

ATBI: E-Learning Task 1

1. go to: <https://www.omim.org/> and search for PLAT
2. choose "Plasminogen Activator, Tissue; PLAT"
3. click on "DNA" and navigate to "Ensembl (MANE Select)"
4. click on "Download sequence" > "Preview" > search (CTRL+F) for "Intron 8" > copy the sequence to file (or as string to python script)
5. close this window and click on "Show transcript table" > click on "NM_000930.5" > you can see all genetic relevant information about the PLAT gene
6. search next to "Nucleotide" for "PLAT Alu sequence" in NCBI Nucleotides > select first entry (GenBank: K03021.1)
7. download FASTA sequence (use "Send to" + "File" + "FASTA" + "Create File") > save as "PLATwithALUsequence.fasta" (or as string to python script)
8. process raw sequences and extract sequence between primers: GTGAAAAGCAAGGTCTACCAG and GACACCGAGTTCATCTTGAC
! Hint: remember DNA strands – you won't find the second primer if you don't use the reverse complementary version: GTCAAGATGAACTCGGTGTC
9. go to <https://dotlet.vital-it.ch/> > add both sequences > take a screenshot
10. go to https://www.ebi.ac.uk/jdispatcher/psa/emboss_needle > enter the two sequences > submit
11. Note the following parameters: Number of Gaps, Alignment Score, Start position of the Gap
12. (optional) search for ORFs (using ORFfinder: <https://www.ncbi.nlm.nih.gov/orffinder/>) > insert sequence with Alu > how many ORFs are found?
13. (optional) go to <https://alfred.med.yale.edu/> and enter PLAT > choose "Plasminogen activator, tissue"
 - a. select "TPA25 Alu insertion" > click on "Frequency Display Formats: Graph"
 - b. learn something about human migration ;)