Task-1: Protein Sequence Analysis Using BLAST

Objective

This study aims to analyze the protein sequence of Inhibin beta A using BLAST to identify similar sequences and conserved areas.

Sequence Information

Protein name: Inhibin beta A

Organism: Homo sapiens

Sequence length: 426 amino acids

Tool used: BLASTp (NCBI)

Database: Clustered NR

Methodology

The amino acid sequence of Inhibin beta A was obtained from the NCBI database. Protein BLAST (BLASTp) was performed against the Clustered NR database with default settings. The results were examined using cluster view, graphic summary, and alignment reports from BLAST.

Results

The BLASTp analysis revealed several significant matches with similar proteins from various species. There was a high sequence identity and query coverage, which pointed to the strong conservation of the protein. Conserved domains like TGFβ_propeptide and TGF_beta_SF were identified in the graphic summary. The alignment results showed 100% identity with a statistically significant E-value of 0.0.

Conclusion

The sequence analysis of Inhibin beta A using BLAST confirmed that the protein is highly conserved and is part of the TGF-β superfamily. BLAST analysis proved to be a useful tool for spotting sequence similarities and conserved functional domains.

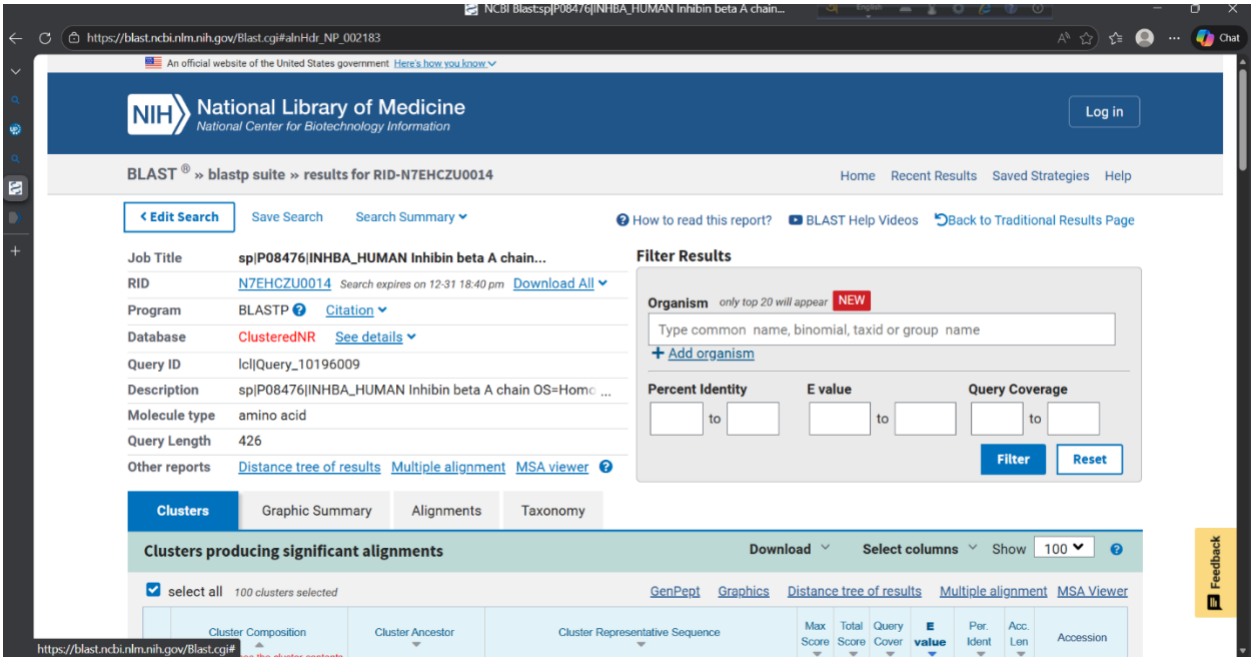

Figure – 1:ClusteredNR_Info

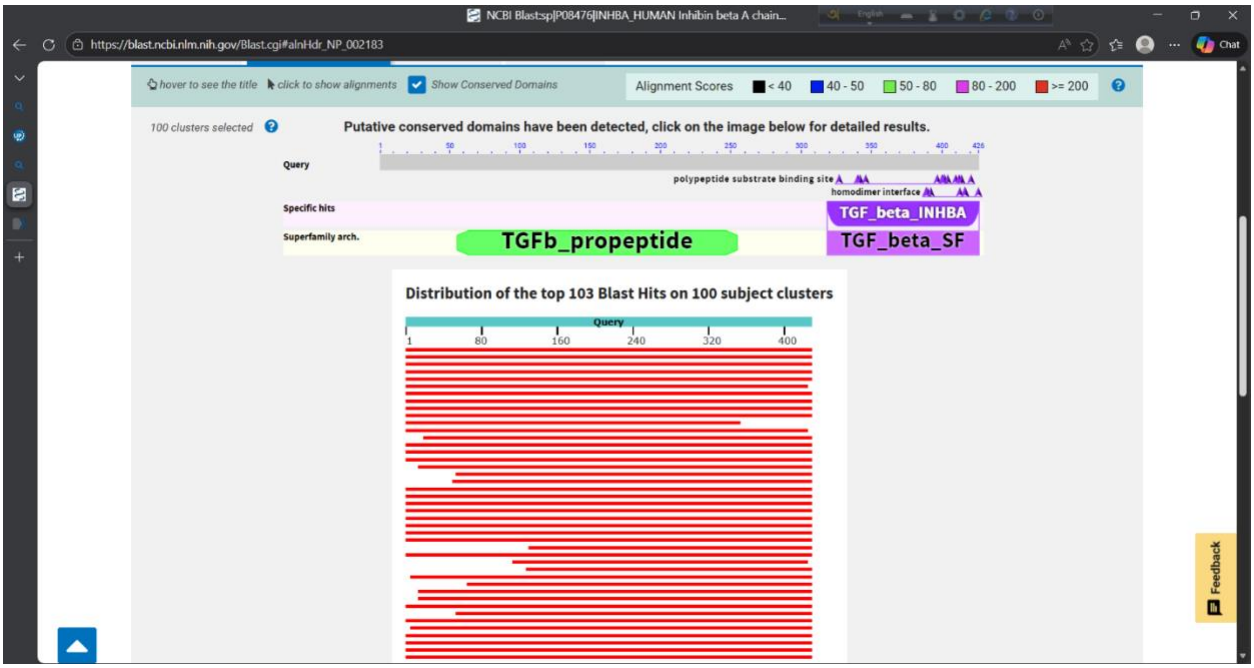

Figure – 2 : GraphicSummary_Domains

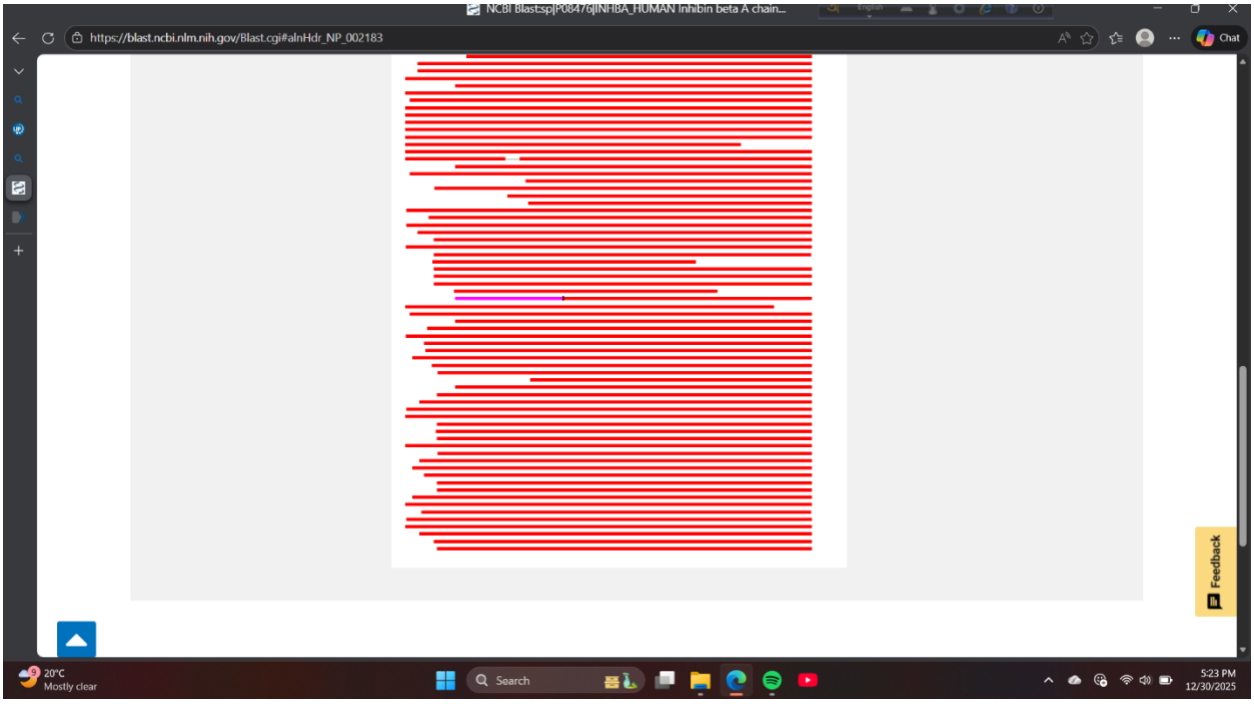

Figure – 3 : GraphicSummary_Distribution

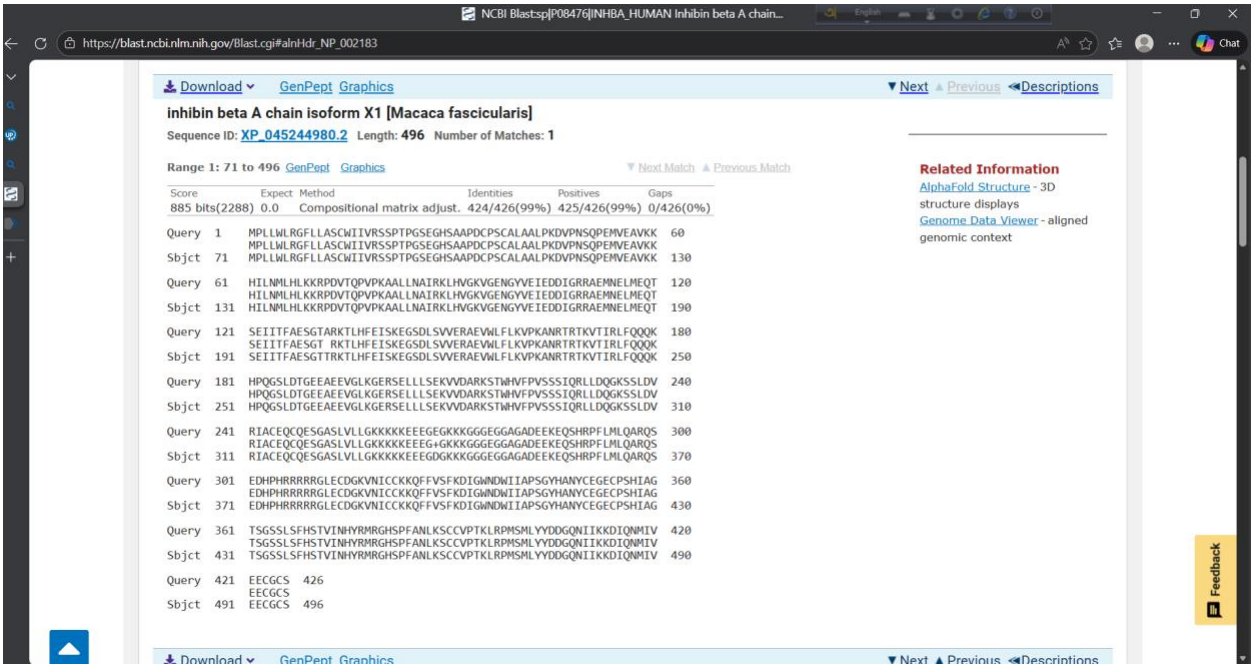

Figure – 4 : Alignment