# HMMER Opdracht Sander Bouwman

## Generating HMM

Previously created MSA is used for creation of HMM.

HMM is built by using command:

*hmmbuild alligned.hmm alligned.faa*

Graphical user interface, text

Description automatically generated Text

Description automatically generated

## Downloading refseq

Then a refseq human protein was downloaded from ncbi:

Using wget:

❯ wget <ftp://ftp.ncbi.nlm.nih.gov:21/refseq/H_sapiens/mRNA_Prot/human.1.protein.faa.gz>

Which was then unzipped with gunzip:

❯ gunzip human.1.protein.faa.gz

## HMMSearch

Then hmmsearch was performed with:

❯ hmmsearch -o search\_log.txt alligned.hmm human.1.protein.faa

Log file is saved as search\_log.txt and is included in this repository.

HMMScan

Before HMMScan is performed, file aligned.hmm should be compressed:

❯ hmmpress alligned.hmm

Whichafter HMMScan is performed:

❯ hmmscan --notextw --tblout table.tbl alligned.hmm human.1.protein.faa > allignment\_scan.out

Hmmscan  
A picture containing graphical user interface

Description automatically generated