



# WIPO Sequence Version 1.1.0

## User Manual

*The purpose of this document is to provide the users with instructions on how to perform basic operations with the WIPO Sequence desktop application. Typically, the users are a patent applicant, or their representative, seeking to submit a patent application which includes a sequence listing.*

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# WIPO SEQUENCE Version 1.1.0

## USER MANUAL

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# 1 INTRODUCTION

## 1.1 OVERVIEW

WIPO Sequence is a desktop tool which enables a user to:

- (i) create/edit a sequence listing in XML format compliant with WIPO Standard ST.26**
- (ii) verify the compliance of a sequence listing in XML format against WIPO ST.26 requirements.**

The WIPO Standard ST.26 can be found at:

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

This document describes how to use WIPO Sequence as an applicant or a representative of an applicant. A full list of the functionality of the tool can be found in section 2 of this document.

## 1.2 SYSTEM REQUIREMENTS

The WIPO Sequence tool was developed to support the following Operating Systems:

- Windows 10 version 1803 (32- and 64-bits versions)
- Linux: Ubuntu version 18.04 and CentOS 7 version 1804
- MacOS version 10.13 (64 bits version)

Besides these versions above, it also supports the following operating systems:

- Windows 7 and higher (both 32bits and 64 bits)
- Ubuntu version 12.04 and newer
- MacOS version 10.9 (64 bits version)

The WIPO Sequence tool requires the following minimum hardware specifications:

- CPU: 1.6 GHz
- RAM: 4 Gb
- Free Hard Disk: 1 GB (additional HD can be required for storing the sequence listing information)
- Screen resolution: 1366x768

## 1.2.1 Installation

### 1.2.1.1 Windows

WIPO Sequence provides a single installation file for both 32- and 64-bits versions of Windows. The user should follow the process shown in the installation wizard.

We have to specify that users will have performance problems, or the tool will not work properly if the 32bit version is used.

The database files used for storing the project information along with the log of the tool are stored at the following location:

```
C:\Users\\AppData\Roaming\ST26_authoring
```

When the application is updated or uninstalled, these files are not removed, so the projects data will remain if the application is reinstalled.

### 1.2.1.2 Linux

WIPO Sequence is provided as an “AppImage” file (<https://appimage.org/>) that will run on most Linux distributions, including CentOS and Ubuntu. In order to run the file, the user can execute the file by double-clicking on it or executing using the command line.

Initially, the user will be prompted with a message to select whether or not a shortcut on the desktop should be created.

### 1.2.1.3 OSX

WIPO Sequence provides a “dmg” file for installing the application on a MacOS 64-bit operating system. In order to install it, the user should double-click on the file and follow the wizard.

The database files used for storing the project information along with the log of the tool are stored at the following location:

```
/Users/<username>/Library/Application Support/ST26_authoring
```

When the application is updated or uninstalled, these files are not removed, so the projects data will remain if the application is reinstalled.

### 1.2.1.4 Silent install

WIPO Sequence supports a silent install by use of the following flags during installation (with .exe installer file):

- /S : to launch a silent install

- `/allusers` : to installs the tool so it is available for all Windows users on the desktop machine (this has to be launched when logged in as an admin user).

## 1.2.2 Uninstall

### 1.2.2.1 Windows

WIPO Sequence provides an uninstall wizard that can be launched under the “Add or Remove Programs” option in Windows.

In order to completely remove the log files and the files used to store the projects information, the following folder must be deleted:

```
C:\Users\\AppData\Roaming\ST26_authoring
```

### 1.2.2.2 Linux

By removing the Linux “Applmage” file, the application is uninstalled from the computer. Additionally, the menu entry can be removed by deleting the desktop file from the location:

```
$HOME/.local/share/applications/.
```

In order to completely remove the log files and the files used to store the projects information, the following folder must be deleted:

```
/Users/<username>/.config/ST26_authoring
```

### 1.2.2.3 OSX

The application can be uninstalled from Finder on OSX, under the Applications section.

In order to completely remove the log files and the files used to store the projects information, the following folder must be deleted:

```
/Users/<username>/Library/Application Support/ST26_authoring
```

### 1.2.3 Auto update process

After opening, the tool will check for available updates and if an update is found, it will inform the user to download and install the new version.

**Note:**

*In order to enable the auto update, the computer must be connected to the internet and the tool must have permissions to access the WIPO website through HTTP. Please also note that no information is sent from the user to the WIPO update server.*

## 2 TOOL FUNCTIONALITIES

This section outlines all of the functionalities that are implemented by the tool, in the current version of the tool, version 1.0.0. The list of functionalities is provided here in alphabetical order.

ID	Functionality
1	Add a custom organism name & description to the list of organism names of the system
2	Add an invention title and its corresponding language code to a project
3	Add application information (either current or prior application) to a project
4	Add feature information to a sequence
5	Add a source feature and its mandatory qualifiers to a sequence
6	Add new organism names to the list of organism names stored in this system
7	Add qualifier information to a feature
8	Add sequence listing general information data to a project
9	Add a sequence name to a selected sequence
10	Change the order in which the sequences will be listed in the generated sequence listing
11	Create a workspace in which data related to one sequence listing is stored
12	Create an instance of the sequence data structure and set its attributes to the values obtained from a ST.26 sequence data XML node received as input
13	Create and insert a sequence in another position in the listing
14	Create a translation qualifier for a selected CDS feature and its associated translated sequence
15	Create a new person or organization name

16	Delete a sequence
17	Display the generated sequence listing
18	Display the data changed upon import of a sequence
19	Edit the attributes of an instance of “Qualifier” data structure
20	Edit the attributes of a project
21	Edit the attributes of a sequence
22	Edit the attributes of an instance of “Feature” data structure
23	Enable or disable selected verification rules
24	Export of free text qualifiers, for the purpose of translation in XLIFF format
25	Export all data stored in a project so that it can be later imported into the same or a different instance of the system
26	Export the list of custom organism names to a file that can be later on imported into a different instance of this system
27	Export Generated sequence listing in human readable format (.html & .txt)
28	Generate sequence listing
29	Import a list of custom organism names from a file
30	Import all data stored in a project file
31	Import data from a ST.25 sequence listing file into a newly created project
32	Import data from a ST.26 sequence listing file into a newly created project
33	Import data from a FASTA file into an existing project
34	Import multiple sequences from a file in “one go”
35	Import into the current project (target project) the data from another project (origin project)

36	Parse a multi-sequence format sequence and review it returns the four parts (sequence name, molecule type, organism, and residues)
37	Print data from the project or generated ST.26 sequence listing
38	Provide location information to a selected feature
39	Provide the system with a string of residues containing invalid symbols and verify the process residues reformatted
40	Record data that has been changed upon import, so that the original data and the changed data can be displayed after import
41	Remove from the project all data associated with a sequence and renumber the remaining sequences accordingly
42	Set the "INSDQualifierMolType" attribute of a sequence to one of the predefined values
43	Set and store the system preferences (maximum number of residues symbols displayed per line, etc.)
44	Store in the system information about an applicant or inventor, (for example, name, its corresponding language code and its translation or transliteration into Latin characters (if applicable), address etc.) so that it can be used later in various projects;
45	Translate a nucleic acids sequence according to a specified genetic code table number
46	Verify a ST.26 sequence listing file and list the issues as a verification report containing warning and error messages;
47	Verify the data stored in a project and list the issues as a verification report containing warning and error messages;



---

## 3 TOOL OVERVIEW

### 3.1 TOOL MAIN ELEMENTS

This section details the main elements of the tool. The goal in providing this detail is for the user to be familiar with the common components provided within the desktop tool.

#### 3.1.1 Page

The Page is the main container for views within the tool. There are two main pages that contain views within them:

- Main Page
  - Projects list View
  - Persons and Organizations View
  - Custom Organisms View
  - Preferences View
- Project Page (accessible from the Projects View)
  - Project Detail View
  - Verification Report View
  - Free Text Qualifiers View
  - Import Report View
  - Display Sequence Listing View

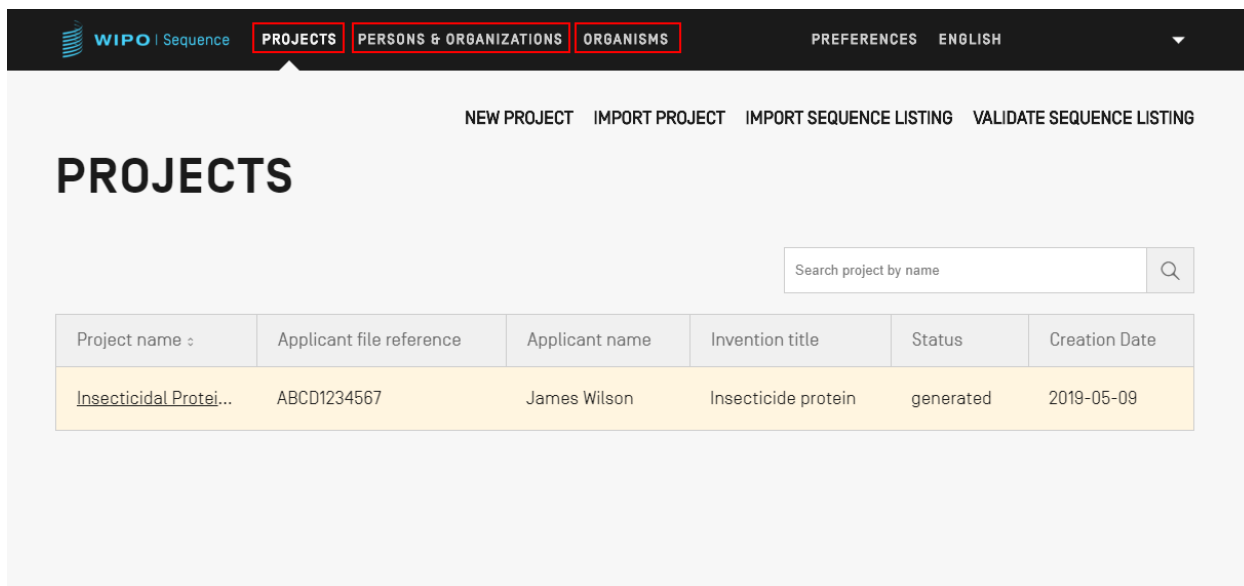


Figure 1 Main Page

### 3.1.2 View

The different displays of information that can be seen within a same page are termed Views.

### 3.1.3 Sections

Some views can have Sections. Sections provide a convenient way of compartmentalizing different parts of a large View.

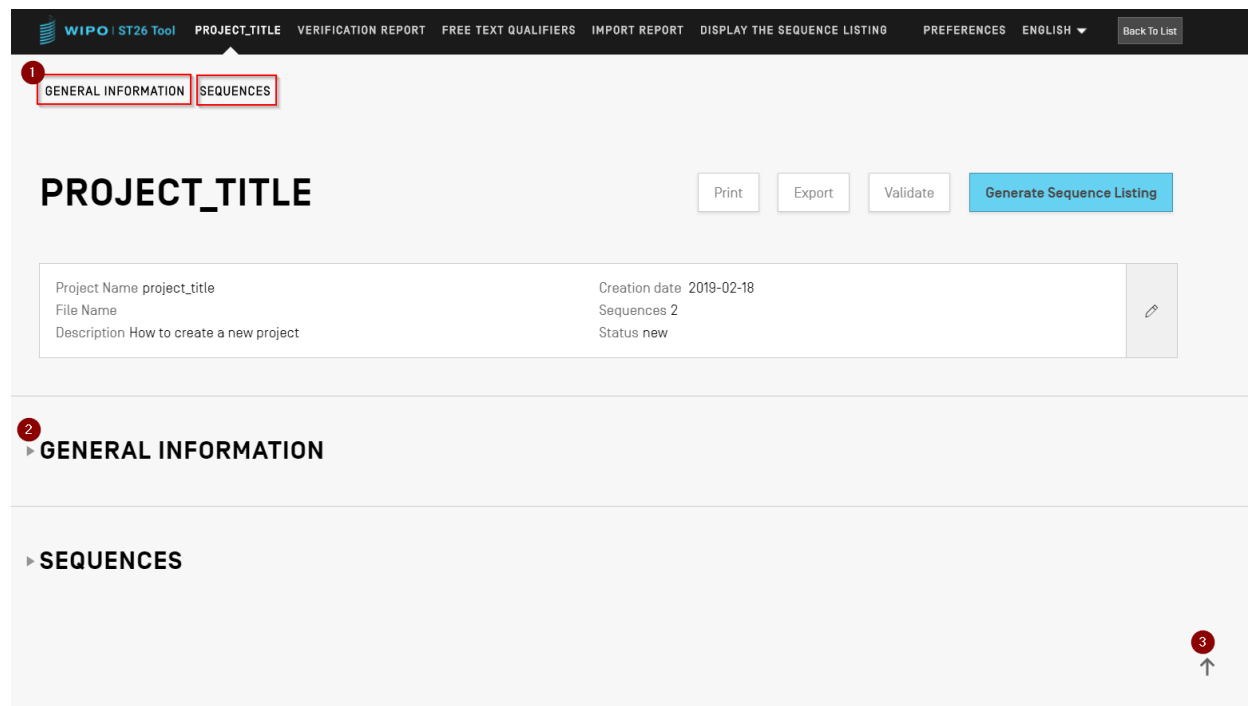


Figure 2 Project Detail view

Within the Project Detail View, shown in Figure 2, there are 2 collapsible sections: General Information & Sequences. At the top of the Project Detail View, there are two links that will navigate the user to the corresponding sections (1); each section is collapsible (indicated by the small triangle to the left) for the sake of ease of navigation (2); the user can click on the arrow icon to scroll to the top of the Project Detail view (3).

### 3.1.4 Overlay

When a Panel needs to be filled out or modified, sometimes an Overlay will appear over the current view, greying out the background as shown in the following example captured in Figure 3.

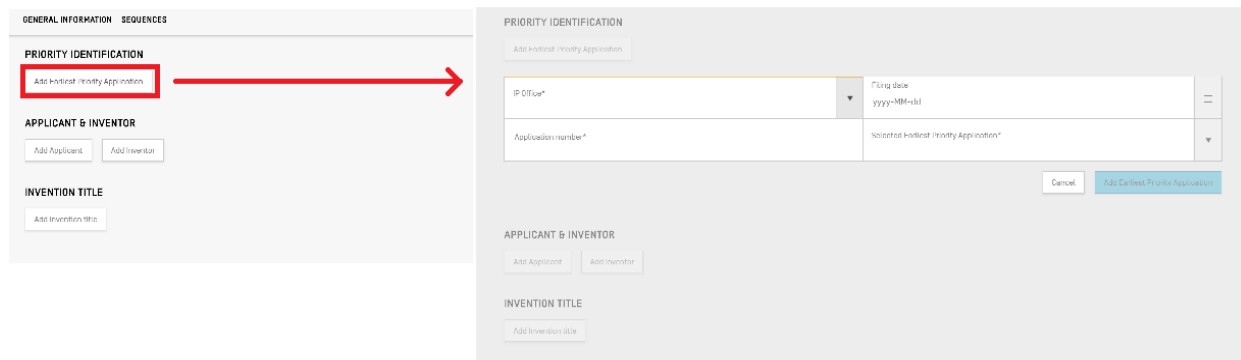


Figure 3 Overlay

When the Overlay is visible, all elements behind the Overlay are non-functional, and only the items in focus will be modifiable.

### 3.1.5 Tables

Name	Language Code	Name Latin	Residence Address	Correspondence Address
הילה בן אברהם	he - Hebrew	Hila Ben Avraham		
Juan Rodriguez Garcia	es - Spanish; Castilian		Spain, Valencia, Calle Cardenal ...	Spain, Valencia, Calle Cardenal ...
John Smith	en - English		England, Leeds, Eden Mount, 26	England, Leeds, Eden Mount

Figure 4 Tables

An example of a Table is shown in Figure 4. When search is enabled for the Table, the user can enter some search data and click on the search icon to the right of the search bar (1). To return to the full list of elements within the table, clear the search input box and click on the search icon (1).

The user can navigate through the pages of rows in a Table by clicking on the buttons below the table, in the case that all the entries do not fit in one page (2). To delete an entry in a Table, the user can click on the trash icon to the right of the corresponding row (3). To open the edit view

of an entry in a Table, the user must click on the underlined value in the row (underlining indicates it is clickable) (4).

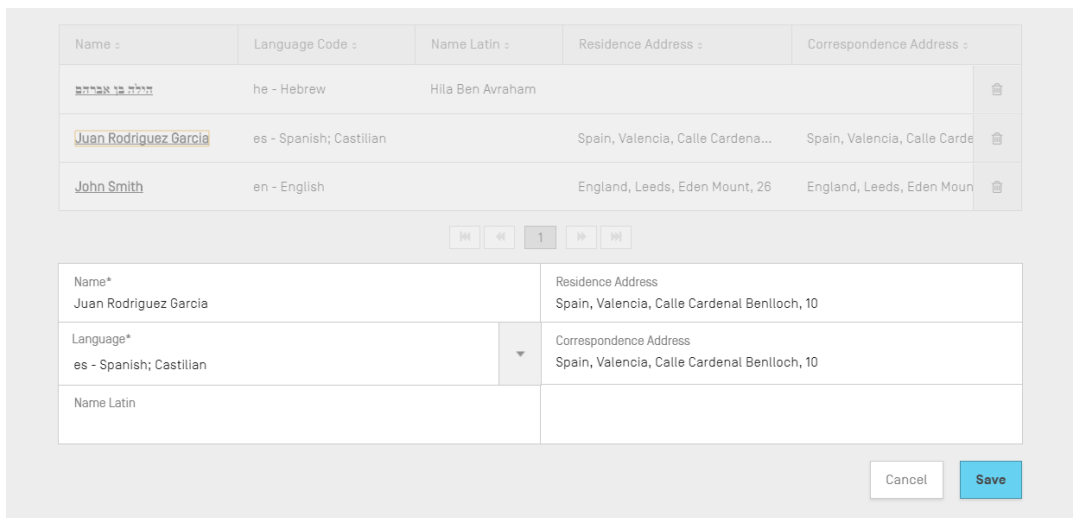


Figure 5 Table edit

Once this entry has been selected, an Overlay will appear over the screen and an editable panel will open beneath the Table.

### 3.1.6 Panel Views

Panel Views display a group of data. Items in a Panel View can be distributed across several columns. Each item has a label and a (optional) value.

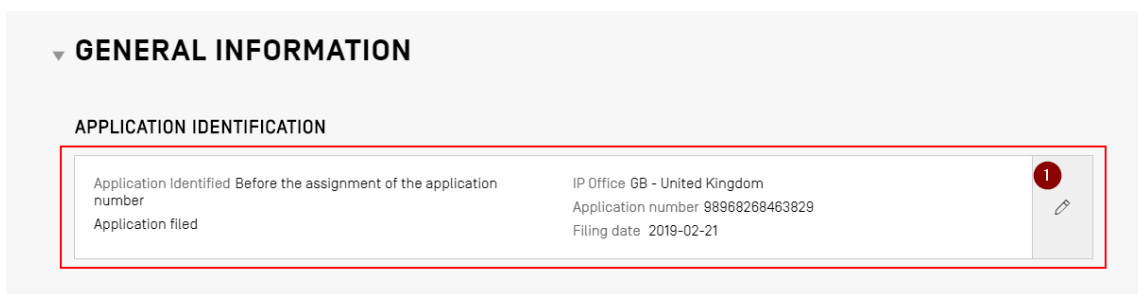


Figure 6 Panel View

As shown in Figure 6, when the button with the pencil icon (1) is clicked on a panel view, the Panel View is replaced with an Edit Panel.

### 3.1.7 Edit Panel

Once an Edit Panel has been opened, the fields that can be modified are presented to the user. Once the user has finished editing values, they will be able to either save the changes made, or discard them by clicking on the “Save” (1) or “Cancel” (2) buttons respectively (shown in Figure 7).

**Note:**

*Fields that are only for display, and not modifiable, will appear greyed out.*

▼ GENERAL INFORMATION

APPLICATION IDENTIFICATION

IP Office GB	Applicant file reference* ABC1234
Application Identification* <input checked="" type="radio"/> Before the assignment of the application number <input type="radio"/> After the assignment of the application number	Application File Reference is a mandatory field when 'Before the assignment of the application number' is provided.
Application number 98968268463829	Filing date 2019-02-21

Cancel Save

Figure 7 Edit Panel

### 3.1.8 Date Picker

Whenever a user is required to enter a date, they will use the Date Picker interface. By clicking on the calendar icon (1), the Date Picker component will open (2), as shown in Figure 8.

Year: 2019, Month: Feb

Calendar grid showing dates from 27 to 09.

Filing date: 2019-02-22

Figure 8 Date picker

The currently selected date is marked with a grey background (22<sup>nd</sup>), and the day of use is indicated with a black underline (26<sup>th</sup>). The first day of the week is considered to be a Sunday.

Conversely, the user can also simply type in the desired date in the appropriate format (“YYYY-MM-DD”) (3).

### 3.2 PDF READER

When a user prints a Verification report for a particular sequence listing, an Import report or Project information, a PDF file will be generated and opened in a PDF Reader. To download the file and save it, the user must click on the download icon at the top right of the viewer (1), shown in Figure 9.



Figure 9 PDF Viewer

### 3.3 KEYBOARD NAVIGATION

WIPO Sequence supports basic keyboard navigation. The 'TAB' key is used to navigate between items and the 'SPACE' key is used to select items.

## 4 MAIN PAGE

The main page of the tool consists of 3 main Views:

The **Project** View (Figure 10), the **Persons & Organizations** View (Figure 11) and the **Organisms** View (Figure 12).

The screenshot shows the 'PROJECTS' view. At the top, there is a navigation bar with 'PROJECTS' highlighted in a red box. Below the navigation bar, there are links for 'NEW PROJECT', 'IMPORT PROJECT', 'IMPORT SEQUENCE LISTING', and 'VALIDATE SEQUENCE LISTING'. The main heading is 'PROJECTS'. Below the heading is a search bar with the text 'Search project by name' and a magnifying glass icon. Below the search bar is a table with the following data:

Project name :	Applicant file reference	Applicant name	Invention title	Status	Creation Date :
Q	222222	Tom Jons	Copolymer including uncharged hydrophilic block	modified	2021-05-12
1	IMM343US1	LIU, DONGLIN	ANTI-MUCIN ANTIBODIES FOR EARLY DETECTION AND TREATMENT OF PANCREATIC CANCER	modified	2021-05-05
1000K	2093.1300PCT	CAMP4 THERAPEUTICS CORPORATION	IDENTIFICATION AND TARGETED MODULATION OF GENE SIGNALING NETWORKS	new	2021-06-02
10^11	AB123	Tom Jons	Copolymer including uncharged hydrophilic block	modified	2021-06-03

Figure 10 ProjectsView

The screenshot shows the 'PERSONS & ORGANIZATIONS' view. At the top, there is a navigation bar with 'PERSONS & ORGANIZATIONS' highlighted in a red box. Below the navigation bar, there are links for 'CREATE NEW PERSON OR ORGANIZATION'. The main heading is 'PERSONS & ORGANIZATIONS'. Below the heading is a search bar with the text 'Search person or organization by name' and a magnifying glass icon. Below the search bar is a table with the following data:

Name :	Language Code :	Name Latin :	Residence Address :	Correspondence Address :
Джо. Смит				
Джейн. Эйр				
Влад	ru - Russian	test name		

Figure 11 Persons& Organizationspage



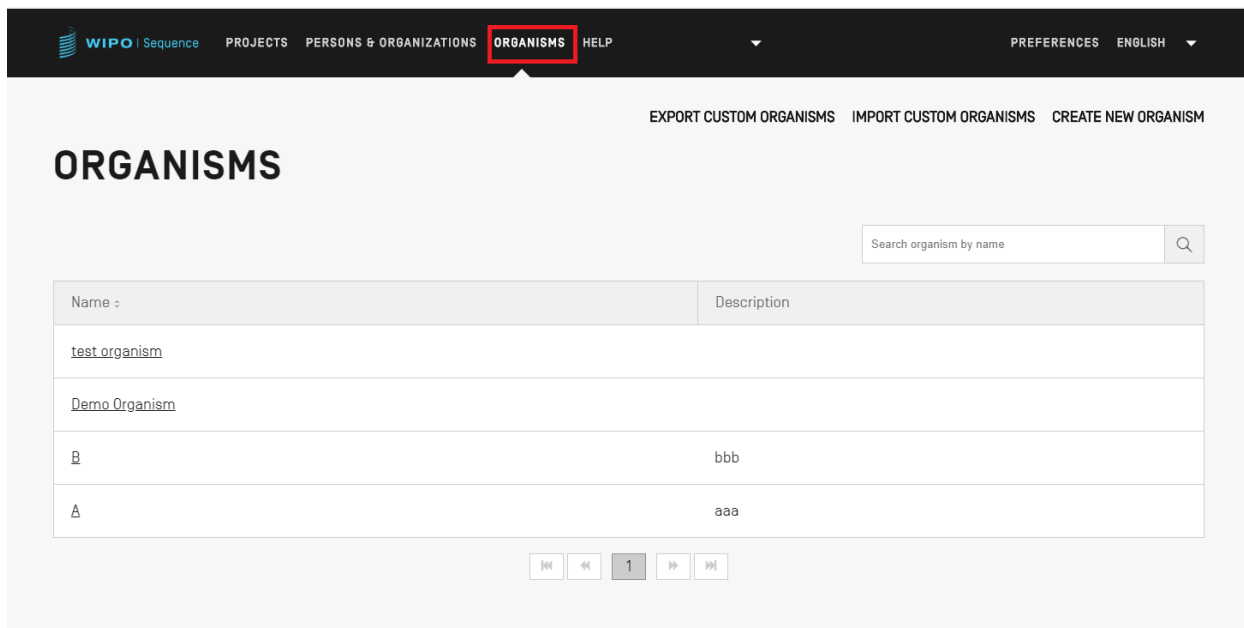


Figure 12 Organismsview

## 4.1 PROJECTS VIEW

This section details the different options accessible in the Projects View.

A project is the object structure that the tool uses to store data necessary to generate a sequence listing. The tool uses data stored in the project, once this data has been validated as compliant with WIPO Standard ST.26, as the values within the generated sequence listing.

### 4.1.1 Create Project

To create a new project, the user must begin from the main Projects list View (see Figure 13).

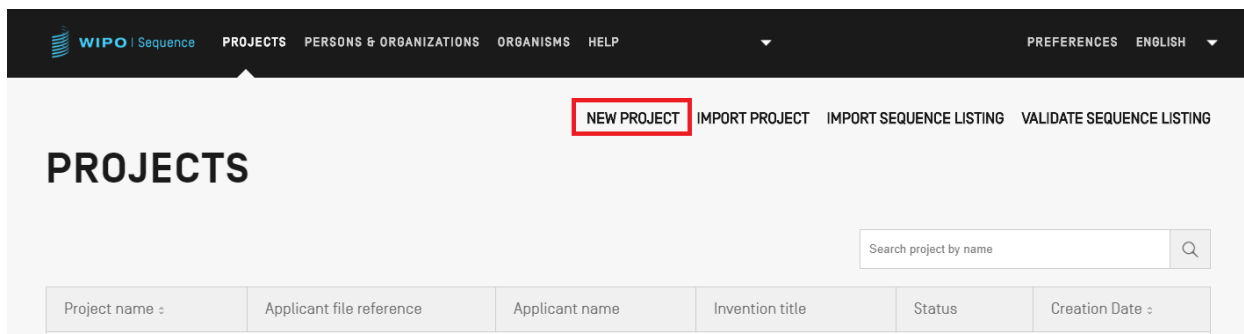


Figure 13 New project (a)

- 1) Click on the “NEW PROJECT” link at the top of the View indicated in Figure 13. In the following view, the tool will request a Name (mandatory) and a Description (optional).

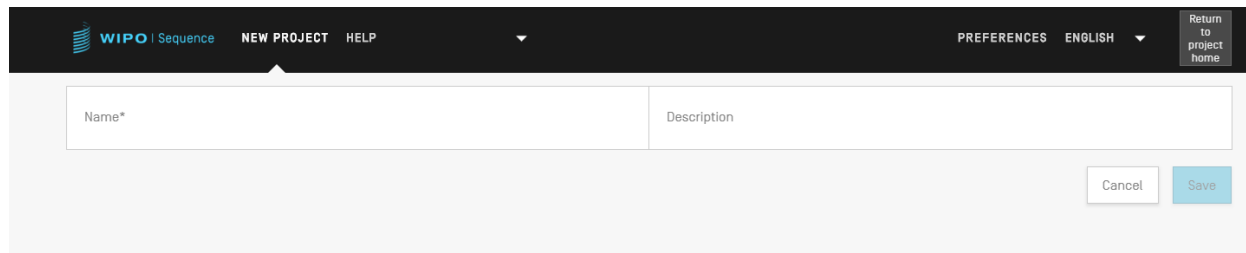
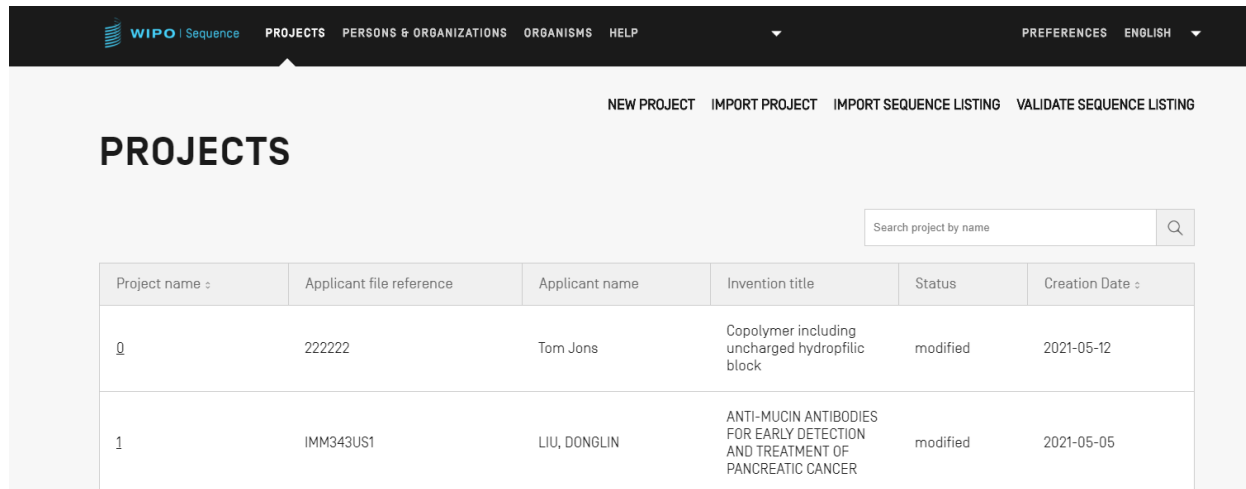


Figure 14 New project (b)

- 2) When a value is entered in the name field, the “Save” button will be enabled for the user to save the new project. The list of projects which includes this new project is shown in Figure 15.



Project name	Applicant file reference	Applicant name	Invention title	Status	Creation Date
0	222222	Tom Jons	Copolymer including uncharged hydrophilic block	modified	2021-05-12
1	IMM343US1	LIU, DONGLIN	ANTI-MUCIN ANTIBODIES FOR EARLY DETECTION AND TREATMENT OF PANCREATIC CANCER	modified	2021-05-05

Figure 15 New project (c)

## 4.1.2 Import Project

This functionality allows the import into the tool of a previously exported project as described in section 5.1.1.4 Export Project. To import a project file, the user must begin from the Projects list View.

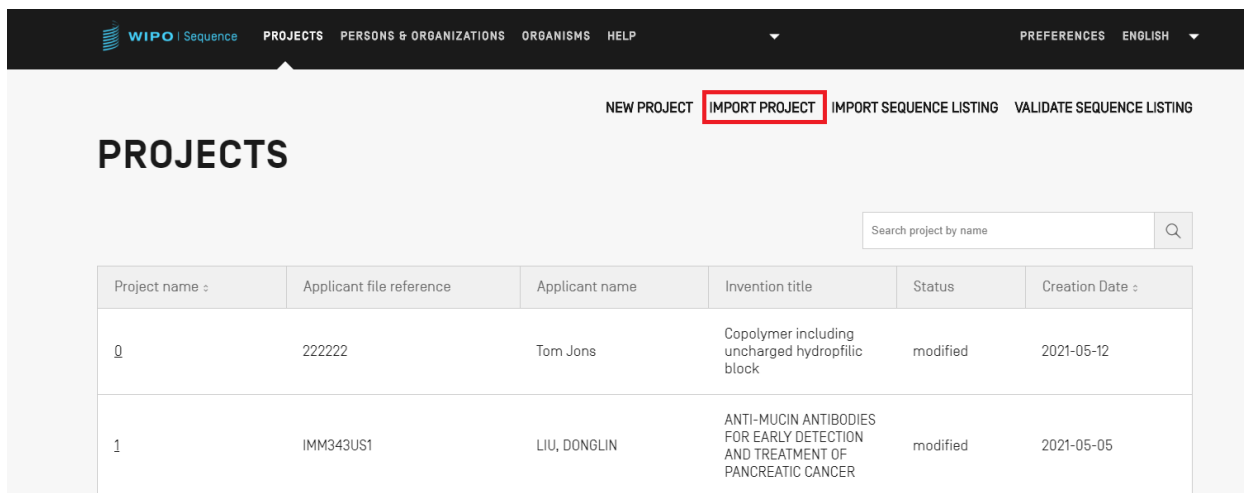


Figure 16 Import project

- 1) Click on the “IMPORT PROJECT” link at the top of the view as indicated in Figure 17.

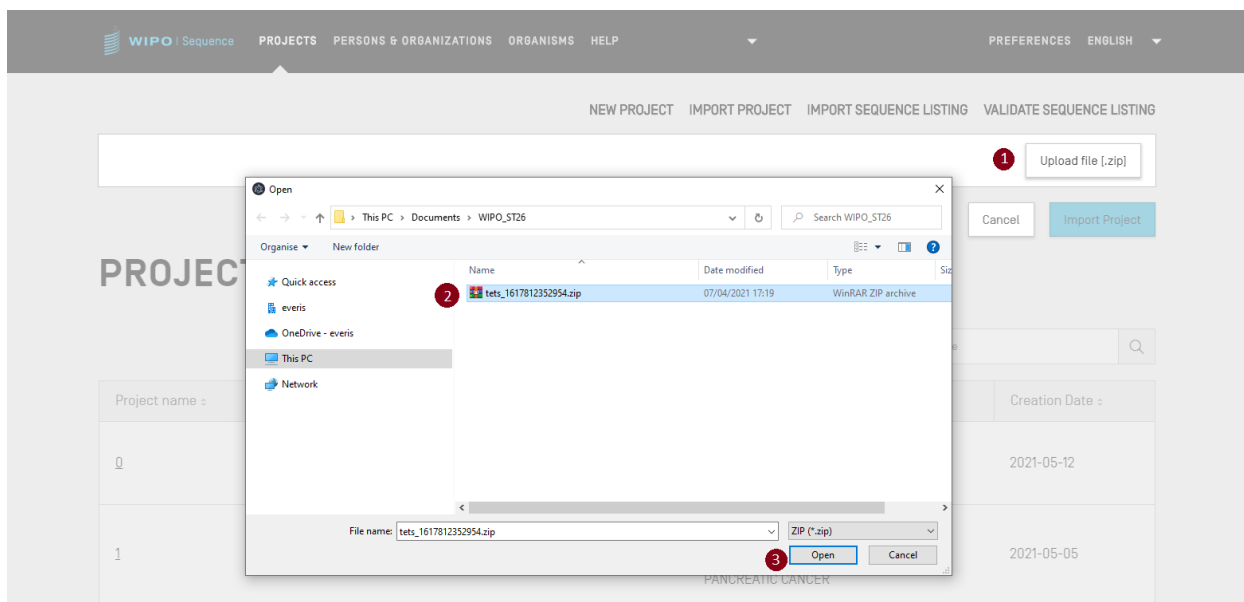


Figure 17 Import project dialog box

- 2) On the Overlay screen shown in Figure 17, click the “Upload file [.zip]” button (1).
- 3) In the dialog box that opens, shown in Figure 18, select the project file to be imported (2 & 3).

2008\_1617871543027.zip

Select Range of Sequence IDs

Sequence Number [ID]	Position
1	
2	

<< < 1 > >>

Select Range of Sequence IDs [Empty is All].

Use "," to separate yours ids selection, to select a range use "-" between the ids

Figure 18 Import project sequence select

- 4) If “Select Range Sequences” remains unchecked, all the sequences will be imported. If the user wishes to select which sequences to import into the project, check the “Select Range Sequences” checkbox (1) and enter the ID numbers of the desired sequences in the appropriate field (2) shown in Figure 19. A single sequence can be entered, as well as a list of sequences separated by commas or a range of sequences in the form x-y.

Example: “1, 3, 7, 13-20, 30-50”

- 5) The final step is to click on the blue “Import Project” button (3), as shown in Figure 19.

If the project is successfully imported, the following blue banner and message will appear at the top of the View.

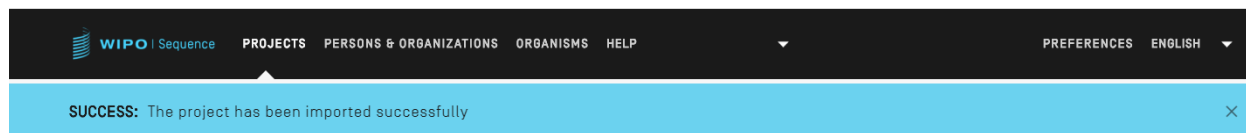


Figure 19 Import project banner

Known issue: System generate a lot of unexpected errors while importing the project: it is not clear what the error is. Possibly no error in the code, but this error is most of the times due to the tool that is hanging. Suggestion to add a 'please try again' message.

### 4.1.3 Import Sequence Listing

From the Projects View, the user can import exclusively the sequence information from a ST.26 **or** ST.25 compliant sequence listing. The file formats for each are \*.xml for ST.26 format and \*.txt for ST.25 files.

- 1) First, click the “IMPORT SEQUENCE LISTING” button at the top of the view shown in Figure 20.

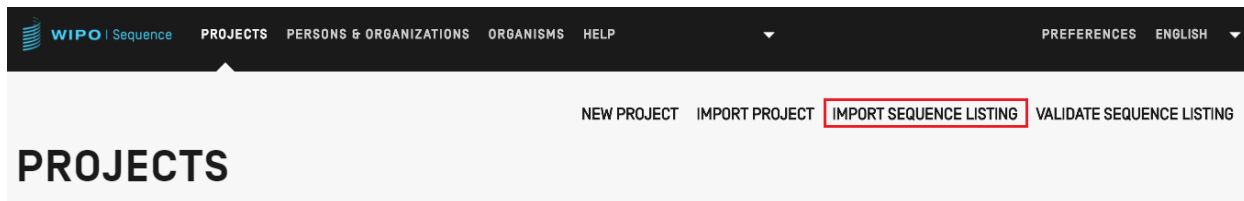


Figure 20 Import sequence listing

- 2) In the Overlay that opens, click on the “Upload file ST.25 [.txt] or ST.26 [.xml]” button (1), and select the desired sequence listing file in the dialog box that opens (2). Then enter a name for the new project that is being created under the name given in the “Project Name” field (3).

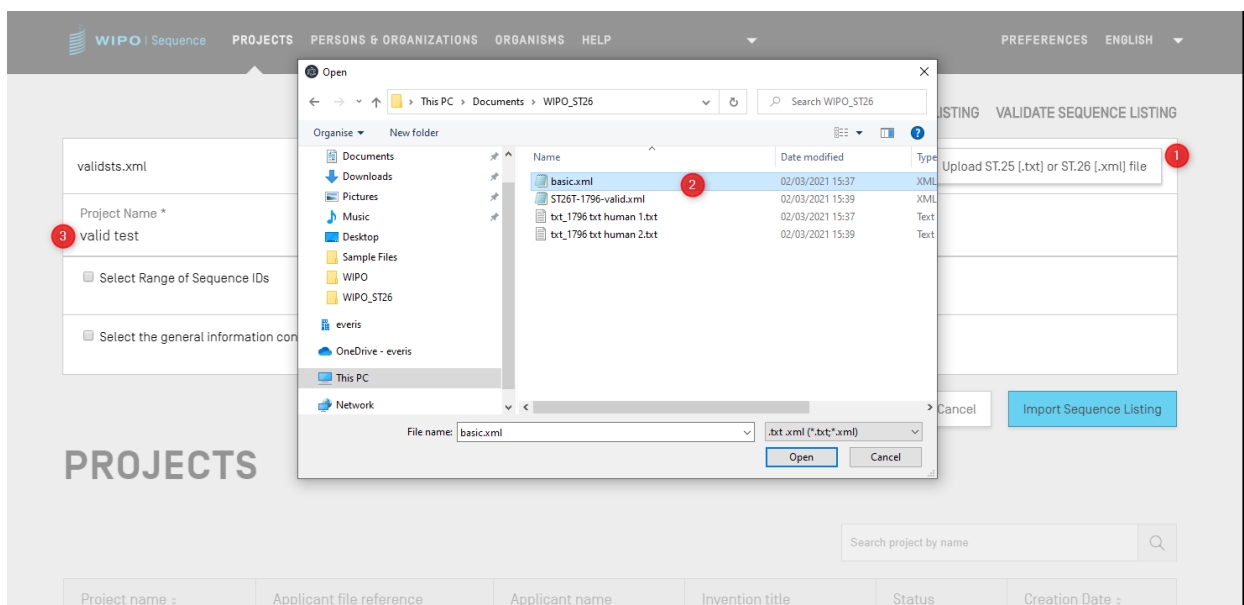


Figure 21 Import sequence listing (dialog box)

Two primary checkboxes shown in Figure 22 will allow the user to specify which sections are to be imported into the new project, “Select Range Sequences” and “Select the general information contents to be imported”.

validation\_testing\_app2.xml Upload ST.25 [.txt] or ST.26 [.xml] file

Project Name  
Insecticidal Protein Project

Select Range Sequences

Sequence Number [ID]	Position
[1]	1
[2]	2
[3]	3

⏪ ⏩ 1 ⏪ ⏩

Select range Sequence ID Numbers (Empty is All)

Use "," to separate yours ids selection, to select a range use "-" between the ids

Select the general information contents to be imported

Cancel Import Sequence Listing

Figure 22 Import sequence listing, select range

The first checkbox will allow the user to enter which specific sequences they wish to import from the sequence listing. A single sequence can be entered, as well as a list of sequences separated by commas or a range of sequences in the form x-y.

Example: "1, 3, 7, 13-20, 30-50"

The Table shown in Figure 22 has two columns, one gives the Sequence ID Number to identify the corresponding sequence and the other gives the "position" in which it will appear in the sequence listing.

Project Name  
Insectidal Proteins |

Select Range Sequences

Select the general information contents to be imported

<input checked="" type="checkbox"/>	Element	Origin Element Value	Target Element Value
<input checked="" type="checkbox"/>	Application Identification		IP Office = GB Application number = 34892756 Filing date = 2019-05-02
<input checked="" type="checkbox"/>	Applicant File Reference		Applicant file reference = ABCD1234567
<input checked="" type="checkbox"/>	Earliest Priority Application Identification		IP Office = GB Application number = 128432643875345 Filing date = 2019-05-01
<input checked="" type="checkbox"/>	Applicant Name		Name = James Wilson
<input checked="" type="checkbox"/>	Invention Title Bag		Invention title = Insecticide protein, Language code = en

The data for the selected attributes will be overwritten

Figure 23 Import Sequence Listing, select General Information

Checking the second checkbox will enable a list of additional checkboxes which allow the user to individually select which properties are to be imported or ignored, as shown above in Figure 23.

3) Finally, click on the blue “Import Project” button to create the new project.

If the Sequence listing was imported correctly, the Change Data Table shown in Figure 24 will be displayed informing the user of the automatic changes made to the ST.25, multi-sequence and raw sequence listing data during import, in order to adapt it to the requirements of ST.26.

**Import Report** Print Report

**Change Data**

Origin Tag	Origin Element Name	Origin Element Value	Target Element Name	Target Element Value	Transformation	Sequence ID Number
INSDQualifier	ID		Qualifier ID	q1	The qualifier ID was created since one was not specified.	1

⏪ ⏴ 1 ⏵ ⏩

Figure 24 Import sequence listing, Change data

If the file format was ST.25, then the Import Report View will include an Import Report Table first, as well as the Change Data Table. An example of the Change Data report is shown in Figure 24 and an example Import Report is shown in Figure 25.

**Import Report** Print Report

**Import Report Messages**

Type of Note	Data Element	Message Text	Detected Sequence
Global		Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences.	
Global	<222>	The following transformations have been applied to the location values: removed parentheses, replaced '-' and '...' with '.', and simplified all single residue locations, e.g. '[5].[5]' replaced by '5'.	
Global	<221>	Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences.	

Figure 25 Import sequence listing, Import report

At this point, the user can return to the Projects View (2) or print a report of these changes in PDF format (1): see Figure 25.



For instructions on how to download the PDF file, see section **2.2**.

Conversely, the import process can fail if there are errors in the sequence listing file. In this case, after attempting to import, the user will be notified with a red banner indicating an error has occurred during import, see Figure 26. .

The screenshot shows the WIPO Sequence web application interface. At the top, there is a navigation bar with the WIPO logo and menu items: PROJECTS, PERSONS & ORGANIZATIONS, ORGANISMS, HELP, PREFERENCES, and ENGLISH. Below the navigation bar, a red error banner displays the message: "ERROR: An error occurred while importing the ST.25 sequence listing." Below the error banner, there are navigation links: NEW PROJECT, IMPORT PROJECT, IMPORT SEQUENCE LISTING, and VALIDATE SEQUENCE LISTING. The main heading is "PROJECTS". Below the heading is a search bar with the placeholder text "Search project by name" and a magnifying glass icon. Below the search bar is a table with the following data:

Project name :	Applicant file reference	Applicant name	Invention title	Status	Creation Date :
<a href="#">qv_42_xqv_42</a>	AB123	Tom Jons	Copolymer including uncharged hydrophilic block	new	2021-07-07

Figure 26 Import ST.26 sequence listing, Import report

Please **note** that for importing a Sequence Listing, the ST.26 files should comply with the following requirements:

- Must be encoded in UTF-8 and must contain valid characters according to XML 1.0 specification<sup>1</sup>
- Must contain a DOCTYPE line as follows:

```
<!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.3//EN"
"ST26SequenceListing_V1_3.dtd">
```

- Attribute dtdVersion should be compliant with the DTD version:

```
<ST26SequenceListing dtdVersion="V1_3"...
```

- The file must comply with DTD file ST26SequenceListing\_V1\_3.dtd.

<sup>1</sup> See <https://www.w3.org/TR/2006/REC-xml-20060816/Overview.html#charsets>

#### 4.1.4 Validate Sequence Listing

The user can validate an ST.26 sequence listing file by clicking on the “VALIDATE SEQUENCE LISTING” button at the top right of the Projects View, shown in Figure 27.

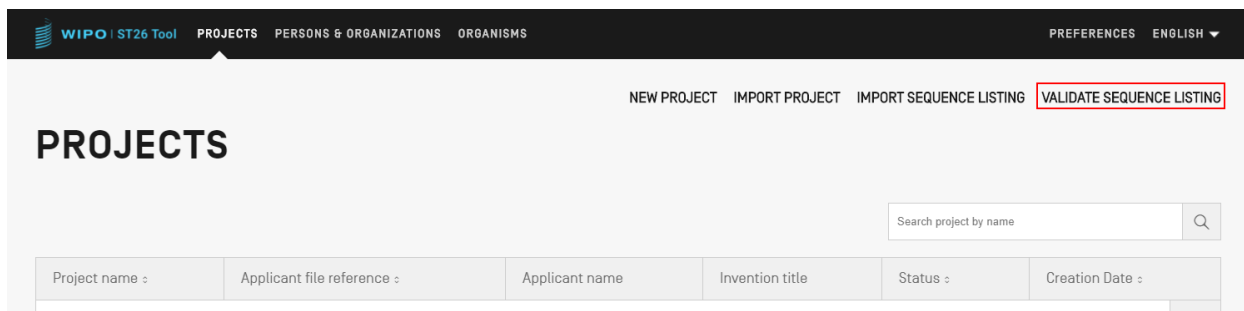


Figure 27 Validate sequence listing

Next, the user must click on the “Upload file ST.26 [.xml]” button (1), and then select the file in the dialog box (2).

Lastly, click the “Validate Sequence Listing” button (3).

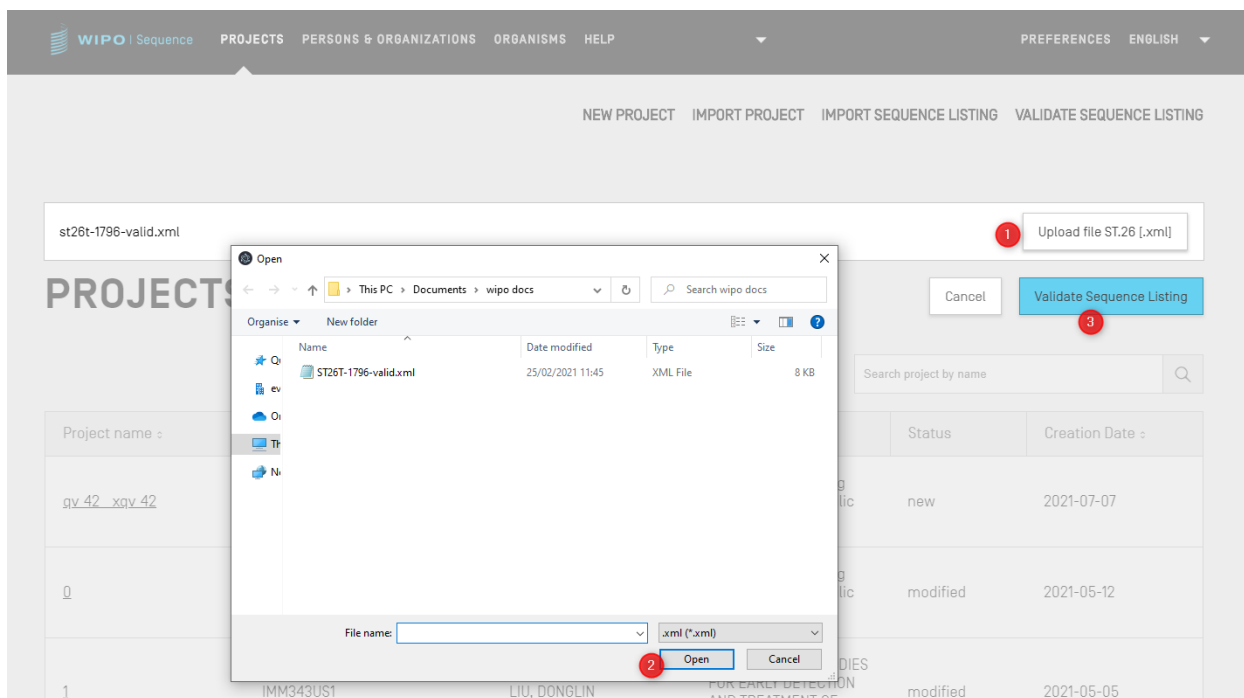


Figure 28 Validate sequence listing (dialog box)

If the sequence listing passes validation, a banner will appear as shown in Figure 29:

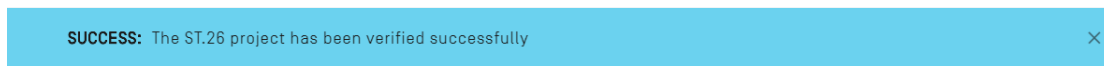


Figure 29 Validate sequence listing, Success banner

If the sequence listing fails the validation, a verification report will be opened in the user's browser with the validation errors listed in a table as shown in Figure 30.

**VERIFICATION REPORT**

**FILE INFORMATION**

Production date	2019-07-17
Verification Report XML file path	C:\Users\bmcmlle\AppData\Roaming\ST26_authoring\Invalid_project.xml
Verification Report HTML file path	C:\Users\bmcmlle\AppData\Roaming\ST26_authoring\Invalid_project.html

**VERIFICATION MESSAGES**

Severity	Data Element	Message	Detected Value	Detected Sequence
WARNING	Qualifier Value	Verify that the value for the qualifier 'lab_host' contains the full binomial scientific name for the host organism.	source_free_text	1
ERROR	Qualifier Value	The mandatory qualifier value for qualifier EC_number is missing.		1
WARNING	Qualifier Value	Verify that the value for the qualifier 'EC_number' is in the format specified in WIPO ST.26 Annex I, Section 6, for this qualifier.	mat_peptide_free_text	1
WARNING	Feature Qualifiers	Verify that the 'note' qualifier describes the 'OTHER' value for the 'mod_base' qualifier.	modified_base_free_text	1
WARNING	Qualifier Value	Verify that the value for the qualifier 'frequency' is a fraction.	modified_base_free_text	1
WARNING	Feature Qualifiers	Verify that the 'note' qualifier describes the 'OTHER' or 'other' value for the "ncRNA_class", recombination_class, or regulatory_class qualifiers.	ncRNA_free_text	1

Figure 30 Validate sequence listing, verification error table

The location of the HTML file will be displayed in the navigation bar (1) of the user's browser in case the user wishes to copy the file to a different location.

The user must allow internal script to be run on his machine for the format to display correctly, ActiveX control on IE browser. It should be clicked to: 'allow blocked content' for the format to load correctly.

Please **note** that for validating a Sequence Listing, the ST.26 file should comply with the following requirements:

- Must be encoded in UTF-8 and must contain valid characters according to XML 1.0 specification
- Must contain a DOCTYPE line as follows:

```
<!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.3//EN" "ST26SequenceListing_V1_3.dtd">
```

- Attribute dtdVersion should be compliant with the DTD version:
- The file must comply with DTD file ST26SequenceListing\_V1\_3.dtd.

### 4.1.5 Delete Project

To delete a project, the user must begin from the Projects View, shown in Figure 31.

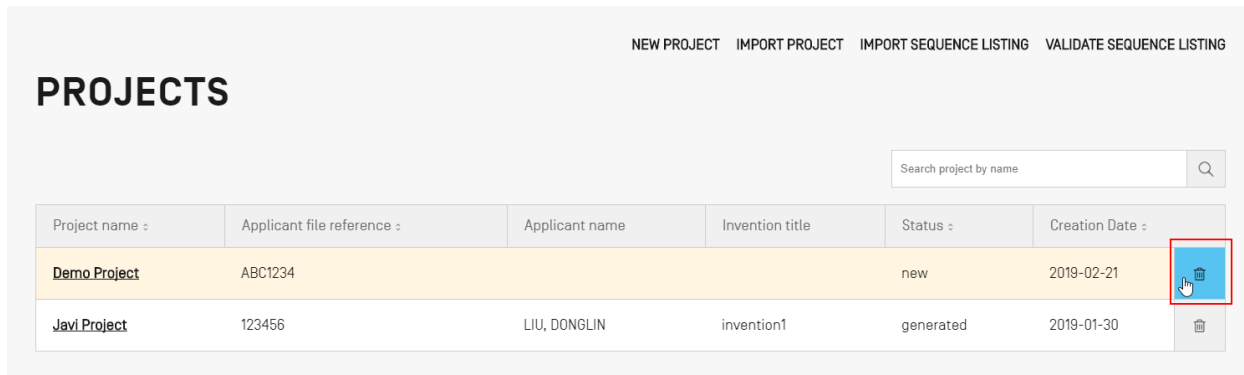


Figure 31 Delete project

Click on the button with the trash can icon on the row within the Projects View Table that the user wishes to delete.

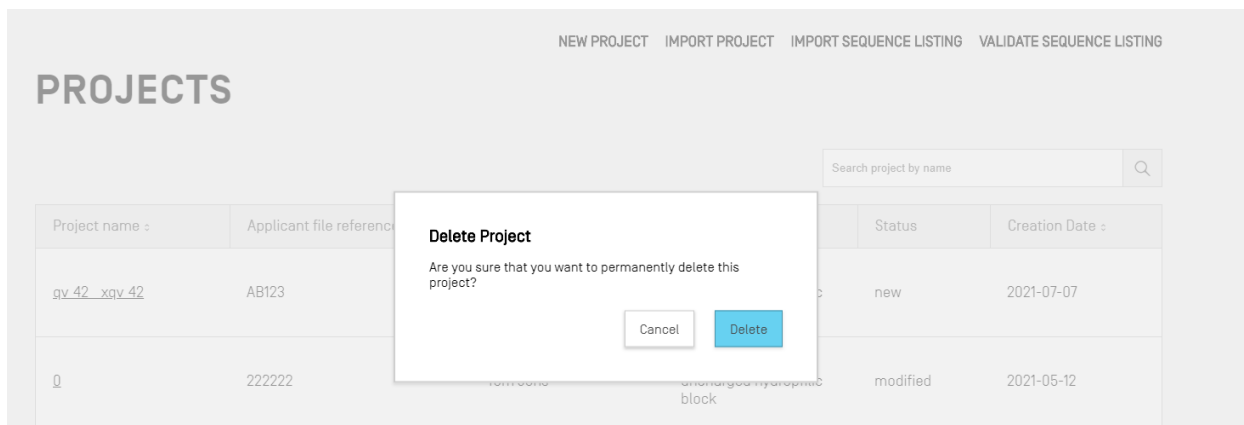


Figure 32 Delete project (confirmation)

In the pop-up click “Delete” to confirm that you want to delete the selected project.

## 4.2 PERSON & ORGANIZATIONS

### 4.2.1 Create

To create a new Person or Organization, the user must begin from the Persons & Organizations View.

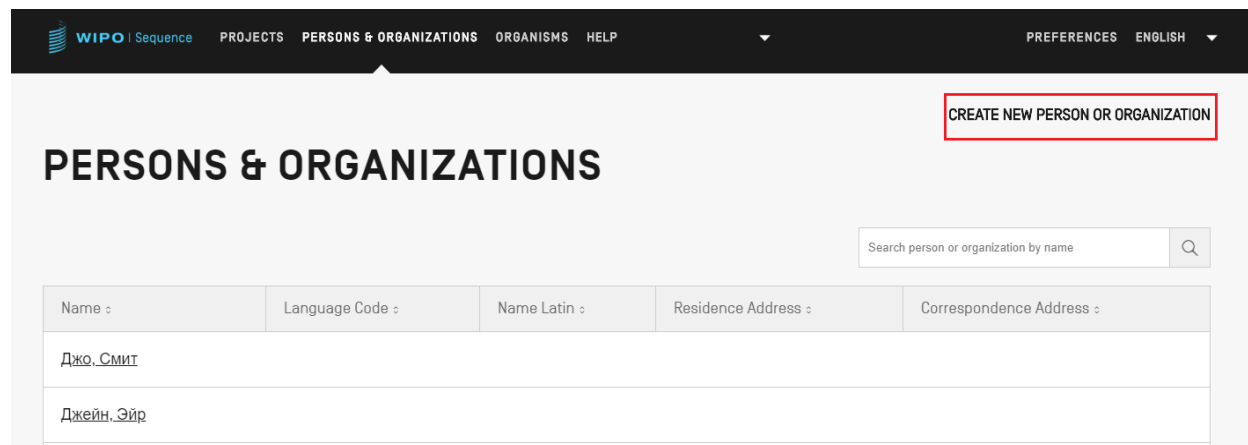


Figure 33 Create new person/organization

First, the user must click on the “CREATE NEW PERSON OR ORGANIZATION” link at the top of the View, as shown in Figure 34.

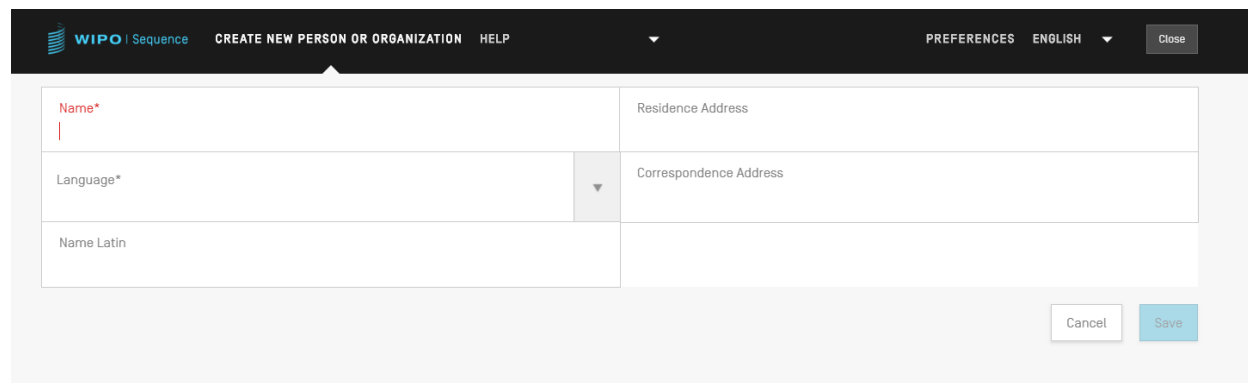


Figure 34 Create new person/organization Panel

In the new View, the user must at least fill in the mandatory fields (indicated with a ‘\*’) corresponding to the details of the new person/organization.

When the name of the person or organization is not in Latin characters, then the Latin version of the name should be provided in the “Name Latin” field. If this information is not provided then the project will not validate when the ST.26 sequence listing is generated.

### 4.3 CUSTOM ORGANISMS

To create, edit, import, export or delete Custom Organisms, the user must begin from the Organisms View.

#### 4.3.1 Create Custom Organism

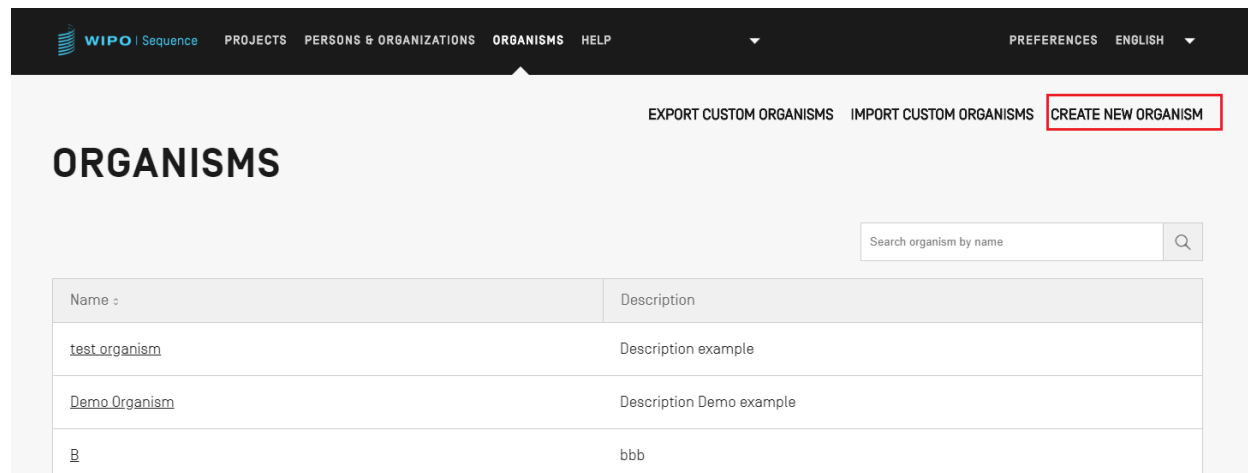


Figure 35 Create new organism

To create a new custom organism, click the “CREATE NEW ORGANISM” link at the top of the view, shown in Figure 35. In the screen that follows (Figure 36), enter the name of the new Organism and click “Save”.

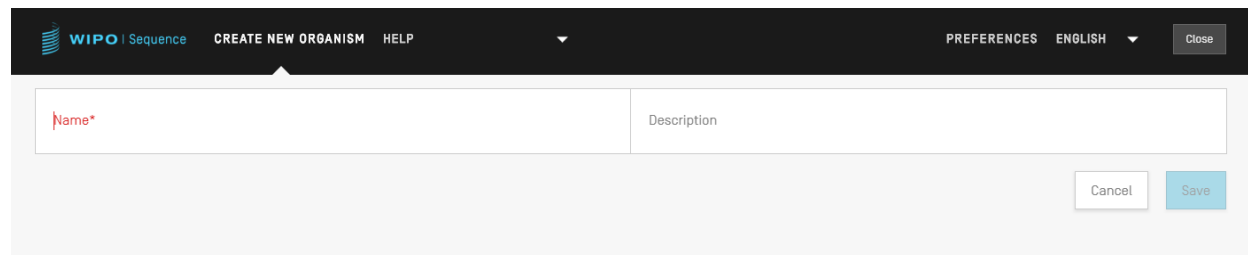


Figure 36 Create new organism (form)

#### 4.3.2 Export Custom Organisms

All the custom organisms and their description that are stored in the tool can be exported and saved to a text file to be modified outside the tool or imported on a later date. To export this list, start by selecting 'EXPORT CUSTOM ORGANISMS', as highlighted in Figure 37:

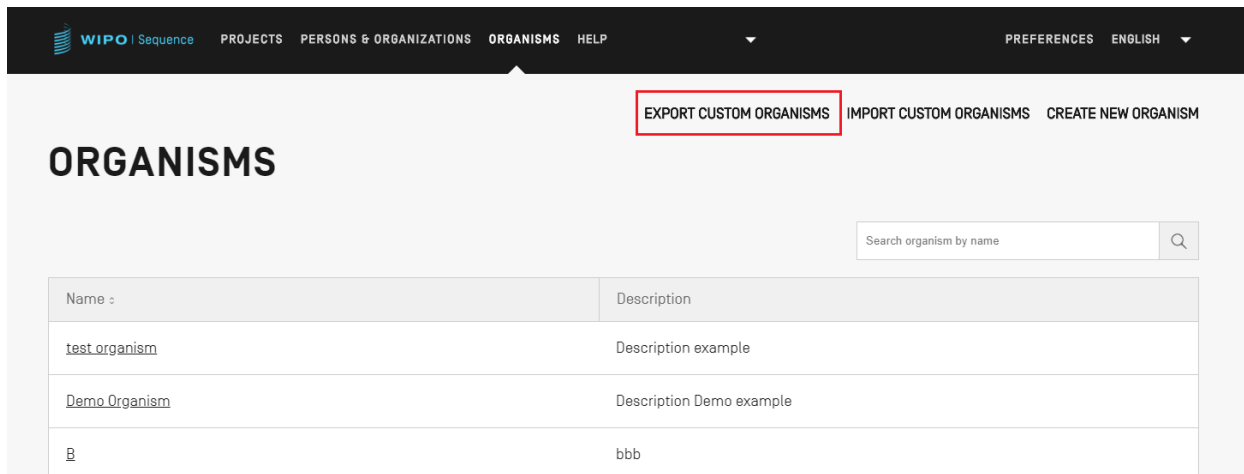


Figure 37 Export custom organisms

Next, a dialog box will open allowing the user to choose the name of the file and the desired file location, see Figure 38.

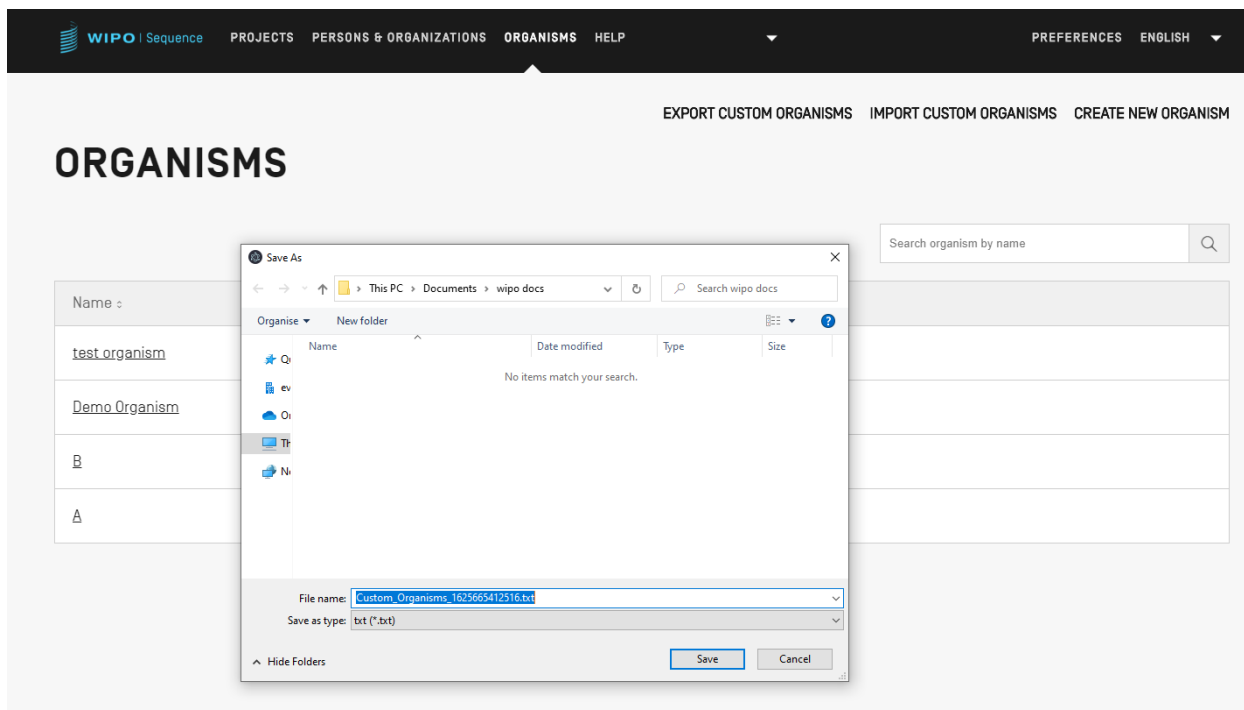
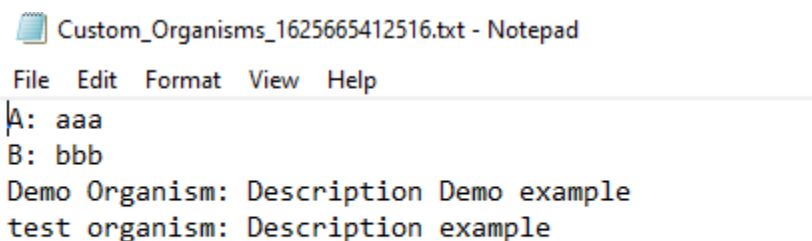


Figure 38 Export custom organisms dialog box

The file that is exported is txt file including both the name and the description of the organism which could be Edited and imported into the tool (see Figure 39).



```
Custom_Organisms_1625665412516.txt - Notepad
File Edit Format View Help
A: aaa
B: bbb
Demo Organism: Description Demo example
test organism: Description example
```

Figure 39 Example of Custom organism file

### 4.3.3 Import Custom Organisms

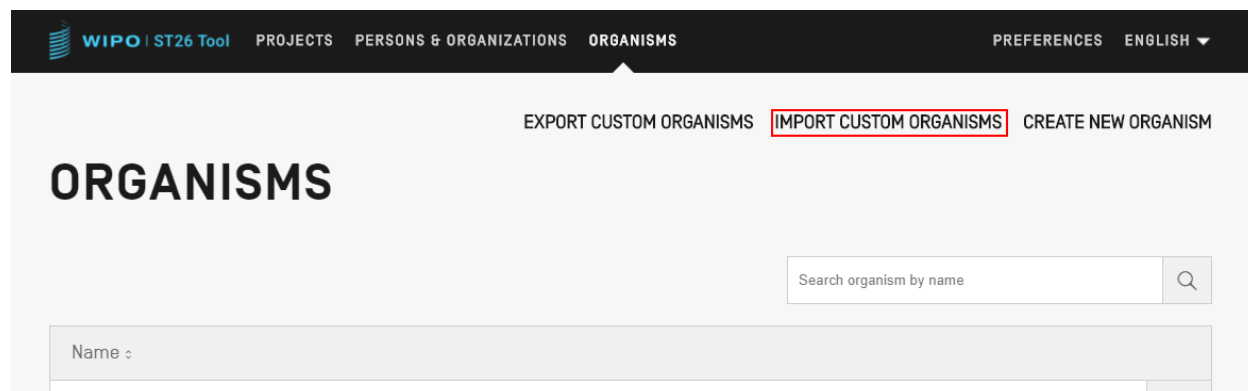


Figure 40 Import custom organisms

Firstly, in order to import a list of custom organisms, the user must click on the “IMPORT CUSTOM ORGANISMS” link at the top of the View, as shown in Figure 40. This will open an Overlay below the Organisms Table, as shown in Figure 41.



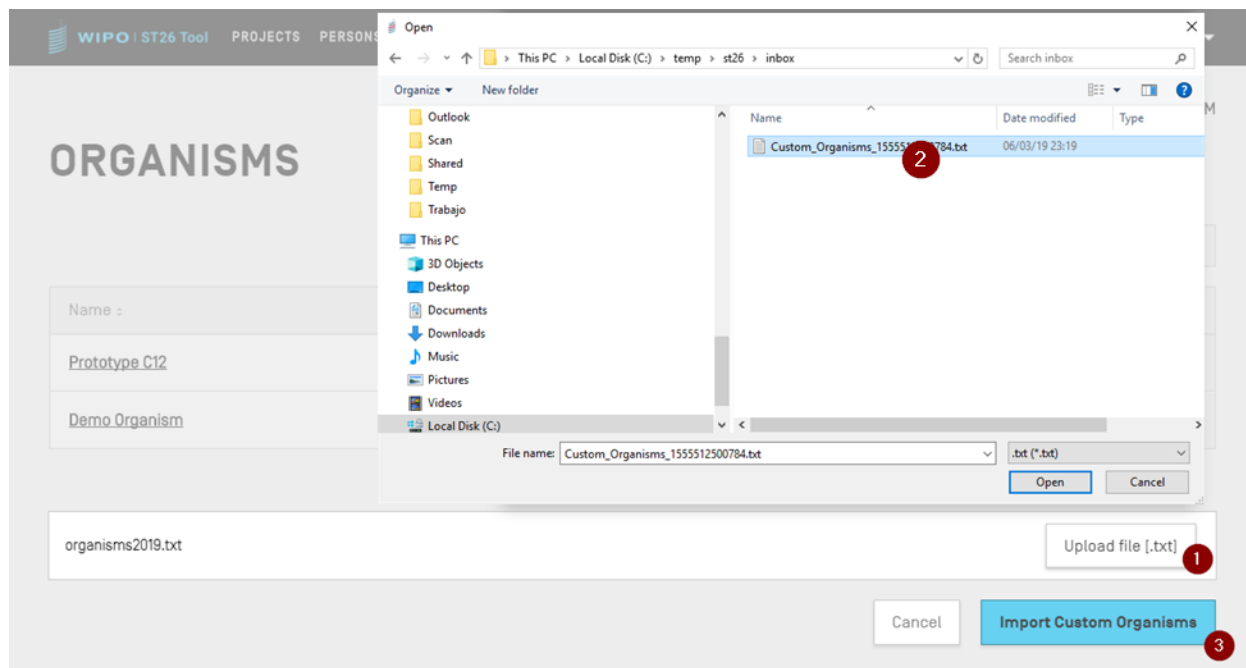


Figure 41 Import custom organisms(dialog box)

- 1) Click on the “Upload file [.txt]” button (1)
- 2) Select the file with the custom organism names from within the dialog box (2)
- 3) Finally, click on the blue “Import Custom Organisms” button (3)

**Note:**

The file to be imported will be a text file (\*.txt) with a list of custom organism names in plain text (UTF-8), each item on a new line.

#### 4.4 SYSTEM PREFERENCES

The System Preferences View allows the modification of several configuration parameters of WIPO Sequence. These parameters will apply to every project created or edited by the tool (see Figure 42).

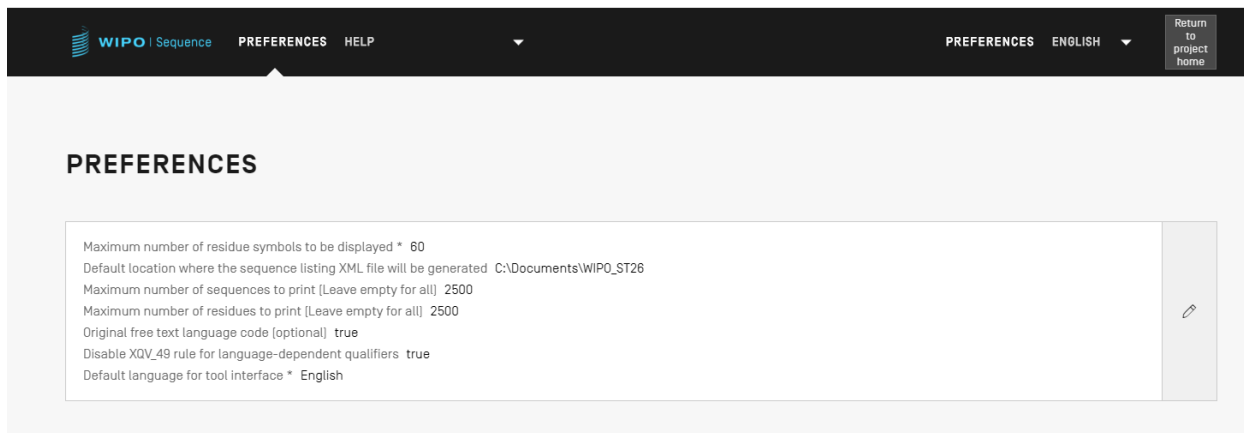


Figure 42 Summary of System Preferences

In order to modify the system preferences, the user should click on the pencil icon shown above to open the Edit Panel shown in Figure 43:

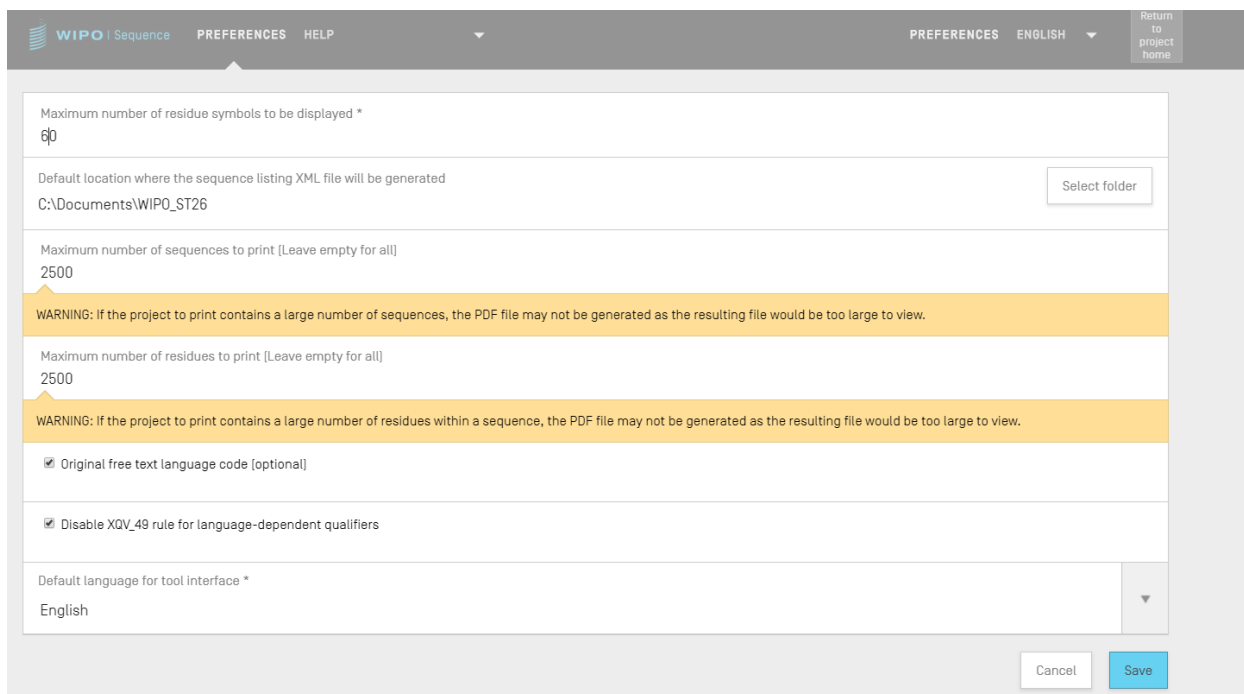


Figure 43 Configuring system preferences

The list of configuration items that can be modified from this View are:

- Maximum number of residue symbols to be displayed. This parameter sets the number of residues that will be displayed per row when displaying a sequence: the default is 60 residues;
- Default location where the ST.26 sequence listing file (.xml) will be generated;
- Maximum number of sequences to print (leave empty for all): default is 1000 sequences;
- Maximum number of residues to print (leave empty for all): default is 1200 residues.
- Original Free Text language code default : checked
- Disable XQV\_49 : checked
- Default interface language : English

---

---

**Note:**

*The 3<sup>rd</sup> and 4<sup>th</sup> items are relevant when Printing the project as a PDF. For very large sequence listings, the resulting PDF can have several thousand pages and be impossible to display.*

---

---

## 5 PROJECT PAGE

The project page is composed of six Views that can be used to navigate between different portions of the workflow, as shown in Figure 44:

1. Project Detail View (1) (indicated by the name of the project),
2. Verification Report View (2),
3. Free Text Qualifiers View (3),
4. Import Report View (4),
5. Display Sequence Listing View (5) and
6. Help Menu
7. Preferences View (6).

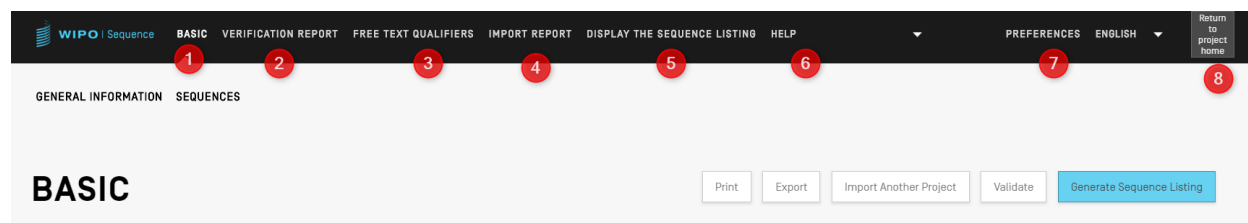


Figure 44 Project page header

To return to the Projects View (main home page), the user can click on the “return to project home” button (8) at the right end of the header.

### 5.1 PROJECT DETAIL

#### 5.1.1 Basic Information

A Table containing the basic information about the project can be found at the top of the Project Detail View, shown in Figure 45.

This section contains:

- Name of Project
- Date of Creation
- Project status (possible values: ‘new’/‘modified’/‘generated’/‘invalid’/‘valid’/‘warnings’)
- Name of the imported file (in the case that the project was imported)

- Project description
- Number of Sequences (labelled: ‘Sequences’)
- Source language code for free text qualifiers
- Non English free text language code
- Original free text language code
- Automatic add a translation qualifier when a CDS feature is created

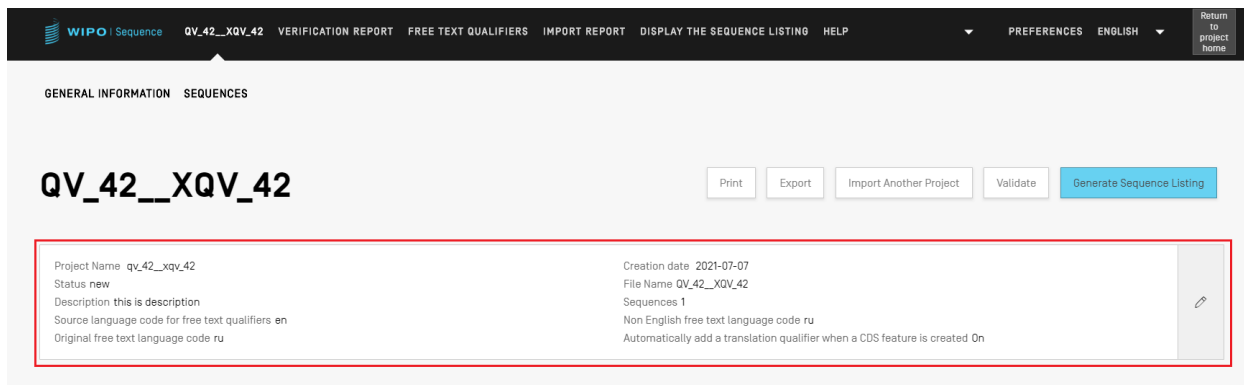


Figure 45 Basic Information Section

### 5.1.1.1 Print a project

To print a project, the user must enter the Project Detail View of the desired project and click on the “Print” button at the top of the view, see Figure 46.

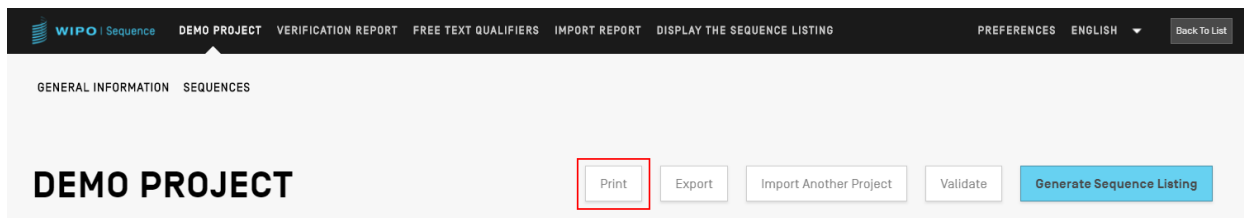


Figure 46 Print project

Next, the user will be shown two checkboxes to clarify what information the user wants to print from the project: General Information and/or Sequence Information (see Figure 47).

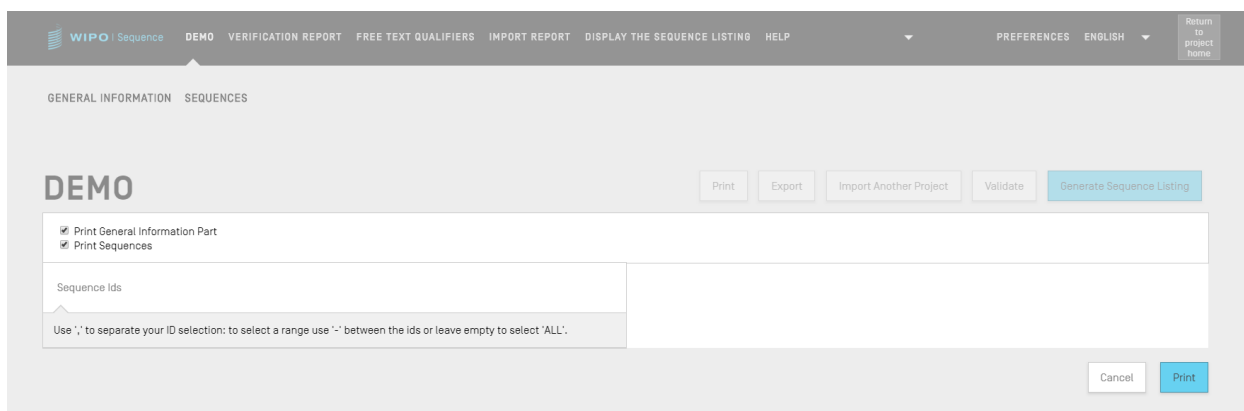


Figure 47 Print project, Section selection

If “Print Sequences” is selected, the user will have the choice to specify which sequences are to be printed by specifying the range of ID numbers within the “Sequence IDs” field, or simply print all if this field is left blank.

Once the blue “Print” button has been clicked, if the PDF file was generated correctly, the tool will open the file in a PDF reader for the user’s review.

For instructions on how to download the PDF file, see Section 3.2.

### 5.1.1.2 Import Information From Another Project

The user can copy information from other projects stored in the tool, into the currently open project. This imported information can be either the “General Information” Section, “Sequences” Section, or both.

*Note: imported General Information will replace the currently existing General Information in the project, while imported Sequences will be appended to the current list of sequences within the project.*

To begin, the user must click on the “Import Another Project” button at the top of the Project Detail View, see Figure 48.

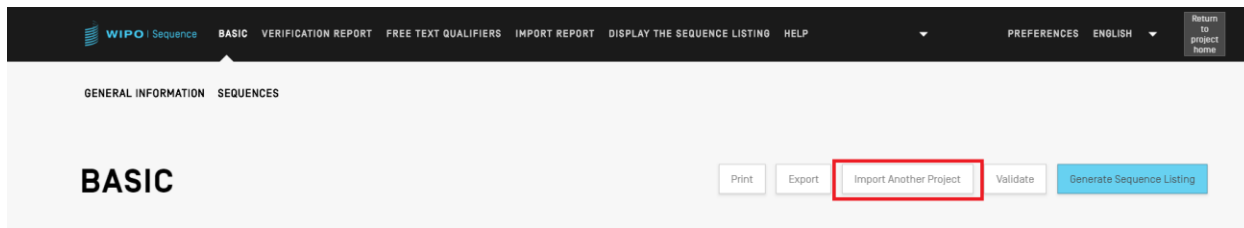


Figure 48 Import Another Project

The tool will open an Overlay, as shown in Figure 49. The user must first select the project from which they wish to import information.

**BASIC**

Print Export Import Another Project Validate Generate Sequence Listing

Project\*

Select the general information contents to be imported

Select the sequences to be imported. If the box is left unchecked then no sequences will be imported.

Cancel Import Project

Figure 49 Import Another Project, select target

Next, as shown in Figure 50, the user can select whether they wish to include parts of the details provided in the General Information (1) Section of the project and also enter a range of sequence ID numbers (2) to specify which of the sequences are to be imported into the project.

Project\*  
mixed

Select the general information contents to be imported

Select the sequences to be imported. If the box is left unchecked then no sequences will be imported.

1

Select Range of Sequence IDs (Empty is All).	Total Sequences
2	2

Use "," to separate yours ids selection, to select a range use "-" between the ids

Cancel Import Project

Figure 50 Import Another Project, Panel

If the General Information checkbox is checked then a Table will appear displaying all the General Information Section of both projects: the currently selected (origin) project, and the target project (destination).

The user must then select which of the General Information elements are to be replaced by the corresponding target project's General Information, as shown in Figure 51.

**BASIC**

Project\*  
mixed

Select the general information contents to be imported

<input type="checkbox"/>	Element	Origin Element Value	Target Element Value
<input checked="" type="checkbox"/>	Application Identification	IP Office = FR Application number = 1234	Application number = 18675309 Filing date = 2017-03-24
<input checked="" type="checkbox"/>	Applicant File Reference	Applicant file reference = 4586789415231	Applicant file reference = S3C test file
<input checked="" type="checkbox"/>	Applicant Name	Name = Mazinger Language code = tk	Name = Kalafus, Kathleen
<input checked="" type="checkbox"/>	Applicant List	Applicant name = Mazinger	Applicant name = Kalafus, Kathleen
<input checked="" type="checkbox"/>	Invention Title Bag	Invention title = mi titulo de invención, Language code = es Invention title = my title of invention bro, Language code = en Invention title = le titulé de la inventé, Language code = fr	Invention title = PatentIn and Checker Test File

The data for the selected attributes will be overwritten

Select the sequences to be imported. If the box is left unchecked then no sequences will be imported.

Cancel Import Project

Figure 51 Import Another Project, select general information elements

Finally, when the user has decided on which General Information elements and sequences are to be imported into the project, then the user must click on the blue “Import Project” button, shown at the bottom of Figure 51.

**SUCCESS:** The project has been imported successfully.

Figure 52 Import Another Project, success banner

If the elements were imported correctly, a blue banner will appear as shown in Figure 52.

### 5.1.1.3 Validate Project

Before generating the sequence listing as an ST.26-compliant XML file, a project can pass through a validation check, beforehand. This step is always conducted prior to generating the sequence listing but can also be performed on its own.

To validate a project, the user must click on the “Validate” button at the top of the Project Detail View, shown in Figure 53.



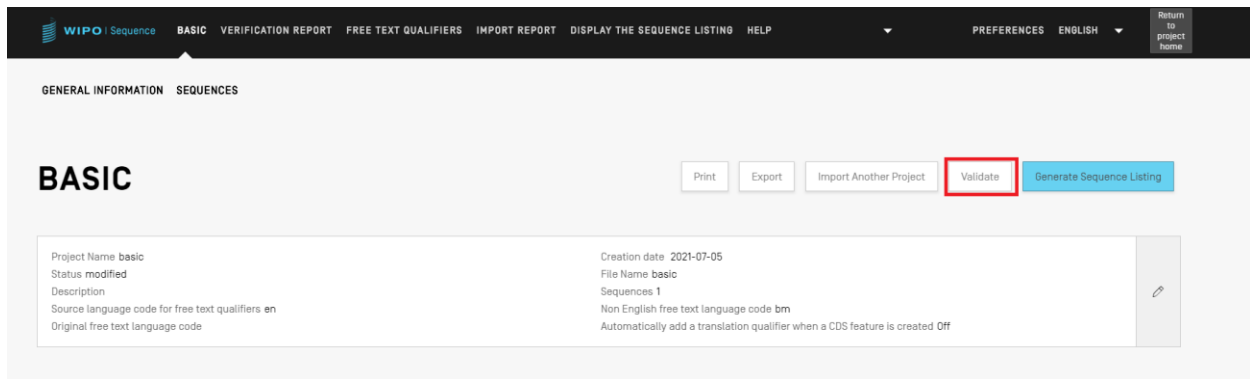


Figure 53 Project validation

Once the validation has finished, the user will be brought to the “Verification Report” View, displaying any the verification errors/warnings that may be generated. Figure 54 shows the screen that will be displayed in the case of successful validation.

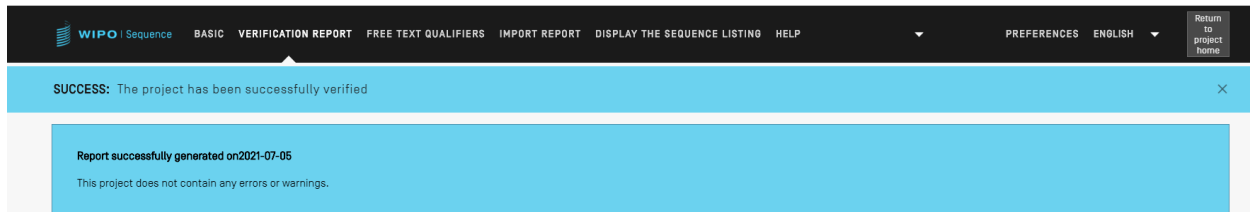


Figure 54 Project validate, no errors

If the validation process finds any errors or warnings, a Verification Report will be generated with a Table detailing the detected verification rules and guidelines that have been broken. An example report is shown in Figure 55. Each row is also identifies whether this is an error, which must be addressed, or a warning, must can be ignored by the user.

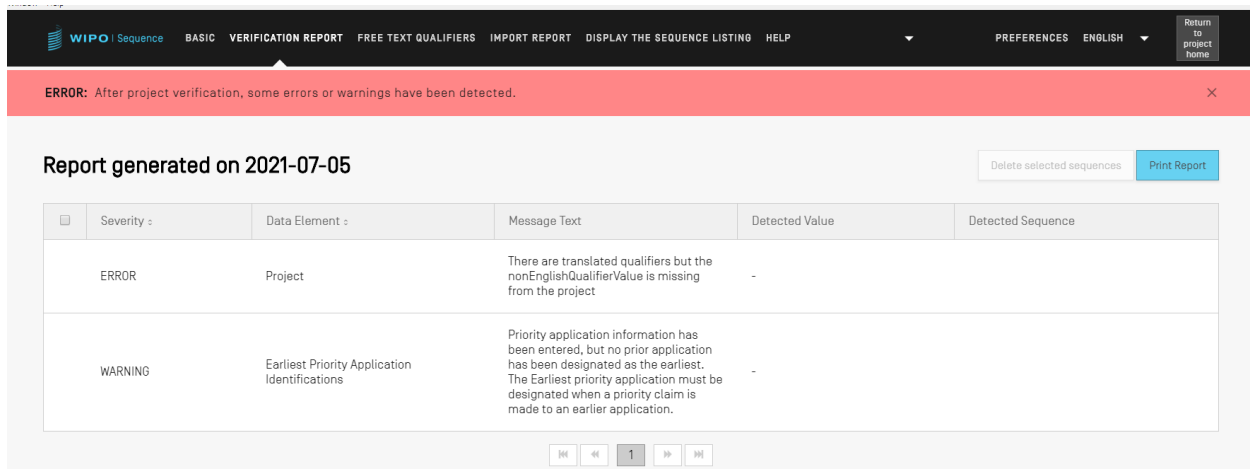


Figure 55 Project validate, errors/warnings

### 5.1.1.4 Export Project

A project can be exported to a .zip file for the user to back-up project data or alternatively import with another desktop computer with WIPO Sequence installed, as shown in Figure 56.

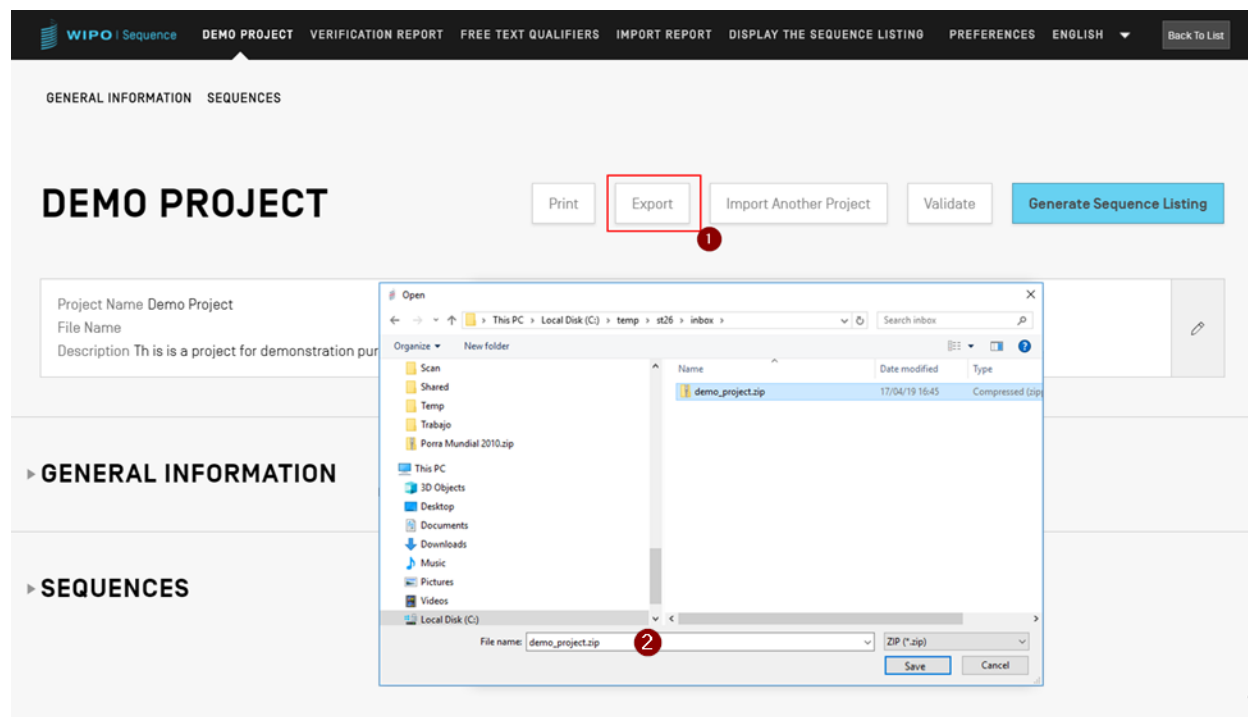


Figure 56 Export Project

- 1) Click on the “Export” button at the top of the Project Detail view.
- 2) In the dialog box that appears, select the file name and desired location to save the project.

If the project is successfully exported, a blue banner with the saved name and location will appear at the top of the screen as shown in Figure 57.

The screenshot shows the top navigation bar with the WIPO Sequence logo and menu items: DEMO PROJECT, VERIFICATION REPORT, FREE TEXT QUALIFIERS, IMPORT REPORT, DISPLAY THE SEQUENCE LISTING, PREFERENCES, ENGLISH, and a Back To List button. Below the navigation bar is a blue success message box: "SUCCESS: The project has been exported successfully at 'C:\Users\...Documents\Import projects\Export-project.zip'". The main content area has tabs for GENERAL INFORMATION and SEQUENCES. The title "DEMO PROJECT" is displayed. Below the title are buttons for Print, Export, Import Another Project, Validate, and Generate Sequence Listing. A table below the buttons shows project details:

Project Name Demo Project	Creation date 2019-02-21
File Name	Sequences 36
Description Th is is a project for demonstration purposes of the manual.	Status new

Figure 57 Export Project, success

### 5.1.1.5 Generate Sequence Listing

The final action that can be performed on a project, and perhaps the most important, is to generate the sequence listing. To generate the sequence listing, the user must click on the blue “Generate Sequence Listing” button, at the top of the Project Detail view, highlighted in Figure 58. This will automatically trigger the validation process to be run on the project first (see 39 5.1.1.3).

This screenshot is identical to Figure 57, but the "Generate Sequence Listing" button is highlighted with a red rectangular box. The success message is no longer present.

Figure 58 Generate Sequence Listing

If the project passes the validation process, a dialog box will open for the user to select where to save the generated ST.26 compliant sequence listing (.xml), as highlighted in Figure 59.

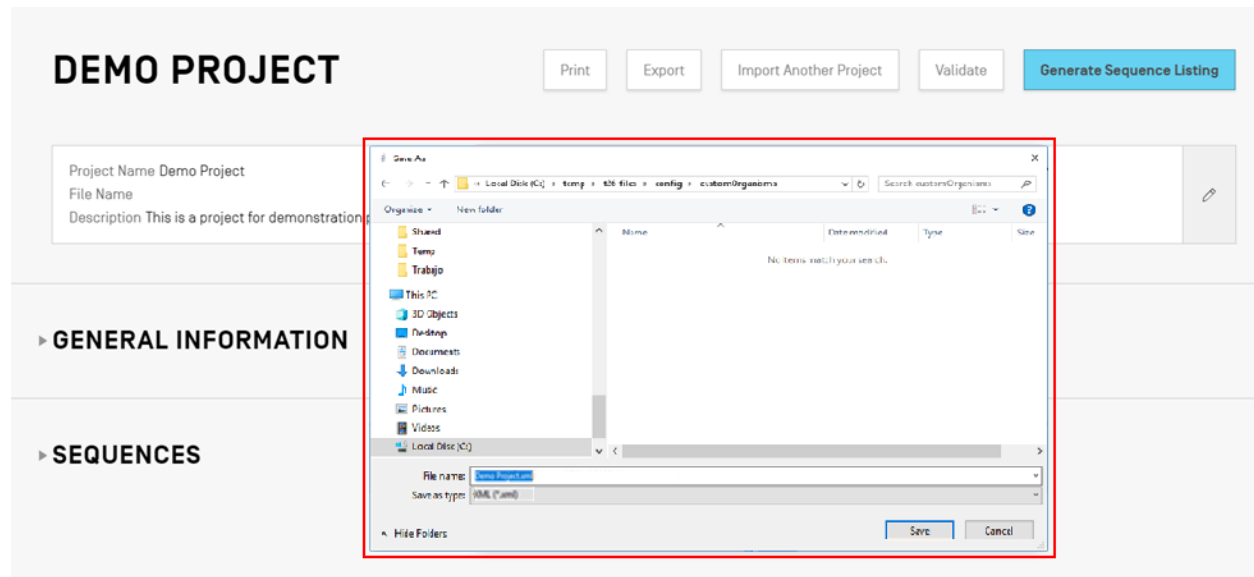


Figure 59 Generate Sequence Listing Dialog box

If the project fails validation, then the Verification Report View will instead be presented along with a red banner as shown in Figure 60.

**ERROR:** The ST.26 sequence listing file cannot be generated because the project contains errors.

[Print Report](#)

**Report generated on 28 Feb 2019, 16:19**

Severity	Data Element	Message Text	Detected Value	Detected Sequence
WARN	earliest priority application identification	Earliest priority application information has not been entered. It must be entered when a priority claim is made to an earlier application.	{ "IPOfficeCode": "", "applicationNumb...	
ERROR	invention title bag	The invention title is missing. At least one invention title must be entered.		
ERROR	applicant name name	The person or organization name has not been entered. At least one name must be entered.		
ERROR	inventor name name	The person or organization name has not been entered. At least one name must be entered.		

⏪
⏩
1
⏪
⏩

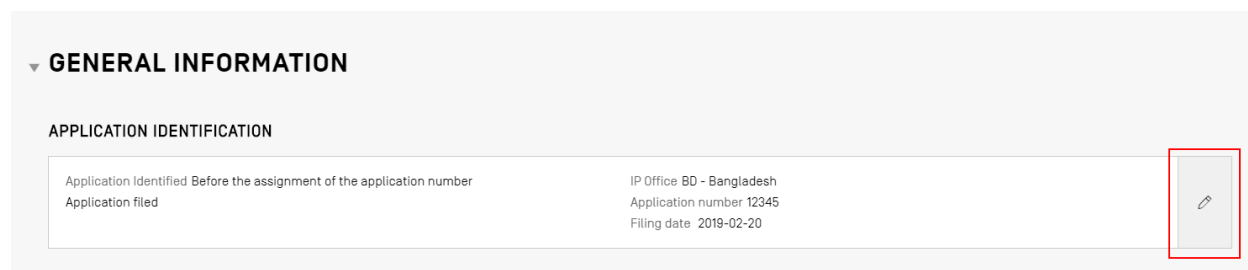
Figure 60 Generate Sequence Listing, Failed

## 5.1.2 General Information

This Section allows the user to enter information related to the patent application itself, which is used to associate the generated sequence listing with this application.

### 5.1.2.1 Application Identification

The “Application Identification” subsection of the General Information Section is related to the patent application status and information of the selected project, see Figure 61.



▼ **GENERAL INFORMATION**

APPLICATION IDENTIFICATION

Application Identified Before the assignment of the application number	IP Office BD - Bangladesh
Application filed	Application number 12345
	Filing date 2019-02-20

Figure 61 Application Identification

To edit information within the Application Identification subsection, click on the pencil icon highlighted, to the right of the subsection. Then the user must provide information based on the following steps shown in Figure 62:

- 1) If the application already has an assigned application number, the user must select the code of the Intellectual Property Office (IP Office) at which the application was filed. This is the WIPO ST.3 code.
- 2) The user must select whether or not they have already been notified of the application number or else just provided within an application file, by selecting the appropriate radio button.
- 3) In the case of not having the application number, the user **MUST** provide the applicant file reference in this field.
- 4) If an application number has already been assigned, the user should enter the application number provided for the patent.
- 5) Select the filing date of the application with the Date Picker if a date has been assigned.
- 6) Click the blue “Save” button

Figure 62 Application Identification Edit Panel

### 5.1.2.2 Priority Identification

To add a priority application to the project, the user must click on the “Add Earliest Priority Application” button in the General Information Section of the Project Detail View, shown in Figure 63.

Figure 63 Earliest Priority Application

To set the currently selected priority application as the earliest, the user must select “Yes” in the “Selected Earliest Priority Application” dropdown. This will set or modify this as the priority application established as the earliest priority application when the sequence listing is generated.

To finish, click on the blue “Add Earliest Priority Application” button in the Overlay, shown in Figure 64.

Figure 64 Earliest Priority Application Edit Panel

### 5.1.2.3 Applicant & Inventor

To add data regarding a new applicant or inventor to the project, the user must click on the “Add Inventor” or “Add Applicant” button within the General Information Section of the Project Detail View. The steps for performing both these actions are identical so only general instructions will be provided but this process must be repeated twice if both an applicant and an inventor are to be included within the project, even if the applicant is also the inventor.

An Overlay will open with two radio buttons, shown in Figure 65. If “Existing applicant/inventor” is selected, the user can choose from a drop-down box which lists currently saved persons and organizations within the local instance of the desktop tool. Figure 65 shows a list of three existing applicants, including “John Smith”.

Figure 65 Add existing Applicant/Inventor

If “New applicant/inventor” is selected, the user must fill out the Edit Panel in the same manner as when a new person/organization is being created (see Section 4.2.1 and Figure 66).

Finally, once the details are complete, the user clicks on the “Add Applicant/Inventor” button shown in Figure 66.

Add Applicant		Add Inventor	
Select the option*			
<input type="radio"/> Existing applicant			
<input checked="" type="radio"/> New applicant			
Name*		Residence Address	
Language*	▼	Correspondence Address	
Name Latin			
		Cancel	Add Applicant

Figure 66 Add new Applicant/Inventor

#### 5.1.2.4 *Invention Title*

The “Invention Title” is the last subsection within the General Information Section.

- 1) To add a new invention title, click on the “Add Invention title” button, as shown in Figure 67.

INVENTION TITLE		
Add Invention title		
Invention title*	Language* ▼	
	Cancel	Add Invention title

Figure 67 Add Invention title

- 2) In this Overlay, the user must enter the title of the invention and also indicate what language the title is provided in.
- 3) Click the blue “Add Invention title” button.

According to the WIPO ST.26, it is mandatory for a sequence listing to have the invention title provided in the language of filing. However a project can also optionally include more than one invention title, in additional languages. Each new invention title can be added using the steps above.



### 5.1.3 Sequences

The “Sequences” Section of the Project Detail View is where the user provides the technical information related to the sequences themselves.

To create/import/insert/reorder a sequence, the user must scroll down to the ‘Sequences’ section at the bottom of the Project Detail View. The subsections below provide further details on the steps required to perform these actions.

#### 5.1.3.1 Create Sequence

- 1) Click the “Create new sequence” button, as shown in Figure 68.

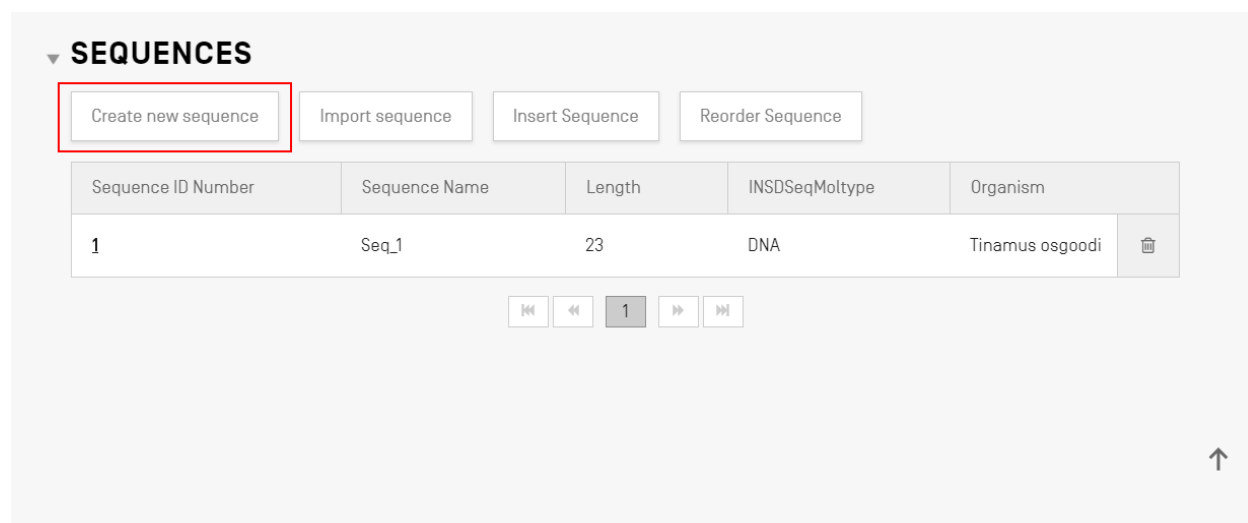


Figure 68 Create new sequence

The remainder of the steps are shown in Figure 69:

- 2) The user can optionally provide a name by providing a value in the ‘Sequence name’ field, to make it easier to distinguish this sequence. If left blank, the desktop tool will assign a default value with the default name for each new sequence starting with ‘Seq’ and then an iteratively increasing number (‘Seq\_1’, ‘Seq\_2’, ‘Seq\_3’) (1).

The user must select one of the three molecule types allowable in ST.26 and provided by the dropdown box (‘DNA’, ‘RNA’ & ‘AA’) (2). The sequence itself must be entered in the

“Residues”<sup>2</sup> text field (3). Note, if the user wishes to create a sequence with both DNA & RNA segments, DNA must be selected as the main molecule type.

The user must also select an organism name for the sequence being created, as this is a mandatory field. This can be either selected from a list of pre-defined organisms in the desktop tool database or one of the custom organisms created and saved locally by the user. For this, the “Existing organism” radio button must be selected (4).

The user also has the option to enter a new (custom) organism name directly by selecting the “New organism” radio button (4).

The user can also classify the organism by selecting a Qualifier Molecule Type<sup>3</sup> from a dropdown box (5) which provides values which vary depending on the Molecule Type previously selected.

If “Mark as an intentionally skipped sequence” (6) is checked, the Sequence panel will remove all constraints on providing values for mandatory elements and the resulting saved sequence will be ignored when validating the project and generating a sequence listing (the residues value will be provided as ‘000’).

If “The sequence contains both DNA & RNA segments” is checked (6), the panel will expand to include fields allowing the user to describe each DNA and RNA segments with a feature “misc\_feature”. The location of each of the defined segments will be stored in a different “misc\_feature” feature (7) of the Sequence, along with a “note” qualifier inside each “misc\_feature” with the molecule type followed by the “Further Text” text field value in each “misc\_feature”. A user can create as many of these features as is necessary by clicking on the “Add new ‘misc\_feature’ feature” button, and this must be done so for all the segments in the whole sequence: both for DNA **and** RNA segments.

---

<sup>2</sup> See WIPO Standard ST.26 – Annex I, Sections 1 & 3 for the tables of valid Nucleotide symbols & Amino acid symbols

<sup>3</sup> See WIPO Standard ST.26 – Annex I, Sections 6 & 8 for the Qualifier values for the mol type entry under the Nucleotides and Amino acid tables respectively

The screenshot shows a web form for creating a new sequence. It includes the following elements:

- 1**: Sequence Name field with the placeholder text "Name/Description for sequence".
- 2**: Molecule Type\* dropdown menu currently set to "DNA".
- 3**: Residues\* text area containing a long DNA sequence.
- 4**: Radio buttons for "Existing organism." (selected) and "New organism.".
- 5**: Qualifier Molecule Type\* dropdown menu currently set to "genomic DNA".
- 6**: Checkboxes for "Mark as an intentionally skipped sequence" (unchecked) and "The sequence contains both DNA & RNA fragments" (checked).
- 7**: A table with columns "Molecule Type", "Location", and "Further Text". The first row shows "RNA" in the Molecule Type column and "7..13" in the Location column.

At the bottom of the form are four buttons: "Cancel", "Add new 'misc\_feature' feature", "Create sequence", and "Create & Display Sequence".

Figure 69 Create new Sequence Panel

3) To finish, the user can click on the grey “Create sequence” button or the blue “Create & Display Sequence” button.

If the user clicks on the blue “Create & Display sequence” button, a collapsible sequence display will open after creating the sequence, beneath the Sequences Section within the Project Detail View, for the user to review the values.

The newly created sequence can be found in the last position in the list of sequences, with the next available Sequence ID Number.

(To see details on how to reorder the Sequence list, see Section 5.1.3.4)

**WIPO ST26 Tool** DEMO PROJECT VERIFICATION REPORT FREE TEXT QUALIFIERS IMPORT REPORT DISPLAY THE SEQUENCE LISTING PREFERENCES ENGLISH Back To List

GENERAL INFORMATION SEQUENCES

▶ **SEQUENCES**

▼ **SEQUENCE 2**

Sequence Number (ID) 2	Molecule Type DNA
Sequence Name Seq_2	Organism Demo Organism
Length 100000	Skipped Sequence No

▼ **FEATURES**

Add feature

Feature Key	Location	Qualifiers
source	1..100000	mol_type = genomic DNA organism = Demo Organism

1

▼ **SEQUENCE**

```

atagtaaaaa  tggtagaaat  taaggggaagt  aggggatattt  ttaagttaat  atagataaaa  gatgtatgga  70
gaaagtgtta  gtgttgtgtt  agtatgttgg  tggggaaggt  gatattagga  ataattataa  tttggggatg  140
ggagttttg  gttattaatt  tttaggtagg  tatataagtg  gtatagggag  taggatatta  taatgttgag  210
atataagaaa  tagtaagggg  aaagtgattt  aggtatattg  ggaatatgta  ggtaaaaata  gtgttgatac  280
taagggtaat  gaagttaaaa  aaaaaaagtg  taaggtaagt  ggttattagg  gtagtgatga  ggaagggttg  350
-----
    
```

Figure 70 Display sequence

### 5.1.3.2 Import Sequence

Sequences can also be imported directly from files into a project. The accepted file formats<sup>4</sup> are **raw**, **multi-sequence**, **FASTA**, **ST.26** and **ST.25**. When selected, the desktop tool will automatically detect the format used in the file.

<sup>4</sup> See File Formats section of this document (Section 6)

1) Click on the “Import sequence button”, highlighted in Figure 71.



Figure 71 Import Sequence

2) Click on the “Upload file [.txt, .xml]”, shown in Figure 72.

When the dialog box opens, select the file containing sequence data to be imported. The desktop tool will detect the format being used and will perform some validation checks on import.

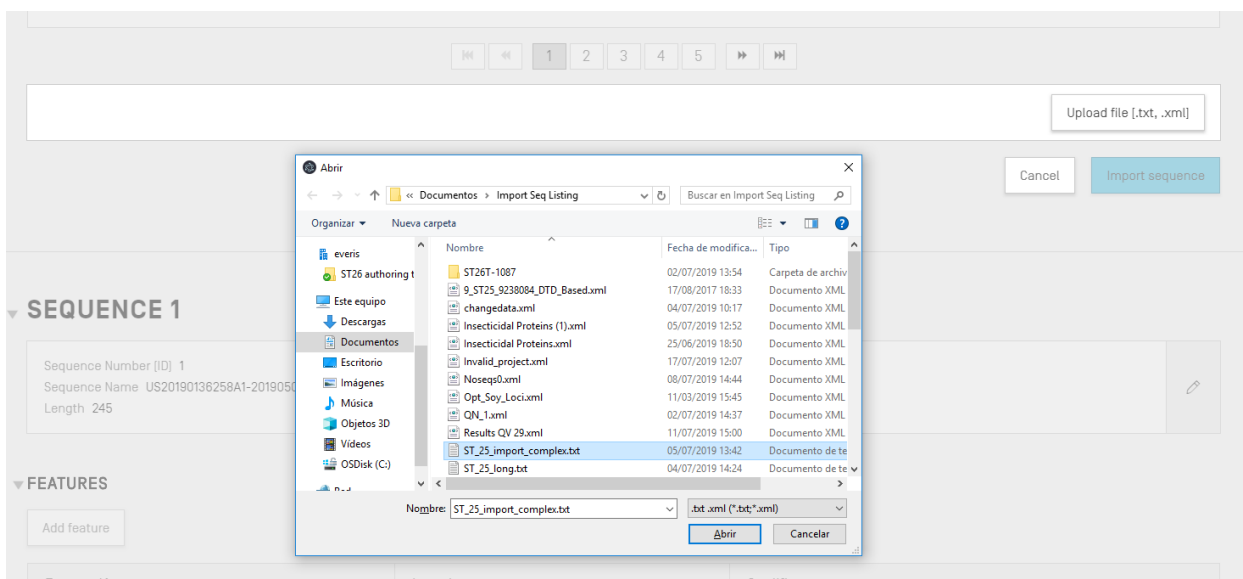


Figure 72 Import Sequence (dialog box)

There are five formats that the tool will accept for importing sequences: raw, multi-sequence, FASTA, ST.26 and ST.25. The format these files must be provided in are outlined in section 6 of this document.

In the case of selecting a file that is in ST.25 or ST.26 format (see Figure 73), the user will first see a “Select Range Sequences” checkbox (1). When checked, this will open a Table (2) with the Sequence ID Numbers of each sequence in the file and the order in which they will be appended to the list of sequence provided in the project.

If the user does not wish to import all of the sequences to the project, they can provide the desired range of sequence ID numbers (3).

A single sequence can be entered, as well as a list of sequences separated by commas or a range of sequences in the form  $x-y$ .

For example: "1, 3, 7, 13-20, 30-50".

C:\Users\... \ST26 authoring tool - Desarrollo 2018\02 Delivery\09- Development\ ficheros extremos de test\St25\ST\_25\_extralong.txt Upload file [.txt, .xml]

Select Range Sequences

Sequence Number [ID]	Detail
[1]	1
[2]	2
[3]	3
[4]	4
[5]	5

1 2

Select range Sequence ID Numbers [Empty is All]

Use "," to separate yours ids selection, to select a range use "-" between the ids

Cancel Import sequence

Figure 73 Import Sequence, ST.25/ ST.26 format

In the case of importing a multi-sequence format file (see Section 6.1 for information on this format and Figure 74), the user will see a "Select Range Sequences" checkbox (1), which when checked, will display a preview Table showing the Sequence ID Numbers of the corresponding sequences in the file as well as the details of each sequence under the "Detail" column (2): including sequence name, molecule type and organism name.

The user must select the range of Sequence ID numbers that they wish to import to the list of sequences within the project (3).

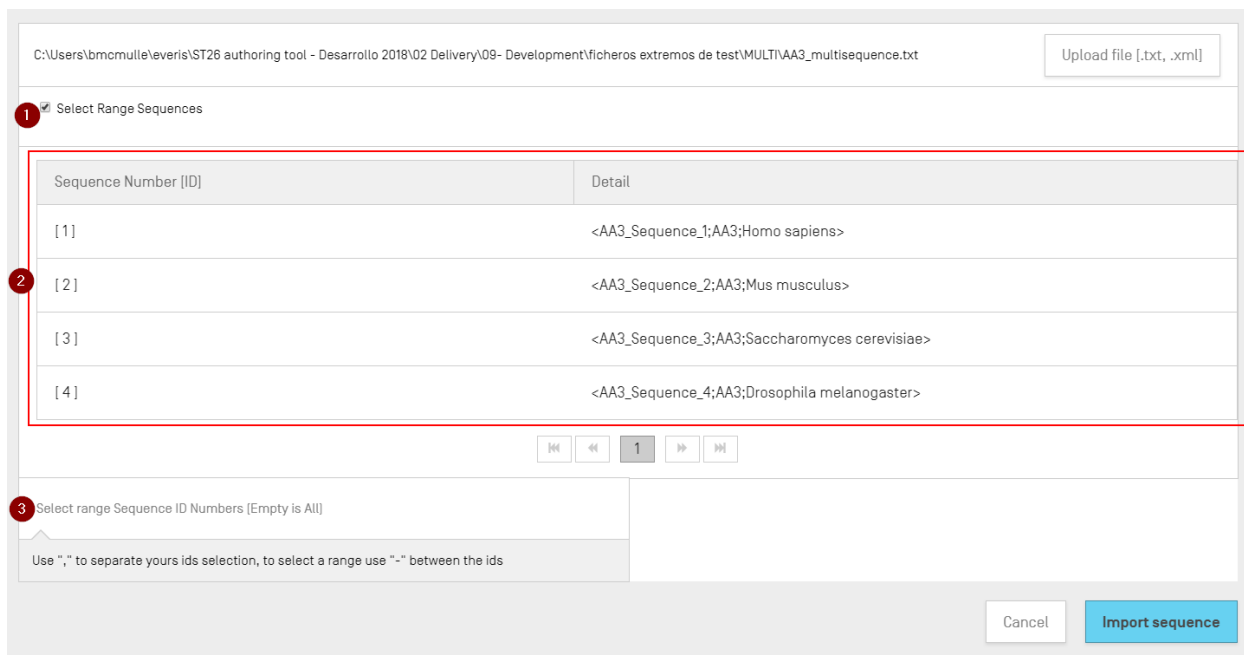


Figure 74 Import Sequence, multi-sequence format

The last case for formats that are accepted by the import Sequence process is the raw file format (see Section 6.3). This format only defines a single sequence per file. When a raw file is selected for import, the tool will display the Edit Panel shown in Figure 75. The molecule type of the sequence is the only mandatory field.

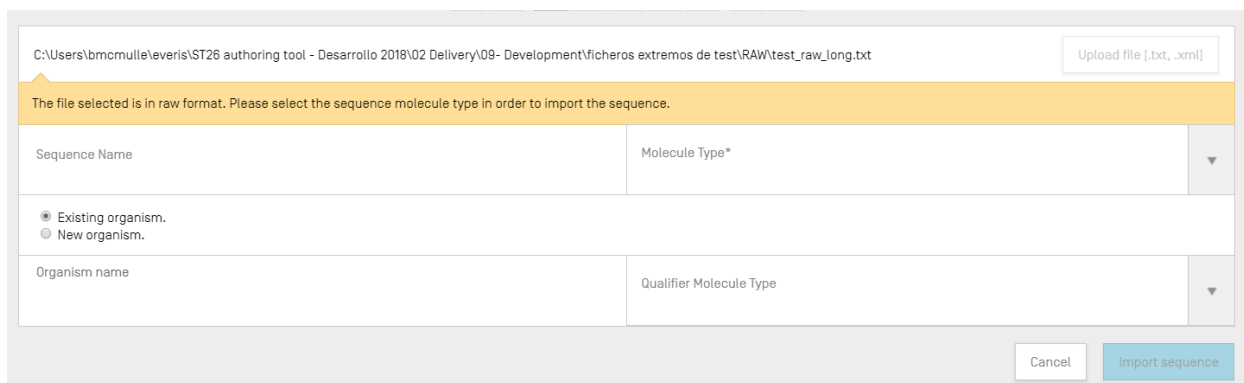


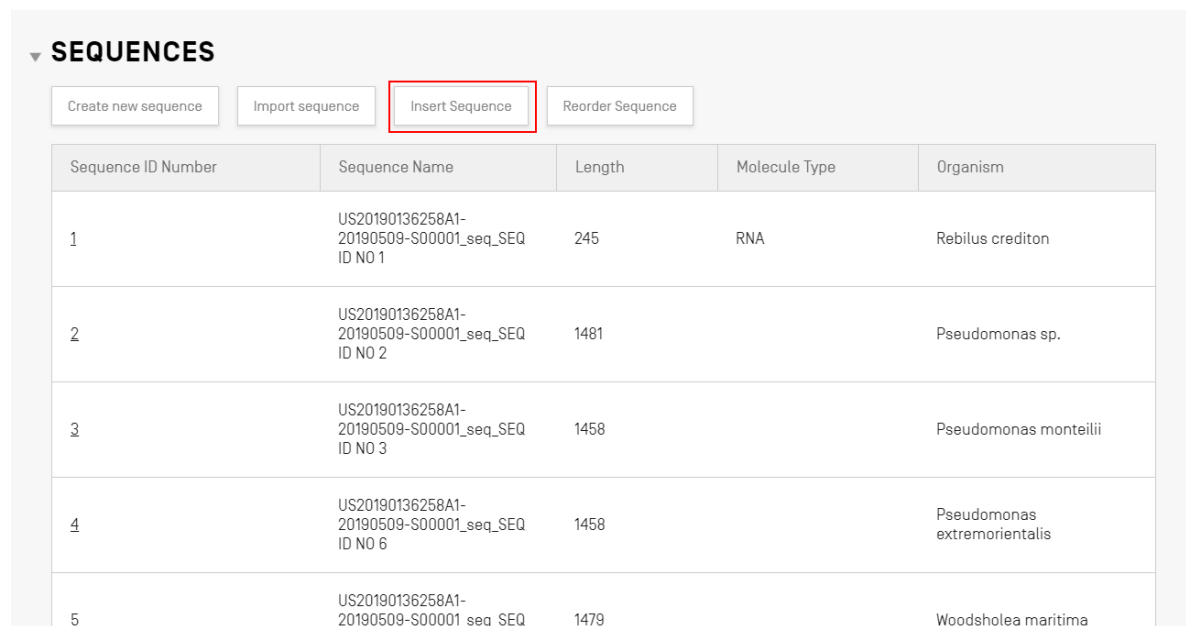
Figure 75 Import Sequence, RAW format

3) To finish, the user should click on the “Import sequence” blue button.

After the import, the tool will navigate to the “Import Report” View, detailed in Section 5.4

### 5.1.3.3 Insert Sequence

To insert a sequence into a specific position of the list of sequences, the user must click on the “Insert Sequence” button at the top of the Sequences Section (highlighted in Figure 76 ).



Sequence ID Number	Sequence Name	Length	Molecule Type	Organism
1	US20190136258A1-20190509-S00001_seq_SEQ ID NO 1	245	RNA	Rebilus crediton
2	US20190136258A1-20190509-S00001_seq_SEQ ID NO 2	1481		Pseudomonas sp.
3	US20190136258A1-20190509-S00001_seq_SEQ ID NO 3	1458		Pseudomonas monteilii
4	US20190136258A1-20190509-S00001_seq_SEQ ID NO 6	1458		Pseudomonas extremorientalis
5	US20190136258A1-20190509-S00001_seq_SEQ	1479		Woodsholea maritima

Figure 76 Insert sequence

An Overlay with a panel will appear (see Figure 77). The user must fill out all the information required for creating a sequence (see Section 5.1.3.1), and in addition, at the top-left of the panel, the user must enter the position in which the sequence should appear in the list of sequences (highlighted in Figure 77).



Figure 77 Insert sequence panel

To finish, the user can click on the insert “Insert sequence” or “Insert & Display Sequence”, also highlighted in Figure 77.

**SEQUENCES**

Create new sequence   Import sequence   Insert Sequence   Reorder Sequence

Sequence ID Number	Sequence Name	Length	Molecule Type	Organism
1	US20190136258A1-20190509-S00001_seq_SEQ ID NO 1	245	RNA	Rebilus crediton
2	US20190136258A1-20190509-S00001_seq_SEQ ID NO 2	1481		Pseudomonas sp.
3	Inserted sequence	41	DNA	Wohlfahrtiopsis bishoppi
4	US20190136258A1-20190509-S00001_seq_SEQ ID NO 3	1458		Pseudomonas monteilii

Figure 78 Sequence Inserted

If the user clicks on the blue “Insert & Display sequence” button, a collapsible sequence Table will open after creating the sequence, beneath the list of sequences within the Project Detail view, as shown in Figure 78.

### 5.1.3.4 Reorder Sequence

The user can reorganize in what order the sequences should appear within the list of sequences provided in a project by using the following steps. The sequence order transformation is shown from Figure 79 (start) to Figure 81 (result).

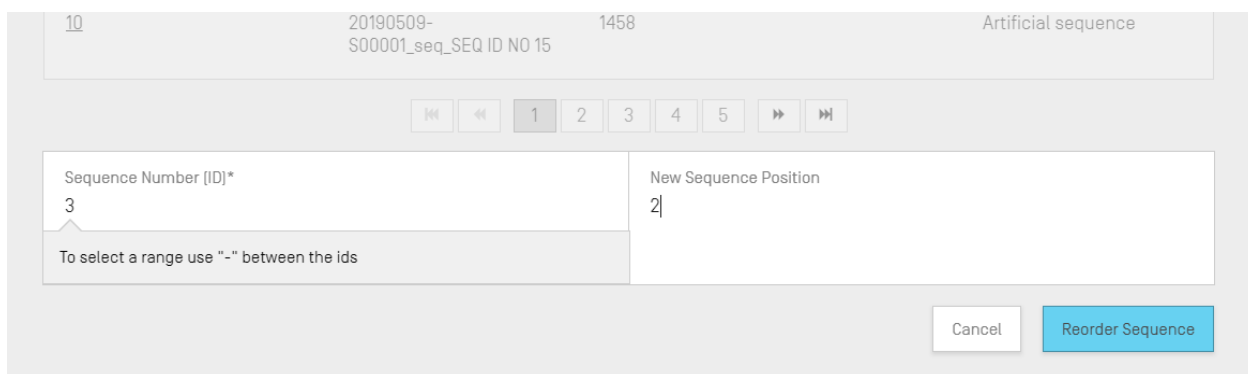
- 1) Click on the “Reorder Sequence” button, shown in Figure 79.



Sequence ID Number	Sequence Name	Length	Molecule Type	Organism
1	US20190136258A1-20190509-S00001_seq_SEQ ID NO 1	245	RNA	Rebilus crediton
2	US20190136258A1-20190509-S00001_seq_SEQ ID NO 2	1481		Pseudomonas sp.
3	Inserted sequence	41	DNA	Wohlfahrtiopsis bishoppi
4	US20190136258A1-20190509-S00001_seq_SEQ ID NO 3	1458		Pseudomonas monteilii

Figure 79 Reorder Sequence

- 2) Select the sequence(s) to be moved and select the position in which they are to be placed with respect to the current sequence list order, as shown in Figure 80.



10 20190509-S00001\_seq\_SEQ ID NO 15 1458 Artificial sequence

1 2 3 4 5

Sequence Number (ID)\*  
3

New Sequence Position  
2

To select a range use "-" between the ids

Cancel Reorder Sequence

Figure 80 Reorder Sequence panel

- 3) The sequence now appears in Figure 81 in the second position.

**SEQUENCES**

Create new sequence   Import sequence   Insert Sequence   Reorder Sequence

Sequence ID Number	Sequence Name	Length	Molecule Type	Organism
1	US20190136258A1-20190509-S00001_seq_SEQ ID NO 1	245	RNA	Rebilus crediton
2	Inserted sequence	41	DNA	Wohlfahrtiopsis bishoppi
3	US20190136258A1-20190509-S00001_seq_SEQ ID NO 2	1481		Pseudomonas sp.
4	US20190136258A1-20190509-S00001_seq_SEQ ID NO 2	1458		Pseudomonas monteilii

Figure 81 Reordered Sequence

### 5.1.3.5 Edit Sequence

To edit a sequence, the user must click on the Sequence ID Number of the corresponding sequence to be modified, as highlighted in Figure 82 (Sequence ID ‘1’).

**SEQUENCES**

Create new sequence   Import sequence   Insert Sequence   Reorder Sequence

Sequence ID Number	Sequence Name	Length	INSDSeqMoltype	Organism
1	Seq_1	23	DNA	Tinamus osgoodi

Figure 82 Edit sequence

This will open a new Section in the Project Detail View beneath the Sequences Section, as shown in Figure 83.

This Sequence Section is composed of the “Basic Information” Edit Panel (1), the “Features” list Table (2) and the “Sequence” residues Edit Panel (3).

**GENERAL INFORMATION** SEQUENCES

**SEQUENCE 2**

1 Sequence Number (ID) 2 Molecule Type DNA  
 Sequence Name Inserted sequence Organism Wohlfahrtiopsis bishoppi  
 Length 41

**FEATURES**

2 Add feature

Feature Key	Location	Qualifiers
source	1..41	mol_type = genomic DNA organism = Wohlfahrtiopsis bishoppi

**SEQUENCE**

3 gatagtatgt atatatagta gtatgatgat gatgatgatga t 41

Figure 83 Edit sequence, display sequence

### 5.1.3.6 Features

According to WIPO ST.26, every sequence MUST have at least one feature associated with it: source or SOURCE, depending on the molecule type.

The Features Table has three columns: the feature key, the location of the feature within the genetic sequence and the qualifiers associated with an individual sequence feature.

The feature location indicates in which segment of the sequence the feature exists. The allowable formats to specify the feature location are provided in WIPO ST.26 and are as follows:

- Single residue number: x
- Residue numbers delimiting a sequence span: x..y
- Residues before the first or beyond the last specified residue number: <x, >x, <x..y, x..>y, <x..>y
- A site between two adjoining nucleotides: x^y
- Residue numbers joined by an intrachain cross-link: x..y

Location **operators** can be used to form complex location descriptions:

- “**join** (location, location, ... location)”<sup>5</sup>: The locations are joined (placed end-to-end) to form one contiguous sequence.
- “**order** (location, location, ... location)”<sup>5</sup>: The elements are found in the specified order, but nothing is implied about whether joining those elements is reasonable.
- “**complement** (location)”<sup>5</sup>: Indicates that the feature is located on the strand complementary to the sequence span specified by the location descriptor, when read in the 5’ to 3’ direction or in the direction that mimics the 5’ to 3’ direction.

To add a new feature to the sequence, click the “Add feature” button in the Features Section of the selected Sequence, highlighted below in Figure 84.

The screenshot shows the 'SEQUENCE 2' interface. At the top, there is a summary box with the following information:

Sequence Number (ID) 2	Molecule Type DNA
Sequence Name Inserted sequence	Organism Wohlfahrtiopsis bishoppi
Length 41	

Below this is the 'FEATURES' section, which contains an 'Add feature' button highlighted with a red box. Underneath the button is a table of features:

Feature Key	Location	Qualifiers
source	1..41	mol_type = genomic DNA organism = Wohlfahrtiopsis bishoppi

Below the table is a navigation bar with buttons for first, previous, 1, next, and last. At the bottom, there is a 'SEQUENCE' section showing the sequence: gatagtatgt atatatagta gtatgatgat gatgatgatga t, with a length of 41.

Figure 84 Add feature

Next, in the Overlay that opens (shown in Figure 85) select an entry from the feature key<sup>5</sup> dropdown list and specify the feature location within the sequence that the feature applies to.

<sup>5</sup> See WIPO Standard ST.26 – Annex I, Sections 5 & 7 for tables of feature keys for Nucleotides and Amino acids

▼ FEATURES

Add feature

Feature Key	Location	Qualifiers	
source	1..23	mol_type = genomic DNA organism = Tinamus osgoodi	

1

**Feature 1**

Feature Key*	▼	Feature Location*
D_segment		4..15

For a detailed explanation of the format of the feature location please [click here](#)

▼ QUALIFIERS

Add qualifier

Cancel Create Feature

Figure 85 Add feature, overlay

Qualifiers can also be added to the feature at this stage, but they will be covered in the next section (Section 5.1.3.7).

Feature 1

Feature Key*	▼	Feature Location*
CDS		1..13

Automatic addition of a translation qualifier is currently on. This means a separate sequence will be generated and a protein\_id qualifier created if the translation qualifier value meets the minimum length requirement.

For a detailed explanation of the format of the feature location please [click here](#)

A link has been added to have a detailed explanation of the format of the feature location. The link is located at the end of the sentence 'click here'. The link has been underlined in Figure 86 to make it easier for the user to identify it.

Figure 86 Feature Location Link

To finish, click the blue "Create Feature" button, shown in Figure 85.

#### 5.1.3.6.1 CDS Features

The CDS Feature type is used to convert a segment of the sequence to which it belongs, into a separate associated amino acid Sequence in the list of sequence provided in the project. Within the CDS Feature of the original sequence, the ID reference of the translated Amino Acid Sequence will be provided in the "protein\_id" qualifier.

When creating a “CDS” feature for a Sequence, a ‘translation’ qualifier (with default “Genetic Code” value of 1 – “Standard Code”) can be automatically added to the feature in order to translate a residue chunk of the sequence by checking the checkbox in Basic Information (see Figure 87 and Figure 88). However, this qualifier is not mandatory and can be deleted after generation. The user can also manually create a “protein\_id” qualifier of their own and reference the associated translated Sequence ID.

Project Name* demo	Creation date 2021-04-30
Status modified	File Name ST26 demo1
Description this is a description	Sequences 144
Source language code for free text q... en - English	Non English free text language code ru - Russian
Original free text language code ru - Russian	<input checked="" type="checkbox"/> Automatically add a translation qualifier when a CDS feature is created <small>Automatically add a translation qualifier, its value, and a protein_id qualifier and associated separate amino acid sequence (if appropriate) when a CDS feature is added to a nucleotide sequence.</small>

Figure 87 Automatic CDS translation treatment: check to turn on

**DEMO**

Project Name demo      Creation date 2021-04-30

Status modified      File Name ST26 demo1

Description this is a description      Sequences 144

Source language code for free text qualifiers en      Non English free text language code ru

Original free text language code ru       Automatically add a translation qualifier when a CDS feature is created On

Figure 88: Automatic CDS translation treatment is On

If the user wishes to automatically generate the translation qualifier, the translation table value and sequence name can be set from the Edit Panel of the qualifier. When the user creates the feature, the tool will perform the translation and then add a “protein\_id” qualifier to the feature and a new sequence with the value of the translation.

The translation will be performed again, only if the feature location or one of the qualifiers “transl\_table”, “transl\_except”, or “codon\_start” changes its values, in which case the linked sequence will be updated.

**Note:**

*If the translation value is changed, the linked sequence will update its value automatically. However, if the linked nucleotide sequence is modified, the value of the translation qualifier will not change. If the “protein\_id” qualifier is modified after creation, then the linked sequence will lose its association to the original sequence.*

**Advice around use of stop codon:**

Initially, stop codons should only be found at the end of a CDS feature, indicating the end of the encoded amino acid sequence. They should never be found in the middle of a CDS feature unless there is a transl\_except qualifier that indicates that the stop codon is to be translated into a particular amino acid.

If a stop codon is found in the middle of a CDS feature, and there is no transl\_except qualifier indicating that the stop codon is to be translated into a particular amino acid, as shown in Figure 89, then the tool should stop translation at that point and a red banner would be displayed informing the user that no translation will be generated.

The screenshot shows the WIPO Sequence interface. At the top, there is a navigation bar with options: WIPO Sequence, DEMO, VERIFICATION REPORT, FREE TEXT QUALIFIERS, IMPORT REPORT, DISPLAY THE SEQUENCE LISTING, HELP, PREFERENCES, ENGLISH, and a 'Return to project home' button. Below the navigation bar, a red error banner reads: "ERROR: No translated sequence will be generated as the CDS feature contains an improper internal stop codon. Please ensure that the correct genetic code table has been selected or whether qualifiers 'transl\_except' or 'codon\_start' are required." Below the error banner, the 'FEATURES' section is visible, containing an 'Add feature' button and a table with the following data:

Feature Key	Location	Qualifiers
<a href="#">CDS</a>	1..14	translation
<a href="#">source</a>	1..342	mol_type = other DNA organism = synthetic construct

Below the features table, there are navigation arrows and a page number '1'. The 'SEQUENCE' section shows a sequence of nucleotides: atcctaaactc atcatcatca ctcatcaaca tcatcactca tcatcatcac tcatcatcat. The sequence is displayed in two lines, with the first line ending at position 60 and the second line ending at position 120. The stop codon 'taa' in the first line is highlighted in yellow.

Figure 89: Automatic translation checkbox is On and the sequence contains an improper stop codon

And an error should be listed in the validation report to alert the user that there is a problem with their coding sequence, as shown in Figure 90.



The screenshot shows the top navigation bar with options: WIPO | Sequence, DEMO, VERIFICATION REPORT, FREE TEXT QUALIFIERS, IMPORT REPORT, DISPLAY THE SEQUENCE LISTING, HELP, PREFERENCES, ENGLISH, and a 'Return to project home' button. Below the navigation bar, the report title is 'Report generated on 2021-07-08'. There are two buttons: 'Delete selected sequences' and 'Print Report'. The main content is a table with the following data:

Severity	Data Element	Message Text	Detected Value	Detected Sequence
ERROR	Feature Key	The CDS feature contains an improper internal stop codon. Please ensure that the correct genetic code table has been selected or whether qualifiers 'transl_except' or 'codon_start' are required.	CDS	Sequence 1

Below the table, there is a note: 'The value of the qualifier'.

Figure 90: sequence contains an improper stop codon verification error

### Automatic CDS Feature creation

The steps for automatically creating a CDS feature qualifier are as follows:

- 1) In the specific sequence display, click the “Add feature” button and select “CDS” as the feature key. If the checkbox ‘automatically add a translation qualifier’ in Basic Information is checked, it will automatically add a translation qualifier, its value, and a protein\_id qualifier and its associated separate amino acid sequence (if appropriate) when a CDS feature is added to a nucleotide sequence.
- 2) The user also has the option to manually create a translation qualifier.

The screenshot shows a form titled 'QUALIFIERS' with an 'Add qualifier' button. The form contains the following fields and options:

- Qualifier Name \*: translation
- Select Genetic Code: 1 - Standard Code
- Sequence Name: (empty field)
- Qualifier Value: (empty field)

Below the fields, there is a note: 'Automatic Translation is ON. Leave this field blank to automatically generate the translation qualifier value, protein\_id qualifier, and associated amino acid sequence.' At the bottom right, there are 'Cancel' and 'Create Qualifier' buttons.

Figure 91: Create translation qualifier

- 3) When the user is finished editing the feature and its related qualifiers, they must click the “Create Feature” button to save it. A resulting CDS feature is shown in Figure 92.

▼ FEATURES

Add feature

Feature Key	Location	Qualifiers
<a href="#">CDS</a>	1..14	protein_id = 145 translation = ITHH
<a href="#">source</a>	1..339	mol_type = other DNA organism = synthetic construct

« ‹ 1 › »


Figure 92: CDS feature

The tool then **creates a new sequence\*** for the project with the following attributes:

- **Sequence ID Number** = the next available value for Sequence ID Number
- **Length** = length of the translated sequence
- **Sequence Name** = the value given in the “Sequence Name” field of the “translation” qualifier (see **Error! Reference source not found.**). If no name was provided, the default sequence name will be provided (“Seq\_#”).
- **Molecule Type** = “AA”
- **Organism Name** = the same value as provided for the original sequence
- **Qualifier Molecule Type** = “protein”
- **Sequence Residues** = translated values of the original sequence

A resulting example after this process has completed is shown in Figure 93.

**SEQUENCE 20**

Sequence Number (ID) 20 Sequence Name ST26 demo_seq_8 Length 4	Molecule Type AA Organism synthetic construct	
--	--	---

▼ FEATURES

Add feature

Feature Key	Location	Qualifiers
<u>COILED</u>	1..4	NOTE = qual val
<u>SOURCE</u>	1..4	MOL_TYPE = protein ORGANISM = synthetic construct




Figure 93: CDS feature, generated sequence

**\*Note, regarding the creation of the translated sequence:**

The translated sequence is created only if its length is at least 4 characters long, excluding any "X" chars from the count (i.e., AXTG counts as 3 characters).

In the case of modifying the qualifier "translation", if the qualifier value decreases below 4 characters, then the associated sequence translation will be removed, as will the 'protein\_id' qualifier.

**5.1.3.7 Qualifiers**

To view the qualifiers for a feature, the user must first select the relevant feature from the Feature Table of the relevant sequence. In the example shown in Figure 94 the 'source' feature is highlighted.

GENERAL INFORMATION SEQUENCES

▶ SEQUENCES

▼ SEQUENCE 1

Sequence Number (ID) 1	Molecule Type DNA
Sequence Name Seq_1	Organism Tinamus osgoodi
Length 23	Skipped Sequence No

▼ FEATURES

Add feature

Feature Key	Location	Qualifiers
source	1..23	mol_type = genomic DNA organism = Tinamus osgoodi

Navigation: [Home] [Left] [1] [Right] [End]

Figure 94: View qualifiers

Clicking on a Feature Key will open the following feature Overlay, as shown in Figure 95.

Feature Key	Location	Qualifiers
source	1..23	mol_type = genomic DNA organism = Tinamus osgoodi

Navigation: [Home] [Left] [1] [Right] [End]

**Feature 1**

Feature Key source	Feature Location* 1..23
-----------------------	----------------------------

For a detailed explanation of the format of the feature location please [click here](#)

▼ QUALIFIERS

Add qualifier

Qualifier Name mol_type	Qualifier Value genomic DNA	[Edit]
Qualifier Name organism	Qualifier Value Tinamus osgoodi	[Edit]

Buttons: Cancel Update feature

Figure 95: Add/Edit qualifiers

Existing qualifiers can be edited by clicking on the pencil icon to the right of each row (1), or the user can add a new qualifier to the currently selected feature by clicking the “Add qualifier” button (2).

When editing or adding a qualifier, the user will be presented with the two fields shown in Figure 96: the 'Qualifier name'<sup>6</sup> (to be selected from a dropdown list) and the 'Qualifier value'.

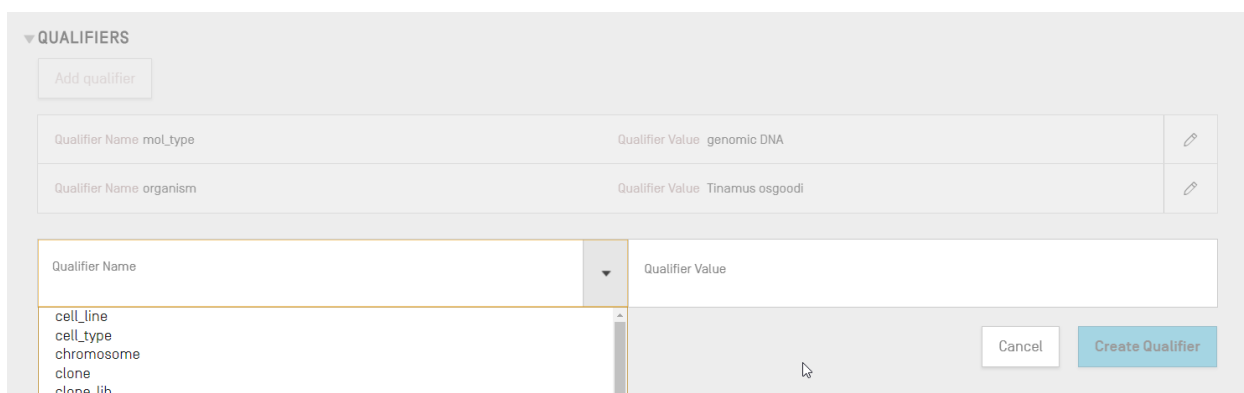
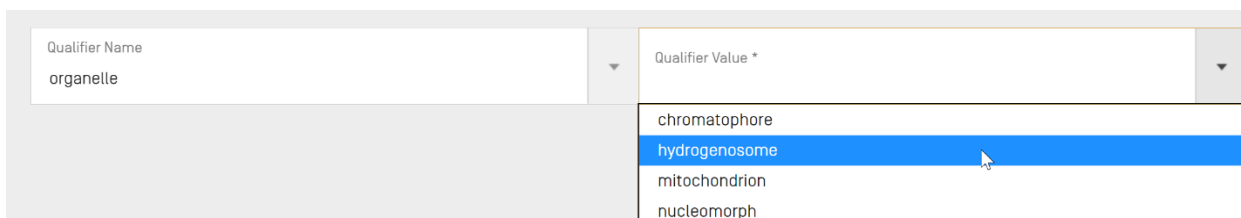


Figure 96 Qualifier Panel

The Qualifier Value field will have a different behaviour depending on the type of qualifier:

- **Qualifiers with pre-defined values.** The value field is a dropdown field where the user can select one of the predefined values for the qualifier, as shown in the example below:



- **Qualifiers with free text.** The value field is a free-text field. In addition to the Qualifier Name and the Qualifier Value, which holds the English value only, two additional fields appear to allow the user to provide both the language code (e.g., 'ru') and the corresponding language value in the Non English Qualifier Value, as shown in the example below:

---

<sup>6</sup> See *WIPO Standard ST.26 – Annex I, Sections 6 & 8* for all possible Qualifiers for Nucleotides and Amino acids

The Language code field is assigned the same value as the 'Non English Free text language code' filed in the Project Detail Information.

The user can provide a series of Non English values for each selected language either by manual input or by importing the proper associated language from an XLIFF File (see section 5.1.3.2 for more details on Import).

- **Qualifiers with pre-defined format.** The value field is a free-text field, but the value entered is validation to ensure it matches the specific rules provided in WIPO ST.26 Annex I, Section 6<sup>7</sup>. In the example shown, the date has not been provided in the correct format:

- **Qualifiers with no value allowed.** The qualifier value field is not editable, as indicated below in the example:

When finished, the user must click the blue “Create Qualifier” button to add the newly created qualifier, or “Save”, to save the changes made to the existing qualifier.

The last step, once the qualifier(s) have been added/modified, the user must click on the “Update feature” button at the bottom of the Feature Overlay, shown in Figure 97 to proceed.

<sup>7</sup> See WIPO Standard ST.26 – Annex I, Section 6 for rules regarding these qualifiers.

**Feature 2**

Feature Key source	Feature Location* 1..339
-----------------------	-----------------------------

For a detailed explanation of the format of the feature location please [click here](#)

**QUALIFIERS**

Add qualifier

Qualifier Name mol_type	Qualifier Value other DNA	
Qualifier Name organism	Qualifier Value synthetic construct	

Cancel **Update feature**

Figure 97: Update feature

## 5.2 VERIFICATION REPORT

To open the verification report of the sequence listing of a project, from the Project Details View, the user can click on the “VERIFICATION REPORT” link in the menu bar at the top of the View.

For further details on how to generate the verification report, see Section 5.1.1.3.

WIPO Sequence **VALID** VERIFICATION REPORT FREE TEXT QUALIFIERS IMPORT REPORT DISPLAY THE SEQUENCE LISTING HELP PREFERENCES ENGLISH Return to project home

**GENERAL INFORMATION** SEQUENCES

**VALID** Print Export Import Another Project Validate **Generate Sequence Listing**

Project Name valid	Creation date 2021-07-06	
Status modified	File Name validSTS	
Description	Sequences 3	
Source language code for free text qualifiers en	Non English free text language code	
Original free text language code	Automatically add a translation qualifier when a CDS feature is created Off	

**GENERAL INFORMATION**

Figure 98 Verification view/button

Depending on whether the project sequence listing is valid or not there will be two resulting Views: Figure 99, where errors/warnings have been generated and Figure 100, after a successful validation.

Report generated on 2021-07-06

<input type="checkbox"/>	Severity	Data Element	Message Text	Detected Value	Detected Sequence
<input checked="" type="checkbox"/>	ERROR	Feature Location	The feature location includes a residue number less than 1, which is invalid.	-2	Sequence 10
<input type="checkbox"/>	ERROR	Sequence Residue	The sequence contains the invalid nucleotide symbol u at position 10. Nucleotide sequences must only contain the symbols set forth in WIPO ST.26 Annex I, Section 1.	-	Sequence 14
<input type="checkbox"/>	ERROR	Sequence Residue	The sequence contains the invalid nucleotide symbol u at position 2. Nucleotide sequences must only contain the symbols set forth in WIPO ST.26 Annex I, Section 1.	-	Sequence 14
<input type="checkbox"/>	ERROR	Sequence Residue	The sequence contains the invalid nucleotide symbol u at position 8. Nucleotide sequences must only contain the symbols set forth in WIPO ST.26 Annex I, Section 1.	-	Sequence 14
<input type="checkbox"/>	ERROR	Sequence Residue	The sequence contains the invalid nucleotide symbol u at position 18. Nucleotide sequences must only contain the symbols set forth in WIPO ST.26 Annex I, Section 1.	-	Sequence 14

Figure 99 Verification report, errors

The user has the option to bulk delete sequences by checking the checkbox in the first column and clicking the button delete selected sequences (see Figure 99).

The Verification Report can be exported as a PDF by clicking on the “Print Report” button, shown in the top-right-hand corner of Figure 99Figure . The generated report will be displayed in the PDF viewer as explained in Section 3.2.

Report successfully generated on 27 Feb 2019, 18:11

This project does not contain any errors or warnings.

Figure 100 Verification report, no errors



### 5.3 FREE TEXT QUALIFIERS

The qualifiers which allow a “free text” value in a project are further referenced within the “FREE TEXT QUALIFIERS” view of the Project page.

Whenever a free text qualifier is added to the current project, the qualifier will also be added to this View, shown in Figure 101.

Sequence ID Number	Sequence Name	Feature Key	Feature Location	Qualifier ID	Qualifier Name	Qualifier Value	Non English Qualifier Value-[ko]	Available language codes
1	basic_seq_1	source	1..26	q1	organism	Una virus	organism Ko	ko

Figure 101 Free-text qualifiers view

The user can modify a qualifier’s associated translated free-text value by clicking on the ‘Qualifier Name’ value, as shown in Figure 95, which will open an Overlay with an Edit Panel.

#### 5.3.1 IMPORT FREE TEXT QUALIFIERS

If the user clicks on the “IMPORT FREE TEXT QUALIFIERS” button, the tool will open our file explorer and we will be able to browse through our folders until we find and select the (.XLIFF) file we want to import and will display multiple validation step to ensure that the correct mappings are conducted.

The selected file must contain the following items of data:

- Project name
- The target language code
- The source language code
- For each XLIFF unit element:

The qualifier unique id (following the format: a number preceded by the letter ‘q’)

The qualifier value in the source language tag

The qualifier value in the target language tag

```
<xliff xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xsi:schemaLocation="urn:oasis:names:tc:xliff:document:1.2 http://docs.oasis-open.org/xliff/v1.2/os/xliff-core-1.2.xsd" original="basic1" datatype="plaintext" source-language="en" target-language="fr">
  <body>
    <trans-unit id="q1" sequenceIDNumber="1" sequenceName="basic_seq_1" featureKey="source" featureLocation="1..26" qualifierName="organism">
      <source>Una virus</source>
      <target>organism fr</target>
    </trans-unit>
    <trans-unit id="q2" sequenceIDNumber="2" sequenceName="basic_seq_2" featureKey="source" featureLocation="1..26" qualifierName="organism">
      <source>Una virus</source>
      <target>organism fr</target>
    </trans-unit>
  </body>
</file>
</xliff>
```

Figure 102: an example of a valid XLIFF File

Once we have selected the file we want to import, the tool will ask us to verify if we really want to proceed by confirming verification steps (see Figure 103 to Figure 107).

- The system compares the project name from the input file with the name of the selected project:

The screenshot shows the 'FREE TEXT QUALIFIERS' section of the WIPO Sequence tool. A table lists the imported qualifiers. A modal dialog box is open, displaying a validation error. The error message states: 'No matching project names. The current project name basic does not match with the name specified in the XLIFF file basic1.' The text 'basic1' is highlighted with a red box. The dialog includes 'Cancel' and 'Continue' buttons.

Sequence ID Number	Sequence Name	Feature Key	Feature Location	Qualifier ID	Qualifier Name	Qualifier Value	Non English Qualifier Value-(bm)	Available language codes
1	basic_seq_1	source	1..26	q1	organism	Una virus	organism	bm

Figure 103: Projectname validation

- The system will inform user if any qualifiers could not be mapped:

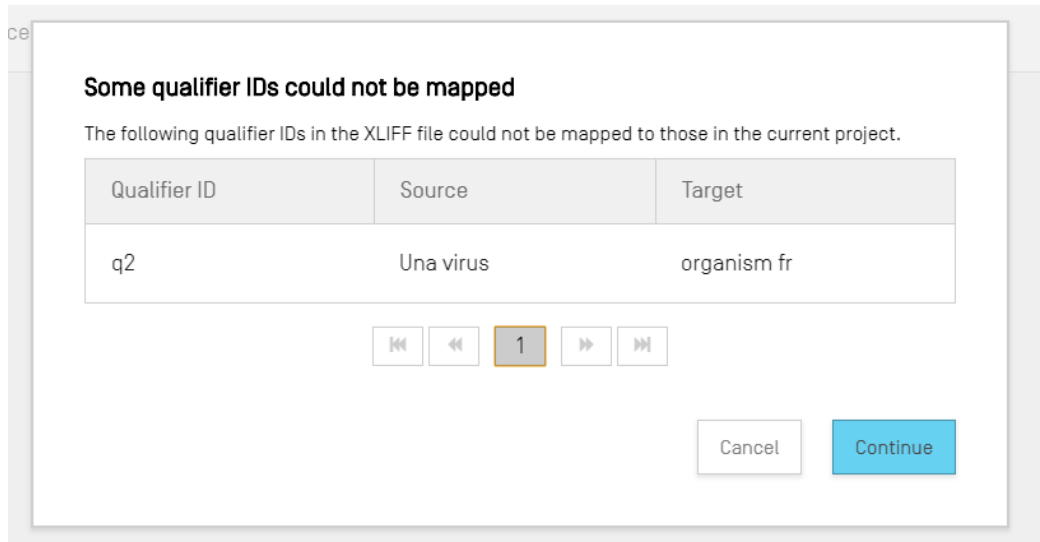


Figure 104: qualifiersmapping validation

- The system will inform the user of the changes related to the source language and the Qualifiers values:

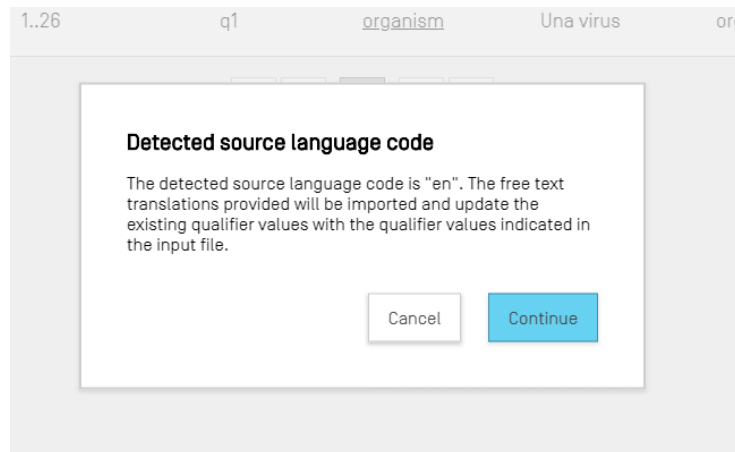


Figure 105: Source language validation

- The system will inform the user of the changes related to the Target language and the Qualifiers Translated values:

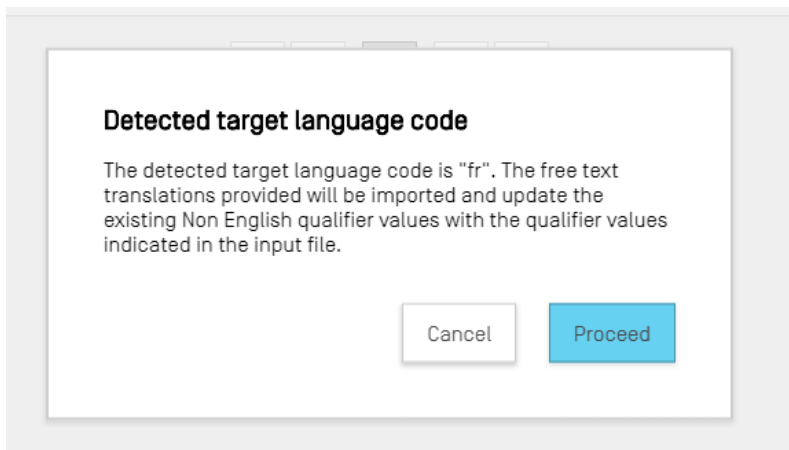


Figure 106: Target language validation

After that we will receive the following message at the top in blue: ‘SUCCESS: THE FREE TEXT QUALIFIER HAS BEEN IMPORTED SUCCESSFULLY’ and a report displaying in details the affected filed its previous and current imported values.

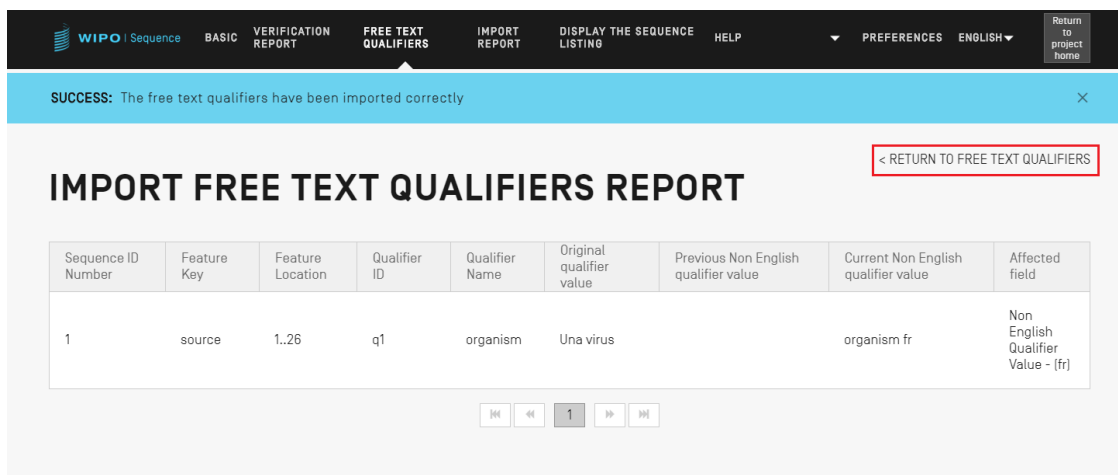


Figure 107: Import Free text qualifier report

User can get back to the Free text Qualifier view by clicking the 'RETURN TO FREE TEXT QUALIFIERS' , highlighted in Figure 107.

### 5.3.2 EXPORT FREE TEXT QUALIFIERS

If the user clicks on the “EXPORT FREE TEXT QUALIFIERS” button at the top of the View, and then in the dialog box, select the file name and location to save the qualifier text file, **all** of the free-text qualifiers of the project will be exported and saved to an XLIFF file format.

The file will include:

- The project source language.
- The project target language.
- The free-text qualifiers values.
- The translated qualifier free-text values<sup>8</sup>.
- The associated Qualifier and Feature information provided in the Table shown in Figure 107.

This file can be viewed, edited and imported in the tool again after providing the appropriate translation following the steps shown in section 5.3.1.

## 5.4 IMPORT REPORT

If a project is imported from a sequence listing (ST.25 or ST.26) or when the user imports multiple sequences from a file (with formats ST.26, ST.25, raw, FASTA or multi-sequence), then the corresponding Import Report will include a Table with all the changes made to the data to adapt the imported sequence listing to the correct format.

If a project was not created by process of importing and no sequence has been imported into the project, the Import Report view will display the banner shown in Figure 108.

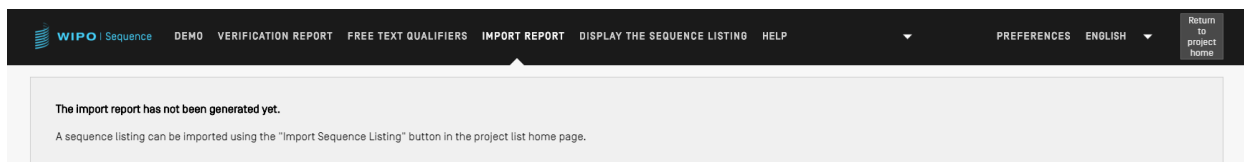


Figure 108: Import report view, no import performed

If an import has been successfully completed and the project has been created, the View could display the following two Tables:

- Import Report Table (see section 5.4.1)

---

<sup>8</sup> The translation of the selected Non English free text language code provided in the project during export

- Change Data Table (see section 5.4.2)

## 5.4.1 Import Report Table

Type of Note	Data Element	Message Text	Detected Sequence
Global		Please provide appropriate value(s) for the qualifier 'mol_type' of the following SEQ ID NO(s): 5, as prescribed by Annex VII, ST.26.	
Global		Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences.	
Global	<300> - <313>	SEQ ID NOs: [4] contain publication information (ST.25 numeric identifiers <300> to <313>) that has not been imported into the project. This information can be inserted into the accompanying application body, if not already contained therein: SEQ ID: 4 => fields	
Global	<221>	Mandatory features source/SOURCE have been automatically created with the exception of intentionally skipped sequences.	
Global	<400>	Three-letter amino acid symbols have been replaced with their corresponding one-letter codes.	

Figure 109: Import report, generated

The Import Report Table is shown only when importing a file results in errors and displays the following columns:

- **Type of note:** “INDIVIDUAL” for a message related to a specific sequence or “GLOBAL” for one or more sequences generally;
- **Data element code:** from the source file, for ST.25 sequence listings;
- **Message text:** Detailed message with information on the identified issue in question and the changes made to rectify it (if any);
- **Detected sequence:** Sequence number of the imported sequence related to the message (when the type is “INDIVIDUAL” otherwise this field is blank).

## 5.4.2 Change Data Table

The screenshot displays the 'Change Data' table within the WIPO Sequence application. The table lists transformations applied to sequence elements during the import process. The columns are: Origin Tag, Origin Element Name, Origin Element Value, Target Element Name, Target Element Value, Transformation, and Sequence ID Number. The table contains four rows of data, each representing a different transformation. Below the table, there are navigation controls including a 'Return to project home' button and page navigation buttons for pages 1 and 2.

Origin Tag	Origin Element Name	Origin Element Value	Target Element Name	Target Element Value	Transformation	Sequence ID Number
<222>	Feature Location		Feature Location	1..184	A feature location has been specified automatically since one was not provided.	4
<221>	Name/Key		Feature Key	REGION	The custom feature key has been replaced with a recommended key [see Annex VII, ST.26].	4
<223>	Other information		Qualifier Name	NOTE	A 'Note' qualifier has been created.	4
<223>	Other information		Qualifier Value	synthetically generated sequence	A value has been added to qualifier.	4

Figure 110: ChangeData table

This Table displays any data that has undergone a transformation or change during the importing process. This following data is presented in Table columns (see Figure 110):

- **Origin Tag:** data element code for the element type, for ST.25 sequence listings;
- **Origin Element Name:** corresponding name for the element type;
- **Origin Element Value:** corresponding value of the original element in the source file
- **Target Element Name:** equivalent ST.26 element name where the information is going to be stored in the project;
- **Target Element Value:** value that will be set for the Target Element Name in the project;
- **Transformation:** description of the change(s)/transformation made to the element;
- **Sequence ID Number:** ID number of the relevant sequence of the transformed element in the project.

## 5.5 DISPLAY SEQUENCE LISTING

WIPO Sequence allows the user to generate a sequence listing in a more human-readable format than XML. When the “DISPLAY THE SEQUENCE LISTING” View is accessed, it will first present a blue banner indicating that the sequence listing file has generated successfully, along with two options to display the aforementioned sequence listing as (.html) or (.txt) format (see Figure 111).

For further details on how to generate a sequence listing, go to section 5.1.1.5.

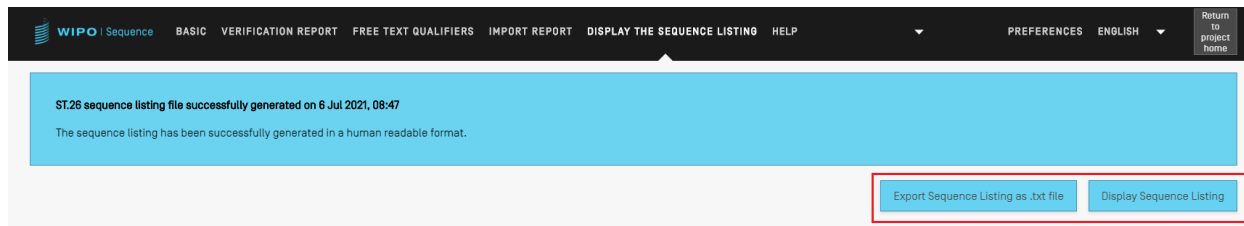


Figure 111 Display Sequence Listing, generated

If a sequence listing has not been successfully generated for a given project, then the Display Sequence Listing View will disable the “Display Sequence Listing” & “Export Sequence Listing as .txt file” buttons and the user will see the error shown in Figure 112.

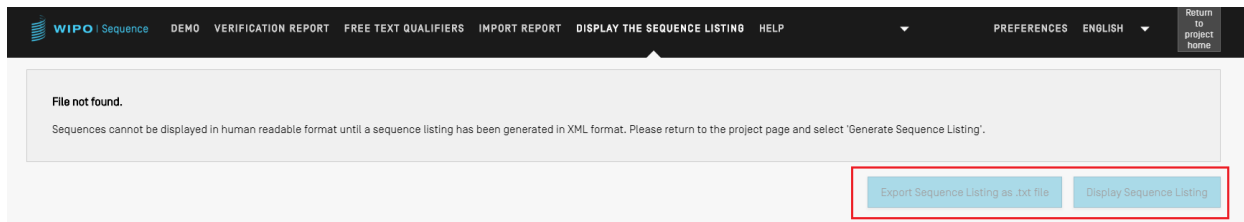


Figure 112: Display Sequence Listing, not generated

When the user clicks on the “Display Sequence Listing” button, a HTML file will be opened in the default browser. This provides a formatted view of the ST.26-compliant XML file so that the values of particular fields are more visible to the user. An example is shown in Figure 113.

**Note:**

*To display the sequence listing in another language, the sequence listing must be generated again. First the new language for the interface is selected within the tool and then the steps above can be repeated.*



← → ↻ 🏠 ⓘ File | C:/Users/ /AppData/Roaming/ST26\_authoring/Project\_458/generated.html

## Sequence Listing

### Sequence Listing Information

File Name	validSTS.xml
DTD Version	V1_3
Software Name	WIPO Sequence
Software Version	1.1.0-beta.7
Production Date	2021-07-06

### General Information

Current application: IP Office	US
Current application: Application number	1231123343
Current application: Filing date	2019-05-02
Current application: Applicant file reference	app_file_ref
Earliest priority application: IP Office	US
Earliest priority application: Application number	1231123343
Earliest priority application: Filing date	2019-04-30
Applicant name	Vault Tec
Applicant name: Language	en
Applicant name: Name Latin	
Inventor name	Vault Tec
Inventor name: Language	en
Inventor name: Name Latin	
Invention title	FEV ( en )
Invention title	fd̂f ( ru )
Sequence Total Quantity	3

### Sequences

Figure 113: Display Sequence Listing, HTML

**Note: the location of the HTML file will be displayed in the navigation bar of the user's browser, in case the user wishes to copy the file into a different location.**

When the user clicks on the “Export Sequence Listing as .txt file” button, a txt file will be opened. This provides a formatted view of the ST.26-compliant XML file so that the values of particular fields are more visible to the user. An example is shown in Figure 114.

## Sequence Listing Information:

DTD Version: V1\_3  
 File Name: validSTS.xml  
 Software Name: WIPO Sequence  
 Software Version: 1.1.0-beta.7  
 Production Date: 2021-07-06

## General Information:

Current application / IP Office: US  
 Current application / Application number: 1231123343  
 Current application / Filing date: 2019-05-02  
 Current application / Applicant file reference: app\_file\_ref  
 Earliest priority application / IP Office: US  
 Earliest priority application / Application number: 1231123343  
 Earliest priority application / Filing date: 2019-04-30  
 Applicant name: Vault Tec  
 Applicant name / Language: en  
 Inventor name: Vault Tec  
 Inventor name / Language: en  
 Invention title: FEV ( en )  
 Invention title: fdf' ( ru )  
 Sequence Total Quantity: 3

## Sequences:

Sequence Number (ID): 1  
 Length: 368  
 Molecule Type: DNA  
 Features Location/Qualifiers:  
 - source, 1..368  
     > mol\_type, other DNA  
     > organism, synthetic construct  
 - STS, 1  
 - STS, 2..4

## Residues:

atcatgctaa	tcatgctagc	tagtagctga	tgatcatgct	agcatcatgc	taatcatgct	60
agctagtagc	tgatgatcat	gctagctagt	agctgatgat	catgctagct	agtagctgat	120
gatcatgcta	gctagtagct	gatgatcatg	ctagctagta	gctgatgctc	atgctagcta	180
gtagctgatg	atcatgctag	ctagtagctg	atggctagta	gctgatgtag	tagctgatga	240
tcatgctagc	tagtagctga	tgatcatgct	agctagtagc	tgatgatcat	gctagctagt	300
agctgatgat	catgctagct	agtagctgat	gatcatgcta	gctagtagct	gatggctagt	360
agctgatg						368

## Sequence Number (ID): 2

Length: 368  
 Molecule Type: RNA  
 Features Location/Qualifiers:  
 - source, 1..368  
     > mol\_type, genomic RNA  
     > organism, Asaccus elisae  
 - gene, 1  
 - gene, 2..4

Figure 114: Display Sequence Listing, TXT

## 5.6 HELP

The tool will allow the user to view the help options available to get assistance using this tool (see Figure 115).

Help options direct to information that will:

- Provide a link to the User Manual
- Provide a link to the FAQ
- Provide a link to Contact WIPO
- Provide a link to the Standard ST.26
- Describe the Tool

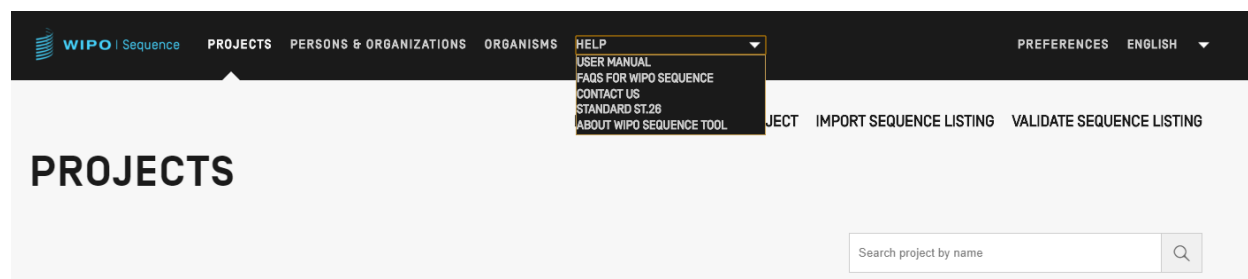


Figure 115 Help

## 5.7 PREFERENCES

The last View is where the user can set specific properties which apply to all projects which has been detailed previously.

For further details refer to the section **4.4**.

## 6 FILE FORMATS

### 6.1 ST.25

For details on the format of WIPO Standard ST.25 files please refer to:

<https://www.wipo.int/export/sites/www/standards/en/pdf/03-25-01.pdf>

### 6.2 MULTI-SEQUENCE

The multi-sequence format<sup>9</sup> can describe one or multiple sequences, along with their name, the type of molecule and the name of the organism and is one of the allowable formats for import using PatentIn.

The first line of non-blank text is the header and is comprised of the following components:

```
<SequenceName; SequenceType; OrganismName>
```

Sequence data begins on the line after the header. A new sequence is delineated by a new line in the file, after the end of the genetic code of the previous sequence. The following is an example of a set of two sequences defined in multi-sequence format.

Example:

```
<First Sequence; RNA; Albies alba>
```

```
uuuucuuauuguuuucuccuacugcuuaucauaaugauugucguaguggcuuccuauugucuccccacc  
gccuaccacaacgacugccgcagcggauuacuaauaguaucaccaacagcauaacaaaagaauagacgaa  
gagggauugcugaugggugucgcgcagcggcguagcagaaggaguggcggagggg
```

```
<Second Sequence; DNA; Albies alba>
```

```
attgaugtuagtgauguggtautgaugtuagutguagtautgaugtauuaauuauagtggtagututuga  
uatguaautgautugtugutattgaugtuagtgauguggtautgaugtuagutguagtautgaugtauua  
auuauagtggtagututugauatguaautgautugtugutuagt
```

---

<sup>9</sup> [https://www.uspto.gov/sites/default/files/patents/resources/tools/checker/patentin351\\_20110214\\_6.pdf](https://www.uspto.gov/sites/default/files/patents/resources/tools/checker/patentin351_20110214_6.pdf)

### 6.3 RAW

This format can only describe one sequence. The genetic code is written in its basic form with no additional information. When imported, molecule type, features and name must be added to the sequence through the tool.

Example:

```
aggat atagatag tata tgat agtat gat atgat gat gtat gtat agtg tagt tatga
```

### 6.4 FASTA

This format contains residues and description and while importing the user has the option to save the description as a note qualifier

#### 6.4.1 FASTA file with one sequence

```
>AJ011880.1 Artificial oligonucleotide sequence SSR primer  
(CAC13R)
```

```
CTCAACAATCTGAAGCATCG
```

See <https://www.ncbi.nlm.nih.gov/nuccore/3724029?report=fasta> (accessed on 22 May 2017)

#### 6.4.2 FASTA file with several sequences (FASTA-Multi)

```
>SEQUENCE_1  
MTEITAAMVKELRESTGAGMMDCKNALSETNGDFDKAVQLLREKGLGKAAKKADRLAAEG  
LVSVKVSDDFTIAAMRPSYLSYEDLDMTFVENEYKALVAELEKENEERRRLKDPNKPEHK  
IPQFASRKQLSDAILKEAEEKIKEELKAQGKPEKIWDNIIPGKMNSFIADNSQLDSKLTLL  
MGQFYVMDDKKTVEQVIAEKEKEFGGKIKIVEFICFEVGEGLKKTEDFAAEVAAQL  
>SEQUENCE_2  
SATVSEINSETDFVAKNDQFIALTKD'TTAHIQSNSLQSVEELHSSTINGVKFEEYLKSQI  
ATIGENLVRRFATLKA GANGVVNGYIHTNGRVGVVIAACDSAEVASKSRDLRQICMH
```

See [https://en.wikipedia.org/wiki/FASTA\\_format](https://en.wikipedia.org/wiki/FASTA_format) (accessed on 22 May 2017)

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