

# **WIPO Sequence Suite**

Release notes version 1.1.0



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## **WIPO Sequence Suite version 1.1.0**

#### Overview

- Public release date: 28/10/2021
- Public stable release
- This stable release is based on a series of 8 beta releases the contents of which are described in detail below.

### WIPO Sequence 1.1.0 artefacts

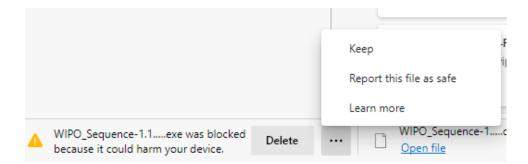
If you have not yet installed WIPO Sequence, please find below the location where the different distributions can be downloaded.

Stable release binaries (hosted the production environment of the WIPO Sequence Server)

- Linux: http://wiposequence.wipo.int/download/latest/linux\_64
- Mac: http://wiposequence.wipo.int/download/latest/osx
- Windows: http://wiposequence.wipo.int/download/latest/windows\_64

#### Known installation issues

1. The **Windows version** is marked as unsafe by Microsoft upon download: Please continue the download by clicking on 'Keep'



2. The **Windows version** may cause a security warning from Defender SmartScreen to popup (in Windows 10). To bypass this click on 'More Info" and then "Run Anyway".

**Installation instructions** for the desktop tool are available in the user manual on the <u>WIPO</u> <u>Sequence homepage</u>



#### **Highlights**

The focus of this release is on the use cases with highest priorities, the so called 'MH' ("Must-Have's").

Most of the improvements made for the WIPO Sequence desktop tool focus on the implementation of many verification rules. A detailed description of the implemented changes is available in section 0.

Not all the "must-have" requirements are implemented yet but development on these are planned for the next release v1.1.0-beta-2, which will be ready for release on 25<sup>th</sup> January 2021.

#### **New Functionalities**

No new functionalities have been added.

#### **Improvements**

In reference to the <u>requirements catalogue</u> (task force access only) the following improvements (use cases) have been implemented:

| Туре        | Key        | Summary   | Ref 1                    | Ref. 2      | Ref. 3      | Ref. 4      | Ref.5       |
|-------------|------------|---|--------------------------|-------------|-------------|-------------|-------------|
| Improvement | ST26T-1782 | Validator response to provide a response once the validation has completed and provide a response with additional fields to the end point which made the call - MHV04 | SequenceValidator        |             |             |             |             |
| Improvement | ST26T-1781 | Validator Request: Pass additional parameters as part of the request to the service, as requested by the USPTO - MHV03  | SequenceValidator        | UC23        | <u>UC31</u> | <u>UC62</u> |             |
| Sub-task    | ST26T-1770 | Feature location FL_22 - MHD24<br>MHD02   | <u>VerificationRules</u> | <u>UC20</u> |             |             |             |
| Sub-task    | ST26T-1769 | Feature location FL_21 - MHD24<br>MHD02   | <u>VerificationRules</u> |             |             |             |             |
| Story       | ST26T-1685 | Original Free Text Language Code & Non-English Free Text Language Code fields - MHD03   | <u>VerificationRules</u> | <u>UC01</u> | <u>UC20</u> |             |             |
| Improvement | ST26T-1755 | NonEnglishQualifierValue - MHD03  | VerificationRules        | <u>UC09</u> | <u>UC23</u> | <u>UC31</u> | <u>UC62</u> |
| Improvement | ST26T-1788 | Feature location - MHD24 MHD02  | <u>VerificationRules</u> |             |             |             |             |
| Sub-task    | ST26T-1790 | qualifierID attribute for newly created qualifiers  |                          | <u>UC05</u> |             |             |             |



| Improvement | ST26T-1787 | Export from Free text Qualifier tab format change to XLIFF - MHD03 | <u>UC31</u>              |             |             |             |  |
|-------------|------------|--|--------------------------|-------------|-------------|-------------|--|
| Sub-task    | ST26T-1759 | Feature location FL_11 replacing FL_3 - MHD24 MHD02                |                          |             |             |             |  |
| Sub-task    | ST26T-1758 | Feature location FL_10 replacing FL_3 - MHD24 MHD02                | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1757 | Feature location FL_6 - MHD24<br>MHD02                             | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1756 | Feature location FL_5 - MHD24<br>MHD02                             | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1760 | Feature location FL_12 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1777 | Feature location FL_27 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1776 | Feature location FL_26 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1775 | Feature location FL_25 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1774 | Feature location FL_24 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1773 | Feature location FL_23 ter - MHD24<br>MHD02                        | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1772 | Feature location FL_23 bis - MHD24<br>MHD02                        | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1771 | Feature location FL_23 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1768 | Feature location FL_20 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1767 | Feature location FL_19 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1766 | Feature location FL_18 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1765 | Feature location FL_17 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1764 | Feature location FL_16 - MHD24<br>MHD02                            | VerificationRules        |             |             |             |  |
| Sub-task    | ST26T-1763 | Feature location FL_15 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1762 | Feature location Fl_14 - MHD24<br>MHD02                            | <u>VerificationRules</u> |             |             |             |  |
| Sub-task    | ST26T-1761 | Feature location FL_13 -MHD24<br>MHD02                             | <u>VerificationRules</u> |             |             |             |  |
| Story       | ST26T-1754 | id attribute for Language dependent<br>qualifiers                  | <u>UC09</u>              | <u>UC31</u> | <u>UC43</u> | <u>UC62</u> |  |



| Improvement | ST26T-1780 | Reserved characters should be transformed back for HTML Display SL - MHD18               | GUI               |             |
|-------------|------------|--|-------------------|-------------|
| Improvement | ST26T-1783 | Convert nucleotide sequence data in uppercase to lowercase - MHD04                       | GUI               |             |
| Improvement | ST26T-1784 | Display applicant file reference<br>number in Application Information<br>section - MHD05 | GUI               | <u>UC05</u> |
| Improvement | ST26T-1786 | After deleting a sequence, do not reorder the sequence ID - MHD17                        | <u>UC28</u>       |             |
| Improvement | ST26T-1785 | Allow project to be validated without having a priority date - MHD12                     | VerificationRules | <u>UC05</u> |
| Improvement | ST26T-1779 | HTML Display Sequence List layout to be adjusted - NWD01                                 | <u>UC21</u>       |             |

As this is the first release in this development project, this release does not contain any bug fixes.

### Version 1.1.0-beta.2

### **Highlights**

This release provides a mix of the use cases with the highest priorities: the so called 'MH' ("Must-Have") and 'HD' ("Highly-Desirable").

A detailed description of the implemented changes is available in section 0.

<u>Note:</u> not all the MH requirements have been implemented yet but development for these is planned for the next two releases (version 1.1.0-beta-3 & version 1.1.0-RC1), which will be available on February 12 and March 5 respectively.

#### **New Functionalities**

No new functionalities have been added.

#### **Improvements**

In reference to the <u>requirements catalogue</u>, the following improvements (use cases) have been implemented:

| Type Key Summary Ref 1 Ref |
|----------------------------|
|----------------------------|



| Improvement | ST26T-1778 | Adding additional applicant/inventor names - MHD01   | UC5                 |             |
|-------------|------------|--|---------------------|-------------|
| Improvement | ST26T-1797 | How to handle white spaces in imported ST26 file - MHD11   | Import              |             |
| Improvement | ST26T-1798 | Remove trash icon for Source feature - HDD05   | GUI                 |             |
| Improvement | ST26T-1800 | Update the version number in the DTD automatically to reflect the one being used - HDB03   | DTD                 |             |
| Improvement | ST26T-1801 | Sort verification report to show only errors or warnings - HDD08   | GUI                 |             |
| Improvement | ST26T-1802 | Import of FASTA format - MHD22   | <u>UC36</u>         |             |
| Improvement | ST26T-1803 | Page persistence - Verification Report - HDD04   | GUI                 |             |
| Improvement | ST26T-1804 | Progress bar or message for Import/Validate processes - HDD20  | Tool Behaviour      |             |
| Improvement | ST26T-1805 | The original language code attribute is mandatory or optional. Sequence Validator - MHV06  | <u>UC31</u>         |             |
| Improvement | ST26T-1806 | Validator - the service provides a response, once validation is completed - MHV01  | Validator           |             |
| Improvement | ST26T-1807 | Refresh the database which stores project data when moving between projects - MHD07  | Database            |             |
| Improvement | ST26T-1808 | Automatically create source/SOURCE feature when importing an ST.26 file - MHD14  | <u>UC20</u>         | <u>UC43</u> |
| Improvement | ST26T-1809 | Import of grouped nucleotides and proteins from ST.25 sequence listing - MHD15   | <u>UC12</u>         |             |
| Improvement | ST26T-1810 | Different label for 'name' dependent upon whether an Applicant or an Inventor name is added MHD23  | Translations        |             |
| Improvement | ST26T-1811 | Feature location and <222> field don't include a negative number - HDD06   | <u>UC12</u>         |             |
| Improvement | ST26T-1817 | Date Validation: must be in ST.2 format - HDD10  | UC5                 |             |
| Improvement | ST26T-1818 | 'Preferences' and a 'System Preferences' inconsistency - HDD15   | GUI                 |             |
| Improvement | ST26T-1819 | Jump to the relevant portion of the sequence that caused the error - HDD19   | Verification Report |             |
| Improvement | ST26T-1820 | Sequence view Pane to display 20 sequences - HDD21   | UC6                 |             |
| Improvement | ST26T-1822 | Allow only one clone qualifier per source feature - HDB05  | UC9                 |             |
| Improvement | ST26T-1828 | Each label/notification message/etc. that needs to be translated should be represented by a unique ID that should replace the existing key MHD21 | Translations        |             |
| Improvement | ST26T-1829 | Error/warning codes need to be added for each type of distinct error or warning - HDD24  | Verification Report |             |



In total 24 bugs were reported during testing of the Sprint 1 release and two of them were fixed in this release:

| <b>T</b> ype | Key        | Summary  | Reported By |
|--------------|------------|--|-------------|
| Bug          | ST26T-1813 | Intermittently WIPO module stops writing content into the file   | USPTO       |
| Bug          | ST26T-1814 | Sometime WIPO validation status service call returns "NOT_FOUND" | USPTO       |

#### Version 1.1.0-beta.3

#### **Highlights**

This release provides a mix of the use cases with the highest priorities: those classified as 'MH' ("Must-Have") and 'HD' ("Highly-Desirable"). Some new requirements were also implemented.

A detailed description of the implemented changes is available in section 0.

Note: not all the MH requirements have been implemented yet but development for these is planned for the next two releases (version 1.1.0-beta-4 & version 1.1.0-RC1), which will be available on March 5 and March 26 respectively.

#### **New Functionalities**

New functionalities that have been added:

- Provide help in the tool
- Generation of human-readable format for generated ST.26 sequence listing

#### **Improvements**

In reference to the <u>requirements catalogue</u> (task force access only) the following improvements (use cases) have been implemented:

| Т           | Key            | Summary   | <u>Ref 1</u> | <u>Ref.</u><br><u>2</u> | <u>Ref.</u><br><u>3</u> | <u>Ref.</u><br><u>4</u> | <u>Ref.</u><br><u>5</u> | <u>Ref.</u><br><u>6</u> | <u>Ref. 7</u> |
|-------------|----------------|---|--------------|-------------------------|-------------------------|-------------------------|-------------------------|-------------------------|---------------|
| Story       | ST26T-<br>1796 | Generation of human-readable format for generated ST.26 sequence listing - MHB01    |              |                         |                         |                         |                         |                         |               |
| Improvement | ST26T-<br>1815 | CDS feature updates in all relevant fields - HDD07                                  | <u>UC08</u>  |                         |                         |                         |                         |                         |               |
| Improvement | ST26T-<br>1816 | Provide default location for missing feature locations while importing ST25 - HDD13 | UC12         |                         |                         |                         |                         |                         |               |



| Improvement | 1827           | Optional "translation" qualifier SHOULD NOT be automatically generated whenever a CDS feature key is created - MHD13 | <u>UC08</u> | <u>UC09</u> | <u>UC10</u> | <u>UC12</u> | <u>UC13</u> | <u>UC32</u> | Verification rules |
|-------------|----------------|--|-------------|-------------|-------------|-------------|-------------|-------------|--------------------|
| Improvement | ST26T-<br>1865 | WAR reference to DTD should be in class path - MHV05   |             |             |             |             |             |             |                    |
| Story       | ST26T-<br>1866 | Provide help in the tool - MHD06   |             |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1867 | Notify when <300>-<313> are discarded after a ST.25 Sequence import - MHD16  | UC12        |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1868 | Include the custom list of organisms displayed in the autocomplete field - HDD12                                     | <u>UC38</u> |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1869 | Report "3-letter codes" which cannot be converted and abort the import itself - MHD20                                | <u>UC12</u> |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1880 | Ability to (copy/cut and) paste entries into text boxes - NWD03  |             |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1881 | Sort projects on the project list home page by creation date - NWD12   |             |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1882 | Harmonize how "pencil"/"trash" icons appear on fields - NWD14  |             |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1883 | Ensure all links appear the same way in the tool - HDD16   |             |             |             |             |             |             |                    |
| Improvement | ST26T-<br>1884 | All mandatory fields should be identified with a '*' - HDD17   |             |             |             |             |             |             |                    |

In total 24 bugs were reported during testing of the Sprint 1 release and 21 of them were fixed (and ready for retesting) in this release:

| Т   | Key            | Summary  | Labels           | Resolution |
|-----|----------------|--|------------------|------------|
| Bug | ST26T-<br>1825 | Version number in desktop tool header is incorrect   | WIPO-<br>Testing | Done       |
| Bug | ST26T-<br>1832 | Entering the location "join(complement(1897>2100),complement(1999))" for a CDS feature is not recognised as a valid location | USPTO            | Done       |
| Bug | ST26T-<br>1833 | Entering the location "join(complement(18972100),complement(1>999))" generates wrong error message                           | USPTO            | Done       |
| Bug | ST26T-<br>1834 | Chinese characters not rendered when printing verification report  | WIPO-<br>Testing | Done       |
| Bug | ST26T-<br>1835 | Unable to update feature after removing the ">" in the location the location "join(complement(>2100),complement(1999))"      | USPTO            | Done       |



| Bug | ST26T-<br>1836 | After playing around with a CDS feature with different locations, entering and then deleting multiple CDS features, somehow the sequence lost the source feature | USPTO | Done |
|-----|----------------|--|-------|------|
| Bug | ST26T-<br>1837 | The location "join(complement(10062100),complement(<102999))" should not return an error   | USPTO | Done |
| Bug | ST26T-<br>1838 | The location "join(complement(<10062100),complement(102999))" generates an incorrect error message   | USPTO | Done |
| Bug | ST26T-<br>1839 | The location "join(complement(10062100),complement(<999))" was not accepted as a valid location  | USPTO | Done |
| Bug | ST26T-<br>1841 | If one sets the project non-English qualifier language code, and enters a non-English qualifier value, then the value cannot be deleted                          | USPTO | Done |
| Bug | ST26T-<br>1842 | If the project non-English language code was set, then removed generates an incorrect error  | USPTO | Done |
| Bug | ST26T-<br>1843 | The translated qualifier value and language code are not shown after changing/removing project language code   | USPTO | Done |
| Bug | ST26T-<br>1844 | "en", i.e., English, should not be included in the drop down for non-<br>English qualifier   | USPTO | Done |
| Bug | ST26T-<br>1845 | When no project language code is set, one cannot enter a translated value (good), however one can set the language code  | USPTO | Done |
| Bug | ST26T-<br>1847 | Only able to enter single numbers into any feature, not allowed to enter any other formats as listed in paragraph 66 of the standard.                            | USPTO | Done |
| Bug | ST26T-<br>1848 | No error indicating that the locations were all outside of the 12100 sequence range  | USPTO | Done |
| Bug | ST26T-<br>1849 | No notification to user to allow the user to indicate the sequence as skipped  | USPTO | Done |
| Bug | ST26T-<br>1850 | HTML display is a continuous sequence without breaks or 10 residue separations IE  | USPTO | Done |
| Bug | ST26T-<br>1858 | Pagination is not working on Import Report   | FAT   | Done |
| Bug | ST26T-<br>1870 | Cannot read property featureKey of undefined   | FAT   | Done |

### **Highlights**

This release provides a mix of the use cases with the highest priorities: the so called 'MH' ("Must-Have") and 'HD' ("Highly-Desirable"). Some new requirements were implemented during this sprint but it had a focus on resolving bus reported during testing.

A detailed description of the implemented changes is available in section 0.

Note: not all the MH & HDD requirements have been implemented yet but final development for these is planned for the next release (version 1.1.0-RC1), which will be available on March 26.



#### **New Functionalities**

No new functionalities have been added

### **Improvements**

In reference to IDs shown from the <u>requirements catalogue</u> (task force access only) the following improvements have been implemented during this sprint:

| Туре        | Кеу        | Summary  | Use<br>case |
|-------------|------------|--|-------------|
| Improvement | ST26T-1942 | MHD02 - Implement verification rule FL_28 for "Features"   |             |
| Improvement | ST26T-1981 | HDB06 - Add General Information - Only report a single error when Applicant File Reference is absent                       | <u>UC05</u> |
| Improvement | ST26T-1821 | HDD22 - Import language-dependent free text from language file to create new language version                              | <u>UC63</u> |
| Improvement | ST26T-1982 | HDB07 - when adding General Information, if there is no ApplicationIdentification then a single error should be reported   | <u>UC05</u> |
| Improvement | ST26T-1980 | HDB04 - Add General Information - When Applicant File reference is absent, generate an error                               | <u>UC05</u> |
| Improvement | ST26T-1969 | NHD07: change label for 'back to list' and 'close' buttons   | GUI         |
| Improvement | ST26T-1979 | NWD16 - Import ST.25 Sequence Listing  | <u>UC12</u> |
| Improvement | ST26T-1941 | NWD02 - Translation of codons that encode an ambiguous amino acid (B, Z, J)  | <u>UC33</u> |
| Improvement | ST26T-1984 | HDV02 - During formality check If the ApplicationIdentification element is present then a single error should be reported. |             |
| Improvement | ST26T-1983 | HDV01 - Validator - Formality Check If there is no ApplicationIdentification , a single error should be reported           |             |
| Improvement | ST26T-1918 | NWD17 - Importing skipped sequences from ST.25 Sequence Listing  | <u>UC12</u> |
| Improvement | ST26T-1892 | HDD07 - CDS feature updates in all relevant fields (changes in residues)   | UC8         |
| Improvement | ST26T-1917 | NWB02 - Correct error in the XQV_23 rule   | <u>UC25</u> |
| Improvement | ST26T-2001 | MHD06 - Add more information to the ABOUT WIPO pop-up  |             |

## **Bug Fixing – Issues Done**

During this sprint, 46 bugs were fixed and are ready for retest which are detailed as follows:

| Type | Key        | Summary  | Reporter     |
|------|------------|--|--------------|
| Bug  | ST26T-1940 | Cannot import skipped sequences in ST.25 SLs   | WIPO-Testing |
| Bug  | ST26T-1962 | Location Source feature does not update  | FAT          |
| Bug  | ST26T-1963 | Multiple inventor and applicant marked all as primary  | FAT          |
| Bug  | ST26T-1948 | Error message when update residues   | FAT          |
| Bug  | ST26T-1996 | when validate a project with Applicant File reference is absent, don't generate the error expected | FAT          |



| D   | CTACT 40CC | Individe aution agreed in account of the second  | ГАТ                        |
|-----|------------|--|----------------------------|
| Bug | ST26T-1966 | Include option cancel in sequence delete pop up  | FAT                        |
| Bug | ST26T-1978 | The error is not directly accessed through the hyperlink   | FAT                        |
| Bug | ST26T-1993 | Sequence is automatically marked as skipped when has exactly 10 specifically defined nucleotides   | FAT                        |
| Bug | ST26T-1958 | QV 48 error when there is a translation except qualifier and stop codon  | FAT                        |
| Bug | ST26T-1960 | There is no way to ask the tool to import the information line as a note/NOTE qualifier when importing multiple sequences from a FASTA file. | FAT                        |
| Bug | ST26T-1959 | Import ST.25: Error message when importing PRT sequence  | FAT                        |
| Bug | ST26T-1995 | Non English free text language code is not updated after import  | FAT                        |
| Bug | ST26T-1977 | Non English Qualifier Value is not updated when editing from Validation report   | FAT                        |
| Bug | ST26T-1947 | When importing a ST25 or ST25 mix-mode file with CDS feature and unchecked "Automatic translation" one qualifier is created without a name   | FAT                        |
| Bug | ST26T-1938 | Date Validation: must be in ST.2 format is not fixed   | USPTO, User-testing-cycle2 |
| Bug | ST26T-1846 | Import RNA: incorrect feature location inserted for 'u' and 't'  | USPTO                      |
| Bug | ST26T-1895 | Import: join(24,68) produces an error message: Invalid location operator format.   | EPO, User-testing-cycle2   |
| Bug | ST26T-1903 | FL_23 bis: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1920 | ST.25 Import: Several errors including negative numbers in feature location  | EPO, User-testing-cycle2   |
| Bug | ST26T-1853 | Source language for XLIFF is not original language code  | WIPO-Testing               |
| Bug | ST26T-1904 | FL_23: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1913 | MHD24/MHD02, FL_14: Wrong error message is generated   | EPO, User-testing-cycle2   |
| Bug | ST26T-1911 | FL_18: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1912 | Import: feature location 0^1 fails FL_10 but not FL_15   | EPO, User-testing-cycle2   |
| Bug | ST26T-1906 | Feature location FL_20 - MHD24 MHD02: Error msg contains placeholder {{featureKey}} instead of the feature key name.                         | EPO, User-testing-cycle2   |
| Bug | ST26T-1908 | FL_17: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1931 | Import of a FASTA file with a single sequence; the screen displayed is confusing   | USPTO, User-testing-cycle2 |



| Bug | ST26T-1932 | When the "mark to save the sequence description" box is checked, Validation gives an error   | USPTO, User-testing-cycle2 |
|-----|------------|--|----------------------------|
| Bug | ST26T-1937 | NO Source feature was automatically created on import  | USPTO, User-testing-cycle2 |
| Bug | ST26T-1902 | FL_23 ter: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1907 | FL_19: The verification message contains a placeholder {{featureKey}}, not a name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1899 | Import: complement(order(5)) fails FL_5.   | EPO, User-testing-cycle2   |
| Bug | ST26T-1894 | FL_21: The verification message contains a placeholder {{featureKey}},not the name   | EPO, User-testing-cycle2   |
| Bug | ST26T-1893 | FL_22 The verification message contains a placeholder {{featureKey}} not the name  | EPO, User-testing-cycle2   |
| Bug | ST26T-1891 | The buttons of the pop-up confirmation for deleting should be "cancel" and "delete"  | FAT                        |
| Bug | ST26T-1924 | Feature location and <222> field don't include a negative number - test failed   | EPO, User-testing-cycle2   |
| Bug | ST26T-1933 | There is no way to ask the tool to import the information line as a note/NOTE qualifier when importing multiple sequences from a FASTA file. | USPTO, User-testing-cycle2 |
| Bug | ST26T-1926 | When editing the sequence residues by inserting or deleting a residue, the feature locations are not updated                                 | EPO, User-testing-cycle2   |
| Bug | ST26T-1943 | Version number is missing in the ABOUT option included in the Help   | FAT                        |
| Bug | ST26T-2000 | Complementary sequence is not translating 'r' to 'y' correctly   | FAT                        |
| Bug | ST26T-1994 | During import, continue button don't reset after cancel selected   | FAT                        |
| Bug | ST26T-1914 | Qualifier name isn't mandatory when editing  | FAT                        |
| Bug | ST26T-1961 | Incorrect message when creating misc_feature with errors in feature location   | FAT                        |
| Bug | ST26T-1991 | Source feature duplicated when importing ST25  | FAT                        |

## **Highlights**

This release provides a mix of the use cases with the highest priorities: the 'MH' ("Must-Have") and 'HD' ("Highly-Desirable") requirements. Additionally some of the bugs reported during testing have been resolved.

A detailed description of the implemented changes is available in section 0.



Note: not all the MH & HDD requirements have been implemented yet however the next release (version 1.1.0-RC2), will contain all of them. That release will be available on 16/4/2021

## **Improvements**

In reference to the <u>requirements catalogue</u> (task force access only) the following improvements (use cases) have been implemented:

| Туре        | Key            | Summary  |
|-------------|----------------|--|
| Story       | ST26T-<br>1971 | NWD10 - Generate a warning for missing tags for a "n" nucleotide - UC12  |
| Improvement | ST26T-<br>1823 | HDD09 - Bulk modifications   |
| Improvement | ST26T-<br>1877 | Verification rule FL_4 no longer required  |
| Improvement | ST26T-<br>1632 | Validator: Response provided once validation complete  |
| Improvement | ST26T-<br>2048 | Update Qualifier value field in order to be consistent with Free text qualifier tab and preventing the use of non Latin characters |
| Improvement | ST26T-<br>1826 | If there is a non english qualifier value provided it should be visible in the qualifier summary value                             |
| Improvement | ST26T-<br>1990 | HDB04: Application number all in letters did not generate an error or warning!   |
| Improvement | ST26T-<br>1998 | Package naming convention: not com.wipo but org.wipo (WIPO internal issue)   |
| Improvement | ST26T-<br>1964 | MHD02: Missing feature location rules from functional specification  |
| Improvement | ST26T-<br>1873 | Original free text language code or Non English free text language code cannot be removed  |
| Improvement | ST26T-<br>1922 | The only way to stop processing is to exit the application (no cancel button)  |
| Improvement | ST26T-<br>1859 | Provide default language for GUI   |
| Improvement | ST26T-<br>1633 | Additional fields to include in Validation service request (input)   |
| Improvement | ST26T-<br>2024 | HTML human readable format: reformat the sequence summary table  |
| Improvement | ST26T-<br>2023 | HTML human readable format: Replace the '/' separator with ':' for each field  |
| Improvement | ST26T-<br>1982 | HDB07 - Add General Information - If there is no ApplicationIdentification , a single error should be reported                     |
| Improvement | ST26T-<br>1981 | HDB06 - Add General Information - Only report a single error when Applicant File Reference is absent                               |
| Improvement | ST26T-<br>1980 | HDB04 - Add General Information - When Applicant File reference is absent, generate an error                                       |
| Improvement | ST26T-<br>2047 | Update description Help : About WIPO Sequence Tool popup, add released date and Copyright  |



45 bugs were fixed (and are ready for retest) in this release:

| Туре | Key            | Summary  | Labels                              | Resolution |
|------|----------------|--|-------------------------------------|------------|
| Bug  | ST26T-<br>1992 | Printing verification report: French non-Latin characters are not rendered   | CIPO, GUI                           | Done       |
| Bug  | ST26T-<br>1923 | When I open the project after import the applicant's name and/or Inventor are not visible  | EPO, User-testing-cycle2            | Done       |
| Bug  | ST26T-<br>1901 | Verification Rule FL_6 is not being triggered on imports   | EPO, User-testing-cycle2            | Done       |
| Bug  | ST26T-<br>1897 | Feature location '10^11' SHOULD NOT be allowable for sequence span 10  | EPO, User-testing-cycle2            | Done       |
| Bug  | ST26T-<br>1909 | Feature location 'join(4,>69)' generates wrong error message: 'The format of the feature location descriptor is invalid' while expected: 'The location descriptors of the 'join' operator of the feature <feature key=""> are invalid'</feature> | EPO, User-testing-<br>cycle2        | Done       |
| Bug  | ST26T-<br>1921 | Applicant file reference entered but error in verification report mentions that it is absent   | EPO, User-testing-<br>cycle2        | Done       |
| Bug  | ST26T-<br>1907 | When a feature with key and location is created incorrectly, the verification message contains a placeholder {{featureKey}} (FL_19), instead of the name of the feature.   | EPO, USPTO, User-<br>testing-cycle2 | Duplicate  |
| Bug  | ST26T-<br>1910 | Import: location 'join(3)' generates wrong error message<br>'Invalid location operator format', while expected: 'The<br>location descriptors of the 'join' operator of the feature<br><feature key=""> are invalid'</feature>                    | EPO, User-testing-<br>cycle2        | Done       |
| Bug  | ST26T-<br>1886 | Navigation in Import/Change Data Reports - jumping to wrong pages  | EPO                                 | Done       |
| Bug  | ST26T-<br>2041 | Imported features not displayed when importing ST.25 sequences   | FAT                                 | Done       |
| Bug  | ST26T-<br>2008 | Cannot validate project when feature location has format 'x0'  | FAT                                 | Done       |
| Bug  | ST26T-<br>1959 | When importing an ST.25 file with skipped sequences (residues = 000), the application is displaying an error message for PRT and AA molecules  | FAT, USPTO                          | Done       |
| Bug  | ST26T-<br>2036 | The selected page number persists when you cancel the import of an XLIFF file  | FAT                                 | Done       |
| Bug  | ST26T-<br>2075 | Tool allows the user to leave blank Qualifier value / Non<br>English Qualifier value on Free Text Qualifiers   | FAT                                 | Done       |
| Bug  | ST26T-<br>2059 | The button "Bulk Edit" is enabled even though there is no sequences to be updated in a project   | FAT                                 | Done       |
| Bug  | ST26T-<br>2074 | Organism Name label has not changed to Qualifier Value on project qualifier form   | FAT                                 | Done       |
| Bug  | ST26T-<br>2049 | Default language for tool interface should have an asterisk when editing preferences   | FAT                                 | Done       |
| Bug  | ST26T-<br>1996 | When a project is validated through "Validate Sequence Listing" the error indicates that Applicant File reference is   | FAT                                 | Done       |



|     |                | absent. But if the File is imported and then validated, the error does not appear.  |                                |                     |
|-----|----------------|---|--------------------------------|---------------------|
| Bug | ST26T-<br>2010 | Sequence listing length not updating after delete   | FAT                            | Done                |
| Bug | ST26T-<br>1997 | When importing a Fasta file with one sequence and a new organism is created, the new organism only exists within the sequence but not in the Organism list  | FAT                            | Done                |
| Bug | ST26T-<br>2011 | Import ST26: sequences are not imported but the inventor and applicant are  | FAT                            | Done                |
| Bug | ST26T-<br>2033 | The error displayed for missing project name is not correct when importing XLIFF  | FAT                            | Done                |
| Bug | ST26T-<br>2050 | Import ST.25 file: a message for missing tags <221> to <223> of nucleotide "n" of last sequences is not generated in import report  | FAT                            | Done                |
| Bug | ST26T-<br>2007 | Duplicated qualifiers on source feature after editing residues  | FAT                            | Done                |
| Bug | ST26T-<br>2042 | Import ST.25 and Import Report: Error message contains placeholder {{featureKey}} instead of the feature key name.  | FAT                            | Done                |
| Bug | ST26T-<br>2063 | The "name of the organism" and / or the qualifier "type of molecule", are mandatory but are not identified with a '*'   | ROSPATENT                      | Duplicate           |
| Bug | ST26T-<br>1874 | In the General information and Sequences section there are mandatory fields which are not identified with a '*'   | ROSPATENT                      | Duplicate           |
| Bug | ST26T-<br>1872 | An error is thrown unless both the applicant file reference and the application file number are provided  | RSPO                           | Done                |
| Bug | ST26T-<br>1840 | The feature location "join(complement(<1006>2100),complement(<102>999))" in the feature "gene" did not generate any errors, while 2 errors are expected for verification rules FL_21 & FL_22                                | USPTO                          | Obsolete            |
| Bug | ST26T-<br>2066 | When adding General Information, if there is no ApplicationIdentificationthen a single error should be reported, but ApplicantFileReference value is not detected by Tool when present.                                     | USPTO                          | Duplicate           |
| Bug | ST26T-<br>2070 | If the ApplicationIdentification element is present but ApplicationNumberText element contains no numerals, and the ApplicantFileReference element is absent, no error is generated during formality check                  | USPTO                          | Done                |
| Bug | ST26T-<br>2112 | Fasta file import with a single nucleotide sequence in upper case letters: the sequence was imported into the project as upper case residues. Validation led to an error for every one of the 5K+ residues in the sequence. | USPTO                          | Cannot<br>Reproduce |
| Bug | ST26T-<br>2102 | Import of DNA sequences FASTA: numerous SR_2_SR_3 errors and SR_6 errors, for all sequences: sequences were not converted to lower case, while this should be done  | USPTO                          | Duplicate           |
| Bug | ST26T-<br>1936 | Validation after import generates wrong error message:<br>ERROR that both the application identification # and file<br>reference # are absent, which is not true  | USPTO, User-testing-<br>cycle2 | Done                |
| Bug | ST26T-<br>2067 | When Applicant File reference is absent, generate an error, but - No error on verification report when  | USPTO                          | Done                |



|     |                | ApplicationNumberText is only letters and ApplicationFileReference is absent  |                                |           |
|-----|----------------|---|--------------------------------|-----------|
| Bug | ST26T-<br>1935 | Applicant File Reference: After generating the SL, a message appears that the SL could not be generated due to errors in the project. The alleged error is that both an application number and a file reference number are missing, which is not true | USPTO, User-testing-<br>cycle2 | Duplicate |
| Bug | ST26T-<br>2065 | While adding general information the<br>ApplicantFileReference value is not detected by the Tool<br>when present, while it should be detected   | USPTO                          | Done      |
| Bug | ST26T-<br>2098 | Tool generates an error even though the project contains a file reference number: "Both the Application Identification number and the Applicant File Reference number are absent. At least one must be present"                                       | USPTO                          | Duplicate |
| Bug | ST26T-<br>2068 | Import of DNA from an ST.25 sequence listing, a RNA sequence with exactly 10 residues, 9 specifically defined and one "n" residue is not marked skipped, while it should be marked  | USPTO                          | Done      |
| Bug | ST26T-<br>1988 | Bug MHD20: Report "3-letter codes" which cannot be converted and abort the import itself  | USPTO                          | Done      |
| Bug | ST26T-<br>2094 | Import ST25: aa sequence with two features: "PROPEP" and "mat_peptide": message contains the placeholder "{{featureKey}}" instead of stating the relevant feature name. It should say "PROPEP".   | USPTO                          | Duplicate |
| Bug | ST26T-<br>2100 | Verification report shows warnings/errors that correspond to (i.e. derive from) validation of a different project, or to same project as it existed prior to editing Sequence List. The old/remembered report data should not be displayed            | USPTO                          | Duplicate |
| Bug | ST26T-<br>1838 | The feature location "join(complement(<10062100),complement(102999))" generates an incorrect error message  | USPTO                          | Done      |
| Bug | ST26T-<br>1888 | Import of protein sequence is case sensitive, it should be not be the case  | end_users                      | Done      |
| Bug | ST26T-<br>1887 | Sequence listing of exactly 10 nucleotides SHOULD be allowable  | end_users                      | Done      |

## **Highlights**

This is the second last release containing improvements before the final release v1.1. The last so called 'MH' ("Must-Have") and 'HD' ("Highly-Desirable") are implemented.

A detailed description of the implemented changes is available in section 0.

Many bugs have been resolved and are ready for retest. The next and final release will be only to address necessary bug-fixes (next planned is RC3 on May 28).



### **New Functionalities**

No new functionalities have been added.

### **Improvements**

In reference to the  $\underline{\text{requirements catalogue}}$ , the following improvements (use cases) have been implemented:

| Туре        | Key        | Summary  |
|-------------|------------|--|
| Improvement | ST26T-1454 | Relabel "Add Earliest Priority Application" button   |
| Improvement | ST26T-1824 | Order of languages provided in dropdown list   |
| Improvement | ST26T-1927 | Update feature location of annotation feature after updating position of ambiguous residue           |
| Improvement | ST26T-1945 | New verification rule: error provided if qualifier value is not in English                           |
| Improvement | ST26T-1946 | New verification rule desktop tool: warning provided if qualifiers are not in English                |
| Improvement | ST26T-1952 | MHD13: new verification rules  |
| Improvement | ST26T-2019 | Provide a link to WIPO Standard ST.26 under Help   |
| Improvement | ST26T-2030 | If 'note' qualifier value is empty for mod_base/ncRNA_class/regulatory qualifiers: report only error |
| Improvement | ST26T-2031 | Allow only one bound_moiety qualifier per feature during drafting of project                         |
| Improvement | ST26T-2034 | Skipped sequences should be identifiable in sequence summary table                                   |
| Improvement | ST26T-2044 | GUI: Increase the height of the 'Sequence' text box  |
| Improvement | ST26T-2046 | Improve XML header in generated sequence listing   |
| Improvement | ST26T-2056 | Stop Codon   |
| Improvement | ST26T-2140 | MHD13: implementing CDS automatic translation functionality  |

## **Bug Fixing – Issues Done**

68 bugs were fixed (and are ready for retest) in this release:

| Typ<br>e | Key                | Summary  | Labels | Resoluti<br>on |
|----------|--------------------|--|--------|----------------|
| Bug      | ST26<br>T-<br>2235 | Linux: Application hangs if Project contains a lot of Sequences  | WP2    | Done           |
| Bug      | ST26<br>T-<br>2106 | Delete the Non English free text language code from a project will prevent a user from generating a sequence listing, this should still be possible  | USPTO  | Done           |
| Bug      | ST26<br>T-<br>2089 | Editing the sequence of an amino acid sequence identified in a protein_id qualifier SHOULD NOT have any impact on the "automatically add a translation qualifier when a CDS feature is added" functionality: | USPTO  | Done           |



| Bug | ST26<br>T-<br>2088 | Editing the translation qualifier value manually SHOULD NOT change the associated amino acid sequence.  | USPTO        | Done  |
|-----|--------------------|---|--------------|-------|
| Bug | ST26<br>T-<br>2101 | Import of FASTA sequences: error in SEQ ID numbering - 2 is duplicated in Sequence ID Number and Sequence Name, and no Sequence ID Number 3 of Seq_3. However, as shown by the length of both SEQ ID Numbers 2, the sequences are different                 | USPTO        | Done  |
| Bug | ST26<br>T-<br>2087 | Import RNA sequence ST.25 file: inserts a "mod_base" qualifier with the value "OTHER" and a "note" qualifier with the value "thymine" for each u residue in the original sequence, while should ONLY be inserted when original RNA sequence has "t" residue | USPTO        | Done  |
| Bug | ST26<br>T-<br>1989 | Bug HDD17: All mandatory fields should be identified with a '*'   | GUI, USPTO   | Done  |
| Bug | ST26<br>T-<br>2103 | Changing the value of a "translation" qualifier value with an associated protein_id qualifier resulted in associated protein sequence identified in the protein_id qualifier was updated to match, which should not happen                                  | USPTO        | Done  |
| Bug | ST26<br>T-<br>2095 | Import ST25: aa sequence with two features: "PROPEP" and "mat_peptide": PROPEP feature was not imported.  | USPTO        | Done  |
| Bug | ST26<br>T-<br>2093 | Import ST25: aa sequence with two features: "PROPEP" and "mat_peptide"; message is saying wrongly that ther is no location  | USPTO        | Done  |
| Bug | ST26<br>T-<br>2119 | Imported an ST.25 sequence listing with only one sequence: A problem with the format of a qID was given as an error before the generation of a sequence listing   | USPTO        | Done  |
| Bug | ST26<br>T-<br>2155 | Unable to add mol_type to new sequence  | WIPO-Testing | Done  |
| Bug | ST26<br>T-<br>2163 | The pagination doesn't work and doesn't display in the Feature list section when the feature keys are more than 10  | WP2          | Done  |
| Bug | ST26<br>T-<br>2118 | Imported an ST.25 sequence listing with only one sequence: after verification the report shows a sequence listing verification error, not a project error code. Why is it showing up in a project verification report?                                      | USPTO        | Done  |
| Bug | ST26<br>T-<br>2162 | Linux: "Import sequence" doesn't work on Project details screen   | WP2          | Fixed |
| Bug | ST26<br>T-<br>1814 | Sometimes when a WIPO validation status service call is made it returns "NOT_FOUND" even though it was showing "Running" as its status earlier for the same Verification ID   | USPTO        | Done  |



| ST26<br>T-         | Error is appeared after editing "Name" field of Applicant and Inventor in the imported project.  | WP2  | Done                              |
|--------------------|--|--|-----------------------------------|
|                    | , , , , , , , , , , , , , , , , , , ,  |  |                                   |
| ST26<br>T-<br>2091 | Import ST.26 file containing 480nt DNA sequence: in the project, the Length is noted at 960, but the source feature location is 1480 and the sequence clearly has only 480 residues  | USPTO  | Cannot<br>Reprodu<br>ce           |
| ST26<br>T-<br>2234 | ST25 import is failing when CDS feature has not translation  |  | Done                              |
| ST26<br>T-<br>2142 | UC24 reordering sequences doesn't work properly - additional sequence appears  | WP2  | Done                              |
| ST26<br>T-<br>2143 | Added qualifiers aren't actually added after "Update feature"  | WP2  | Done                              |
| ST26<br>T-<br>2055 | ST.25 Import: source feature disappears after an attempt to add a feature  | WP2  | Done                              |
| ST26<br>T-<br>2114 | When importing sequence files – the import processes correctly but when updating the project information to include free text language code information I am not able to save after selecting the languages                                | USPTO  | Done                              |
| ST26<br>T-<br>2240 | warning banner not displayed after updating position of ambiguous residue for feature location LOC_DESC_FORMAT_1   | FAT  | Done                              |
| ST26<br>T-<br>2325 | It is not possible to add a "non English free text language code" without entering a file name   | USPTO  | Done                              |
| ST26<br>T-<br>2324 | Detected value is incorrect. Actual result, Error "Message text" was correct; "Detected value" is "{"0":"j","1":"o","2":"i","3":"n","4":"(","5":"3","6":")","filingD ate":"Invalid Date"}". Expected result, "Detected value" is "join(3)" | USPTO  | Done                              |
| ST26<br>T-<br>2323 | ST.25 import – presence of tab in amino acid sequence causes problems in imported sequence   | USPTO  | Done                              |
| ST26<br>T-<br>2282 | Verification rule QV_47 (Verify that the value for the qualifier 'rpt_unit_seq' is in the format specified in WIPO ST.26 Annex I, Section 6, for this qualifier): The verification report isn't generated                                  | WP2  | Done                              |
| ST26<br>T-<br>2246 | Missing localized text for verification rule XOSID_1 (The element 'INSDSeq' must not contain any element 'INSDSeq_other-seqids')   | WP2  | Done                              |
| ST26<br>T-<br>2151 | 'Validating' processing hangs if Project contains a lot of Sequences   | WP2  | Done                              |
|                    | T- 2057 ST26 T- 2091  ST26 T- 2234 ST26 T- 2142 ST26 T- 2143 ST26 T- 2144  ST26 T- 2055 ST26 T- 2114  ST26 T- 2325 ST26 T- 2324                           | T- 2057  ST26  Import ST.26 file containing 480nt DNA sequence: in the project, the Length is noted at 960, but the source feature location is 1.480 and the sequence clearly has only 480 residues  ST26  ST25 import is failing when CDS feature has not translation  T- 2234  ST26  UC24 reordering sequences doesn't work properly - additional sequence appears  Added qualifiers aren't actually added after "Update feature"  T- 2143  ST26  ST.25 Import: source feature disappears after an attempt to add a feature  When importing sequence files — the import processes correctly but when updating the project information to include free text language code information I am not able to save after selecting the languages  Warning banner not displayed after updating position of ambiguous residue for feature location  LOC_DESC_FORMAT_1  ST26  T- 2325  Detected value is incorrect. Actual result, Error "Message text" was correct; "Detected value" is "join(3)"  ST26  ST.25 import - presence of tab in amino acid sequence causes problems in imported sequence  T- 2323  ST26  Verification rule QV_47 (Verify that the value for the qualifier 'rpt_unit_seq' is in the format specified in WIPO ST.26 Annex I, Section 6, for this qualifier): The verification report isn't generated  Missing localized text for verification rule XOSID_1 (The element 'INSDSeq' must not contain any element  1NSDSeq_other-seqids')  T- Validating' processing hangs if Project contains a lot of Sequences  Sequences | Inventor in the imported project. |



| Bug | ST26<br>T-         | Verification report: sorting stops working on other columns after applying once  | WP2        | Done                    |
|-----|--------------------|--|------------|-------------------------|
|     | 2153               | arter apprying once  |            |                         |
| Bug | ST26<br>T-<br>2158 | A JavaScript error appears in projects when trying to Edit Inventor (wrongly imported from ST25 listing)   | IPOBSD     | Done                    |
| Bug | ST26<br>T-<br>2159 | System did not automatically set the attribute qualifier Ids while testing the extraction of information about the qualifiers with language dependent free text  | IPOBSD     | Done                    |
| Bug | ST26<br>T-<br>1843 | The translated qualifier value and language code are not shown after changing/removing project language code   | USPTO      | Done                    |
| Bug | ST26<br>T-<br>2061 | Sometimes (not always), an error is reported when "Create Feature" is selected, after manually creating CDS Feature key in imported sequence   | RSPO       | Done                    |
| Bug | ST26<br>T-<br>2136 | Problem with importing test files, many of the test files could not be imported, while they should   | EPO        | Pending                 |
| Bug | ST26<br>T-<br>1900 | Input: complement(join(6)) passes FL_25, while it should fail FL_25 because it fails FL_17   | EPO        |                         |
| Bug | ST26<br>T-<br>2051 | Project is created even though an error occurs and its not possible to create features   | FAT        | Done                    |
| Bug | ST26<br>T-<br>2084 | Imported an ST.26 file where SEQ ID NO:1 contained a feature table with a CDS feature but NO source feature: a source feature was created and added to the sequence, but the sequence length was erroneously doubled from 480 to 960 | USPTO      | Done                    |
| Bug | ST26<br>T-<br>1890 | The message of protein ID doesn't appear when select automatic translation and the translation has 4 letters   | FAT        | Cannot<br>Reprodu<br>ce |
| Bug | ST26<br>T-<br>1871 | If the project non-English language code was set and you intentionally skip all the sequences you also get the error that there are translated qualifier values but no language code   | FAT        | Cannot<br>Reprodu<br>ce |
| Bug | ST26<br>T-<br>1903 | When creating a feature location, the verification message contains a placeholder {{featureKey}} (FL_23 bis FAIL), instead of the name of the feature  | EPO, USPTO | Done                    |
| Bug | ST26<br>T-<br>2082 | Import RNA: the tool is putting in modified_base features with mod_base qualifiers for imported RNA sequences with u residues, which should not happen   | USPTO      | Done                    |
| Bug | ST26<br>T-<br>1842 | If the project non-English language code was set, then removed, and all sequences are intentionally skipped, an incorrect error is generated on validation.  | USPTO      | Cannot<br>Reprodu<br>ce |



| Bug | ST26<br>T-<br>1896 | Feature location xx: rule FL_6 fails but not rule FL_5  | EPO        | Done         |
|-----|--------------------|---|------------|--------------|
| Bug | ST26<br>T-<br>2043 | When import ST.25 with sequence containing 000 is not marked as skipped and subsequent sequences are not, an error import message is displayed imported. It is expected that all sequences are imported successfully and the sequence 5 is marked as skipped  | FAT        | Done         |
| Bug | ST26<br>T-<br>1848 | After entering the following location into a "C_region" feature in a 2100 nt long sequence: no error indicating that the locations were all outside of the 12100 sequence range was thrown  | USPTO      | Done         |
| Bug | ST26<br>T-<br>1904 | When creating a feature with location, the verification message contains a placeholder {{featureKey}} (FL_23), it is expected that it contains the name of the feature  | EPO, USPTO | Done         |
| Bug | ST26<br>T-<br>2083 | ST25 - Import: amino acid numbering was changed from beginning with -21 to beginning with 1, the message should be in the "Change Data" section and say, the first amino acid was renumbered 1., the wrong message was show in Import Report Messages section | USPTO      | Done         |
| Bug | ST26<br>T-<br>1931 | Import of a FASTA file with a single sequence; the screen displayed is confusing because it's not understandable that you need to click on the sequence number to get to the information input box.   | USPTO      | Done         |
| Bug | ST26<br>T-<br>2148 | ST.25 Import: The sequences with CDS feature doesn't import without error   | WP2        | Done         |
| Bug | ST26<br>T-<br>2152 | Not all sequences are imported into the project in some cases   | WP2        | Done         |
| Bug | ST26<br>T-<br>2160 | Tool should provide a Warning instead of an Error for the new verification rule when qualifiers are presented only in english   |            | Done         |
| Bug | ST26<br>T-<br>2085 | Import: complement(order(5)) fails FL_5: after project validation the location is not flagged as an error, only a warning is seen, while an error should be shown   | USPTO      | Done         |
| Bug | ST26<br>T-<br>2150 | The sequence containing both DNA and RNA fragments is not created with a filled "Location" field  | WP2        | Done         |
| Bug | ST26<br>T-<br>2125 | Display The Sequence Listing: Last step in test case when TXT format expected: Check data in file is the same like in the application.  | EPO        | Won't<br>Fix |
| Bug | ST26<br>T-<br>1898 | Input 'join(complement(1215),complement(811)) for AA moltype': fails FL_27, as expected but also FL_4. Expected: It should not fail fail for FL_4. FL_4 can be removed since we have FL_27.   | EPO        | Done         |



| Bug | ST26<br>T-<br>1902 | When a feature with key and location is created incorrectly, the verification message contains a placeholder {{featureKey}} (FL_23), and the expected is to have the name of the feature. | EPO, USPTO                      | Done          |
|-----|--------------------|---|---------------------------------|---------------|
| Bug | ST26<br>T-<br>1894 | When a feature with key and location is created incorrectly, the verification message contains a placeholder {{featureKey}} (FL_21), and the expected is to have the name of the feature. | EPO, USPTO                      | Done          |
| Bug | ST26<br>T-<br>1893 | When a feature with key and location is created incorrectly, the verification message contains a placeholder {{featureKey}} (FL_22), and the expected is to have the name of the feature. | EPO, USPTO                      | Done          |
| Bug | ST26<br>T-<br>1948 | Error message when updating residues, an error message appears but the sequence is still updated.   | FAT, USPTO                      | Done          |
| Bug | ST26<br>T-<br>2009 | Importing a project with no ApplicantFileReference and ApplicationNumberTest with white spaces. The FillingDate is not displayed correctly when validating the project                    | FAT                             | Done          |
| Bug | ST26<br>T-<br>2003 | Organism Name should be mandatroy and generate an error on validate report  | FAT                             | Done          |
| Bug | ST26<br>T-<br>2062 | When importing ST25 listing without inventor names, in the Inventor name field in the project the name of the applicant appears   | RSPO,<br>ST26_existing_b<br>ugs | Done          |
| Bug | ST26<br>T-<br>2113 | When importing multisequence FASTA files, the check box should say "Check to save all descriptions as a note." The note currently says "this description", which is confusing             | USPTO                           | Done          |
| Bug | ST26<br>T-<br>2002 | Export XML: If the fields are filled manually, the exported values for "filling date" and "priority date" are not correct   | FAT                             | Done          |
| Bug | ST26<br>T-<br>2122 | The "Cancel validation" button does not look like a button. It should be made obviously a button, in a blue box like other buttons in the tool  | USPTO                           | Done          |
| Bug | ST26<br>T-<br>2123 | A non English language code or original free text language code cannot be saved in a newly created project unless a "File Name" is entered, which should be possible                      | USPTO                           | Duplicat<br>e |

## Highlights

This is the first release during warranty period. It contains no new functionality, only bugs fixes.



#### **New Functionalities**

As indicated above, no new functionalities have been added.

### **Improvements**

None, this is a bug fix release.

## **Bug Fixing – Issues Done**

106 bugs were fixed (and are ready for retest) in this release. The label indicates the original reporter of the bug:

| Туре | Key        | Summary  | Status | Severity | Label  | Resolution |
|------|------------|--|--------|----------|--------|------------|
| Bug  | ST26T-2299 | Performance: validating an external ST26 file with 500 sequences and low complexity is nearly impossible when trying to edit   | Done   | Major    | BASF   | Duplicate  |
| Bug  | ST26T-2298 | Performance: validating an external ST26 file with 4000 sequences and low complexity is nearly impossible when trying to edit as it is very slow   | Done   | Major    | BASF   | Done       |
| Bug  | ST26T-2297 | A qualifier "mol_type" having no value is not detected as Error during validation within the project, while it should, further actions should stop   | Done   | Major    | BASF   | Done       |
| Bug  | ST26T-2296 | Import add. sequences from ST.26 sequence listing file into project, which is already holding sequences, Qualifier-ID is not auto-changed during import, while Unique Qualifier-IDs over the complete project after any kind of sequence import are expected | Done   | Major    | BASF   | Done       |
| Bug  | ST26T-2359 | A number of errors were reported with the Rule ID: SR_2_SR_3, SR_6. Errors reported in an imported sequence which should not have been   | Done   | Major    | CIPO   | Duplicate  |
| Bug  | ST26T-2358 | Not all the sequences in a sequence listing were imported  | Done   | Major    | CIPO   | Done       |
| Bug  | ST26T-2357 | Existing Applicant List is not arranged in alphabetical order.   | Done   | Major    | CIPO   | Done       |
| Bug  | ST26T-2356 | Wrong title in the remove custom organism confirmation dialog, Title is "Create new organism" while it should be "Remove custom organism".   | Done   | Major    | CIPO   | Done       |
| Bug  | ST26T-2355 | The tool does not recognize Portuguese characters when importing a Portuguese sequence list  | Done   | Major    | Daniel | Done       |
| Bug  | ST26T-2354 | The tool does not recognize Portuguese characters  | Done   | Major    | Daniel | Done       |
| Bug  | ST26T-2352 | Wrong number of dates on the priority identification: tool selects one day before the one selected by the user   | Done   | Major    | Daniel | Duplicate  |
| Bug  | ST26T-2368 | Test files ST_26_short and ST_26_long_amended DTD version cannot be imported   | Done   | Major    | EPO    | Obsolete   |
| Bug  | ST26T-2367 | When I click on the hyperlink "feature location" after import of SEQ ID1 that generated an error, it does not direct me to such a feature, but to the project page with an error message   | Done   | Major    | EPO    | Done       |
| Bug  | ST26T-2366 | The information in field 110, 120 and 130 of the original ST.25 file is not imported as expected   | Done   | Major    | EPO    | Done       |



| Bug | ST26T-2364 | Importing a St.25 sequence characterized as DNA and containing u residues generates an error in the validation report  | Done | Major   | EPO    | Done                |
|-----|------------|--|------|---------|--------|---------------------|
| Bug | ST26T-2363 | Importing nucleotide sequences written in upper case generates an error upon validation saying that nucleotide sequences should be in lower case, while it should be changed automatically to upper case | Done | Major   | EPO    | Done                |
| Bug | ST26T-2362 | In the case of RNA: not all u residues are identified  | Done | Major   | EPO    | Done                |
| Bug | ST26T-2360 | All errors relating to one SEQ ID NO should be grouped together.   | Done | Major   | EPO    | Done                |
| Bug | ST26T-2139 | UC28 -currently it is possible to delete an aa sequence associated with a translation qualifier and the protein_id is NOT updated!   | Done | Major   | EPO    | Done                |
| Bug | ST26T-2138 | UC24 - Sequences table: sequence name, molecule type, organism removed, they should not. Length set to 0, it should not  | Done | Major   | EPO    | Duplicate           |
| Bug | ST26T-2137 | UC24 - Move to position 0 Value 0 is accepted. It should not   | Done | Major   | EPO    | Duplicate           |
| Bug | ST26T-2136 | Problem with importing test files, many of the test files could not be imported, while they should   | Done | Major   | EPO    | Done                |
| Bug | ST26T-2131 | Skip sequences are automatically assigned the feature(s) of a previously entered sequence. This is odd and should not happen. They should not show any feature   | Done | Major   | EPO    | Done                |
| Bug | ST26T-2157 | Title in remove custom organism confirmation dialog, is 'Create new organism' while it should be 'Remove'  | Done | Minor   | IPOBSD | Duplicate           |
| Bug | ST26T-2400 | Priority Identification - filing date shown in edit window is one day before the selected date   | Done | Blocker | USPTO  | Duplicate           |
| Bug | ST26T-2397 | Application Identification box – filing date shown in edit window is one day before the selected date  | Done | Blocker | USPTO  | Done                |
| Bug | ST26T-2387 | Wrong title in the remove custom organism confirmation dialog  | Done | Major   | USPTO  | Duplicate           |
| Bug | ST26T-2378 | Cannot add a "transl_table" qualifier to an existing CDS feature   | Done | Major   | USPTO  | Duplicate           |
| Bug | ST26T-2377 | During the creation of new sequence with DNA/RNA fragments, proper location formats are not accepted and the "create" buttons are inactive   | Done | Major   | USPTO  | Done                |
| Bug | ST26T-2376 | Inappropriate "feature table missing" error message (XFT_1) seen in project validation, this error should never be seen on project validation as it is not applicable to a project                       | Done | Major   | USPTO  | Done                |
| Bug | ST26T-2375 | Cannot save a "replace" qualifier with an empty value during the addition of a feature key ("replace" can have an empty value to signify a deletion of the indicated residue)                            | Done | Major   | USPTO  | Cannot<br>Reproduce |
| Bug | ST26T-2349 | Import of sequences from multisequence file results in confusing messages, one 'success, one 'no import'   | Done | Major   | USPTO  | Done                |
| Bug | ST26T-2348 | Import of protein sequence from ST.25 with a lowercase/lowercase amino acid abbreviation – three letter abbreviations are treated as three separate amino acids, which should not happen                 | Done | Major   | USPTO  | Done                |
| Bug | ST26T-2347 | Error correction: Link from 'organism' error listed on verification report does not open a window that allows for correction of the error by adding and saving the missing organism information.         | Done | Major   | USPTO  | Done                |
|     |            |  |      |         |        |                     |



| Bug | ST26T-2346 | The verification report displayed following project validation is often erroneous.   | Done | Major | USPTO | Duplicate |
|-----|------------|--|------|-------|-------|-----------|
| Bug | ST26T-2345 | Faulty import of NonEnglishQualifier values during import of ST.26 sequences into new project  | Done | Major | USPTO | Done      |
| Bug | ST26T-2342 | XML error that seen on project validation  | Done | Major | USPTO | Done      |
| Bug | ST26T-2341 | Project validation does not match the validation that occurs when "generate sequence listing" is selected  | Done | Major | USPTO | Done      |
| Bug | ST26T-2337 | Tool does not provide message for sequence that is not imported.   | Done | Major | USPTO | Done      |
| Bug | ST26T-2336 | Incorrect error message for missing applicant 'At least one of the Applicants provided must be marked as the primary' is displayed, while 'The applicant name is missing. An applicant must be entered' is expected        | Done | Major | USPTO | Done      |
| Bug | ST26T-2332 | After import of XML with both English and non-English qualifier values, only the English is visible in the project.  | Done | Minor | USPTO | Done      |
| Bug | ST26T-2326 | Inappropriate qID error after importing a FASTA file sequence  | Done | Major | USPTO | Done      |
| Bug | ST26T-2322 | ST.25 import – cannot manually add protein_id qualifier to CDS feature.  | Done | Major | USPTO | Done      |
| Bug | ST26T-2321 | Project verification does not catch empty translation qualifier value, after Import ST.25 with a DNA sequence that has a CDS   | Done | Minor | USPTO | Obsolete  |
| Bug | ST26T-2319 | Project verification does not catch empty mol_type qualifier value   | Done | Major | USPTO | Done      |
| Bug | ST26T-2317 | Export of free text qualifiers does not give an option to choose the "source" (UC31, step 5.1.3)   | Done | Major | USPTO | Won't Fix |
| Bug | ST26T-2316 | Import of ST.25 sequence listing with Xaa residue generates and old message (UC12) while it should generate the one defined in UC10  | Done | Major | USPTO | Done      |
| Bug | ST26T-2315 | Wrong important report message due to an incorrect implementation of Story ST26T-1971  | Done | Major | USPTO | Done      |
| Bug | ST26T-2313 | Calendar function in the "filing date" field puts in a date one day before the chosen date   | Done | Major | USPTO | Done      |
| Bug | ST26T-2312 | It is not possible to delete filing date in "Application Identification" box   | Done | Major | USPTO | Done      |
| Bug | ST26T-2311 | Conflicting messages displayed in the process of validating a project  | Done | Major | USPTO | Duplicate |
| Bug | ST26T-2309 | XQID_3 wrongly considered as a project error instead of a validation error.  | Done | Major | USPTO | Duplicate |
| Bug | ST26T-2307 | Wrong error message displayed on validation of the project - 'The format of the feature location operator is invalid.' while 'The location descriptors of the 'join' operator of the feature exon are invalid' is expected | Done | Major | USPTO | Done      |
| Bug | ST26T-2306 | Bulk editing does not allow to edit just one detail of the sequence  | Done | Major | USPTO | Won't Fix |
| Bug | ST26T-2305 | Bulk edit sequence list not updated after bulk edit  | Done | Major | USPTO | Done      |
| Bug | ST26T-2302 | The title for the remove custom organism confirmation dialog is not correct and has to be changed  | Done | Major | USPTO | Duplicate |
| Bug | ST26T-2120 | General information: if "Before the assignment of the application number" is selected and IPO is mistakenly entered, it is not possible to remove IPO code   | Done | Major | USPTO | Done      |



| Bug | ST26T-2111 | No feature table available when SEQ ID NO:3 clearly has a source feature and a CDS feature   | Done | Critical | USPTO                      | Done      |
|-----|------------|--|------|----------|----------------------------|-----------|
| Bug | ST26T-2110 | XML validation error codes are showing up in project validation reports, this should not be the case   | Done | Major    | USPTO                      | Done      |
| Bug | ST26T-2072 | XQV23 Rule: The sub-element value of "location" of anticodon is (pos:3,aa:Leu,seq:atg), LOC_DESC_FORMAT_1, generates no WARNING, while it should   | Done | Major    | USPTO                      | Done      |
| Bug | ST26T-1853 | The source language for the XLIFF export of free text qualifiers is wrongly derived from the original free text language code. Only English, the original non-English language and the target translation non-English language may be present in a project | Done | Major    | USPTO,<br>WIPO-<br>Testing | Done      |
| Bug | ST26T-1831 | Import report: SEQ ID information missing regarding mol_type   | Done | Major    | WIPO-<br>Testing           | Done      |
| Bug | ST26T-2289 | The system doesn't notice that " <x" "="" and="">x" location descriptor is not valid for CDS feature</x">  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2283 | 'Validating' processing disappears if button is clicked before all sequences have loaded   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2274 | The "Help" menu doesn't return in the original state on MAC OS   | Done | Minor    | WP2                        | Done      |
| Bug | ST26T-2263 | Rule_ID is wrong PO_N_1, PO_NL_1, 2  | Done | Minor    | WP2                        | Duplicate |
| Bug | ST26T-2262 | PAFD_1 and PAFD_2 trigger in the .jar / .war WIPO Sequence Validator and in the application  | Done | Minor    | WP2                        | Done      |
| Bug | ST26T-2255 | Validator: FileNotFoundException appears in console  | Done | Minor    | WP2                        | Done      |
| Bug | ST26T-2248 | Application might unexpectedly close during validation operation   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2245 | ST.25 Import: The "note" qualifier is not created for keys "3'clip" and "5'clip" and custom feature if <223> element isn't presented   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2244 | Verification rule QV_1 ("The qualifier value for the qualifier <qualifier name=""> is missing.") rule doesn't trigger</qualifier>  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2243 | "Name Latin" is not displayed in GUI after importing the XML ST.26 file  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2242 | Preferences: 'Default location' doesn't work properly and it's populated by path+fileName after generate sequence listing  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2241 | Verification rule XNEFTLC_2 (The non-English free text language code is mandatory) doesn't trigger in .jar /.war WIPO Sequence Validator   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2238 | Verification rule XQV_46 (The value of this qualifier cannot be empty) the rule doesn't trigger  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2236 | The file gets stuck in the process folder during validation in WIPO Sequence Validator   | Done | Critical | WP2                        | Done      |
| Bug | ST26T-2231 | The system grants duplicate IDs for qualifiers with language dependent values  | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2230 | Import FASTA sequence: mol_type qualifier is not created automatically for nucleotides   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2228 | Unused or redundant code (Validator)   | Done | Minor    | WP2                        | Done      |
| Bug | ST26T-2222 | The validator version is hard coded to v0.1 while it should be 1.0   | Done | Major    | WP2                        | Done      |
| Bug | ST26T-2217 | Combined indicator: the informational message is displayed near another field  | Done | Trivial  | WP2                        | Done      |
|     |            |  |      |          |                            |           |



| Bug | ST26T-2212 | Rule_ID is wrong AEPAI_ANT_2   | Done | Minor | WP2 | Duplicate |
|-----|------------|--|------|-------|-----|-----------|
| Bug | ST26T-2211 | Rule_ID is wrong AEPAI_ANT_1   | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2210 | Rule_ID is wrong for AEPAI_OC_2  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2209 | Rule_ID is wrong AEPAI_OC_1  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2208 | Rule_ID is wrong PA_1  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2205 | After validation of import xml file Rule_ID is wrong CA_1, while it should be CA_2   | Done | Minor | WP2 | Done      |
| Bug | ST26T-2202 | 'UI.MESSAGE.VERIFICATION.Cannot read property 'length' of undefined  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2200 | Rule_ID is wrong AEPAI_FD_3  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2199 | Rule_ID is wrong for FL rules  | Done | Minor | WP2 | Duplicate |
| Bug | ST26T-2193 | Verification rule QV_26 (Invalid qualifier value format) doesn't trigger when the value of the mandatory qualifier "mobile_element_type" is empty  | Done | Major | WP2 | Done      |
| Bug | ST26T-2192 | ST.25 Import: The system doesn't set the attribute "skippedIndicator" of the sequence to 'yes' when this sequence contains less than 10 nucleotide simbols that are not 'n'                                    | Done | Major | WP2 | Duplicate |
| Bug | ST26T-2191 | ST.25 Import: The ST.25 .txt file doesn't import if <110> element is empty   | Done | Major | WP2 | Done      |
| Bug | ST26T-2190 | Verification rule FL_20bis (The location descriptors of the 'join' operator of the feature {{feature key}} are invalid) doesn't trigger  | Done | Major | WP2 | Done      |
| Bug | ST26T-2187 | Verification rule XQV_2a (A qualifier value for qualifier <qualifier name=""> is not permitted.): the Message Text / Localized Message and Message Key are not correct.</qualifier>                            | Done | Minor | WP2 | Done      |
| Bug | ST26T-2185 | Verification rule NEQV_4 (Non-English qualifier free text is permitted only for a qualifier that allows language-dependent free text) - there is no way to fix the validation error, the message text is empty | Done | Major | WP2 | Done      |
| Bug | ST26T-2184 | Verification rules QV_36 / QV_37 and XQV_38 / XQV_39 (Invalid qualifier value format) don't trigger for certain descriptors  | Done | Major | WP2 | Done      |
| Bug | ST26T-2183 | ST.25 Import: The obsolete feature key "scRNA" is replaced with the wrong qualifier value  | Done | Major | WP2 | Done      |
| Bug | ST26T-2181 | Anti-patterns and wrong code (Improper Use of Truthly and Falsely Evaluation & Missing 'break' before 'default' in switch statement)   | Done | Major | WP2 | Done      |
| Bug | ST26T-2179 | Internationalization and localization issues   | Done | Major | WP2 | Done      |
| Bug | ST26T-2175 | Licensing: the type of application license is not defined in the main package.json   | Done | Major | WP2 | Done      |
| Bug | ST26T-2168 | The qualifier IDs aren't renumbered properly during import .xml file where qualifier IDs attributes aren't unique  | Done | Major | WP2 | Done      |
| Bug | ST26T-2165 | Verification rule XQID_2 (The format of the qualifier id attribute is invalid. It must be the character 'q' followed by a positive integer.) doesn't trigger if Qualifier ID = "q0"                            | Done | Major | WP2 | Done      |
| Bug | ST26T-2149 | Verification rule QV_25 (Invalid qualifier value format of the qualifier anticodon) doesn't trigger if the anticodon seq sub-element contains less or more than 3 nucleotide                                   | Done | Major | WP2 | Done      |



| Bug | ST26T-2147 | Import ST26: Editing of Priority Identification is NOT possible where .xml file doesn't contain "ApplicationNumberText" element | Done | Major | WP2 | Done      |
|-----|------------|---|------|-------|-----|-----------|
| Bug | ST26T-2058 | Application hangs if Project contains a lot of Sequences  | Done | Major | WP2 | Duplicate |

## **Highlights**

This is the second release during warranty period. It contains no new functionality, only bugs fixes.

### **New Functionalities**

No new functionalities have been added.

## **Improvements**

None, this is a bug fix release.

## **Bug Fixing – Issues Done**

106 bugs were fixed (and are ready for retest) in this release:

| Туре | key            | Summary  | Status | Priority | Resolution          | Labels         |
|------|----------------|--|--------|----------|---------------------|----------------|
| Bug  | ST26T-<br>1875 | Windows 32bit OS version is unstable and 'hangs' while trying to generate a sequence listing | Done   | Minor    | Won't Fix           | ROSPATENT      |
| Bug  | ST26T-<br>1905 | Import: join(complement(79)) generates wrong error message                                   | Done   | Minor    | Won't Fix           | EPO            |
| Bug  | ST26T-<br>2413 | Auto-update feature does not download latest binary  | Done   | Major    | Cannot<br>Reproduce | EPO            |
| Bug  | ST26T-<br>2233 | Large sequence listing (50k sequences) causes desktop tool to crash                          | Done   | Major    | Cannot<br>Reproduce | non-functional |
| Bug  | ST26T-<br>2534 | Replace qualifier: different behavior in project/XML verification                            | Done   | Critical | Done                | USPTO          |



| Bug      | ST26T-<br>2386 | Multiple issues detected   | Done | Minor    | Done                |       |
|----------|----------------|--|------|----------|---------------------|-------|
| Bug      | ST26T-<br>2541 | Sequences with all EMPTY values cannot be imported into desktop tool                                     | Done | Major    | Done                | USPTO |
| Bug      | ST26T-<br>2540 | Verification report: applicant not marked primary after language code selected                           | Done | Minor    | Done                | USPTO |
| Bug      | ST26T-<br>2411 | 'Application filed' appears after saving the application information                                     | Done | Minor    | Done                | GUI   |
| Sub-task | ST26T-<br>1999 | When non-Latin characters are entered in a qualifier value, the language dropdown is no longer available | Done | Major    | Done                | CIPO  |
| Bug      | ST26T-<br>2539 | Detected sequence not reported for reserved character error  | Done | Major    | Done                | USPTO |
| Bug      | ST26T-<br>2535 | "numeric" residue QV_1A not being invoked  | Done | Critical | Done                |       |
| Bug      | ST26T-<br>2532 | Sequence length is wrong due to counting of  | Done | Critical | Done                | USPTO |
| Bug      | ST26T-<br>2530 | Value of translation<br>qualifier does not update<br>when residues changed<br>(UC19, step 4.5)           | Done | Major    | Done                | USPTO |
| Bug      | ST26T-<br>2528 | Update of source feature location not accurate after editing residues in a sequence                      | Done | Major    | Done                | USPTO |
| Bug      | ST26T-<br>2529 | Protein sequence linked to protein_id qualifier empty  | Done | Major    | Cannot<br>Reproduce | USPTO |
| Bug      | ST26T-<br>2531 | Certain Language-<br>Dependent Free Text<br>Qualifiers do not export to<br>XLIFF                         | Done | Critical | Cannot<br>Reproduce | USPTO |
| Bug      | ST26T-<br>2533 | Cannot edit a replace qualifier value from a residue to empty  | Done | Major    | Done                |       |



| Bug | ST26T-<br>2201 | Installation -> Windows 10 (64-bit): Additional folders are left in the System after uninstall application   | Done | Minor | Won't Fix           | WP2            |
|-----|----------------|--|------|-------|---------------------|----------------|
| Bug | ST26T-<br>2289 | The system doesn't notice that " <x" "="" and="">x" location descriptor is not valid for CDS feature</x">  | Done | Major | Done                | WP2            |
| Bug | ST26T-<br>2264 | FQ_1 and XFQ_3 rules don't trigger (only more generic error message returned)  | Done | Minor | Won't Fix           | functional_gap |
| Bug | ST26T-<br>2259 | "Cancel validation" button doesn't work  | Done | Minor | Cannot<br>Reproduce | WP2            |
| Bug | ST26T-<br>2253 | OFTLC_2 doesn't trigger  | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2187 | Verification rule XQV_2a (A qualifier value for qualifier <qualifier ame=""> is not permitted.): the Message Text / Localized Message and Message Key are not correct.</qualifier> | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2204 | SF_1: The wrong link from verification report  | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2203 | Detected Sequence is non-<br>empty and there should be<br>no link for PO_N_1   | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2058 | Application hangs if Project contains a lot of Sequences (Linux)   | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2426 | Installation -> problem with reinstalling the application if previous installed application was deleted by user manually   | Done | Minor | Declined            | WP2            |
| Bug | ST26T-<br>2293 | Internationalization -<br>Incomplete translation<br>cases  | Done | Minor | Done                | WP2            |
| Bug | ST26T-<br>2514 | The rules NEQV_3/XNEQV_3 aren't triggered  | Done | Minor | Done                | WP2            |



| Bug | ST26T-<br>2513 | The system doesn't inform about wrong format of "transl_except" qualifier value (space characters)   | Done | Minor | Done | WP2         |
|-----|----------------|--|------|-------|------|-------------|
| Bug | ST26T-<br>2510 | Import ST.25: The system doesn't support the several date formats that mention in the messages in the Import Report for <140/141> and <150/151> elements | Done | Minor | Done | WP2         |
| Bug | ST26T-<br>2502 | The system sees space characters as a part of "source" feature location  | Done | Minor | Done | WP2         |
| Bug | ST26T-<br>2435 | Huge ST25 (97k) file import is interrupted by error on last sequence   | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2433 | Validation process stops in a middle   | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2170 | Variables, fields, methods, classes, and packages defects  | Done | Minor | Done | CODE_REVIEW |
| Bug | ST26T-<br>2176 | Tests reasonability criteria defects   | Done | Minor | Done | CODE_REVIEW |
| Bug | ST26T-<br>2434 | Huge ST25 (71k) file import is interrupted by error  | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2512 | Import ST.25: The system doesn't add the note to the Import Report for each amino acid sequence of the mixed mode  | Done | Minor | Done | WP2         |
| Bug | ST26T-<br>2511 | There are two errors during validation if there is no ApplicationIdentification  | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2385 | Import another project -<br>primary inventor is not<br>imported  | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2384 | Bulk edit - "empty is all" in<br>the sequence range field<br>misleads the user   | Done | Major | Done | WP2         |
| Bug | ST26T-<br>2175 | Licensing: the type of application license is not  | Done | Major | Done | CODE_REVIEW |



|     |                | defined in the main   |      |       |      |                    |
|-----|----------------|---|------|-------|------|--------------------|
| Bug | ST26T-<br>2174 | package.json Clean code criteria defects  | Done | Minor | Done | CODE_REVIEW        |
| Bug | ST26T-<br>2506 | ST.25 Import: The system doesn't import some dates correctly from <141> and <151> elements  | Done | Major | Done | WP2                |
| Bug | ST26T-<br>2181 | Anti-patterns and wrong code (Improper Use of True and False Evaluation & Missing 'break' before 'default' in switch statement)                                   | Done | Major | Done | CODE_REVIEW        |
| Bug | ST26T-<br>2180 | Unused or redundant code  | Done | Minor | Done | CODE_REVIEW        |
| Bug | ST26T-<br>2232 | Change data report is not complete at first   | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2424 | The .xliff file with empty source or target language is not suitable for import   | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2425 | Input fields aren't cleared after cancelling and reopening "Reorder Sequence"   | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2521 | Import ST.25: The message in the Import Report contains placeholder if the <140> element is absent  | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2505 | Import ST.25: The radio button "After the assignment of the application number" isn't automatically checked when "Application Number" is present in <140> element | Done | Minor | Done | ST26_existing_bugs |
| Bug | ST26T-<br>2520 | XAFR_1 rule isn't triggered   | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2504 | Import ST.25: The system creates empty "Invention Title" instance if the <120>  | Done | Minor | Done | WP2                |



|     |                | element value is missed in ST.25 .txt file   |      |       |      |                    |
|-----|----------------|--|------|-------|------|--------------------|
| Bug | ST26T-<br>2519 | After cancelling the XLIFF file import in the case of "No matching project names", further import attempts are terminated    | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2515 | The rule AEPAI_FD_3 isn't triggered for Earliest Priority Application  | Done | Major | Done | WP2                |
| Bug | ST26T-<br>2507 | Warning rules "Verify that<br>the 'note' qualifier<br>describes the 'OTHER' or<br>'other' value" don't trigger               | Done | Major | Done | WP2                |
| Bug | ST26T-<br>2509 | Feature table pagination: current page number is shared between sequences  | Done | Major | Done | WP2                |
| Bug | ST26T-<br>2516 | When the rule AEPAI_FD_3 applies, detected value for Filing date is wrong  | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2417 | The "Cancel" button does not work in the "bulk edit" form  | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2429 | Detected Value is non-<br>descriptive and has<br>different formats for the<br>language code validation<br>(LC_1, LC_2 rules) | Done | Minor | Done | ST26_existing_bugs |
| Bug | ST26T-<br>2432 | Import Report: Sequence ID<br>Number in the Change Data<br>report doesn't match with<br>Sequence ID into the<br>project      | Done | Minor | Done | ST26_existing_bugs |
| Bug | ST26T-<br>2431 | The system import or displays the wrong number of imported sequences   | Done | Minor | Done | WP2                |
| Bug | ST26T-<br>2412 | Qualifier values are not displayed properly in some circumstances  | Done | Major | Done | WP2                |
| Bug | ST26T-<br>2518 | The rule QV_1A doesn't work  | Done | Major | Done | WP2                |



| Bug | ST26T-<br>2517 | The QV_39 rule doesn't work. XQV_2 rule is triggered instead  | Done | Major    | Done                | WP2                |
|-----|----------------|---|------|----------|---------------------|--------------------|
| Bug | ST26T-<br>2508 | Generation process stops in the middle (Linux)  | Done | Major    | Done                | WP2                |
| Bug | ST26T-<br>2227 | Concurrency issues (Validator)  | Done | Minor    | Done                | CODE_REVIEW        |
| Bug | ST26T-<br>2421 | The tool does not recognize Portuguese characters   | Done | Major    | Won't fix           | Daniel             |
| Bug | ST26T-<br>2405 | Inappropriate warning on validation report  | Done | Critical | Done                | USPTO              |
| Bug | ST26T-<br>2403 | Inappropriate global<br>message in import report<br>regarding import of ST.25<br>SL   | Done | Major    | Won't Fix           | ST26_existing_bugs |
| Bug | ST26T-<br>2393 | Project validation: a stop<br>codon at the end of a CDS<br>location (last 3 positions of<br>the CDS location) is being<br>incorrectly erred   | Done | Major    | Done                | USPTO              |
| Bug | ST26T-<br>2391 | Warning regarding Non-<br>English free text language<br>code appears when it<br>shouldn't   | Done | Major    | Duplicate           | USPTO              |
| Bug | ST26T-<br>2389 | Reordering sequences led to mis-numbering or duplicates   | Done | Major    | Cannot<br>Reproduce | USPTO              |
| Bug | ST26T-<br>2501 | When importing a ST25 parse file and the element <212> contains value is not equal "DNA", "RNA", "ADN", "ARN", "PRT" or missed, The information should be skipped, and the field should be set blank, which is not the case | Done | Major    | Done                | JPO                |
| Bug | ST26T-<br>2497 | Sometimes, when created a new project, the project initially contained several sequences in the "SEQUENCES" section while it should not contain any   | Done | Major    | Cannot<br>Reproduce | JPO                |



| Bug | ST26T-<br>2496 | While extracting free text qualifiers, It seems that ""source-language"" in XLIFFs is set based on ""Source language code for free text qualifiers"", NOT on ""Original free text language code"", and if the former is empty, automatically set as "en". | Done | Major    | Done                | JPO   |
|-----|----------------|---|------|----------|---------------------|-------|
| Bug | ST26T-<br>2495 | While extracting all free text qualifiers qualifier ID's are not unique, while they should  | Done | Major    | Done                | JPO   |
| Bug | ST26T-<br>2494 | While creating a sequence manually, a new sequence was able to be created without keeping the field blank, although organism name is mandatory, it isn't needed to save, while it should  | Done | Major    | Done                | JPO   |
| Bug | ST26T-<br>2491 | During import of multiple sequences in a raw multisequence text file, Tool assigns the same qID to all sequences  | Done | Critical | Done                | USPTO |
| Bug | ST26T-<br>2484 | Import report for multisequence and raw file import is empty when Printed   | Done | Minor    | Done                | USPTO |
| Bug | ST26T-<br>2483 | Project with only warnings created an XML with a sequence with no feature table   | Done | Critical | Cannot<br>Reproduce | USPTO |
| Bug | ST26T-<br>2477 | Inconsistent error<br>messaging upon import of<br>ST25 files  | Done | Minor    | Cannot<br>Reproduce | USPTO |
| Bug | ST26T-<br>2475 | Inappropriate error for missing qualifier value when enterering a feature (protein_bind) qualifier (bound_moiety) and   | Done | Major    | Duplicate           | USPTO |



| Bug | ST26T-<br>2464 | including a value with only a non-English value, this should not generate an error  Clicked on the trash can icon to delete CDS feature in a project with a nucleotide sequence and a CDS feature key, the CDS feature should be deleted, but it isn't | Done | Critical | Cannot<br>Reproduce     | USPTO |
|-----|----------------|--|------|----------|-------------------------|-------|
| Bug | ST26T-<br>2462 | Validation report lists an ERROR saying that the applicant name is missing or none have been selected as primary, while there is primary selected  | Done | Major    | Duplicate               | USPTO |
| Bug | ST26T-<br>2446 | FQS03 step9 and 11 not possible to create it   | Done | Major    | Cannot<br>Reproduce     | EPO   |
| Bug | ST26T-<br>2466 | Empty translation qualifier value not detected on project validation (QV_1) while validating a CDS feature with an empty translation qualifier value.  | Done | Major    | Done                    | USPTO |
| Bug | ST26T-<br>2139 | UC28 -currently it is possible to delete an aa sequence associated with a translation qualifier and the protein_id is NOT updated!   | Done | Major    | Done                    | EPO   |
| Bug | ST26T-<br>2463 | Rule QV_44 did not trigger as expected while deleting seq. corresponding to seq. indicated in protein_id qualifier. Subsequent seq. was renumbered and matched seq. in protein_id qualifier, but seq. does not match value of translation qualifier    | Done | Major    | Done                    | USPTO |
| Bug | ST26T-<br>2395 | In the Verification Report, sorting stops working on   | Done | Minor    | Won't fix<br>(obsolete) | USPTO |



|     |                | other columns after applying once.   |      |       |      |       |
|-----|----------------|--|------|-------|------|-------|
| Bug | ST26T-<br>2470 | Locations " <x" "="" and="">x" not permitted for CDS features, while it should</x">  | Done | Major | Done | USPTO |
| Bug | ST26T-<br>2468 | Project rule QV_48 did not trigger while validating a CDS feature with an empty translation qualifier value and a protein_id qualifier with a value that matched SEQ ID Number of related protein sequence | Done | Major | Done | USPTO |
| Bug | ST26T-<br>2392 | New verification rule desktop tool: warning provided if qualifiers are not in English error seen when qualifier value provided only in non-English language  | Done | Major | Done | USPTO |
| Bug | ST26T-<br>2467 | Project rule QV_44 did not trigger while validating a CDS feature with an empty translation qualifier value and a protein_id qualifier with a value that matched SEQ ID Number of related protein sequence | Done | Major | Done | USPTO |
| Bug | ST26T-<br>2473 | Alphabetical sorting of persons and organizations list should ignore letter case   | Done | Minor | Done | USPTO |
| Bug | ST26T-<br>2396 | Incorrect detected value in Verification Report  | Done | Minor | Done | USPTO |
| Bug | ST26T-<br>2402 | Missing global message in import report regarding import of ST.25 RNA sequences with 'u' symbols   | Done | Major | Done | USPTO |
| Bug | ST26T-<br>2476 | Date entered into<br>'Application Identification'<br>filing date field in a project<br>is not accurate when a  | Done | Major | Done | USPTO |



|     |                | sequence listing is generated  |      |          |      |                    |
|-----|----------------|--|------|----------|------|--------------------|
| Bug | ST26T-<br>2401 | Renumbering amino acid sequence from ST.25 with a negative number incorrect message in Change Data of Import Report                      | Done | Minor    | Done | USPTO              |
| Bug | ST26T-<br>2479 | Import with improper feature location for CDS does not generate an error   | Done | Major    | Done | ST26_existing_bugs |
| Bug | ST26T-<br>2478 | Import report messages<br>and change data only list 5<br>messages each per page, at<br>least 10 would be better                          | Done | Minor    | Done | USPTO              |
| Bug | ST26T-<br>2482 | Create New Sequence edit window has inappropriate non-functional "Add new 'misc_feature' feature" button.                                | Done | Minor    | Done | USPTO              |
| Bug | ST26T-<br>2481 | Project status is not updated on the project home page when returning immediately to main project page after sequence listing generation | Done | Major    | Done | ST26_existing_bugs |
| Bug | ST26T-<br>2492 | Even after adding a new "primary" applicant, the first inventor, was still marked as Primary, too.                                       | Done | Major    | Done | JPO                |
| Bug | ST26T-<br>2498 | Errors while importing invalid files are not shown   | Done | Major    | Done | JPO                |
| Bug | ST26T-<br>2487 | Free text translation required not recognized  | Done | Major    | Done | USPTO              |
| Bug | ST26T-<br>2485 | QV_36 rule and QV_37 rule in GUI: enforcement is not immediate   | Done | Major    | Done | USPTO              |
| Bug | ST26T-<br>2489 | The second sequence is removed when reordering sequences - related to ST26T-2138   | Done | Critical | Done | USPTO              |



| Bug | ST26T-<br>2488 | Incomplete Import Report (text file in FASTA multisequence or raw multisequence format): Import report does not show an entry for the last sequence  | Done | Major | Done                | USPTO |
|-----|----------------|--|------|-------|---------------------|-------|
| Bug | ST26T-<br>2499 | During editing the sequence residues, when the user entered multiple "spaces" within the residue box and then clicked "Update residue", the spaces were removed from the "SEQUENCE" display, but the number of the spaces were also counted up | Done | Major | Done                | JPO   |
| Bug | ST26T-<br>2445 | UTB QT05 case 2: It not possible to save and do step 3   | Done | Major | Done                | EPO   |
| Bug | ST26T-<br>2449 | Small problem, when you click on a ID NO (e.g., 4: the page of features opens on page 2 of changes and not page 1, while for ID NO 5 it opened on page 1   | Done | Minor | Cannot<br>reproduce | EPO   |
| Bug | ST26T-<br>2448 | Clicking on the warning<br>Organism (in the<br>Verification Report),<br>doesn't open at the correct<br>place   | Done | Minor | Done                | EPO   |
| Bug | ST26T-<br>2461 | Inconsistent GUI interface<br>"Priority Identification: Edit<br>pencil should always be<br>visible, but it isn't   | Done | Minor | Done                | USPTO |
| Bug | ST26T-<br>2460 | FASTA import: mol_type value not saved in project  | Done | Major | Done                | USPTO |
| Bug | ST26T-<br>2321 | Project verification does<br>not catch empty translation<br>qualifier value, after Import<br>ST.25 with a DNA sequence<br>that has a CDS   | Done | Minor | Won't Fix           | USPTO |



| Bug | ST26T-<br>2315 | Wrong important report message due to an incorrect implementation of Story ST26T-1971  | Done | Major | Won't Fix | USPTO       |
|-----|----------------|--|------|-------|-----------|-------------|
| Bug | ST26T-<br>2307 | Wrong error message displayed on validation of the project - 'The format of the feature location operator is invalid.' while 'The location descriptors of the join operator of the feature exon are invalid' is expected | Done | Major | Done      | USPTO       |
| Bug | ST26T-<br>2372 | Not understanding what<br>the source language code<br>for free text qualifier refers<br>to and by searching in ST.26<br>itself for source language<br>code and it did not return<br>any results.                         | Done | Minor | Done      | EPO         |
| Bug | ST26T-<br>2367 | When I click on the hyperlink feature location after import of SEQ ID1 that generated an error, it does not direct me to such a feature, but to the project page with an error message                                   | Done | Minor | Duplicate | EPO         |
| Bug | ST26T-<br>1994 | When starting an import process and cancelling, the continue button doesn't reset and is displaying a proceed button instead   | Done | Minor | Done      | FAT         |
| Bug | ST26T-<br>2161 | Non English qualifier value disappears from summary when cancel qualifier edition  | Done | Minor | Done      | FAT         |
| Bug | ST26T-<br>2272 | Sonarqube: failed metrics  | Done | Major | Done      | CODE_REVIEW |

## Known Issues in version 1.1.0

As such, two minor bugs reported by WP2 are still open.



| Туре | key            | Summary   | Status  | Priority | Resolution | Labels |
|------|----------------|---|---------|----------|------------|--------|
| Bug  | ST26T-<br>2430 | Application is closed time to time after finish generation sequence listing for more than 40k sequences | Blocked | Minor    | Unresolved | WP2    |
| Bug  | ST26T-<br>2285 | Application closed on validating 200k sequences   | Blocked | Minor    | Unresolved | WP2    |

## List of 15 minor/trivial 'st26-existing' bugs planned to be resolved during maintenance:

| Т   | Key            | Summary   | Status         | Р       | Resolution | Labels                    |
|-----|----------------|---|----------------|---------|------------|---------------------------|
| Bug | ST26T-         | Tests reasonability criteria  | In             | Trivial | Pending    | CODE_REVIEW,              |
|     | 2225           | defects (Validator)   | Progress       |         |            | WP2,ST26_existing_bugs    |
| Bug | ST26T-<br>2216 | ST.25 Import: There are two text message "Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences." in the Import report | Blocked        | Trivial |            | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2045 | Linux: No icon appears for application  | To Do          | Trivial |            | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2330 | Tool won't allow complex locations in "anticodon" location sub-element (QV_23)  | To Do          | Minor   | Pending    | ST26_existing_bugs, USPTO |
| Bug | ST26T-<br>2295 | Internationalization - Problems with layout   | Blocked        | Minor   |            | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2278 | Internationalization - Dropdown menus are not translated after changing language  | Blocked        | Minor   |            | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2277 | Arabian localization issues   | Blocked        | Minor   |            | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2275 | XQV_29 doesn't trigger, XQV_28 triggers instead   | In<br>Progress | Minor   | Pending    | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2258 | XDECL_1 rule triggers in the case of wrong .XML declaration but does NOT trigger in the case of empty declaration   | In<br>Progress | Minor   | Pending    | ST26_existing_bugs, WP2   |
| Bug | ST26T-<br>2257 | ST.25 Import: The "D-segment" feature key is not imported properly  | To Do          | Minor   | Pending    | ST26_existing_bugs, WP2   |



| Bug | ST26T-<br>2256 | ST.25 Import: 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" | In<br>Progress | Minor | Pending | ST26_existing_bugs, WP2                 |
|-----|----------------|--|----------------|-------|---------|---|
| Bug | ST26T-2178     | Incorrect logic implementation   | Blocked        | Minor |         | CODE_REVIEW,<br>ST26_existing_bugs, WP2 |
| Bug | ST26T-2172     | Architectural implementation defects   | To Do          | Minor |         | CODE_REVIEW,<br>ST26_existing_bugs, WP2 |
| Bug | ST26T-2167     | ST.25 Import: The system creates<br>the extra qualifier "note/NOTE"<br>for some ST.25 obsoleted feature<br>keys where <223> element is<br>presented  | To Do          | Minor |         | ST26_existing_bugs, WP2                 |
| Bug | ST26T-2144     | The qualifier name "organism/ORGANISM" for the feature other than source/SOURCE can't be changed and deleted. The value is set as a name of organism in the basic panel of sequence                                    | Blocked        | Minor |         | ST26_existing_bugs, WP2                 |



## **Glossary**

| Glossary              |  |
|-----------------------|--|
| Term                  | Definition   |
| CODE_REVIEW           | Defects that relate to the quality of code, this is not a criteria to move to the next phase in the project, they are only a criteria at the end of the warranty phase |
| ST26_existing_defects | Defects that were identified, and validated by WIPO & WP2, as defects already existing before development for this project started                                     |
| Non-functional        | A bug not related to the functional specification for the tool   |
| FAT                   | Factory Acceptance Testing – testing performed by development team   |
| WP2                   | Testing performed by Quality Assurance & Acceptance team   |
| ЕРО                   | Reported by the European Patent Office   |
| Daniel                | Reported by Daniel law patent attorney firm  |
| USPTO                 | Reported by the United States Patent and Trademark Office  |
| JPO                   | Reported by the Japanese Patent Office   |
| ROSPATENT             | Reported by ROSPATENT  |