Worked on literature review. Papers on know PETase were examined to find out the temperature, pH and location at which these enzymes were found. After this, Pyza database was used to figure out the biological samples of these PETase enzymes. I also wrote the aggregate temperature of different subgroups for our phylogenetic network. Then, I used Jalview to reorient the amino acid sequence to figure out the residue numbers of different enzymes and figure out the sites. After this, Pymol was used to measure the cleft distance. This was done again with the Ancestral reconstruction data.