The EPO would like to thank the users who took part in the consultation. The comments received on the proposed new standard, while limited in number, were concise and relevant and covered all major stakeholders (attorneys, IP associations, biotech/pharma industry, search and sequence listing firms).

The EPO has grouped by topic all the comments received as follows:

1. **XML FORMAT**
   - focus on further developing TXT-based ST.25; less favoured alternative: co-existence of both standards
   - much harder for humans to read, interpret and review (e.g. spotting errors, manual correction)
   - not possible to make “last minute” changes without having access to specialised software
   - extra work and costs for applicants
   - use of text editors difficult or impossible
   - adaptation of PCT applications for European phase more cumbersome (requires special software even for minor changes, e.g. bibliographic data)
   - larger files (issue of acceptance by Electronic Filing and Submission (EFS) portal(s)?)
   - no numbering of residues in sequences
   - no mixed mode (amino acids displayed below coding sequence, codons displayed as triplets)
   - more difficult to refer to specific parts of a sequence
   - legal uncertainty when referring to computer-generated display of sequence listing (and not original version), risk of mistakes or variability introduced by computer
   - possible to introduce spaces or blank lines to break up the text for improved readability?

2. **MAIN BODY**
   - missing requirement for SEQ ID NOs in description should be made explicit
   - paragraph 7: replication of sequences can be difficult to detect/avoid; is such replication explicitly prohibited? software support (e.g. BiSSAP) possible?
   - paragraphs 9, 28, 37: “intentionally skipped sequence” is unclear, should be replaced by “empty sequence”
   - table 2: additional column should be introduced: “corresponding preferred unmodified base”; spelling mistake: “queuosine”
   - table 4: two additional columns should be introduced: “corresponding preferred unmodified amino acid” and “MOD_RES or SITE”
   - paragraph 22: examples should be given for each situation, add fourth situation for consensus sequences
• paragraph 28: “ApplicationFilingDate” cannot be mandatory because not known at filing (proposal: use same explanation as for “ApplicationNumber”)
• paragraph 35: “u” instead of “t” for RNA in example
• paragraph 59 (“Fields for patent office's use only”): patent offices should not be allowed to write something into a sequence listing which is an elementary part of the disclosure of the invention and which is the sole responsibility of the applicant
• indication of inventor’s name should be deleted (problems with national provisions)

2.1. Prohibited sequences
• will branched sequences and sequences containing fewer than ten defined nucleotides or four defined amino acids be rejected?
• what about sequences containing only “Xaa” (required by some offices for search purposes)?

2.2. Modified nucleotides
• does each individual chemical moiety have to be defined explicitly?

2.3. D-amino acids
• requirement to indicate for each residue whether it is D- or L-?

2.4. Variants
• one entry per variant will result in overly long sequence listings
• variants with less than four defined residues (e.g. ambiguous positions) to be included?

3. ANNEX: CONTROLLED VOCABULARY
• too many optional feature keys
• qualifiers relating to geographical origin should be removed (optional, serve no purpose)
• reduce number of feature keys to two: one to define “n” in a nucleotide sequence and one to define “Xaa” in an amino acid sequence
• many optional feature keys have mandatory qualifiers
• delete optional feature keys (“most applicants choose to ignore any key which is not mandatory”)
• some modifications are abbreviated while others must be described in full. why is this?
• why is the “Source” feature mandatory?
• remove Section 10 (“Country” qualifier values)
4. SOFTWARE

- “WIPO ST.26 [should not be] required until the software for generating ST.26-formatted sequence listings and for their ex officio conversion for publications is fit for purpose”
- sequence-listing authoring tool required
- quick and reliable software program required for conversion between conventional PatentIn-generated ST.25-compliant sequence listing files (TXT format) and the proposed ST.26-compliant sequence listing files (XML format)
- why should there be different authoring tools from different offices (e.g. BiSSAP, planned USPTO developments)?
- ensure compatibility between different software tools (e.g. PatentIn, BiSSAP)
- software should be developed by WIPO or office which adopts ST.26
- applicants should be provided with software
- easy-to-understand manual
- sufficient test period to ensure stable use of tool
- output should be easy to check (NA-, AA-sequences, types, positions, sequences of modifications)
- more efficient “post-processing” options in new listing-generation software?
- “reliance on BiSSAP’s infallibility is unacceptable”

5. TRANSITION

- if standard is not accepted by other offices, this will generate extra work and costs for applicants
- “ensure that existing sequence listings can be used”
- transitional provision (“that the EPO only requires use of the new WIPO ST.26 on applications where the earliest of the date of filing and any date of priority is after the relevant “start” or “cut-off” date”)
- “ensure that the introduction of a new WIPO ST.26 does not cause unnecessary expense, inconvenience, or possible loss of rights for applicants where sequence listings have already been prepared and filed for applications"
- existing applications/divisionals: no new sequence listing should be required, offices should do the conversion
- provide long overlap period during which both formats will be accepted
- one-year grace period (wherein both ST.25 and ST.26 are allowed) seems appropriate
- national/regional compliance with different standards makes process longer and more costly
- EPO should co-ordinate implementation with other major IPOs

6. CONVERSION

- EPO should formally propose style sheets (for each official language) and any ancillary files for check and review
- EPO should formally adopt style sheets and any ancillary files for use by BiSSAP and subsequent conversion
• conversion carries risk of errors, potential loss of rights
• consistent use of style sheets for sequence-listing generation and conversion
• “ensure that whatever information is contained in the WIPO ST.26-formatted XML file is both correct and complete in the converted document produced by the EPO”
• rights of applicant should not be affected by incorrect or incomplete *ex officio* conversion
• rights of third parties should not be adversely affected by incorrect or incomplete *ex officio* conversion
• applicants should always be allowed to submit ST.25-compliant sequence listings, patent offices should do conversion

7. PROCEDURAL

• introduce standard to harmonise the differences in national or regional practices (e.g. reference to database accession numbers, representation of consensus sequences)
• problems with description of PCR primers
• correction of “feature keys” upon registration should be possible
• amendment of sequence listing based on specification should be allowed
• lower fees for pages of sequence listing

8. PUBLIC ACCESS/INFORMATION

• make original sequence-listing files available online (as WIPO does for PCT) because conversion of sequence listings to PDF (Art. 6(2) Dec. of the President of the EPO dated 28 April 2011 on the filing of sequence listings, OJ EPO 2011, 372) does not allow third parties to inspect originally filed data