*First get summary (?) of 1000 hits*

blastn -db nr -query week1\_query.fa -out blastresult -remote -max\_target\_seqs 1000

*After checking E value is less than 0.0001, get alignments from all 1000 hits.*

blastn -db nr -query week1\_query.fa –evalue 0.0001 –outfmt "6 sseqid qstart qend sseq"

*Change FASTA to amino acid seq*

transeq blast.fa

blast.pep

*align the AA sequences*

mafft fakeoutput > align

aligned

$ blastn -db nr -query week1\_query.fa -evalue 0.0001 -max\_target\_seqs 1000 -remote -outfmt "6 sseqid qstart qend sseq" > alignment.out

# running the blast file

awk '$2 == 1 {print ">"$1"\t"$3"\t"$4}' alignment.out | sed 's| - ||g' | awk '$2 == 10293 {print $1"\n"$3}' > alignment.fa

#converting to fa file and getting rid of gaps

transeq alignment.fa codon.fa

mafft codon.fa > mafft.out