

Botrytis/Sclerotinia Resources and Tools

BSPGW, Sept 17th, 2011



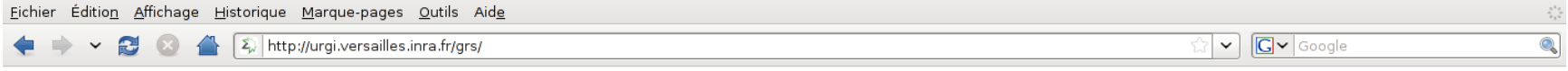
J. Amselem, N. Lapalu

ALIMENTATION
AGRICULTURE
ENVIRONNEMENT



- Get Info on a specific gene :
 - ◆ *Genome Report System*
- Get Info on a set of genes:
 - ◆ *BioMart*
- Combine data from several sources:
 - ◆ *Galaxy*
- Gene Ontology Analysis:
 - ◆ *Blast2GO*
- Blast environment and further analysis
 - ◆ *Mobyle Blast*
 - ◆ *Mobyle Blast-Koriviewer*
 - ◆ *SRS*

Get Info on a specific gene :
Genome Report System



Genome Report System

Access to Reports

[Leptosphaeria maculans](#)

[Botrytis cinerea T4](#)

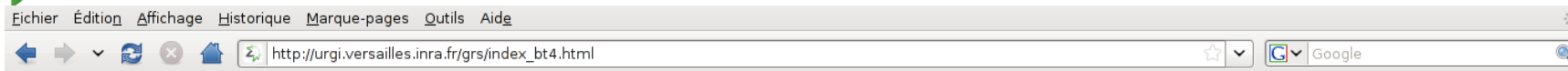
[Sclerotinia sclerotiorum](#)

[Botrytis cinerea B0510](#)



Genome Report System - copyright INRA 2011

<http://urgi.versailles.inra.fr/grs>



Homepage	GnpGenome	FunAnnot Browser	Blast	Downloads
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Botrytis cinerea T4 GRS


Search by ontology (ID or term)

(Use the autocomplete proposition in order to find a GO term, example: *Transport, Lipase or GO:000..*)

Search by gene name

(Use the autocomplete proposition in order to find a Gene, example: *BofuT4_P000020.1, BofuT4_P000200.1*)

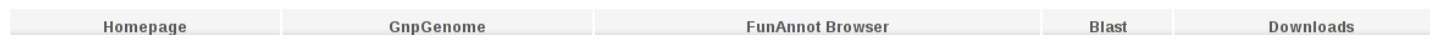
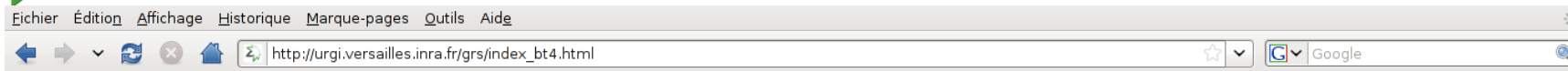
Search by keyword on whole GnpIS

For a multiple search based criteria, please use the [GnpIS portal](#) . Build your queries with either keywords or wildcards or various features of gene (name, function, InterPro entries, PFAM domains, PROSITE motifs,...).
example:

- submit *PF01529* to show genes sharing this PFAM domain
- submit *Palmitoyltransferase* to show genes matching with public or private database entries defined as Palmitoyltransferase



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Botrytis cinerea T4 GRS

Search by ontology (ID or term)

- GO:0000079 : regulation of cyclin-dependent protein **kinase** activity
- GO:0000285 : 1-phosphatidylinositol-3-phosphate 5-**kinase** activity
- GO:0000307 : cyclin-dependent protein **kinase** holoenzyme complex
- GO:0000308 : cytoplasmic cyclin-dependent protein **kinase** holoenzyme complex

GO Form :
Auto complete form

Search by keyword on whole GnrpS

For a multiple search based criteria, please use the [GnrpS portal](#) . Build your queries with either keywords or wildcards or various features of gene (name, function, InterPro entries, PFAM domains, PROSITE motifs,...).

- submit **PF01529** to show genes sharing this PFAM domain
- submit **Palmitoyltransferase** to show genes matching with public or private database entries defined as Palmitoyltransferase



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Botrytis cinerea T4 GRS

Functional annotation

GO:0046873

Description

Accession	GO:0046873
Name	metal ion transmembrane transporter activity
Ontology	molecular_function
Definition	Catalysis of the transfer of metal ions from one side of a membrane to the other
Synonyms	narrow : heavy metal ion porter activity narrow : heavy metal ion transporter activity narrow : heavy metal ion:hydrogen symporter activity narrow : heavy metal-exporting ATPase activity narrow : high affinity metal ion uptake transporter activity narrow : low affinity metal ion uptake transporter activity
Cross-refs.	GOC:ai
Comment	none
Gene Product	none
	Go to gene products section

GO term:
Info and Navigation tree

TreeView

```

graph TD
  GO0003674[GO:0003674 : molecular_function] --> GO0005215[GO:0005215 : transporter activity]
  GO0005215 --> GO0022892[GO:0022892 : substrate-specific transporter activity]
  GO0022892 --> GO0022891[GO:0022891 : substrate-specific transmembrane transporter activity]
  GO0022891 --> GO0015075[GO:0015075 : ion transmembrane transporter activity]
  GO0015075 --> GO0046873[GO:0046873 : metal ion transmembrane transporter activity]
  GO0046873 --> GO0015083[GO:0015083 : aluminum ion transmembrane transporter activity]
  GO0046873 --> GO0015085[GO:0015085 : calcium ion transmembrane transporter activity]
  GO0046873 --> GO0005261[GO:0005261 : cation channel activity]
  GO0046873 --> GO0015094[GO:0015094 : lead ion transmembrane transporter activity]
  GO0046873 --> GO0015095[GO:0015095 : magnesium ion transmembrane transporter activity]
  GO0046873 --> GO0042888[GO:0042888 : molybdenum ion transmembrane transporter activity]
  GO0046873 --> GO0015079[GO:0015079 : potassium ion transmembrane transporter activity]
  GO0046873 --> GO0015081[GO:0015081 : sodium ion transmembrane transporter activity]
  GO0046873 --> GO0046915[GO:0046915 : transition metal ion transmembrane transporter activity]
  GO0022857[GO:0022857 : transmembrane transporter activity] --> GO0022891
  
```




Homepage	GnpGenome	FunAnnot Browser	Blast	Downloads
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Botrytis cinerea T4 GRS

Search by ontology (ID or term)

(Use the autocomplete proposition in order to find a GO term, example: *Transport, Lipase or GO:000..*)

Search by gene name

- BofuT4_P000020.1
- BofuT4_P000030.1
- BofuT4_P000040.1
- BofuT4_P000050.1
- BofuT4_P000070.1
- BofuT4_P000080.1
- BofuT4_P000090.1
- BofuT4_P000100.1
- BofuT4_P000110.1

to find a Gene, example: *BofuT4_P000*

use the [GnpIS portal](#) . Build y

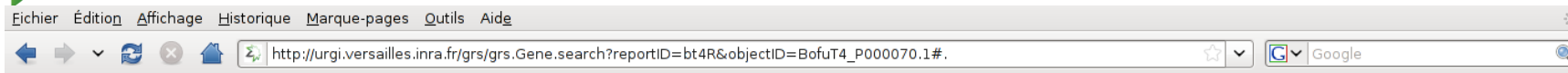
show genes sharing this PFAM domain

- submit *Palmitoyltransferase* to show genes matching with public or private database entries defined as Palmitoyltransferase

Gene request form :
Auto complete form



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Homepage	GnpGenome	FunAnnot Browser	Blast	Downloads
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***Botrytis cinerea* T4 GRS**

Functional annotation

BofuT4_P000070.1

- + [Gene Identifier](#)
- + [DbXrefs](#)
- + [Domain/Motif \(Interproscan results\)](#)
- + [Localization / Targeting](#)
- + [Predicted function](#)
- + [Blast based analysis](#)
- + [Other analysis](#)
- + [Functional Gbrowse](#)
- + [Structural Gbrowse](#)
- + [Genome Mapping at gene locus](#)
- + [Current manual annotation](#)
- + [Ortholog](#)



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Functional annotation

BofuT4_P000070.1

Gene Identifier

Located on : bt4_SuperContig_0_1

Analysis	Type	ID	RefStart	RefEnd
gene		BofuT4_G000070.1	13607	14962
egn5_orf	mRNA	BofuT4_T000070.1	13607	14962
	polypeptide	BofuT4_P000070.1	13607	14962

Gene locus and sequence

```
>BofuT4_P000070.1 | 387 aa
MKLTNLSLLALSASLASARFIEQHETDQVILNSNVVDSERYLIETAPGKQQWVTEEEKWELRRNGQNFMDITI
```

DbXrefs

DB	Accession
DB:GenBank_protein	-
DB:uniprot	-

DbXref : INSD accession (submitted to EMBL)

Domain/Motif (Interproscan results)

Analysis	Domains	Begin	End	Length	Gene Ontology	Cross Ref	InterPro
HMMPFam	PF04389	181	367	187	GO:0006508 proteolysis GO:0008233 peptidase activity	↔ ↔	IPR007484
HMMSmart					no results		
HMMTigr					no results		
HMMPanther					no results		
superfamily	SSF53187	90	387	298			none
coils					no results		
gene3d	G3DSA:3.40.630.10	90	383	294			none
seg					no results		
proflescan					no results		
PRODOM					no results		
FPRINTScan					no results		
patternscan					no results		

Domains, motifs

---> : Genes sharing the same GOID

Localization / Targeting

Analysis	Start	End	Length	Location	Reliability class	Signal Peptide CutOff	Mitochondrion CutOff
targetp	1	18	18	Secretory pathway 2		0.808	0.073

Cellular Localization

Analysis	Start	End	Length
signalp	1	18	17
tmhmm	Not result		

Predicted function

Predicted function submitted to Public database (EMBL): similar to leucine aminopeptidase 1

Predicted function

Blast based analysis

Analysis	Hit	start	end	length	Note	Hit coverage	Hit length	Hit pident	Hit pcons	eValue	Hit description
blastp_kegg	afv:AFLA_114830	28	387	360	Caps:6	94.06	387	59.34	14.01	1e-122	aminopeptidase putative
	pcs:Pc13q06380	27	387	361	Caps:6	94.81	385	58.90	14.52	1e-124	Pc13q06380
	cim:CIMC_06741	39	387	349	Caps:2	90.46	388	63.82	11.68	1e-130	hypothe
	ure:UREG_03719	39	387	349	Caps:8	90.38	395	65.27	9.52	1e-132	LAP2 p
	pno:SNOG_12603	28	387	360	Caps:8	93.57	389	67.58	10.44	1e-142	hypothe
	pan:PODANSg7635	41	385	345	Caps:6	88.35	395	70.77	10.03	1e-144	hypothe
	ncr:NCU04479	1	385	385	Caps:7	97.01	402	66.15	10.77	1e-148	similar
	mgr:MGG_10171	19	387	369	Caps:5	93.27	401	67.91	11.23	1e-149	MG10171.4 hypothetical protein
	fgr:FG05245.1	1	384	384	Caps:8	94.06	404	68.42	8.95	1e-150	hypothetical protein
sst:SS1G_08618	1	387	387	n/a	100.00	387	84.75	3.62	0.0	LAP2	
blastp_uniprot_sprot	spiA7U10 LAP2_TRITO	168	275	108	Caps:14	19.39	495	38.54	19.79	7e-07	Leucine aminopeptidase 2 OS Trichophyton tonsurans GN LAP2 PE 3 SV 1
	spiP37302 APE3_YEAST	167	288	122	Caps:21	21.04	537	38.05	15.93	3e-08	Aminopeptidase Y OS Saccharomyces cerevisiae GN APE3 PE 1 SV 1
	spiQ01693 AMPX_VIBPR	109	382	274	Caps:23	52.58	504	37.74	17.74	2e-34	Bacterial leucyl aminopeptidase OS Vibrio proteolyticus PE 1 SV 1
	spiQ04033 YD415_YEAST	53	383	331	Caps:16	89.04	374	46.25	16.22	5e-78	Probable aminopeptidase YDR415C OS Saccharomyces cerevisiae GN YDR415C PE 1 SV 1
	spiC5FNBS LAP5_NANOT	42	387	346	Caps:14	93.00	357	47.89	15.06	6e-83	Probable leucine aminopeptidase MCGY_04170 OS Nannizzia otae (strain CBS 113480) GN MCGY_04170 PE 3 SV 1
	spiC5G0A8 LAP3_NANOT	36	385	350	Caps:7	92.20	372	48.98	16.62	5e-91	Probable leucine aminopeptidase MCGY_08380 OS Nannizzia otae (strain CBS 113480) GN MCGY_08380 PE 3 SV 1
	spiC5FLR8 LAP4_NANOT	36	385	350	Caps:6	92.47	372	47.67	17.15	2e-91	Probable leucine aminopeptidase MCGY_03459 OS Nannizzia otae (strain CBS 113480) GN MCGY_03459 PE 3 SV 1
	spiA7U11 LAP1_TRIEQ	38	383	346	Caps:2	92.76	373	52.02	17.34	1e-106	Leucine aminopeptidase 1 OS Trichophyton equinum GN LAP1 PE 3 SV 1
spiQ5QHG5 LAP1_TRIRU	38	383	346	Caps:2	92.76	373	52.60	17.05	1e-107	Leucine aminopeptidase 1 OS Trichophyton rubrum GN LAP1 PE 1 SV 1	
spiC5FFM0 LAP1_NANOT	39	383	345	n/a	92.49	373	52.46	16.23	1e-108	Leucine aminopeptidase 1 OS Nannizzia otae (strain CBS 113480) GN LAP1 PE 3 SV 1	
blastp_pdb	2dea_A	109	382	274	Caps:23	88.63	299	37.74	17.74	4e-35	mol:protein length:299 Bacterial leucyl aminopeptidase
	2nyq_A	109	382	274	Caps:23	88.63	299	37.74	17.74	4e-35	mol:protein length:299 Aminopeptidase
	3fn4_A	109	382	274	Caps:23	88.63	299	37.74	17.74	4e-35	mol:protein length:299 Bacterial leucyl aminopeptidase
	1amp_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 AMINOPEPTIDASE
	1cp6_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 PROTEIN (AMINOPEPTIDASE)
	1ft7_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 BACTERIAL LEUCYL AMINOPEPTIDASE
	1iqb_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 AMINOPEPTIDASE
	1lok_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 Bacterial leucyl aminopeptidase
2iq6_A	109	382	274	Caps:23	91.07	291	37.74	17.74	3e-35	mol:protein length:291 Bacterial leucyl aminopeptidase	

Blast results

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http://urgi.versailles.inra.fr/grs/grs.Gene.search?reportID=bt4R&objectID=BofuT4_P000070.1# Google

Other analysis

cazy	
Not result	
blast2GO	
description	lamina-associated polypeptide 2
Gene ontology	GO:0006508 – proteolysis →
	GO:0008233 – peptidase activity →
EST	
nbEST	26
...> : Genes sharing the same GOID	

Cazy, GO (blast2GO)

Functional Gbrowse



Gene domains Browser

Structural Gbrowse



Genome Browser

Genome Mapping at gene locus

Analysis	Hit name								
RepeatMasker_ALL_Rebase									
TRF									
REPET									
	YCHA_541152	13607	14296	643	99.84	100.00	n/a	Botrytis cinerea HortResearch libraries	
	YCHA_544633	13607	14214	561	99.82	100.00	n/a	Botrytis cinerea HortResearch libraries	
	AL112673	13686	14081	515	91.81	68.74	n/a	BT4 Mycelium - nitrate starvation library	
	PD0ABA3YC15FM1	13606	14375	723	100.00	100.00	n/a	BT4 young mycelium library	
	PD0ABA40YD19FM1	13605	14375	725	99.86	100.00	n/a	BT4 young mycelium library	
	PD0ACA5YN07FM1	13604	14375	725	100.00	100.00	n/a	BT4 mycelium - pH stress library	
	PD0ACA4YJ14FM1	13622	14375	707	100.00	100.00	n/a	BT4 mycelium - pH stress library	
	PD0ACA22YC24FM1	13681	14533	725	100.00	100.00	n/a	BT4 mycelium - pH stress library	
	PD0ACA14YO08FM1	13654	14513	732	100.00	100.00	n/a	BT4 mycelium - pH stress library	
	PD0ACA15YO08FM1	13699	14253	508	99.80	100.00	n/a	BT4 mycelium - pH stress library	
	PD0ACA12YO08FM1	13898	14210	313	99.04	100.00	n/a	BT4 mycelium - pH stress library	

Other features at the same locus, TEs, ESTs

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http://urgi.versailles.inra.fr/grs/grs.Gene.search?reportID=bt4R&objectID=BofuT4_P000070.1#

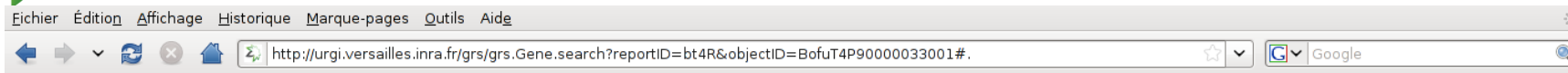
	nr7055	13007	14935	330	97.00	99.23	n/a	protein translation 391 aa
sim4_B0510_genes	BC1G_08767.1	13759	13964	150	100.00	100.00	n/a	n/a
sim4_SS_genes	SS1G_08618.1	13607	14962	1164	86.37	97.08	n/a	n/a
blastn_b0510_supercontig	B0510_supercontig_1.58	8080	13993	255615	99.93	n/a	n/a	n/a
	SS_supercontig_1.11	14453	14671	1419214	85.84	n/a	n/a	n/a
blastn_SS_supercontig	SS_supercontig_1.11	14888	14962	1419214	93.33	n/a	n/a	n/a
	SS_supercontig_1.11	13584	14375	1419214	85.98	n/a	n/a	n/a
blat_oligo	botrytisP00036521	13681	13740	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:46.59 . min_over_threshold:7.63 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036523	13687	13746	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:45.1 . min_over_threshold:6.17 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036524	13693	13752	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:42.49 . min_over_threshold:8.48 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036525	14016	14075	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:114.23 . min_over_threshold:21.77 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036526	14167	14226	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:161 . min_over_threshold:31.05 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036527	14354	14494	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:83.22 . min_over_threshold:15.55 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036528	14618	14741	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:124.12 . min_over_threshold:35.69 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036529	14765	14824	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:147.06 . min_over_threshold:31.08 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0
	botrytisP00036530	14789	14848	60	n/a	n/a	n/a	array_gene:BofuT4_P000070_1 . max_over_threshold:109.51 . min_over_threshold:20.36 . percent_hyb_over_threshold:100 . flag_cross_hyb_gene:0 . flag_cross_hyb_organism:0

[+ Current manual annotation](#)

[- Ortholog](#)

Analysis	Specie	Link
ortho	sclero	SS1G_08618.1
	bofub0510	BC1G_07770.1

Orthologs



Homepage	GnpGenome	FunAnnot Browser	Blast	Downloads
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***Botrytis cinerea* T4 GRS**

Functional annotation

BofuT4P90000033001

- + Gene Identifier
- + DbXrefs
- + Domain/Motif (Interproscan results)
- + Localization / Targeting
- + Predicted function
- + Blast based analysis
- + Other analysis
- + Functional Gbrowse
- + **Structural Gbrowse**
- + Genome Mapping at gene locus
- + Current manual annotation
- + Ortholog


Manually curated gene: access to functional edition



[Link to edition](#)



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Le site <http://urgi.versailles.inra.fr> demande un nom d'utilisateur et un mot de passe.
Le site indique : « URGI »

Utilisateur :

Mot de passe :

Authenticated access



Homepage	GnpGenome	FunAnnot Browser	Blast	Downloads
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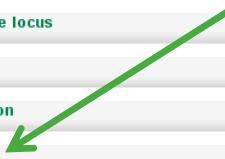
Botrytis cinerea T4 GRS

Functional annotation

BofuT4P90000033001

- + Sequence
- + Domain/Motif (Interproscan results)
- + Localization / Targeting
- + Blast based analysis
- + Other analysis
- + Genome Mapping at gene locus
- + Ortholog
- + Current manual annotation
- + **Functional edition**
- + Gene prediction at gene locus
- + TreeView

Edition category



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http://urgi.versailles.inra.fr/grs/editionBt4.htm?reportID=bt4E&objectID=BofuT4P90000033001#.

GRS - Genome Report Syst... GRS - Genome Report Syst...

+ Ortholog

+ Current manual annotation

- Functional edition

Gene ID:

Gene Name:

Synonym:

BofuT4_uP139390.1	<input type="button" value="<< Add"/>
BofuT4P1942139390001	<input type="button" value="Delete >>"/>
BofuT4P90000033001	

PMID:

Functional validation status: Not validate Validate

Evidence Code:

IDA	<input type="button" value="Add"/>
IPI	
IMP	

Gene function:

Comments:

Search ontology by term or ID (for this enter only number):

Gene Ontology:

+ Gene prediction at gene locus

+ TreeView

Evidence Code:
<http://www.geneontology.org/GO.evidence.shtml>

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http://urgi.versailles.inra.fr/grs/editionBt4.htm?reportID=bt4E&objectID=BofuT4P90000033001#.

GRS - Genome Report Syst... GRS - Genome Report Syst...

+ Ortholog

+ Current manual annotation

- Functional edition

Gene ID:

Gene Name:

Synonym:

BofuT4_uP139390.1	<< Add
BofuT4P1942139390001	
BofuT4P90000033001	Delete >>

PMID:

Functional validation status: Not validate Validate

Evidence Code :

IDA
IMP
IGI

Gene function:

Comments:

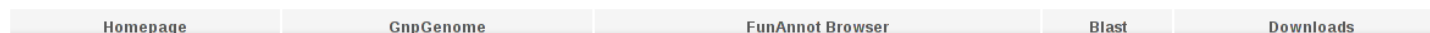
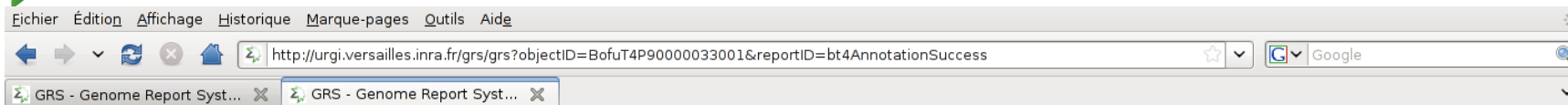
Search ontology by term or ID (for this enter only number):

Gene Ontology:

+ Gene prediction at gene locus

+ TreeView

Evidence Code:
<http://www.geneontology.org/GO.evidence.shtml>



Botrytis cinerea T4 GRS

Functional annotation

BofuT4P90000033001

■ EditionSuccess

Results save in database	
Gene ID	BofuT4P90000033001
Comments	need validation
Gene function	kinase
functional_annot_last_modif_date	Thu Sep 08 17:08:37 CEST 2011
Gene name	
Status	in progress
functional_annot_author	nlapalu
Gene Ontology	
Evidence code	IPI : Inferred from Physical Interaction
	BofuT4P90000033001
Synonyms	BofuT4P1942139390001
	BofuT4_uP139390.1

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Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/grs/editionBt4.htm?reportID=bt4E&objectID=BofuT4P90000033001#.

GRS - Genome Report Syst... GRS - Genome Report Syst...

- + Domain/Motif (Interproscan results)
- + Localization / Targeting
- + Blast based analysis
- + Other analysis
- + Genome Mapping at gene locus
- + Ortholog
- + Current manual annotation
- + Functional edition
- Gene prediction at gene locus

Analysis	Type	ID	Start	End
egn5_orf	polypeptide	BofuT4 tP139390.1	487784	488004

- TreeView

- GO:0008150 : biological_process
 - GO:0022610 : biological adhesion
 - GO:0065007 : biological regulation
 - GO:0001906 : cell killing
 - GO:0009987 : cellular process
 - GO:0032502 : developmental process
 - GO:0051234 : establishment of localization
 - GO:0040007 : growth
 - GO:0002376 : immune system process
 - GO:0051179 : localization
 - GO:0040011 : locomotion
 - GO:0051235 : maintenance of localization
 - GO:0008152 : metabolic process
 - GO:0051704 : multi-organism process
 - GO:0032501 : multicellular organismal process
 - GO:0043473 : pigmentation
 - GO:0000003 : reproduction
 - GO:0022414 : reproductive process
 - GO:0050896 : response to stimulus
 - GO:0048511 : rhythmic process
 - GO:0016032 : viral reproduction
 - GO:0005575 : cellular_component
 - GO:0003674 : molecular_function

Help:


- Co-located gene predictions
- GO tree

Get Info on a set of genes:
Biomart

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

Google



GnpIS advanced search

New Count Results

★ URL XML Perl Help

Dataset

[None selected]


- CHOOSE DATABASE -
- CHOOSE DATABASE -
- Query local mart: GnpMap (markers, Qtls), GnpSNP (snps, genes) with GnpGenome (annotations)
- Query local mart: GnpGenome (annotations) with GnpMap (genetic markers..) for Grapevine 8x
- Query local mart: GnpGenome (annotations) with GnpMap (genetic markers..) for Grapevine 12x
- Query local single mart: GnpGenome (annotations) for Poplar
- Query local single mart: GnpGenome (annotations) for Poplar V2.0
- GnpGenome Botrytis cinerea T4, genes annotation**
- GnpGenome Leptosphaeria maculans, genes functional annotation
- Query local single mart: GnpGenome Arabidopsis, Rice (gene annotations) with GnpSNP (snps)
- Query local single mart: GnpGenome (annotations) with GnpMap (genetic markers..) and GnpSNP (snps) for Wheat

<http://urgi.versailles.inra.fr/biomart/martview>

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

Google



GnpIS advanced search

New Count Results URL XML Perl Help

Dataset: GnpGenome Botrytis cinerea T4, genes annotation

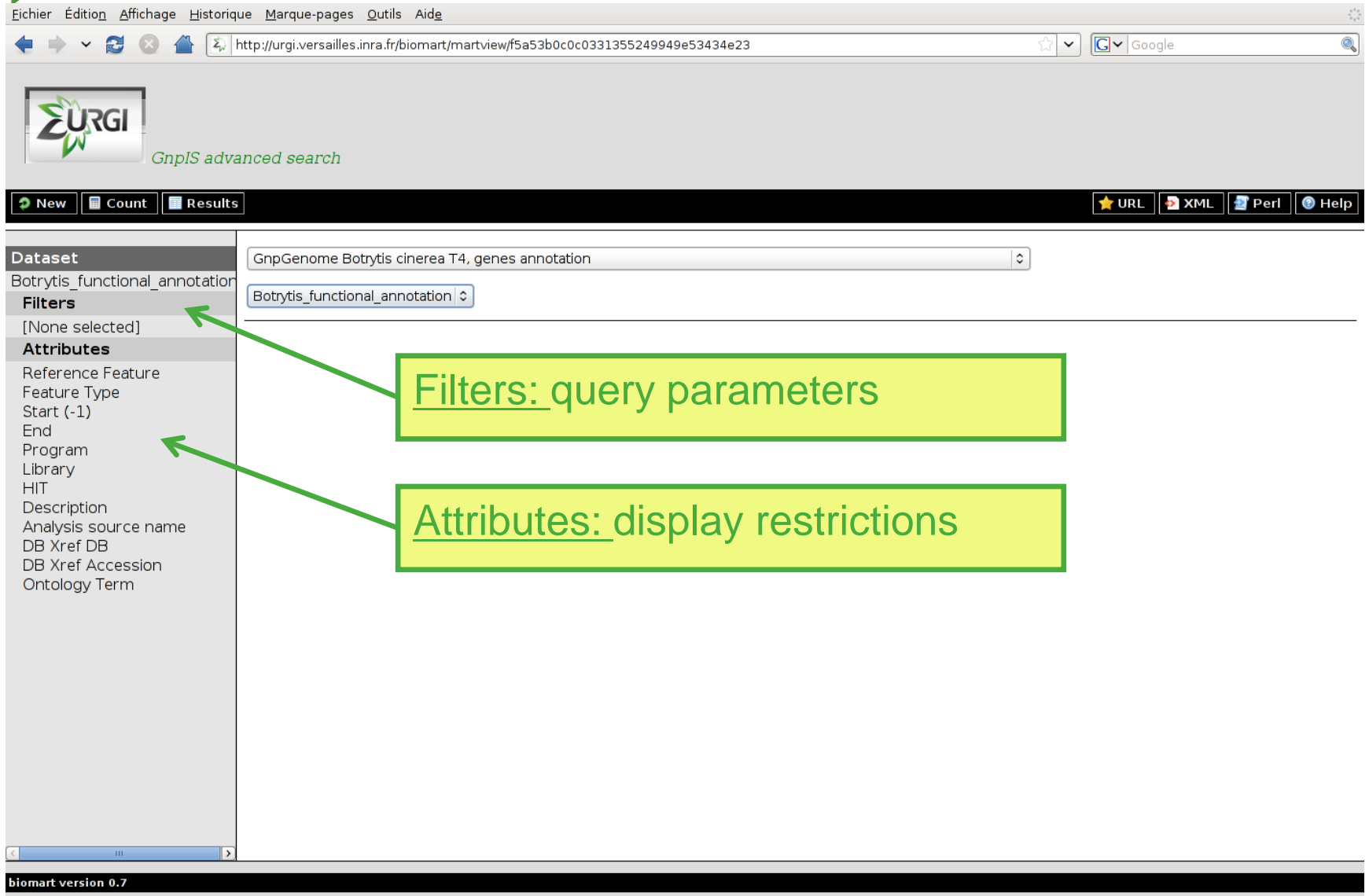
Botrytis_functional_annotation

Filters: [None selected]

Attributes:

- Reference Feature
- Feature Type
- Start (-1)
- End
- Program
- Library
- HIT
- Description
- Analysis source name
- DB Xref DB
- DB Xref Accession
- Ontology Term

biomart version 0.7



The screenshot shows the URGI web interface. At the top, there is a menu bar with options: [Eichier](#), [Édition](#), [Affichage](#), [Historique](#), [Marque-pages](#), [Outils](#), and [Aide](#). Below the menu bar is a browser address bar showing the URL: <http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23>. The main content area features the URGI logo and the text "GnplS advanced search". Below this, there are buttons for "New", "Count", and "Results". On the right side, there are icons for "URL", "XML", "Perl", and "Help". The main interface is divided into two main sections. The left section is titled "Dataset" and contains a dropdown menu with the selected value "GnpGenome Botrytis cinerea T4, genes annotation". Below this, there is a section for "Filters" with the text "[None selected]". The "Attributes" section lists various attributes: Reference Feature, Feature Type, Start (-1), End, Program, Library, HIT, Description, Analysis source name, DB Xref DB, DB Xref Accession, and Ontology Term. The right section is a large empty area. Two green callout boxes with arrows point to the "Filters" and "Attributes" sections. The first callout box contains the text "Filters: query parameters" and the second callout box contains the text "Attributes: display restrictions". At the bottom left of the interface, there is a footer that reads "biomart version 0.7".

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

GnpIS advanced search

New Count Results ★ URL XML Perl Help

Get result count for the query with any filters applied

Dataset 13 / 366639 Entries
Botrytis_functional_annotation

Filters
 Feature Type : polypeptide
 Ontology Term (% for wildcard). Example: %kinase% : metal%ion%transmembrane

Attributes
 Reference Feature
 Feature Type
 Start (-1)
 End
 Program
 Library
 HIT
 Description
 Analysis source name
 DB Xref DB
 DB Xref Accession
 Ontology Term

Please restrict your query using criteria below

Feature

Reference Feature (% for Wildcard). Example: BofuT4_P0001%

Feature Type

Feature Name (% for wildcard). Example: BofuT4_P009%

Feature Location

Start <

Start >

End <

End >

HIT (% for wildcard). Example: 3b95_%

Description (% for wildcard). Example: %Euchromatic%

Ontology Term (% for wildcard). Example: %kinase%

Program

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

GnpIS advanced search

New Count Results URL XML Perl Help

Get result count for the query with any filters applied

Please restrict your query using criteria below

Dataset 13 / 366639 Entries
Botrytis_functional_annotation

Filters
Feature Type : polypeptide
Ontology Term (% for wildcard). Example: %kinase% : metal%ion%transmembrane

Attributes
Reference Feature
Feature Type
Start (-1)

Feature

Reference Feature (% for Wildcard). Example: BofuT4_P0001%

Feature Type

match
polypeptide
polypeptide_domain
signal_peptide

HIT (% for wildcard). Example: 3b95_%

Description (% for wildcard). Example: %Euchromatic%

Ontology Term (% for wildcard). Example: %kinase%
metal%ion%transmembran

Program
FPRINTSscan

Filters:

- Type : *polypeptide*
- GO term : *metal%ion%transmembrane%transport%activity*

[Fichier](#) [Édition](#) [Affichage](#) [Historique](#) [Marque-pages](#) [Outils](#) [Aide](#)

[http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c331355249949e53434e23](#)

GnPS advanced search

[New](#) [Count](#) [Results](#)

[★ URL](#) [XML](#) [Perl](#) [Help](#)

Dataset 13 / 366639 Entries
 Botrytis_functional_annotation

Filters
 Feature Type : polypeptide
 Ontology Term (% for wildcard). Example: %kinase% : metal%ion%transmembrane

Attributes
 Reference Feature
 Feature Type
 Start (-1)
 End
 Program
 Library
 HIT
 Description
 Analysis source name
 DB Xref DB
 DB Xref Accession
 Ontology Term

Export all results to Unique results only

Email notification to

View rows as Unique results only

Reference Feature	Feature Type	Start (-1)	End	Program	Library	HIT	Description	Analysis source name	DB Xref DB	DB Xref Accession	Ontology Term
BofuT4_P015570.1	polypeptide	0	636	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P036480.1	polypeptide	0	305	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P042940.1	polypeptide	0	444	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P064350.1	polypeptide	0	485	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P068270.1	polypeptide	0	404	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P072600.1	polypeptide	0	549	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P083030.1	polypeptide	0	469	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P087510.1	polypeptide	0	369	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P096110.1	polypeptide	0	239	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P117450.1	polypeptide	0	405	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P123040.1	polypeptide	0	747	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P129290.1	polypeptide	0	953	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity
BofuT4_P141740.1	polypeptide	0	634	blast2go					GFF_source	general_info	metal ion transmembrane transporter activity

biomart version 0.7


Results :
13 polypeptides

Attributes: limit result

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

Google

 *GnplS advanced search*

New Count Results URL XML Perl Help

Dataset 13 / 366639 Entries
Botrytis_functional_annotation

Filters
Feature Type : polypeptide
Ontology Term (% for wildcard). Example: %kinase% : metal%ion%transmembrane

Attributes
Reference Feature
Ontology Term

Please select columns to be included in the output and hit 'Results' when ready

Feature

Feature

- Reference Feature
- Feature Type
- Start (-1)
- End
- Program
- Library
- HIT
- Description
- Analysis source name
- DB Xref DB
- DB Xref Accession
- Ontology Term
- Feature Unique Name

biomart version 0.7


Attributes:
Select columns to display

Attributes: limit result

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

BioMart - MartView Galaxy

 *GnPlS advanced search*

New Count Results URL XML Perl Help

Dataset: Botrytis_functional_annotation

Filters: Ontology Term (% for wildcard), Example: %kinase% ; metal%ion%transmembrane ; Feature Type : polypeptide

Attributes: Reference Feature ; Ontology Term ; Feature Type ; Program

Export all results to: File XLS Unique results only Go

Email notification to:

View: 50 rows as HTML Unique results only

Reference Feature	Ontology Term	Feature Type	Program
BofuT4_P015570.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P036480.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P042940.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P064350.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P068270.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P072600.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P083030.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P087510.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P096110.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P117450.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P123040.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P129290.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P11740.1	metal ion transmembrane transporter activity	polypeptide	blast2go

biomart version 0.7

Link:
to Genome Report System

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/f5a53b0c0c0331355249949e53434e23

URGI
GnPS advanced search

New Count Results URL XML Perl Help

Dataset 47 / 366639 Entries
Botrytis_functional_annotation

Filters
Ontology Term (% for wildcard). Example: %kinase% : metal%ion%transmembrane
Feature Type : polypeptide, polypeptide_dom

Attributes
Reference Feature
Ontology Term
Feature Type
Program

Export all results to Unique results only

Email notification to

View rows as Unique only

Reference Feature	Ontology Term	Feature Type	Program
BofuT4_P015570.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P036480.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P042940.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P064350.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P068270.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P072600.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P083030.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P087510.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P096110.1	metal ion transmembrane transporter activity	polypeptide	blast2go
BofuT4_P055370.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P064350.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P068270.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P072600.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPanther
BofuT4_P072600.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P075720.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P083030.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P087350.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMTigr
BofuT4_P087510.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPanther
BofuT4_P087510.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam
BofuT4_P096110.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPanther
BofuT4_P096110.1	metal ion transmembrane transporter activity	polypeptide_domain	HMMPFam

Export:
Save and Export your results (HTML, CSV, EXCEL)

Combine data from several sources:
Galaxy

The screenshot shows the Galaxy web interface at <http://urgi.versailles.inra.fr/galaxy/>. The interface includes a top navigation bar with menu items like 'Fichier', 'Édition', 'Affichage', 'Historique', 'Marque-pages', 'Outils', and 'Aide'. Below this is a browser address bar and a 'Galaxy' header with navigation links: 'Analyze Data', 'Workflow', 'Shared Data', 'Help', and 'User'.

The main content area is divided into three panels:

- Tools panel (left):** A list of tools under the 'Get Data' section, including 'Upload File from your computer', 'UCSC Main table browser', 'UCSC Test table browser', 'UCSC Archaea table browser', 'BX main browser', 'Get Microbial Data', 'BioMart Central server', 'BioMart INRA URGI Gnpls', 'CBI Rice Mart rice mart', 'GrameneMart Central server', 'modENCODE fly server', 'Flymine server', 'Flymine test server', 'modMine server', 'Patmine server', 'modENCODE worm server', 'Wormbase server', 'Wormbase test server', 'EuPathDB server', 'EncodeDB at NHGPI', 'EpiGRAPH server', 'EpiGRAPH test server', and 'HbVar Human Hemoglobin Variants and Thalassemias'. Other sections include 'Send Data', 'ENCODE Tools', 'Lift-Over', 'Text Manipulation', 'Filter and Sort', 'Unix Tools', 'Join, Subtract and Group', and 'Convert Formats'.
- Central visualization:** A graphic with the text 'Unité Recherche Génomique Info' at the top, the URGI logo in the center, and several DNA double helix structures around it.
- History panel (right):** A panel titled 'History' with an 'Options' dropdown. It contains a message: 'Your history is empty. Click 'Get Data' on the left pane to start'. There is an 'Edit attributes' button next to the message.

Annotations on the screenshot include:

- A green box labeled 'Tools panel' with an arrow pointing to the left-hand tools list.
- A green box labeled 'History panel (data)' with an arrow pointing to the right-hand history panel.
- The INRA logo is visible in the bottom right area of the visualization.

At the bottom of the screenshot, the URL <http://urgi.versailles.inra.fr/galaxy> is displayed in green text.

Tools panel

History panel (data)

<http://urgi.versailles.inra.fr/galaxy>

Galaxy GnpIS - URGI URGI - Gene list results

Gene list results

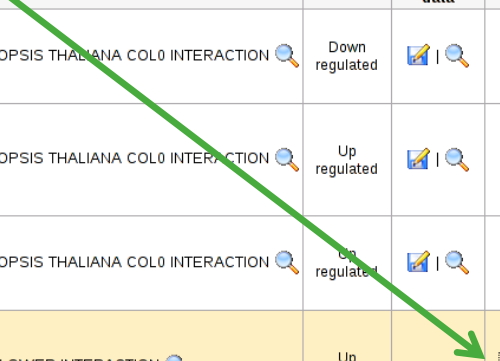
Results

Number of unique reporters in your query: 211
 Number of unique genes in your query: 35690

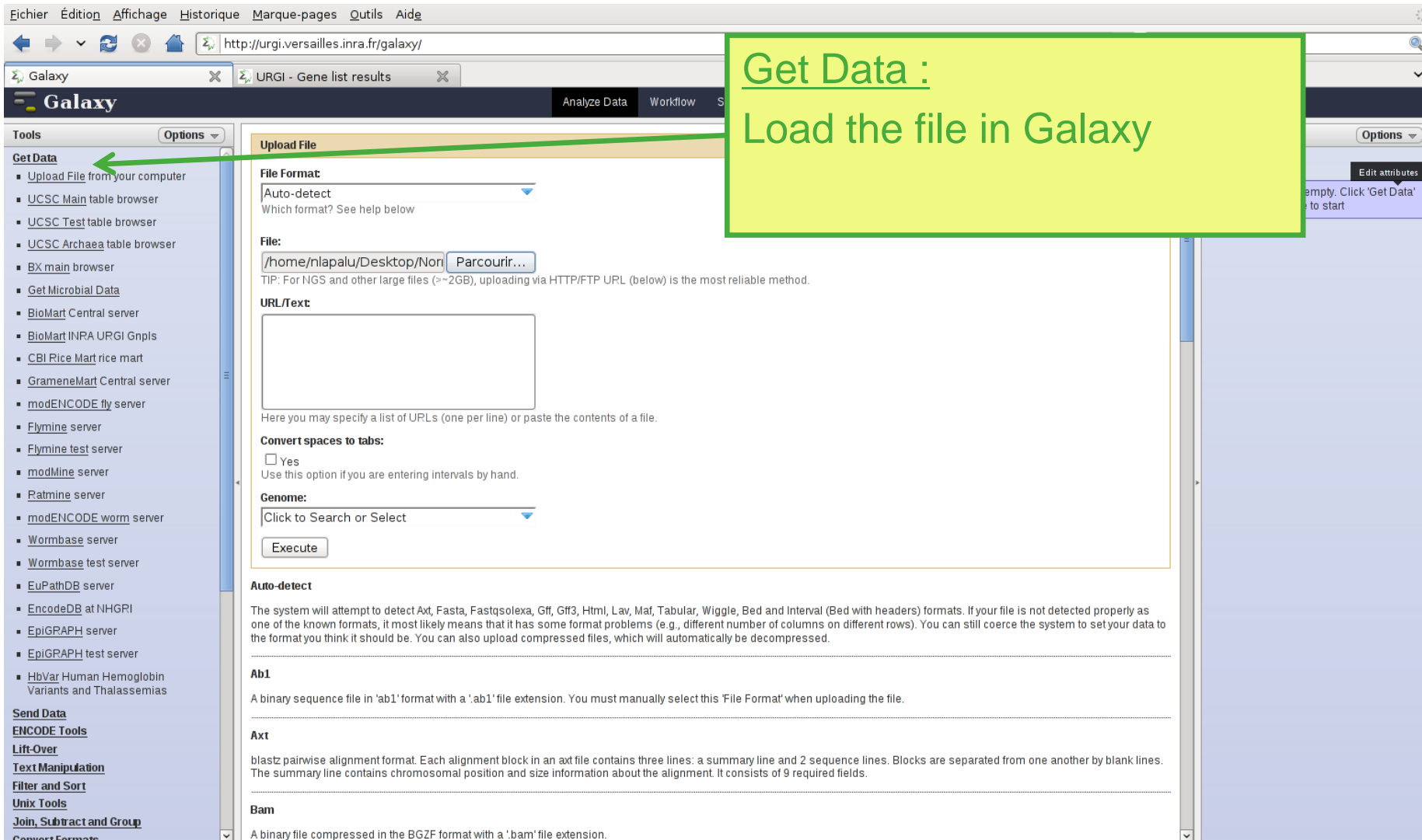
9 items found, displaying 1 to 9 | Display 10 results per page

#	Gene list name	Creation date	Description	Project	Regulation	Reporter normalized data	Gene normalized data
1	Bc2 - In planta Down (Botrytis-Arabidopsis interaction) (113 reporters)	2005/04/15	Variance analysis wa... > more	INRA_AFGBC	Down regulated		
2	Bc3 - Consolidated In planta Up (Botrytis-Arabidopsis interaction) (32 reporters)	2005/04/15	Expression values of... > more	INRA_AFGBC	Up regulated		
3	Bc1 - In planta Up (Botrytis-Arabidopsis interaction) (98 reporters)	2005/04/15	Variance analysis wa... > more	INRA_AFGBC	Up regulated		
4	Bc1 - in planta Up (Botrytis-B0510 : in vitro vs in planta[sunflower]) (277 genes)	2009/03/09	Variance analysis wa... > more	Botrytis on Sunflower 2008	Up regulated		
5	Bc1 - In planta Down (Botrytis-B0510 : in vitro vs in planta[sunflower]) (306 genes)	2009/03/09	Variance analysis wa... > more	Botrytis on Sunflower 2008	Down regulated		

Get Data from GnpArray:
 download up-regulated Botrytis genes



Load Data in Galaxy



Get Data :
Load the file in Galaxy

The screenshot shows the Galaxy web interface. The left sidebar contains a 'Tools' menu with a 'Get Data' section. A yellow callout box highlights the 'Get Data' section and the 'Upload File' tool. A green arrow points from the callout to the 'Upload File' tool. The 'Upload File' tool interface includes a 'File Format' dropdown set to 'Auto-detect', a 'File:' input field with a file path and a 'Parcourir...' button, a 'URL/Text' text area, and an 'Execute' button. Below the tool interface, there are sections for 'Auto-detect', 'Ab1', 'Axt', and 'Bam' with their respective descriptions.

Tools Options

Get Data

- Upload File from your computer
- UCSC Main table browser
- UCSC Test table browser
- UCSC Archaea table browser
- BX main browser
- Get Microbial Data
- BioMart Central server
- BioMart INRA URGI Gnpls
- CBI Rice Mart rice mart
- GrameneMart Central server
- modENCODE fly server
- Flymine server
- Flymine test server
- modMine server
- Patmine server
- modENCODE worm server
- Wormbase server
- Wormbase test server
- EuPathDB server
- EncodeDB at NHGRI
- EpiGRAPH server
- EpiGRAPH test server
- HbVar Human Hemoglobin Variants and Thalassemias

Send Data

ENCODE Tools

Lift-Over

Text Manipulation

Filter and Sort

Unix Tools

Join, Subtract and Group

Convert Formats

Upload File

File Format
Auto-detect
Which format? See help below

File:
/home/nlapalu/Desktop/Nori Parcourir...

TIP: For NGS and other large files (>~2GB), uploading via HTTP/FTP URL (below) is the most reliable method.

URL/Text

Here you may specify a list of URLs (one per line) or paste the contents of a file.

Convert spaces to tabs:
 Yes
Use this option if you are entering intervals by hand.

Genome:
Click to Search or Select

Execute

Auto-detect
The system will attempt to detect Axt, Fasta, Fastqsolexa, Gff, Gff3, Html, Lav, Maf, Tabular, Wiggle, Bed and Interval (Bed with headers) formats. If your file is not detected properly as one of the known formats, it most likely means that it has some format problems (e.g., different number of columns on different rows). You can still coerce the system to set your data to the format you think it should be. You can also upload compressed files, which will automatically be decompressed.

Ab1
A binary sequence file in 'ab1' format with a '.ab1' file extension. You must manually select this 'File Format' when uploading the file.

Axt
blastz pairwise alignment format. Each alignment block in an axt file contains three lines: a summary line and 2 sequence lines. Blocks are separated from one another by blank lines. The summary line contains chromosomal position and size information about the alignment. It consists of 9 required fields.

Bam
A binary file compressed in the BGZF format with a '.bam' file extension.

Load Data in Galaxy

Fichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/galaxy/

Galaxy URG1 - Gene list results

Analyze Data Workflow Shared Data Help User

Tools Options

- Get Data
 - Upload File from your computer
 - UCSC Main table browser
 - UCSC Test table browser
 - UCSC Archaea table browser
 - BX main browser
 - Get Microbial Data
 - BioMart Central server
 - BioMart INRA URG1 GnpIs
 - CBI Rice Mart rice mart
 - GrameneMart Central server
 - modENCODE fly server
 - Flymine server
 - Flymine test server
 - modMine server
 - Patmine server
 - modENCODE worm server
 - Wormbase server
 - Wormbase test server
 - EuPathDB server
 - EncodeDB at NHGRI
 - EpiGRAPH server
 - EpiGRAPH test server
 - HbVar Human Hemoglobin Variants and Thalassemias
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Unix Tools
- Join, Subtract and Group
- Convert Formats

Reporter name	Sequence db ID	FOLD CHANGE	pVALUE	Normalized_Variance
B4BC_116_249_C09	B4BC_116_249_C09	8.0	2.129635E-6	0.97
B5BC_116_281_B07	B5BC_116_281_B07	4.5	7.856555E-7	0.97
BC1G_00109.1	BC1G_00109.1	2.2	6.83884E-7	0.97
BC1G_00913.1	BC1G_00913.1	1.7	1.424435E-6	0.97
BC1G_01483.1	BC1G_01483.1	23.0	4.262601E-7	0.99
BC1G_03803.1	BC1G_03803.1	29.0	1.299432E-6	0.98
BC1G_04307.1	BC1G_04307.1	1.8	2.289414E-6	0.94
BC1G_05330.1	BC1G_05330.1	4.3	1.193244E-6	0.97
BC1G_05859.1	BC1G_05859.1	4.6	1.015448E-6	0.98
BC1G_06363.1	BC1G_06363.1	3.3	2.623233E-6	0.97
BC1G_06588.1	BC1G_06588.1	3.2	6.603145E-7	0.91
BC1G_07638.1	BC1G_07638.1	2.6	4.994546E-7	0.99
BC1G_08995.1	BC1G_08995.1	6.8	7.061857E-7	0.98
BC1G_09422.1	BC1G_09422.1	3.9	2.404327E-6	0.95
BC1G_09889.1	BC1G_09889.1	2.6	1.378184E-6	0.97
BC1G_10542.1	BC1G_10542.1	8.3	2.324573E-6	0.94
BC1G_12051.1	BC1G_12051.1	2.2	2.988155E-6	0.93
BC1G_12341.1	BC1G_12341.1	2.0	2.609739E-6	0.95
BC1G_12847.1	BC1G_12847.1	9.9	2.262815E-7	0.91
BC1G_12848.1	BC1G_12848.1	11.0	5.841038E-7	0.96
BC1G_12849.1	BC1G_12849.1	7.0	4.852249E-7	0.94
BC1G_13809.1	BC1G_13809.1	10.0	2.803728E-7	0.99
BC1G_13810.1	BC1G_13810.1	13.0	5.707901E-7	0.99
BC1G_13833.1	BC1G_13833.1	6.2	3.874826E-7	0.97
BC1G_14128.1	BC1G_14128.1	3.9	1.310243E-6	0.98
BC1G_14540.1	BC1G_14540.1	4.0	1.679697E-6	0.95
BC1G_14688.1	BC1G_14688.1	54.0	1.363408E-7	0.99
BC1G_15681.1	BC1G_15681.1	2.9	2.419977E-6	0.9
BC1G_15887.1	BC1G_15887.1	15.0	1.21429E-6	0.98
BC1G_15967.1	BC1G_15967.1	4.5	2.462145E-6	0.96
BC1G_15968.1	BC1G_15968.1	13.0	4.523991E-7	0.98
BC1G_16001.1	BC1G_16001.1	5.4	1.007591E-6	0.97
BC1G_16034.1	BC1G_16034.1	2.6	1.563056E-7	0.98
BC1G_16093.1	BC1G_16093.1	4.0	2.00237E-6	0.98
BC1G_16127.1	BC1G_16127.1	15.0	2.078083E-6	0.97
BC1G_16165.1	BC1G_16165.1	5.4	1.377053E-6	0.98
BC1G_16184.1	BC1G_16184.1	6.6	6.001744E-7	0.99
BC1G_16341.1	BC1G_16341.1	30.0	2.572288E-7	0.99
BC1G_16358.1	BC1G_16358.1	3.9	2.440423E-6	0.97
BofuT4_P001930.1	BofuT4_P001930.1	13.0	1.885913E-7	0.99
BofuT4_P002750.1	BofuT4_P002750.1	5.6	8.712867E-7	0.99
BofuT4_P003870.1	BofuT4_P003870.1	18.0	2.209389E-7	0.99
BofuT4_P003990.1	BofuT4_P003990.1	18.0	1.283808E-6	0.96
BofuT4_P004830.1	BofuT4_P004830.1	39.0	1.956912E-7	0.99
BofuT4_P005160.1	BofuT4_P005160.1	6.8	1.077158E-6	0.98
BofuT4_P005170.1	BofuT4_P005170.1	6.0	1.569941E-6	0.98
BofuT4_P006510.1	BofuT4_P006510.1	2.7	2.681189E-6	0.88
BofuT4_P006540.1	BofuT4_P006540.1	24.0	2.941267E-7	0.99
BofuT4_P007640.1	BofuT4_P007640.1	13.0	1.087957E-6	0.97
BofuT4_P007740.1	BofuT4_P007740.1	2.3	1.882424E-6	0.96
BofuT4_P008190.1	BofuT4_P008190.1	4.3	9.539359E-7	0.98

History Options

31: Normalized_Data_1.3643098867419643
278 lines, format: tabular, database: ?
Info: uploaded tabular file

1	2	3
Reporter name	Sequence db ID	FOLD CHANG
B4BC_116_249_C09	B4BC_116_249_C09	8.0
B5BC_116_281_B07	B5BC_116_281_B07	4.5
BC1G_00109.1	BC1G_00109.1	2.2
BC1G_00913.1	BC1G_00913.1	1.7
BC1G_01483.1	BC1G_01483.1	23.0

Display your data

Galaxy interface showing the 'Select' tool configuration. The tool is set to select lines from '31: Normalized_Data_1.9643E11.csv' using a 'Matching' operation with the pattern '^BofuT4'. A green callout box highlights the 'Filter and Sort' section and the pattern.

Filter and Sort section :
Select lines matching with :
"^BofuT4" pattern;

Syntax

The select tool searches the data for lines containing or not containing a certain amount of text.

- `{ } [] . * ? + ^ $` are all special characters. `\` can be used to escape them.
- `^` matches the beginning of a string (but not an internal line).
- `\d` matches a digit, same as `[0-9]`.
- `\D` matches a non-digit.
- `\s` matches a whitespace character.
- `\S` matches anything BUT a whitespace.
- `\t` matches a tab.
- `\w` matches an alphanumeric character.
- `\W` matches anything but an alphanumeric character.
- `[...]` groups a particular pattern.
- `\z` matches the end of a string (but not an internal line).
- `{ n or n, or n,m }` specifies an expected number of repetitions of the preceding pattern.
 - `{n}` The preceding item is matched exactly n times.
 - `{n,}` The preceding item is matched n or more times.
 - `{n,m}` The preceding item is matched at least n times but not more than m times.
- `[...]` creates a character class. Within the brackets, single characters can be placed. A dash (`-`) may be used to indicate a range such as `a-z`.
- `.` Matches any single character except a newline.
- `*` The preceding item will be matched zero or more times.
- `?` The preceding item is optional and matched at most once.
- `+` The preceding item will be matched one or more times.
- `^` has two meanings: `-` matches the beginning of a line or string. `-` indicates negation in a character class. For example, `[^..]` matches every character except the ones inside brackets.
- `$` matches the end of a line or string.
- `|` Separates alternate possibilities.

Example

`chr(10)Z` would match lines that begin with chromosome 10, such as lines in a BED format file.

select lines by text pattern

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Galaxy URGI - Gene list results

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BofuT4_P001930.1	BofuT4_P001930.1	13.0	1.885913E-7	0.99
BofuT4_P002750.1	BofuT4_P002750.1	5.6	8.712867E-7	0.99
BofuT4_P003870.1	BofuT4_P003870.1	18.0	2.209389E-7	0.99
BofuT4_P003990.1	BofuT4_P003990.1	18.0	1.283808E-6	0.96
BofuT4_P004830.1	BofuT4_P004830.1	39.0	1.956912E-7	0.99
BofuT4_P005160.1	BofuT4_P005160.1	6.8	1.077158E-6	0.98
BofuT4_P005170.1	BofuT4_P005170.1	6.0	1.569941E-6	0.98
BofuT4_P006510.1	BofuT4_P006510.1	2.7	2.681189E-6	0.88
BofuT4_P006540.1	BofuT4_P006540.1	24.0	2.941267E-7	0.99
BofuT4_P007640.1	BofuT4_P007640.1	13.0	1.087957E-6	0.97
BofuT4_P007740.1	BofuT4_P007740.1	2.3	1.882424E-6	0.96
BofuT4_P008190.1	BofuT4_P008190.1	4.3	9.539359E-7	0.98
BofuT4_P008630.1	BofuT4_P008630.1	2.9	7.737233E-7	0.96
BofuT4_P008670.1	BofuT4_P008670.1	4.0	1.574286E-6	0.98
BofuT4_P008680.1	BofuT4_P008680.1	1.1	1.73574E-7	0.98
BofuT4_P010370.1	BofuT4_P010370.1	5.4	1.059331E-6	0.98
BofuT4_P010380.1	BofuT4_P010380.1	58.0	2.482903E-7	0.99
BofuT4_P010920.1	BofuT4_P010920.1	2.2	1.312561E-7	0.95
BofuT4_P011170.1	BofuT4_P011170.1	9.8	9.651431E-8	0.99
BofuT4_P011330.1	BofuT4_P011330.1	4.3	2.055745E-6	0.97
BofuT4_P011370.1	BofuT4_P011370.1	2.9	6.80443E-7	0.88
BofuT4_P011380.1	BofuT4_P011380.1	5.9	1.831534E-6	0.97
BofuT4_P011810.1	BofuT4_P011810.1	61.0	2.404901E-7	0.99
BofuT4_P012350.1	BofuT4_P012350.1	16.0	5.079203E-7	0.99
BofuT4_P012360.1	BofuT4_P012360.1	16.0	7.85463E-7	0.98
BofuT4_P012400.1	BofuT4_P012400.1	12.0	2.733368E-7	0.98
BofuT4_P012420.1	BofuT4_P012420.1	96.0	1.514637E-7	0.99
BofuT4_P012560.1	BofuT4_P012560.1	1.9	2.884356E-6	0.71
BofuT4_P013210.1	BofuT4_P013210.1	3.4	2.399235E-6	0.96
BofuT4_P013310.1	BofuT4_P013310.1	4.6	2.854698E-7	0.93
BofuT4_P013640.1	BofuT4_P013640.1	6.9	3.997133E-7	0.99
BofuT4_P014290.1	BofuT4_P014290.1	6.8	2.97187E-6	0.92
BofuT4_P014350.1	BofuT4_P014350.1			
BofuT4_P015750.1	BofuT4_P015750.1			
BofuT4_P015800.1	BofuT4_P015800.1			
BofuT4_P016040.1	BofuT4_P016040.1			
BofuT4_P018370.1	BofuT4_P018370.1			
BofuT4_P019100.1	BofuT4_P019100.1			
BofuT4_P019510.1	BofuT4_P019510.1			
BofuT4_P020150.1	BofuT4_P020150.1			
BofuT4_P024150.1	BofuT4_P024150.1			
BofuT4_P024480.1	BofuT4_P024480.1			
BofuT4_P025640.1	BofuT4_P025640.1			
BofuT4_P026680.1	BofuT4_P026680.1			
BofuT4_P026710.1	BofuT4_P026710.1	4.5	1.797477E-6	0.97
BofuT4_P028100.1	BofuT4_P028100.1	11.0	8.213926E-7	0.98
BofuT4_P030610.1	BofuT4_P030610.1	1.4	2.561869E-6	0.86
BofuT4_P030940.1	BofuT4_P030940.1	3.3	1.119613E-6	0.91
BofuT4_P031660.1	BofuT4_P031660.1	74.0	1.093146E-7	0.99
BofuT4_P032210.1	BofuT4_P032210.1	2.5	1.135655E-6	0.97
BofuT4_P033100.1	BofuT4_P033100.1	4.9	2.967344E-6	0.97
BofuT4_P033780.1	BofuT4_P033780.1	2.8	1.810585E-6	0.97

History

32: Select on data 31
228 lines, format: tabular, database: ?
Info: Matching pattern: *BofuT4

1	2	3	4
BofuT4_P001930.1	BofuT4_P001930.1	13.0	1.885913E-7
BofuT4_P002750.1	BofuT4_P002750.1	5.6	8.712867E-7
BofuT4_P003870.1	BofuT4_P003870.1	18.0	2.209389E-7
BofuT4_P003990.1	BofuT4_P003990.1	18.0	1.283808E-6
BofuT4_P004830.1	BofuT4_P004830.1	39.0	1.956912E-7
BofuT4_P005160.1	BofuT4_P005160.1	6.8	1.077158E-6

31:
Normalized Data_1.3643098867419643
278 lines, format: tabular, database: ?
Info: uploaded tabular file

1	2	3
Reporter name	Sequence db ID	FOLD CHANGE
B4BC_116_249_C09	B4BC_116_249_C09	8.0
B5BC_116_281_B07	B5BC_116_281_B07	4.5
BC16_00109.1	BC16_00109.1	2.2
BC16_00913.1	BC16_00913.1	1.7
BC16_01483.1	BC16_01483.1	23.0

Match :
You get a new file, with only BT4 genes

Galaxy interface showing the 'Cut' tool configuration and execution results.

Tools (left sidebar):

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
 - Add column to an existing query
 - Compute an expression on every row
 - Concatenate queries tail-to-head
 - Cut columns from a table
 - Merge Columns together
 - Convert delimiters to TAB
 - Create single interval as a new query
 - Change Case of selected columns
 - Paste two files side by side
 - Remove beginning of a file
 - Select random lines from a file
 - Select first lines from a Query
 - Select last lines from a Query
 - Trim leading or trailing characters
 - Filter on ambiguities in polymorphism datasets
 - Arithmetic Operations on tables
- Filter and Sort
- Unix Tools
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics

Cut tool configuration:

- Cut columns:
- Delimited by:
- From:

Execute

WARNING: This tool breaks column assignments. To

i The output of this tool is always in tabular format (e.g.,

Cutting columns 1 and 3 from:

```
apple,1s,good
windows,1s,bad
```

will give:

```
apple good
windows bad
```

What it does

This tool selects (cuts out) specified columns from the dataset.

- Columns are specified as **c1, c2,** and so on. Column count begins with **1**
- Columns can be specified in any order (e.g., **c2,c1,c6**)
- If you specify more columns than actually present - empty spaces will be filled with dots

Example

Input dataset (six columns: c1, c2, c3, c4, c5, and c6):

```
chr1 10 1000 gene1 0 +
chr2 100 1500 gene2 0 +
```

cut on columns "**c1,c4,c6**" will return:

```
chr1 gene1 +
chr2 gene2 +
```

cut on columns "**c6,c5,c4,c1**" will return:

```
+ 0 gene1 chr1
+ 0 gene2 chr2
```

cut on columns "**c8,c7,c4**" will return:

```
... gene1
```

History (right sidebar):

- 32: Select on data 31
 - 228 lines, format: tabular, database: ?
 - Info: Matching pattern: "BofuT4"
- 31: Normalized Data_1.3643098867419643
 - 278 lines, format: tabular, database: ?
 - Info: uploaded tabular file

1	2	3
Reporter name	Sequence db ID	FOLD CHANGE
B4BC_116_249_C09	B4BC_116_249_C09	8.0
BSBC_116_281_B07	BSBC_116_281_B07	4.5
BC1G_00109.1	BC1G_00109.1	2.2
BC1G_00913.1	BC1G_00913.1	1.7
BC1G_01483.1	BC1G_01483.1	23.0

Text manipulation section :
Cut , merge , paste , convert

Cut columns

Galaxy interface showing a workflow step: **33: Cut on data 32**. The tool description indicates: "228 lines, format: tabular, database: ?". The input data is shown as a list of gene identifiers (e.g., BofuT4_P001930.1).

The **History** panel shows the previous step: **32: Select on data 31**, with a matching pattern of "BofuT4".

The **Tools** panel on the left lists various operations, including "Cut columns from a table" under the **Text Manipulation** section.

Two green arrows point from the **33: Cut on data 32** tool description to the **32: Select on data 31** tool description and the **Tools** panel, indicating the workflow and the tool used.

A green callout box contains the text: **Cut first column: You get a new file with gene names only.**

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Galaxy URG1 - Gene list results



Analyze Data Workflow Shared Data Help User

Tools Options



- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
 - Add column to an existing query
 - Compute an expression on every row
 - Concatenate queries tail-to-head
 - Cut columns from a table
 - Merge Columns together
 - Convert delimiters to TAB
 - Create single interval as a new query
 - Change Case of selected columns
 - Paste two files side by side
 - Remove beginning of a file
 - Select random lines from a file
 - Select first lines from a Query
 - Select last lines from a Query
 - Trim leading or trailing characters
 - Filter on ambiguities in polymorphism datasets
 - Arithmetic Operations on tables
- Filter and Sort
- Unix Tools
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics

Attributes updated



History Options

33: gene list 228 lines, format: tabular, database: ?
Info:  

1
BoFuT4_P001930.1
BoFuT4_P002750.1
BoFuT4_P003870.1
BoFuT4_P003990.1
BoFuT4_P004830.1
BoFuT4_P005160.1

32: Select on data 31 228 lines, format: tabular, database: ?
Info: Matching pattern: ^BoFuT4  

1	2	3	4
BoFuT4_P001930.1	BoFuT4_P001930.1	13.0	1.885
BoFuT4_P002750.1	BoFuT4_P002750.1	5.6	8.71
BoFuT4_P003870.1	BoFuT4_P003870.1	18.0	2.205
BoFuT4_P003990.1	BoFuT4_P003990.1	18.0	1.28
BoFuT4_P004830.1	BoFuT4_P004830.1	39.0	1.954
BoFuT4_P005160.1	BoFuT4_P005160.1	6.8	1.07

31: Normalized Data_1.3643098867419643 278 lines, format: tabular, database: ?
Info: uploaded tabular file  

1	2	3
Reporter name	Sequence db ID	FOLD CHANG
B4BC_116_249_C09	B4BC_116_249_C09	8.0
B5BC_116_281_B07	B5BC_116_281_B07	4.5
BC16_00109.1	BC16_00109.1	2.2
BC16_00913.1	BC16_00913.1	1.7
BC16_01483.1	BC16_01483.1	23.0

Edit Attributes (click on pen):
Give a name to your file.

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http://urgi.versailles.inra.fr/biomart/martview/9ad9a9289d80ee670fd1a35ddd60279a

Galaxy URGI - Gene list results BioMart - MartView

ZURGI
GnplS advanced search

New Count Results

Dataset 968 / 366639
Entries
Botrytis_functional_annotation

Filters

Reference Feature (% for Wildcard). Example: BofuT4_P0001% : [ID-list specified]
Feature Type : polypeptide_domain
DB Xref DB : DB:PFAM

Attributes

Reference Feature
Feature Type
Start (-1)
End
Program
Library
HIT
Description
Analysis source name
DB Xref DB
DB Xref Accession
Ontology Term

Please restrict your query

Feature

Reference Feature (% for Wildcard). Example: BofuT4_P0001%

BofuT4_uP106990.1
BofuT4_uP127940.1
BofuT4_uP128130.1
BofuT4_uP131510.1

Parcourir...

Feature Type

match
polypeptide
polypeptide_domain
signal_peptide

Feature Name (% for wildcard). Example: BofuT4_P009%

Parcourir...

Feature Location

Start <
Start >
End <
End >

HIT (% for wildcard). Example: 3b95_%

Parcourir...

Edit Filters:
Paste your gene list

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/9ad9a9289d80ee670fd1a35ddd60279a

Galaxy URGI - Gene list results BioMart - MartView

polypeptide_domain
DB Xref DB : DB:PFAM

Attributes

- Reference Feature
- Feature Type
- Start (-1)
- End
- Program
- Library
- HIT
- Description
- Analysis source name
- DB Xref DB
- DB Xref Accession
- Ontology Term

Feature Type

match
polypeptide
polypeptide_domain
signal_peptide

Feature Name (% for wildcard). Example: BofuT4_P009%

Feature Location

Start <
Start >
End <
End >

HIT (% for wildcard). Example: 3b95_%

Parcourir...

Description (% for wildcard). Example: %Euchromatic%

Ontology Term (% for wildcard). Example: %kinase%

Program

FPRINTScan

Analysis source name

polypeptide_iprscan_annotation
polypeptide_vs_Cdd_profiles
polypeptide_vs_Kog_profiles
polypeptide_vs_kegg
polypeptide_vs_pdb

DB Xref DB

DB:PFAM
DB:PIR
DB:PRINTS
DB:PRODOM
DB:PROFILE


DB Xref Accession (% for wildcard)

Edit Filters:
Get PFAM domains of selected genes

Eichier Édition Affichage Historique Marque-pages Outils Aide

http://urgi.versailles.inra.fr/biomart/martview/9ad9a9289d80ee670fd1a35ddd60279a

Galaxy URGI - Gene list results BioMart - MartView



GnpIS advanced search

New Count Results URL XML Perl Help

Dataset 968 / 366639
 Entries
 Botrytis_functional_annotation

Filters
 Reference Feature (% for Wildcard). Example: BofuT4_P0001% : [ID-list specified]
 Feature Type : polypeptide_domain
 DB Xref DB : DB:PFAM

Attributes
 Reference Feature
 Start (-1)
 End
 DB Xref Accession

Export all results to Unique results only

Email notification to

View rows as Unique results only

Reference Feature	Start (-1)	End	DB Xref Accession
BofuT4_P001930.1	6	198	PF00857
BofuT4_P003870.1	6	217	PF03443
BofuT4_P003990.1	3	194	PF06101
BofuT4_P004830.1	791	819	PF00734
BofuT4_P004830.1	61	271	PF00933
BofuT4_P004830.1	353	601	PF01915
BofuT4_P005160.1	3	283	PF00067
BofuT4_P006540.1	269	574	PF00732
BofuT4_P006540.1	815	846	PF00734
BofuT4_P006540.1	685	801	PF05199
BofuT4_P007640.1	90	152	PF00775
BofuT4_P007740.1	22	444	PF00171
BofuT4_P008190.1	50	386	PF01301
BofuT4_P008190.1	394	575	PF10435
BofuT4_P008630.1	80	117	PF08545
BofuT4_P008630.1	273	365	PF02803
BofuT4_P010370.1	34	288	PF00657
BofuT4_P010380.1	26	86	PF05730
BofuT4_P010920.1	18	164	PF09792
BofuT4_P011330.1	986	1118	PF00156

biomart version 0.7

Export:
Export your result in tab file

Load the new file

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http://urgi.versailles.inra.fr/galaxy/

Galaxy URGI - Gene list results BioMart - MartView

Analyze Data Workflow Shared Data Help User

Tools Options

- Get Data
 - Upload File from your computer
 - UCSC Main table browser
 - UCSC Test table browser
 - UCSC Archaea table browser
 - BX main browser
 - Get Microbial Data
 - BioMart Central server
 - BioMart INRA URGI Gnpls
 - CBI Rice Mart rice mart
 - GrameneMart Central server
 - modENCODE fly server
 - Flymine server
 - Flymine test server
 - modMine server
 - Patmine server
 - modENCODE worm server
 - Wormbase server
 - Wormbase test server
 - EuPathDB server
 - EncodeDB at NHGRI
 - EpiGRAPH server
 - EpiGRAPH test server
 - HbVar Human Hemoglobin Variants and Thalassemias
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Unix Tools
- Join, Subtract and Group
- Convert Formats

Reference Feature	Start (-1)	End	DB Xref	Accession
BofuT4_P001930.1	6	198	PF00857	
BofuT4_P003870.1	6	217	PF03443	
BofuT4_P003990.1	3	194	PF06101	
BofuT4_P004830.1	791	819	PF00734	
BofuT4_P004830.1	61	271	PF00933	
BofuT4_P004830.1	353	601	PF01915	
BofuT4_P005160.1	3	283	PF00067	
BofuT4_P006540.1	269	574	PF00732	
BofuT4_P006540.1	815	846	PF00734	
BofuT4_P006540.1	685	801	PF05199	
BofuT4_P007640.1	90	152	PF00775	
BofuT4_P007740.1	22	444	PF00171	
BofuT4_P008190.1	50	386	PF01301	
BofuT4_P008190.1	394	575	PF10435	
BofuT4_P008630.1	80	117	PF08545	
BofuT4_P008630.1	273	365	PF02803	
BofuT4_P010370.1	34	288	PF00657	
BofuT4_P010380.1	26	86	PF05730	
BofuT4_P010920.1	18	164	PF09792	
BofuT4_P011330.1	986	1118	PF00156	
BofuT4_P011330.1	769	847	PF04275	
BofuT4_P011330.1	317	459	PF01565	
BofuT4_P011380.1	1	83	PF03006	
BofuT4_P011810.1	17	140	PF12296	
BofuT4_P012350.1	34	253	PF00701	
BofuT4_P012360.1	17	282	PF00248	
BofuT4_P012400.1	98	374	PF00501	
BofuT4_P012400.1	571	636	PF00550	
BofuT4_P012400.1	680	920	PF07993	
BofuT4_P012420.1	69	441	PF07690	
BofuT4_P013210.1	98	284	PF03235	
BofuT4_P013640.1	0	59	PF04119	
BofuT4_P014290.1	116	195	PF01822	
BofuT4_P014290.1	239	465	PF11790	
BofuT4_P014350.1	62	232	PF01083	
BofuT4_P015800.1	115	295	PF00544	
BofuT4_P016040.1	6	80	PF03992	
BofuT4_P019100.1	173	858	PF03639	
BofuT4_P019510.1	3	309	PF03060	
BofuT4_P020150.1	38	213	PF00106	
BofuT4_P025640.1	38	541	PF00135	
BofuT4_P026680.1	83	537	PF00067	
BofuT4_P026710.1	268	662	PF05592	
BofuT4_P028100.1	54	514	PF00083	
BofuT4_P030610.1	245	392	PF06985	
BofuT4_P030940.1	5	240	PF12138	
BofuT4_P031660.1	287	315	PF00734	
BofuT4_P031660.1	6	234	PF03443	
BofuT4_P032210.1	89	760	PF03169	
BofuT4_P033100.1	529	702	PF08760	
BofuT4_P033780.1	287	312	PF00006	

Get Data :
Load the Biomart result file in
Galaxy

History Options

34: mart_export.txt
228 lines, format: tabular, database: ?
Info: uploaded tabular file

1	2	3	4
Reference Feature	Start (-1)	End	DB Xref Acc
BofuT4_P001930.1	6	198	PF00857
BofuT4_P003870.1	6	217	PF03443
BofuT4_P003990.1	3	194	PF06101
BofuT4_P004830.1	791	819	PF00734
BofuT4_P004830.1	61	271	PF00933

33: gene list
228 lines, format: tabular, database: ?
Info:

BofuT4_P001930.1
BofuT4_P002750.1
BofuT4_P003870.1
BofuT4_P003990.1
BofuT4_P004830.1
BofuT4_P005160.1

32: Select on data 31

31:
Normalized_Data_1.3643098867419643

Join files

Join, Subtract and Group section:
Join the gene list file with Biomart result file by column with gene name

Gene Name	Count 1	Count 2	PFAM Domain
BofuT4_P001930.1		217	PF03443
BofuT4_P002750.1			
BofuT4_P003870.1		194	PF06101
BofuT4_P003990.1		791	PF00734
BofuT4_P004830.1		61	PF00933
BofuT4_P004830.1		353	PF01915
BofuT4_P005160.1		3	PF00067
BofuT4_P005170.1			
BofuT4_P006510.1			
BofuT4_P006540.1	269	574	PF00732
BofuT4_P006540.1	815	846	PF00734
BofuT4_P006540.1	685	801	PF05199
BofuT4_P007640.1	90	152	PF00775
BofuT4_P007740.1	22	444	PF00171
BofuT4_P008190.1	50	386	PF01301
BofuT4_P008190.1	394	575	PF10435
BofuT4_P008630.1	80	117	PF08545
BofuT4_P008630.1	273	365	PF02803
BofuT4_P008670.1			
BofuT4_P008680.1			
BofuT4_P010370.1	34	288	PF00657
BofuT4_P010380.1	26	86	PF05730
BofuT4_P010920.1	18	164	PF09792
BofuT4_P011170.1			
BofuT4_P011330.1	986	1118	PF00156
BofuT4_P011330.1	769	847	PF04275
BofuT4_P011330.1	317	459	PF01565
BofuT4_P011370.1			
BofuT4_P011380.1	1	83	PF03006
BofuT4_P011810.1	17	140	PF12296
BofuT4_P012350.1	34	253	PF00701
BofuT4_P012360.1	17	282	PF00248
BofuT4_P012400.1	98	374	PF00501
BofuT4_P012400.1	571	636	PF00550
BofuT4_P012400.1	680	920	PF07993
BofuT4_P012420.1	69	441	PF07690
BofuT4_P012560.1			
BofuT4_P013210.1	98	284	PF03235
BofuT4_P013310.1			
BofuT4_P013640.1	0	59	PF04119
BofuT4_P014290.1	116	133	PF01822
BofuT4_P014290.1	239	465	PF11790
BofuT4_P014350.1	67	222	PF01383
BofuT4_P015750.1			
BofuT4_P015800.1	115	295	PF00544
BofuT4_P016040.1	6	80	PF03992
BofuT4_P018370.1			
BofuT4_P019100.1	173	858	PF03639
BofuT4_P019510.1	3	309	PF03060
BofuT4_P020150.1	38	213	PF00106
BofuT4_P021150.1			

Blanks are genes without PFAM domain

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http://urgi.versailles.inra.fr/galaxy/

Galaxy URGI - Gene list results BioMart - MartView

Analyze Data Workflow Shared Data Help User

1	BofuT4_P073850.1	PF05378
1	BofuT4_P076160.1	PF05368
1	BofuT4_P080640.1	PF00083
1	BofuT4_P081980.1	PF00106
1	BofuT4_P082390.1	PF00732
1	BofuT4_P086620.1	PF00933
1	BofuT4_P086620.1	PF01915
2	BofuT4_P087430.1	PF00168
1	BofuT4_P090010.1	PF07690
1	BofuT4_P091380.1	PF03443
1	BofuT4_P092510.1	PF07690
1	BofuT4_P093130.1	PF02036
3	BofuT4_P093940.1	PF00023
1	BofuT4_P093940.1	PF05729
1	BofuT4_P096750.1	PF00106
1	BofuT4_P097870.1	PF00246
1	BofuT4_P098790.1	PF00107
1	BofuT4_P098790.1	PF08240
1	BofuT4_P098800.1	PF00122
1	BofuT4_P098800.1	PF00689
1	BofuT4_P098800.1	PF00690
1	BofuT4_P098800.1	PF00702
1	BofuT4_P098960.1	PF01565
1	BofuT4_P098960.1	PF08031
1	BofuT4_P101100.1	PF00106
1	BofuT4_P101740.1	PF00561
1	BofuT4_P102850.1	PF03022
1	BofuT4_P103120.1	PF00657
1	BofuT4_P103800.1	PF00264
1	BofuT4_P103810.1	PF11807
1	BofuT4_P103870.1	PF11807
1	BofuT4_P106980.1	PF00795
5	BofuT4_P107170.1	PF00023
1	BofuT4_P107170.1	PF05729
1	BofuT4_P108520.1	PF01039
1	BofuT4_P108740.1	PF02515
1	BofuT4_P108760.1	PF06985
1	BofuT4_P109330.1	PF03443
1	BofuT4_P112680.1	PF01565
1	BofuT4_P112680.1	PF08031
1	BofuT4_P112910.1	PF00150
1	BofuT4_P113100.1	PF00441
1	BofuT4_P113100.1	PF02770
1	BofuT4_P113100.1	PF02771
1	BofuT4_P114590.1	PF00150
1	BofuT4_P114590.1	PF00734
1	BofuT4_P114590.1	PF03442
1	BofuT4_P115120.1	PF00278
1	BofuT4_P115120.1	PF02784
1	BofuT4_P117020.1	PF08241
1	BofuT4_P117260.1	PF00326
1	BofuT4_P118670.1	PF00150

Tools Options

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Unix Tools
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
 - Summary Statistics for any numerical column
 - Count occurrences of each record
 - Correlation for numeric columns
 - Generate A Matrix for using PC and LDA
 - Perform LDA Linear Discriminant Analysis
 - Draw ROC Receiver Operating Characteristic plot
 - T Test for Two Samples
 - Compute q-values based on multiple simultaneous tests p-values
- Wavelet Analysis
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Metagenomic analyses
- FASTA manipulation
- NGS: OC and manipulation

History Options

39: Count on data 34

33: gene list

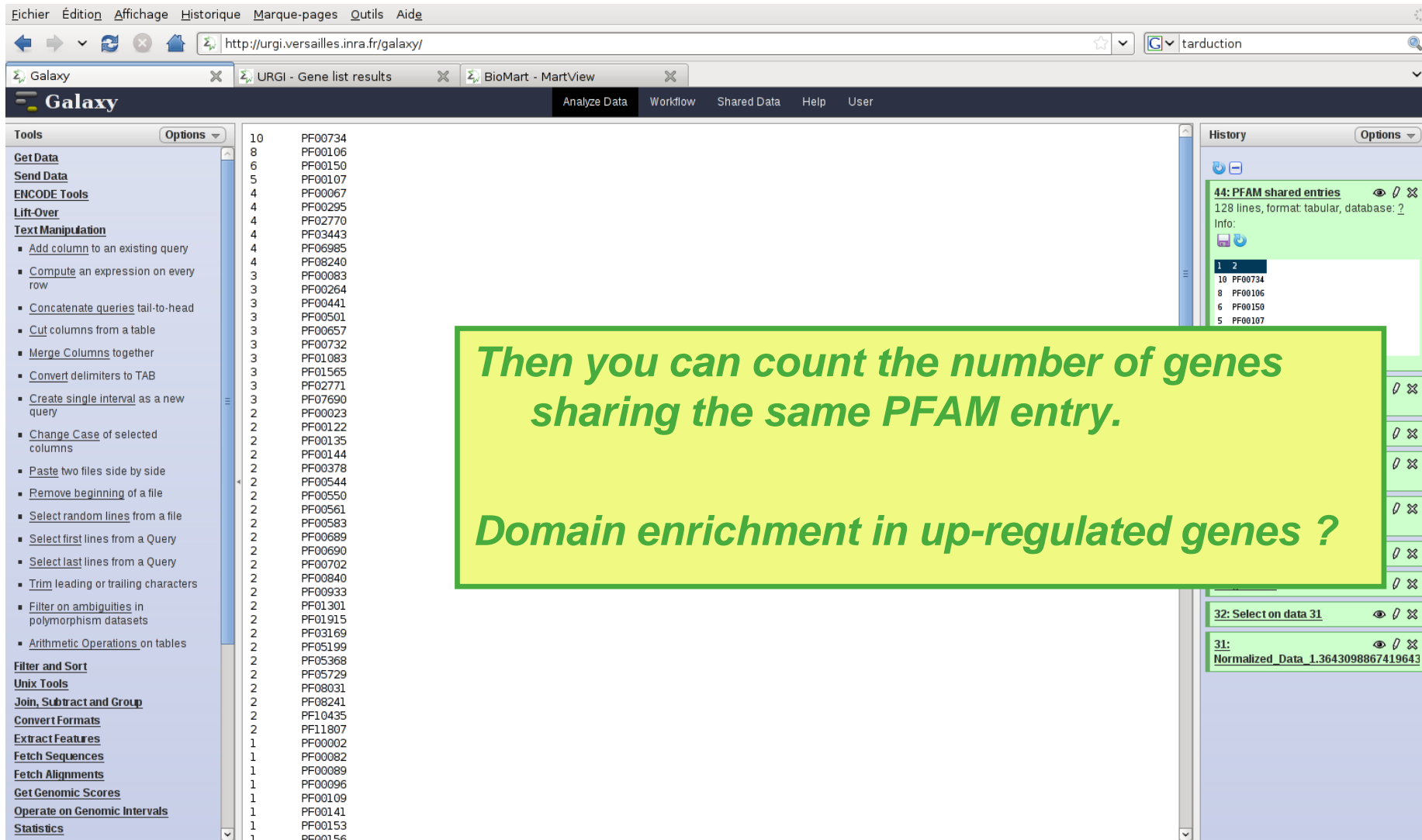
32: Select on data 31

31: Normalized_Data_1.3643098867419643

Statistics section:

From Biomart result, get gene names and PFAM entries. Then count the number of identical PFAM entry / gene.

The aim is to remove duplicates.



The screenshot shows the Galaxy web interface with a table of gene list results. The table has two columns: a count and a PFAM ID. The counts range from 1 to 10, and the PFAM IDs are listed in the second column.

Count	PFAM ID
10	PF00734
8	PF00106
6	PF00150
5	PF00107
4	PF00067
4	PF00295
4	PF02770
4	PF03443
4	PF06985
4	PF08240
3	PF00083
3	PF00264
3	PF00441
3	PF00501
3	PF00657
3	PF00732
3	PF01083
3	PF01565
3	PF02771
3	PF07690
2	PF00023
2	PF00122
2	PF00135
2	PF00144
2	PF00378
2	PF00544
2	PF00550
2	PF00561
2	PF00583
2	PF00689
2	PF00690
2	PF00702
2	PF00840
2	PF00933
2	PF01301
2	PF01915
2	PF03169
2	PF05199
2	PF05368
2	PF05729
2	PF08031
2	PF08241
2	PF10435
2	PF11807
1	PF00002
1	PF00082
1	PF00089
1	PF00096
1	PF00109
1	PF00141
1	PF00153
1	PF00156

The interface also shows a 'Tools' sidebar on the left with various options like 'Get Data', 'Send Data', and 'Statistics'. On the right, there is a 'History' panel showing recent actions like '44: PFAM shared entries' and '32: Select on data 31'.

Then you can count the number of genes sharing the same PFAM entry.

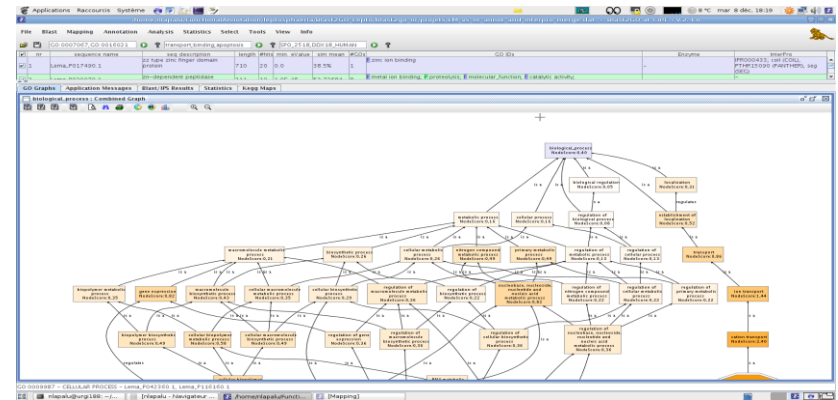
Domain enrichment in up-regulated genes ?

Gene Ontology Analysis:

Blast2GO

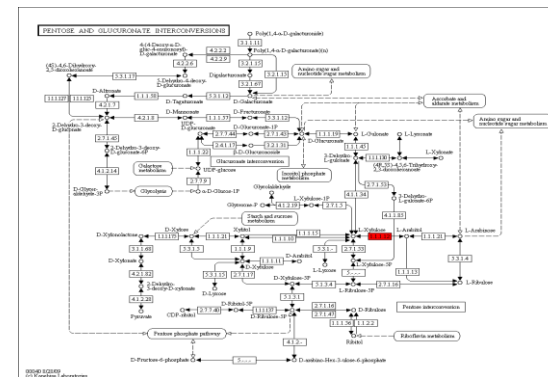
Aim:

- GO annotation from Blast Results and Identified domains (Ana Conesa, et al, Bioinformatics, Sept 2005)



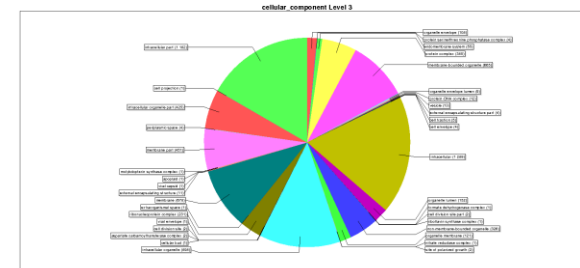
Export:

- annotations, table
- full project (re-usable data)



Display:

- blast statistics
- GO distributions
- kegg map



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- Venturia
- Arabidopsis
- Oryza
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Genomic sequences

- [bt4_supctq.fsa.gz](#) (11.34 MB) Botrytis T4 Supercontigs
- [bt4_ctq.fsa.gz](#) (11.29 MB) Botrytis T4 contigs (virtual contigs extracted from supercontigs after final assembly they are separated by gap of at least one nucleotide N)
- [bt4_ctq_exclus.fsa.gz](#) (667.17 kB) Botrytis T4 excluded contigs (from excluded supercontigs (length < 20Kb or Ns > 10%))

Genes

- [BofuT4_orfnucall_1.fsa.gz](#) (5.32 MB) Botrytis T4 predicted genes:
It contains reliable and unreliable Eugene predicted gene (without UTRs)
BofuT4_Pxxxxx.1 : gene with length > 300 Nucl OR (gene with length < 300 aa with EST Evidence)
BofuT4_uPxxxxx.1 : gene with length < 300 aa without EST evidence (at the time of prediction pipeline))
- [BofuT4_orfprotall_1.fsa.gz](#) (3.45 MB) Botrytis T4 predicted protein:
It contains reliable and unreliable Eugene predicted protein
BofuT4_Pxxxxx.1 : protein with length > 100 aa OR (protein with length < 100 aa with EST Evidence)
BofuT4_uPxxxxx.1 : protein with length < 100 aa without EST evidence (at the time of prediction pipeline))
- [Bot_chips.fsa.gz](#) (6.00 MB) Botrytis T4 (genes and ESTs) and B05.10 (genes) sequences used for Botrytis Nimblegen design

Supplementary downloads

- [bt4_supctq_ctq.fsa.off.gz](#) (11.34 MB) Gff file for Botrytis T4 contigs mapping on supercontig
- [bt4_ctq_supctq_coordinates.gz](#) (26.59 kB) Botrytis T4 contigs mapping on supercontig
- [bt4_ctq_supctq_size.gz](#) (14.98 kB) Botrytis T4 contigs and supercontig sizes
- [BofuT4_orfnucall_1.cusp.gz](#) (1.04 kB) Codon usage table calculated on Botrytis T4 genes (BofuT4_orfallnuc_1.fsa)
- [blast2go_botrytis.dat](#) (20.45 MB) Blast2GO project (Gene Ontologie Annotation)

Download
project

Blast2GO


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http://blast2go.org/start_blast2go

- Downloads/Docu
- B2G in Papers
- B2G-FAR
- B2G Courses

Blast2GO Survey



INSTALL JAVA:
The minimum requirement to run Blast2GO is a working Java installation (version > 1.5) (on Win,Linux,Mac etc.) In case you do not have that already please install the actual Java Runtime Environment (JRE) from <http://www.java.com/download>

JAVA WEB START
By Java Web Start technology (which is included in JAVA) you will be provided with the latest Blast2GO update each time you start the application. If your browser hasn't been set up to run Java WebStart JNLP files, the link above will download a file called blast2go_cipf.jnlp. Some browsers will ask you what you want to do with the JNLP file (instead of automatically downloading it somewhere, or presenting it to you as text). If a dialog appears with "Open using application..." on it, use the javaws application to run your file (and check the box marked "Don't ask me again"):

- <path to java runtime installation>/bin/javaws
- <path to jdk installation>/jre/bin/javaws
- javaws.exe

Download Blast2GO

Please select the amount of your system memory (RAM) to improve the performance of Blast2GO:

Please select:						
256 MB	512 MB	1000 MB	1500 MB	1800 MB	2000 MB	3000 MB
very small projects	default	> 10000 seqs	> 15000 seqs	> 20000 seqs	> 25000 seqs and 64 bit CPU	> 40000 seqs and 64 bit CPU

Blast2GO needs more memory? → Use the dynamic memory JNLP URL:
<http://bioinfo.cipf.es/blast2go/webstart/makejnlp.php?mem=<put here the amount of memory you need>>

Blast2GO Database Issues

To connect to the B2G database you (your computer settings, your personal firewall) and your institute (institutes firewall, providers network settings) has to permit outgoing tcp connections on port 3306. Normally outgoing connections of this type are always permitted unless you have a highly restrictive network policy. (To easily test if B2G works fine press one of the green arrows in the B2G main frame, some GO graphs should appear more or less instantly).

- The current DB is called **b2g_jun11**, older one: b2g_may10
- The database server IP is: **80.86.82.44**
- Older DBs: b2g_may10 at 193.144.127.204

Other Blast2GO database servers with the possibility to request access

Location	Institution	Version (Month/Year)	Contact	E-Mail
Indiana, USA	Purdue University	09/2009	Rick Westerman	westerman(at)purdue(dot)edu

http://www.blast2go.org/start_blast2go

Blast2GO

Menu: File > Load B2G-Project > Blast2go_botrytis.dat

C:\Users\Nicolas Lapalu\Downloa

File Blast Mapping Annota

GO:0007067,GO:0016021

<input type="checkbox"/>	nr	sequence name	seq description	length	#hits	min. eValue	sim mean	#GOS	GO IDs	Enzyme	InterPro
<input type="checkbox"/>	1	BofuT4_P000020.1	het domain protein	753	20	0,0E0	66.1%	0			IPR002110; IPR010730; G3D.1.25.40.20 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF302 (PANTHER)
<input checked="" type="checkbox"/>	2	BofuT4_P000030.1	hypothetical protein BC1G_08771 [Botryotinia fuckeliana B05.10]	530	20	0,0E0	64.55%	3	F:ATP binding; P:metabolic process; F:catalytic activity		SSF51735 (SUPERFAMILY), SSF56059 (SUPERFAMILY)
<input checked="" type="checkbox"/>	3	BofuT4_P000040.1	predicted protein [Botryotinia fuckeliana B05.10]	742	3	0,0E0	86.333333...	7	P:fatty acid biosynthetic process; F:holo-[acyl-carrier-protein] synthase activity; P:macromolecule biosynthetic process; C:intracellular; F:magnesium ion binding; F:zinc ion binding; P:pantothenate biosynthetic process	EC:2.7.8.7	IPR001876; IPR004568; IPR008278; coil (COIL), seg (SEG), SSF54928 (SUPERFAMILY), SSF90209 (SUPERFAMILY)
<input type="checkbox"/>	4	BofuT4_P000050.1	hypothetical protein BC1G_08769 [Botryotinia fuckeliana B05.10]	292	20	0,0E0	71.15%	2	F:molecular_function; P:biological_process		IPR013920; SSF88633 (SUPERFAMILY)
<input checked="" type="checkbox"/>	5	BofuT4_P000070.1	lamina-associated polypeptide 2	387	20	0,0E0	84.25%	3	F:inositol or phosphatidylinositol phosphatase activity; P:proteolysis; F:aminopeptidase activity	EC:3.4.11.0	IPR007484; G3D.3.40.630.10 (GENE3D), seg (SEG), SSF54433 (SUPERFAMILY)

GO Graphs Application Messages Blast/IPS Results Statistics Kegg Maps

Blast2GO - Latest updates!

- Please visit B2G-FAR: The Blast2GO Functional Annotation Repository (<http://www.b2gfar.org>)
- Please help to improve B2G. Suggest and vote new ideas at <http://blast2go.uservice.com>
- A new SELECT menu to filter/query your data-set for InterProScan results:
- Try the new Keyboard shortcuts
- Find more information in the BlastResult table (frame, hit/query ratio...)
- We added automatic internet browser detection
- Improved interface for the enrichment results export, filtering and visualization
- Export pie and bar charts in plain text-format
- Find a new Java memory monitor under TOOLS

Extract list of genes:

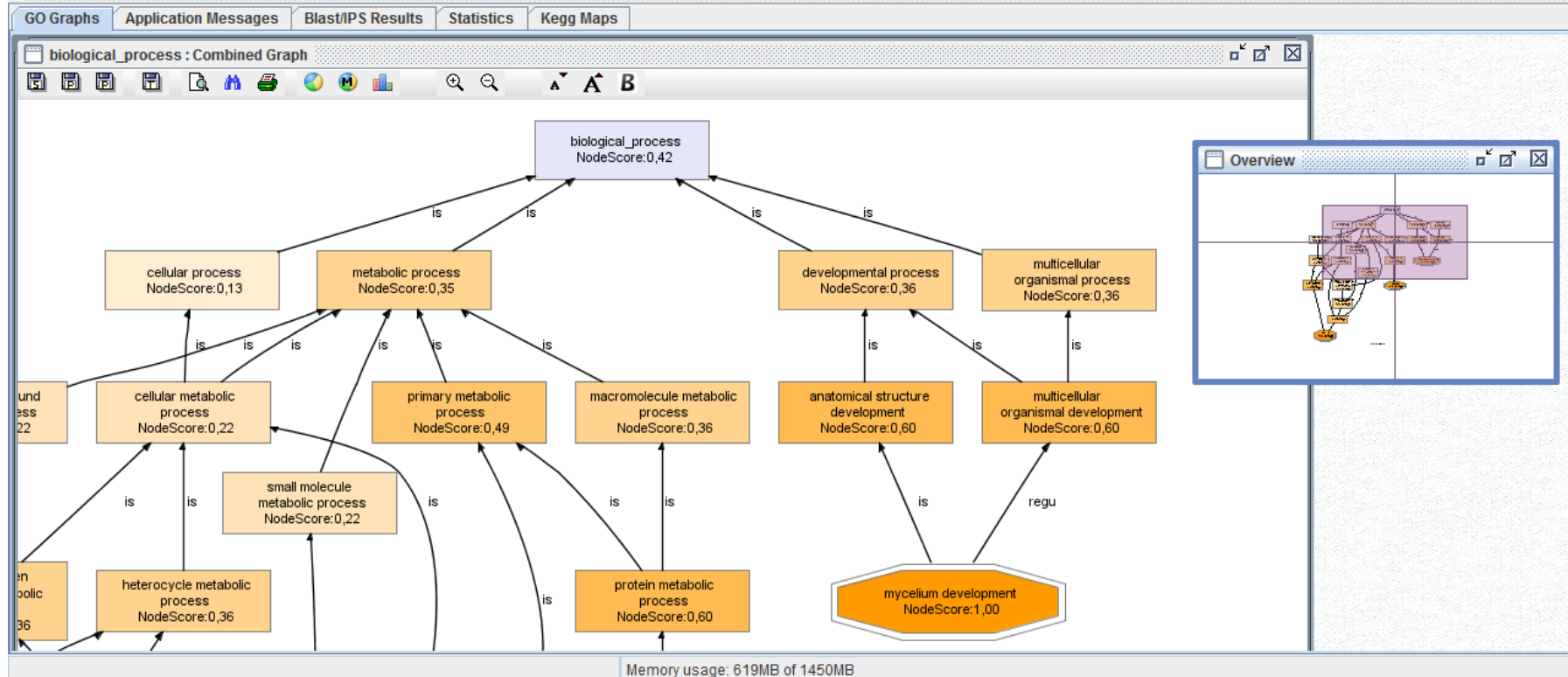
- enrichment analysis

C:\Users\Nicolas Lapalu\Downloads\blast2go_botrytis.dat - Blast2GO V.2.5.0

File Blast Mapping Annotation Analysis Statistics Select Tools View Support

GO:0007067,GO:0016021

nr	sequence name	seq description	length	#hits	min. eValue	sim mean	#GOs	GO IDs	Enzyme	InterPro
1	BofuT4_P000020.1	het domain protein	753	20	0,0E0	66.1%	0			IPR002110; IPR010730; G3D:1.25.40.20 (GENE3D), PTHR18958 (PANTHER), PTHR18958:SF302 (PANTHER)



C:\Users\Nicolas Lapalu\Downloads\blast2go_botrytis.dat - Blast2GO V.2.5.0

File Blast Mapping Annotation Analysis Statistics Select Tools View Support

GO:0007067,GO:0016021

nr	sequence name	seq description	length	#hits	min. eValue	sim mean	#GOs	GO IDs	Enzyme	InterPro
5	BofuT4_P000070.1	lamina-associated polypeptide 2	387	20	0,0E0	84.25%	3	F:inositol or phosphatidylinositol phosphatase activity; P:proteolysis; F:aminopeptidase activity	EC:3.4.11.0	IPR007484; G3D:3.40.630.10 (GENE3D), seg (SEG), SSF53187 (SUPERFAMILY)
6	BofuT4_P000080.1	hypothetical protein SS1G_08619 Sclerotinia sclerotiorum	318	20	0,0E0	76.35%	1	P:mycelium development	-	coil (COIL), seg (SEG), SSF82708 (SUPERFAMILY)

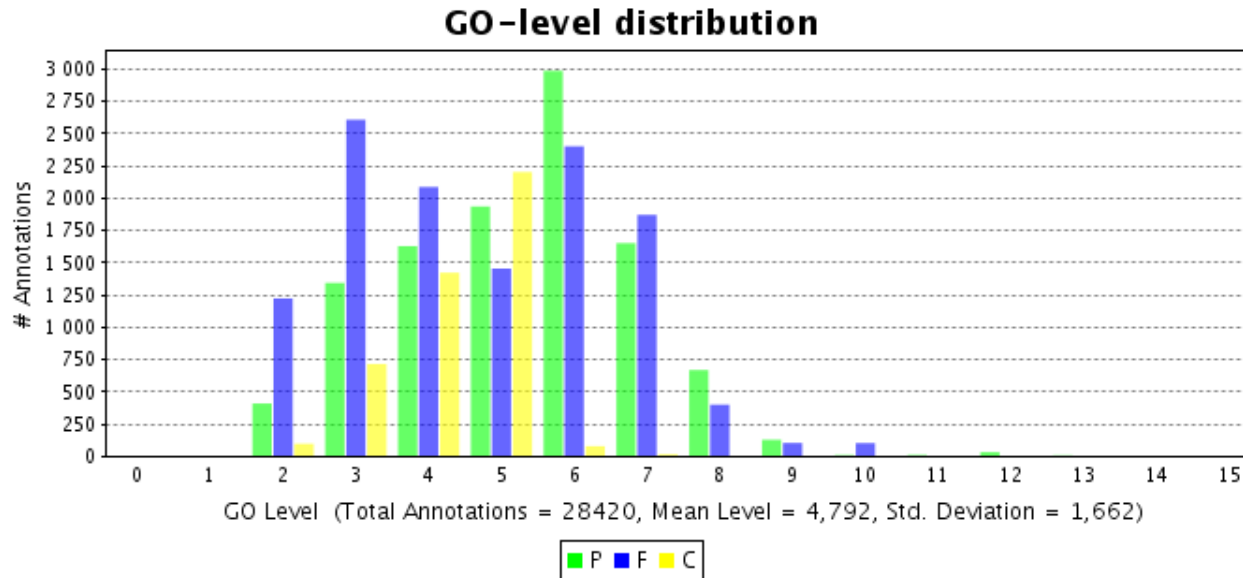
GO Graphs Application Messages Blast/IPS Results Statistics **Kegg Maps**

Enzyme: ec:3.6.1.3 - adenosinetriphosphatase

Sequences: BofuT4_P000090.1

Purine Pathways (KEGG Map):
BofuT4_P000090.1 -> EC 3.6.1.3

Project statistics



annotations	28420
annotated sequences	7316
Mean GO level	4.792
GO Standard deviation	1.662
number of Enzyme Codes	2567
sequences with EC	2229

Blast environment and further analysis

Mobyle Blast

Mobyle Blast-Koriviewer

SRS

Mobyle

<div data-bbox="92 468 517 885"> <p>Programs</p> <input type="text"/> <input type="button" value="Search"/></div> <div data-bbox="92 539 305 656"> <ul style="list-style-type: none"> ▼ blast <ul style="list-style-type: none"> ○ blast2 ○ blast2-koriviewer ▶ blat ▶ extractseq </div> <div data-bbox="92 678 517 706"> <p>Data Bookmarks refresh</p> </div> <div data-bbox="92 714 517 742"> <p>Jobs refresh</p> </div> <div data-bbox="92 749 517 885"> <p>Tutorials refresh</p> <ul style="list-style-type: none"> How to use Mobyle? A step by step tutorial Sequence formats Alignment formats </div>	<div data-bbox="537 468 1814 885"> <p style="text-align: center;">Welcome to Mobyle, a portal for bioinformatics analyses</p> <div style="display: flex; justify-content: space-around; border-bottom: 1px solid black; margin-bottom: 10px;"> Welcome Programs Data Bookmarks Jobs Tutorials </div> <div style="border: 1px solid black; padding: 5px; margin-bottom: 10px;"> <p>Select an analysis in the Programs menu.</p> </div> <div style="border: 1px solid black; padding: 5px;"> <p>Tutorials are available. See our interactive guided tour.</p> </div> <p>Credits</p> <p>Mobyle is a platform developed jointly by the Institut Pasteur "Logiciels et Banques de Données" Team and the Ressource Parisienne en Bioinformatique Structurale. More information about this project can be found here.</p> </div>
--	--

<http://urgi/mobyle/cgi-bin/portal.py?form=blast2>

Mobylye

([guest](#))
[set email](#) | [sign-out](#)

Programs

▼ blast
 ○ blast2
 ○ blast2-koriviewer
▶ blat
▶ extractseq

Data Bookmarks

Jobs refresh

Tutorials refresh

[How to use Mobylye? A step by step tutorial](#)
[Sequence formats](#)
[Alignment formats](#)

Welcome | **Programs** | Data Bookmarks | Jobs | Tutorials

BLAST2 x

BLAST2

NCBI BLAST, with gaps

* Blast program (-p) ?

Database

Protein db (-d) ?

Nucleotid db (-d) ?

Query Sequence

* Query (-i) (Sequence) ?

Paste | File

Start of required region in query sequence (-L) ?

End of required region in query sequence (-L) ?

Number of concatenated queries (blastn or tblastn) (-B)

Scoring options

Cost to open a gap (-G) ?

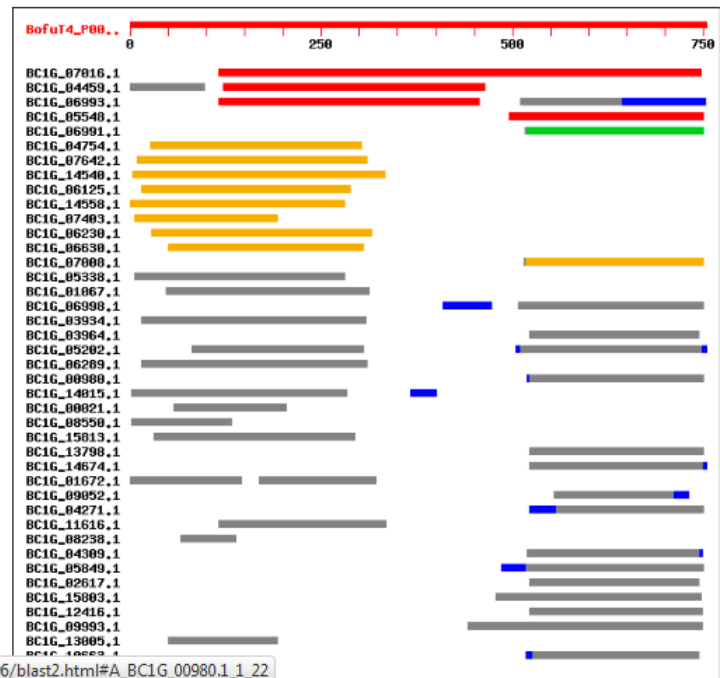
Cost to extend a gap (-E) ?

Protein penalty (not for blastn)

Blast Result

BC1G_000711.1	hypothetical protein (translation)	33	0.15
BC1G_12943.1	hypothetical protein (translation)	34	0.15
BC1G_02595.1	hypothetical protein (translation)	33	0.19
BC1G_12741.1	hypothetical protein (translation)	33	0.28
BC1G_06261.1	hypothetical protein (translation)	33	0.29
BC1G_08139.1	hypothetical protein (translation)	33	0.31
BC1G_04895.1	hypothetical protein (translation)	33	0.38
BC1G_01191.1	hypothetical protein (translation)	33	0.38
BC1G_05929.1	hypothetical protein (translation)	32	0.47
BC1G_09479.1	hypothetical protein (translation)	32	0.51
BC1G_16152.1	hypothetical protein (translation)	32	0.55
BC1G_03492.1	hypothetical protein (translation)	32	0.55
BC1G_02711.1	hypothetical protein (translation)	32	0.59
BC1G_04226.1	hypothetical protein (translation)	31	1.1
BC1G_14609.1	hypothetical protein (translation)	31	1.3
BC1G_12527.1	hypothetical protein (translation)	30	3.0
BC1G_03609.1	hypothetical protein (translation)	29	4.8
BC1G_03476.1	predicted protein (translation)	29	5.0
BC1G_06440.1	hypothetical protein (translation)	29	5.1
BC1G_12528.1	hypothetical protein (translation)	29	5.6
BC1G_14865.1	hypothetical protein (translation)	28	6.3
BC1G_12502.1	hypothetical protein (translation)	28	6.6
BC1G_14004.1	hypothetical protein (translation)	28	8.4
BC1G_03296.1	hypothetical protein (translation)	28	8.4
BC1G_02615.1	predicted protein (translation)	28	8.9

usual display -> html, text



http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2/U12797899396896/blast2.html#A_BC1G_00980.1_1_22

Mobyle

Programs

- ▼ blast
 - blast2
 - blast2-koriviewer
- ▶ blat
- ▶ extractseq

Data Bookmarks

Sequence: query_seq.data

Jobs

- ✓ blast2 - 09/07/11 11:47:44
- ✓ blast2 - 09/07/11 11:48:32
- ✓ blast2-koriviewer - 09/07/11 11:50:13

Tutorials

- [How to use Mobyle? A step by step tutorial](#)
- [Sequence formats](#)
- [Alignment formats](#)

[Welcome](#) | [Programs](#) | [Data Bookmarks](#) | [Jobs](#) | [Tutorials](#)

blast2-koriviewer 09/07/11 11:50:13 × blast2 09/07/11 11:47:44 ×

<http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2/U12797899396896>

results

Blast text report (BlastTextOutput)

blast2.txt

"Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= BofuT4_P000020.1 | 753 aa
 (753 letters)

as: blast2.txt

Blast html report (BlastHtmlOutput)

... Madden, Alejandro A. Schaffer,
 ... and David J. Lipman (1997),
 ... tion of protein database search
 ... 02.
 ... adjustment: Altschul, Stephen F.,

Job management during one session.

Allow to Re-do jobs with different parameters

Mobyle

<div data-bbox="92 468 517 885"> <p>Programs</p> <input type="text"/> <input type="button" value="Search"/></div> <div data-bbox="92 539 517 664"> <ul style="list-style-type: none"> ▼ blast <ul style="list-style-type: none"> ○ blast2 ○ blast2-koriviewer ▶ blat ▶ extractseq </div> <div data-bbox="92 678 517 706"> <p>Data Bookmarks refresh</p> </div> <div data-bbox="92 721 517 749"> <p>Jobs refresh</p> </div> <div data-bbox="92 763 517 878"> <p>Tutorials refresh</p> <ul style="list-style-type: none"> How to use Mobyle? A step by step tutorial Sequence formats Alignment formats </div>	<div data-bbox="537 468 1810 492"> <p> Welcome Programs Data Bookmarks Jobs Tutorials </p> </div> <div data-bbox="537 506 1810 549" style="text-align: center;"> <p>Welcome to Mobyle, a portal for bioinformatics analyses</p> </div> <div data-bbox="537 564 1284 763"> <div style="border: 1px solid black; padding: 5px; margin-bottom: 10px;"> <p>← Select an analysis in the Programs menu.</p> </div> <div style="border: 1px solid black; padding: 5px;"> <p>← Tutorials are available. See our interactive guided tour.</p> </div> </div> <div data-bbox="537 771 1810 871"> <p>Credits</p> <p>Mobyle is a platform developed jointly by the Institut Pasteur "Logiciels et Banques de Données" Team and the Ressource Parisienne en Bioinformatique Structurale. More information about this project can be found here.</p> </div>
--	---

<http://urgi/mobyle/cgi-bin/portal.py?form=blast2-koriviewer>

Launch Koriviewer

nicolas.lapalu@versailles.inra.fr (guest)
[set email](#) | [sign-out](#)

Mobyle

Programs

Search

- blast
 - blast2
 - blast2-koriviewer
- blat
- extractseq

Data Bookmarks

Sequence: query_seq.data refresh

Jobs

- blast2 - 09/13/11 10:17:39 refresh
- blast2-koriviewer - 09/13/11 10:18:07

Tutorials

- [How to use Mobyle? A step by step tutorial](#)
- [Sequence formats](#)
- [Alignment formats](#)

Welcome Programs Data Bookmarks Jobs Tutorials

blast2 09/13/11 10:17:39 x blast2-koriviewer 09/13/11 10:18:07 x

✓ <http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2-koriviewer/Q21332044632912>

update job status ask for help back to program form remove this job

results

Click to run koriviewer (HtmlOutput)

koriviewer.html save

Click to run Koriviewer

full screen view bookmark as: koriviewer.h

parameters

Query (-i) (Sequence)

file	format detection program	re-formatted file
query_seq_data.ori (RAW format)	squizz	query_seq_data.fasta (FASTA format)

Blast program (-p) (Choice)
Value: blastp

Protein db (-d) (Choice)
Value: BofuT4_orfprotall_1

Command line

```
echo \

```

Html link :
Download and run
Koriviewer

KoriViewerWS - [urgi.versailles.inra.fr]

BLAST results

result_3
blastp vs. B051...
BofuT4_P0000...

Analyse

Preferences

Help and Tutorial

URGI

Hits

Results for: Seq 1: 119 hits Hits: 119 HSPs: 252

List Conserved regions Alignment & Tree Position Specific Matrix Taxonomy

#	Accession	Definition	Quality	# HSPs
1	7015	BC1G_07016.1 hypothetical protein (translation)	😊	4
2	4458	BC1G_04459.1 hypothetical protein (translation)	😊	2
3	6992	BC1G_06993.1 hypothetical protein (translation)	😊	7
4	5547	BC1G_05548.1 hypothetical protein (translation)	😊	7
5	6990	BC1G_06991.1 hypothetical protein (translation)	😊	3
6	4753	BC1G_04754.1 hypothetical protein (translation)	😊	1
7	7641	BC1G_07642.1 hypothetical protein (translation)	😊	1
8	14539	BC1G_14540.1 hypothetical protein (translation)	😊	1
9	6124	BC1G_06125.1 hypothetical protein (translation)	😊	1
10	14557	BC1G_14558.1 hypothetical protein (translation)	😊	1
11	7402	BC1G_07403.1 hypothetical protein (translation)	😊	1
12	6229	BC1G_06230.1 hypothetical protein (translation)	😊	1
13	6629	BC1G_06630.1 hypothetical protein (translation)	😊	1
14	7007	BC1G_07008.1 hypothetical protein (translation)	😊	8
15	5337	BC1G_05338.1 hypothetical protein (translation)	😊	1
16	1066	BC1G_01067.1 hypothetical protein (translation)	😊	1
17	6997	BC1G_06998.1 hypothetical protein (translation)	😊	5
18	3933	BC1G_03934.1 hypothetical protein (translation)	😊	1
19	3963	BC1G_03964.1 hypothetical protein (translation)	😊	6
20	5201	BC1G_05202.1 hypothetical protein (translation)	😊	8
21	6288	BC1G_06289.1 hypothetical protein (translation)	😊	1
22	979	BC1G_00980.1 hypothetical protein (translation)	😊	7
23	14014	BC1G_14015.1 hypothetical protein (translation)	😊	2
24	20	BC1G_00021.1 hypothetical protein (translation)	😊	1
25	8549	BC1G_08550.1 hypothetical protein (translation)	😊	1
26	15812	BC1G_15813.1 hypothetical protein (translation)	😊	1
27	13797	BC1G_13798.1 hypothetical protein (translation)	😊	2
28	14673	BC1G_14674.1 hypothetical protein (translation)	😊	5
29	1671	BC1G_01672.1 hypothetical protein (translation)	😊	2
30	9051	BC1G_09052.1 hypothetical protein (translation)	😊	3
31	4270	BC1G_04271.1 hypothetical protein (translation)	😊	5
32	11615	BC1G_11616.1 hypothetical protein (translation)	😊	1
33	8237	BC1G_08238.1 hypothetical protein (translation)	😊	1

Alignment: Query (753 aa) vs. 6229 (464 aa)

Loading: <http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2-koriviewer/R12820310177088/blast2.xml>

49Mo/123Mo

See conserved regions

KoriviewerWS - [urgi.versailles.inra.fr]

BLAST results
result_3
blastp vs. B051...
BofuT4_P0000...

Analyse

Hits

Results for: Seq 1: 119 hits Hits: 119 HSPs: 252

List Conserved regions Alignment & Tree Position Specific Matrix Taxonomy

#	Hit	HSP	E-Value	Query From	Query To	Hit From	Hit To
12	6229	1	2,E-24	29	316	45	359
13	6629	1	3,E-24	50	306	114	380
14	7007	1	7,E-23	518	750	542	768
14	7007	2	2,E-21	515	750	406	669
14	7007	3	1,E-19	516	750	442	702
14	7007	4	2,E-19	526	711	813	994
14	7007	5	1,E-18	518	750	707	933
14	7007	6	2,E-18	526	750	747	966
14	7007	7	9,E-15	580	750	404	570
14	7007	8	4,E-7	526	725	912	1160
15	5337	1	3,E-21	7	280	11	338
16	1066	1	6,E-21	47	313	118	384
17	6997	1	9,E-21	508	750	748	981
17	6997	2	2,E-18	518	750	850	1080

Sort by: Hit order Display: Ungroup HSPs Header: Identities Features:

Alignment: Query (753 aa) vs. 6229 (464 aa)

HSP Map Definition Statistics Alignment Features SeqInfo Status

Query: from 29 to 316
6229: from 45 to 359
length: 321

30 40 50 60 70 80 90 100 110

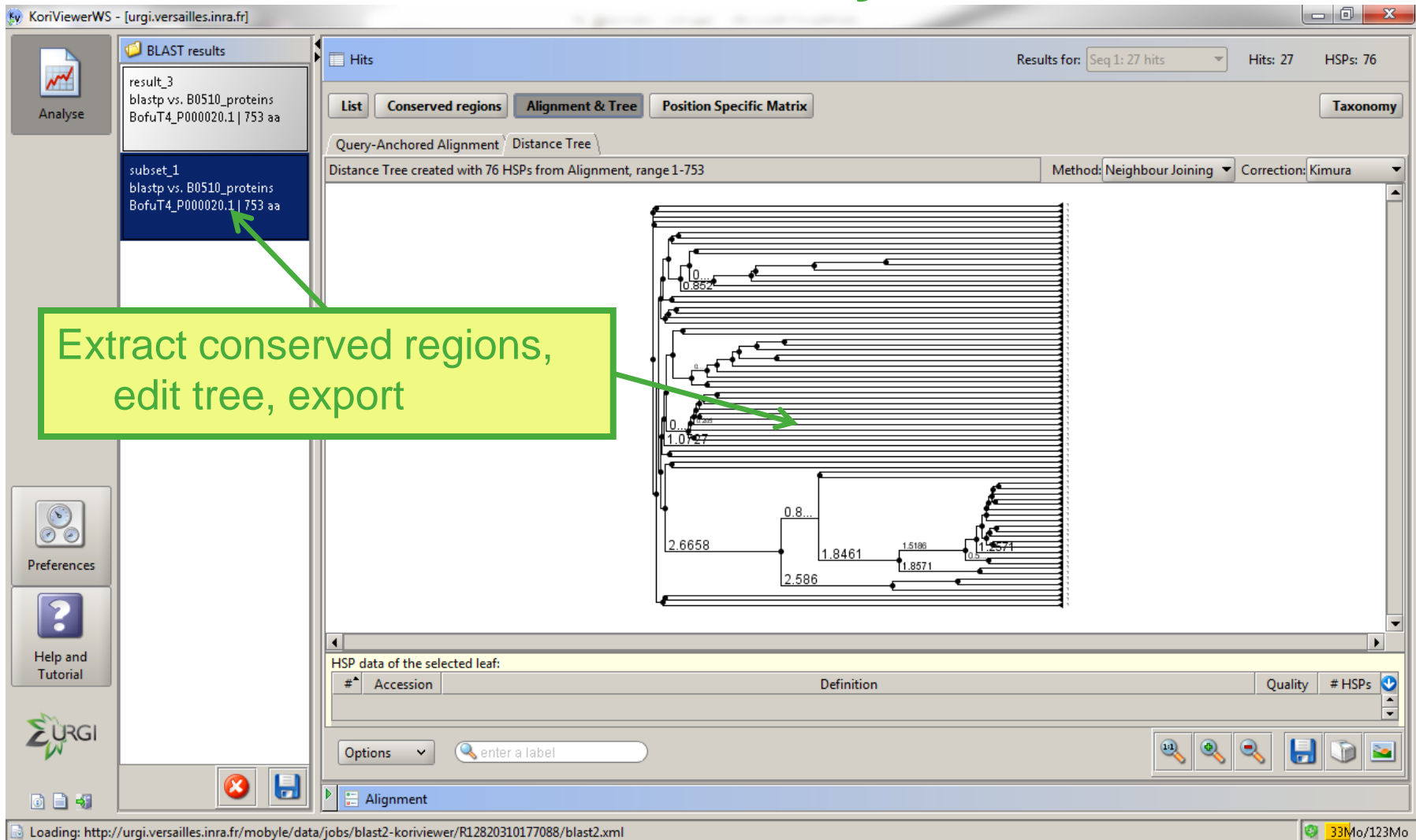
A P L H C E L R D Y S L - Q R S T P R T H L Y E A L S Y V W G D P H N T L P I S V N E K Q F Q V T I N L H D A L L R L R D H S F E R I L W V
+ P L C S L + L + N P Y A L S Y V W G D + N + V + E K + L + L R D + + + W
S P L S C L I H S N L F Y C + R P L I D N Y S A L S Y V W G D A N N R K T V L V D E K + L L V S A S L D L A L R L R D S K K D I M I W A

HSP: 1/1

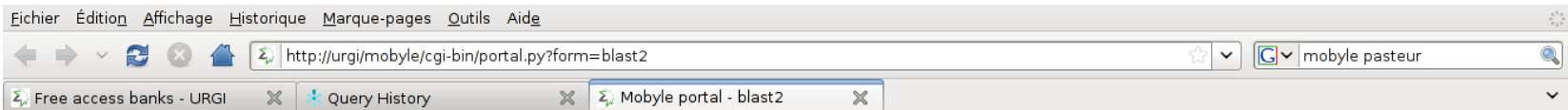
Loading: http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2-koriviewer/R12820310177088/blast2.xml

17Mo/123Mo

See conserved regions...
Browse the alignment



The screenshot shows the KoriViewerWS interface. On the left, under 'BLAST results', two entries are listed: 'result_3' and 'subset_1'. 'subset_1' is highlighted in blue, and a green arrow points from a callout box to it. The callout box contains the text: 'Extract conserved regions, edit tree, export'. Another green arrow points from the callout box to a distance tree in the main area. The tree is titled 'Distance Tree created with 76 HSPs from Alignment, range 1-753'. Below the tree, there is a table for 'HSP data of the selected leaf:' with columns for '#', 'Accession', 'Definition', 'Quality', and '# HSPs'. The bottom status bar shows the URL: 'http://urgi.versailles.inra.fr/mobyle/data/jobs/blast2-koriviewer/R12820310177088/blast2.xml' and system information: '33Mo/123Mo'.



nicolaslap@versailles.fr (guest)
[set email](#) | [sign-out](#)

Mobyle

Programs

Search

- blast
- blat
- extractseq
 - extractseq-urgi

Data Bookmarks

Sequence: query_seq.data refresh

Jobs

blast2 - 09/09/11 17:21:56 refresh

Tutorials

- [How to use Mobyle? A step by step tutorial](#)
- [Sequence formats](#)
- [Alignment formats](#)

Welcome Programs Data Bookmarks Jobs Tutorials

BLAST2 x extractseq-urgi x

extractseq-urgi

Reset Help Pages

Extract regions from an URGI databank

Run

* Database: Plantgene non redundant proteins (february 2003)

Required section

- * Sequence ID
- * Regions to extract ?

Additional section

Write regions to separate sequences ?

Output section

Name of the output sequence file (outseq)

Choose the sequence output format

* : mandatory parameter

Reference: <http://emboss.sourceforge.net/>

Author(s): EMBOSS

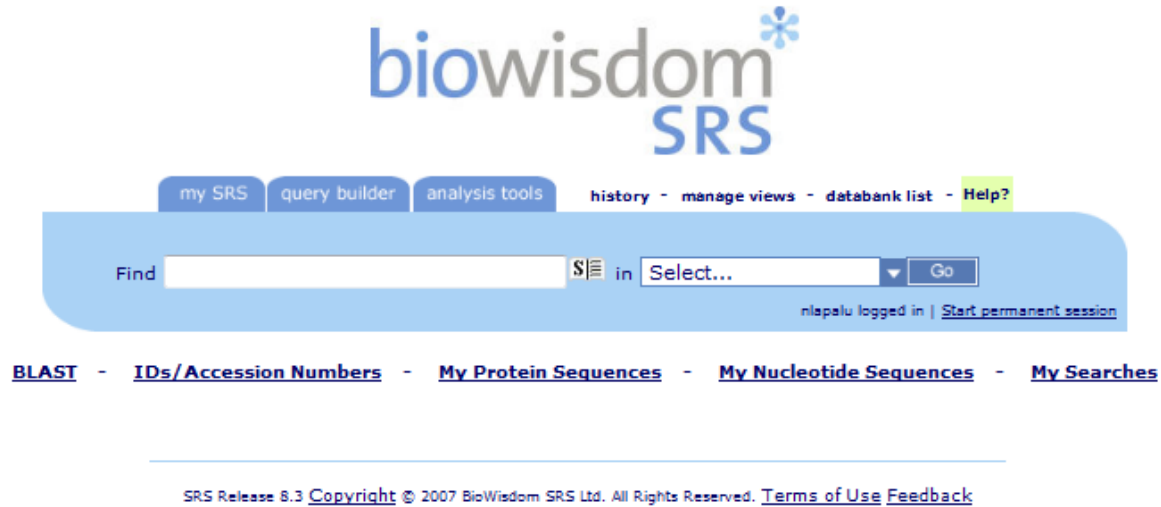
Program help pages:

- <http://bioweb2.pasteur.fr/docs/EMBOSS/extractseq.html>

Other tool interfaces:

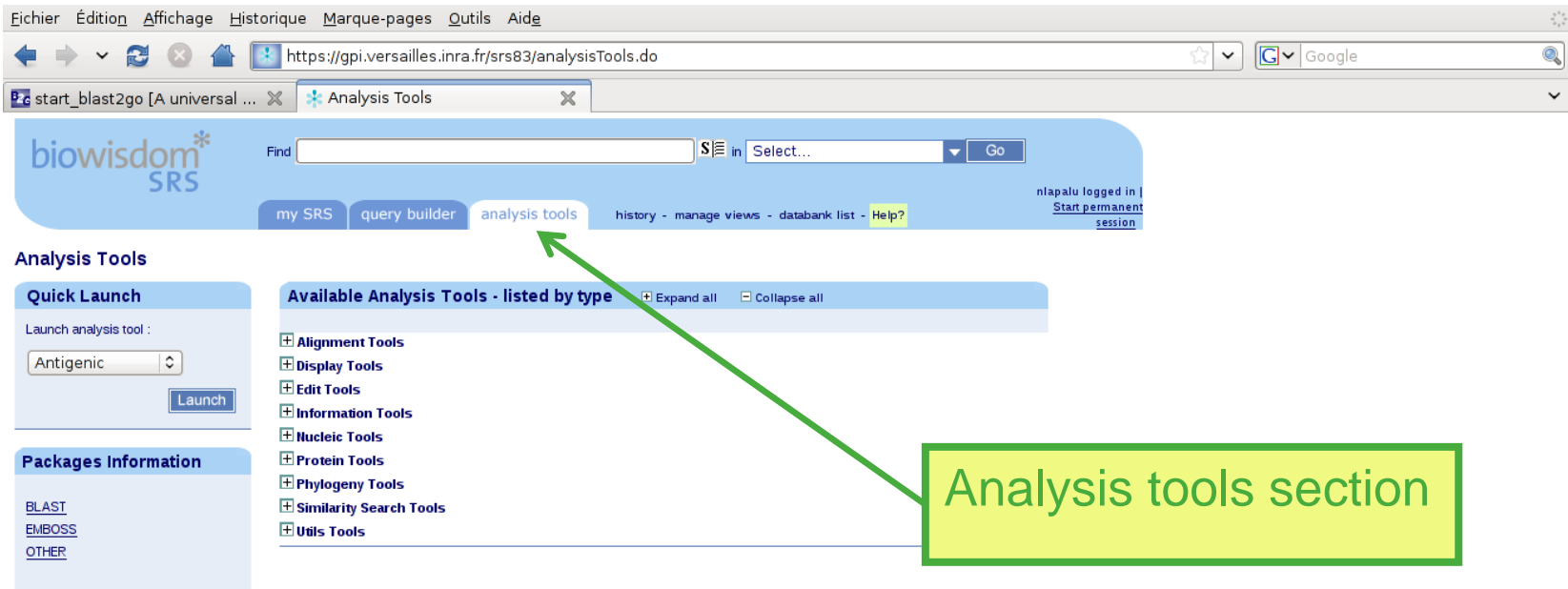
- Blat vs EST
- Extract Sequence

SRS : Databanks and tools



The screenshot shows the BioWisdom SRS web interface. At the top, the logo "biowisdom SRS" is displayed in blue. Below the logo is a navigation bar with several tabs: "my SRS", "query builder", "analysis tools", "history", "manage views", "databank list", and "Help?". The "Help?" tab is highlighted in yellow. Below the navigation bar is a search bar with the text "Find" on the left, a text input field, a dropdown menu with "S" and "in" and "Select..." options, and a "Go" button. Below the search bar, it says "nlapalu logged in | [Start permanent session](#)". At the bottom of the page, there is a horizontal line and a footer with the text "SRS Release 8.3 Copyright © 2007 BioWisdom SRS Ltd. All Rights Reserved. [Terms of Use](#) [Feedback](#)".

<https://gpi.versailles.inra.fr/srs83>



Fichier Édition Affichage Historique Marque-pages Outils Aide

https://gpi.versailles.inra.fr/srs83/analysisTools.do

start_blast2go [A universal ...] Analysis Tools

biowisdom SRS

Find S in Select... Go

my SRS query builder **analysis tools** history - manage views - databank list - Help?

nlapalu logged in | [Start permanent session](#)

Analysis Tools

Quick Launch

Launch analysis tool :

Antigenic

Launch

Packages Information

[BLAST](#)

[EMBOSS](#)

[OTHER](#)

Available Analysis Tools - listed by type Expand all Collapse all

- Alignment Tools
- Display Tools
- Edit Tools
- Information Tools
- Nucleic Tools
- Protein Tools
- Phylogeny Tools
- Similarity Search Tools
- Utils Tools

Analysis tools section

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[Fichier](#) [Édition](#) [Affichage](#) [Historique](#) [Marque-pages](#) [Outils](#) [Aide](#)

[https://gpi.versailles.inra.fr/srs83/packageinfo.do?packageName=BLAST](#)

[start_blast2go](#) [A universal ...] [Package Information](#)

biowisdom
SRS

Find [S](#) in [Select...](#) [Go](#)

[my SRS](#) [query builder](#) [analysis tools](#) [history - manage views - databank list - Help?](#)

nlapalu logged in | [Start permanent session](#)

Package Information

Name	BLAST
Version	2.2.18
Description	BLAST (Basic Local Alignment Search Tool) package from NCBI is a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. The BLAST programs have been designed for speed, with a minimal sacrifice of sensitivity to distant sequence relationships. The scores assigned in a BLAST search have a well-defined statistical interpretation, making real matches easier to distinguish from random background hits. BLAST uses an heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions of similarity (Atschul et al., J Mol Biol 1990 215:403-10).
WWW	http://www.ncbi.nlm.nih.gov/BLAST/
Tools	BlastP Launch BlastX Launch BlastN Launch TBlastX Launch TBlastI Launch

SRS Release 8.3 [Copyright](#) © 2007 BioWisdom SRS Ltd. All Rights Reserved.

Launch your Blast Program:
BlastP, BlastN, ...

Fichier Édition Affichage Historique Marque-pages Outils Aide

https://gpi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastP

start_blast2go [A universal ...] Tool Launch

biowisdom SRS

Find in Go

my SRS query builder analysis tools history - manage views - databank list - Help?

nlapalu logged in | [Start permanent session](#)

Tool Launch : BlastP

Step 1 : Data Source

Upload from file : Parcourir...

Paste/Create your own sequence(s) or type in the sequence ID(s) :

```
LQEVAAARHIIIVCGSTTIDGYAFCLGVKSLKLYTDPSSGLETLLSVIDI
KANLSERFSLQIRPLAELIDMFYTRQATDIRDKLFALLGMSDDPGKAGL
VFEQLVKFVLGKDISFRASSQTPRIKCRGIVVGQIYSVRMNSRQVIFTS
REWTLPASAKPIRERDII CL IYGASTPSIIRLCKDHFSMI VI AVTPLNGL
SKTQFLRDFELVMDWESSSGDMRDEGEYKTLIETFQSQSVFSKVEPGGYL
ATLDDLVEVKEADERFIAAQDEYYLAAFQKMPSWYESGSKCGRTILAFAA
LLETIHPDIKDGKVGRTPLFFAAEHGHEAIVKLLLATGQVNTESKDESGE
HESVVKLLLSIQIEVNSKDGSDRTPCWAAINGHKSVIKLLSIDQIEV
LCWAAREGHESVIKLLLSIRQIEVNSKDGFDQTPCLAAREGHESVVKLL
KDRFERTPLYANMKNHVSVKLLLEDHAKDHTT*
```

Save my sequence in **USERPROTEIN**

Step 2 : Launch Options

Views: HomologyView

You may continue to alter the tool settings below, or you can [Launch Now!](#)

Save my settings as a parameter set

Step 3 : Tool Settings

Database to search:

Currently Selected : Botrytis T4 ORFs protein
Botrytis T4 ORFs protein (Unreliable)
Sclerotinia ORFs protein
Stagnosporum nodorum ORFs protein

Main Databases

Kyoto Encyclopedia of Genes NCBI nr - All Non-redundant Genbank CDS Repbase REPET

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https://gpi.versailles.inra.fr/srs83/displayTool.do?toolName=BlastP

start_blast2go [A universal ...] Tool Launch

Database to search:

Currently Selected : Botrytis T4 ORFs protein
Botrytis T4 ORFs protein (Unreliable)
Sclerotinia ORFs protein
Stagnosporum nodorum ORFs protein

Main Databases

Kyoto Encyclopedia of Genes and Genomes (24feb11) NCBI nr - All Non-redundant Genbank CDS translation+PDB+Swissprot+PIR Refbase REPET Edition (16_03)

Botrytis databases

All databases in group
 Botrytis B05.10 ORFs protein Botrytis T4 ORFs protein Botrytis T4 ORFs protein (Unreliable)
 Botrytis Cineria T4 orf all BofuT4_orfprotall_1

Leptosphaeria maculans databases

All databases in group
 Leptosphaeria maculans ORFs protein Leptosphaeria maculans Fgenesh ORFs protein

Sclerotinia databases

All databases in group
 Sclerotinia ORFs protein

Stagnosporum databases

All databases in group
 Stagnosporum nodorum ORFs protein

UniProtKB

All databases in group
 UniProtKB UniProtKB/Swiss-Prot UniProtKB/TrEMBL
 Fungi-not in TrEMBL

MaizeSequence.org databases (march 2011)

Maize 5a WGS translations (Peptide sequences)

Other Protein Databases

Arabidopsis thaliana predicted chloroplast protein from TIGR (may 2003) Arabidopsis thaliana proteins (1503 sequences) from Genefarm (may 2003) Oryza sativa TIGR V5 Proteome/Oryza sativa TIGR V5 proteome (january 2007)
 Plant repeats from TREP (october 2006) RCSB World Wide Protein Data Bank (3.2)

Job name: temp

Select several databanks and run one blast job

Ex: run blast against Sclerotinia and Botrytis ORFs

Fichier Édition Affichage Historique Marque-pages Outils Aide

https://gpi.versailles.inra.fr/srs83/launchTool.do

start_blast2go [A universal ...] Query Results

my SRS query builder analysis tools history - manage views - databank list - Help?

nlapalu logged in | Start permanent session

Query Results

Primary Search ☆ Refine **Query Expression:** [BLASTP-JobName.temp_job1]

Found 50 entries

Tools

Related Information

Protein Sequence

Options: Selected Entries View Results/Page Page 1/2 >

Choose Colouring Scheme: Score E Value Percent Id Redraw

<40 **40-50** **50-80** **80-200** **>=200** - Coloured by Score

BofuT4_P000020.1

0 100 200 300 400 500 600 700

>BofuT4_P000020.1
 >BofuT4_P005460.1
 >BofuT4_P143800.1
 >BofuT4_P095000.1
 >BofuT4_P085470.1
 >BofuT4_P107170.1
 >BofuT4_P108560.1
 >BofuT4_P098020.1
 >BofuT4_P108570.1
 >SS16_01503.1
 >BofuT4_P037430.1
 >BofuT4_P025600.1
 >SS16_03889.1
 >SS16_07172.1
 >BofuT4_P021220.1
 >SS16_03086.1
 >SS16_02890.1
 >SS16_02602.1
 >BofuT4_P152300.1

ID: temp_job1_1
Accession:
Database: BofuT4_P000020.1
Description: 753
Score: 1552.000000
Expect: 0
% ID: 100

Blast result View

Tools

Related Information

Protein Sequence

Options: Selected Entries View Results/Page

Page 1/1

Select: All, None

BLASTP:temp job7_1

>BofuT4_P000030.1 530
Length = 530

Score = 1105 bits (2859), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 530/530 (100%), Positives = 530/530 (100%)

Query: 1 MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS 60
MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS
Sbjct: 1 MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS 60

Query: 61 KSPFRTILVTGVGMSKGLSIARSFYRAGHRVIGADFEPPYIPVSGHFSKSLRKFYRLRKP 120
KSPFRTILVTGVGMSKGLSIARSFYRAGHRVIGADFEPPYIPVSGHFSKSLRKFYRLRKP
Sbjct: 61 KSPFRTILVTGVGMSKGLSIARSFYRAGHRVIGADFEPPYIPVSGHFSKSLRKFYRLRKP 120

Query: 121 NGKSGAEYTRDIVNIIEKERVLDLWVSCGVASAIEDGEAAEMVQRNTRCAVVQFGVGLT 180
NGKSGAEYTRDIVNIIEKERVLDLWVSCGVASAIEDGEAAEMVQRNTRCAVVQFGVGLT
Sbjct: 121 NGKSGAEYTRDIVNIIEKERVLDLWVSCGVASAIEDGEAAEMVQRNTRCAVVQFGVGLT 180

Query: 181 EMLHEKFAFIKYTMELGLNVPLTYRIHSCCEALEILHPENGESVDKFKIMKPEMVDDSVR 240
EMLHEKFAFIKYTMELGLNVPLTYRIHSCCEALEILHPENGESVDKFKIMKPEMVDDSVR
Sbjct: 181 EMLHEKFAFIKYTMELGLNVPLTYRIHSCCEALEILHPENGESVDKFKIMKPEMVDDSVR 240

Query: 241 ADMTLLPSPSRTQTDTHIQKLNPAKRPFVLQQYIKGREYCTHSIVLKGKIHAFVSCRSS 300
ADMTLLPSPSRTQTDTHIQKLNPAKRPFVLQQYIKGREYCTHSIVLKGKIHAFVSCRSS
Sbjct: 241 ADMTLLPSPSRTQTDTHIQKLNPAKRPFVLQQYIKGREYCTHSIVLKGKIHAFVSCRSS 300

Query: 301 DMLMHYQALPSSSALAKAMFHYTTLTIQRAAERTPNSPITGHFSLDFLIDEEIAQKAEGS 360
DMLMHYQALPSSSALAKAMFHYTTLTIQRAAERTPNSPITGHFSLDFLIDEEIAQKAEGS
Sbjct: 301 DMLMHYQALPSSSALAKAMFHYTTLTIQRAAERTPNSPITGHFSLDFLIDEEIAQKAEGS 360

Query: 361 LHPSSKEVEKLQKELFPIECNPRAHAVLLNDSAEEMAEAYLSLLSDYNTNGNGDTYLP 420
LHPSSKEVEKLQKELFPIECNPRAHAVLLNDSAEEMAEAYLSLLSDYNTNGNGDTYLP
Sbjct: 361 LHPSSKEVEKLQKELFPIECNPRAHAVLLNDSAEEMAEAYLSLLSDYNTNGNGDTYLP 420

Query: 421 ALQRNEDPITPLSQAVNGGYWIGHDFVTKVLLPIPHLISFQKGITNLVREWWFQKHYL 480
ALQRNEDPITPLSQAVNGGYWIGHDFVTKVLLPIPHLISFQKGITNLVREWWFQKHYL
Sbjct: 421 ALQRNEDPITPLSQAVNGGYWIGHDFVTKVLLPIPHLISFQKGITNLVREWWFQKHYL 480

Query: 481 LWKDGTYEIWDPFPAWCLYVLFPLGCFWVSIWERKWSRCNVSTGKFFGV 530
LWKDGTYEIWDPFPAWCLYVLFPLGCFWVSIWERKWSRCNVSTGKFFGV
Sbjct: 481 LWKDGTYEIWDPFPAWCLYVLFPLGCFWVSIWERKWSRCNVSTGKFFGV 530

Choose your result view and select specific result to perform further analysis

BLASTP:temp job7_2

>BC1G_08771.1 hypothetical protein (translation)
Length = 416

Score = 803 bits (2075), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 387/390 (99%), Positives = 389/390 (99%)

Query: 1 MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS 60
MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS
Sbjct: 1 MFLDARSPVILHYLQNLFLIAICAAFTPFLTSIAILSTLISPLITSKQIQHPLKWRDSS 60

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my SRS query builder analysis tools history - manage views - databank list - Help?

Quick Searches

- BLAST
- IDs/Accession Numbers
- My Protein Sequences
- My Nucleotide Sequences
- Favorite Searches
- Other Searches

Customize...

My Protein Sequences

- >SRS:set_2|BLASTP:temp_iobl_1

```
MSSHYSLLPASGDNIRLLRLLPSEDEAAPLHCELRDYSLQRSTPRTHLYEALSYVWGD
P HNTLPI SVNEKQFQVT VNLHDALLRLRDHSFERI LWVD AI C IDOYNHEERNHQVIMAKI
YSSAHRVI VWL GEEKVEVKGALEDIQLAANEQPKNLPKKELKQORILKLLRNPFORIWV
LQEVAAARHII I VCGSTTIDGYAFCLGVKSLKLYTDSGLTLLSVIDI I ERAGLRPKF
KANLSERFSLQIRPLAELIDMFYTRQATDIRDKLFALLGMSDDPGKAGLQPNYEASWEE
VFQQLVKFVLGKDISFRASSQTPRIKCRGIVVGOIYSVRMNSRORVIFTKFGDRELGGT
REWTLPASAKPIRERDIICLIYGASTPSIIRLCKDHFSMI VI AVTPLNGLIRHEWPFQSR
SKTQFLRDFELVNDWESSGDMPEDEGEYKTLIETFSSQSVFSKVEPGGYLEKVTKLWNDI
ATLDDLVEVKEADERFIAAQDEYYLAAFQKMPSWYVESGSKCGRTILAFAAEKGHENI VKL
LLETIHPIKDKGVGRTPLFFAAEHGHEAIVKLLLATGOVNTESKDESGETLLQWAAREG
HESVVKLLLSI.GQIEVNSKDGSDRTPLCWAAINGHKSIVKLLLSIDQIEVNSKDEFDRTPL
CWAAREGHESIVKLLLSIRQIEVNSKDGFDOTPLCWAAREGHESVVKLLLSIDQIKVDS
KDRFERTPLYYANMNHVSVVKLLEDHAKDHTT
```

Launch tool... [Remove](#)
- >SRS:set_2|BLASTP:temp_iobl_2

```
MSSHLYSLLPENNIRMLRLLPSEDEAAPLHCEL CNYSLQRSSIRTHLYEALSYVWGD
P KQTLISYVDKQFQVT VNLHAALLQLRDYSFERI IWVD AI C IDONKKEERKQVQLMAQI
YISAHRI VWL GEOTVEKQGALEDIQLAANNEELIEHKSKEIKQQQILNLLQNPWFORTW
VLQEVAAARDVVMCGST AIDGYIFCLGVKSLKLYTASPELKT A IYLI E H A G F R P K F R T
DL SK R F S L N I R S L A E L I D M F H T R Q A T D N R P K V Y A L L G M S D D L E K A G L Q P D Y N T S W E E L F
Q Q L I K F V L S E N I S V E V S G O R A V I Q C K G
```

Launch tool... [Remove](#)

Displaying the total of 2 sequences [View all](#)

[Add to My Protein Sequences](#)

Import sequences and results in your personal library.

Projects

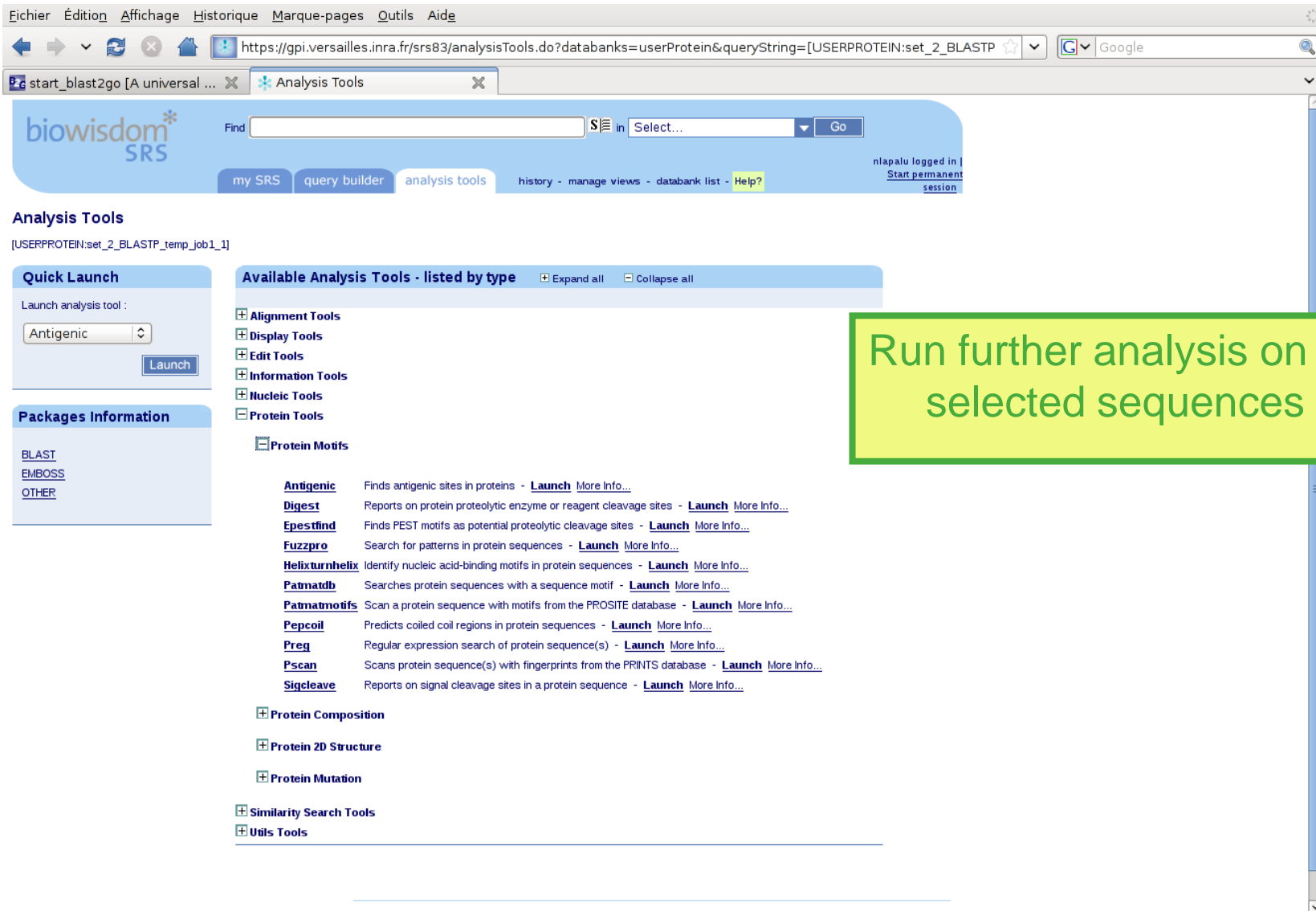
Current Project : **Temporary**

Import

Import existing project: [Parcourir...](#) [Go](#)

Export

Export current project [Export](#)



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https://gpi.versailles.inra.fr/srs83/analysisTools.do?databanks=userProtein&queryString=[USERPROTEIN:set_2_BLASTP

start_blast2go [A universal ... Analysis Tools

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Analysis Tools

[USERPROTEIN:set_2_BLASTP_temp_job1_1]

Quick Launch

Launch analysis tool :

Packages Information

[BLAST](#)

[EMBOSS](#)

[OTHER](#)

Available Analysis Tools - listed by type

Expand all Collapse all

- Alignment Tools
- Display Tools
- Edit Tools
- Information Tools
- Nucleic Tools
- Protein Tools
- Protein Motifs
- Protein Composition
- Protein 2D Structure
- Protein Mutation
- Similarity Search Tools
- Utils Tools

Antigenic Finds antigenic sites in proteins - [Launch](#) [More Info...](#)

Digest Reports on protein proteolytic enzyme or reagent cleavage sites - [Launch](#) [More Info...](#)

Epestfind Finds PEST motifs as potential proteolytic cleavage sites - [Launch](#) [More Info...](#)

Fuzzipro Search for patterns in protein sequences - [Launch](#) [More Info...](#)

Helixturnhelix Identify nucleic acid-binding motifs in protein sequences - [Launch](#) [More Info...](#)

Patmatdb Searches protein sequences with a sequence motif - [Launch](#) [More Info...](#)

Patmatmotifs Scan a protein sequence with motifs from the PROSITE database - [Launch](#) [More Info...](#)

Peppcoil Predicts coiled coil regions in protein sequences - [Launch](#) [More Info...](#)

Preg Regular expression search of protein sequence(s) - [Launch](#) [More Info...](#)

Pscan Scans protein sequence(s) with fingerprints from the PRINTS database - [Launch](#) [More Info...](#)

Sigcleave Reports on signal cleavage sites in a protein sequence - [Launch](#) [More Info...](#)

Run further analysis on selected sequences

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SRS

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Entry view - OCTANOL:temp_job8 [bookmark](#)

Options: [Actions](#) [View](#) [View Summary Sheet](#) [Get PDF version](#) [View Databank](#) Page 1 of 1

Tools

White-Wimley Plot

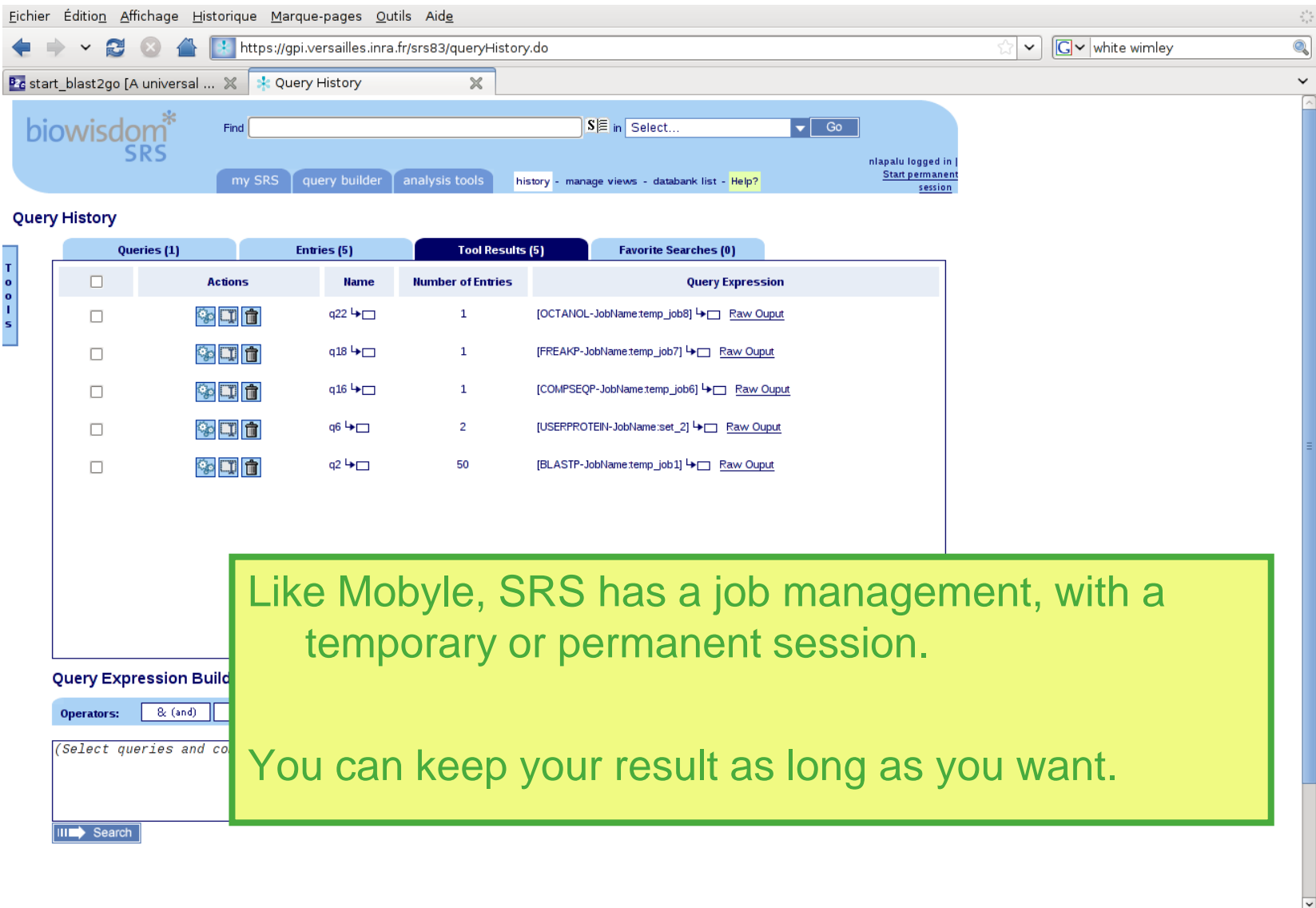
Total Free Energy (Kcal/mol)

0
-10
-20
















0 100 200 300

set:2-BLASTP-temp:job1-2

Ex : Hydropathy plot on blast Hit sequence



The screenshot shows the SRS Query History page. At the top, there is a navigation bar with 'my SRS', 'query builder', 'analysis tools', and 'history'. Below this is a table titled 'Query History' with columns for 'Actions', 'Name', 'Number of Entries', and 'Query Expression'. The table lists five queries, with the last one, 'q2', having 50 entries.

Actions	Name	Number of Entries	Query Expression
  	q22	1	[OCTANOL-JobName.temp_job8] Raw Output
  	q18	1	[FREAKP-JobName.temp_job7] Raw Output
  	q16	1	[COMPSEQP-JobName.temp_job6] Raw Output
  	q6	2	[USERPROTEIN-JobName.set_2] Raw Output
  	q2	50	[BLASTP-JobName.temp_job1] Raw Output

Below the table is a 'Query Expression Builder' section with a search bar and a 'Search' button.

Like Mobyale, SRS has a job management, with a temporary or permanent session.

You can keep your result as long as you want.

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