

Reference:

NCBI – Subsection Gene database

UNIPROT

Information Retrieval:

1. Gene Name:
2. Chromosome:
3. Gene Size:
4. Gene orientation:
5. mRNA sequence (in FASTA format):
6. Number of exons:
7. Number of transcripts:
8. Protein name:
9. Protein function:
10. Homologs- Different species from which it is studied and reported:
11. Protein Size: (Longest and Shortest homolog)
12. Protein Sequence (in FASTA Format):
13. Structure:
14. Expression:
15. Subcellular localisation:
16. Interacting partners:
17. Variants/ mutations:
18. Implications in diseases:
19. Phylogenic Gene tree analysis:
20. Pathways/ Biological process:
21. Analysis from Protein sequence alignment:
22. Post Translation Modifications (if any)
23. Recent publications

(Answer should always be accompanied with reference-parent Database from where the information is taken and/or Cross-referenced database if accessed)