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Webinar: WIPO Sequence

hosted by the International Bureau of WIPO

Virtual, April 28, 2021
12:00 – 13:30 (CEST)

RESPONSES TO QUESTIONS

prepared by the International Bureau of WIPO

Following are the responses to the questions raised at the Webinar.

Q1: Are mandatory fields and optional fields marked within the interface of the WIPO Sequence desktop tool?

A1: Yes, all fields mandatory for inclusion in order to save the data within the tool are marked with an asterisk. However, in terms of mandatory/optional qualifiers for a particular feature key, these can only be identified during validation.

Q2: Can I share my custom lists with co-workers who have WIPO Sequence running on their own computers?

A2: In terms of custom lists, it is possible to export your list of custom organisms as an Excel file and share it with your colleagues. However, it is not possible to export any 'person/organizations' saved locally in order to share this information with them.

Please note, custom list data is only stored locally within your own instance of the tool.

Q3: Are there examples of how to import the multi-sequence and raw upload formats into a WIPO Sequence project?

A3: Examples of how to import multi-sequence and raw formats were shown during the presentation. The slide deck is published here: https://www.wipo.int/meetings/en/details.jsp?meeting_id=62849

Q4: What are skipped sequences used for in a sequence listing?

A4: As in WIPO ST.25, it is possible to mark a particular sequence as 'skipped'. This is so that the residue data of a particular sequence can be ignored but the subsequent sequences do not need to be renumbered. See paragraph 3(d) and 58 of WIPO ST.26.

Q5: If a validated ST.26 Sequence listing is re-imported into WIPO Sequence, can there be situations where it can generate any errors?

A5: A validated ST.26-compliant sequence listing which has been exported from WIPO Sequence should not generate any errors when re-imported into the tool, unless it was generated using a different DTD or edits were made to the XML document after generation.

Q6: Can you download an Excel file in which all sequences have been entered? This is possible with PatentIn and very useful when we have a huge number of sequences.

A6: While it is not possible to export the sequences from a project to an Excel file, it is possible to print a project and specify whether only the general information or only the sequence section of the project are included. This will produce as a PDF file all of the sequences saved within a project.

Q7: Is the first webinar (Introduction to WIPO ST.26) recorded and available to watch online?

A7: Yes, the session was recorded and the video was published along with the slide deck on the webinar event page at: https://www.wipo.int/meetings/en/details.jsp?meeting_id=62849

Q8: If applicants have any queries on this tool about creating a sequence listing, will WIPO be providing support directly to applicants?

A8: At the moment, WIPO is finalizing development of a series of improvements of the tool. During this period, prior to the big bang date, all queries regarding implementation of the tool, or reports of bugs or requests for improvement should be sent to standards@wipo.int.
After the big-bang date, the expectation is that patent Offices serve as a Level 1 support and only if their queries cannot be resolved will it then be forwarded onto WIPO.

Q9: Is it possible to import the data contained in an excel file into the tool?

A9: Currently there is no means of importing sequence data contained within an Excel sheet. We were unaware of the need to implement this function and if end users consider this important, further details regarding the exact format that should be supported should be sent to standards@wipo.int.

Q10: Is it possible to demonstrate how to import a FASTA file into a WIPO Sequence project?

A10: How to import a FASTA sequence is captured on slide 22 of the slide deck published on the webinar event page at: https://www.wipo.int/meetings/en/details.jsp?meeting_id=62849

Additionally, the updated user desktop manual will provide full details on how to proceed with importing this type of sequence and this will be published along with the new version of WIPO Sequence in August 2021.

Q11: Can the WIPO Sequence desktop be run offline after we have installed it?

A11: Yes. The tool is designed to be used offline. There is no need to be connected to the internet in order to author a WIPO Sequence project nor validate or generate an ST.26 sequence listing.

Q12: Is there a format suitable for importing branched sequences? If so, what does it look like or where can I find an example of it?

A12: ST.26 Annex VI is a guidance document which provides various example sequences, advises whether they should form part of an ST.26 sequence listing and how to provide this information. Example 7(a)-1 has an example of a branched nucleotide sequence listing and Examples 7(b)-2 & 3 are examples of a branched amino acid sequence listing.

Q13: Is the information contained within a project protected even when there are errors reported with the desktop tool? Can we retrieve previously typed information if the system cannot move on to the next phase due to error?

A13: Yes. The tool will save with the edit or save button any information which is entered into the project. If the tool then crashes or any error occurs when you reopen the project later it will have all the information saved prior to the error occurring.

Q14: If I want to manually copy in a sequence (raw) that has line numbering in it, will WIPO Sequence remove the line numbering automatically or will I need to do this in advance?

A14: No. The desktop tool will strip white space and line numbers when you cut-and-paste sequence data into the sequence text box within the interface.

Q15: Where can I find a .txt file listing the names of organisms that can be imported into the program? Do I need to generate this list by myself?

A15: The list is provided in the tool as a series of 26 JSON files (one for each letter of the alphabet).

The list of predefined organism names, which is provided in the tool, is put together from two industry databases annually (see question 8 of the ST.26 Implementation FAQ). In the future, we are investigating whether custom organisms provided by applicants should also be reviewed by the sequence listing task force for inclusion within the list.

Q16: While it is possible to "import" sequences in various formats into WIPO Sequence, can one simply copy and paste a sequence into the platform (say from a word doc. or from NCBI website)?

A16: Yes, it is possible to cut-and-paste sequence data from a word doc or website directly into the residues box (labelled 'Sequences') in the WIPO Sequence desktop interface. It is also possible to cut-and-paste qualifier values into the qualifier value boxes, however the type of qualifier will still need to be manually selected from the dropdown box.

Q17: If a validated sequence listing is generated using the WIPO Sequence Desktop Tool, is there a need for the offices to validate this sequence listing using the WIPO Validator Tool?

A17: While a sequence listing generated by WIPO Sequence will be compliant with WIPO ST.26, it is still recommended that Offices validate any sequences they have received. Even if the sequence listing is generated by WIPO Sequence, it can also be edited using a basic text editor so Offices need to ensure that the sequence listing is still compliant.

Additionally, there are checks at the Office level at filing which the Validator service performs. For example, checking to see if English translations have been provided if the free text qualifiers were originally provided in a language other than English.

Q18: Is it possible to import the human readable format to WIPO sequence?

A18: No. The only allowable ST.26 format for import into the tool is the XML document.

The human readable format is provided only to make the content of the sequence listing more digestible for users who are not familiar with XML documents, after generation.

Q19: Can custom lists be imported from elsewhere?

A19: In terms of custom lists, the only one which can be imported or exported from the tool is the custom organism name list. If one instance of WIPO Sequence exports their list of custom organisms, as an Excel file, this can then be reimported into another instance of WIPO Sequence.

Q20: Is there a format suitable for importing amino acid sequences having D-AA's in them? If so, what does it look like or where can I find an example of it?

A20: Although ST.25 sequence listings do not allow D-Amino acids, the definition of what is defined as an amino acid is expanded in ST.26 and ST.26 compliant-sequence listings require their inclusion. For an example, see Example 3(a)-1 in Annex VI of WIPO ST.26. Examples 29-1 and 30-1 may also be useful in this instance.

Q21: After testing the tool, I could not find a way to delete imported sequences in batch (e.g., delete 10 sequences at a time). Is this possible?

A21: During the current development project we have introduced this new feature. On the verification report, it is possible to select multiple sequences (by checking the box next to the relevant SEQ ID) and bulk deleting these sequences. The latest version of the desktop tool also supports the bulk editing of sequences, for instance to apply a particular molecule type.

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