**Version A1**

1. Work with following sequence:

GCCTTCATCGAGTTTAAGAATTTCAAAAAGGAAAAGGAAACCCCCTTTAACCAAGTCCCC

ATACTCGAAATGGACAACATCATATTTGCCCAAAGTCAAGCCATAGTAAGGTACCTCTCC

AAGAAATACAAAATAAGTGGGAACAGCGAGCTGAACGAATTTTACGCCGACATGATTTTT

TGTGGAGTACAAGACATACATTATAAATTTAACAATACAAATTTATTTAAGCAGAATGAG

ACCACCTTTCTTAATGAGGAGTTGCCGAAGTGGTCAGGTTACTTTGAGAATATTTTGAAA

CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAG

GCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGA

TAACAATTTCACACAGGAAA

* Find out if there is any vector contamination.
* If yes, get the “purified” sequence and write it down in FASTA format
* Would be the purified sequence cut by restriction endonucleases KpnI, HpaII or RsaI?
* How long is the longest peptide after translation? In which open reading frame (ORF) is it encoded?
* From which organism does this sequence likely come from?

1. Download the sequence of the accession number: NM\_000771.4

* How long is the coding sequence and how long will the translated protein be?
* Design primers for the detection of this gene for amplification of the product no longer than 500nt.
* How many prolines does corresponding protein have?
* How many times would be the sequence cut by pepsin (pH1.3)?
* Compare the corresponding protein with protein with accession number: P10632. What is the level of identity?