Guião

- Laboratórios de Bioinformática –

To carry out this research about the HBB gene, several bioinformatic software tools were used.

Firstly, a theoretical research was developed on the chosen gene (HBB) to gather knowledge about the sequence in question using NCBI, UniProt and Pubmed.

> Acquire protein structure – Through the UniProt database, a tridimensional image of Hemogloblin subunit Beta was obtained. This enabled us to see specific details, such as the spatial arrangement of different regions of the protein.

> Homologous sequences – To get the 10 homologous sequences of the HBB protein, we used the BLASTp website. This allowed us to compare and analyze the sequences and the evolutive parameters between species.

> Multiple Sequence Alignment (MSA) and logo – Using Clustal Omega and the previous homologous sequences of the HBB protein, we were able to generate a multiple sequence alignment. This was crucial to identify conserved regions among species. We also generated a logo using Weblogo to better understand the similarities and disparities between them.

> Phylogenetic tree – To generate a phylogenetic tree, we have used both Clustal Omega and iTOL to be able to get different prespectives of the relationship between genes and their evolutionary course.

> Motifs – Regarding the identification of motifs, we have opted to use GenomeNet to have a better understanding of which parts of the sequences have a higher role in the protein.

> Functional domains – Through the use of Interpro, we were able to understand better the main roles that the proteins carry on.

Website created: <https://sites.google.com/view/hemoglobinsubunitbetab/p%C3%A1gina-inicial>

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