

➤ MyGenomeBrowser

Adeline Simon, Nicolas Lapalu
Atelier Bioinfo BIOGER - 25 février 2025

➤ Genome Visualization

Introduction to genome browsers

➤ How to access genome browsers implemented by the bioinfobioger platform ?

➤ MyGenomeBrowser Presentation, main features

➤ Play with the GenomeBrowser of your favorite fungus



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➤ Genome Visualization

Introduction to genome browsers



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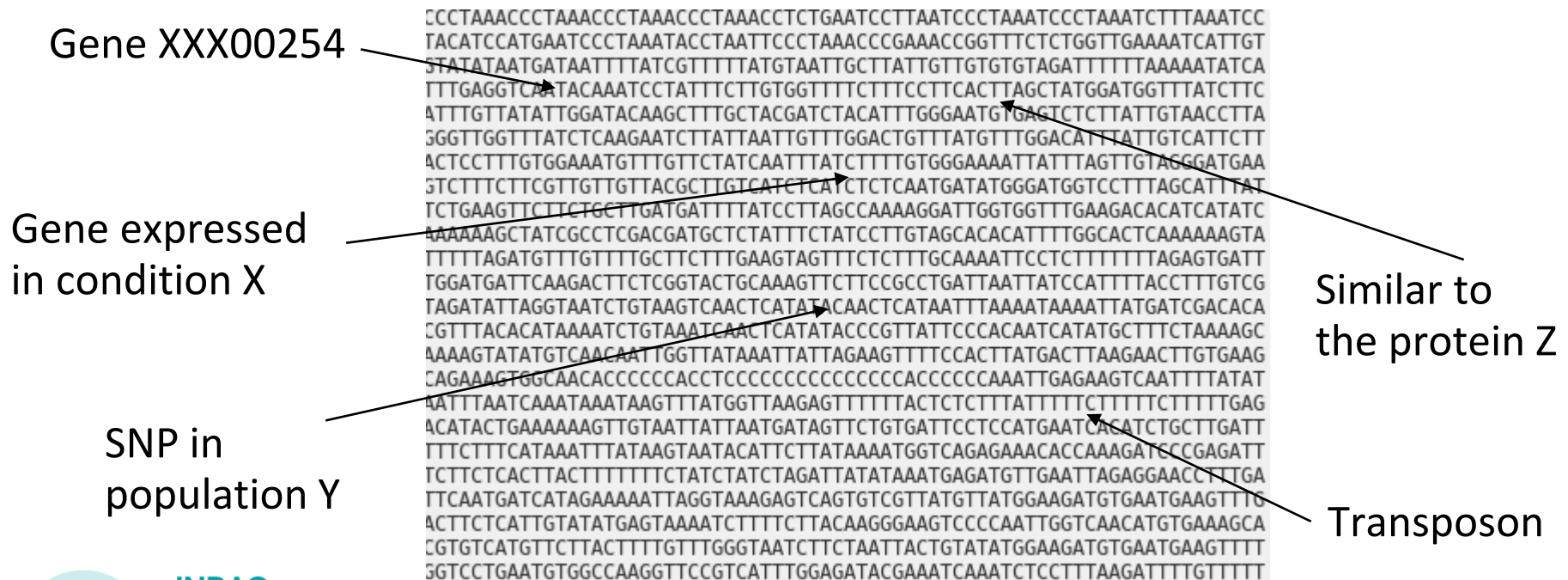
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➤ Genome Visualization

A challenge in bioinformatics.

How to display data on a genomic sequence ?

- The sequence of a genome alone is rather poor in information
- A multitude of elements that can be positioned on this sequence



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➤ Genome Browsers

A genome browser is a graphical interface to display information for genomic data.

It allows to visualize and browse entire genomes with various annotated data including gene structure, gene expression, regulation, variation...

Visualisation: cross-referencing of information at each position in the genome

Browsing: global or local vision, information on the neighbourhood



➤ Formats

A **genome browser** displays different graphical views, depending on the type of data and the associated file format.

Starting point : The genomic sequence (in fasta format)

GFF3 to display gene structure

BAM/SAM to display mapping informations

VCF to display variant informations

BED to display basic features

All the files
contain
coordinates
positioned on the
genomic fasta
sequence

➤ Genome Browsers

Public genome browsers with predefined data

Browsers available on the web for the most studied genomes (e.g. NCBI)

Custom genome browsers

IGV (<https://software.broadinstitute.org/software/igv/>)

Jbrowse2 (<https://jbrowse.org/jb2/download/>)

Available genome browsers for fungal genomes at BIOGER

Based on My GenomeBrowser

(Carrere & Gouzy 2017, <https://doi.org/10.1093/bioinformatics/btw800>)

Public or private access

>> You don't have to manage formats

>> The data are shared, everybody works on the same version



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➤ How to access genome browsers implemented by the bioinfobioger platform ?

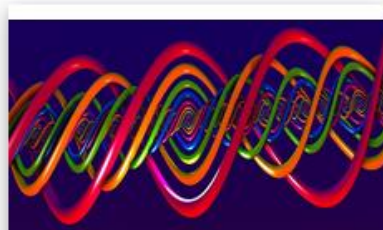


Genomic resources for phytopathogenic fungi

BioinfoBioger is a platform dedicated to the management and analysis of genomic data for plant pathogenic fungi. It is part of the BIOGER unit, within INRAE's Plant Health and Environment division.

The platform is involved in multiple projects producing fungal genomes and populations omics data. The web portal provides access to different tools to explore these genomes and populations data through genome browsers or dedicated tools, and a data browser with raw and processed files and their related metadata. We also provide access to bioinformatics tools developed as part of our projects.

List of scientific publications/productions involving the members of the platform.



Genomes & populations



Tools



Data browser



About us

➤ Genomes & Populations

(Public)

Genomes & Populations



Botrytis cinerea

Genome : [B0510](#)

Genome : [S13](#)

Genome : [Vv3](#)

Population : [Daphne 35 genomes](#)



Colletotrichum destructivum

Genome : [LARS 709 \(CBS 520.97\)](#)



Colletotrichum higginsianum

Genome : [IMI 349063](#)



Leptosphaeria biglobosa

Genome : [G12-14](#)



Leptosphaeria maculans

Genome : [JN3](#)



Septoria linicola

Genome : [SE14017](#)

Genome : [SE15195](#)



Zymoseptoria tritici

Genome : [IPO323](#)

Population : [ANU 2015](#)

Population : [ETH 2016](#)

Population : [GANDALF 2013](#)



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Colletotrichum higginsianum

Genome : IMI 349063

General info resources:

Class: [Sordariomycetes](#) Taxonomy ID: [759273](#) Sequencing technology: [PacBio RS II](#) Publication: [Dallery et al., 2017](#) Isolated from: [Not defined](#)
 Region: [Not defined](#) MAT: [Not defined](#) Genome repository: [NCBI](#)

Gene annotations:

# Id Gene	Len protein	Pos genome : chr	Pos genome : start	Pos genome : end	Description (Dallery et al, 2017)	Sumr
CH63R_00001	226	chr1	23988	24919	C6 zinc finger protein (681 nt)	
CH63R_00002	844	chr1	26447	29173	Beta-glucosidase (2535 nt)	CAZ
CH63R_00003	809	chr1	29646	32499	Alpha-L-rhamnosidase (2430 nt)	CAZ
CH63R_00004	520	chr1	34904	36526	Lactose permease (1563 nt)	
CH63R_00005	300	chr1	37257	38159	Low-density lipoprotein receptor YWTD (903 nt)	
CH63R_00006	321	chr1	38897	39862	3-hydroxyacyl-CoA dehydrogenase (966 nt)	
CH63R_00007	576	chr1	40985	42715	Alpha methylacyl-CoA racemase, putative (1731 nt)	
CH63R_00008	791	chr1	44175	46631	Ank-repeat protein mbp1 (2376 nt)	
CH63R_00009	446	chr1	46843	48256	C6 zinc finger protein (1341 nt)	
CH63R_00010	310	chr1	49227	50330	Phytanoyl-CoA dioxygenase (933 nt)	
CH63R_00011	533	chr1	52671	54951	ATP-dependent rRNA helicase RRP3 (1602 nt)	
CH63R_00012	813	chr1	55539	58096	Kinesin-like protein (2442 nt)	
CH63R_00013	574	chr1	61221	63006	hypothetical protein (1725 nt)	
CH63R_00014	79	chr1	63675	63914	Antigenic cell wall (240 nt)	
CH63R_00015	734	chr1	65216	67420	Brf1-like TBP-binding domain-containing protein (2205 nt)	
CH63R_00016	191	chr1	69040	69668	hypothetical protein (576 nt)	
CH63R_00017	134	chr1	69752	70218	hypothetical protein (405 nt)	
CH63R_00018	245	chr1	71310	72168	hypothetical protein (738 nt)	
CH63R_00019	175	chr1	73077	73801	Signal peptidase complex catalytic subunit SEC11 (528 nt)	
CH63R_00020	351	chr1	75089	76431	hypothetical protein (1056 nt)	

◀ ▶

Page Size **20** First Prev 1 2 3 4 5 Next Last

Download as: [.tsv \(tab\)](#) [.csv \(.\)](#)

➤ Tools

Explore fungal genomic data



Genome browsers
Display, search and extract features on a fungal genome

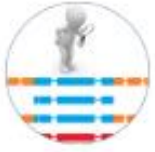


Variant explorer
Extract genomic regions on a fungal population

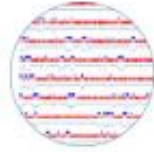


Botrytis mutants
List of manually curated *Botrytis cinerea* mutants (genes and publications)

Bioinformatics tools



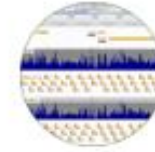
InGenAnnot
Inspect gene annotations



Karyoplot
Draw genome karyoplot/ideogram



Segmental Duplication
Detect duplications in genomes



MNase-Seq Tool Suite
Analyze MNase-Seq data

Other tools



Device booking system
(for BIOGER only)

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➤ Genome browsers

(Public)

Fungal Genome Browsers

Organism	Link to Genome Browser	Link to Project
Botrytis cinerea	GB Vv3	Vv3
Botrytis cinerea	GB SI3	SI3
Colletotrichum destructivum	GB Cdes LARS709	LARS 709 (CBS 520.97)
Colletotrichum higginsianum	GB Chig IMI349063	IMI 349063
Leptosphaeria biglobosa	GB G1214	G12-14
Leptosphaeria maculans	GB JN3	JN3
Septoria linicola	GB SE14017	SE14017
Septoria linicola	GB SE15195	SE15195
Zymoseptoria tritici	GB IPO323	IPO323

The Genome Browsers are based on : *myGenomeBrowser: building and sharing your own genome browser*. Sébastien Carrere, Jérôme Gouzy. *Bioinformatics* (2017) 33 (8): 1255-1257. <https://doi.org/10.1093/bioinformatics/btw800>



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➤ MyGenomeBrowser

Presentation, main features



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➤ Visualization on chromosomes & browsing

Colletotrichum_higginsianum_IMI349063

Browse Open in a new window Search Blast Extract

Genome Track View Help

500,000 1,000,000 1,500,000 2,000,000 2,500,000 3,000,000 3,500,000 4,000,000 4,500,000 5,000,000 5,500,000 6,000,000

Select tracks

Reference sequence

4,432,500 4,435,000 4,437,500 4,440,000 4,442,500

Zoom in to see sequence

Chromosome

Displayed region

Surf along the sequence

Zoom

Select a region to visualize



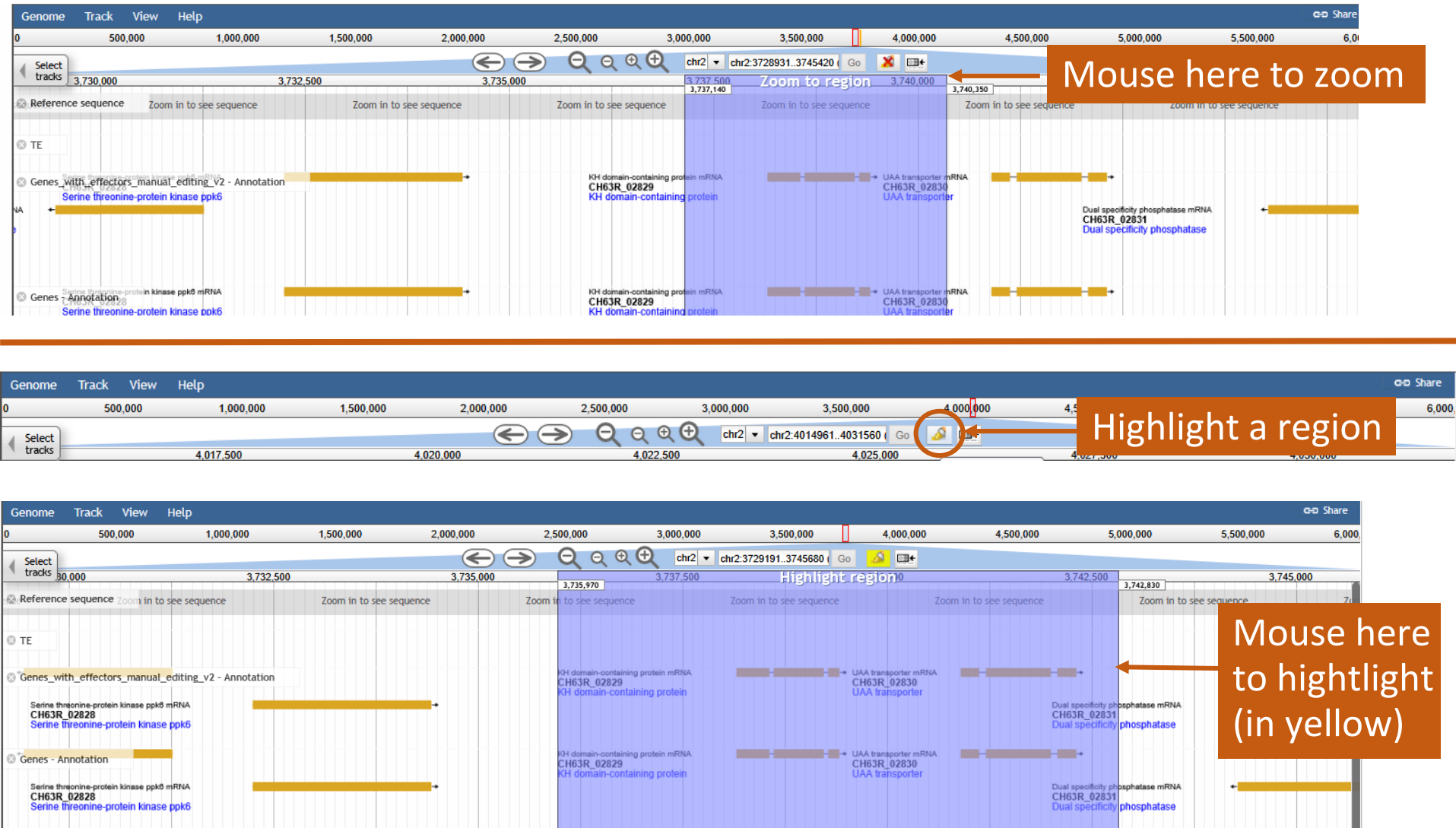
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myGenomeBrowser– INRAE / BIOGER

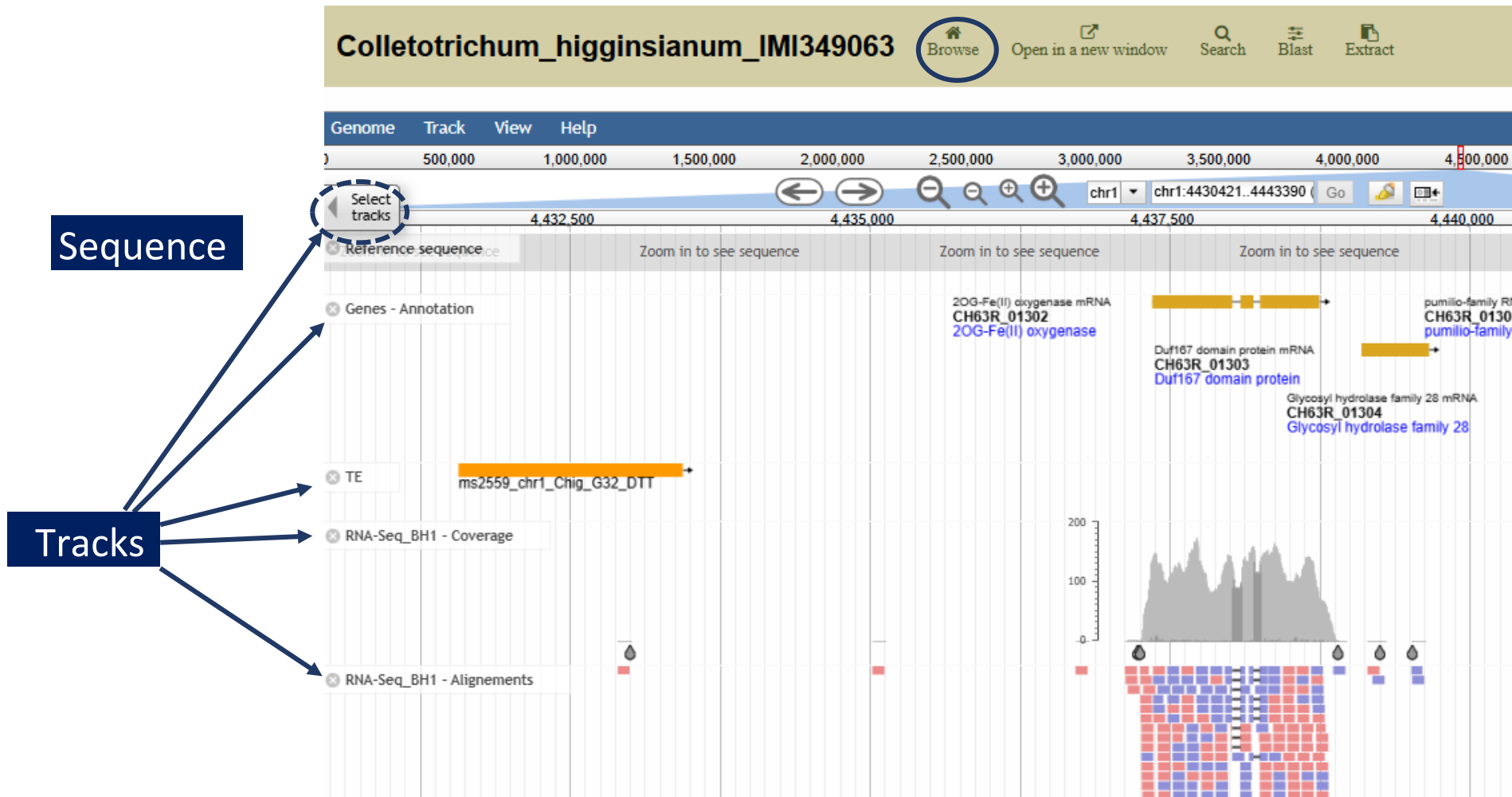
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Visualization on chromosomes & browsing

Difference between **Zoom to region** and **Highlight region**



➤ Visualization of tracks



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➤ Types of track

Alignments

Generic Alignments [GFF3]

Blast hits [TSV]

Annotations

Generic features [BED]

Structural Annotation [GFF3]

Generic features [GFF3]

InterPro [InterPro match table format]

Mapping

Coverage [BAM]

Mapping [BAM]

Modification

Variants [VCF]

Quantitative

Generic measure [bigWig]

Generic Barplots [TSV]



➤ Select tracks to display

Select Tracks

My Tracks

Currently Active

Recently Used

Category

3 Annotations

20 Mapping

1 Reference sequence

Date

1 (no data)

2 Fri Sep 11 14:07:42 CEST 2020

1 Mon Jun 29 09:49:48 UTC 2020

2 Thu Sep 10 14:35:05 CEST 2020

2 Thu Sep 10 14:57:54 CEST 2020

2 Thu Sep 10 15:02:55 CEST 2020

2 Thu Sep 10 17:50:46 CEST 2020

1 Tue Oct 26 13:21:38 UTC 2021

1 Tue Sep 15 08:56:18 UTC 2020

2 Tue Sep 15 15:06:15 UTC 2020

2 Wed Jul 1 11:04:38 CEST 2020

2 Wed Jul 1 11:17:53 CEST 2020

2 Wed Jul 1 11:25:52 CEST 2020

2 Wed Jul 1 11:37:54 CEST 2020

Description

1 (no data)

2 454 mid2_MQ_cDNA_norm_Cle

2 C.higginsianum_SfiAprimer_20

2 EST_Sanger_assembled_reads

2 ESTs

2 in_vitro_appressoria_sanger_r

2 FACS_biotrophic_hyphae_Sang

1 Genes

1 Genes_with_effectors_manua

8 Mapping STAR RNASeq

1 Transposable elements (REPET

2 mid3_cDNA_norm_Clean_2009

Legend

Back to browser

✗ Clear All Filters

Contains text

24 matching tracks

☐	Category	Date	Description	Name	Legend	Rawdata	Track type
☐		2020	an_2009-01-15	Alignments		87225887c45d41400cd212-Chig_genome_mid2_MQ_cDNA_norm_Clean_2009_01_15_sorted.bam>Download	
☐	Mapping	Thu Sep 10 17:50:46 CEST 2020	454 mid2_MQ_cDNA_norm_Cle an_2009-01-15	454_biotrophic_hyphae - Coverage	...	Download 	JBrowse/View/Track/SNPCo verage
☒	Mapping	Wed Jul 1 11:04:38 CEST 2020	Mapping STAR RNASeq	RNA-Seq_BH1 - Alignments	...	Download	JBrowse/View/Track/Alignm ents2
☒	Mapping	Wed Jul 1 11:04:38 CEST 2020	Mapping STAR RNASeq	RNA-Seq_BH1 - Coverage	...	Download	JBrowse/View/Track/SNPCo verage
☐	Mapping	Fri Sep 11 14:07:42 CEST 2020	C.higginsianum_SfiAprimer_ 2010_01_21	454_in-vitro-appressoria - Alignments	...	Download	JBrowse/View/Track/Alignm ents2
☐	Mapping	Fri Sep 11 14:07:42 CEST 2020	C.higginsianum_SfiAprimer_ 2010_01_21	454_in-vitro-appressoria - Coverage	...	Download	JBrowse/View/Track/SNPCo verage

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p. 19

➤ Display customization

Colletotrichum_higginsianum_IMI349063

Browse Open in a new window Search Blast Extract

Genome Track View Help

0 500,000 1,000,000 1,500,000 2,000,000 2,500,000 3,000,000 3,500,000

Select tracks

4,432,500 4,435,000 4,437,500

Reference sequence Zoom in to see sequence Zoom in to see sequence Zoom in

Genes - Annotation

Left click to display track context menu

TE

About this track

☐ Pin to top

☐ Edit config

☒ Delete track

☐ Save track data

Display mode

☒ normal

☐ compact

☐ collapsed

☒ Show labels

RNA-Seq_BH1 - Alignments

ig_G32_DTT

2OG-Fe(II) oxygenase mRNA
CH63R_01302
2OG-Fe(II) oxygenase

Duf167 domain protein n
CH63R_01303
Duf167 domain prote

200

100

0

The screenshot displays the myGenomeBrowser interface for the Colletotrichum_higginsianum_IMI349063 genome. The top navigation bar includes 'Browse', 'Open in a new window', 'Search', 'Blast', and 'Extract'. The main interface shows a genomic track with a scale from 0 to 3,500,000. A specific region on chromosome 1 (chr1:4430771) is highlighted. The 'Genes - Annotation' track shows two genes: '2OG-Fe(II) oxygenase mRNA' (CH63R_01302) and 'Duf167 domain protein n' (CH63R_01303). A context menu is open for the 'TE' track, showing options like 'About this track', 'Pin to top', 'Edit config', 'Delete track', 'Save track data', 'Display mode' (normal, compact, collapsed), and 'Show labels'. A green box with an arrow points to the 'TE' track header, indicating that a left click opens this context menu. The bottom right corner shows a heatmap of RNA-Seq alignments.

» « Search » functions

Colletotrichum_higginsianum_IMI349063

Browse

Open in a new window

Search

Blast

Extract

Gene name,
function...
(ex. kinase)

myGenomeBrowser



Search

keyword, accession, pfam

in

Colletotrichum_higginsianum_IMI349063

portal

Go

Colletotrichum_higginsianum_IMI349063

Browse

Open in a new window

Search

Blast

Extract

Found in structural annotation files

Click to display browser

#	Name	ocus_tag	Type	Product	Note	Seqid	Start	End	Strand	Dbxr
	Phosphoglycerate kinase CDS		CDS	Phosphoglycerate kinase		chr1	127663	127728	+	
	CH63R_00036_exon_1		exon	Phosphoglycerate kinase		chr1	127663	127728	+	
	Phosphoglycerate kinase mRNA		mRNA	Phosphoglycerate kinase		chr1	127663	129329	+	
	Phosphoglycerate kinase CDS		CDS	Phosphoglycerate kinase		chr1	128060	128483	+	
	CH63R_00036_exon_2		exon	Phosphoglycerate kinase		chr1	128060	128483	+	
	Phosphoglycerate kinase CDS		CDS	Phosphoglycerate kinase		chr1	128563	129329	+	
	CH63R_00036_exon_3		exon	Phosphoglycerate kinase		chr1	128563	129329	+	

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» « Search » functions

Gene name,
chromosome

Colletotrichum_higginsianum_IMI349063

Browse Open in a new window Search Blast Extract

Genome Track View Help

500,000 1,000,000 1,500,000 2,000,000 2,500,000 3,000,000 3,500,000 4,000,000 4,500,000

Select tracks

Reference sequence

Zoom in to see sequence

Genes - Annotation

Phosphoglycerate kinase mRNA
CH63R_00036
Phosphoglycerate kinase

TE

RNA-Seq_BH1 - Coverage

RNA-Seq_BH1 - Alignments

chr1 CH63R_00001 CH63R_00002 CH63R_00003 CH63R_00004 CH63R_00005 CH63R_00006 CH63R_00007 chr1 chr10 chr11 chr12 chr2 chr3 chr4 chr5 chr6 chr7 chr7_5 chr8 chr9

» « Extract » functions

Colletotrichum_higginsianum_IMI349063

Browse

Open in a new window

Search

Blast

Extract

Extract features from name/accession

Extract features from genomic regions

Complete Fasta files

Genes prot - prot sequences

accession

Chr.begin..end

Based on annotation

Submit

Envoyer

Réinitialiser

Colletotrichum_higginsianum_IMI349063

- Genes_with_effectors_manual_editing_v2 cds - Nucleotide, cds, 14686 sequences
- Genes_with_effectors_manual_editing_v2 gene - Nucleotide, gene, 14686 sequences
- Genes_with_effectors_manual_editing_v2 mrna - Nucleotide, mrna, 14686 sequences
- Genes_with_effectors_manual_editing_v2 prot - Protein, prot, 14684 sequences
- Genes cds - Nucleotide, cds, 14651 sequences
- Genes gene - Nucleotide, gene, 14651 sequences
- Genes mrna - Nucleotide, mrna, 14651 sequences
- Genes prot - Protein, prot, 14651 sequences
- Colletotrichum_higginsianum_IMI349063 genomic sequences - Nucleotide, IMI349063.refseq, 14 sequences

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➤ « Extract » functions

Colletotrichum_higginsianum_IMI349063

Browse Open in a new window Search Blast Extract

Genome Track View Help

0 500,000 1,000,000 1,500,000 2,000,000 2,500,000 3,000,000 3,500,000 4,000,000 4,500,000

Select tracks

Reference sequence Zoom in to see sequence

Genes - Annotation

2OG-Fe(II) oxygenase mRNA
CH63R_01302
2OG-Fe(II) oxygenase

Duf167 domain protein mRNA
CH63R_01303
Duf167 domain protein

Extract feature sequences
IPR-Chig: InterProScan_v5 Galaxy
Highlight this gene

Right click
to display
feature context menu



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» « Extract » functions

Colletotrichum_higginsianum_IMI349063

Browse Open in a new window Search Blast Extract

Genome Track View Help

0 500,000 1,000,000 1,500,000

Select tracks 126,250

Reference sequence

Genes - Annotation

TE

RNA-Seq

RNA-Seq_BH1 - Alignments

Left click to display track context menu

About this track
To save original downloaded data

Save track data associated with the visible region or whole reference sequence

(« Save track » Context menu depends on track type)
(See examples on next slide)

» « Extract » functions

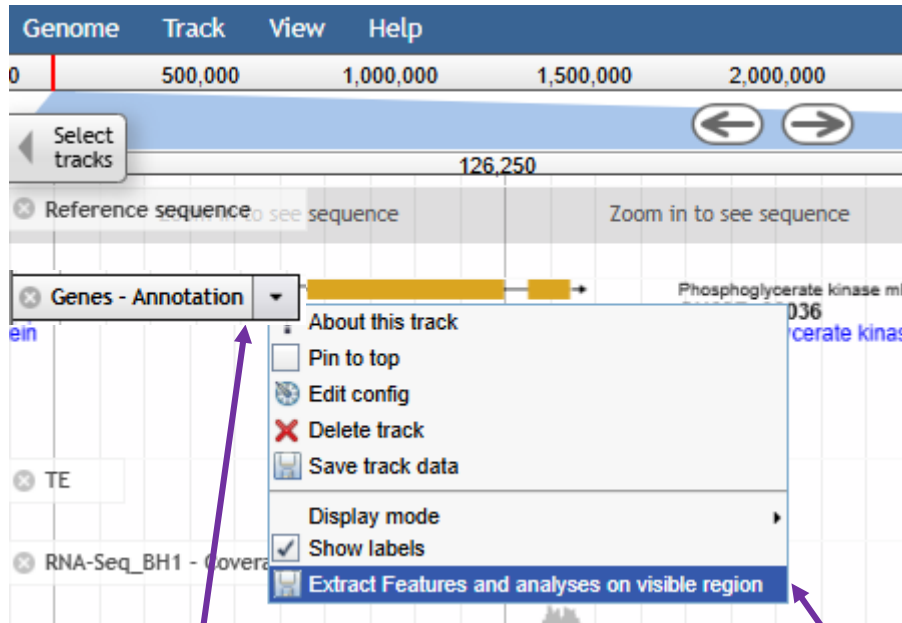
The screenshot displays the myGenomeBrowser interface for the organism *Colletotrichum_higginsianum_IMI349063*. The top navigation bar includes a 'Browse' button (circled in purple), 'Open in a new window', 'Search', 'Blast', and 'Extract'.

Two examples of the 'Extract' function are shown:

- Example 1: Reference sequence**
 - The 'Reference sequence' track is selected.
 - The context menu shows 'Save track data' (circled in purple).
 - The 'Save track data' dialog box shows:
 - Region to save:** ☒ Highlighted region - chr2:3735970..3742819 (6.85 Kb)
 - Format:** ☒ FASTA
 - Filename:** Reference sequence-chr2-3735970..3742819.fasta
- Example 2: Genes - Annotation**
 - The 'Genes - Annotation' track is selected.
 - The context menu shows 'Save track data' (circled in purple).
 - The 'Save track data' dialog box shows:
 - Region to save:** ☒ Highlighted region - chr2:3735970..3742819 (6.85 Kb)
 - Format:** ☒ GFF3
 - Filename:** Genes - Annotation-chr2-3735970..3742819.gff3

Etc... for other track types

» « Extract » functions



Left click
to display Annotation
feature context menu

Extract Features and analyses on visible region /myGenomeBrowser/cgi/jbrowse-extract-app.cgi/cgi/index.cgi?dataset=6b4642563b3bf098e75169d1b1ffc25d9&ion=chr1:124870..131300&cfg_dir=L3Zhc193d3cvbXIHZW5vbWVCcm93c2Vyl2RhdGEvOGZh

Extract features from genomic regions

Colletotrichum_higginsianum_IMI349063 / Genes Datasets | Data from region chr1:124870..131300

- refseq/chr1:124870..131300 [1]
- gff/Genes_with_effectors_manual_editing_v2 [26]
- gff/Genes [26]
- fasta/Genes_with_effectors_manual_editing_v2 cds [3]
- fasta/Genes_with_effectors_manual_editing_v2 gene [3]
- fasta/Genes_with_effectors_manual_editing_v2 mma [3]
- fasta/Genes_with_effectors_manual_editing_v2 prot [3]
- fasta/Genes gene [3]
- tsv/IPR-Chig [45]
- bam/454_biotrophic_hyphae [163]
- bam/RNA-Seq_BH1 [1084]
- bam/454_in-vitro-appressoria [173]
- bam/RNA-Seq_SW1 [4255]
- bam/RNA-Seq_VAV1 [4722]
- bam/454_necrotrophic_hyphae [38]
- bam/RNA-Seq_PA1 [1247]

Input File Number:23

➤ Blast function

Colletotrichum_higginsianum_IMI349063
[Browse](#) [Open in a new window](#) [Search](#) [Blast](#) [Extract](#)

Genes prot - Protein, 14651 prot sequences

GCAGGCTCAGTAGCGCGGTGAGGTTACCACCAGCGGCAAGGCGATCAGCATGCTCTTGGGGCGATGCAGTAG
CGCGCCCCGCATGGTCTCTGCGTCAGGGAATCGCTAGGCGGCGGGTCTGCTCGCCCCCTGGAACACGGCGG
TATTCCTTCGATGCTTCTTTCGGCACC

blastp: Protein-Protein BLAST

Envoyer

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blastp options

Input query options

General search options

Formatting options

Query filtering options

Restrict search or results

Statistical options

Extension options

Miscellaneous options

> Blast function

Colletotrichum_higginsianum_IMI349063 [Browse](#) [Open in a new window](#) [Search](#) **Blast** [Extract](#)

Genes prot - Protein, 14651 prot sequences ▼

```
GCAGGCTCAGTAGCGCGGTGAGGTTCCACCACCAGCGGCAAGGCGATCAGCATGCTCTTGGGGCGATGCAGTAG
CGCGCCCCGCATGGTCTCTGCGTCAGGGAATCGCTAGGCGGCGGTCTGCTCGCCCGCCTGGAACACGGCGG
TATTCCTTCGATGCTTCTTCTCGGCACC
```

blastp: Protein-Protein BLAST ▼

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blast options

blastp: 2.2.31+
Package: blast 2.2.31, build Jun 2 2015 10:20:04
database:Genes prot

qseqid	saccver	stitle	pcq	pcs	eval	pid
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_00003	Alpha-l-rhamnosidase note=Alpha-l-rhamnosidase	100	100	0	100
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_01976	alpha-L-rhamnosidase A note=alpha-L-rhamnosidase A	39	42	3e-05	24.14
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_01735	Alpha-L-rhamnosidase note=Alpha-L-rhamnosidase	33	31	0.0009	25.77
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_12308	Alpha-L-rhamnosidase note=Alpha-L-rhamnosidase	18	27	0.003	23.87
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_09776	Alpha-l-rhamnosidase note=Alpha-l-rhamnosidase	15	12	1.9	25.6
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_03910	CipC-like antibiotic response protein, putative note=CipC-like antibiotic response protein, putative	12	61	2.5	25
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_00494	Sec1 family protein note=Sec1 family protein	9	11	5.7	33.33
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_10768	Acetylornithine aminotransferase note=Acetylornithine aminotransferase	9	14	7.5	29.87

➤ Blast function

Colletotrichum_higginsianum_IMI349063 [Browse](#) [Open in a new window](#) [Search](#)

Genes prot - Protein, 14651 prot sequences

GCAGGCTCAGTAGCGCGGTGAGGTTACCAACAGCGCAAGGCGATCAGCATGCTCTTGGGGCGATGCAGTAGCGCGCCCCGCATGGTCTCTGCGTCAGGAATCGCTAGGCGCGGGTCTGCTCGCCCGCCTGGAACACGGCGGTATTTCTCTTCGATGCTCTTCTTCGGCACC

blast: Protein-Protein BLAST

Envoyer Réinitialiser

blast options

ThonCIALE:CH63R_00003 1 MDRSFLOTTWIWHPDQDHGVDTAGRLVHFRKIDLTTPVSAPLTIQITADTRYKLFVNSHCVITG
ThonCIALE:CH63R_00003 1 MDRSFLOTTWIWHPDQDHGVDTAGRLVHFRKIDLTTPVSAPLTIQITADTRYKLFVNSHCVITG

FHATPYATSFPRLSFPGLFVRTPDPSQDHAALALQSDASWECAIDHTTVLRVDQKEDDFLHIYENV
FHATPYATSFPRLSFPGLFVRTPDPSQDHAALALQSDASWECAIDHTTVLRVDQKEDDFLHIYENV

IPVPESVPVRPAAIHNVRSPIIDHAAMEQVWLGSLGRLPAGTSHHIEIEAEHHLTAHITFRFRRP
IPVPESVPVRPAAIHNVRSPIIDHAAMEQVWLGSLGRLPAGTSHHIEIEAEHHLTAHITFRFRRP

GKGLYGPEDRYVFAAGRLGAQGNALGYQSDPTAFEVFSPFHRTLRYSIDIDVAQNSOLDMVGIG
GKGLYGPEDRYVFAAGRLGAQGNALGYQSDPTAFEVFSPFHRTLRYSIDIDVAQNSOLDMVGIG

RTLRCMHDCYEDCPFYELQYAMDVRSCLFTYALSGDDRMARQAIQVLHNSYRPSLGLIASRSP
RTLRCMHDCYEDCPFYELQYAMDVRSCLFTYALSGDDRMARQAIQVLHNSYRPSLGLIASRSP

LSTCDGILNSFARRLSPDTGLLSSSLEAIQAHMDFVNDTEWRPMGIPTASRRGTGTFTNFIYAY
LSTCDGILNSFARRLSPDTGLLSSSLEAIQAHMDFVNDTEWRPMGIPTASRRGTGTFTNFIYAY

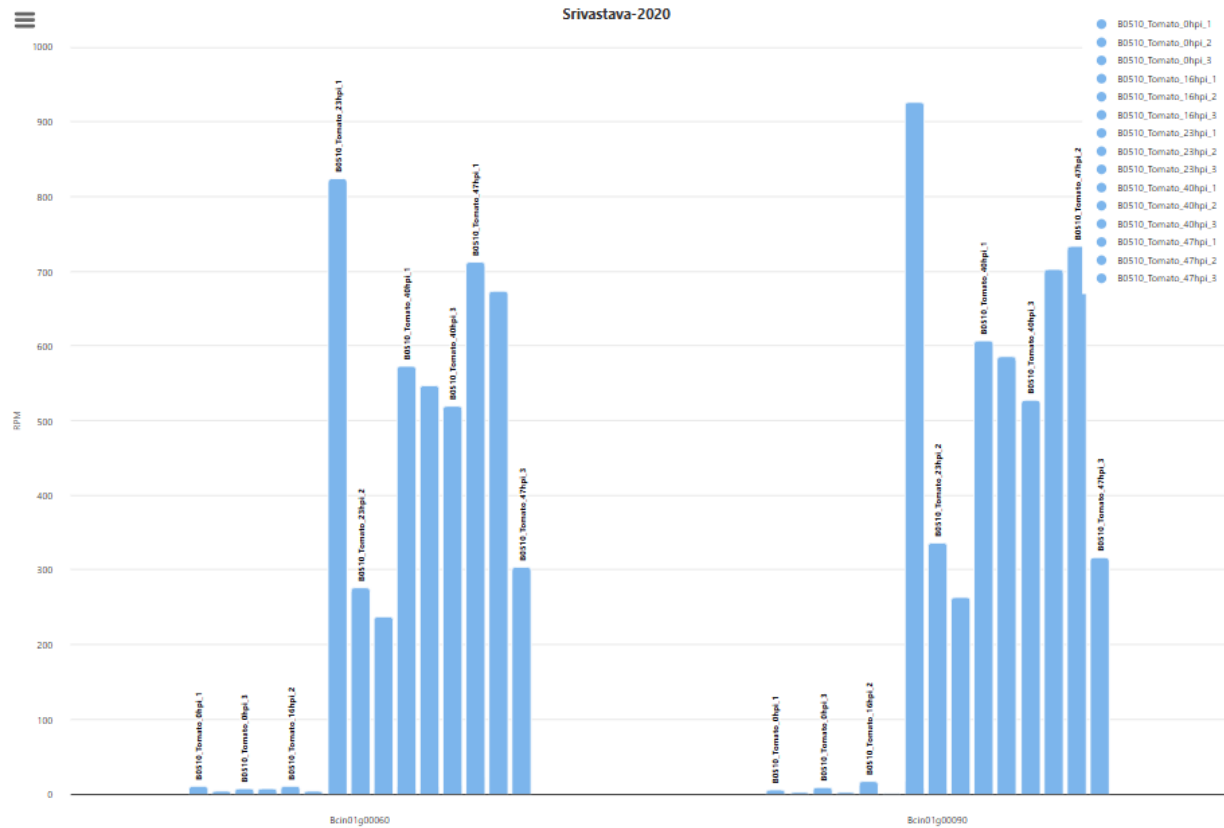
Close

blastp: 2.2.31+
Package: blast 2.2.31, build Jun 2 2015 10:20:04
database: Genes prot

qseqid	saccver		pcq	pcs	eval	pident
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_00003	Alpha-l-rhamnosidase note=Alpha-l-rhamnosidase	100	100	0	100
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_01976	alpha-L-rhamnosidase A note=alpha-L-rhamnosidase A	39	42	3e-05	24.14
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_01735	Alpha-L-rhamnosidase note=Alpha-L-rhamnosidase	33	31	0.0009	25.77
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_12308	Alpha-L-rhamnosidase note=Alpha-L-rhamnosidase	18	27	0.003	23.87
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_09776	Alpha-l-rhamnosidase note=Alpha-l-rhamnosidase	15	12	1.9	25.6
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_03910	CipC-like antibiotic response protein, putative note=CipC-like antibiotic response protein, putative	12	61	2.5	25
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_00494	Sec1 family protein note=Sec1 family protein	9	11	5.7	33.33
ThonCIALE:CH63R_00003	ThonCIALE:CH63R_10768	Acetylornithine aminotransferase note=Acetylornithine aminotransferase	9	14	7.5	29.87

➤ Barplots

Only available on Botrytis B05.10



#id	B0510_Tomato_0hpi_1	B0510_Tomato_0hpi_2	B0510_Tomato_0hpi_3	B0510_Tomato_16hpi_1	B0510_Tomato_16hpi_2	B0510_Tomato_16hpi_3
Bcin01g00060	10.6803212	3.4235945	7.2031956	7.777304658	10.79913308	4.72539288
Bcin01g00090	5.340160602	2.282396334	8.512867527	2.72205663	16.33715004	0.72698352

Export

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