

Annotating Proteins

Predicting function of proteins.

- [Pfam site docs](#)
- [Pfam manual](#) # Finding homologs

For Protein to Protein searches BLASTP, phmmer ([HMMER](#)), FASTA

```
module load fasta
fasta36 query database > results.FASTA
fasta36 -m 8c -E 1e-3 query database > results.FASTA.tab
```

To Find Domains

See Overview lecture [Domains lecture](#)

Searching with [HMMer](#) against [Pfam](#)

See the HMMER [tutorial](#)

Searching with [Interpro](#)

Searchin Intepro on HPCC

Note this can be slow.

```
#SBATCH -p batch -N 1 -n 8
module load iprscan
CPU=4
interproscan.sh --goterms --pathways -f tsv -i PROTEINFILE.fa --cpu $CPU > SEARCH.log
```

The results will contain information like

Gene Ontology <http://geneontology.org/>

Running Analyses on Biocluster

```
module load hmmer
module load db-pfam
hmmsearch --domtbl domtbl_results.out $PFAM_DB/Pfam-A.hmm proteins.fa > proteins.hmmsearch
hmmsearch --domtbl domtbl_results.out $HMM protein-db.fa > protein.hmmsearch
```

Pfam2GO - <http://current.geneontology.org/ontology/external2go/pfam2go>

Workshop

1. Searching for Pfam domains in sets of proteins - [Bioinformatics_4](#) See [search_SOD1.sh](#)

2. Parsing report files