Ashlee Gardiner

Bioinformatics for Biologists

Assignment 5 - updated

**Number 3-**

**(fasta file)** raxmlHPC-HYBRID-AVX -T 4 -s infile -N autoMRE -n result -f a -p 12345 -x 12345 -m PROTCATDAYHOFF

**(newick file)** muscle -in infile.fasta -seqtype protein -maxiters 16 -maxmb 30000000 -hydro 5 -hydrofactor 1.2 -log logfile.txt -weight1 clustalw -distance1 kmer6\_6 -cluster1 upgmb -sueff 0.1 -root1 pseudo -maxtrees 1 -weight2 clustalw -distance2 pctidkimura -cluster2 upgmb -sueff 0.1 -root2 pseudo -objscore sp -noanchors -out output.fasta

**Number 4-**

Syconycteris\_australis\_ace2

Dobsonia\_viridis\_ace2

Cynopterus\_sphinx\_ace2

Rousettus\_leschenaultii\_ace2

Epomophorus\_wahlbergi\_ace2

**Number 5-**

Phylogeny enriches our understanding of how these specific receptors (ace2 and bats) relate to their common ancestors and other receptors. This helps us to be study and understand the pathogenesis and mode of transmission of COVID which caused the last world-wide pandemic.