**Proposed new Examples for Annex VI of Standard ST.26**

### *Paragraph 94 – Variant sequence disclosed as a single sequence with enumerated alternative residues*

**Example 94-2 – Representation of single sequence with enumerated alternative amino acids that may be modified amino acids**

A patent application describes the following polypeptide:

Leu-Glu-Tyr-Cys-Leu-Lys-Arg-Trp-Xaa-Glu-Thr-Ile-Ser-His-Cys-Ala-Trp

where Xaa can be Ile, Ala, Phe, Tyr, aIle, MeIle, or Nle.

**Question 1: Does ST.26 require inclusion of the sequence(s)?**

**YES**

The enumerated peptide provides 16 specifically defined amino acids. Therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph (7)(b).

**Question 3: How should the sequence(s) be represented in the sequence listing?**

The most restrictive ambiguity symbol that can encompass “Ile, Ala, Phe, Tyr, aIle, MeIle, or Nle” is “X”. Therefore, the sequence must be included in a sequence listing as:

LEYCLKRWXETISHCAW (SEQ ID NO: xx)

ST.26 paragraph 30 requires that “[a] modified amino acid must be further described in the feature table”. However, paragraph 30 does not require any specific feature key be used to describe modified amino acids. While paragraph 30 describes the use of feature keys “CARBOHYD”, “LIPID”, “MOD\_RES”, and “SITE”, these feature keys are more appropriate for scenarios where the modified amino acid is not within a list of alternatives for a specific location. In this example, the feature key “VARIANT” satisfies the requirement of paragraph 30 since it allows for the inclusion of all of the alternatives for the variant site. So, the feature key “VARIANT” with the qualifier “note” “Ile, Ala, Phe, Tyr, aIle, MeIle, or Nle” as a qualifier value should be used to describe the variant site at position 9. The use of a second feature key such as “SITE” with a qualifier “note” may be used to further identify the modified amino acids found at position 9.

**Relevant ST.26 paragraph(s):** 3(a), 7(b), 27, 30, **94**, 96, and Annex I, Section 4, Table 4

### *Paragraph 30 – Annotation of a modified amino acid*

**Example 30-2 – Post-translationally modified amino acids**

A patent application describes the following polypeptide:

Leu-Glu-Tyr-Cys-Leu-Lys-**Arg**-Trp-Glu-Thr-Ile-Ser-His

wherein the Arg at position 7 may be post-translationally deiminated to citrulline.

**Question 1: Does ST.26 require inclusion of the sequence(s)?**

**YES**

The enumerated peptide provides 13 specifically defined amino acids. Therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph (7)(b).

**Question 3: How should the sequence(s) be represented in the sequence listing?**

According to ST.26 paragraph 29, a modified amino acid should be represented in the sequence as the corresponding unmodified amino acid whenever possible.

Therefore, the sequence should be included in a sequence listing as:

LEYCLKRWETISH (SEQ ID NO: xx)

where the symbol “R” is used to represent the arginine at position 7.

A further description indicating that the arginine at position 7 may be modified to citrulline is required. The modification of arginine to citrulline is a post-translational modification. Therefore, the feature key “MOD\_RES” should be used together with the mandatory qualifier “note” to indicate that the arginine may be deiminated to form citrulline. The location descriptor in the feature location element is the residue position number of the modified arginine.

**Relevant ST.26 paragraph(s):** 3(a), 7(b), **30**, and Annex I, Section 7, Feature Key 7.18

### *Paragraph 12 – Circular nucleotide sequence*

**Example 12-1: Circular nucleotide sequence**

A patent application contains the following figure, disclosing the DNA sequence of plasmid pCIRC1:



**Question 1: Does ST.26 require inclusion of the sequence(s)?**

**YES**

The enumerated nucleotide sequence has more than 10 specifically defined nucleotides. Therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph (7)(a).

**Question 3: How should the sequence(s) be represented in the sequence listing?**

According to ST.26 paragraph 12, when nucleotide sequences are circular in configuration, the applicant must choose the nucleotide in residue position number 1. For the purposes of this example, the “a” residue identified by the arrow in the figure will be used as position 1. However, any residue may be chosen as position 1. With the residue indicated by the arrow as position 1, the sequence should be included in a sequence listing as:

atggataatgaagaagttaacgaagaatgtatgagattatttttcaagaacgctcgtgcgcatctggataaacatctaacatcaaggttgacatgcgatgaaaatgaaaatgcatatatcacgttcagatgcttcctggatggaatacatcgcaaatctactaggtttctcgaagagctacttttgaaacaagaaaatatgtaccaccaatg (SEQ ID NO: xx)

The sequence should be further described using feature key “misc\_feature” with a location of “212^1”, which indicates that the last residue in the sequence, position 212, is linked to residue 1. A “note” qualifier must be included with a value indicating that the molecule is circular.

**Relevant ST.26 paragraphs:** 7(a), **12**, and Annex I, Section 5, Feature Key 5.15

[后接附件二（附件六附录）]