



WIPO Sequence
Release notes version 2.0.0

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WIPO Sequence

1. Binaries

1.1. Overview

This is a stable version of the WIPO Sequence released to the public and published [on our website](#) in the week commencing May 16, 2022.

1.2. Download version 2.0.0

Current users who installed version 1.1.0 will receive an auto-update message. Please select 'OK' to proceed with the installation but do not minimize the desktop tool while performing this task.

If you are a new user, the binaries are available to download from the [WIPO Sequence website](#). WIPO Sequence distributions are provided for three platforms: Windows, Mac OSX and Linux.

Installation instructions for the WIPO Sequence desktop tool are available in the user manual which is published at the same location.

2. Release notes

2.1 Highlights

This is the third stable release provided by the World Intellectual Property Organization (WIPO) and the next public version available after version 1.1.0. It incorporates both improvements and bug fixes reported during testing. The basis of this release is to satisfy what was defined by patent Offices as the Minimum Viable Product (MVP) that would be required by applicants to generate an ST.26-compliant sequence listing.

2.2 Improvements

Since version 1.1.0, the following main improvements have been implemented in the latest version of WIPO Sequence:

- Incorporating a Terms of Use when the desktop tool is first installed;
- Necessary updates which resulted from the revision to WIPO Standard ST.26 at the last session of the Committee on WIPO Standards (CWS);
- New verification rules to ensure the appropriate anticodon format for optional qualifiers for CDS features;
- Improving the performance of the import of ST.25 sequence listings by limiting what is reported to the user;
- Validation checks to ensure that the appropriate feature locations for CDS and other features using location operators;
- Validation checks to ensure appropriate format for location of anticodon and transl_except qualifiers;
- Improvement to the import of ST.25 files including the automatic transformation of uracil to thymine for a DNA sequence;
- Validation checks for skipped sequences, including ensuring no feature table is present;
- Improvements to the language dependent free text qualifier tab, for use in exporting and importing, in XLIFF format, language dependent free text qualifier values in a target language;
- Improving the formatting for the sequence listing when provided in HTML format;
- Improvements to the information provided in the import and verification reports;
- Improvements to the sorting of the projects provided on the project home page;
- Improvements to the bulk editing function; and
- Improvements to keyboard navigation to ensure the accessibility of the desktop tool.

According to the results of our non-performance testing, the threshold of the WIPO Sequence performance (version 2.0.0) is as follows¹:

- (1) When importing sequence data:
 - Import ST.25: 71 k sequences
 - Printing of the import report: 47.5k sequences
- (2) When validating and generating ST.26 files
 - for simple sequences: 180k sequences

¹ This is also impacted by the distribution which is being used e.g., Linux versus Windows

- for complex sequences: 6.5k sequences
- XLIFF import/export: 3k sequences containing approximately 12.6k non-English qualifier values

2.4 Bug Fixing – Issues resolved

In total 235 bugs, which were reported with the previous versions of WIPO Sequence (the stable version 1.1.0 and beta versions provided during development) were resolved during this period. These include fixes for the following main defects:

- Problems caused by qIDs not being numbered appropriately (these identify language dependent free text qualifiers);
- Issues related to the export/import of language dependent free text qualifiers;
- Translation qualifier value is no longer limited to just 1000 residues;
- Issues with the implementation of the validation checks for the location of the transl_except qualifier;
- Issues with the implementation of the CDS feature verification rules;
- Problems with import of mixed-mode sequences;
- Issues with printing of the project and printing of the reports;
- Issues with the general information dates being imported from ST.25 sequence listings; and
- Problems with degrading performance.

2.5 Bug Fixing - Known Issues

Some of the minor and trivial bugs reported during testing are still open and reported below for user information. Additionally there are two known major bugs which occur after multiple XLIFF exports which have not been resolved for this version:

- Sequences from another project can spontaneously appear in a new empty project; and
- Qualifiers can disappear in a new empty project after saving.

If you wish to provide a feedback regarding any of these known issues, please reference the relevant 'Key'.

Type	Key	Summary
Bug (performance)	ST26T-2837	Windows, CentOS, Ubuntu: complex sequences validate processes thresholds
Bug (performance)	ST26T-2836	Windows,CentOs,Linux: complex sequences import process threshold
Bug (performance)	ST26T-2835	XML validation: thresholds for simple sequences
Bug (performance)	ST26T-2834	ST.25 large file with 1million sequences 300Mb and file with 444k sequences 1.02Gb cannot be imported
Bug (performance)	ST26T-2833	Thresholds for import process ("simple sequences")
Bug (performance)	ST26T-2832	Thresholds for validating process of simple sequences

Bug (performance)	ST26T-2831	Import report for large SL cannot be printed
Bug (performance)	ST26T-2830	ST.25 large file 39 Sequences 3 Gb: 2 or more sequences, imported at the same time, cannot be imported correctly
Bug (performance)	ST26T-2829	Verification report for large SL cannot be printed
Bug (performance)	ST26T-2828	The single case of Generate sequence listing finished with Error
Bug (performance)	ST26T-2827	XML validation of files with >180000 simple sequences failed
Bug (performance)	ST26T-2824	XLIFF export: tool fails to export more than 980 Language Dependent Qualifiers
Bug (performance)	ST26T-2799	Delay when the user uploads the file for import after consistent use of large projects
Bug (performance)	ST26T-2743	Performance issues with the large project data
Bug (performance)	ST26T-2739	Validation of .xml file in WIPO Sequence: the bigger test data file, the more time is needed to create a report after validation
Bug	ST26T-2294	When Rules XQV_9 and XQV_45 thrown, the detected value is empty
Bug	ST26T-2292	The wrong link label in the verification report
Bug (localization)	ST26T-2278	Drop-down menus are not translated after changing language of interface
Bug	ST26T-2275	More generic error thrown when invalid qualifier value for PCR_primer
Bug	ST26T-2258	No error in the case of empty DOCTYPE declaration
Bug (ST.25 Import)	ST26T-2257	The "D-segment" feature key is not imported properly
Bug (ST.25 Import)	ST26T-2256	The mandatory value of the <223> element which describe organism <213> with value: "Artificial Sequence" or "Unknown" should be included in the qualifier "note/NOTE" of the feature key "source/SOURCE"

Bug (ST.25 Import)	ST26T-2216	There are two text message "Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences." in the Import report
Bug	ST26T-2144	The qualifier name "organism/ORGANISM" for the feature other than source/SOURCE can't be changed/deleted
Bug (performance)	ST26T-2837	Windows, CentOS, Ubuntu: complex sequences validate processes thresholds
Bug (performance)	ST26T-2835	XML validation: thresholds for simple sequences
Bug (ST.25 Import)	ST26T-2216	There are two text message "Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences." in the Import report
Bug (MAJOR)	ST26T-2854	Sequences from another project erroneously appear in empty project
Bug (MAJOR)	ST26T-2856	Qualifiers disappeared after clicking "Update feature" button

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