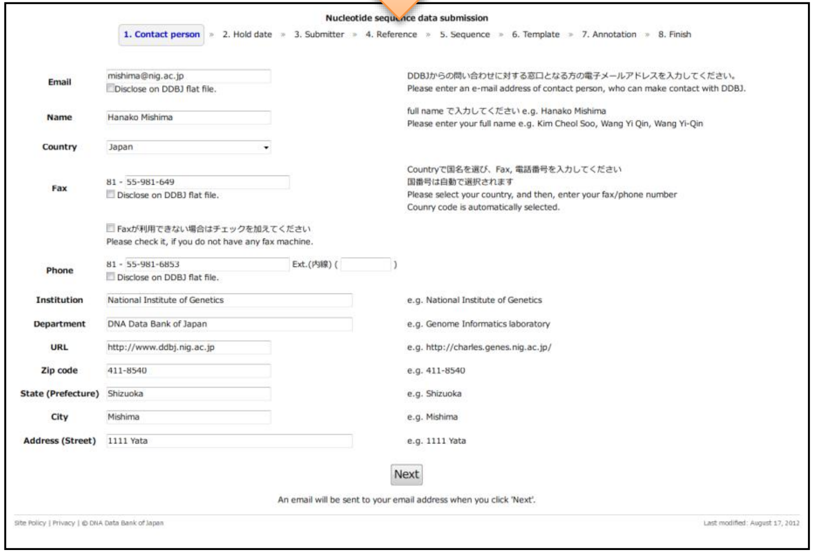
DDBJ Nucleotide Sequence Submission System

Outline of the submission

Open http://ddbj.nig.ac.jp/submission/
and click "Create new submission"



Nucleotide sequence data submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Email	mishima@nig.ac.jp ☐ Disclose on DDBJ flat file.	DDBJからの問い合わせに対する窓口となる方の電子メールアドレスを入力してください。 Please enter an e-mail address of contact person, who can make contact with DDBJ.
Name	Hanako Mishima	full name で入力してください e.g. Hanako Mishima Please enter your full name e.g. Kim Cheol Soo, Wang Yi Qin, Wang Yi-Qin
Country	Japan	
Fax	81 - 55-981-649 ☐ Disclose on DDBJ flat file.	Countryで国名を選び、Fax, 電話番号を入力してください 国番号は自動で選択されます Please select your country, and then, enter your fax/phone number Counry code is automatically selected.
	☐ Faxが利用できない場合はチェックを加えてください Please check it, if you do not have any fax machine.	
Phone	81 - 55-981-6853 Ext.(内線) ( ) ☐ Disclose on DDBJ flat file.	
Institution	National Institute of Genetics	e.g. National Institute of Genetics
Department	DNA Data Bank of Japan	e.g. Genome Informatics laboratory
URL	http://www.ddbj.nig.ac.jp	e.g. http://charles.genes.nig.ac.jp/
Zip code	411-8540	e.g. 411-8540
State (Prefecture)	Shizuoka	e.g. Shizuoka
City	Mishima	e.g. Mishima
Address (Street)	1111 Yata	e.g. 1111 Yata

An email will be sent to your email address when you click 'Next'.

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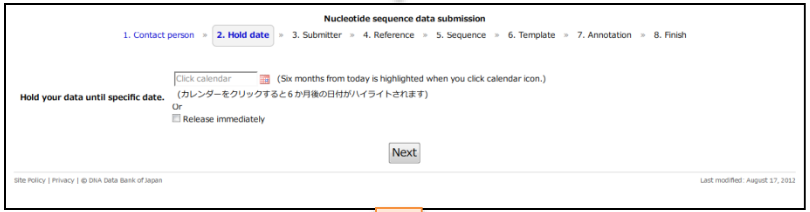
1. Enter "Contact person"
Receive an email and click a link to activate your submission



Nucleotide sequence data submission

1. Contact person » **2. Hold date** » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Hold your data until specific date. Click calendar (Six months from today is highlighted when you click calendar icon.)
(カレンダーをクリックすると６か月後の日付がハイライトされます)
Or
☐ Release immediately

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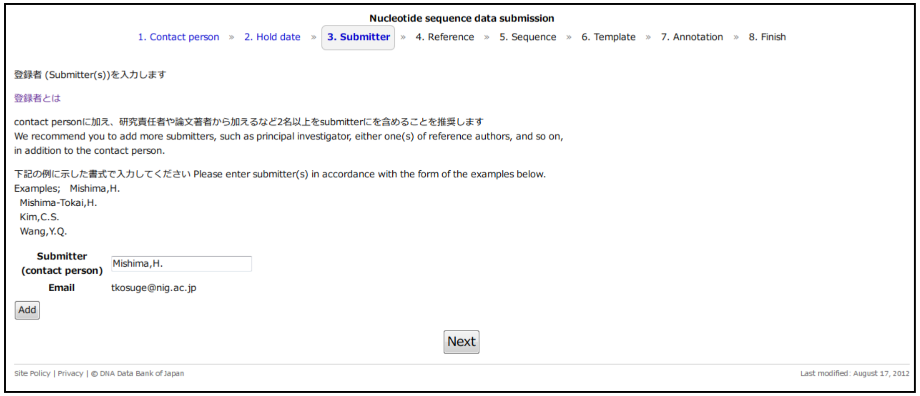
Last modified: August 17, 2012

2. Enter "Hold date"

3. Enter “Submitter”



Nucleotide sequence data submission

登録者 (Submitter(s))を入力します

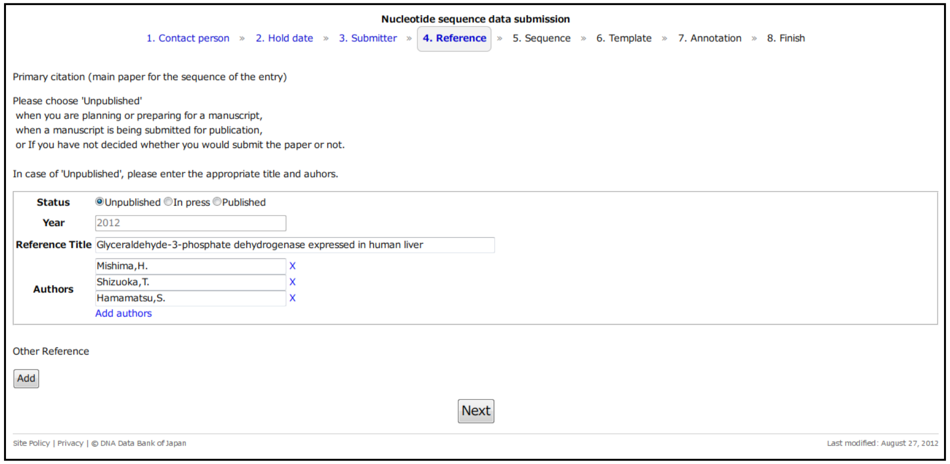
登録者とは

contact personに加え、研究責任者や論文著者から加えるなど2名以上をsubmitterにを含めることを推奨します
We recommend you to add more submitters, such as principal investigator, either one(s) of reference authors, and so on, in addition to the contact person.

下記の例に示した書式で入力してください Please enter submitter(s) in accordance with the form of the examples below.
Examples; Mishima,H.
Mishima-Tokai,H.
Kim,C.S.
Wang,Y.Q.

Submitter (contact person)	Mishima,H.
Email	tkosuge@nig.ac.jp

4. Enter “Reference”



Nucleotide sequence data submission

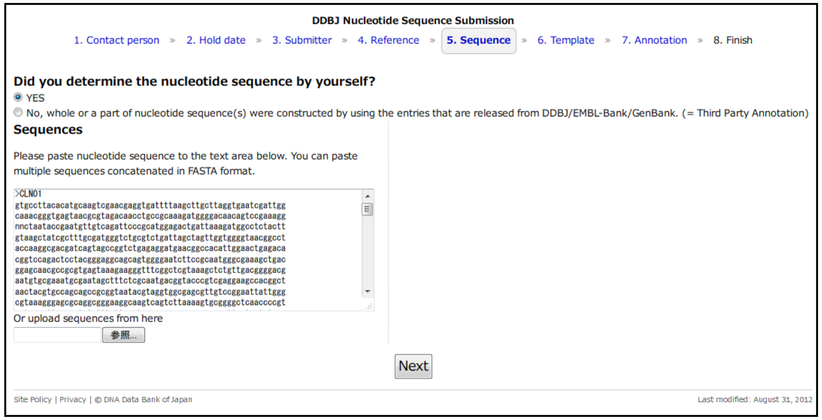
Primary citation (main paper for the sequence of the entry)

Please choose 'Unpublished'
when you are planning or preparing for a manuscript,
when a manuscript is being submitted for publication,
or If you have not decided whether you would submit the paper or not.

In case of 'Unpublished', please enter the appropriate title and auhors.

Status	● Unpublished ○ In press ○ Published
Year	2012
Reference Title	Glyceraldehyde-3-phosphate dehydrogenase expressed in human liver
Authors	Mishima,H. X Shizuoka,T. X Hamamatsu,S. X Add authors

Other Reference



DDBJ Nucleotide Sequence Submission

Did you determine the nucleotide sequence by yourself?

● YES

○ No, whole or a part of nucleotide sequence(s) were constructed by using the entries that are released from DDBJ/EMBL-Bank/GenBank. (= Third Party Annotation)

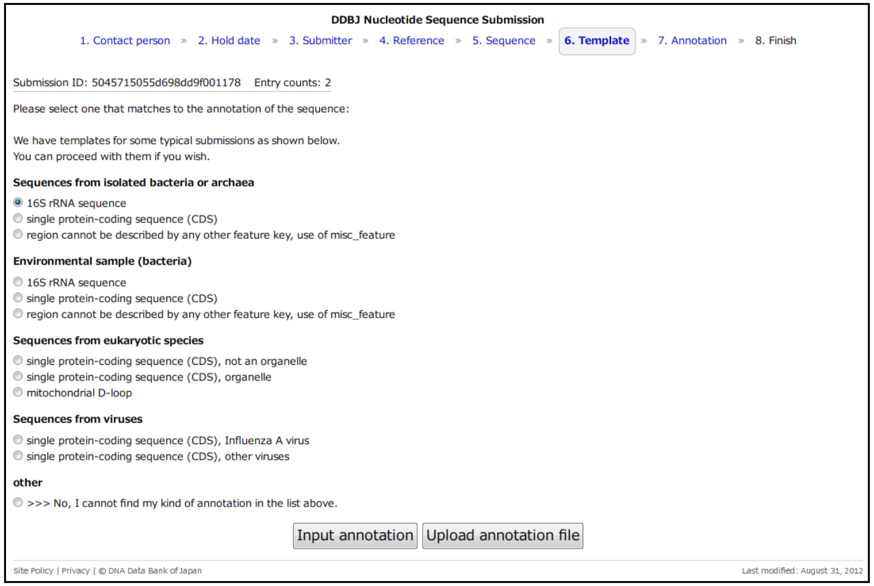
Sequences

Please paste nucleotide sequence to the text area below. You can paste multiple sequences concatenated in FASTA format.

```
>CLN01
gtgccttacacatgcaagtcgaacgaggtgattttaagcttgcttaggtgaatcgattgg
caaacgggtgagtaacgcgtagacaacctgccgcaaagatggggacaacagtccgaaagg
nnctaataccgaatgttgtcagattcccgcatggagactgattaaagatggcctctactt
gtaagctatcgctttgcgatgggtctgcgtctgattagctagttggtggggtaacggcct
accaaggcgacgatcagtagccggtctgagaggatgaacggccacattggaactgagaca
cggtccagactcctacgggaggcagcagtggggaatcttccgcaatgggcgaaagctgac
ggagcaacgccgcgtgagtaaagaagggtttcggctcgtaaagctctgttgacggggacg
aatgtgcgaaatgcgaatagctttctcgcaatgacggtacccgtcgaggaagccacggct
aactacgtgccagcagccgcggtaatacgtaggtggcgagcgttgtccggaattattggg
cgtaaagggagcgcaggcgggaaggcaagtcagtcttaaaagtgcggggctcaaccccgt
```

Or upload sequences from here

5. Enter nucleotide sequences
Enter assembly information for TPA



DDBJ Nucleotide Sequence Submission

Submission ID: 5045715055d698dd9f001178 Entry counts: 2

Please select one that matches to the annotation of the sequence:

We have templates for some typical submissions as shown below.
You can proceed with them if you wish.

Sequences from isolated bacteria or archaea

● 16S rRNA sequence
○ single protein-coding sequence (CDS)
○ region cannot be described by any other feature key, use of misc_feature

Environmental sample (bacteria)

○ 16S rRNA sequence
○ single protein-coding sequence (CDS)
○ region cannot be described by any other feature key, use of misc_feature

Sequences from eukaryotic species

○ single protein-coding sequence (CDS), not an organelle
○ single protein-coding sequence (CDS), organelle
○ mitochondrial D-loop

Sequences from viruses

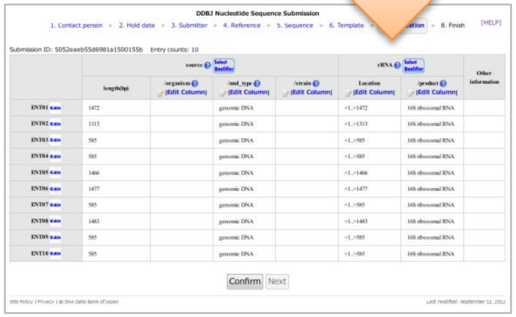
○ single protein-coding sequence (CDS), Influenza A virus
○ single protein-coding sequence (CDS), other viruses

other

○ >>> No, I cannot find my kind of annotation in the list above.

6. Select template that matches to the annotation. You can choose input annotation or upload annotation from file.

7. Input annotation or upload a file that contains annotation.


DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » …ation » 8. Finish [HELP]

Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

	source				rRNA		Other information
	length(bp)	/organism	/mol_type	/strain	Location	/product	
ENT01	1472		genomic DNA		<1..>1472	16S ribosomal RNA	
ENT02	1313		genomic DNA		<1..>1313	16S ribosomal RNA	
ENT03	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT04	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT05	1466		genomic DNA		<1..>1466	16S ribosomal RNA	
ENT06	1477		genomic DNA		<1..>1477	16S ribosomal RNA	
ENT07	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT08	1483		genomic DNA		<1..>1483	16S ribosomal RNA	
ENT09	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT10	585		genomic DNA		<1..>585	16S ribosomal RNA	

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DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish [HELP]

Submission ID: 50581dac55d6981a12000918 Entry counts: 3

sample1

source: length=658, genetic code=, /organism =, /mol_type =

CDS: location=1..658, /codon_start =, /note =, /product =

misc_feature: location=1..658

sample2

source: length=632, genetic code=, /organism =, /mol_type =

CDS: location=1..632, /codon_start =, /gene =, /product =

sample3

source: length=632, genetic code=, /organism =, /mol_type =

exon: location=1..632, /gene =, /number =

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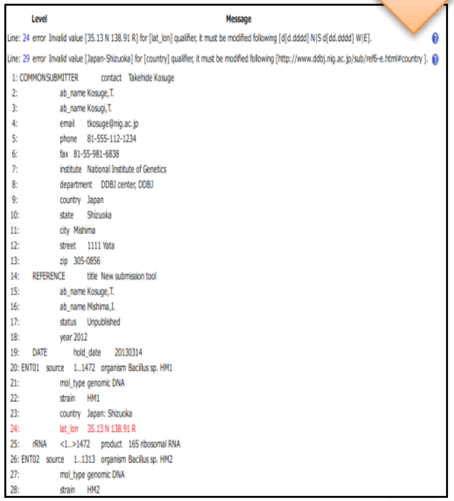
Repeat annotation check until error is completely corrected.



```
Level                Message
Line: 24 error Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E].
Line: 29 error Invalid value [Japan-Shizuoka] for [country] qualifier, it must be modified following [http://www.ddbj.nig.ac.jp/sub/ref6-e.html#country ].
1: COMMONSUBMITTER    contact   Takehide Kosuge
2:           ab_name Kosuge,T.
3:           ab_name Kosugi,T.
4:           email     tkosuge@nig.ac.jp
5:           phone     81-555-112-1234
6:           fax  81-55-981-6838
7:           institute   National Institute of Genetics
8:           department    DDBJ center, DDBJ
9:           country   Japan
10:          state     Shizuoka
11:          city  Mishima
12:          street    1111 Yata
13:          zip  305-0856
14:   REFERENCE       title  New submission tool
15:          ab_name Kosuge,T.
16:          ab_name Mishima,I.
17:          status    Unpublished
18:          year 2012
19:   DATE        hold_date     20130314
20: ENT01   source    1..1472   organism Bacillus sp. HM1
21:          mol_type genomic DNA
22:          strain    HM1
23:          country   Japan: Shizuoka
24:          lat_lon   35.13 N 138.91 R
25:   rRNA     <1..>1472    product   16S ribosomal RNA
26: ENT02   source    1..1313   organism Bacillus sp. HM2
27:          mol_type genomic DNA
28:          strain    HM2
```


DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish [HELP]

Contact person

Email	tkosuge@nig.ac.jp
Name	Takehide Kosuge
Country	Japan
Fax	55-981-6838
Phone	555-112-1234
Phone extension	
Institution	National Institute of Genetics
Department	DDBJ center, DDBJ
Zip code	305-0856
State (Prefecture)	Shizuoka
City	Mishima
Address (Street)	1111 Yata

Publication

Hold date	2013-03-14

Submitters

Name	Kosuge,T.
Email	tkosuge@nig.ac.jp
Name	Kosugi,T.
Email	

References

Status	Unpublished
Year	2012
Reference Title	New submission tool
Name	Kosuge,T.
Name	Mishima,I.

Submission information

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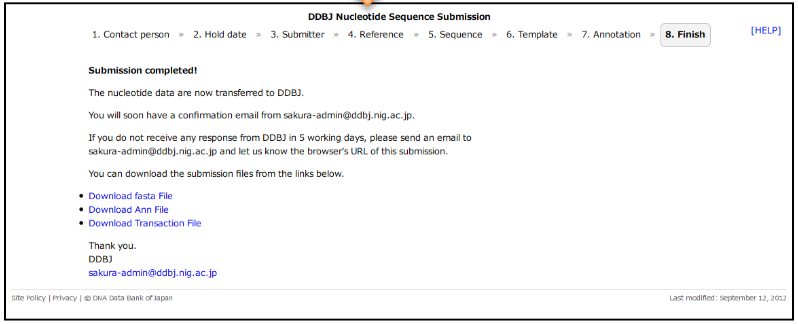
8. Finish, you will soon receive an email from DDBJ.


DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish [HELP]

Submission completed!

The nucleotide data are now transferred to DDBJ.

You will soon have a confirmation email from sakura-admin@ddbj.nig.ac.jp.

If you do not receive any response from DDBJ in 5 working days, please send an email to sakura-admin@ddbj.nig.ac.jp and let us know the browser's URL of this submission.

You can download the submission files from the links below.

- Download fasta File
- Download Ann File
- Download Transaction File

Thank you.
DDBJ
sakura-admin@ddbj.nig.ac.jp

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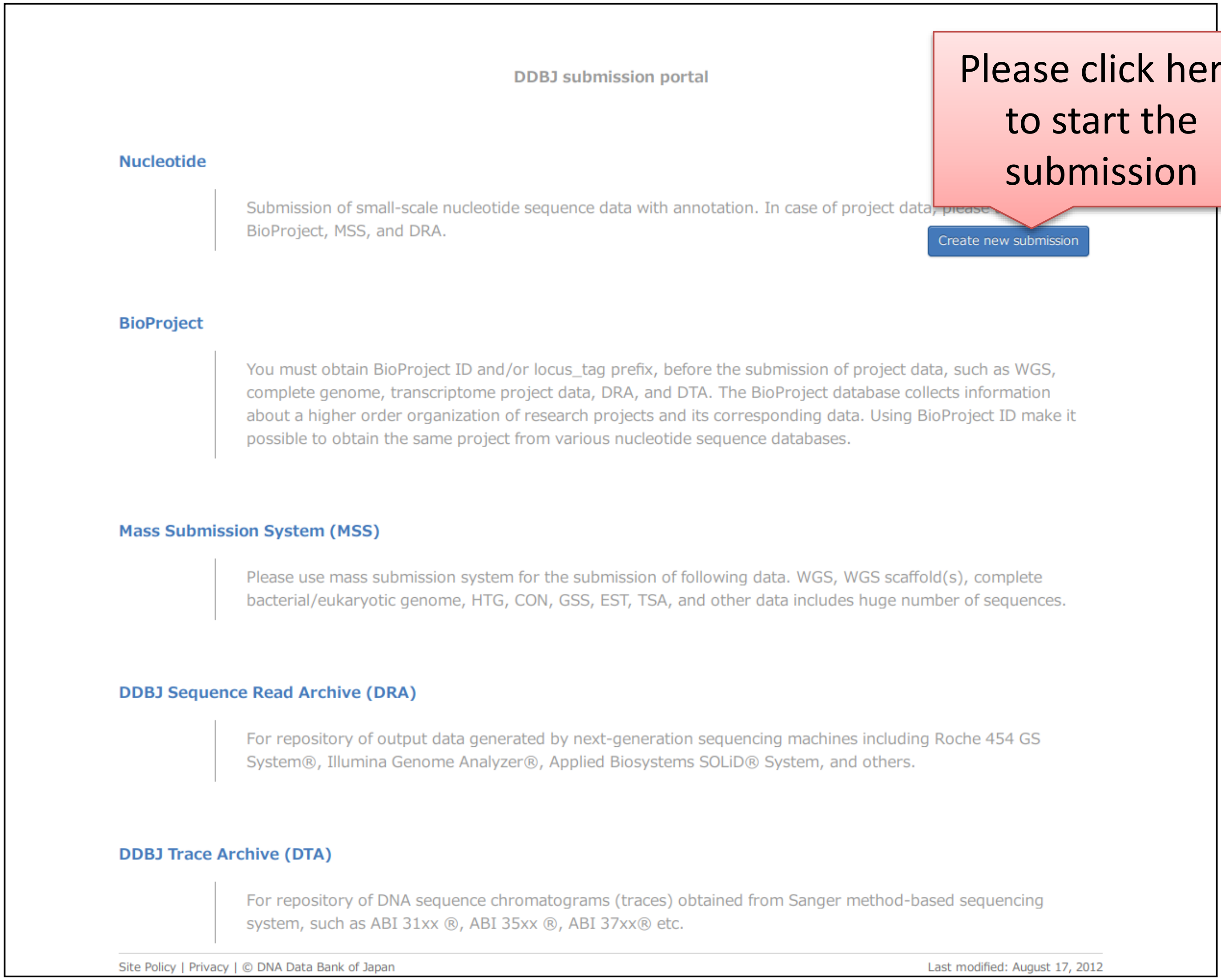
Start the submission from http://ddbj.nig.ac.jp/submission/



DDBJ submission portal

Nucleotide

Submission of small-scale nucleotide sequence data with annotation. In case of project data, please BioProject, MSS, and DRA.

BioProject

You must obtain BioProject ID and/or locus_tag prefix, before the submission of project data, such as WGS, complete genome, transcriptome project data, DRA, and DTA. The BioProject database collects information about a higher order organization of research projects and its corresponding data. Using BioProject ID make it possible to obtain the same project from various nucleotide sequence databases.

Mass Submission System (MSS)

Please use mass submission system for the submission of following data. WGS, WGS scaffold(s), complete bacterial/eukaryotic genome, HTG, CON, GSS, EST, TSA, and other data includes huge number of sequences.

DDBJ Sequence Read Archive (DRA)

For repository of output data generated by next-generation sequencing machines including Roche 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD® System, and others.

DDBJ Trace Archive (DTA)

For repository of DNA sequence chromatograms (traces) obtained from Sanger method-based sequencing system, such as ABI 31xx ®, ABI 35xx ®, ABI 37xx® etc.

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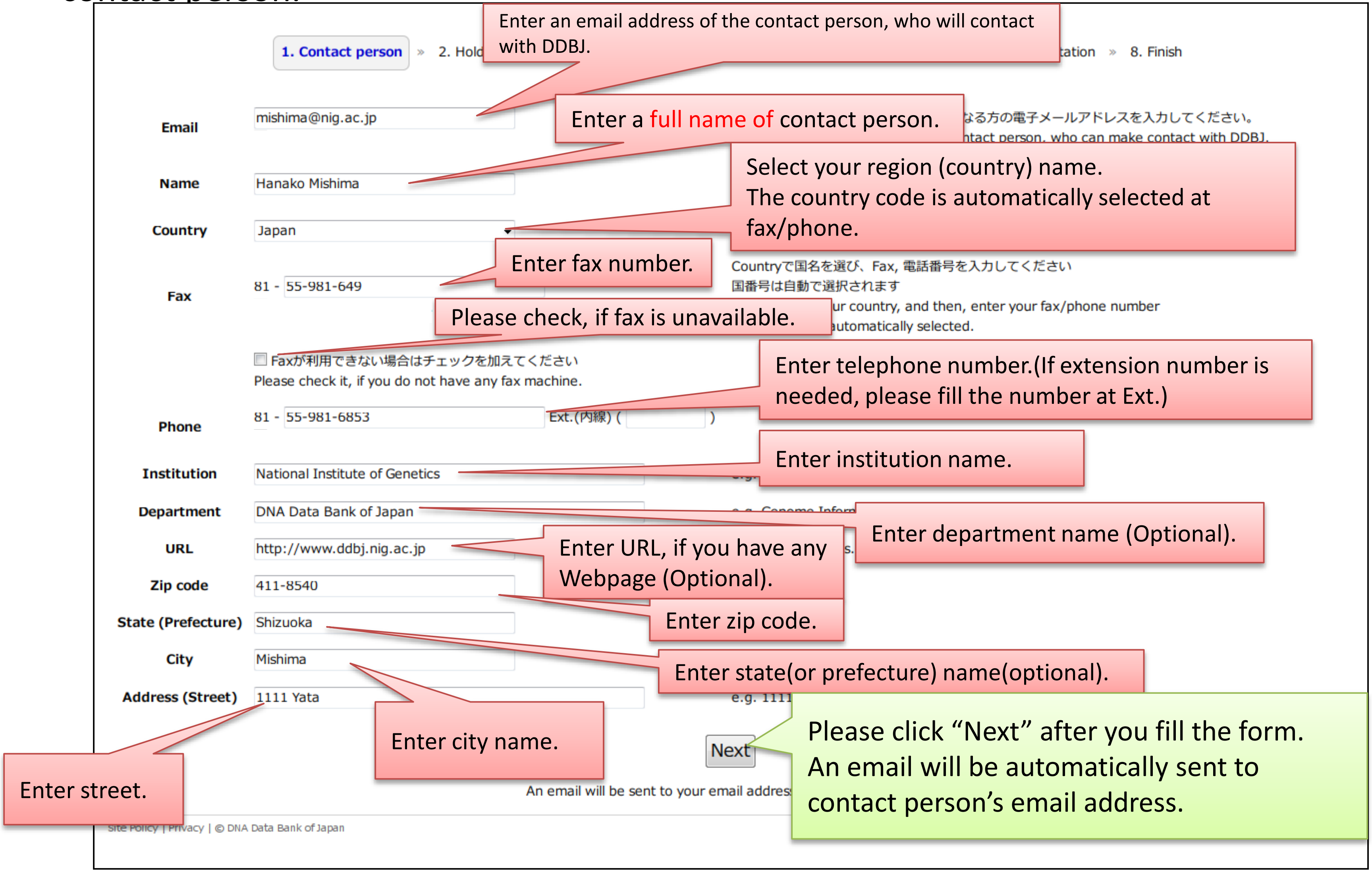
Please click here to start the submission

1. Contact person

Contact person is the person who will make contact with DDBJ and DDBJ users about the entry, in principle. One of the submitter can become a contact person.



Email mishima@nig.ac.jp

なる方の電子メールアドレスを入力してください。
ntact person, who can make contact with DDBJ.

Name Hanako Mishima

Country Japan

Fax 81 - 55-981-649

Countryで国名を選び、Fax, 電話番号を入力してください
国番号は自動で選択されます
ur country, and then, enter your fax/phone number
automatically selected.

☐ Faxが利用できない場合はチェックを加えてください
Please check it, if you do not have any fax machine.

Phone 81 - 55-981-6853 Ext.(内線) ( )

Institution National Institute of Genetics

Department DNA Data Bank of Japan

URL http://www.ddbj.nig.ac.jp

Zip code 411-8540

State (Prefecture) Shizuoka

City Mishima

Address (Street) 1111 Yata

e.g. 1111

An email will be sent to your email addres

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Enter an email address of the contact person, who will contact with DDBJ.

Enter a full name of contact person.

Select your region (country) name.
The country code is automatically selected at fax/phone.

Enter fax number.

Please check, if fax is unavailable.

Enter telephone number.(If extension number is needed, please fill the number at Ext.)

Enter institution name.

Enter department name (Optional).

Enter URL, if you have any Webpage (Optional).

Enter zip code.

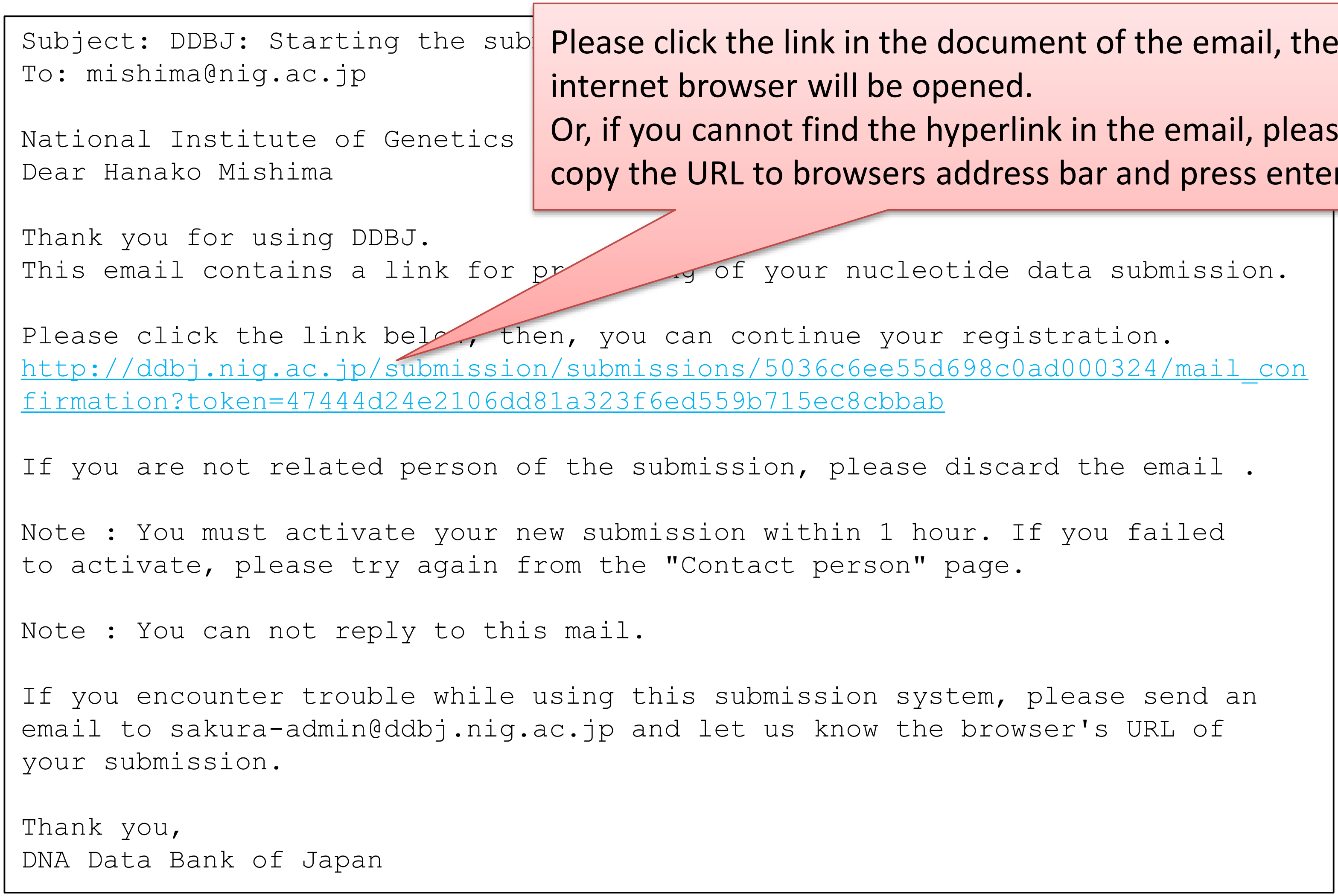
Enter state(or prefecture) name(optional).

Enter city name.

Enter street.

Please click “Next” after you fill the form. An email will be automatically sent to contact person’s email address.

An email, which contains a link to start the submission, is automatically sent to the contact person's email address.



Subject: DDBJ: Starting the sub
To: mishima@nig.ac.jp

National Institute of Genetics
Dear Hanako Mishima

Thank you for using DDBJ.
This email contains a link for pr g of your nucleotide data submission.

Please click the link bel then, you can continue your registration.
http://ddbj.nig.ac.jp/submission/submissions/5036c6ee55d698c0ad000324/mail_confirmation?token=47444d24e2106dd81a323f6ed559b715ec8cbbab

If you are not related person of the submission, please discard the email .

Note : You must activate your new submission within 1 hour. If you failed
to activate, please try again from the "Contact person" page.

Note : You can not reply to this mail.

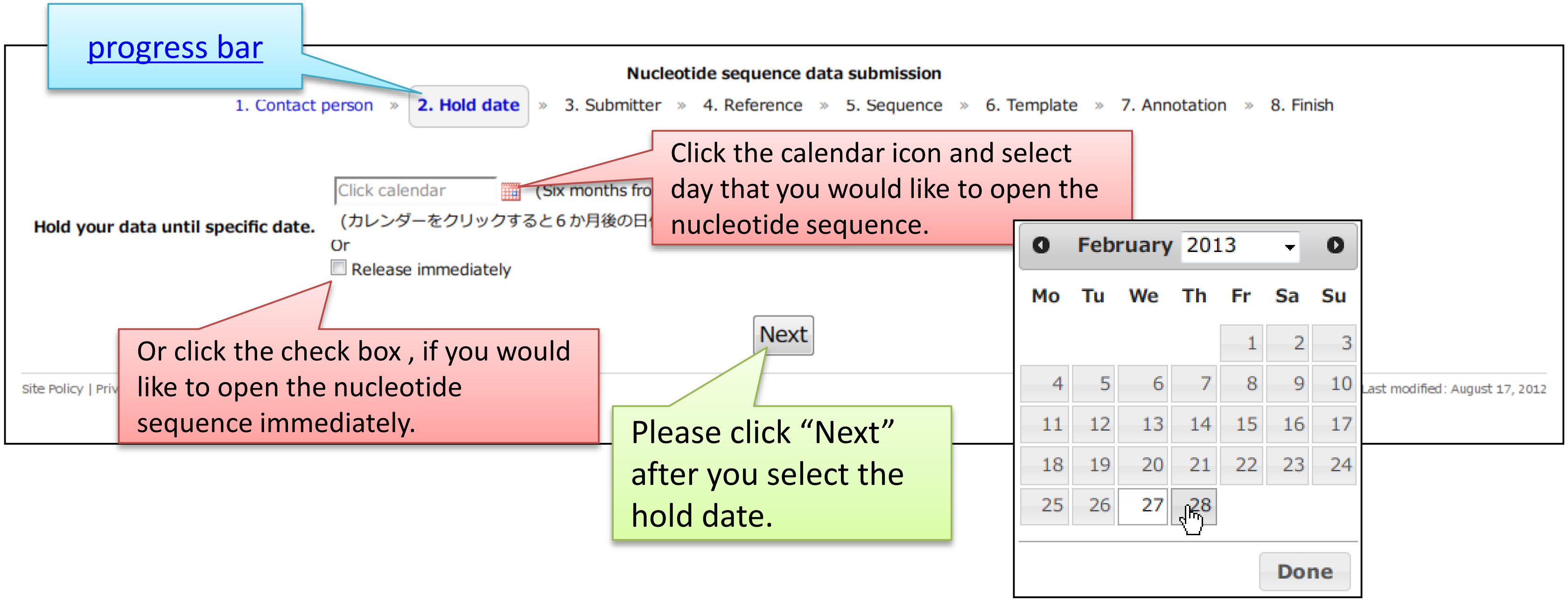
If you encounter trouble while using this submission system, please send an
email to sakura-admin@ddbj.nig.ac.jp and let us know the browser's URL of
your submission.

Thank you,
DNA Data Bank of Japan

Please click the link in the document of the email, then internet browser will be opened.
Or, if you cannot find the hyperlink in the email, please copy the URL to browsers address bar and press enter.

2. Hold date

Enter hold date or select “Release immediately” on the page.



progress bar

Nucleotide sequence data submission

1. Contact person » **2. Hold date** » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Hold your data until specific date. Click calendar (Six months fro
（カレンダーをクリックすると6か月後の日
Or
☐ Release immediately

Next

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ast modified: August 17, 2012

February 2013

Mo	Tu	We	Th	Fr	Sa	Su
				1	2	3
4	5	6	7	8	9	10
11	12	13	14	15	16	17
18	19	20	21	22	23	24
25	26	27	28			

Done

Click the calendar icon and select day that you would like to open the nucleotide sequence.

Or click the check box , if you would like to open the nucleotide sequence immediately.

Please click “Next” after you select the hold date.

- A day six months from today is highlighted when you click the calendar icon.
- You cannot select the several days on end or begin of the year as a hold date because DDBJ usually suspends the work to release the nucleotide sequences during the days.
- The selectable hold date is limited within three yeas from today.

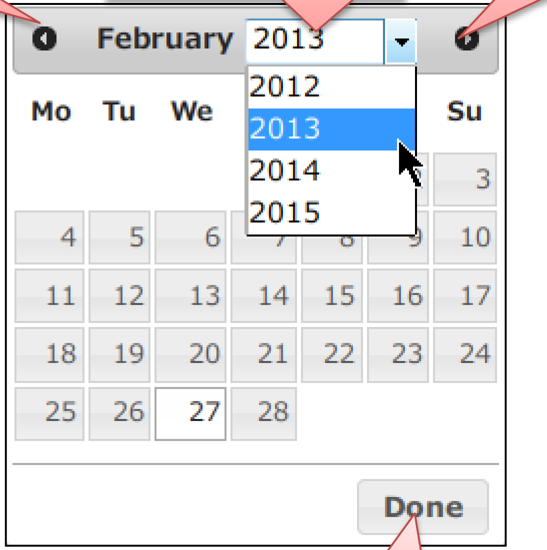
How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

How to use calendar

Move to previous month

You can select the year from the list.

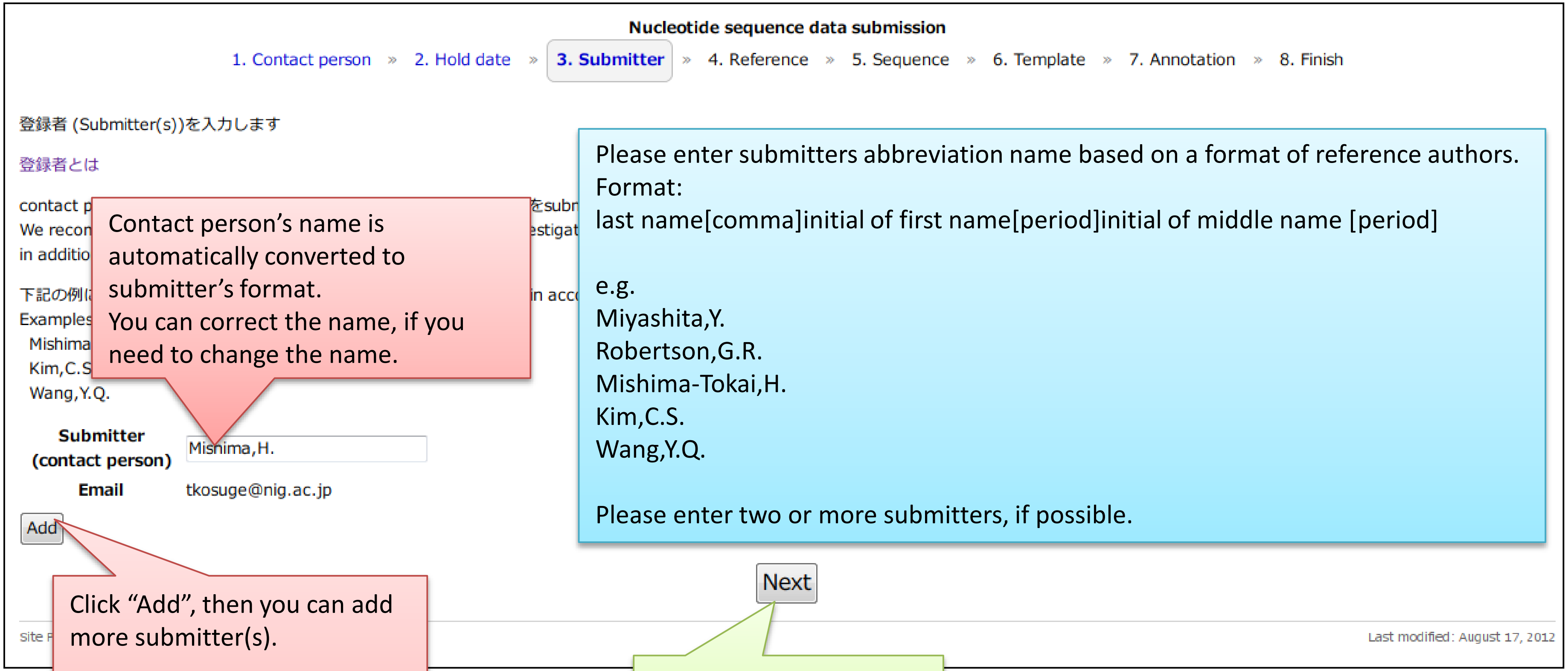
Move to next month



If you would like to close the calendar, please click.

3. Submitter

Enter Submitter (s) on the page.



Nucleotide sequence data submission

登録者 (Submitter(s))を入力します

登録者とは

contact p … をsubm
We recon … estigat
in additio

下記の例に … in acc
Examples
Mishima
Kim,C.S
Wang,Y.Q.

Submitter (contact person) Mishima,H.

Email tkosuge@nig.ac.jp

Contact person's name is automatically converted to submitter's format.
You can correct the name, if you need to change the name.

Please enter submitters abbreviation name based on a format of reference authors.
Format:
last name[comma]initial of first name[period]initial of middle name [period]

e.g.
Miyashita,Y.
Robertson,G.R.
Mishima-Tokai,H.
Kim,C.S.
Wang,Y.Q.

Please enter two or more submitters, if possible.

Click "Add", then you can add more submitter(s).

DDBJ recommend you to include two or more submitters in the submission.

Submitters name will be displayed in the flat file according to the submitters order of this page.

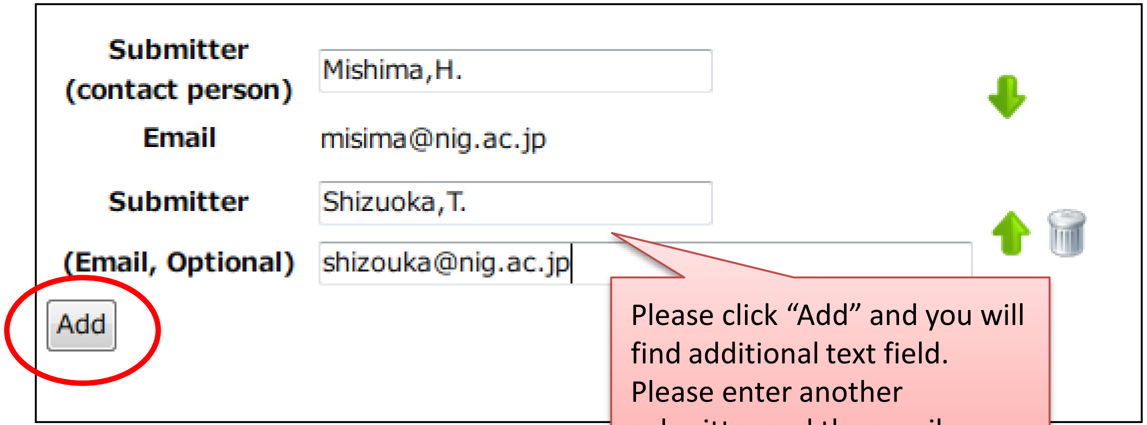
Please click "Next" after you fill the form.

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

We would like to ask you to include two or more submitters.

We occasionally meet the situation where we cannot contact to the submitter in case of entries which have only one submitter. In our rule, submitter is responsible for the data and only the submitter can update own entries. Without contacting to the submitter, we cannot fulfill necessary corrections.
Of course, you can register your entries with only one submitter, but we recommend you to add more submitters, such as principal investigator, to your entries.

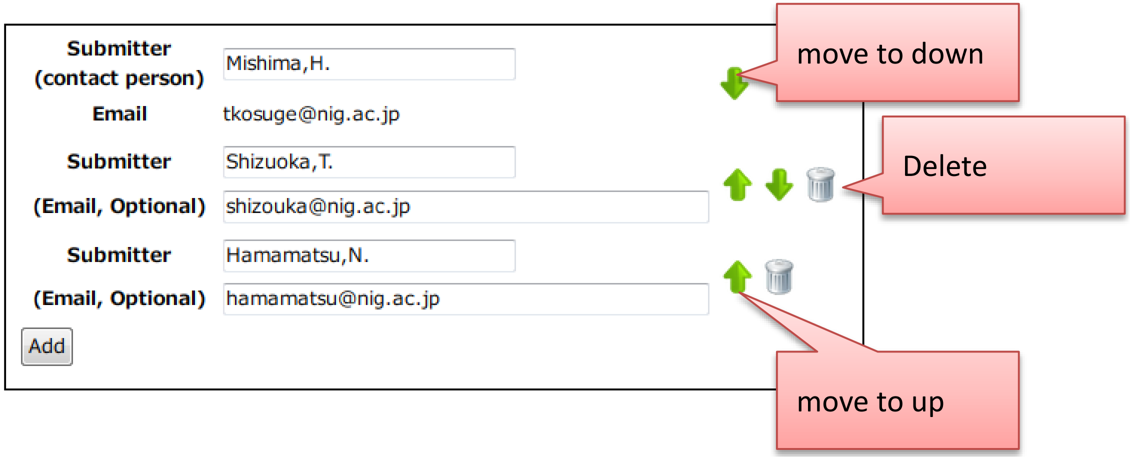
How to add a submitter



Submitter (contact person)	Mishima,H.
Email	misima@nig.ac.jp
Submitter	Shizuoka,T.
(Email, Optional)	shizouka@nig.ac.jp

Please click “Add” and you will find additional text field. Please enter another submitter and the email address.

How to change the order of submitter
How to delete a submitter



Submitter (contact person) Mishima,H.

Email tkosuge@nig.ac.jp

Submitter Shizuoka,T.

(Email, Optional) shizouka@nig.ac.jp

Submitter Hamamatsu,N.

(Email, Optional) hamamatsu@nig.ac.jp

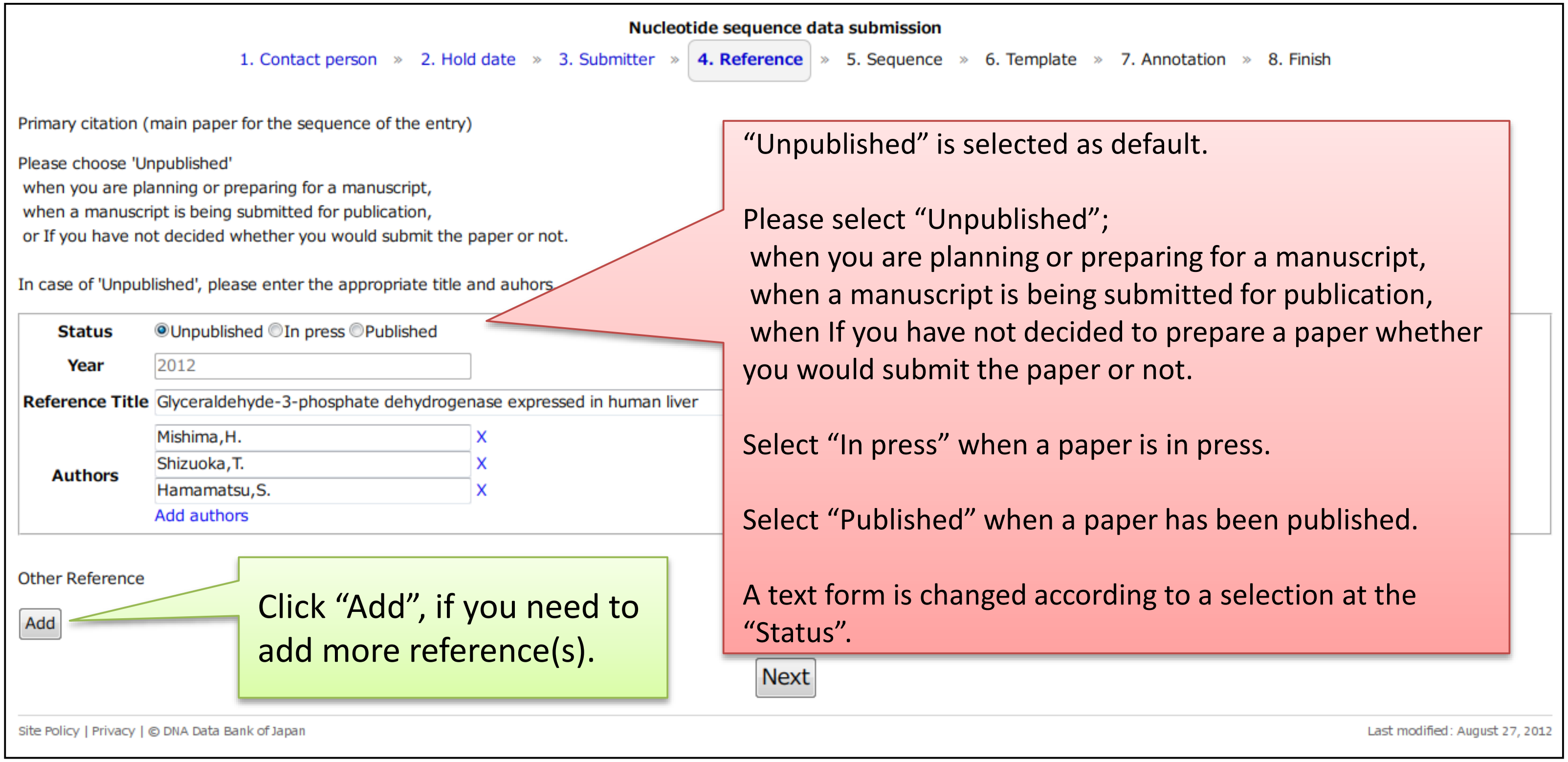
move to down

Delete

move to up

4. Reference

Enter reference information on the page.
Please enter primary citation on the 1st reference.



Nucleotide sequence data submission

Primary citation (main paper for the sequence of the entry)

Please choose 'Unpublished'
when you are planning or preparing for a manuscript,
when a manuscript is being submitted for publication,
or If you have not decided whether you would submit the paper or not.

In case of 'Unpublished', please enter the appropriate title and auhors

Status	● Unpublished ○ In press ○ Published
Year	2012
Reference Title	Glyceraldehyde-3-phosphate dehydrogenase expressed in human liver
Authors	Mishima,H. Shizuoka,T. Hamamatsu,S.

Other Reference

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Last modified: August 27, 2012

"Unpublished" is selected as default.

Please select "Unpublished";
when you are planning or preparing for a manuscript,
when a manuscript is being submitted for publication,
when If you have not decided to prepare a paper whether you would submit the paper or not.

Select "In press" when a paper is in press.

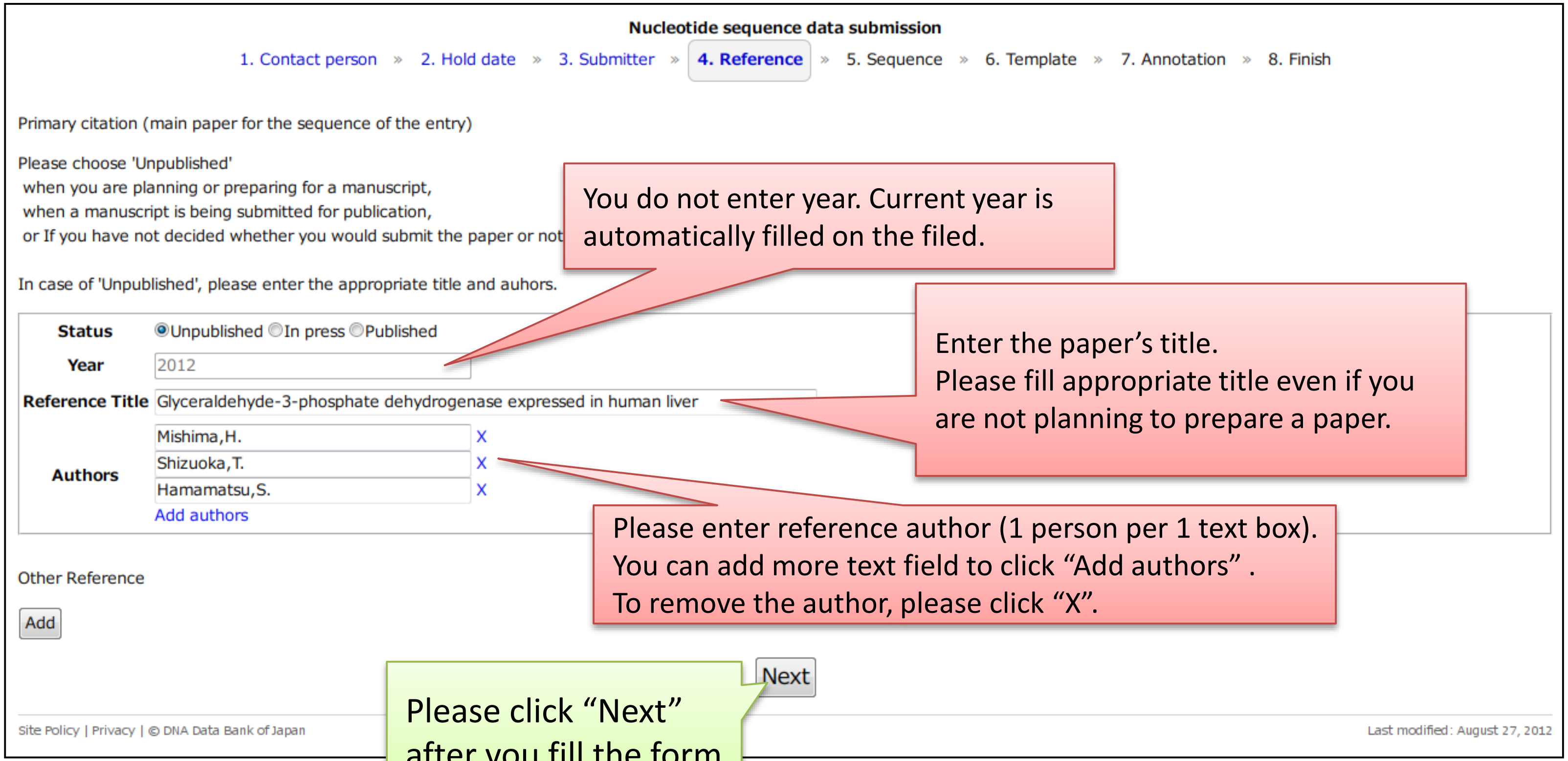
Select "Published" when a paper has been published.

A text form is changed according to a selection at the "Status".

Click "Add", if you need to add more reference(s).

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Status: Unpublished



Nucleotide sequence data submission

1. Contact person » 2. Hold date » 3. Submitter » **4. Reference** » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Primary citation (main paper for the sequence of the entry)

Please choose 'Unpublished'
when you are planning or preparing for a manuscript,
when a manuscript is being submitted for publication,
or If you have not decided whether you would submit the paper or not

In case of 'Unpublished', please enter the appropriate title and auhors.

Status	● Unpublished ○ In press ○ Published
Year	2012
Reference Title	Glyceraldehyde-3-phosphate dehydrogenase expressed in human liver
Authors	Mishima,H. X Shizuoka,T. X Hamamatsu,S. X Add authors

Other Reference

You do not enter year. Current year is automatically filled on the filed.

Enter the paper's title.
Please fill appropriate title even if you are not planning to prepare a paper.

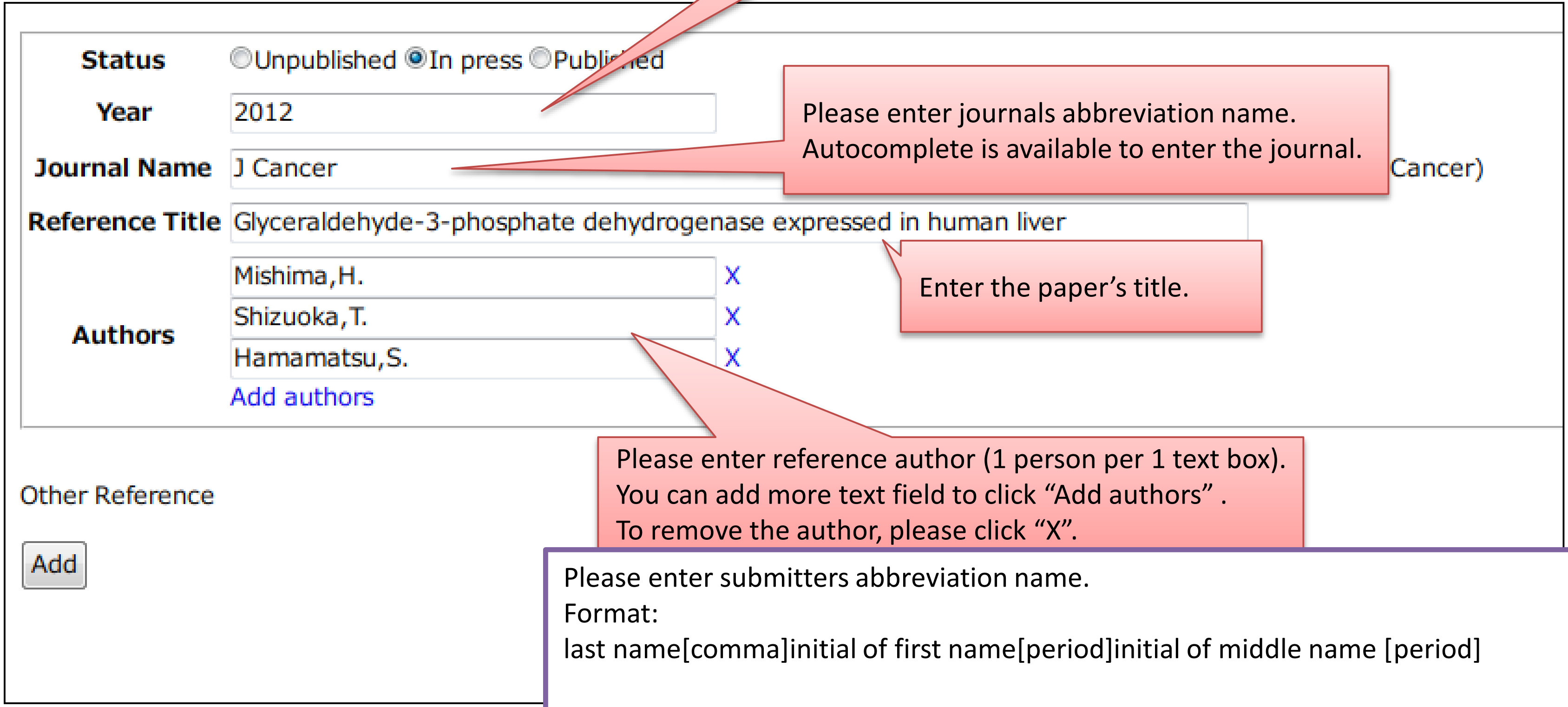
Please enter reference author (1 person per 1 text box).
You can add more text field to click "Add authors" .
To remove the author, please click "X".

Please click "Next" after you fill the form.

Please enter submitters abbreviation name.
Format:
last name[comma]initial of first name[period]initial of middle name [period]

e.g.
Miyashita,Y.
Robertson,G.R.
Mishima-Tokai,H.
Kim,C.S.
Wang,Y.Q.

Status: In press



Status ○Unpublished ●In press ○Published

Year 2012

Journal Name J Cancer

Cancer)

Reference Title Glyceraldehyde-3-phosphate dehydrogenase expressed in human liver

Authors

Mishima,H. X

Shizuoka,T. X

Hamamatsu,S. X

Enter year

Please enter journals abbreviation name.
Autocomplete is available to enter the journal.

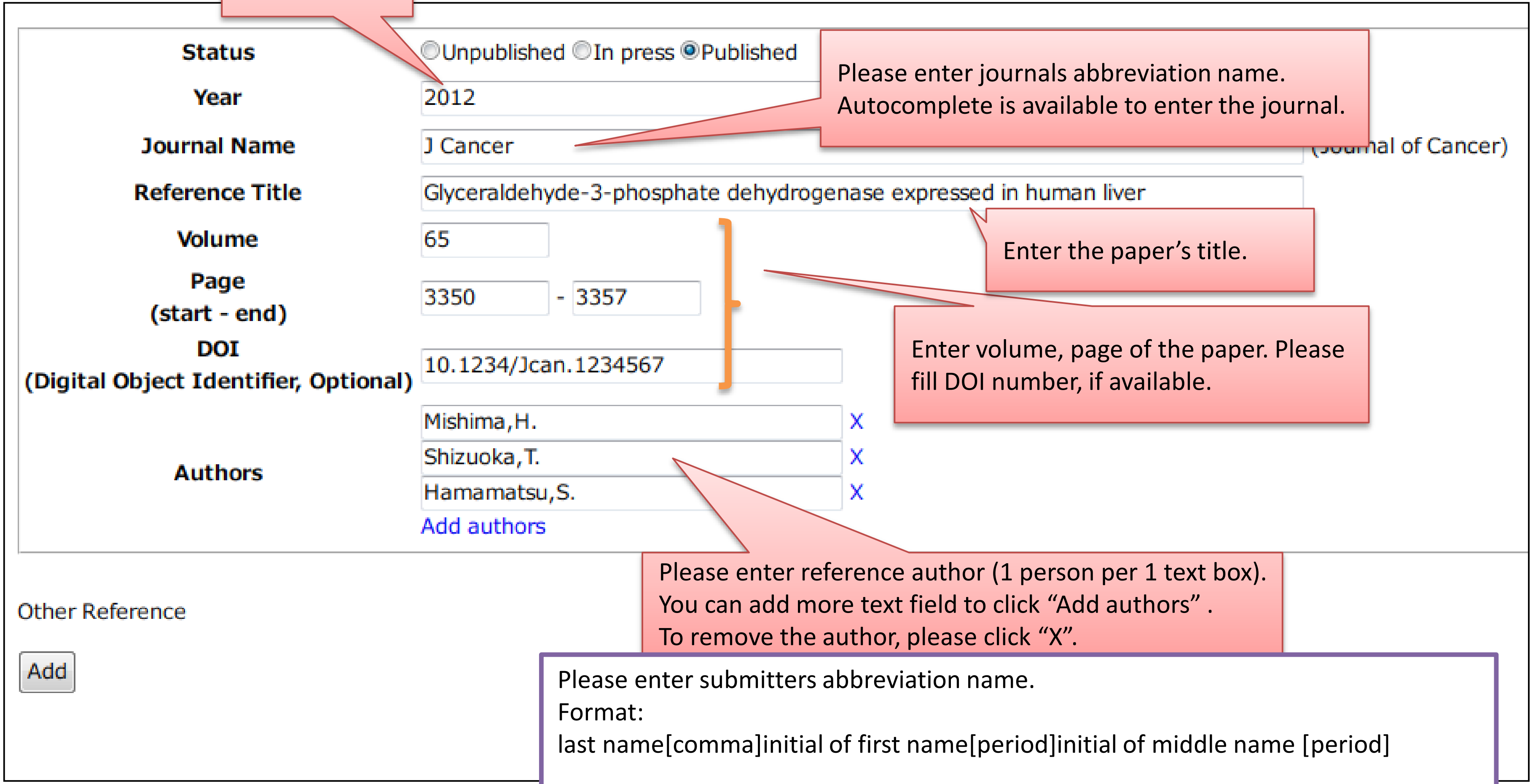
Enter the paper's title.

Please enter reference author (1 person per 1 text box).
You can add more text field to click "Add authors" .
To remove the author, please click "X".

Please enter submitters abbreviation name.
Format:
last name[comma]initial of first name[period]initial of middle name [period]

e.g.
Miyashita,Y.
Robertson,G.R.
Mishima-Tokai,H.
Kim,C.S.
Wang,Y.Q.

Status: Published



Status	○Unpublished ○In press ●Published
Year	2012
Journal Name	J Cancer (Journal of Cancer)
Reference Title	Glyceraldehyde-3-phosphate dehydrogenase expressed in human liver
Volume	65
Page (start - end)	3350 - 3357
DOI (Digital Object Identifier, Optional)	10.1234/Jcan.1234567
Authors	Mishima,H. X Shizuoka,T. X Hamamatsu,S. X Add authors

Other Reference

Enter year

Please enter journals abbreviation name.
Autocomplete is available to enter the journal.

Enter the paper’s title.

Enter volume, page of the paper. Please fill DOI number, if available.

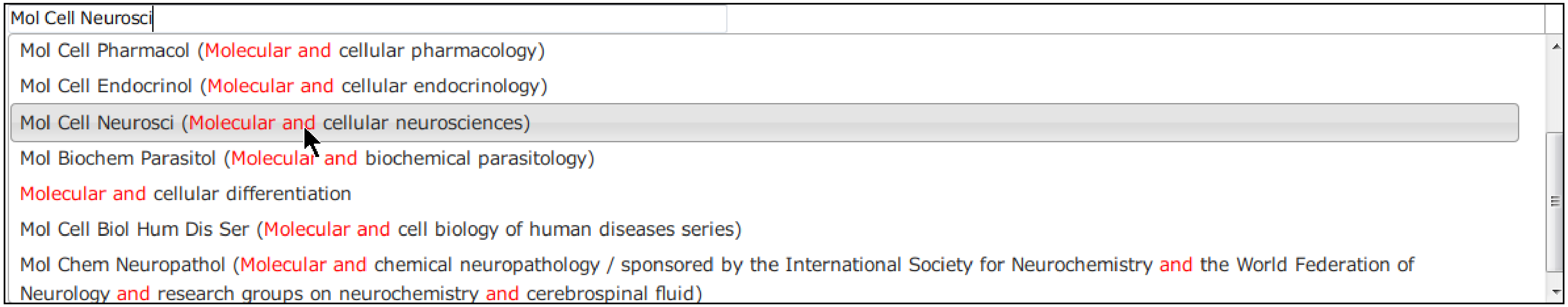
Please enter reference author (1 person per 1 text box).
You can add more text field to click “Add authors” .
To remove the author, please click “X”.

Please enter submitters abbreviation name.
Format:
last name[comma]initial of first name[period]initial of middle name [period]

e.g.
Miyashita,Y.
Robertson,G.R.
Mishima-Tokai,H.
Kim,C.S.
Wang,Y.Q.

Autocomplete function at the input field of journal name

You will see the candidate of journal's name when you enter a full or part of the beginning name of a journal. You can enter the journal's abbreviation name by select one from the list.



Mol Cell Neurosci

Mol Cell Pharmacol (Molecular and cellular pharmacology)

Mol Cell Endocrinol (Molecular and cellular endocrinology)

Mol Cell Neurosci (Molecular and cellular neurosciences)

Mol Biochem Parasitol (Molecular and biochemical parasitology)

Molecular and cellular differentiation

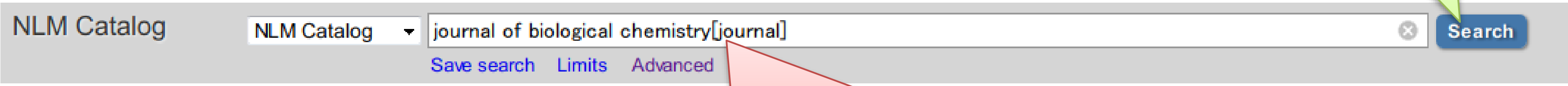
Mol Cell Biol Hum Dis Ser (Molecular and cell biology of human diseases series)

Mol Chem Neuropathol (Molecular and chemical neuropathology / sponsored by the International Society for Neurochemistry and the World Federation of Neurology and research groups on neurochemistry and cerebrospinal fluid)

The system uses [NLM Catalog] for its Input dictionary. You can search journal's ISO abbreviation at [NLM Catalog].

e.g. How to search ISO abbreviation of “Journal of biological chemistry”

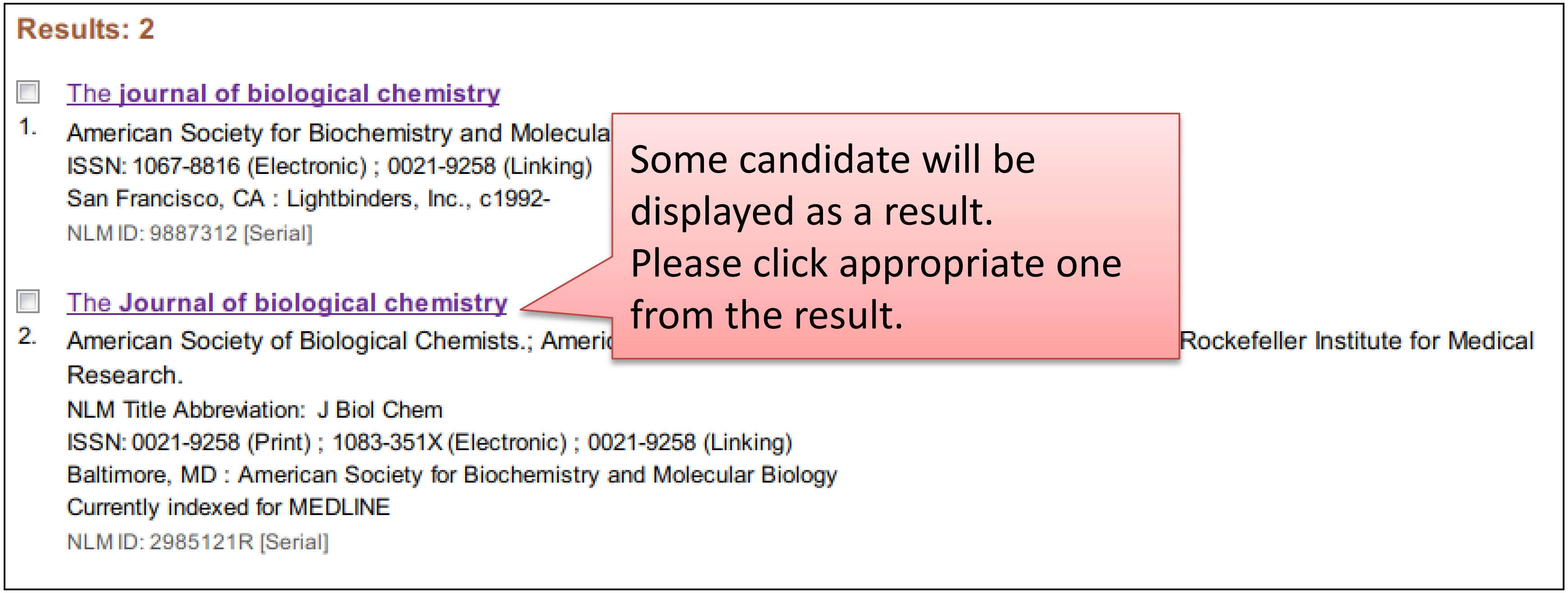
Open [NLM Catalog]() on the internet browser and enter keyword “journal name[journal]” and click search.



journal of biological chemistry[journal]

Click

Enter a full journal name[journal] to the search box and click search.



Results: 2

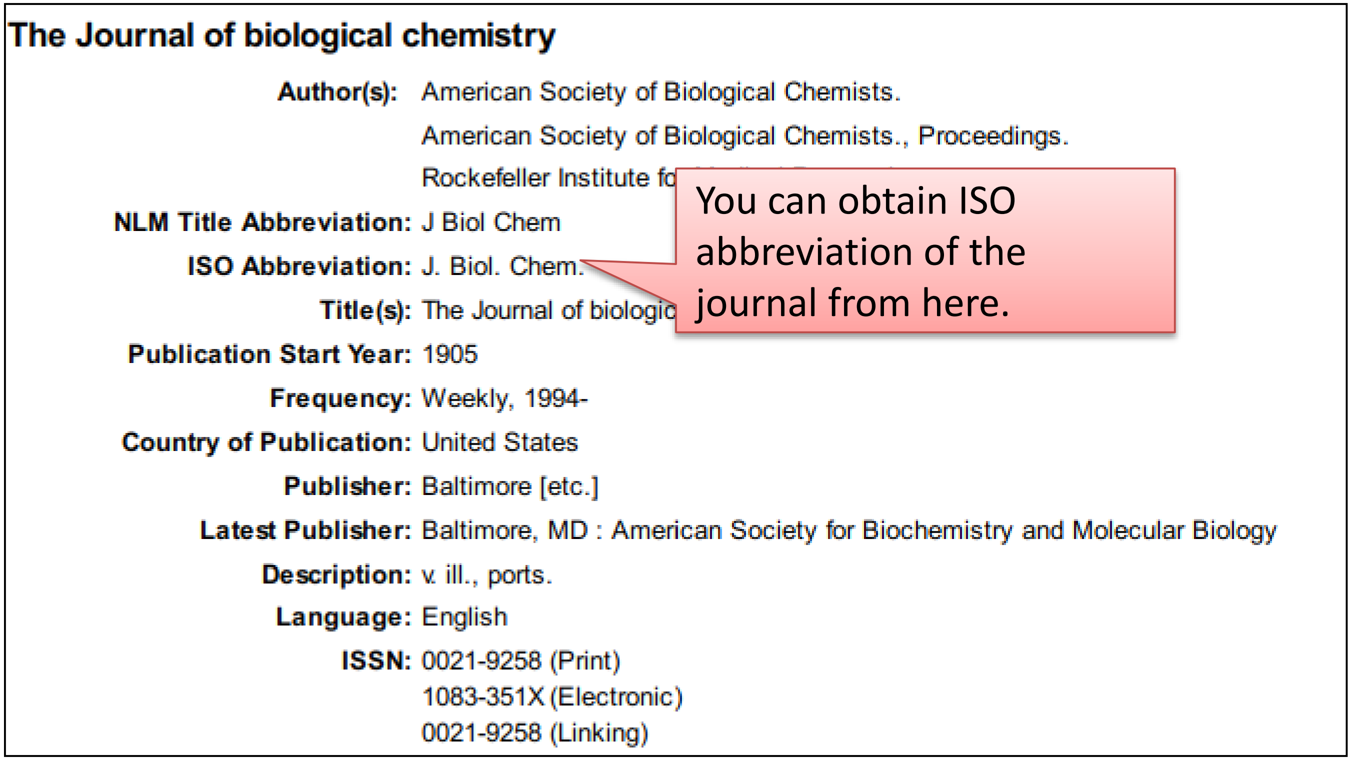
☐ The journal of biological chemistry

1. American Society for Biochemistry and Molecula
ISSN: 1067-8816 (Electronic) ; 0021-9258 (Linking)
San Francisco, CA : Lightbinders, Inc., c1992-
NLM ID: 9887312 [Serial]

☐ The Journal of biological chemistry

2. American Society of Biological Chemists.; Americ Rockefeller Institute for Medical Research.
NLM Title Abbreviation: J Biol Chem
ISSN: 0021-9258 (Print) ; 1083-351X (Electronic) ; 0021-9258 (Linking)
Baltimore, MD : American Society for Biochemistry and Molecular Biology
Currently indexed for MEDLINE
NLM ID: 2985121R [Serial]

Some candidate will be displayed as a result.
Please click appropriate one from the result.



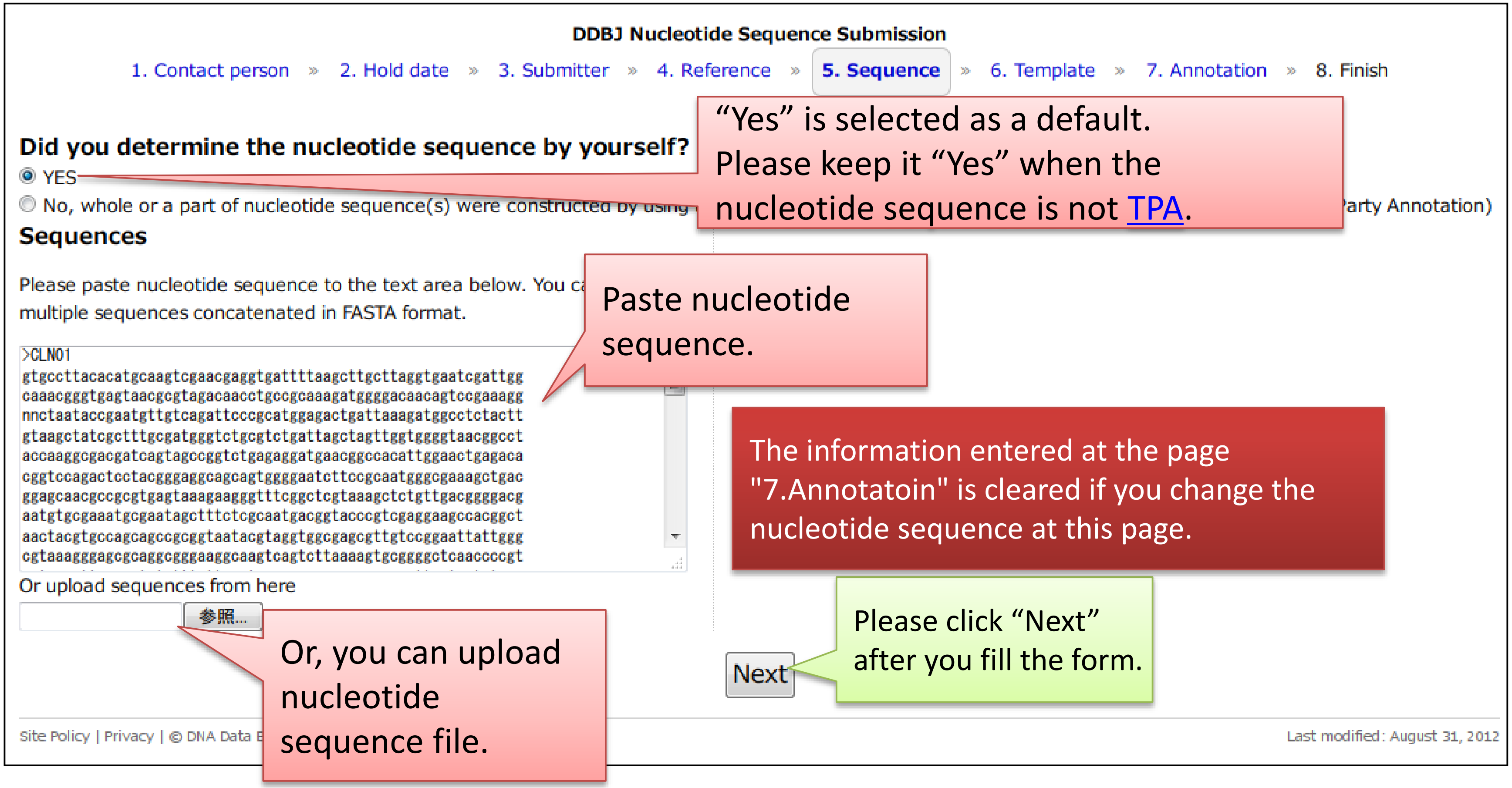
The Journal of biological chemistry

Author(s): American Society of Biological Chemists.
American Society of Biological Chemists., Proceedings.
Rockefeller Institute fo
NLM Title Abbreviation: J Biol Chem
ISO Abbreviation: J. Biol. Chem.
Title(s): The Journal of biologic
Publication Start Year: 1905
Frequency: Weekly, 1994-
Country of Publication: United States
Publisher: Baltimore [etc.]
Latest Publisher: Baltimore, MD : American Society for Biochemistry and Molecular Biology
Description: v. ill., ports.
Language: English
ISSN: 0021-9258 (Print)
1083-351X (Electronic)
0021-9258 (Linking)

You can obtain ISO abbreviation of the journal from here.

5.Sequence

Enter nucleotide sequence.
Assembly information is also needed for the case of TPA



DDBJ Nucleotide Sequence Submission

Did you determine the nucleotide sequence by yourself?

● YES

○ No, whole or a part of nucleotide sequence(s) were constructed by using … arty Annotation)

Sequences

Please paste nucleotide sequence to the text area below. You ca… multiple sequences concatenated in FASTA format.

```
>CLN01
gtgccttacacatgcaagtcgaacgaggtgattttaagcttgcttaggtgaatcgattgg
caaacgggtgagtaacgcgtagacaacctgccgcaaagatggggacaacagtccgaaagg
nnctaataccgaatgttgtcagattcccgcatggagactgattaaagatggcctctactt
gtaagctatcgctttgcgatgggtctgcgtctgattagctagttggtggggtaacggcct
accaaggcgacgatcagtagccggtctgagaggatgaacggccacattggaactgagaca
cggtccagactcctacgggaggcagcagtggggaatcttccgcaatgggcgaaagctgac
ggagcaacgccgcgtgagtaaagaagggtttcggctcgtaaagctctgttgacggggacg
aatgtgcgaaatgcgaatagctttctcgcaatgacggtacccgtcgaggaagccacggct
aactacgtgccagcagccgcggtaatacgtaggtggcgagcgttgtccggaattattggg
cgtaaagggagcgcaggcgggaaggcaagtcagtcttaaaagtgcggggctcaaccccgt
```

Or upload sequences from here

Site Policy | Privacy | © DNA Data B

Last modified: August 31, 2012

"Yes" is selected as a default. Please keep it "Yes" when the nucleotide sequence is not TPA.

Paste nucleotide sequence.

The information entered at the page "7.Annotatoin" is cleared if you change the nucleotide sequence at this page.

Please click "Next" after you fill the form.

Or, you can upload nucleotide sequence file.

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Nucleotide sequence that you can paste/upload

You can paste or upload nucleotide sequence consists of multi-FASTA format.

Double slash(//) is not needed for separate the entries. Of course, you can include double slash (//) as a separation mark of the entries.(e.g.1 & e.g.2)

This system automatically insert double slash (//) between entries when the nucleotide sequence that contains no double slash (//) is entered.

Entry name is required to be described in less than 24 letters of characters which do not contain [space], " [double-quote], ? [question], ¥, [back-slash].

Entry names must be unique in one submission.
If the same entry name are contained in the submission, you must correct the entry name to avoid an error.

The sequence must consists of a, c, g, t, m, r, w, s, y, k, v, h, d, b, or n.

Spaces, numeric characters within the nucleotide sequence are automatically removed.

Upper cases of the nucleotide residue id automatically converted into lower cases.

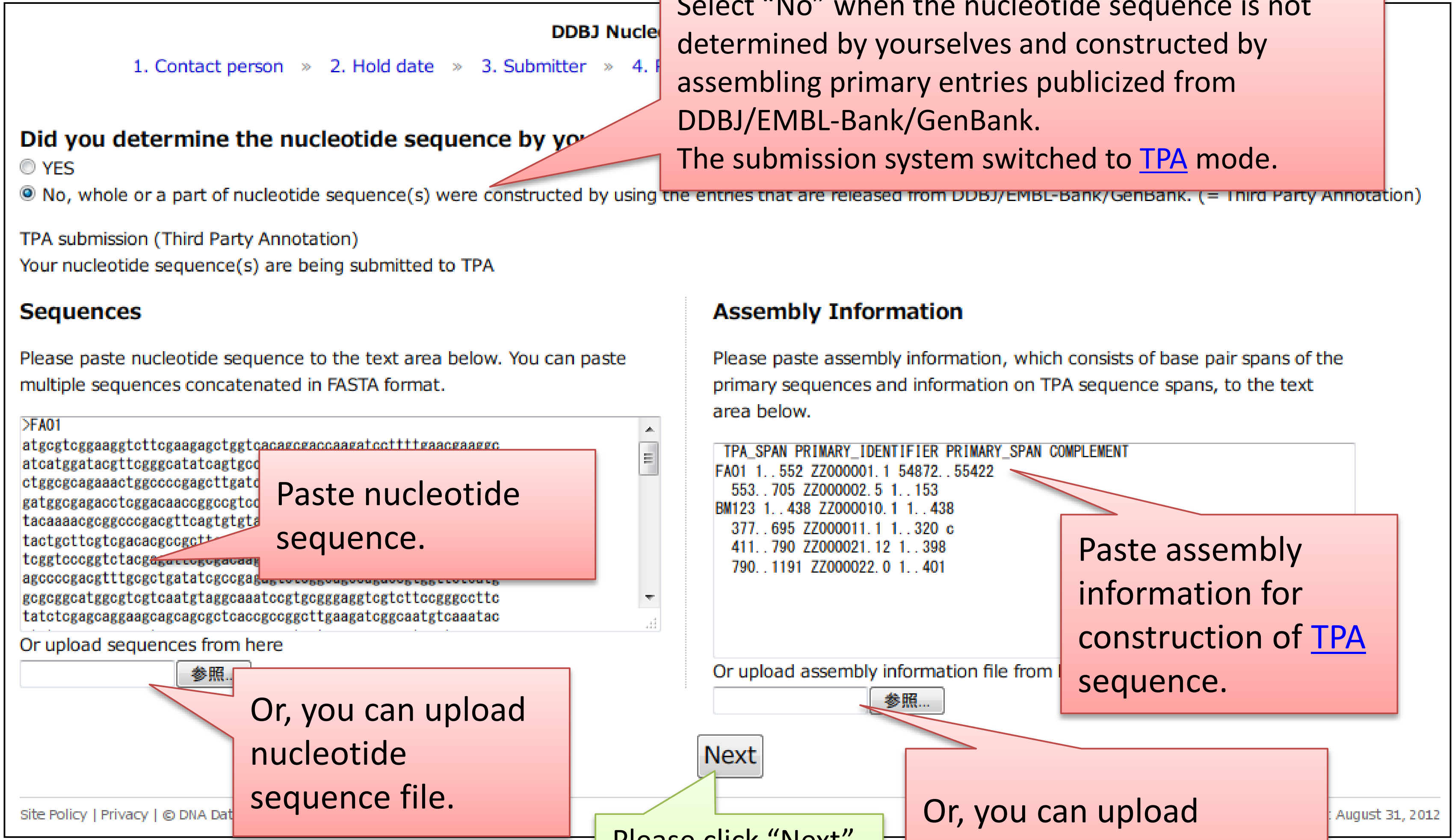
e. g. 1

```
>CLN01
ggacaggctgccgcaggagccaggccgggagcaggtggtggaagacagacctgtaggtgg
aagaggcttcgggggagccggagaactgggccagaccccacaggtgcaggctgccctgtc
tgcgcttcagtcgtgggcgaagcctgaggaaaaagagagagaggctcaaggaagagagga
tgaggcaggagaatcgcttgaaccccggaggcggaggttgcagtgagccgagattacgcc
accgcactccagcctgggcgacagagtgagactccatctcaaaaaaaaaaaaaaaaaa
>CLN02
ctcacacagatgctgcgcacaccagtggttgtaacaatgccgtttgcctccttcaggtct
gaagcctgaggtgcgctcgtggtcagtgaagagggcaaaaagagagagaggctcaaagga
tgcgcttcagtcgtgggcgaagcctgaggaaaaagagagagaggctcaaggaagagagga
tagtcattcatataaatttgaacacacctgctgtgcctagacaagtgtctttctgtaaga
gctgtaactctgagatgtgctaaataaaccctctttctcaaaaaaaaaaaaaaaa
```

e. g. 2

```
>CLN01
ggacaggctgccgcaggagccaggccgggagcaggtggtggaagacagacctgtaggtgg
aagaggcttcgggggagccggagaactgggccagaccccacaggtgcaggctgccctgtc
tgcgcttcagtcgtgggcgaagcctgaggaaaaagagagagaggctcaaggaagagagga
tgaggcaggagaatcgcttgaaccccggaggcggaggttgcagtgagccgagattacgcc
accgcactccagcctgggcgacagagtgagactccatctcaaaaaaaaaaaaaaaaaa
//
>CLN02
ctcacacagatgctgcgcacaccagtggttgtaacaatgccgtttgcctccttcaggtct
gaagcctgaggtgcgctcgtggtcagtgaagagggcaaaaagagagagaggctcaaagga
tgcgcttcagtcgtgggcgaagcctgaggaaaaagagagagaggctcaaggaagagagga
tagtcattcatataaatttgaacacacctgctgtgcctagacaagtgtctttctgtaaga
gctgtaactctgagatgtgctaaataaaccctctttctcaaaaaaaaaaaaaaaa
//
```

Sequence for TPA submission



DDBJ Nucle

Did you determine the nucleotide sequence by yo

○ YES

● No, whole or a part of nucleotide sequence(s) were constructed by using the entries that are released from DDBJ/EMBL-Bank/GenBank. (= Third Party Annotation)

TPA submission (Third Party Annotation)
Your nucleotide sequence(s) are being submitted to TPA

Sequences

Please paste nucleotide sequence to the text area below. You can paste multiple sequences concatenated in FASTA format.

```
>FA01
atgcgtcggaaggtcttcgaagagctggtcacagcgaccaagatcctttttgaacgaaggc
atcatggatacgttcgggcatatcagtgcc
ctggcgcagaaactggccccgagcttgatc
gatggcgagacctcggacaaccggccgtcc
tacaaaacgcggcccgacgttcagtgtgta
tactgcttcgtcgacacgccgct
tcggtcccggtctacg
agccccgacgtttgcgctgatatcgccgag
gcgcggcatggcgtcgtcaatgtaggcaaatccgtgcgggaggtcgtcttccgggccttc
tatctcgagcaggaagcagcagcgctcaccgccggcttgaagatcggcaatgtcaaatac
```

Or upload sequences from here

Assembly Information

Please paste assembly information, which consists of base pair spans of the primary sequences and information on TPA sequence spans, to the text area below.

```
 TPA_SPAN PRIMARY_IDENTIFIER PRIMARY_SPAN COMPLEMENT
FA01 1..552 ZZ000001.1 54872..55422
  553..705 ZZ000002.5 1..153
BM123 1..438 ZZ000010.1 1..438
  377..695 ZZ000011.1 1..320 c
  411..790 ZZ000021.12 1..398
  790..1191 ZZ000022.0 1..401
```

Or upload assembly information file from

Select "No" when the nucleotide sequence is not determined by yourselves and constructed by assembling primary entries publicized from DDBJ/EMBL-Bank/GenBank.
The submission system switched to TPA mode.

Paste nucleotide sequence.

Paste assembly information for construction of TPA sequence.

Or, you can upload nucleotide sequence file.

Please click "Next" after you fill the form.

Or, you can upload assembly information file.

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Format of assembly Information for TPA submission

e.g.

	TPA_SPAN	PRIMARY_IDENTIFIER	PRIMARY_SPAN	COMPLEMENT
FA01	1-552	ZZ000001.1	54872-55422	
	553-705	ZZ000002.5	1-153	
BM123	1-438	ZZ000010.1	1-438	
	377-695	ZZ000011.1	1-320	c
	411-790	ZZ000021.12	1-398	
	790-1191	ZZ000022.0	1-401	

“c” is designated when complementary region of primary span is used.

Entry Name

Location of TPA sequence

Accession number with version of primary entry.

Region of primary entry.

The table means;

As for Entry name FA01
TPA sequence:1-552 corresponds to ZZ000001.1:54872-55422
TPA sequence:553-705 corresponds to ZZ000002.5:1-153

As for Entry name BM123
TPA sequence:1-438 corresponds to ZZ000010.1 :1-438
TPA sequence:377-695 corresponds to ZZ000011.1:complement(1-320)
TPA sequence:411-790 corresponds to ZZ000021.12:1-398
TPA sequence:790-1191 corresponds to ZZ000022.0 :1-401

Their correspondence is subject to the rule, “The sequence alignment rule between TPA and primary entries”

Rule: Description of Assembly Information

- The 1st line must be

[tab or space]TPA_SPAN[tab or space]PRIMARY_IDENTIFIER[tab or space]PRIMARY_SPAN[tab or space]COMPLEMENT

- Do not include null line(s)

- Entry name must be entered at the 1st column. Assembly information is separated with each entry at the line of entry name.

- TPA_SPAN:

  X..Y or X-Y (X and Y are numeric, X<Y)
  Location on TPA sequence is described.
  e.g.
  100..2000
  100-2000

- PRIMARY_IDENTIFIER:

  accession number.version
  Accession number with version of primary entry is described. Please use 0 for the version number if primary entry is not released.
  e.g.
  AB123456.1
  AB987654.0

- PRIMARY_SPAN:

  X..Y or X-Y (X and Y are numeric, X<Y)
  The region from primary entry, which was used for construct TPA sequence, is described. The region must match to the TPA_SPAN.
  Please see "The sequence alignment rule between TPA and primary entries"

- COMPLEMENT:

  null or c
  Enter "c" when complementary region is used from primary entry.

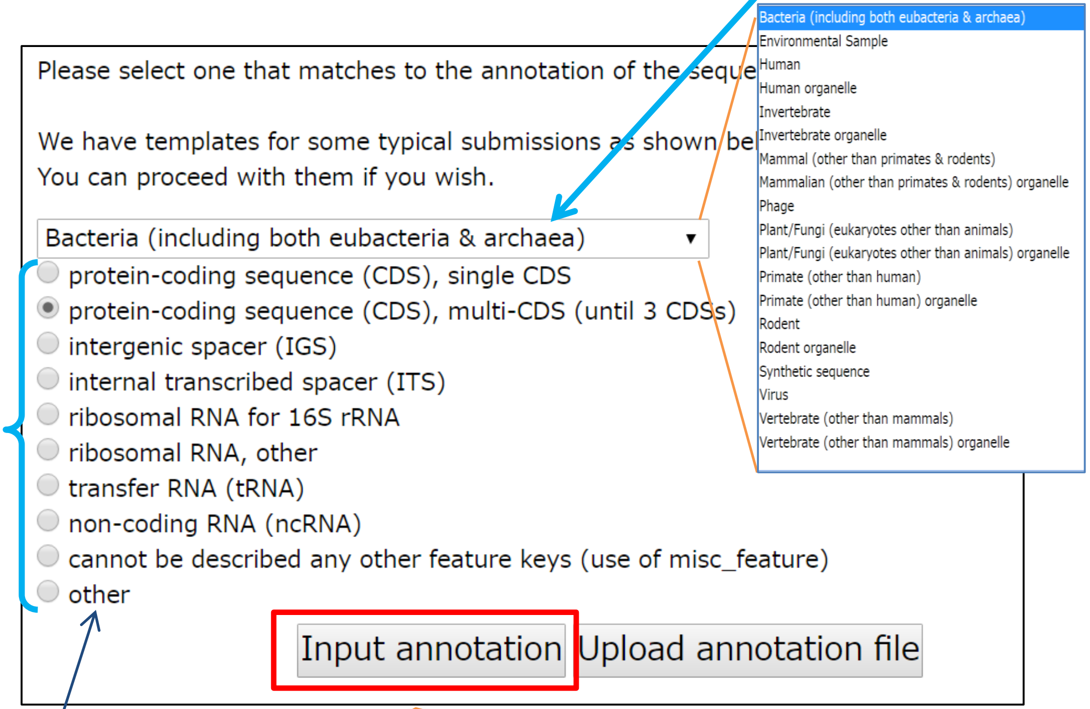
6. Template

① Please select a taxonomic division of the sequenced organism. When nucleotide sequences have been obtained from organelle, you should select one whose name includes ‘organelle’ to automatically add /organelle under source feature.
Available qualifier keys under source feature vary with the selected taxonomic division.
If you cannot find an appropriate taxonomic division, we recommend you to choose "Plant/Fungi (eukaryotes other than animals)" because almost qualifier keys are available in "Plant/Fungi" division.
(Link: taxonomic divisions, http://www.ddbj.nig.ac.jp/sub/locus-e.html#division)

② You will see an available annotation template.
Please select one and click "Input annotation".

① Taxonomic division

②



Please select one that matches to the annotation of the seque

We have templates for some typical submissions as shown be
You can proceed with them if you wish.

Bacteria (including both eubacteria & archaea) ▾

- ○ protein-coding sequence (CDS), single CDS
- ● protein-coding sequence (CDS), multi-CDS (until 3 CDSs)
- ○ intergenic spacer (IGS)
- ○ internal transcribed spacer (ITS)
- ○ ribosomal RNA for 16S rRNA
- ○ ribosomal RNA, other
- ○ transfer RNA (tRNA)
- ○ non-coding RNA (ncRNA)
- ○ cannot be described any other feature keys (use of misc_feature)
- ○ other

Bacteria (including both eubacteria & archaea)
Environmental Sample
Human
Human organelle
Invertebrate
Invertebrate organelle
Mammal (other than primates & rodents)
Mammalian (other than primates & rodents) organelle
Phage
Plant/Fungi (eukaryotes other than animals)
Plant/Fungi (eukaryotes other than animals) organelle
Primate (other than human)
Primate (other than human) organelle
Rodent
Rodent organelle
Synthetic sequence
Virus
Vertebrate (other than mammals)
Vertebrate (other than mammals) organelle

Select "other" if you cannot find an appropriate annotation template from the list . In the case, you cannot use a spreadsheet-type editor for entering annotation.

After the selection, please click "Input annotation" and move to "7. Annotation" page.

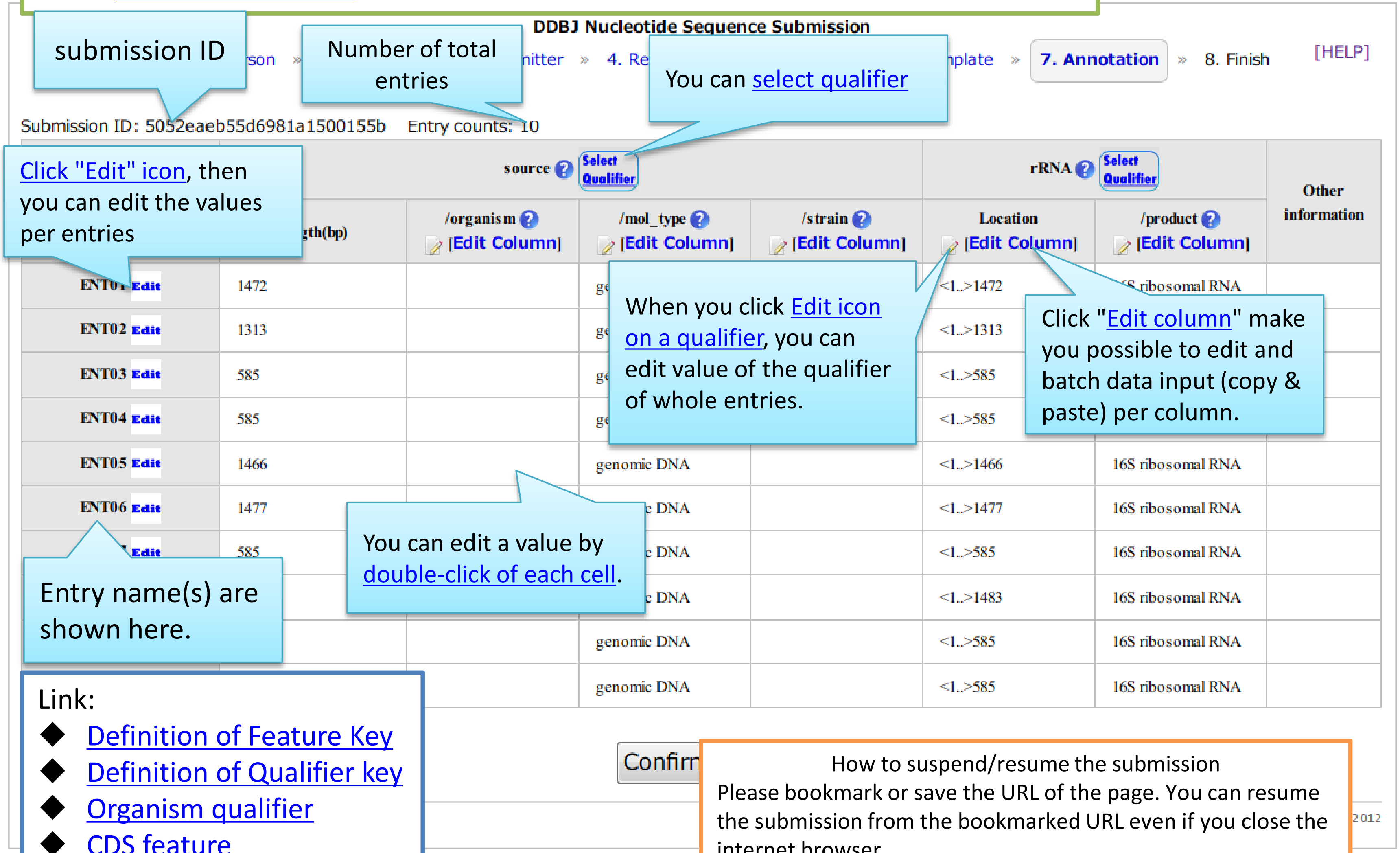
How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

The information entered at the "7.Annotatoin" page are disappeared if you change the template at this page.

7.Annotation

Four kinds of input method are available for spreadsheet-type annotation template.

- Click "Edit" icon (recommended)
- Double click a cell
- Click edit icon at a qualifier
- Click "Edit Column"



DDBJ Nucleotide Sequence Submission

Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

		source ? Select Qualifier			rRNA ? Select Qualifier		Other information
	gth(bp)	/organism ? [Edit Column]	/mol_type ? [Edit Column]	/strain ? [Edit Column]	Location [Edit Column]	/product ? [Edit Column]	
ENT01 Edit	1472		ge		<1..>1472	S ribosomal RNA	
ENT02 Edit	1313		ge		<1..>1313		
ENT03 Edit	585		ge		<1..>585		
ENT04 Edit	585		ge		<1..>585		
ENT05 Edit	1466		genomic DNA		<1..>1466	16S ribosomal RNA	
ENT06 Edit	1477		c DNA		<1..>1477	16S ribosomal RNA	
Edit	585		c DNA		<1..>585	16S ribosomal RNA	
			c DNA		<1..>1483	16S ribosomal RNA	
			genomic DNA		<1..>585	16S ribosomal RNA	
			genomic DNA		<1..>585	16S ribosomal RNA	

submission ID

Number of total entries

You can select qualifier

Click "Edit" icon, then you can edit the values per entries

When you click Edit icon on a qualifier, you can edit value of the qualifier of whole entries.

Click "Edit column" make you possible to edit and batch data input (copy & paste) per column.

You can edit a value by double-click of each cell.

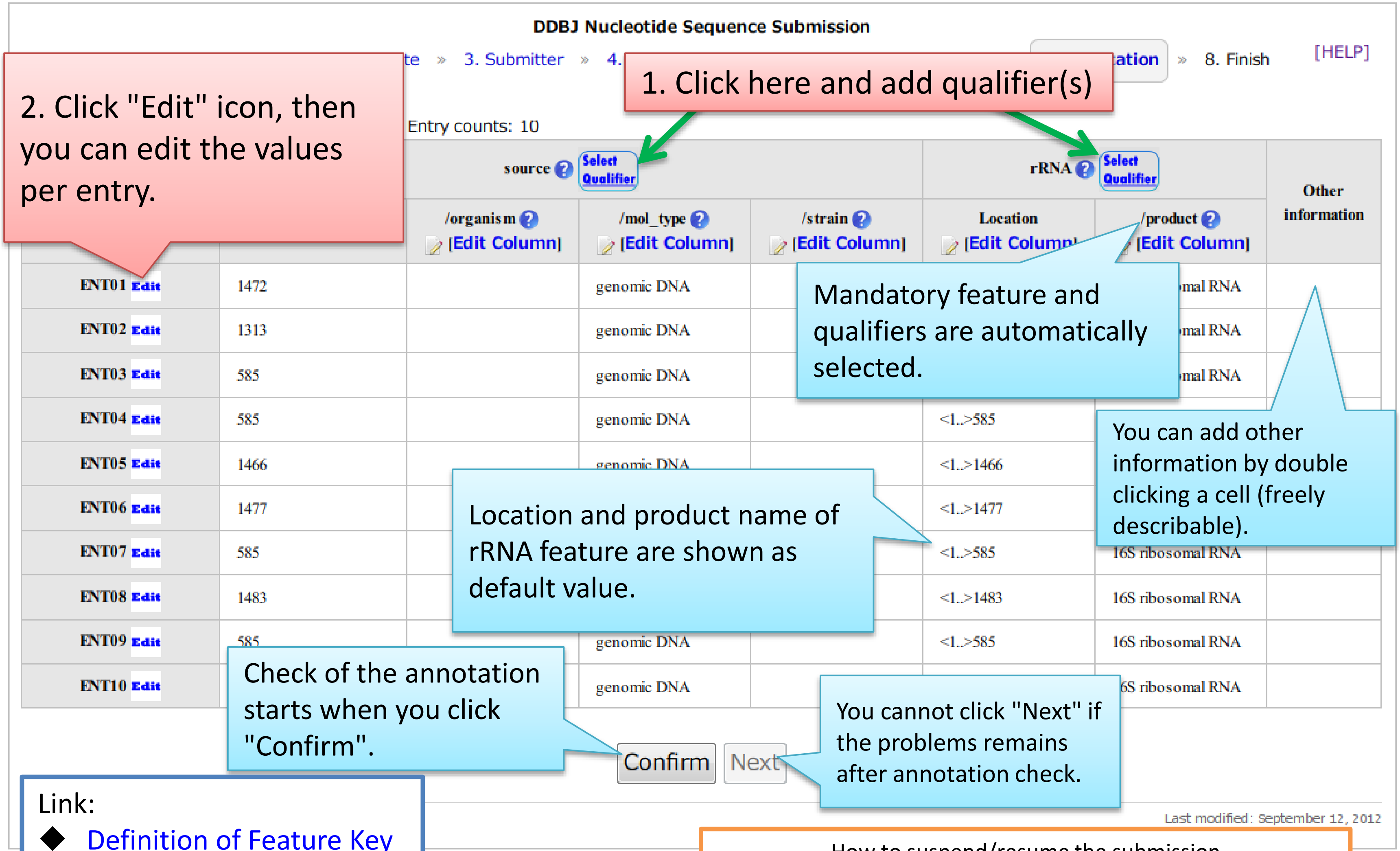
Entry name(s) are shown here.

Link:

- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

e.g. How to enter annotation of 16S rRNA



DDBJ Nucleotide Sequence Submission

Entry counts: 10

		source ? Select Qualifier			rRNA ? Select Qualifier		Other information
		/organism ? [Edit Column]	/mol_type ? [Edit Column]	/strain ? [Edit Column]	Location [Edit Column]	/product ? [Edit Column]	
ENT01 Edit	1472		genomic DNA			mal RNA	
ENT02 Edit	1313		genomic DNA			mal RNA	
ENT03 Edit	585		genomic DNA			mal RNA	
ENT04 Edit	585		genomic DNA		<1..>585		
ENT05 Edit	1466		genomic DNA		<1..>1466		
ENT06 Edit	1477				<1..>1477		
ENT07 Edit	585				<1..>585	16S ribosomal RNA	
ENT08 Edit	1483				<1..>1483	16S ribosomal RNA	
ENT09 Edit	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT10 Edit			genomic DNA			6S ribosomal RNA	

Last modified: September 12, 2012

1. Click here and add qualifier(s)

2. Click "Edit" icon, then you can edit the values per entry.

Mandatory feature and qualifiers are automatically selected.

You can add other information by double clicking a cell (freely describable).

Location and product name of rRNA feature are shown as default value.

Check of the annotation starts when you click "Confirm".

You cannot click "Next" if the problems remains after annotation check.

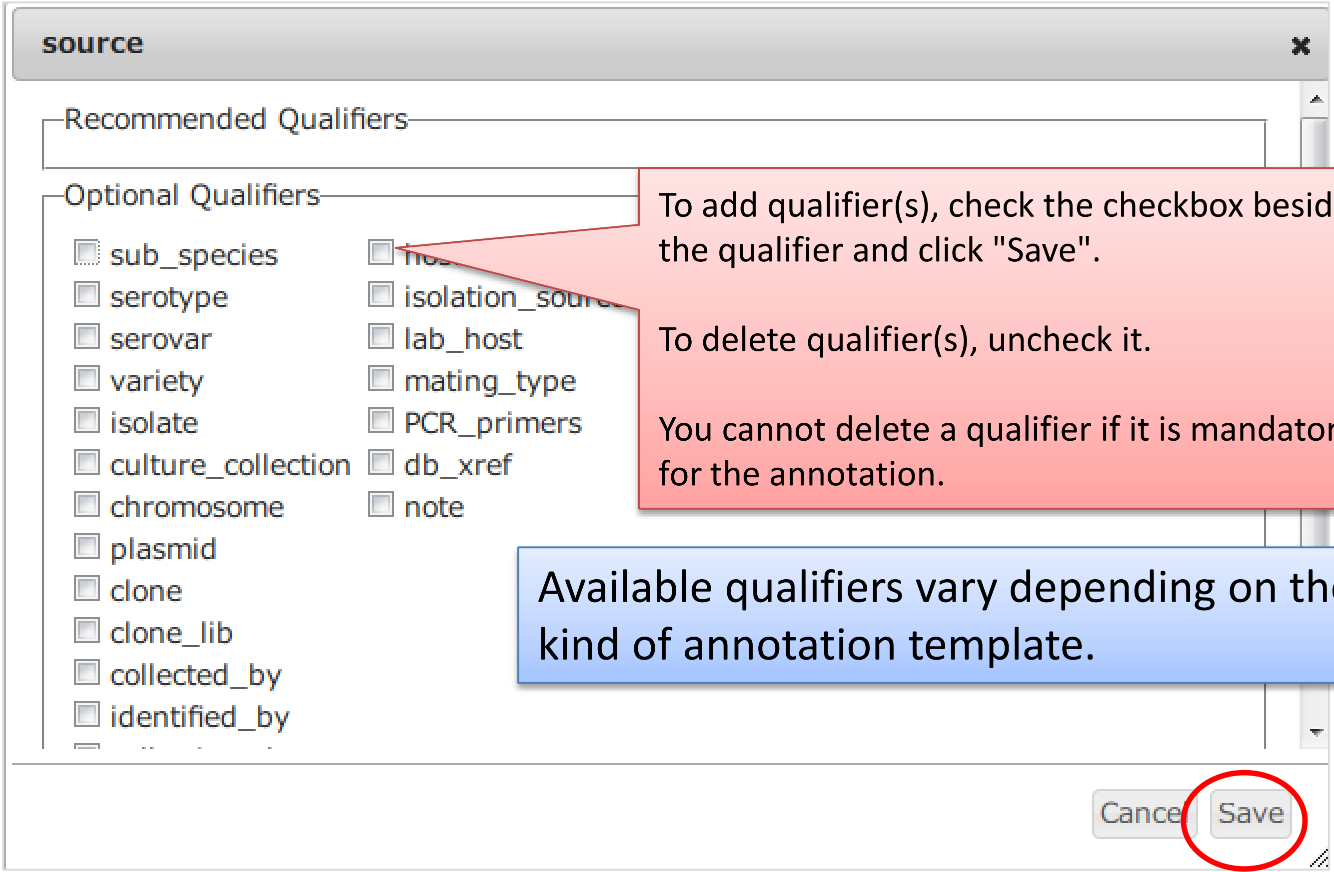
Link:

- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

How to suspend/resume the submission

Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Select qualifier



To add qualifier(s), check the checkbox beside the qualifier and click "Save".

To delete qualifier(s), uncheck it.

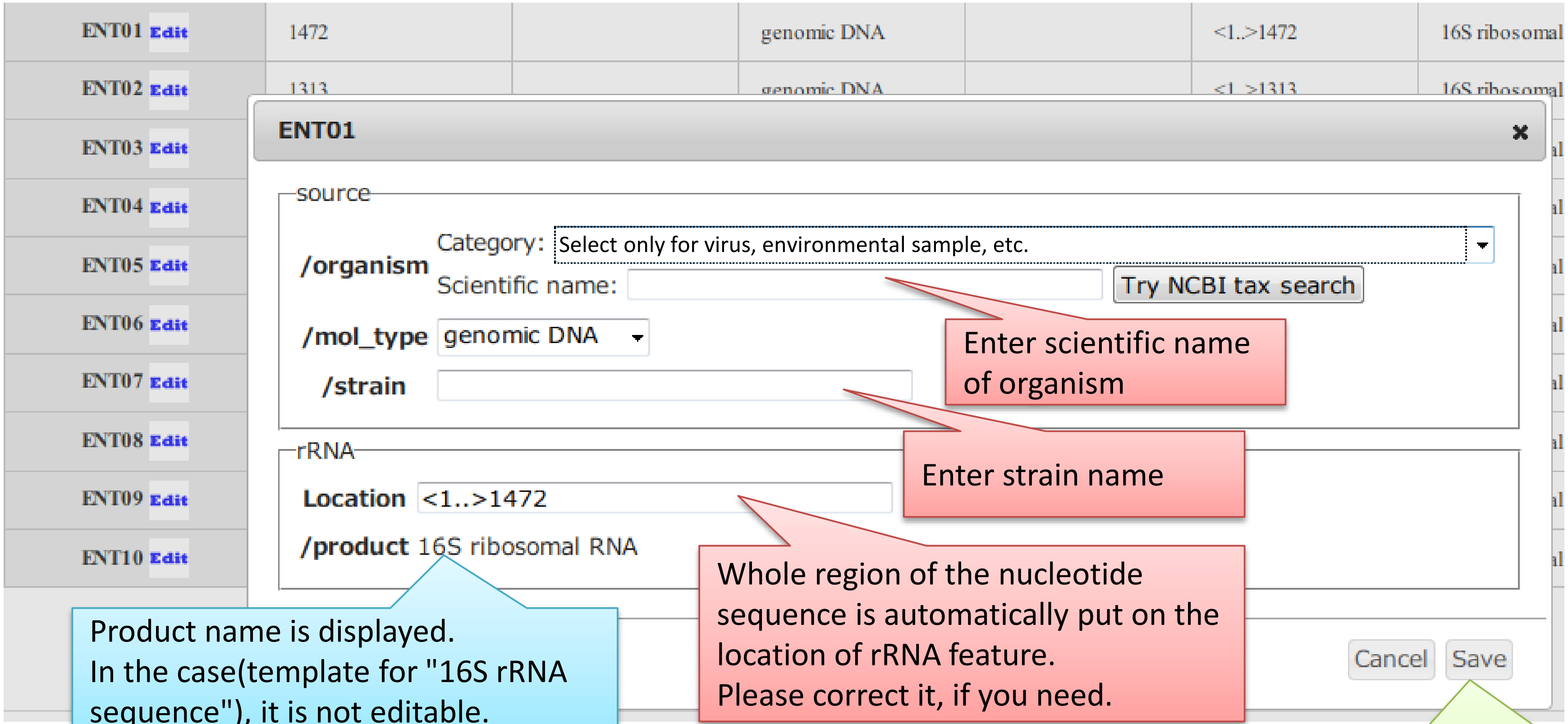
You cannot delete a qualifier if it is mandatory for the annotation.

Available qualifiers vary depending on the kind of annotation template.

Link:
[7.Annotation]
[Annotation screen when "Other" is selected at "Template"]
[e.g. Input annotation of mitochondrial DNA]

Link:
- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

Edit feature/qualifier values of a entry



source

/organism Category: Select only for virus, environmental sample, etc.

Scientific name:

/mol_type genomic DNA

/strain

rRNA

Location <1..>1472

/product 16S ribosomal RNA

Enter scientific name of organism

Enter strain name

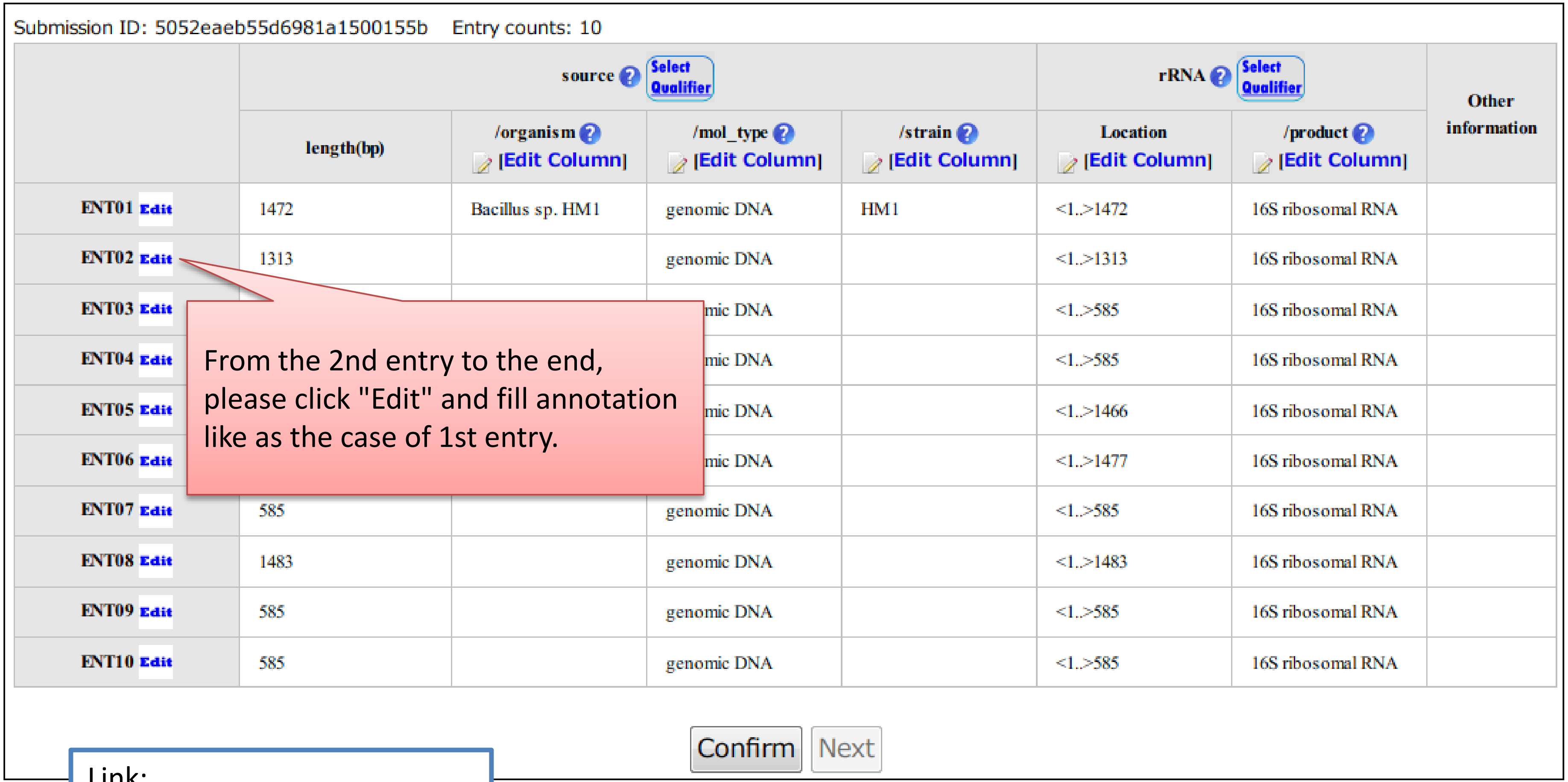
Whole region of the nucleotide sequence is automatically put on the location of rRNA feature.
Please correct it, if you need.

Product name is displayed.
In the case(template for "16S rRNA sequence"), it is not editable.

Please click “Next” after you fill the form.

Link:
[7.Annotation]()
[Annotation screen when "Other" is selected at "Template"]()
[e.g. Input annotation of mitochondrial DNA]()
[How to input an organism name]()

Annotation screen just after edit the 1st entry.



Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

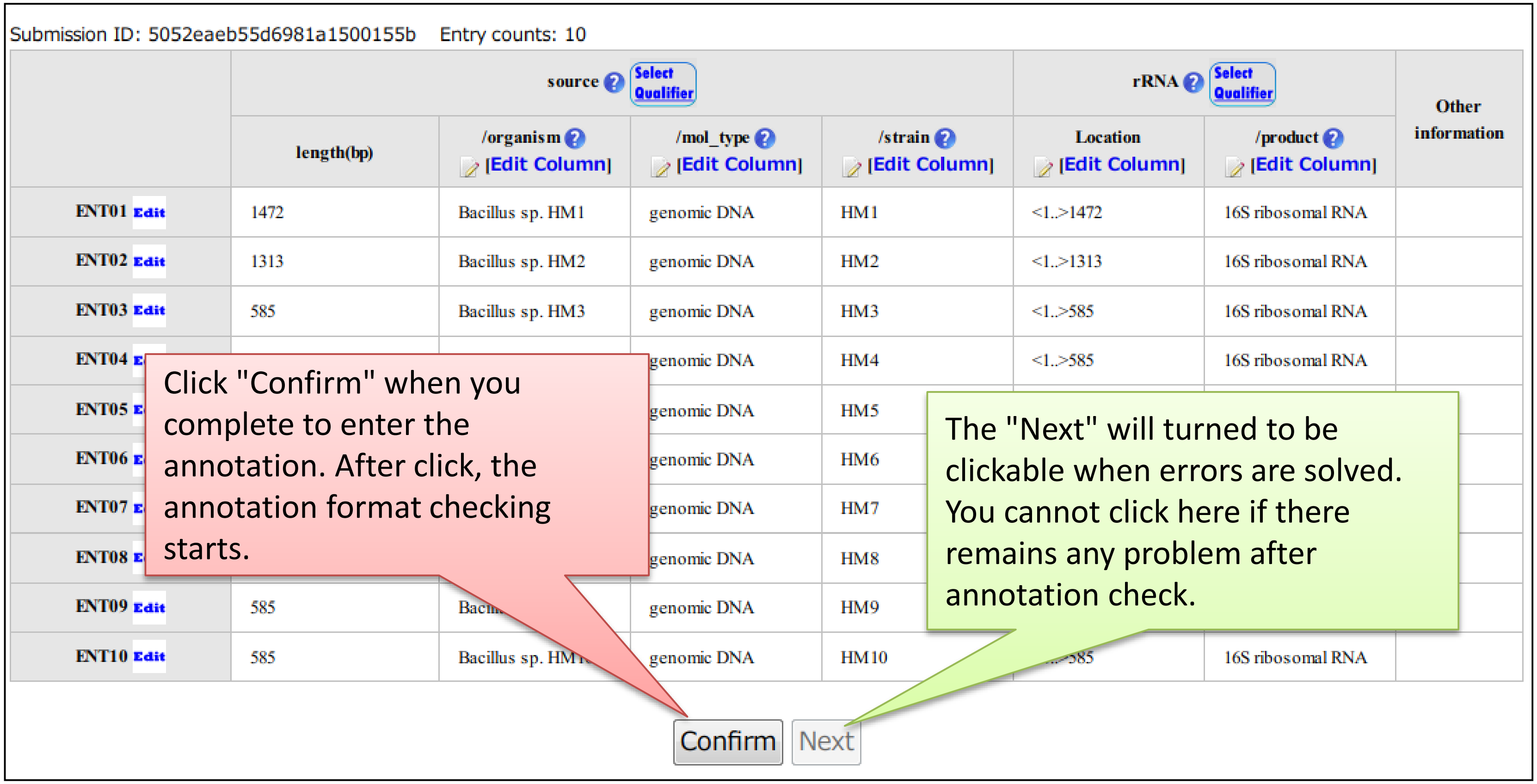
	source ? Select Qualifier				rRNA ? Select Qualifier		Other information
	length(bp)	/organism ? [Edit Column]	/mol_type ? [Edit Column]	/strain ? [Edit Column]	Location [Edit Column]	/product ? [Edit Column]	
ENT01 Edit	1472	Bacillus sp. HM1	genomic DNA	HM1	<1..>1472	16S ribosomal RNA	
ENT02 Edit	1313		genomic DNA		<1..>1313	16S ribosomal RNA	
ENT03 Edit			mic DNA		<1..>585	16S ribosomal RNA	
ENT04 Edit			mic DNA		<1..>585	16S ribosomal RNA	
ENT05 Edit			mic DNA		<1..>1466	16S ribosomal RNA	
ENT06 Edit			mic DNA		<1..>1477	16S ribosomal RNA	
ENT07 Edit	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT08 Edit	1483		genomic DNA		<1..>1483	16S ribosomal RNA	
ENT09 Edit	585		genomic DNA		<1..>585	16S ribosomal RNA	
ENT10 Edit	585		genomic DNA		<1..>585	16S ribosomal RNA	

From the 2nd entry to the end, please click "Edit" and fill annotation like as the case of 1st entry.

Link:
- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Annotation check starts when you click "Confirm"



Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

	source ? Select Qualifier				rRNA ? Select Qualifier		Other information
	length(bp)	/organism ? [Edit Column]	/mol_type ? [Edit Column]	/strain ? [Edit Column]	Location [Edit Column]	/product ? [Edit Column]	
ENT01 Edit	1472	Bacillus sp. HM1	genomic DNA	HM1	<1..>1472	16S ribosomal RNA	
ENT02 Edit	1313	Bacillus sp. HM2	genomic DNA	HM2	<1..>1313	16S ribosomal RNA	
ENT03 Edit	585	Bacillus sp. HM3	genomic DNA	HM3	<1..>585	16S ribosomal RNA	
ENT04			genomic DNA	HM4	<1..>585	16S ribosomal RNA	
ENT05			genomic DNA	HM5			
ENT06			genomic DNA	HM6			
ENT07			genomic DNA	HM7			
ENT08			genomic DNA	HM8			
ENT09 Edit	585	Bacil	genomic DNA	HM9			
ENT10 Edit	585	Bacillus sp. HM1	genomic DNA	HM10	>585	16S ribosomal RNA	

Click "Confirm" when you complete to enter the annotation. After click, the annotation format checking starts.

The "Next" will turned to be clickable when errors are solved. You cannot click here if there remains any problem after annotation check.

Link:
Confirm => no errors
Confirm => You can proceed to the next step even though there are some warnings
Confirm => There are any errors
Direct links of the page that explains translation error s and warnings
Progress bar
final confirmation screen

How to suspend/resume the submission

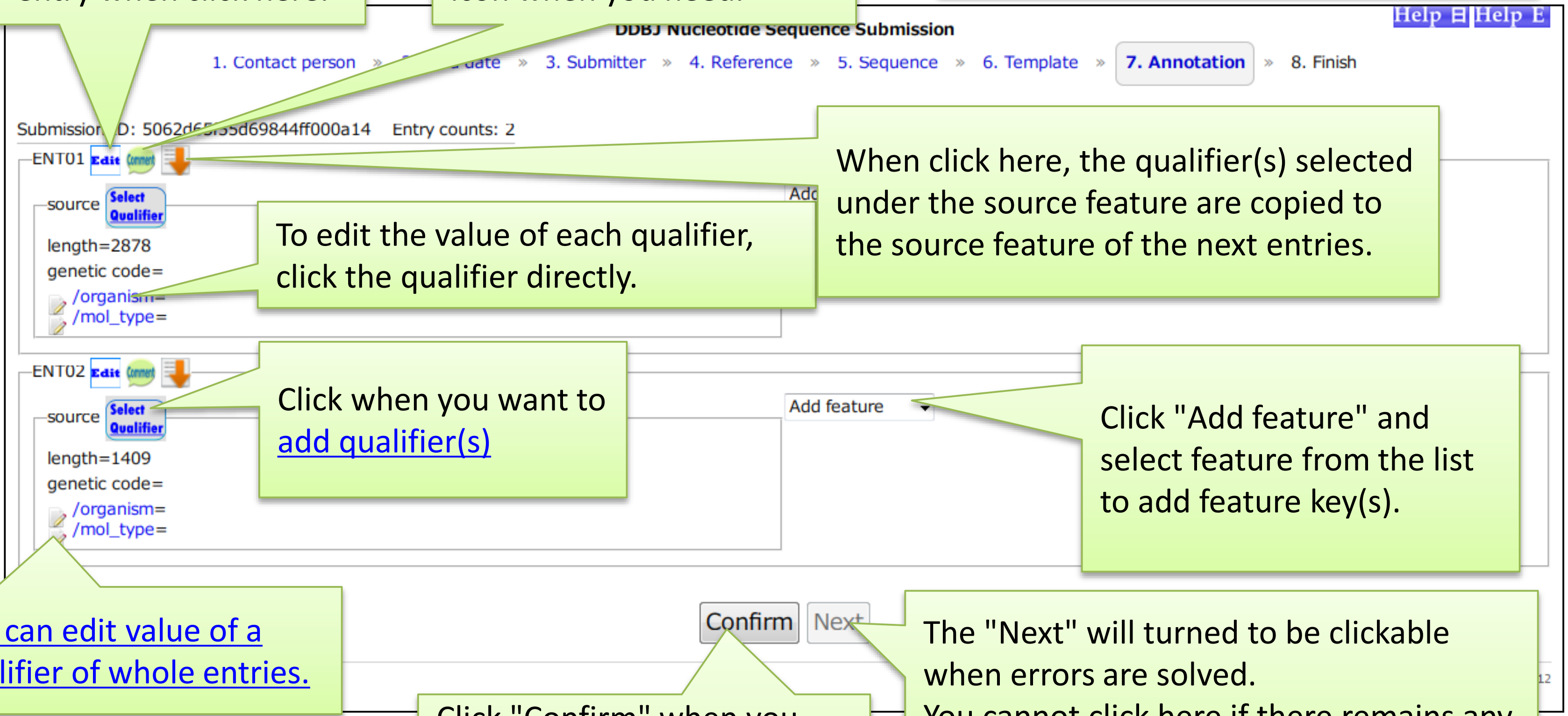
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Annotation screen when "Other" is selected at "Template"

You will see edit window to edit the entry when click here.

You can add additional information by clicking the icon when you need.

In the template (other), you must select (add) feature and qualifier, which are needed for the annotation of the submitted sequences, by yourself



ENT01 source: length=2878, genetic code=, /organism=, /mol_type=

ENT02 source: length=1409, genetic code=, /organism=, /mol_type=

When click here, the qualifier(s) selected under the source feature are copied to the source feature of the next entries.

To edit the value of each qualifier, click the qualifier directly.

Click when you want to add qualifier(s)

Click "Add feature" and select feature from the list to add feature key(s).

You can edit value of a qualifier of whole entries.

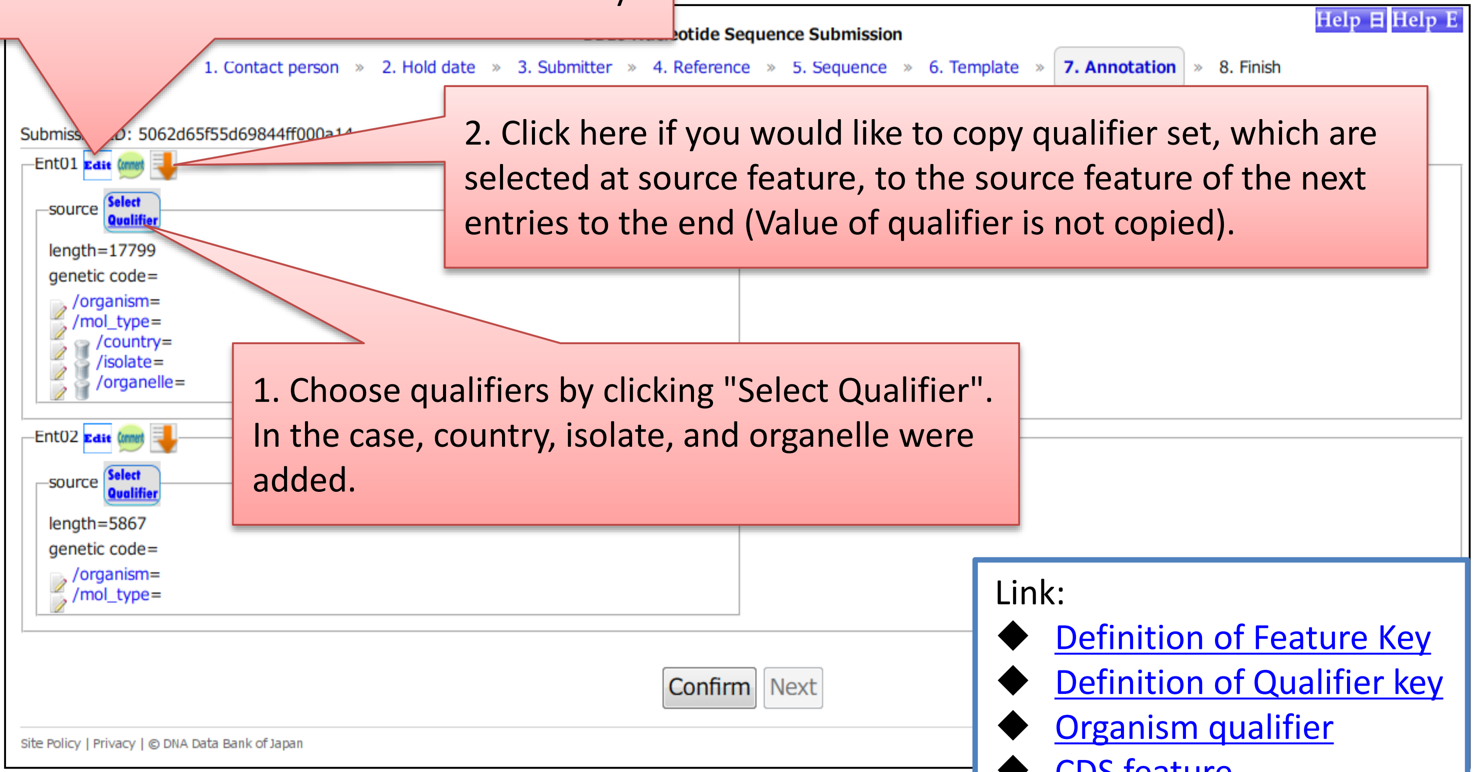
Click "Confirm" when you complete to enter the annotation. After click, the annotation format checking starts.

The "Next" will turned to be clickable when errors are solved.
You cannot click here if there remains any problem after annotation check.

Link:
- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

e.g. Input annotation of mitochondrial DNA



Ent01

source

length=17799
genetic code=
/organism=
/mol_type=
/country=
/isolate=
/organelle=

Ent02

source

length=5867
genetic code=
/organism=
/mol_type=

3. Click "Edit" and enter annotation of the entry.

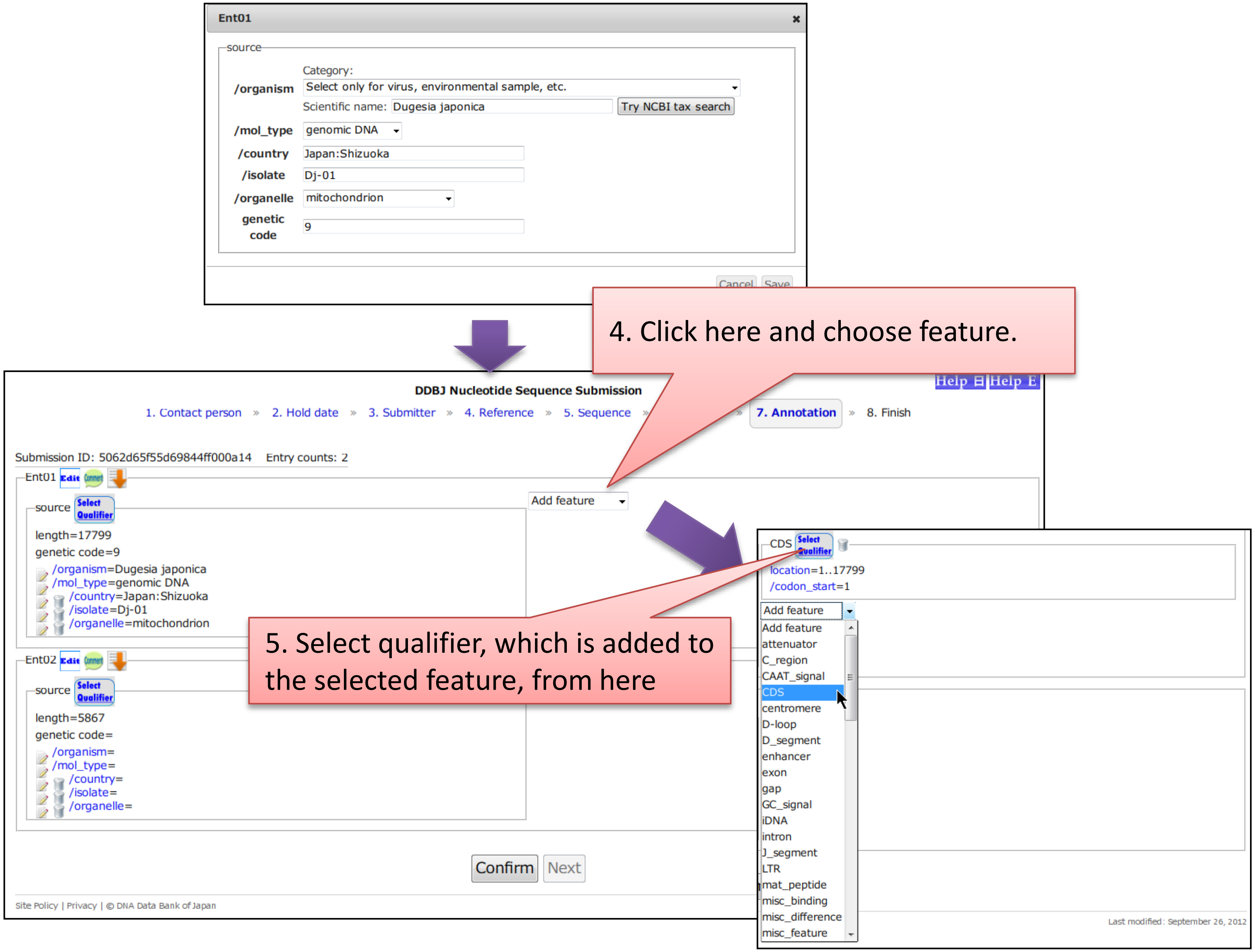
2. Click here if you would like to copy qualifier set, which are selected at source feature, to the source feature of the next entries to the end (Value of qualifier is not copied).

1. Choose qualifiers by clicking "Select Qualifier". In the case, country, isolate, and organelle were added.

Link:
- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

Link:
Select qualifier
Edit feature/qualifier values of a entry

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.



Ent01

source

/organism Category: Select only for virus, environmental sample, etc.

Scientific name: Dugesia japonica

/mol_type genomic DNA

/country Japan:Shizuoka

/isolate Dj-01

/organelle mitochondrion

genetic code 9

4. Click here and choose feature.

DDBJ Nucleotide Sequence Submission

Submission ID: 5062d65f55d69844ff000a14 Entry counts: 2

Ent01

source

length=17799

genetic code=9

/organism=Dugesia japonica

/mol_type=genomic DNA

/country=Japan:Shizuoka

/isolate=Dj-01

/organelle=mitochondrion

Ent02

source

length=5867

genetic code=

/organism=

/mol_type=

/country=

/isolate=

/organelle=

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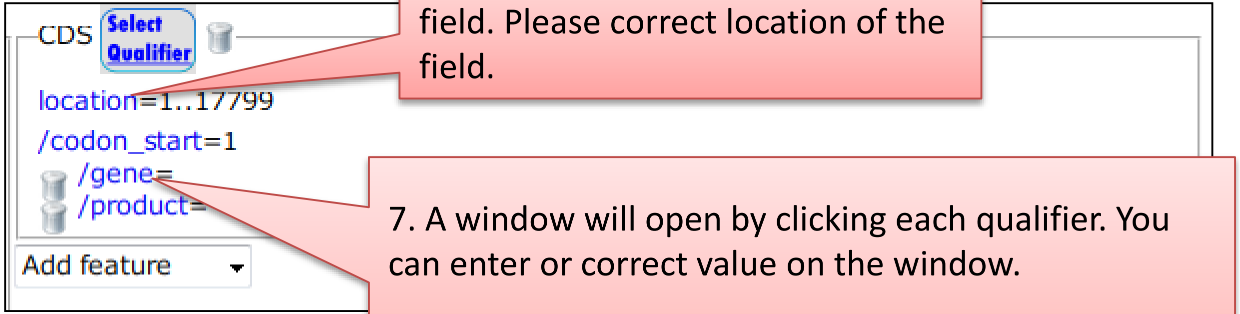
CDS

location=1..17799

/codon_start=1

Last modified: September 26, 2012

5. Select qualifier, which is added to the selected feature, from here

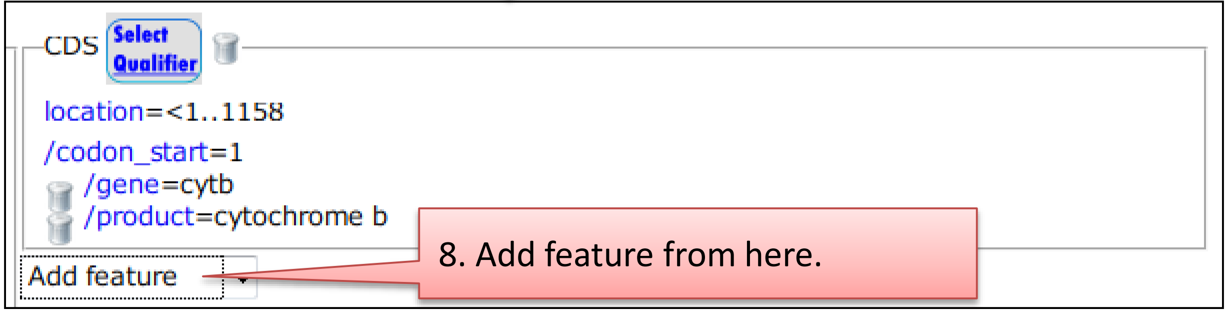


location=1..17799
/codon_start=1
/gene=
/product=

6. Click here and you will see input field. Please correct location of the field.

7. A window will open by clicking each qualifier. You can enter or correct value on the window.

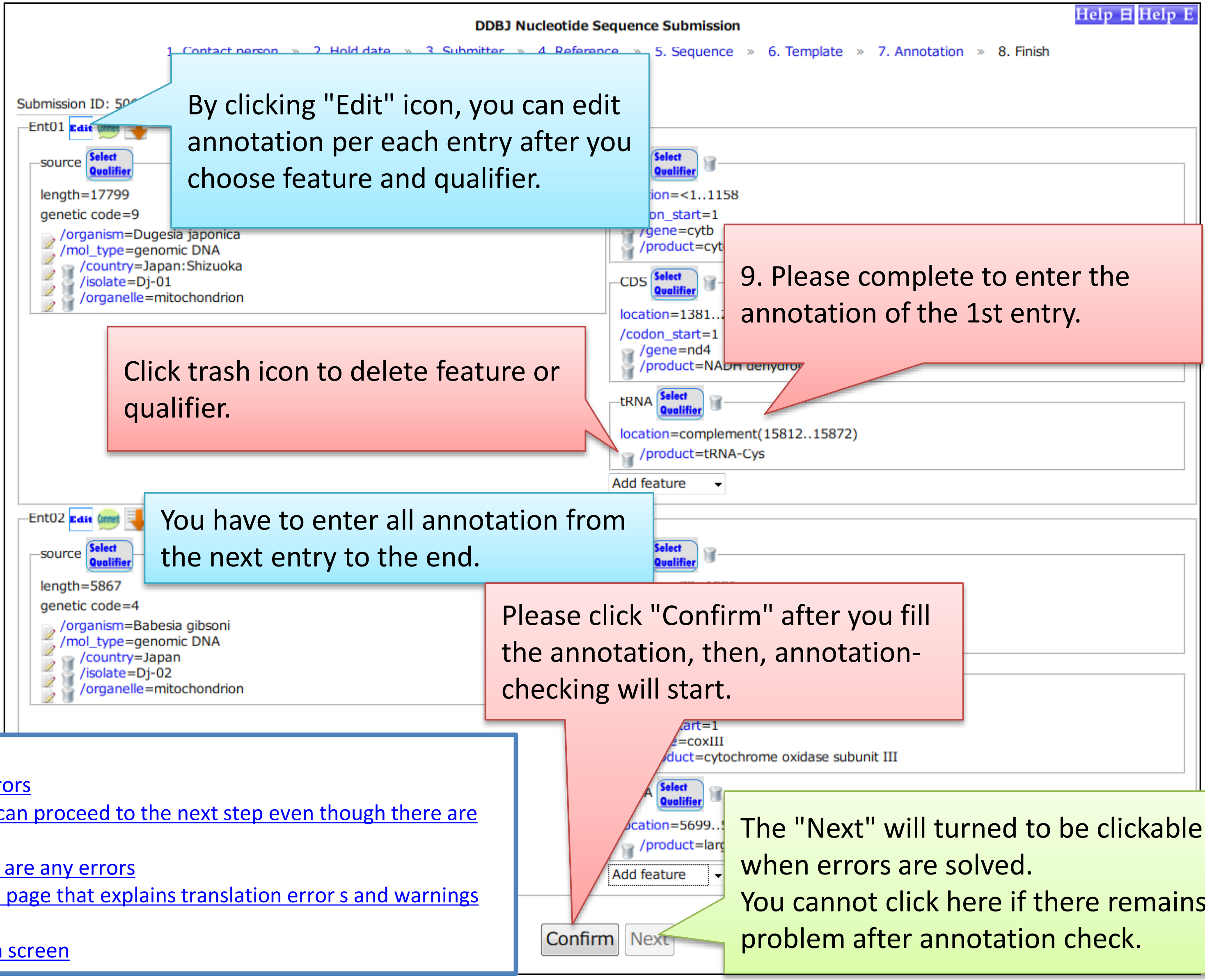
/codon_start is automatically set to "1" in the case of CDS feature. You should correct the value if you need.



location=<1..1158
/codon_start=1
/gene=cytb
/product=cytochrome b

8. Add feature from here.

Clicking "Confirm" on annotation screen



DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Submission ID: 50

length=17799
genetic code=9
/organism=Dugesia japonica
/mol_type=genomic DNA
/country=Japan:Shizuoka
/isolate=Dj-01
/organelle=mitochondrion

ion=<1..1158
on_start=1
/gene=cytb
/product=cyt

location=1381..
/codon_start=1
/gene=nd4
/product=NADH dehydro

location=complement(15812..15872)
/product=tRNA-Cys

length=5867
genetic code=4
/organism=Babesia gibsoni
/mol_type=genomic DNA
/country=Japan
/isolate=Dj-02
/organelle=mitochondrion

art=1
=coxIII
duct=cytochrome oxidase subunit III

location=5699..
/product=larg

By clicking "Edit" icon, you can edit annotation per each entry after you choose feature and qualifier.

9. Please complete to enter the annotation of the 1st entry.

Click trash icon to delete feature or qualifier.

You have to enter all annotation from the next entry to the end.

Please click "Confirm" after you fill the annotation, then, annotation-checking will start.

The "Next" will turned to be clickable when errors are solved.
You cannot click here if there remains any problem after annotation check.

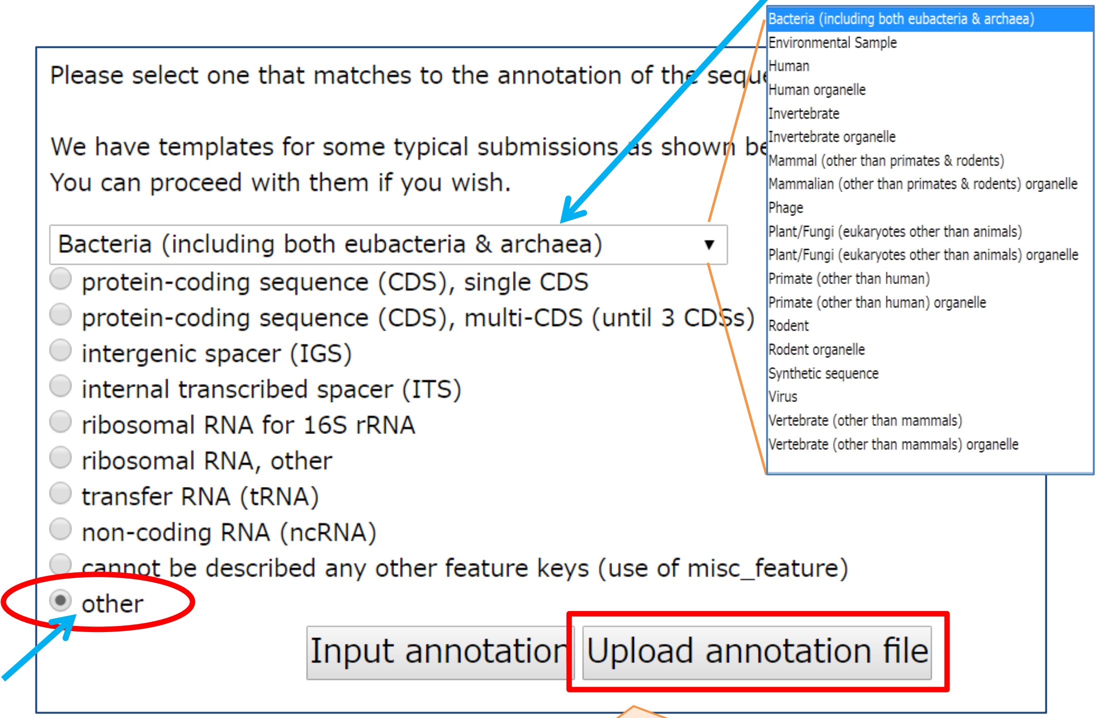
Link:
Confirm => no errors
Confirm => You can proceed to the next step even though there are some warnings
Confirm => There are any errors
Direct links of the page that explains translation error s and warnings
Progress bar
final confirmation screen

How to upload annotation from a tab-deliminated text-file

① Please select a taxonomic division of the sequenced organism. When nucleotide sequences have been obtained from organelle, you should select one whose name includes ‘organelle’.
Available qualifier keys under source feature vary with the selected taxonomic division.
If you cannot find an appropriate taxonomic division, we recommend you to choose "Plant/Fungi (eukaryotes other than animals)" because almost qualifier keys are available in "Plant/Fungi" division.
(Link: taxonomic divisions, http://www.ddbj.nig.ac.jp/sub/locus-e.html#division)

② Select “other” when you would like to upload annotation by using a tab-deliminated text-file.

①Taxonomic division


Please select one that matches to the annotation of the seque

We have templates for some typical submissions as shown be
You can proceed with them if you wish.

Bacteria (including both eubacteria & archaea) ▾

- Bacteria (including both eubacteria & archaea)
- Environmental Sample
- Human
- Human organelle
- Invertebrate
- Invertebrate organelle
- Mammal (other than primates & rodents)
- Mammalian (other than primates & rodents) organelle
- Phage
- Plant/Fungi (eukaryotes other than animals)
- Plant/Fungi (eukaryotes other than animals) organelle
- Primate (other than human)
- Primate (other than human) organelle
- Rodent
- Rodent organelle
- Synthetic sequence
- Virus
- Vertebrate (other than mammals)
- Vertebrate (other than mammals) organelle

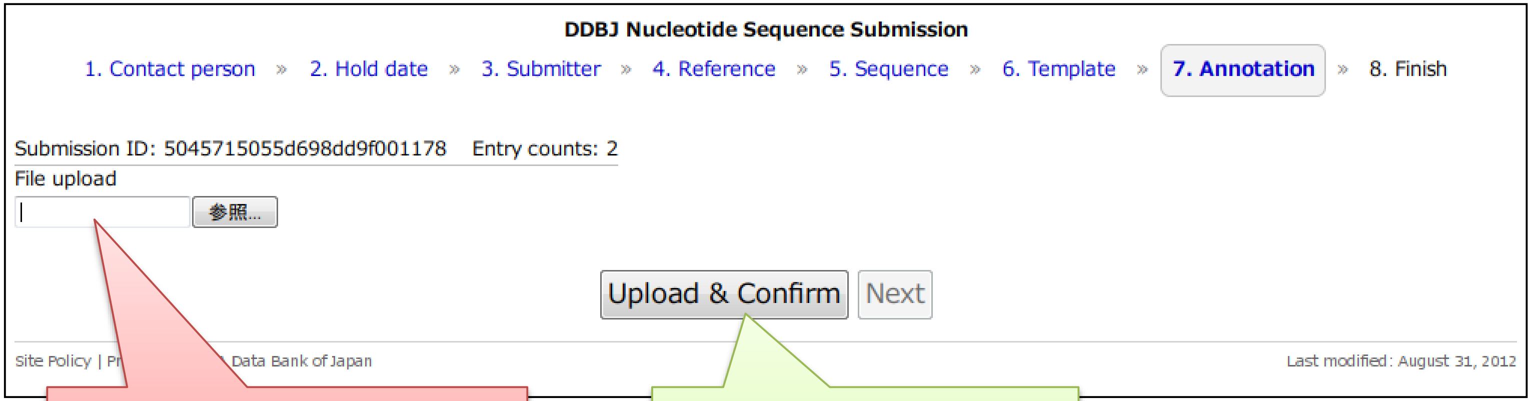
○ protein-coding sequence (CDS), single CDS
○ protein-coding sequence (CDS), multi-CDS (until 3 CDSs)
○ intergenic spacer (IGS)
○ internal transcribed spacer (ITS)
○ ribosomal RNA for 16S rRNA
○ ribosomal RNA, other
○ transfer RNA (tRNA)
○ non-coding RNA (ncRNA)
○ cannot be described any other feature keys (use of misc_feature)
● other

②

After the selection, please click "Upload annotation file".

The information entered at the "7.Annotatoin" page are disappeared if you change the template at this page.

Submission by uploading the annotation file



DDBJ Nucleotide Sequence Submission

Submission ID: 5045715055d698dd9f001178 Entry counts: 2

File upload

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Last modified: August 31, 2012

Set an annotation file here.

Click "Upload & Confirm" to start checking of annotation file.

Annotation file that is able to be uploaded

- ✓ You can see some examples on ‘sample annotation file’ page.
- ✓ Please include only annotation section in annotation file.
- ✓ You cannot upload WGS, CON, AGP, EST, GSS, STS, HTG, HTC, TSA files. Please contact DDBJ mass submission system (MSS) to submit such submission files.
- ✓ Information that you entered on the pages, "1. Contact person", "2. Hold date", "3. Submitter", and "4. Reference", are added in front of uploaded annotation file as COMMON section.
- ✓ When COMMON is included in the uploaded annotation file, if will be replaced with information obtained from "1. Contact person", "2. Hold date", "3. Submitter", and "4. Reference."
- ✓ For TPA, you should not include PRIMARY_CONTIG section in annotation file. PRIMARY_CONTIG section is automatically inserted to the uploaded annotation file by converting information of the "5.Sequence" page.

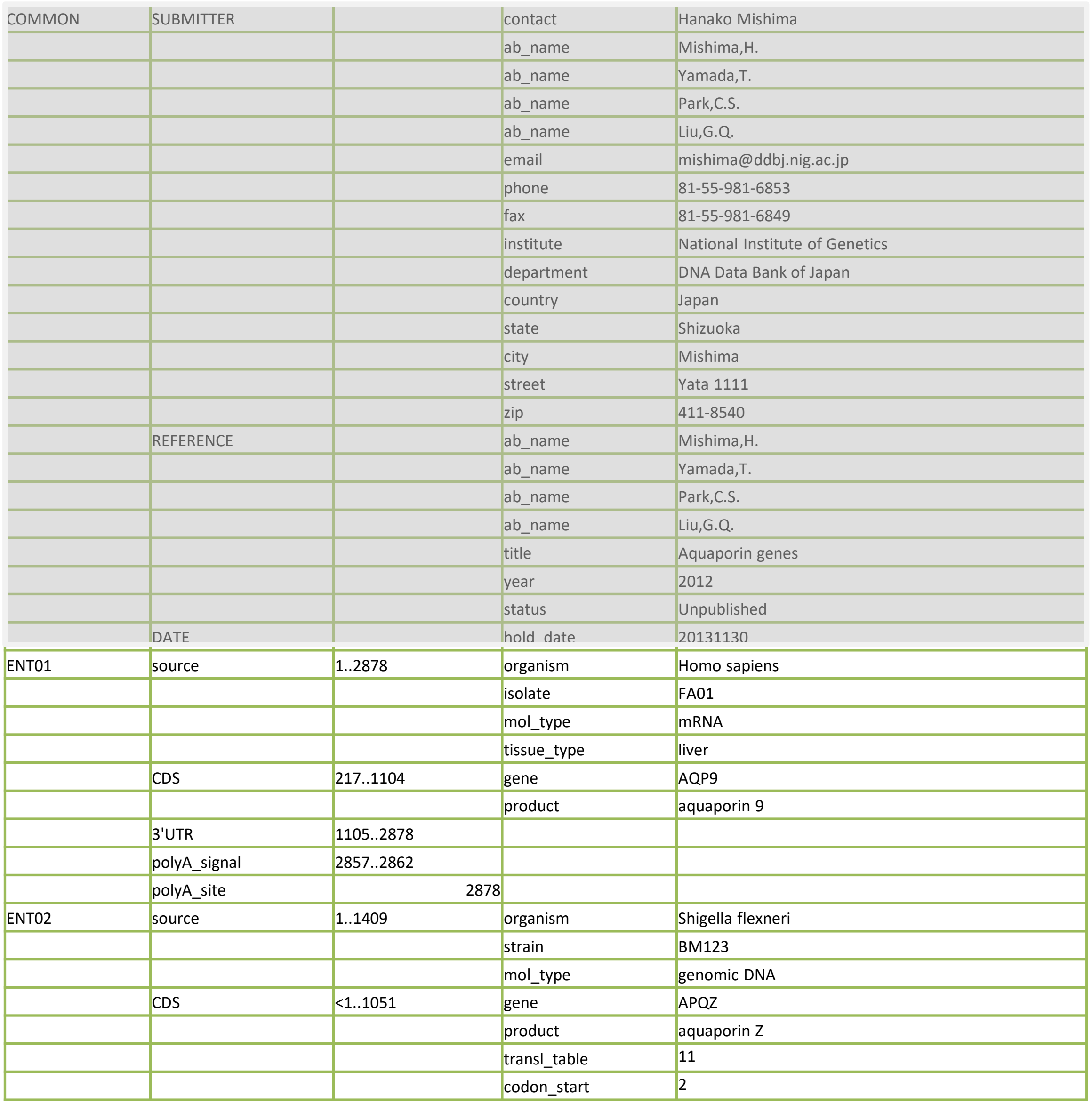
Link:

- ◆ Definition of Feature Key
- ◆ Definition of Qualifier key
- ◆ Organism qualifier
- ◆ CDS feature

Example annotation file used for upload

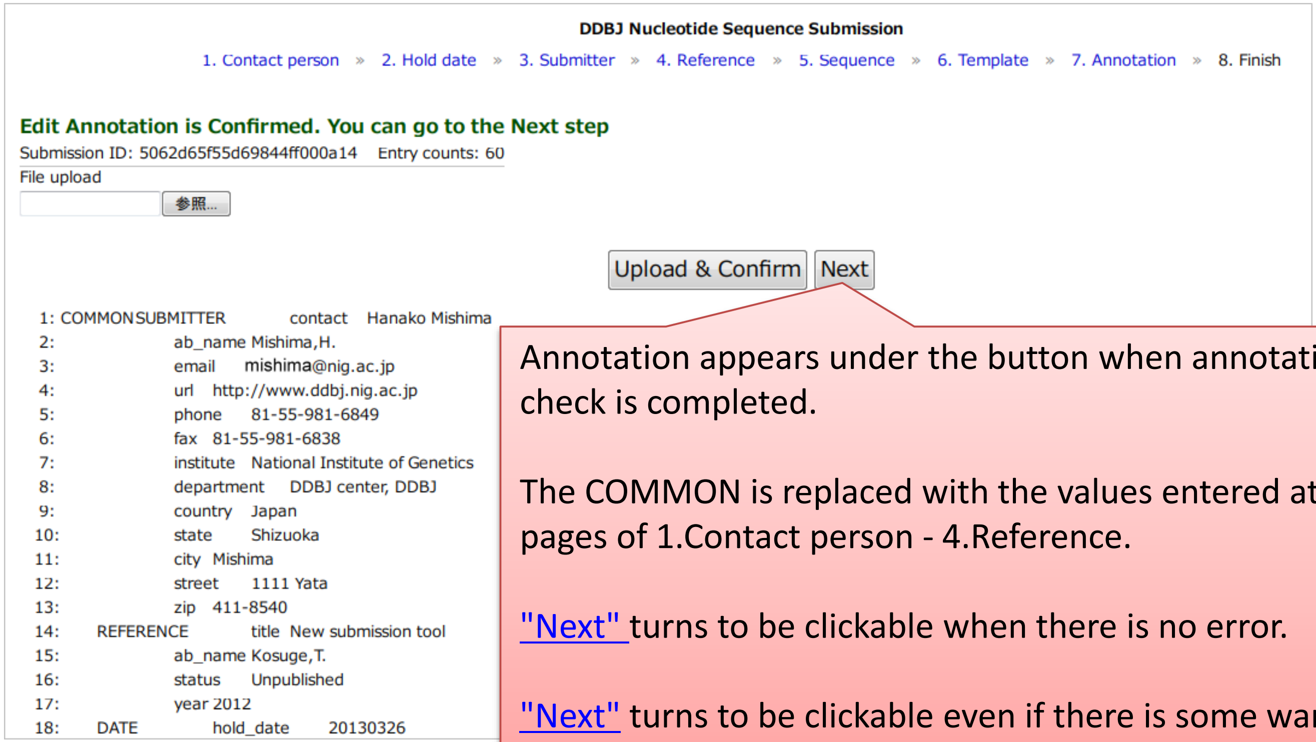
You do not have to include the area to the annotation file.
If it is included in the annotation file, it will be replaced with the information entered at the pages such as 1. Contact person, 2. Hold date, 3. Submitter, and 4. Reference

You should include only this region (= section consists of biological features) in annotation file.



COMMON	SUBMITTER		contact	Hanako Mishima
			ab_name	Mishima,H.
			ab_name	Yamada,T.
			ab_name	Park,C.S.
			ab_name	Liu,G.Q.
			email	mishima@ddbj.nig.ac.jp
			phone	81-55-981-6853
			fax	81-55-981-6849
			institute	National Institute of Genetics
			department	DNA Data Bank of Japan
			country	Japan
			state	Shizuoka
			city	Mishima
			street	Yata 1111
			zip	411-8540
	REFERENCE		ab_name	Mishima,H.
			ab_name	Yamada,T.
			ab_name	Park,C.S.
			ab_name	Liu,G.Q.
			title	Aquaporin genes
			year	2012
			status	Unpublished
	DATE		hold_date	20131130
ENT01	source	1..2878	organism	Homo sapiens
			isolate	FA01
			mol_type	mRNA
			tissue_type	liver
	CDS	217..1104	gene	AQP9
			product	aquaporin 9
	3'UTR	1105..2878		
	polyA_signal	2857..2862		
	polyA_site	2878		
ENT02	source	1..1409	organism	Shigella flexneri
			strain	BM123
			mol_type	genomic DNA
	CDS	<1..1051	gene	APQZ
			product	aquaporin Z
			transl_table	11
			codon_start	2

"Upload & Confirm" => no error



Edit Annotation is Confirmed. You can go to the Next step

Submission ID: 5062d65f55d69844ff000a14 Entry counts: 60

File upload

```
 1: COMMON SUBMITTER        contact    Hanako Mishima
 2:                 ab_name Mishima,H.
 3:                 email      mishima@nig.ac.jp
 4:                 url   http://www.ddbj.nig.ac.jp
 5:                 phone     81-55-981-6849
 6:                 fax   81-55-981-6838
 7:                 institute   National Institute of Genetics
 8:                 department     DDBJ center, DDBJ
 9:                 country   Japan
10:                 state       Shizuoka
11:                 city  Mishima
12:                 street      1111 Yata
13:                 zip   411-8540
14:     REFERENCE          title  New submission tool
15:                 ab_name Kosuge,T.
16:                 status      Unpublished
17:                 year 2012
18:     DATE            hold_date       20130326
```

Annotation appears under the button when annotation file check is completed.

The COMMON is replaced with the values entered at the pages of 1.Contact person - 4.Reference.

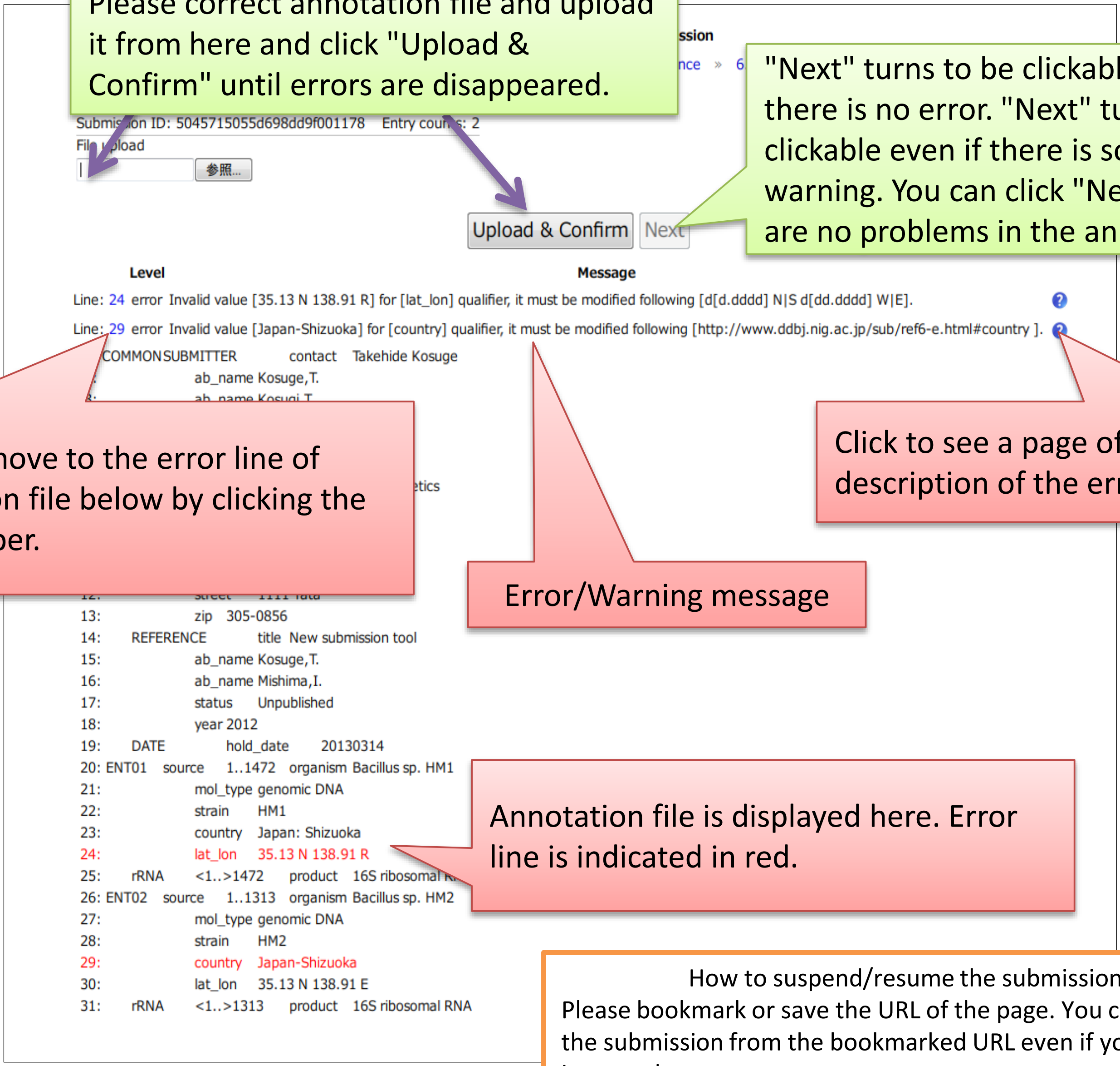
"Next" turns to be clickable when there is no error.

"Next" turns to be clickable even if there is some warning. You should correct the annotation if needed.

Link :
final confirmation screen

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

"Upload & Confirm" => Error/Warning occurred



Please correct annotation file and upload it from here and click "Upload & Confirm" until errors are disappeared.

"Next" turns to be clickable when there is no error. "Next" turns to be clickable even if there is some warning. You can click "Next" if there are no problems in the annotation.

Level	Message
Line: 24 error	Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E].
Line: 29 error	Invalid value [Japan-Shizuoka] for [country] qualifier, it must be modified following [http://www.ddbj.nig.ac.jp/sub/ref6-e.html#country].

You can move to the error line of annotation file below by clicking the line number.

Error/Warning message

Click to see a page of detailed description of the error.

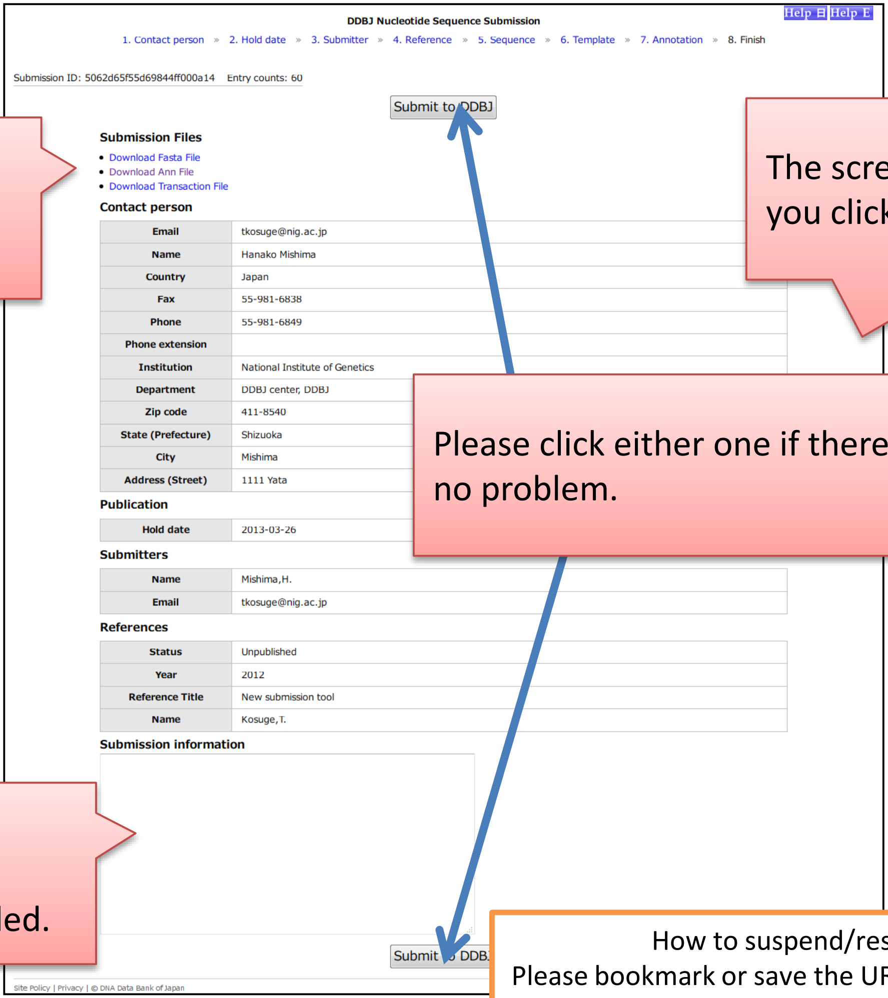
```
    COMMONSUBMITTER         contact    Takehide Kosuge
                    ab_name Kosuge,T.
13:                 zip   305-0856
14:      REFERENCE          title  New submission tool
15:                 ab_name Kosuge,T.
16:                 ab_name Mishima,I.
17:                 status     Unpublished
18:                 year 2012
19:      DATE          hold_date       20130314
20: ENT01    source     1..1472    organism Bacillus sp. HM1
21:                 mol_type genomic DNA
22:                 strain     HM1
23:                 country    Japan: Shizuoka
24:                 lat_lon    35.13 N 138.91 R
25:      rRNA       <1..>1472     product    16S ribosomal
26: ENT02    source     1..1313    organism Bacillus sp. HM2
27:                 mol_type genomic DNA
28:                 strain     HM2
29:                 country    Japan-Shizuoka
30:                 lat_lon    35.13 N 138.91 E
31:      rRNA       <1..>1313     product    16S ribosomal RNA
```

Annotation file is displayed here. Error line is indicated in red.

How to suspend/resume the submission

Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

final confirmation screen



DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

Submission ID: 5062d65f55d69844ff000a14 Entry counts: 60

Submission Files

- Download Fasta File
- Download Ann File
- Download Transaction File

Contact person

Email	tkosuge@nig.ac.jp
Name	Hanako Mishima
Country	Japan
Fax	55-981-6838
Phone	55-981-6849
Phone extension	
Institution	National Institute of Genetics
Department	DDBJ center, DDBJ
Zip code	411-8540
State (Prefecture)	Shizuoka
City	Mishima
Address (Street)	1111 Yata

Publication

Hold date	2013-03-26

Submitters

Name	Mishima,H.
Email	tkosuge@nig.ac.jp

References

Status	Unpublished
Year	2012
Reference Title	New submission tool
Name	Kosuge,T.

Submission information

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You can browse the information of pages 1 to 7 in text format.

The screen will appear after you click "Next".

Please click either one if there is no problem.

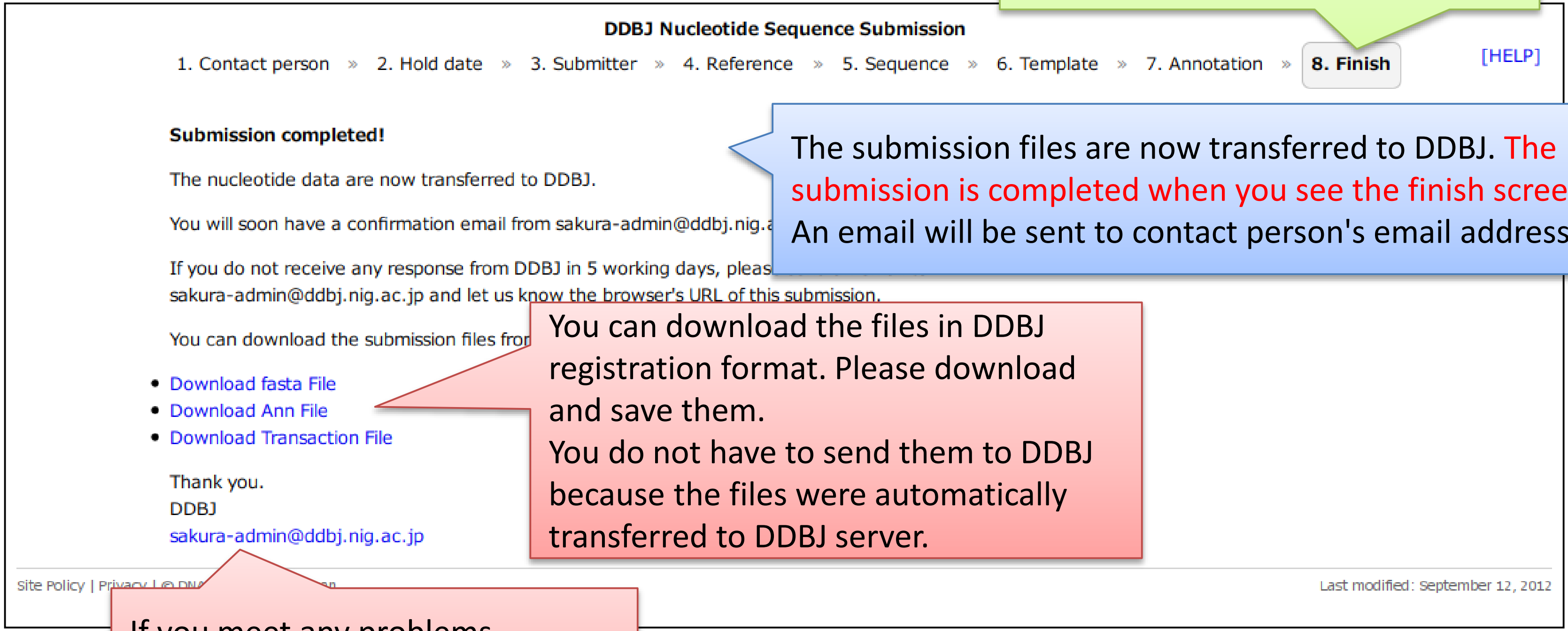
Please describe here if there are any other information when needed.

How to suspend/resume the submission
Please bookmark or save the URL of the page. You can resume the submission from the bookmarked URL even if you close the internet browser.

Link：
Annotation check starts when you click "Confirm"
Clicking "Confirm" on annotation screen (when Template: other was selected)
"Upload & Confirm" => no error

8. Finish

Please bookmark the page. You can browse the page from the bookmark for a certain period even though you close the browser.



DDBJ Nucleotide Sequence Submission

Submission completed!

The nucleotide data are now transferred to DDBJ.

You will soon have a confirmation email from sakura-admin@ddbj.nig.a

If you do not receive any response from DDBJ in 5 working days, pleas
sakura-admin@ddbj.nig.ac.jp and let us know the browser's URL of this submission.

You can download the submission files fror

- Download fasta File
- Download Ann File
- Download Transaction File

Thank you.
DDBJ
sakura-admin@ddbj.nig.ac.jp

The submission files are now transferred to DDBJ. The submission is completed when you see the finish screen. An email will be sent to contact person's email address.

You can download the files in DDBJ registration format. Please download and save them.
You do not have to send them to DDBJ because the files were automatically transferred to DDBJ server.

If you meet any problems regarding of the tool, please email to the address.

Link:
[final confirmation screen]

You will receive an email when submission completed

From: sakura-admin@ddbj.nig.ac.jp
Subject: DDBJ: Web submission completed

Contact person : mishima@nig.ac.jp
Hanako Mishima
National Institute of Genetics
DDBJ center, DDBJ
1111 Yata
Mishima, Shizuoka, 411-8540
Japan

Thank you very much for choosing DDBJ for data submission.

We have received your data. We will soon check and annotate them on the basis of the manual and rules common to the DDBJ, EMBL-Bank, and GenBank.

If you do not hear from DDBJ after 5 working days after receiving this notice, please contact us at the following address indicating your Entry Name.

Email address: sakura-admin@ddbj.nig.ac.jp

Sincerely,

DNA Data Bank of Japan
DDBJ Center
National Institute of Genetics
Research Organization of Information
and Systems
Mishima, Shizuoka 411-8540, Japan
fax: +81-55-981-6849

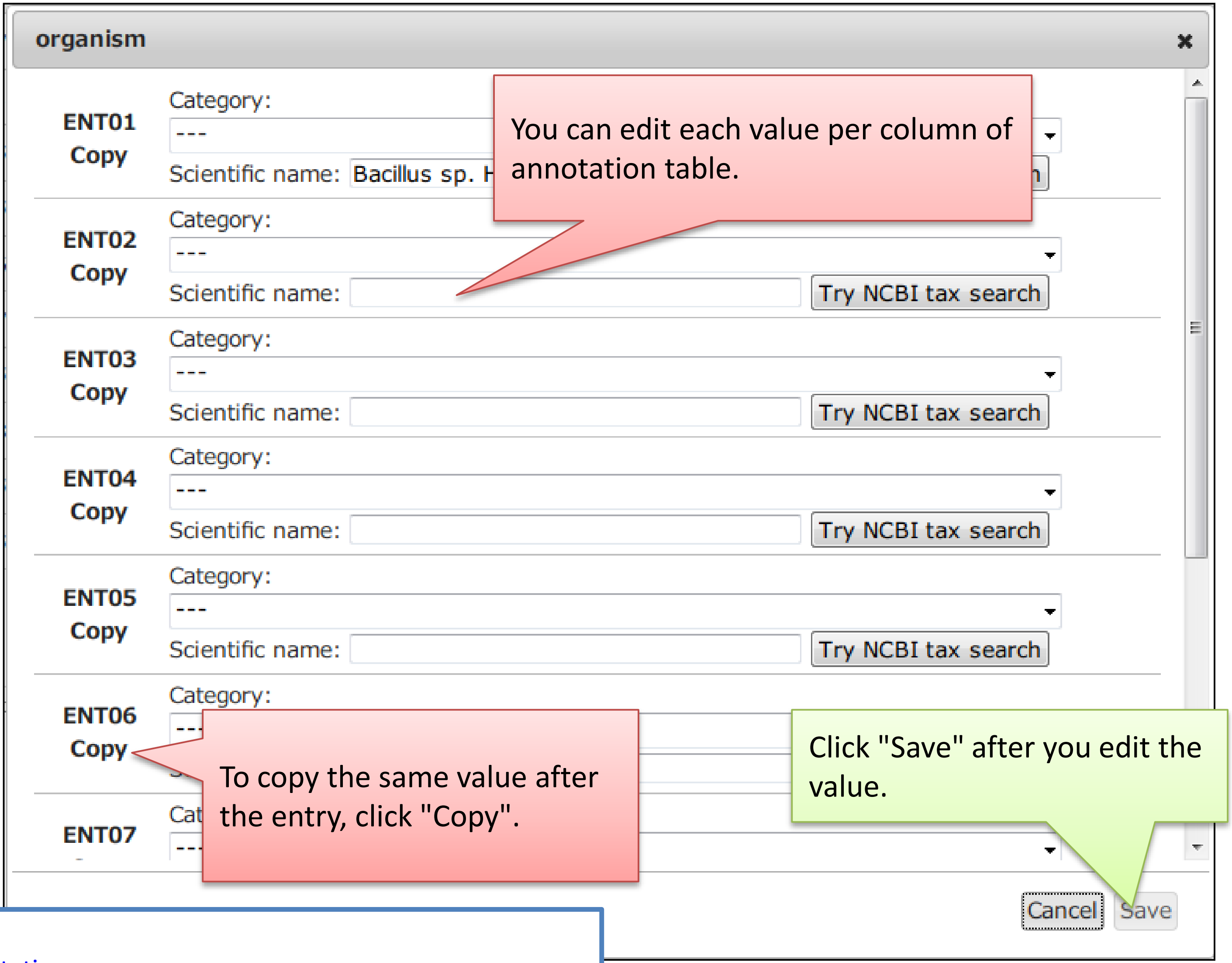
[Hold-date]
2013-03-29

[Entry ID]
5065382e55d69849870005fe.entry01
5065382e55d69849870005fe.entry02

Link:
[8. Finish]

Illustrations of text input field

Edit icon at each qualifier



organism

ENT01 **Copy**	Category: --- Scientific name: Bacillus sp. H
ENT02 **Copy**	Category: --- Scientific name:
ENT03 **Copy**	Category: --- Scientific name:
ENT04 **Copy**	Category: --- Scientific name:
ENT05 **Copy**	Category: --- Scientific name:
ENT06 **Copy**	Category: ---
ENT07	Cat ---

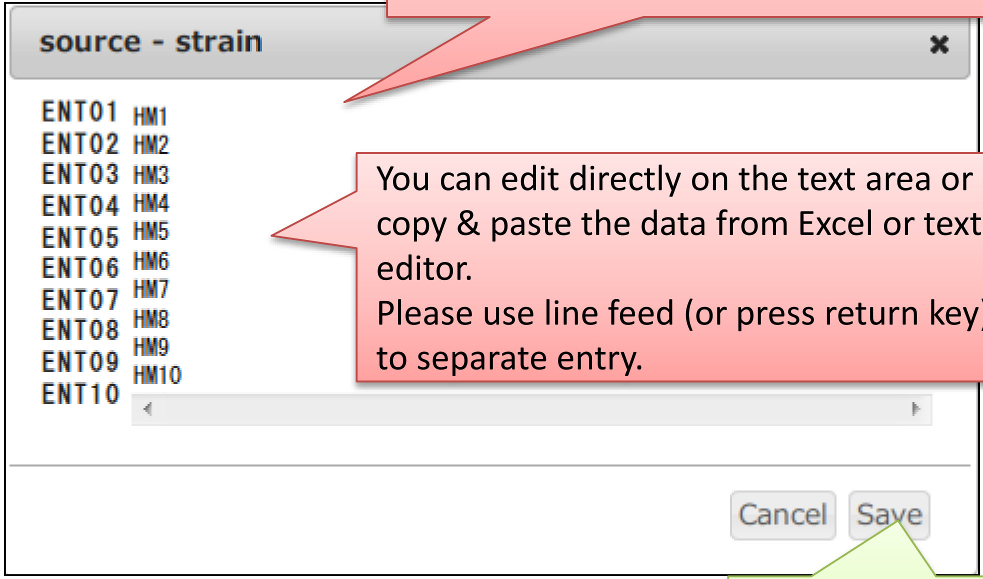
You can edit each value per column of annotation table.

To copy the same value after the entry, click "Copy".

Click "Save" after you edit the value.

Link:
[7.Annotation]()
[Annotation screen when "Other" is selected at "Template"]()
[e.g. Input annotation of mitochondrial DNA]()

Edit column



source - strain

ENT01	HM1
ENT02	HM2
ENT03	HM3
ENT04	HM4
ENT05	HM5
ENT06	HM6
ENT07	HM7
ENT08	HM8
ENT09	HM9
ENT10	HM10

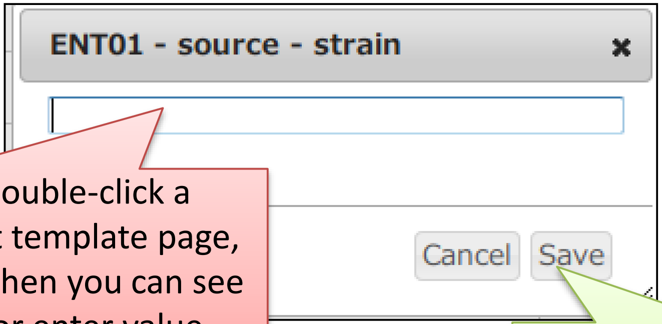
You can edit each value per column of annotation table.

You can edit directly on the text area or copy & paste the data from Excel or text editor.
Please use line feed (or press return key) to separate entry.

Click "Save" after edit/enter the value.

Link:
[7.Annotation]
[Annotation screen when "Other" is selected at "Template"]
[e.g. Input annotation of mitochondrial DNA]

Double-click a cell
(Click qualifier for "Other" template)



A window will open when you double-click a cell (When you select "other" at template page, you should click each qualifier, then you can see the same window). Please edit or enter value against the input field.

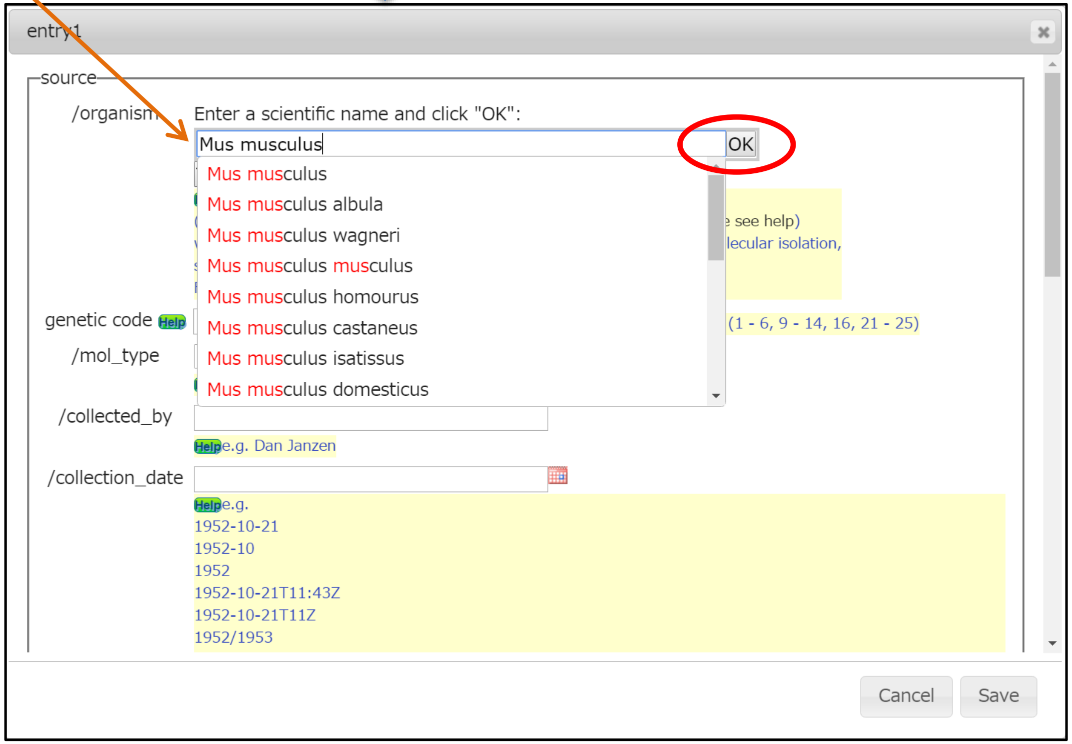
Click "Save" after edit/enter the value.

Link:
[7.Annotation]()
[Annotation screen when "Other" is selected at "Template"]()
[e.g. Input annotation of mitochondrial DNA]()

How to input organism name

Please click "Edit"

Enter a correct scientific name here. When you type a name, candidates are automatically searched from the GenBank taxonomy database and displayed on the screen. Please select one from the list and click "OK".



entry1

source

/organism Enter a scientific name and click "OK":

Mus musculus

- Mus musculus
- Mus musculus albula
- Mus musculus wagneri
- Mus musculus musculus
- Mus musculus homourus
- Mus musculus castaneus
- Mus musculus isatissus
- Mus musculus domesticus

see help)
lecular isolation,

genetic code Help (1 - 6, 9 - 14, 16, 21 - 25)

/mol_type

/collected_by

Help e.g. Dan Janzen

/collection_date

Help e.g.
1952-10-21
1952-10
1952
1952-10-21T11:43Z
1952-10-21T11Z
1952/1953

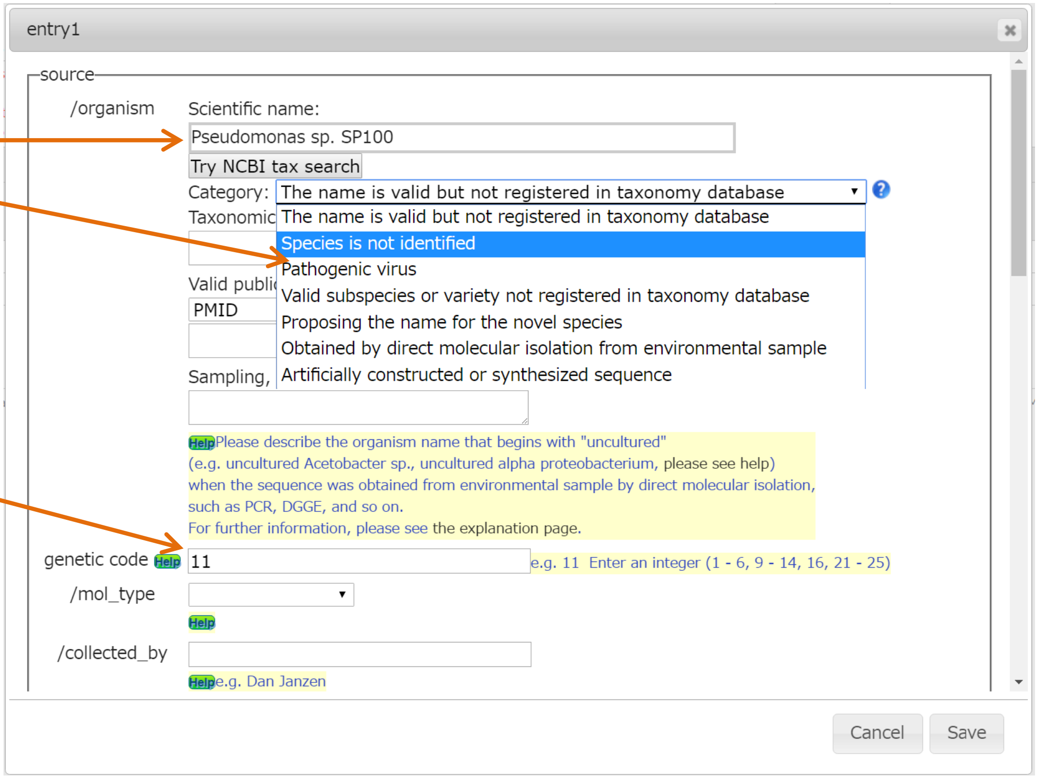
How to input an organism not registered in taxonomy database

When you enter a new organism, which has not been registered to the GenBank taxonomy database, you must select "Category" and input information about the organism such as taxonomic lineage, valid publication, and so on.

Link: http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

After input of an organism name, genetic code (must be an integer) is automatically entered to the text box when the organism name is included in the GenBank taxonomy database.

You must manually enter a genetic code (e.g. 1 for universal, 11 for Bacteria, 2 for vertebrate mitochondrion, 5 for invertebrate mitochondrion) when the organism name is not registered to the taxonomy database and an integer is not automatically entered.



/organism Scientific name: Pseudomonas sp. SP100

Category: The name is valid but not registered in taxonomy database

- The name is valid but not registered in taxonomy database
- Species is not identified
- Pathogenic virus
- Valid subspecies or variety not registered in taxonomy database
- Proposing the name for the novel species
- Obtained by direct molecular isolation from environmental sample
- Artificially constructed or synthesized sequence

PMID

Help Please describe the organism name that begins with "uncultured" (e.g. uncultured Acetobacter sp., uncultured alpha proteobacterium, please see help) when the sequence was obtained from environmental sample by direct molecular isolation, such as PCR, DGGE, and so on. For further information, please see the explanation page.

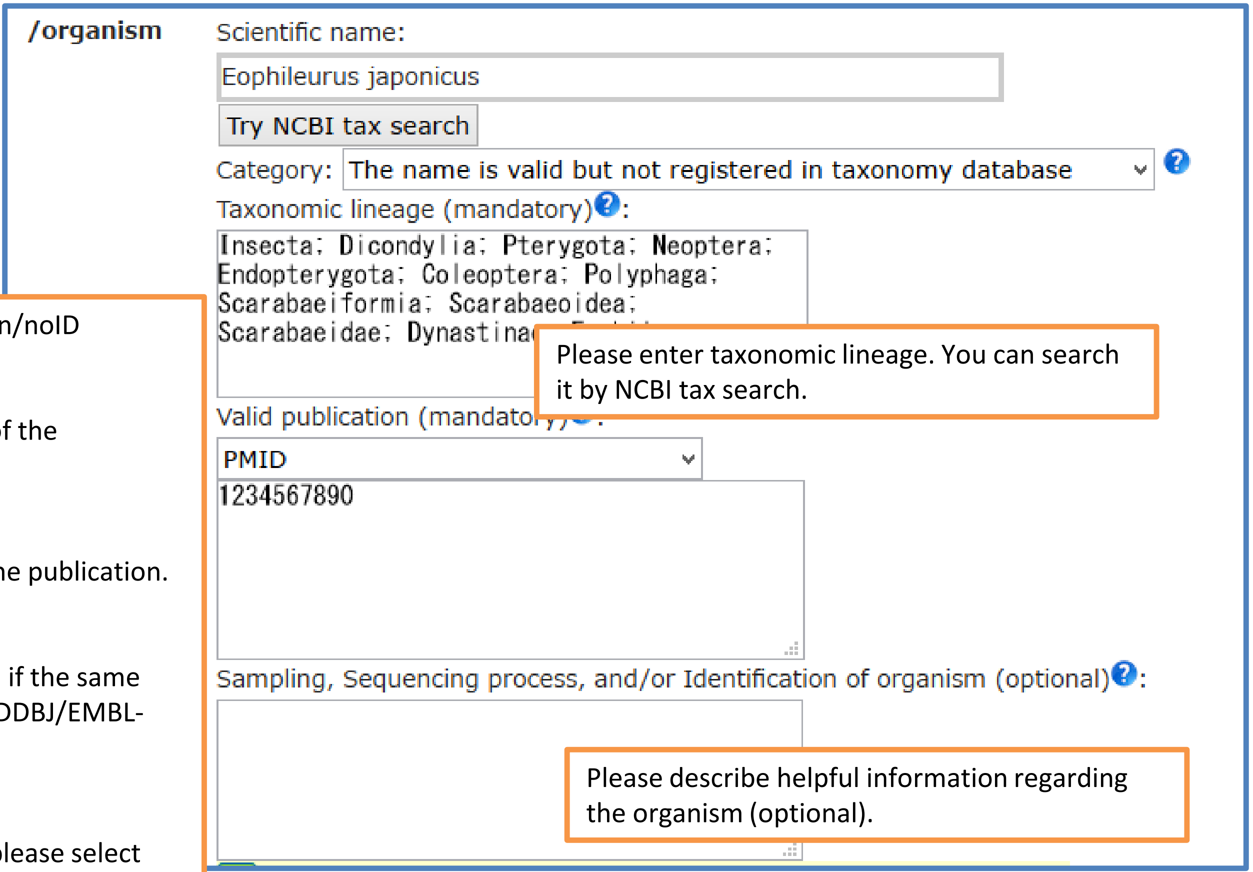
genetic code Help 11 e.g. 11 Enter an integer (1 - 6, 9 - 14, 16, 21 - 25)

/collected_by

Help e.g. Dan Janzen

Category: The name is valid but not registered in taxonomy database

Example



/organism

Scientific name:

Eophileurus japonicus

Category: The name is valid but not registered in taxonomy database

Taxonomic lineage (mandatory):

Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia; Scarabaeoidea; Scarabaeidae; Dynastina

Valid publication (mandatory):

PMID

1234567890

Sampling, Sequencing process, and/or Identification of organism (optional):

Please select PMID/DOI/Accession/noID

PMID
Enter PubMed unique identifier of the publication.

DOI
Enter digital object identifier of the publication.

Accession number
Please enter accession number(s) if the same organism has been registered to DDBJ/EMBL-Bank/GenBank.

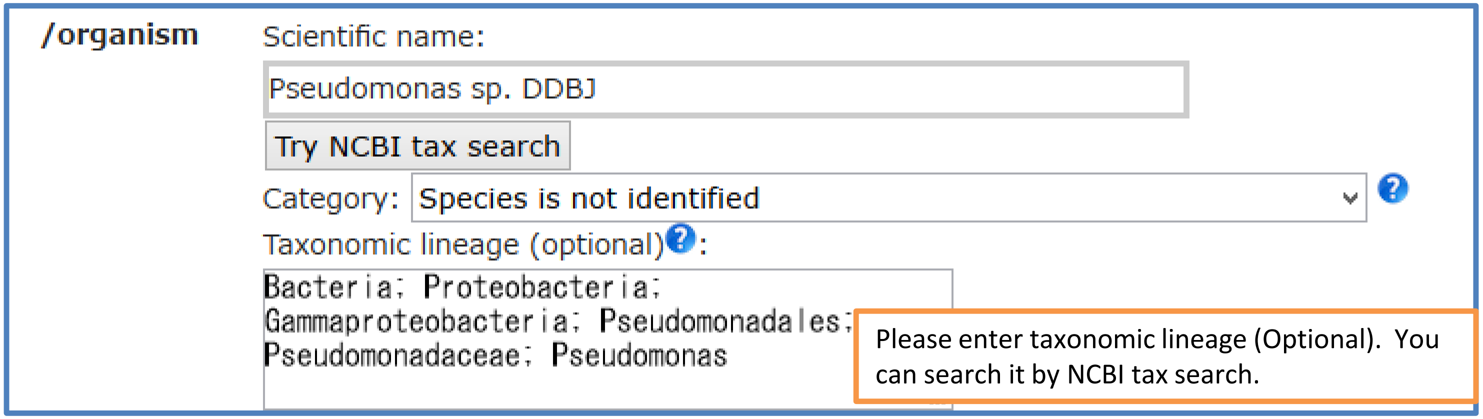
noID
When the publication has no id, please select "noID" and describe the information of the publication such as title, authors, year, volume, pages, and journal name.

Please enter taxonomic lineage. You can search it by NCBI tax search.

Please describe helpful information regarding the organism (optional).

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Species is not identified



/organism

Scientific name: Pseudomonas sp. DDBJ

Category: Species is not identified

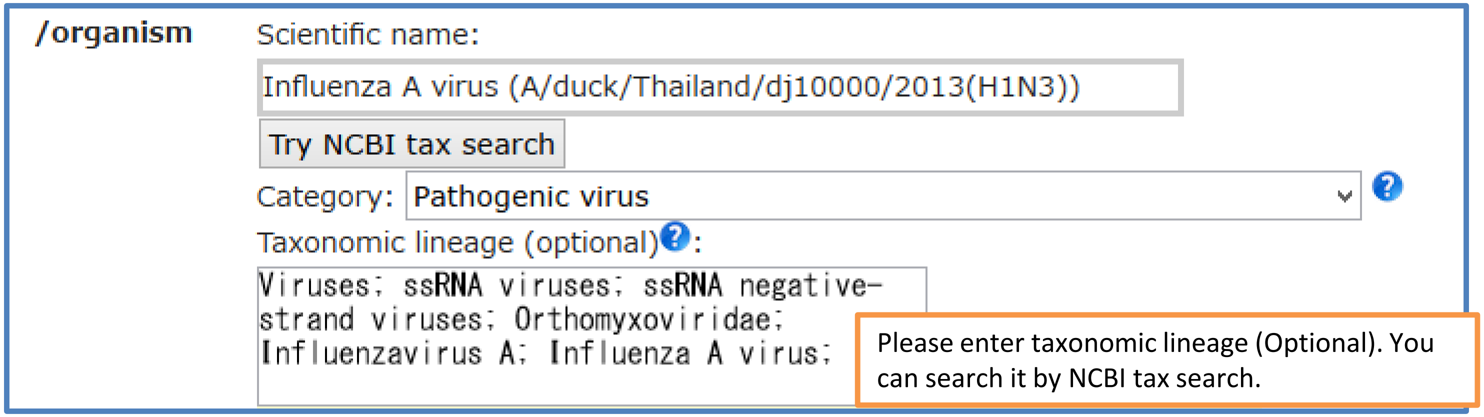
Taxonomic lineage (optional):

Bacteria; Proteobacteria;
Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas

Please enter taxonomic lineage (Optional). You can search it by NCBI tax search.

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Pathogenic virus



/organism Scientific name:

Influenza A virus (A/duck/Thailand/dj10000/2013(H1N3))

Category: Pathogenic virus

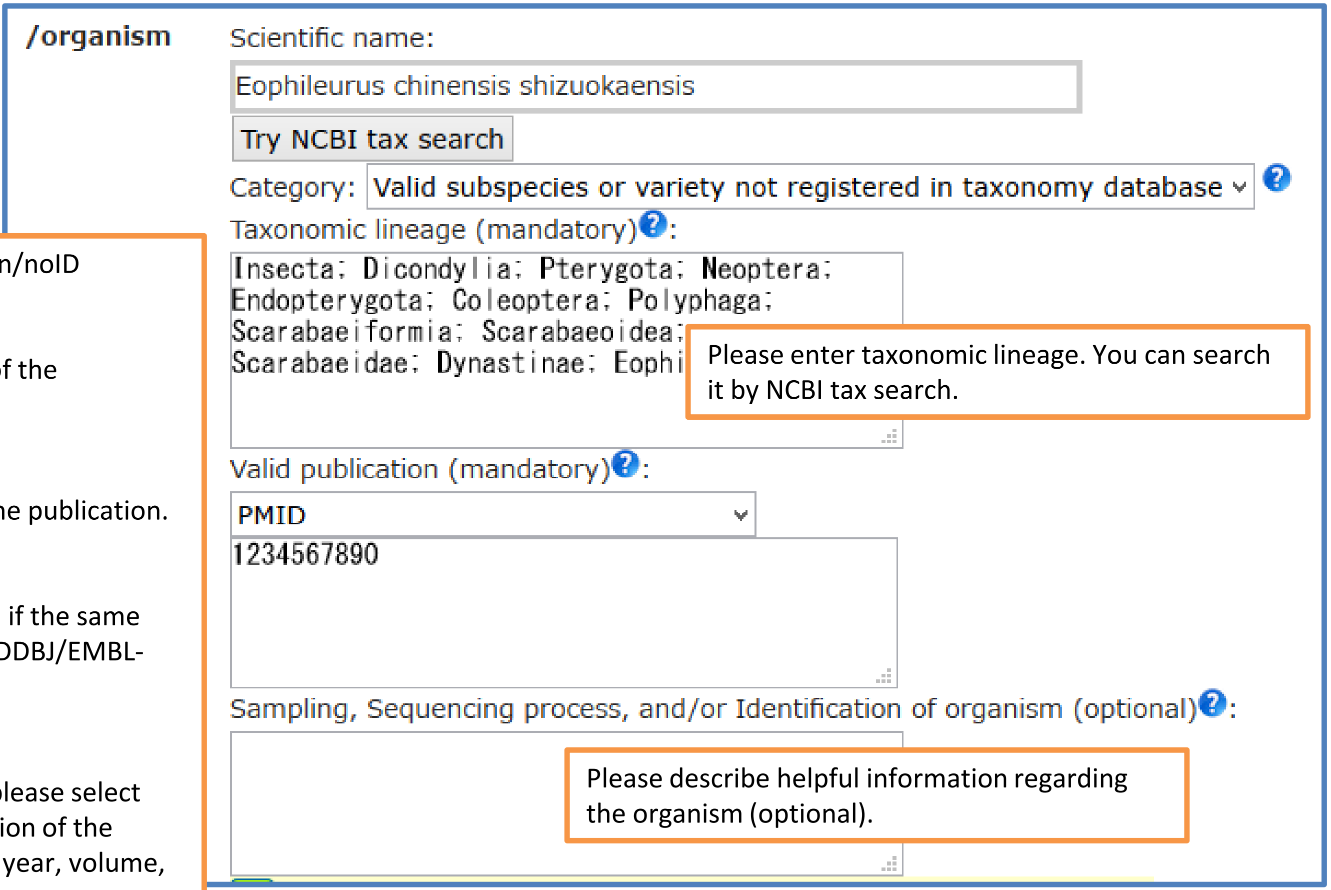
Taxonomic lineage (optional):

Viruses; ssRNA viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A; Influenza A virus;

Please enter taxonomic lineage (Optional). You can search it by NCBI tax search.

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Valid subspecies or variety not registered in taxonomy database



/organism

Scientific name:

Eophileurus chinensis shizuokaensis

Category: Valid subspecies or variety not registered in taxonomy database

Taxonomic lineage (mandatory):

Insecta; Dicondylia; Pterygota; Neoptera;
Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeoidea;
Scarabaeidae; Dynastinae; Eophi

Valid publication (mandatory):

PMID

1234567890

Sampling, Sequencing process, and/or Identification of organism (optional):

Please enter taxonomic lineage. You can search it by NCBI tax search.

Please describe helpful information regarding the organism (optional).

Please select PMID/DOI/Accession/noID

PMID
Enter PubMed unique identifier of the publication.

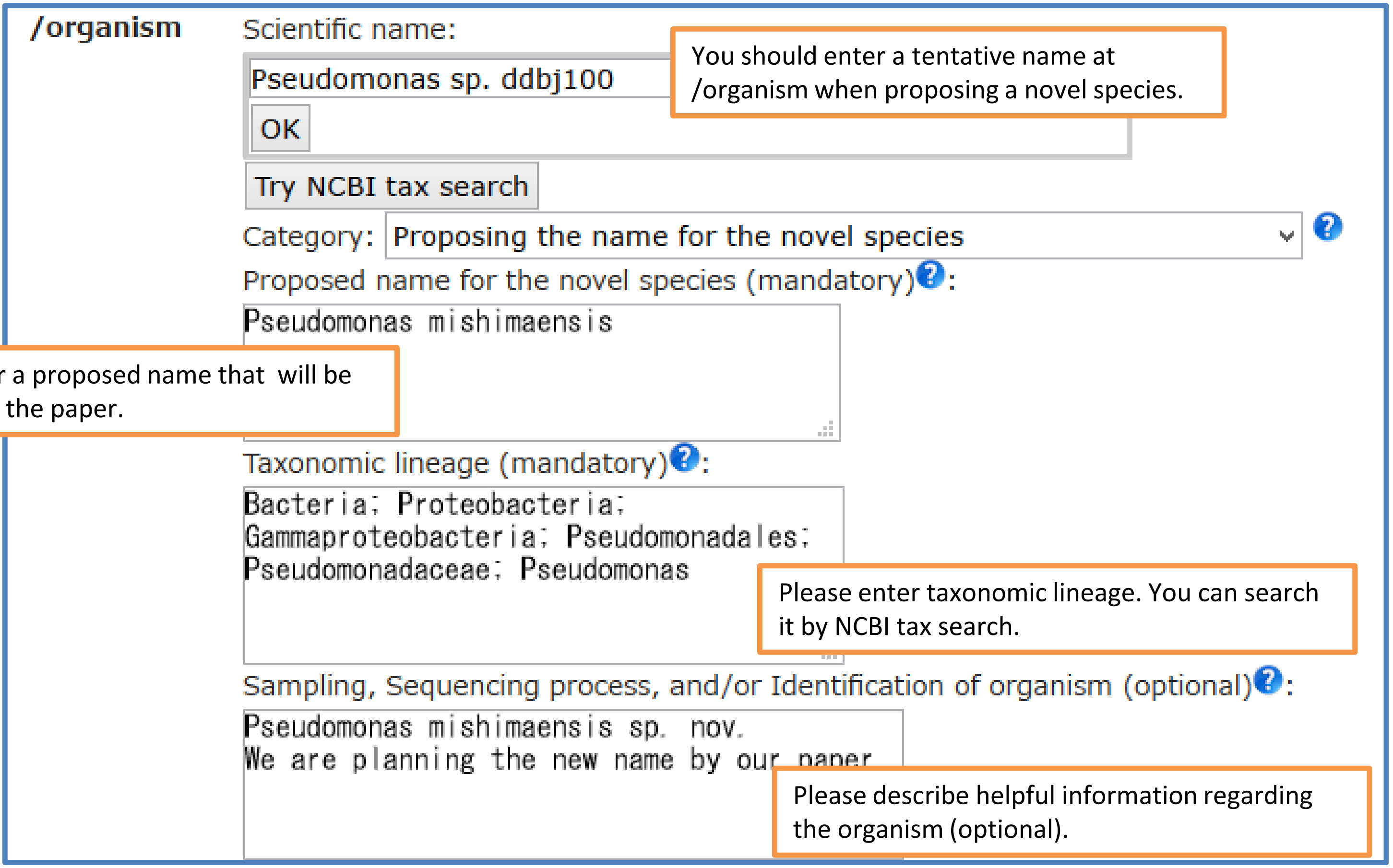
DOI
Enter digital object identifier of the publication.

Accession number
Please enter accession number(s) if the same organism has been registered to DDBJ/EMBL-Bank/GenBank.

noID
When the publication has no id, please select "noID" and describe the information of the publication such as title, authors, year, volume, pages, and journal name.

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Proposing the name for the novel species



/organism

Scientific name: Pseudomonas sp. ddbj100

Category: Proposing the name for the novel species

Proposed name for the novel species (mandatory): Pseudomonas mishimaensis

Taxonomic lineage (mandatory): Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas

Sampling, Sequencing process, and/or Identification of organism (optional):

Pseudomonas mishimaensis sp. nov.
We are planning the new name by our paper

You should enter a tentative name at /organism when proposing a novel species.

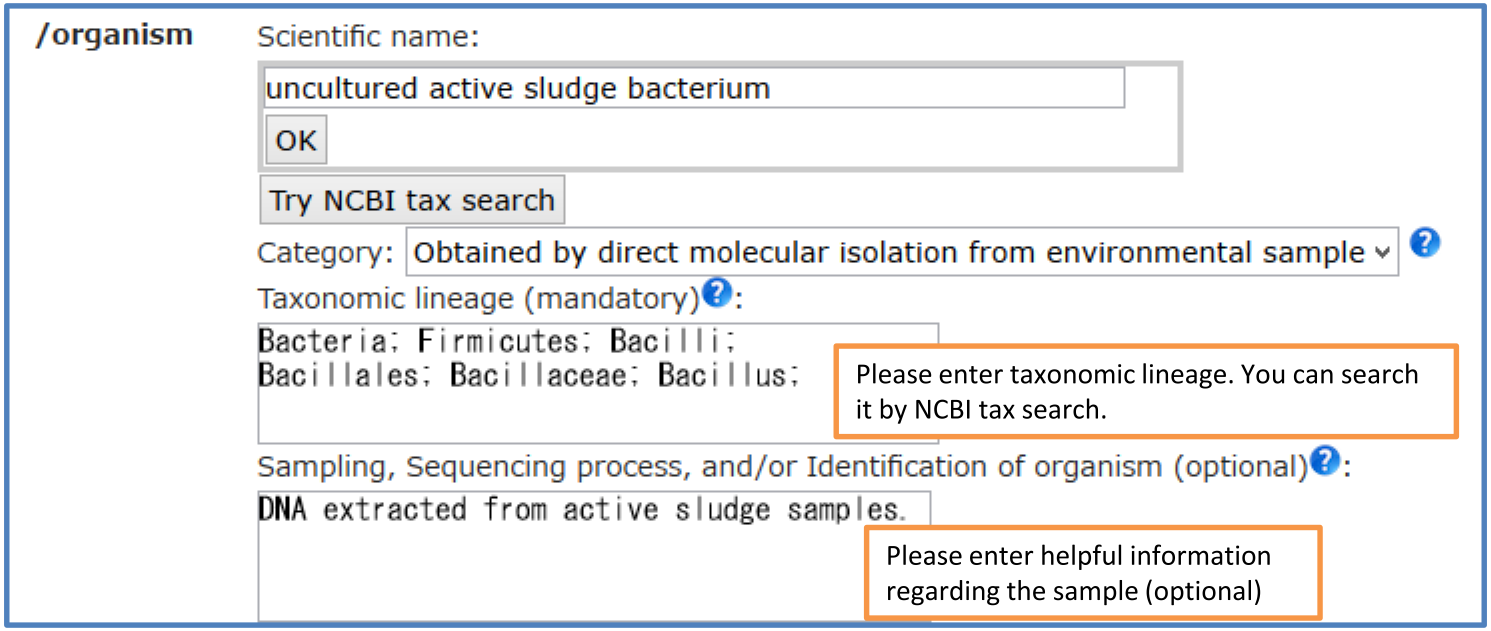
Please enter a proposed name that will be reported by the paper.

Please enter taxonomic lineage. You can search it by NCBI tax search.

Please describe helpful information regarding the organism (optional).

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Obtained by direct molecular isolation from environmental sample



/organism

Scientific name: uncultured active sludge bacterium

Category: Obtained by direct molecular isolation from environmental sample

Taxonomic lineage (mandatory):

Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;

Please enter taxonomic lineage. You can search it by NCBI tax search.

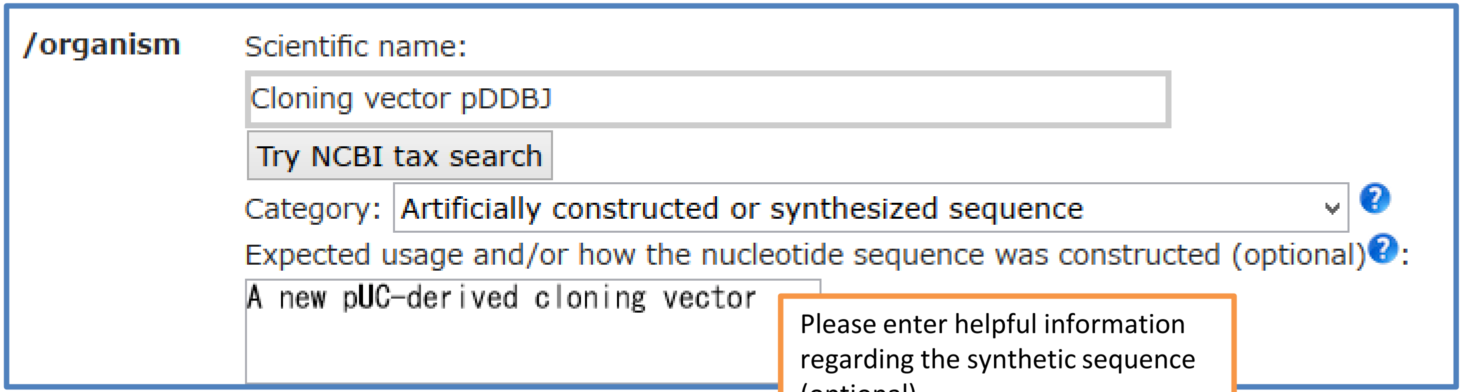
Sampling, Sequencing process, and/or Identification of organism (optional):

DNA extracted from active sludge samples.

Please enter helpful information regarding the sample (optional)

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Category: Artificially constructed or synthesized sequence



/organism

Scientific name: Cloning vector pDDBJ

Category: Artificially constructed or synthesized sequence

Expected usage and/or how the nucleotide sequence was constructed (optional): A new pUC-derived cloning vector

Please enter helpful information regarding the synthetic sequence (optional)

Link:
http://www.ddbj.nig.ac.jp/sub/ref8-e.html#deasy

Link to the pages for detailed description of errors & warnings

You can see detailed explanation of Errors and Warning at;
http://www.ddbj.nig.ac.jp/sub/validator-j.html

Regarding the errors and warnings about amino acid translation of CDS feature, you can see their explanation at;
http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC

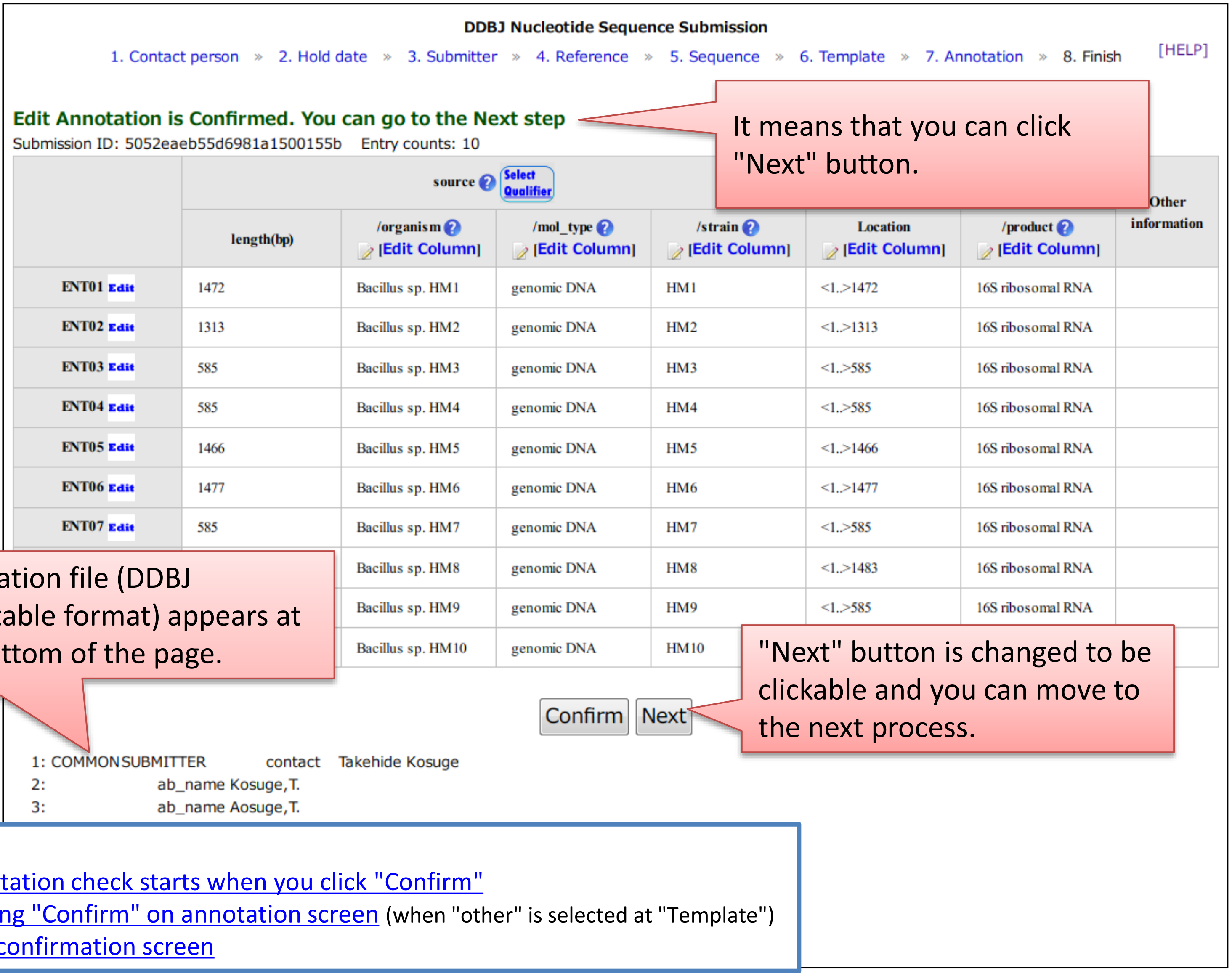
Please refer the following links for preparation of annotation.

- Definition of Feature Key
- Definition of Qualifier key
- Organism qualifier
- CDS feature

Direct links of the page that explains translation errors and warnings

Message	Link
[WARNING] 'codon_start' qualifier should be selected. The value is automatically set 1.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC22
[WARNING] 'transl_table' qualifier should be selected. The value is automatically set 1.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC23
[WARNING] Amino acid of 'transl_except' qualifier [#Value] is not [Met].	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC24
[ERROR] Untranslatable codon [#Codon] is found in the sequence range.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC18
[ERROR] First codon [#Codon] is not a start codon.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC19
[ERROR] Final codon [#Codon] is not a stop codon.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC20
[ERROR] Stop codon '*' is found in the range.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC21
[ERROR] Description of Location [#location of CDS feature] is illegal.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC04
[ERROR] 'codon_start' qualifier is duplicated. The value is automatically set 1.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC05
[ERROR] 'codon_start' qualifier has invalid value [#Value].	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC06
[ERROR] 'transl_table' qualifier is duplicated. The value is automatically set 1.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC07
[ERROR] 'transl_table' qualifier has invalid value [#Value].	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC08
[ERROR] Amino acid abbreviation [#abbreviation] in 'transl_except' qualifier is illegal.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC09
[ERROR] 'transl_except' qualifier has invalid value [#Value].	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC10
[ERROR] Location of 'transl_except' qualifier [#Value] is overlapped.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC11
[ERROR] Location of 'transl_except' qualifier [#Value] is invalid.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC12
[ERROR] Base range of 'transl_except' qualifier [#Value] is mismatched in reading frame.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC13
[ERROR] Amino acid of 'transl_except' qualifier [#Value] is not changed from conceptual translation.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC14
[ERROR] Amino acid of 'transl_except' qualifier [#Value] is not [TERM].	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC15
[ERROR] Stop codon is specified by 'transl_except' qualifier [#Value] in mid of CDS location.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC16
[ERROR] Entry [#Entry name] is NOT found in sequence entries.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#TC17
[FATAL] Proper 'Codon Table' is not found in 'src' folder.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#T01
[FATAL] Proper 'Amino Table' is not found in 'src' folder.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#T02
[FATAL] Unable to execute Translation.	http://www.ddbj.nig.ac.jp/sub/validator-j.html#T03

Confirm => no errors



Edit Annotation is Confirmed. You can go to the Next step

Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

		source ? Select Qualifier					Other information
	length(bp)	/organism ? [Edit Column]	/mol_type ? [Edit Column]	/strain ? [Edit Column]	Location [Edit Column]	/product ? [Edit Column]	
ENT01 Edit	1472	Bacillus sp. HM1	genomic DNA	HM1	<1..>1472	16S ribosomal RNA	
ENT02 Edit	1313	Bacillus sp. HM2	genomic DNA	HM2	<1..>1313	16S ribosomal RNA	
ENT03 Edit	585	Bacillus sp. HM3	genomic DNA	HM3	<1..>585	16S ribosomal RNA	
ENT04 Edit	585	Bacillus sp. HM4	genomic DNA	HM4	<1..>585	16S ribosomal RNA	
ENT05 Edit	1466	Bacillus sp. HM5	genomic DNA	HM5	<1..>1466	16S ribosomal RNA	
ENT06 Edit	1477	Bacillus sp. HM6	genomic DNA	HM6	<1..>1477	16S ribosomal RNA	
ENT07 Edit	585	Bacillus sp. HM7	genomic DNA	HM7	<1..>585	16S ribosomal RNA	
		Bacillus sp. HM8	genomic DNA	HM8	<1..>1483	16S ribosomal RNA	
		Bacillus sp. HM9	genomic DNA	HM9	<1..>585	16S ribosomal RNA	
		Bacillus sp. HM10	genomic DNA	HM10			

```
1: COMMON SUBMITTER          contact   Takehide Kosuge
2:                  ab_name Kosuge,T.
3:                  ab_name Aosuge,T.
```

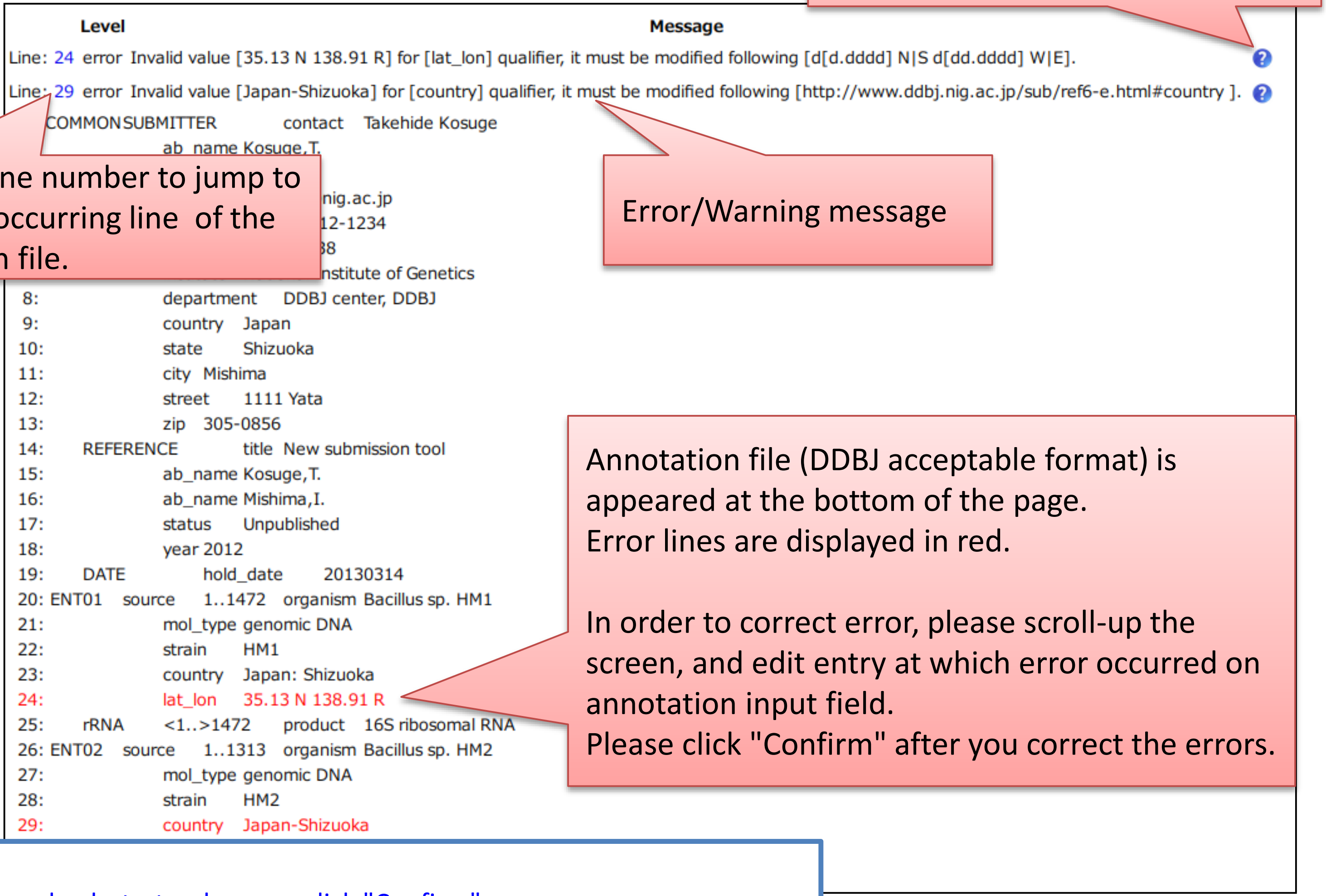
It means that you can click "Next" button.

Annotation file (DDBJ acceptable format) appears at the bottom of the page.

"Next" button is changed to be clickable and you can move to the next process.

Link:
[Annotation check starts when you click "Confirm"]
[Clicking "Confirm" on annotation screen] (when "other" is selected at "Template")
[final confirmation screen]

Error/warning messages are displayed beneath input area



Level	Message
Line: 24 error	Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E]. ?
Line: 29 error	Invalid value [Japan-Shizuoka] for [country] qualifier, it must be modified following [http://www.ddbj.nig.ac.jp/sub/ref6-e.html#country]. ?

```
     COMMONSUBMITTER          contact    Takehide Kosuge
                    ab_name Kosuge,T.
                                     nig.ac.jp
                                     12-1234
                                     38
                                     nstitute of Genetics
 8:                 department    DDBJ center, DDBJ
 9:                 country    Japan
10:                 state      Shizuoka
11:                 city   Mishima
12:                 street     1111 Yata
13:                 zip    305-0856
14:     REFERENCE          title   New submission tool
15:                 ab_name Kosuge,T.
16:                 ab_name Mishima,I.
17:                 status     Unpublished
18:                 year 2012
19:     DATE           hold_date      20130314
20: ENT01   source     1..1472   organism  Bacillus sp. HM1
21:                 mol_type genomic DNA
22:                 strain     HM1
23:                 country    Japan: Shizuoka
24:                 lat_lon    35.13 N 138.91 R
25:     rRNA        <1..>1472     product    16S ribosomal RNA
26: ENT02   source     1..1313   organism  Bacillus sp. HM2
27:                 mol_type genomic DNA
28:                 strain     HM2
29:                 country    Japan-Shizuoka
```

Click the icon to open a page that contains detailed description.

Click the line number to jump to the error-occurring line of the annotation file.

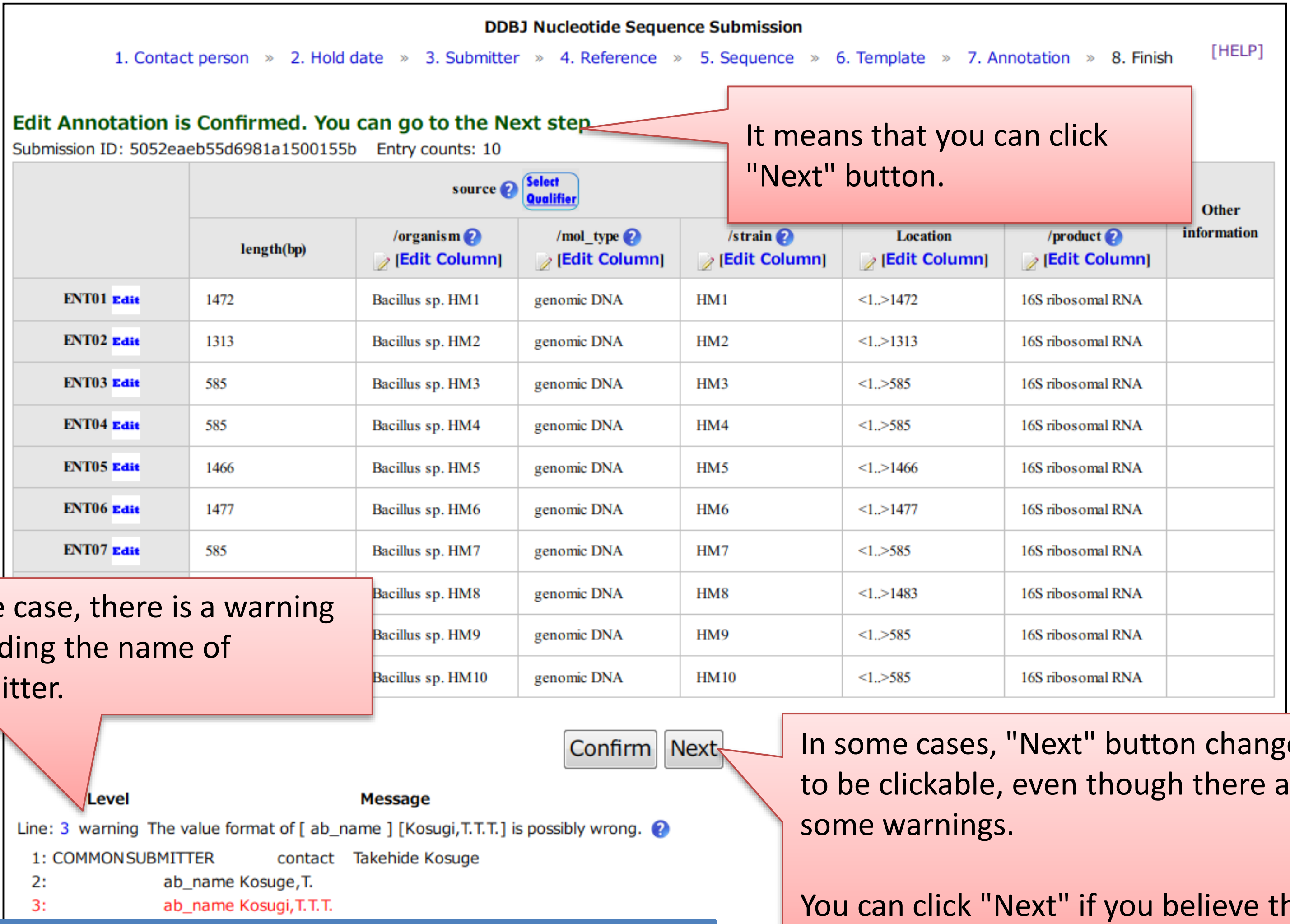
Error/Warning message

Annotation file (DDBJ acceptable format) is appeared at the bottom of the page.
Error lines are displayed in red.

In order to correct error, please scroll-up the screen, and edit entry at which error occurred on annotation input field.
Please click "Confirm" after you correct the errors.

Link:
[Annotation check starts when you click "Confirm"]
[Clicking "Confirm" on annotation screen] (when "other" is selected at "Template")

Confirm => You can proceed to the next step even though there are some warnings



Edit Annotation is Confirmed. You can go to the Next step

Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

	source						Other information
	length(bp)	/organism [Edit Column]	/mol_type [Edit Column]	/strain [Edit Column]	Location [Edit Column]	/product [Edit Column]	
ENT01 Edit	1472	Bacillus sp. HM1	genomic DNA	HM1	<1..>1472	16S ribosomal RNA	
ENT02 Edit	1313	Bacillus sp. HM2	genomic DNA	HM2	<1..>1313	16S ribosomal RNA	
ENT03 Edit	585	Bacillus sp. HM3	genomic DNA	HM3	<1..>585	16S ribosomal RNA	
ENT04 Edit	585	Bacillus sp. HM4	genomic DNA	HM4	<1..>585	16S ribosomal RNA	
ENT05 Edit	1466	Bacillus sp. HM5	genomic DNA	HM5	<1..>1466	16S ribosomal RNA	
ENT06 Edit	1477	Bacillus sp. HM6	genomic DNA	HM6	<1..>1477	16S ribosomal RNA	
ENT07 Edit	585	Bacillus sp. HM7	genomic DNA	HM7	<1..>585	16S ribosomal RNA	
		Bacillus sp. HM8	genomic DNA	HM8	<1..>1483	16S ribosomal RNA	
		Bacillus sp. HM9	genomic DNA	HM9	<1..>585	16S ribosomal RNA	
		Bacillus sp. HM10	genomic DNA	HM10	<1..>585	16S ribosomal RNA	

Level	Message
Line: 3 warning	The value format of [ab_name] [Kosugi,T.T.T.] is possibly wrong.

```
1: COMMONSUBMITTER          contact    Takehide Kosuge
2:                 ab_name Kosuge,T.
3:                 ab_name Kosugi,T.T.T.
```

It means that you can click "Next" button.

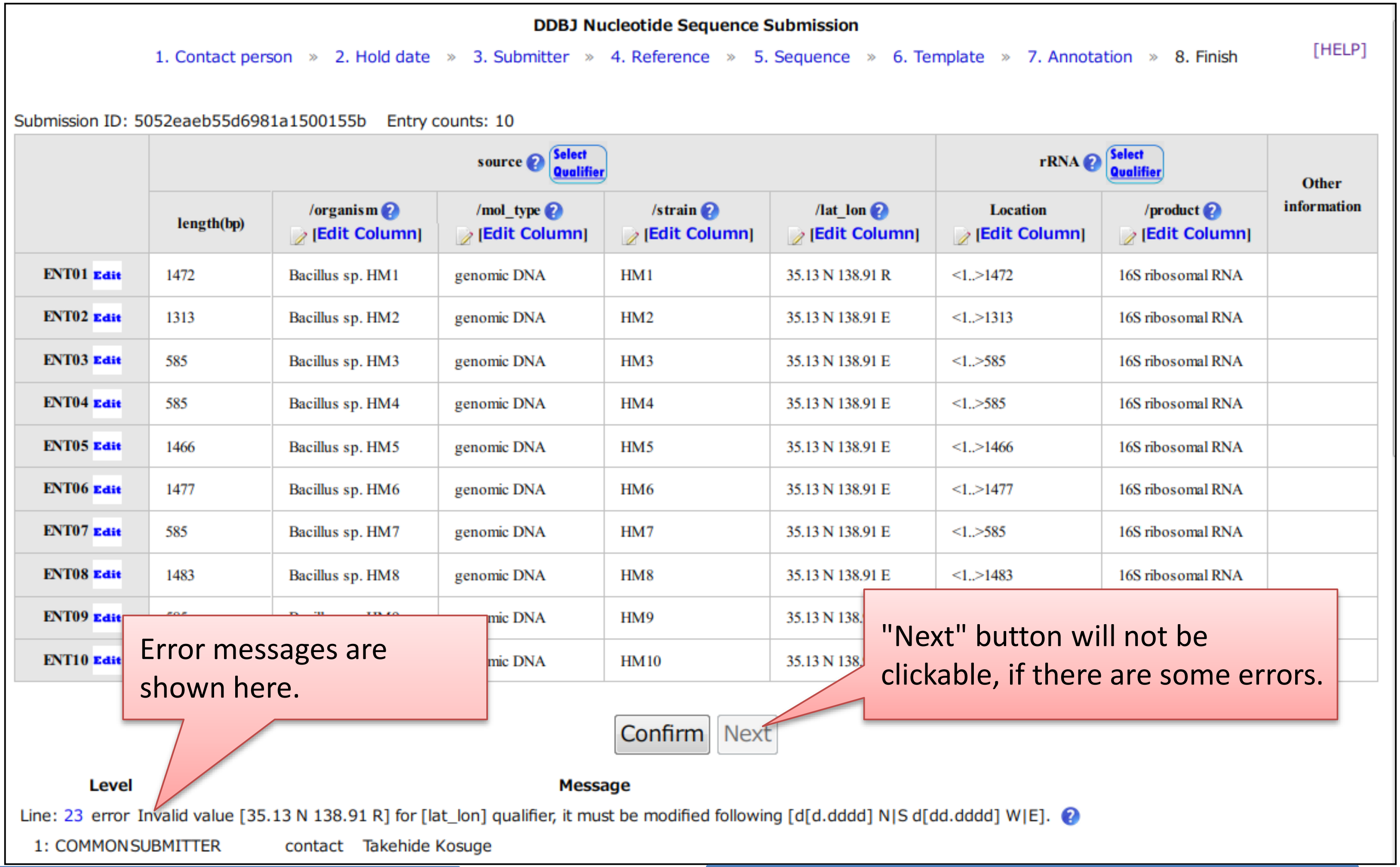
In the case, there is a warning regarding the name of submitter.

In some cases, "Next" button changes to be clickable, even though there are some warnings.

You can click "Next" if you believe that there is no problem in the input data.

Link:
[Annotation check starts when you click "Confirm"]
[Clicking "Confirm" on annotation screen] (when "other" is selected at "Template")
[final confirmation screen]

Confirm => There are any errors



DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

[HELP]

Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

	source					rRNA		Other information
	length(bp)	/organism [Edit Column]	/mol_type [Edit Column]	/strain [Edit Column]	/lat_lon [Edit Column]	Location [Edit Column]	/product [Edit Column]	
ENT01 Edit	1472	Bacillus sp. HM1	genomic DNA	HM1	35.13 N 138.91 R	<1..>1472	16S ribosomal RNA	
ENT02 Edit	1313	Bacillus sp. HM2	genomic DNA	HM2	35.13 N 138.91 E	<1..>1313	16S ribosomal RNA	
ENT03 Edit	585	Bacillus sp. HM3	genomic DNA	HM3	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT04 Edit	585	Bacillus sp. HM4	genomic DNA	HM4	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT05 Edit	1466	Bacillus sp. HM5	genomic DNA	HM5	35.13 N 138.91 E	<1..>1466	16S ribosomal RNA	
ENT06 Edit	1477	Bacillus sp. HM6	genomic DNA	HM6	35.13 N 138.91 E	<1..>1477	16S ribosomal RNA	
ENT07 Edit	585	Bacillus sp. HM7	genomic DNA	HM7	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT08 Edit	1483	Bacillus sp. HM8	genomic DNA	HM8	35.13 N 138.91 E	<1..>1483	16S ribosomal RNA	
ENT09 Edit			mic DNA	HM9	35.13 N 138.			
ENT10 Edit			mic DNA	HM10	35.13 N 138.			

Level	Message
Line: 23 error	Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E].

1: COMMONSUBMITTER contact Takehide Kosuge

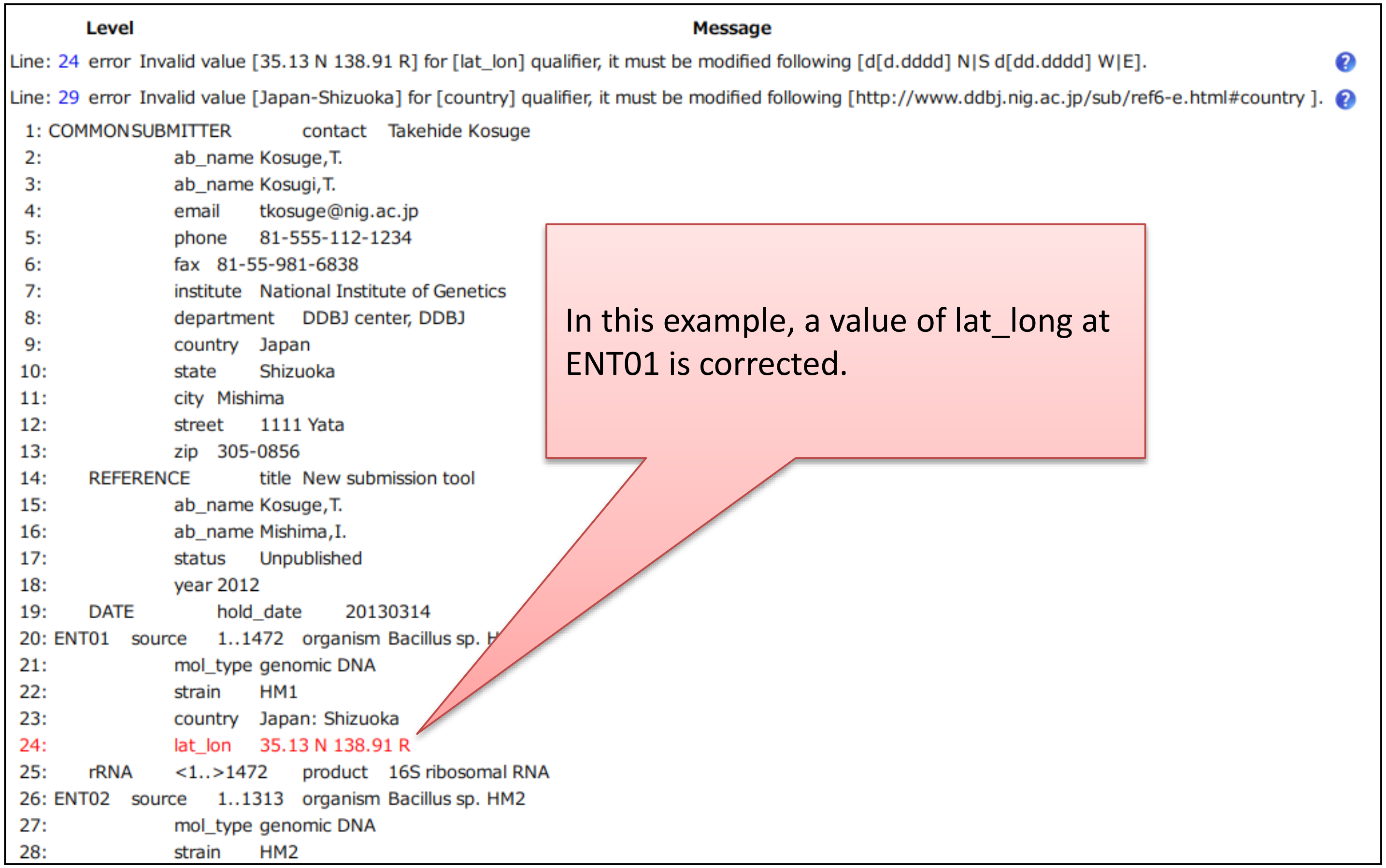
Error messages are shown here.

"Next" button will not be clickable, if there are some errors.

Link:
[Errors/Warnings occurred in entry]()
[Errors/Warnings occurred in Submitter]()
[Errors/Warnings occurred in Reference]()

[Annotation check starts when you click "Confirm"]()
[Clicking "Confirm" on annotation screen]() (when "other" is selected at "Template")

Errors/Warnings occurred in entry



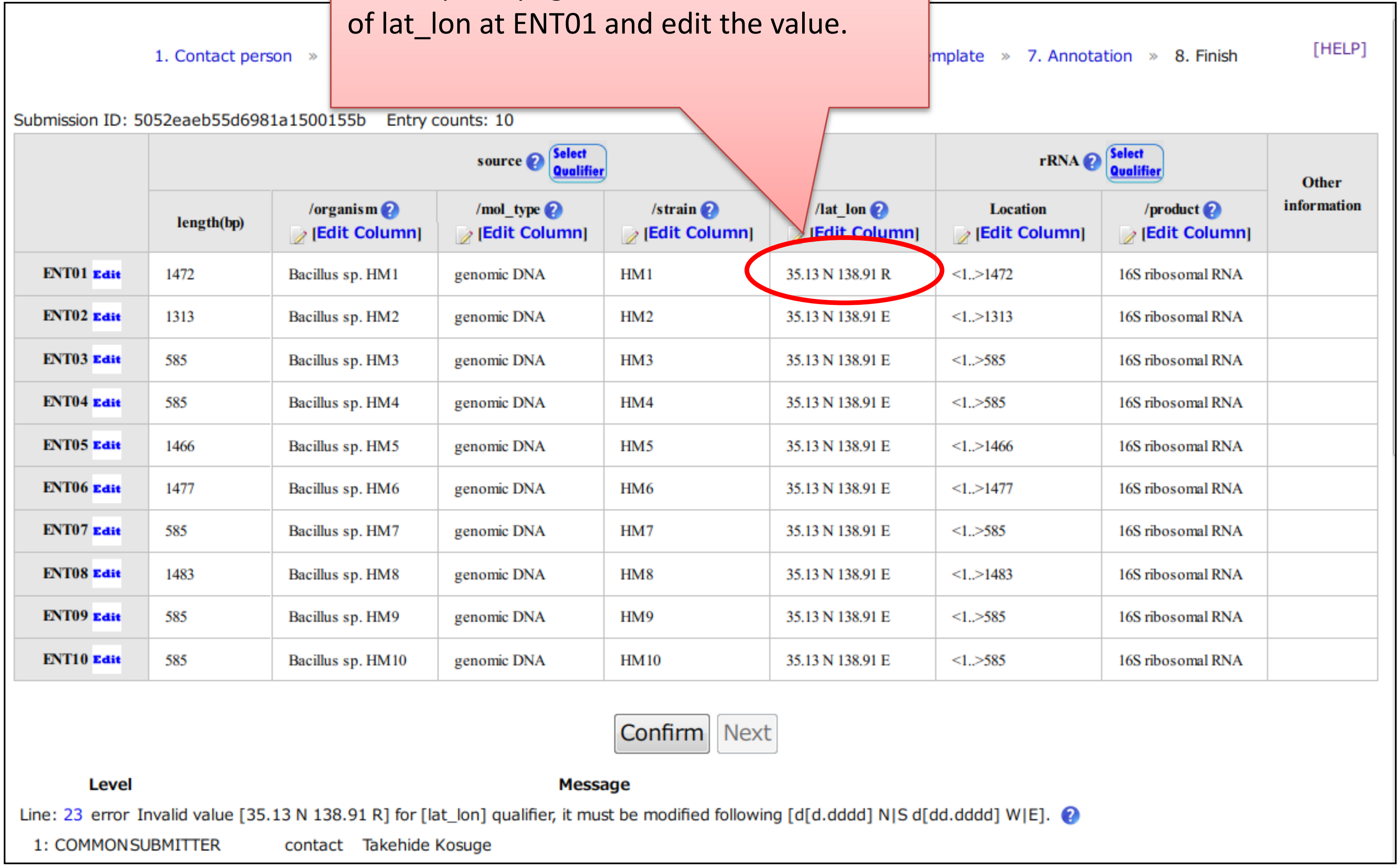
Level	Message
Line: 24 error	Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E].
Line: 29 error	Invalid value [Japan-Shizuoka] for [country] qualifier, it must be modified following [http://www.ddbj.nig.ac.jp/sub/ref6-e.html#country].

```
 1: COMMON SUBMITTER          contact    Takehide Kosuge
 2:                  ab_name Kosuge,T.
 3:                  ab_name Kosugi,T.
 4:                  email      tkosuge@nig.ac.jp
 5:                  phone      81-555-112-1234
 6:                  fax   81-55-981-6838
 7:                  institute   National Institute of Genetics
 8:                  department     DDBJ center, DDBJ
 9:                  country    Japan
10:                  state       Shizuoka
11:                  city   Mishima
12:                  street      1111 Yata
13:                  zip   305-0856
14:       REFERENCE             title  New submission tool
15:                  ab_name Kosuge,T.
16:                  ab_name Mishima,I.
17:                  status      Unpublished
18:                  year 2012
19:       DATE             hold_date       20130314
20: ENT01   source     1..1472   organism  Bacillus sp. H
21:                  mol_type genomic DNA
22:                  strain      HM1
23:                  country    Japan: Shizuoka
24:                  lat_lon     35.13 N 138.91 R
25:       rRNA       <1..>1472      product    16S ribosomal RNA
26: ENT02   source     1..1313   organism  Bacillus sp. HM2
27:                  mol_type genomic DNA
28:                  strain      HM2
```

In this example, a value of lat_long at ENT01 is corrected.

Link:
[Annotation check starts when you click "Confirm"]
[Clicking "Confirm" on annotation screen] (when "other" is selected at "Template")
[Confirm => There are any errors]

Scroll up the page and double click the cell of lat_lon at ENT01 and edit the value.



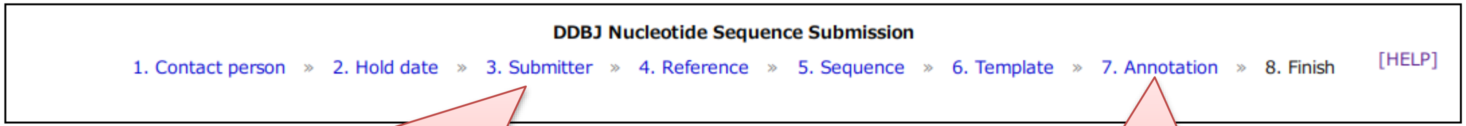
Submission ID: 5052eaeb55d6981a1500155b Entry counts: 10

	source					rRNA		Other information
	length(bp)	/organism	/mol_type	/strain	/lat_lon	Location	/product	
ENT01	1472	Bacillus sp. HM1	genomic DNA	HM1	35.13 N 138.91 R	<1..>1472	16S ribosomal RNA	
ENT02	1313	Bacillus sp. HM2	genomic DNA	HM2	35.13 N 138.91 E	<1..>1313	16S ribosomal RNA	
ENT03	585	Bacillus sp. HM3	genomic DNA	HM3	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT04	585	Bacillus sp. HM4	genomic DNA	HM4	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT05	1466	Bacillus sp. HM5	genomic DNA	HM5	35.13 N 138.91 E	<1..>1466	16S ribosomal RNA	
ENT06	1477	Bacillus sp. HM6	genomic DNA	HM6	35.13 N 138.91 E	<1..>1477	16S ribosomal RNA	
ENT07	585	Bacillus sp. HM7	genomic DNA	HM7	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT08	1483	Bacillus sp. HM8	genomic DNA	HM8	35.13 N 138.91 E	<1..>1483	16S ribosomal RNA	
ENT09	585	Bacillus sp. HM9	genomic DNA	HM9	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	
ENT10	585	Bacillus sp. HM10	genomic DNA	HM10	35.13 N 138.91 E	<1..>585	16S ribosomal RNA	

Level	Message
Line: 23 error	Invalid value [35.13 N 138.91 R] for [lat_lon] qualifier, it must be modified following [d[d.dddd] N|S d[dd.dddd] W|E].

1: COMMON SUBMITTER contact Takehide Kosuge

Errors/Warnings occurred in Submitter



Click "3.Submitter" at progress bar. Please correct submitter at "3.Reference page" and click "Next".

You can return by clicking "7.Annotation".

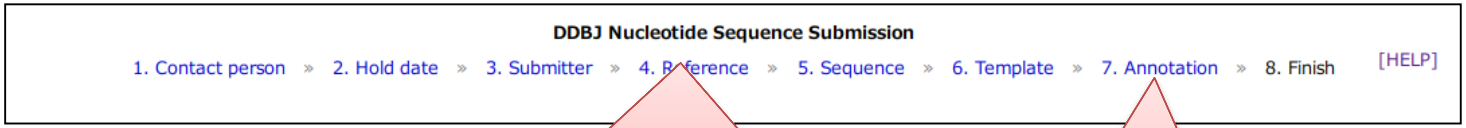
Click "3.Submitter" at progress bar.

You can move to "3.Submitter" page. Please correct submitter and click "Next" at the bottom of the page.

Please click "7.Annotation" at progress bar to return to annotation screen.

Link:
Progress bar
Annotation check starts when you click "Confirm"
Clicking "Confirm" on annotation screen (when "other" is selected at "Template")
"Upload & Confirm" => Error/Warning occurred
Confirm => There are any errors

Errors/Warnings occurred in Reference



Click "4.Reference" at progress bar.
Please correct reference at
"4.Reference page" and click "Next".

You can return by clicking
"7.Annotation".

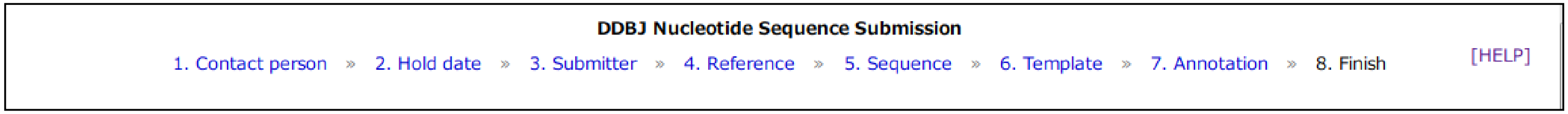
Click "4.Reference" at progress bar.

You can move to "4.Reference" page. Please correct reference and click "Next" at the bottom of the page.

Please click "7.Annotation" at progress bar to return to annotation screen.

Link:
Progress bar
Annotation check starts when you click "Confirm"
Clicking "Confirm" on annotation screen (when "other" is selected at "Template")
"Upload & Confirm" => Error/Warning occurred
Confirm => There are any errors

Progress bar



DDBJ Nucleotide Sequence Submission

1. Contact person » 2. Hold date » 3. Submitter » 4. Reference » 5. Sequence » 6. Template » 7. Annotation » 8. Finish

[HELP]

- ✓ You can go back to previous page by clicking each page name. Please click "Next" at the bottom of each page if you correct the value at the previous page.
- ✓ The annotation is disappeared if you change nucleotide sequence at "5.Sequence" page.
- ✓ The annotation is also disappeared if you change kind of template at "6.Template" page.

Link:
2.Hold date
Errors/Warnings occurred in Submitter
Errors/Warnings occurred in Reference
Annotation check starts when you click "Confirm"
Clicking "Confirm" on annotation screen (when "other" is selected at "Template")
"Upload & Confirm" => Error/Warning occurred
Confirm => There are any errors