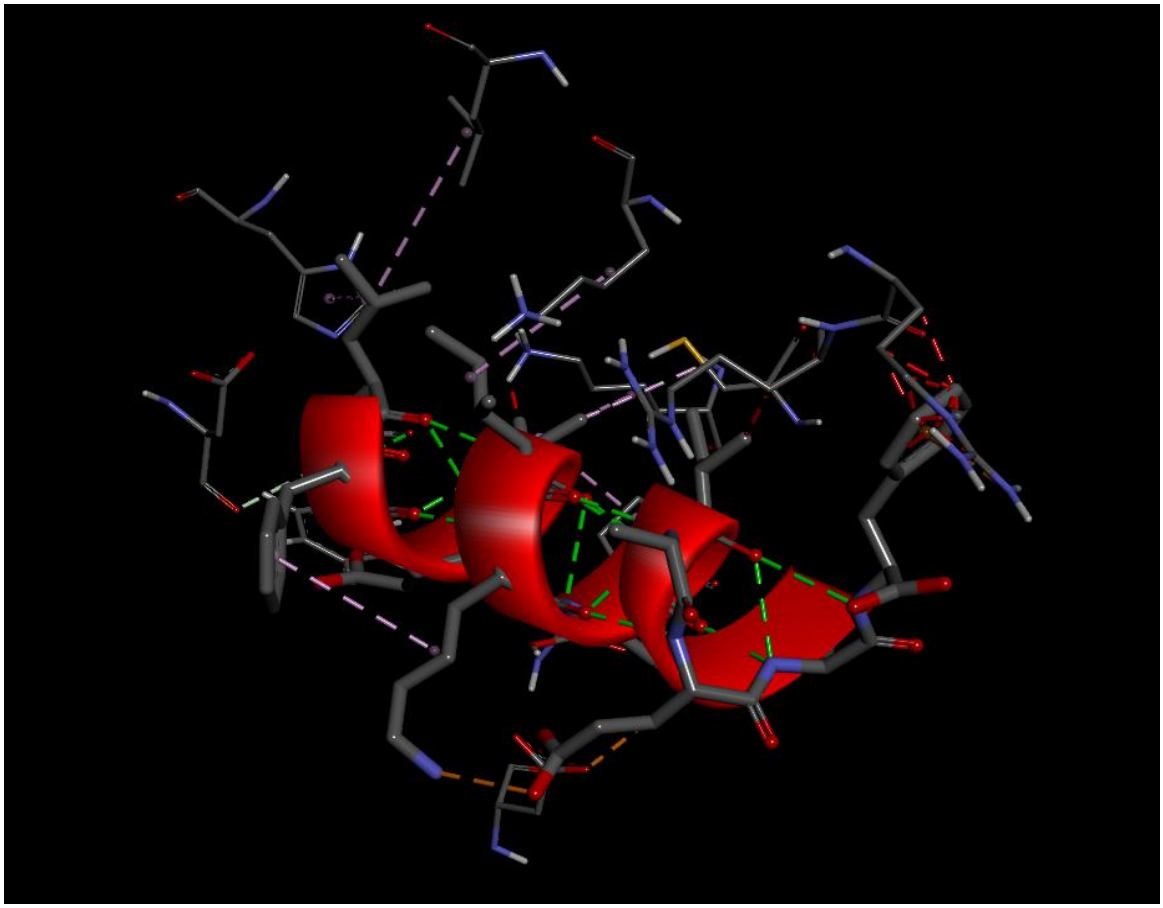
	Score	Area	ACE
Model 1	7362	1030.90	295.70
Model 2	7260	958.90	63.68
Model 3	7386	1129.40	-41.46
Model 4	7418	1094.20	-83.15
Model 5	7494	975.90	130.20

Non bonding interaction image of these 5 peptides model with the protein by *Discovery Studio*.

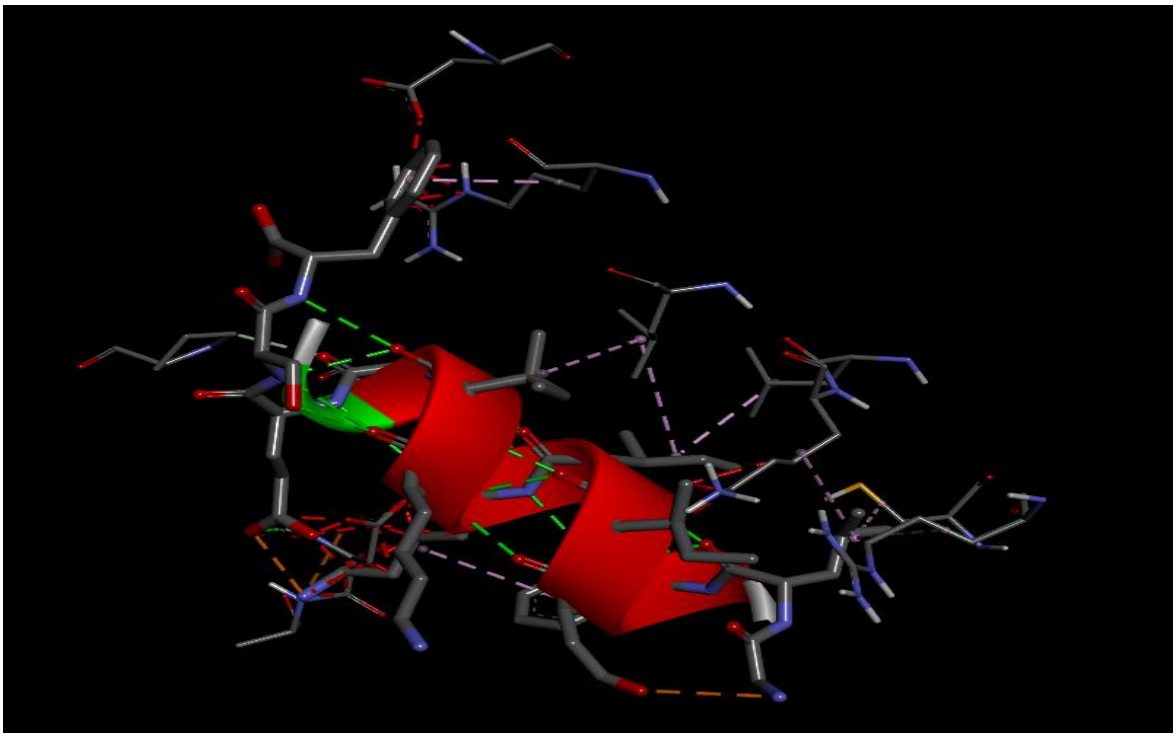
Non bonding interaction image of Model 1 with the protein



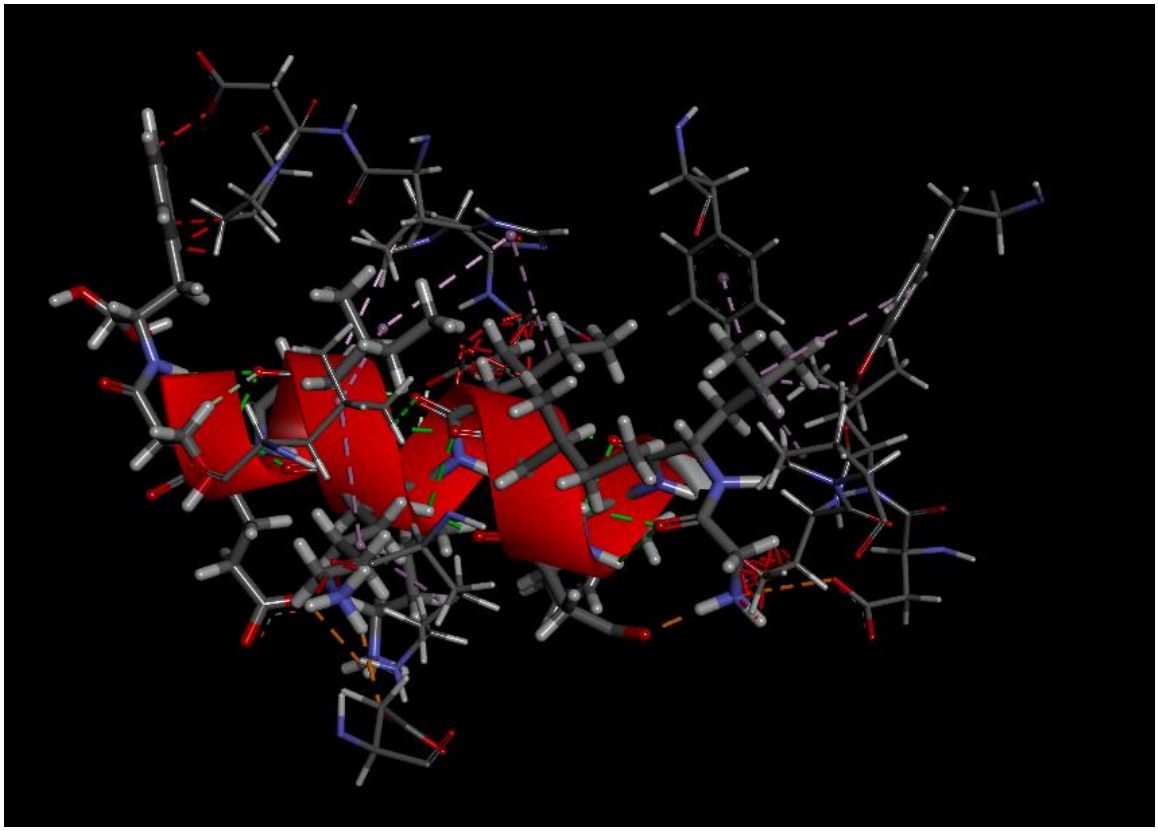
Non bonding interaction image of Model 2 with protein



Non bonding interaction image of Model 3 with protein



Non bonding interaction image of Model 4 with protein



Non bonding interaction image of Model 5 with protein