

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 TGF β _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.

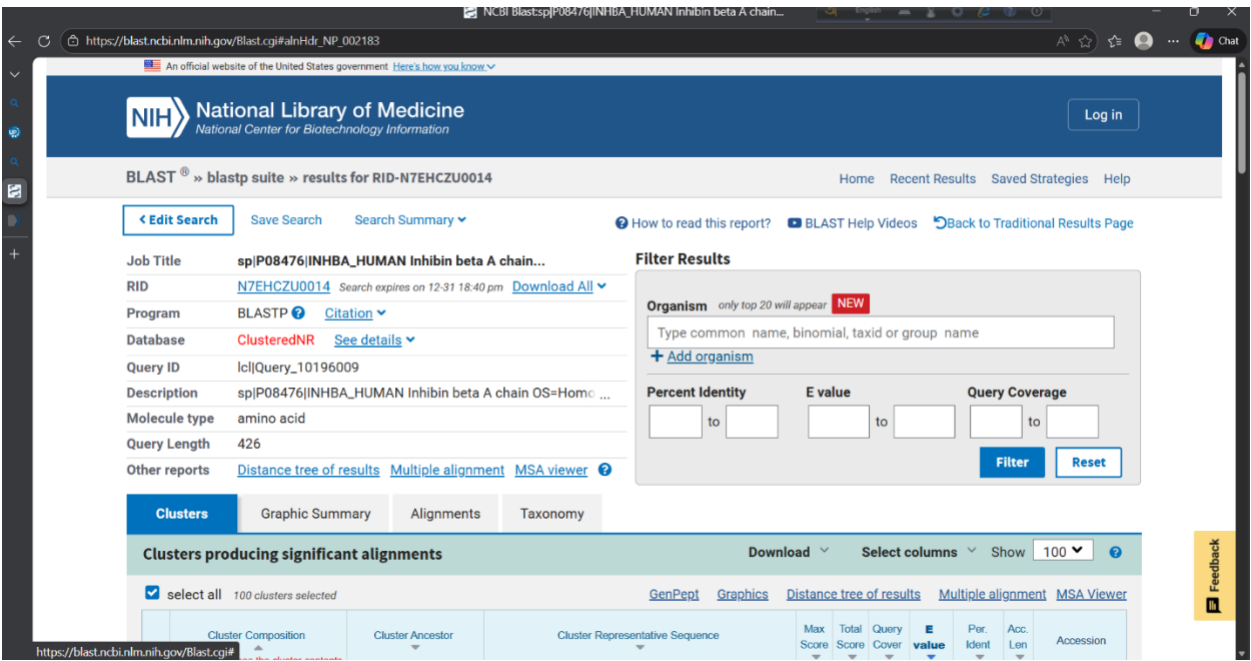


Figure – 1:ClusteredNR_Info

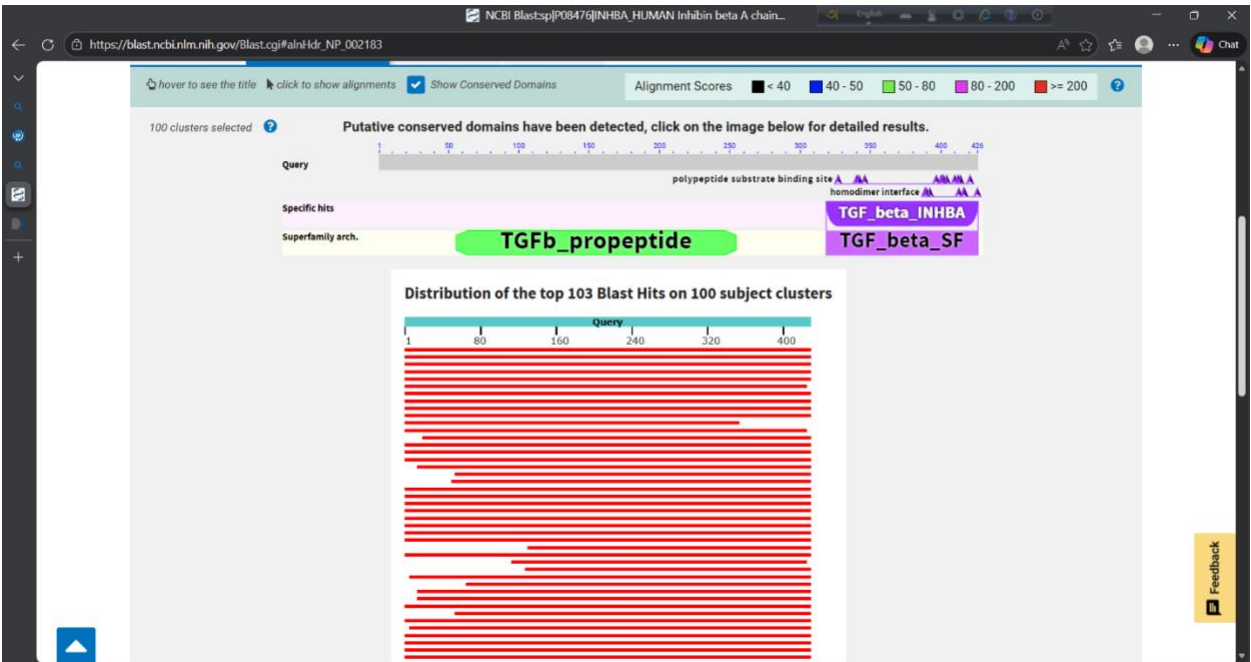


Figure – 2 : GraphicSummary_Domains

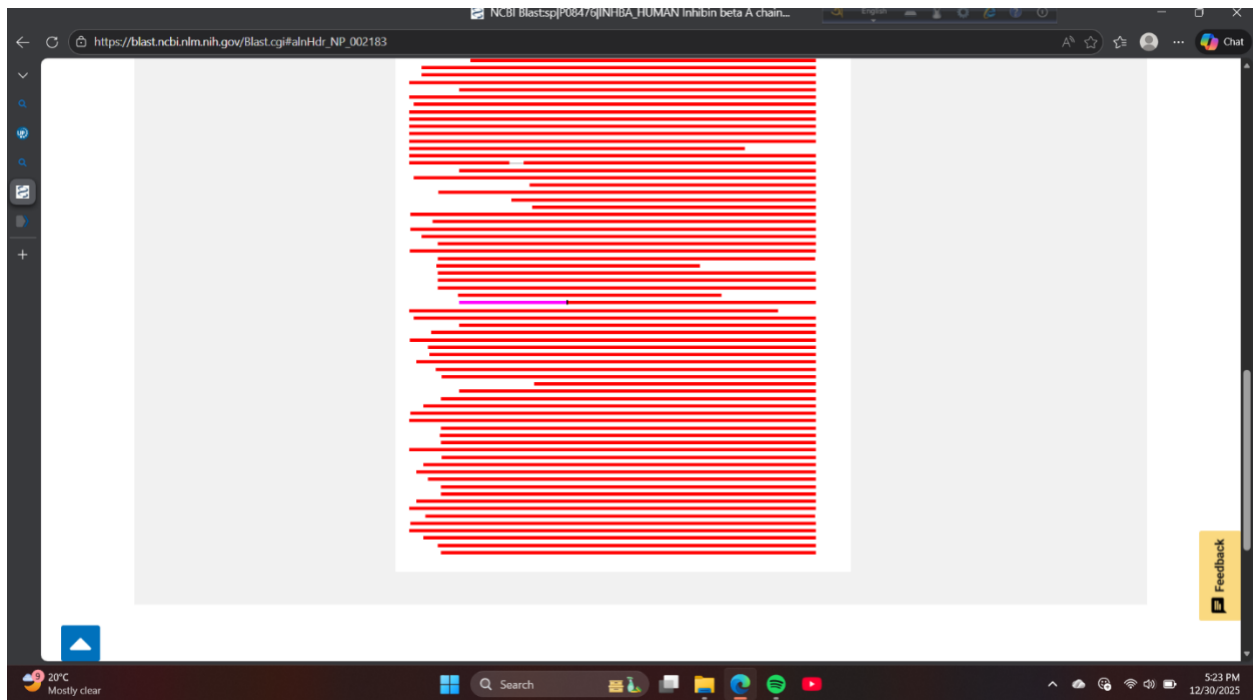


Figure – 3 : GraphicSummary_Distribution

NCBI Blastsp|08476|INHBA_HUMAN Inhibin beta A chain...
https://blast.ncbi.nlm.nih.gov/Blast.cgi?alnHdr_NP_002183

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inhibin beta A chain isoform X1 [Macaca fascicularis]
 Sequence ID: [XP_045244980.2](#) Length: 496 Number of Matches: 1

Range 1: 71 to 496 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
885 bits (2288)	0.0	Compositional matrix adjust.	424/426(99%)	425/426(99%)	0/426(0%)
Query 1	MPLLWLRGFLASCWIIVRSSPTPGSEGHSAAPDCPSALAAALPKDVPSQPEMVEAVKK	60			
Sbjct 71	MPLLWLRGFLASCWIIVRSSPTPGSEGHSAAPDCPSALAAALPKDVPSQPEMVEAVKK	130			
Query 61	HILNMLHLKKRPDVTQVPKAAALLNAIRKLHVGKVGNGYVEIEDDIGRAEMNELMEQT	120			
Sbjct 131	HILNMLHLKKRPDVTQVPKAAALLNAIRKLHVGKVGNGYVEIEDDIGRAEMNELMEQT	190			
Query 121	SEITTFASGTARKTLHFEISKEGSDLSVVERAEVWFLKVPKANRTRTKVIRLFQQQK	180			
Sbjct 191	SEITTFASGTARKTLHFEISKEGSDLSVVERAEVWFLKVPKANRTRTKVIRLFQQQK	250			
Query 181	HPQGLDTGEEAEVGLKGERSELLSEKVVDAKSTNHVFPVSSSIQRLLDQGSLLDV	240			
Sbjct 251	HPQGLDTGEEAEVGLKGERSELLSEKVVDAKSTNHVFPVSSSIQRLLDQGSLLDV	310			
Query 241	RIACEQCQESGASLVLLGKKKKKEEGEGKKGGGGAGADEEKEQSHRPFMLQARQS	300			
Sbjct 311	RIACEQCQESGASLVLLGKKKKKEEGEGKKGGGGAGADEEKEQSHRPFMLQARQS	370			
Query 301	EDPHRRRRRGLCEDGVNICKKQFVFSFKDIGNDWIAPSGYHANYCEGCPSHIAG	360			
Sbjct 371	EDPHRRRRRGLCEDGVNICKKQFVFSFKDIGNDWIAPSGYHANYCEGCPSHIAG	430			
Query 361	TSGSSLSFHSVTINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIKKDIQNMIV	420			
Sbjct 431	TSGSSLSFHSVTINHYRMRGHSPFANLKSCCVPTKLRPMSMLYYDDGQNIKKDIQNMIV	490			
Query 421	EEGCS 426				
Sbjct 491	EEGCS 496				

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Related Information
[AlphaFold Structure - 3D](#)
[structure displays](#)
[Genome Data Viewer](#) - aligned genomic context

Figure – 4 : Alignment