How to use
EPPO-Q-bank?

https://qbank.eppo.int/

- Guidelines for users -

Contents

This document includes guidance for the users of the EPPO Q-bank database. Guidance on Sanger sequencing, consensus preparation and data analysis can be found in EPPO PM 7/129.

Video tutorials of barcoding training sessions produced in the framework of the PRACTIBAR a Euphresco project (Giovani et al., 2020) are available on YouTube (https://www.youtube.com/playlist?list=PLoVf4Pt04Db53pUVTI8qwcWkWgUgg46gm).

Presentation of the EPPO-Q-bank databases

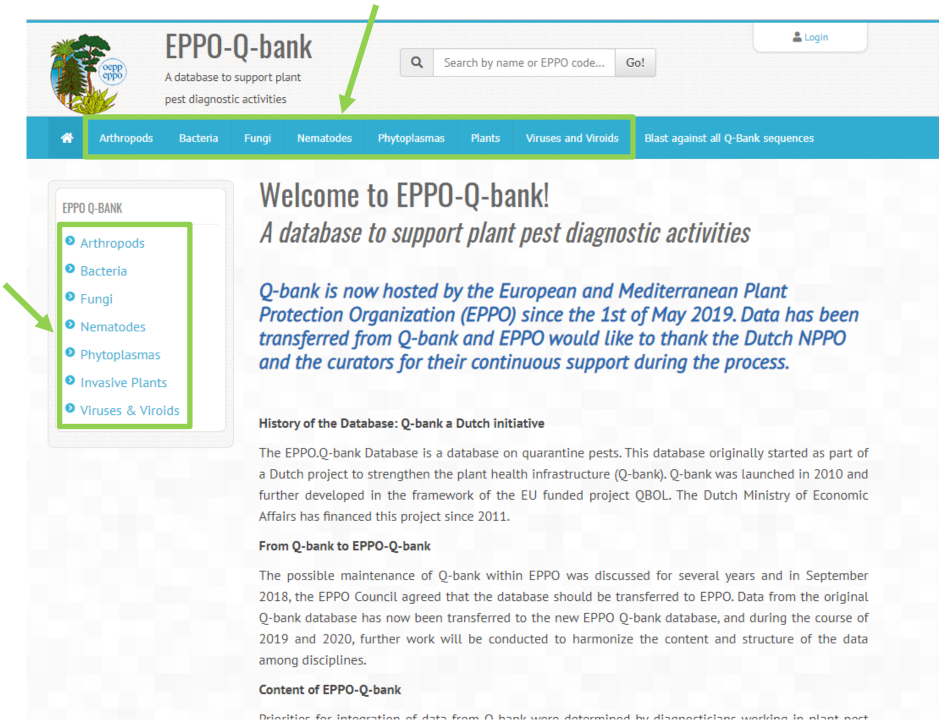
EPPO-Q-bank is composed of 7 specific databases, one for each of the following disciplines:

- Arthropods
- Bacteria
- Fungi
- Nematodes
- Phytoplasmas
- Invasive Plants
- Viruses & Viroids

The specific databases can be accessed from the **EPPO-Q-bank home page**.

Access to the database specific to a discipline

Access to the database specific to a discipline



Welcome to EPPO-Q-bank!

A database to support plant pest diagnostic activities

Q-bank is now hosted by the European and Mediterranean Plant Protection Organization (EPPO) since the 1st of May 2019. Data has been transferred from Q-bank and EPPO would like to thank the Dutch NPPO and the curators for their continuous support during the process.

History of the Database: Q-bank a Dutch initiative

The EPPO.Q-bank Database is a database on quarantine pests. This database originally started as part of a Dutch project to strengthen the plant health infrastructure (Q-bank). Q-bank was launched in 2010 and further developed in the framework of the EU funded project QBOL. The Dutch Ministry of Economic Affairs has financed this project since 2011.

From Q-bank to EPPO-Q-bank

The possible maintenance of Q-bank within EPPO was discussed for several years and in September 2018, the EPPO Council agreed that the database should be transferred to EPPO. Data from the original Q-bank database has now been transferred to the new EPPO Q-bank database, and during the course of 2019 and 2020, further work will be conducted to harmonize the content and structure of the data among disciplines.

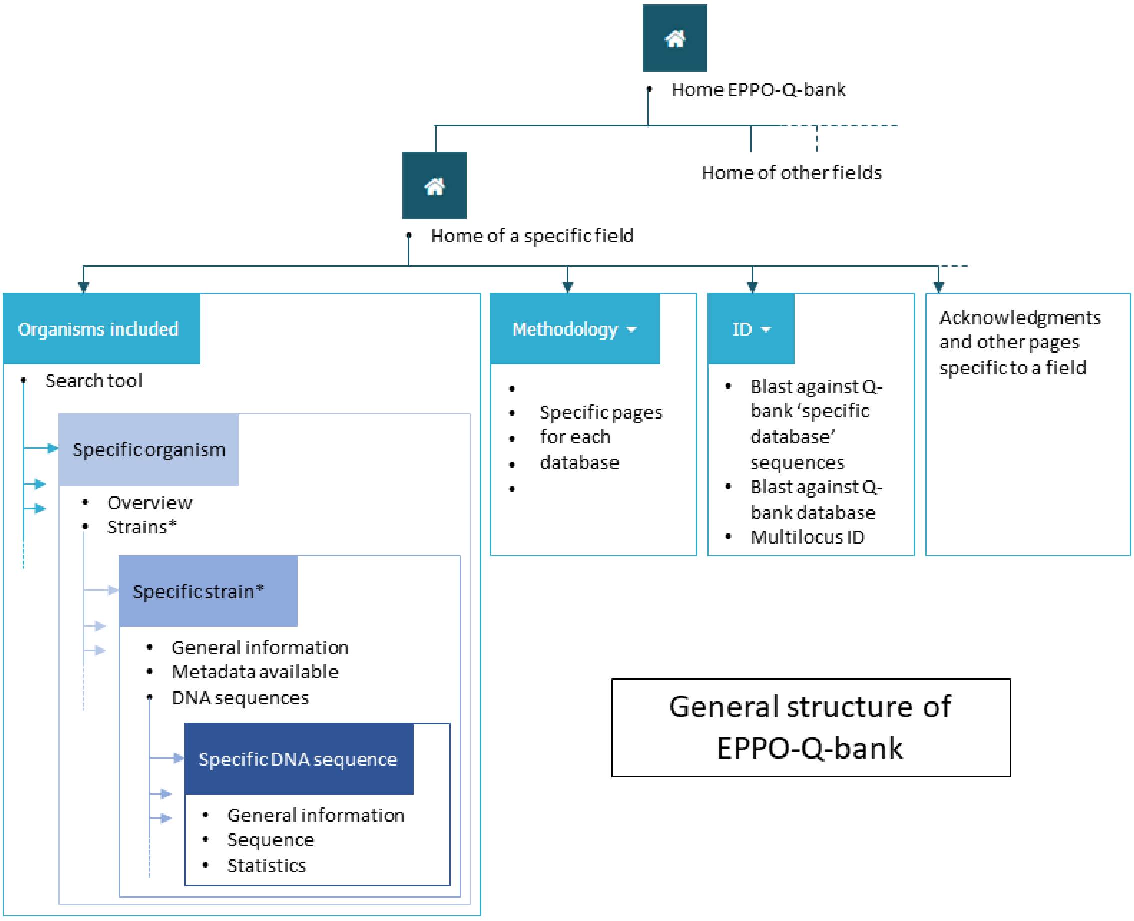
Content of EPPO-Q-bank

Priorities for integration of data from Q bank were determined by diagnosticians working in plant pest

For each discipline, the website is built similarly and is composed of the following pages:

- A home page which presents the specific discipline and information available for that discipline.

- One page listing the organisms included in EPPO-Q-bank for that specific discipline. Each organism (species and specimen/strain/isolate) has a specific page with relevant information including DNA sequences
- One or more pages regarding the methodology that should be used to identify a specimen/strain/isolate.
- Several pages to blast specific sequences to EPPO-Q-bank database
- And, possibly, other specific pages.



General structure of EPPO-Q-bank

What can I do as a user of the EPPO-Q-bank database?

As a user of the EPPO-Q-bank database, you can:

- Search for specimens/strains/isolates and see in which collection they are available (however this does not mean that they can be provided)
- Access sequences on each specimen/strain/isolate page (once logged in)
- Check barcoding protocols and other pest identification tests
- Blast (barcode) sequences.

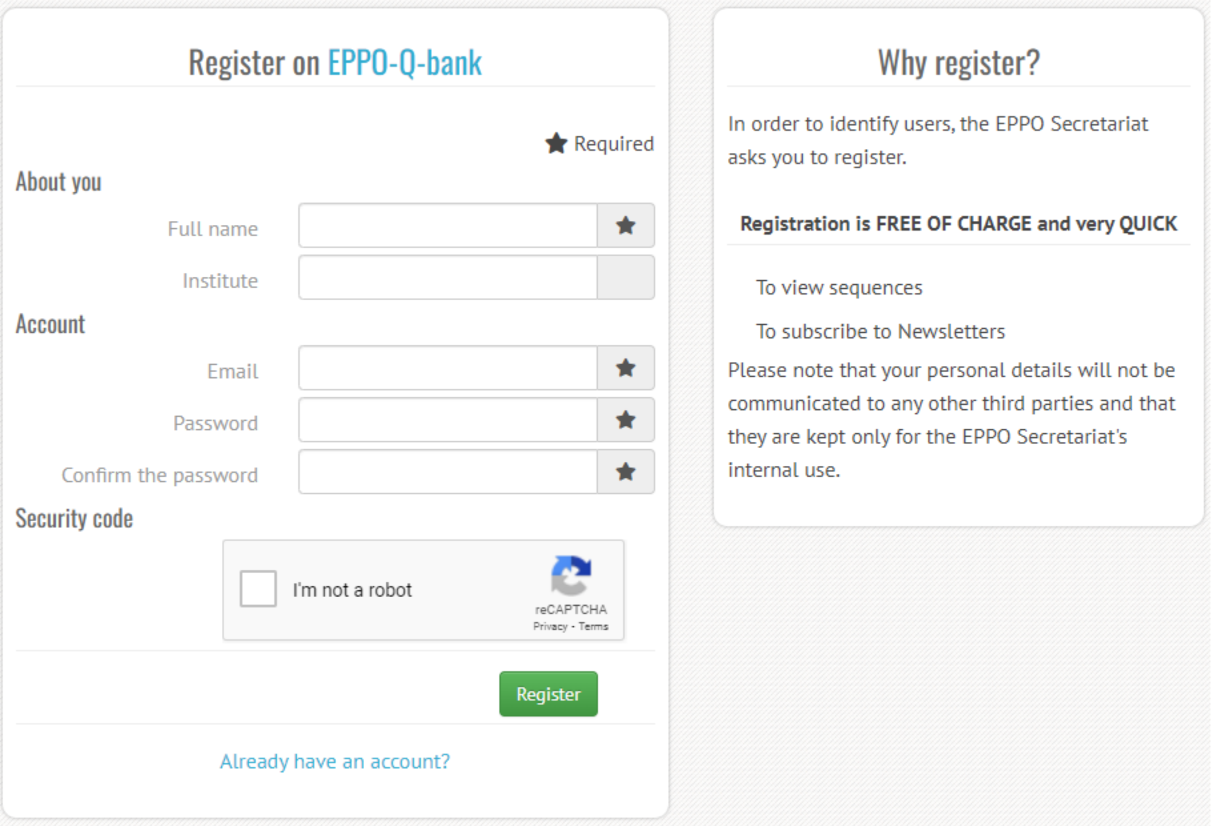
Information is provided per discipline (arthropods, bacteria, fungi, nematodes, phyto-plasmas, viruses & viroids, and invasive plants). Data of the database is accessible through the website only.

You can find more information on EPPO-Q-bank in our factsheet (https://qbank.eppo.int/data/files/general/factsheet_EPPO-Q-bank.pdf)

General information about your account

How to create a user account?

In order to create an account, click on register and fill in the required information.



Register on EPPO-Q-bank

★ Required

About you

Full name ★

Institute

Account

Email ★

Password ★

Confirm the password ★

Security code

☐ I'm not a robot

Why register?

In order to identify users, the EPPO Secretariat asks you to register.

Registration is FREE OF CHARGE and very QUICK

To view sequences

To subscribe to Newsletters

Please note that your personal details will not be communicated to any other third parties and that they are kept only for the EPPO Secretariat's internal use.

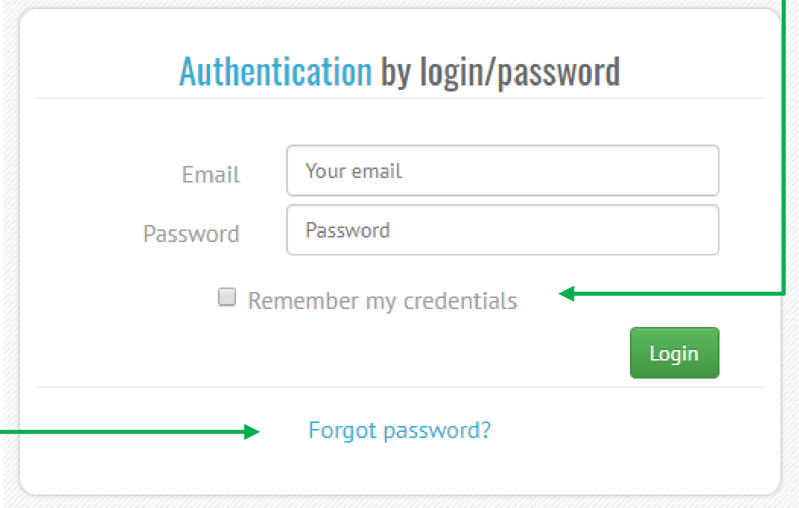
Registration is mandatory to view sequences in the database.

How to log in (already registered user)?

You are registered on EPPO-Q-bank and want to access your user account:

- click on the 'login' button on the top right of the Database home screen

- enter your email and password (if you wish, tick the box 'Remember my credentials' to be recognized automatically at your next visit).


Authentication by login/password

Email: Your email

Password: Password

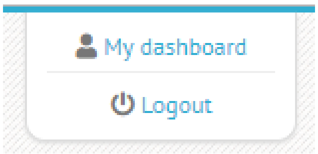
☐ Remember my credentials

If you have lost your password, click on 'Forgot password?' to receive an email with a link allowing you to reset your password.

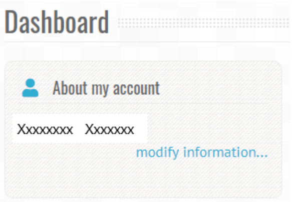
How to manage your account information (including password)

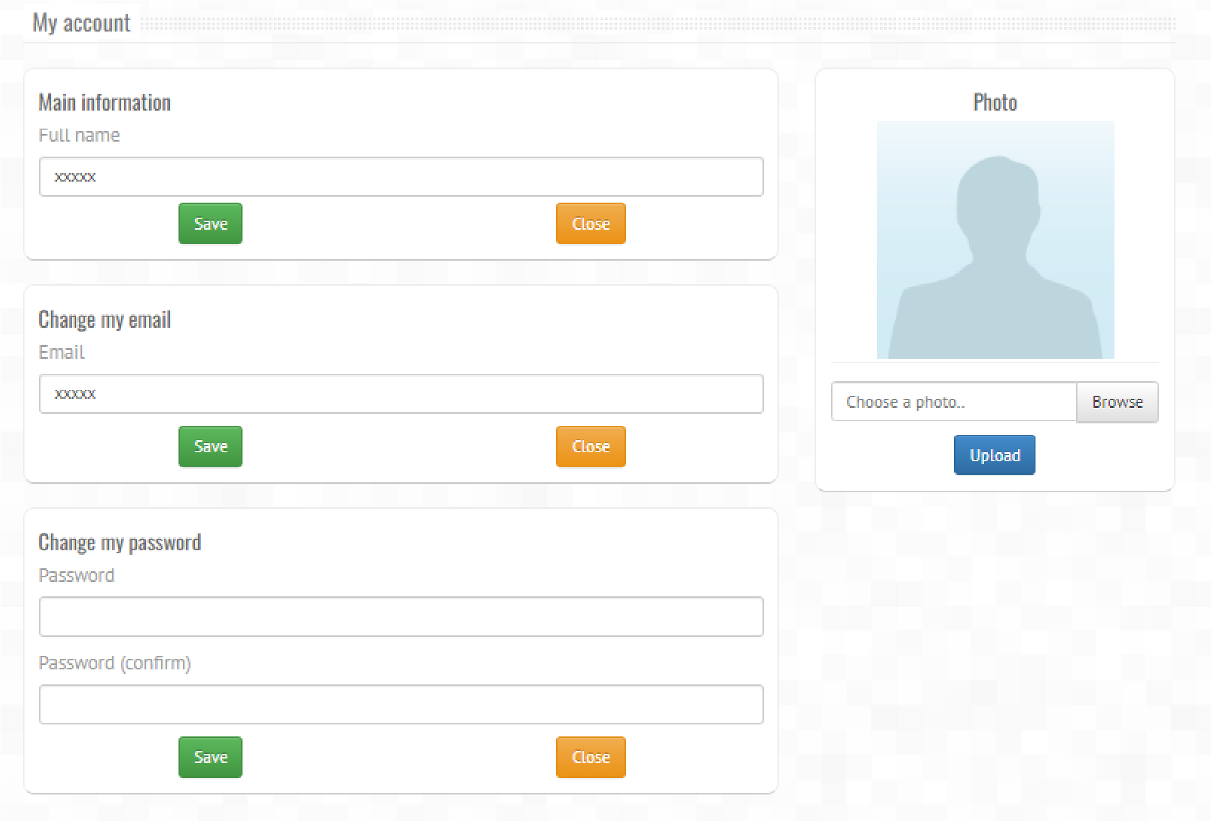
To change your account information (name, e-mail, photo and password):

- click on the 'My dashboard' button on the top right of the Database home screen



- Click on 'modify information…' in the About my account section of the dashboard





My account

Main information

Full name: xxxxx

Change my email

Email: xxxxx

Change my password

Password:

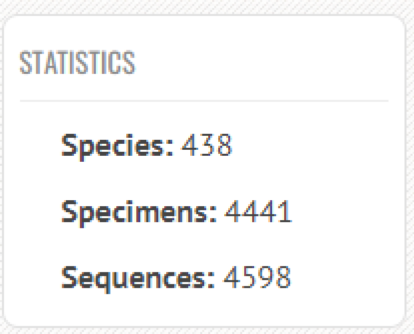
Password (confirm):

You can modify your name, your email, and your password. You can also add a picture.

Searching the database

Statistics

In the Home page of each discipline, statistics regarding the number of species, strains/specimens/isolates and sequences appears.



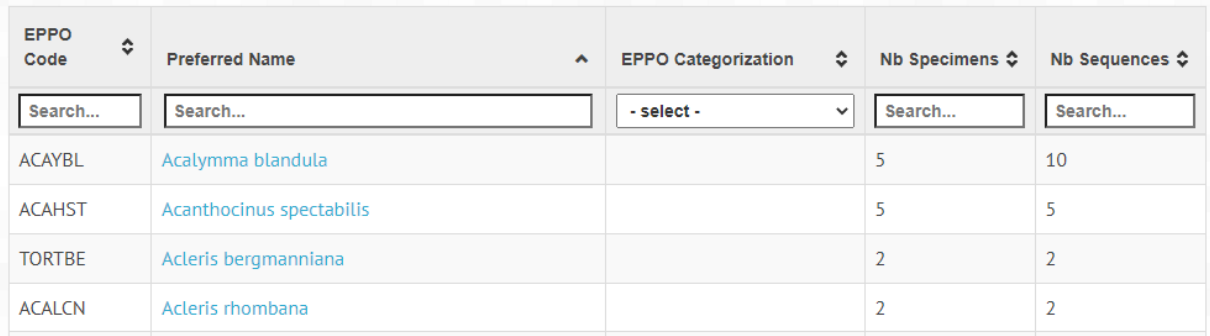
STATISTICS

Species: 438

Specimens: 4441

Sequences: 4598

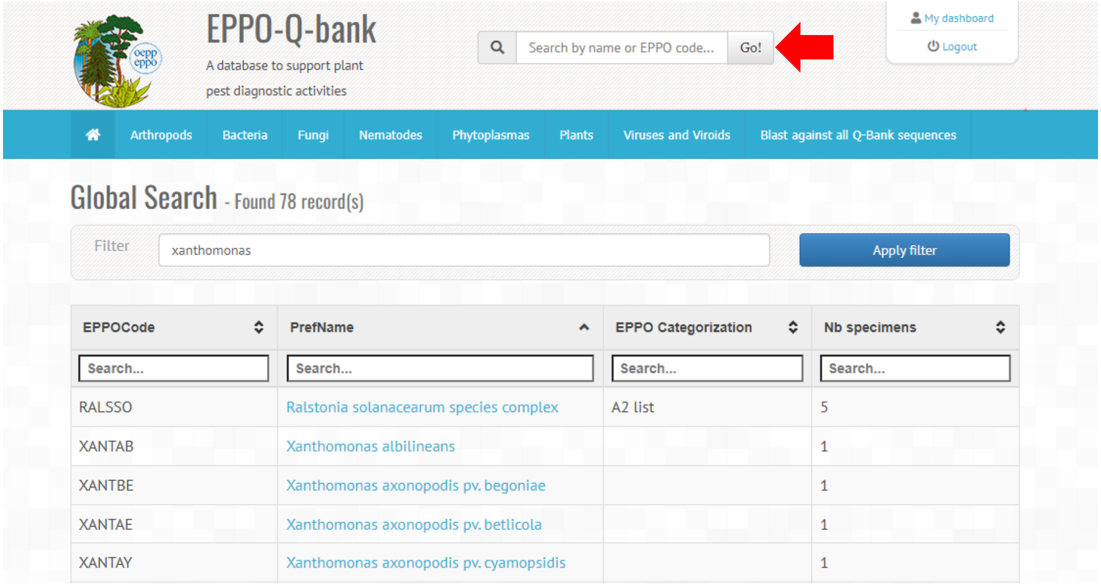
In the Organisms included page of each discipline, statistics regarding the number of strains/specimens/isolates and sequences for each species appears.



EPPO Code	Preferred Name	EPPO Categorization	Nb Specimens	Nb Sequences
Search...	Search...	- select -	Search...	Search...
ACAYBL	Acalymma blandula		5	10
ACAHST	Acanthocinus spectabilis		5	5
TORTBE	Acleris bergmanniana		2	2
ACALCN	Acleris rhombana		2	2

How to search for a specific species?

Global search: Search by name or EPPO code in the global search tool (red arrow).



Global Search - Found 78 record(s)

Filter: xanthomonas

EPPOCode	PrefName	EPPO Categorization	Nb specimens
Search...	Search...	Search...	Search...
RALSSO	Ralstonia solanacearum species complex	A2 list	5
XANTAB	Xanthomonas albilineans		1
XANTBE	Xanthomonas axonopodis pv. begoniae		1
XANTAE	Xanthomonas axonopodis pv. betlicola		1
XANTAY	Xanthomonas axonopodis pv. cyamopsidis		1

Search by discipline: for each discipline, go to the Organisms included tab.

1 – search for a species using scientific name, common name or EPPO Code; reduce the number of species appearing in the table

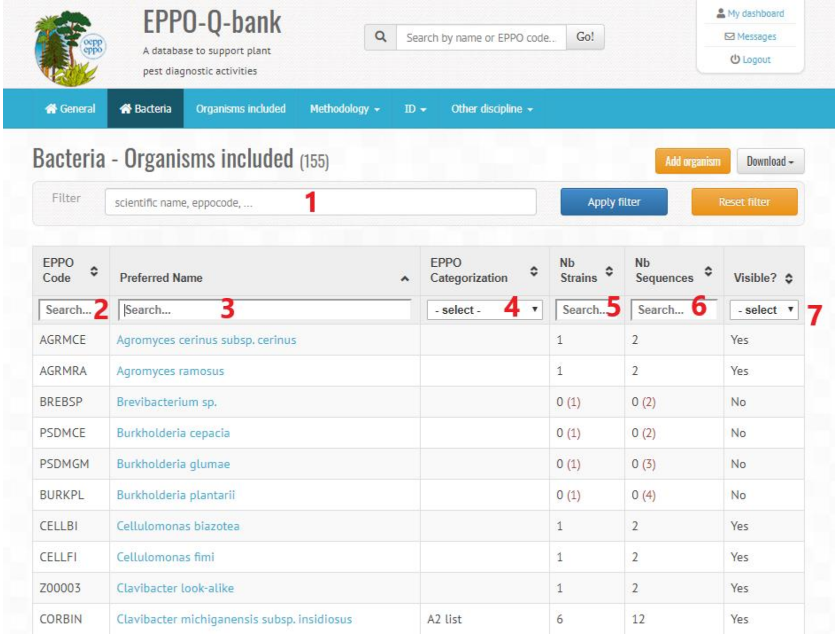
2 – search the table using EPPO Codes

3 – search the table using preferred scientific name

4 – search the table based on EPPO categorization

5 & 6 – number of visible strains and sequences (number of strains and sequences invisible)

7 – search for a species based on whether they are visible or not in EPPO-Q-bank

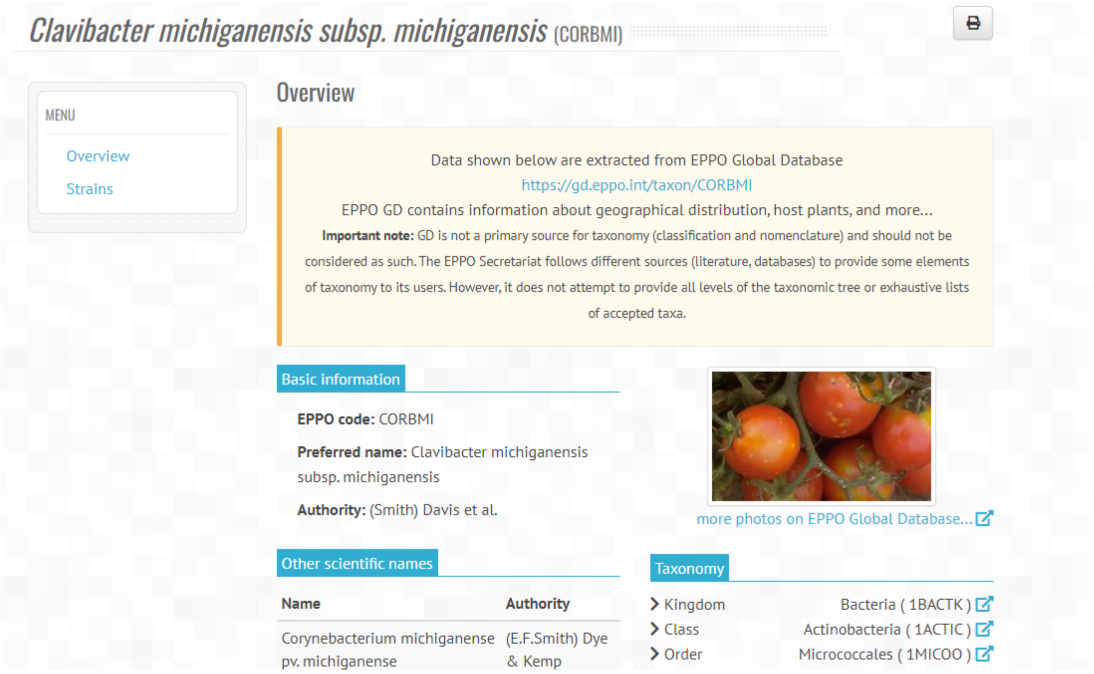


Bacteria - Organisms included (155)

EPPO Code	Preferred Name	EPPO Categorization	Nb Strains	Nb Sequences	Visible?
Search...	Search...	- select -	Search...	Search...	- select
AGRMCE	Agromyces cerinus subsp. cerinus		1	2	Yes
AGRMRA	Agromyces ramosus		1	2	Yes
BREBSP	Brevibacterium sp.		0 (1)	0 (2)	No
PSDMCE	Burkholderia cepacia		0 (1)	0 (2)	No
PSDMGM	Burkholderia glumae		0 (1)	0 (3)	No
BURKPL	Burkholderia plantarii		0 (1)	0 (4)	No
CELLBI	Cellulomonas biazotea		1	2	Yes
CELLFI	Cellulomonas fimi		1	2	Yes
Z00003	Clavibacter look-alike		1	2	Yes
CORBIN	Clavibacter michiganensis subsp. insidiosus	A2 list	6	12	Yes

Species pages

For each species in the database, an overview of the species is provided and contains information from EPPO Global database and when available, relevant PM 7 Diagnostic protocols.



Clavibacter michiganensis subsp. michiganensis (CORBMI)

Overview

Data shown below are extracted from EPPO Global Database
https://gd.eppo.int/taxon/CORBMI
EPPO GD contains information about geographical distribution, host plants, and more...
Important note: GD is not a primary source for taxonomy (classification and nomenclature) and should not be considered as such. The EPPO Secretariat follows different sources (literature, databases) to provide some elements of taxonomy to its users. However, it does not attempt to provide all levels of the taxonomic tree or exhaustive lists of accepted taxa.

EPPO code: CORBMI

Preferred name: Clavibacter michiganensis subsp. michiganensis

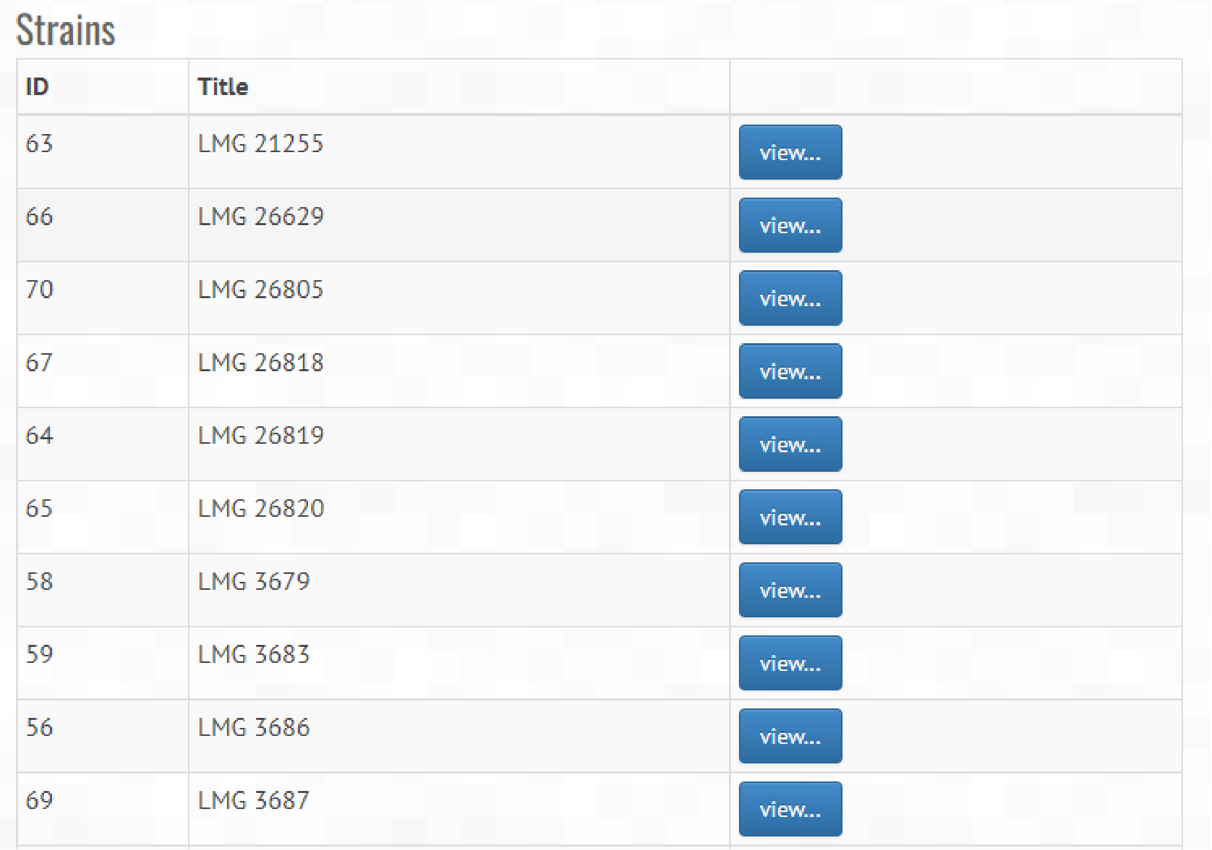
Authority: (Smith) Davis et al.

more photos on EPPO Global Database...

Name	Authority
Corynebacterium michiganense pv. michiganense	(E.F.Smith) Dye & Kemp

Kingdom	Bacteria (1BACTK)
Class	Actinobacteria (1ACTIC)
Order	Micrococcales (1MICOO)

The list of specimens/strains/isolates for which sequences are available is listed in the **Strains** page.



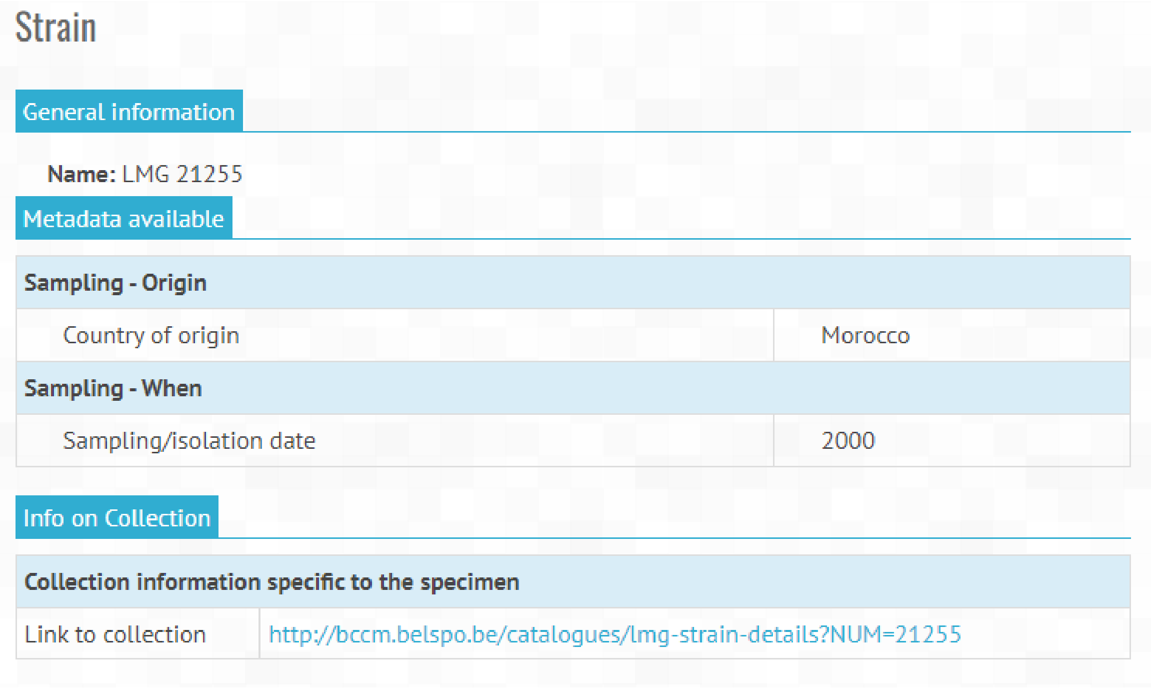
Strains

ID	Title	
63	LMG 21255	view...
66	LMG 26629	view...
70	LMG 26805	view...
67	LMG 26818	view...
64	LMG 26819	view...
65	LMG 26820	view...
58	LMG 3679	view...
59	LMG 3683	view...
56	LMG 3686	view...
69	LMG 3687	view...

More information can be found for each specimen/strain/isolate by clicking on the button **view…**

Specimen/strain/isolate pages

For each specimen/strain/isolate, several metadata are available. The exact list of metadata depends on the disciplines and on the specimen. Links to collections where the specimen/strain/isolate can be found are usually available.



Strain

General information

Name: LMG 21255

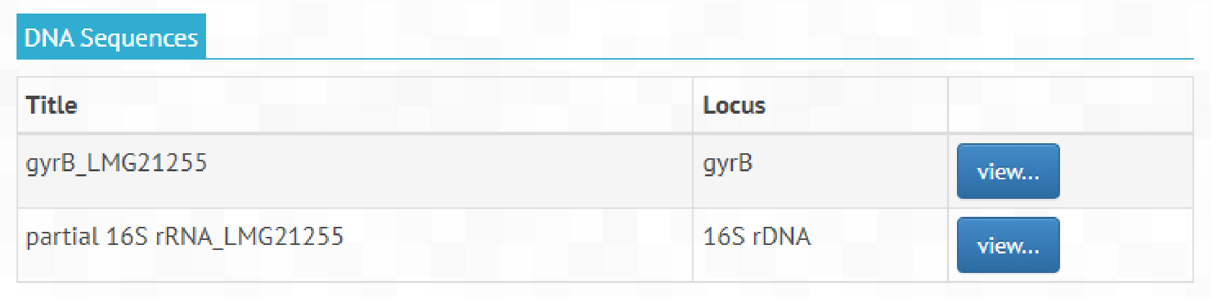
Metadata available

Sampling - Origin	
Country of origin	Morocco
Sampling - When	
Sampling/isolation date	2000

Info on Collection

Collection information specific to the specimen	
Link to collection	http://bccm.belspo.be/catalogues/lmg-strain-details?NUM=21255

DNA sequences available for the specimen also appear:



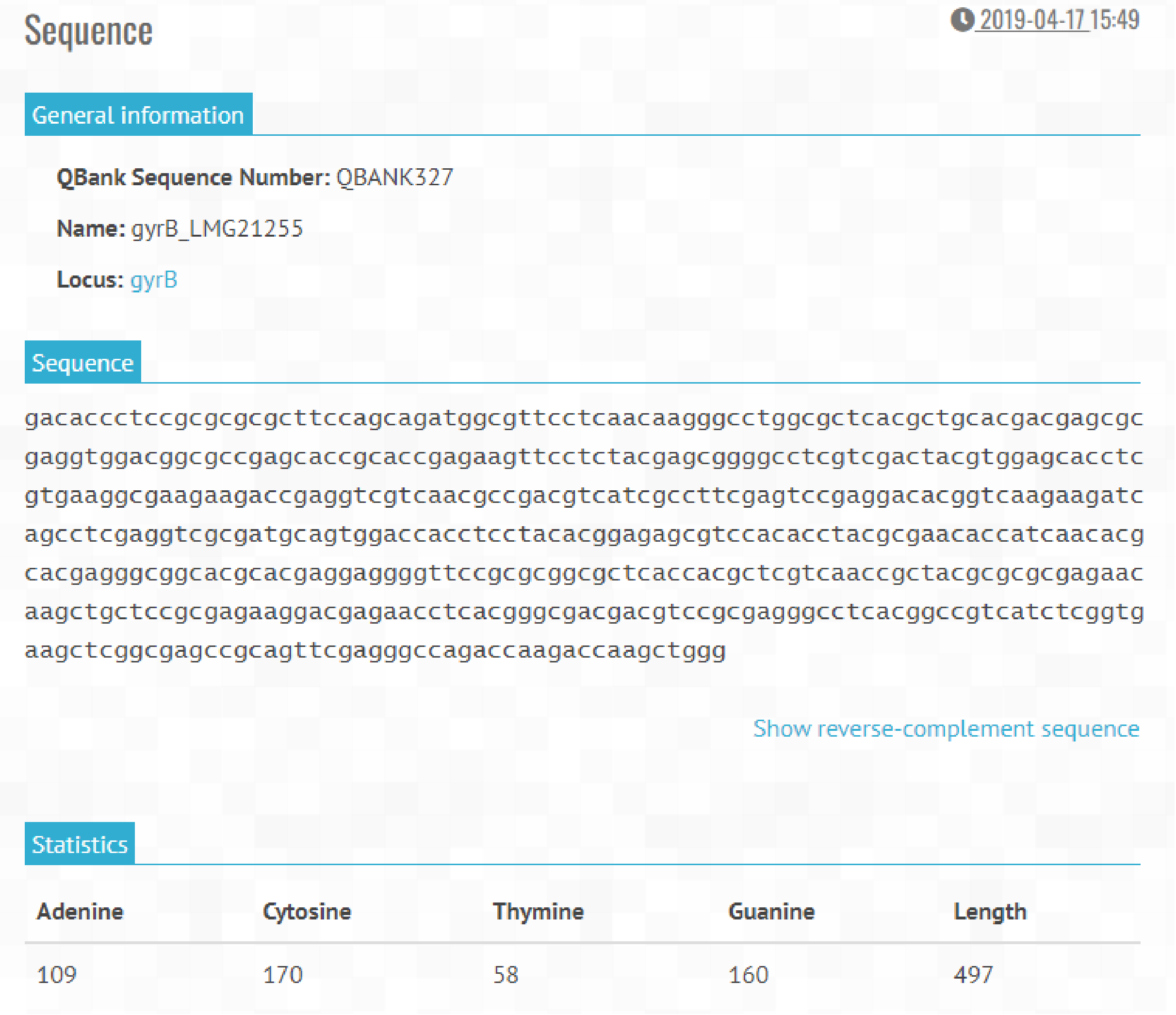
DNA Sequences

Title	Locus	
gyrB_LMG21255	gyrB	view...
partial 16S rRNA_LMG21255	16S rDNA	view...

To view the sequence, logged on and click on **view…**

Sequence pages

Sequences can only be viewed if you are logged in.



Sequence

2019-04-17 15:49

General information

QBank Sequence Number: QBANK327

Name: gyrB_LMG21255

Locus: gyrB

Sequence

```
gacaccctccgcgcgcgcttccagcagatggcgttcctcaacaagggcctggcgctcacgctgcacgacgagcgc
gaggtggacggcgccgagcaccgcaccgagaagttcctctacgagcggggcctcgtcgactacgtggagcacctc
gtgaaggcgaagaagaccgaggtcgtcaacgccgacgtcatcgccttcgagtccgaggacacggtcaagaagatc
agcctcgaggtcgcgatgcagtggaccacctcctacacggagagcgtccacacctacgcgaacaccatcaacacg
cacgagggcggcacgcacgaggaggggttccgcgcggcgctcaccacgctcgtcaaccgctacgcgcgcgagaac
aagctgctccgcgagaaggacgagaacctcacgggcgacgacgtccgcgagggcctcacggccgtcatctcggtg
aagctcggcgagccgcagttcgagggccagaccaagaccaagctggg
```

Show reverse-complement sequence

Statistics

Adenine	Cytosine	Thymine	Guanine	Length
109	170	58	160	497

Methodology

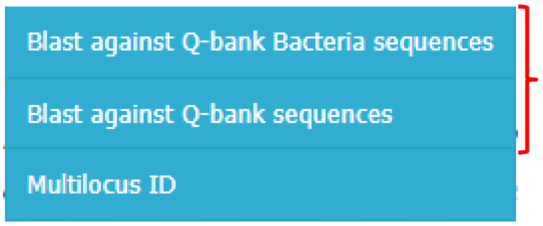
The methodology section lists molecular tests published in PM 7/129. Other tests considered as useful by curators of a discipline may also be listed.

Molecular decision schemes are provided.

Tools

2 blast tools are available:

- Blast
- Multilocus blast



BLAST (+ Tree visualisation)

Multilocus BLAST

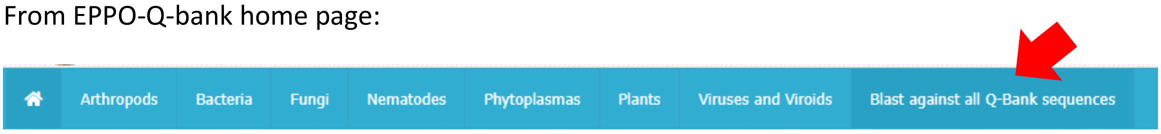
Blast

The Blast tool is available from the menu of the home page of EPPO-Q-bank and from the menu of the discipline specific databases.

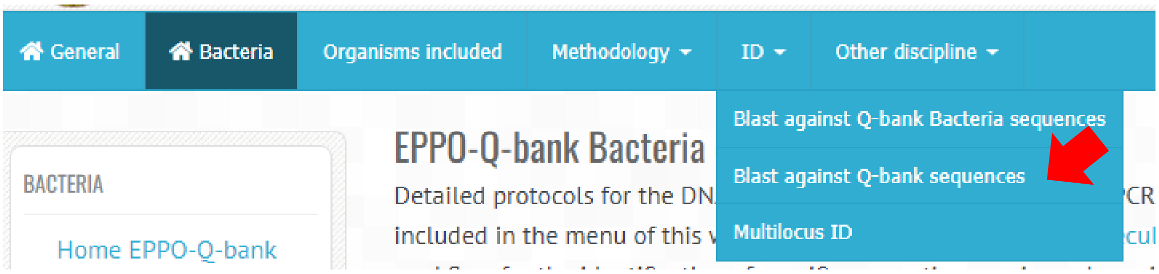
You can blast against all EPPO-Q-bank sequences or just against a subset of sequences corresponding to one discipline

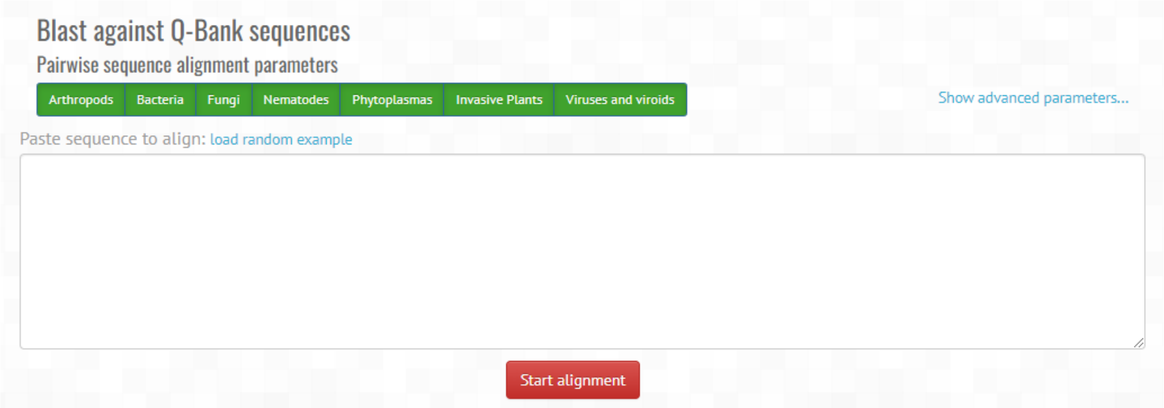
Blast against all EPPO-Q-bank sequences

From EPPO-Q-bank home page:

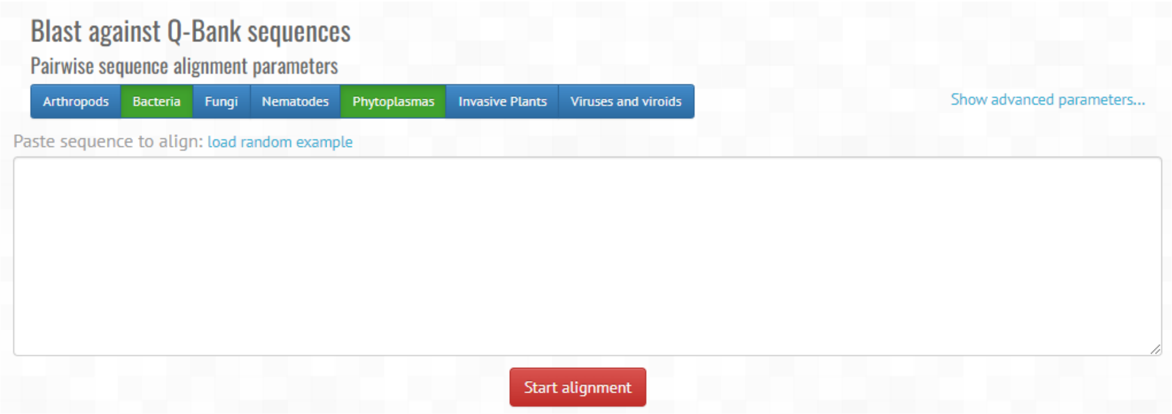


From discipline specific home page (e.g. bacteria)



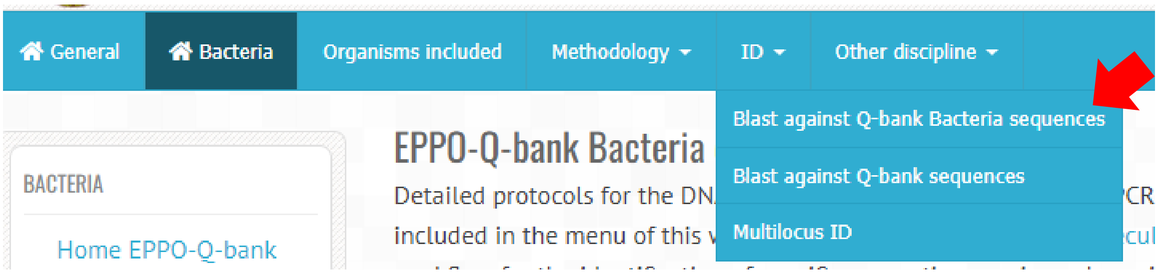


You can further select (remove) the databases you are (not) interested in by clicking on them. Selected databases appear in green (e.g. Bacteria and Phytoplasmas)

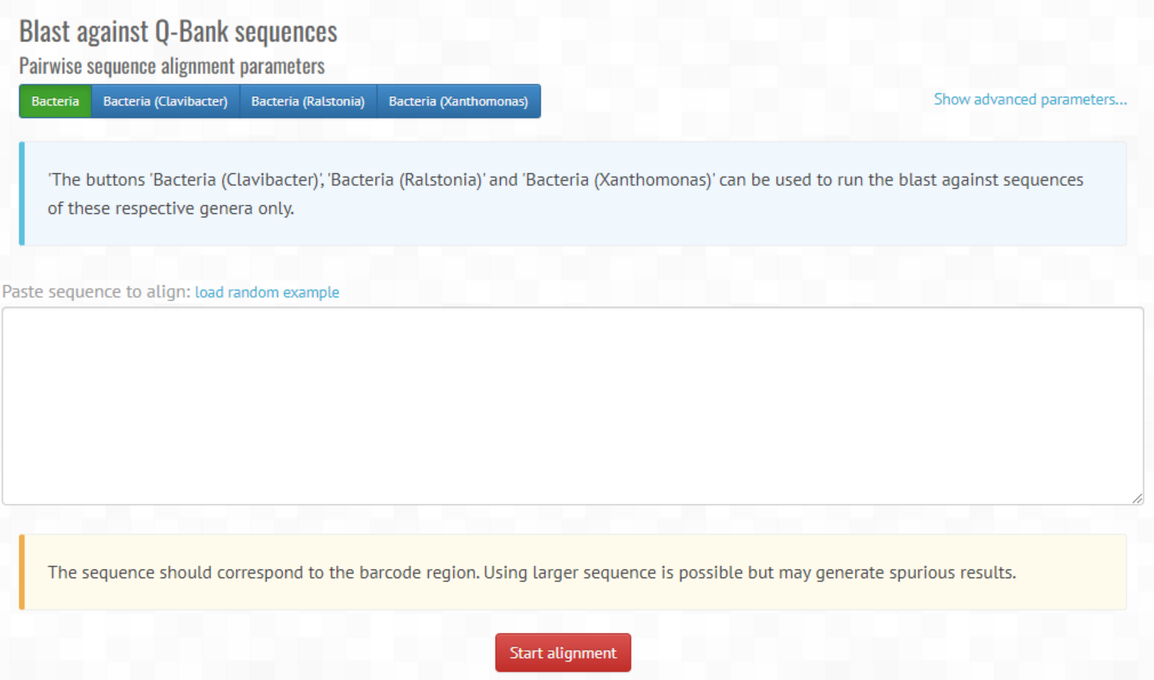


Blast against discipline specific sequences

From a discipline specific home page (e.g. bacteria)



Only the database of the discipline of interest will be searched (e.g. bacteria).



Blast against Q-Bank sequences

Pairwise sequence alignment parameters

'The buttons 'Bacteria (Clavibacter)', 'Bacteria (Ralstonia)' and 'Bacteria (Xanthomonas)' can be used to run the blast against sequences of these respective genera only.

Paste sequence to align: load random example

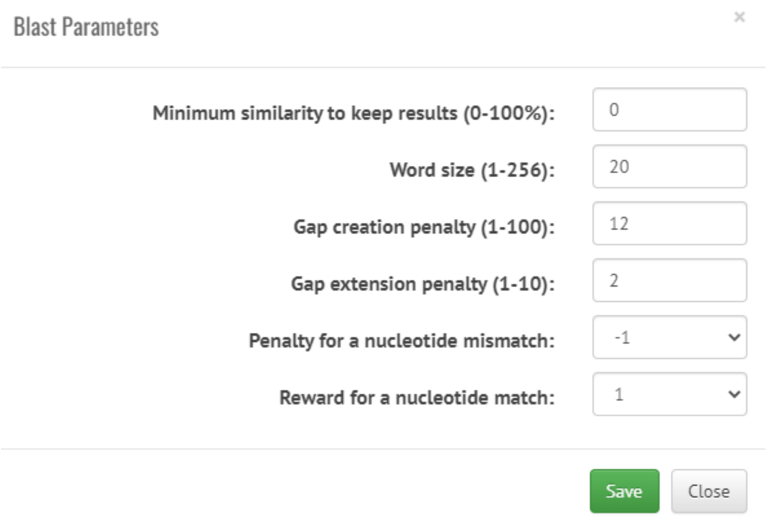
The sequence should correspond to the barcode region. Using larger sequence is possible but may generate spurious results.

For bacteria, you also have the possibility to run the blast against a specific subset of sequences (i.e. Clavibacter, Ralstonia or Xanthomonas). Select the database of interest by clicking on them. Selected databases appear in green (e.g. Bacteria)

Blast run

Paste your sequence in the box. Sequences should only contain the codes ATGC (no other characters are permitted)

By default, the BLAST parameters are the ones from NCBI Blastn. Click on Show advanced parameters... to see these BLAST parameters and if relevant to modify them .



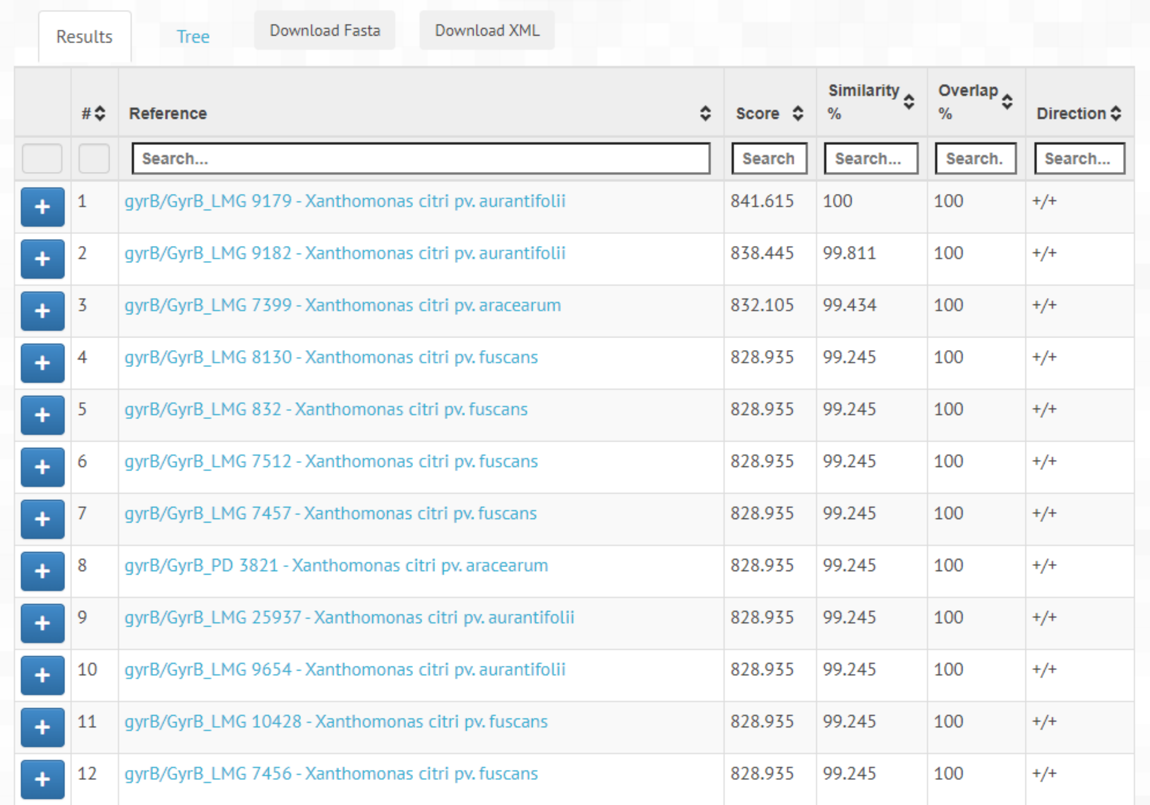
Blast Parameters

Minimum similarity to keep results (0-100%):	0
Word size (1-256):	20
Gap creation penalty (1-100):	12
Gap extension penalty (1-10):	2
Penalty for a nucleotide mismatch:	-1
Reward for a nucleotide match:	1

Click on Start alignment to run the BLAST.

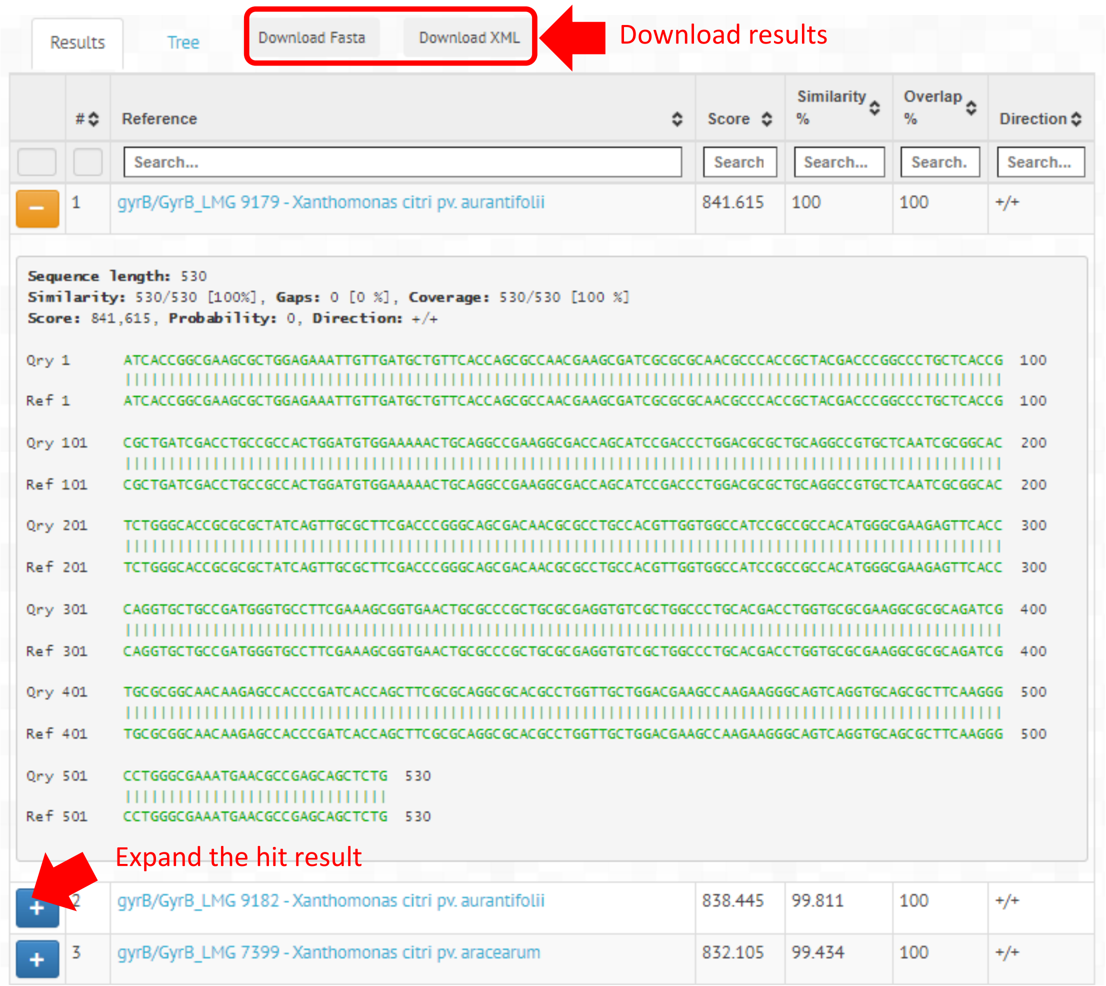
Blast results

BLAST results (first 100 hits) are displayed as a hit table showing, for example, the name of the hits, the coverage with respect to the query sequence (% overlap) and the percentage similarity. Furthermore, the orientation of inputted sequence with respect to the hit is displayed under Direction (+/+ or +/–). In EPPO-Q-bank, the E-value is referred to as probability. In addition, the score is shown. By default, the results are sorted out based on the E-score. You can sort the results based on other parameters (e.g. similarity).



	#	Reference	Score	Similarity %	Overlap %	Direction
		Search...	Search	Search...	Search.	Search...
+	1	gyrB/GyrB_LMG 9179 - Xanthomonas citri pv. aurantifolii	841.615	100	100	+/+
+	2	gyrB/GyrB_LMG 9182 - Xanthomonas citri pv. aurantifolii	838.445	99.811	100	+/+
+	3	gyrB/GyrB_LMG 7399 - Xanthomonas citri pv. aracearum	832.105	99.434	100	+/+
+	4	gyrB/GyrB_LMG 8130 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+
+	5	gyrB/GyrB_LMG 832 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+
+	6	gyrB/GyrB_LMG 7512 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+
+	7	gyrB/GyrB_LMG 7457 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+
+	8	gyrB/GyrB_PD 3821 - Xanthomonas citri pv. aracearum	828.935	99.245	100	+/+
+	9	gyrB/GyrB_LMG 25937 - Xanthomonas citri pv. aurantifolii	828.935	99.245	100	+/+
+	10	gyrB/GyrB_LMG 9654 - Xanthomonas citri pv. aurantifolii	828.935	99.245	100	+/+
+	11	gyrB/GyrB_LMG 10428 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+
+	12	gyrB/GyrB_LMG 7456 - Xanthomonas citri pv. fuscans	828.935	99.245	100	+/+

Alignments can be accessed by expanding the hit results (click on the + sign next to the hit).



Download results

Expand the hit result

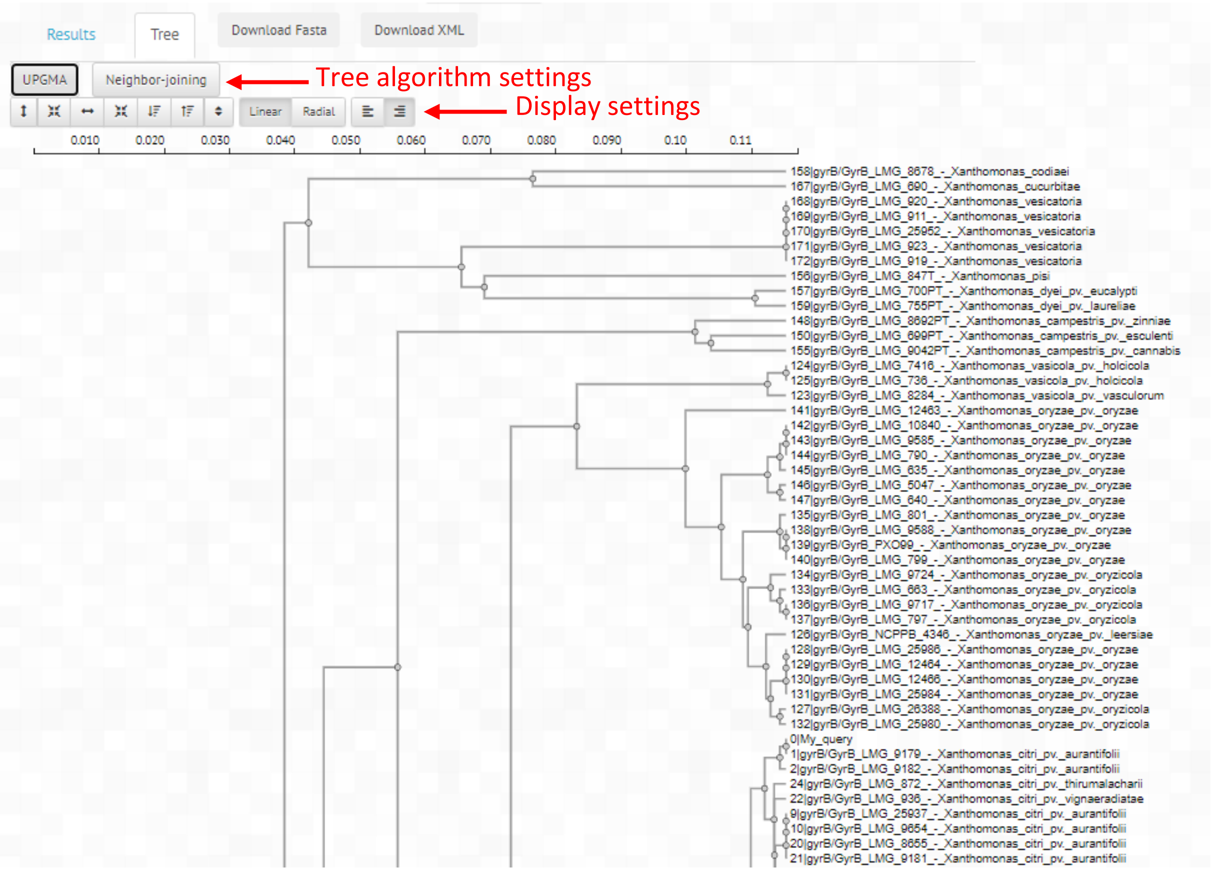
	#	Reference	Score	Similarity %	Overlap %	Direction
		Search...	Search	Search...	Search.	Search...
−	1	gyrB/GyrB_LMG 9179 - Xanthomonas citri pv. aurantifolii	841.615	100	100	+/+
+	2	gyrB/GyrB_LMG 9182 - Xanthomonas citri pv. aurantifolii	838.445	99.811	100	+/+
+	3	gyrB/GyrB_LMG 7399 - Xanthomonas citri pv. aracearum	832.105	99.434	100	+/+

```
Sequence length: 530
Similarity: 530/530 [100%], Gaps: 0 [0 %], Coverage: 530/530 [100 %]
Score: 841,615, Probability: 0, Direction: +/+

Qry 1      ATCACCGGCGAAGCGCTGGAGAAATTGTTGATGCTGTTCACCAGCGCCAACGAAGCGATCGCGCGCAACGCCCACCGCTACGACCCGGCCCTGCTCACCG  100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ref 1      ATCACCGGCGAAGCGCTGGAGAAATTGTTGATGCTGTTCACCAGCGCCAACGAAGCGATCGCGCGCAACGCCCACCGCTACGACCCGGCCCTGCTCACCG  100

Qry 101    CGCTGATCGACCTGCCGCCACTGGATGTGGAAAAACTGCAGGCCGAAGGCGACCAGCATCCGACCCTGGACGCGCTGCAGGCCGTGCTCAATCGCGGCAC  200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ref 101    CGCTGATCGACCTGCCGCCACTGGATGTGGAAAAACTGCAGGCCGAAGGCGACCAGCATCCGACCCTGGACGCGCTGCAGGCCGTGCTCAATCGCGGCAC  200

Qry 201    TCTGGGCACCGCGCGCTATCAGTTGCGCTTCGACCCGGGCAGCGACAACGCGCCTGCCACGTTGGTGGCCATCCGCCGCCACATGGGCGAAGAGTTCACC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ref 201    TCTGGGCACCGCGCGCTATCAGTTGCGCTTCGACCCGGGCAGCGACAACGCGCCTGCCACGTTGGTGGCCATCCGCCGCCACATGGGCGAAGAGTTCACC  300

Qry 301    CAGGTGCTGCCGATGGGTGCCTTCGAAAGCGGTGAACTGCGCCCGCTGCGCGAGGTGTCGCTGGCCCTGCACGACCTGGTGCGCGAAGGCGCGCAGATCG  400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ref 301    CAGGTGCTGCCGATGGGTGCCTTCGAAAGCGGTGAACTGCGCCCGCTGCGCGAGGTGTCGCTGGCCCTGCACGACCTGGTGCGCGAAGGCGCGCAGATCG  400

Qry 401    TGCGCGGCAACAAGAGCCACCCGATCACCAGCTTCGCGCAGGCGCACGCCTGGTTGCTGGACGAAGCCAAGAAGGGCAGTCAGGTGCAGCGCTTCAAGGG  500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Ref 401    TGCGCGGCAACAAGAGCCACCCGATCACCAGCTTCGCGCAGGCGCACGCCTGGTTGCTGGACGAAGCCAAGAAGGGCAGTCAGGTGCAGCGCTTCAAGGG  500

Qry 501    CCTGGGCGAAATGAACGCCGAGCAGCTCTG  530
           ||||||||||||||||||||||||||||||
Ref 501    CCTGGGCGAAATGAACGCCGAGCAGCTCTG  530
```

Blast results can also be downloaded in FASTA or XML format.

Tree views

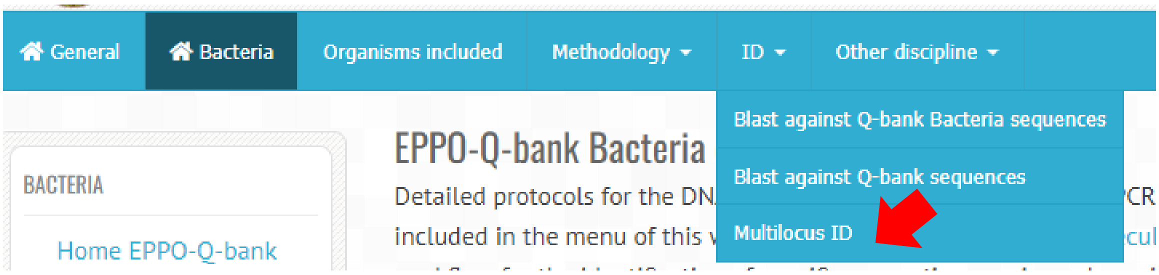
Single BLAST hit results can be displayed using different tree views by selecting ‘Tree’ on the BLAST results page and then by clicking on ‘Neighbour joining’ or ‘UPGMA’. The query sequence is indicated with ‘My_query’. In addition to choosing the tree algorithm, the display of the trees can be adjusted.



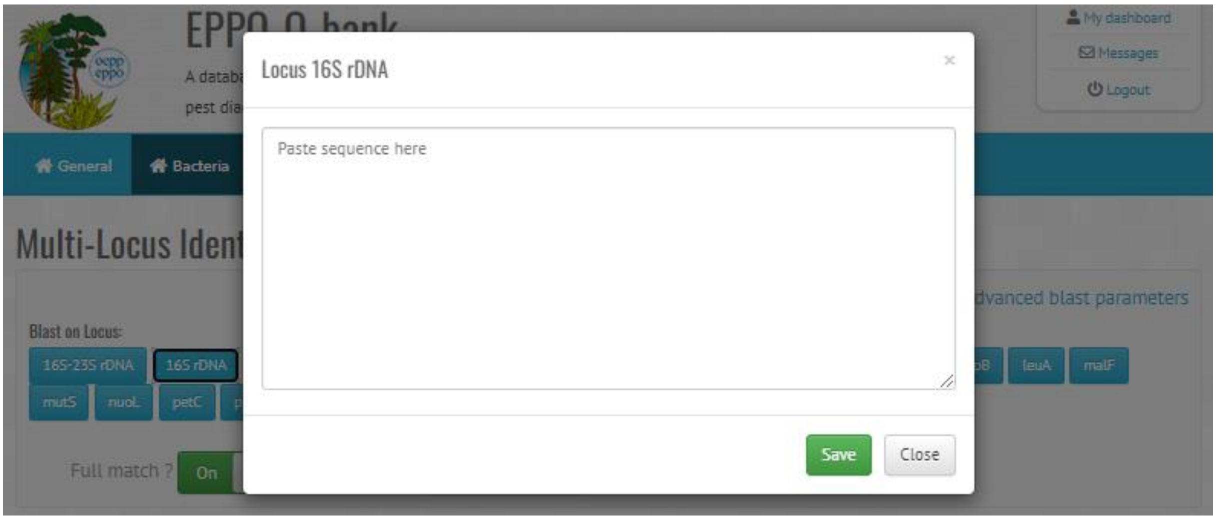
For the interpretation of tree views, see EPPO PM 7/129.

Multi-locus blast (MLSA)

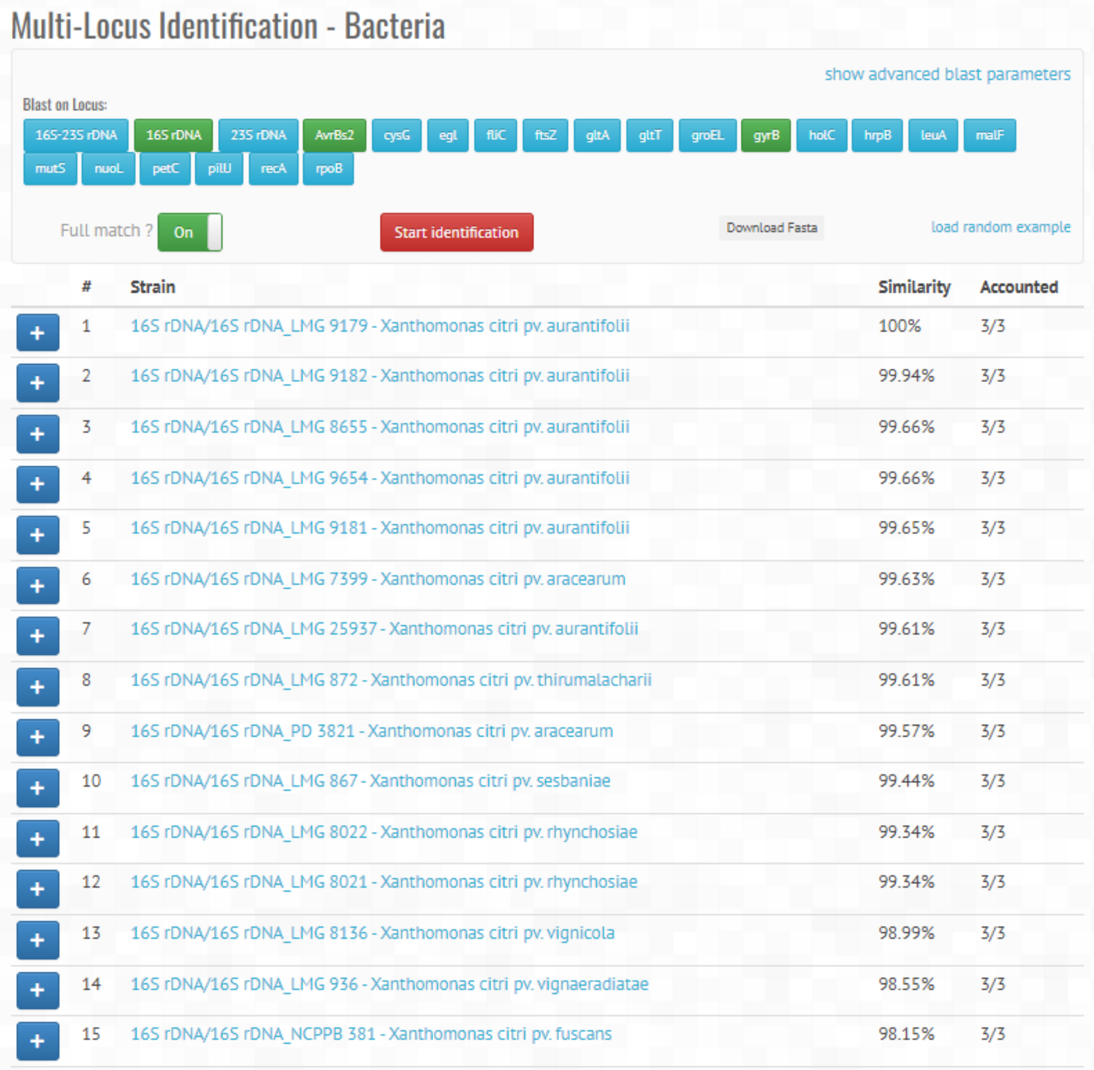
MLSA is accessed under Multilocus ID in the discipline-specific subsets of the database. Sequences of different loci can be submitted.



Paste your sequence in the box. Sequences should only contain the codes ATGC (no other characters are permitted)

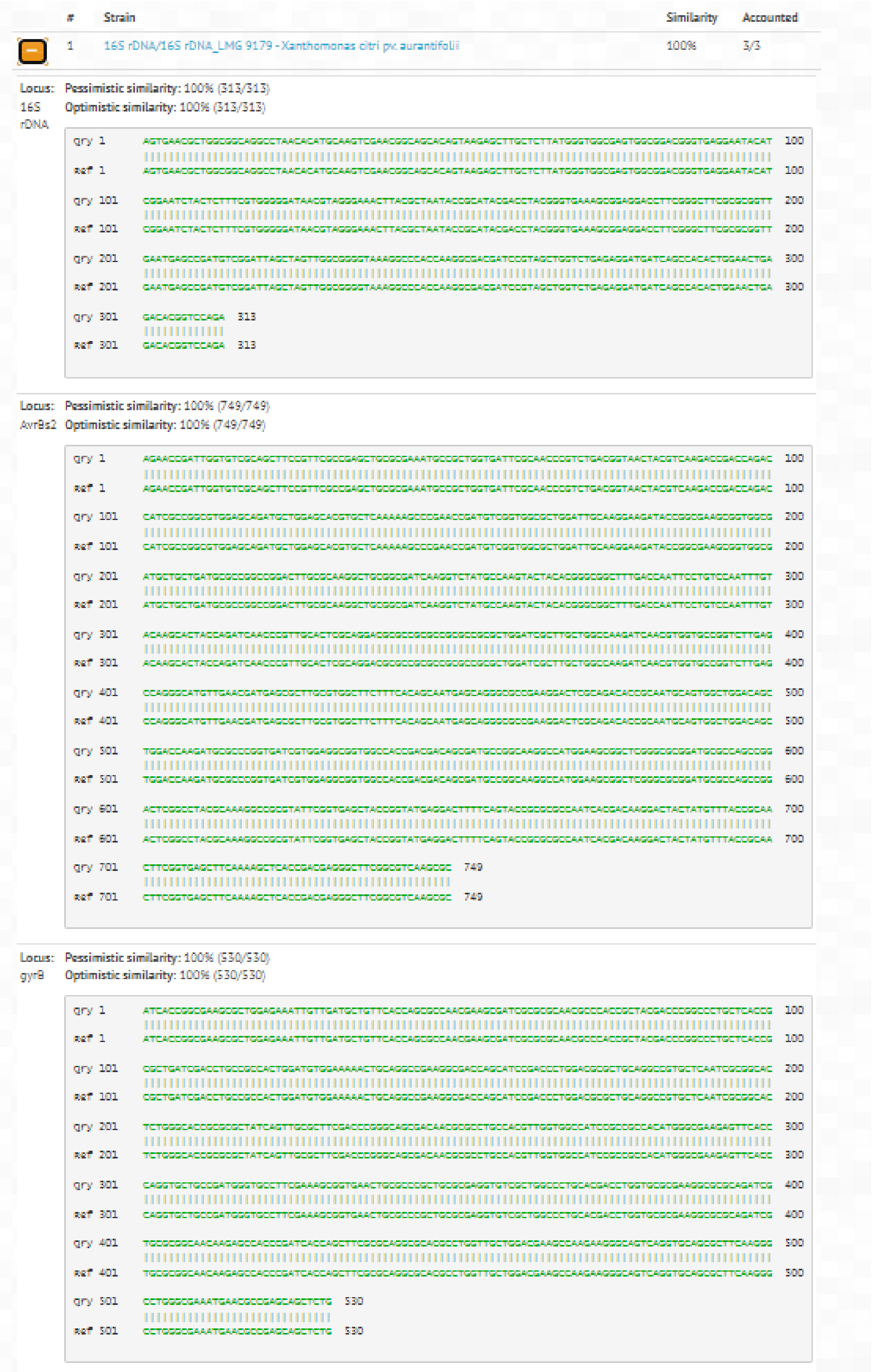


Click on Start identification to start the analysis. As for the BLAST, under 'show advanced parameters', different BLAST settings such as word size, maximum alignments to display, and cut-off settings for minimum similarity and overlap can be adjusted. Set 'Full match' on to only get results with all the loci accounted for.



#	Strain	Similarity	Accounted
1	16S rDNA/16S rDNA_LMG 9179 - Xanthomonas citri pv. aurantifolii	100%	3/3
2	16S rDNA/16S rDNA_LMG 9182 - Xanthomonas citri pv. aurantifolii	99.94%	3/3
3	16S rDNA/16S rDNA_LMG 8655 - Xanthomonas citri pv. aurantifolii	99.66%	3/3
4	16S rDNA/16S rDNA_LMG 9654 - Xanthomonas citri pv. aurantifolii	99.66%	3/3
5	16S rDNA/16S rDNA_LMG 9181 - Xanthomonas citri pv. aurantifolii	99.65%	3/3
6	16S rDNA/16S rDNA_LMG 7399 - Xanthomonas citri pv. aracearum	99.63%	3/3
7	16S rDNA/16S rDNA_LMG 25937 - Xanthomonas citri pv. aurantifolii	99.61%	3/3
8	16S rDNA/16S rDNA_LMG 872 - Xanthomonas citri pv. thirumalacharii	99.61%	3/3
9	16S rDNA/16S rDNA_PD 3821 - Xanthomonas citri pv. aracearum	99.57%	3/3
10	16S rDNA/16S rDNA_LMG 867 - Xanthomonas citri pv. sesbaniae	99.44%	3/3
11	16S rDNA/16S rDNA_LMG 8022 - Xanthomonas citri pv. rhynchosiae	99.34%	3/3
12	16S rDNA/16S rDNA_LMG 8021 - Xanthomonas citri pv. rhynchosiae	99.34%	3/3
13	16S rDNA/16S rDNA_LMG 8136 - Xanthomonas citri pv. vignicola	98.99%	3/3
14	16S rDNA/16S rDNA_LMG 936 - Xanthomonas citri pv. vignaeradiatae	98.55%	3/3
15	16S rDNA/16S rDNA_NCPPB 381 - Xanthomonas citri pv. fuscans	98.15%	3/3

In the MLSA results, EPPO-Q bank shows the number of loci that are included in the analysis (“Accounted”). Also, the degree of similarity is displayed. Alignments of different loci can be accessed by expanding the hit (click the ‘+’ sign next to the hit).



	#	Strain	Similarity	Accounted
−	1	16S rDNA/16S rDNA_LMG 9179 - Xanthomonas citri pv. aurantifolii	100%	3/3

Locus: 16S rDNA
Pessimistic similarity: 100% (313/313)
Optimistic similarity: 100% (313/313)

Locus: AvrBs2
Pessimistic similarity: 100% (749/749)
Optimistic similarity: 100% (749/749)

Locus: gyrB
Pessimistic similarity: 100% (530/530)
Optimistic similarity: 100% (530/530)

Feedback and comments on this user guide

We hope that this User guide answers any questions you may have.

If you have suggestions to improve it, please contact us. You can use the contact form available in EPPO-Q-bank (https://qbank.eppo.int/contact).