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***WIPO Sequence***  
**Release Notes**

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**Version 1.0.0**

## ***Table of Content***

<b>1. Binaries</b> .....	<b>3</b>
<b>1.1. WIPO Sequence Tool 1.0.0</b> .....	3
<b>1.2. WIPO Sequence Validator 1.0.0</b> .....	3
<b>2. Release notes</b> .....	<b>3</b>
<b>2.1. New Functionalities</b> .....	3
<b>2.2. Bug Fixing</b> .....	3
<b>2.3. Specific details on reported bugs</b> .....	4
<b>2.4. Known Issues</b> .....	8

# WIPO Sequence Software Tool

## 1. Binaries

### 1.1. WIPO Sequence Tool 1.0.0

The binaries for the desktop tool are available for the following three platforms:

- Windows: [http://wiposequence.wipo.int/download/latest/windows\\_64](http://wiposequence.wipo.int/download/latest/windows_64) (.exe)
- Mac OSX: <http://wiposequence.wipo.int/download/latest/osx> (.dpm)
- Linux: [http://wiposequence.wipo.int/download/latest/linux\\_64](http://wiposequence.wipo.int/download/latest/linux_64) (.appimage)

### 1.2. WIPO Sequence Validator 1.0.0

- Service as WAR: <https://wiposequence.wipo.int/download/validator/latest/wipo-sequence-validator.war>
- Service as JAR: <https://wiposequence.wipo.int/download/validator/latest/wipo-sequence-validator.jar>

## 2. Release notes

### 2.1. New Functionalities

No new functionalities have been added from 1.0.0-beta2, the last publicly available release.


### 2.2. Bug Fixing

Broadly, the changes provided within this release can be summarized as follows:

1. Inclusion of the values missing in the qualifier drop-down list in the desktop tool interface.
2. Translation now using the latest version of the Genetic Code Tables 27-30 from Annex I, WIPO ST.26.
3. Additional “NOTE” qualifiers incorrectly being included during WIPO ST.25 import are no longer provided as a duplicate.
4. Validation of the feature location have been improved to cover complex scenarios, for instance the use of ‘<’ and ‘>’ in the same feature location (which is allowable).
5. Several fixes in the translation of a CDS feature when referencing a complex feature location, variable residues and `transl_except` qualifiers.
6. Filing date no longer displays the wrong date when entered manually.
7. An error is now generated during validation when `INSDFeature_key` was empty.
8. The right severity-level is now provided, WARNING instead of ERROR, for the following verification rules:
  - a. XQV\_23: The location sub-element of the value of the qualifier “anticodon” must be a location descriptor with the format `LOC_DESC_FORMAT_1` specified in the section “Predefined vocabularies”, “Location descriptor formats”.
  - b. XQV\_24: The `amino_acid` sub-element of the value of the qualifier “anticodon” must be one of the values listed in the section “Predefined vocabularies”, “Amino acid symbols for the value of qualifier /anticodon”.

- c. XQV\_25: The text sub-element of the value of the qualifier “anticodon” must be a sequence of 3 nucleotide symbols as set forth in the section “Predefined vocabularies”, “Nucleotide symbols”.
9. Verification Rule XQV\_37 (*If the element INSDQualifier\_name has the value “protein\_id”, then the associated INSDQualifier\_value must be an integer greater than 0 and less than or equal to the total number of sequences of this sequence listing file*) is now correctly detected when the protein\_id was exactly equal to the number of sequences + 1.
  10. The correct number of sequences specified in the system preferences is printed. Previously the number of printed sequences was out by 1.
  11. Problems with the sequence length have been fixed. Previously sequence length was incorrectly updated after adding new characters and spaces in the “Residues” field.
  12. When importing an ST.25 sequence with a non-valid feature key, the feature key (element <221>) is now concatenated to the generated “note/NOTE” qualifier.
  13. Import can proceed without error when the applicant/inventor name or invention title includes more than one coded character entity.

### 2.3. Specific details on reported bugs

Type	Summary	Details
Bug	CDS Feature: Incorrect validation error for complex CDS locations with format 'complement(join(a..b,c..d))'	 <p>The screenshot shows a table with columns: Severity, Data Element, Message Text, Detected Value, and Detected Sequence. The row contains: Error, Feature Location, Invalid location operator format, complement(join(1..10,10..10)), and Sequence 1.</p>
Bug	WIPO ST.25 Import: Different position features grouped in misc_feature	For an WIPO ST.25 import, the tool must be able to handle different features located at different positions but grouped as a single misc_feature
Bug	WIPO ST.25 Import: Incorrect identification of "t" symbols when an importing WIPO ST.25 file with RNA sequences	For a WIPO ST.25 import, mixing replacement of uracil with thymine. WIPO WIPO ST.26 does not allow the presence of “u” (uracil) in the sequences. It defines that “t” should be construed as thymine (“t”) if the molecule type is DNA and as uracil (“u”) if the molecule type is RNA. (See WIPO ST.26, paragraph 14). It further defines that in special cases where there is uracil in DNA or thymine in RNA, they are considered as modified nucleotide that must be further described in the feature table as defined in WIPO ST.26, paragraph 19, namely as “t” in the sequence with a feature key modified_base as follows: mod_base = other note = uracil or thymine
Bug	WIPO ST.25 Import: AA features with mandatory qualifiers aren't handled properly	The tool creates a new instance of Qualifier with the name note (or NOTE, as appropriate), sets its value to the value of element 223 and adds it to the attribute featureQuals of this feature.  However, in this case, note qualifier is not appropriate for amino acid feature. Only one NOTE qualifier with the value of element <223> value should be enough in this case.
Bug	CDS feature: feature cannot be created if the location includes	A CDS feature cannot be created if the location includes both the 'join' and 'complement' location

	both the 'join' and 'complement' location operators	operators. WIPO Sequence attempts to process the CDS feature but then displays an error message.
Bug	CDS translation: not working for variable residues	It seems the tool translates any codon that has a variable residue (m, r, w, s, y, k, v, h, d, b, and n)
Bug	Feature location: Issues related to validation of complex locations	When entering a CDS location= 'complement(join(1..99,300..4212))' receives an error message.
Bug	WIPO Sequence Server: logo	An outdated logo was used for the WIPO Sequence Server <sup>1</sup>
Bug	CDS feature: Errors creating a CDS feature with location including 'complement'	An error was generated for a valid feature location.
Bug	When adding a transl_except qualifier to a CDS that is on the complement (i.e. the location of the CDS is 'complement(x..y)', one cannot enter the correct qualifier value	Related to the bug above – unable to use 'complement' for a feature location
Bug	Feature location: tool will not allow the use of "<" and ">" at the same time	For feature location, tool will not allow the use of '<' and '>' at the same which is allowable. Removal of either '<' or '>' in the example below, then the location is OK, and no error is posted (no error should be posted in these cases either).  e.g. '>1..<300'
Bug	Qualifier values: for the rpt_type Qualifier Value the option "terminal" is missing	This is in contrast to Annex I, WIPO ST.26
Bug	CDS feature: a Protein sequence is marked as skipped when editing location of a CDS feature.	If a CDS feature is saved, and then it is edited to change the feature location such that a new amino acid sequence results, the translation qualifier value is correctly updated and the sequence of the associated protein sequence (indicated in the protein_id qualifier) is also correctly updated.  However, the associated protein sequence is now marked as intentionally skipped.
Bug	If a user changes the default file name given to an XML upon generation, that new name should be inserted into the fileName attribute	Although the filename was updated at the point of saving the XML file, afterwards the filename was not recorded in the Project.
Bug	Qualifier value: if the value in the mobile element name field	Certain special characters could not be used for qualifier value ((!, -, @, #, \$, %, ^, &, *, for example) so the qualifier cannot be saved.)

<sup>1</sup> WIPO Sequence Server available to WIPO Staff only

	includes whitespaces or special characters	
Bug	Importing a Multisequence file or Raw file: Import Report is showing an error message concerning “u” symbols not being permitted when the sequence is amino acid, 3-letter symbols.	This is an inappropriate error message. This error message should only ever be applied to nucleotide sequences
Bug	Feature location: Issues creating CDS features from complex locations including both join and complement and large sequences	<p>For location format contains join and complement, the following valid feature locations can be entered into a project for a CDS feature: ‘complement(join(1..12,16..27))’ and ‘join(complement(16..27))’, ‘complement(1..12))’, and the feature is generated with translation and protein_id qualifiers and the associated protein sequence with separate SEQ ID NO (as indicated in protein_id qualifier)</p> <p>With respect to generating a CDS feature with a ‘join(complement ...)’ or ‘complement(join...)’ location, the tool is unable to generate the CDS feature for larger coding sequences. The problem appears to be creating a CDS feature with a ‘complement’ location operator for larger coding sequences, though there may be a further problem with ‘complement + join’ operators too.</p>
Bug	Nucleotide feature key prim_transcript is missing the optional qualifiers from the qualifier drop-down menu.	For nucleotide feature key prim_transcript is missing the optional qualifiers: function, gene, gene_synonym, map, and note from the qualifier drop-down menu.
Bug	Add values for rep_origin optional qualifier drop down list	For the nucleotide feature key rep_origin, the optional qualifier drop-down does not have the optional qualifiers: function, gene, gene_synonym, map, note
Bug	Inconsistency between interface and validation for “unassigned RNA” mol_type qualifier value	The tool allows you to select “unassigned RNA” as the mol_type qualifier value, however, upon validation “unassigned RNA” is listed as an error
Bug	CDS feature: there should be no limit to the number of transl_except qualifiers that can be added to this feature	Currently only one transl_except qualifier can be entered into a CDS feature; if one transl_except qualifier is already present, transl_except is no longer listed in the Qualifier Name dropdown.
Bug	Update required for Genetic Code Tables 27-30: errors in translation using Tables 27-30	The tool needs to be updated in line with the latest version of INSDC feature tables after update to WIPO ST.26
Bug	WIPO ST.25 Import: An additional NOTE qualifier is added with value OTHER	When a DISULFID feature has a <223> with a value, the tool is erroneously creating a NOTE qualifier with the value OTHER, and a note qualifier with the value from the <223> line. Only one NOTE qualifier should be created for DISULFID and it should contain the value of the <223>.
Bug	Manually entered Filing date incorrectly saved	When editing the “Application Identification” box, if you manually type in a date in the “Filing date” field (not using the pop-up calendar) and then click outside of the box (for example, in the medium grey area just

		<p>below the “Application Identification” box), the date in the “Filing date” field goes back by one day. If you click “Save”, the incorrect date is shown in the “Application Identification” box.</p> <p>If the date is improper (for example, in the future) and you validate, the validation report shows the date as originally typed in. If a sequence listing is generated, it contains the originally entered filing date even though the project displays the incorrect date that is one day earlier than the entered date.</p>
Bug	Error in stop codon translation	When the codon specified in the transl_except value is not a stop codon, the amino acid specified in the value is not replacing the initial amino acid in either the translation qualifier or the associated protein sequence
Bug	Defects in the validation of Source/SOURCE defects in a WIPO ST.26 sequence listing	<p>When the sequence listing has no &lt;INSDFeature_qual&gt; element under a source/SOURCE feature, sequence listing validation does not list any errors, e.g. organism and mol_type qualifiers are missing.</p> <p>In contrast, if &lt;INSDFeature_qual&gt; element is present, e.g., with note qualifier, and the organism and mol_type qualifiers are missing, then the appropriate errors are listed. Also, upon import, project validation does list the appropriate errors if the source feature is missing; source is present with no &lt;INSDFeature_qual&gt; element or is present with an &lt;INSDFeature_qual&gt; element that is missing organism and mol_type qualifiers. These can be corrected in the project.</p>
Bug	When the sequence listing has no <INSDFeature_qual> element under a source/SOURCE feature (SEQ ID NO: 3), sequence listing validation does not list any errors	Major bug and needs correction by applicant/user
Bug	Validation of an XML including element INSDSeq_other-seqids should raise an ERROR instead of a WARNING	Major bug as the sequence listing can be generated with a warning
Bug	During import of ST.25 SL, when applicant name field contained more than 1 coded character entity, import could not proceed	Bug as tool should be able to interpret any and all coded character and predefined character entities during import. WIPO ST.26 provides allowable predefined entities.
Bug	System preference for number of sequences to be printed does not work.	When printing the sequence listing, the number of sequence printed was out by one.
Bug	Sequence length incorrectly updated after “Residues” new characters and spaces added.	If the user edited the sequence text box to include new characters including spaces then the sequence length did not correctly update in value.

## 2.4. Known Issues

The following bugs are pending resolution but will be addressed in the WIPO Sequence improvement project:

Type	Summary	Priority
Bug	Auto-update does not work for non-stable releases, such as beta releases	Minor
Bug	Discrepancy in errors listed when the source feature key value is empty. One error listed when the XML is validated, but two errors seen when the XML is imported and validated	Trivial
Bug	The sprint 11 authoring tool does not capture the complete file name with '.xml' extension in the XML header	Trivial
Bug	Verification rule XQV_23 was incorrectly stated in the functional specification and so much be corrected for in the next release.	Major

## 3. Annexes: Previous Release Notes

The Release Notes for the previous two publicly available beta releases, 1.0.0-beta1 and 1.0.0-beta2, are provided as Annexes for the reference of the reader.

[Annexes follow]



## Annex 1: Release notes Beta2

### Introduction

Broadly the changes provided within this release can be summarized as follows:

- Several inconsistencies for validation were reported during the last Quality Assurance period. These were validation functionalities of the tool which worked differently for project and sequence-listing validation. Any additional functionalities which were required to ensure consistency for validation were included; and
- WIPO Sequence Server now allows addition of a version name which include basic Latin characters. This will allow labelling of new beta versions as '-betaX' where X is a number.

### Bug Fixing

The following list indicates both previously identified bugs, highlighted in bold, and the resolution which is provided within this release:

- 1. Inconsistencies for validation which were previously identified have been fixed. The following specific validation rules should now be applied consistently both in the project validation and the sequence listing validation:**
  - The attribute `fileName` of a project must contain only the characters specified in WIPO Standard<sup>2</sup> ST.26 par. 40(b);
  - The attribute `applicationIdentification` of a project is mandatory when the attribute `applicantFileReference` of the project is missing;
  - The attribute `filingDate` is a date less than or equal to the current date;
  - The element `FilingDate` of `EarliestPriorityApplicationIdentification` must be less or equal to the element `FilingDate` of `ApplicationIdentification`;
  - The element `INSDFeature_qual` associated with the element `INSDFeature_key` "source" may contain one and only one `INSDQualifier` node with `INSDQualifier_name` "clone";
  - The attribute `applicationNumberText` must contain only the characters specified in WIPO ST.26 par. 40(b);
  - If the element `ApplicantName` contains characters other than those as set forth in WIPO ST.26, par. 40 (b), then the element `ApplicantNameLatin` is mandatory;
  - The element `INSDSeq_moltype` is mandatory;
  - The attribute `featureTable` of the sequence contains one and only one instance of "Feature" with the attribute `INSDFeatureKey` equal to either 'source' or 'SOURCE';

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<sup>2</sup> <https://www.wipo.int/export/sites/www/standards/en/pdf/03-26-01.pdf>

- If the element `INSDSeq_moltype` of a sequence is 'DNA' or 'RNA', then the element `INSDSeq_feature-table` must contain one and only one `INSDFeature` node with the element `INSDFeature_key` "source";
  - If the element `INSDSeq_moltype` of a sequence is 'AA', then the element `INSDSeq_feature-table` must contain one and only one `INSDFeature` node with the element `INSDFeature_key` "SOURCE";
  - The 'join' location operator must be used to indicate the location of the `ribosomal_slippage` (qualifier name "ribosomal\_slippage") or (ii) `trans_splicing` event (qualifier name "trans\_splicing");
  - If the name of the qualifier is "transl\_table", then the value of the qualifier is one of the numbers assigned to genetic code tables as listed in the section WIPO ST.26 Annex I "Predefined vocabularies";
  - The element `IPOfficeCode` is mandatory;
  - The attribute `featureTable` of the sequence contains one and only one instance of "Feature" with the attribute `INSDFeatureKey` equal to either 'source' or 'SOURCE'. (Note: *WIPO Sequence now shows an error if the sequence does not have a feature table*);
  - If the element `INSDQualifier_name` has the value "PCR\_primers", then the sub-elements  `fwd_seq` and  `rev_seq` of the associated element `INSDQualifier_value` must have the format specified in the section WIPO ST.26 Annex I "Predefined vocabularies" (*Modified: now a WARNING*);
  - If the element `INSDQualifier_name` has the value "rpt\_unit\_seq", then the associated `INSDQualifier_value` must be a string containing the symbols <set of chars - to be provided>;
  - If the name of the qualifier is "rpt\_unit\_seq", then the attribute `qualifierValue` of the qualifier must be a string containing only symbols from the set: [a-zA-Z1-9());
  - If the element `INSDSeq_moltype` of a sequence is 'DNA' or 'RNA', then the element `INSDFeature_key` must have one of the values listed in the section WIPO ST.26 Annex I "Predefined vocabularies". In addition, the values "3'UTR" or "5'UTR" are allowed.
2. **Previously there was no check to ensure that INSDSeq did not contain INSDSeq\_other-seqids:** the following error is now triggered in WIPO Sequence Validator: "the element `INSDSeq` must not contain this element `INSDSeq_other-seqids`" The element `INSDSeq_other-seqids` is intended to hold publication information that will be added by the IP Office after the publication of the application/grant; hence it is out of the applicant's concern.
  3. **In French language interface, the English term "add qualifier" was used instead of the French term. In this release the French term "Ajouter un qualificateur" replaces it.**
  4. **The Validator failed when trying to validate an XML with a missing Applicant Name tag:** an error is now thrown by the Validator when validating an XML with a missing Applicant Name tag.
  5. **The following issues related to validation of complex feature locations were fixed:**

- **A CDS feature was not created if the location includes both the join and complement location operators** (i.e., “complement(join(1..99,300..4212))”). WIPO Sequence attempts to process the CDS feature, it displays an error message.
- The following incorrect formats were not detected by the WIPO Sequence but are now detectable:
  - -1..y
  - complement(-1..y)
  - join(-1..y1,x2..y2)
  - 0^y
  - x-y

### Known Issues

There are currently no known bugs identified for correction in the next release.

There have been some issues detecting during testing in regards to the translations provided for the different language interfaces. Improvements to these translations will be provided in the next beta release.

## Annex 2: Release notes Beta1

### New Functionalities

The following features and tasks have been implemented:

- Correct all issues detected by external formal acceptance team and other 'Major' issues detected during testing;
- Code Signing of Windows release to establish WIPO as the publisher;
- Update code quality metrics including the comment density to improve maintainability of source code.

### Bug Fixing – Issues Summary

The following previously identified bugs have been resolved within this release:

Title	Priority	Description	Components
Configure final classification of free text qualifiers	Critical	Implement the summary of which of the 51 free text qualifiers should be classified as 'language-dependent' versus 'language-independent':	WIPO Sequence Tool
Search project by name doesn't work properly	Minor	Previously this feature did not work	WIPO Sequence Tool
Organism import: need to reopen "Organisms" page to see imported organisms	Trivial	New imported organism were not added to the custom list	WIPO Sequence Tool
Document type declaration and root element requirements aren't fulfilled.	Major	Error associated with the wrong DTD file being declared were not being triggered	WIPO Sequence Validator
QF_1 case: WIPO Sequence ignores DTD errors during import, without any error message	Major	Errors within the schema due to the DTD file were not being ignored by the Tool	WIPO Sequence Tool
Absence of filing date might be ignored by the validator	Minor	If both the filing date and earliest priority date are missing, only one is reported on.	WIPO Sequence Tool, WIPO Sequence Validator
Error on import st25 using a file	Minor	Tool was freezing if the ST.25 input file had not sequences.	WIPO Sequence Tool

without sequences			
The application imports sequences by their sequenceID value which is not always correct	Minor	SEQ ID value was used during import to identify the sequence position in the imported sequence listing.	WIPO Sequence Tool
Error "The sequence don't exist" when removing a sequence from a project with a large number of sequences	Minor	Improve reporting when deleting and renumbering sequences when listing contains a large number of sequences	WIPO Sequence Tool
ST25 Import - DISULFID feature in an AA sequence	Minor	When a DISULFID feature has a <223> with a value, the tool is erroneously creating a NOTE qualifier with the value "OTHER", and a "note" qualifier with the value from the <223> line. Only one "NOTE" qualifier should be created for DISULFID and it should contain the value of the <223>.	WIPO Sequence Tool
Presumably, multithreading doesn't work	Major	Files should be validated concurrently. Tool now uses threads for validation (at least up to 5).	WIPO Sequence Validator
Fixes russian translation	Minor	Improved Russian labels based on feedback from ROSPATENT	WIPO Sequence Tool
In the process of generating several projects and validating as I made edits, I keep getting the validation report of a project I am not working on.	Minor	Validation report of a different project appears	WIPO Sequence Tool
Intermittent defect in "New Project" function, prepopulating sequences in the project: 'New Project' was selected, then the project was named and saved.	Minor	Intermittent defect in "New Project" function, prepopulating sequences in the project: 'New Project' was selected, then the project was named and saved. When the project opened, sequences were already listed for the project. The steps were repeated twice more, and the same thing happened, and it appeared to be the same set of sequences listed. The tool was closed and relaunched. Repeated 'New Project' about 10 times, and 50% of the new projects had sequences listed (same set each time, but a different set than observed in the first instance), the others were as expected, the only data showing was the project name.	WIPO Sequence Tool

For the rpt_type Qualifier Value the option “terminal” is missing versus Annex I, as USPTO noted for the Feb2019 Annex I.	Major	For the rpt_type Qualifier Value the option “terminal” is missing versus Annex I, as USPTO noted for the Feb2019 Annex I.	WIPO Sequence Tool
Mobile_element_type: started with “other” and a name in the mobile element name field	Minor	Mobile element types other than “other” do not require a mobile element name, so this is a bug.	WIPO Sequence Tool
The terms “Verification”/“verify” and “Validation”/“validate” are both used in the tool without a definition of their meaning, only one term should be used throughout	Major	These terms, verify vs validate, must be used consistently through the tool as they are different in scope.	WIPO Sequence Tool
The softwareName is listing "ST26 authoring and validation tool" instead of "WIPO Sequence" when displayed in the tool and in the downloaded XML file.	Minor	The software tool name must be updated to reflect the new brand name	WIPO Sequence Tool
The translation provided for Table 11 “Bacterial, Archaeal and Plant Plastid Code” is incorrect.	Minor	<p>The translation provided for Table 11 “Bacterial, Archaeal and Plant Plastid Code” is incorrect. The Tool translation (which, as noted, ignores stop codons) compared to the Table 11 translation (bottom) in Annex 1 (and in the INSDC Table) is:</p> <p>FFLLSSSSYYCCWLLLLPPPPHHQRRRRRIIMTT TTNKKSSRRVVVAAAADDEEGGGG</p> <p>FFLLSSSSYY**CC*WLLLLPPPPHHQRRRRRIIMT TTNKKSSRRVVVAAAADDEEGGGG (Verified on second test that there is an extra “C”).</p>	WIPO Sequence Tool

Mixed language, not all text translated into German (same for other languages: e.g. French, Spanish)	Major	Translations to not apply to all terms. The EPO reported for the German/French language interface that only some terms were translated.	WIPO Sequence Tool
Wrong translation of "Import report" should be "Import Bericht"	Major	Wrong translation of "Import report" should be "Import Bericht"	WIPO Sequence Tool
MOD_RES creating NOTE and note qualifiers in Import ST.25	Minor	Import ST.25 : An amino acid sequence with MOD_RES in <221> and "sarcosine" in <223>. Upon import, the tool created a 'NOTE' qualifier with 'OTHER' and a lower-case 'note' qualifier with 'sarcosine". The 'note' should have been upper-case 'NOTE'. When the sequence listing is validated, an error is given for 'note', as it should.	WIPO Sequence Tool
Case insensitivity to SOURCE/source during validation	Major	Does not apply error when SOURCE is lowercase for a DNA molecule and source is uppercase for an amino acid	WIPO Sequence Tool, WIPO Sequence Validator
WIPO Sequence update doesn't work	Critical	A new version exists, the binary file is uploaded. Initiate update: run WIPO Sequence and confirm the launch of the update procedure. After confirmation, nothing happens	WIPO Sequence Server, WIPO Sequence Tool
Not possible to import only the General Information from a different project	Minor	Not possible to import only the General Information from a different project, without importing any sequences (i.e. empty would import all sequences) Entering "0" leads to stalling of the system, program has to be stopped.	WIPO Sequence Tool
Import of ST_25_long: strange characters in Import report: <212>, etc.	Minor	Import of ST_25_long: strange characters in Import report: <212>, etc.	WIPO Sequence Tool
Get current sequence listing path logic error	Critical	Project ID, which identifies a project is not initialized. Can result in a project not found error. Result of code review.	WIPO Sequence Tool
Linter doesn't work in the front part of the tool	Minor	TSLint is an extensible static analysis tool that checks TypeScript code for readability, maintainability, and functionality errors. There is command to run linter in the project.json. Try to run the liner and get an exception. Result of code review.	WIPO Sequence Tool

Error handling architecture for algorithms based on EventEmitter is not correct	Major	When an EventEmitter instance experiences an error, the typical action is to emit an 'error' event. Error events are treated as a special case in NodeJS. If there is no listener for it, then the default action is to print a stack trace and exit the program. Thus, if an error is generated in an 'error' handler of an EventEmitter it will never be caught and user will see ugly stack trace. Result of code review.	WIPO Sequence Tool
Wrong "Import Sequence Listing Validation"	Major	Wrong "Import Sequence Listing Validation". XML validation errors return an empty array. Result of code review.	WIPO Sequence Tool
Translated messages issues	Minor	Improved translation messages for Japanese, Chinese and Russian.	WIPO Sequence Tool
Unique bound_moiety issues (QV_40/XFQ_6, XFQ_7)	Major	Functional gap issue: bound_moiety feature key not mandatory for oRit feature key.	WIPO Sequence Tool, WIPO Sequence Validator
XQV_37 doesn't trigger reliably	Major	WIPO Sequence Validator does not return error for invalid qualifier value when protein_id is not in the range 0..number_sequences	WIPO Sequence Validator
FQ_1 doesn't apply	Minor		WIPO Sequence Tool
Unhandled error messages (using the example of XFL_6)	Major	Appropriate error message not returned during ST.26 import. Result of code review.	WIPO Sequence Tool, WIPO Sequence Validator
XFL_1 rule doesn't apply	Major	Empty feature location but no error thrown by WIPO Sequence Validator	WIPO Sequence Validator
Values composed of invalid characters are unreadable in xml-report	Trivial	Unreadable characters returned in Verification report XML	WIPO Sequence Validator
Some symbols are displayed incorrectly in the report message text	Minor	Brackets and quotation marks are not displayed in report message texts. All language, except English. Russian, Japan and Chinese languages have problems only with brackets.	WIPO Sequence Tool
Some elements aren't translated	Minor	Several labels within the interface have not been translated.	WIPO Sequence Tool



Import ST25: if ST25 file contains source feature, there are two source features in the imported project	Minor	There are duplicate source feature produced in the project after ST.25 import.	WIPO Sequence Tool
ST.25 repeat_unit feature transfers into ST.26 inaccurately	Major	Same result whether repeat_region qualifier is used or not used for repeat_unit feature key. ST.26 there should be a different result.	WIPO Sequence Tool
ST25 import: incorrect value of the satellite qualifier	Minor	During ST.25 import, 'satellite' qualifier value is "satellite (or microsatellite or minisatellite - if supported)" which is taken from the scenario 8, ST.26, Annex VII. Suggest accepting 'satellite' value as default.	WIPO Sequence Tool
ST.25 Import: AA features with mandatory qualifiers aren't handled properly	Major	The ST.25 file which contains AA features with mandatory qualifiers (BINDING, CARBOHYD, DISULFID, DNA_BIND, DOMAIN, LIPID, METAL, MOD_RES, NP_BIND, SITE, ZN_FING). The element 223 of every feature is present and not empty. All features mentioned above have qualifiers "NOTE" with value "OTHER", and second qualifier "note" with value taken from <223> field.	WIPO Sequence Tool
Import st.25 process returns error if file contains "promoter" feature	Major	ST.25 File which contains "promoter" feature. Message: ERROR: An error occurred while importing the ST.25 sequence listing.	WIPO Sequence Tool
QV_44 doesn't trigger in the case of import another project	Major	QV_44: IF an attribute featureQuals contains a qualifier qt with the name "translation" and a qualifier 'qp' with the name "protein_id", then, the attribute INSDSeqSequence of the sequence with the attribute sequenceIDNumber equal to the value of 'qp', must be identical to the value of qt.	WIPO Sequence Tool
Import from another project: if check-uncheck-check general info during import, the general info isn't imported	Trivial	Unchecking after selecting the checkbox to import general information from a project stopped the import from occurring.	WIPO Sequence Tool
Wrong software name shown in reports/generated sequence listings	Minor	The old software name is show in the human readable generated sequence listing.	WIPO Sequence Tool
WIPO Sequence	Critical	CentOS, a Linux variant, was one of the platforms selected that WIPO Sequence must work on.	WIPO Sequence Tool

doesn't work on CentOS			
Characters not rendered when exporting free text qualifiers	Minor	The USPTO has reported that when they include non-Latin characters within the 'Qualifier Value Translated' field in the WIPO Sequence tool (see snapshot), these characters are rendered when shown in the 'Free Text Qualifiers' screen within the Tool interface but not once they are exported. If these characters are included within the Tool as a translation and can be rendered within the Tool then they should also be visible once exported from the Tool.	WIPO Sequence Tool
Unidentified developer	Major	WIPO Sequence could not be installed by some users as there was no publisher identified. It should be WIPO.	WIPO Sequence Tool
IT_IT_1, PO_N_1 don't trigger	Major	The user can enter invalid characters in applicant name or invention title but an error must be returned during validation.	WIPO Sequence Tool
There are a lot of "magic" numbers and strings in codes. Instead of them constants should be defined	Minor	Improve code by using global constants.	WIPO Sequence Tool
A lot of commented out code.	Minor	Result of code review. Remove redundant code.	WIPO Sequence Tool
Order by Project name doesn't work properly	Major	Ordering by project name does not sort in alphabetical order.	WIPO Sequence Tool
Fake validation	Major	Sometimes the validation process returns feedback instantly, displaying the report without any reports. It's not a real validation report. The issue is hard to reproduce. It might happen after some work with features and qualifiers.	WIPO Sequence Tool
Non user friendly verification messages	Minor	Several verification messages were improved as the result of code review.	WIPO Sequence Tool, WIPO Sequence Validator

## Known Issues

The following bugs are pending resolution and will be corrected in the next release. They are mostly related to 'functional gaps' between the functional specification document, the WIPO ST.26 Standard and the implementation of the tool:

Summary	Priority	Description	Components
Error in XML Validation when the Applicant Name tag is missing	Major	The Validator fails when trying to validate an XML with a missing Applicant Name tag	WIPO Sequence Validator
Minor "functional gaps"	Minor	Certain validation rules that became redundant and must be removed from the implementation.	WIPO Sequence Tool, WIPO Sequence Validator
XQV_44 doesn't apply in WIPO Sequence	Minor	XQV_44: If the element INSDQualifier_name has the value "rpt_unit_seq", then the associated INSDQualifier_value must be a string containing the symbols <set of chars - to be provided>.	WIPO Sequence Tool
When the tool imports the filing date and priority dates from the ST.25 sequence listing, the dates are always off by one day	Major	When the tool imports the filing date and priority dates from the ST.25 sequence listing, the dates are always off by one day.	WIPO Sequence Tool
XFT_1 case works incorrectly in WIPO Sequence application after import	Major	For a sequence which is NOT an intentionally skipped sequence, The element INSDSeq_feature-table is mandatory but no errors are reported.	WIPO Sequence Tool
AEPAL_OC_1 doesn't apply to XML	Major	IP Office code is missing: rule for project doesn't have equivalent for XML. However, we assume that WIPO Sequence Validator also should apply this rule.	WIPO Sequence Validator
QV_38 doesn't apply to XML	Major	If the name of the qualifier is "transl_table", then the value of the qualifier is one of the numbers assigned to genetic code tables as listed in the section "Predefined vocabularies", "Genetic code table numbers and names". Default selected: 1.	WIPO Sequence Validator
XFL_8 doesn't trigger for trans_splicing	Major	XFL_8: If the element INSDQualifier_name is "ribosomal_slippage", then the element INSDFeature_location of the associated INSDFeature element (i.e. the one with the INSDFeature_key a 'CDS') must include the 'join' location operator. This should apply for trans_splicing qualifiers.	WIPO Sequence Validator
SF_1, XFT_2, XFT_3 issues	Major	WIPO Sequence should take into account cases of missing source/SOURCE.	WIPO Sequence Tool, WIPO

		For WIPO Sequence Validator need to fix notification messages for double source/SOURCE features (only one is allowed).	Sequence Validator
SM_1 doesn't apply on XML	Major	SM_1: The attribute INSDSeqMoltype of a sequence is mandatory. This rule is not applied for WIPO Sequence Validator.	WIPO Sequence Validator
XANL_1 rule doesn't apply to Inventor (xml validation)	Major	When verifying ST.26 XML, there is no check to see if there is a Latin equivalent for inventor name when the inventor name is not provided in Basic Latin characters.	WIPO Sequence Validator
AEPAL_ANT_1 doesn't apply on XML	Major	AEPAL_ANT_1: The attribute applicationNumberText must contain only the characters specified in ST.26 par. 40(b). Does not apply for WIPO Sequence Validator.	WIPO Sequence Validator
XFQ_19 rule doesn't work in the application	Major	XFQ_19: The element INSDFeature_qual associated with the element INSDFeature_key "source" may contain one and only one INSDQualifier node with INSDQualifier_name "clone". Works for WIPO Sequence Validator but not for WIPO Sequence.	WIPO Sequence Tool
QV_29 and XQV_30 rules don't apply accurately	Minor	<p>These rules are very similar and scope but one is an error and one is a warning.</p> <p>QV_29: If the name of the qualifier is "PCR_primers", then the subelements "fwd_seq" and "rev_seq" of the qualifier value must contain only symbols from (i) ST.26, Annex I, Section 1 "List of nucleotides", Table 1, column 'Symbol' and (ii) ST.26, Annex I, Section 2 "List of modified nucleotides", Table 2, column 'Abbreviation'.</p> <p>The abbreviations from point (ii) above must be written between angle brackets, for example: cg&lt;i&gt;gtgtatcttact (error)</p> <p>XQV_30: If the element INSDQualifier_name has the value "PCR_primers", then the sub-elements fwd_seq and rev_seq of the associated element INSDQualifier_value must have the format specified in the section "Predefined vocabularies", "Predefined qualifier values – Qualifiers values with predefined format" id. 6.45. (warning)</p>	documentation, WIPO Sequence Tool, WIPO Sequence Validator
Cases PAFD_2, XFD_4 are processing incorrectly	Major	PAFD_2: The filingDate attribute of the earliestPriorityApplicationIdentification attribute of a project is a date less than or equal to the filingDate attribute of the	WIPO Sequence Tool, WIPO Sequence Validator

		<p>applicationIdentification attribute of that project.</p> <p>XFD_4: The value of the element FilingDate must be a date less than or equal to the current date.</p> <p>Function of both WIPO Sequence and WIPO Sequence Validator should be the same for filing date validation.</p>	
CA_2 doesn't trigger after XML-validation	Major	<p>CA_2: The attribute applicationIdentification of a project is mandatory when the attribute applicantFileReference of the project is missing. WIPO Sequence Validator should also apply this rule.</p>	WIPO Sequence Validator
FN_1 doesn't trigger after xml-validation	Major	<p>FN_1: The attribute fileName of a project must contain only the characters specified in ST.26 par. 40(b).</p> <p>Clarification: The tool allows the user to enter and it stores whatever characters, however, in order to generate the sequence listing, this verification rules must pass. WIPO Sequence Validator should also apply this rule.</p>	WIPO Sequence Validator

[End of Release Notes]