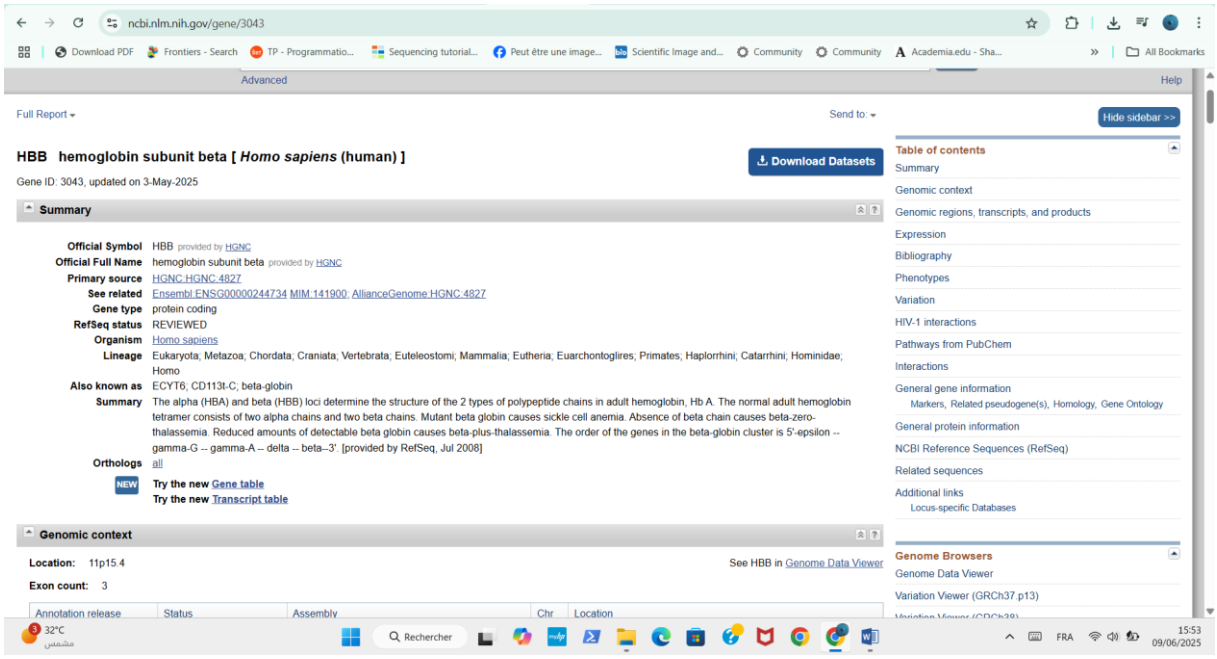
BIOINFROMHER MODULE 2 PROJECT

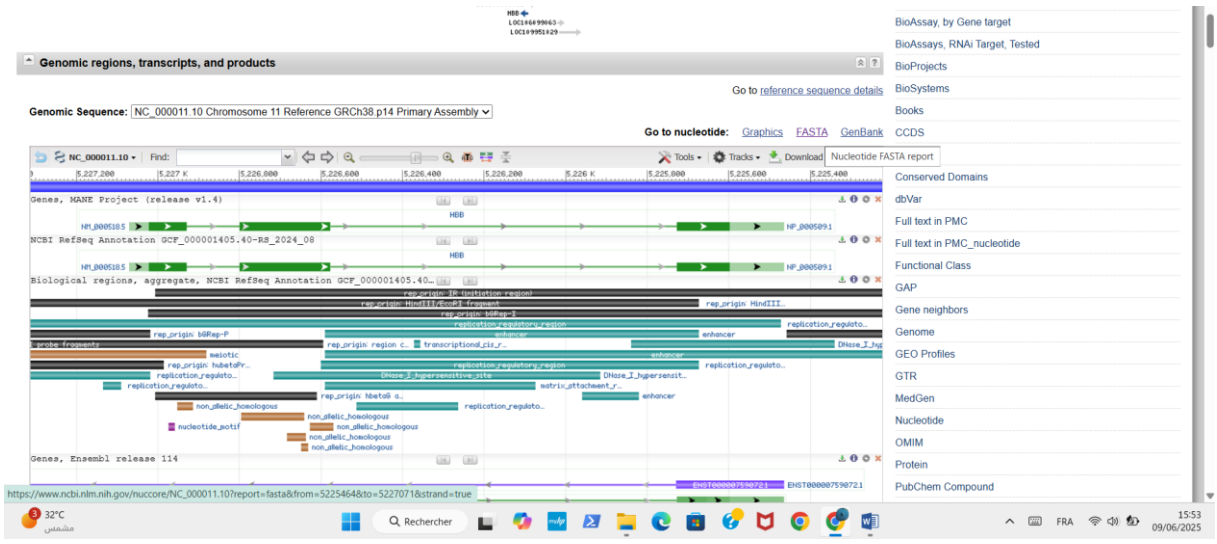
Tracking the Evolution of the Hemoglobin Beta (HBB) Gene across Species

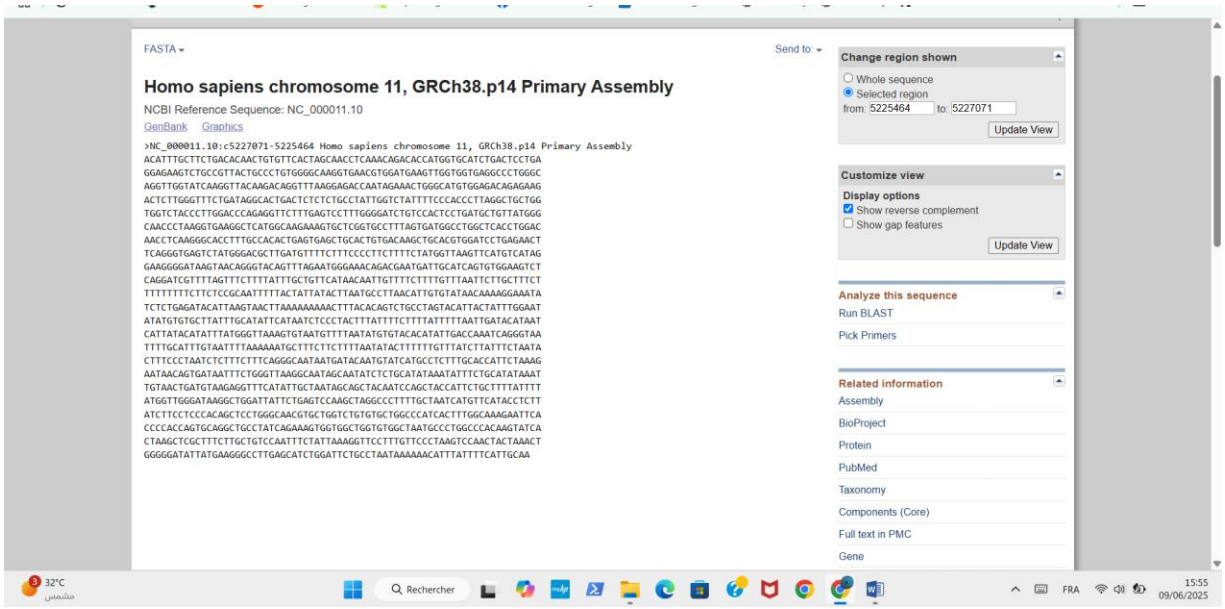
CONDUCTED BY :
Maram Nhaili

1 Sequence Retrieval and blast search:

1.1 Sequence Retrieval:







HBB for humain:

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>NC_000011.10:c5227071-5225464 Homo sapiens chromosome 11, GRCh38.p14
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1.2 Fasta formet for other species:

1.2.1 COW:

Accession number: M63453.1

>M63453.1 Bovine Beta globin gene and globin (PSI-3) pseudogene, complete cds

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1.2.2 Chimpanzee :

Accession number : X02345.1

>X02345.1 P.troglodytes beta-globin gene, exons 1-3
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TACCTCTTGTCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA
AG

1.2.3 Zebrafish :

No significant similarity found

1.2.4 Chicken :

No significant similarity found

1.2.5 Mouse :

>EF605360.1 Mus musculus isolate Lima138A beta-globin (Hbbt1) gene, complete cds

GCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTC
ACATTTGCTTCTGACATAGTTGTGTTGACTCACAACCCCAGAAACAGACATCATGGTGCACCTGACTGAT
GCTGAGAAGGCTGCTGTCTCTGGCCTGTGGGGAAAGGTGAACGCCGATGAAGTTGGTGGTGAGGCCCTGG
GCAGGTTGGTATCCAGGTTACAAGGCAGCTCACAAGTAGAAGTTGGGTGCTTGGAGACAGAGGTCTGCTT
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GGACCCAGCGGTACTTTGATAGCTTTGGAGACCTATCCTCTGCCTCTGCTATCATGGGTAATGCCAAAGT
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CACTAAACCCCCTTTCCTGCTCTTGCCTGTGAACAATGGTTAATTGTTCCCAAGAGAGCATCTGTC

1.3 Blast search :

Species	Acession Number	Identity
Cow	M63453.1	81.09%
Mouse	EF605360	79.61%
Zebrafish		No significant similarity found
Chicken		No significant similarity found
Champanzee	X02345.1	98.71%

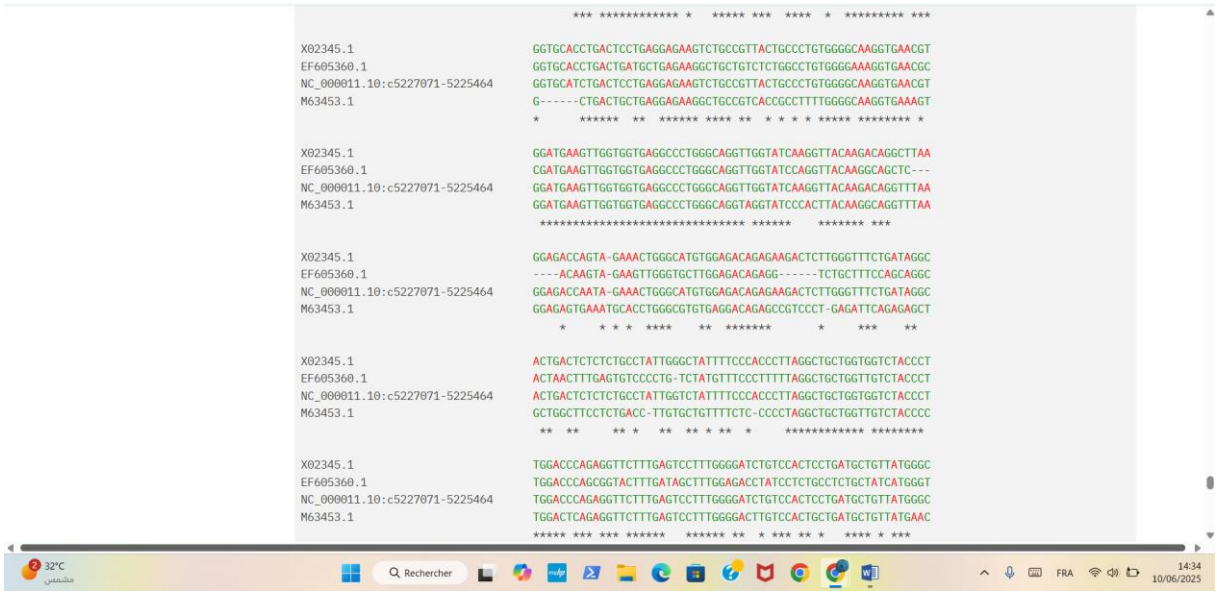
2 Pairwaise sequence Alignment :

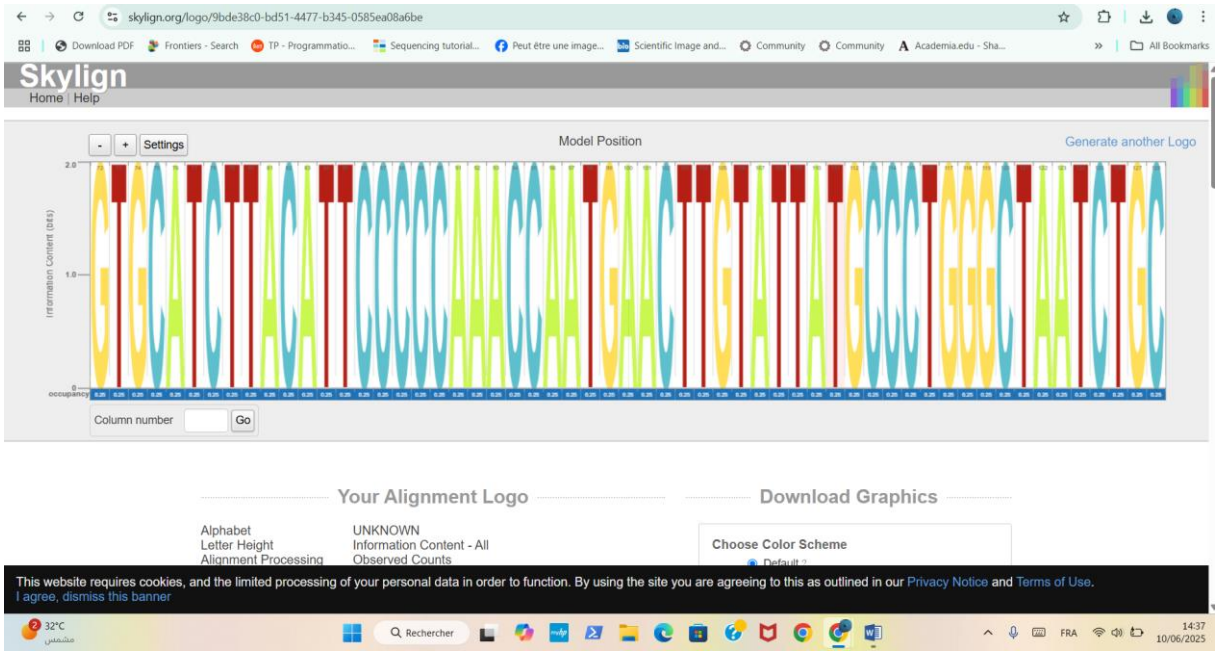
Species	Similarity	Identity	Number of gaps
Cow	8.9%	8.9%	89.1%
Champanzee	99%	99%	0%

Interpretation:

Based on the data provided from the table above we can confirm that the chimpanzee has more conserved regions that the cow because its similarity and identity (99%) is higher than the one found in the cow which represents 8.9%.Moreover, we can see that the number of gaps is higher in the cow that the chimpanzee.

3 Multiple sequence alignment:





The sequence logo shows that each columns correspond to a position in MSA (multiple sequence alignment).we observe high conserved regions due to the height of the nucleotide at each position where their total height correspond to 2 bits.

Additionally, there are highly conserved residues meaning there is little variation across sequences at those sites.

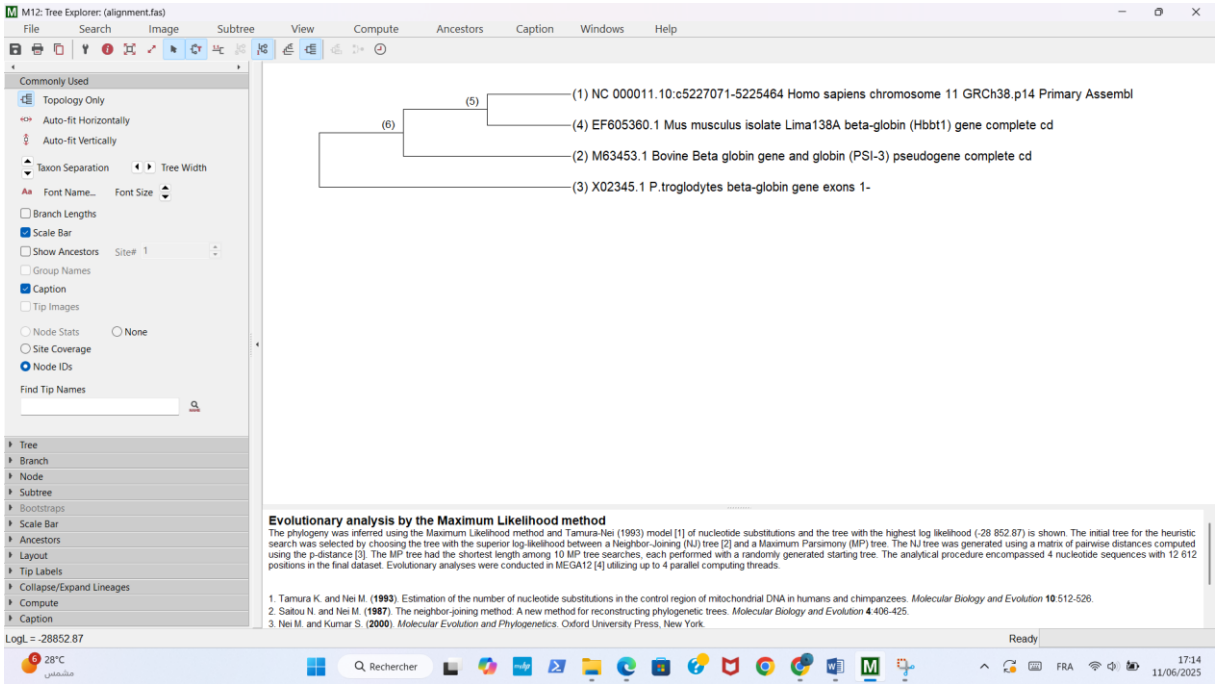
These conserved regions play critical role. They are functional importance where these regions could be :

- A promoter
- An enhancer
- A biding site for transcription factors or regulatory proteins

Structural stability

Evolutionary conservation

4 Phylogenetic tree construction:



- Human and Mouse beta-globin sequences cluster together more closely than with the other species, suggesting a more recent common ancestor between them for this gene region (which might reflect conserved functional regions rather than strict evolutionary distance).
- Chimpanzee (P. troglodytes) appears more distant, which is biologically unexpected given its close relation to humans. This suggests:

The chimpanzee sequence may be shorter (only "exons 1–"), or

There could be alignment gaps or divergence in the sequenced region used.

- Bovine (cow) gene shows greater divergence, as expected due to larger evolutionary distance from primates and rodents.

Does this tree match what you expect evolutionarily?

No, this tree does not match the expected evolutionary relationships of the species involved — especially not in the broad evolutionary sense.