GenEpi Webinar

Focus on the Agents of Whooping Cough

A virtual training workshop within GenEpi-BioTrain.

# Pratical exercices on BIGSdb Bordetella database

**Valérie Bouchez & Martin Rethoret-Pasty**

**November, 5th**

slido

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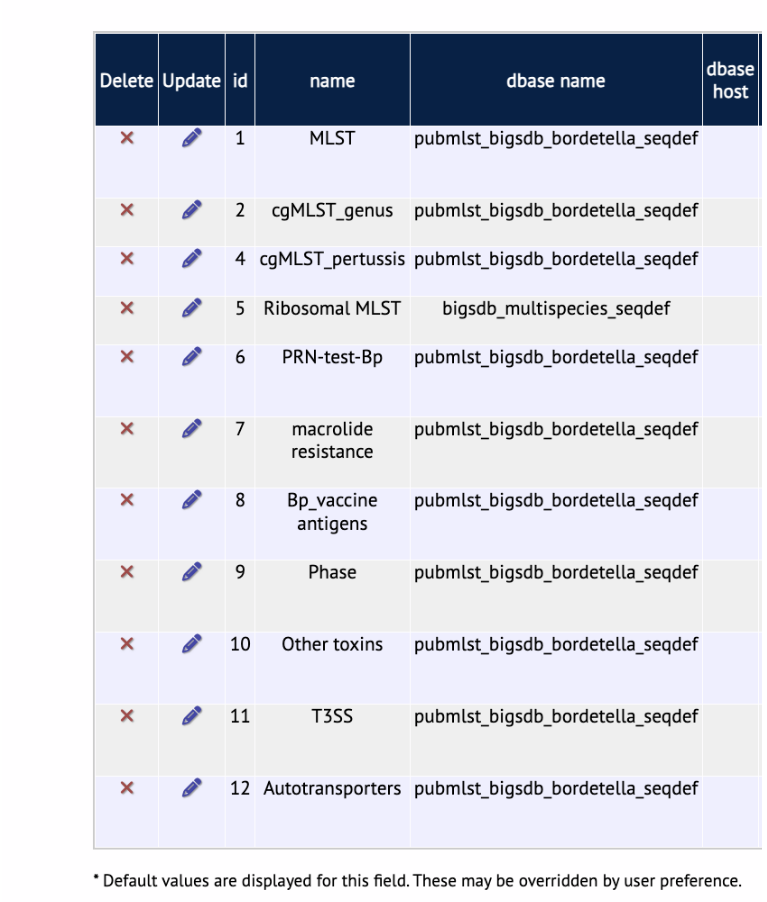
# Did you already use BIGSD for Bordetella genotyping?

ⓘ Start presenting to display the poll results on this slide.

# BigsDB Database for Bordetellae spp.
# Genotyping schemes



| Delete | Update | id | name | dbase name | dbase host |
|---|---|---|---|---|---|
| ✕ | ✎ | 1 | MLST | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 2 | cgMLST_genus | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 4 | cgMLST_pertussis | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 5 | Ribosomal MLST | bigsdb_multispecies_seqdef | |
| ✕ | ✎ | 6 | PRN-test-Bp | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 7 | macrolide resistance | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 8 | Bp_vaccine antigens | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 9 | Phase | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 10 | Other toxins | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 11 | T3SS | pubmlst_bigsdb_bordetella_seqdef | |
| ✕ | ✎ | 12 | Autotransporters | pubmlst_bigsdb_bordetella_seqdef | |

* Default values are displayed for this field. These may be overridden by user preference.

**MLST** (*adk, fumC, glyA, icd, pepA, pgm, tyrB*)

**cgMLST genus** (1415 core gene loci) : for all Bordetella spp.
**cgMLST_pertussis** (2038 core gene loci) : only for B. pertussis

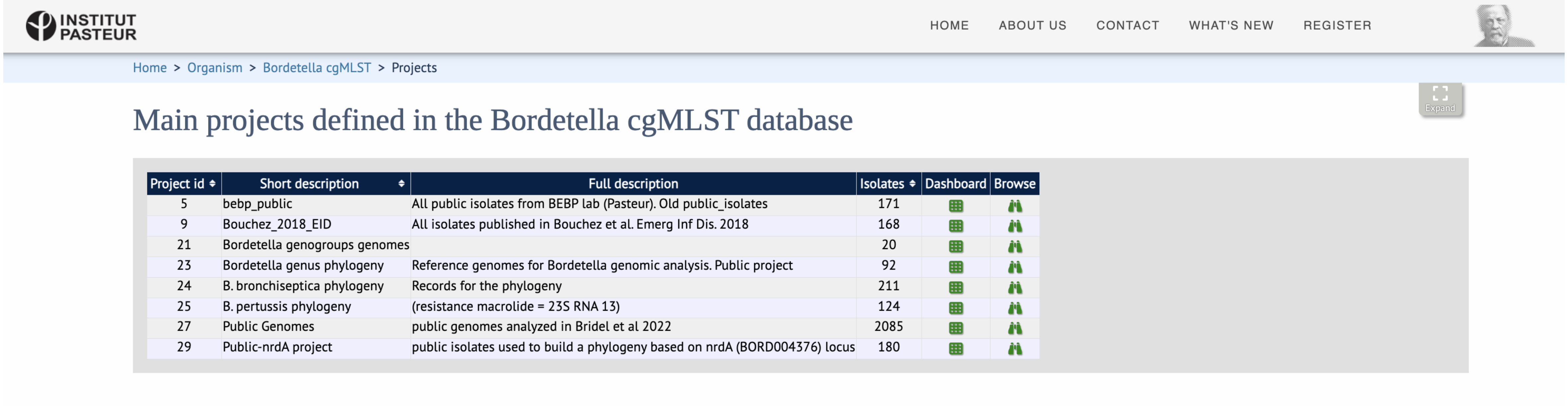
***Ribosomal MLST*** :Ribosomal Multilocus Sequence Typing (rMLST) is an approach that indexes variation of the 53 genes encoding the bacterial ribosome protein subunits (*rps* genes) as a means of integrating microbial taxonomy and typing.
rMLST is described in Jolley *et al.* 2012 *Microbiology* **158:**1005-15

**Macrolide resistance** (23S_rRNA, fhaB loci)
**Bp_vaccine antigens** (ptxP, ptxA to E, fim2, fim3, FhaB-2500-5550)
**Phase** (bipA, bvgA, bvgS)
**Other toxins** (cyaA, dnt)
**T3SS** (bopB, bopD, bopN, bsp22, bteA)
**Autotransporters** (bapC, brkA, prn, tcfA, vag8)

https://bigsdb.pasteur.fr

# BigsDB Database for Bordetellae spp.

## Public projects



### Main projects defined in the Bordetella cgMLST database

| Project id | Short description | Full description | Isolates | Dashboard | Browse |
|---|---|---|---|---|---|
| 5 | bebp_public | All public isolates from BEBP lab (Pasteur). Old public_isolates | 171 | ▦ | 🔍 |
| 9 | Bouchez_2018_EID | All isolates published in Bouchez et al. Emerg Inf Dis. 2018 | 168 | ▦ | 🔍 |
| 21 | Bordetella genogroups genomes |  | 20 | ▦ | 🔍 |
| 23 | Bordetella genus phylogeny | Reference genomes for Bordetella genomic analysis. Public project | 92 | ▦ | 🔍 |
| 24 | B. bronchiseptica phylogeny | Records for the phylogeny | 211 | ▦ | 🔍 |
| 25 | B. pertussis phylogeny | (resistance macrolide = 23S RNA 13) | 124 | ▦ | 🔍 |
| 27 | Public Genomes | public genomes analyzed in Bridel et al 2022 | 2085 | ▦ | 🔍 |
| 29 | Public-nrdA project | public isolates used to build a phylogeny based on nrdA (BORD004376) locus | 180 | ▦ | 🔍 |

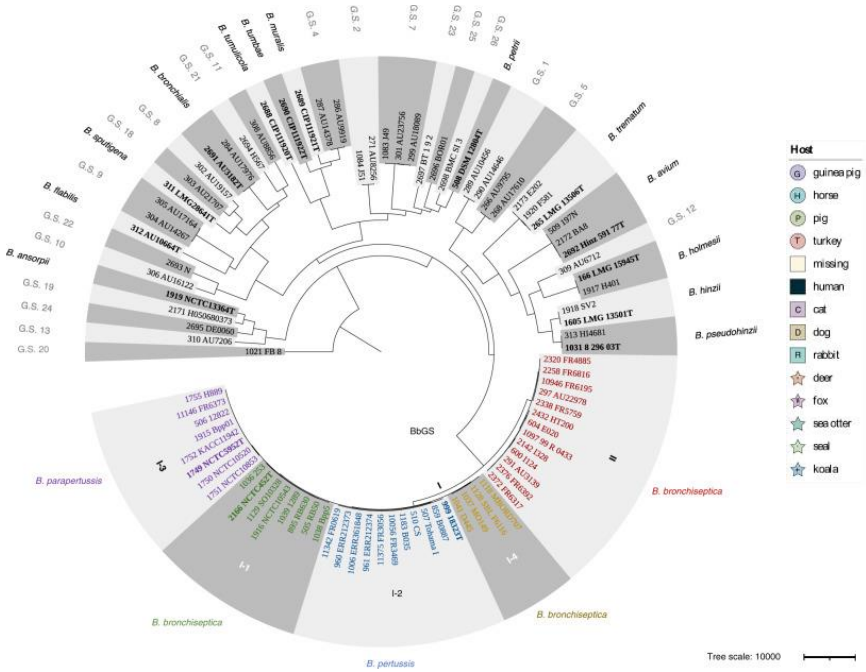
https://bigsdb.pasteur.fr/bordetella/

# BIGSdb Bordetella : overview of Isolates database, genotyping schemes and public projects

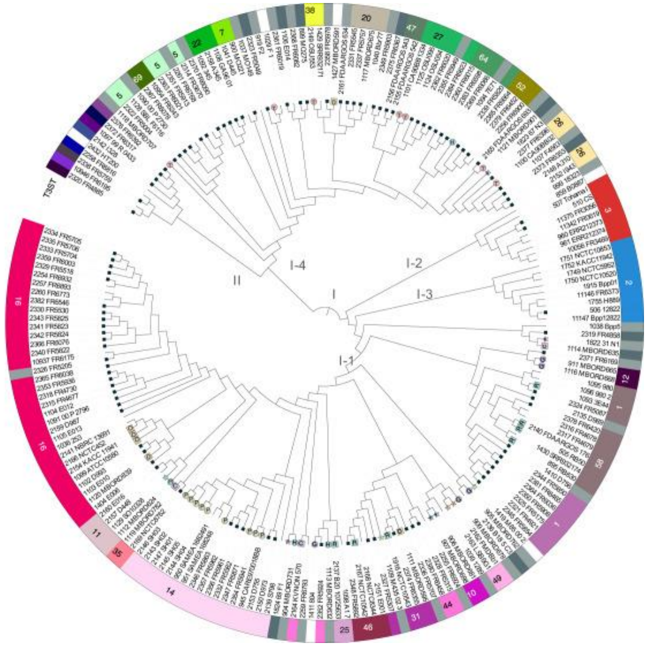
Bordetella genus Phylogeny
**Project id=23**. *B. genus*

Bordetella Bronchiseptica
**Project id=24.**
*B. bronchiseptica (T3SS-ST))*

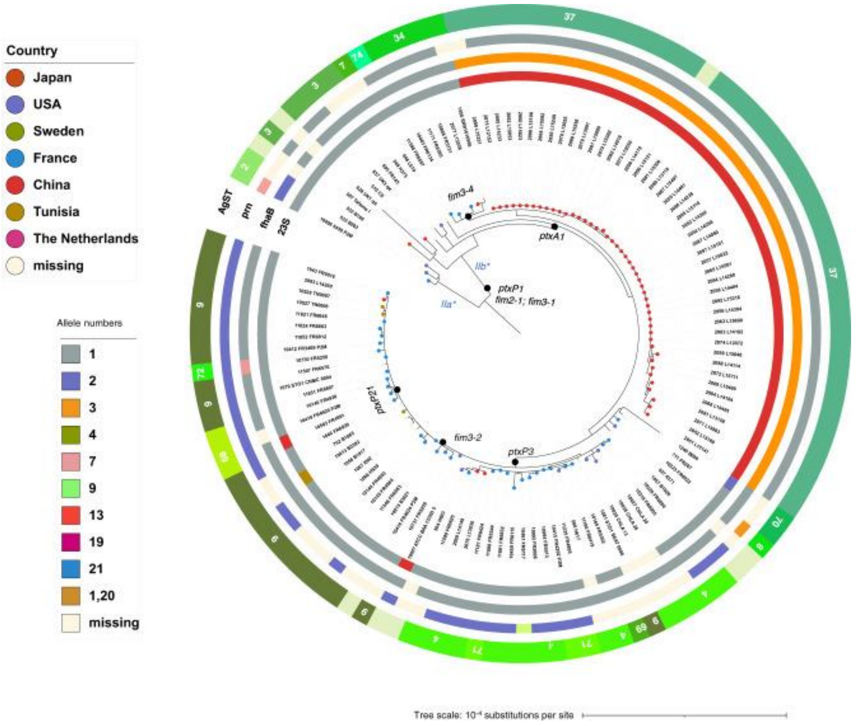
Bordetella genus Phylogeny
**Project id=25**. *B. pertussis (macrolide resistance)*



**92 Bordetella genomes**
1415 core gene sequences
*cgMLST_genus* scheme
https://itol.embl.de/shared/1l7Fw0AvKOoCF.



**186 *Bb* genomes, 9 *Bp* genomes and 9 *Bpp* genomes**
1415 core gene loci
*cgMLST_genus* scheme
https://itol.embl.de/shared/1l7Fw0AvKOoCF



**124 Bp genomes**
2038 core genome loci
*cgMLST_pertussis* scheme
https://itol.embl.de/shared/1l7Fw0AvKOoCF

A comprehensive resource for Bordetella genomic epidemiology and biodiversity studies
Bridel et al., 2022, Nat. Com. PMID: 35778384, https://pubmed.ncbi.nlm.nih.gov/35778384/

slido

Please download and install the
Slido app on all computers you use

# Do you intend to use BIGSdb Bordetella platform for

ⓘ Start presenting to display the poll results on this slide.

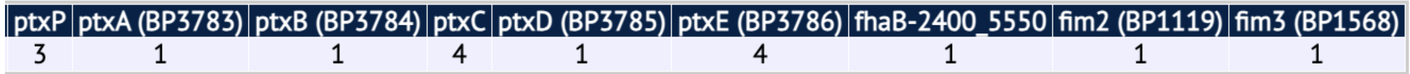
# Practical session on BIGSdb Bordetella

**Part1 :**

**In BIGSdb Bordetella Alleles & profiles database :**

Considering locus *fim3*, compare alleles 1 and 2 (i.e  fim3-1 and fim 3-2) using locus explorer;

What Bp-agST correspond to the following profiles :



| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 1 |

| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 2 |

**Part2 :**

**In BIGSdb Bordetella Isolates database :**

Considering all isolates from the public project 25,

Visualize the percentage of isolates per country in a pie chart (Field breakdown option)

Visualize the number of isolates resistant to macrolide per country (Two field breakdown option)

Using genome comparator, compare isolates FR5015 and FR5016, is it the same strain?

Using genome comparator, compare isolates FR5015 and FR4964, is it the same strain?

**Part 3 :**

**In BIGSdb Bordetella Isolates database :**

Considering all isolates from the public **project 25,**

Perform a first GrapeTree analysis based on Bp-vaccine-Antigen scheme

Color isolates per country, label BpAg-ST, indicate branch length

Visualize metadata

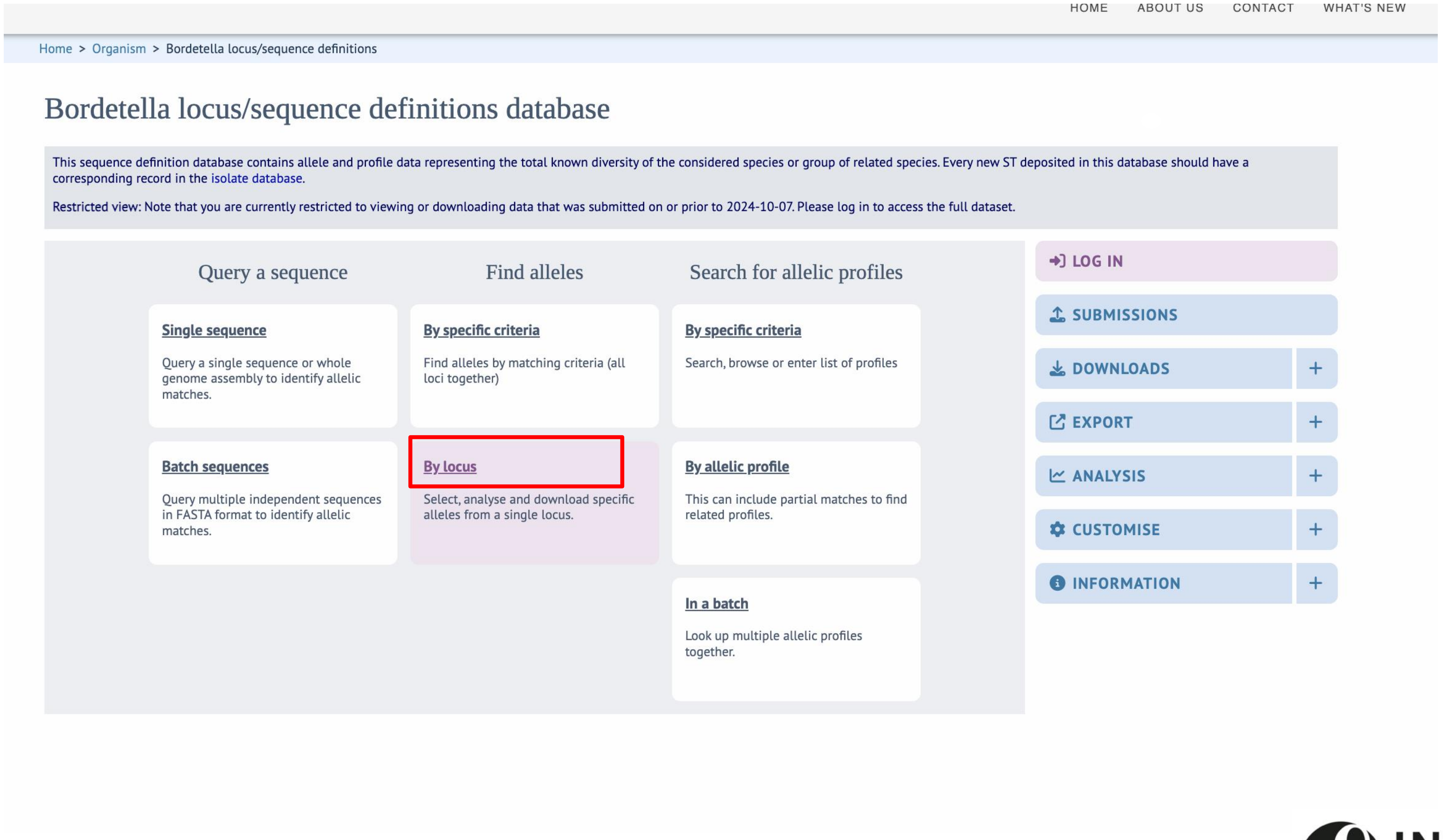
Perform a second GrapeTree based on cgMLST_pertussis

Color isolates per BpAg-ST, indicate branch length

Export image

Use Microreact to visualize analysis based on Bp-vaccine antigens and explore Microreact functions

https://bigsdb.pasteur.fr/bordetella/



# Bordetella locus/sequence definitions database

This sequence definition database contains allele and profile data representing the total known diversity of the considered species or group of related species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-10-07. Please log in to access the full dataset.

## Query a sequence

**Single sequence**

Query a single sequence or whole genome assembly to identify allelic matches.

**Batch sequences**

Query multiple independent sequences in FASTA format to identify allelic matches.

## Find alleles

**By specific criteria**

Find alleles by matching criteria (all loci together)

**By locus**

Select, analyse and download specific alleles from a single locus.

## Search for allelic profiles

**By specific criteria**

Search, browse or enter list of profiles

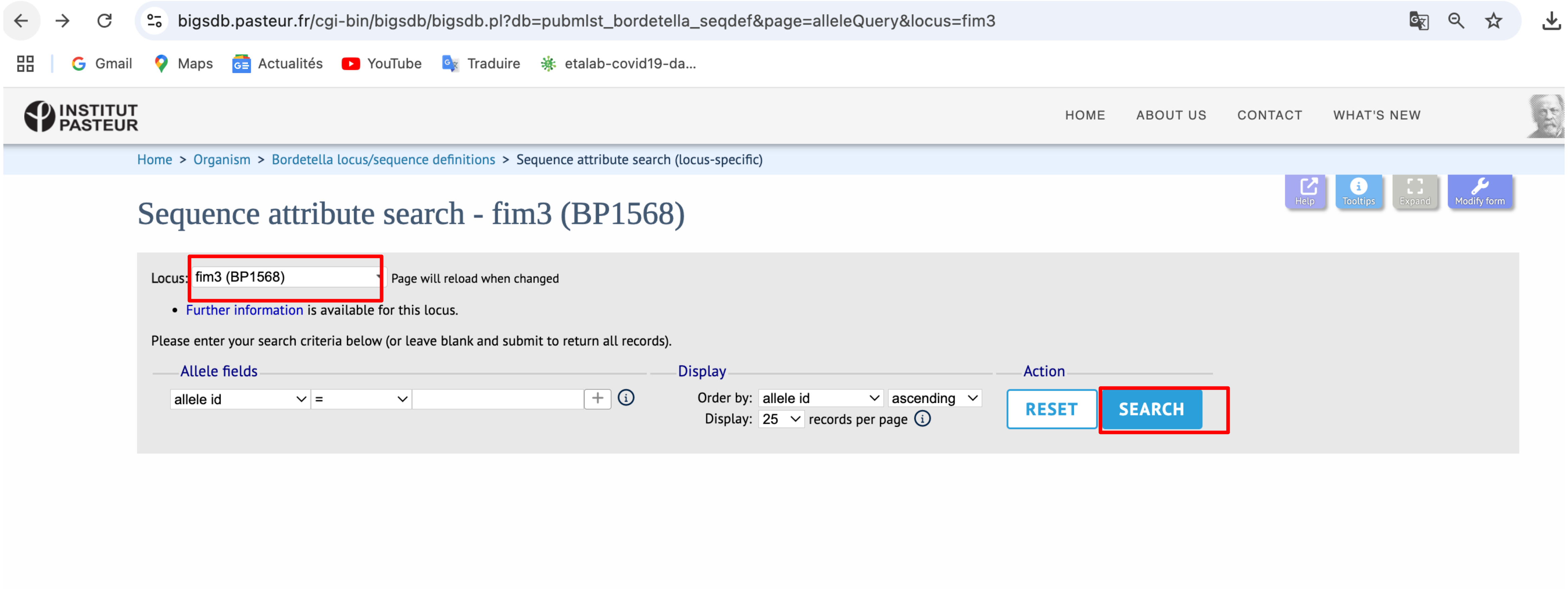
**By allelic profile**

This can include partial matches to find related profiles.

**In a batch**

Look up multiple allelic profiles together.

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Sequence attribute search (locus-specific)

## Sequence attribute search - fim3 (BP1568)

Locus: fim3 (BP1568) Page will reload when changed

- Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

**Allele fields**

allele id =

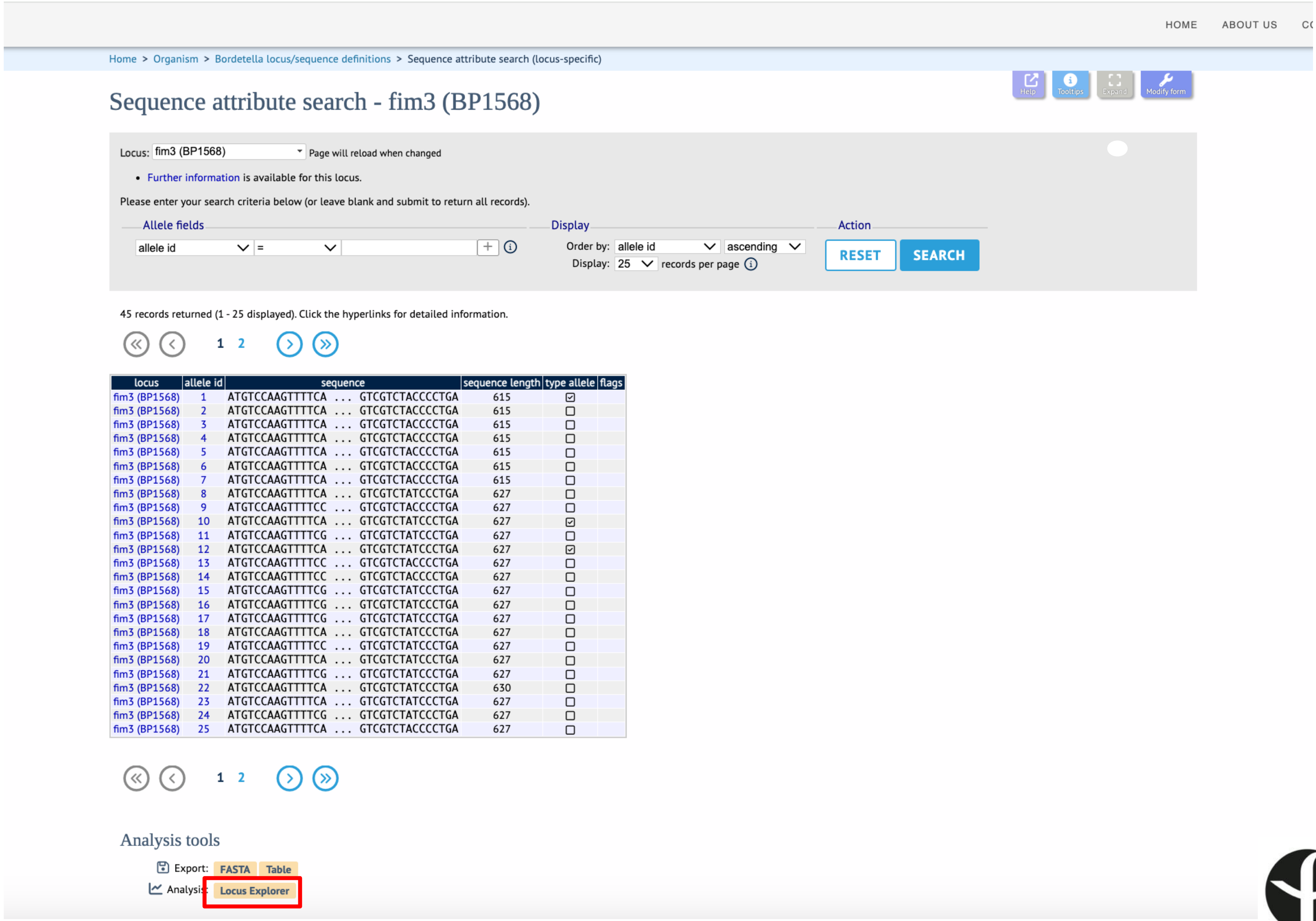
**Display**

Order by: allele id ascending

Display: 25 records per page

**Action**

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Sequence attribute search (locus-specific)

## Sequence attribute search - fim3 (BP1568)

Locus: fim3 (BP1568) Page will reload when changed

- Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

**Allele fields**

allele id =

**Display**

Order by: allele id ascending

Display: 25 records per page

**Action**

45 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

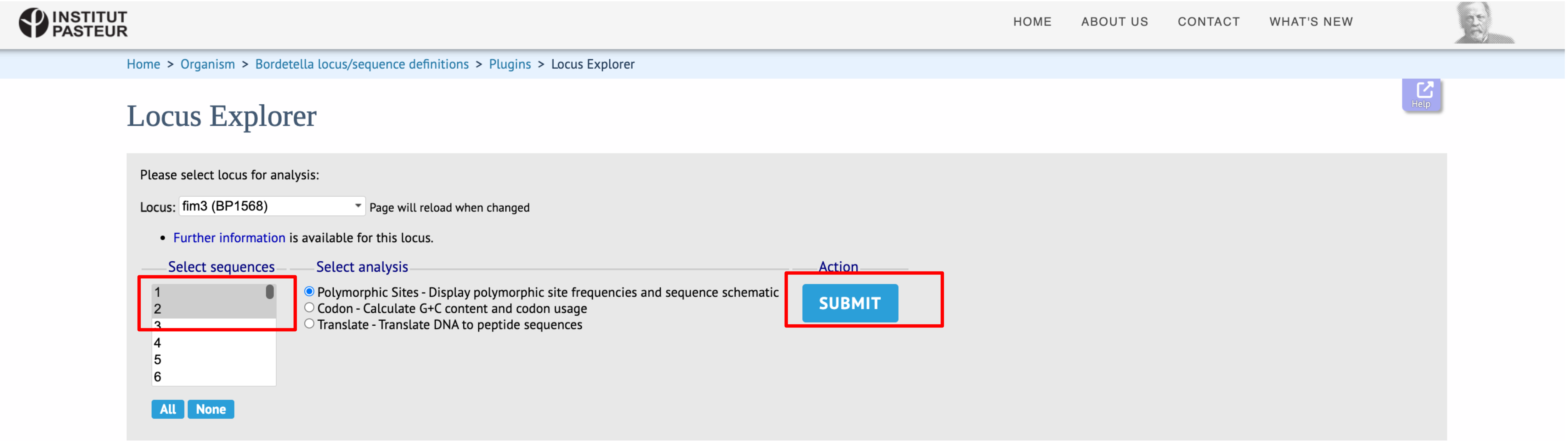
| locus | allele id | sequence | sequence length | type allele | flags |
|---|---|---|---|---|---|
| fim3 (BP1568) | 1 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☑ | |
| fim3 (BP1568) | 2 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 3 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 4 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 5 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 6 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 7 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 615 | ☐ | |
| fim3 (BP1568) | 8 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 9 | ATGTCCAAGTTTTCC ... GTCGTCTACCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 10 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☑ | |
| fim3 (BP1568) | 11 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 12 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☑ | |
| fim3 (BP1568) | 13 | ATGTCCAAGTTTTCC ... GTCGTCTACCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 14 | ATGTCCAAGTTTTCC ... GTCGTCTACCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 15 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 16 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 17 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 18 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 19 | ATGTCCAAGTTTTCC ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 20 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 21 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 22 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 630 | ☐ | |
| fim3 (BP1568) | 23 | ATGTCCAAGTTTTCA ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 24 | ATGTCCAAGTTTTCG ... GTCGTCTATCCCTGA | 627 | ☐ | |
| fim3 (BP1568) | 25 | ATGTCCAAGTTTTCA ... GTCGTCTACCCCTGA | 627 | ☐ | |

### Analysis tools

Export: FASTA Table

Analysis: Locus Explorer

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Plugins > Locus Explorer

# Locus Explorer

Please select locus for analysis:

Locus: fim3 (BP1568) Page will reload when changed

- Further information is available for this locus.

Select sequences

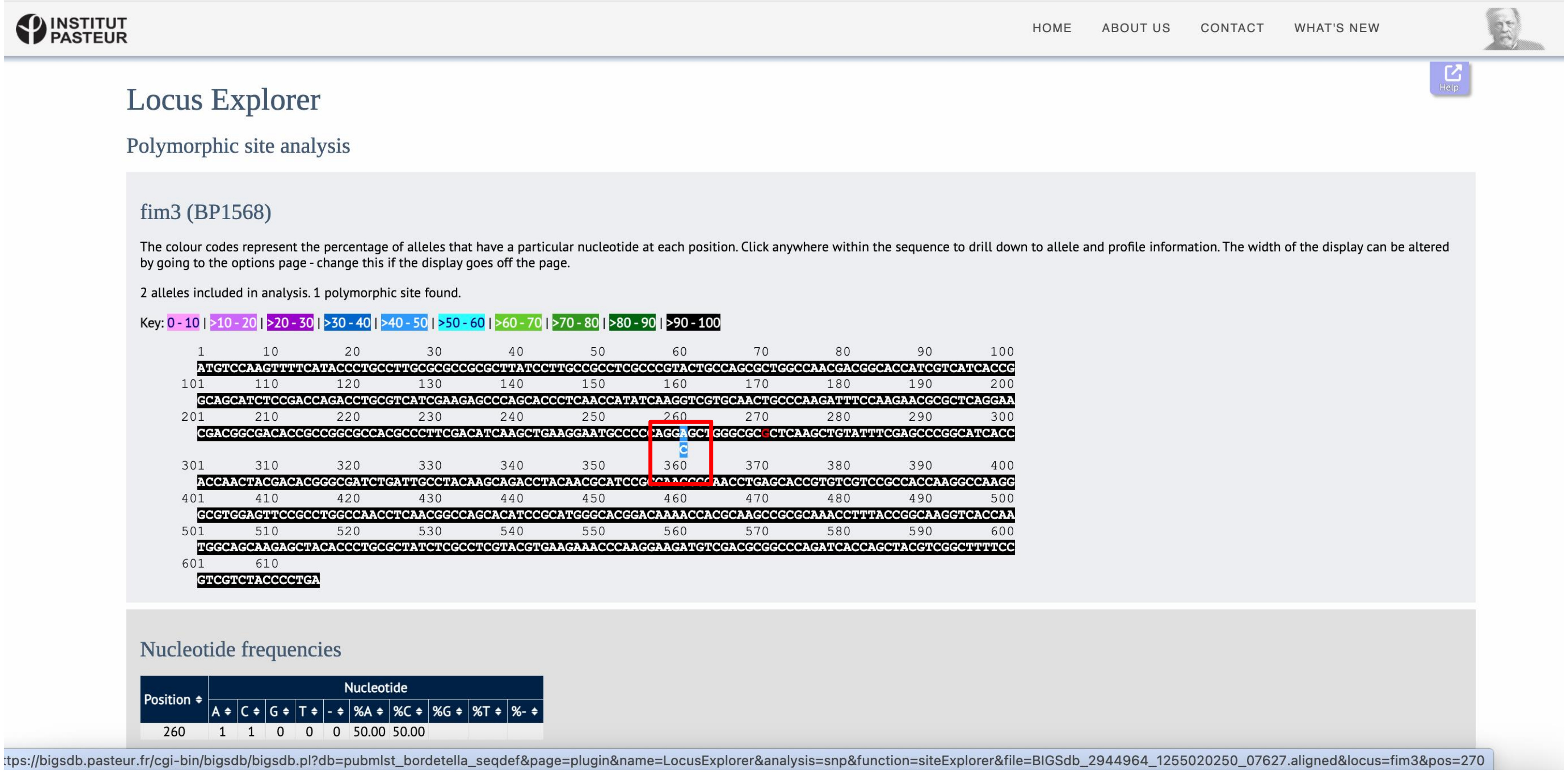
1
2
3
4
5
6

Select analysis

● Polymorphic Sites - Display polymorphic site frequencies and sequence schematic
○ Codon - Calculate G+C content and codon usage
○ Translate - Translate DNA to peptide sequences

Action

https://bigsdb.pasteur.fr/bordetella/



# Locus Explorer

## Polymorphic site analysis

### fim3 (BP1568)

The colour codes represent the percentage of alleles that have a particular nucleotide at each position. Click anywhere within the sequence to drill down to allele and profile information. The width of the display can be altered by going to the options page - change this if the display goes off the page.

2 alleles included in analysis. 1 polymorphic site found.

Key: 0 - 10 | >10 - 20 | >20 - 30 | >30 - 40 | >40 - 50 | >50 - 60 | >60 - 70 | >70 - 80 | >80 - 90 | >90 - 100

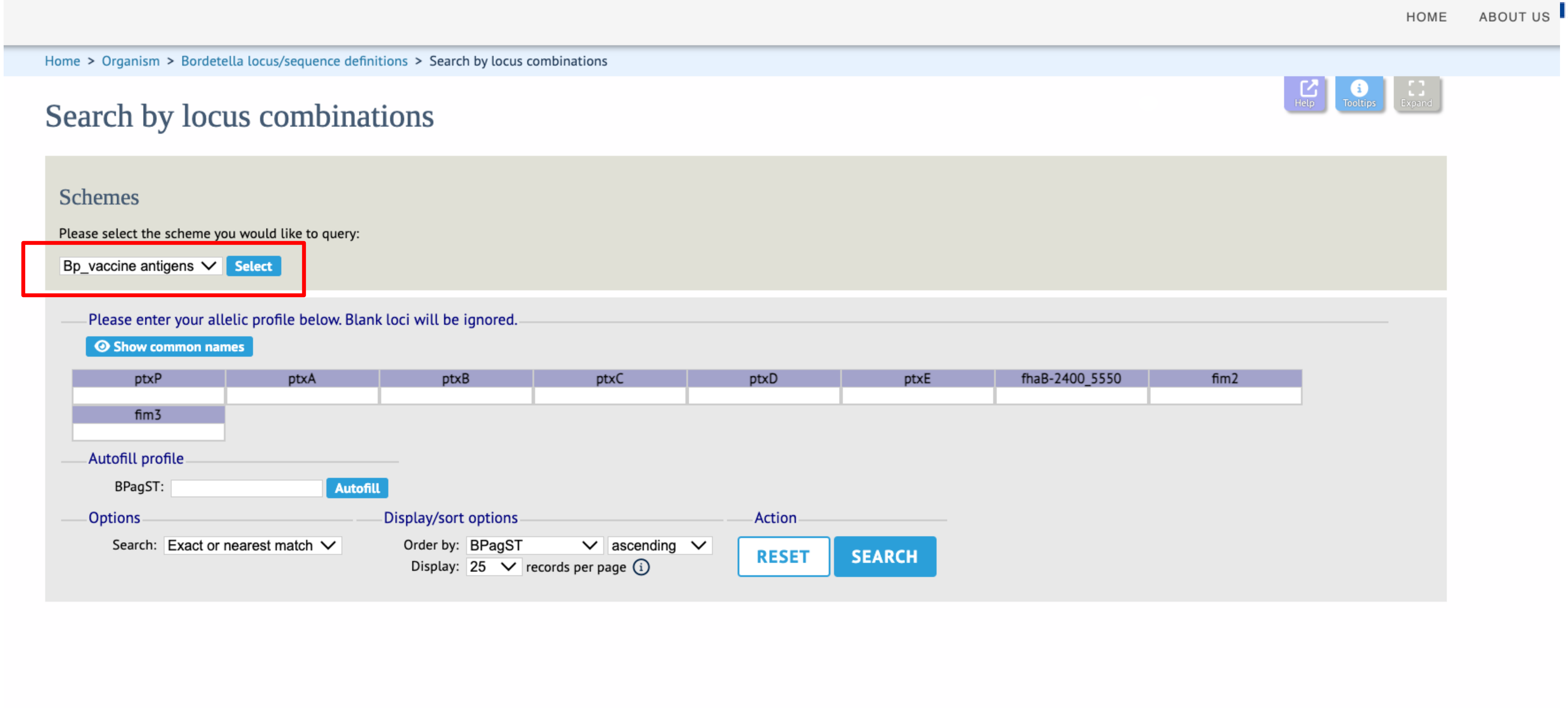
```
  1        10         20         30         40         50         60         70         80         90         100
 ATGTCCAAGTTTTCATACCCTGCCTTGCGCGCCGCGCTTATCCTTGCCGCCTCGCCCGTACTGCCAGCGCTGGCCAACGACGGCACCATCGTCATCACCG
101       110        120        130        140        150        160        170        180        190        200
 GCAGCATCTCCGACCAGACCTGCGTCATCGAAGAGCCCAGCACCCTCAACCATATCAAGGTCGTGCAACTGCCCAAGATTTCCAAGAACGCGCTCAGGAA
201       210        220        230        240        250        260        270        280        290        300
 CGACGGCGACACCGCCGGCGCCACGCCCTTCGACATCAAGCTGAAGGAATGCCCCCAGGAGCTGGGCGCGCTCAAGCTGTATTTCGAGCCCGGCATCACC
                                                            C
301       310        320        330        340        350        360        370        380        390        400
 ACCAACTACGACACGGGCGATCTGATTGCCTACAAGCAGACCTACAACGCATCCGCCAACGCCAACCTGAGCACCGTGTCGTCCGCCACCAAGGCCAAGG
401       410        420        430        440        450        460        470        480        490        500
 GCGTGGAGTTCCGCCTGGCCAACCTCAACGGCCAGCACATCCGCATGGGCACGGACAAAACCACGCAAGCCGCGCAAACCTTTACCGGCAAGGTCACCAA
501       510        520        530        540        550        560        570        580        590        600
 TGGCAGCAAGAGCTACACCCTGCGCTATCTCGCCTCGTACGTGAAGAAACCCAAGGAAGATGTCGACGCGGCCCAGATCACCAGCTACGTCGGCTTTTCC
601       610
 GTCGTCTACCCCTGA
```

### Nucleotide frequencies

| Position | Nucleotide | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | A | C | G | T | - | %A | %C | %G | %T | %- |
| 260 | 1 | 1 | 0 | 0 | 0 | 50.00 | 50.00 | | | |

ttps://bigsdb.pasteur.fr/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst_bordetella_seqdef&page=plugin&name=LocusExplorer&analysis=snp&function=siteExplorer&file=BIGSdb_2944964_1255020250_07627.aligned&locus=fim3&pos=270

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Search by locus combinations

# Search by locus combinations

## Schemes

Please select the scheme you would like to query:

Bp_vaccine antigens

Please enter your allelic profile below. Blank loci will be ignored.

| ptxP | ptxA | ptxB | ptxC | ptxD | ptxE | fhaB-2400_5550 | fim2 |
|---|---|---|---|---|---|---|---|
| | | | | | | | |

| fim3 |
|---|
| |

Autofill profile

BPagST:

Options

Search: Exact or nearest match

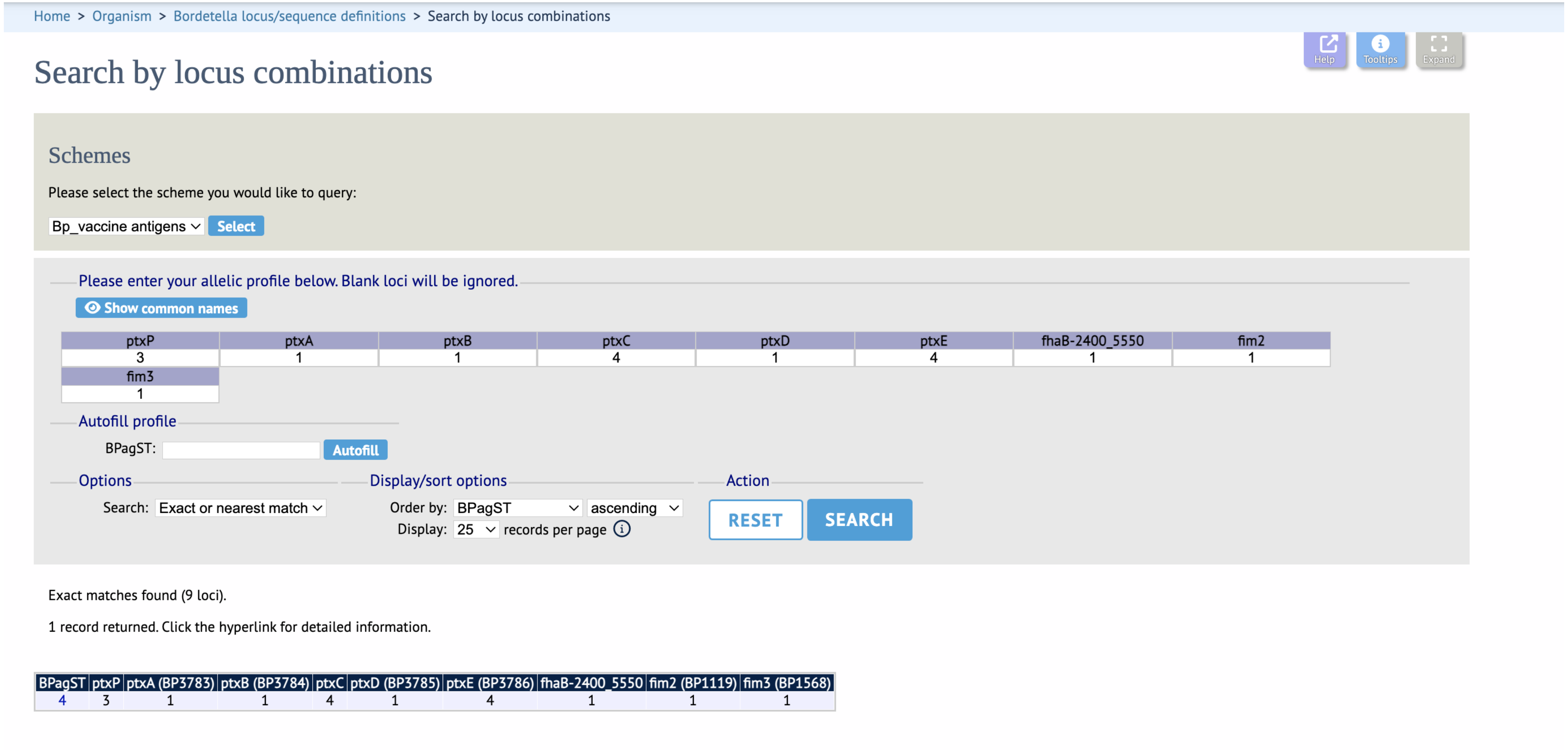
Display/sort options

Order by: BPagST ascending

Display: 25 records per page

Action

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Search by locus combinations

# Search by locus combinations

## Schemes

Please select the scheme you would like to query:

Bp_vaccine antigens

Please enter your allelic profile below. Blank loci will be ignored.

| ptxP | ptxA | ptxB | ptxC | ptxD | ptxE | fhaB-2400_5550 | fim2 |
|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 |

| fim3 |
|---|
| 1 |

Autofill profile

BPagST:

Options

Search: Exact or nearest match

Display/sort options

Order by: BPagST ascending

Display: 25 records per page

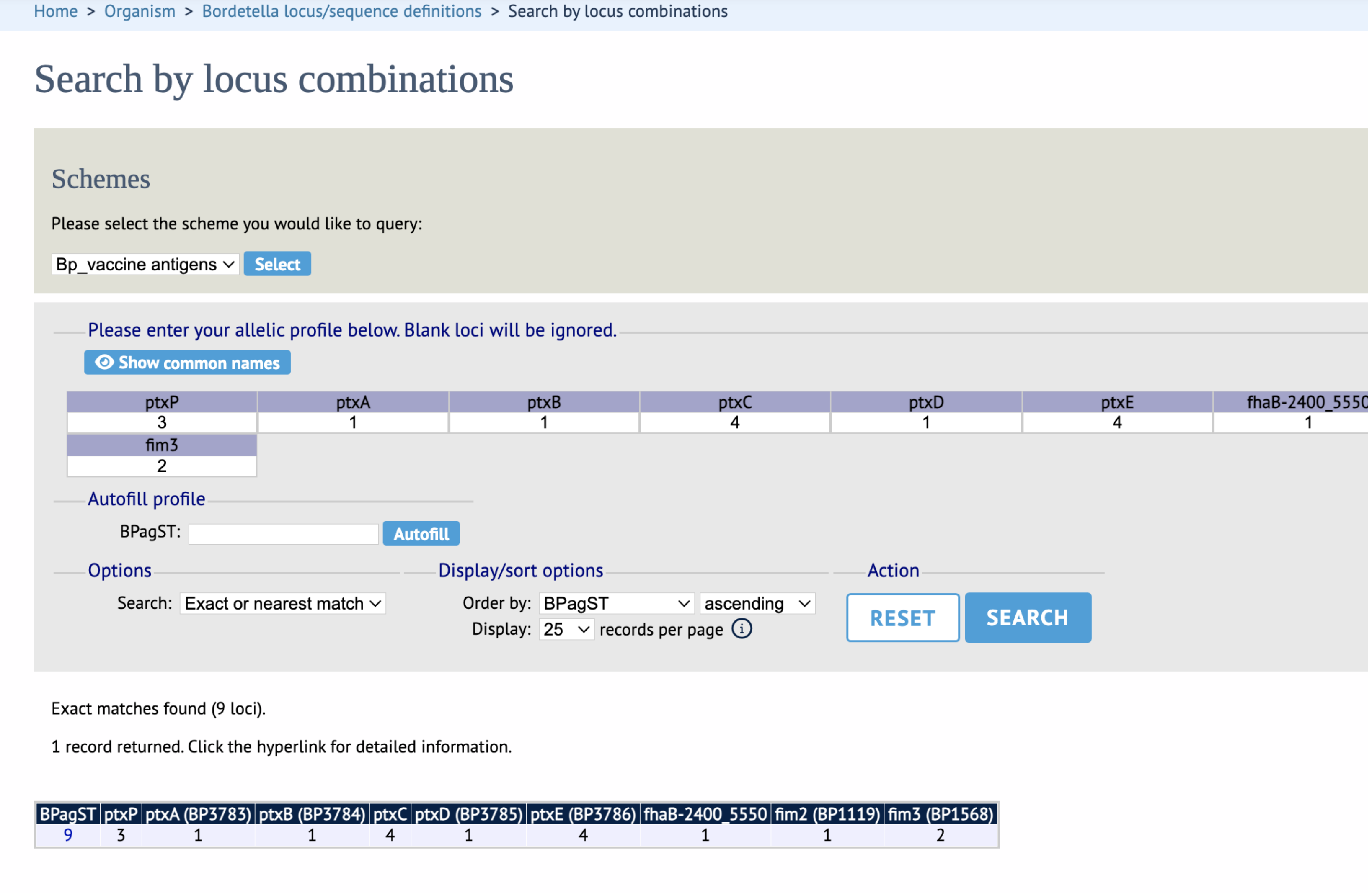
Action

Exact matches found (9 loci).

1 record returned. Click the hyperlink for detailed information.

| BPagST | ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|---|
| 4 | 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 1 |

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella locus/sequence definitions > Search by locus combinations

# Search by locus combinations

## Schemes

Please select the scheme you would like to query:

Bp_vaccine antigens

Please enter your allelic profile below. Blank loci will be ignored.

| ptxP | ptxA | ptxB | ptxC | ptxD | ptxE | fhaB-2400_555 |
|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 |

| fim3 |
|---|
| 2 |

Autofill profile

BPagST:

Options

Search: Exact or nearest match

Display/sort options

Order by: BPagST ascending

Display: 25 records per page

Action

Exact matches found (9 loci).

1 record returned. Click the hyperlink for detailed information.

| BPagST | ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|---|
| 9 | 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 2 |

https://bigsdb.pasteur.fr/bordetella/

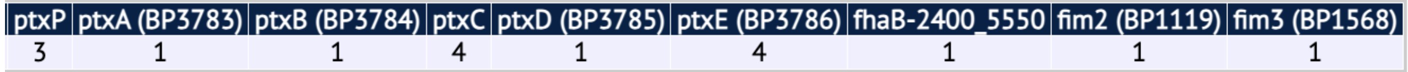
# Practical session on BIGSdb Bordetella

## Part1 :

**In BIGSdb Bordetella Alleles & profiles database :**

Considering locus *fim3*, compare alleles 1 and 2 (i.e  fim3-1 and fim 3-2) using locus explorer;

What Bp-agST correspond to the following profiles :



| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 1 |

| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 2 |

## Part2 :

In BIGSdb Bordetella Isolates database :

Considering all isolates from the public project 25,

Visualize the percentage of isolates per country in a pie chart (Field breakdown option)

Visualize the number of isolates resistant to macrolide per country (Two field breakdown option)

Using genome comparator, compare isolates FR5015 and FR5016, is it the same strain?

Using genome comparator, compare isolates FR5015 and FR4964, is it the same strain?

## Part 3 :

**In BIGSdb Bordetella Isolates database :**

Considering all isolates from the public **project 25,**

Perform a first GrapeTree analysis based on Bp-vaccine-Antigen scheme

Color isolates per country, label BpAg-ST, indicate branch length

Visualize metadata

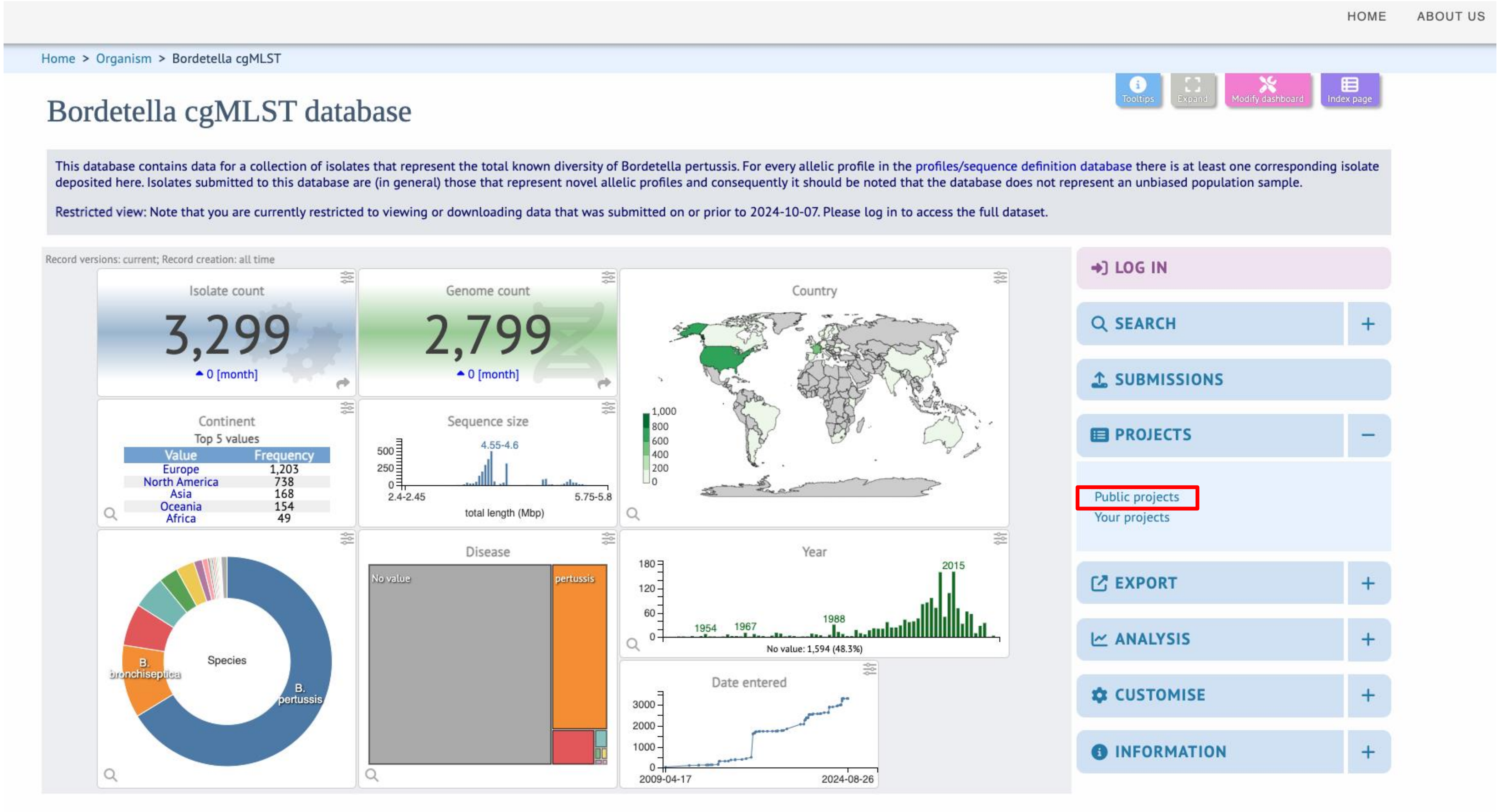
Perform a second GrapeTree based on cgMLST_pertussis

Color isolates per BpAg-ST, indicate branch length

Export image

Use Microreact to visualize analysis based on Bp-vaccine antigens and explore Microreact functions

https://bigsdb.pasteur.fr/bordetella/



# Bordetella cgMLST database

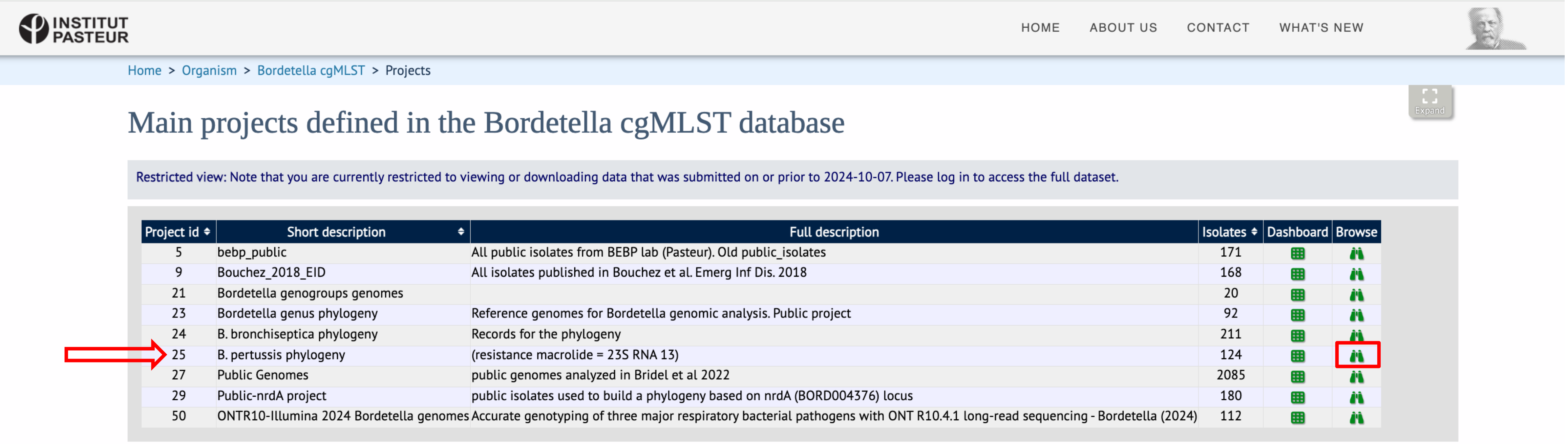
This database contains data for a collection of isolates that represent the total known diversity of Bordetella pertussis. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Isolates submitted to this database are (in general) those that represent novel allelic profiles and consequently it should be noted that the database does not represent an unbiased population sample.

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-10-07. Please log in to access the full dataset.

Record versions: current; Record creation: all time

| Value | Frequency |
|---|---|
| Europe | 1,203 |
| North America | 738 |
| Asia | 168 |
| Oceania | 154 |
| Africa | 49 |

https://bigsdb.pasteur.fr/bordetella/



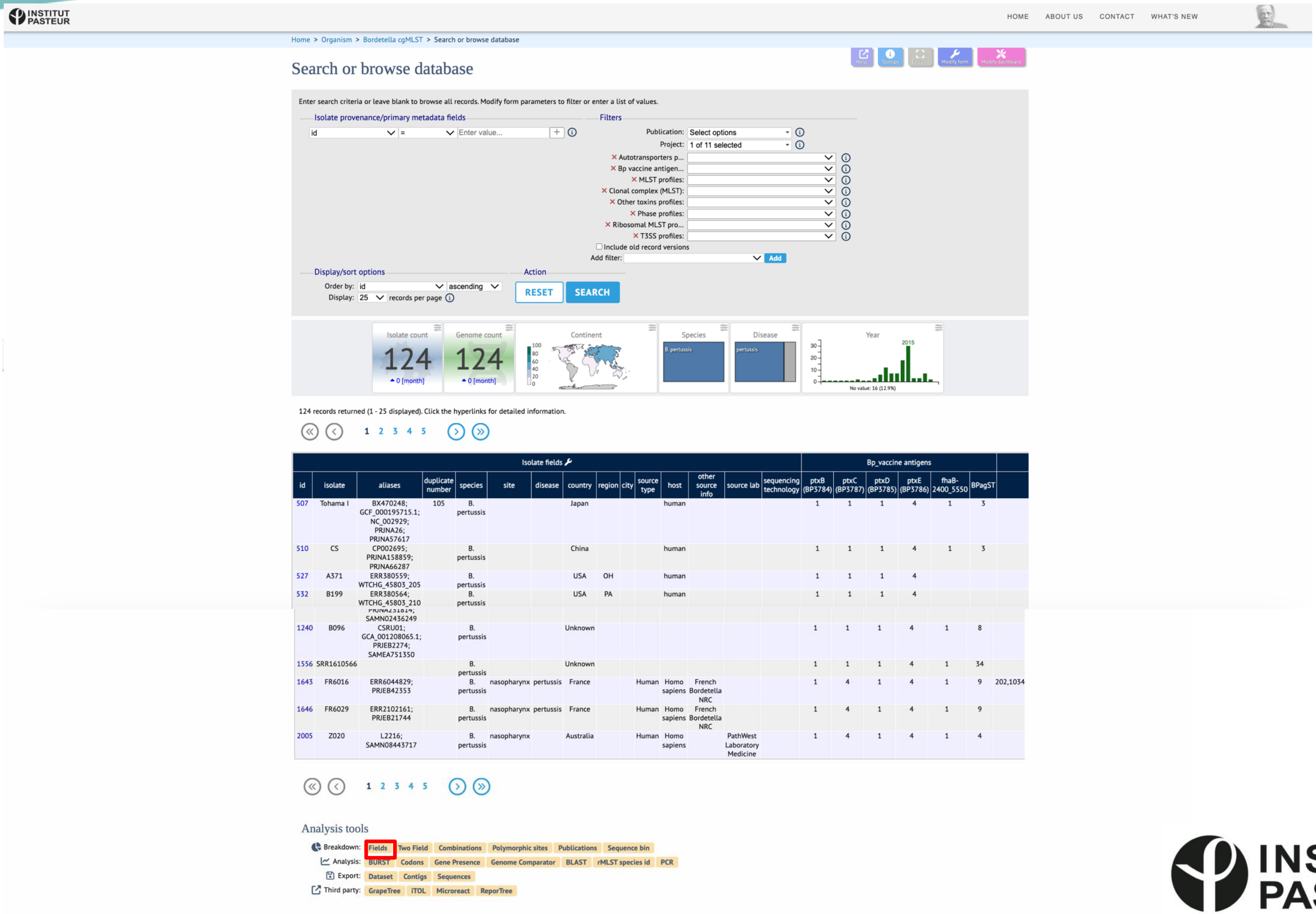
Home > Organism > Bordetella cgMLST > Projects

## Main projects defined in the Bordetella cgMLST database

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-10-07. Please log in to access the full dataset.

| Project id | Short description | Full description | Isolates | Dashboard | Browse |
|---|---|---|---|---|---|
| 5 | bebp_public | All public isolates from BEBP lab (Pasteur). Old public_isolates | 171 | ▦ | 🔍 |
| 9 | Bouchez_2018_EID | All isolates published in Bouchez et al. Emerg Inf Dis. 2018 | 168 | ▦ | 🔍 |
| 21 | Bordetella genogroups genomes | | 20 | ▦ | 🔍 |
| 23 | Bordetella genus phylogeny | Reference genomes for Bordetella genomic analysis. Public project | 92 | ▦ | 🔍 |
| 24 | B. bronchiseptica phylogeny | Records for the phylogeny | 211 | ▦ | 🔍 |
| 25 | B. pertussis phylogeny | (resistance macrolide = 23S RNA 13) | 124 | ▦ | 🔍 |
| 27 | Public Genomes | public genomes analyzed in Bridel et al 2022 | 2085 | ▦ | 🔍 |
| 29 | Public-nrdA project | public isolates used to build a phylogeny based on nrdA (BORD004376) locus | 180 | ▦ | 🔍 |
| 50 | ONTR10-Illumina 2024 Bordetella genomes | Accurate genotyping of three major respiratory bacterial pathogens with ONT R10.4.1 long-read sequencing - Bordetella (2024) | 112 | ▦ | 🔍 |

https://bigsdb.pasteur.fr/bordetella/



## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance/primary metadata fields**

id = Enter value... +

**Filters**

Publication: Select options
Project: 1 of 11 selected
Autotransporters p...:
Bp vaccine antigen...:
MLST profiles:
Clonal complex (MLST):
Other toxins profiles:
Phase profiles:
Ribosomal MLST pro...:
T3SS profiles:
☐ Include old record versions
Add filter: Add

**Display/sort options**

Order by: id ascending
Display: 25 records per page

**Action**

RESET SEARCH

124 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« ‹ 1 2 3 4 5 › »

| Isolate fields | | | | | | | | | | | | | | | Bp_vaccine antigens | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| id | isolate | aliases | duplicate number | species | site | disease | country | region | city | source type | host | other source info | source lab | sequencing technology | ptxB (BP3784) | ptxC (BP3787) | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | BPagST | |
| 507 | Tohama I | BX470248;<br>GCF_000195715.1;<br>NC_002929;<br>PRJNA26;<br>PRJNA57617 | 105 | B. pertussis | | | Japan | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 510 | CS | CP002695;<br>PRJNA158859;<br>PRJNA66287 | | B. pertussis | | | China | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 527 | A371 | ERR380559;<br>WTCHG_45803_205 | | B. pertussis | | | USA | OH | | | human | | | | 1 | 1 | 1 | 4 | | | |
| 532 | B199 | ERR380564;<br>WTCHG_45803_210 | | B. pertussis | | | USA | PA | | | human | | | | 1 | 1 | 1 | 4 | | | |
| | | PRJNA231814;<br>SAMN02436249 | | | | | | | | | | | | | | | | | | | |
| 1240 | B096 | CSRU01;<br>GCA_001208065.1;<br>PRJEB2274;<br>SAMEA751350 | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 8 | |
| 1556 | SRR1610566 | | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 34 | |
| 1643 | FR6016 | ERR6044829;<br>PRJEB42353 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | 202,1034 |
| 1646 | FR6029 | ERR2102161;<br>PRJEB21744 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | |
| 2005 | Z020 | L2216;<br>SAMN08443717 | | B. pertussis | nasopharynx | | Australia | | | Human | Homo sapiens | | PathWest Laboratory Medicine | | 1 | 4 | 1 | 4 | 1 | 4 | |

« ‹ 1 2 3 4 5 › »

### Analysis tools

https://bigsdb.pasteur.fr/bordetella/

Home > Organism > Bordetella cgMLST > Plugins > Field breakdown

# Field breakdown of dataset

Isolate records: 124

Field selection

Select field: country

List: ● fields ○ loci ○ schemes

Controls

Theme:

Range:

Projection: Natural Earth

https://bigsdb.pasteur.fr/bordetella/

Home > Organism > Bordetella cgMLST > Plugins > Field breakdown

# Field breakdown of dataset

Isolate records: 124

Field selection

Select field: country

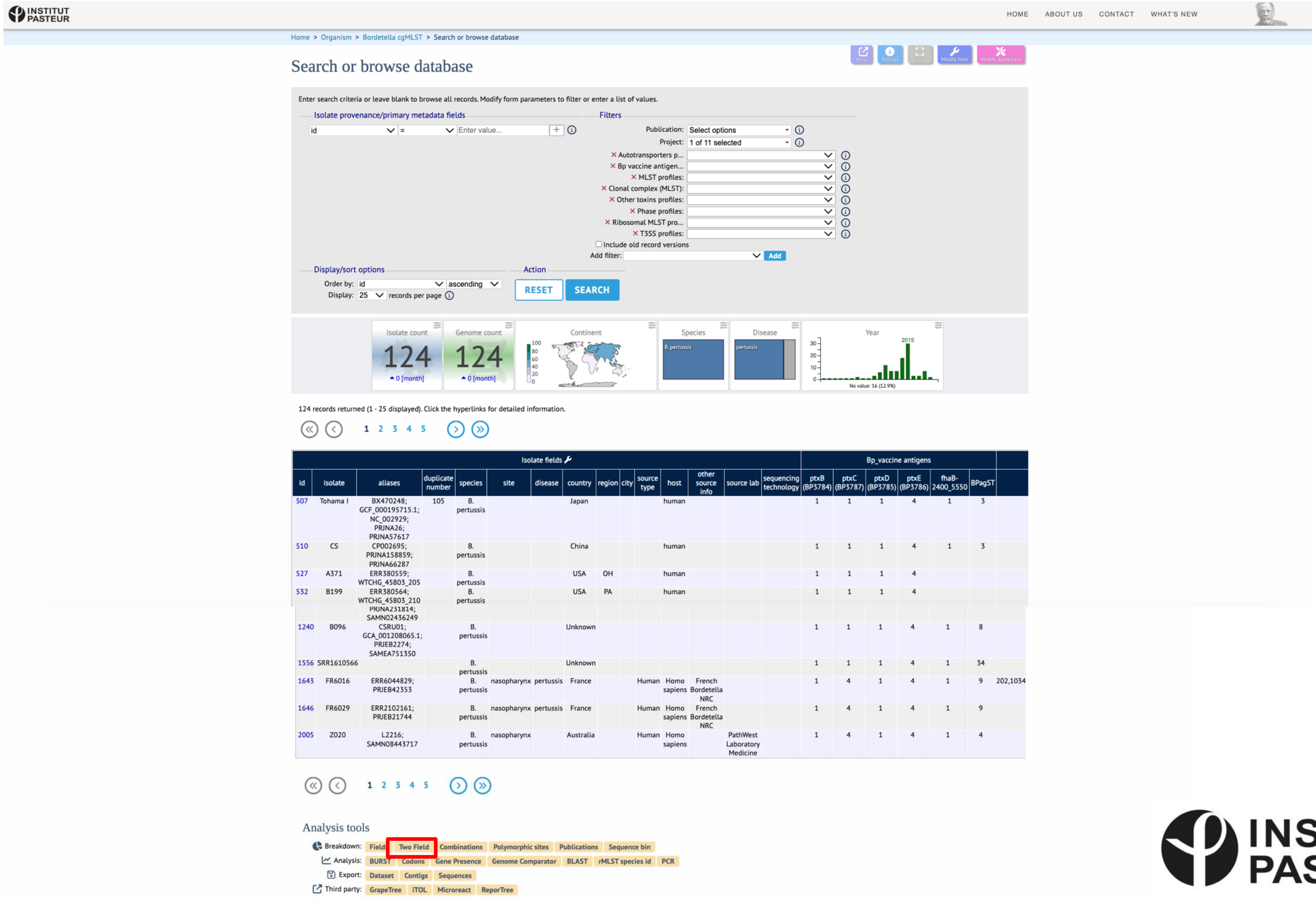
List: ● fields ○ loci ○ schemes

Max segments: 20

country (9 values)

https://bigsdb.pasteur.fr/bordetella/

Bridel & Bouchez, Nature Comm. 2022



Home > Organism > Bordetella cgMLST > Search or browse database

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance/primary metadata fields**

id = Enter value...

**Filters**

Publication: Select options
Project: 1 of 11 selected
Autotransporters p...:
Bp vaccine antigen...:
MLST profiles:
Clonal complex (MLST):
Other toxins profiles:
Phase profiles:
Ribosomal MLST pro...:
T3SS profiles:
☐ Include old record versions
Add filter: Add

**Display/sort options**

Order by: id ascending
Display: 25 records per page

**Action**

RESET SEARCH

124 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« ‹ 1 2 3 4 5 › »

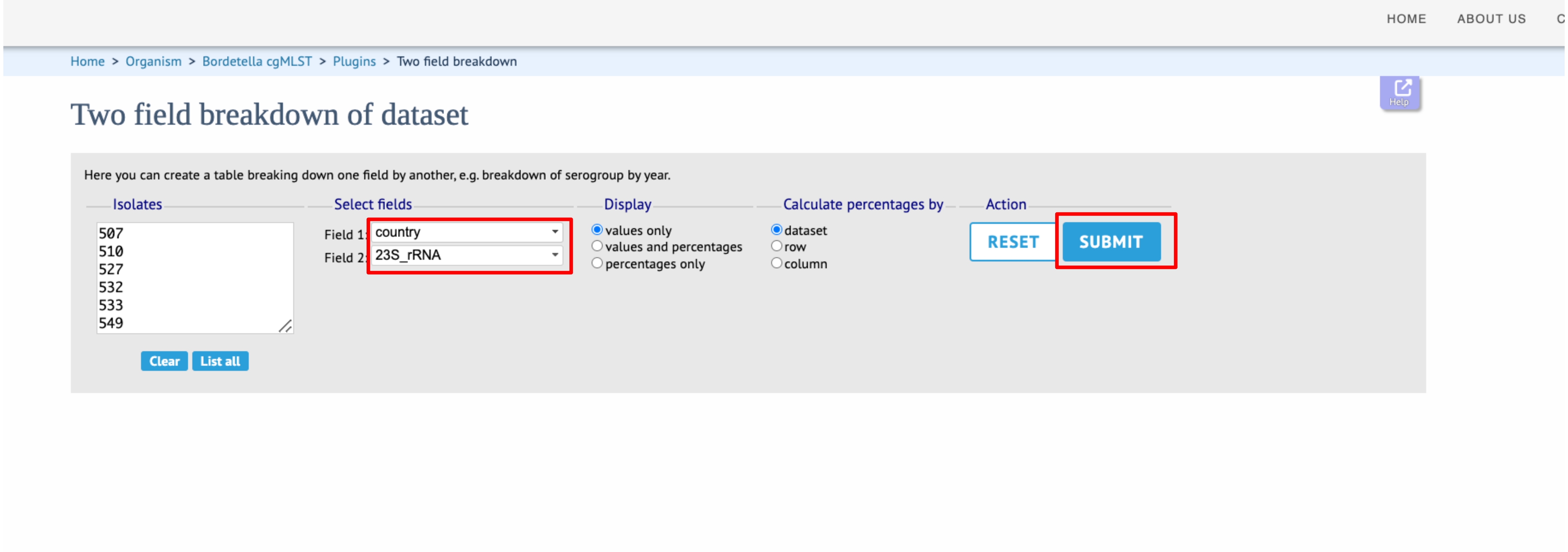
| Isolate fields | | | | | | | | | | | | | | | Bp_vaccine antigens | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| id | isolate | aliases | duplicate number | species | site | disease | country | region | city | source type | host | other source info | source lab | sequencing technology | ptxB (BP3784) | ptxC (BP3787) | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | BPagST | |
| 507 | Tohama I | BX470248;<br>GCF_000195715.1;<br>NC_002929;<br>PRJNA26;<br>PRJNA57617 | 105 | B. pertussis | | | Japan | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 510 | CS | CP002695;<br>PRJNA158859;<br>PRJNA66287 | | B. pertussis | | | China | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 527 | A371 | ERR380559;<br>WTCHG_45803_205 | | B. pertussis | | | USA | OH | | | human | | | | 1 | 1 | 1 | 4 | | | |
| 532 | B199 | ERR380564;<br>WTCHG_45803_210 | | B. pertussis | | | USA | PA | | | human | | | | 1 | 1 | 1 | 4 | | | |
| | | PRJNA231814;<br>SAMN02436249 | | | | | | | | | | | | | | | | | | | |
| 1240 | B096 | CSRU01;<br>GCA_001208065.1;<br>PRJEB2274;<br>SAMEA751350 | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 8 | |
| 1556 | SRR1610566 | | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 34 | |
| 1643 | FR6016 | ERR6044829;<br>PRJEB42353 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | 202,1034 |
| 1646 | FR6029 | ERR2102161;<br>PRJEB21744 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | |
| 2005 | Z020 | L2216;<br>SAMN08443717 | | B. pertussis | nasopharynx | | Australia | | | Human | Homo sapiens | | PathWest Laboratory Medicine | | 1 | 4 | 1 | 4 | 1 | 4 | |

« ‹ 1 2 3 4 5 › »

### Analysis tools

Breakdown: Fields | Two Field | Combinations | Polymorphic sites | Publications | Sequence bin
Analysis: BURST | Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR
Export: Dataset | Contigs | Sequences
Third party: GrapeTree | iTOL | Microreact | ReporTree

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella cgMLST > Plugins > Two field breakdown

Two field breakdown of dataset

Here you can create a table breaking down one field by another, e.g. breakdown of serogroup by year.

Isolates
507
510
527
532
533
549

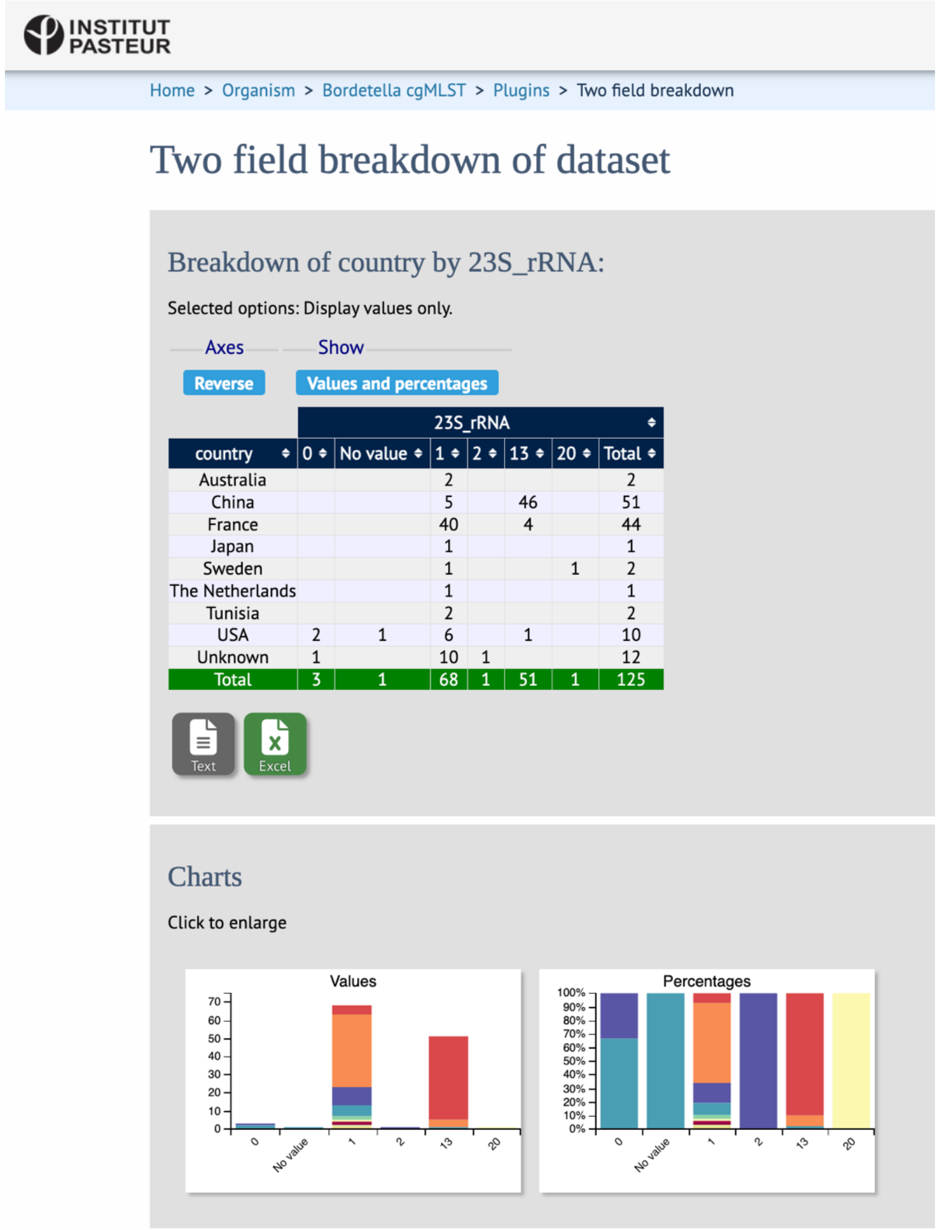
Select fields
Field 1: country
Field 2: 23S_rRNA

Display
● values only
○ values and percentages
○ percentages only

Calculate percentages by
● dataset
○ row
○ column

Action

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella cgMLST > Plugins > Two field breakdown

# Two field breakdown of dataset

## Breakdown of country by 23S_rRNA:

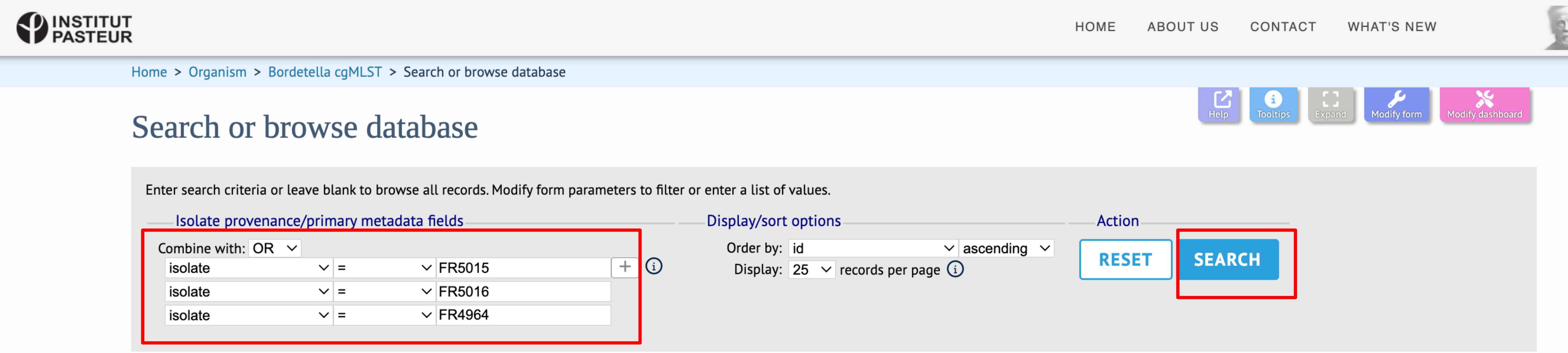
Selected options: Display values only.

| | 23S_rRNA | | | | | | |
|---|---|---|---|---|---|---|---|
| country | 0 | No value | 1 | 2 | 13 | 20 | Total |
| Australia | | | 2 | | | | 2 |
| China | | | 5 | | 46 | | 51 |
| France | | | 40 | | 4 | | 44 |
| Japan | | | 1 | | | | 1 |
| Sweden | | | 1 | | | 1 | 2 |
| The Netherlands | | | 1 | | | | 1 |
| Tunisia | | | 2 | | | | 2 |
| USA | 2 | 1 | 6 | | 1 | | 10 |
| Unknown | 1 | | 10 | 1 | | | 12 |
| Total | 3 | 1 | 68 | 1 | 51 | 1 | 125 |

## Charts

Click to enlarge

[https://bigsdb.pasteur.fr/bordetella/](https://bigsdb.pasteur.fr/bordetella/)



Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

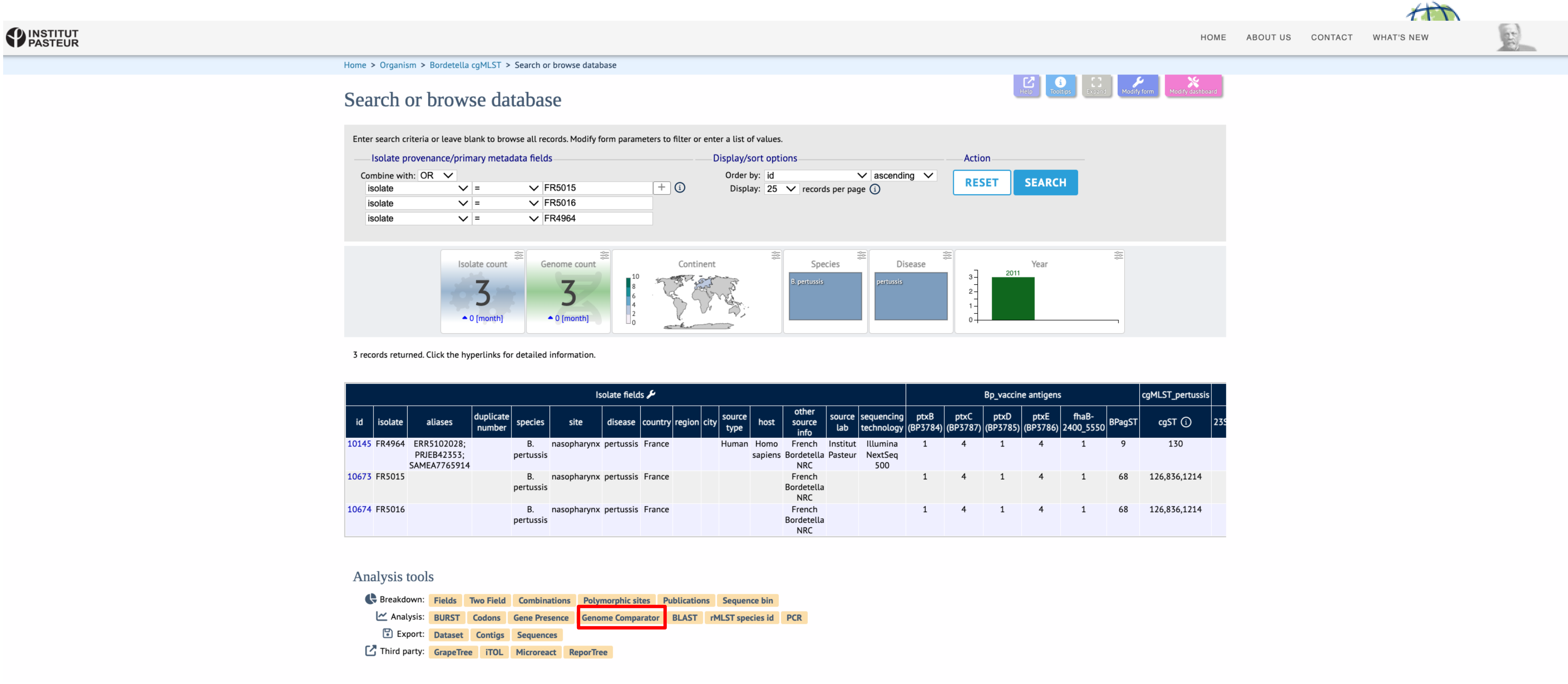
Combine with: OR
isolate = FR5015
isolate = FR5016
isolate = FR4964

Display/sort options

Order by: id ascending
Display: 25 records per page

Action

https://bigsdb.pasteur.fr/bordetella/



## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance/primary metadata fields**

Combine with: OR

isolate = FR5015

isolate = FR5016

isolate = FR4964

**Display/sort options**

Order by: id ascending

Display: 25 records per page

**Action**

RESET SEARCH

3 records returned. Click the hyperlinks for detailed information.

| Isolate fields | | | | | | | | | | | | | | | Bp_vaccine antigens | | | | | | cgMLST_pertussis | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| id | isolate | aliases | duplicate number | species | site | disease | country | region | city | source type | host | other source info | source lab | sequencing technology | ptxB (BP3784) | ptxC (BP3787) | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | BPagST | cgST | 23 |
| 10145 | FR4964 | ERR5102028;<br>PRJEB42353;<br>SAMEA7765914 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | Institut Pasteur | Illumina NextSeq 500 | 1 | 4 | 1 | 4 | 1 | 9 | 130 | |
| 10673 | FR5015 | | | B. pertussis | nasopharynx | pertussis | France | | | | | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 68 | 126,836,1214 | |
| 10674 | FR5016 | | | B. pertussis | nasopharynx | pertussis | France | | | | | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 68 | 126,836,1214 | |

### Analysis tools

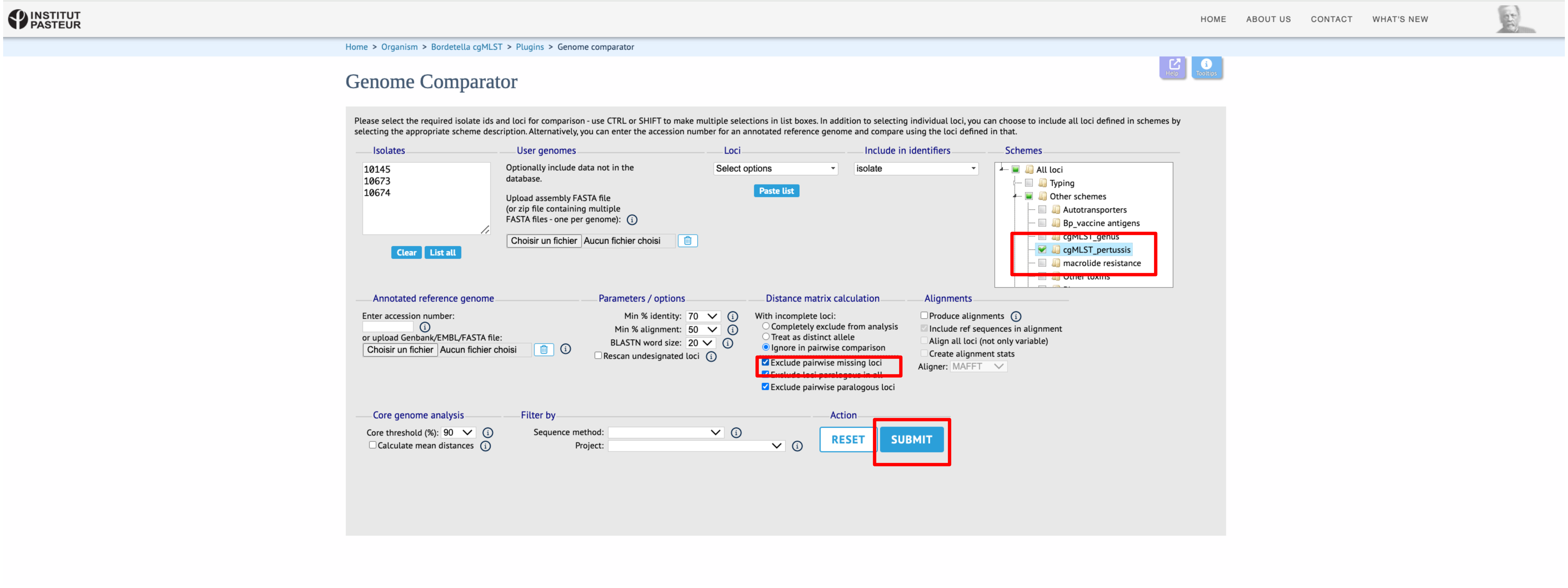
Breakdown: Fields | Two Field | Combinations | Polymorphic sites | Publications | Sequence bin

Analysis: BURST | Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR

Export: Dataset | Contigs | Sequences

Third party: GrapeTree | iTOL | Microreact | ReporTree

https://bigsdb.pasteur.fr/bordetella/



# Genome Comparator

Please select the required isolate ids and loci for comparison - use CTRL or SHIFT to make multiple selections in list boxes. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

**Isolates**

10145
10673
10674

**User genomes**

Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome):

Choisir un fichier Aucun fichier choisi

**Loci**

Select options

**Include in identifiers**

isolate

**Schemes**

- All loci
  - ☐ Typing
  - Other schemes
    - ☐ Autotransporters
    - ☐ Bp_vaccine antigens
    - ☐ cgMLST_genus
    - ☑ cgMLST_pertussis
    - ☐ macrolide resistance
    - ☐ Other toxins

**Annotated reference genome**

Enter accession number:

or upload Genbank/EMBL/FASTA file:

Choisir un fichier Aucun fichier choisi

**Parameters / options**

Min % identity: 70
Min % alignment: 50
BLASTN word size: 20
☐ Rescan undesignated loci

**Distance matrix calculation**

With incomplete loci:
○ Completely exclude from analysis
○ Treat as distinct allele
● Ignore in pairwise comparison
☑ Exclude pairwise missing loci
☑ Exclude loci paralogous in all
☑ Exclude pairwise paralogous loci

**Alignments**

☐ Produce alignments
☑ Include ref sequences in alignment
☐ Align all loci (not only variable)
☐ Create alignment stats
Aligner: MAFFT

**Core genome analysis**

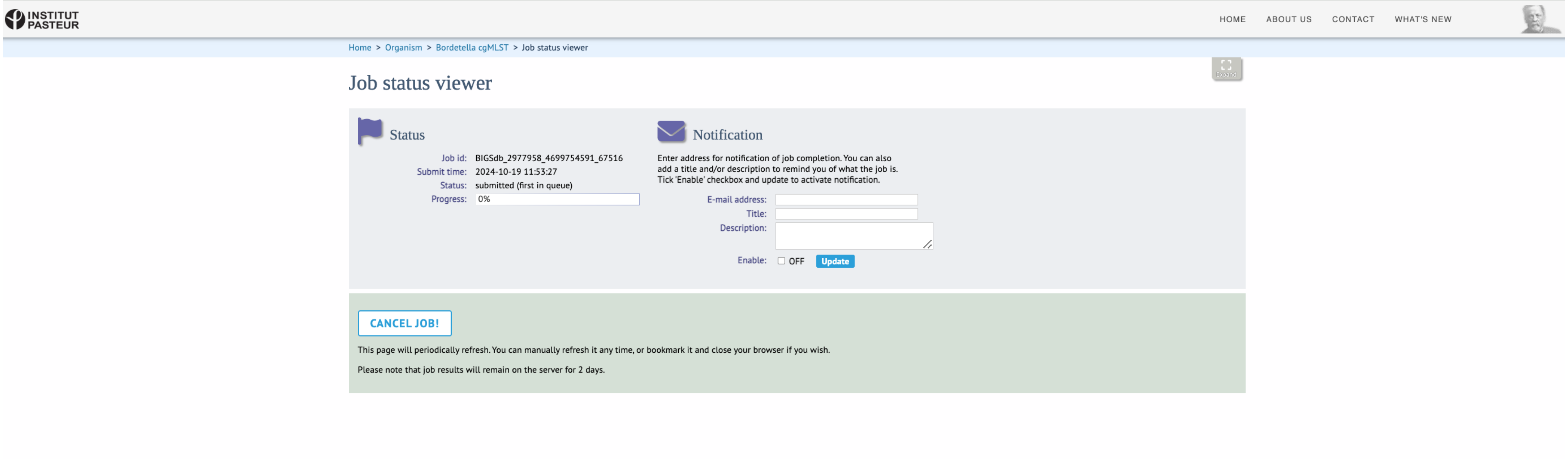
Core threshold (%): 90
☐ Calculate mean distances

**Filter by**

Sequence method:
Project:

**Action**

https://bigsdb.pasteur.fr/bordetella/



## Job status viewer

### Status

Job id: BIGSdb_2977958_4699754591_67516
Submit time: 2024-10-19 11:53:27
Status: submitted (first in queue)
Progress: 0%

### Notification

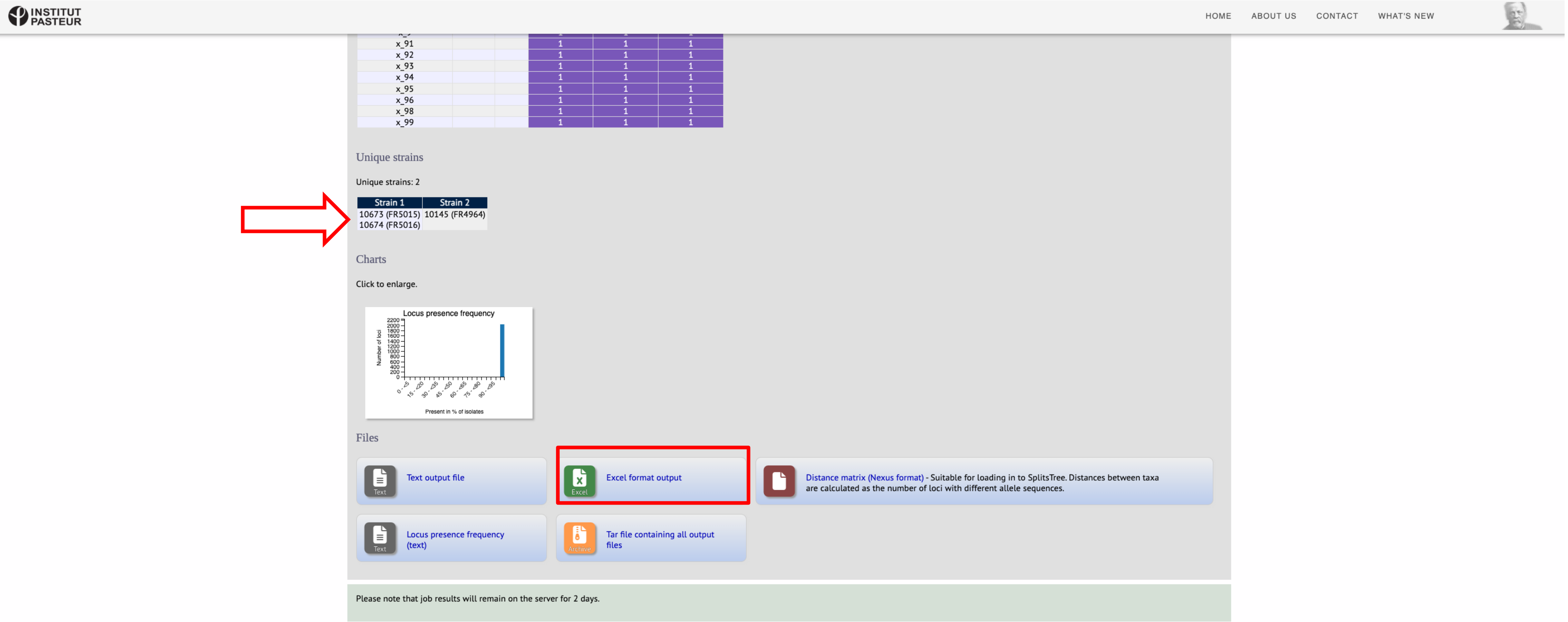
Enter address for notification of job completion. You can also add a title and/or description to remind you of what the job is. Tick 'Enable' checkbox and update to activate notification.

E-mail address:
Title:
Description:
Enable: ☐ OFF

This page will periodically refresh. You can manually refresh it any time, or bookmark it and close your browser if you wish.

Please note that job results will remain on the server for 2 days.

https://bigsdb.pasteur.fr/bordetella/



| | | | | | |
|---|---|---|---|---|---|
| x_91 | | | 1 | 1 | 1 |
| x_92 | | | 1 | 1 | 1 |
| x_93 | | | 1 | 1 | 1 |
| x_94 | | | 1 | 1 | 1 |
| x_95 | | | 1 | 1 | 1 |
| x_96 | | | 1 | 1 | 1 |
| x_98 | | | 1 | 1 | 1 |
| x_99 | | | 1 | 1 | 1 |

## Unique strains

Unique strains: 2

| Strain 1 | Strain 2 |
|---|---|
| 10673 (FR5015)<br>10674 (FR5016) | 10145 (FR4964) |

## Charts

Click to enlarge.

## Files

Text output file

Excel format output

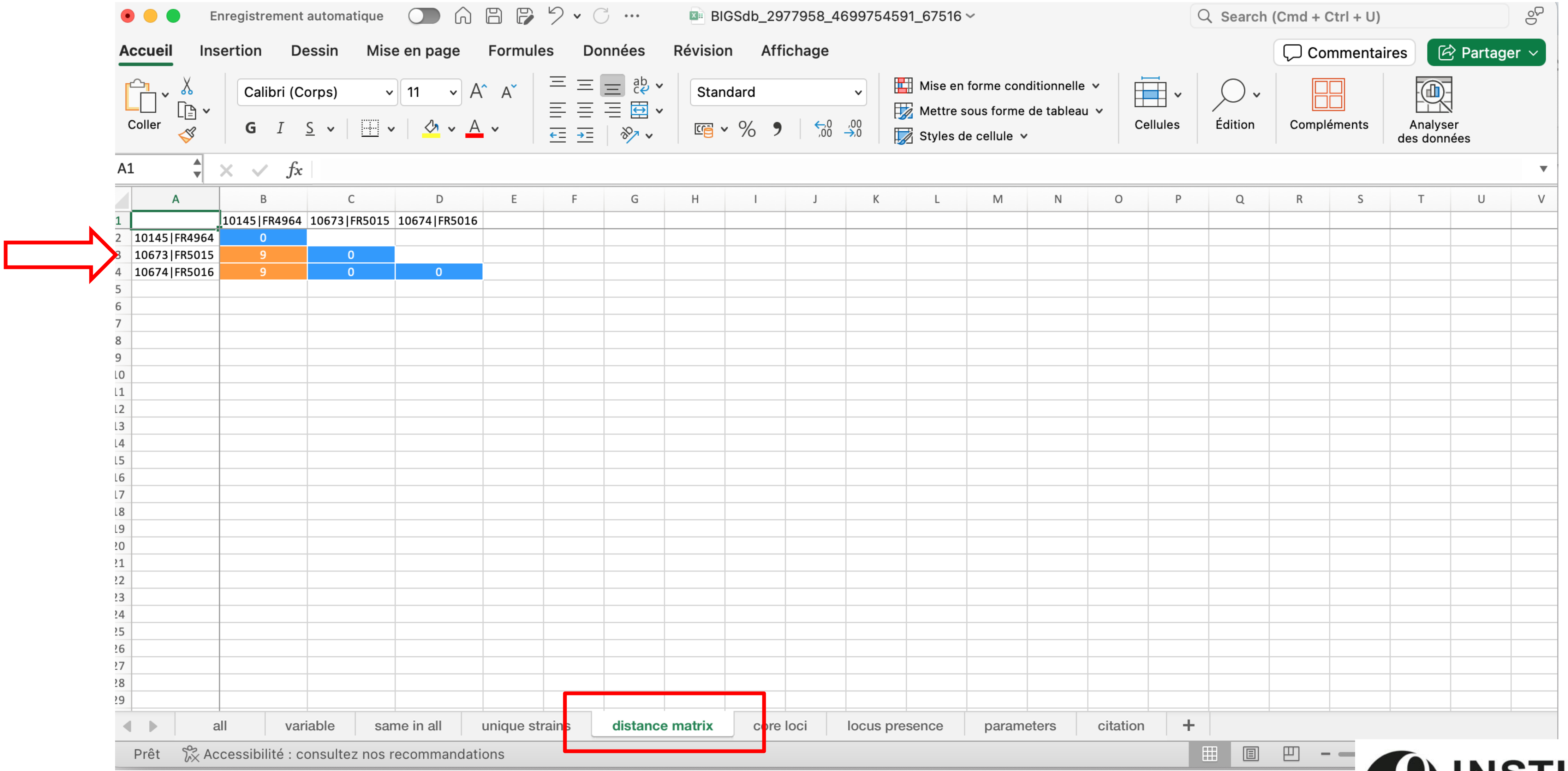
Distance matrix (Nexus format) - Suitable for loading in to SplitsTree. Distances between taxa are calculated as the number of loci with different allele sequences.

Locus presence frequency (text)

Tar file containing all output files

Please note that job results will remain on the server for 2 days.

https://bigsdb.pasteur.fr/bordetella/



| | 10145\|FR4964 | 10673\|FR5015 | 10674\|FR5016 |
|---|---|---|---|
| 10145\|FR4964 | 0 | | |
| 10673\|FR5015 | 9 | 0 | |
| 10674\|FR5016 | 9 | 0 | 0 |

https://bigsdb.pasteur.fr/bordetella/

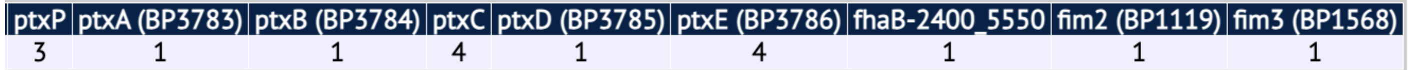
# Practical session on BIGSdb Bordetella

## Part1 :

**In BIGSdb Bordetella Alleles & profiles database :**

Considering locus *fim3*, compare alleles 1 and 2 (i.e fim3-1 and fim 3-2) using locus explorer;

What Bp-agST correspond to the following profiles :



| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 1 |

| ptxP | ptxA (BP3783) | ptxB (BP3784) | ptxC | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | fim2 (BP1119) | fim3 (BP1568) |
|---|---|---|---|---|---|---|---|---|
| 3 | 1 | 1 | 4 | 1 | 4 | 1 | 1 | 2 |

## Part2 :

In BIGSdb Bordetella Isolates database :

Considering all isolates from the public project 25,

Visualize the percentage of isolates per country in a pie chart (Field breakdown option)

Visualize the number of isolates resistant to macrolide per country (Two field breakdown option)

Using genome comparator, compare isolates FR5015 and FR5016, is it the same strain?

Using genome comparator, compare isolates FR5015 and FR4964, is it the same strain?

## Part 3 :

**In BIGSdb Bordetella Isolates database :**

Considering all isolates from the public **project 25,**

Perform a first GrapeTree analysis based on Bp-vaccine-Antigen scheme

Color isolates per country, label BpAg-ST, indicate branch length

Visualize metadata

Perform a second GrapeTree based on cgMLST_pertussis

Color isolates per BpAg-ST, indicate branch length

Export image

Use Microreact to visualize analysis based on Bp-vaccine antigens and explore Microreact functions

https://bigsdb.pasteur.fr/bordetella/

# **GrapeTree :** generate minimum spanning trees trees from allelic profiles. **Analysis available on BIGSdb**

**Eurosurveillance**

Europe's journal on infectious disease epidemiology, prevention and control since 1996

Publisher: European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Euro Surveill. 2024 Aug 1; 29(31): 2400459. PMCID: PMC11295439

doi: 10.2807/1560-7917.ES.2024.29.31.2400459 PMID: 39092529

Resurgence of *Bordetella pertussis*, including one macrolide-resistant isolate, France, 2024

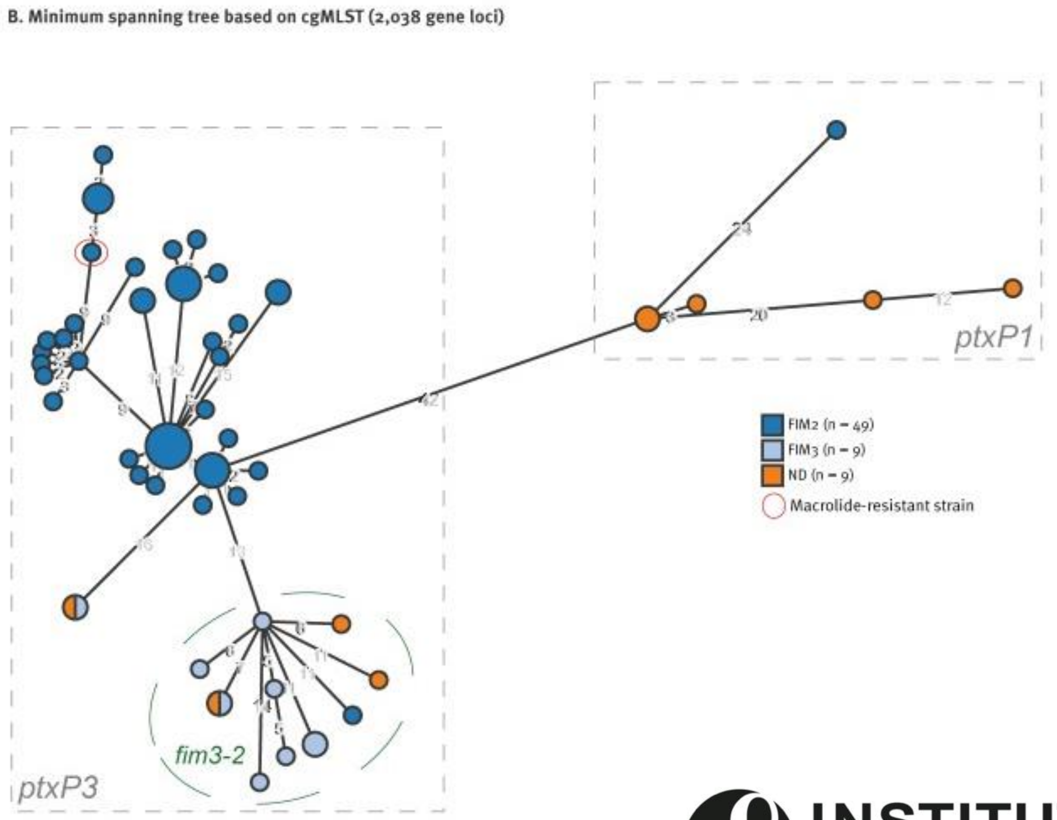
Carla Rodrigues,[1,2,*] Valérie Bouchez,[1,2,*] Anaïs Soares,[3] Sabine Trombert-Paolantoni,[4] Fatima Aït El Belghiti,[5] Jérémie F Cohen,[6,7] Nathalie Armatys,[1,2] Annie Landier,[1,2] Thomas Blanchot,[3] Marie Hervo,[3] REMICOQ study group,[8] Julie Toubiana,[1,2,6,**] and Sylvain Brisse[1,2,**]

Journal Article

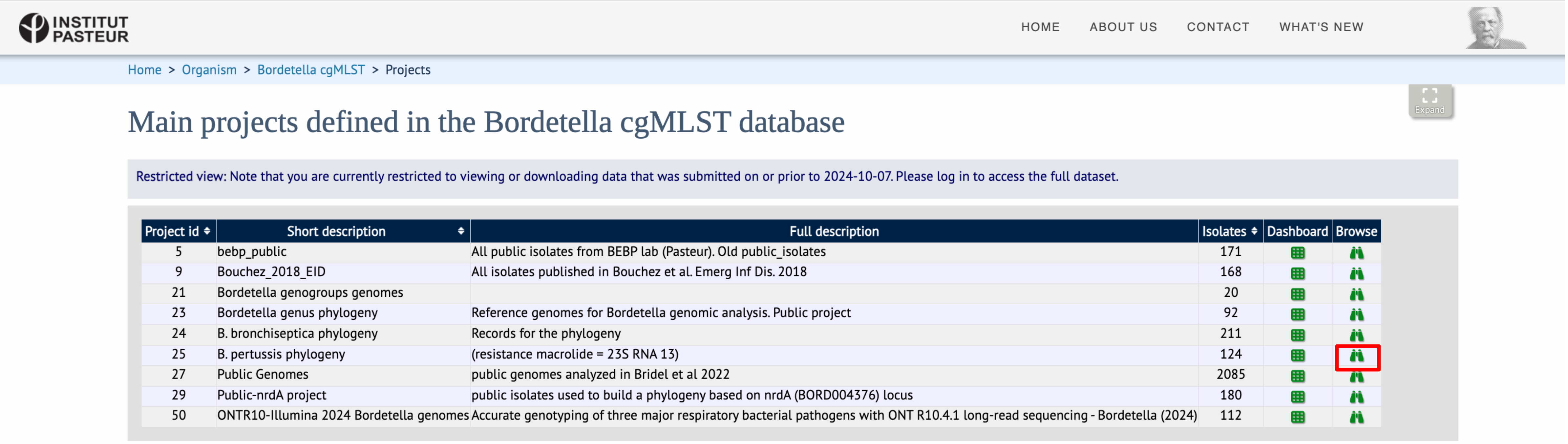
**Minimum spaninning tree based on cgMLST_pertussis (2038 loci)**

The numbers on the branches indicate the number of allelic differences among cgST profiles. Each circle represents a cgST type, coloured by FIM serotype. The diameter of circles is related to the number of isolates they comprise

https://bigsdb.pasteur.fr/bordetella/



B. Minimum spanning tree based on cgMLST (2,038 gene loci)



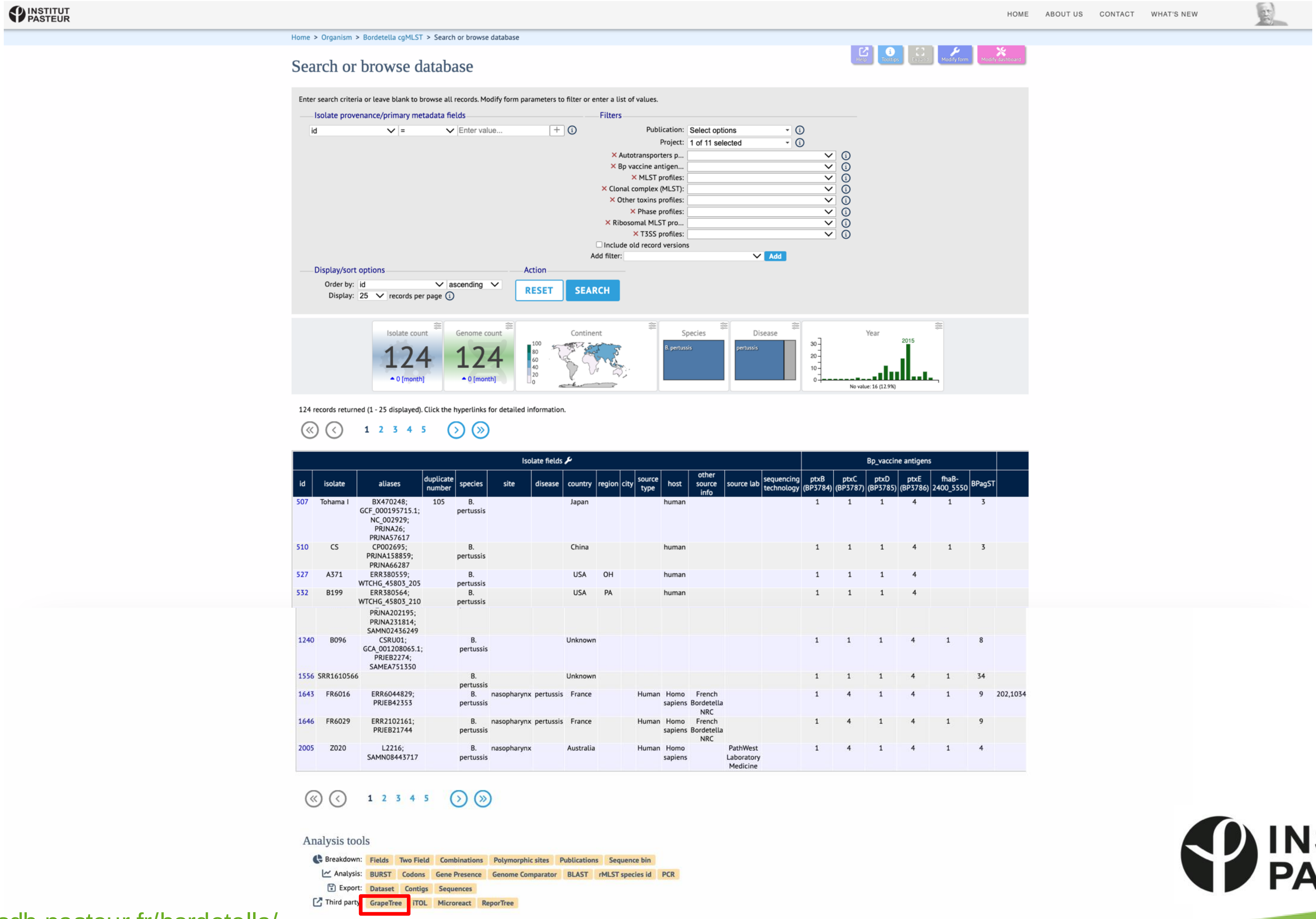
Home > Organism > Bordetella cgMLST > Projects

# Main projects defined in the Bordetella cgMLST database

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-10-07. Please log in to access the full dataset.

| Project id | Short description | Full description | Isolates | Dashboard | Browse |
|---|---|---|---|---|---|
| 5 | bebp_public | All public isolates from BEBP lab (Pasteur). Old public_isolates | 171 | ▦ | 🔍 |
| 9 | Bouchez_2018_EID | All isolates published in Bouchez et al. Emerg Inf Dis. 2018 | 168 | ▦ | 🔍 |
| 21 | Bordetella genogroups genomes |  | 20 | ▦ | 🔍 |
| 23 | Bordetella genus phylogeny | Reference genomes for Bordetella genomic analysis. Public project | 92 | ▦ | 🔍 |
| 24 | B. bronchiseptica phylogeny | Records for the phylogeny | 211 | ▦ | 🔍 |
| 25 | B. pertussis phylogeny | (resistance macrolide = 23S RNA 13) | 124 | ▦ | 🔍 |
| 27 | Public Genomes | public genomes analyzed in Bridel et al 2022 | 2085 | ▦ | 🔍 |
| 29 | Public-nrdA project | public isolates used to build a phylogeny based on nrdA (BORD004376) locus | 180 | ▦ | 🔍 |
| 50 | ONTR10-Illumina 2024 Bordetella genomes | Accurate genotyping of three major respiratory bacterial pathogens with ONT R10.4.1 long-read sequencing - Bordetella (2024) | 112 | ▦ | 🔍 |

https://bigsdb.pasteur.fr/bordetella/



Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

id = Enter value...

Filters

Publication: Select options

Project: 1 of 11 selected

× Autotransporters p...:

× Bp vaccine antigen...:

× MLST profiles:

× Clonal complex (MLST):

× Other toxins profiles:

× Phase profiles:

× Ribosomal MLST pro...:

× T3SS profiles:

☐ Include old record versions

Add filter: Add

Display/sort options

Order by: id ascending

Display: 25 records per page

Action

RESET SEARCH

124 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

| Isolate fields |  |  |  |  |  |  |  |  |  |  |  |  |  |  | Bp_vaccine antigens |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| id | isolate | aliases | duplicate number | species | site | disease | country | region | city | source type | host | other source info | source lab | sequencing technology | ptxB (BP3784) | ptxC (BP3787) | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | BPagST |  |
| 507 | Tohama I | BX470248; GCF_000195715.1; NC_002929; PRJNA26; PRJNA57617 | 105 | B. pertussis |  |  | Japan |  |  |  | human |  |  |  | 1 | 1 | 1 | 4 | 1 | 3 |  |
| 510 | CS | CP002695; PRJNA158859; PRJNA66287 |  | B. pertussis |  |  | China |  |  |  | human |  |  |  | 1 | 1 | 1 | 4 | 1 | 3 |  |
| 527 | A371 | ERR380559; WTCHG_45803_205 |  | B. pertussis |  |  | USA | OH |  |  | human |  |  |  | 1 | 1 | 1 | 4 |  |  |  |
| 532 | B199 | ERR380564; WTCHG_45803_210 |  | B. pertussis |  |  | USA | PA |  |  | human |  |  |  | 1 | 1 | 1 | 4 |  |  |  |
|  |  | PRJNA202195; PRJNA231814; SAMN02436249 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1240 | B096 | CSRU01; GCA_001208065.1; PRJEB2274; SAMEA751350 |  | B. pertussis |  |  | Unknown |  |  |  |  |  |  |  | 1 | 1 | 1 | 4 | 1 | 8 |  |
| 1556 | SRR1610566 |  |  | B. pertussis |  |  | Unknown |  |  |  |  |  |  |  | 1 | 1 | 1 | 4 | 1 | 34 |  |
| 1643 | FR6016 | ERR6044829; PRJEB42353 |  | B. pertussis | nasopharynx | pertussis | France |  |  | Human | Homo sapiens | French Bordetella NRC |  |  | 1 | 4 | 1 | 4 | 1 | 9 | 202,1034 |
| 1646 | FR6029 | ERR2102161; PRJEB21744 |  | B. pertussis | nasopharynx | pertussis | France |  |  | Human | Homo sapiens | French Bordetella NRC |  |  | 1 | 4 | 1 | 4 | 1 | 9 |  |
| 2005 | Z020 | L2216; SAMN08443717 |  | B. pertussis | nasopharynx |  | Australia |  |  | Human | Homo sapiens |  | PathWest Laboratory Medicine |  | 1 | 4 | 1 | 4 | 1 | 4 |  |

Analysis tools

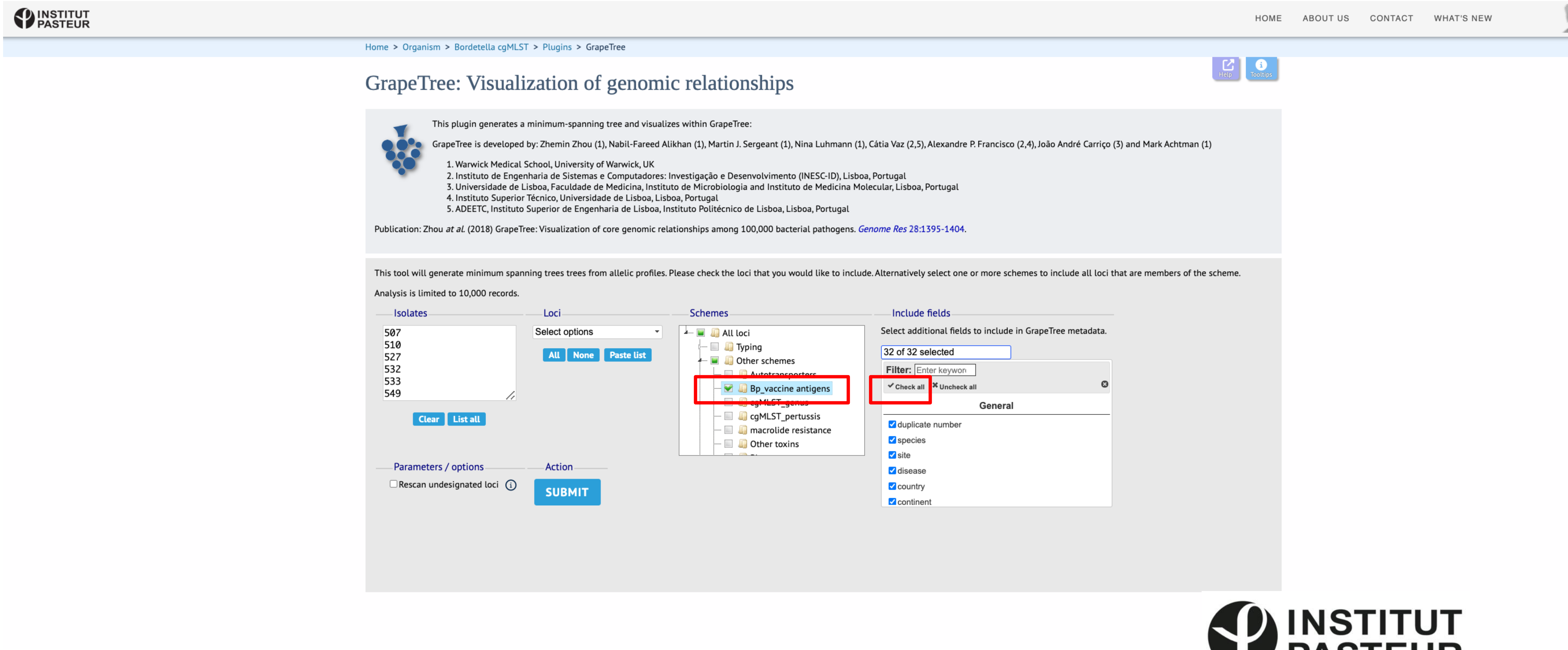
Breakdown: Fields | Two Field | Combinations | Polymorphic sites | Publications | Sequence bin

Analysis: BURST | Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR

Export: Dataset | Contigs | Sequences

Third party: GrapeTree | iTOL | Microreact | ReporTree

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella cgMLST > Plugins > GrapeTree

# GrapeTree: Visualization of genomic relationships

This plugin generates a minimum-spanning tree and visualizes within GrapeTree:

GrapeTree is developed by: Zhemin Zhou (1), Nabil-Fareed Alikhan (1), Martin J. Sergeant (1), Nina Luhmann (1), Cátia Vaz (2,5), Alexandre P. Francisco (2,4), João André Carriço (3) and Mark Achtman (1)

1. Warwick Medical School, University of Warwick, UK
2. Instituto de Engenharia de Sistemas e Computadores: Investigação e Desenvolvimento (INESC-ID), Lisboa, Portugal
3. Universidade de Lisboa, Faculdade de Medicina, Instituto de Microbiologia and Instituto de Medicina Molecular, Lisboa, Portugal
4. Instituto Superior Técnico, Universidade de Lisboa, Lisboa, Portugal
5. ADEETC, Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, Lisboa, Portugal

Publication: Zhou *at al.* (2018) GrapeTree: Visualization of core genomic relationships among 100,000 bacterial pathogens. *Genome Res* 28:1395-1404.

This tool will generate minimum spanning trees trees from allelic profiles. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 10,000 records.

Isolates
507
510
527
532
533
549

Loci
Select options

Schemes
All loci
☐ Typing
Other schemes
☐ Autotransporters
☑ Bp_vaccine antigens
☐ cgMLST_genus
☐ cgMLST_pertussis
☐ macrolide resistance
☐ Other toxins

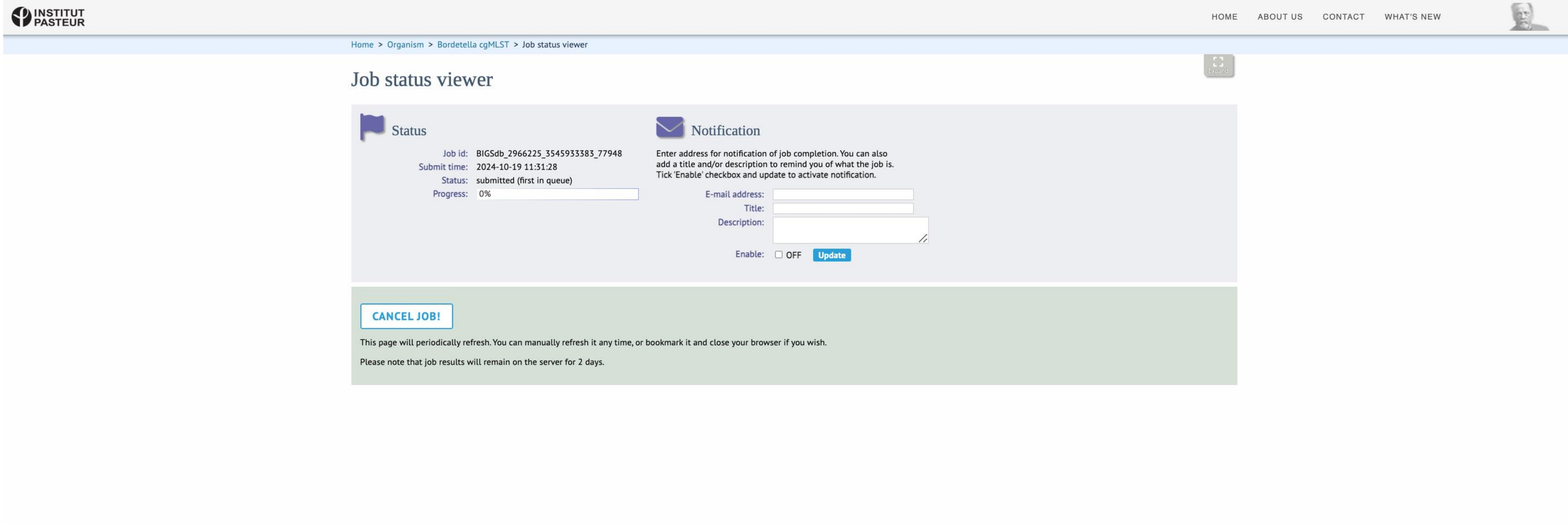
Include fields
Select additional fields to include in GrapeTree metadata.
32 of 32 selected
Filter: Enter keyword
✓ Check all ✖ Uncheck all

General
☑ duplicate number
☑ species
☑ site
☑ disease
☑ country
☑ continent

Parameters / options
☐ Rescan undesignated loci

Action

https://bigsdb.pasteur.fr/bordetella/



# Job status viewer

## Status

Job id: BIGSdb_2966225_3545933383_77948
Submit time: 2024-10-19 11:31:28
Status: submitted (first in queue)
Progress: 0%

## Notification

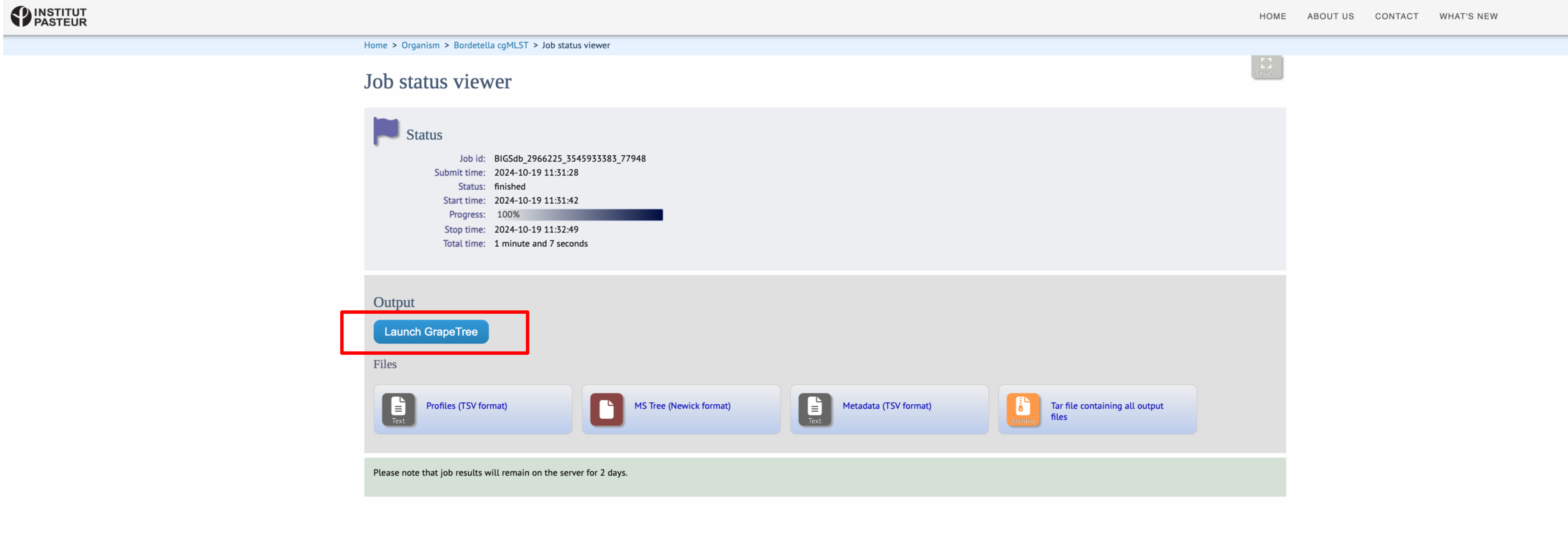
Enter address for notification of job completion. You can also add a title and/or description to remind you of what the job is. Tick 'Enable' checkbox and update to activate notification.

E-mail address:
Title:
Description:
Enable: ☐ OFF

This page will periodically refresh. You can manually refresh it any time, or bookmark it and close your browser if you wish.

Please note that job results will remain on the server for 2 days.

https://bigsdb.pasteur.fr/bordetella/



# Job status viewer

## Status

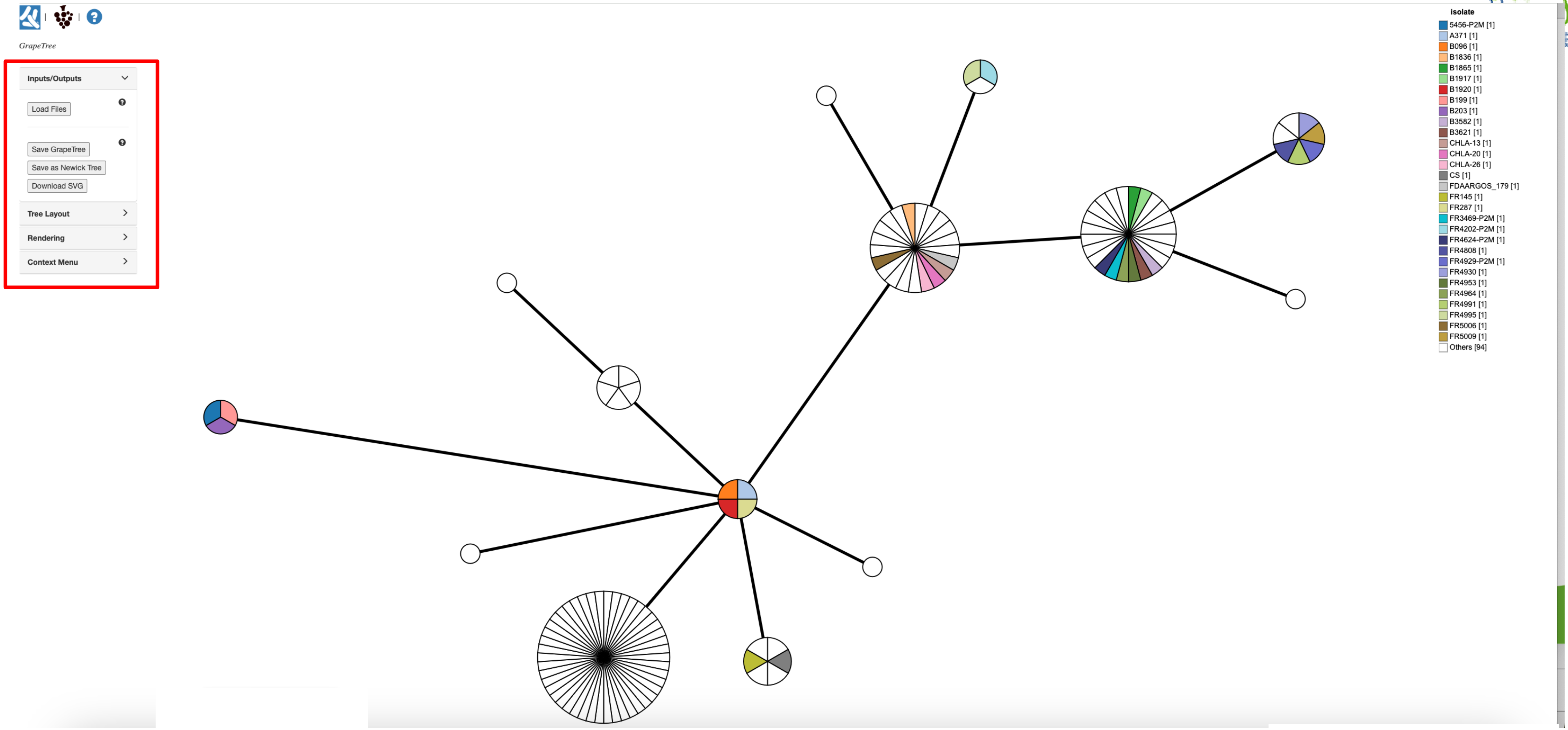
Job id: BIGSdb_2966225_3545933383_77948
Submit time: 2024-10-19 11:31:28
Status: finished
Start time: 2024-10-19 11:31:42
Progress: 100%
Stop time: 2024-10-19 11:32:49
Total time: 1 minute and 7 seconds

## Output

Files

Please note that job results will remain on the server for 2 days.

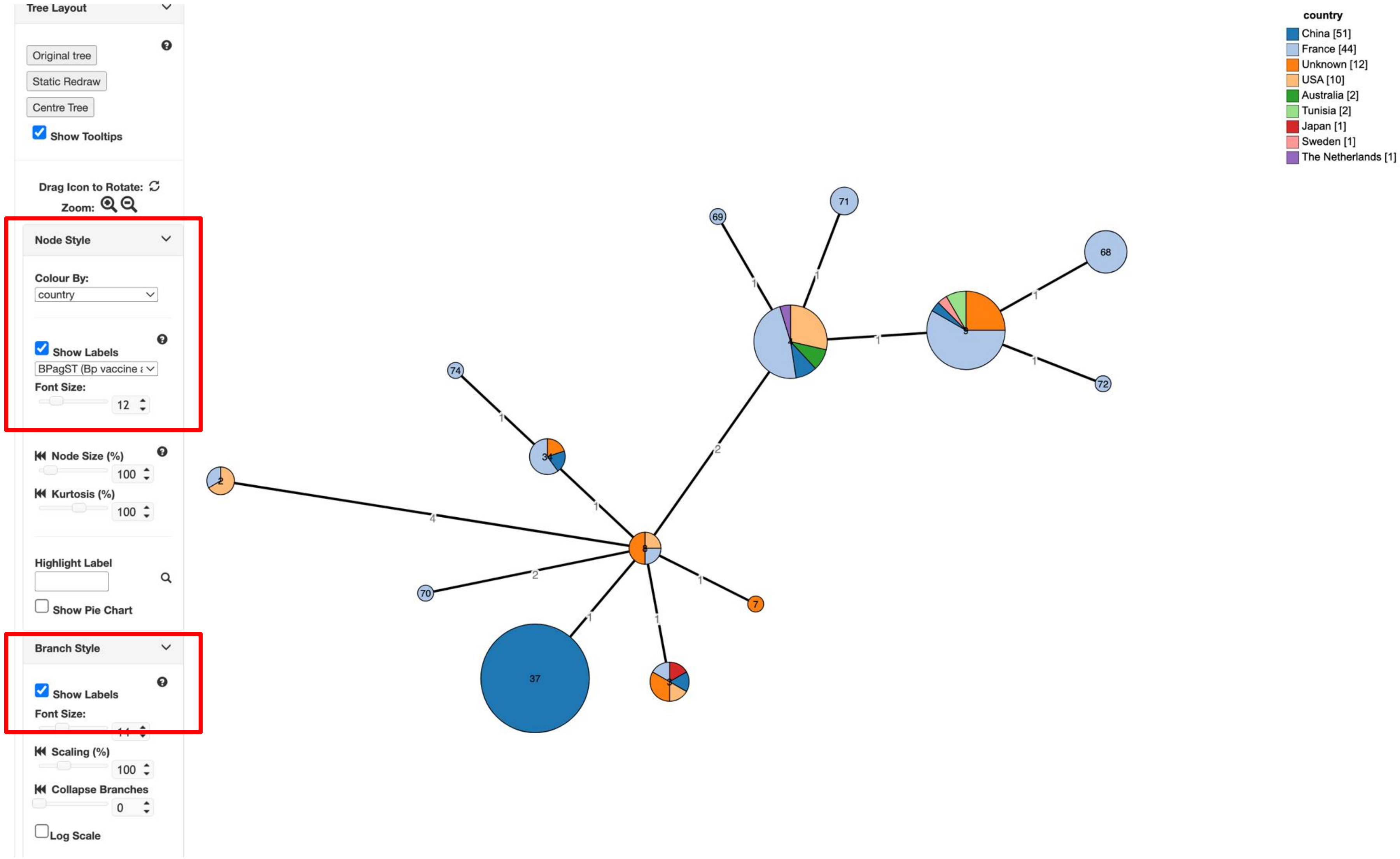
https://bigsdb.pasteur.fr/bordetella/



Public project 25
GrapeTree/Bp_vaccine antigen scheme

https://bigsdb.pasteur.fr/bordetella/

# GrapeTree :



Tree Layout

Original tree
Static Redraw
Centre Tree
☑ Show Tooltips

Drag Icon to Rotate:
Zoom:

Node Style

Colour By: country

☑ Show Labels
BPagST (Bp vaccine a
Font Size: 12

Node Size (%) 100
Kurtosis (%) 100

Highlight Label
☐ Show Pie Chart

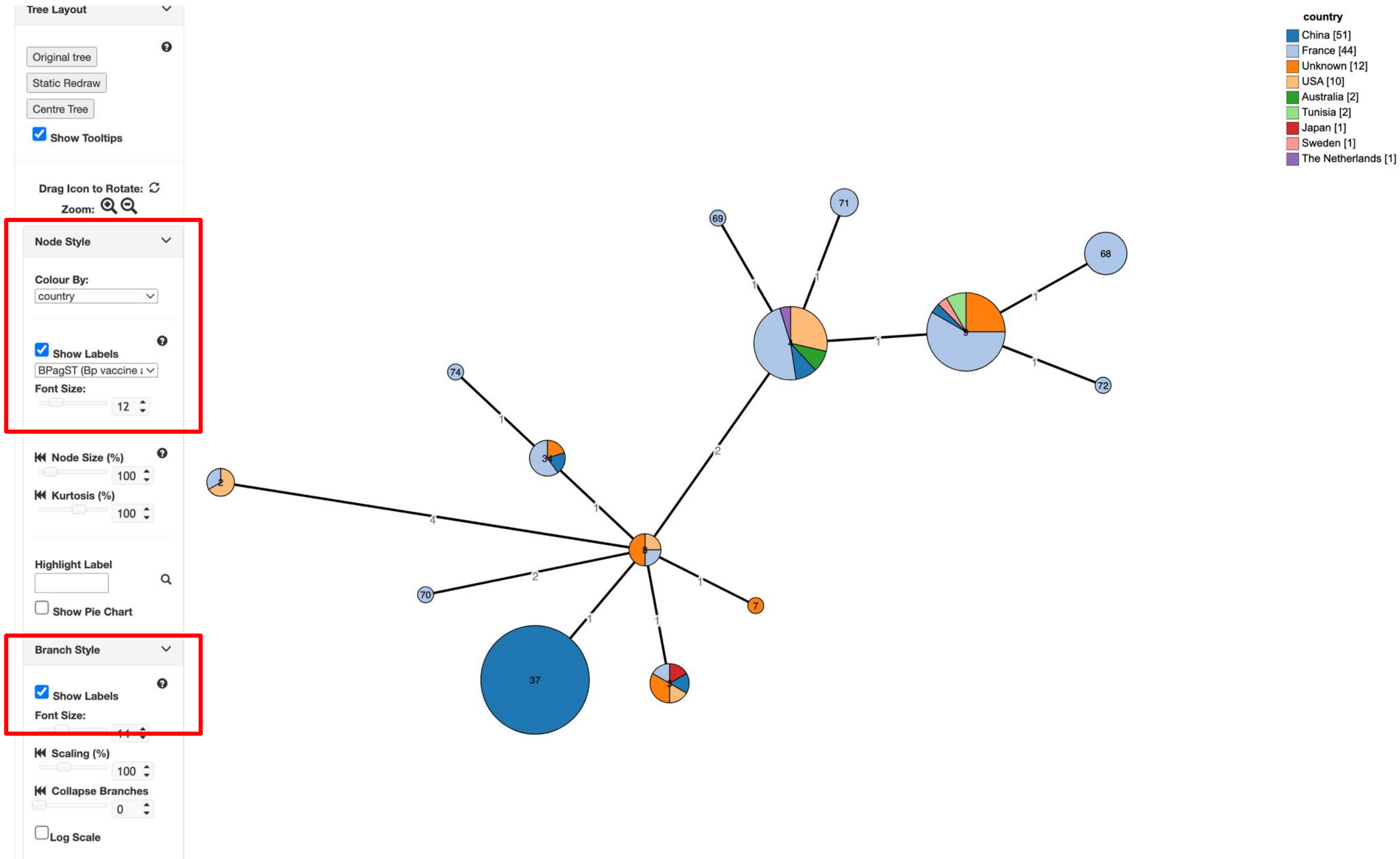
Branch Style

☑ Show Labels
Font Size: 11
Scaling (%) 100
Collapse Branches 0
☐ Log Scale

https://bigsdb.pasteur.fr/bordetella/

Public project 25
GrapeTree/Bp_vaccine antigen scheme

# GrapeTree :



Tree Layout

Original tree
Static Redraw
Centre Tree
☑ Show Tooltips

Drag Icon to Rotate:
Zoom:

**Node Style**

Colour By: country

☑ Show Labels
BPagST (Bp vaccine a
Font Size: 12

Node Size (%) 100
Kurtosis (%) 100

Highlight Label

☐ Show Pie Chart

**Branch Style**

☑ Show Labels
Font Size: 11

Scaling (%) 100
Collapse Branches 0
☐ Log Scale

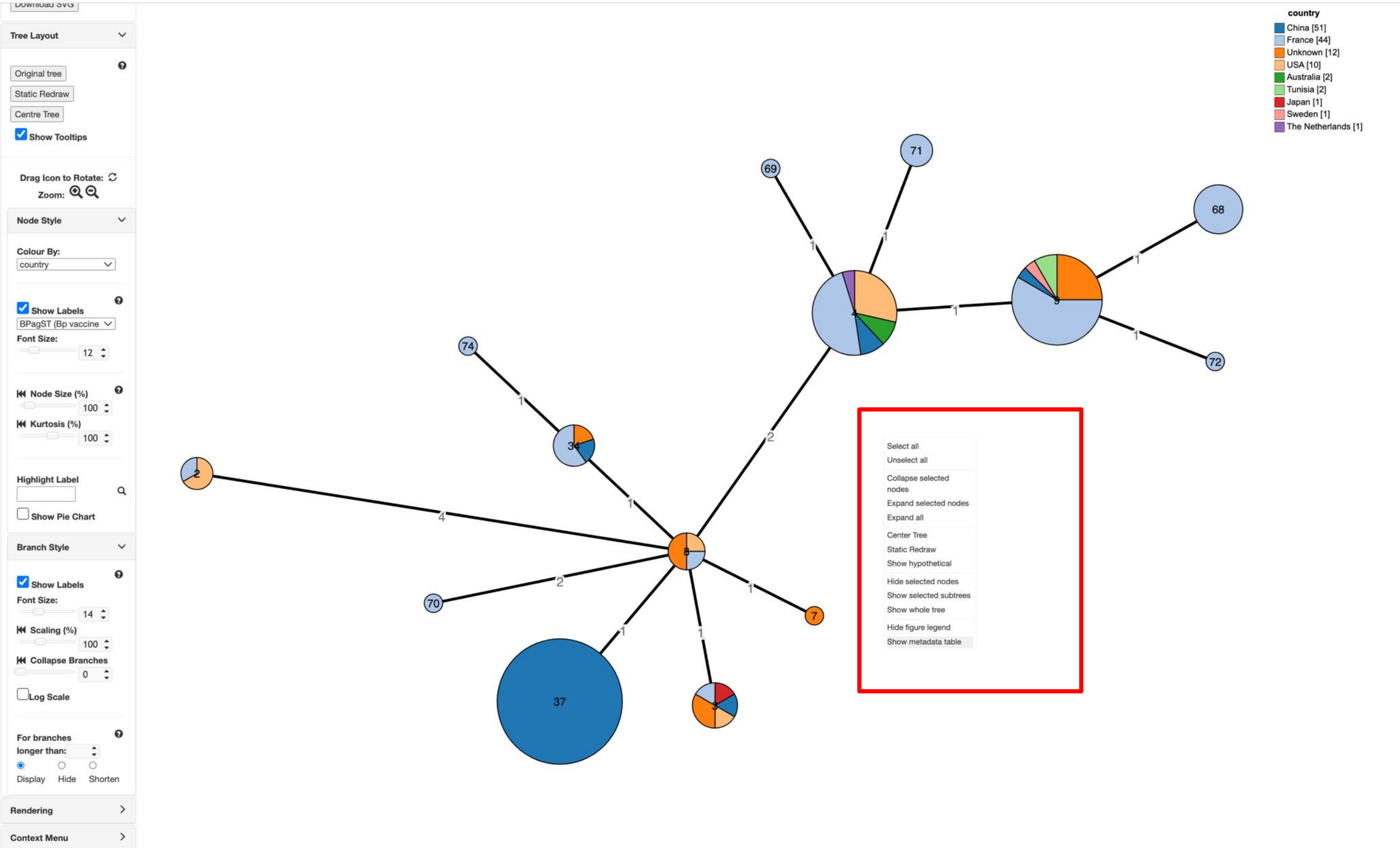
country

- 🟦 China [51]
- 🟦 France [44]
- 🟧 Unknown [12]
- 🟧 USA [10]
- 🟩 Australia [2]
- 🟩 Tunisia [2]
- 🟥 Japan [1]
- 🟥 Sweden [1]
- 🟪 The Netherlands [1]

[https://bigsdb.pasteur.fr/bordetella/](https://bigsdb.pasteur.fr/bordetella/)

Public project 25
GrapeTree/Bp_vaccine antigen scheme

# GrapeTree :



☑ Show Tooltips

Colour By: country

☑ Show Labels BPagST (Bp vaccine

Font Size: 12

Node Size (%) 100

Kurtosis (%) 100

Highlight Label

☐ Show Pie Chart

Branch Style

☑ Show Labels

Font Size: 14

Scaling (%) 100

Collapse Branches 0

☐ Log Scale

For branches longer than:

● Display ○ Hide ○ Shorten

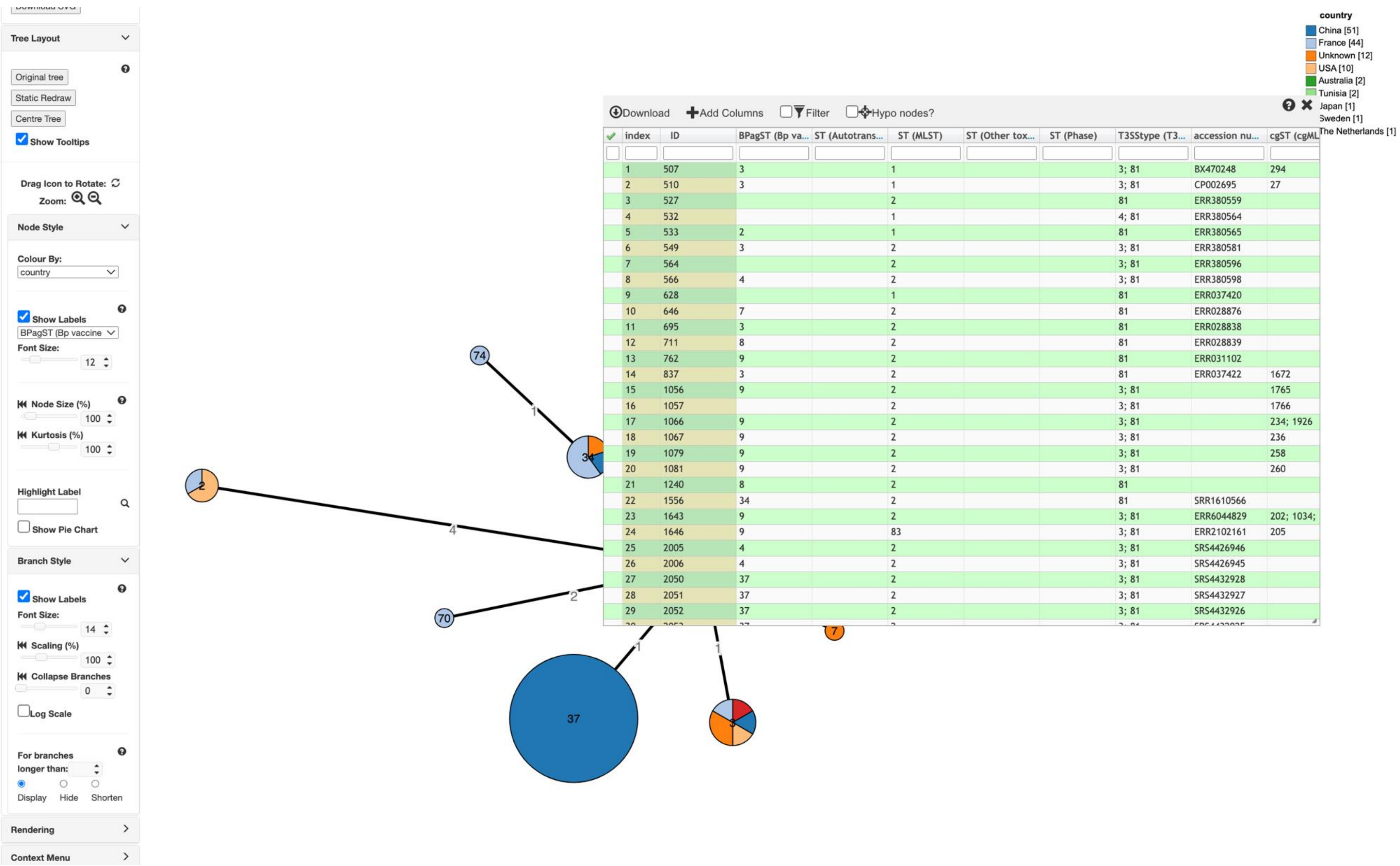
country

| | |
|---|---|
| 🟦 | China [51] |
| 🟦 | France [44] |
| 🟧 | Unknown [12] |
| 🟧 | USA [10] |
| 🟩 | Australia [2] |
| 🟩 | Tunisia [2] |
| 🟥 | Japan [1] |
| 🟥 | Sweden [1] |
| 🟪 | The Netherlands [1] |

[https://bigsdb.pasteur.fr/bordetella/](https://bigsdb.pasteur.fr/bordetella/)

Public project 25
GrapeTree/Bp_vaccine antigen scheme

# GrapeTree :



☑ Show Tooltips

Colour By: country

☑ Show Labels: BPagST (Bp vaccine

Font Size: 12

Node Size (%): 100

Kurtosis (%): 100

Highlight Label

☐ Show Pie Chart

☑ Show Labels

Font Size: 14

Scaling (%): 100

Collapse Branches: 0

☐ Log Scale

For branches longer than:

● Display ○ Hide ○ Shorten

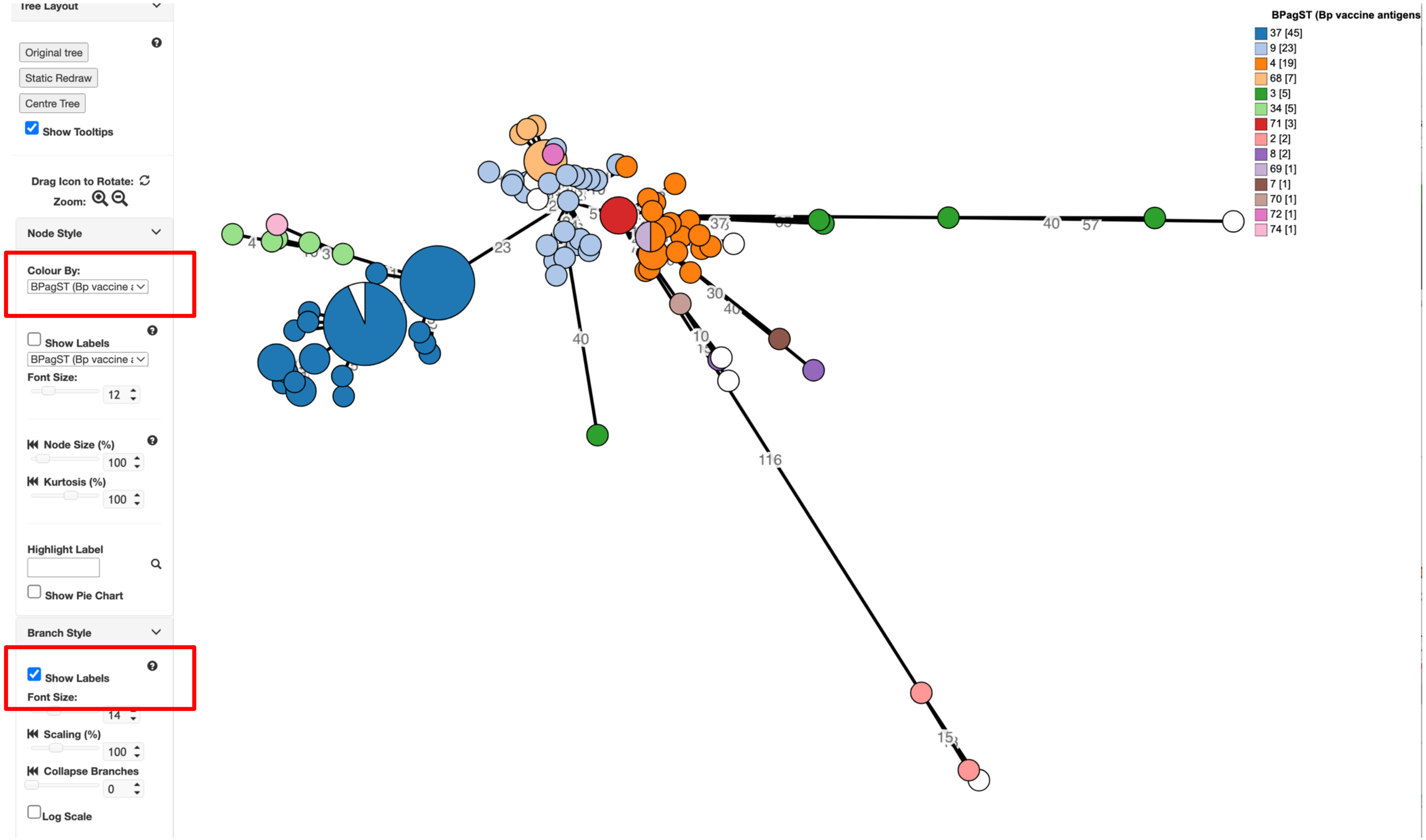
☐ Filter ☐ Hypo nodes?

| ✓ | index | ID | BPagST (Bp va... | ST (Autotrans... | ST (MLST) | ST (Other tox... | ST (Phase) | T3SStype (T3... | accession nu... | cgST (cgML |
|---|---|---|---|---|---|---|---|---|---|---|
| | 1 | 507 | 3 | | 1 | | | 3; 81 | BX470248 | 294 |
| | 2 | 510 | 3 | | 1 | | | 3; 81 | CP002695 | 27 |
| | 3 | 527 | | | 2 | | | 81 | ERR380559 | |
| | 4 | 532 | | | 1 | | | 4; 81 | ERR380564 | |
| | 5 | 533 | 2 | | 1 | | | 81 | ERR380565 | |
| | 6 | 549 | 3 | | 2 | | | 3; 81 | ERR380581 | |
| | 7 | 564 | | | 2 | | | 3; 81 | ERR380596 | |
| | 8 | 566 | 4 | | 2 | | | 3; 81 | ERR380598 | |
| | 9 | 628 | | | 1 | | | 81 | ERR037420 | |
| | 10 | 646 | 7 | | 2 | | | 81 | ERR028876 | |
| | 11 | 695 | 3 | | 2 | | | 81 | ERR028838 | |
| | 12 | 711 | 8 | | 2 | | | 81 | ERR028839 | |
| | 13 | 762 | 9 | | 2 | | | 81 | ERR031102 | |
| | 14 | 837 | 3 | | 2 | | | 81 | ERR037422 | 1672 |
| | 15 | 1056 | 9 | | 2 | | | 3; 81 | | 1765 |
| | 16 | 1057 | | | 2 | | | 3; 81 | | 1766 |
| | 17 | 1066 | 9 | | 2 | | | 3; 81 | | 234; 1926 |
| | 18 | 1067 | 9 | | 2 | | | 3; 81 | | 236 |
| | 19 | 1079 | 9 | | 2 | | | 3; 81 | | 258 |
| | 20 | 1081 | 9 | | 2 | | | 3; 81 | | 260 |
| | 21 | 1240 | 8 | | 2 | | | 81 | | |
| | 22 | 1556 | 34 | | 2 | | | 81 | SRR1610566 | |
| | 23 | 1643 | 9 | | 2 | | | 3; 81 | ERR6044829 | 202; 1034; |
| | 24 | 1646 | 9 | | 83 | | | 3; 81 | ERR2102161 | 205 |
| | 25 | 2005 | 4 | | 2 | | | 3; 81 | SRS4426946 | |
| | 26 | 2006 | 4 | | 2 | | | 3; 81 | SRS4426945 | |
| | 27 | 2050 | 37 | | 2 | | | 3; 81 | SRS4432928 | |
| | 28 | 2051 | 37 | | 2 | | | 3; 81 | SRS4432927 | |
| | 29 | 2052 | 37 | | 2 | | | 3; 81 | SRS4432926 | |

https://bigsdb.pasteur.fr/bordetella/

Public project 25
GrapeTree/Bp_vaccine antigen scheme

# GrapeTree :



Tree Layout

Original tree

Static Redraw

Centre Tree

☑ Show Tooltips

Drag Icon to Rotate:

Zoom:

Node Style

Colour By: BPagST (Bp vaccine a

☐ Show Labels

BPagST (Bp vaccine a

Font Size: 12

Node Size (%) 100

Kurtosis (%) 100

Highlight Label

☐ Show Pie Chart

Branch Style

☑ Show Labels

Font Size: 14

Scaling (%) 100

Collapse Branches 0

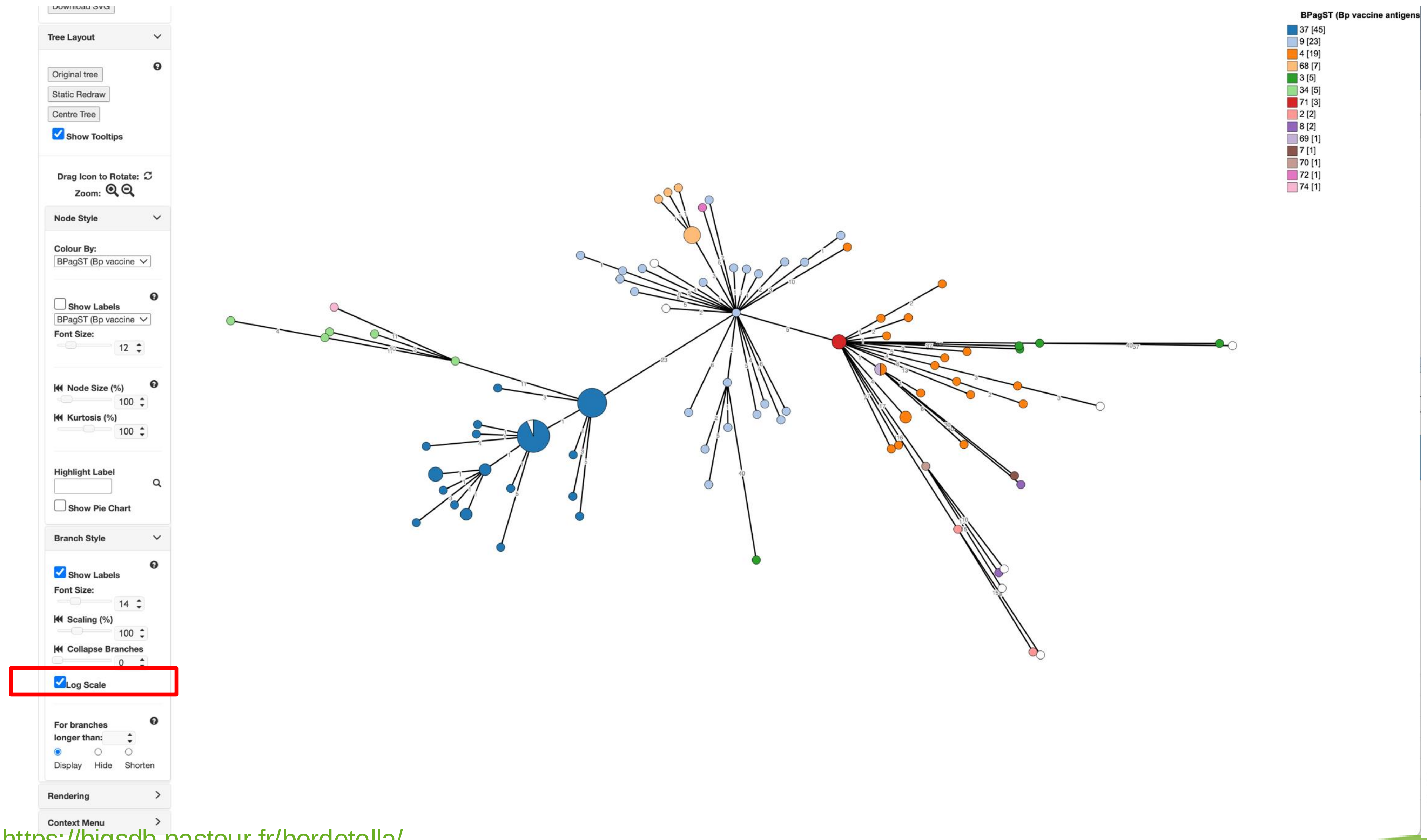
☐ Log Scale

BPagST (Bp vaccine antigens

- 37 [45]
- 9 [23]
- 4 [19]
- 68 [7]
- 3 [5]
- 34 [5]
- 71 [3]
- 2 [2]
- 8 [2]
- 69 [1]
- 7 [1]
- 70 [1]
- 72 [1]
- 74 [1]

https://bigsdb.pasteur.fr/bordetella/

# GrapeTree :



☑ Show Tooltips

Colour By: BPagST (Bp vaccine

☐ Show Labels BPagST (Bp vaccine

Font Size: 12

Node Size (%) 100

Kurtosis (%) 100

☐ Show Pie Chart

☑ Show Labels

Font Size: 14

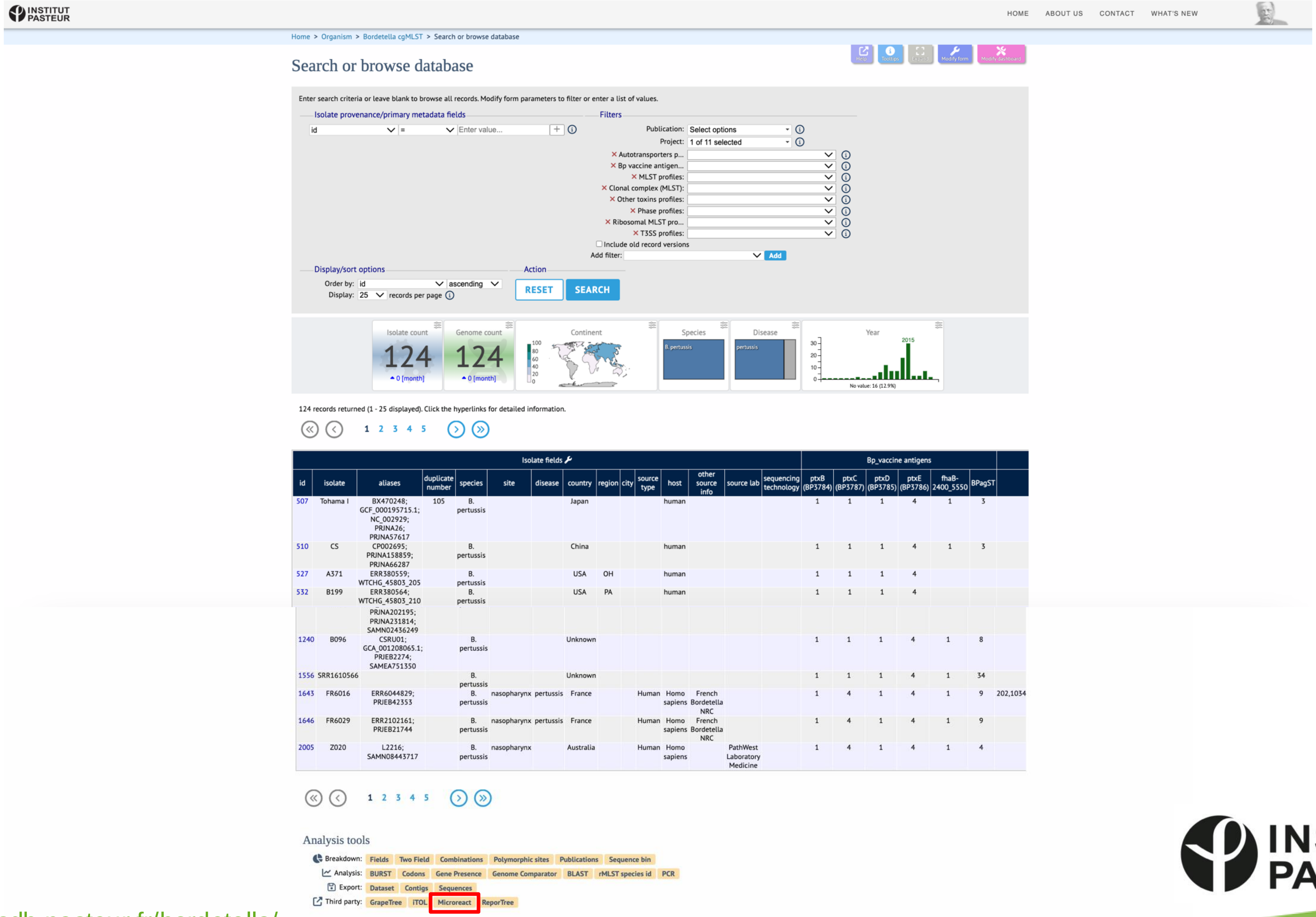
Scaling (%) 100

Collapse Branches 0

☑ Log Scale

For branches longer than: ● Display ○ Hide ○ Shorten

https://bigsdb.pasteur.fr/bordetella/



Home > Organism > Bordetella cgMLST > Search or browse database

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance/primary metadata fields**

id = Enter value...

**Filters**

Publication: Select options
Project: 1 of 11 selected
✕ Autotransporters p...
✕ Bp vaccine antigen...
✕ MLST profiles:
✕ Clonal complex (MLST):
✕ Other toxins profiles:
✕ Phase profiles:
✕ Ribosomal MLST pro...
✕ T3SS profiles:
☐ Include old record versions
Add filter: Add

**Display/sort options**

Order by: id ascending
Display: 25 records per page

**Action**

RESET SEARCH

124 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« ‹ 1 2 3 4 5 › »

| Isolate fields | | | | | | | | | | | | | | Bp_vaccine antigens | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| id | isolate | aliases | duplicate number | species | site | disease | country | region | city | source type | host | other source info | source lab | sequencing technology | ptxB (BP3784) | ptxC (BP3787) | ptxD (BP3785) | ptxE (BP3786) | fhaB-2400_5550 | BPagST | |
| 507 | Tohama I | BX470248;<br>GCF_000195715.1;<br>NC_002929;<br>PRJNA26;<br>PRJNA57617 | 105 | B. pertussis | | | Japan | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 510 | CS | CP002695;<br>PRJNA158859;<br>PRJNA66287 | | B. pertussis | | | China | | | | human | | | | 1 | 1 | 1 | 4 | 1 | 3 | |
| 527 | A371 | ERR380559;<br>WTCHG_45803_205 | | B. pertussis | | | USA | OH | | | human | | | | 1 | 1 | 1 | 4 | | | |
| 532 | B199 | ERR380564;<br>WTCHG_45803_210 | | B. pertussis | | | USA | PA | | | human | | | | 1 | 1 | 1 | 4 | | | |
| | | PRJNA202195;<br>PRJNA231814;<br>SAMN02436249 | | | | | | | | | | | | | | | | | | | |
| 1240 | B096 | CSRU01;<br>GCA_001208065.1;<br>PRJEB2274;<br>SAMEA751350 | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 8 | |
| 1556 | SRR1610566 | | | B. pertussis | | | Unknown | | | | | | | | 1 | 1 | 1 | 4 | 1 | 34 | |
| 1643 | FR6016 | ERR6044829;<br>PRJEB42353 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | 202,1034 |
| 1646 | FR6029 | ERR2102161;<br>PRJEB21744 | | B. pertussis | nasopharynx | pertussis | France | | | Human | Homo sapiens | French Bordetella NRC | | | 1 | 4 | 1 | 4 | 1 | 9 | |
| 2005 | Z020 | L2216;<br>SAMN08443717 | | B. pertussis | nasopharynx | | Australia | | | Human | Homo sapiens | | PathWest Laboratory Medicine | | 1 | 4 | 1 | 4 | 1 | 4 | |

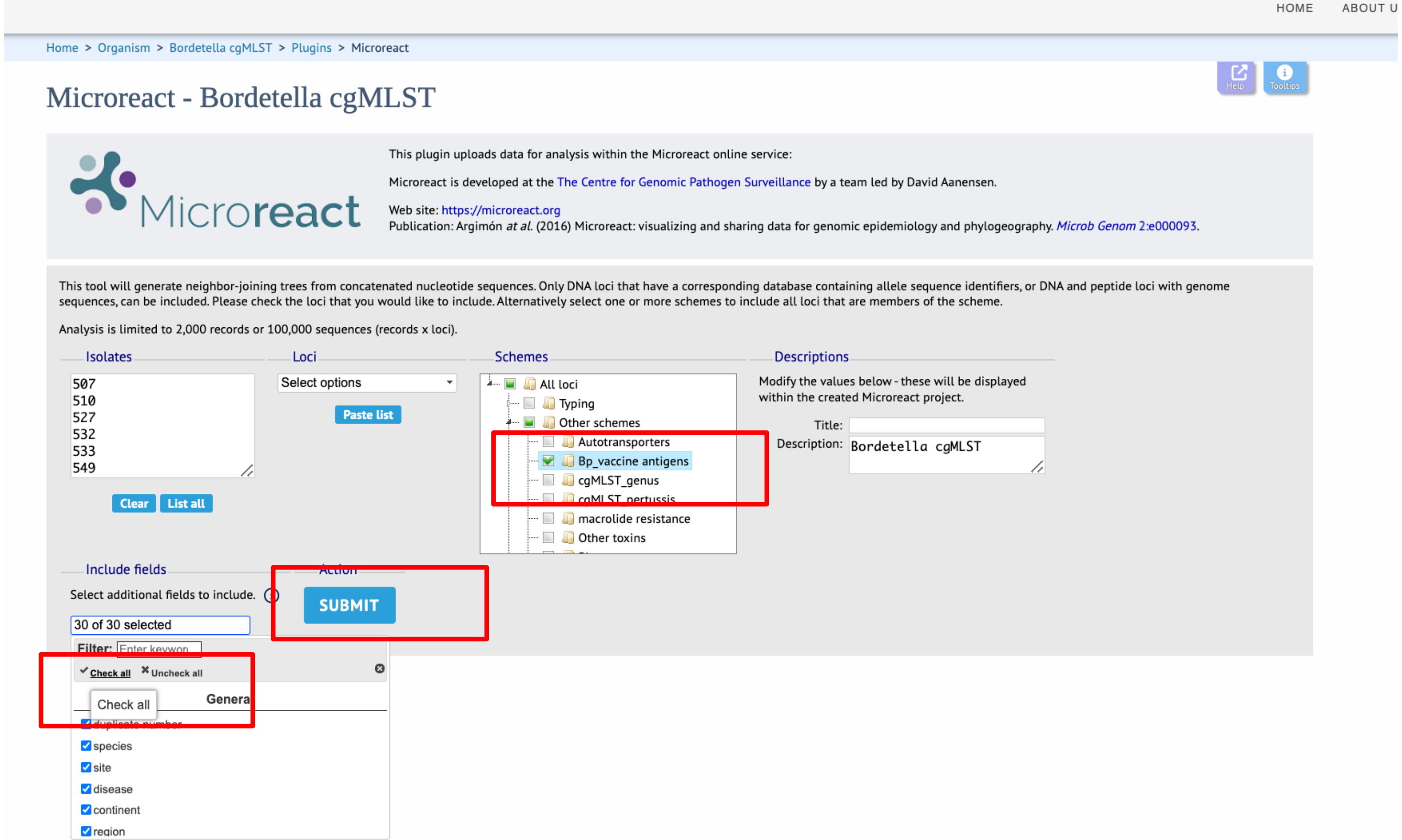
« ‹ 1 2 3 4 5 › »

### Analysis tools

Breakdown: Fields | Two Field | Combinations | Polymorphic sites | Publications | Sequence bin
Analysis: BURST | Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR
Export: Dataset | Contigs | Sequences
Third party: GrapeTree | iTOL | Microreact | ReporTree

https://bigsdb.pasteur.fr/bordetella/

# GrapeTree :



## Microreact - Bordetella cgMLST

This plugin uploads data for analysis within the Microreact online service:

Microreact is developed at the The Centre for Genomic Pathogen Surveillance by a team led by David Aanensen.

Web site: https://microreact.org
Publication: Argimón *at al.* (2016) Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. *Microb Genom* 2:e000093.

This tool will generate neighbor-joining trees from concatenated nucleotide sequences. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA and peptide loci with genome sequences, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 2,000 records or 100,000 sequences (records x loci).

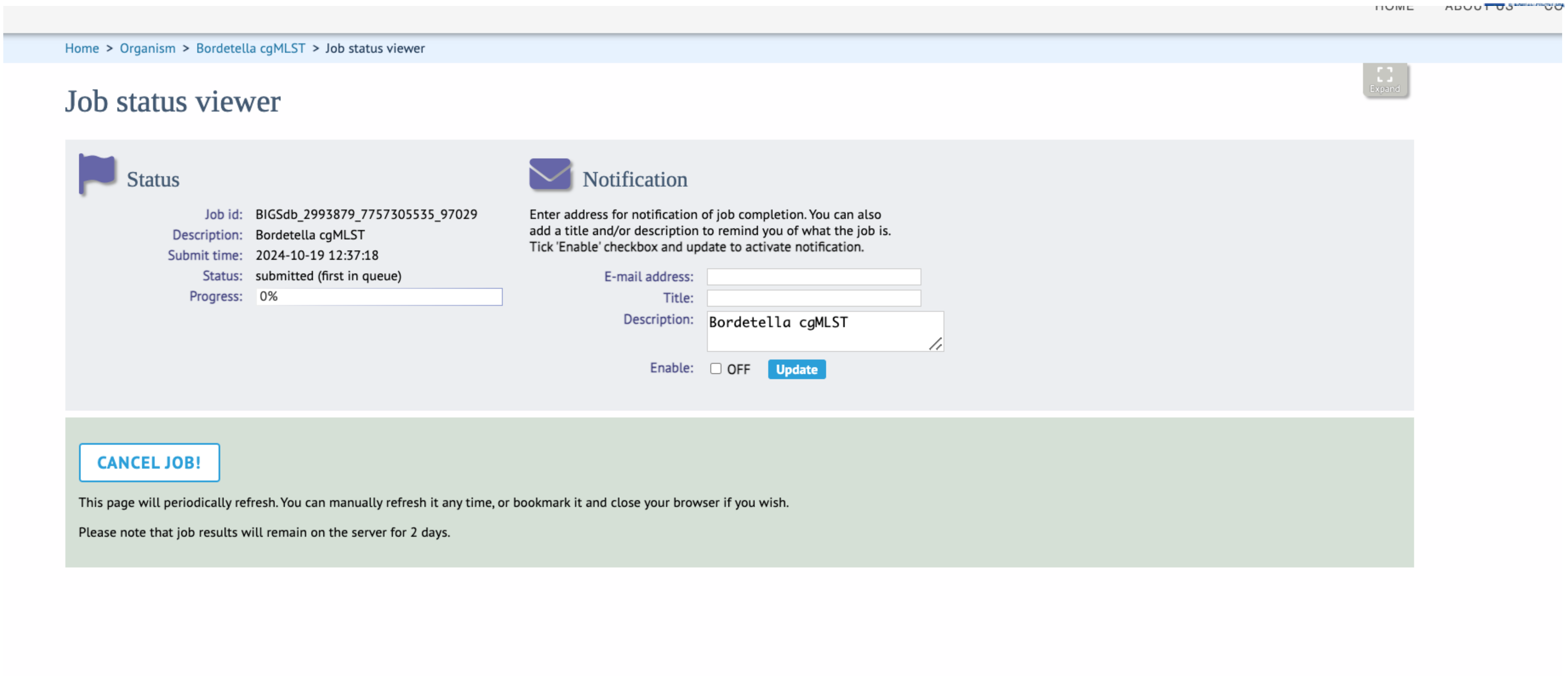
Modify the values below - these will be displayed within the created Microreact project.

Title:
Description: Bordetella cgMLST

Select additional fields to include.

https://bigsdb.pasteur.fr/bordetella/

# GrapeTree :



## Job status viewer

### Status

| | |
|---|---|
| Job id: | BIGSdb_2993879_7757305535_97029 |
| Description: | Bordetella cgMLST |
| Submit time: | 2024-10-19 12:37:18 |
| Status: | submitted (first in queue) |
| Progress: | 0% |

### Notification

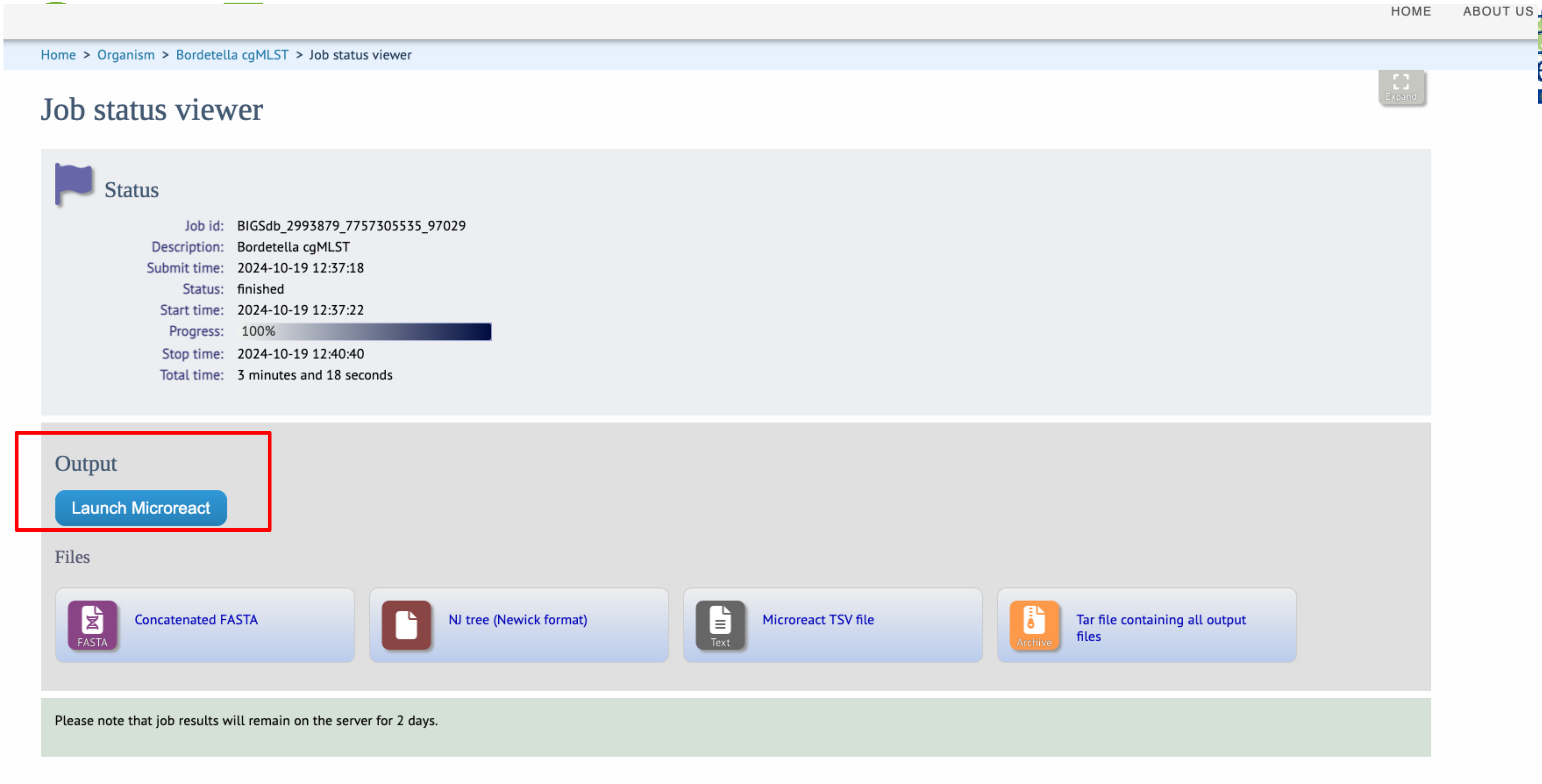
Enter address for notification of job completion. You can also add a title and/or description to remind you of what the job is. Tick 'Enable' checkbox and update to activate notification.

| | |
|---|---|
| E-mail address: | |
| Title: | |
| Description: | Bordetella cgMLST |
| Enable: | ☐ OFF |

This page will periodically refresh. You can manually refresh it any time, or bookmark it and close your browser if you wish.

Please note that job results will remain on the server for 2 days.

https://bigsdb.pasteur.fr/bordetella/



# Job status viewer

## Status

| | |
|---|---|
| Job id: | BIGSdb_2993879_7757305535_97029 |
| Description: | Bordetella cgMLST |
| Submit time: | 2024-10-19 12:37:18 |
| Status: | finished |
| Start time: | 2024-10-19 12:37:22 |
| Progress: | 100% |
| Stop time: | 2024-10-19 12:40:40 |
| Total time: | 3 minutes and 18 seconds |

## Output

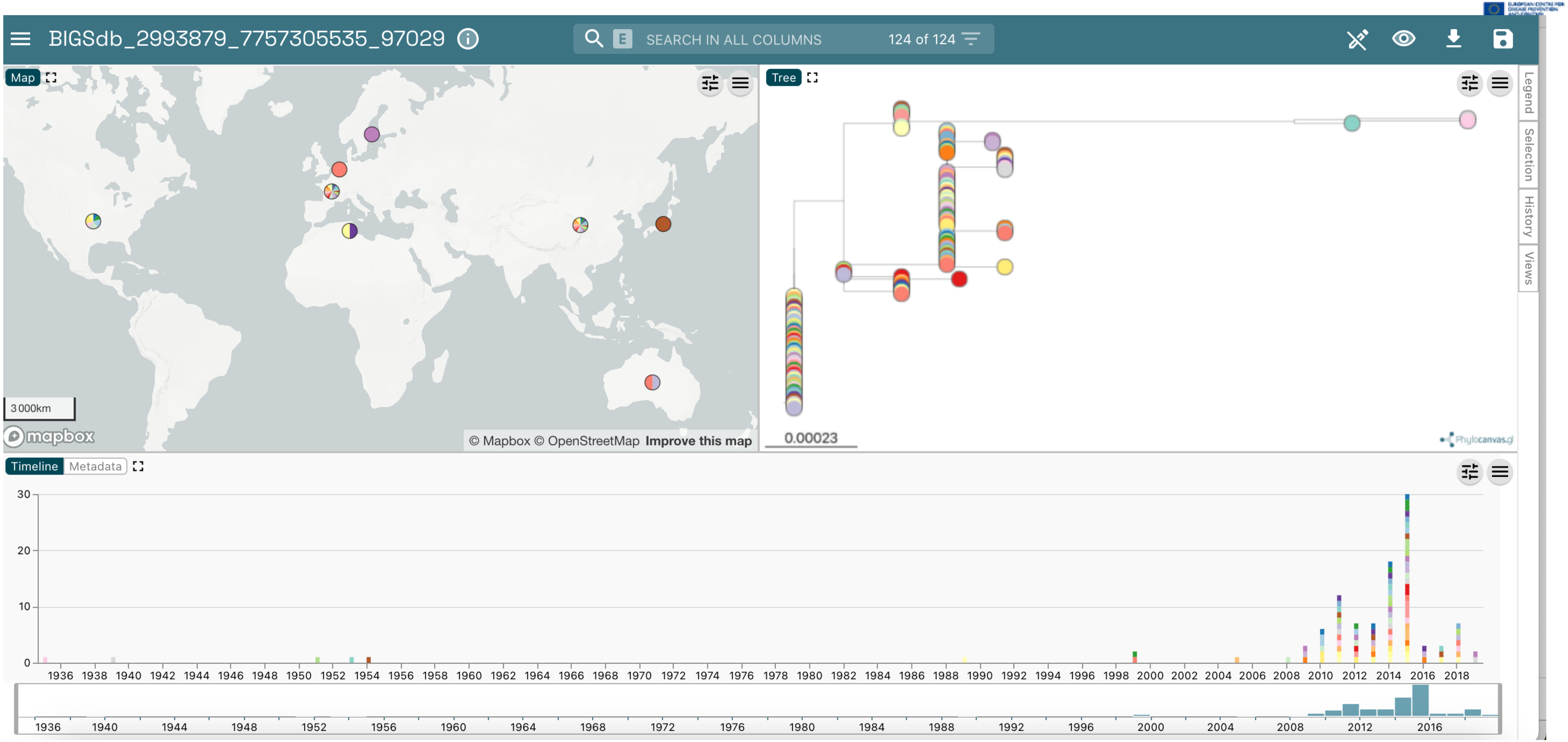
### Files

- Concatenated FASTA
- NJ tree (Newick format)
- Microreact TSV file
- Tar file containing all output files

Please note that job results will remain on the server for 2 days.

https://bigsdb.pasteur.fr/bordetella/

# GrapeTree :



https://bigsdb.pasteur.fr/bordetella/

# Acknowledgements

**The creation of this training material was commissioned by ECDC to Institut Pasteur with the direct involvement of Valérie Bouchez.**