

Sequence Listings

```

AGGACCATAAACTCCAGTCAGTGAAC TTTCGCAGTCTGA
AAACAAGTTAATAAACTAAAAC TTTCAACAACGGATCTC
TGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATA
GTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTT
GAACGCACATTGCGCCCCTTGGTATTCCGAGGGGGCATGC
TGTTTCGAGCGTCATTTCAACCCTCAAGCTCTGCTTGGTA
TGGGCTCCGTCCCTCCACGGACGCGCCTTAAAGACCTCGG

```

If a nucleotide or amino acid sequence is disclosed in a European patent application, it must be represented in a sequence listing, irrespective of whether the sequence is claimed. The application must contain a sequence listing in an annex to the description. The sequence listing must conform to WIPO Standard ST.25 and be submitted electronically. The sequence listing should ideally be provided when filing the patent application (including divisional applications). Deficiencies of the sequence listing may lead to refusal of the application or to the award of a later date of filing. It may be possible to remedy deficiencies within a specified period, but compliance with the sequence filing requirements from the date of filing of the application is strongly recommended.

Sequence listings should be filed in electronic form which conform to the requirements and standards found in [Annex C](#) of the Administrative Instructions under the Patent Cooperation Treaty. Typically, 'PatentIn' software is used to prepare the sequence listings for patent applications.

Each sequence listing should be given a separate sequence identifier and identified according to this identifier in the patent application.

Nucleotide and amino acid sequences should be represented by at least one of the following three possibilities:

- (i) a pure nucleotide sequence
- (ii) a pure amino acid sequence
- (iii) a nucleotide sequence together with its corresponding amino acid sequence

A **nucleotide sequence** should be presented as a single strand in the 5' to 3' direction from left to right. The bases of a nucleotide sequence should be represented using a one letter code ([Appendix 2, Table 1](#) of the PCT Instructions).

Any modified bases should be represented as the corresponding unmodified bases or as "n". The modification should be further described in the sequence listing, using the codes in [Appendix 2, Table 2](#) of the PCT Instructions. The symbol "n" is the equivalent of only one unknown or modified nucleotide.

An **amino acid sequence** in a protein or peptide sequence should be listed in the amino to carboxy direction from left to right. The amino acids should be represented using a three-letter code as per [Appendix 2, Table 3](#) of the PCT Instructions.

Modified and unusual amino acids should be represented as the corresponding unmodified amino acids or as “Xaa”. The modification should be further described in the sequence listing using the codes given in [Appendix 2, Table 4](#) of the PCT Instructions. The symbol “Xaa” is the equivalent of only one unknown or modified amino acid.

When nucleotide and amino acid sequences are provided together the amino acids should be placed under the corresponding codons of the nucleotide sequence.

More details regarding the format of the sequences can be found in [Annex C](#) of the Administrative Instructions under the Patent Cooperation Treaty.

In addition to the actual sequence the sequence listing should also include the applicant name, title of invention, number of sequence ID numbers, the sequence ID number, length (of sequence), type (of sequence) and the organism.

If the sequence contains a modified base or modified or unusual amino acid the sequence listing should also contain details of the feature, the name/key, location and any other information.

The sequence listing may also contain free text which can be used to describe the sequence. The text should be limited to a few short terms indispensable for understanding the sequence. This free text and any further information regarding the sequence listing should be contained within the description.

We have explained the general principles of sequence listings in this AL Factsheet but it is only an introduction, and any live situation will need individual assessment. Please contact us if you need more detailed information.