

PCNT_HUMAN Analysis Report

Input Protein

PCNT_HUMAN

Searching in

10_uniprot_mammals.fasta

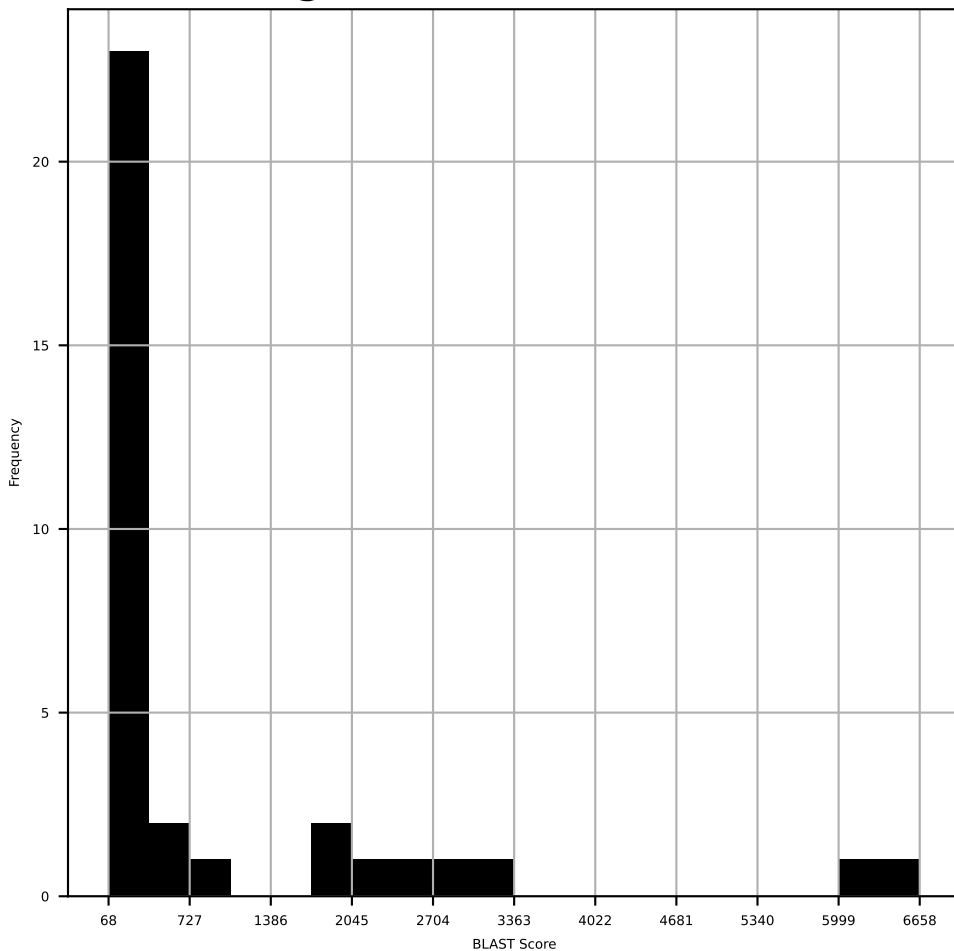
Programs used

blastp, muscle.exe

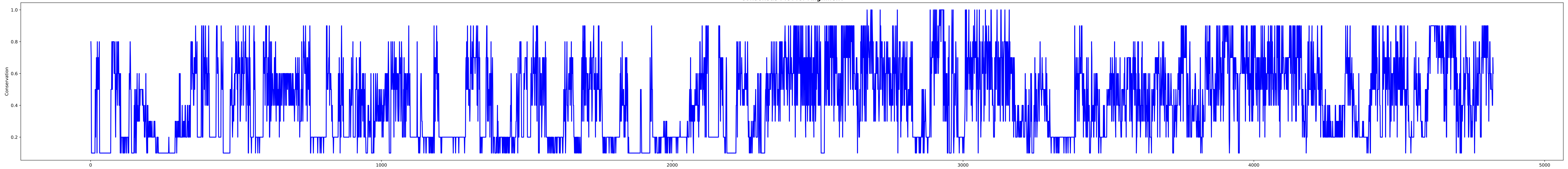
Top 5 Blast Hits for PCNT_HUMAN

Hit_Sequence	E_value	BLAST Score
sp O95613 PCNT_HUMAN	0.0	6662.0
tr H2R0F3 H2R0F3_PANTR	0.0	6216.0
tr E1BKZ0 E1BKZ0_BOVIN	0.0	3036.0
tr G5C7V2 G5C7V2_HETGA	0.0	2907.0
tr G5C7V2 G5C7V2_HETGA	0.0	2417.0

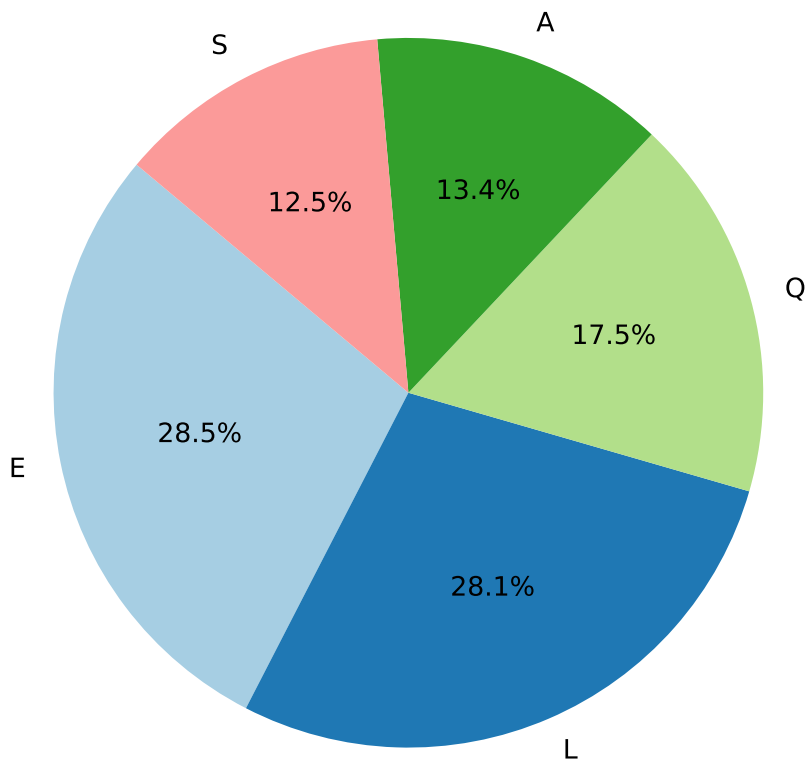
Histogram of the BLAST Scores



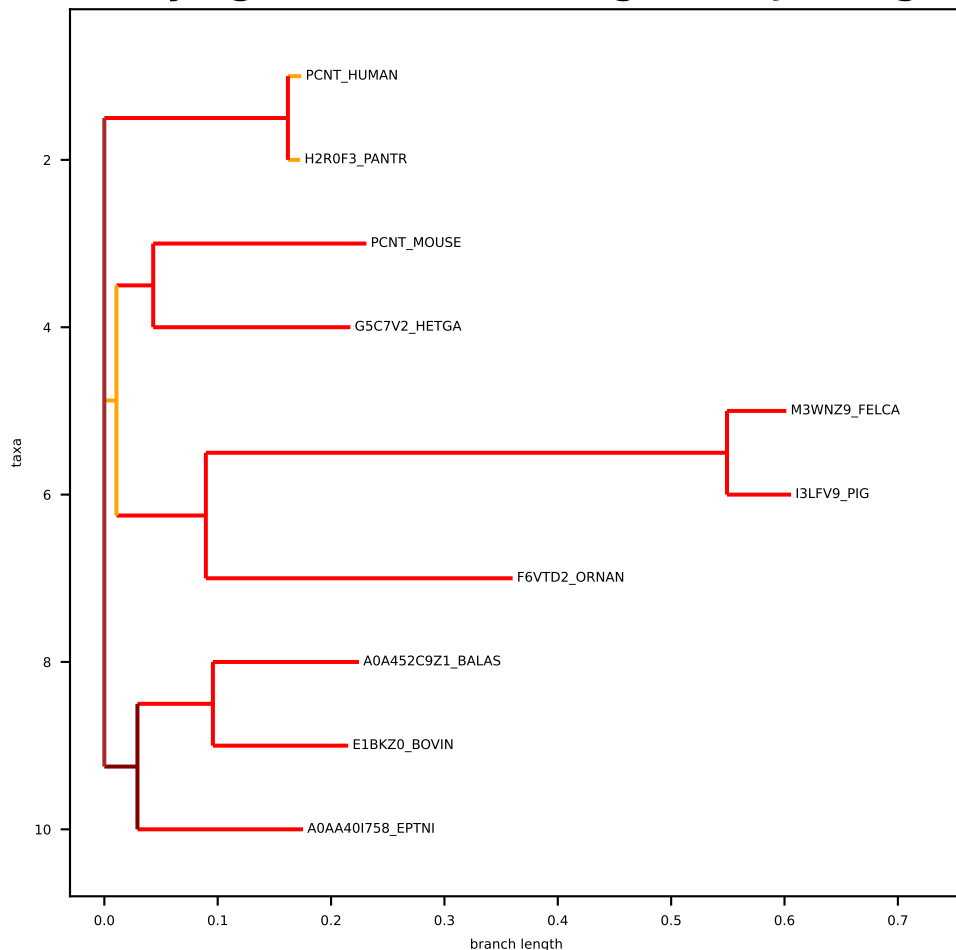
Consensus Plot for Alignment



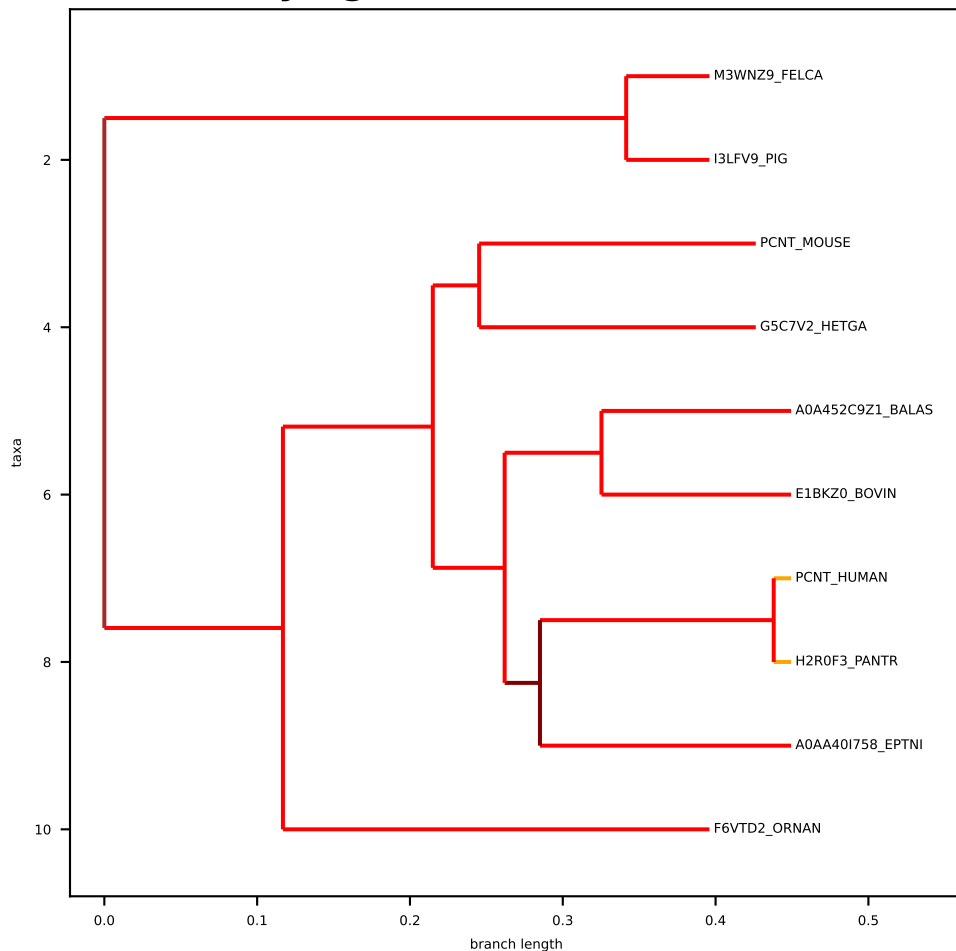
Top 5 Most Conserved Amino Acids in Alignment



Phylogenetics Tree--Neighbour Joining



Phylogenetics Tree--UPGMA



Raw Files

Blast Input

temp_9809_blast_input.txt

Blast Output

temp_9809_blast_output.txt

Filtered Blast Output(contains E-values of less than $1E-5$)

filtered_blast_output_9809.tsv

Alignment Input

temp_9809_msa_input.fasta

Alignment Output

temp_9809_msa_output.fasta