

represented as a single amino acid sequence, but shall be presented as separate amino acid sequences.

(e) A sequence with a gap or gaps shall be presented as a plurality of separate sequences, with separate sequence identifiers, with the number of separate sequences being equal in number to the number of continuous strings of sequence data. A sequence that is made up of one or more non-contiguous segments of a larger sequence or segments from different sequences shall be presented as a separate sequence.

[63 FR 29635, June 1, 1998, as amended at 69 FR 18803, Apr. 9, 2004; 70 FR 10489, Mar. 4, 2005]

**§ 1.823 Requirements for nucleotide and/or amino acid sequences as part of the application.**

(a)(1) If the “Sequence Listing” required by §1.821(c) is submitted on paper: The “Sequence Listing,” setting forth the nucleotide and/or amino acid sequence and associated information in accordance with paragraph (b) of this section, must begin on a new page and must be titled “Sequence Listing.” The pages of the “Sequence Listing” preferably should be numbered independently of the numbering of the remainder of the application. Each page of the “Sequence Listing” shall contain no more than 66 lines and each line shall contain no more than 72 characters. The sheet or sheets presenting a sequence listing may not include material other than part of the sequence listing. A fixed-width font should be used exclusively throughout the “Sequence Listing.”

(2) If the “Sequence Listing” required by §1.821(c) is submitted on compact disc: The “Sequence Listing” must be submitted on a compact disc in compliance with §1.52(e). The compact disc may also contain table information if the application contains table information that may be submitted on a compact disc (§1.52(e)(1)(iii)). The specification must contain an incorporation-by-reference of the Sequence Listing as required by §1.52(e)(5). The presentation of the “Sequence Listing” and other materials on compact disc under §1.821(c) does not substitute for the Computer Readable Form that must be submitted on disk, compact disc, or tape in accordance with §1.824.

(b) The “Sequence Listing” shall, except as otherwise indicated, include the actual nucleotide and/or amino acid sequence, the numeric identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the “Sequence Listing.” The order and presentation of the items of information in the “Sequence Listing” shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an “M” is mandatory. The submission of those items of information designated with an “O” is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the “Sequence Listing.” The following table illustrates the numeric identifiers.

Numeric identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<110> .....	Applicant .....	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials.	M.
<120> .....	Title of Invention .....	.....	M.
<130> .....	File Reference .....	Personal file reference .....	M when filed prior to assignment of appl. number.
<140> .....	Current Application Number.	Specify as: US 07/999,999 or PCT/US96/99999.	M, if available.
<141> .....	Current Filing Date	Specify as: yyyy-mm-dd .....	M, if available.
<150> .....	Prior Application Number.	Specify as: US 07/999,999 or PCT/US96/99999.	M, if applicable include priority documents under 35 USC 119 and 120.
<151> .....	Prior Application Filing Date.	Specify as: yyyy-mm-dd .....	M, if applicable.
<160> .....	Number of SEQ ID NOs.	Count includes total number of SEQ ID NOs.	M.
<170> .....	Software .....	Name of software used to create the Sequence Listing.	O.

Numeric identifier	Definition	Comments and format	Mandatory (M) or optional (O).
<210> .....	SEQ ID NO:#: .....	Response shall be an integer representing the SEQ ID NO shown.	M.
<211> .....	Length .....	Respond with an integer expressing the number of bases or amino acid residues.	M.
<212> .....	Type .....	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M.
<213> .....	Organism .....	Scientific name, i.e. Genus/ species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220> .....	Feature .....	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence..	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA"
<221> .....	Name/Key .....	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<222> .....	Location .....	Specify location within sequence; where appropriate state number of first and last bases/amino acids in feature.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<223> .....	Other Information ...	Other relevant information; four lines maximum.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300> .....	Publication Information.	Leave blank after <300> .....	O.
<301> .....	Authors .....	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials.	O.
<302> .....	Title .....		O.
<303> .....	Journal .....		O.
<304> .....	Volume .....		O.
<305> .....	Issue .....		O.
<306> .....	Pages .....		O.
<307> .....	Date .....	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy.	O.
<308> .....	Database Accession Number.	Accession number assigned by database including database name.	O.
<309> .....	Database Entry Date.	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy.	O.
<310> .....	Patent Document Number.	Document number; for patent-type citations only. Specify as, for example, US 07/999,999.	O.
<311> .....	Patent Filing Date ...	Document filing date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<312> .....	Publication Date ....	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<313> .....	Relevant Residues	FROM (position) TO (position) .....	O.
<400> .....	Sequence .....	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence.	M.

[63 FR 29636, June 1, 1998, as amended at 65 FR 54681, Sept. 8, 2000; 68 FR 38630, June 30, 2003]