**Exercise 2 - GENSCAN**

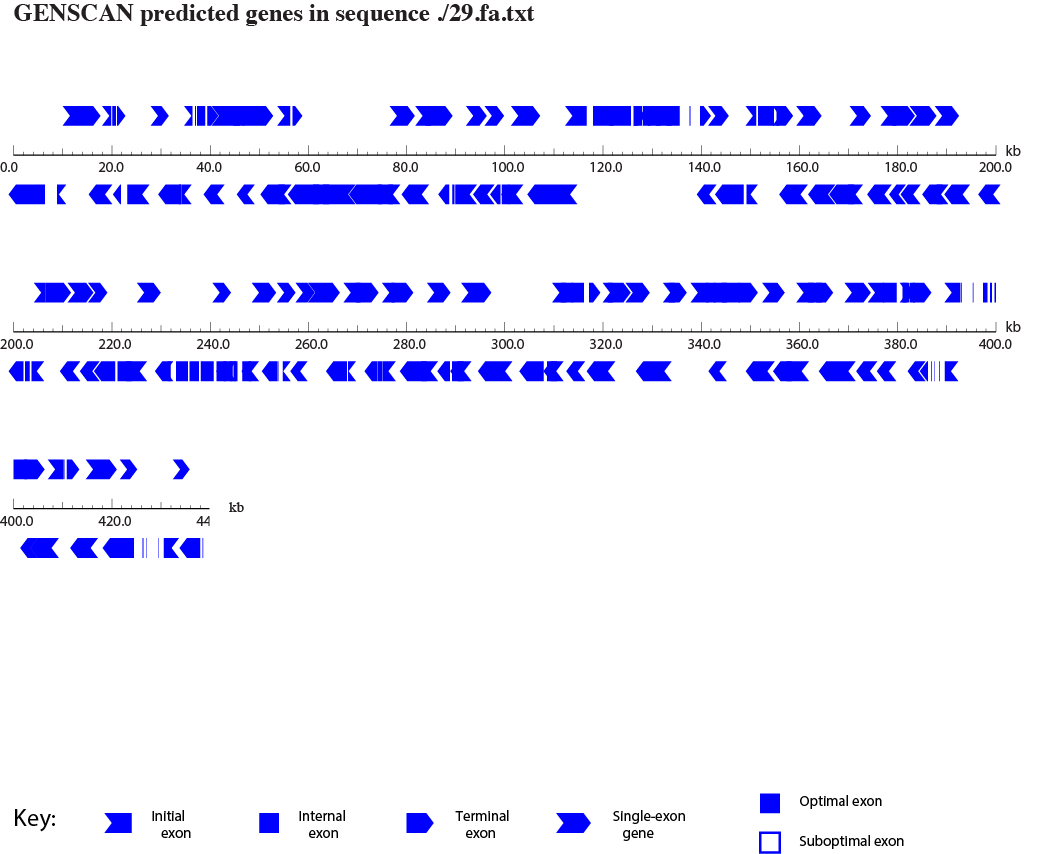
*Steps for the second part of the exercise.*

Run **GENSCAN** for the eukaryote provided in Practical 1. Run it, using **HumanIso.smat** .

1. From GENSCAN output, extract the amino acid and nucleotide sequences and make separate files for each.

The files are called peptide\_out and nucleotide\_out respectively.

1. Create the PostScript (graphical) output, which is a diagram of the locations and DNA strand of all predicted exons/genes.



1. Using BLAST and the nucleotide sequences extracted from GENSCAN output, tell me the protein names of the first two nucleotide sequences.

>./29.fa.txt|GENSCAN\_predicted\_peptide\_1|2058\_aa: Y' element ATP-dependent helicase protein 1

>./29.fa.txt|GENSCAN\_predicted\_peptide\_2|1549\_aa: Signal sequence-binding protein