Questions to explore protein -aa files

-stop codons in middle 🡪 how to deal with this

-how can we differentiate a mutated (non-funtional) protein from others? 🡪 guessing they wouldn’t meet the threshold and would not occur in occur in output file

- mutuation such as insertion or deletion (in aas that really matter) in this case, not early stop ,

- would just have to use logic and protein maker software?

-how would proteins with low probability of occurring be classified? Or do we disregard that

-how do we differentiate unencountered/uncategorized proteins from unviable sequences 🡪 use protein folding rules?

-HHM + annotation questions

-what is the threshold we set for proteins?

-output seems as though it gives protein name and probability of that sequence happening by chance (assuming that’s either i-value or c-value)