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.
# 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 and (ii) verify the compliance of a sequence listing in XML format against WIPO ST.26 requirements.

The WIPO ST.26 can be found at:


This document describes how to use WIPO Sequence as an applicant or a representative of an applicant.

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 support 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 specification:

- 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 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.

The database files used for storing the project information along with the log of the tool are stored under this path:

C:\Users\<user>\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 through the command line.

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

1.2.1.3 OSX

WIPO Sequence provides a dmg file for installing the application on a MacOS 64 bits. 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 under this path:

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

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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.

In order to enable the auto update, the computer must have internet connection and the tool must have permissions to access the WIPO website through HTTP

1.2.4 Uninstall

1.2.4.1 Windows

WIPO Sequence provides a 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 removed:

C:\Users\<user>\AppData\Roaming\ST26_authoring

1.2.4.2 Linux

By removing Linux AppImage file the application is uninstalled from the computer. Additionally the menu entry can be removed by deleting the desktop file from $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 removed:

/Users/<username>/.config/ST26_authoring
1.2.4.3 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 removed:

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

1.2.5 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.

---

In order to enable the auto update, the computer must have internet connection and the tool must have permissions to access the WIPO website through HTTP
2 TOOL OVERVIEW

2.1 TOOL MAIN ELEMENTS

This section details the main elements of the tool. The goal is for the user to be familiar with the common interaction concepts that each of these components provide.

2.1.1 Page

The Page is the main container for views within the tool. There are 2 main pages that contain views within them:

- Main Page
  - Project List view
  - Persons and Organizations view
  - Custom Organisms view
- Project Page (accessible from the Project List view)
  - Project Detail view
  - Verification Report view
  - Free Text Qualifiers view
  - Import Report view
  - Display Sequence Listing view
Figure 1 Main Page containing three views
2.1.2 View

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

2.1.3 Sections

Some views can have Sections. Sections provide a convenient way of accessing different parts of a large view.

Within the Project Detail view, there are 2 collapsible sections: General Information & Sequences.

(1) At the top of the Project Detail view there are 2 links that will navigate the user to the corresponding sections. (2) Each section is collapsible for the sake of ease of navigation, collapsibility is indicated by the small triangle to the left. (3) The user can click on the arrow icon to scroll to the top of the screen.
2.1.4 Overlay

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

![Figure 3 Overlay](image)

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

2.1.5 Tables

![Figure 4 Tables](image)

Tables appear as in Figure 4. When search is enabled for the table, the user can enter some characters 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).

![Table edit](Image)

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

### 2.1.6 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.

![Panel View](Image)

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

Once an edit panel has been opened, the user is presented with fields that can be modified. 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, appear greyed out.

Figure 7 Edit Panel
2.1.8 Date picker

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

![Figure 8 Date picker](image)

The currently selected date is marked with a grey background (22nd), and the day of use is indicated with a black underline (26th). The weekday order of the columns is Sunday -> Saturday. Conversely, the user can also simply type in the desired date in the format YYYY-MM-DD (3).
2.2 PDF VIEWER

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.

![PDF Viewer](image-url)
3 MAIN PAGE

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

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

![Figure 10 Project list view](image)

![Figure 11 Persons & Organizations page](image)
3.1 PROJECT LIST VIEW

This section details the different options accessible in the Project List 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 data, once it has passed the validation process to generate sequence Listings.

3.1.1 Create Project

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

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).
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 project list which includes this new project is shown in Figure 15.

### 3.1.2 Import Project

This functionality allows the import into the tool of a previously exported project as described in section 4.1.1.4 Export Project. To import a project file, the user must begin from the Projects list screen.
1) Click on the “IMPORT PROJECT” link at the top of the view as indicated in Figure 17.

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).
4) If “Select Range Sequences” remains unchecked, all the sequences will be imported. If the user wishes to select which of the sequences to import with the project, check the “Select Range Sequences” checkbox (1) and enter the ID numbers of the desired sequences in the “Select range Sequence Id Numbers” field (2) that appears as 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.
3.1.3 Import Sequence Listing

From the Project list 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.

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).

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”.

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The first checkbox will allow the user to discriminate which of the sequences they wish to import from the list in the file.

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 has two columns, one gives the Sequence ID Number to identify to the corresponding sequence and the other gives the “position” in which it will appear in the list.
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 by checking the corresponding checkbox for each element, 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 following view shown in Figure 24 will be displayed with the automatic changes made to the ST.25, RAW and MULTI sequence listing data in order to adapt it to the requirements of ST.26.
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.

<table>
<thead>
<tr>
<th>Type of Note</th>
<th>Data Element</th>
<th>Message Text</th>
<th>Detected Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>INDIVIDUAL</td>
<td>&lt;223&gt;</td>
<td>In SEQ ID NO.1, the mandatory qualifier for SITE has been added with no value, together with the provisional qualifier &quot;note&quot; or &quot;NOTE&quot; with the value from the associated &lt;223&gt; field in the ST.25 sequence listing. Consult the User’s Manual for further instructions.</td>
<td>1</td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>&lt;400&gt;</td>
<td>The first amino acid should be numbered 1.</td>
<td>1</td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>&lt;222&gt;</td>
<td>No location information has been found for the feature misc_feature of SEQ ID NO.2. The user can add the location information as recommended in Annex VII, ST.25.</td>
<td>2</td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>&lt;223&gt;</td>
<td>For sequence SEQ ID 2 with feature CDS, the &lt;223&gt; value is missing, please review it in consultation with the User’s Manual.</td>
<td>2</td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>&lt;221&gt;</td>
<td>SEQ ID NO.2 contains a CDS feature. The Standard genetic code (Genetic Code Table I) is assumed; if a different Genetic Code Table is needed for translation, then a qualifier 'nonstandard_table' may be used to specify the appropriate table (Consult Annex VII, ST.25 for further guidance).</td>
<td>2</td>
</tr>
</tbody>
</table>

Figure 25 Import sequence listing, Import report

At this point, the user can return to the Project list 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 brought to an Import report view with information on the errors identified, see Figure 26.
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**
- **Must contain a DOCTYPE line as follows:**

  ```xml
  <!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.2//EN"
  "ST26SequenceListing_V1_2.dtd">
  
  Attribute dtdVersion should be compliant with the DTD version:
  
  ```xml
  <ST26SequenceListing dtdVersion="V1_2">
  
  The file must comply with DTD file ST26SequenceListing_V1_2.dtd.
  ```

To return to the Project list, the user must click on the “Back to list” button in the header shown in Figure 26.

---

1 See [https://www.w3.org/TR/2006/REC-xml-20060816/Overview.html#charsets](https://www.w3.org/TR/2006/REC-xml-20060816/Overview.html#charsets)
3.1.4 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 list view, shown in Figure 27.

![Figure 27 Validate sequence listing](image)

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 Project” button (3).

![Figure 28 Validate sequence listing (dialog box)](image)

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

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.

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\(^2\)

- Must contain a DOCTYPE line as follows:

```xml
<!DOCTYPE ST26SequenceListing PUBLIC "//WIPO//DTD Sequence Listing 1.2//EN" "ST26SequenceListing_V1_2.dtd">
```

- Attribute dtdVersion should be compliant with the DTD version:

```xml
<ST26SequenceListing dtdVersion="V1_2">
```

- The file must comply with DTD file ST26SequenceListing_V1_2.dtd.

\(^2\) See [https://www.w3.org/TR/2006/REC-xml-20060816/Overview.html#charsets](https://www.w3.org/TR/2006/REC-xml-20060816/Overview.html#charsets)
3.1.5 Delete Project

To delete a project, the user must begin from the projects list screen.

Click on the button with the trash can icon on the row within the project list table that the user wishes to delete.

In the pop-up click “Yes” to confirm that you want to delete the selected project.
3.2 PERSON & ORGANIZATIONS

3.2.1 Create

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

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

In the new screen, the user must fill the fields corresponding to the person/organization that is being created in the tool.

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.
3.3 CUSTOM ORGANISMS

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

3.3.1 Create Custom 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”.

3.3.2 Export Custom Organisms

All the custom organisms 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:
Next, a dialog box will open for the user to choose the name of the file and the location to which said file should be saved with the custom organisms, see Figure 38.
3.3.3 Import Custom Organisms

In order to import a list of custom organisms, first, the user must click on the “IMPORT CUSTOM ORGANISMS” link at the top of the view, as shown in Figure 39. This will open an overlay below the Organisms table, as shown in Figure 40.

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)
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.

3.4 PREFERENCES

The preferences view allows the modification of several configuration parameters of WIPO Sequence. These parameters will apply to every project handled by the tool:

![System Preferences Panel]

In order to modify the system preferences the user should click on the pencil icon shown above to open the edit panel:
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 in when displaying a sequence: default is 60.
- Default location where the sequence listing XML file will be generated
- Maximum number of sequences to print (Leave empty for all): default is 1000
- Maximum number of residues to print (Leave empty for all): default is 1200

*The two last items refer to the print of the project as a PDF. For very large sequence listings, the resulting PDF can have several thousand pages and impossible to display.*
4 PROJECT PAGE

The project page is composed of 6 views that can be used to navigate between different portions of the workflow, as shown in Figure 41:

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

![Project page header]

To return to the Project List view of the Main page, the user can click on the “Back To List” button (7) at the right end of the header.

4.1 PROJECT DETAIL

4.1.1 Basic Information

A table containing the basic information about the project can be found at the top of the Project Detail view, see Figure 42.

This section contains:

- Name of Project
- Date of Creation
- Name of import file (in the case that the project was imported)
- Number of Sequences (labelled: ‘Sequences’)
- Project description
- Project status (new/modified/generated/invalid/valid/warnings)

Figure 42 Basic Information section

4.1.1.1 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 43.

Next, the user will be shown two check boxes to clarify what information the user wants to print of the project, General Information and/or Sequence Information, see Figure 44.
If “Print Sequences” is selected, the user will have the choice to specify which sequences are to be printed with their associated information by means of their ID numbers through 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.

To download the PDF file, see section (2.2).

4.1.1.2 Import Information From Another Project

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

Note: imported General Information will replace the currently existing General Information in the project.

On the other hand, 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 45.
The tool will open an overlay, as shown in Figure 46. The user must first select the project from which they wish to import information.

Next, as shown in Figure 47, the user can select whether they wish to include parts of the information from the General Information (1) section of the project and also enter a set of sequence ID numbers (2) to specify which of the sequences are to be imported in the project.
If the General Information checkbox is selected then a table will appear displaying all the General Information of both projects, the currently selected (origin) project, and the target import (target) project.

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 48.

![Figure 48 Import Another Project, select general information elements](image)

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 48.

![Figure 49 Import Another Project, success banner](image)

If the elements were imported correctly, a banner will appear as shown in Figure 49.

4.1.1.3 Validate Project
A project can have its information passed through a validation check, to ensure that all the data follows the format descriptions of the Standard WIPO ST.26, before generating the sequence listing.

To validate a project, the user must click on the “Validate” button at the top of the Project Detail view, shown in Figure 50.

Once the validation test has finished, the user will be brought to the “Verification Report” view of the Project page, displaying the verification errors/warnings, if any. Figure 51 shows the screen that will be displayed in the case of successful validation.

If the validation process finds any errors or warnings, a validation report will be generated with a table of the detected verification rules and guidelines that have been broken. An example report is shown in Figure 52.
**ERROR:** After project verification, some errors or warnings have been detected.

<table>
<thead>
<tr>
<th>Severity</th>
<th>Data Element</th>
<th>Message Text</th>
<th>Detected Value</th>
<th>Detected Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>WARNING</td>
<td>Feature Qualifiers</td>
<td>Verify that the ‘note’ qualifier describes the ‘OTHER’ or ‘other’ value for the ‘mod_base’, ‘ncRNA_class’, or ‘regulatory_class’ qualifiers.</td>
<td>xyz</td>
<td>Sequence 392</td>
</tr>
<tr>
<td>WARNING</td>
<td>Organism</td>
<td>The organism name has not been found in the list of predefined and custom organism names stored in this system. Suggestion: this organism may be added to the list of custom organism names.</td>
<td>Phytobacteria sp.</td>
<td>Sequence 394</td>
</tr>
<tr>
<td>ERROR</td>
<td>Qualifier Value</td>
<td>The mandatory qualifier value is missing.</td>
<td>mol_type</td>
<td>Sequence 394</td>
</tr>
</tbody>
</table>

Figure 52 Project validate, errors/warnings
4.1.1.4 Export Project

A project can be exported to a .zip file for the user to back-up this data or alternatively import with another computer with WIPO Sequence, shown in Figure 53.

1) Click on the “Export” button at the top of the Project Detail view.

2) In the dialog box that appears, select the name and location with which to save the project.

If the project is successfully exported, a success banner with the saved name and location will appear at the top of the screen as shown in Figure 54.
The final action that can be performed on a project from the Basic Information section 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 55. This will automatically trigger the validation process to be run on the project first.

If the project passes the validation test, a dialog box will open for the user to select where to save the generated .xml file with the sequence listing data, shown in Figure 56.
If the project fails the validation test, then the verification report view will be opened along with a red banner as shown in Figure 57.

Figure 56 Generate Sequence Listing Dialog box

Figure 57 Generate Sequence Listing, Failed
4.1.2 General Information

This section allows the user to enter information about the project itself, not related to the technical sequence information.

4.1.2.1 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 58.

<table>
<thead>
<tr>
<th>GENERAL INFORMATION</th>
</tr>
</thead>
<tbody>
<tr>
<td>APPLICATION IDENTIFICATION</td>
</tr>
<tr>
<td>Application identified before the assignment of the application number</td>
</tr>
<tr>
<td>Application filed</td>
</tr>
<tr>
<td>IP Office BD - Bangladesh</td>
</tr>
<tr>
<td>Application number 12345</td>
</tr>
<tr>
<td>Filing date: 2005-02-20</td>
</tr>
</tbody>
</table>

To enter/modify application identification information, click on the edit button, the pencil icon highlighted, to the right of the section. Then the user must conduct the following steps shown in Figure 59:

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.

2) The user must select whether or not the application file reference has been provided at the time of requesting an application number or not.

3) In the case of not yet having the application number, the user MUST provide the Applicant file reference in this field.

4) If an application number has already been assigned, 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
4.1.2.2 Priority Identification

To add a Priority Application to the project, the user must click on the “Add Earliest Priority Identification” button in the General Information section of the Project Detail view, shown in Figure 60.

To set the currently selected priority application as the earliest, the user must select “Yes” in the “Selected Earliest Priority Application”. This will replace whatever priority application that was previously established as the Earliest Priority Application.

To finish, click on the blue “Add Earliest Priority Application” button in the overlay, shown in Figure 61.
4.1.2.3 Applicant & Inventor

To add 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 both are identical from here). Note, 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 62. If “Existing applicant/inventor” is selected, the user can choose from a drop-down box a list of currently saved persons and organizations within this instance of the Tool.

If “New applicant/inventor” is selected, the user must fill out the panel that appears just as when a new person/organization is being created (see Section 3.2.1 and Figure 63)
4.1.2.4 Invention Title

The invention title is the last part of the General Information section.

1) To add a new invention title, click on the “Add Invention title” button, see Figure 64.

2) In the overlay, the user must enter the title of the invention and also indicate what language the given title is in.

3) Click the blue “Add Invention title” button.

According to the Standard, a project can only have one Invention Title value provided in each language.
4.1.3 Sequences

This 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 of the Project Detail view. Further details on the steps required are set-out below.

4.1.3.1 Create Sequence

1) Click the “Create new sequence” button, as shown in Figure 65.

![Figure 65 Create new sequence](image)

The remainder of the steps are shown in Figure 66:

2) The user can select a name to make it easier to distinguish between other sequences. It is not compulsory to fill out this field. If left blank, the tool will assign a default value with each 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 provided by the select box (DNA, RNA & AA) (2), the sequence itself must be entered in the “Residues” text field (3). If the user wishes to create a sequence with both DNA & RNA segments, DNA must be selected as the main Molecule Type.

---

3 See ST.26 standard – Annex I, Sections 1 & 3 for the tables of valid Nucleotide symbols & Amino acid symbols
The user must also select an organism name for the sequence being created, this can be either from a list of existing organisms in the tool database or one of the custom organisms created by the user. For this, the “Existing organism” radio button must be selected (4).

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

The user can also classify the organism by selecting a Qualifier Molecule Type\(^4\) from a select box (5) that varies depending on the Molecule Type previously selected.

If “Mark as an intentionally skipped sequence” (6) is checked, the sequence panel will remove all mandatory constraints and the resulting saved sequence will be ignored when validating the project and generating a sequence listing.

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 in 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, DNA and RNA segments.

---

\(^4\) See ST.26 standard – Annex I, Sections 6 & 8 for the Qualifier values for the mol type entry under the Nucleotides and Amino acids tables respectively
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 “Display & Create sequence” button, a collapsible sequence display will open after creating the sequence, beneath the sequences section within the Project Detail view.

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

(To see details on how to reorder the Sequence list, see Section 4.1.3.4)
4.1.3.2 Import Sequence

Sequences can also be imported directly from files into a project. The accepted file formats are RAW, MULTI, ST.26 and ST.25. When selected, the tool will automatically detect the format used in the file.

5 See File Formats (section 5)
1) Click on the “Import sequence button”, as shown in Figure 68.

2) Click on the “Upload file [.txt, .xml]”, shown in Figure 69.

When the dialog box opens, select the sequence file to be imported. The tool will detect the format being used and will validate the sequence data to be imported.

There are four formats that the tool will accept for importing sequences, RAW, MULTI, ST.26 and ST.25. These are outlined in the file formats section 5.

In the case of selecting a file that is in ST.25 or ST.26 format (see Figure 70), 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 project sequence list.

If the user does not wish to import all of the sequences to the project, they can select the set of sequences that they are interested in by entering their 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.
Example: “1,3,7,13-20,30-50”

In the case of selecting a **MULTI** file (see Section 5.1 for information on this format and fig 71), the user will see a “Select Range Sequences” checkbox (1), which when checked, will display a table showing the Sequence ID Numbers of the corresponding sequences in the file and also the details of each sequence under the “Detail” column (2), including sequence name, Molecule Type and Organism name.

The user must select the set of Sequence ID’s that they wish to import to the list of sequences (3).
The last case for formats that are accepted by the import Sequence process is the **RAW** file format (see section 5.3 for information on the format). This format only defines a single sequence per file. When a RAW file is selected, the tool will display an edit panel that requests as a minimum, the Molecule Type of the sequence being imported Figure 72.

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

After the import, the tool will navigate to the Import Report view, detailed in section 4.4
4.1.3.3  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 (see Figure 73).

<table>
<thead>
<tr>
<th>Sequence ID Number</th>
<th>Sequence Name</th>
<th>Length</th>
<th>Molecule Type</th>
<th>Organism</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>US20190136258A1-20190509-000001_seq_SEQ ID NO 1</td>
<td>245</td>
<td>RNA</td>
<td>Rebilus crediton</td>
</tr>
<tr>
<td>2</td>
<td>US20190136258A1-20190509-000001_seq_SEQ ID NO 2</td>
<td>1481</td>
<td></td>
<td>Pseudomonas sp.</td>
</tr>
<tr>
<td>3</td>
<td>US20190136258A1-20190509-000001_seq_SEQ ID NO 3</td>
<td>1458</td>
<td></td>
<td>Pseudomonas montellii</td>
</tr>
<tr>
<td>4</td>
<td>US20190136258A1-20190509-000001_seq_SEQ ID NO 6</td>
<td>1458</td>
<td></td>
<td>Pseudomonas extremozonatis</td>
</tr>
<tr>
<td>5</td>
<td>US20190136258A1-20190509-000001_seq_SEQ</td>
<td>1470</td>
<td></td>
<td>Woodsholes maritima</td>
</tr>
</tbody>
</table>

An overlay with a panel will appear (see Figure 74). The user must fill out all the information required for creating a sequence (4.1.3.1), and in addition, at the top of the panel, the user must enter the position in which the sequence should appear in the list of sequences (Sequence Number ID Number field highlighted).
To finish, the user can click on the insert “Insert sequence” or “Insert & Display Sequence”, highlighted in Figure 74.

If the user clicks on the blue “Insert & Display sequence” button, a collapsible sequence display will open after creating the sequence, beneath the sequences section within the Project Detail view, as shown in Figure 75.

Figure 74 Insert sequence panel

Figure 75 Sequence Inserted

Figure 75 Sequence Inserted
4.1.3.4 Reorder Sequence

The user can reorganize in what order the sequences should appear within the project sequence list by using the following steps.

1) Click on the “Reorder Sequence” button, shown in Figure 76.

![Figure 76 Reorder Sequence](image)

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 77.

![Figure 77 Reorder Sequence panel](image)

The sequence order transformation is shown from Figure 76(start) to Figure 78(result).
4.1.3.5  Edit Sequence

To edit a sequence, the user must click on the Sequence ID Number of the corresponding sequence to be modified, as shown in Figure 79.

This will open a new section in the Project Detail view beneath the Sequences section, as shown in Figure 80.
The sequence display is composed of the basic info panel (1), the features list section (2) and the sequence section (3).

4.1.3.6 Features

According to the Standard, every sequence has at least one feature associated with it: source or SOURCE.

- The Features table has 3 columns, the Feature Key, the location of the feature within the genetic sequence and the qualifiers associated with each individual sequence feature.

The location format indicates in what segment of the sequence the feature exists.

The possible location formats are as follows, according to Standard ST.26: Structure of the Sequence Listing, Feature Location:

- Single residue number: 467
- Residue numbers delimiting a sequence span: 340..565
- Residues before the first or beyond the last specified residue number: <42
• A site between two adjoining residue numbers: 123^124

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

• “join (location, location, ... location)”: The locations are joined (placed end-to-end) to form one contiguous sequence.

• “order (location, location, ... location)”: The elements are found in the specified order but nothing is implied about whether joining those elements is reasonable.

• “complement (location)”: 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 feature section of the selected sequence display section, shown in Figure 81.

![Figure 81 Add feature](image)

Next, in the overlay that opens shown in Figure 82, select an entry from the Feature Key list and specify the start and end positions within the sequence that the feature applies to.

---

6 See ST.26 standard – Annex I, Sections 5 & 7 for tables of feature keys for Nucleotides and Amino acids
Qualifiers can also be added to the feature at this stage, but they will be covered in the next section (4.1.3.7).

To finish, click the blue “Create Feature” button, shown in Figure 82.

4.1.3.6.1 **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 Project. Within the CDS Feature of the original Sequence the ID of the translated Amino Acid Sequence will be referenced by the “protein_id” qualifier.

When creating a “CDS” feature for a Sequence, a ‘translation’ Qualifier (with default “Genetic Code” value of 1 – Standard Code) is automatically added to the feature in order to translate a residue chunk of the sequence. However this qualifier is not mandatory and can be deleted after generation. The user can manually create a “protein_id” qualifier of their own and associate the translated Sequence ID to the qualifier value.

If the user wishes to follow the automatic process, 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 their values, in which case the linked sequence will be updated.

**NOTE:** If the translation value is changed, the linked sequence will update its value. On the other hand, if the linked nucleotide sequence has its residues modified, the qualifier translation value will not change. If the “protein_id” qualifier is modified after creation, then the linked sequence will lose its association to the original sequence.

### Automatic CDS Feature creation

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

1) In the sequence display, click the “Add feature” button and select “CDS” for the Feature Key. This will create a “translation” qualifier.

2) Click the pencil icon on the translation qualifier to modify the values. The resulting overlay is shown in Figure 83.

![Figure 83 Add CDS feature](image-url)
3) If the genetic code\textsuperscript{7} is changed from its default value (1 – Standard Code), then another qualifier, “transl_table” will be generated automatically.

4) When the user is finished with 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 84.

The tool then \textbf{creates a new sequence}\textsuperscript{*} 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 (Figure 83), if none was provided, the default Sequence naming format will be followed (Seq_#).
- Molecule Type = “AA”
- Organism Name = the same value as for the original sequence
- Qualifier Molecule Type = “protein”
- Residues = translated values of the original sequence
- A resulting example of this process is shown in Figure 85.

\textsuperscript{7} See \textit{ST.26 standard – Annex I, Section 9} for the list of possible Genetic Code Tables. A reference to the Standard is provided at the end of this document.
Figure 85 CDS feature, generated sequence

*Please 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 well as the protein_id qualifier.

4.1.3.7 Qualifiers

To view the qualifiers for a feature, the user must first select the desired feature from the feature table of the sequence being viewed, as shown in Figure 86.
Clicking on a Feature Key will open the following feature overlay, as shown in Figure 87.

Existing qualifiers can be modified 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 two fields, the Qualifier name (to be selected from a list) and the Qualifier value, as shown in Figure 88.

![Figure 88 Qualifier Panel](image)

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

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

![Predefined Values](image)

- **Qualifiers with free text.** The value field is a free-text field. An additional field appears to allow the user to provide the translated value of the free-text value, as shown below:

![Free Text](image)

---

8 See *ST.26 Standard – Annex I, Sections 6 & 8* for all possible Qualifiers for Nucleotides and Amino acids.
- **Qualifiers with predefined format.** The value field is a free-text field, but a validation is run on the format of the introduced text so it matches the specific rules for this value as per WIPO ST.26 Annex I, Section 6:\n
```
Qualifier Name
collection_date
```

```
Qualifier Value
2002-09-1
```

> Invalid qualifier value format. The value for the qualifier ‘collection_date’ must have the format ‘YYYY-MM-DD’, ‘YYYY-MM’ or ‘YYYY’.

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

```
Qualifier Name
gene
```

When finished, the user must click the blue “Create Qualifier” 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 89.

---

Figure 89 Update feature
4.2 VERIFICATION REPORT

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

To generate the verification report, see section (4.1.1.3)

The following view will have one of two resulting pages: depending on if the project sequence listing is valid or not. These are shown as Figure 91 (errors/warnings) and Figure 92 (successful validation).
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 91. The generated report will be displayed in the PDF viewer as explained in section (2.2) PDF Viewer

<table>
<thead>
<tr>
<th>Severity</th>
<th>Data Element</th>
<th>Message Text</th>
<th>Detected Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>WARN</td>
<td>earliest priority application</td>
<td>Earliest priority application information has not been entered. It must be</td>
<td>&quot;IPDcode&quot;:&quot;&quot;,&quot;applicationNumb...</td>
</tr>
<tr>
<td></td>
<td>Identification</td>
<td>entered when a priority claim is made to an earlier application.</td>
<td></td>
</tr>
<tr>
<td>ERROR</td>
<td>invention title</td>
<td>The invention title is missing. At least one invention title must be entered.</td>
<td></td>
</tr>
<tr>
<td>ERROR</td>
<td>applicant name</td>
<td>The person or organization name has not been entered. At least one name</td>
<td></td>
</tr>
<tr>
<td></td>
<td>name</td>
<td>must be entered.</td>
<td></td>
</tr>
<tr>
<td>ERROR</td>
<td>inventor name</td>
<td>The person or organization name has not been entered. At least one name</td>
<td></td>
</tr>
<tr>
<td></td>
<td>name</td>
<td>must be entered.</td>
<td></td>
</tr>
</tbody>
</table>

Figure 92 Verification report, no errors

This project does not contain any errors or warnings.
4.3 FREE TEXT QUALIFIERS

The qualifiers with a “free text” value format of a project are stored in 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.

The user can modify a qualifier’s associated translation by clicking on the Qualifier Value, as shown in Figure 93, which will open an overlay with an editable panel (1).

If the user clicks on the “EXPORT FREE TEXT QUALIFIERS” button (2), all of the free text qualifiers of the Project will be exported and saved to a .csv file, along with their qualifier values and their translated qualifier free text values.

The user can export all the free-text qualifiers of a project to a .csv file along with the associated sequence and feature information provided in the table shown by clicking on the “EXPORT FREE TEXT QUALIFIERS” button at the top of the view and then in the dialog box, selecting the name and location to save the qualifiers (2).

This file can be viewed and used in any spreadsheet tool such as Excel, Google Sheets or LibreOffice.
4.4 IMPORT REPORT

If a project is imported from a sequence listing (ST.25 or ST.26) or when the user imports a set of sequences from a file (with formats ST.26, ST.25, Raw or Multisequence), 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 following, shown in Figure 94.

If an import has been performed, the view could display two tables:

- Import Report table (4.4.1)
- Change Data table (4.4.2)
4.4.1 Import Report Table

The Import Report table is shown only when importing a file that has 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

- Detailed message with information on the identified issue in question and the changes made to rectify it (if any).

- Sequence number of the imported sequence related to the message (when type is INDIVIDUAL)
4.4.2 Change Data Table

This table displays the data that has undergone a transformation or change during the importing process. This following data is presented in table columns:

- **Origin Tag**: code for the element type
- **Origin Element Name**: name for the element type
- **Origin Element Value**: value of the original element in the source file
- **Target Element Name**: element name of the resulting ST.26 project where the information is going to be stored
- **Target Element Value**: value that will be set in the resulting ST.26 project
- **Transformation**: description of the change(s) made to the element
- **Sequence ID Number**: identification number of the Sequence to which the resulting transformed element is stored in the ST.26 project

<table>
<thead>
<tr>
<th>Origin Tag</th>
<th>Origin Element Name</th>
<th>Origin Element Value</th>
<th>Target Element Name</th>
<th>Target Element Value</th>
<th>Transformation</th>
<th>Sequence ID Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;221&gt;</td>
<td>Name/Key</td>
<td>repeat_unit</td>
<td>Feature Key</td>
<td>repeat_region</td>
<td>The absolute feature key has been replaced with the recommended key (see Annex VI, ST.26)</td>
<td>1</td>
</tr>
<tr>
<td>&lt;223&gt;</td>
<td>Other information</td>
<td>repeat_unit</td>
<td>Qualifier Name</td>
<td>note</td>
<td>A 'Note' qualifier has been created.</td>
<td>1</td>
</tr>
<tr>
<td>&lt;225&gt;</td>
<td>Other information</td>
<td>repeat_unit</td>
<td>Qualifier Value</td>
<td>adh1-1</td>
<td>A value has been added to qualifier.</td>
<td>1</td>
</tr>
<tr>
<td>&lt;227&gt;</td>
<td>Name/Key</td>
<td>repeat_unit</td>
<td>Feature Key</td>
<td>misc_feature</td>
<td>The absolute feature key has been replaced with the recommended key (see Annex VI, ST.26)</td>
<td>1</td>
</tr>
<tr>
<td>&lt;227&gt;</td>
<td>Other information</td>
<td>repeat_unit</td>
<td>Qualifier Name</td>
<td>note</td>
<td>A 'Note' qualifier has been created.</td>
<td>1</td>
</tr>
</tbody>
</table>

Figure 96. Change Data table
4.5 DISPLAY SEQUENCE LISTING

The last view of the project page header is the “DISPLAY THE SEQUENCE LISTING” view. When this view is accessed, it will display an information box of the last sequence listing file generated, along with a button to display the aforementioned sequence listing.

To see how to generate a sequence Listing, go to section (4.1.1.5).

If a sequence listing has not been successfully generated for a given project, then the Display Sequence Listing view will notify the user of this condition and will disable the “Display Sequence Listing” button and the user will see the error shown below in Figure 98.

When the user clicks on the “Display Sequence Listing” button, a HTML file will be opened in the default browser. An example is shown in Figure 99.

Note: To display the sequence listing in another language, the sequence listing must be generated again, while the tool is in the desired language mode, before clicking the “Display Sequence Listing” button again.
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.
5 FILE FORMATS

5.1 ST.25

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


5.2 MULTI

The MULTI format can describe one or multiple sequences, along with their name, the type of molecule and the name of the organism. The format for a single sequence is as follows:

*Sequence_name; molecule_type; Organism_name*

Genetic_code

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 format.

Example:

<First Sequence; RNA; Albies alba>

uuuuuuauuuuuuucuucucuacugcuuaucaauauggauugucguagggcuucccucaucgcucuccccacc
gccuaccacacaccacucgccccgacgccaauauacuauaguaucaccacaacagcauaaacaagaugauggcgaagaaggggaggguucugauggugucgccccgacgcaacagcagagagucgaggccggaggaggg

<Second Sequence; DNA; Albies alba>

atggauugttgauguggtatugtuaguuatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugtuaatgtaurttaaaauaauugggtggtgagututuguatuagttuaautugt
5.3 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:

```
Aggatatagatagtatgatagtatgatagtatgatagtttatghtatgtatgtatgtatgtatgtatgtagttatga
```

[End of Manual]