BioinformHer Mini Project – Module 2

Tracking the Evolution of the Hemoglobin Beta (HBB) Gene Across Species

Project Objective

To investigate the evolutionary conservation of the HBB gene across six species using nucleotide sequences. This includes sequence retrieval, alignment, sequence logo generation, and phylogenetic tree construction.

1. Sequence Retrieval & BLAST Search

Nucleotide sequences of the HBB gene were retrieved from NCBI for six species. A BLAST search was used to identify orthologs, and percentage identity with the human gene was noted.

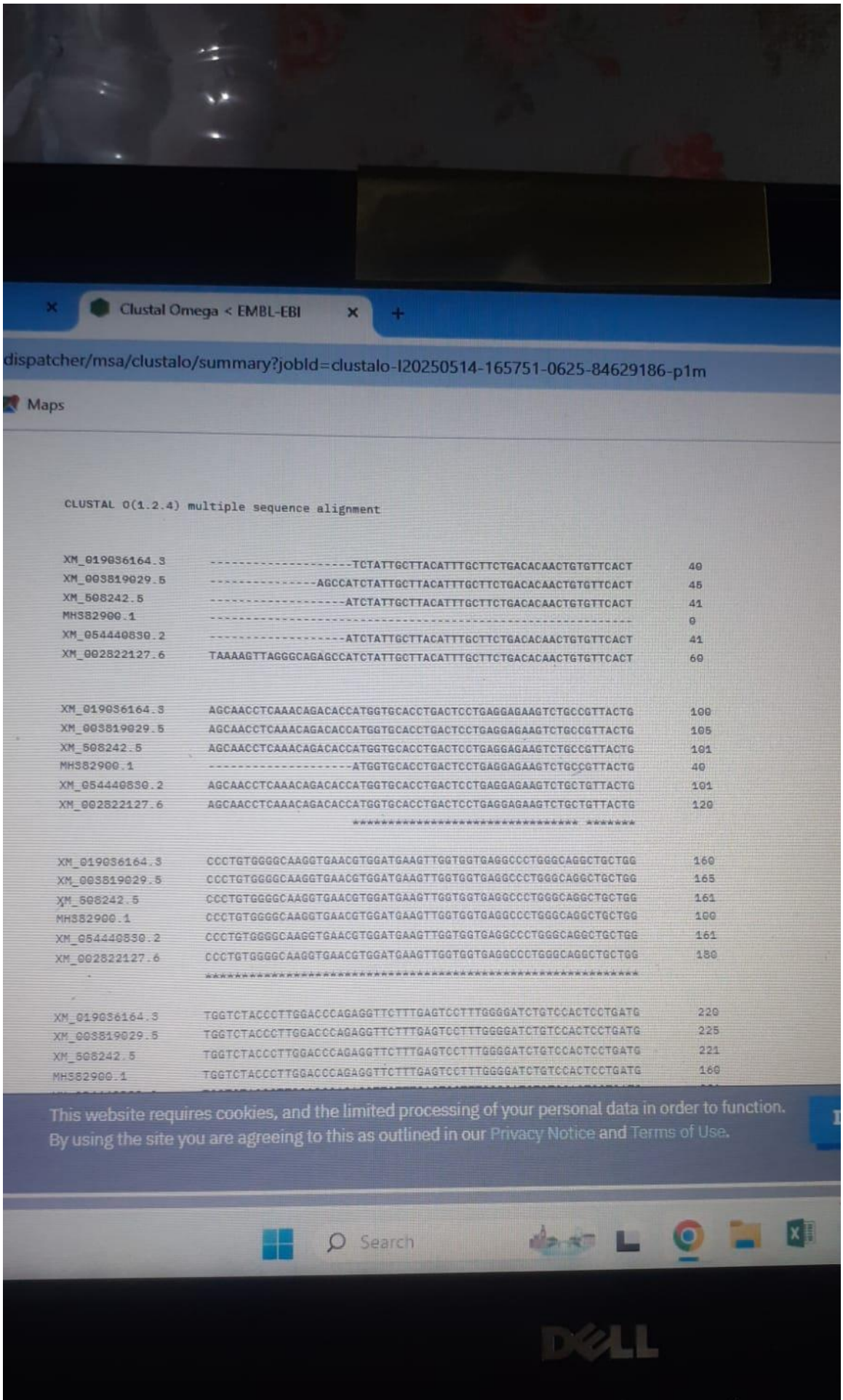
Species	Accession Number	Gene Symbol	% Identity with Human HBB
Human	NM_000518.5	HBB	100%
Chimpanzee	XM_508242.5	HBB	100%
Cow	NM_17391.7	HBB	100%
Mouse	NM_198776	Hbb-b1	100%
Chicken	NM_205489.3	HBBA	100%
Zebrafish	NM_131020.3	hbba1	100%
Zebra fish	NM-001013027	hb1	97.73%

2. Pairwise & Multiple Sequence Alignment

Table: Pairwise Comparison to Human HBB

Species	% Identity	No. of Gaps	Conservation Notes
Human	628/628	0/628	
Chimpanzee	626/628	0/628	Highly conserved, nearly identical

Zebrafish	603/617	0/617	Least conserved, most distantly related
Zebrafish	716/716	0/716	



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Maps

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CLUSTAL O(1.2.4) multiple sequence alignment


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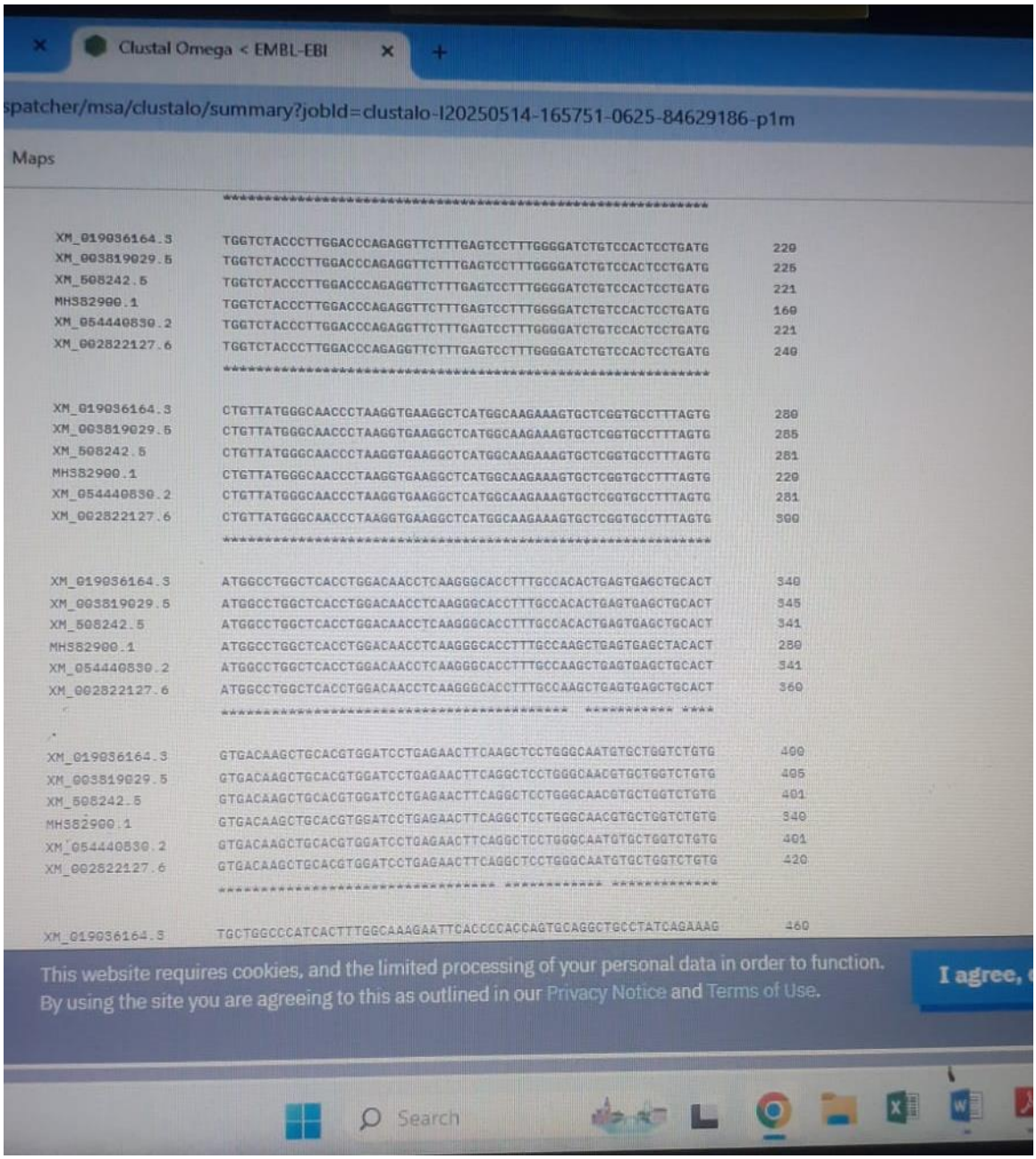
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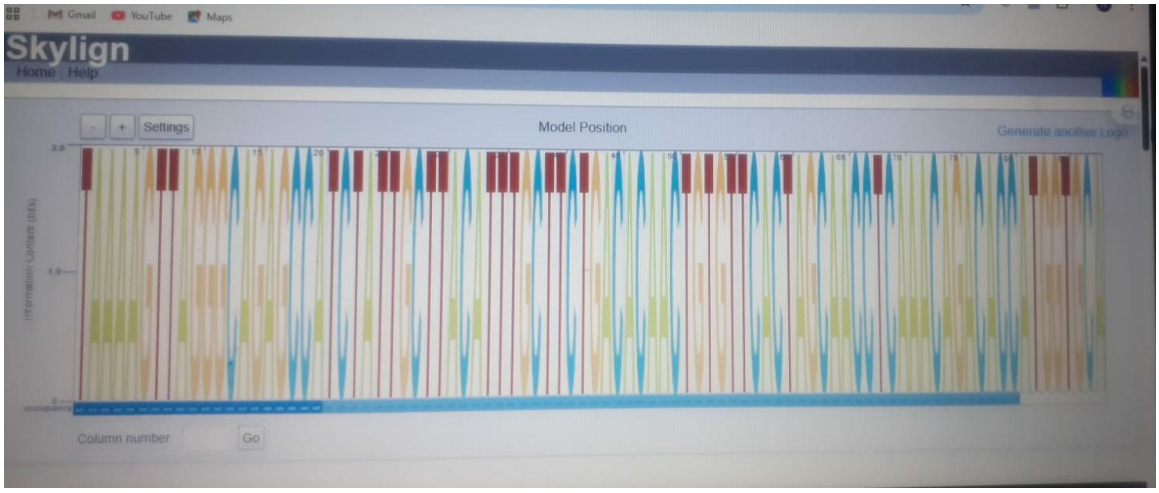
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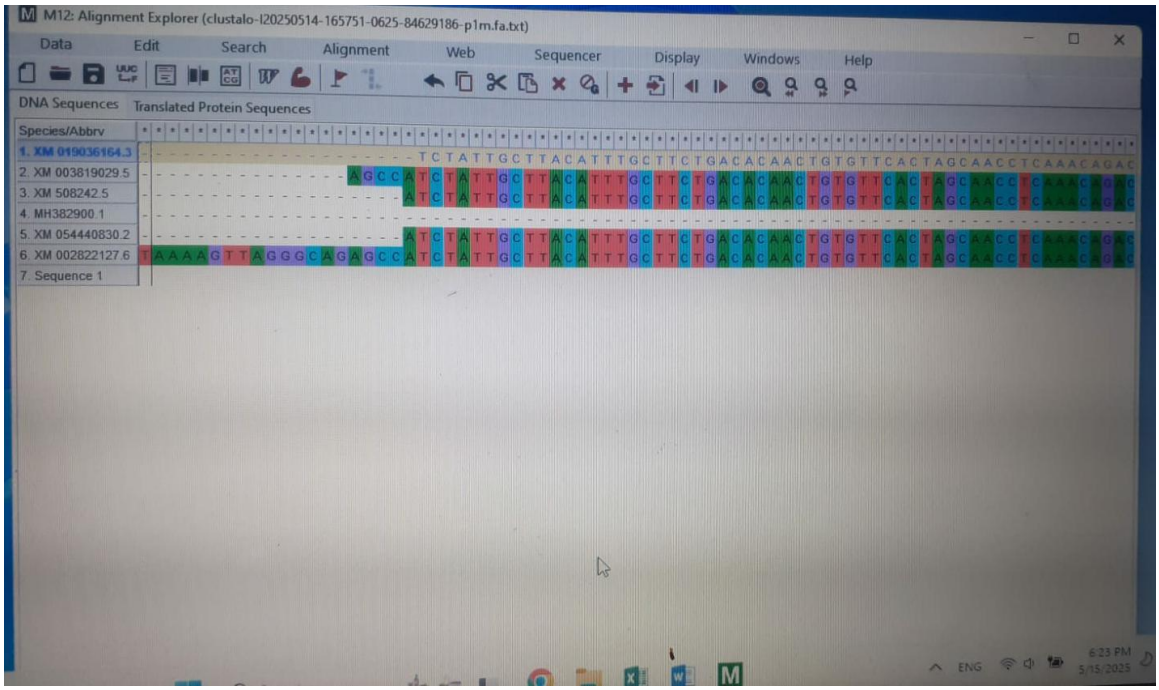
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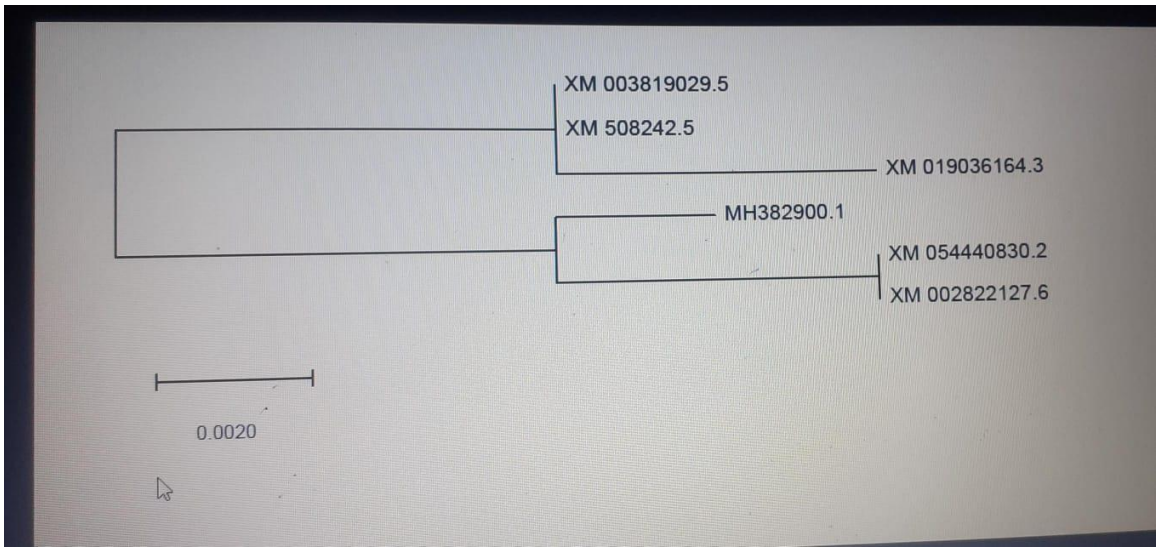
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