Practical Session:

Pertussis vaccine antigen detection

Valérie Bouchez

GenEpi Webinar :

Antigen Surveillance: from Evolution to Immune Escape

A virtual training workshop within GenEpi-BioTrain.

March 23rd, 2026

Intended Learning Objectives

Live demonstration of genomic tools used for the exercises

-Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb

-Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb

-Focus on Pertactin *B. pertussis* vaccine antigen (exploring diversity of prn using BIGSdb and blastN)

Presentation of the exercises to be carried out on public project 81

Session of March 25th, 2026- Correction of the practical exercises

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

https://blast.ncbi.nlm.nih.gov/

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Have you already used BIGSdb platform for genotyping purpose?

Rapid general BIGSdb presentation

BIGSdb (Bacterial Isolate Genome Sequence Database) is a software platform designed to manage bacterial genomic sequence data.

It serves as a public **nomenclature database**, but is also a **database of bacterial genomes**.

Used by
- Microbiologists
- Epidemiologists
- Bioinformaticians
- Public health researchers

Usefull for
- Surveillance of bacterial infections
- Pathogen traceability
- Real-time epidemic management.

Two different databases can be used depending on the pathogen of interest :

- **BIGSdb** (Pasteur) (https://bigsdb.pasteur.fr)
  - 13 pathogens (including **Bordetella**)

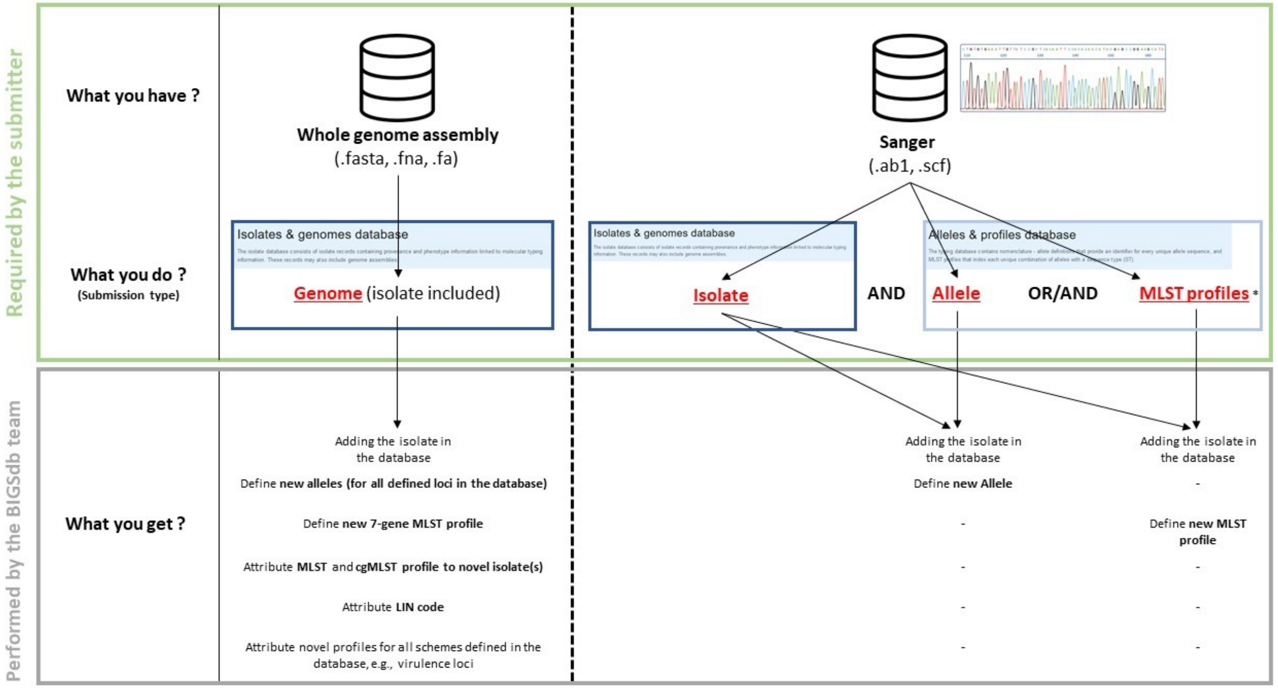
- **PubMLST** (Oxford) (https://pubmlst.org)
  - 139 organisms

Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb

✓ All BIGSdb databases are **subdivided** into **two databases**

Alleles & profiles (Seqdef)	**Isolates & genomes**
Contains the nomenclature : - **Allele** (Id for every unique ellele sequence) - **Profiles** (MLST, cgMLST, LINcode ...)	Contains isolates: - **Metadata** associated with isolates (Provenance, phenotype ...) - **Molecular typing** based on the nomenclature of the SeqDef database - Isolates can be linked to a **genome assembly**

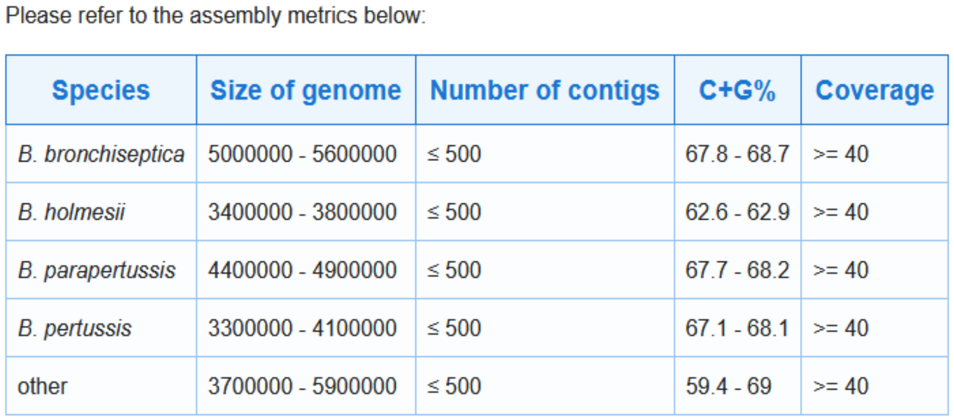
✓ Type of data accepted



*If all the alleles of the MLST profile are already known and the combination of these alleles is new, the Sanger data may not be required. The procedure to follow is also detailed in the Sanger data submission guidelines.

✓ Whole genome sequencing data requirements

only high-quality assemblies generated from pure cultures sequenced at a minimum coverage of 40X.



Please refer to the assembly metrics below:

Species	Size of genome	Number of contigs	C+G%	Coverage
B. bronchiseptica	5000000 - 5600000	≤ 500	67.8 - 68.7	>= 40
B. holmesii	3400000 - 3800000	≤ 500	62.6 - 62.9	>= 40
B. parapertussis	4400000 - 4900000	≤ 500	67.7 - 68.2	>= 40
B. pertussis	3300000 - 4100000	≤ 500	67.1 - 68.1	>= 40
other	3700000 - 5900000	≤ 500	59.4 - 69	>= 40

https://bigsdb.pasteur.fr/bordetella/genomes-quality-criteria/

Submission guidelines : https://bigsdb.pasteur.fr/submission-procedure-for-data-curation/

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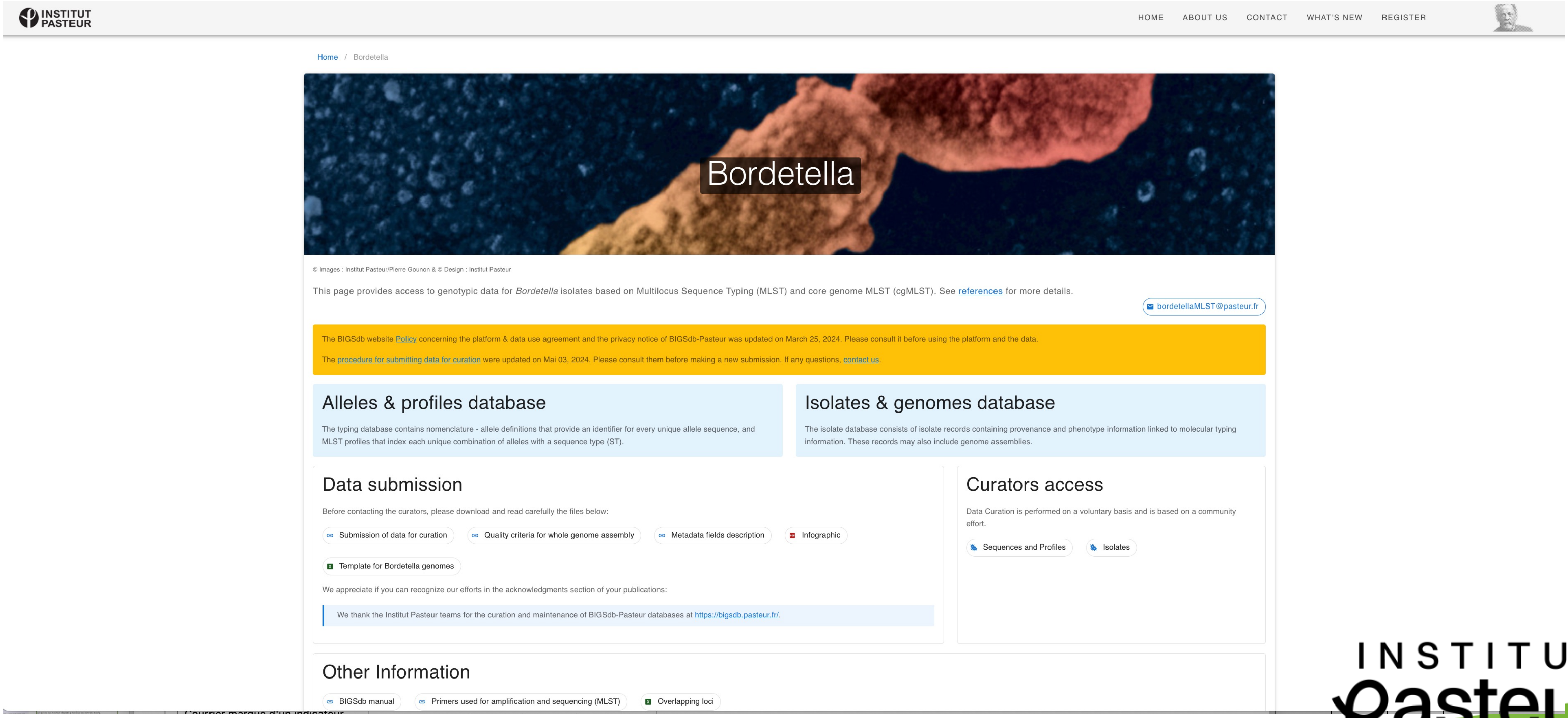
→ https://bigsdb.pasteur.fr/bordetella/



© Images : Institut Pasteur/Pierre Gounon & © Design : Institut Pasteur

This page provides access to genotypic data for *Bordetella* isolates based on Multilocus Sequence Typing (MLST) and core genome MLST (cgMLST). See references for more details.

bordetellaMLST@pasteur.fr

The BIGSdb website Policy concerning the platform & data use agreement and the privacy notice of BIGSdb-Pasteur was updated on March 25, 2024. Please consult it before using the platform and the data.

The procedure for submitting data for curation were updated on Mai 03, 2024. Please consult them before making a new submission. If any questions, contact us.

Alleles & profiles database

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Isolates & genomes database

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Data submission

Before contacting the curators, please download and read carefully the files below:

We appreciate if you can recognize our efforts in the acknowledgments section of your publications:

> We thank the Institut Pasteur teams for the curation and maintenance of BIGSdb-Pasteur databases at https://bigsdb.pasteur.fr/.

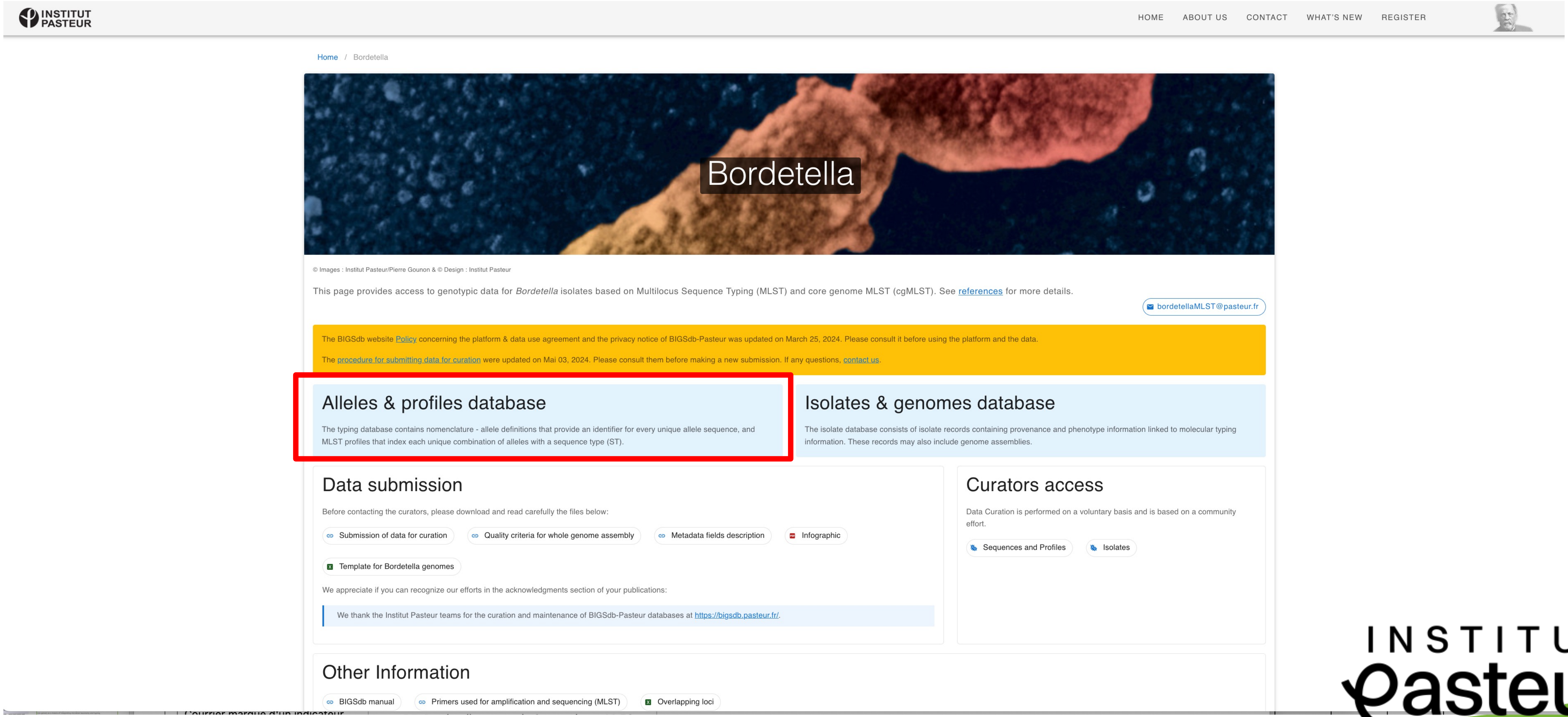
Curators access

Data Curation is performed on a voluntary basis and is based on a community effort.

Other Information

Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb

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



© Images : Institut Pasteur/Pierre Gounon & © Design : Institut Pasteur

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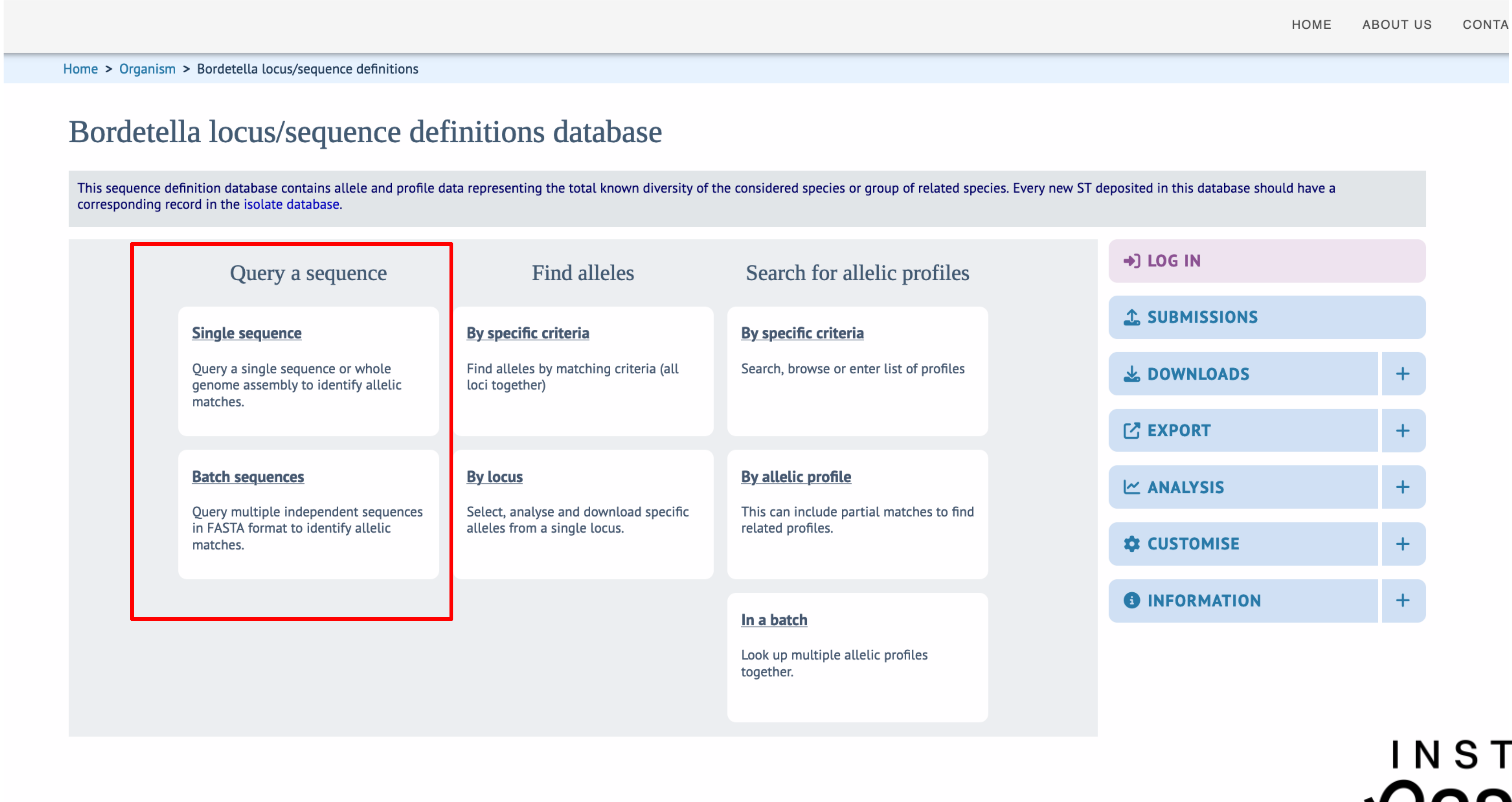


Bordetella locus/sequence definitions database

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.

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

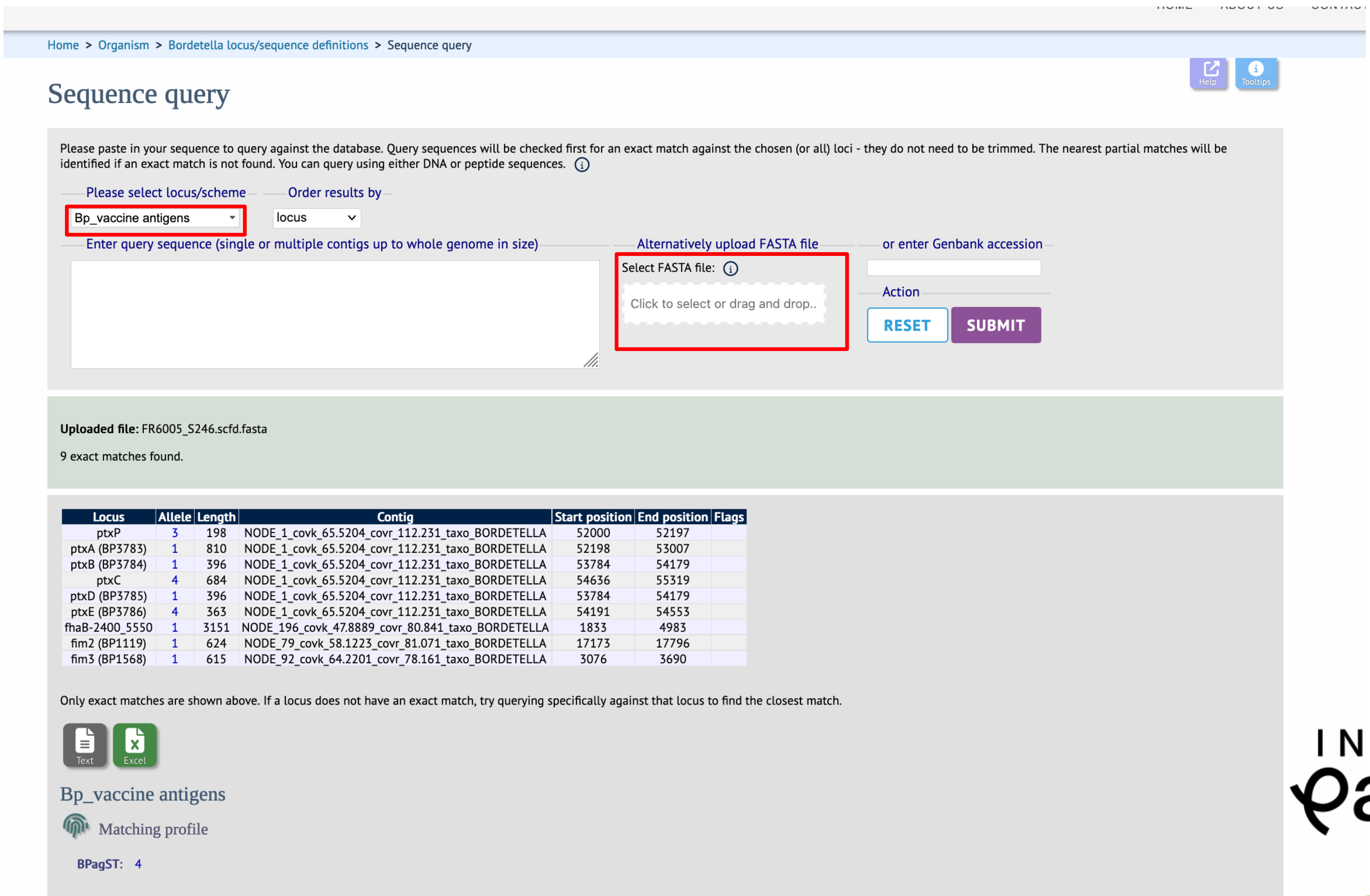
This can include partial matches to find related profiles.

In a batch

Look up multiple allelic profiles together.

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

Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb



Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences.

Please select locus/scheme: Bp_vaccine antigens

Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file:

Uploaded file: FR6005_S246.scfd.fasta

9 exact matches found.

Locus	Allele	Length	Contig	Start position	End position	Flags
ptxP	3	198	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	52000	52197	
ptxA (BP3783)	1	810	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	52198	53007	
ptxB (BP3784)	1	396	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	53784	54179	
ptxC	4	684	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	54636	55319	
ptxD (BP3785)	1	396	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	53784	54179	
ptxE (BP3786)	4	363	NODE_1_covk_65.5204_covr_112.231_taxo_BORDETELLA	54191	54553	
fhaB-2400_5550	1	3151	NODE_196_covk_47.8889_covr_80.841_taxo_BORDETELLA	1833	4983	
fim2 (BP1119)	1	624	NODE_79_covk_58.1223_covr_81.071_taxo_BORDETELLA	17173	17796	
fim3 (BP1568)	1	615	NODE_92_covk_64.2201_covr_78.161_taxo_BORDETELLA	3076	3690	

Only exact matches are shown above. If a locus does not have an exact match, try querying specifically against that locus to find the closest match.

Bp_vaccine antigens

Matching profile

BPagST: 4

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

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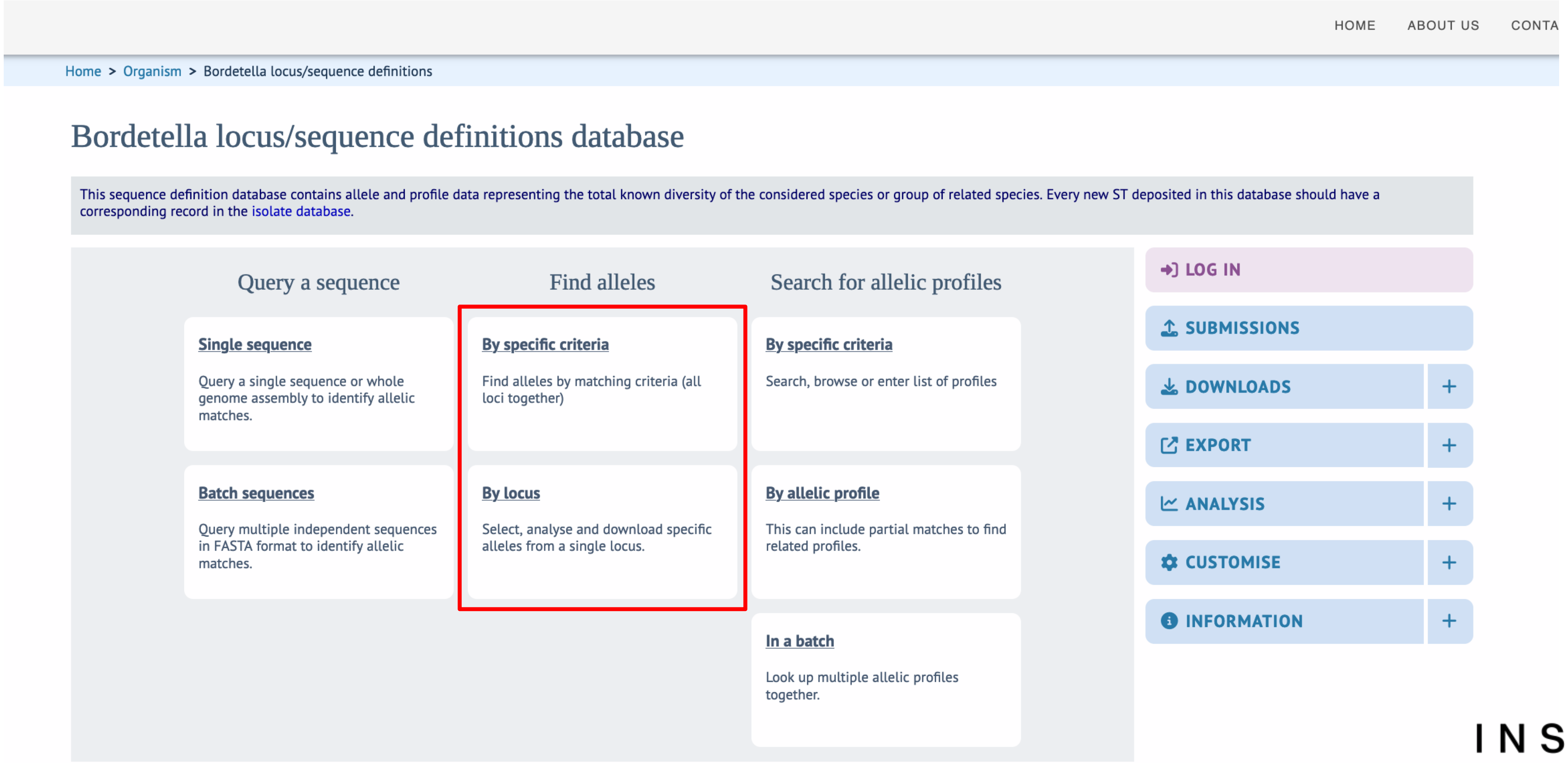

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Single sequence Query a single sequence or whole genome assembly to identify allelic matches.	**By specific criteria** Find alleles by matching criteria (all loci together)	**By specific criteria** Search, browse or enter list of profiles
Batch sequences Query multiple independent sequences in FASTA format to identify allelic matches.	**By locus** Select, analyse and download specific alleles from a single locus.	**By allelic profile** This can include partial matches to find related profiles.
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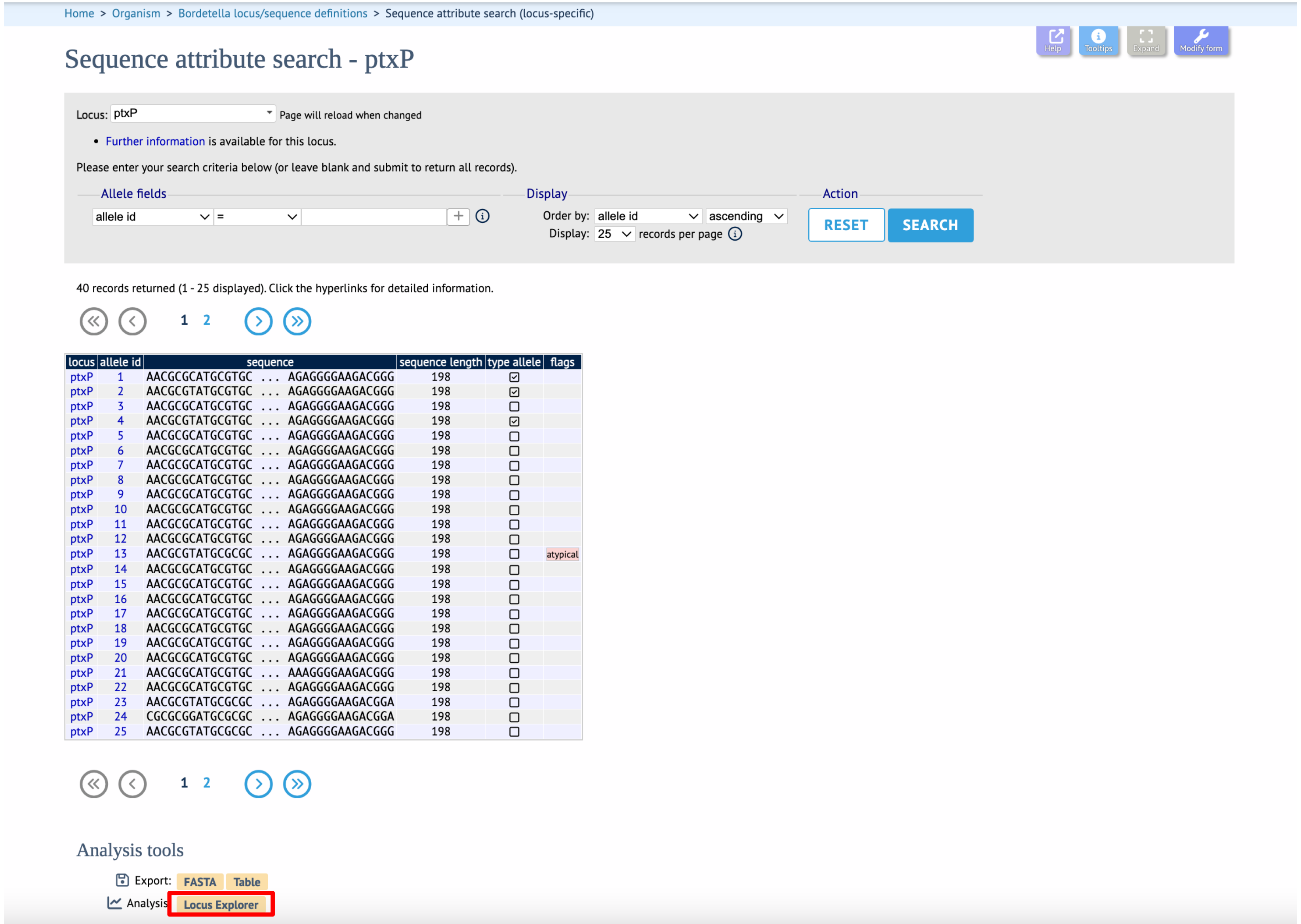

Home > Organism > Bordetella locus/sequence definitions > Sequence attribute search (locus-specific)

Sequence attribute search - ptxP

Locus: ptxP 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

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

locus	allele id	sequence	sequence length	type allele	flags
ptxP	1	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☑	
ptxP	2	AACGCGTATGCGTGC ... AGAGGGGAAGACGGG	198	☑	
ptxP	3	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	4	AACGCGTATGCGTGC ... AGAGGGGAAGACGGG	198	☑	
ptxP	5	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	6	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	7	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	8	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	9	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	10	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	11	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	12	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	13	AACGCGTATGCGCGC ... AGAGGGGAAGACGGG	198	☐	atypical
ptxP	14	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	15	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	16	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	17	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	18	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	19	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	20	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	21	AACGCGCATGCGTGC ... AAAGGGGAAGACGGG	198	☐	
ptxP	22	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	23	AACGCGTATGCGCGC ... AGAGGGGAAGACGGA	198	☐	
ptxP	24	CGCGCGGATGCGCGC ... AGAGGGGAAGACGGA	198	☐	
ptxP	25	AACGCGTATGCGCGC ... AGAGGGGAAGACGGG	198	☐	

Analysis tools

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

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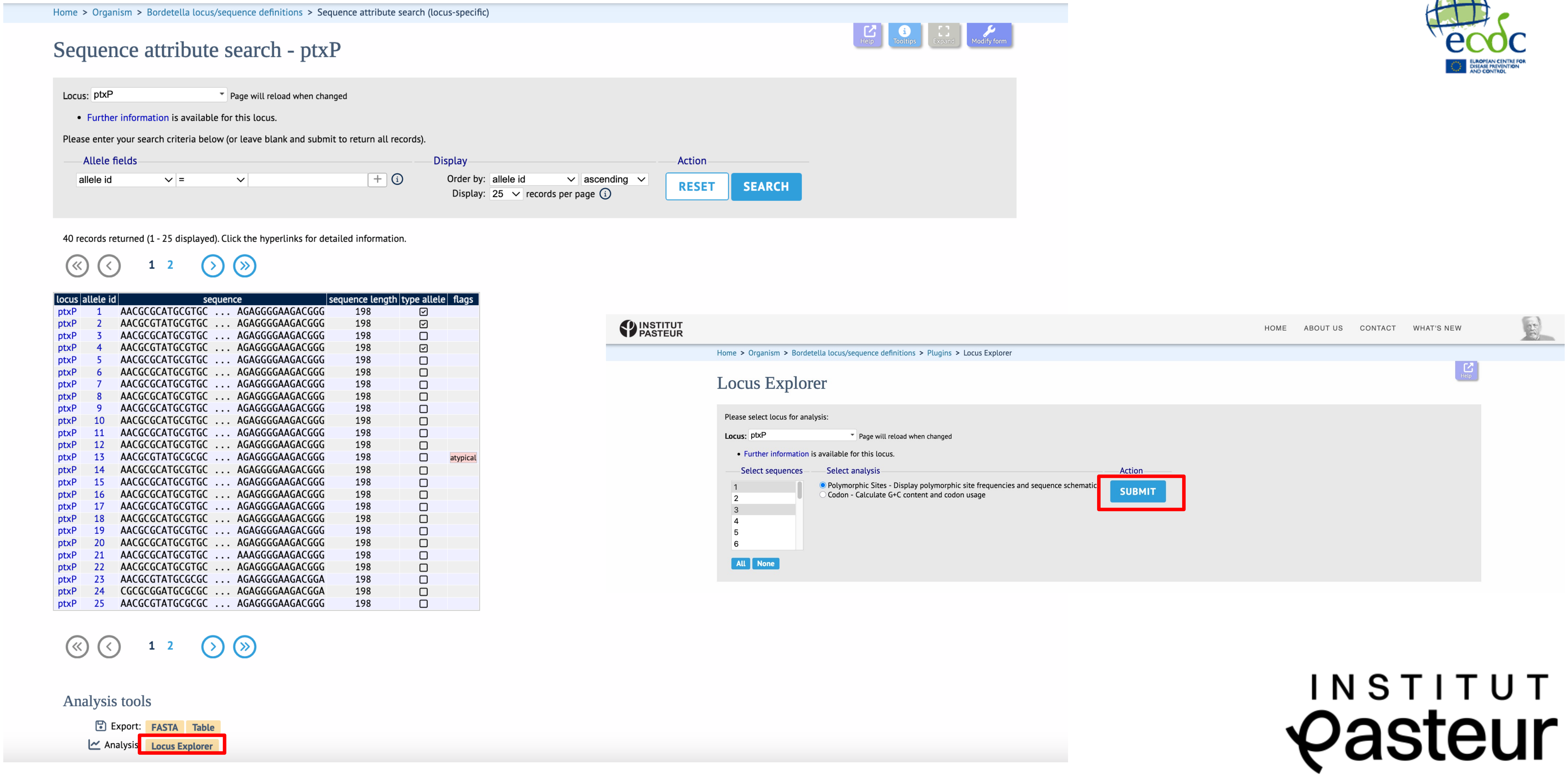

Sequence attribute search - ptxP

Locus: ptxP 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).

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ptxP	3	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	4	AACGCGTATGCGTGC ... AGAGGGGAAGACGGG	198	☑	
ptxP	5	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	6	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	7	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	8	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	9	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	10	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	11	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	12	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	13	AACGCGTATGCGCGC ... AGAGGGGAAGACGGG	198	☐	atypical
ptxP	14	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	15	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	16	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	17	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	18	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	19	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	20	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	21	AACGCGCATGCGTGC ... AAAGGGGAAGACGGG	198	☐	
ptxP	22	AACGCGCATGCGTGC ... AGAGGGGAAGACGGG	198	☐	
ptxP	23	AACGCGTATGCGCGC ... AGAGGGGAAGACGGA	198	☐	
ptxP	24	CGCGCGGATGCGCGC ... AGAGGGGAAGACGGA	198	☐	
ptxP	25	AACGCGTATGCGCGC ... AGAGGGGAAGACGGG	198	☐	

Analysis tools

Locus Explorer

Please select locus for analysis:

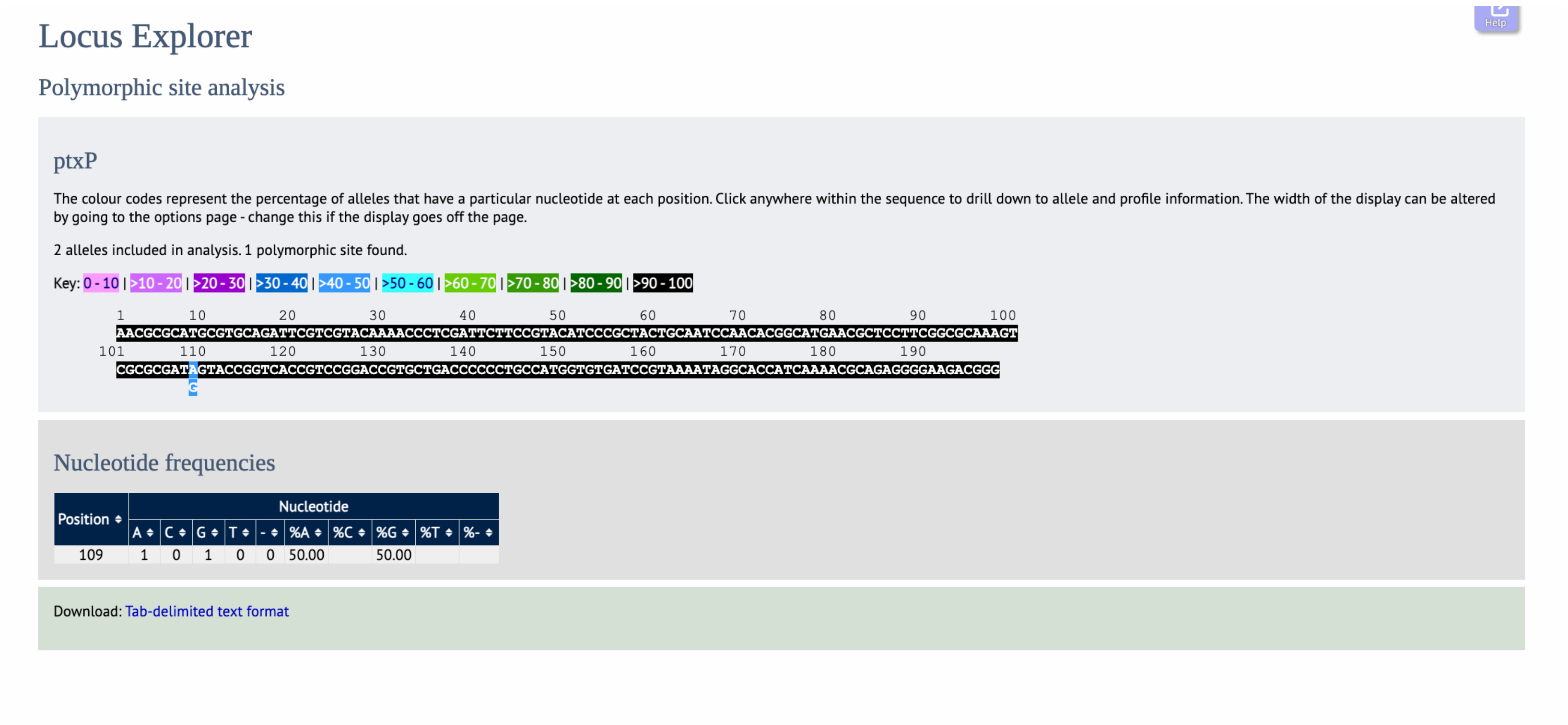
Locus: ptxP Page will reload when changed

- Further information is available for this locus.

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

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

Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb



Locus Explorer

Polymorphic site analysis

ptxP

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
   AACGCGCATGCGTGCAGATTCGTCGTACAAAACCCTCGATTCTTCCGTACATCCCGCTACTGCAATCCAACACGGCATGAACGCTCCTTCGGCGCAAAGT
 101        110       120       130       140       150       160       170       180       190
   CGCGCGATAGTACCGGTCACCGTCCGGACCGTGCTGACCCCCCTGCCATGGTGTGATCCGTAAAATAGGCACCATCAAAACGCAGAGGGGAAGACGGG
           G
```

Nucleotide frequencies

Position	Nucleotide									
	A	C	G	T	-	%A	%C	%G	%T	%-
109	1	0	1	0	0	50.00		50.00		

Download: Tab-delimited text format

22/09/2024

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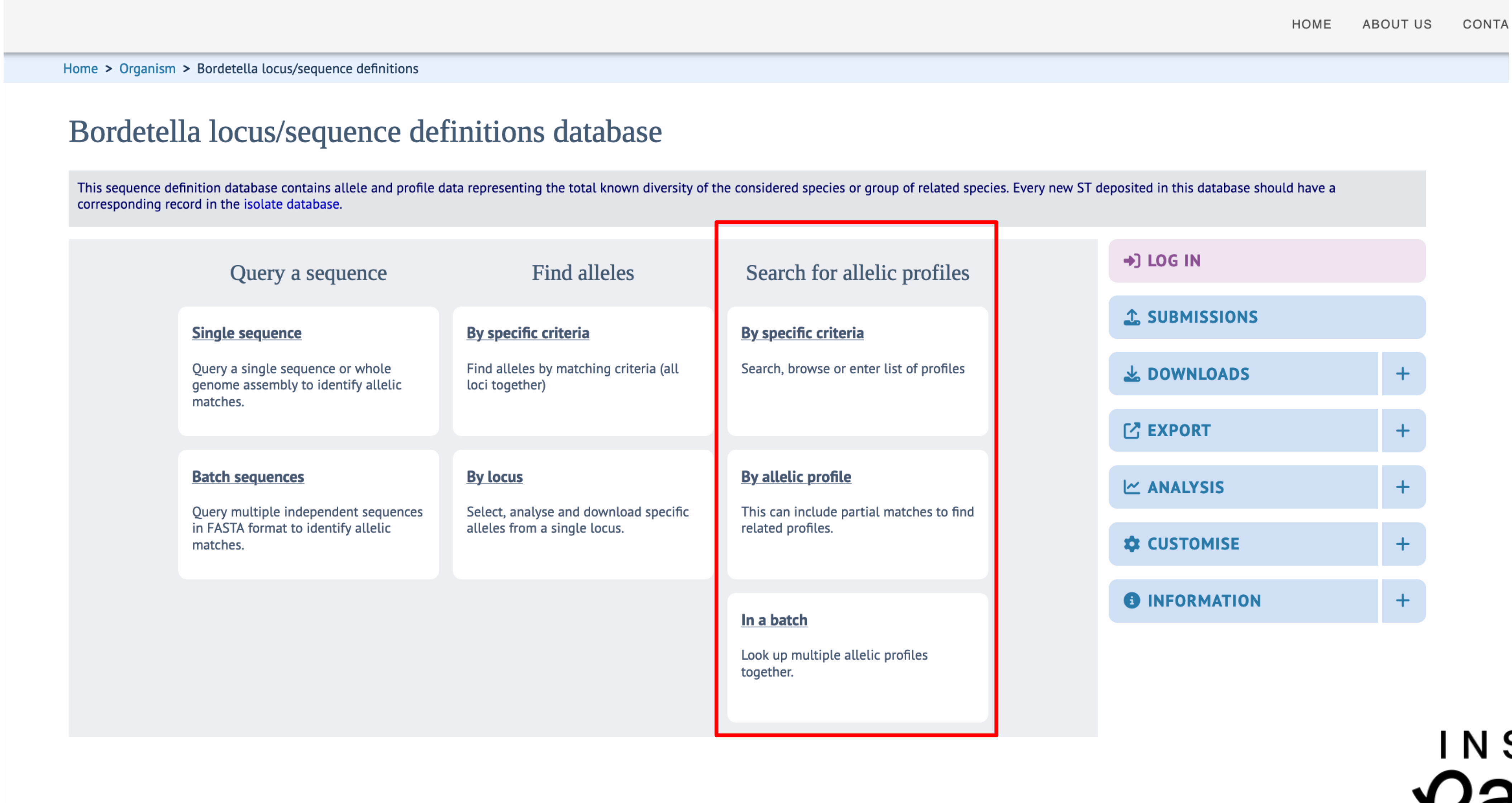

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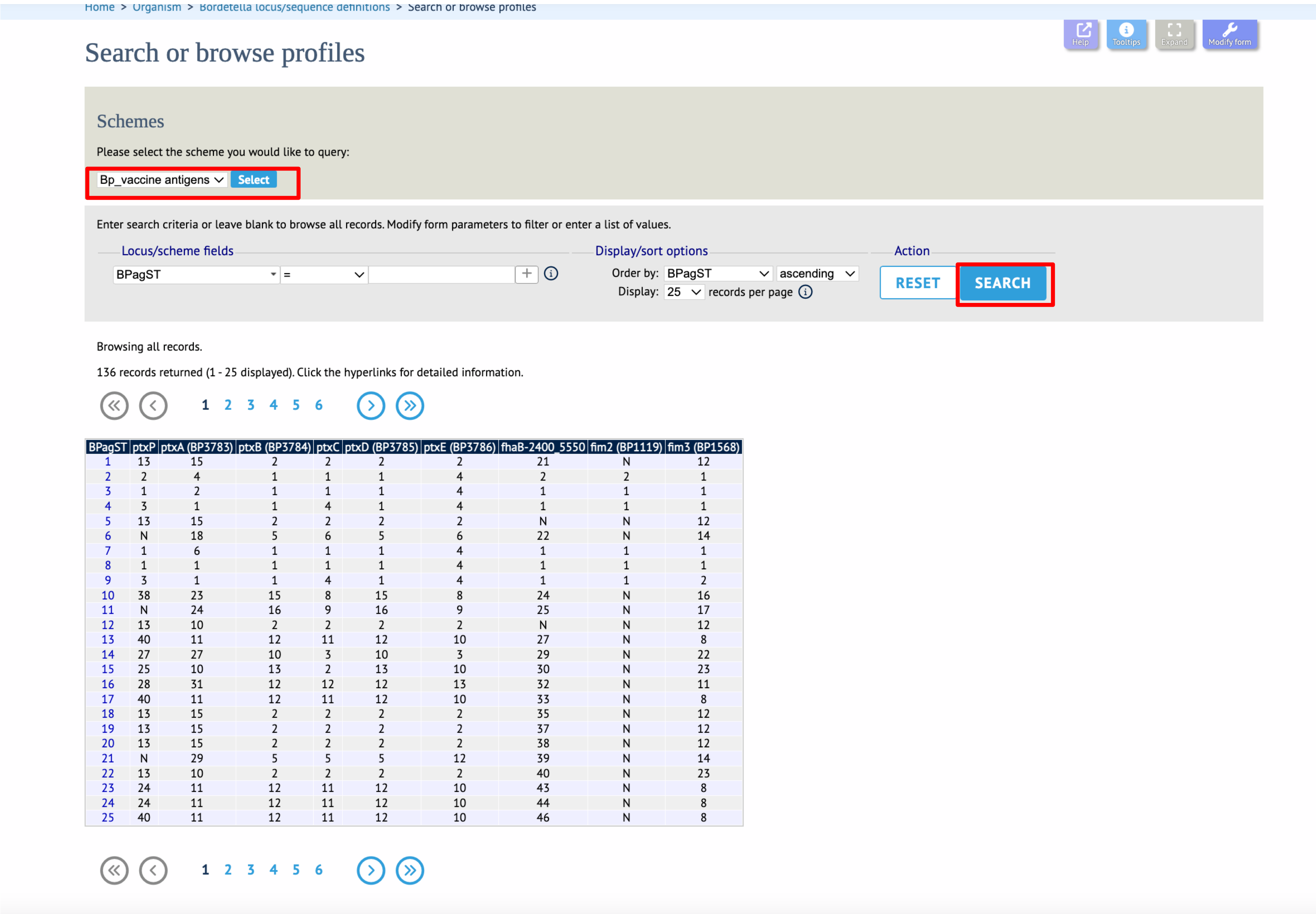

Search or browse profiles

Schemes

Please select the scheme you would like to query:

Bp_vaccine antigens

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

Locus/scheme fields: BPagST =

Display/sort options: Order by: BPagST ascending; Display: 25 records per page

Browsing all records.

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

BPagST	ptxP	ptxA (BP3783)	ptxB (BP3784)	ptxC	ptxD (BP3785)	ptxE (BP3786)	fhaB-2400_5550	fim2 (BP1119)	fim3 (BP1568)
1	13	15	2	2	2	2	21	N	12
2	2	4	1	1	1	4	2	2	1
3	1	2	1	1	1	4	1	1	1
4	3	1	1	4	1	4	1	1	1
5	13	15	2	2	2	2	N	N	12
6	N	18	5	6	5	6	22	N	14
7	1	6	1	1	1	4	1	1	1
8	1	1	1	1	1	4	1	1	1
9	3	1	1	4	1	4	1	1	2
10	38	23	15	8	15	8	24	N	16
11	N	24	16	9	16	9	25	N	17
12	13	10	2	2	2	2	N	N	12
13	40	11	12	11	12	10	27	N	8
14	27	27	10	3	10	3	29	N	22
15	25	10	13	2	13	10	30	N	23
16	28	31	12	12	12	13	32	N	11
17	40	11	12	11	12	10	33	N	8
18	13	15	2	2	2	2	35	N	12
19	13	15	2	2	2	2	37	N	12
20	13	15	2	2	2	2	38	N	12
21	N	29	5	5	5	12	39	N	14
22	13	10	2	2	2	2	40	N	23
23	24	11	12	11	12	10	43	N	8
24	24	11	12	11	12	10	44	N	8
25	40	11	12	11	12	10	46	N	8

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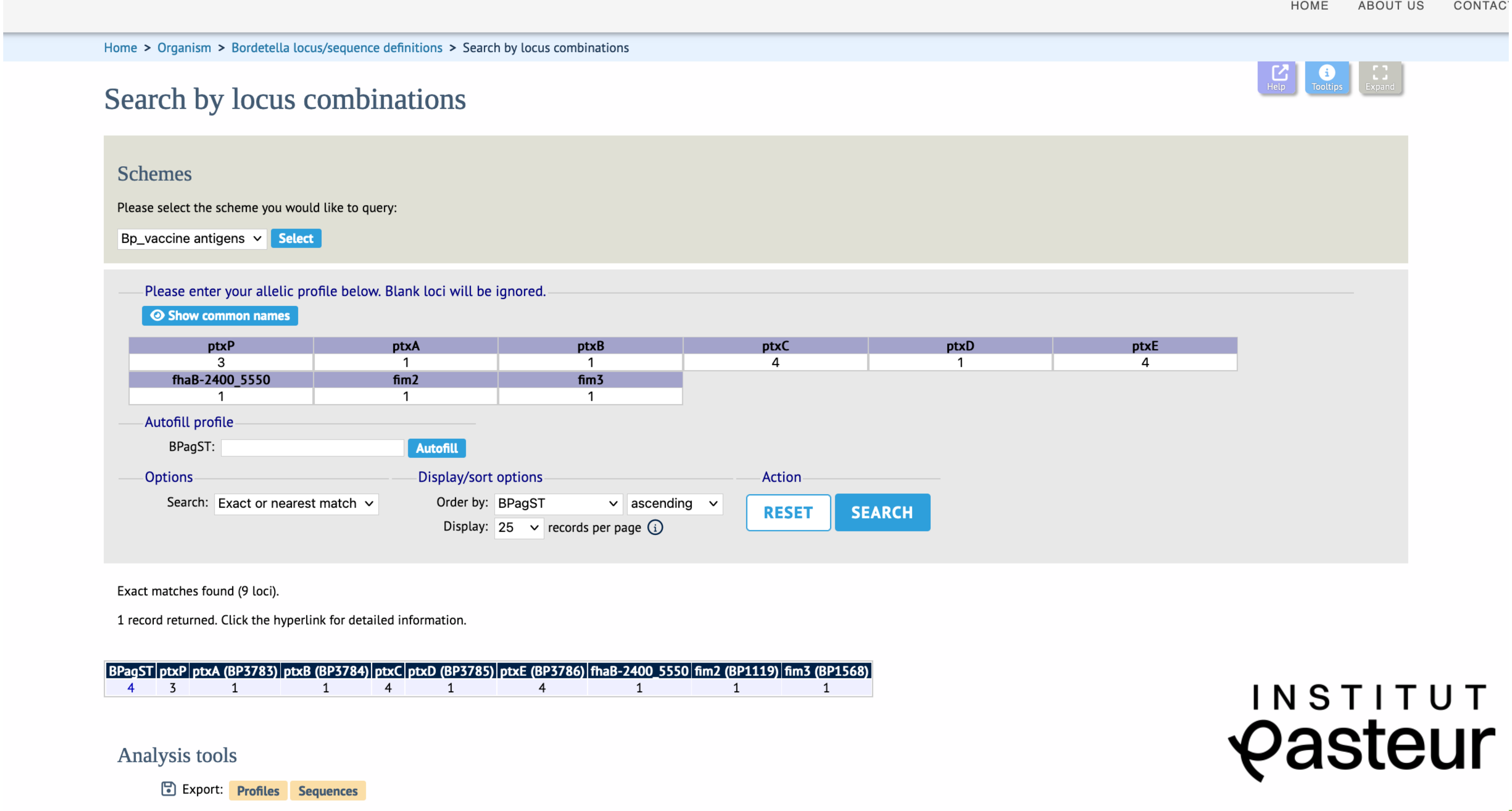

Home > Organism > Bordetella locus/sequence definitions > Search by locus combinations

Search by locus combinations

Schemes

Please select the scheme you would like to query:

Bp_vaccine antigens Select

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

Show common names

ptxP	ptxA	ptxB	ptxC	ptxD	ptxE
3	1	1	4	1	4

fhaB-2400_5550	fim2	fim3
1	1	1

Autofill profile

BPagST: Autofill

Options

Search: Exact or nearest match

Display/sort options

Order by: BPagST ascending

Display: 25 records per page

Action

RESET SEARCH

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

Analysis tools

Export: Profiles Sequences

INSTITUT Pasteur

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

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-Focus on Pertactin *B. pertussis* vaccine antigen (exploring diversity of prn using BIGSdb and blastN)

Presentation of the exercises to be carried out on public project81

Session of March 25th, 2026- Correction of the practical exercises

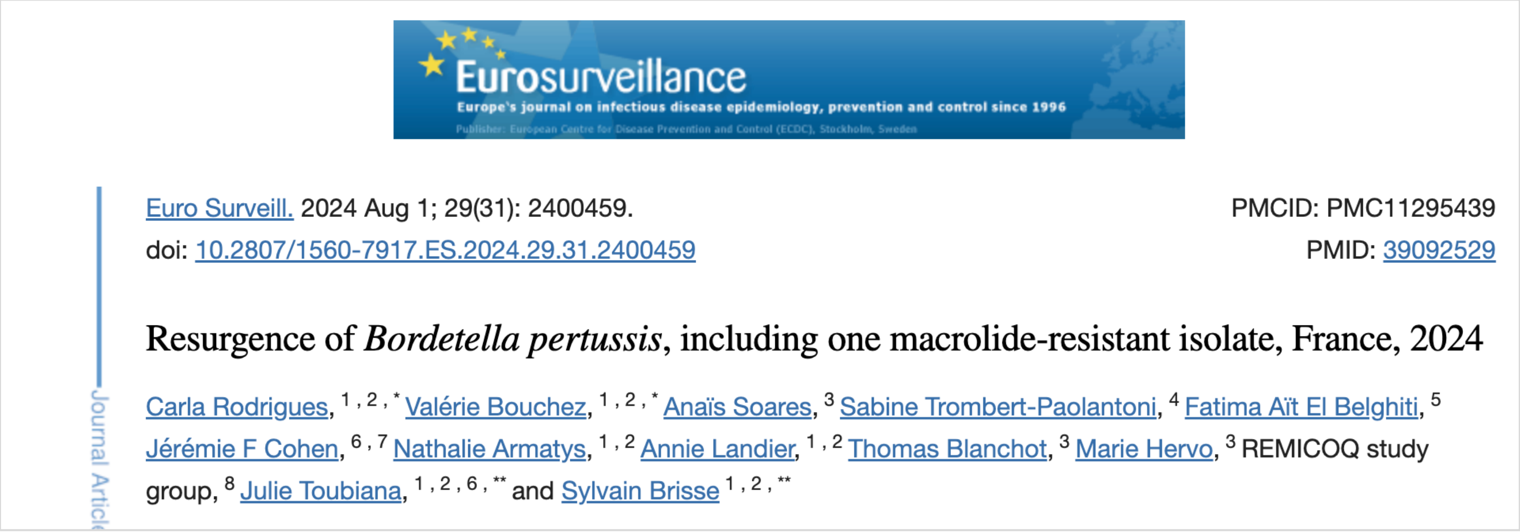
https://bigsdb.pasteur.fr/bordetella/

https://blast.ncbi.nlm.nih.gov/

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb

How to perform a Minimum spaninning tree based on cgMLST_pertussis, displaying Bp-agST and number of allelic differences

public project 55 in Bordetella Isolates & genomes database



Euro Surveill. 2024 Aug 1; 29(31): 2400459.
doi: 10.2807/1560-7917.ES.2024.29.31.2400459

PMCID: PMC11295439
PMID: 39092529

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

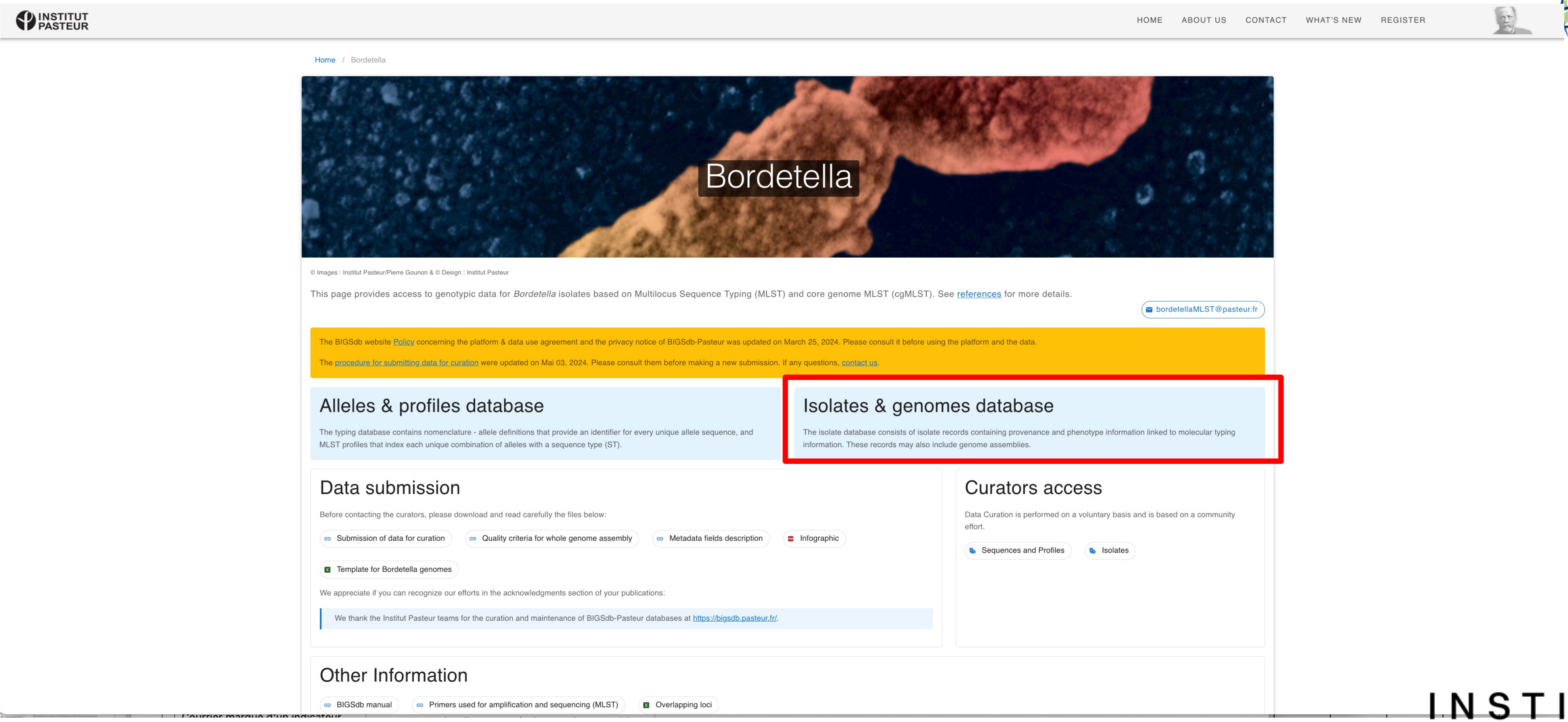
Carla Rodrigues,[1,2,*] Valérie Bouchez,[1,2,*] Anaïs Soares,[3] Sabine Trombert-Paolantoni,[4] Fatima Aït El Belghiti,[5] Jérémie F Cohen,[6,7] Nathalie Armatys,[1,2] Annie Landier,[1,2] Thomas Blanchot,[3] Marie Hervo,[3] REMICOQ study group,[8] Julie Toubiana,[1,2,6,**] and Sylvain Brisse[1,2,**]

Abstract

As other European countries, France is experiencing a resurgence of pertussis in 2024. Between 1 January and 31 May 2024, 5,616 (24.9%) positive *Bordetella pertussis* qPCR tests were identified, following a 3-year period of almost null incidence. Of 67 cultured and whole genome sequenced *B. pertussis* isolates, 66 produced pertactin and 56 produced FIM2, in contrast to pre-COVID-19 years. One isolate of genotype Bp-AgST4 was resistant to macrolides. Pertussis resurgence may favour isolates that produce FIM2 and pertactin.

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



© Images : Institut Pasteur/Pierre Gounon & © Design : Institut Pasteur

This page provides access to genotypic data for *Bordetella* isolates based on Multilocus Sequence Typing (MLST) and core genome MLST (cgMLST). See references for more details.

bordetellaMLST@pasteur.fr

The BIGSdb website Policy concerning the platform & data use agreement and the privacy notice of BIGSdb-Pasteur was updated on March 25, 2024. Please consult it before using the platform and the data.

The procedure for submitting data for curation were updated on Mai 03, 2024. Please consult them before making a new submission. If any questions, contact us.

Alleles & profiles database

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Isolates & genomes database

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Data submission

Before contacting the curators, please download and read carefully the files below:

- Submission of data for curation
- Quality criteria for whole genome assembly
- Metadata fields description
- Infographic
- Template for Bordetella genomes

We appreciate if you can recognize our efforts in the acknowledgments section of your publications:

> We thank the Institut Pasteur teams for the curation and maintenance of BIGSdb-Pasteur databases at https://bigsdb.pasteur.fr/.

Curators access

Data Curation is performed on a voluntary basis and is based on a community effort.

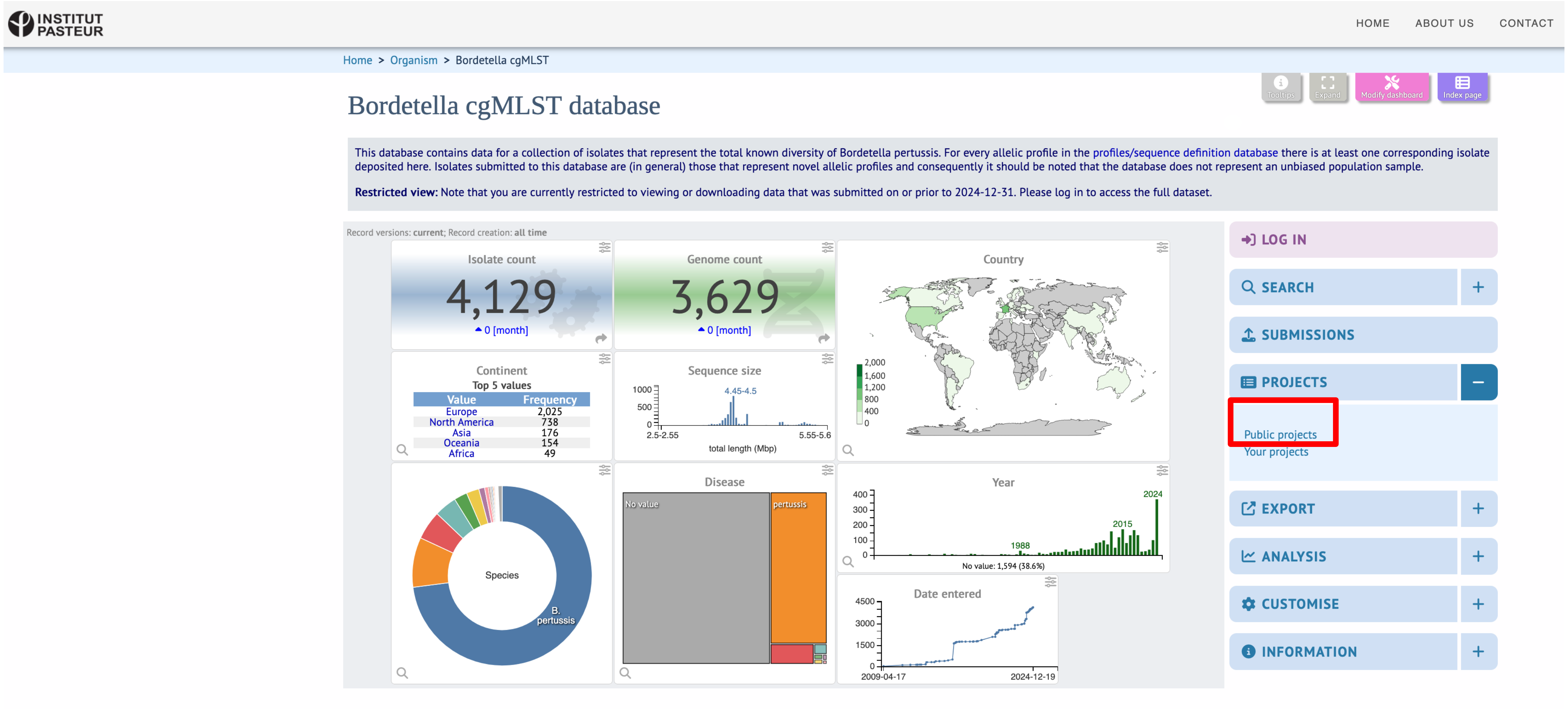
- Sequences and Profiles
- Isolates

Other Information

- BIGSdb manual
- Primers used for amplification and sequencing (MLST)
- Overlapping loci

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



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 2024-12-31. Please log in to access the full dataset.

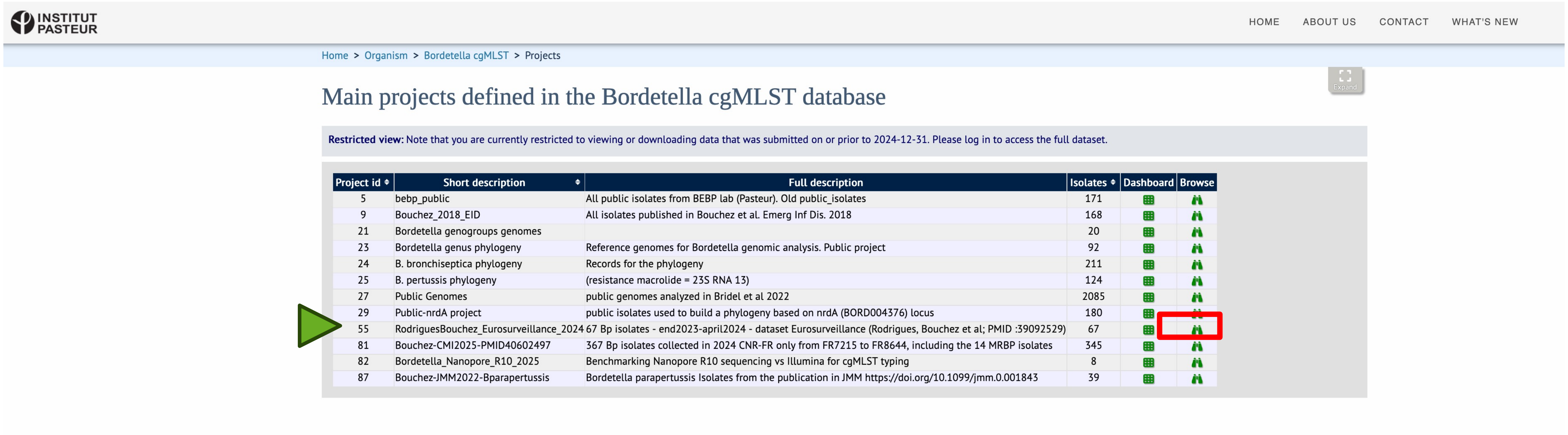
Continent

Top 5 values

Value	Frequency
Europe	2,025
North America	738
Asia	176
Oceania	154
Africa	49

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



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 2024-12-31. 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	▦	🔍
55	RodriguesBouchez_Eurosurveillance_2024	67 Bp isolates - end2023-april2024 - dataset Eurosurveillance (Rodrigues, Bouchez et al; PMID :39092529)	67	▦	🔍
81	Bouchez-CMI2025-PMID40602497	367 Bp isolates collected in 2024 CNR-FR only from FR7215 to FR8644, including the 14 MRBP isolates	345	▦	🔍
82	Bordetella_Nanopore_R10_2025	Benchmarking Nanopore R10 sequencing vs Illumina for cgMLST typing	8	▦	🔍
87	Bouchez-JMM2022-Bparapertussis	Bordetella parapertussis Isolates from the publication in JMM https://doi.org/10.1099/jmm.0.001843	39	▦	🔍

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb

Home > Organism > Bordetella cgMLST > Search or browse database

Search or browse database

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-12-31. Please log in to access the full dataset.

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 14 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

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

1 2 3

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
4063	FR7184			B. pertussis	nasopharynx	pertussis	France	IDF		Human	human		NRC for Whooping Cough, Instiut	illumina	1	4	1	4	1	4		
4816	FR7285			B. pertussis		pertussis	France	ARA		Human	human		NRC for Whooping Cough, Instiut Pasteur Paris		1	4	1	4	1	4		

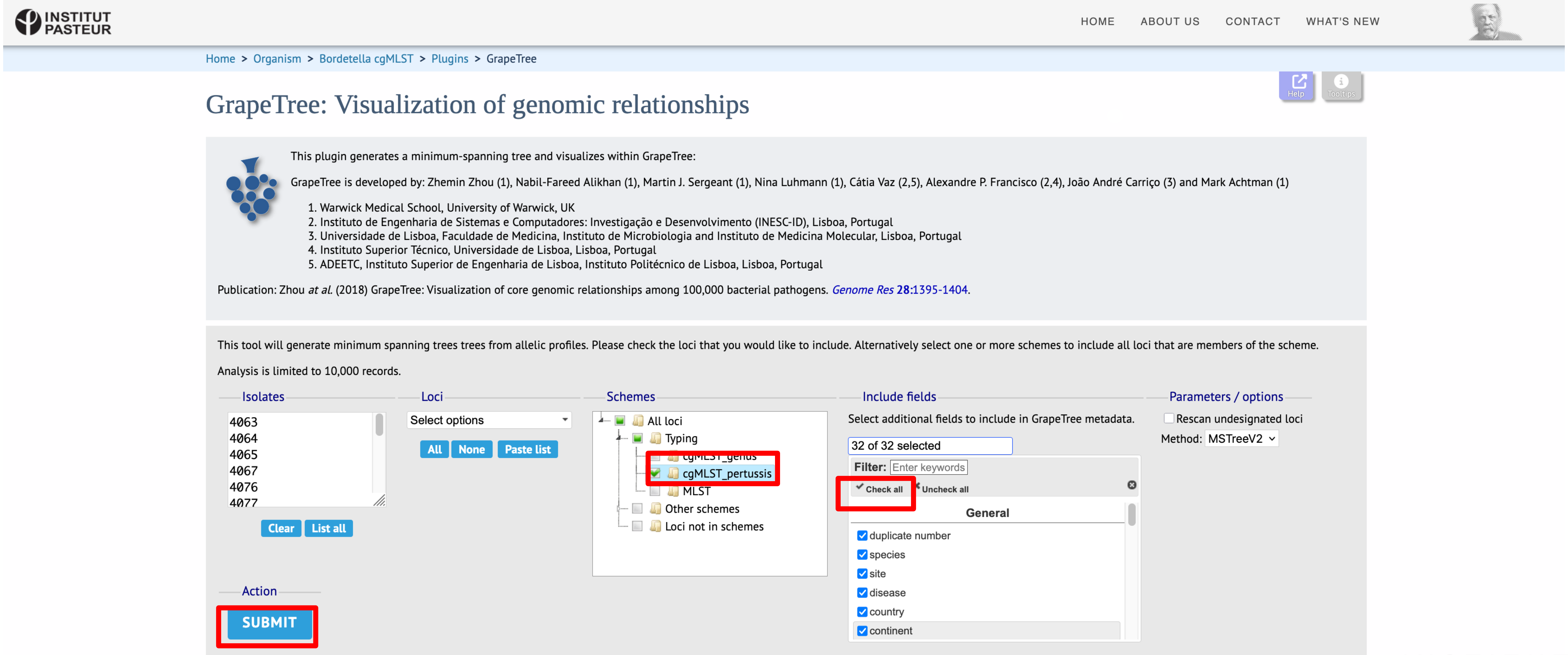
1 2 3

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: ntigs | Sequences
Third party: GrapeTree | iTOL | Microreact | ReporTree

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



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

4063
4064
4065
4067
4076
4077

Clear | List all

Loci

Select options

All | None | Paste list

Schemes

- ☐ All loci
  - ☐ Typing
    - ☐ cgMLST_genus
    - ☑ cgMLST_pertussis
    - ☐ MLST
  - ☐ Other schemes
  - ☐ Loci not in schemes

Include fields

Select additional fields to include in GrapeTree metadata.

32 of 32 selected

Filter: Enter keywords

✓ Check all | ✗ Uncheck all

General

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

Parameters / options

☐ Rescan undesignated loci

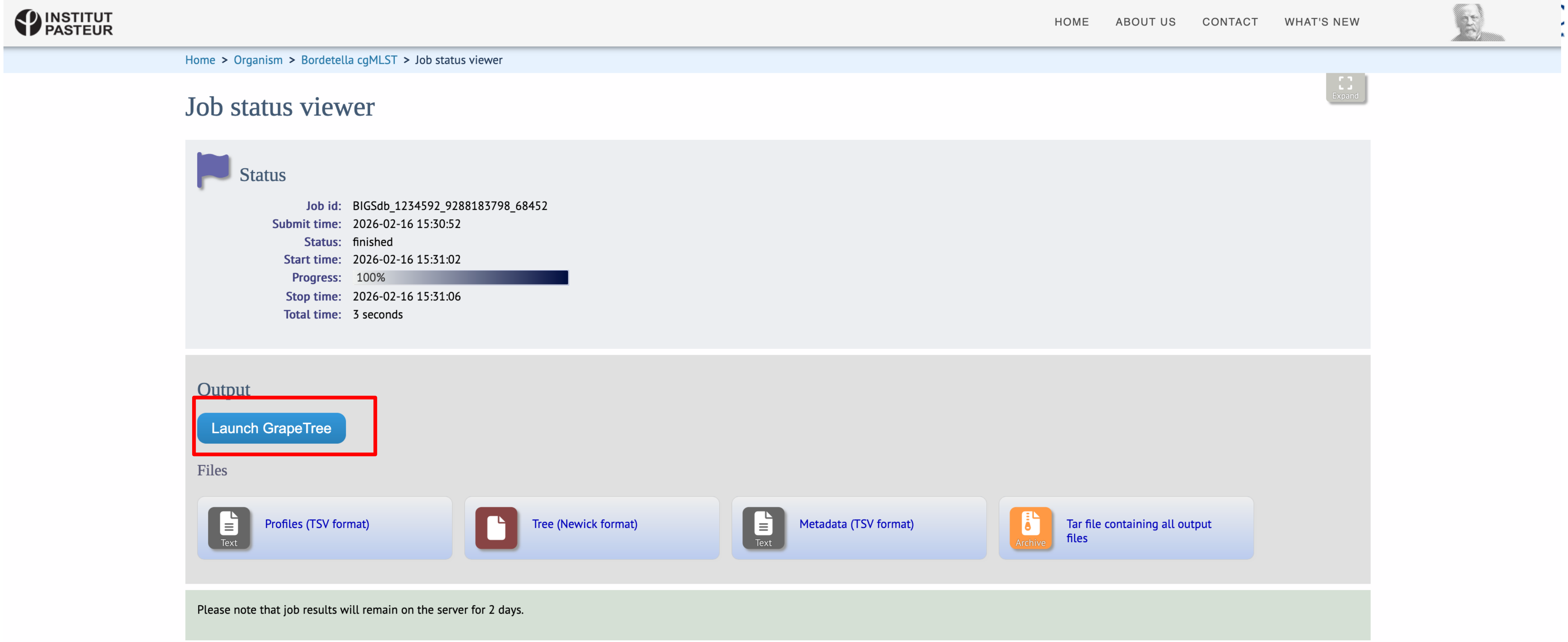
Method: MSTreeV2

Action

SUBMIT

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



Job status viewer

Status

Job id: BIGSdb_1234592_9288183798_68452
Submit time: 2026-02-16 15:30:52
Status: finished
Start time: 2026-02-16 15:31:02
Progress: 100%
Stop time: 2026-02-16 15:31:06
Total time: 3 seconds

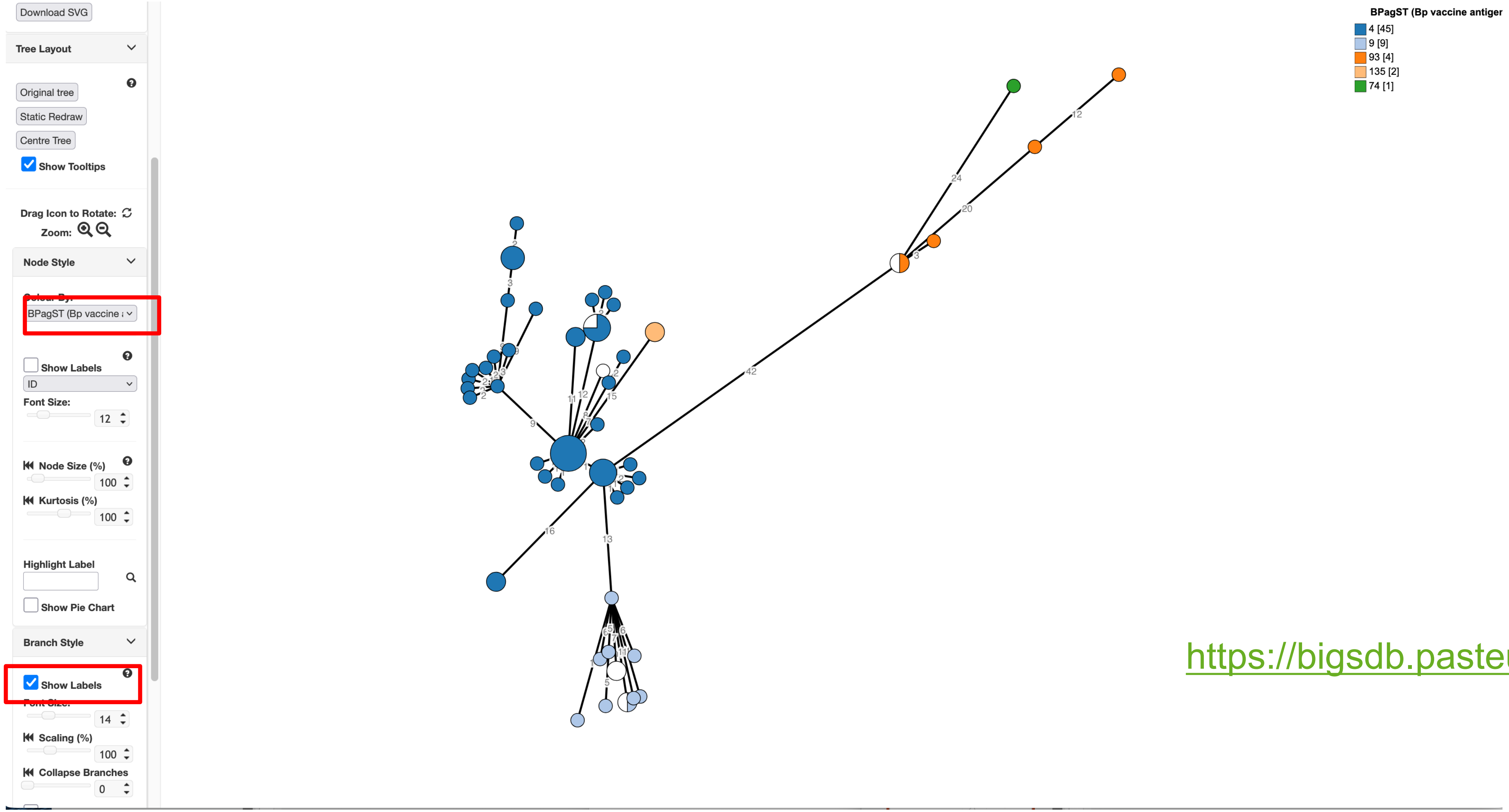
Output

Files

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

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

Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb



Download SVG

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

ID

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

BPagST (Bp vaccine antiger

🟦	4 [45]
🟦	9 [9]
🟧	93 [4]
🟧	135 [2]
🟩	74 [1]

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

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 Bp-agST. The diameter of circles is related to the number of isolates they comprise

Intended Learning Objectives

Live demonstration of genomic tools used for the exercises

-Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb

-Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb

-Focus on Pertactin *B. pertussis* vaccine antigen (exploring diversity of prn using BIGSdb and blastN)

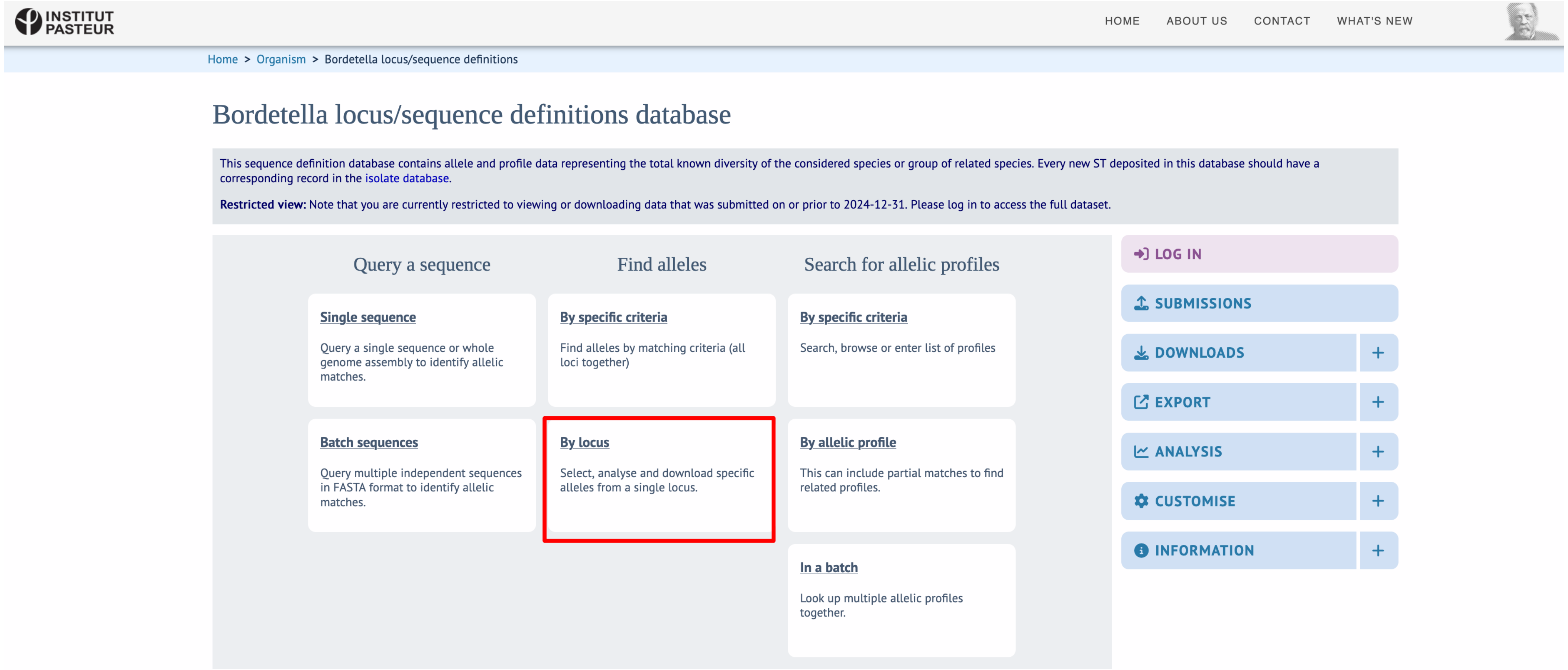
Presentation of the exercises to be carried out on public project81

Session of March 25th, 2026- Correction of the practical exercises

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

https://blast.ncbi.nlm.nih.gov/

Some alleles of prn gene can be detected on BIGSdb platform using prn(BP1054) locus



Bordetella locus/sequence definitions database

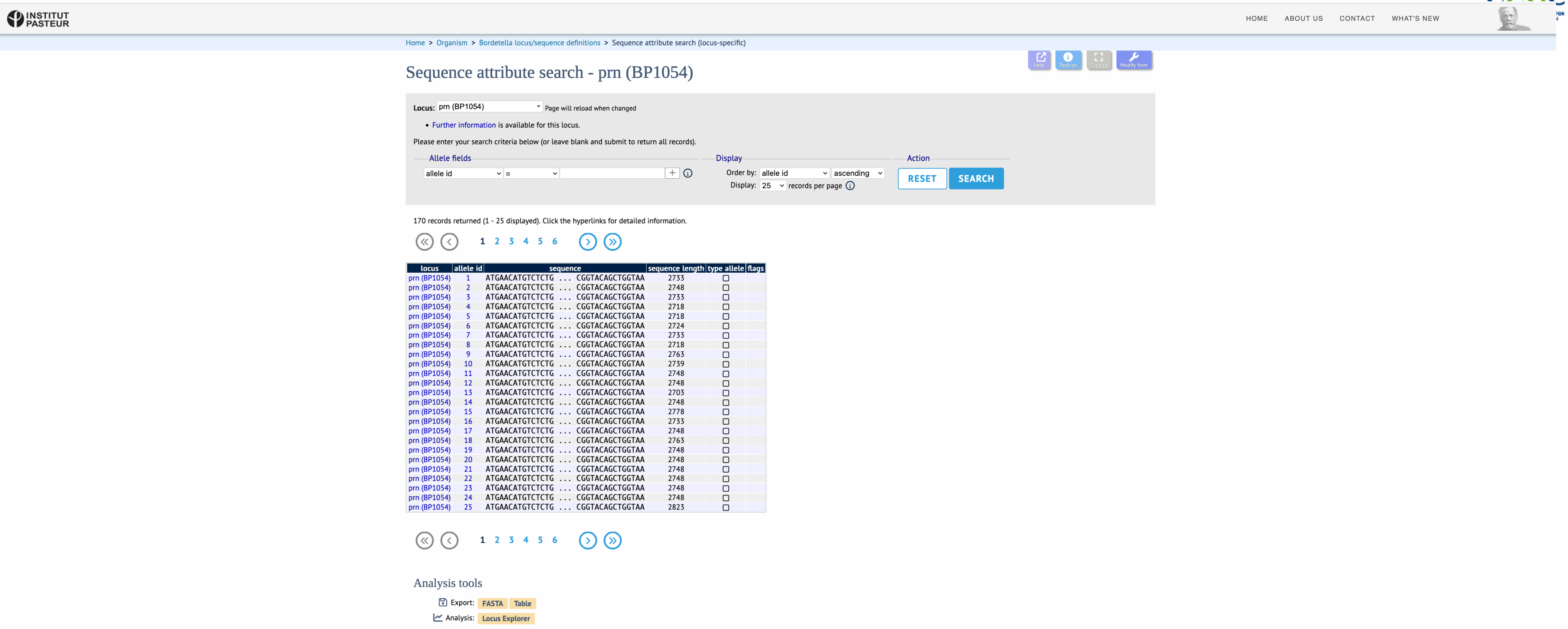
This sequence definition database contains allele and profile data representing the total known diversity of the considered species or group of related species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Restricted view: Note that you are currently restricted to viewing or downloading data that was submitted on or prior to 2024-12-31. Please log in to access the full dataset.

Query a sequence	Find alleles	Search for allelic profiles
Single sequence Query a single sequence or whole genome assembly to identify allelic matches.	**By specific criteria** Find alleles by matching criteria (all loci together)	**By specific criteria** Search, browse or enter list of profiles
Batch sequences Query multiple independent sequences in FASTA format to identify allelic matches.	**By locus** Select, analyse and download specific alleles from a single locus.	**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/

Some alleles of prn gene can be detected on BIGSdb platform using prn(BP1054) locus



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

Sequence attribute search - prn (BP1054)

Locus: prn (BP1054) 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

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

1 2 3 4 5 6

locus	allele id	sequence	sequence length	type allele	flags
prn (BP1054)	1	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2733	☐	
prn (BP1054)	2	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	3	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2733	☐	
prn (BP1054)	4	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2718	☐	
prn (BP1054)	5	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2718	☐	
prn (BP1054)	6	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2724	☐	
prn (BP1054)	7	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2733	☐	
prn (BP1054)	8	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2718	☐	
prn (BP1054)	9	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2763	☐	
prn (BP1054)	10	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2739	☐	
prn (BP1054)	11	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	12	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	13	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2703	☐	
prn (BP1054)	14	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	15	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2778	☐	
prn (BP1054)	16	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2733	☐	
prn (BP1054)	17	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	18	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2763	☐	
prn (BP1054)	19	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	20	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	21	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	22	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	23	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	24	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748	☐	
prn (BP1054)	25	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2823	☐	

1 2 3 4 5 6

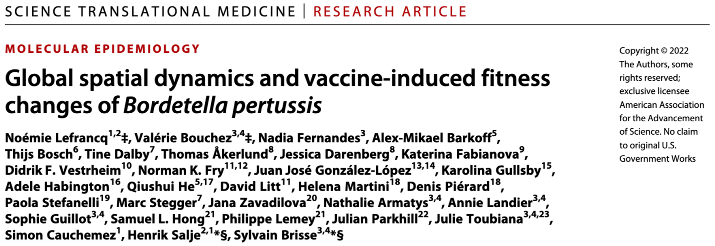
Analysis tools

Export: FASTA Table

Analysis: Locus Explorer

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

In some cases it is moreususeful to perform a blastN search using fasta query file (used in Lefrancq & Bouchez et al., Sc Tr Med 2022


SCIENCE TRANSLATIONAL MEDICINE | RESEARCH ARTICLE

MOLECULAR EPIDEMIOLOGY

Global spatial dynamics and vaccine-induced fitness changes of *Bordetella pertussis*

Noémie Lefrancq[1,2]‡, Valérie Bouchez[3,4]‡, Nadia Fernandes[3], Alex-Mikael Barkoff[5], Thijs Bosch[6], Tine Dalby[7], Thomas Åkerlund[8], Jessica Darenberg[8], Katerina Fabianova[9], Didrik F. Vestrheim[10], Norman K. Fry[11,12], Juan José González-López[13,14], Karolina Gullsby[15], Adele Habington[16], Qiushui He[5,17], David Litt[11], Helena Martini[18], Denis Piérard[18], Paola Stefanelli[19], Marc Stegger[7], Jana Zavadilova[20], Nathalie Armatys[3,4], Annie Landier[3,4], Sophie Guillot[3,4], Samuel L. Hong[21], Philippe Lemey[21], Julian Parkhill[22], Julie Toubiana[3,4,23], Simon Cauchemez[1], Henrik Salje[2,1]*§, Sylvain Brisse[3,4]*§

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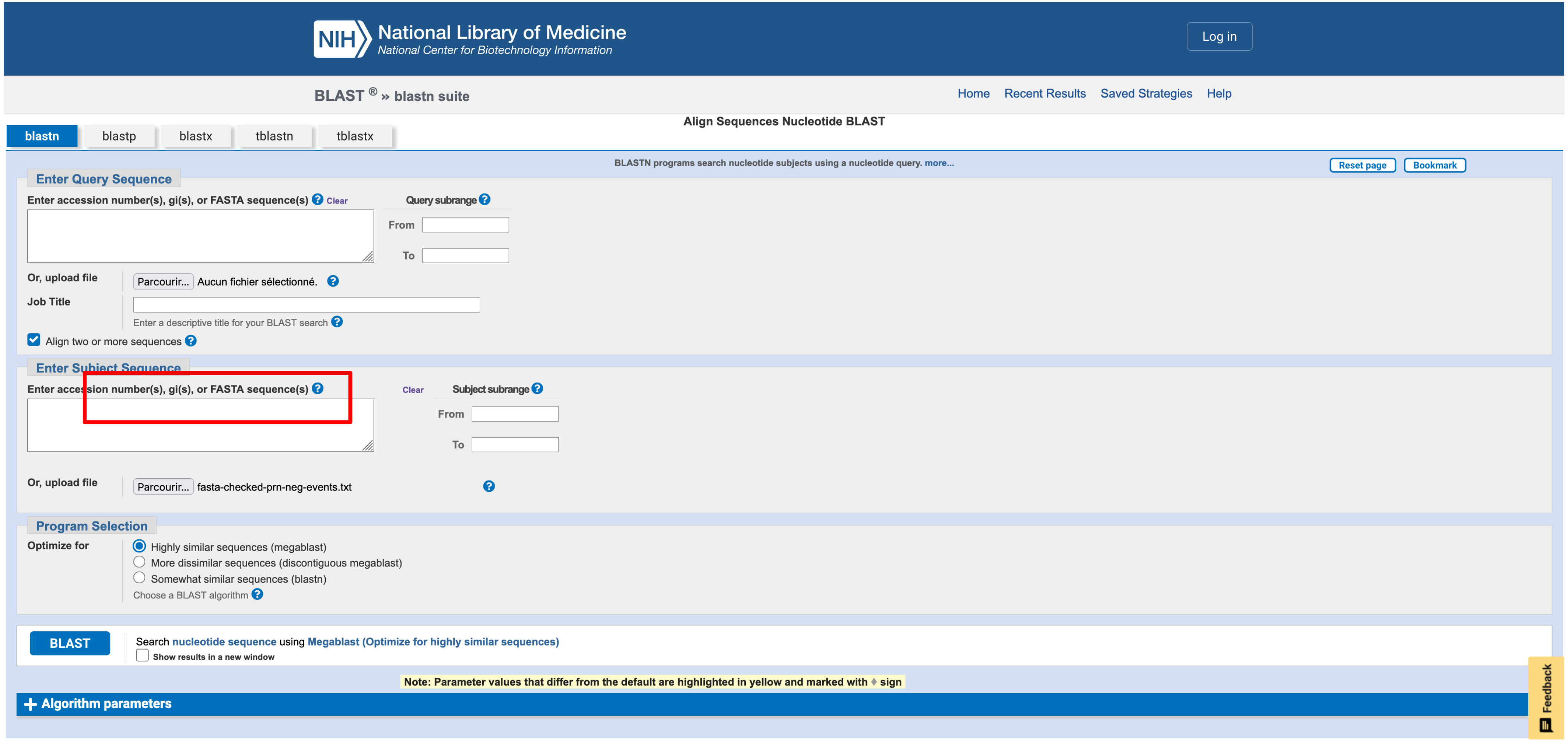

Align Sequences Nucleotide BLAST

BLASTN programs search nucleotide subjects using a nucleotide query. more...

Enter accession number(s), gi(s), or FASTA sequence(s)

Or, upload file: Parcourir... Aucun fichier sélectionné.

Job Title: Enter a descriptive title for your BLAST search

☑ Align two or more sequences

Enter accession number(s), gi(s), or FASTA sequence(s)

Or, upload file: Parcourir... fasta-checked-prn-neg-events.txt

Optimize for
● Highly similar sequences (megablast)
○ More dissimilar sequences (discontiguous megablast)
○ Somewhat similar sequences (blastn)
Choose a BLAST algorithm

Search nucleotide sequence using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow and marked with ♦ sign

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

Intended Learning Objectives

Live demonstration of genomic tools used for the exercises

-Genotyping of *B. pertussis* vaccine antigens (Bp-agST) using BIGSdb

-**Exploring genomic evolution of *B. pertussis* vaccine antigens using BIGSdb**

-Focus on Pertactin *B. pertussis* vaccine antigen (exploring diversity of prn using BIGSdb and blastN)

Presentation of the exercises to be carried out on public project81

Session of March 25th, 2026- Correction of the practical exercises

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

https://blast.ncbi.nlm.nih.gov/

Practical session

Case study (Bouchez-CMI2025-PMID40602497)

public project81

Clinical Microbiology and Infection 31 (2025) 1737–1739

Contents lists available at ScienceDirect

Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

Letter to the Editor

Microbes know no borders: importation of macrolide-resistant *Bordetella pertussis* into France in 2024

Valérie Bouchez [1, 2, 3], Noémie Lefrancq [4, 5], Julie Toubiana [1, 2, 3, 6], Carla Rodrigues [1, 2, 3, †],
Sylvain Brisse [1, 2, 3, *, †]

Explore the genomic evolution of vaccine antigens using BIGSdb: https://bigsdb.pasteur.fr/bordetella/

In Bordetella Isolates & genomes database:

-perform a GrapeTree analysis based on Bp-vaccine-Antigen scheme, Color isolates per country of origin, indicate branch length

-perform a GrapeTree analysis based on cgMLST_pertussis, color isolates by Bp-agST. Note the 3 main Bp-agST

In Bordetella Alleles & profiles database :

-Find the genotypes of vaccine antigen for the main Bp-agST profiles

-Compare prn150 and prn2 alleles

Corrections of pratical exercice on

March 25th, 2026

Acknowledgements

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