

# Sequence alignment: Practice problems

## Easy

### *DNA sequences:*

- ☐ DNA structure - <https://rosalind.info/problems/dna/>
- ☐ RNA translation - <https://rosalind.info/problems/rna/>
- ☐ DNA reverse complement - <https://rosalind.info/problems/revc/>

### *Sequence alignment warm-up*

- ☐ Hamming distance - <https://rosalind.info/problems/hamm/>

## Medium

- ☐ Dynamic programming - <https://rosalind.info/problems/fib/>
- ☐ Edit distance - <https://rosalind.info/problems/edit/>
- ☐ Edit distance alignment - <https://rosalind.info/problems/edta/>

## Advanced

*Note:* [Protein sequences](#) are used in the problems that follow. These are sequences that describe the primary structure of proteins (peptide chains) and not DNA molecules. The basic units of protein sequences are [amino acids](#), which can also be indicated with one letter codes. The sequences can be saved in FASTA (aa) files. The set of symbols is bigger (there are more letters), but the same principles for alignment apply. There are specific scoring matrices that are indicated in the problem descriptions.

### *Global alignment*

- ☐ Global alignment with scoring matrix - <https://rosalind.info/problems/glob/>
- ☐ Global alignment with constant gap penalty - <https://rosalind.info/problems/gcon/>

### *Local alignment*

- ☐ Local alignment with scoring matrix - <https://rosalind.info/problems/loca/>