Problem 1. Dynamic Programming (10 points).

With the following scoring function: *MATCH: 5 MISMATCH: -10 GAP: -5*
Consider the task of finding the optimal global alignment of the following
two sequences: ATC and ATATCTC. Construct the dynamic
programming table.

Answer:

Problem 2. Gene Ontology database (10 points).

Write down at least two **Homo Sapiens** genes or proteins that are annotated to GO:0006285 (base-excision repair, AP site formation) based on experimental evidence (IDA, IMP). Please use the AmiGO2 database (http://amigo.geneontology.org/)

Answer:

Problem 3. UniProt database (10 points).

UniProt database (https://www.uniprot.org/) is where you can find the sequence of a specific gene. Please use the UniProt database to find the amino acid sequence of the gene **KMT2A_HUMAN** and the gene **KMT2A_MOUSE**.
Write down the first 50 amino acids of **KMT2A_HUMAN (5 points)** and the first 50 amino acids of **KMT2A_MOUSE (5 points)** here.

Answer: