

# **PAXI\_HUMAN Analysis Report**

Input Protein

PAXI\_HUMAN

Searching in

10\_uniprot\_mammals.fasta

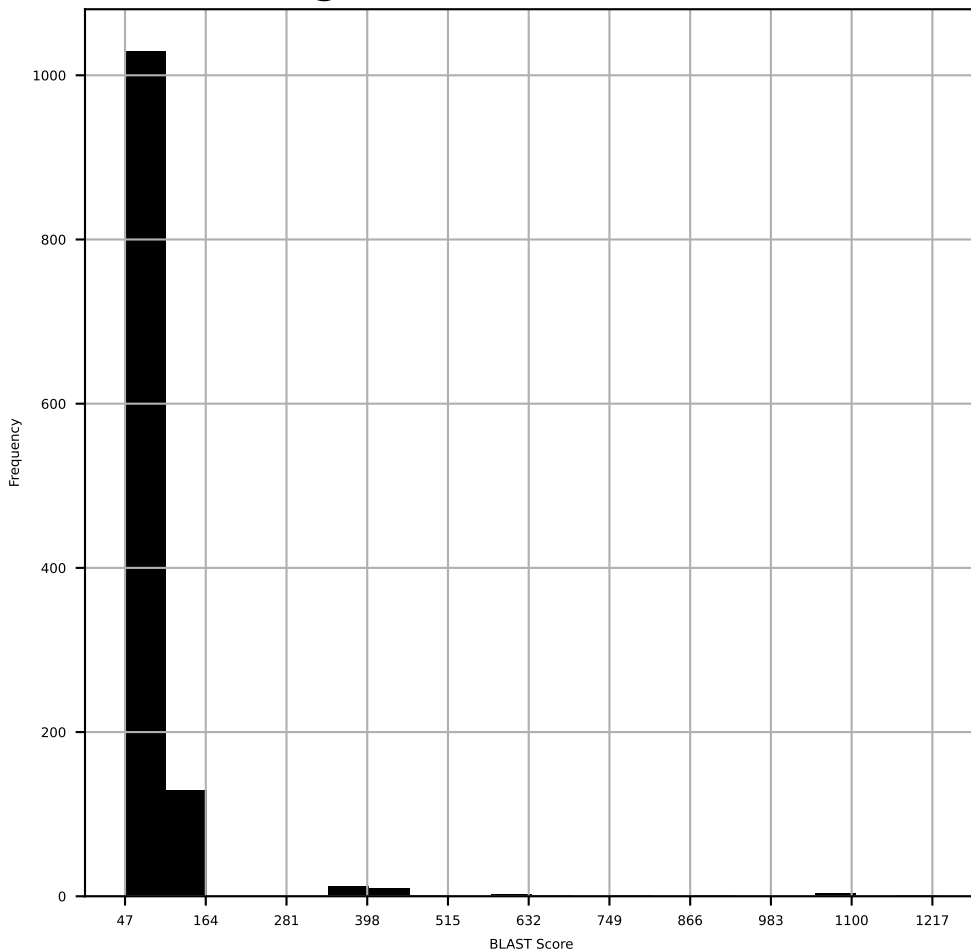
Programs used

blastp, muscle.exe

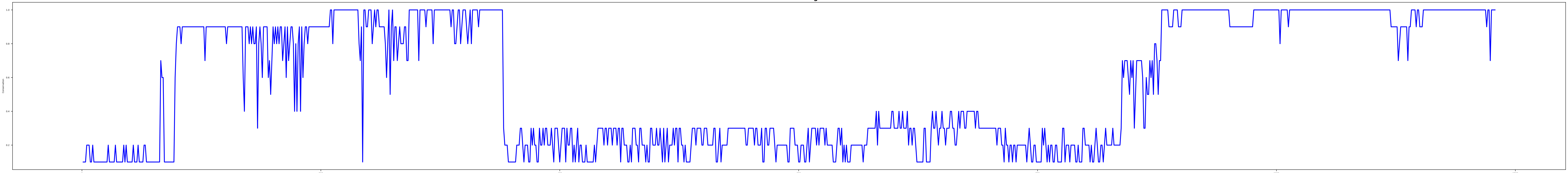
## Top 5 Blast Hits for PAXI\_HUMAN

Hit_Sequence	E_value	BLAST Score
sp P49023 PAXI_HUMAN	0.0	1224.0
tr A0A383Z8D4 A0A383Z8D4_BALAS	0.0	1098.0
sp Q8VI36 PAXI_MOUSE	0.0	1085.0
tr M3WPB0 M3WPB0_FELCA	0.0	1084.0
tr A0A5G2QT44 A0A5G2QT44_PIG	0.0	1065.0

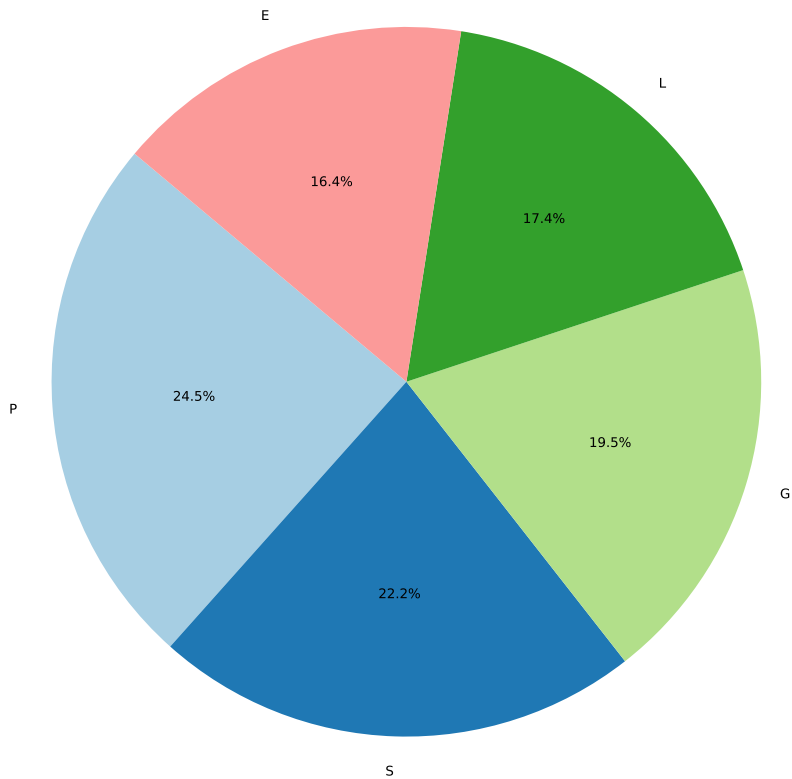
# Histogram of the BLAST Scores



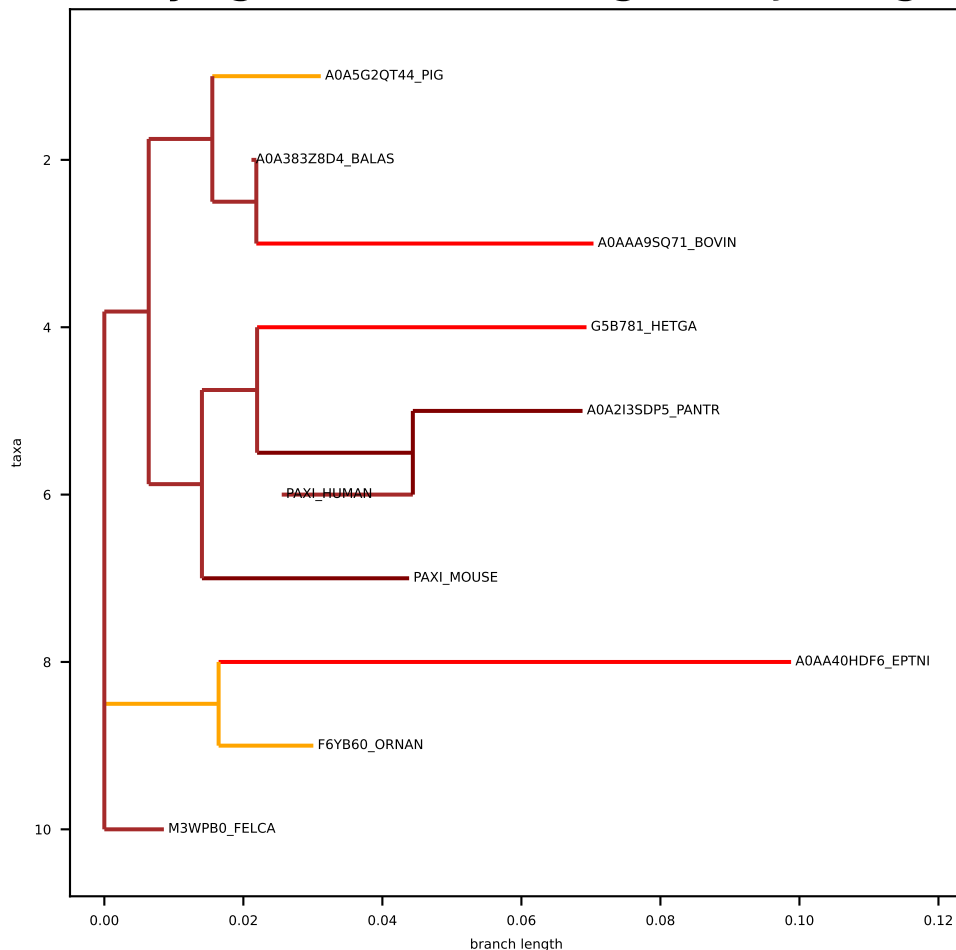
Consensus Plot for Alignment



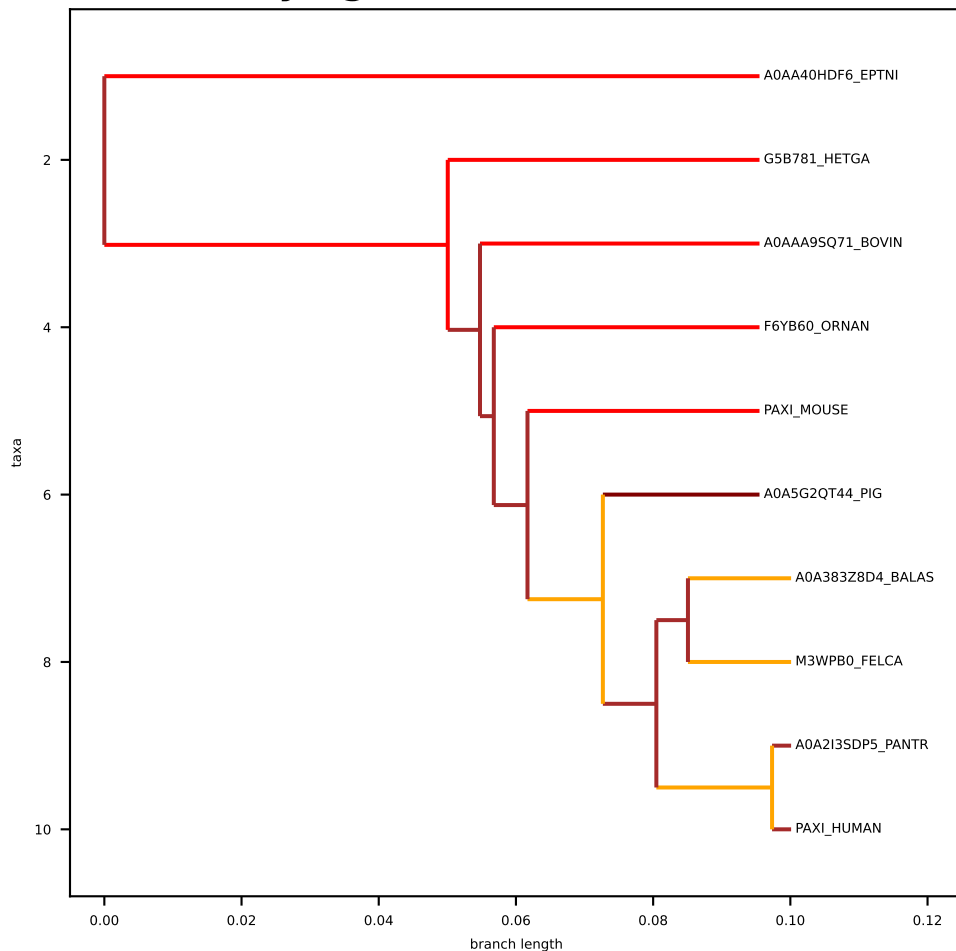
# Top 5 Most Conserved Amino Acids in Alignment



# Phylogenetics Tree--Neighbour Joining



# Phylogenetics Tree--UPGMA



# Raw Files

Blast Input

temp\_2088\_blast\_input.txt

Blast Output

temp\_2088\_blast\_output.txt

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

filtered\_blast\_output\_2088.tsv

Alignment Input

temp\_2088\_msa\_input.fasta

Alignment Output

temp\_2088\_msa\_output.fasta