assignment 2

Mats Slik

HMMbuild:

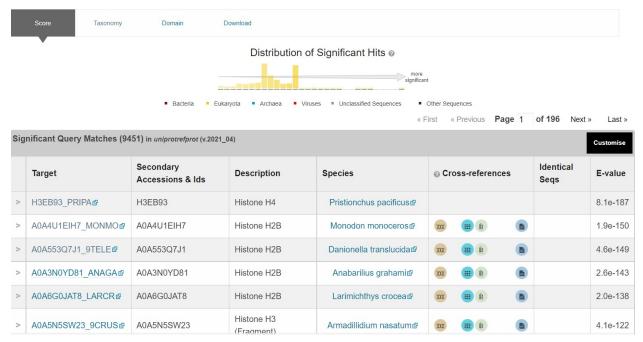
command:= hmmbuild H2bc hmm.mo MSA1.fasta

Hmmscan

command:= hmmbuild H2bc_hmm.mo MSA1.fasta output created: H2bc_hmm.mo subsequently this file was used for the next step.

Hmmsearch

a search was tried on the Bioinf.nl linux network bus found no connection to a refseq DB, so this was used. https://www.ebi.ac.uk/Tools/hmmer/search/hmmsearch



the Results id : 66987292-5D3C-11ED-A5D5-AC9B9F870EE0.1 results link

this gave us multiple results I selected the top three hits: 1.A0A4U1EIH7 2.A0A553Q7J1 3.A0A3N0YD81

these files where combined with the existing homologene 2.fasta multi fasta file that contained the original homologe family of proteins. the new combination file is called "homologene_new.fasta"

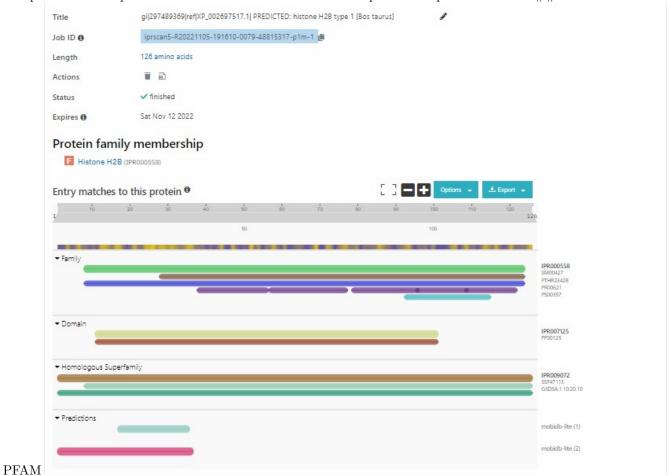
a new alignment was carried out with clustal W using this fasta, the results are stored in: 1."homologene_new1.fast" 2."homologene_new.aln"

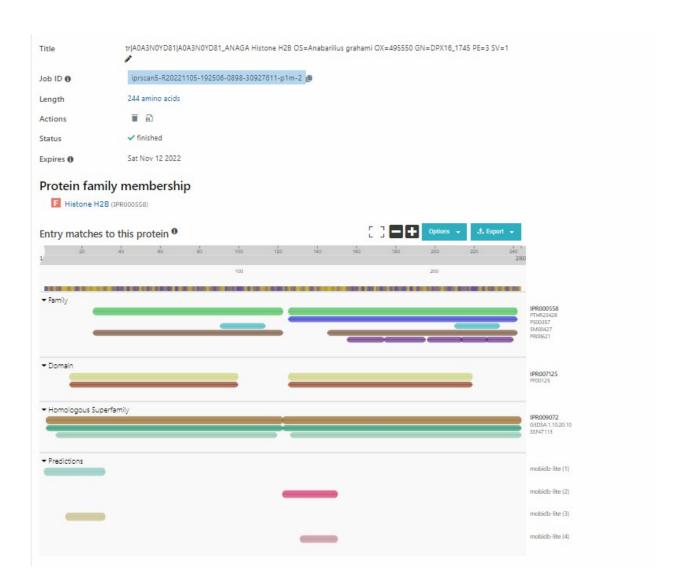
HMMbuild number 2:

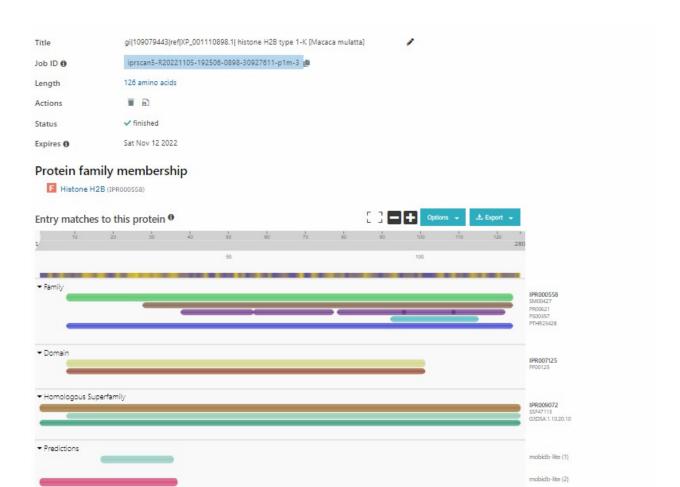
command:= hmmbuild H2bc_hmm_new.mo homologene_new1.fasta

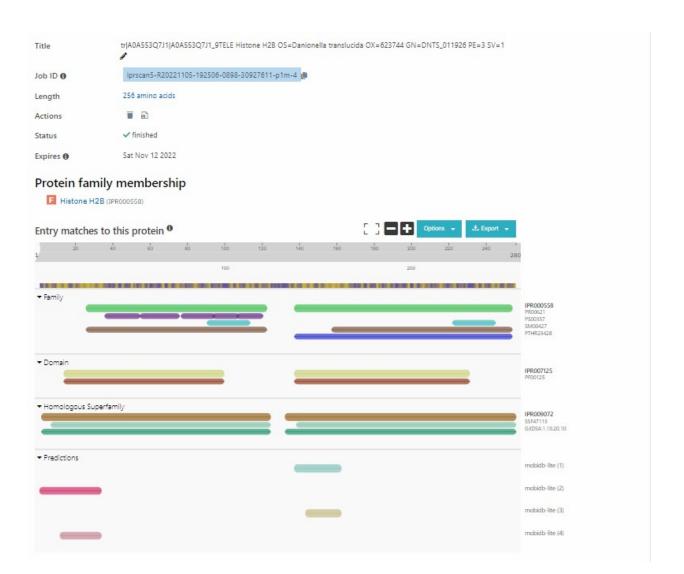
Pfam search

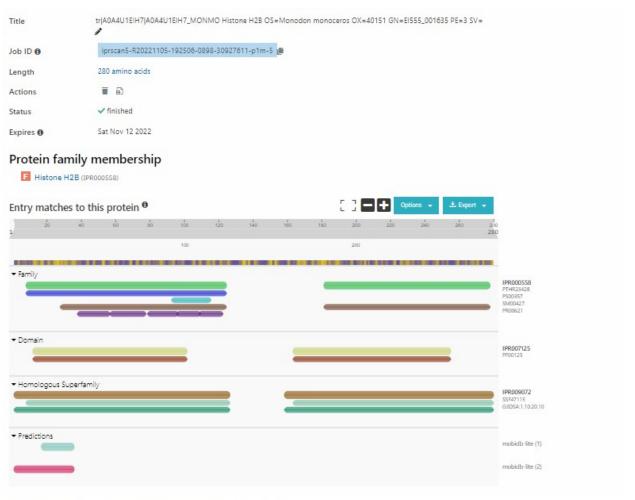
interpro search ID: iprscan5-R20221105-192506-0898-30927611-p1m-1 interpro Pfam search ## screenshots











☆ / Result / InterProScan / Iprscan5-R20221105-192506-0898-30927611-P1m-5 / Entry / InterPro

