## 1. Collect Pfam "seed" entry:

Select the Pfam entry of your protein of interest. Go to the "Alignment" tab, and from "Available alignments" select the "seed" alignment. Download the seed alignment in clustal2 format.

## 2. Use the "Visual" sequence specific selection pairwise sequencing code:

To find the pairwise sequence alignment between 2 homologous sequences of the neurotransmitter membrane channel, a stockholm file from Pfam was input into a biopython code using the pairwise 2 package. This step was repeated with 2 homologous sequences of the protein of interest: Legumain. This was also done using a stockholm file of the protein of interest found on Pfam. This was done using the code below:

```
from Bio import AlignIO, pairwise2

sto_file = r"C:\Users\Tania\Downloads\PF01650.alignment.seed\PF01650.alignment.seed" #Insert your .seed stockholm/clustal2 filepath here

alignment = AlignIO.read(r"C:\Users\Tania\Downloads\PF01650.alignment.seed\PF01650.alignment.seed", "stockholm") #Insert your .seed stockholm/clustal2 filepath again

seq1 = alignment[0].seq

seq2 = alignment[1].seq

alignments = pairwise2.align.globalxx(seq1, seq2)

for alignment in alignments:

print(pairwise2.format_alignment(*alignment))
```

You should receive an output like this:

```
NAMI WASSE GOMMRHADWICHAYO, LLUX GOLDGHLIVFHYOD TAHLE - EMPROYLT TISSPH. 6. D. DOVYK G. - MODY GOTHA-. VTA HISE LAN T. GOMBA. ALS. - GOSGOVES-SCRIPDINFTFYSDHGGP-G. - VLOMP - S - G. PYLYADD-LIDV - LKR. KHASCTYKSLUF - YTEACESGSTFEG-L-UPG-LIDV - LYG. - DO LS-L - Y. BGT - LYG. - LYG. - LYG. - DO LS-L - Y. BGT - LYG. - LYG. - LYG. - DO LS-L - Y. BGT - LYG. - LYG. - LYG. - LYG. - DO LS-L - Y. BGT - LYG. - LYG.
```

## Complete pairwise sequencing code:

WARNING, PLEASE READ: You can use the code below to conduct a sequence alignment between each sequence in the SEED file; however, this will take up a lot of memory, a lot of computer processing power, and it may even crash your computer. Running the code on VS studio may give you a bunch of random numbers in the terminal. You can simply exit VS studio, and you should still have some, if not all pairwise sequences, analyzed on the output .txt file.