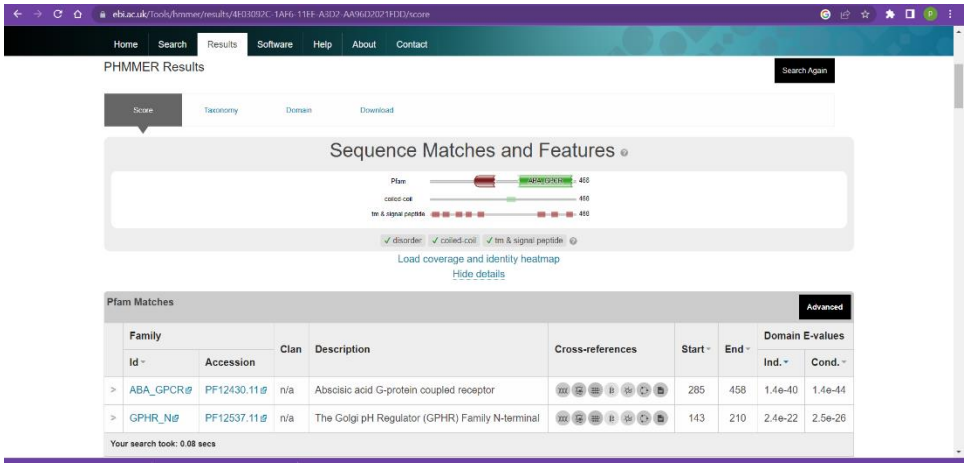
Day 2:

Gene Annotation

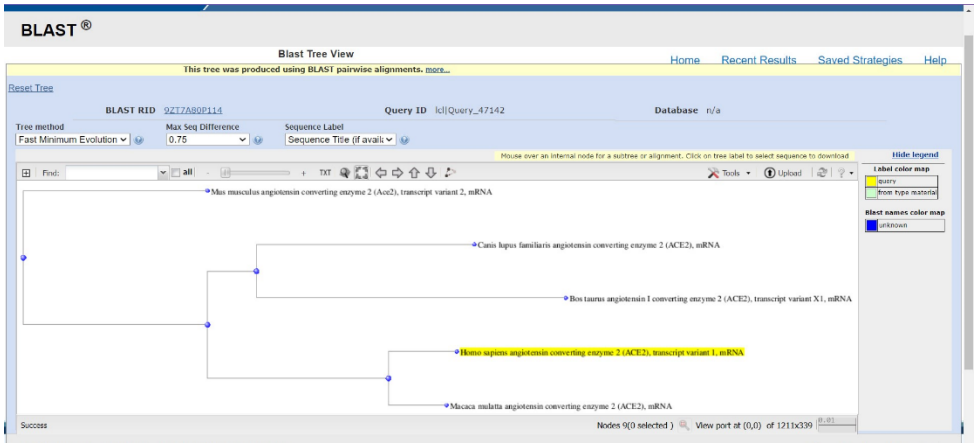
Protein Name: GPCR-type G protein 1
Protein ID - Q9XIP7. GTG1_ARATH
Find the following Gene function details
Location-Start and end: 143 and 210
Family: Golgi pH regulator (TC 1.A.38) family.
Clan: n/a
Domain: GPHR_N,
E value: 2.4e-22 and 2.5e-26
Description of function: The Golgi pH Regulator (GPHR) Family N-terminal.



Day 3: Phylogenetics

Construct a Phylogenetic tree for components of Corona virus.

You can choose any gene/protein/component associated with Corona virus for atleast 5 different species/variants. Add the screenshot of the tree here.



Day 4:
Genome name (the one of your interests): SARS coronavirus Tor2

From RAST results:

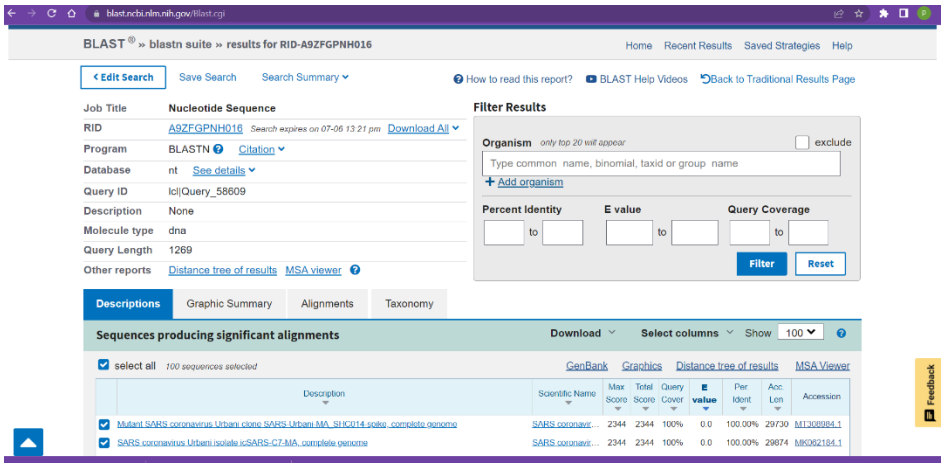
Mention the desired nucleotide sequence that you choose to perform BLAST on and fill in the following:

1) Nucleotide sequence:

atgtctgataatggaccccaatcaaaccaacgtagtgccccccgcattacatttggtggacccacagattcaactgacaataaccagaatgg
aggacgcaatggggcaaggccaaaacagcgccgaccccaaggtttacccaataatactgcgtcttggttcacagctctcactcagcatggc
aaggaggaacttagattccctcgaggccagggcgttccaatcaacaccaatagtggtccagatgaccaaattggctactaccgaagagcta
cccgacgagttcgtggtggtgacggcaaaatgaaagagctcagccccagatggtacttctattacctaggaactggcccagaagcttcacttc
cctacggcgctaacaaagaaggcatcgtatgggttgcaactgagggagccttgaatacacccaaagaccacattggcacccgcaatccta
ataacaatgctgccaccgtgctacaacttcctcaaggaacaacattgccaaaaggcttctacgcagagggaagcagaggcggcagtcaag
cctcttctcgctcctcatcacgtagtcgcggtaattcaagaaattcaactcctggcagcagtaggggaaattctcctgctcgaatggctagcgga
ggtggtgaaactgccctcgcgctattgctgctagacagattgaaccagcttgagagcaaagtttctggtaaaggccaacaacaacaaggcca
aactgtcactaagaaatctgctgctgaggcatctaaaaagcctcgccaaaaacgtactgccacaaaacagtacaacgtcactcaagcatttg
ggagacgtggtccagaacaaacccaaggaaatttcggggaccaagacctaatcagacaaggaactgattacaaacattggccgcaaatt
gcacaatttgctccaagtgcctctgcattctttggaatgtcacgcattggcatggaagtcacaccttcgggaacatggctgacttatcatggagcc
attaaattggatgacaaagatccacaattcaaagacaacgtcatactgctgaacaagcacattgacgcatacaaaacattcccaccaacag
agcctaaaaaggacaaaaagaaaaagactgatgaagctcagcctttgccgcagagacaaaagaagcagcccactgtgactcttcttcctg
cggctgacatggatgatttctccagacaacttcaaaattccatgagtggagcttctgctgattcaactcaggcataa

2) Location on the genome: AY274119.3_28120_29388
3) Start and end nucleotide: 28120 AND 29388
4) Function : hypothetical protein

Perform a BLAST on the nucleotide sequence and paste a screenshot of the obtained BLAST results:



Day 5 & 6:

Molecular Docking

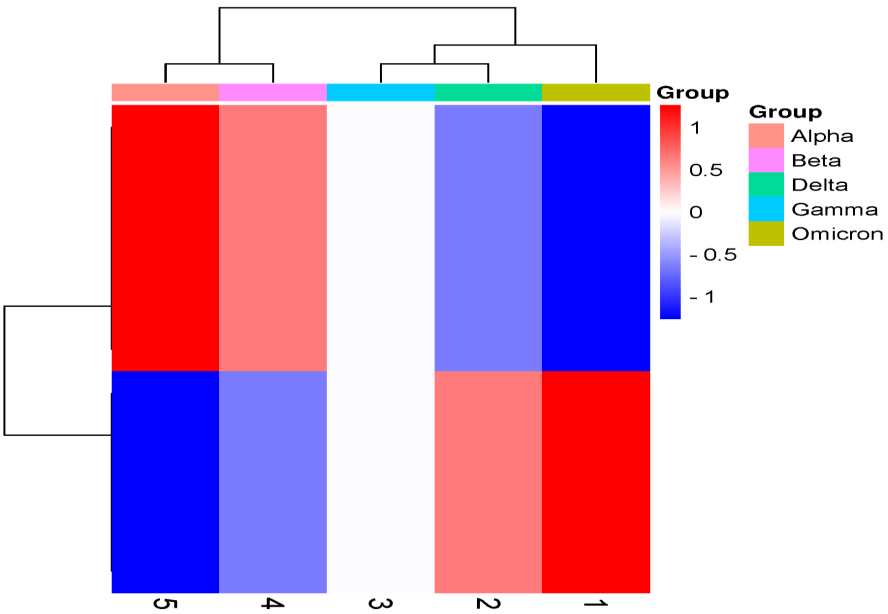
Protein Name: PDE4

Protein ID - 5X74

Ligand Name	Ligand ID	Follows Lipinski Rule?	Energy value	Dock Image

Theophylline	2153	YES	-	
Apremilast	11561674	YES	-	
Roflumilast	449193	YES	-	

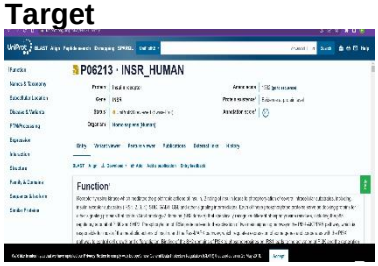
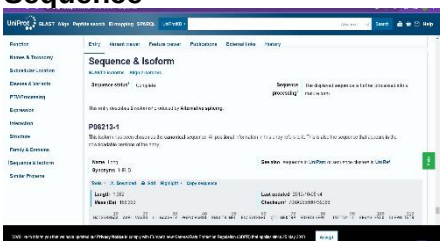
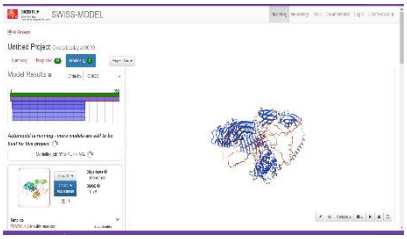
Day 7:
INPUT LINK: https://docs.google.com/spreadsheets/d/1ZSR8D3ex8heS7n-vmDDsYBPCBZ6dOZVk/edit?usp=drive_link&ouid=116553913411753756421&rtpof=true&sd=true



INTERPRETATION:

Day 8 & 9: Homology Modelling:
You can choose any protein which is involved in SARS CoV-2 Pathogenesis (Eg: ACE2 receptor, any envelope protein) and can take at least 2 homologous sequences with sequence similarity >30%. Try to develop a hypothesis around it (Like Why you want to use Homology modelling for your protein of interest, Purpose and outcome of it) and more importantly how it is going to add value to your hypothesis.

Protein: Angiotensin-converting Enzyme 2
Gene: ACE2
PDB: Q9BYF1 (First Isoform)

Target	Sequence	Result
		

Day 10:

Please paste your GitHub account link: https://github.com/praneethareddy07/FIRST-career-project