

How to use EPPO-Q-bank?

<https://qbank.eppo.int/>

- Guidelines for users -

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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

The screenshot shows the EPPO-Q-bank website. At the top, there is a header with the EPPO-Q-bank logo and a search bar. Below the header is a navigation menu with links to Arthropods, Bacteria, Fungi, Nematodes, Phytoplasmas, Plants, and Viruses and Viroids. A sidebar on the left contains a list of disciplines with a green box highlighting the 'Arthropods' link. The main content area displays a welcome message and information about the database's history and content.

EPPO-Q-bank
A database to support plant pest diagnostic activities

Search by name or EPPO code... Go!

Arthropods Bacteria Fungi Nematodes Phytoplasmas Plants Viruses and Viroids Blast against all Q-Bank sequences

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.

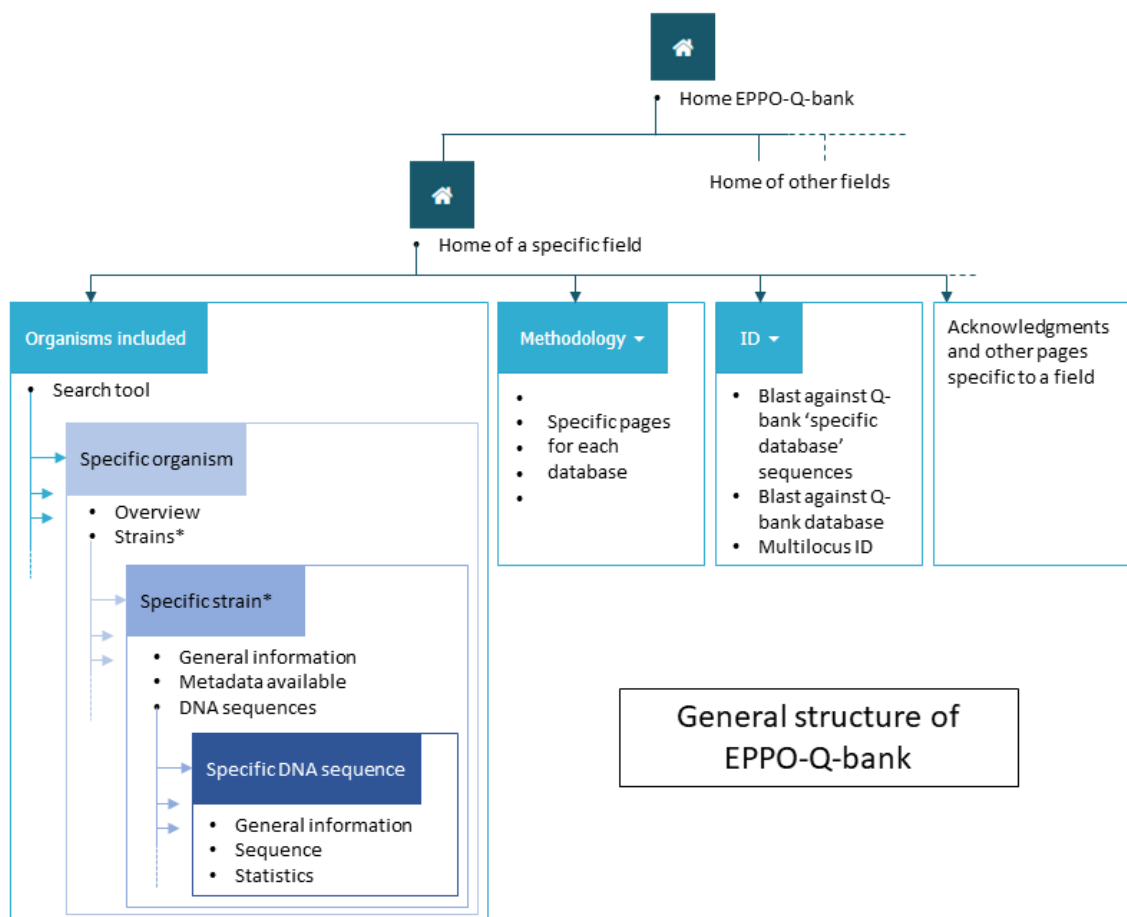
Content of EPPO-Q-bank

Priority for integration of data from Q-bank was determined by disciplines 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.



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  reCAPTCHA
Privacy - Terms

Register

[Already have an account?](#)

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

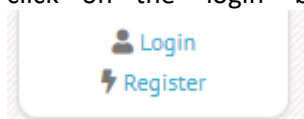
Please note that your personal details will not be communicated to any other third parties and that they are kept only for the EPPO Secretariat's internal use.

Registration is mandatory to view sequences in the database.

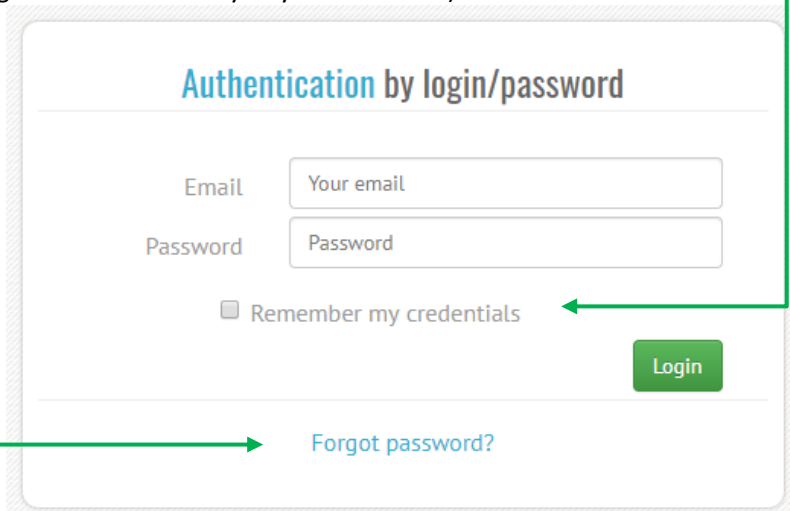
How to log in (already registered user)?

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).



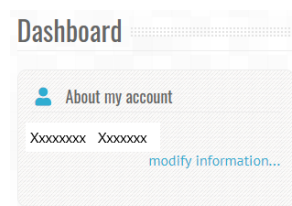
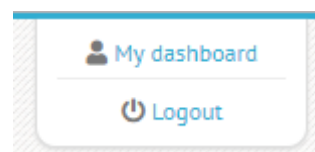
The image shows a login form titled "Authentication by login/password". It contains two input fields: "Email" with the placeholder text "Your email" and "Password" with the placeholder text "Password". Below these fields is a checkbox labeled "Remember my credentials". To the right of the checkbox is a green "Login" button. Below the "Login" button is a blue link that says "Forgot password?". A green arrow points from the text "Remember my credentials" in the list above to the checkbox. Another green arrow points from the text "Forgot password?" in the list below to the "Forgot password?" link.

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

Change my email


Email

Change my password

Password

Password (confirm)

Photo



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
<input type="text" value="Search..."/>	<input type="text" value="Search..."/>	- select -	<input type="text" value="Search..."/>	<input type="text" value="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).



EPPO-Q-bank
 A database to support plant
 pest diagnostic activities

[My dashboard](#)
[Logout](#)

[Home](#)
[Arthropods](#)
[Bacteria](#)
[Fungi](#)
[Nematodes](#)
[Phytoplasmas](#)
[Plants](#)
[Viruses and Viroids](#)
[Blast against all Q-Bank sequences](#)

Global Search - Found 78 record(s)

EPPOCode	PrefName	EPPO Categorization	Nb specimens
<input type="text" value="Search..."/>	<input type="text" value="Search..."/>	<input type="text" value="Search..."/>	<input type="text" value="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

EPPO-Q-bank
A database to support plant pest diagnostic activities

Search by name or EPPO code... Go!

My dashboard
Messages
Logout

General Bacteria **Organisms included** Methodology ID Other discipline

Bacteria - Organisms included (155) Add organism Download

Filter: scientific name, eppocode, ... (1) Apply filter Reset filter

EPPO Code	Preferred Name	EPPO Categorization	Nb Strains	Nb Sequences	Visible?
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 blazotea		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

Menu: Overview, Strains

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.

Basic information

EPPO code: CORBMI

Preferred name: *Clavibacter michiganensis subsp. michiganensis*

Authority: (Smith) Davis et al.

Other scientific names

Name	Authority
<i>Corynebacterium michiganense</i>	(E.F.Smith) Dye & Kemp
<i>pv. michiganense</i>	

Taxonomy

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

more photos on EPPO Global Database...

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

```

gacaccctccgcgcgcgcttccagcagatggcggttcctcaacaagggcctggcgctcacgctgcacgacgagcgc
gaggtggacggcgccgagcaccgcaccgagaagtctctacgagcggggcctcgctcgactacgtggagcacctc
gtgaaggcgaagaagaccgaggtcgtaacgccgacgtcatcgcttcgagtcgaggacacgggtcaagaagatc
agcctcgaggtcgcatgtagtgaccacctctacacggagagcggtccacacctacgcgaacaccatcaacacg
cacgagggcgccgacgcacgaggaggggttccgcgcggcgctcaccacgctcgtaaccgctacgcgcgcgagaac
aagctgctccgcgagaaggacgagaacctcacgggcgacgacgtccgcgagggcctcacggccgctatctcggtg
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 against Q-bank Bacteria sequences	}	BLAST (+ Tree visualisation)
Blast against Q-bank sequences		
Multilocus ID		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.

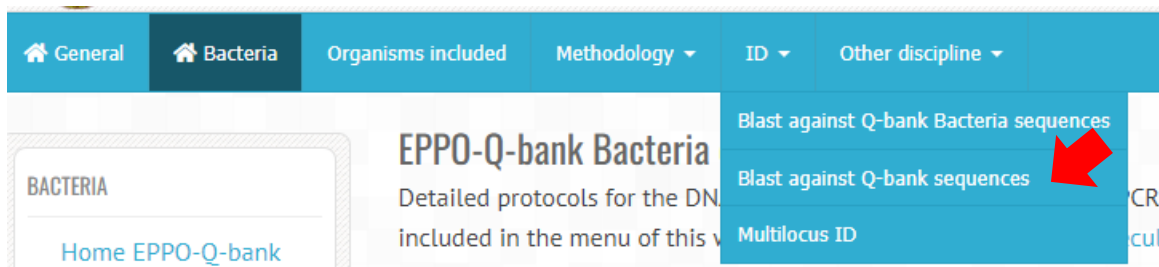
You can blast against all EPPO-Q-bank sequences or just against a subset of sequences corresponding to one discipline

Blast against all EPPO-Q-bank sequences

From EPPO-Q-bank home page:



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



Blast against Q-Bank sequences
Pairwise sequence alignment parameters

Arthropods Bacteria Fungi Nematodes **Phytoplasmas** Invasive Plants Viruses and viroids [Show advanced parameters...](#)

Paste sequence to align: [load random example](#)

[Start alignment](#)

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 Q-Bank sequences
Pairwise sequence alignment parameters

Arthropods **Bacteria** Fungi Nematodes **Phytoplasmas** Invasive Plants Viruses and viroids [Show advanced parameters...](#)

Paste sequence to align: [load random example](#)

[Start alignment](#)

Blast against discipline specific sequences

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

🏠 General 🏠 **Bacteria** Organisms included Methodology ▾ ID ▾ Other discipline ▾

BACTERIA

[Home EPPO-Q-bank](#)

EPPO-Q-bank Bacteria

Detailed protocols for the DN
included in the menu of this v

[Blast against Q-bank Bacteria sequences](#)

[Blast against Q-bank sequences](#)

[Multilocus ID](#)

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

Blast against Q-Bank sequences

Pairwise sequence alignment parameters

[Bacteria](#)
[Bacteria \(Clavibacter\)](#)
[Bacteria \(Ralstonia\)](#)
[Bacteria \(Xanthomonas\)](#)
[Show advanced 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.

[Start alignment](#)

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 .

[Show advanced parameters...](#)

Blast Parameters

Minimum similarity to keep results (0-100%):

Word size (1-256):

Gap creation penalty (1-100):

Gap extension penalty (1-10):

Penalty for a nucleotide mismatch:

Reward for a nucleotide match:


[Save](#) [Close](#)


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).

Results						
Tree		Download Fasta		Download XML		
#	Reference	Score	Similarity %	Overlap %	Direction	
<input type="checkbox"/>	<input type="text" value="Search..."/>	<input type="button" value="Search"/>	<input type="text" value="Search..."/>	<input type="button" value="Search..."/>	<input type="button" value="Search..."/>	<input type="button" value="Search..."/>
<input type="button" value="+"/> 1	gyrB/GyrB_LMG 9179 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	841.615	100	100	+/+	
<input type="button" value="+"/> 2	gyrB/GyrB_LMG 9182 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	838.445	99.811	100	+/+	
<input type="button" value="+"/> 3	gyrB/GyrB_LMG 7399 - <i>Xanthomonas citri</i> pv. <i>aracearum</i>	832.105	99.434	100	+/+	
<input type="button" value="+"/> 4	gyrB/GyrB_LMG 8130 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 5	gyrB/GyrB_LMG 832 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 6	gyrB/GyrB_LMG 7512 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 7	gyrB/GyrB_LMG 7457 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 8	gyrB/GyrB_PD 3821 - <i>Xanthomonas citri</i> pv. <i>aracearum</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 9	gyrB/GyrB_LMG 25937 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 10	gyrB/GyrB_LMG 9654 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 11	gyrB/GyrB_LMG 10428 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	
<input type="button" value="+"/> 12	gyrB/GyrB_LMG 7456 - <i>Xanthomonas citri</i> pv. <i>fuscans</i>	828.935	99.245	100	+/+	

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

Results Tree Download Fasta Download XML  Download results

#	Reference	Score	Similarity %	Overlap %	Direction
1	gyrB/GyrB_LMG 9179 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	841.615	100	100	+/+

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

```

Qry 1      ATCACCGCGAAGCGCTGGAGAAATTGTTGATGCTGTTACCAAGCGCAACGAAGCGATCGCGCAACGCCACCGCTACGACCCGGCCCTGCTACCG 100
Ref 1      ATCACCGCGAAGCGCTGGAGAAATTGTTGATGCTGTTACCAAGCGCAACGAAGCGATCGCGCAACGCCACCGCTACGACCCGGCCCTGCTACCG 100

Qry 101    CGCTGATCGACCTGCCGCCACTGGATGTGGAAGAACTGCAGGCCGAAGGCGACAGCATCCGACCTGGACGCGCTGCAGGCCGTGCTCAATCGCGGCAC 200
Ref 101    CGCTGATCGACCTGCCGCCACTGGATGTGGAAGAACTGCAGGCCGAAGGCGACAGCATCCGACCTGGACGCGCTGCAGGCCGTGCTCAATCGCGGCAC 200


Qry 201    TCTGGGACCGCGCGCTATCAGTTGCGCTTCGACCCGGGCGAGCAACGCGCTGCCACGTTGGTGCCATCCGCCGCCACATGGGCGAAGAGTTTACC 300
Ref 201    TCTGGGACCGCGCGCTATCAGTTGCGCTTCGACCCGGGCGAGCAACGCGCTGCCACGTTGGTGCCATCCGCCGCCACATGGGCGAAGAGTTTACC 300

Qry 301    CAGGTGCTGCCGATGGGTGCTTCAAGAGCGGTGAAGTGCAGGCCGCTGCGCGAGGTGTCGCTGGCCCTGCACGACCTGGTGCGCAAGGCGCGCAGATCG 400
Ref 301    CAGGTGCTGCCGATGGGTGCTTCAAGAGCGGTGAAGTGCAGGCCGCTGCGCGAGGTGTCGCTGGCCCTGCACGACCTGGTGCGCAAGGCGCGCAGATCG 400

Qry 401    TGGCGGGCAACAAGAGCCACCCGATCACCAGCTTCGCGAGGCGCACGCTGGTTGCTGGACGAAGCCAAGAAGGGCAGTCAGGTGCAGCGCTTCAAGGG 500
Ref 401    TGGCGGGCAACAAGAGCCACCCGATCACCAGCTTCGCGAGGCGCACGCTGGTTGCTGGACGAAGCCAAGAAGGGCAGTCAGGTGCAGCGCTTCAAGGG 500

Qry 501    CCTGGGCGAAATGAACGCCGAGCAGCTCTG 530
Ref 501    CCTGGGCGAAATGAACGCCGAGCAGCTCTG 530

```

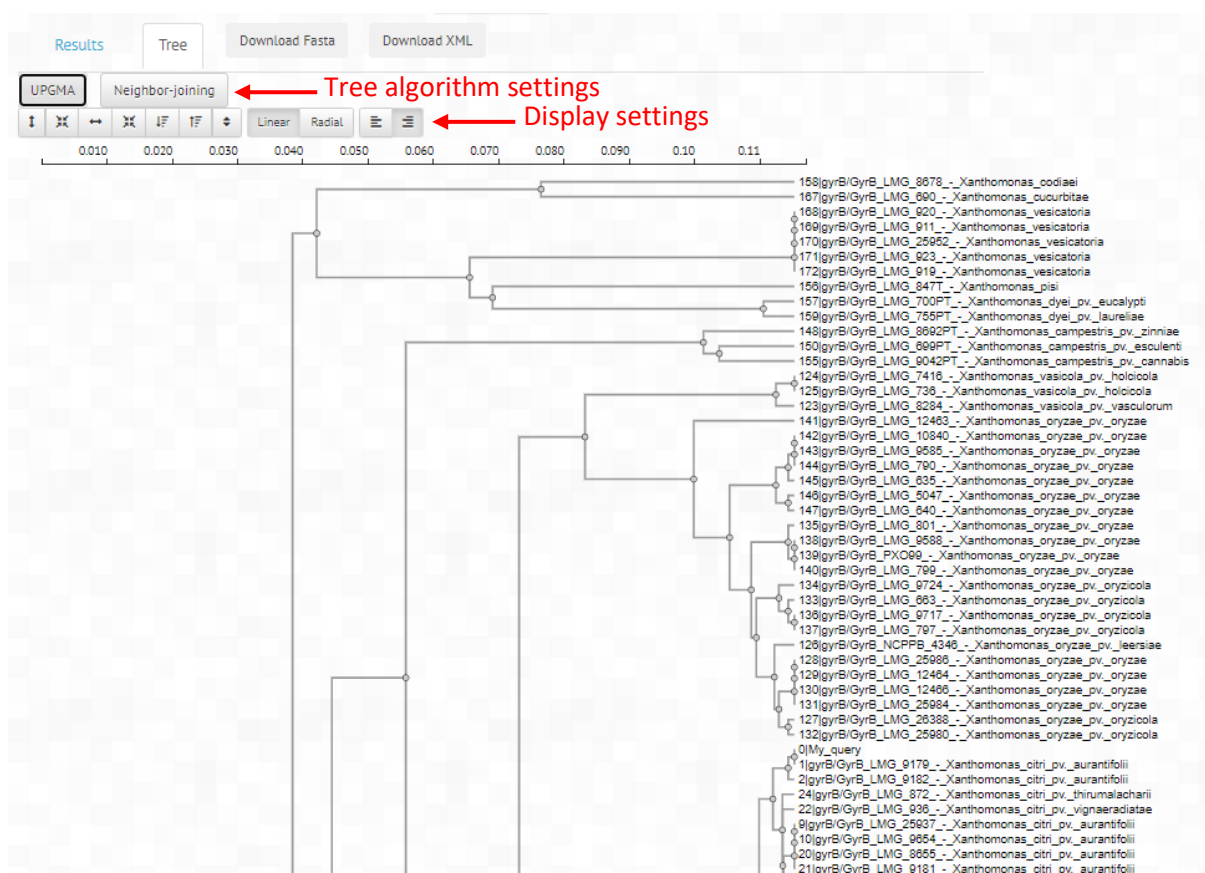
 Expand the hit result

2	gyrB/GyrB_LMG 9182 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	838.445	99.811	100	+/+
3	gyrB/GyrB_LMG 7399 - <i>Xanthomonas citri</i> pv. <i>aracearum</i>	832.105	99.434	100	+/+

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

Tree views

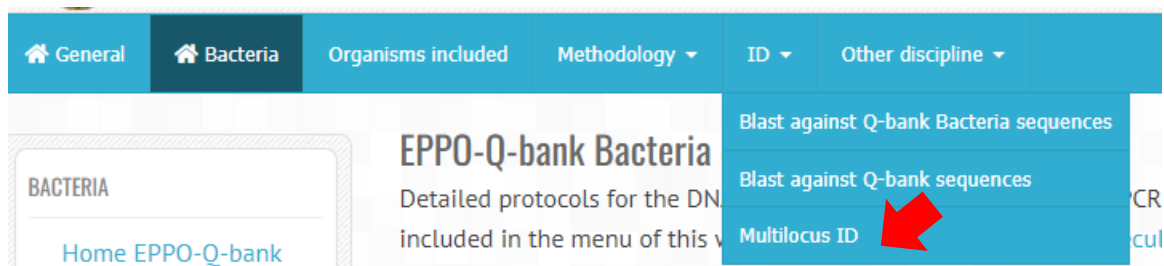
Single BLAST hit results can be displayed using different tree views by selecting 'Tree' on the BLAST results page and then by clicking on 'Neighbour joining' or 'UPGMA'. The query sequence is indicated with 'My_query'. In addition to choosing the tree algorithm, the display of the trees can be adjusted.



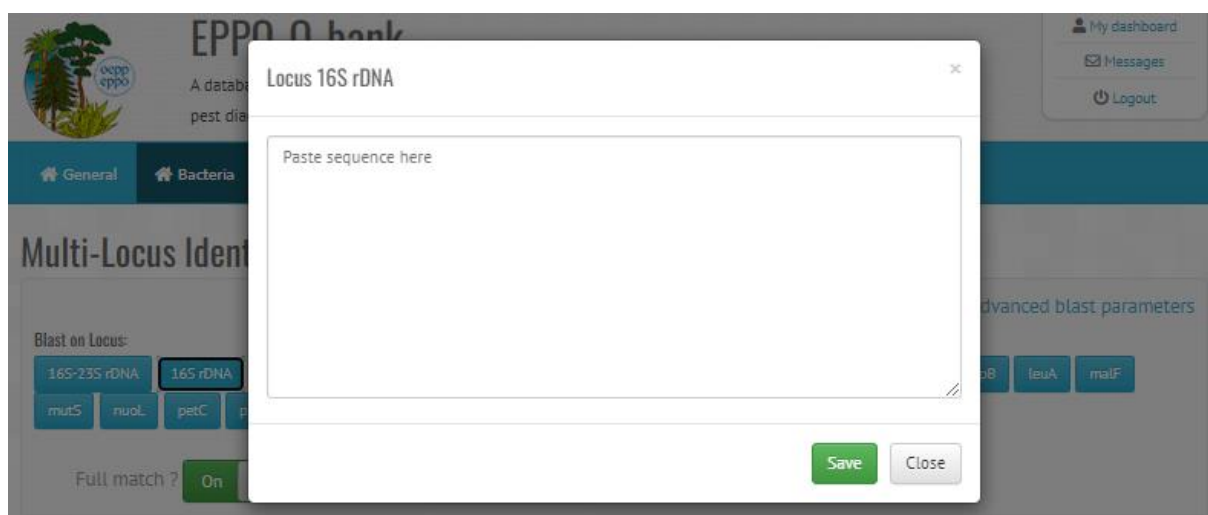
For the interpretation of tree views, see EPPO PM 7/129.

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)



Start identification

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.

Multi-Locus Identification - Bacteria

show advanced blast parameters

Blast on Locus:

16S-23S rDNA 16S rDNA 23S rDNA AvrBs2 cysG egl fljC ftsZ gltA gltT groEL gyrB hcrC hcrB leuA malF

mutS nuoL petC pilU recA rpoB

Full match? ☒ On **Start identification** Download Fasta load random example

#	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 - <i>Xanthomonas citri</i> pv. <i>aurantifolia</i>	100%	3/3

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

qry 1	AGTGAACGCTGGCGGCAAGGCTAACACATGCAAGTGAACGGCAGCAGTAAAGAGCTTGTCTTATGGGTGGCGAGTGGCGGACGGGTGAGGAATACAT	100
ref 1	AGTGAACGCTGGCGGCAAGGCTAACACATGCAAGTGAACGGCAGCAGTAAAGAGCTTGTCTTATGGGTGGCGAGTGGCGGACGGGTGAGGAATACAT	100
qry 101	CGGAATCTACTCTTTGGTGGGGGATAAGTAGGGAACCTACGCTAATACCGCATACGACCTACGGGTGAAGCGGAGGACCTTCGGGCTTCGGCGGGT	200
ref 101	CGGAATCTACTCTTTGGTGGGGGATAAGTAGGGAACCTACGCTAATACCGCATACGACCTACGGGTGAAGCGGAGGACCTTCGGGCTTCGGCGGGT	200
qry 201	GAATGAGCGGATGTGGGATTAGCTAGTTGGCGGGTAAAGGCCACCAAGGCGAGGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAACTGA	300
ref 201	GAATGAGCGGATGTGGGATTAGCTAGTTGGCGGGTAAAGGCCACCAAGGCGAGGATCCGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGAACTGA	300
qry 301	GACACGGTCCAGA	313
ref 301	GACACGGTCCAGA	313

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

qry 1	AGAACCAGATTGGTGTGGCAGCTTCGGTTTCGGCAGCTGGCGGAAATGCCGCTGGTGAATTCGCAACCGCTCTGACGGTAACCTAGCTCAAGACCGACGAC	100
ref 1	AGAACCAGATTGGTGTGGCAGCTTCGGTTTCGGCAGCTGGCGGAAATGCCGCTGGTGAATTCGCAACCGCTCTGACGGTAACCTAGCTCAAGACCGACGAC	100
qry 101	CATCGCGGGGTGGAGCAGATGCTGGAGCAGCTGCTCAAAAAGCCGSAACCGATGTCGGTGGCGCTGGATTGCAAGGAAGATACCGGCGAAGCGGTGGCG	200
ref 101	CATCGCGGGGTGGAGCAGATGCTGGAGCAGCTGCTCAAAAAGCCGSAACCGATGTCGGTGGCGCTGGATTGCAAGGAAGATACCGGCGAAGCGGTGGCG	200
qry 201	ATGCTGCTGATGCGCGCGCGGACTTGGCAAGGCTGCGGGGATCAAGGCTATGCCAAGTACTACACGGCGCGCTTTGACCAATTCCTGTCCAATTTGT	300
ref 201	ATGCTGCTGATGCGCGCGCGGACTTGGCAAGGCTGCGGGGATCAAGGCTATGCCAAGTACTACACGGCGCGCTTTGACCAATTCCTGTCCAATTTGT	300
qry 301	ACAAGCACTACCAAGATCAACCGGTTGCACTCGCAGGACGCGCGCGCGCGCGCGCGCTGGATCGCTTGGTGGCCAAAGATCAACGGTGGTGGGCTTTGAG	400
ref 301	ACAAGCACTACCAAGATCAACCGGTTGCACTCGCAGGACGCGCGCGCGCGCGCGCGCTGGATCGCTTGGTGGCCAAAGATCAACGGTGGTGGGCTTTGAG	400
qry 401	CCAGGCGATGTTGAACGATGAGCGCTTCGGTGGCTTTTTCACAGCAATGAGCAGGCGCGGCAAGGACTCGCAGACACCGCAATGCAAGTGGCTGGAGAC	500
ref 401	CCAGGCGATGTTGAACGATGAGCGCTTCGGTGGCTTTTTCACAGCAATGAGCAGGCGCGGCAAGGACTCGCAGACACCGCAATGCAAGTGGCTGGAGAC	500
qry 501	TGGACCAAGATGCGCGCGGATGCTGGAGCGGCTGGCCACCGACAGGATGCGCGCAAGGCTCATGGAAGCGGCTCGGGCGCGGATGCGCGCAGCGG	600
ref 501	TGGACCAAGATGCGCGCGGATGCTGGAGCGGCTGGCCACCGACAGGATGCGCGCAAGGCTCATGGAAGCGGCTCGGGCGCGGATGCGCGCAGCGG	600
qry 601	ACTCGGCTACGCAAAAGGCGCGCTATTGGTGGCTACCGGATAGGAGCTTTTCACTACCGCGCGCAATCAGCAGGAGTACTATGTTTACCGCAA	700
ref 601	ACTCGGCTACGCAAAAGGCGCGCTATTGGTGGCTACCGGATAGGAGCTTTTCACTACCGCGCGCAATCAGCAGGAGTACTATGTTTACCGCAA	700
qry 701	CTTCGGTGGCTTCAAAAGCTCACCGACGAGGCTTCGGGCTCAAGGCG	749
ref 701	CTTCGGTGGCTTCAAAAGCTCACCGACGAGGCTTCGGGCTCAAGGCG	749

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

qry 1	ATCACCGGCGAAGCGCTGGAGAAATGTTGATGCTGTTACACGAGCGCAACGAGCGATCGCGCGCAACGCGCACCGCTACGACCGCGGCTGCTCACCG	100
ref 1	ATCACCGGCGAAGCGCTGGAGAAATGTTGATGCTGTTACACGAGCGCAACGAGCGATCGCGCGCAACGCGCACCGCTACGACCGCGGCTGCTCACCG	100
qry 101	CGCTGATGACCTGCGCGCACTGGATGTGGAAAACTGCAGGCGGAAGGCGACCGATCGGACCTGGAAGCGCTGCAAGGCGGCTGCTCAATGCGGGCAC	200
ref 101	CGCTGATGACCTGCGCGCACTGGATGTGGAAAACTGCAGGCGGAAGGCGACCGATCGGACCTGGAAGCGCTGCAAGGCGGCTGCTCAATGCGGGCAC	200
qry 201	TCTGGGACCGCGCGCTATCAGTTGCGCTTCGACCGGGCAGCGACACCGCGCTGCCACGTTGGTGGCCATCGCGCGCCACATGGGCGAAGAGTTCAACC	300
ref 201	TCTGGGACCGCGCGCTATCAGTTGCGCTTCGACCGGGCAGCGACACCGCGCTGCCACGTTGGTGGCCATCGCGCGCCACATGGGCGAAGAGTTCAACC	300
qry 301	CAGGTGCTGCGGATGGGTGCTTGAAGCGGTGAACCTGCGCGCTGCGGCGAGGTGCTGCGGCTGCAAGACCTGGTGGCGGAAGGCGCGCAGATCG	400
ref 301	CAGGTGCTGCGGATGGGTGCTTGAAGCGGTGAACCTGCGCGCTGCGGCGAGGTGCTGCGGCTGCAAGACCTGGTGGCGGAAGGCGCGCAGATCG	400
qry 401	TGGCGGGCAACAGAGCCACCGGATCAGGCTTCGCGAGGCGCACCGCTGGTGGTGAAGAGCCAAAGAGGCGAGTCAAGTGCAGCGCTTCAAGGG	500
ref 401	TGGCGGGCAACAGAGCCACCGGATCAGGCTTCGCGAGGCGCACCGCTGGTGGTGAAGAGCCAAAGAGGCGAGTCAAGTGCAGCGCTTCAAGGG	500
qry 501	CCTGGGCGAAATGAACGCGCGAGCAGCTCG	530
ref 501	CCTGGGCGAAATGAACGCGCGAGCAGCTCG	530

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