

Committee on WIPO Standards (CWS)

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NEW WIPO STANDARD ON THE PRESENTATION OF NUCLEOTIDE AND AMINO ACID SEQUENCE LISTINGS USING EXTENSIBLE MARKUP LANGUAGE (XML)

Document prepared by the Secretariat

1. Document CWS/4/7 contains a proposal of a new WIPO Standard ST.26 “Recommended standard for the presentation of nucleotide and amino acid sequence listings using XML” prepared by the SEQL Task Force. This proposal is presented for consideration and adoption by the Committee on WIPO Standards (CWS).
2. Following another round of Task Force discussions, which took place after the submission of the draft new WIPO Standard ST.26 to the International Bureau, the Task Force agreed that further changes to the proposal presented in document CWS/4/7 were necessary. The proposed amendments to draft new standard ST.26, which is presented in document CWS/4/7, are reproduced in the Annex to this document for consideration and approval by the CWS.
3. *The CWS is invited to consider and approve amendments to the draft new standard ST.26, as reproduced in the Annex to this document.*

[Annex follows]

PROPOSAL FOR AMENDMENTS TO THE DRAFT WIPO STANDARD ST.26

Document prepared by the European Patent Office (EPO)

INTRODUCTION

1. Following the submission of the draft new standard ST.26 for consideration by the CWS (see document CWS/4/7), a group of SEQL Task Force members, representing trilateral offices, proposed a number of changes to the main body of the draft new standard and to Annex II thereto. The proposals agreed by the Task Force are presented below.
2. Changes to paragraph 29 of the main body are proposed to facilitate the determination by practitioners, whether a particular amino acid is post-translationally modified or not.
3. Changes to Annex II (DTD) are proposed to align it with the main body with regard to the data element `IPOfficeCode` which was optional for `ApplicationIdentification` and `EarliestPriorityApplicationIdentification` elements and is now defined as mandatory in both cases.

AMENDMENTS TO THE MAIN BODY OF DRAFT NEW STANDARD ST.26

29. A modified amino acid must be further described in a feature table (see paragraph 60 *et seq.*). The feature key "MOD_RES" must **should** be used for post-translationally modified amino acids together with the qualifier "NOTE"; **otherwise,** and the feature key "SITE" ~~for other modified amino acids~~ together with the qualifier "NOTE" **should be used.** The value for the qualifier "NOTE" must either be an abbreviation set forth in Annex I (see Section 4, Table 4), or the complete, unabbreviated name of the modified amino acid. The abbreviations set forth in Table 4 referred to above or the complete, unabbreviated names must not be used in the sequence itself.

AMENDMENTS TO ANNEX II OF DRAFT NEW STANDARD ST.26 (DTD)

```
<!--ApplicationIdentification
Application identification for which the sequence listing is submitted, when available.
-->
<!ELEMENT ApplicationIdentification (IPOfficeCode?,ApplicationNumberText,
FilingDate?) >

<!--EarliestPriorityApplicationIdentification
Application identification of the earliest claimed priority, which Contains
IPOfficeCode, ApplicationNumberText and FilingDate elements.
-->
<!ELEMENT EarliestPriorityApplicationIdentification (IPOfficeCode?,
ApplicationNumberText,FilingDate?) >
```

[End of Annex and of document]