1. Nucleotide BLAST is our preferred BLAST program because we’re using a nucleotide sequence to compare against reference accessions.
2. The top 4 hits:

|  |  |
| --- | --- |
| Name | Accession |
| [Homo sapiens hemoglobin subunit beta (HBB), mRNA](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_1401724401) | [NM\_000518.5](https://www.ncbi.nlm.nih.gov/nucleotide/NM_000518.5?report=genbank&log$=nucltop&blast_rank=1&RID=A781Y5H2014) |
| [PREDICTED: Pan troglodytes hemoglobin subunit beta (HBB), mRNA](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_694943029) | [XM\_508242.4](https://www.ncbi.nlm.nih.gov/nucleotide/XM_508242.4?report=genbank&log$=nucltop&blast_rank=2&RID=A781Y5H2014) |
| [PREDICTED: Pan paniscus hemoglobin subunit beta (LOC100976465), mRNA](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_675751226) | [XM\_003819029.2](https://www.ncbi.nlm.nih.gov/nucleotide/XM_003819029.2?report=genbank&log$=nucltop&blast_rank=3&RID=A781Y5H2014) |
| [Homo sapiens hemoglobin beta chain variant Hb S-Wake (HBB) mRNA, complete cds](https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_23268448) | [AY136510.1](https://www.ncbi.nlm.nih.gov/nucleotide/AY136510.1?report=genbank&log$=nucltop&blast_rank=4&RID=A781Y5H2014) |

1. Percent identities for these hits are 99.57%, 99.36%, 99.36%, and 99.36%, respectively.
2. The top hit has 466 identical and 2 non-identical nucleotides.




8. HBB has a role in alpha & beta thalassemia and sickle cell disease.
9. Accession: NM\_000518.5
10. EXON1 is located between nt positions 1 and 142.
11. The CDS is found between positions 51 and 494.
12. 50
13. A>T in position 20: Glu 🡪 Val. T>A in position 162 (Ala) is a silent mutation.

16. Val6 is located on the protein surface proximate to a heme group that may interefere with its ability to bind oxygen, in addition to being a hydrophobic residue.