

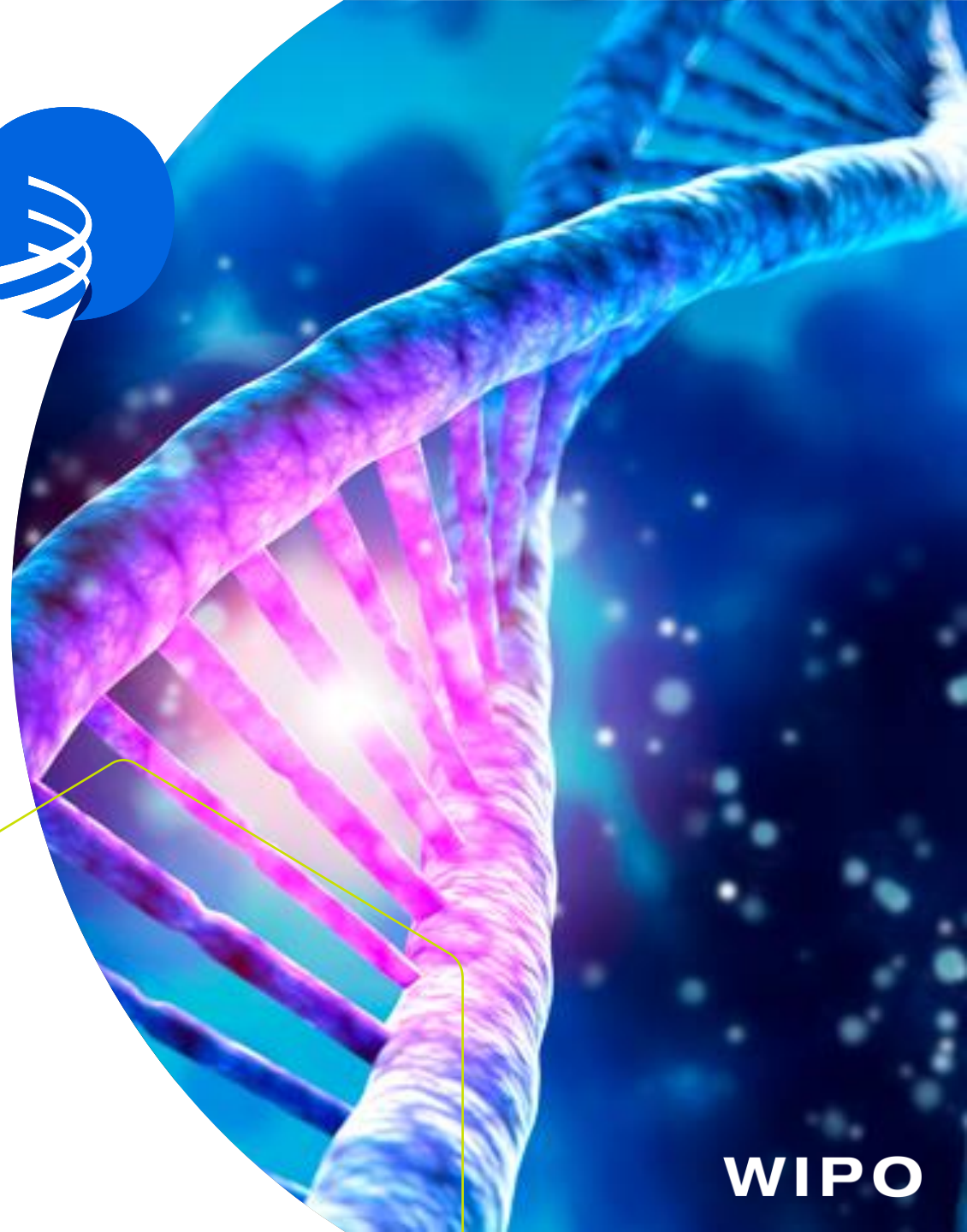
WIPO Standard ST.26 and WIPO Sequence

Emma Francis

WIPO Sequence Product Owner

Understanding the PCT System: A National Webinar for
Georgian Applicants

November 19, 2025



A sequence listing...

- Contains nucleotide and/or amino acid sequences disclosed in a patent application and forms part of the description
- Includes descriptive information about each sequence known as annotations
- Allows for the sequence data of an invention to be searchable:
 - Inside an IP Office
 - In publicly available databases (INSDC databases)
- Conforms to the requirements of the relevant WIPO Standard (WIPO ST.25 or ST.26)

So why a new WIPO Standard?

Sequence listings were filed compliant with WIPO ST.25



However:

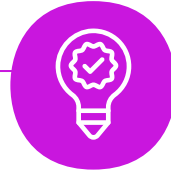
- WIPO ST.25 format is not compliant with INSDC requirements, so data is lost when entered into public databases
- WIPO ST.25 rules are not clear enough, and IP Offices worldwide interpret and enforce the rules differently
- Sequence types that are common today are not covered by WIPO ST.25 rules (nucleotide analogs, D-amino acids, branched sequences) and therefore are not present in searchable databases
- Data is unstructured – WIPO ST.25 format is difficult to use for automated validation and data exchange

Benefits of WIPO Standard ST.26



Acceptance of a single sequence listing worldwide

- Sequence listings should be generated once and then accepted at all patent Offices
- The only exception is if a translation is required



More sequence data is searchable

- Now can include D-amino acids and branched sequences
- In version 2.0, must specify nucleotide and peptide analogs



Enhanced submission quality

- Standardization of feature locations, annotations and qualifiers
- Structured format supports automated checks – results in less corrections
- Data compatibility with public databases like INSDC

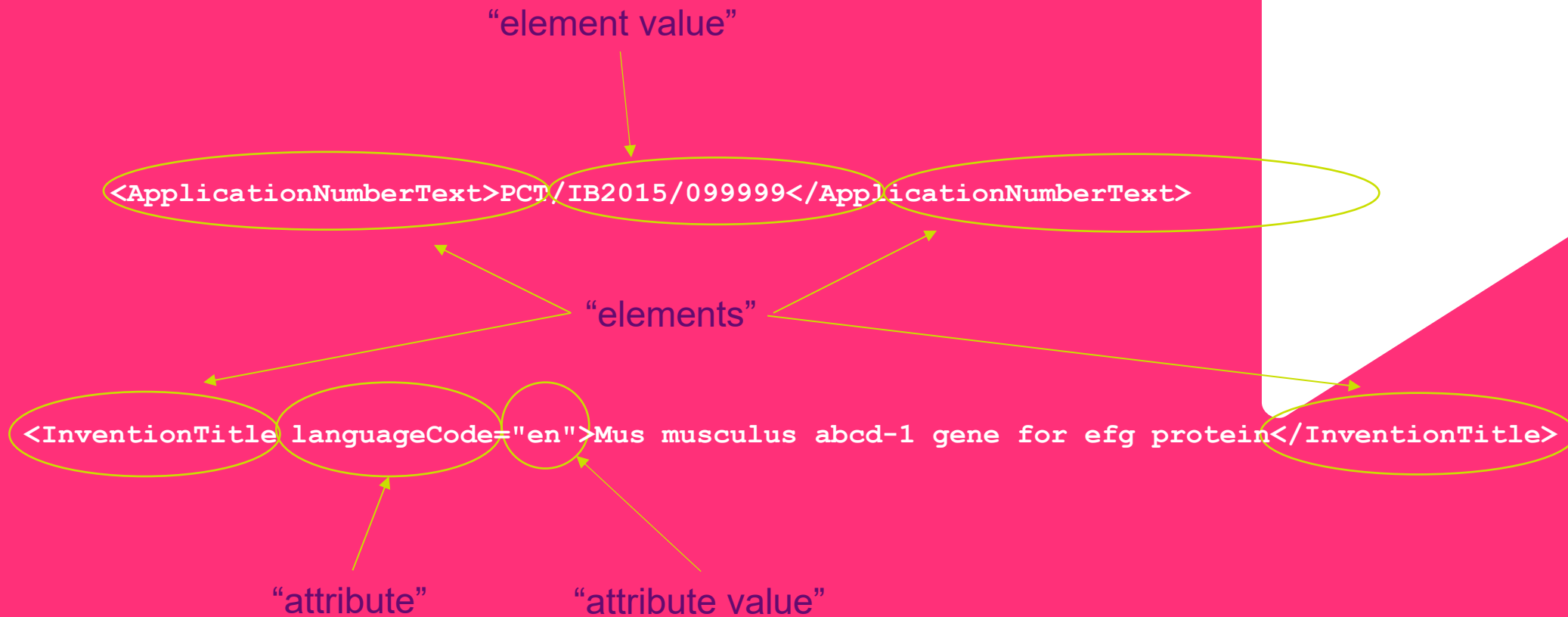
WIPO Standard ST.26 – version 1.7

- **Main Body** – Requirements for inclusion/representation
- **Annex I** – Controlled vocabulary based on INSDC
- **Annex II** – ST.26 Document Type DTD
- **Annex III** – Example ST.26 Sequence Listing XML file
- **Annex IV** – Character Subset of Basic Latin Code for ST.26 XML Instance
- **Annex V** – INDS Data Exchange Requirements (IPOs only)
- **Annex VI** – Guidance Document with Examples
- **Appendix to Annex VI** –XML file including all of the sequence disclosures exemplified in Annex VI
- **Annex VII** – Recommendation for the Transformation of a Sequence Listing from ST.25 to ST.26

XML Basics

- XML = eXtensible Markup Language
- Information is 'tagged' using descriptive elements and attributes
- Standardized means of data exchange that is both human and machine-readable
- DTD = Document Type Definition - defines the structure and the legal elements and attributes of an XML document

Annex II of WIPO ST.26 is the DTD for the sequence listing



XML Basics: Reserved characters

...must be replaced by their predefined entities in an element value.

Reserved Character	Predefined Entities
<	<
>	>
&	&
“	"
'	'

Example: feature location is “<50..62”:

× `<INSDFeature_location><50..62</INSDFeature_location>`

✓ `<INSDFeature_location><50..62</INSDFeature_location>`

WIPO ST.26: XML document

- Must be provided as one XML 1.0 format file
- Must validate against the WIPO ST.26 DTD (Annex II) and business rules derived from the content of the Standard
- Must be encoded using Unicode UTF-8
- Structure of the ST.26 sequence listing:

- XML declaration:

```
<?xml version="1.0" encoding="UTF-8"?>
```

- Document type (DOCTYPE) declaration:

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

- Root element

- General information part
- Sequence data part

XML declaration

```
<?xml version="1.0" encoding="UTF-8"?>
```

DOCTYPE declaration

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

Root element

```
<ST26SequenceListing dtdVersion="V1_3" fileName="st26-annex-iii-sequence-listing-specimen.xml"  
softwareName="WIPO Sequence" softwareVersion="1.2.0" productionDate="2022-01-07"  
originalFreeTextLanguageCode="ja" nonEnglishFreeTextLanguageCode="de">
```

General information

```
<ApplicationIdentification>  
  <IPOfficeCode>IB</IPOfficeCode>  
  <ApplicationNumberText>PCT/IB2015/099999</ApplicationNumberText>  
  <FilingDate>2015-01-31</FilingDate>  
</ApplicationIdentification>  
<ApplicantFileReference>AB123</ApplicantFileReference>  
<EarliestPriorityApplicationIdentification>  
  <IPOfficeCode>IB</IPOfficeCode>  
  <ApplicationNumberText>PCT/IB2014/111111</ApplicationNumberText>  
  <FilingDate>2014-01-30</FilingDate>  
</EarliestPriorityApplicationIdentification>  
<ApplicantName languageCode="ja">出願製薬株式会社</ApplicantName>  
<ApplicantNameLatin>Shutsugan Pharmaceuticals Kabushiki Kaisha</ApplicantNameLatin>  
<InventorName languageCode="ja">特許 太郎</InventorName>  
<InventorNameLatin>Taro Tokkyo</InventorNameLatin>  
<InventionTitle languageCode="ja">efgタンパク質をコードするマウスabcd-1遺伝子</InventionTitle>  
<InventionTitle languageCode="en">Mus musculus abcd-1 gene for efg protein</InventionTitle>  
<SequenceTotalQuantity>11</SequenceTotalQuantity>
```

Sequence data

```
<SequenceData sequenceIDNumber="1">  
  <INSDSeq>  
    <INSDSeq_length>133</INSDSeq_length>  
    <INSDSeq_moltype>DNA</INSDSeq_moltype>  
    <INSDSeq_division>PAT</INSDSeq_division>
```

...

WIPO ST.26 General Information (1)

- The “**Application Identification**” section:
 - - application number, filing date, and IP office code are mandatory if known
 - - otherwise, just the applicant file reference is sufficient
- The “**Priority Application**” section
 - only one priority application can be included in the sequence listing, and it must be the earliest priority application;
 - mandatory where priority is claimed
- The “**Applicant and Inventor Name**” section
 - only one applicant name and one inventor name may be included in the sequence listing, and they must be the “primary” applicant and inventor;
- however multiple applicants/inventors can be saved in a project;
- applicant name is mandatory; inventor name is optional;
- a language code for applicant and inventor names is mandatory;
- if the applicant and/or inventor name contains non-Unicode Basic Latin characters, then a transliteration or translation into Basic Latin characters must be included

WIPO ST.26 General Information (2)

- The “**Invention Title**” section
 - at least one invention title in the language of filing is mandatory;
 - additional titles in other languages may be included;
 - a language code is mandatory for each title;
- The “**Sequence Total Quantity**” element
 - mandatory;
 - the total must include skipped sequences

What is specifically defined?

What is a “specifically defined” nucleotide or amino acid?

- “specifically defined” means any nucleotide other than those represented by the symbol “n” and any amino acid other than those represented by the symbol “X”, listed in Annex I
 - only “specifically defined” residues count towards the minimum length requirement:
 - 10 or more specifically defined nucleotides; or,
 - 4 or more specifically defined amino acids
- × 5'- anctggcaan - 3' only 8 specifically defined nucleotides; must not be included
- ✓ 5'- agctggcaat - 3' ten specifically defined nucleotides; must be included

WIPO ST.26 nucleotide codes

Symbol	Nucleotide
a	adenine
c	cytosine
g	guanine
t	thymine in DNA/uracil in RNA (t/u)
m	a or c
r	a or g
w	a or t/u
s	c or g
y	c or t/u
k	g or t/u
v	a or c or g; not t/u
h	a or c or t/u; not g
d	a or g or t/u; not c
b	c or g or t/u; not a
n	a or c or g or t/u; "unknown" or "other"

Nucleotide sequences:

- all lower-case symbols;
- no spaces, no numbering;
- no "u" symbols; "t" represents uracil in RNA
- "n" has a default value of "any one of 'a', 'c', 'g', or 't/u'"

WIPO ST.26 amino acid codes

Symbol	Definition
A	Alanine
R	Arginine
N	Asparagine
D	Aspartic acid (Aspartate)
C	Cysteine
Q	Glutamine
E	Glutamic acid (Glutamate)
G	Glycine
H	Histidine
I	Isoleucine
L	Leucine
K	Lysine
M	Methionine
F	Phenylalanine
P	Proline
O	Pyrrolysine
S	Serine
U	Selenocysteine
T	Threonine
W	Tryptophan
Y	Tyrosine
V	Valine
B	Aspartic acid or Asparagine
Z	Glutamine or Glutamic acid
J	Leucine or Isoleucine
X	A or R or N or D or C or Q or E or G or H or I or L or K or M or F or P or O or S or U or T or W or Y or V; "unknown" or "other"

Amino acid sequences:

- all single letter, upper case symbols;
- no spaces, no numbering;
- "X" has a default value of "any one of 'A', 'R', 'N', 'D', 'C', 'Q', 'E', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'O', 'S', 'U', 'T', 'W', 'Y', or 'V'"

WIPO ST.26 - Annotation

Feature Keys and Qualifiers

- Annotation in sequence listings comprises of a **feature key** at a particular **feature location** within the sequence length where additional details are provided using **qualifiers**
- In addition to the mandatory “source” feature, applicants can add multiple optional features to further describe the sequence:
 - different feature keys for nucleotide sequences and amino acid sequences;
 - each feature may have one or more optional qualifiers, and may have a mandatory qualifier
 - The full list is defined in Annex I

WIPO ST.26 Sequences – mandatory elements

- Every sequence must have:
 - a “**source**” feature with both a mandatory “**organism**” qualifier and “**mol_type**” qualifier, spanning the entire sequence
 - a unique SEQ ID NO. or Sequence ID Number
 - The molecule type (DNA, RNA or AA)
 - a series of residues or ‘000’ for a skipped sequence
- For an “organism” qualifier, the qualifier value can be:
 - Latin genus and species name e.g., “Mus musculus”
 - Genus name followed by “sp.” e.g., “Mus sp.”
 - Virus name e.g., “Torque teno virus 1”
 - “unidentified”
 - “synthetic construct”
 - Note: Common names, such as “mouse,” must **not** be used as the organism name. If desired, common names can be included in a note qualifier.

WIPO ST.26 – skipped sequences

- Skipped sequences: allow an applicant to delete sequence data from a sequence listing without the need to renumber subsequence sequences.
 - INSDSeq_length, INSDSeq_moltype, INSDSeq_division present, but with no value;
 - No feature table and no source feature;
 - Sequence element must have the value "000"

```
▼ <SequenceData sequenceIDNumber="7">  
  ▼ <INSDSeq>  
    <INSDSeq_length/>  
    <INSDSeq_moltype/>  
    <INSDSeq_division/>  
    <INSDSeq_sequence>000</INSDSeq_sequence>  
  </INSDSeq>  
</SequenceData>
```

Updates for version 2.0

1

The minimum length requirement has now been lifted

- Applicants can now optionally include short sequences in their sequence listing

2

Nucleotide or peptide analogs must use specifically defined symbols

- This will not be checked automatically but Offices are not required to conduct manual checks on filing
- Rather it is a tool for examiners

3

Comes into force on July 1, 2027

- Version 2.0 and its transition plan were approved at CWS/13 last week
- Filing date is only important in relation to nucleotide or peptide analog sequences



WIPO Sequence Suite


- Desktop tool developed by WIPO to support authoring, validation, and generation of ST.26 compliant sequence listings
- Member states requested WIPO develop this common tool for all Offices and applicants at international, national and regional level
- Use of WIPO Sequence simplifies ST.26 XML creation with a user-friendly interface: no need to ever directly edit an XML file
- Beta versions released in 2020 and 2021 and production release 2.3.0
- Currently working on version 3.1.0

!! 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. A Terms of Use has recently been published on our website.

Always update to the
latest version available

Project home

**PROJECTS** PERSONS & ORGANIZATIONS ORGANISMS HELP First level menu PREFERENCES ENGLISH

Second level menu NEW PROJECT IMPORT PROJECT IMPORT SEQUENCE LISTING VALIDATE SEQUENCE LISTING

PROJECTS

Search project by name

Project name	Applicant file reference	Applicant name	Invention title	Status	Creation Date	Last modified
Testing_ST26T-2955	PF Number xyz99	Dingenskirchen Company	Method for the production of gold	invalid	2024-07-10 15:02	2024-07-17 17:44
Better Tropical Soybean	BRIN-ID-01	BRIN	Tropical Soybean Genetic markers	generated	2024-07-04 17:06	2024-07-04 17:06
Tropical Soybean Chr01 Gene	TPD-UID/GM01/V1	BRIN	Tropical Soybean Genetic markers Chr01	generated	2024-07-04 16:16	2024-07-04 16:22

Project detail

The screenshot shows the project detail page for 'TROPICAL SOYBEAN CHR01 GENE'. The top navigation bar includes the WIPO Sequence logo, the project name, and several menu items: VERIFICATION REPORT, LANGUAGE DEPENDENT QUALIFIERS, IMPORT REPORT, DISPLAY THE SEQUENCE LISTING, HELP, PREFERENCES, and ENGLISH. A yellow box highlights the 'Project specific menu' items. Below the navigation bar, there are tabs for 'GENERAL INFORMATION' and 'SEQUENCES'. The main heading is 'TROPICAL SOYBEAN CHR01...' followed by buttons for 'Print', 'Export', 'Import Another Project', 'Validate', and 'Generate Sequence Listing'. A table displays project metadata:

Project Name Tropical Soybean Chr01 Gene	Creation date 2024-07-04 16:16
Last modified 2024-07-04 16:22	Status generated
Description	File Name Tropical Soybean SNP GM01_gene
Original free text language code	Sequences 471
Automatically add a translation qualifier when a CDS feature is created On	Non English free text language code

Below the table is a section for 'GENERAL INFORMATION' with a sub-section 'APPLICATION IDENTIFICATION' containing the following details:

Application Identified Before the assignment of the application number
Applicant file reference TPD-UID/GM01/V1

Getting started: Create a project

WIPO | Sequence PROJECTS PERSONS & ORGANIZATIONS ORGANISMS HELP PREFERENCES ENGLISH


NEW PROJECT IMPORT PROJECT IMPORT SEQUENCE LISTING VALIDATE SEQUENCE LISTING

PROJECTS

Search project by name

Project name	Applicant file reference	Applicant name	Invention title	Status	Creation Date	Last modified
Testing ST26T-2955	PF Number xyz99	Dingenskirchen Company	Method for the production of gold	invalid	2024-07-10 15:02	2024-07-17 17:44
Better Tropical Soybean	BRIN-ID-01	BRIN	Tropical Soybean Genetic markers	generated	2024-07-04 17:06	2024-07-04 17:06
Tropical Soybean Chr01 Gene	TPD-UID/GM01/V1	BRIN	Tropical Soybean Genetic markers Chr01	generated	2024-07-04 16:16	2024-07-04 16:22
ST26T-3410	AB123	Tom Jons	Copolymer including uncharged hydrophilic block	generated	2024-06-24 08:20	2024-06-28 09:27

Provide project details: general information

 **TROPICAL SOYBEAN CHR02 GENE** VERIFICATION REPORT LANGUAGE DEPENDENT QUALIFIERS IMPORT REPORT DISPLAY THE SEQUENCE LISTING HELP PREFERENCES ENGLISH Return to project home

GENERAL INFORMATION SEQUENCES

TROPICAL SOYBEAN CHR02 ...

Print Export Import Another Project Validate Generate Sequence Listing

Project Name Tropical Soybean Chr02 Gene	Creation date 2024-07-19 15:58
Last modified 2024-07-19 15:58	Status new
Description For demo	File Name
Original free text language code	Sequences 0
Automatically add a translation qualifier when a CDS feature is created On	Non English free text language code

GENERAL INFORMATION


APPLICATION IDENTIFICATION

Application Identified Before the assignment of the application number
--

Import a sequence data into a project

The screenshot displays the top navigation bar of the WIPO Sequence application. The navigation items include: WIPO | Sequence, TROPICAL SOYBEAN CHR02 GENE, VERIFICATION REPORT, LANGUAGE DEPENDENT QUALIFIERS, IMPORT REPORT, DISPLAY THE SEQUENCE LISTING, HELP, PREFERENCES, and a 'Return to project home' button. Below the navigation bar, the 'GENERAL INFORMATION' section is active, showing 'Invention title Tropical Soybean Genetic markers Chr02' and 'Language en - English'. The 'SEQUENCES' section is expanded, revealing a row of buttons: 'Create new sequence', 'Import sequence', 'Insert Sequence', 'Reorder Sequence', and 'Bulk Edit'. An upward-pointing arrow is visible in the bottom right corner of the main content area.

Import report/change data report

TROPICAL SOYBEAN CHR01 GENE VERIFICATION REPORT LANGUAGE DEPENDENT QUALIFIERS **IMPORT REPORT** DISPLAY THE SEQUENCE LISTING HELP PREFERENCES ENGLI Return to project home

Import Report

[Print Report](#)

Changed Data

Origin Tag	Origin Element Name	Origin Element Value	Target Element Name	Target Element Value	Transformation	Origin Sequence ID	Sequence ID Number
INSDQualifier	ID	q2	Qualifier ID	q946	The qualifier ID has been updated as the specified value was already taken.	2	2
INSDQualifier	ID	q946	Qualifier ID	q949	The qualifier ID has been updated as the specified value was already taken.	4	4
INSDQualifier	ID	q3	Qualifier ID	q948	The qualifier ID has been updated as the specified value	3	3

Validate sequence listing

GENERAL INFORMATION SEQUENCES

TROPICAL...

Print

Export

Import Another Project

Validate

Generate Sequence Listing

Project Name Tropical Soybean Chr02 Gene

Last modified 2024-07-19 16:30

Description For demo

Original free text language code

Automatically add a translation qualifier when a CDS feature is created On

Creation date 2024-07-19 15:58

Status invalid

File Name

Sequences 458

Non English free text language code



Verification report: errors and warnings

ERROR: After project verification, some errors or warnings have been detected.



Report generated on 2024-07-19

Print Report

Severity	Data Element	Message Text	Detected Value	Detected Sequence
WARNING	originalFreeTextLanguageCode	An original free text language code has not been entered.	-	
WARNING	ApplicationIdentification	The filing date has not been entered. If the filing date has been assigned, it must be entered.	-	
WARNING	ApplicantFileReference	An Applicant File Reference number has not been entered. It must be entered if an application number has not been assigned and entered.	-	
WARNING	Earliest Priority Application Identifications	Earliest priority application information has not been entered. It must be entered when a priority claim is made	-	

Errors and warnings

- **WARNING:** can be ignored but should be addressed by manual review
- **ERROR:** must 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

Language dependent free text qualifiers

- One of two types:
 - Language dependent (may require a translation) e.g., 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

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

Import/export XLIFF

IMPORT FREE TEXT QUALIFIERS EXPORT FREE TEXT QUALIFIERS

LANGUAGE DEPENDENT QUALIFIERS

Source language code for free text qualifiers en

Target language code for free text qualifiers



Sequence ID Number	Sequence Name	Feature Key	Feature Location	Qualifier ID	Qualifier Name	Qualifier Value	Non English Qualifier Value	Available in code
1	SEQ472	source	1..1001	q2	<u>organism</u>	Glycine max		
2	SEQ473	source	1..1001	q4	<u>organism</u>	Glycine max		
3	SEQ474	source	1..1001	q6	<u>organism</u>	Glycine max		

Generate sequence listing

GENERAL INFORMATION SEQUENCES

GENERATE THE SEQUENCE LISTING

Do you really want to continue ignoring the warnings and generate the sequence listing?

Users should be aware that some Offices do not allow certain characters in the filename of the sequence listing. Please refer to the WIPO Sequence knowledge base for further details under help.

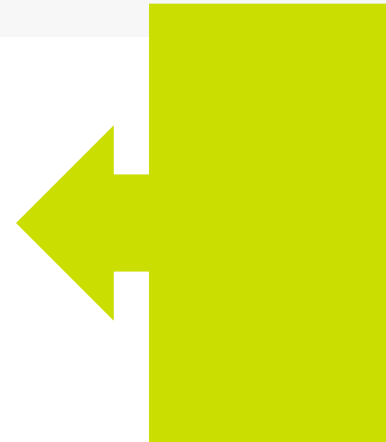
Close

Confirm

Another Project

Validate

Generate Sequence Listing



```
<ST26SequenceListing dtdVersion="V1_3" fileName="st26-annex-iii-sequence-listing-specimen.xml" softwareName="WIPO Sequence" softwareVersion="1.2.0" productionDate="2022-01-07" originalFreeTextLanguageCode="ja" nonEnglishFreeTextLanguageCode="de">
<ApplicationIdentification>
  <IPOfficeCode>IB</IPOfficeCode>
  <ApplicationNumberText>PCT/IB2015/099999</ApplicationNumberText>
  <FilingDate>2015-01-31</FilingDate>
</ApplicationIdentification>
<ApplicantFileReference>AB123</ApplicantFileReference>
<EarliestPriorityApplicationIdentification>
  <IPOfficeCode>IB</IPOfficeCode>
  <ApplicationNumberText>PCT/IB2014/111111</ApplicationNumberText>
  <FilingDate>2014-01-30</FilingDate>
</EarliestPriorityApplicationIdentification>
<ApplicantName languageCode="ja">出願製薬株式会社</ApplicantName>
<ApplicantNameLatin>Shutsugan Pharmaceuticals Kabushiki Kaisha</ApplicantNameLatin>
<InventorName languageCode="ja">特許 太郎</InventorName>
<InventorNameLatin>Taro Tokkyo</InventorNameLatin>
<InventionTitle languageCode="ja">efgタンパク質をコードするマウスabcd-1遺伝子</InventionTitle>
<InventionTitle languageCode="en">Mus musculus abcd-1 gene for efg protein </InventionTitle>
<SequenceTotalQuantity>11</SequenceTotalQuantity>
<SequenceData sequenceIDNumber="1">
  <INSDSeq>
    <INSDSeq_length>133</INSDSeq_length>
    <INSDSeq_moltype>DNA</INSDSeq_moltype>
    <INSDSeq_division>PAT</INSDSeq_division>
    <INSDSeq_feature-table>
      <INSDFeature>
        <INSDFeature_key>source</INSDFeature_key>
        <INSDFeature_location>1..133</INSDFeature_location>
        <INSDFeature_qual>
          <INSDQualifier>
            <INSDQualifier_name>organism</INSDQualifier_name>
            <INSDQualifier_value>Homo sapiens</INSDQualifier_value>
          </INSDQualifier>
          <INSDQualifier>
            <INSDQualifier_name>mol_type</INSDQualifier_name>
            <INSDQualifier_value>genomic DNA</INSDQualifier_value>
          </INSDQualifier>
        </INSDFeature_qual>
      </INSDFeature>
    </INSDSeq_feature-table>
    <INSDSeq_sequence>atgaaattaaacataaaarggatgataaaatgagatttgatataaaaaagggttttagagtttagcagagaaggatgttgagacggcatggagagagacaagggcattaataaaggataaacatattgacaata
    </INSDSeq_sequence>
  </INSDSeq>
</SequenceData>
```

Display sequence listing in txt format

Sequence Listing Information:

dtdVersion: V1_3

fileName: st26-annex-iii-sequence-listing-specimen.xml

softwareName: WIPO Sequence

softwareVersion: 3.0.0

productionDate: 2024-07-28

General Information:

Current application / IP Office: IB

Current application / Application number: PCT/IB2015/099999

Current application / Filing date: 2015-01-31

Current application / Applicant file reference: AB123

Earliest priority application / IP Office: IB

Earliest priority application / Application number: PCT/IB2014/111111

Earliest priority application / Filing date: 2014-01-30

Applicant name: 出願製薬株式会社

Applicant name / Language: ja

Applicant name / Name Latin: Shutsugan Pharmaceuticals Kabushiki Kaisha

Inventor name / Language: ja

Inventor name / Name Latin: Taro Tokkyo

Invention title: efgタンパク質をコードするマウスabcd-1遺伝子 (ja)

Invention title: Mus musculus abcd-1 gene for efg protein (en)

SequenceTotalQuantity: 11

Sequences:

Sequence Number (ID): 1

Length: 133

Molecule Type: DNA

Features Location/Qualifiers:

- source, 1..133

> mol_type, genomic DNA

> organism, Homo sapiens

Residues:

atgaaattaa aacataaaar ggatgataaa algagattg atataaaaaa ggttttagag 60

ttagcagaga aggatttga gacggcatgg agagagacaa gggcattaat aaaggataaa 120

catattgaca ata

133

Display sequence listing in HTML format

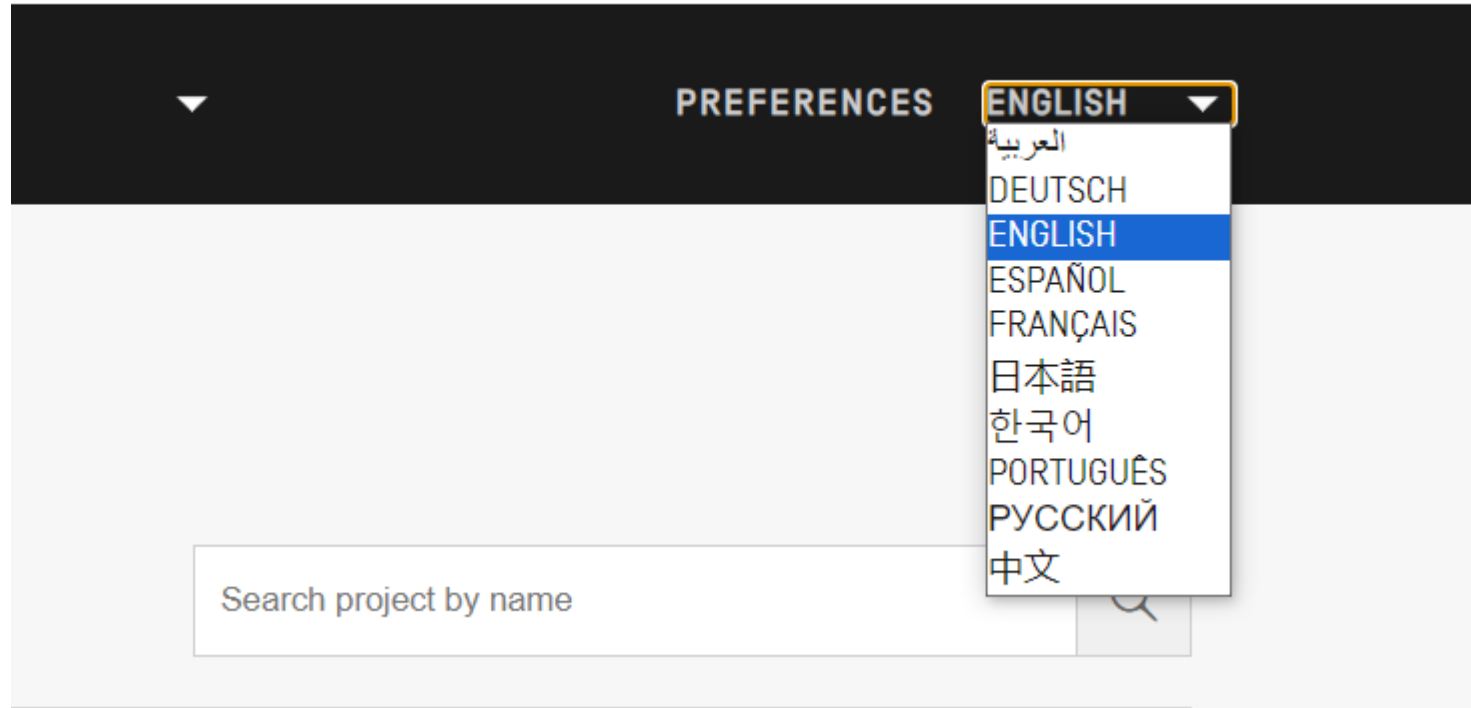
Sequence Listing

1	Sequence Listing Information	
1-1	fileName	st26-annex-iii-sequence-listing-specimen.xml
1-2	dtdVersion	V1_3
1-3	softwareName	WIPO Sequence
1-4	softwareVersion	3.0.0
1-5	productionDate	2024-07-28
1-6	originalFreeTextLanguageCode	ja
1-7	nonEnglishFreeTextLanguageCode	de
2	General Information	
2-1	Current application: IP Office	IB
2-2	Current application: Application number	PCT/IB2015/099999
2-3	Current application: Filing date	2015-01-31
2-4	Current application: Applicant file reference	AB123
2-5	Earliest priority application: IP Office	IB
2-6	Earliest priority application: Application number	PCT/IB2014/111111
2-7	Earliest priority application: Filing date	2014-01-30
2-8ja	Applicant name	出願製薬株式会社
2-8ja	Applicant name: Name Latin	Shutsugan Pharmaceuticals Kabushiki Kaisha
2-9ja	Inventor name	特許 太郎
2-9ja	Inventor name: Name Latin	Taro Tokkyo
2-10ja	Invention title	efgタンパク質をコードするマウスabcd-1遺伝子
2-10en	Invention title	Mus musculus abcd-1 gene for efg protein
2-11	SequenceTotalQuantity	11
3-1	Sequences	
3-1-1	Sequence Number [ID]	1
3-1-2	Molecule Type	DNA
3-1-3	Length	133
3-1-4-1	Features Location/Qualifiers	source 1..133 mol_type= genomic DNA organism= Homo sapiens

Languages available

- 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 WIPO Sequence home page/desktop 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

Setting interface language





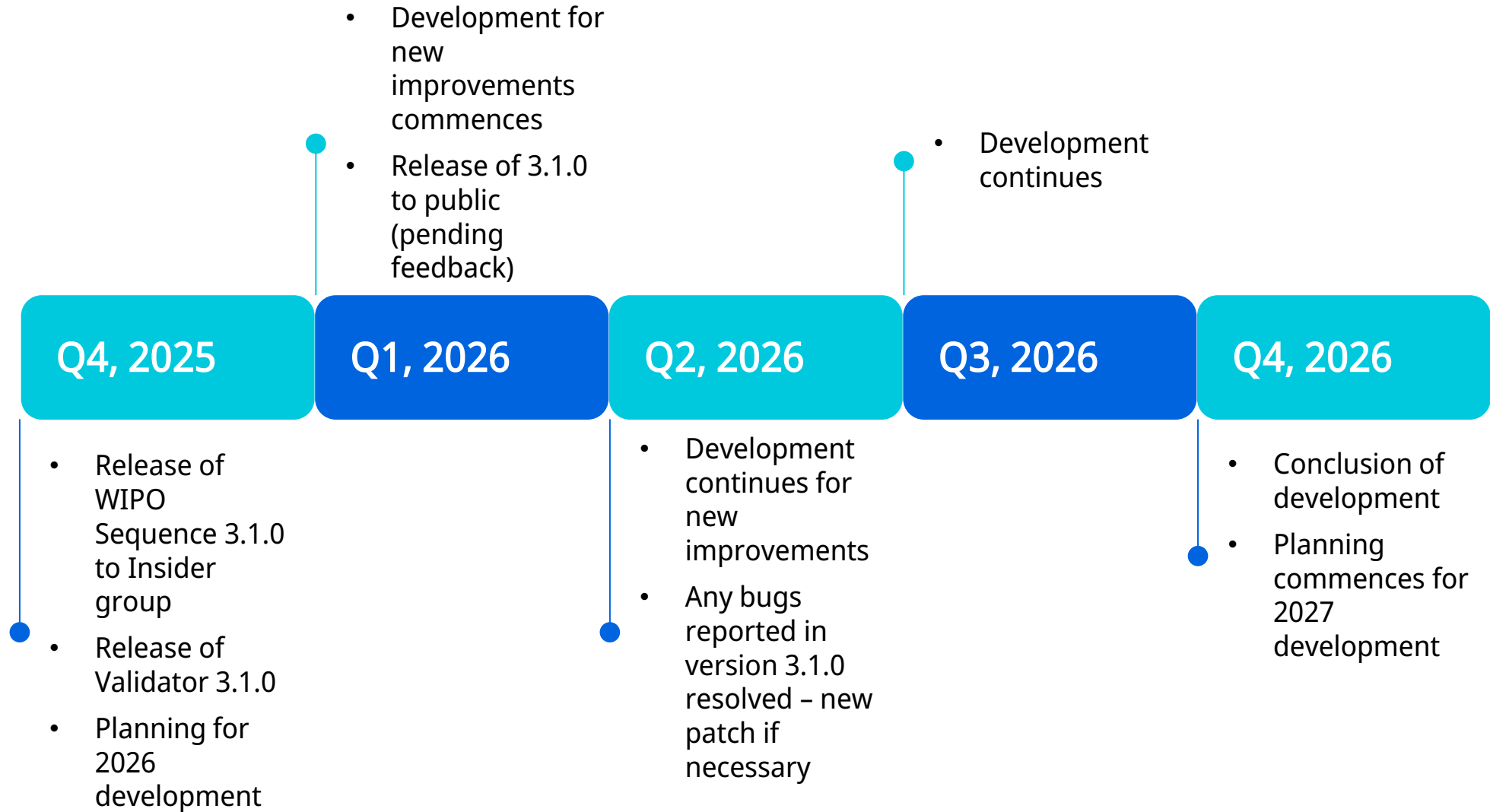
Development 2025-2026

- Technical stakeholder meeting held in October each year.
- Results in improvements being prioritized for development
- Now that WIPO ST.26 version 2.0 is approved, WIPO Sequence will need to be updated to remove verification rules relating to short sequences
- WIPO Sequence Insider group will continue to pilot releases before general release.

Latest improvements implemented in version 3.1.0 include...

- “Jump to” a particular SEQID
- Warnings implemented for skipped sequences
- Bulk “unskip” of selected sequences
- Mandatory qualifiers are automatically added on feature creation
- Bulk add of multiple copies of a feature to a single sequence
- Bulk adding features with a blank feature location
- Bulk FASTA import
- ... and improvements to performance for project validation

Release schedule




WIPO Sequence Insiders

- Pilot new releases before general release
- 150 volunteers
- Generate sequence listings with the new version and report any errors to us
- At the end of the pilot period, inform us whether they are happy for general release to proceed
- Interesting in joining? Contact us at wiposequence@wipo.int





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Contact us:
wiposequence@wipo.int