

WIPO Sequence desktop tool

Webinar training

What we are covering today

- Purpose of the tool
- Main views within the interface: Project Home, Project Detail
- Main features it supports:
 - Creating a project and sequences
 - Import sequence listing data different formats supported
 - Validate sequence listing data verification report
 - Adding project data feature keys and qualifiers
 - Free-text qualifiers and XLIFF export
 - Generating ST.26 compliant sequence listings
- Language support and adjusting preferences



What we will not be covering

- The material covered in the Introduction to WIPO ST.26: https://www.wipo.int/meetings/en/details.jsp?meeting_id=62848
- If you have not completed this module, please refer to WIPO Standard ST.26 at:

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

Progress in current tool development – new stable release 1.1.0 available in August 2021.



Purpose of WIPO Sequence desktop tool

- As of January 1, 2022 all sequence listings filed at the international, national or regional level must be compliant with WIPO Standard ST.26
- WIPO Sequence: common desktop tool produced by WIPO to author and validate WIPO ST.26 compliant sequence listings
- WIPO Sequence produced by WIPO to ensure that all applicants around the world have access to the same free tool



WIPO Sequence: Installation

All installation packages and user support documentation can be download from the WIPO Sequence homepage at:

https://www.wipo.int/standards/en/sequence

- WIPO Sequence desktop tool is available for MS Windows, Mac OSX and Linux operation systems
- An auto-update functionality will prompt the user when a new version is available

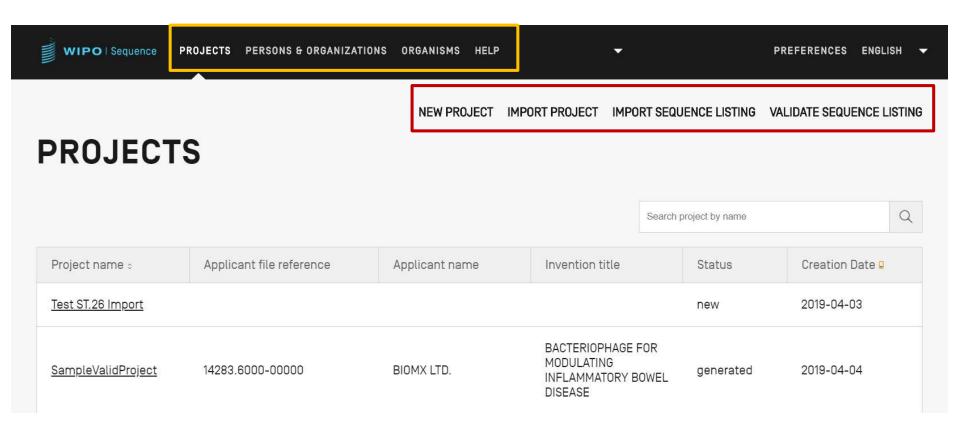


WIPO Sequence: Important

- All generated sequence listings and project data entered into WIPO sequence are stored **locally** (on the user's computer)
- Projects can be created and sequence listings generated while offline but the auto-update feature requires a connection to the internet
- WIPO Sequence is distributed for the free use of all applicants without the provision of the source code.

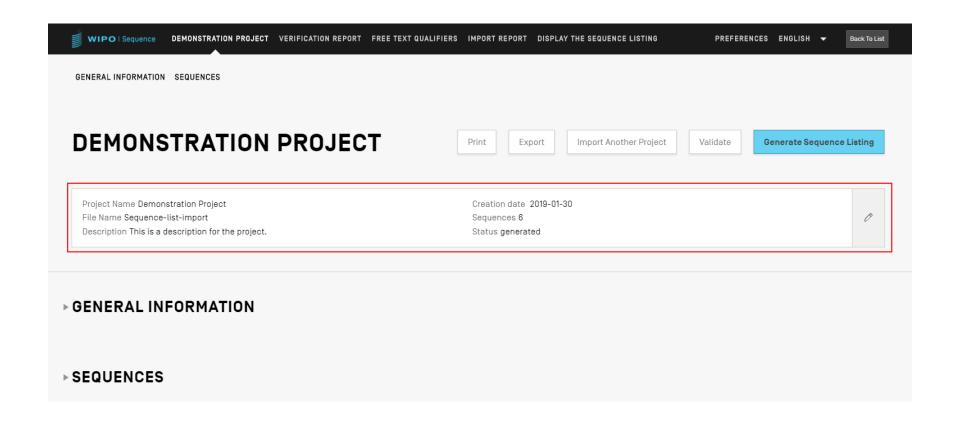


Project Home





Project Detail





Main tool features (1)

- Authoring Project:
 - General Information
 - Sequences
 - Validate Project
 - Generate ST.26 SL
 - Print SL
 - Validate ST.26 SL
- Custom Lists:
 - Custom organisms
 - Person/Organization

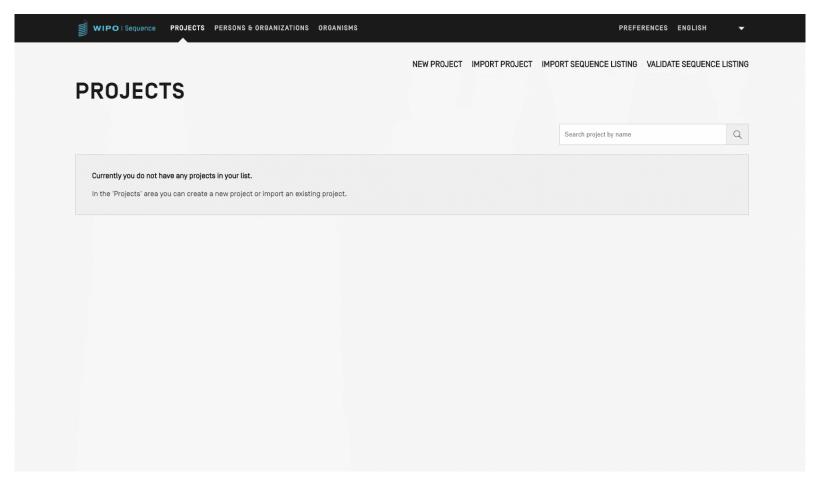


Main tool features (2)

- Import:
 - Existing SL: ST.25/ST.26
 - Common formats: FASTA/multi-sequence/raw
 - Existing ST.26 project
- Tool features:
 - Preferences
 - Multi-language support
 - Auto-update
- Full functionality of the tool is provided in the WIPO Sequence desktop manual at:

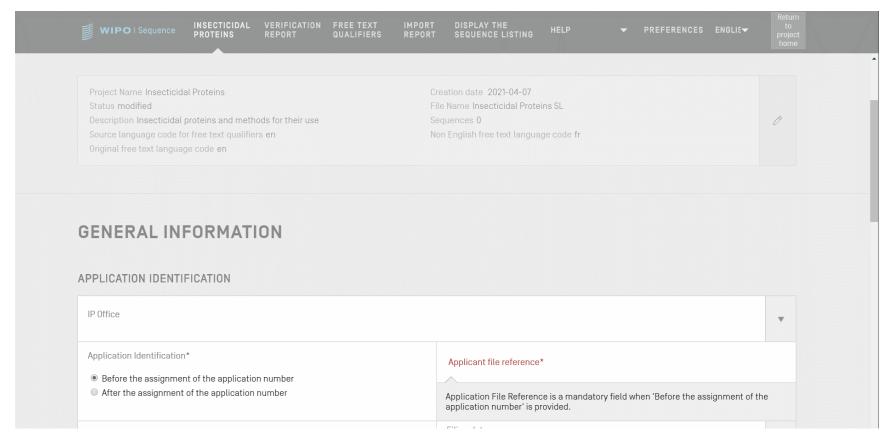
https://www.wipo.int/export/sites/www/standards/en/sequence/wipo_sequence_manual_1_0_0.pdf

Creating a project (demo)



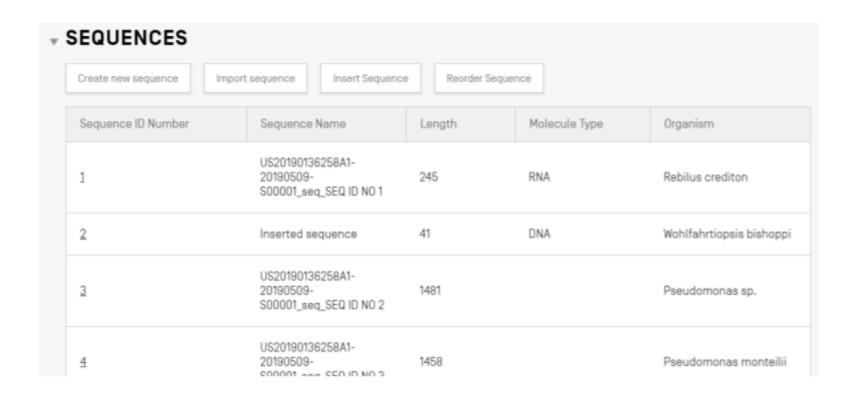


Adding project detail: General Information (demo)





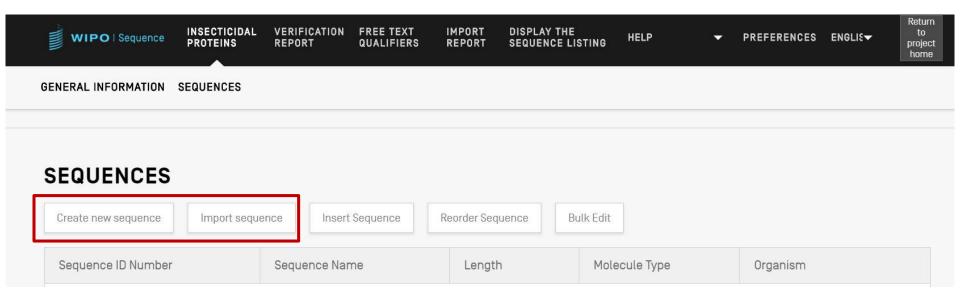
Sequence summary table





Adding project detail: a new sequence

Within project detail view: it is possible to either create a sequence or import a sequence into the project



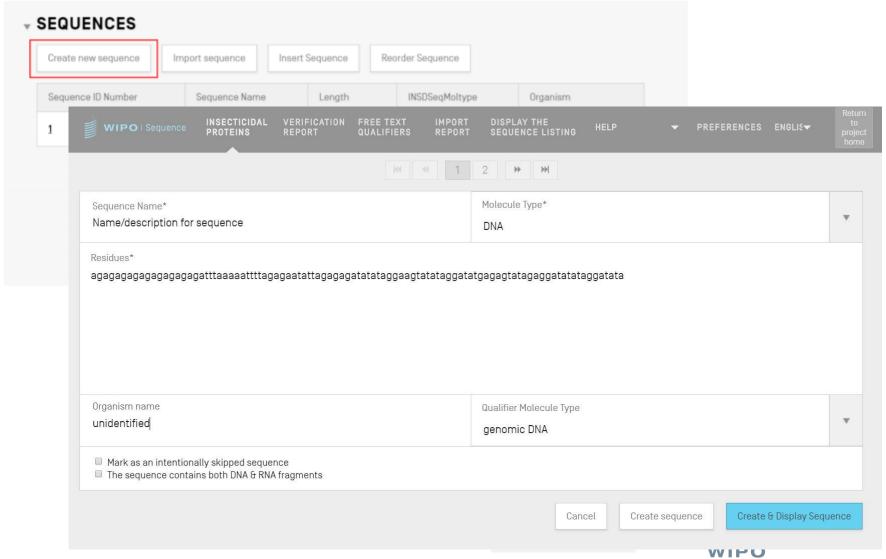


WORLD

ORGANIZATION

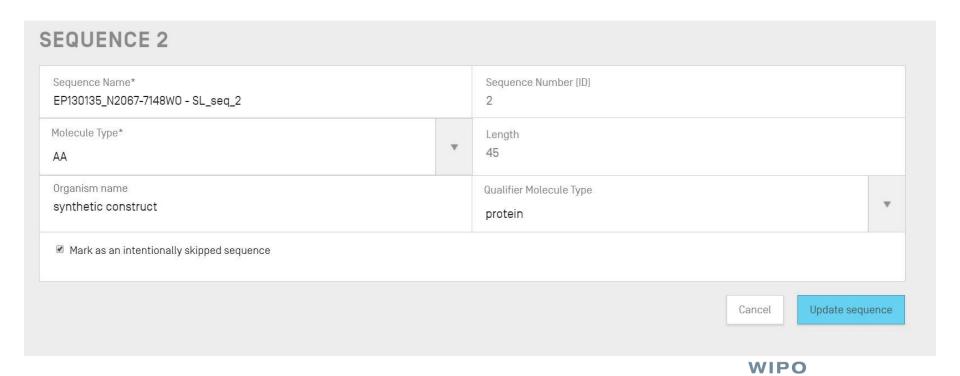
INTELLECTUAL PROPERTY

Creating a sequence

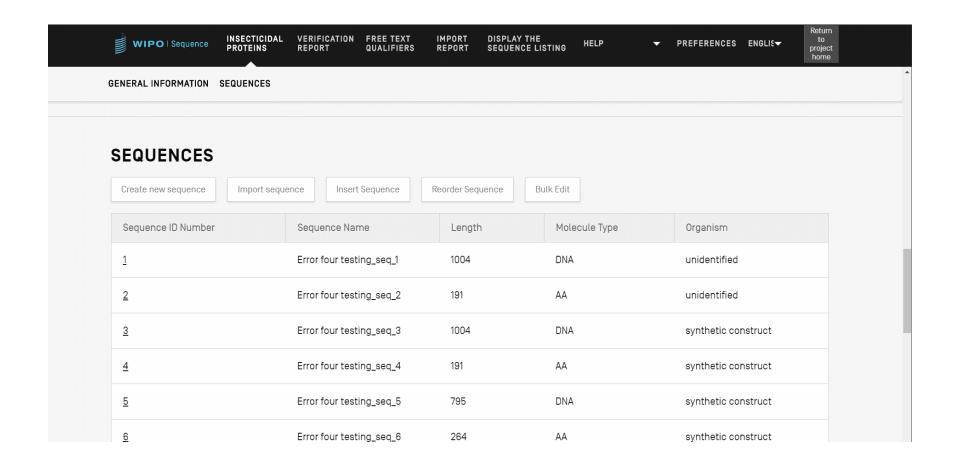


Skipped sequences

- As in ST.25, skipped sequences are represented by the series '000'
- Skipped sequences are indicated by checking the box below:

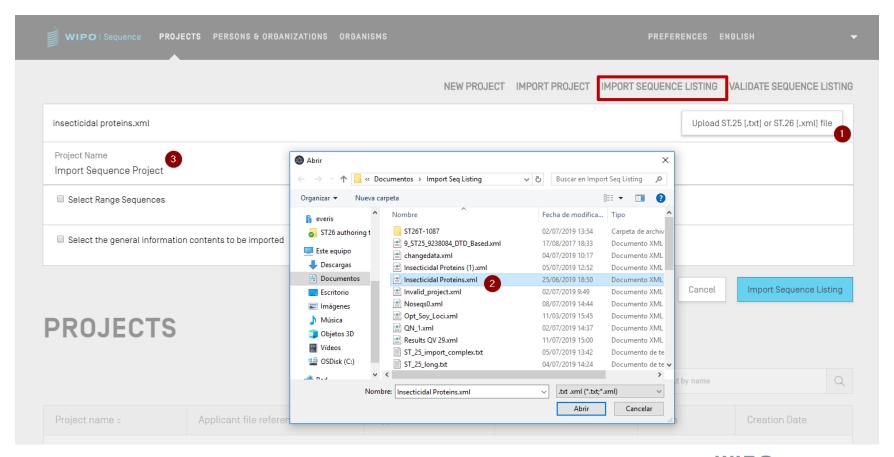


Reordering sequences (demo)





Importing existing sequence listings



WIPO
WORLD
INTELLECTUAL PROPERTY
ORGANIZATION

Import ST.25 sequence listing (1)

- WIPO Sequence supports the import of ST.25 sequence listings
- However, ST.26 mandatory fields missing from the imported file will need to be manually entered by the user including:
 - SOURCE/source: molecule type and organism
 - Mandatory qualifiers for features e.g., modified_base (mod_base)
- On import, WIPO Sequence makes several changes to the imported data before it is included within the project.
- Summarized in "Change Data" report



Import ST.25 sequence listing (2)

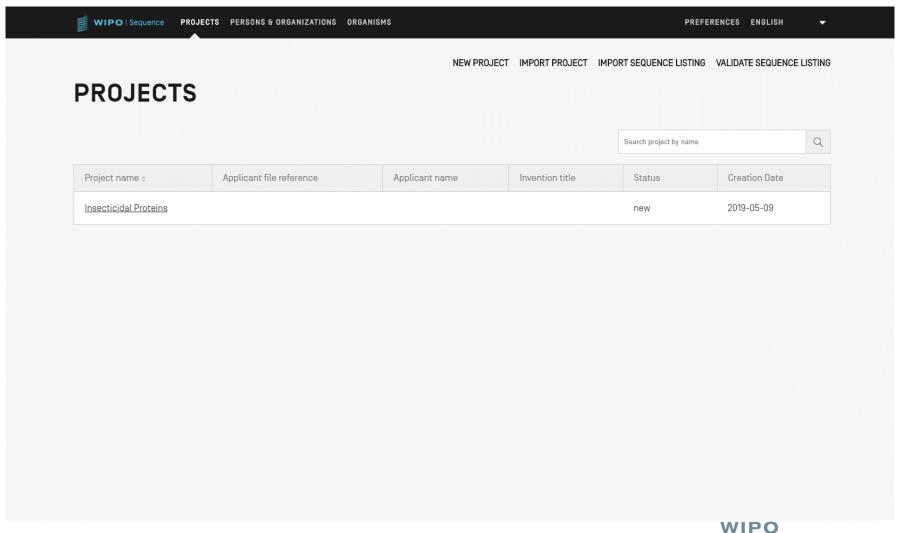
Changes made are implemented according to the recommendations provided in Annex VII (advises on transforming from ST.25 to ST.26 without adding new matter)

These include:

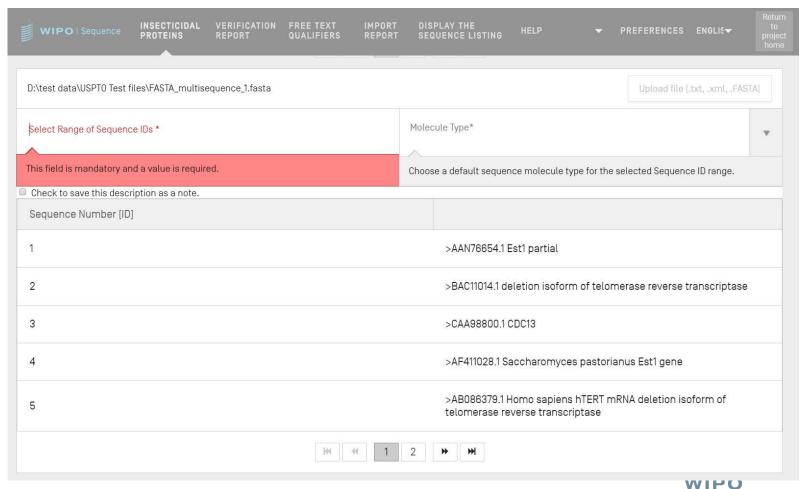
- All 'u' residues are converted to 't'
- Replace molecule type:
 - (i) ADN with DNA, (ii) ARN with RNA, (iii) PRT with AA
- Replace 'artificial sequence' (and specified equivalents) with 'synthetic construct'
- Replace 'unknown' (and specified equivalents) with 'unidentified'
- Replace amino acid symbols in 3-letter code with 1-letter code.



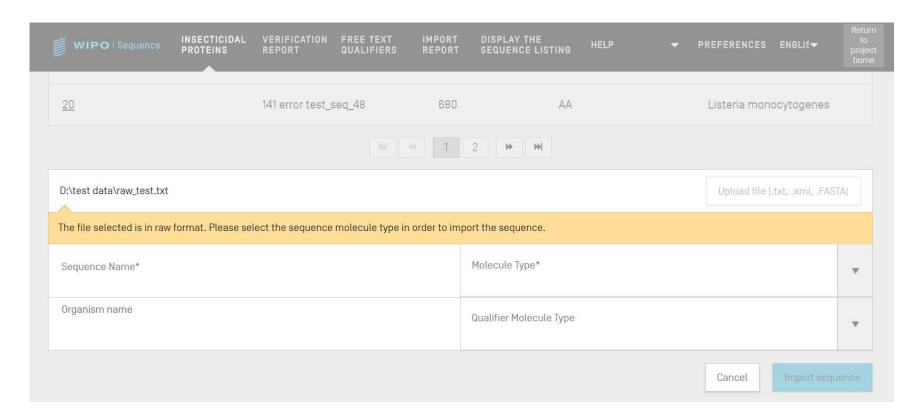
Import sequence listing (demo)



Preview: Import FASTA format

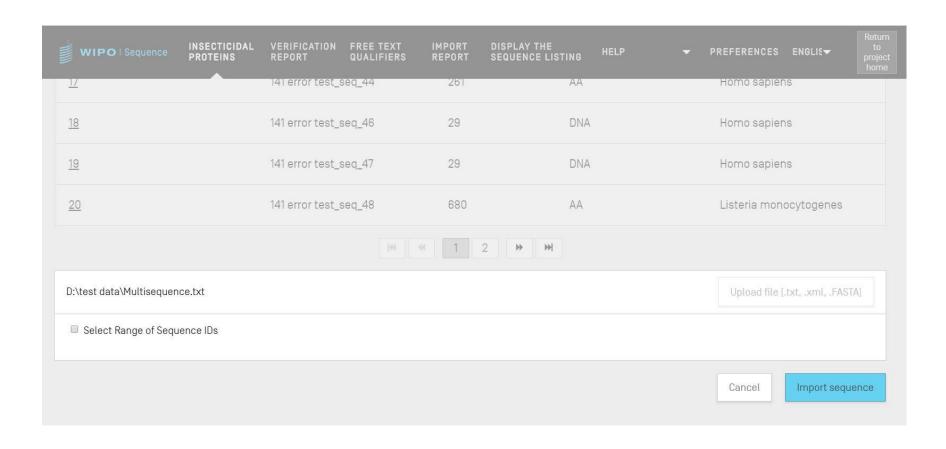


Import RAW format





Import multisequence



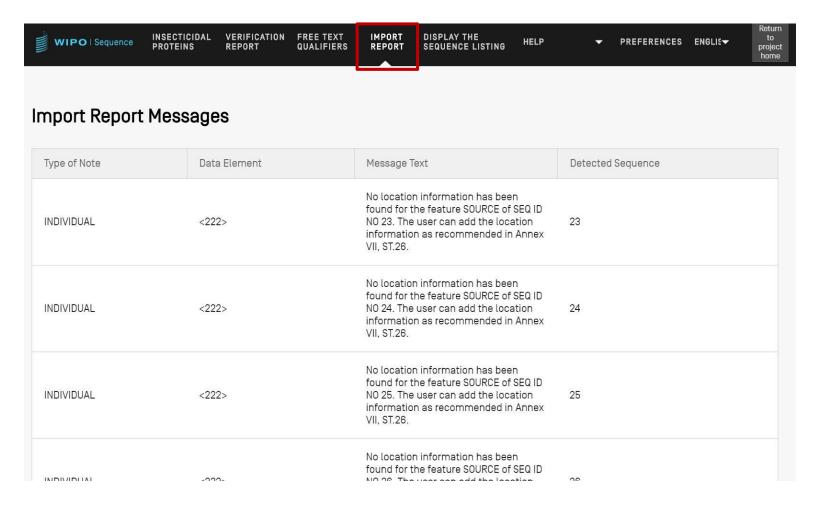


Import report (1)

- If there has been any errors or warnings during import then an import report will be generated
- Messages provided in this report highlight certain sequences that will require manual input by the user
- The import report provides a classification, the relevant ST.25 tag, a message for the user and the SEQ ID
- Messages are classified ('Type of note') as either:
 - INDIVIDUAL: relates to a specific imported sequence
 - GLOBAL: effects all imported sequences



Import Report (2)

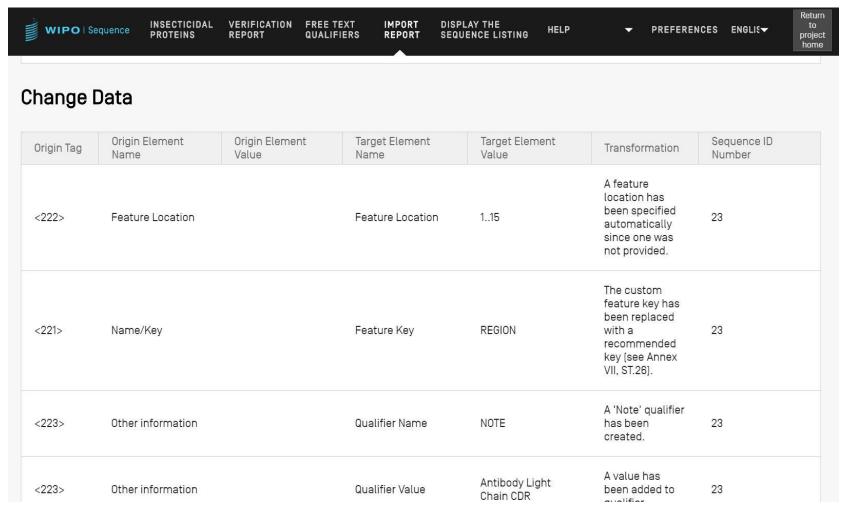




Change data report (1)

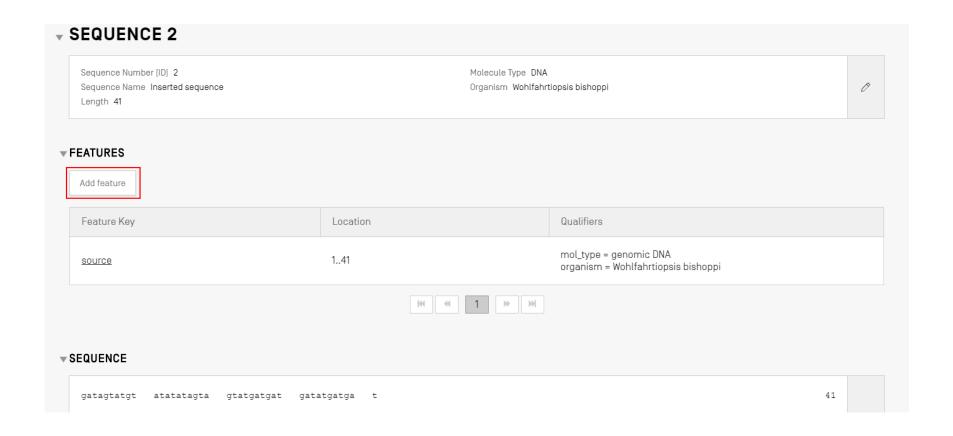
- Specific detail of any changes made during import of an ST.25 sequence listing
- Contrasted with the import report where the user is expected to provide these details
- Lists the original ST.25 tag and the target ST.26 tag as well as the transformation which has been applied and the relevant SEQ ID
- Transformations here however to not change the original content e.g., a 'u' changed to a 't' is still uracil in ST.26 project

Change data report (2)



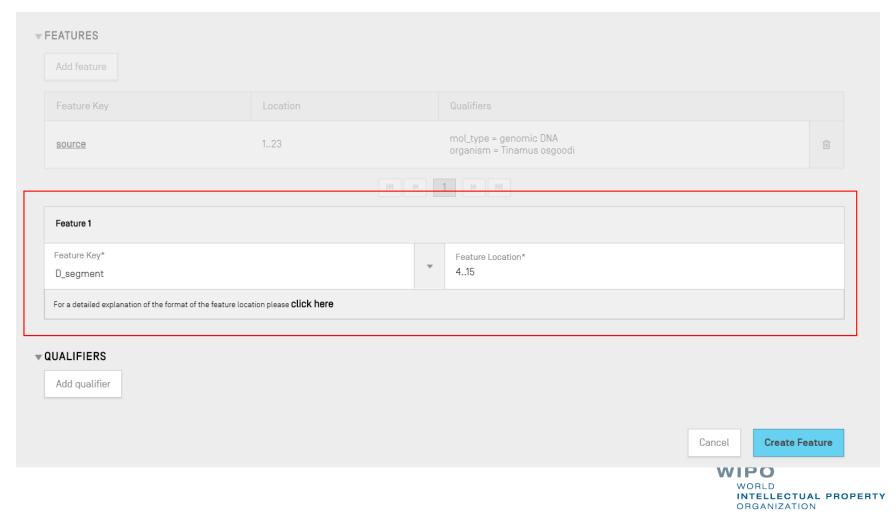


Adding feature keys and qualifiers (1)

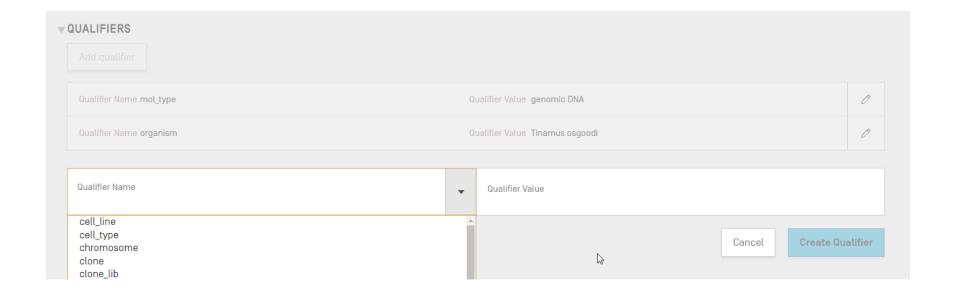




Adding feature keys and qualifiers (2)

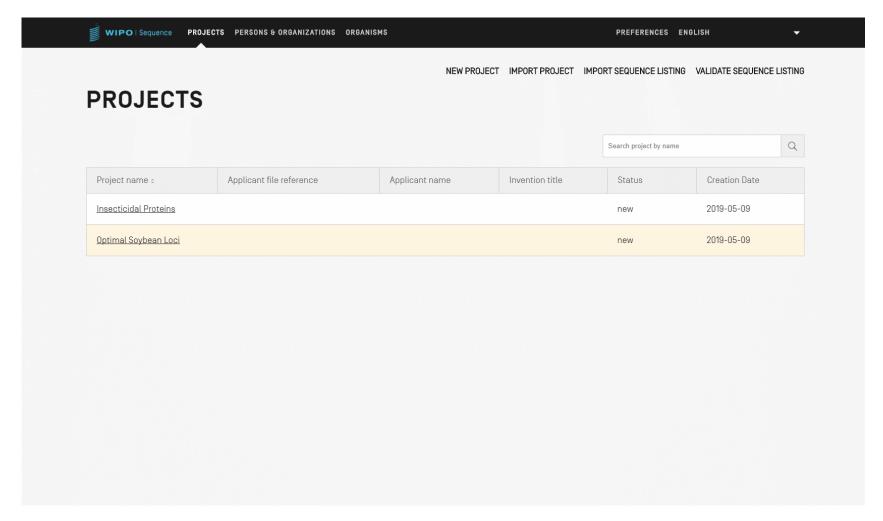


Adding feature keys and qualifiers (3)





Adding feature/qualifier (demo)





Allowable feature locations (1)

Location descriptors for nucleotide and amino acid sequences:

Location	Syntax	Description
Single residue number	X	Points to a single residue in the sequence
Residue numbers delimitating a sequence span	xy	Points to a continuous range of residues bounded by and including the starting and ending residues.
Residues before the first or beyond the last specified residue number	<x >X <xy X>y <x>y</x></xy </x 	Points to a region including a specified residue or span of residues and extending beyond a specified residue. The '<' and '>' symbols may be used with a single residue or the starting and ending residue numbers of a span of residues.

Allowable feature locations (2)

Location descriptors for nucleotide sequences only:

Location	Syntax	Description
A site between two adjoining nucleotides	x^y	Points to a site between two adjoining nucleotides, e.g., endonucleolytic cleavage site. The position numbers for the adjacent nucleotides are separated by a carat (^).



Allowable feature locations (3)

Location descriptors for amino acid sequences only:

Location	Syntax	Description
Residue numbers joined by an intrachain cross-link	xy	Points to amino acids joined by an intrachain linkage when used with a feature that indicates an intrachain cross-link, such as "CROSSLNK" or "DISULFID".



Complex feature locations (nucleotide sequences ONLY)

Location syntax	Location description
<pre>join(location, location,, location)</pre>	The indicated locations are joined (placed end-to- end) to formone contiguous sequence.
order(location, location,, location)	The elements are found in the specified order but nothing is implied about w hether 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.

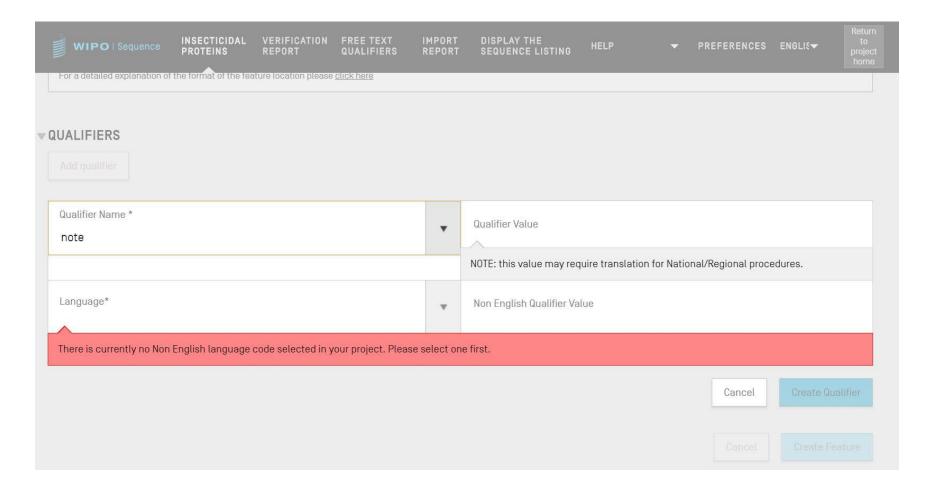


Preview: Free text qualifiers: definition and use

- Free text: "is a type of value format for certain qualifiers, presented in the form of a descriptive text phrase or other specified format"
 ref: WIPO ST.26
- One of two types:
- Language dependent (may require a translation) e.g., note/NOTE
- Language independent e.g., allele
- Must not exceed 1000 characters
- See WIPO ST.26 Annex I Sections 6 and 8: complete list of language dependent free text qualifiers

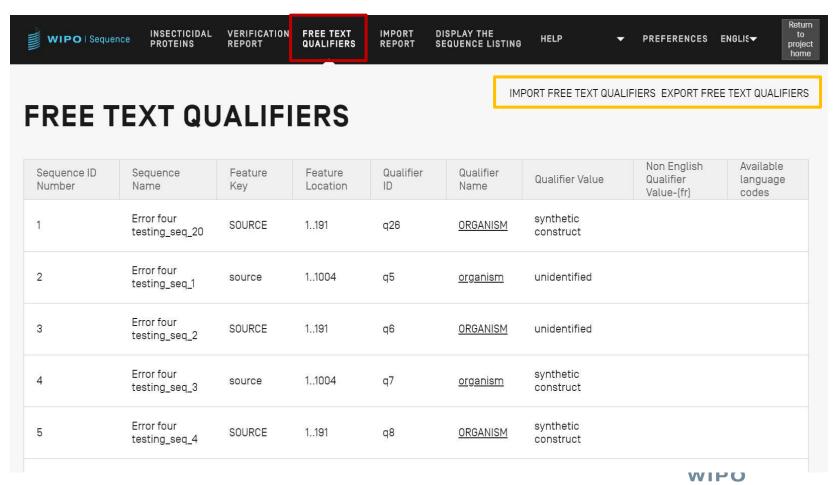


Preview: Adding free text qualifier

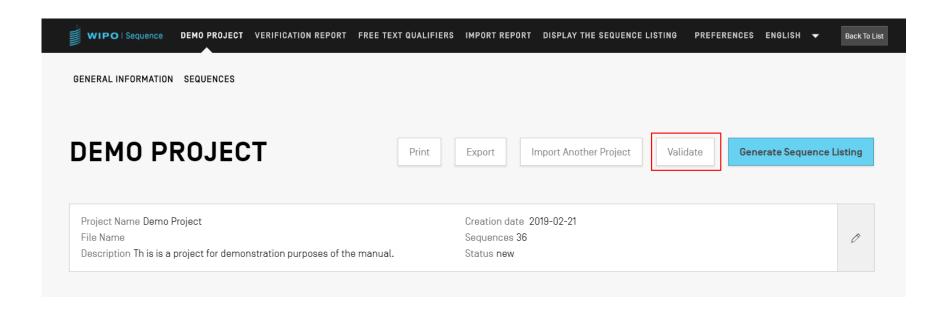




Preview: Free text qualifiers: XLIFF

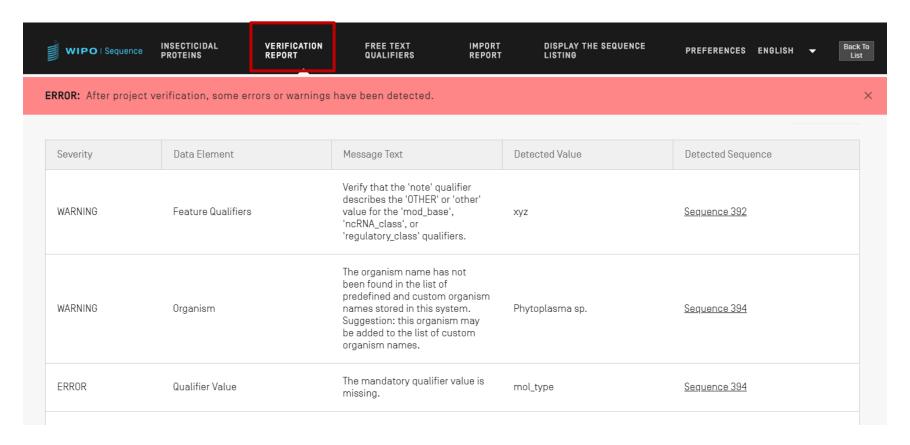


Validating sequence listing





Verification report: errors and warnings





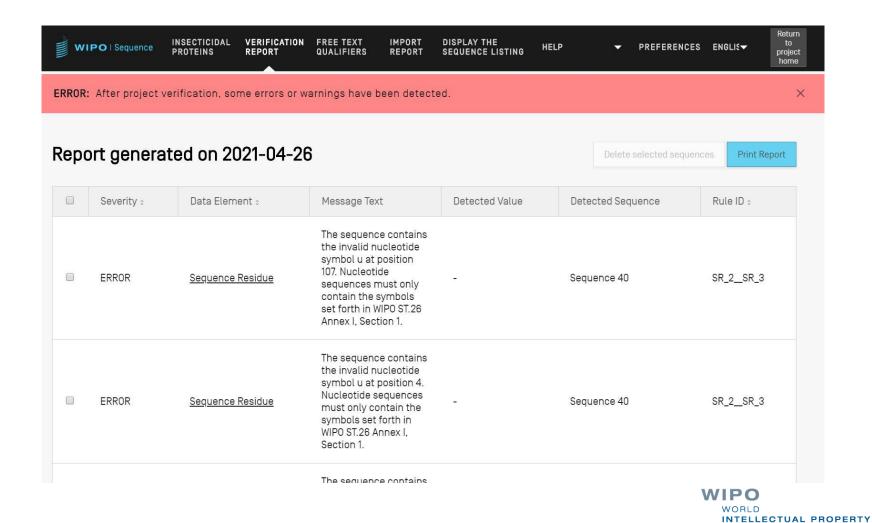
Error/Warning messages

- WARNING: can be ignored but <u>should</u> be addressed by manual review
- ERROR: <u>must</u> be addressed by user
- Link in verification report to specific component within the sequence which was the cause of the error/warning
- Project must be validated again for this error to be removed from the report
- The verification report can be printed for later reference

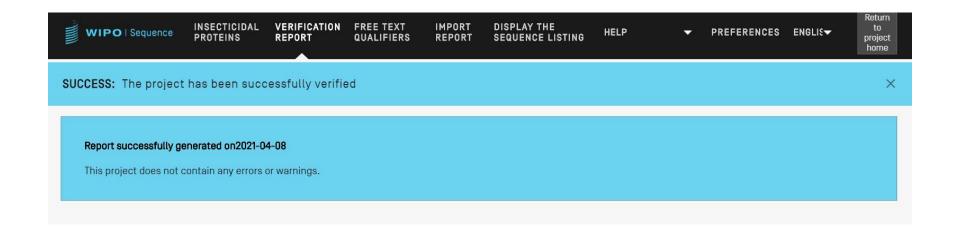


ORGANIZATION

Preview: Improved verification report

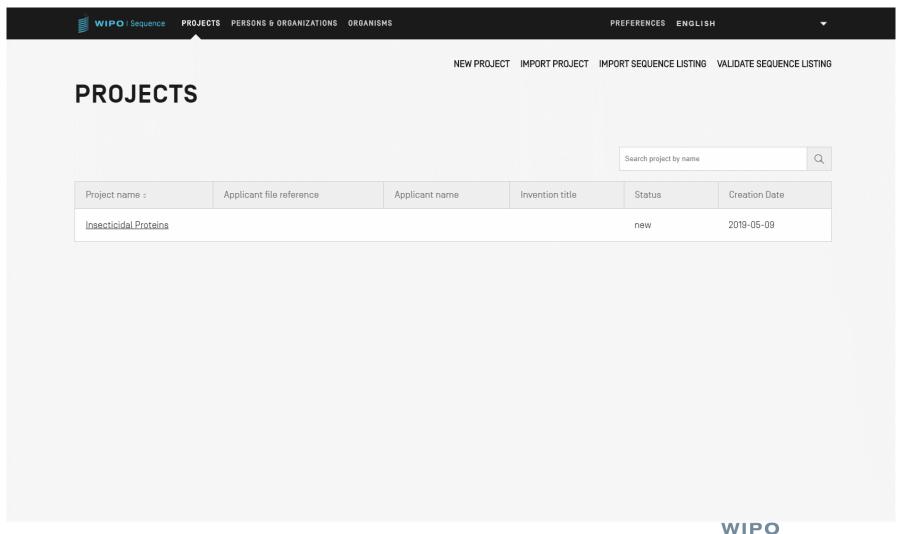


Validation report: no errors

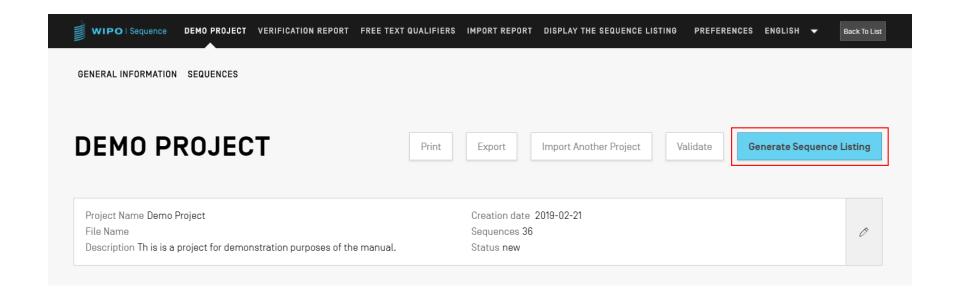




Validate sequence listing (demo)



Generate ST.26 sequence listing





```
<?xml version="1.0" encoding="UTF-8"?>
  <!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.3//EN" "ST26SequenceListing V1 3.dtd">

■ <ST26SequenceListing originalFreeTextLanguageCode="en" dtdVersion="V1 3" fileName="Insecticidal Proteins SL"
</p>
 softwareName="WIPO Sequence" softwareVersion="1.1.0-beta.5" productionDate="2021-04-08">
      <ApplicationIdentification>
          <IPOfficeCode>IB</IPOfficeCode>
         <ApplicationNumberText>PCT/IB2021/000021/ApplicationNumberText>
          <FilingDate>2021-04-07
      </ApplicationIdentification>
      <ApplicantFileReference>WIPO-Insect-Demo</ApplicantFileReference>
      <EarliestPriorityApplicationIdentification>
         <IPOfficeCode>IB</IPOfficeCode>
          <ApplicationNumberText>PCT/IB/2020/000045</applicationNumberText>
         <FilingDate>2020-04-06</FilingDate>
      </EarliestPriorityApplicationIdentification>
      <ApplicantName languageCode="en">Merck Sharpe and Dohme Corp.
      <InventionTitle languageCode="en">Insecticidal proteins and methods of their use</InventionTitle>
      <SequenceTotalQuantity>32</SequenceTotalQuantity>
      <SequenceData sequenceIDNumber="1">
          <INSDSeq>
             <INSDSeq length>440</INSDSeq length>
             <INSDSeq moltype>AA</INSDSeq moltype>
              <INSDSeq_division>PAT</INSDSeq_division>
              <INSDSeq feature-table>
                  <INSDFeature>
                     <INSDFeature key>SOURCE</INSDFeature key>
                     <INSDFeature location>1..440</INSDFeature location>
                     <INSDFeature quals>
                         <INSDQualifier>
                             <INSDQualifier name>MOL TYPE</INSDQualifier name>
                             <INSDQualifier value>protein</INSDQualifier value>
                         </INSDQualifier>
                         <INSDQualifier id="q84">
                             <INSDQualifier name>ORGANISM</INSDQualifier name>
                             <INSDQualifier value>Homo sapiens</INSDQualifier value>
                          </INSDQualifier>
                      </INSDFeature quals>
                  </INSDFeature>
             </INSDSeq feature-table>
             <INSDSeq_sequence>
```

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVS SNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC

Generate ST.26 SL in human-readable format: TXT

Sequence Listing Information:

DTD Version: V1_3

File Name: Insecticidal Proteins SL Software Name: WIPO Sequence Software Version: 1.1.0-beta.5 Production Date: 2021-04-08

General Information:

Current application / IP Office: IB

Current application / Application number: PCT/IB2021/000021

Current application / Filing date: 2021-04-07

Current application / Applicant file reference: WIPO-Insect-Demo

Earliest priority application / IP Office: IB

Earliest priority application / Application number: PCT/IB/2020/000045

Earliest priority application / Filing date: 2020-04-06 Applicant name: Merck Sharpe and Dohme Corp.

Applicant name / Language: en

Invention title: Insecticidal proteins and methods of their use (en)

Sequence Total Quantity: 32

Sequences:

Sequence Number (ID): 1

Length: 440

Molecule Type: AA

Features Location/Qualifiers:

- SOURCE, 1..440

> MOL_TYPE, protein

> ORGANISM, Homo sapiens

WIPO PUBLIC



Generate ST.26 SL in human-readable format: HTML

Sequence Listing

Sequence Listing Information

File Name	Insecticidal Proteins SL	
DTD Version	V1_3	
Software Name	WIPO Sequence	
Software Version	1.1.0-beta.5	
Production Date	2021-04-08	

General Information

Current application: IP Office	IB
Current application: Application number	PCT/IB2021/000021
Current application: Filing date	2021-04-07
Current application: Applicant file reference	WIPO-Insect-Demo
Earliest priority application: IP Office	IB
Earliest priority application: Application number	PCT/IB/2020/000045
Earliest priority application: Filing date	2020-04-06
Applicant name	Merck Sharpe and Dohme Corp.
Applicant name: Language	en
Applicant name: Name Latin	
Inventor name	
Inventor name: Language	
Inventor name: Name Latin	
Invention title	Insecticidal proteins and methods of their use (en)
Sequence Total Quantity	32

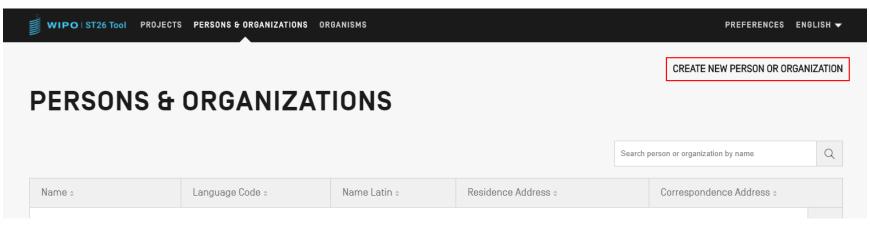
Sequences

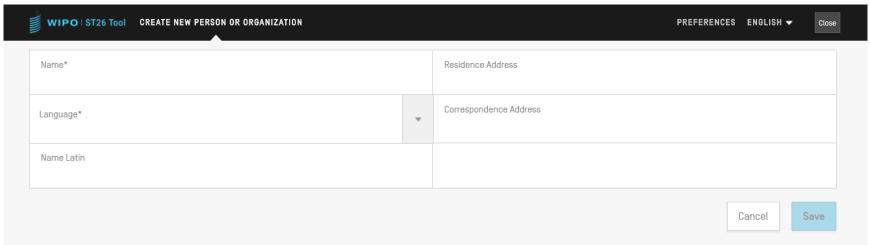
Sequence Number [ID]	1
Molecule Type	AA
Length	440

Features Location/Qualifiers

SOURCE 1..440 /MOL_TYPE= protein /ORGANISM= Homo sapiens WIPO
WORLD
INTELLECTUAL PROPERTY
ORGANIZATION

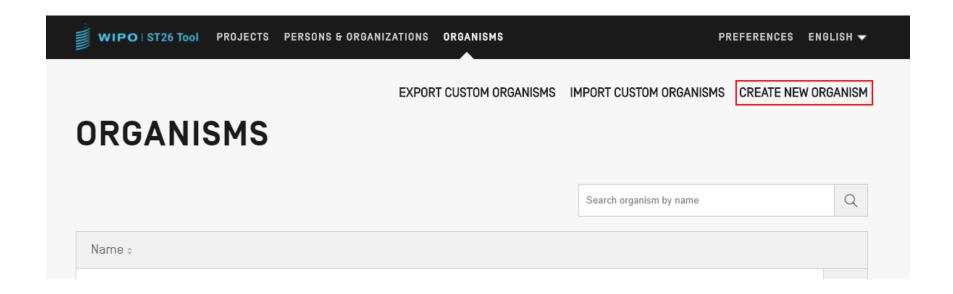
Person/Organizations





WIPO
WORLD
INTELLECTUAL PROPERTY
ORGANIZATION

Custom Organisms



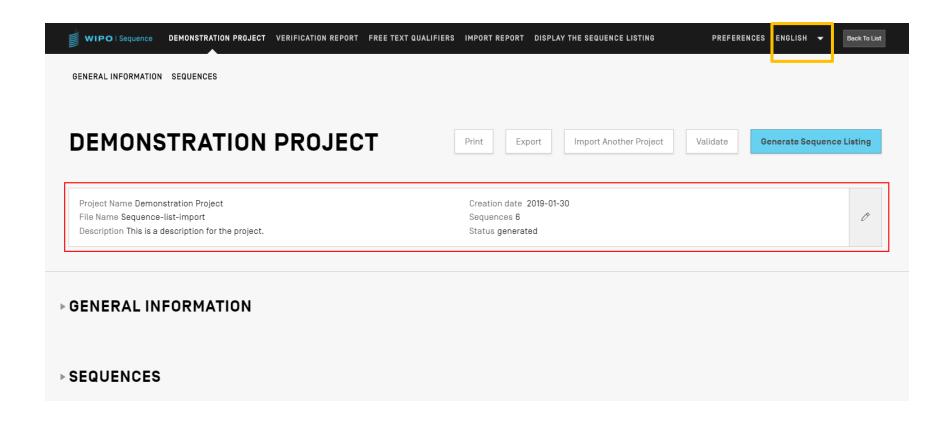


Languages available (1)

- The WIPO Sequence desktop tool provides all labels and notification messages in each of the 10 PCT languages:
 - English, French, Spanish, Arabic, Russian, Chinese, German,
 Portuguese, Korean and Japanese
- The home page/user manual is also provided in these 10 languages
- The language for the interface can be set up in the top right-hand corner of the screen (shown next page)
- The default GUI language can now be set under 'Preferences'
- The verification report will also be generated in this language

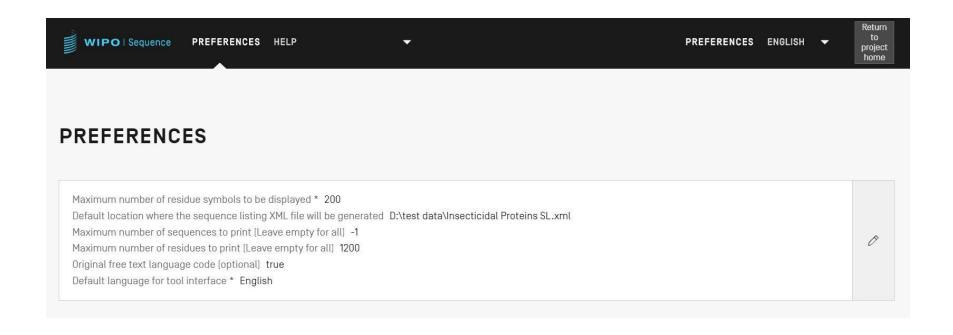


Languages available (2)





Adjusting preferences





Q&A session

standards@wipo.int



Further resources

WIPO Standard ST.26 (in English):

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

WIPO Sequence homepage (in English):

https://www.wipo.int/standards/en/sequence

