

GNPAnnot Community Annotation System applied to sugarcane BAC clone sequences

Valentin GUIGNON

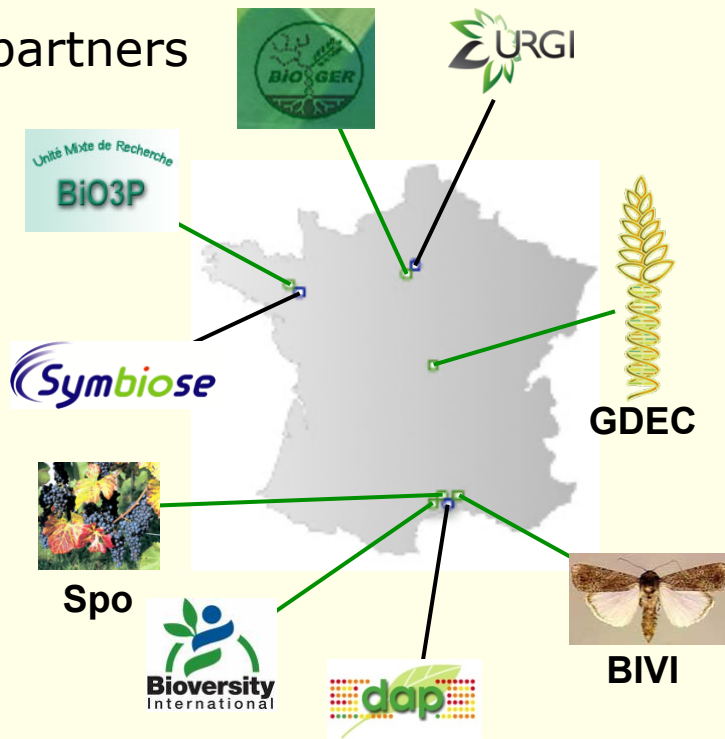
PAG

Sugarcane Genome Sequencing Initiative

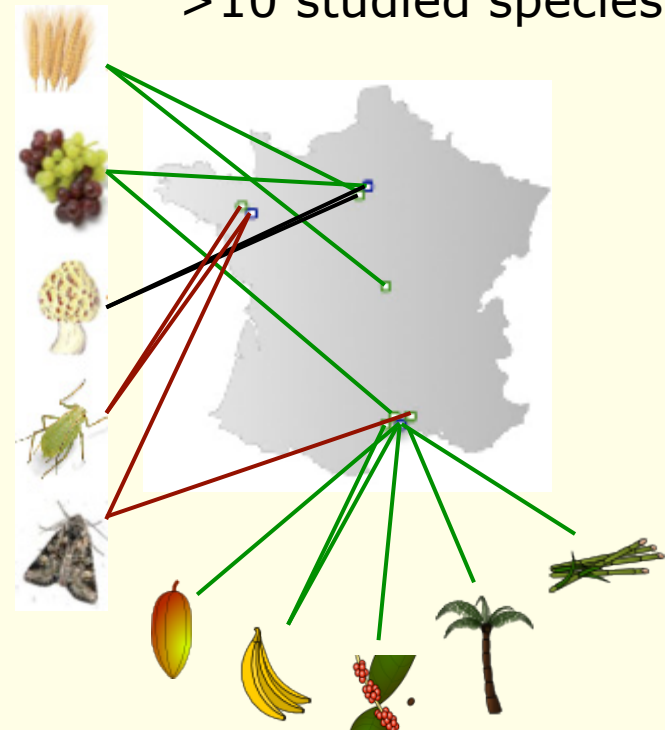
Sunday, 16 January 2011

What is GNPAnnot

9 partners



> 10 studied species



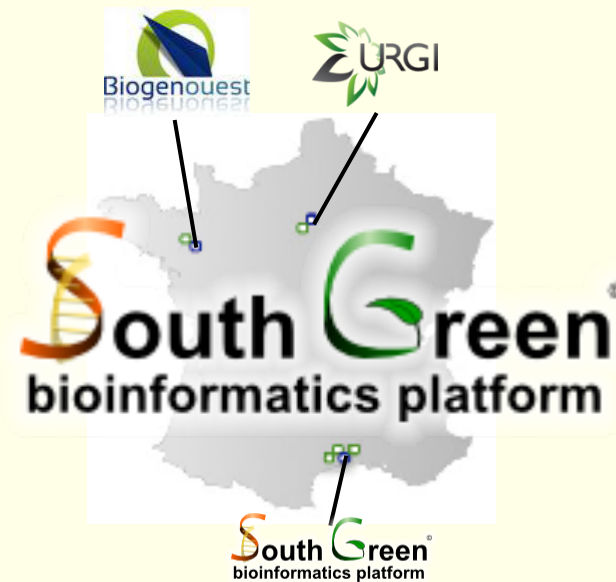
Sunday, 16 January
2011

Valentin GUIGNON

2

What is GNPAnnot

3 bioinformatics platform

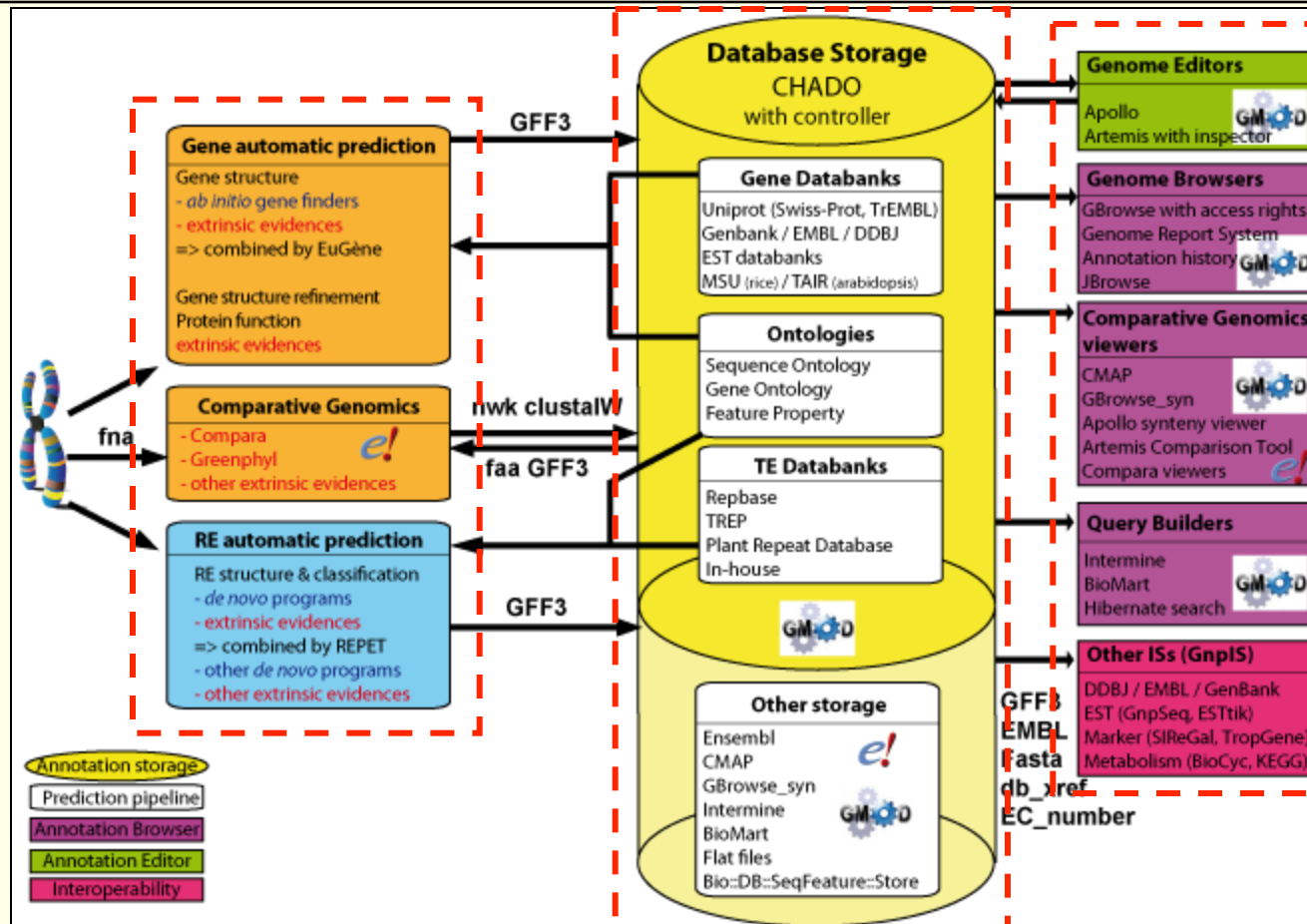




Goals

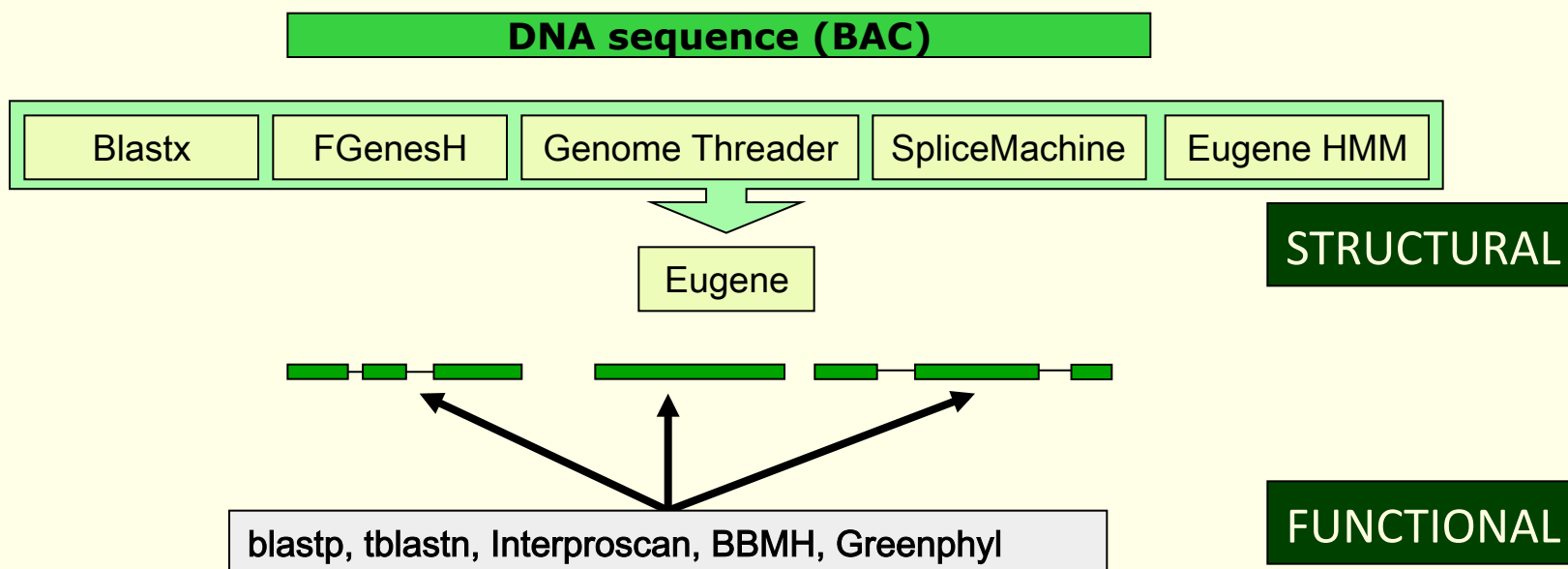
- Automatic annotation pipeline for genes and repeats
- Complete manual annotation framework with
 - Data confidentiality
 - Inspection of manual annotation
 - Annotation history
- Comparative genomics
- Data query and report system

GNPAnnot Concept



In House Annotation Pipeline

Automatic genes structural & functional prediction



Repeats Automatic Annotation

- Dawg Paws
- Repet





About our Annotation Pipelines

- Species-specific parameters
- Sugarcane trained on rice
- Already in use for full-genoms
- We can process your sequences

Portal: <http://www.gnpannot.org>

GNPAnnot Portal

QuickR

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About GNPAnnot

GNPAnnot is a project on green genomics which intends to develop a community system of structural and functional annotation supported by comparative genomics and dedicated to plant, insect and fungus genomes allowing both automatic predictions and manual curations of genomic objects.

[Read more](#)

Community Annotation Systems

- Musa
- Arecaaceae
- SpodoBase
- Cocoa
- Coffee
- AphidBase
- Sugarcane
- TriAnnot Pipeline
- Fungal Platform
- Vitis

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Community Annotation Systems



Musa



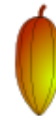
Areaceae



Coffee



SpodoBase



Cocoa



AphidBase



Sugarcane



TriAnnot Pipeline



Vitis



Fungal Platform

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Community Annotation Systems



Musa



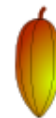
Areaceae



Coffee



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Cocoa



AphidBase



Sugarcane



TriAnnot Pipeline



Fungal Platform



Vitis

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Unique Name	Clone Name	Alias	Accession Number	Length (bp)	Predicted Gene Count	Current Gene Count	Curated Gene Count	Obsolete Gene Count	Current Gene Density (bp/gene)	%Current Gene (scaffold length)	%Curated Gene (scaffold length)	%Curated Gene (overall genes)	Predicted TE Count	Current TE Count	Curated TE Count	Obsolete TE Count	Current TE Density (sc len)	%C TE (sc len)
S scaffold_0023	188C19	Sh188C19		86420	25	22	0	0	3928	66%	0%	0%	0	0	0	0	n/a	n/a
S scaffold_0025				116097	38	30	0	0	3870	60%	0%	0%	1	1	0	0	116097	10%
S scaffold_0026	Sh172H13			113124	40	33	0	0	3428	60%	0%	0%	1	1	0	0	113124	3%
S scaffold_0027	ShCIRB286F09-ShCIRB251D13c			135129	42	29	8	6	4660	37%	24%	19%	4	4	1	0	33782	27%
S Sh186P07	186P07	Sh186P07		94874	38	33	0	0	2875	72%	0%	0%	0	0	0	0	n/a	n/a
S ShCIRB210D07	CIRB210D07	ShCIRB210D07		42796	13	4	9	6	10699	57%	107%	69%	2	3	1	0	14265	75%
S FN431661	ShCIR12E03	ShCIR012E03	FN431661	84926	0	3	0	0	28309	46%	0%	n/a	0	14	14	0	6066	57%
S FN431662	SB_BBc_24P17	Sb024P17c	FN431662	119613	0	19	0	0	6295	29%	0%	n/a	0	5	0	0	23923	15%
S FN431663	Sh15N23	Sh015N23	FN431663	137851	0	13	0	0	10604	26%	0%	n/a	0	5	8	3	27570	27%
S FN431664	Sh53A11	Sh053A11	FN431664	81164	0	9	0	0	9018	34%	0%	n/a	0	4	6	2	20291	24%
S FN431665	Sh135P16		FN431665	142236	0	18	0	0	7902	23%	0%	n/a	0	10	10	0	14224	15%
F FN431666	Sh142J21		FN431666	126547	0	15	0	0	8436	17%	0%	n/a	0	6	6	0	21091	60%
F FN431667	Sh197G04		FN431667	141630	0	10	0	0	14163	10%	0%	n/a	0	9	9	0	15737	39%
F FN431668	Sh253G12		FN431668	158483	0	12	0	0	13207	20%	0%	n/a	0	11	12	1	14408	34%
F FN431669	ShCIR9O20	ShCIR009O20	FN431669	87631	0	7	0	0	12519	19%	0%	n/a	0	7	10	3	12519	53%
F scaffold_0001	265O22	Sh265O22	AM403007	126105	0	17	0	0	7418	45%	0%	n/a	0	31	0	0	4068	24%
F scaffold_0002	51L01	Sh051L01	AM403006	97616	0	10	0	0	9762	38%	0%	n/a	0	21	0	0	4648	32%
Overall: 17 scaffolds				1892242	196	284	17	12	6663	36%	4%	9%	8	132	77	9	14335	28%

Calculation details:

- genes count excludes transposable element genes (TE gene);
- genes length excludes transposable element genes (TE gene) and transposable elements (TE) inside introns;
- predicted genes are genes found by Eugene;
- current gene count includes non-obsolete predicted or curated genes;
- curated genes include obsolete genes;
- genes density is given by the formula: $scaffold\ length / current\ gene\ count$
- percent of genes is given by the formula: $overall\ current\ gene\ length / scaffold\ length$

FN431669 ShCIR9O20 ShCIR009O20 FN431669 87631 0 7 0 0

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Poaceae Statistics

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Unique Name	Clone Name	Alias	Accession Number	Length (bp)	Predicted Gene Count	Current Gene count	Curated Gene Count	Obsolete Gene Count
scaffold_0023	188C19	Sh188C19		86420	25	22	0	0
scaffold_0025				116097	38	30	0	0
scaffold_0026	Sh172H13			113124	40	33	0	0
scaffold_0027	ShCIRB286F09-ShCIRB251D13c			135129	42	29	8	6
Sh186P07	186P07	Sh186P07		94874	38	33	0	0
ShCIRB210D07	CIRB210D07	ShCIRB210D07		42796	13	4	9	6
FN431661	ShCIR12E03	ShCIR012E03	FN431661	84926	0	3	0	0
FN431662	SB_BBc_24P17	Sb024P17c	FN431662	119613	0	19	0	0
FN431663	Sh15N23	Sh015N23	FN431663	137851	0	13	0	0
FN431664	Sh53A11	Sh053A11	FN431664	81164	0	9	0	0
FN431665	Sh135P16		FN431665	142236	0	18	0	0
FN431666	Sh142J21		FN431666	126547	0	15	0	0
FN431667	Sh197G04		FN431667	141630	0	10	0	0
FN431668	Sh253G12		FN431668	158483	0	12	0	0
FN431669	ShCIR9O20	ShCIR009O20	FN431669	87631	0	7	0	0

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Poaceae Statistics

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GNPAnnot Saccharum hybrid cultivar Statistics

	Unique Name	Name	Begin Position	End Position	Length (bp)	Strand	Evidence	Note	Annotators
1	Sh253G12_te010	Sh253G12_te010	16522	18423	1902	forward	curated	retrotransposon: LTR: Copia: RLC_Rhum: Sh253G12_te010	ogarsmeur
2	Sh253G12_te020	Sh253G12_te020	18430	35951	17522	forward	curated	retrotransposon: LTR: Gypsy: RLG_Colada: Sh253G12_te020	sidibeocs, ogarsmeur
3	Sh253G12_te015	Sh253G12_te015	35952	39212	3261	forward	curated	retrotransposon: LTR: Copia: RLC_Rhum: Sh253G12_te015	ogarsmeur
4	Sh253G12_te025	Sh253G12_te025	39213	44212	5000	reverse	curated	Retrotransposon~ LTR~ Gypsy~ RLG_TiPunch~ Sh253G12_te025~ ~ missing_completeness	ogarsmeur
5	Sh253G12_te026	Sh253G12_te026	45474	49321	3848	forward	curated	retrotransposon: LTR: Gypsy: RLG_Colada: Sh253G12_te026	ogarsmeur
6	Sh253G12_te027	Sh253G12_te027	49322	51193	1872	forward	curated	retrotransposon: LTR: Copia: RLC_Caipirinha: Sh253G12_te027	ogarsmeur
7	Sh253G12_te028	Sh253G12_te028	52148	53939	1792	reverse	curated	retrotransposon: LTR: Gypsy: RLG_Planteur: Sh253G12_te028	ogarsmeur

specific protein
nucleotide

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GNPannot Saccharum hybrid cultivar Statistics

	Unique Name	Name	Begin Position	End Position	Length (bp)	Strand	Evidence	Note
1	SUGARP0008000010001	Sh253G12_g010	1284	8611	7328	reverse		Sh253G12_g010~ putative ulp1 protease~ SENP2 missing_complete
2	SUGARP0008000190001	Sh253G12_g190	58155	62144	3990	forward		Sh253G12_g190~ division control protein 2 homolo CDC2~ missing_complete
3	SUGARP0008000220001	Sh253G12_g220	68596	72409	3814	forward		Sh253G12_g220~ putative shrunken seed protein~ PEX16~ missing_complete
4	SUGARP0008000240001	Sh253G12_g240	74674	77664	2991	reverse		Sh253G12_g240~ conserved hypothetical prot OsI_005508~ missing_complete
5	SUGARP0008000250001	Sh253G12_g250	80885	82512	1628	forward		Sh253G12_g250~ putative tyrosine specific protein phosphatase

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Search

Landmark or Region:

FN431668:57650..62649 Search

Reports & Analysis:

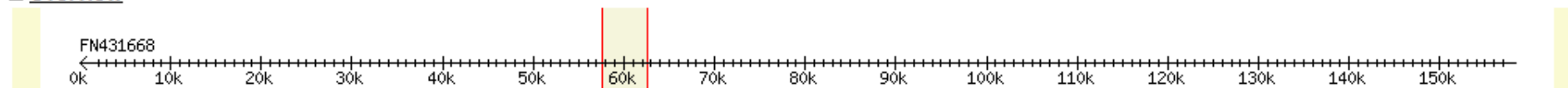
Annotate Restriction Sites Configure... Go

Data Source

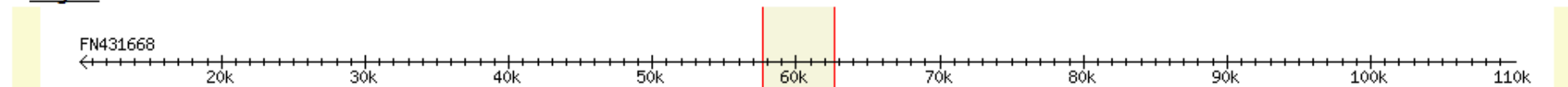
Saccharum hybrid cultivar - GnpAnnot

Scroll/Zoom: <<< < - Show 5 kbp + >>> Flip

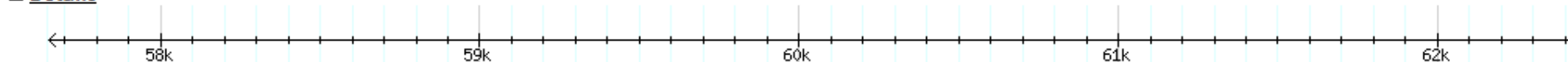
Overview



Region



Details



Eugene (gene)



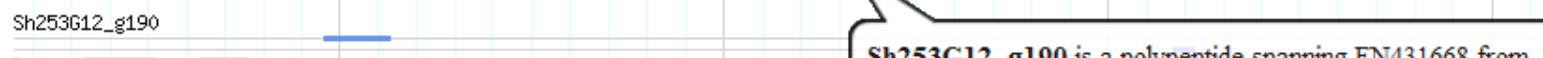
Eugene (mRNA)



Eugene (polypeptide)



Eugene (cds)



Contigs



Sh253G12_g190 is a polypeptide spanning FN431668 from 58155 to 62144. Click for more details.

Clear highlighting

Update Image

Tracks

1. Manual annotation of genes All on All off

Eugene (cds) Eugene (gene) Eugene (mRNA) Eugene (polypeptide)

2. Manual annotation of repetitive elements All on All off

LTR Struct Repet Manual

7. Genomic sequence All on All off

3-frame translation (forward) 3-frame translation (reverse) Contigs DNA/GC Content

Analysis All on All off

Restriction Sites

Configure tracks... Update Image

Search

Landmark or Region:

FN431668:57650..62649 Search

Reports & Analysis:

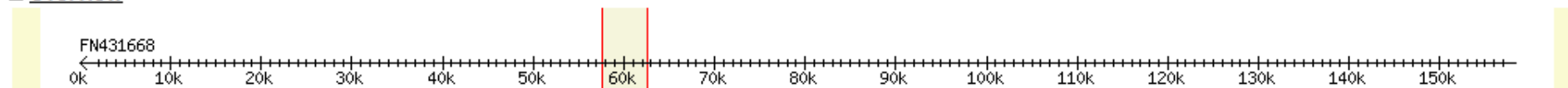
Annotate Restriction Sites Configure... Go

Data Source

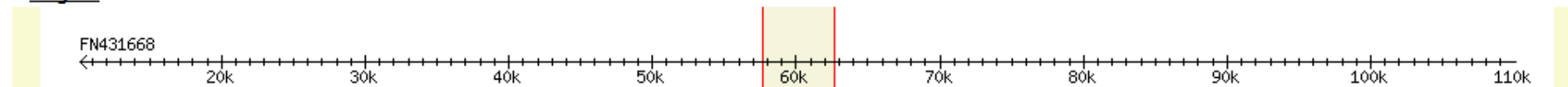
Saccharum hybrid cultivar - GnpAnnot

Scroll/Zoom: <<< < - Show 5 kbp + >>> Flip

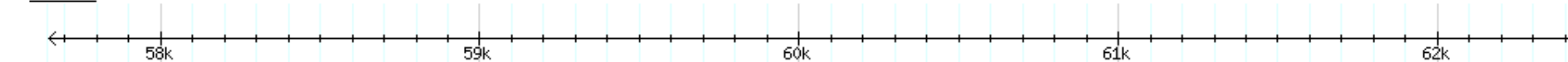
Overview



Region



Details



Eugene (gene)

Sh253G12_g190

Eugene (mRNA)

Sh253G12_g190

Eugene (polypeptide)

Sh253G12_g190

Eugene (cds)

cell division control protein 2 homolog 2; CDC2; missing_completeness

Contigs

Sh253G12_g190

Name Sh253G12_g190

Zoom in FN431668:58155..62144

Link Detailed Report

Annotation History

Edit with apollo

Edit with artemis

Clear highlighting

Update Image

Tracks

1. Manual annotation of genes All on All off

Eugene (cds) Eugene (gene) Eugene (mRNA) Eugene (polypeptide)

2. Manual annotation of repetitive elements All on All off

LTR Struct Repet Manual

7. Genomic sequence All on All off

3-frame translation (forward) 3-frame translation (reverse) Contigs DNA/GC Content

Analysis All on All off

Restriction Sites

Configure tracks... Update Image

Search

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Reports & Analysis:

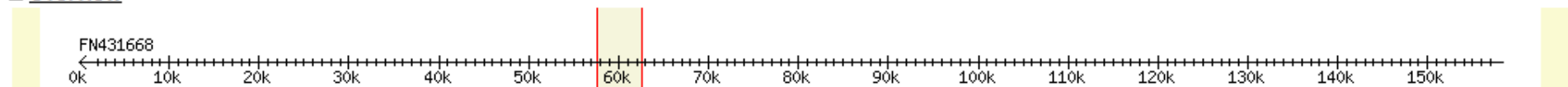
Annotate Restriction Sites Configure... Go

Data Source

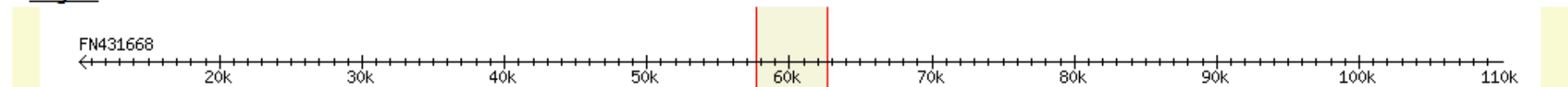
Saccharum hybrid cultivar - GnpAnnot

Scroll/Zoom: <<< < - Show 5 kbp + >>> Flip

Overview



Region



Details

58k 59k 61k 62k

- Eugene (gene) Sh253G12_g190
- Eugene (mRNA) Sh253G12_g190
- Eugene (polypeptide) Sh253G12_g190
- Eugene (cds) cell division control protein
- Contigs Sh253G12_g190

Enter Database Address

Server :
Port :
Database :
User :
Password :
Available databases : Default

OK Annuler

Named Report
Zoom Annotation History
Link Edit with apollo
Edit with artemis

Clear highlighting

Update Image

Tracks

1. Manual annotation of genes All on All off

Eugene (cds) Eugene (gene) Eugene (mRNA) Eugene (polypeptide)

2. Manual annotation of repetitive elements All on All off

LTR Struct Repet Manual

7. Genomic sequence All on All off

3-frame translation (forward) 3-frame translation (reverse) Contigs DNA/GC Content

Analysis All on All off

Restriction Sites

Configure tracks... Update Image

Artemis Gene Builder: Sh253G12_g190

File Edit

SUGARG000800019000

SUGART000800019000

auto3659, auto3659

SUGARP000800019000

Gene Map

Sh253G12_g190

Annotation :: SUGARP0008000190001

Key: polypeptide Add Qualifier: Dbxref

Location: 58155..62144

Complement Refresh Grab Range Remove Range Goto Feature Select Feature TAT ObjectEdit

Properties Core CV Match

Controlled Curation

Term	Dbxref	Evidence	Qualifier	Date	
CDC2				---/--/--	X
CDC2A				---/--/--	X
CDKA-2				---/--/--	X
OsJ_005039				---/--/--	X
CDKA-1				---/--/--	X
cdc2TaB				---/--/--	X
OsI_005505				---/--/--	X
ISS				---/--/--	X

CC_evidence_code

Overview Tab View OK Cancel Apply

Artemis E

File Ent

Entry:

Selected f

000

L # L P

C N C

V T A

TGTAAGTGGC

ACATTGACGG

Q L Q W

T V A

Y S G

gene

CDS

mRNA

polypep

Commit

tag="Sh253

K R M

R E

K E K

AAGAGAA

200

TTCTCTTT

L S V

S F

F L F

ness

Artemis Gene Builder: Sh253G12_g190

File Edit

SUGARG000800019000

SUGART000800019

auto3659, auto

SUGARP00080001

Gene Map

Sh253G12_g190

Annotation :: SUGARP0008000190001

Key: polypeptide Add Qualifier: Dbxref

Location: 58155..62144

Complement Refresh Grab Range Remove Range Goto Feature Select Feature TAT ObjectEdit

Properties Core CV Match

/Dbxref=[UniProtKB/Swiss-Prot:P93101](#)

/Dbxref=[UniProtKB/Swiss-Prot:Q38772](#)

/Dbxref=[UniProtKB/Swiss-Prot:Q41639](#)

/Dbxref=[UniProtKB/TrEMBL:Q9AUH4](#)

/Dbxref=[UniProtKB/TrEMBL:Q92RI0](#)

/Dbxref=[JGI:Sb01g049350.1](#)

/Dbxref=[JGI:Sb04g001920.1](#)

/Dbxref=[JGI:Sb07g027490.1](#)

/Dbxref=[JGI:Sb08g002240.1](#)

/Dbxref=[JGI:Sb10g026160.1](#)

/owner="ogarsmeur"

/date="Mon Aug 24 17:17:45 CEST 2009"

/protein_id="CAZ96199.1"

/note="Sh253G12_g190~ cell division control protein 2 homolog 2~ CDC2~ missing_completeness"

Overview Tab View OK Cancel Apply

Artemis

File Edit

Entry:

Selected

000

L # L

C N C

V T

TGTAACTG

ACATTGAC

Q L Q

T V A

Y S

gene

CDS

mRNA

polyp

Commit

ag="Sh253

K R M

R E

E K

GAGAA

00

CTCTTT

S V

S F

L F

ss

Artemis Gene Builder: Sh253G12_g190

File Edit

SUGARG000800019000
 SUGART000800019000
 auto3659, auto3660, auto3661, auto3662, auto3663, auto3664, auto3665, auto3666
 SUGARP000800019000

Gene Map

Sh253G12_g190

Annotation :: auto3659, auto3660, auto3661, auto3662, auto3663, auto3664, auto3665, auto3666

Key: CDS Add Qualifier: annotator_comment

Location: 3,58332..58516,58638..58755,58957..59130,60621..60784,60882..60969,61169..61222,62055..62144

Complement Refresh Grab Range Remove Range Goto Feature Select Feature TAT ObjectEdit

Properties Core CV Match

ID auto3659, auto3660, auto3661, auto3662, auto3663, auto3664, auto3665, auto3666 +

Parent SUGART0008000190001

Codon Start 1 2 3 Default

partial 5' partial 3' obsolete

24.08.2009 05:33:22 CEST

Overview Tab View OK Cancel Apply

Artemis

File Edit

Entry:

Selected

000

L # L

C N C

V T

TGTAACTG

ACATTGAC

Q L Q

T V A

Y S

gene

CDS

mRNA

polyp

Commit

tag="Sh253

K R M

R E

E K

AGAGAA

00

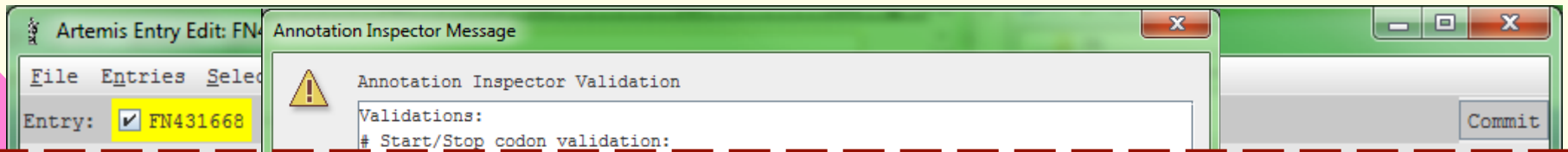
TCTCTT

L S V

S F

L F

ess



Validations:

Start/Stop codon validation:

-Sh253G12_g190:

Start Codon: OK

Stop Codon: OK

Sequence validation:

-Sh253G12_g190:

Length: **ERROR**: coding sequence length (883 bp) is not a multiple of 3!

Introns validation:

-Sh253G12_g190

Intron AG Site: **ERROR**: unrecognized acceptor site (*CA*GAAG at position 62052 from contig sequence beginning) between exons 7 and 8!

Mandatory properties management:

-Sh253G12_g190:

Mandatory properties management: **ERROR**: missing /functional_completeness qualifier!

Mandatory Properties Management: **ERROR**: missing /inference qualifier!

Gene structure validation:

-Sh253G12_g190 (non-obsolete mRNA):

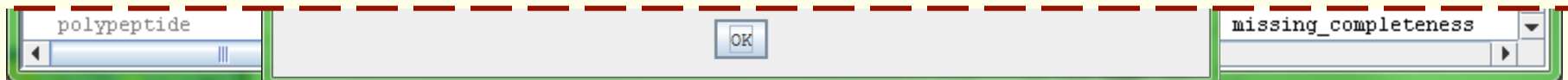
OK

Evidence code coherence management:

-Sh253G12_g190:

Evidence Code Management: **WARNING**: /evidence_code value should be set for gene Sh253G12_g190!

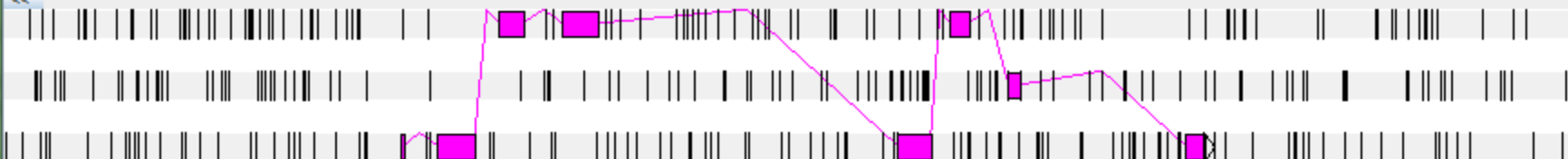
Your changes will be committed to the database and the errors notified above will be reported as qualifiers (when available).



Entry: FN431668

Commit

Selected feature: bases 3990 Sh253G12_g190 (/isObsolete=false /Name=Sh253G12_g190 /ID=SUGARG0008000190001 /locus_tag="Sh253



exon-auto3666

Sh253G12_g190

600 | 56800 | 57600 | 58400 | 59200 | 60000 | 60800 | 61600 | 62400 | 63200

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

TGTAAGTGGCAGTAACACTATTGTGTGTGCTTTCTGTAGTACGCCTTCAGATTGTTTACTTTTGTGCGTGTGCACACAACAGAGCAAGTATTGTCGTATTGAAGCTAAAAATGGAAAGAGAA

60100 | 60120 | 60140 | 60160 | 60180 | 60200

ACATTGACGGTCATTGTGATAAACACACACGAAAAGACATCATGCGGAAGTCTAACAAATGAAAACAGCACACGTGTGTTGTCTCGTTTCATAACAGCATAACTTCGATTTTTACCTTTCTCTTT

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

T V A L L V I Q T H K E T T R R * I T # K Q R T C V V S C T N D Y Q L + F H F S F

Y S G T V S N T H A K R Y Y A K L N N V K T T H V C C L L Y Q R I S A L F P F L F

gene	58155	62144	
CDS	58155	62144	
mRNA	58155	62144	
polypeptide	58155	62144	Sh253G12_g190~ cell division control protein 2 homolog 2~ CDC2~ missing_completeness

Artemis Entry Edit: FN431668

File Entries Select View Goto Edit Create Run Graph Display

Entry: FN431668 Commit

Selected feature: bases 17522 Sh253G12_te020.TE (/isobsolete=false /ID=Sh253G12_te020.TE /feature_id=49418 /timelastmodified=)

Artemis Feature Edit: Sh253G12_te020

Key: Add Qualifier:

Location:

Controlled Curation

Term	Dbxref	Evidence	Qualifier	Date	
curated	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>
retrotransposon	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>
Colada	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>
LTR	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>
Gypsy	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>
missing_rpt_type	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="----/--/--"/>	<input type="button" value="X"/>

Tab View

Sh253G12

Q T V
K R S
T N G C
CAAACGGTCA
GTTTGCCAGT
L R D
F P *
C V T L

exc
253G12_5000

LTR retrotransposon 18430 35951

repeat_region 18430 35951 retrotransposon: LTR: Gypsy: RLG_Colada: Sh253G12_te020

three_prime_LTR 34805 35951

target_site_duplication 35952 35956

Date: 14:20 12/01/2011

Author: guignon

Gene: 58155..62144

mRNA: 58155..62144

Exon: **Join(58155..58163, 58332..58516, 58638..58755, 58957..59130, 60621..60784, 60882..60969, 61169..61222, 62054..62144)**

/owner="guignon"

/note="Sh253G12_g190~ cell division control protein 2 homolog 2~ CDC2~ missing_completeness"

/annotator_comment="Comment test for PAG/SUGESI"

Product="cell division control protein 2 homolog 2"

Structural Completeness="missing_acceptor"

Evidence Code="ISS"

Gene="CDC2A"

Gene="Osl_005505"

Gene="cdc2TaB"

Gene="CDKA-1"

Gene="CDC2"

Gene="OsJ_005039"

Gene="CDKA-2"

Date: 17:59 06/08/2010

Author: gnpannot_admin

Gene: 58155..62144

mRNA: 58155..62144

Exon: **Join(58155..58163, 58332..58516, 58638..58755, 58957..59130, 60621..60784, 60882..60969, 61169..61222, 62055..62144)**

/owner="ogarsmeur"

/note=" [+] "Sh253G12_g190~ cell division control protein 2 homolog 2~ CDC2~ missing_completeness" - 17:59 06/08/2010

Product="cell division control protein 2 homolog 2"

Evidence Code="ISS"

Gene="CDC2A"

Gene="cdc2TaB"

Gene="Osl_005505"

Gene="CDC2"

Gene="CDKA-1"

Gene="OsJ_005039"

Gene="CDKA-2"

Date: 17:33 24/08/2009

Author: gnpannot

Gene: 58155..62144

mRNA: 58155..62144

Exon: **[+]Join(58155..58163, 58332..58516, 58638..58755, 58957..59130, 60621..60784, 60882..60969, 61169..61222, 62055..62144) - 17:33 24/08/2009**


/owner="garsmeur"

/note="Sh253G12g_190 cell division control protein 2 homolog 2"

Product="cell division control protein 2 homolog 2"

Data Confidentiality

GBrowse Access Restriction



User Account
Login:
Password:
Login

The landmark named *ShCIR012E03* is not recognized. See the help

Instructions
Searching: Search using a sequence name
Navigation: Click one of the rulers to center

Examples: *ShCIR012E03*, *Sb024P17c*, *Sh0*
ShCIRB210D07, *Sh186P07*, *Sh188C19*, *Sh0*

[\[Bookmark this\]](#) [\[Upload your own data\]](#) [\[Hide\]](#)

Search
Landmark or Region:
ShCIR012E03 Search

Data Source
Saccharum hybrid cultivar - GnpAnnot

User Account
Welcome guignon!
Change password...
New password:
Confirmation:
Change password

Showing 84.93 kbp from *ShCIR012E03*

Data Confidentiality

Access Restriction Administration

Saccharum hybrid cultivar - GnpAnnot Annotators Management

User Account
Change password...

Logout gnpannot_admin

Database: gnpannot_sugarcane
Authentication module: Bio::Graphics::Browser::AuthExtDB
Authentication database: gnpannot_accounts

Users Menu

- [Create a new user](#)
- [<< Back to Main Menu](#)

ID	User Name	Groups	Flags						Role	Comments	Edit	Remove
			Disabled	Locked	No Password	Password	Write	Gene Admin				
4	dhont	sugarcane_annotators	-	-	-	-	-	√	√	-		
8	droc	sugarcane_annotators	-	-	-	-	-	√	√	√		
10	zini	sugarcane_annotators	-	-	-	-	√	√	√	-	Cyrille Zini	
9	charron	sugarcane_annotators	-	-	-	-	√	√	√	-	Carine Charron	
3	ogarsmeur	sugarcane_annotators	-	-	-	-	-	√	√	-		
5	sidibeboos	sugarcane_annotators	-	-	-	-	-	√	√	√		
7	gaignon	sugarcane_annotators	-	-	-	-	-	√	√	√		
1	gnpannot_admin	sugarcane_annotators	-	-	-	-	-	√	√	√	administrator account	admin access
11	gnpannot_gbrowse		-	-	-	√	-	-	-	√	GBrowse read-only account	Keep "password locked" flag to forbid access to admin interface.

sugarcane

Saccharum hybrid cultivar - GnpAnnot Annotators Management

User Account
Change password...

Logout gnpannot_admin

Database: gnpannot_sugarcane
Authentication module: Bio::Graphics::Browser::AuthExtDB
Authentication database: gnpannot_accounts

Edit Feature Access

Feature: FN431668 (Sh253G12)

Group Name	Change Access				
	Keep current	Use default	Forbidden	Read	Write
anonymous	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>
sugarcane_annotators	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>

Annotator Name	Groups	Change Access				
		Keep current	Use default	Forbidden	Read	Write
dhont	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
droc	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
gnpannot_admin	sugarcane_annotators	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input checked="" type="radio"/>
gnpannot_gbrowse		<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
gaignon	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
ogarsmeur	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
sidibeboos	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
zini	sugarcane_annotators	<input type="radio"/>	<input checked="" type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Update

<< Back to Features Menu

sugarcane

Change data source



Sugarcane BAC Analysis Results

○ Some statistics...

17 scaffolds representing 1892242 bp
196 predicted genes

Currently 284 genes

with an average length of 2420 bp (36% of scaffolds)

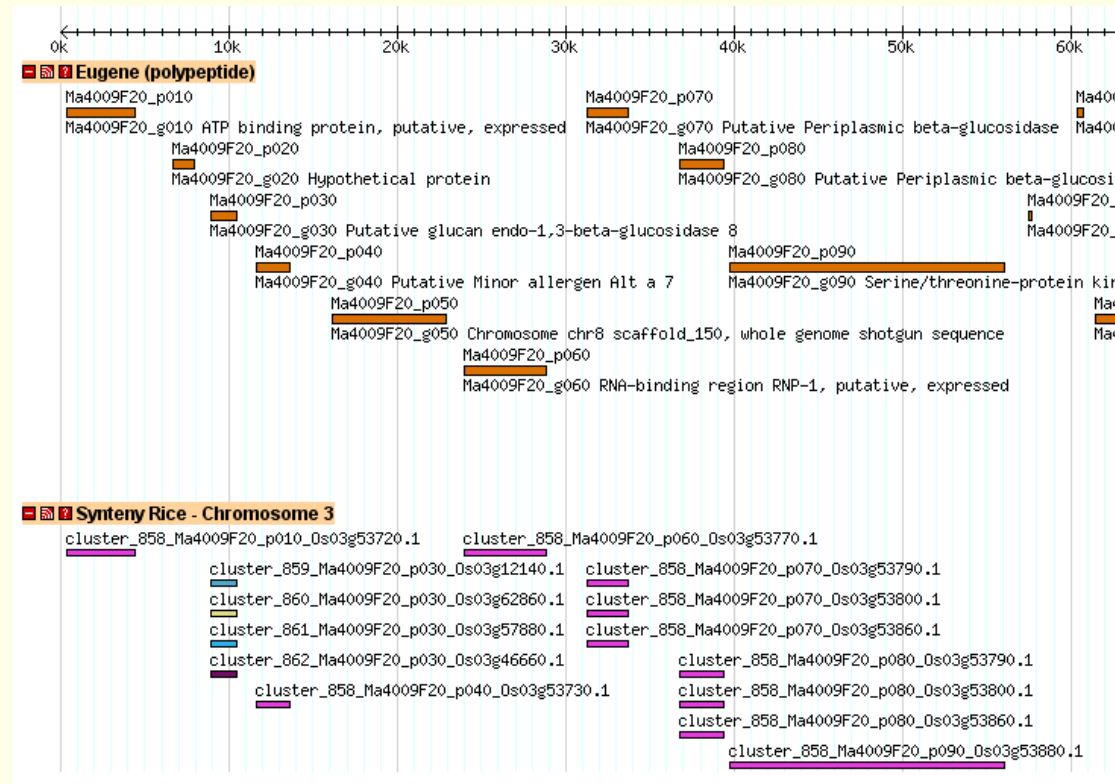
8 predicted TE (transposable elements)

Currently 132 TE

with an average length of 3943 bp (28% of scaffolds)

Other Sequence Analysis Results

○ Synteny Banana BAC / Rice



Other Sequence Analysis Results

URGI - GnpIS - Genetic & Genomic Information System

URGI - Génomique - Info

GnpIS - Genetic & Genomic Information System

Quick search

You can find the indexed databases list here.

Examples: VVI*, VVIF52, gene, transposable_element, arabidopsis, AY109603, Xcfe107-3B

Search: VVIF52 Submit

Specific modules

Terminé

Advanced Search

URGI - Génomique - Info

GnpIS advanced search

Dataset: Botrytis

Filters

Description (% for wildcard): %transport%

Program: blastx

Library: uniprot_sprot

Attributes

Description

Target ID / Hit

Program

Library

Feature Name

Feature Type

Please restrict your query using criteria below

Qualifiers

Description (% for wildcard)

Ontology Term (% for wildcard)

Target ID (% for wildcard)

Program

Export all results to: File TSV Unique results only Go

Email notification to:

View: 20 rows as HTML Unique results only

Description	Target ID / Hit	Program	Library	Feature Name	Feature Type
Monocarboxylate transporter 13 - Bos taurus (Bovine)	uniprot_sprot Q17Q6 MOT13_BOVIN	blastx	uniprot_sprot	bl4cfa_0008_uniprot_sprot Q17Q6 MOT13_BOVIN	match
Monocarboxylate transporter 13 - Homo sapiens (Human)	uniprot_sprot Q7RY0 YOMT13_HUMAN	blastx	uniprot_sprot	bl4cfa_0008_uniprot_sprot Q7RY0 YOMT13_HUMAN	match
Uncharacterized MFS-type transporter CS30_15c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot O74829 YN2F_SCHPO	blastx	uniprot_sprot	bl4cfa_0012_uniprot_sprot O74829 YN2F_SCHPO	match
Uncharacterized transporter B1AT1_01 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q9HDX4 YKN1_SCHPO	blastx	uniprot_sprot	bl4cfa_0019_uniprot_sprot Q9HDX4 YKN1_SCHPO	match
Uncharacterized transporter C11D3_05 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q10084 YAO5_SCHPO	blastx	uniprot_sprot	bl4cfa_0032_uniprot_sprot Q10084 YAO5_SCHPO	match
Uncharacterized transporter C170R_16c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q10487 YDFG_SCHPO	blastx	uniprot_sprot	bl4cfa_0032_uniprot_sprot Q10487 YDFG_SCHPO	match
Uncharacterized transporter YHR048W - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P38776 YHK8_YEAST	blastx	uniprot_sprot	bl4cfa_0032_uniprot_sprot P38776 YHK8_YEAST	match
Protein transport protein SEC9 - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot Q6CSD1 SEC9_KLULA	blastx	uniprot_sprot	bl4cfa_0039_uniprot_sprot Q6CSD1 SEC9_KLULA	match
High-affinity glucose transporter - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot P49374 HGT1_KLULA	blastx	uniprot_sprot	bl4cfa_0047_uniprot_sprot P49374 HGT1_KLULA	match
Iron transport multicopper oxidase FET3 precursor - Candida albicans (Yeast)	uniprot_sprot P78591 FET3_CANAL	blastx	uniprot_sprot	bl4cfa_0048_uniprot_sprot P78591 FET3_CANAL	match
Iron transport multicopper oxidase FET3 precursor - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P38993 FET3_YEAST	blastx	uniprot_sprot	bl4cfa_0048_uniprot_sprot P38993 FET3_YEAST	match
Polyamine transporter TPO5 - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P36029 TPO5_YEAST	blastx	uniprot_sprot	bl4cfa_0080_uniprot_sprot P36029 TPO5_YEAST	match
Iron-sulfur clusters transporter ATM1 mitochondrial precursor - Chaetomium globosum (Soil fungus)	uniprot_sprot Q2HIE9 ATM1_CHAGB	blastx	uniprot_sprot	bl4cfa_0087_uniprot_sprot Q2HIE9 ATM1_CHAGB	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus fumigatus (Soil fungus)	uniprot_sprot Q4WLN7 ATM1_ASPFU	blastx	uniprot_sprot	bl4cfa_0087_uniprot_sprot Q4WLN7 ATM1_ASPFU	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus oryzae	uniprot_sprot Q2ULH4 ATM1_ASPOR	blastx	uniprot_sprot	bl4cfa_0087_uniprot_sprot Q2ULH4 ATM1_ASPOR	match
Iron-sulfur clusters transporter ATM1 mitochondrial precursor - Yarrowia lipolytica (Candida lipolytica)	uniprot_sprot Q6C6N0 ATM1_YARLI	blastx	uniprot_sprot	bl4cfa_0087_uniprot_sprot Q6C6N0 ATM1_YARLI	match
High-affinity hexose transporter HXT6 - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P39004 HXT7_YEAST	blastx	uniprot_sprot	bl4cfa_0112_uniprot_sprot P39004 HXT7_YEAST	match
Galactose transporter - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P13181 GAL2_YEAST	blastx	uniprot_sprot	bl4cfa_0112_uniprot_sprot P13181 GAL2_YEAST	match
Riboflavin transporter MCH5 -	uniprot_sprot P08777 MCH5_YEAST	blastx	uniprot_sprot	bl4cfa_0114_uniprot_sprot P08777 MCH5_YEAST	match

Quick Search:
« Hibernate Search » based

Sunday, 16 January
2011

Valentin GUIGNON

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Other Sequence Analysis Results

○ Methabolic Pathway

ACYPICYC
Acyrtosiphon pisum Metabolic Pathways
Powered by **CYCRS**

The pathways herein are automatically generated and not manually curated, hence users should take caution when interpreting the existence or absence of metabolic pathways.

Search Database Acyr...

Home Search Tools Help Pathway

***Acyrtosiphon pisum* (genome paper version) Pathway: UDP-N-acetyl-D-glucosamine biosynthesis II**

Show Predicted Enzymes More Detail Less Detail Species Comparison

D-fructose-6-phosphate → D-glucosamine-6-phosphate → N-acetyl-D-glucosamine-6-phosphate → N-acetyl-glucosamine-1-phosphate → UDP-N-acetyl-D-glucosamine

Enzymes and EC numbers:
1. ACYPI003246-PA; (ACYPI003246, 2.6.1.16)
2. ACYPI003319-PA; (ACYPI003319, 2.3.1.4)
3. ACYPI006662-PA; (ACYPI006662, 5.4.2.3)
4. ACYPI004621-PA; (ACYPI004621, 2.7.7.23)

Reactants and products:
- L-glutamine → L-glutamate
- acetyl-CoA → coenzyme A + H⁺
- UTP + H⁺ → diphosphate

If an enzyme name is shown in bold, there is experimental evidence for this enzymatic activity.

Synonyms: UDP-N-acetylgalactosamine biosynthesis

Superclasses: [Biosynthesis](#) -> [Amines and Polyamines Biosynthesis](#) -> [UDP-N-acetyl-D-glucosamine Biosynthesis](#)



Sum up

Sum up

- Many annotation tools
- High quality manual annotations
- SouthGreen platform can help you

See also...

Presentations: W315, W107, W069, W152, W511, W327 and W585

Posters: P050, P800, P805 and P820



Thanks for your attention!
