



GenEpi Webinar

Antigen Surveillance: from Evolution to Immune

A virtual training workshop within GenEpi-BioTrain.

Practical exercise on *B. pertussis* vaccine antigens

Valérie Bouchez

March 25th 2026

INSTITUT
pasteur

Practical session
Case study (Bouchez-CMI2025-PMID40602497)
public project 81



Clinical Microbiology and Infection 31 (2025) 1737–1739

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 **ELSEVIER**

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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://bigbdb.pasteur.fr/bordetella/>

In Bordetella Isolates & genomes database use public project 81

- 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.

In Bordetella Alleles & profiles database :

- Find the genotypes of vaccine antigen for the 2 main Bp-agST profiles of the project
- Compare prn150 and prn2 alleles

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



Home > Organism > Bordetella cgMLST

- Tooltips
- Expand
- Modify dashboard
- Index page

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.

Record versions: current; Record creation: all time



- LOG IN
- SEARCH
- SUBMISSIONS
- PROJECTS**
- EXPORT
- ANALYSIS
- CUSTOMISE
- INFORMATION



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

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

Main projects defined in the Bordetella cgMLST database



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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 Bridet 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/>

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



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...
- T3S5 profiles:

Include old record versions

Add filter: Add

Display/sort options

Order by: id ascending

Display: 25 records per page

RESET SEARCH



345 records returned (1 - 25 displayed). 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	23S_rRNA	
3075	FR8323			B. pertussis		pertussis	France			Human	human		NRC for Whooping Cough, Institut Pasteur Paris		1	4	1	4	1	9		1	
3099	FR8472			B. pertussis		pertussis	France			Human	human		NRC for Whooping Cough, Institut Pasteur Paris		1	4	1	4					1



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** TOL Microreact ReporTree

<https://bigsdB.pasteur.fr/bordetella/>

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



HOME ABOUT US CONTACT WHAT'S NEW



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: Zheming 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 *et 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 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

3075
3076
3077
3078
3079
3080

Clear List all

Action

SUBMIT

Loci

Select options

All None Paste list

Schemes

- All loci
 - Typing
 - Other schemes
 - Autotransporters
 - Bp_vaccine antigens**
 - macrotide resistance
 - Other toxins
 - Phase
 - PRN-test-Bp

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

<https://bigsdB.pasteur.fr/bordetella/>



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



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

INSTITUT PASTEUR HOME ABOUT US CONTACT WHAT'S NEW

Home > Organism > Bordetella cgMLST > Job status viewer

Job status viewer

Status

Job id: BIGSdb_1294687_4888264897_36425
Submit time: 2026-02-16 16:02:24
Status: finished
Start time: 2026-02-16 16:02:42
Progress: 100%
Stop time: 2026-02-16 16:02:46
Total time: 4 seconds

Output

Launch GrapeTree

Files

- Profiles (TSV format)
- Tree (Newick format)
- Metadata (TSV format)
- Tar file containing all output files

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

<https://bigbdb.pasteur.fr/bordetella/>

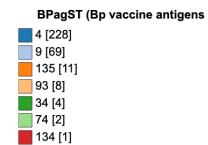
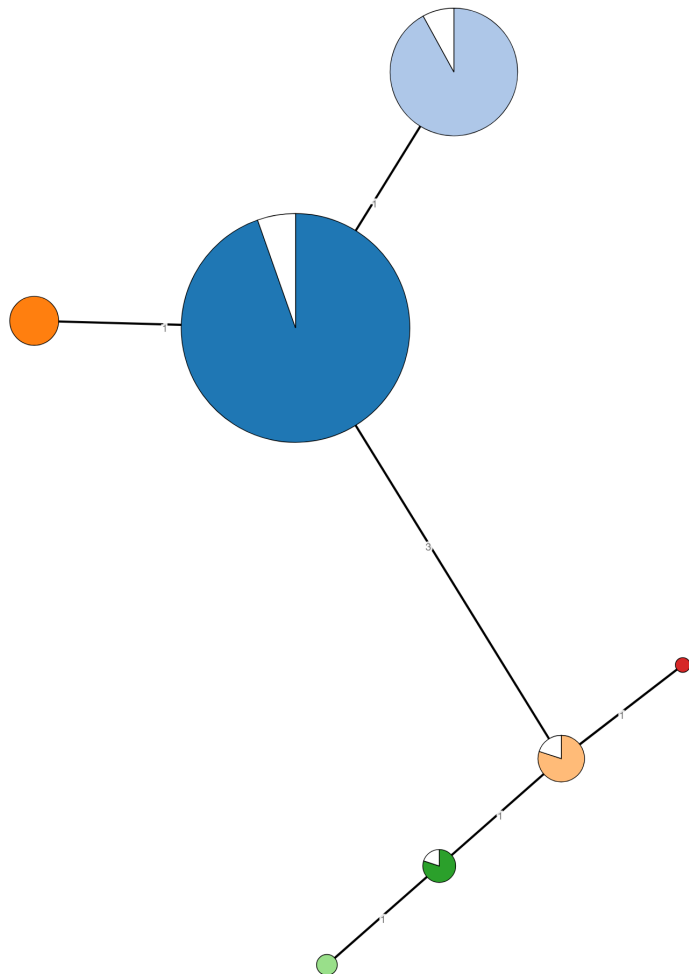
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GrapeTree interface sidebar with the following sections:

- Inputs/Outputs**
 - Load Files
 - Save GrapeTree
 - Save as Newick Tree
 - Download SVG
- Tree Layout**
 - Original tree
 - Static Redraw
 - Centre Tree
 - Show Tooltips
- Drag Icon to Rotate:** [Icon]
- Zoom:** [Magnifying Glass Icon]
- Node Style**
 - Colour By:** BPagST (Bp vaccine : [Dropdown])
 - Show Labels
 - ID [Dropdown]
 - Font Size: [Slider] 12
 - Node Size (%) [Slider] 100
 - Kurtosis (%) [Slider] 100
 - Highlight Label [Input]
 - Show Pie Chart
- Branch Style** [Dropdown]
- Show Labels



<https://bigsdB.pasteur.fr/bordetella/>



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Perform a GrapeTree analysis based on cgMLST_ pertussis, color isolates by Bp-agST



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This tool will generate minimum spanning 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

- 3075
- 3076
- 3077
- 3078
- 3079
- 3080

Clear List all

Action

SUBMIT

Loci

Select options

ALL None Paste list

Schemes

- All loci
- Typing
- 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

Parameters / options

Rescan undesignated loci

Method: MSTreeV2

General

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

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

Perform a GrapeTree analysis based on cgMLST_pertussis, color isolates by Bp-agST



Home > Organism > Bordetella cgMLST > Job status viewer

Job status viewer



Status

Job id: BIGSdb_1284694_2827456469_00068
Submit time: 2026-02-16 15:57:27
Status: finished
Start time: 2026-02-16 15:57:42
Progress: 100%
Stop time: 2026-02-16 15:57:50
Total time: 7 seconds

Output

Launch GrapeTree

Files



Profiles (TSV format)



Tree (Newick format)



Metadata (TSV format)



Tar file containing all output files

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

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

Perform a GrapeTree analysis based on cgMLST_pertussis, color isolates by Bp-agST



BpAgST (Bp vaccine antigen)

4	[228]
9	[69]
135	[11]
93	[8]
34	[4]
74	[2]
134	[1]

GrapeTree

Inputs/Outputs

Load Files

Save GrapeTree

Save as Newick Tree

Download SVG

Tree Layout

Original tree

Static Redraw

Centre Tree

Show Tooltips

Drag Icon to Rotate: ↻

Zoom: 🔍 🔍

Node Style

Colour By: BpAgST (Bp vaccine : ▾)

Show Labels

ID ▾

Font Size: 12

Node Size (%) 100

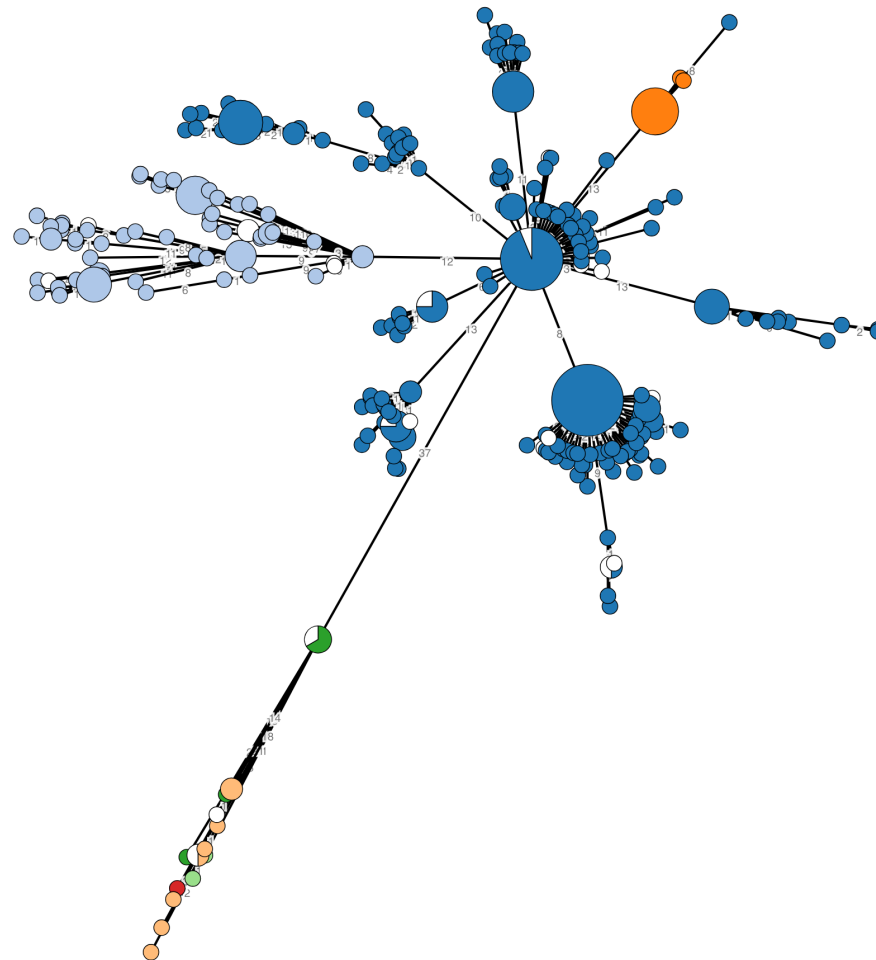
Kurtosis (%) 100

Highlight Label

Show Pie Chart

Branch Style

Show Labels



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In Bordetella Alleles & profiles database :

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In Bordetella Alleles & profiles database :

Find the genotypes of vaccine antigen for the 2 main Bp-agST profiles of the project



Home > Organism > Bordetella locus/sequence definitions

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

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.

➔ LOG IN

↑ SUBMISSIONS

↓ DOWNLOADS +

↗ EXPORT +

↶ ANALYSIS +

⚙ CUSTOMISE +

ℹ INFORMATION +

In Bordetella Alleles & profiles database :

Find the genotypes of vaccine antigen for the 2 main Bp-agST profiles of the project



Search or browse profiles

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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		Display/sort options		Action	
Combine searches with:	OR	Order by:	BPagST ascending	<input type="button" value="RESET"/>	<input type="button" value="SEARCH"/>
BPagST	=	Display:	25 records per page		
BPagST	=				

<https://bigbdb.pasteur.fr/bordetella/>

In Bordetella Alleles & profiles database :

Find the genotypes of vaccine antigen for the 2 main Bp-agST profiles of the project



Home > Organism > Bordetella locus/sequence definitions > Search or browse profiles



Search or browse profiles

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Locus/scheme fields		Display/sort options		Action	
Combine searches with: OR <input type="button" value="v"/>		Order by: BPagST <input type="button" value="v"/> ascending <input type="button" value="v"/>		<input type="button" value="RESET"/> <input type="button" value="SEARCH"/>	
BPagST <input type="button" value="v"/>	= <input type="button" value="v"/> 4 <input type="button" value="+"/> <input type="button" value="i"/>	Display:	25 <input type="button" value="v"/> records per page <input type="button" value="i"/>		
BPagST <input type="button" value="v"/>	= <input type="button" value="v"/> 9 <input type="button" value="v"/>				

2 records returned. Click the hyperlinks 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
9	3	1	1	4	1	4	1	1	2

Analysis tools

Analysis:
 Export:

<https://bigsdB.pasteur.fr/bordetella/>

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Compare *prn150* and *prn2* alleles



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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	LOG IN
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.	SUBMISSIONS
		In a batch Look up multiple allelic profiles together.	DOWNLOADS +
			EXPORT +
			ANALYSIS +
			CUSTOMISE +
			INFORMATION +

Compare *prn150* and *prn2* alleles



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

Combine searches with: **OR**

allele id	=	2	+ ⓘ
allele id	=	150	

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

Compare *prn150* and *prn2* alleles



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

Combine searches with: OR

allele id = 2

allele id = 150

Display

Order by: allele id ascending

Display: 25 records per page

Action

RESET SEARCH

2 records returned. Click the hyperlinks for detailed information.

locus	allele id	sequence	sequence length	type	allele	flags
prn (BP1054)	2	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748			<input type="checkbox"/>
prn (BP1054)	150	ATGAACATGTCTCTG ... CGGTACAGCTGGTAA	2748			<input type="checkbox"/>

Analysis tools

Export: [FASTA](#) [Table](#)

Analysis: [Locus Explorer](#)

Compare *prn150* and *prn2* alleles



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



Sequence attribute search - *prn* (BP1054)

Locus: *prn* (BP1054) Page will reload when changed

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Analysis tools

Export: [FASTA](#) [Table](#)

Analysis: [Locus Explorer](#)

Compare *prn150* and *prn2* alleles



Locus Explorer

Please select locus for analysis:

Locus: Page will reload when changed

- [Further information](#) is available for this locus.

Select sequences

Select analysis

Action

- 1
- 2
- 3
- 4
- 5
- 6

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

SUBMIT

All None

Compare *prn150* and *prn2* alleles



Locus Explorer

Polymorphic site analysis

prn (BP1054)

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



Compare *prn150* and *prn2* alleles



Locus Explorer



Please select locus for analysis:

Locus: Page will reload when changed

• Further information is available for this locus.

Select sequences

- 1
- 2
- 3
- 4
- 5
- 6

All None

Select analysis

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

SUBMIT

Compare *prn150* and *prn2* alleles



Locus Explorer

Translate - aligned protein sequences

prn (BP1054)

ORF used: 1

The width of the alignment can be varied by going to the options page.

2 alleles included in analysis.

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      10      20      30      40      50      60      70      80      90     100
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus MNMSLSRIVKAAPLRRTTLAMALGALGAAPAAHADWNNQSLVKTGERQHGHIHQSDPGGVRTASGTTIKVSGRQAQGLLENPAELQFRNGSVTSSGQ

      110     120     130     140     150     160     170     180     190     200
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus LSDDGIRRFLLGTVTKAGKLVADHATLANVGDWDDGGIALYVAGEQAQASTADSTLQAGAGVQIERGANVTVQRSAIVDGGHLIGALQSLQPEDLPPSR

      210     220     230     240     250     260     270     280     290     300
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus VVLRDNTVAVPASGAPAAVSVLGASELTDGGHITGGRAAGVAAMQGAHVHLQRATIRRGDAPAGGAVPAGGAVPGGFGPQGGFGPVLGDW

      310     320     330     340     350     360     370     380     390     400
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus YGVDVSGSSVELAQSIPEAPELGAATRVGRGARVTVSGGSLSAPHGNVIETGGARRFAPQAAPLSITLQAGAHAQKALLYRVLPEPVKLTLTGGADAQG

      410     420     430     440     450     460     470     480     490     500
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus DIVATLPSIPGTSIGPLDVALASQARWTGATRAVDSLSDNATWMTDMSNVGALRLASDGSVDFQPAEAGRFKVLTVNTLAGSGLFRMNVFADLGLS

      510     520     530     540     550     560     570     580     590     600
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus DKLVVMQDASGQHLRWRNSGSEPASANTLLVQTPLGSAATFTLANKDGKVDIGTYRYRLAANGNQWLSLVGAKAPPKPAQPGPQPQPQPEA

      610     620     630     640     650     660     670     680     690     700
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus PAPQPPAGRELAAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAGRFDQKAVGFEFGADHAVAAGGRWHLGGL

      710     720     730     740     750     760     770     780     790     800
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus AGYTRGDRGFTGDGGHTDSVHVGGYATYIADSGFYLDATLRASRLNDFKVGAGSDGYAVKGYRTHGVASLEAGRRFTHADGWFLPQAEAVFRAGG

      810     820     830     840     850     860     870     880     890     900
2.1  -----|-----|-----|-----|-----|-----|-----|-----|-----|
150_1 -----|-----|-----|-----|-----|-----|-----|-----|-----|
Consensus GAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVPYIKASVLQEFDGAGTHTNGIAHRELRGTRAEGLGMAAALGRGHSLYASYEYKGPK

      910
2.1  -----|-----|
150_1 -----|-----|
Consensus LAMPWTFHAGYRYSW
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Questions?

Acknowledgements

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