

GMOD tools in the frame of GnpAnnot and GnpIS projects at URGI

GMOD Meeting Jan 13th, 2010

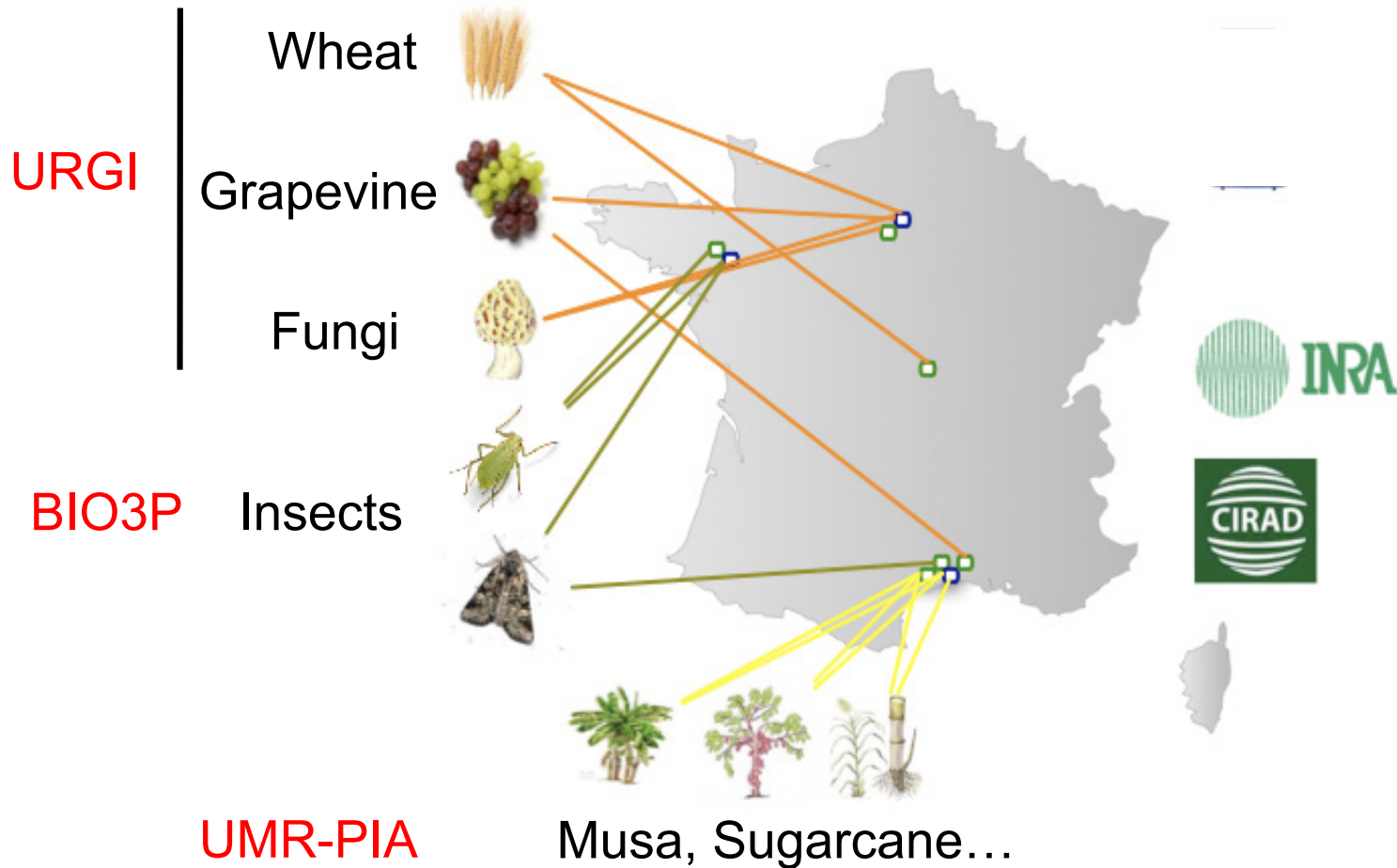


J. Amselem

ALIMENTATION
AGRICULTURE
ENVIRONNEMENT

INRA

- Granted by ANR (French National Research Agency)
- A structural and functional annotation platform supported by comparative genomics and dedicated to plant and bio-aggressor genomes
- 5 work packages
 - ◆ database and flow management
 - ◆ annotator interfaces implementation
 - ◆ interoperability with other systems
 - ◆ sequence exploitation and platform release
 - ◆ manual annotation and platform validation



Structural Automatic prediction

REPET
Fgenesh
Eugene
tRNAscan
...

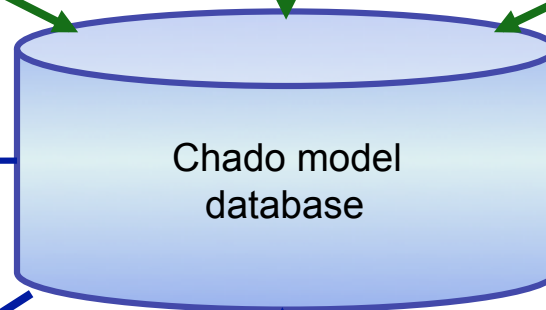
Refinement Analysis

Blast
Blat
Sim4, Gth, GeneSeqer
Comparative genomics
...

Functional Automatic prediction

Interproscan
Blast2GO
Blast based analysis
...

Annotation pipelines



Textual interface

Search

Graphical interfaces

GMC/GMOD Reports
Gene Report
Gene/protein report

Protein Statistics	Accession	Length	Start	End
Locus_PP00001	PP00001	14418	1	14418
Locus_PP00002	PP00002	14418	1	14418
Locus_PP00003	PP00003	14418	1	14418
Locus_PP00004	PP00004	14418	1	14418
Locus_PP00005	PP00005	14418	1	14418
Locus_PP00006	PP00006	14418	1	14418
Locus_PP00007	PP00007	14418	1	14418
Locus_PP00008	PP00008	14418	1	14418
Locus_PP00009	PP00009	14418	1	14418
Locus_PP00010	PP00010	14418	1	14418

Quick search
You can find the indexed databases list here.
Examples: [Virus](#), [WFS2 gene](#), [transposable element arabidopsis](#), [AY108033](#), [Xfa107-3B](#)

Quick search

BioMart advanced search

Description	Target ID(s)	Program	Library	Feature Name	Type
...

Gbrowse

Manual annotation
Apollo
Artemis

Comparative genomics
? GBrowse_syn
ACT
Argo

- A DAS defines a communication protocol used to exchange/share sequences and annotations
 - Relies on sequence references to be annotated
 - A reference sequence server
 - One or more annotation servers
- Set up at URGI : a DAS for manual annotation
 - One annotation server
 - One can upload and display it's own annotation tracks
 - Manual annotations shared by all partners in real time



Write
 "pure JDBC" direct
 communication protocol
 Read

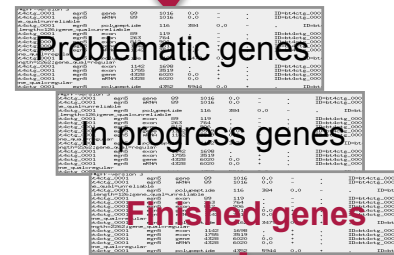


Export Edited genes
 (GFF3)

Automated annotation

- Gene Prediction (Fgenesh, Eugene ...)
- Repeat searching (TEs, TandemRepeats) (REPET pipeline, TRF...)
- Comparison (ESTs, proteins...) (Blastn, Blastx, Sim4...)
- Comparative genomics
- ...

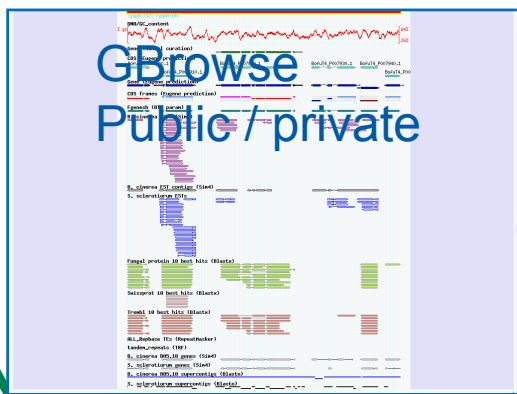
GFF3



New complete
 release



Read





Apollo add...



bt4ctg_0006 Botrytis fuckeliana

File Edit View Tiers Analysis Bookmarks Annotation Window Links Help

- Undo ^U
- Find...
- Preferences
- gene author = DB user login
- gene author = computer user
- Look & Feel:
 - Metal
 - Nimbus
 - CDE/Motif
 - Mac OS X

0 5000 10000 15000 20000 25000

BofuT4_T000580.1 BofuT4_T000620.1 BofuT4_T000650.1

BofuT4_T000590.1 BofuT4_T000600.1 BofuT4_T000630.1 BofuT4_T000640.1

Classes modified :

java/apollo/gui/menus/EditMenu.java

java/apollo/editor/UserName.java

java/apollo/dataadapter/chado/jdbc/JdbcChadoAdapter.java

Position

Zoom Zoom factor = 1.0000 Botrytis fuckeliana:bt4ctg_0006:1-26638

Type	Name	Range	Score
uniprot_trembl	blastx_uniprot_tre...	21835-19697	0.0
uniprot_trembl	blastx_uniprot_tre...	21820-19763	0.0
FNG30_prot	blastx_FNG30_pro...	21613-19760	0.0
FNG30_prot	blastx_FNG30_pro...	21766-19763	0.0
uniprot_trembl	blastx_uniprot_tre...	21613-19763	0.0
FNG30_prot	blastx_FNG30_pro...	21613-19763	0.0

uniprot_trembl: uniprot_trembl Q0U2T4 Q0U2T4_PHANO						
Putative uncharacterized protein - Phaeosphaeria nodorum (Septoria nodorum)						
Genomic...	Genomic...	Score	expect	query_fra...	Match Ra...	Match Le...
21820-1...	2058	0.0		1	1-683	683

Position Feature Action

URGI - GnpIS - Genetic & Genomic Information System

Quick search:

GnpIS - Genetic & Genomic Information System

Quick search (« Hibernate Search » based)

Ex: Search:

Specific modules

Terminé

Results

Display results per p
761 items found, displaying **1**
 <<< < 1 2 3 4 5 6 7 8 9 10 > >>>

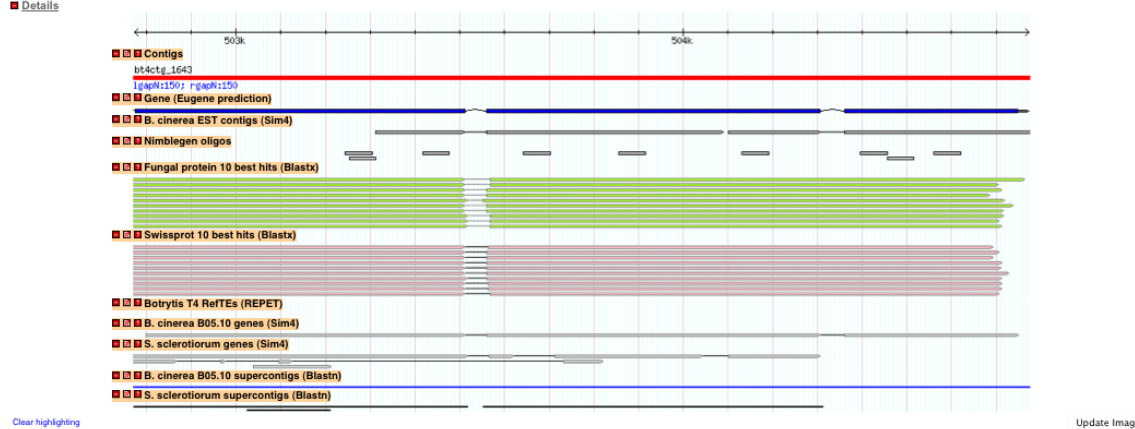
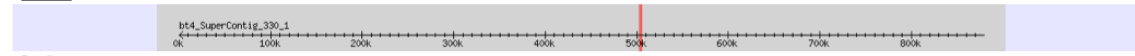
Query parameters: transport*

Botrytis cinerea T4 Supercontigs / contigs annotation

Showing 2 kbp from bt4_SuperContig_330_1, positions 502,773 to 504,772

Instructions
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the ScrollZoom buttons to change magnification and position.
Examples: bt4_SuperContig_0_1:40000..60000, bt4_SuperContig_63_1, bt4ctg_0012, bt4ctg_0198, bt4ctg_0253, bt4ctg_0106:12010..22010, bt4ctg_0111:3858..6529, BofuT4_T004650.1, BofuT4_P000020.1, BofuT4_P000570.1, BofuT4_P015510.1, BofuT4_P001590.1, BofuT4_T005350.1, BofuT4_G005380.1.
[Bookmark this](#) [\[Upload your own data\]](#) [\[Hide banner\]](#) [\[Share these tracks\]](#) [\[Link to Image\]](#) [\[Help\]](#) [\[Reset\]](#)

Search
Landmark or Region: Search
Data Source: Botrytis cinerea T4 genome annotation
Reports & Analysis: Annotate Restriction Sites Go
Scroll/Zoom: Show 2 kbp Flip



Tracks

- Comparative genomics All on All off
- Contigs All on All off
- Gene predictions All on All off
- Proteins All on All off
- Repeats All on All off
- Transcriptomics All on All off
- ncRNA All on All off
- Analysis All on All off

- Feature [genome-arabidopsis] (6)**
- At4g00225 ★★★★★
 - At4g00370 ★★★★★
 - At4g00900 ★★★★★
 - At4g01810 ★★★★★
 - At4g02050 ★★★★★
 - At4g02700 ★★★★★

- Feature [genome-botrytis] (761)**
- BC1G_00425.1 ★★★★★
 - BC1G_00679.1 ★★★★★
 - BC1G_02799.1 ★★★★★
 - BC1G_028... ★★★★★
 - BC1G_03332.1 ★★★★★
 - BC1G_03399.1 ★★★★★

Details

Name: BC1G_02799.1

Unique name: BC1G_02799.1

Type: gene

description: hypothetical protein similar to ABC-transporter

URGI - GnpIS - Genetic & Genomic Information System

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

Quick search:

URGI
Génomique-info

INRA

GnpIS - Genetic & Genomic Information System

Quick
 Advanced
 Biomart
 Galaxy

User guide
 News
 Release notes

About
 Data submission
 GnpArray
 GnpGenome
 GnpMap
 GnpSeq
 GnpSNP
 Siregal

Quick search

You can find the indexed databases list [here](#).

Examples: *VVI**, *VVIF52*, *gene*, *transposable element*, *arabid*

Advanced search

Search:

Advanced search : BioMart

Specific modules

Genetic maps and QTLs

EST and other sequences

Polymorphism data

Plant genetic resources data

Phenotypic and genotypic data

Proteomic data

Microarray data

Genome annotation data



Advanced search : BioMart



GnpIS advanced search



GnpIS advanced search

New Count Results

New Count Results

URL XML Perl Help

Dataset
Botrytis

Filters
Description (% for wildcard) :
%transport%
Program : blastx
Library : uniprot_sprot

Attributes
Description
Target ID / Hit
Program
Library
Feature Name
Feature Type

Dataset
Botrytis

Filters
Description (% for wildcard) :
%transport%
Program : blastx
Library : uniprot_sprot

Attributes
Description
Target ID / Hit
Program
Library
Feature Name
Feature Type

Export all results to Unique results only

Email notification to

View rows as Unique results only

Description	Target ID / Hit	Program	Library	Feature Name	Feature Type
Monocarboxylate transporter 13 - Bos taurus (Bovine)	uniprot_sprot Q17QR6 MOT13_BOVIN	blastx	uniprot_sprot	bl4ctg_0006_uniprot_sprot Q17QR6 MOT13_BOVIN	match
Monocarboxylate transporter 13 - Homo sapiens (Human)	uniprot_sprot Q7R7Y0 MOT13_HUMAN	blastx	uniprot_sprot	bl4ctg_0006_uniprot_sprot Q7R7Y0 MOT13_HUMAN	match
Uncharacterized MFS-type transporter C530.15c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot O74829 YN2F_SCHPO	blastx	uniprot_sprot	bl4ctg_0012_uniprot_sprot O74829 YN2F_SCHPO	match
Uncharacterized transporter B1A11.01 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q9HDX4 YKN1_SCHPO	blastx	uniprot_sprot	bl4ctg_0019_uniprot_sprot Q9HDX4 YKN1_SCHPO	match
Uncharacterized transporter C11D3.05 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q10084 YAO5_SCHPO	blastx	uniprot_sprot	bl4ctg_0032_uniprot_sprot Q10084 YAO5_SCHPO	match
Uncharacterized transporter C17C9.16c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot Q10487 YDFG_SCHPO	blastx	uniprot_sprot	bl4ctg_0032_uniprot_sprot Q10487 YDFG_SCHPO	match
Uncharacterized transporter YHR048W - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P38776 YHK8_YEAST	blastx	uniprot_sprot	bl4ctg_0032_uniprot_sprot P38776 YHK8_YEAST	match
Protein transport protein SEC9 - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot Q6CSD1 SEC9_KLULA	blastx	uniprot_sprot	bl4ctg_0039_uniprot_sprot Q6CSD1 SEC9_KLULA	match
High-affinity glucose transporter - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot P49374 HGT1_KLULA	blastx	uniprot_sprot	bl4ctg_0047_uniprot_sprot P49374 HGT1_KLULA	match
Iron transport multicopper oxidase FET3 precursor - Candida albicans (Yeast)	uniprot_sprot P78591 FET3_CANAL	blastx	uniprot_sprot	bl4ctg_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	bl4ctg_0048_uniprot_sprot P38993 FET3_YEAST	match
Polyamine transporter TPO5 - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P36029 TPO5_YEAST	blastx	uniprot_sprot	bl4ctg_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	bl4ctg_0087_uniprot_sprot Q2HIE9 ATM1_CHAGB	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus fumigatus (Sartoryia fumigata)	uniprot_sprot Q4WLN7 ATM1_ASPFU	blastx	uniprot_sprot	bl4ctg_0087_uniprot_sprot Q4WLN7 ATM1_ASPFU	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus oryzae	uniprot_sprot Q2ULH4 ATM1_ASPOR	blastx	uniprot_sprot	bl4ctg_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	bl4ctg_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	bl4ctg_0112_uniprot_sprot P39004 HXT7_YEAST	match
Galactose transporter - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot P13181 GAL2_YEAST	blastx	uniprot_sprot	bl4ctg_0112_uniprot_sprot P13181 GAL2_YEAST	match
Riboflavin transporter MCH5 -	uniprot_sprot Q09777 MCH5_YEAST	blastx	uniprot_sprot	bl4ctg_0114_uniprot_sprot Q09777 MCH5_YEAST	match





Usecase *Vitis vinifera*



Vitis portal

Why develop grape genomics?

Projects

- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **BOUCALDES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**
- 2009-2011 ANR 2009 **GRAPES**

Genotype table

GnpSNP

Information

Display: 200 (3) results per page
47 items found, displaying 1 to 47

Results

The experiment VVM028_2882009 contains 1 marker (VVM028).

Line	SNP	Position
Line 555Mtp22/Muscad	petra.blancs.B	245 / 267
Line 324Mtp30/Cabernet franc N		227 / 235
Line 3566Mtp1/Sultana		243 / 245
Line 6450Mtp4/Jaquez N		235 / 229
Line 9219Mtp2/Fercal		243 / 218
Line 9157Mtp3/Rohler 99		235 / 218
Line 9221Mtp10/Schwazzenstein		243 / 214
Line 9000Mtp03/Groeth 9		235 / 239
Line 308Mtp2/Muscad of Alexandria B		243 / 267
Line 6430Mtp1/Muscad B		227 / 233
Line 193Mtp1/Print noir N		235 / 215

Marker results

GnpMap

Information

Display: 10 (2) results per page
188 items found, displaying 1 to 10

Results

#	Marker name	Marker type	Marker origin	Dist (Gene function) (annual accession)	Link to list	Anchored clones
1	Vitis.unifolia.VVCF49	SSR	genomic DNA	-	26	VVCF49AF59
2	Vitis.unifolia.VVCF52	SSR	genomic DNA	-	22	VVCF49BA15
3	Vitis.unifolia.VVCF50	SSR	genomic DNA	-	21	VVCF49BF13
4	Vitis.unifolia.VVCF47	SSR	genomic DNA	-	21	VVCF49BF17
5	Vitis.unifolia.VVCF22	SSR	genomic DNA	-	12	VVCF49CG16
6	Vitis.unifolia.VVCF21	SSR	genomic DNA	-	13	VVCF49DE03
7	Vitis.unifolia.VVCF58	SSR	genomic DNA	-	21	VVCF49DBA2
8	Vitis.unifolia.VVCF55	SSR	genomic DNA	-	21	VVCF49DB19
9	Vitis.unifolia.VVCF50	SSR	genomic DNA	-	21	VVCF49DM13
10	Vitis.unifolia.VVCF61	SSR	genomic DNA	-	18	VVCF49EH10

Botrytis cinerea T4 Supercontigs / contigs annotation

Showing 26.64 kbp from 644 SuperContig 0.1, positions 120,110 to 146,747

GnpGenome GBrowse 1.7 Chado

Advanced search

Interoperability (in progress)

BioMart

Apollo 1.11 chado

Quick search + Interoperability

Hibernate Search

GnpIS portal

GnpIS - Genetic & Genomic Information System

Quick search

You can find the indexed databases list using:

Examples: VVCF_VVCF52 gene, transposable_element, analysisData_AVT09003_Vids10730

Search: VVCF52 Submit

Specific modules

- Genetic maps and QTLs
- Polymorphism data
- Plant genetic resources data
- Phenotypic and genotypic data
- Proteomic data
- Microarray data
- Genome annotation data
- GnpGenome
- GnpArray
- GnpMap
- GnpSNP
- GnpSnp
- GnpEphras
- GnpEST
- GnpEST
- GnpEST



URGI Génomique-Info

New Count Results URL XML Perl Help

Export all results to Unique results only

Email notification to

View rows as Unique results only

Map Name	Link Map URGI	Genus	Project Name	Marker Name	Link Marker URGI	Feature Name	Feature Type	Genus	Analysis Name
Grenache_031220	47	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Syrah_031220	46	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Integrated	79	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_F_CS	81	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_Integrated	83	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_M_Bianca	70	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
DG_F_Chardonnay	69	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
SG_031220	48	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
Integrated_fw	78	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation
A1_C_SG	67	Vitis	CI1999076	VVIC51	19586	VVIC51	STS	Vitis	Genoscope_Annotation

GnpMap ↑

GnpGenome ↑

Dataset
GnpMap
Filters
Marker Name (% for wildcard): [ID-list specified]
Attributes
Map Name
Link Map URGI
Genus
Project Name
Marker Name
Link Marker URGI

Dataset
GnpGenome Vitis
Filters
Feature Type: STS
Attributes
Feature Name
Feature Type
Genus
Analysis Name



Usecase *Botrytis cinerea*



Botrytis portal

Botrytis cinerea T4 genome project

The project

Objectives

Results

Post-genomic approaches results

pAscoDB

Functional DB

Letters legend:

- A: pAscoDB Annotations
- B: Broad Annotations
- C: Cytogen Annotations
- F: Fasta Sequence
- M: MIPS Annotations

State:

Numbers between parenthesis correspond to the start and the stop of the domain e.g.: PF00905 HMGB_box(127..193) HMGB_box domain is located from AA 127 to AA 193. You can click on the domain positions to see the corresponding region on the Fasta sequence.

Custom Annotations in Excel like format:

BoFuT4_P0076703.A.F Length: 1011 pt: 8.2188 kDa: 110.73873 Cysteine: 8 Blast Results: ESTs/Matches Elnet/ES

ORTHOLOG	MCLN	Markov Chain	Position	Ortholog	Binding points	First Blast hit
	RC1G_08007.1	1.1E-12	1107	RC1G_08007.1	1107	RC1G_08007.1
	SS1G_10758.1	1.2E-11	1107	SS1G_10758.1	1107	SS1G_10758.1

Botrytis cinerea T4 Supercontigs / contigs annotation

Showing 26.64 Mbp from b44_SuperContig_0_1, positions 120,110 to 146,747

GnpGenome

GBrowse 1.7

Chado

Advanced search

Interoperability (in progress)

BioMart

Export all results to: File CSV TSV Unique results only

Display	Description	Target ID	Library	Feature Name	Feature
match

Gene - BofuT4_P034230.1

GnpArray

Gene details

Name: BofuT4_P034230.1

Associated sequences: BofuT4_P034230.1

Associated gene lists

Associated reporters

Normalized data

Gene list	FOLD CHANGE	Normalized_Variance	pVALUE
BofuT4_P034230.1	-7.9	0.08	1.24E-10

Apollo 1.11

chado

344eq_0006 Botrytis factikiana

Position: 19595

Type	Name	Date	Score
uniprot_trembl	Uniprot_P034230	21851-19597	0.0
uniprot_trembl	Uniprot_P034230	21820-19763	0.0
FNCGO_prot	Uniprot_P034230	21613-19763	0.0
FNCGO_prot	Uniprot_P034230	21766-19763	0.0
uniprot_trembl	Uniprot_P034230	21613-19763	0.0
FNCGO_prot	Uniprot_P034230	21613-19763	0.0

Quick search

+ Interoperability

Hibernate Search

Display: 10 - 20 results per page

Query parameters: BofuT4_P034230.1 BofuT4_P046390.1

Feature [genome-botrytis] (4)	Gene [transcriptome] (1)
BofuT4_P034230.1 ★★★★★	BofuT4_P034230.1 ★★★★★
BofuT4_P046390.1 ★★★★★	BofuT4_P046390.1 ★★★★★
BofuT4_P034230.1 ★★★★★	-
BofuT4_P046390.1 ★★★★★	-

GnpIS portal

GnpIS - Genetic & Genomic Information System

Quick search

You can find the indexed databases list tags.

Examples: VIG_VIGF22 genes, transposable_element, analysis, AC109003, Ude107-30

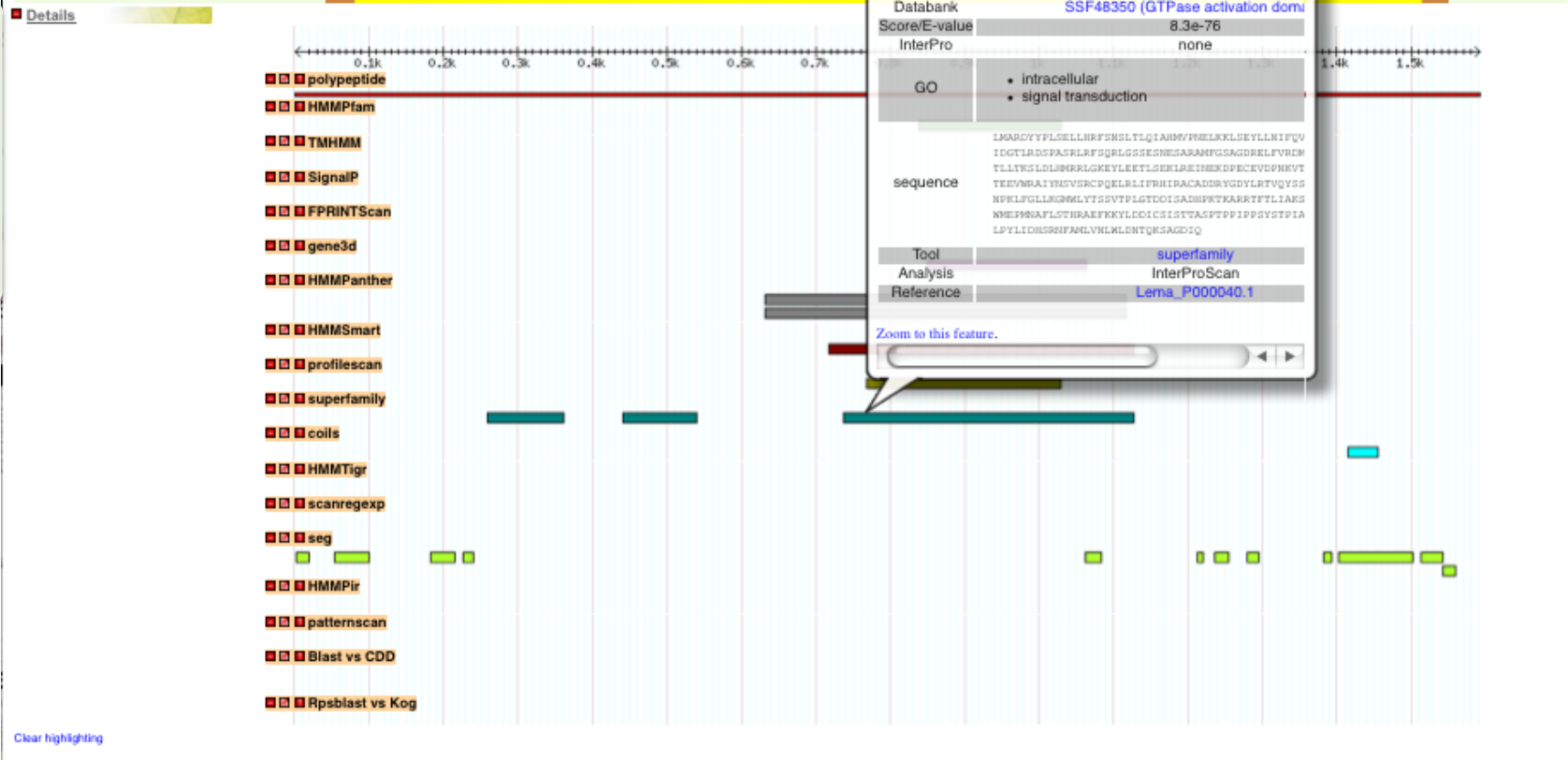
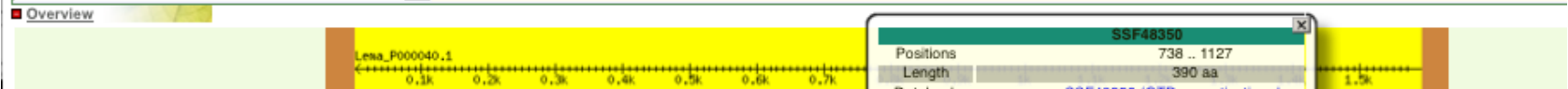
Search: VIGF22 Submit Cancel

Specific modules

Showing 1.591 kbp from Lema_P000040.1, positions 1 to 1,591

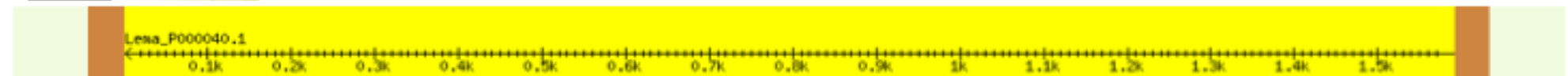
Instructions
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed. To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.
Examples: Lema_P000020.1, Lema_P000040.1, Lema_P000050.1.
[\[Bookmark this\]](#) [\[Upload your own data\]](#) [\[Hide banner\]](#) [\[Share these tracks\]](#) [\[Link to Image\]](#) [\[High-res Image\]](#) [\[Help\]](#) [\[Reset\]](#)

Search
Landmark or Region: Lema_P000040.1 Search
Data Source
 Leptospaeria maculans automated functional annotation
Scroll/Zoom: Show 1.591 kbp Flip



Chado
 Ref
 =
 polypeptide

Overview



Details

← 0.1k 0.2k 0.3k 0.4k 0.5k 0.6k 0.7k 0.8k 0.9k 1k 1.1k 1.2k 1.3k 1.4k 1.5k →

- polypeptide
- HMMPfam
- TMHMM
- SignalP
- FPRINTSscan
- gene3d
- HMMPanther
- HMMSmart
- profilescan
- superfamily
- coils
- HMMTigr
- scanregexp
- seg
- HMMPir
- patternscan
- Blast vs CDD
- Rpsblast vs Kog

Clear highlighting

Lema_P000040.1

Length	1591 aa
CAZy	not identified as CAZy
Blast2GO	<ul style="list-style-type: none"> Description: gtpase activating protein (bud2 cla2) GO: GTPase activator activity GO: intracellular GO: regulation of small GTPase mediated signal transduction

sequence

```

MDQQRRSRREVSASEAAQGLQYTDPRFRDERSKGTTFIRVTFPCOLSIPEEVGCGSGSGSG
GGGGGGGGGGGQNFSPNPSPHSQHSQPGQPGQSSSSSSGQRTTNPRAFVARATSETEYRN
ARDQTRPKRWTLKEERSTRDRSPSSLFAAGRRIGSVASSTYTANFGSLEESVVTSGHIS
TISFPSSSQHQHQHQHQHQPPPTSSSTRSRRLIKQPLRATESPANVAANPNAAAAP
ESNPSVYPASDARKLKALMRSTCGRMQGLLAFRRGESSPWALSFCFINEEAGSLVYEPKH
DTSYTRTLIPDLRGCHVKSAYDGEAFTAYLAWIVHNSKLGVHLRPPQCEFDMMFAALLC
NSPBRPKGIQNRNAKPGAPVTMERRLTDSRRSEVSLKNETPKKEAPIIRVGMNIYMDTS
VTYSNMGTPKGVVSRPQTHRMQSHGSRMRVSVCTLRENGELKLYSOTDVTLVSTVQLSQ
LSRCVAVQLDPSVLDNEFCIAIYPPQYASASALPLLRPIFLSLESRVLYENMIVLLRAFT
VPQLYGPESDLSNDEGTLSPSPGTHDMFMEKSLFIRVIEGRVLPVSPKRVADGATPIRP
SSGANANPGGYLNEILLDGETRAKTMTESEGNAPFWREKFEFLDLPALHTASLLKKRPP
SYTSGEKPLFTSALSTDLAEEGGYAGTFFDQTIGKTDIYLDCLGPNQEMEDMPLIMNYG
NSVGEVLIKVSSEKCAILNARDYYPFLGELLRFNSLTLQIAHWVFNELKLESEYLLNIF
QVSGAAGEMICALVEEKIDGTLRDSFASRLRFSQRLGSSSEKESARAMPFSAGDRELFR
DMGNWAKLEANLLFRGNTLLTKSLDLHMRRLGKEYLEKTLSEKLEINEKDPCEVDPNK
VTSQHELDNRMRRLINCTEKNVRAIYNSVSRCPQELRLIFRHIRACADDRYGDYLRVQY
SSVSGFLFRFFVPAVLNPKLPLGLLQMLYTSVVTPLGTDIISADHPKTKARFTFLIA
KSLQGLIAMSFGTKEAWNEPMNAFLSTRAEFKKYLDLDCISITSTASPTPPIPPSSYTP
IAILHRLPPTFKGFPPLPYLIDHSRNFAMLVNMLDNTQKSAGDIQAGDGLLRFHINIC
VSLNERTKDCCLARAEPAERPSLSSVMEELVEQLGSSRIDNRRGAVTRNGRPIQEKKEF
DAPMSPTPGEKFPSSSTSTPITMQPAPRTRHQNTSISASASSGSSSSGATISYTHPFT
ISKANSGRSAPSGHDSVPASQASSTASADASGAEDTPPGSSDGLIMAFAPSYTPQLTEP
SIAANSFNYSNPMNHINTQGNNSRGGYPPPSAGGGQSMGSEKNGSIQEEYTTALPAFN
SKEGHEKPKERSFRGVLFFNRKPKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDKDK
EENEKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPKKPK
SALGAPTELSLRSKNSQSSHHHNSHNSPMDYNSNFIPISTHTTTTSTTTTTSYSSHN
PLSTLTPNRDEPIFSPRNTSTRDRERDEF
                    
```

Link to URGI SRS environment

Update Image

Entry view - LeptoFunAnnot:P00004

[Bookmark](#)

Options: [Actions](#) [View](#) View Summary Sheet: [?](#) Get PDF version: [?](#) View Databank: [?](#)

Go To: [General](#) [Description](#) [Database Cross-References](#) [Features](#) [Sequence](#)

General Information About The Entry

Entry Name	LeptoFunAnnot:P00004
Identifier	Lema_P000040.1
Prim. Accession	P00004
Created	01-JAN-2000
Last Sequence Update	sequence version 1 01-JAN-2000
Last Annotation Update	entry version 1 01-JAN-2000

Description and Origin of the Protein

Description Automated Functional Annotation.
 Organism Source Leptospaeria maculans "brassicae" group
 Organism Classification Eukaryota; Fungi/Metazoa group; Fungi; Dikarya; Ascomycota; Pazi
 NCBI Taxonomy ID 225342

Similarities

Database Cross-References

PANTHER	PTHR10194-SF24
PANTHER	PTHR10194
PROSITE	PS50018
Pfam	PF00616
SMART	SM00323
superfamily	SSF48350
superfamily	SSF50729
GnpGenome	Lema_P000040.1

Features



Motifs/Domains	Begin	End	Length	Tool
polypeptide	1	1591	1591	reference
G3DSA:1.10_506.10	849	1062	214	gene3d
PF00616	838	1028	191	HMMPfam
PS50018	768	1028	261	proflescan
PTHR10194	632	1115	484	HMMPanther
PTHR10194-SF24	632	1115	484	HMMPanther
SM00323	717	1127	411	HMMSmart
SSF48350	738	1127	390	superfamily
SSF50729	259	360	102	superfamily
SSF50729	441	539	99	superfamily
coil	1415	1455	41	coils
seg	1062	1083	22	seg
seg	1213	1220	8	seg
seg	1236	1254	19	seg
seg	1279	1294	16	seg
seg	1382	1392	11	seg
seg	1402	1501	100	seg
seg	1513	1541	29	seg
seg	1542	1559	18	seg
seg	183	215	33	seg
seg	226	240	15	seg
seg	3	18	16	seg
seg	54	100	47	seg

Sequence

Characteristics Length : 1591, molecular weight: 177773, CRC64 check sum: F9AF690BC383EB5F

Sequence >LeptoFunAnnot:P00004 Automated Functional Annotation.
 NDQQRSRREYVASEAAAGLQTADRPDRERSGGTIRVTFFOOLSIP EEVGCGGGGGGG
 GGGGSSGGGSSQSPSPNSPSPGQISGPGGQSPSSSSGQRTTSPRAFVARATSTETERN
 ASQQTWPFTLERSRTRDRSSSLFAGRRRIGSVASTTARFQSLKESPTSIIGIIS
 TISPPSSSQIQOQHQHQHQHQPRTSTNSRRLIKQPLRTESPANVAAMNPNAAAP
 ESNPSPVPAEDARKLKALNRSPQGRMQGLLAFRRGESSPPALSSCFINEAGSLVYEKFN

Showing 1.591 kbp from Lema_P000040.1, positions 1 to 1,591

Instructions
 Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed. To center on a location, click the ruler. Use the ScrollZoom buttons to change magnification and position.
 Examples: Lema_P000020.1, Lema_P000040.1, Lema_P000050.1

Bookmark this [[Upload your own data](#)] [[Hide banner](#)] [[Share these tracks](#)] [[Link to Image](#)] [[High-res Image](#)] [[Help](#)] [[Reset](#)]

Search
 Landmark or Region: Search
 Data Source: Leptospaeria maculans automated functional annotation
 ScrollZoom: Show 1.591 kbp

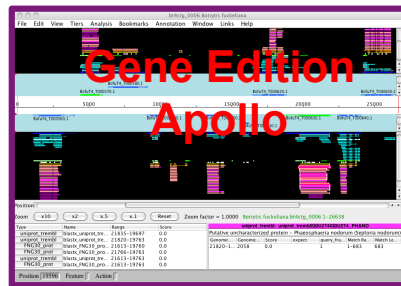
Overview

Details
 polypeptide
 HMMPfam
 TMMH
 SignalP
 PRINTScan
 gene3d
 HMMPanther
 HMMSmart
 proflescan
 superfamily
 coils
 HMMTig
 scarngexp
 seg
 HMMFam
 patternscan
 Blast vs CDD
 Rpsblast vs Kog

Use keyboard Update Image

Tracks
 Blast (vsBlast) All on All of
 Blast vs CDD Rpsblast vs Kog
 General info All on All of
 polypeptide
 InterProScan All on All of
 coils HMMPfam patternscan SignalP
 PRINTScan HMMFam proflescan superfamily
 gene3d HMMSmart scarngexp TMMH
 HMMPanther HMMTig seg

Leptospaeria Leptospaeria maculans complex

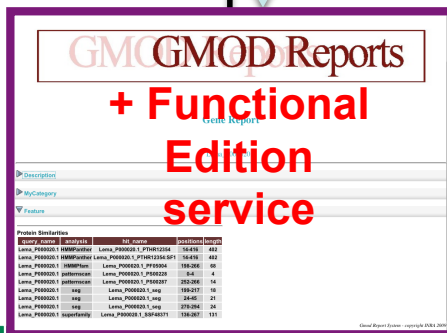


**Gene Edition
Apollo**

Authentication

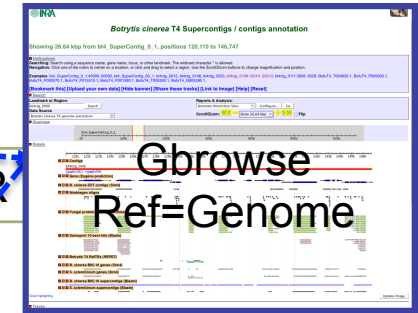
**chado
For
Edition**

Authentication



**GMCGMOD Reports
+ Functional
Edition
service**

Bio::SeqFeat
ure::Store
OR
Bio::DB::Gff



OR

**Gbrowse
Ref=Genome**

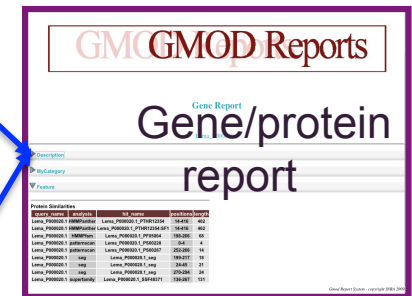
Genes Release (GFF)
= Manually Annotated
Struct + Funct

**chado
Struct. Annot
Ref=genome**

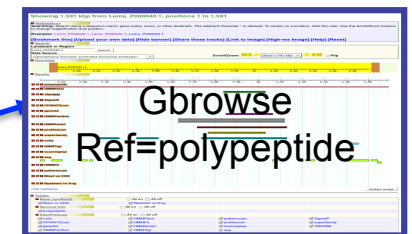
**MediaWiki
+ Semantic Web
+ Halo Extension**

Genes Release (GFF)
= Manually Annotated Struct + Funct.
+ Automatically annotated struct not
overlapping

**Chado
Func. Annot
Ref=polypeptide**



GMCGMOD Reports
Gene Report
Gene/protein
report



**Gbrowse
Ref=polypeptide**



GNPAnnot project
www.gnpannot.org



GMOD Community

Fabrice Legeai (INRA, Bio3P)

Presentation by Michael Alaux (INRA, URGI)

Ensembl release 49: Drosophila melanogaster Gene report for FBgn000363 - Mozilla Firefox

Ensembl Fruitfly GeneView

Ensembl release 49 - Mar 2008

Ensembl Gene Report for FBgn000363

Gene: *cnn* (FlyBaseName gene) To view all Ensembl genes linked to the name [click here](#).

FlyBase Gene ID: FBgn000363

Genomic Location: This gene can be found on Chromosome 2R at location [13,757,595-13,841,516](#). The start of this gene is located in [Chrom 19_275](#).

Description: No description.

Prediction Method: Feature imported from FlyBase gff files (<http://www.flybase.org>)

Transcripts:

Gene ID	Transcript ID	Transcript Name	Transcript Info	Exon Info	Intron Info
FBgn000363	FBtr000363	<i>cnn</i>	Transcript info	Exon info	Intron info

Orthologue Prediction: The following gene(s) have been identified as putative orthologues:
 INR. If you don't find a homologue here, it may be a 'between-species paralogue'. Please view the [gene tree info](#) or export between-species paralogues with [BiMart](#) to see more.)

Species	Type	ENSEMBL Gene Identifier
Done		

Protein features:

- InterPro: [IPR000001](#) RNA recognition motif, [IPR000002](#) RNP-1, [IPR000003](#) Andrew protein type 1
- Protein Family: [PF000001](#) - AMBICOUK
- Transcript structure:
- Protein features:

FlyBase Gene Dmelcnn

Home Tools Files Species Documents Resources News Help Archives Jump to Gene Go

Profile Manager Help Open All Close All

General Information

Symbol	Dmelcnn	Species	<i>D. melanogaster</i>
Name	centrosomin	Annotation symbol	CG4832
Feature type	protein_coding_gene	FlyBase ID	FBgn0013765
Created / Updated	2005-09-09/2005-09-09		

Genomic Location

Chromosome (arm)	2R	Recombination map	2-65
Cytogenetic map	50A8-50A9	Sequence location	2R:9,326,816..9,337,990 [-]

Map (Browse)

Decorated FASTA Get genome region

Gene region Get FASTA

Summary

Automatically generated summary

See sections below for more information

The gene *centrosomin* is referred to in FlyBase by the symbol *cnn* (CG4832, FBgn0013765). It has the cytological map location 50A8-50A9. Its sequence location is 2R:9326816..9337990. Its molecular function is described as: microtubule binding; ATPase activity, coupled. It is involved in the biological processes: microtubule cytoskeleton organization and biogenesis; central nervous system development; midgut development; peripheral nervous system development; nuclear division; centrosome cycle; microtubule-based process; female meiosis chromosome segregation; mitotic spindle organization and biogenesis. 26 alleles are reported. The phenotypes of these alleles are annotated with 14 unique terms, many of which group under: organ system; stage; intracellular organelle part; spindle; cell cycle; gonad; spindle

Browse Apollo Blast Search Documents Data Help

PropriétéTitre: valeurTitre

Catégorie A

propriété1	valeur1
propriété2	valeur2, valeur3
propriété3	valeur4
propriété4	

Feature type 1

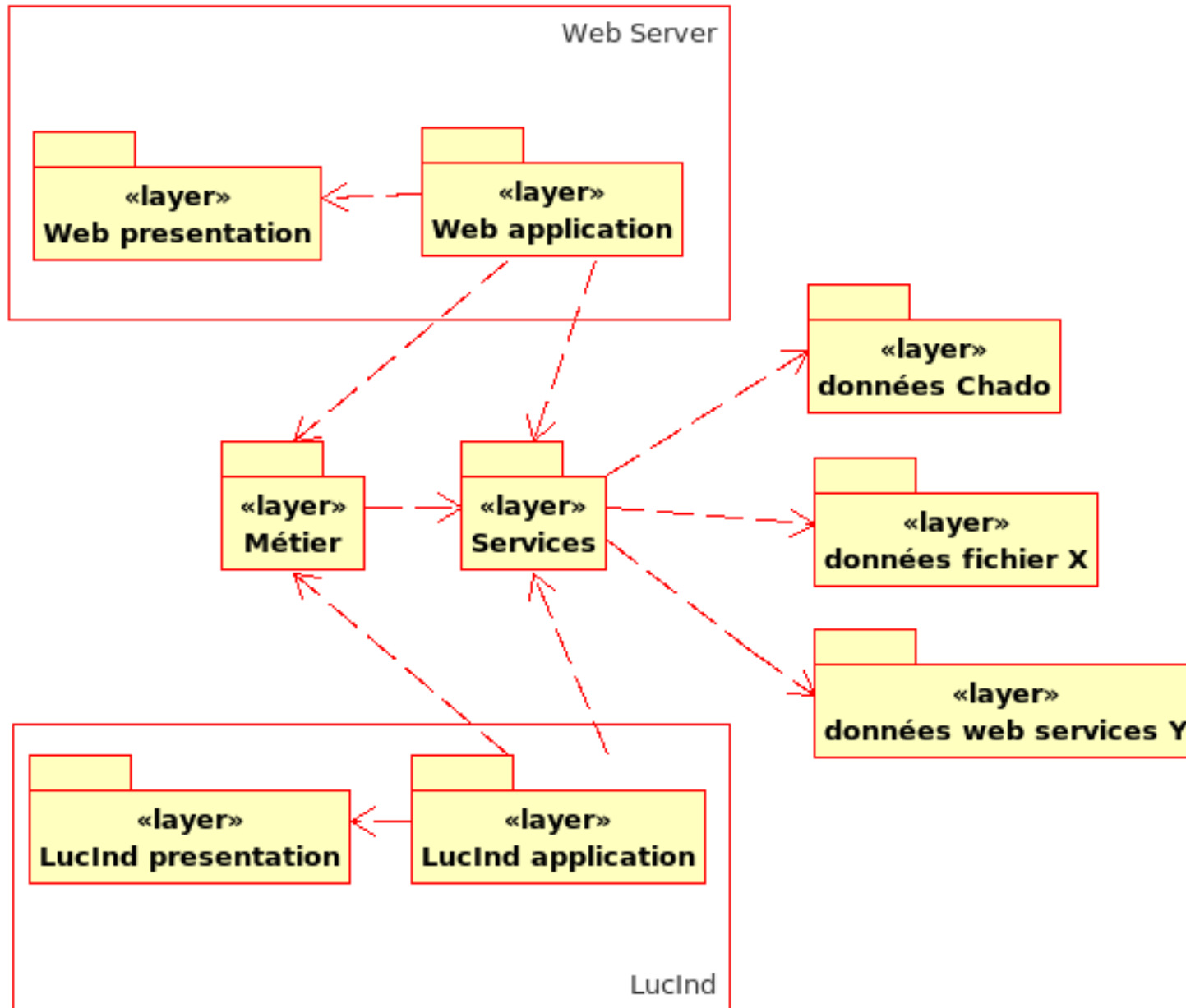
start1 - stop1	propriété5	valeur5
	propriété6	valeur6
start2 - stop2	propriété5	valeur7
	propriété6	valeur8

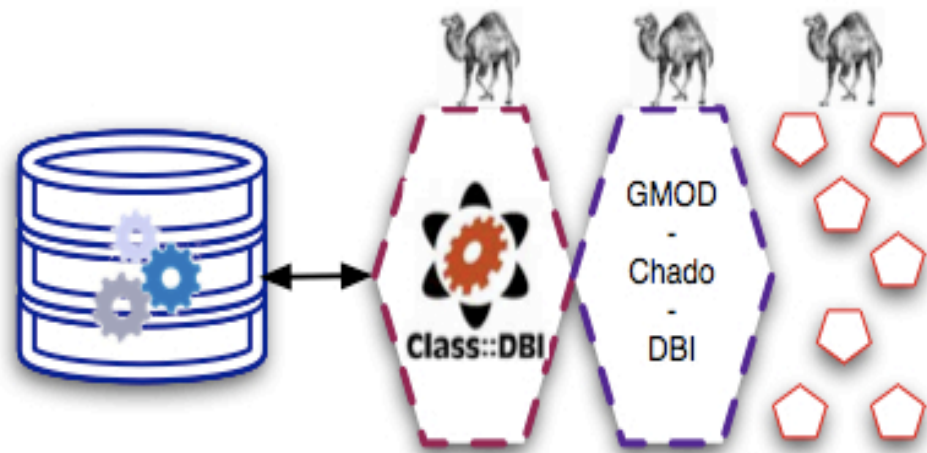
Action X Action Y

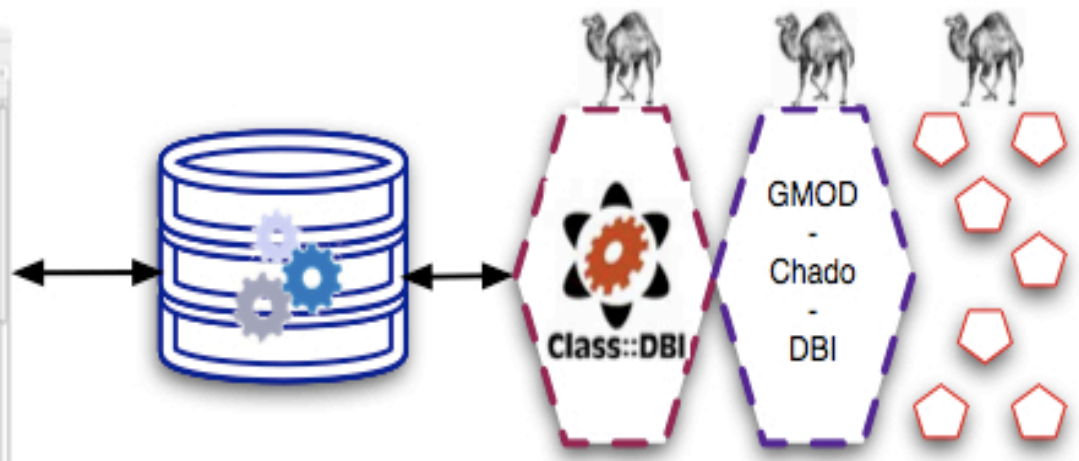
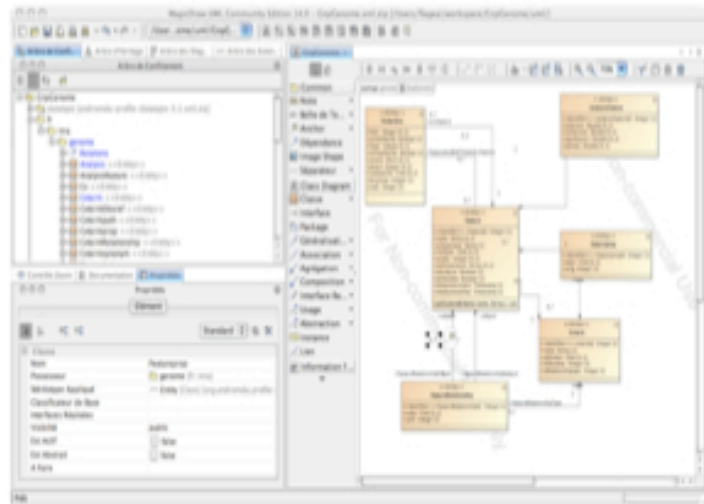
Catégorie B

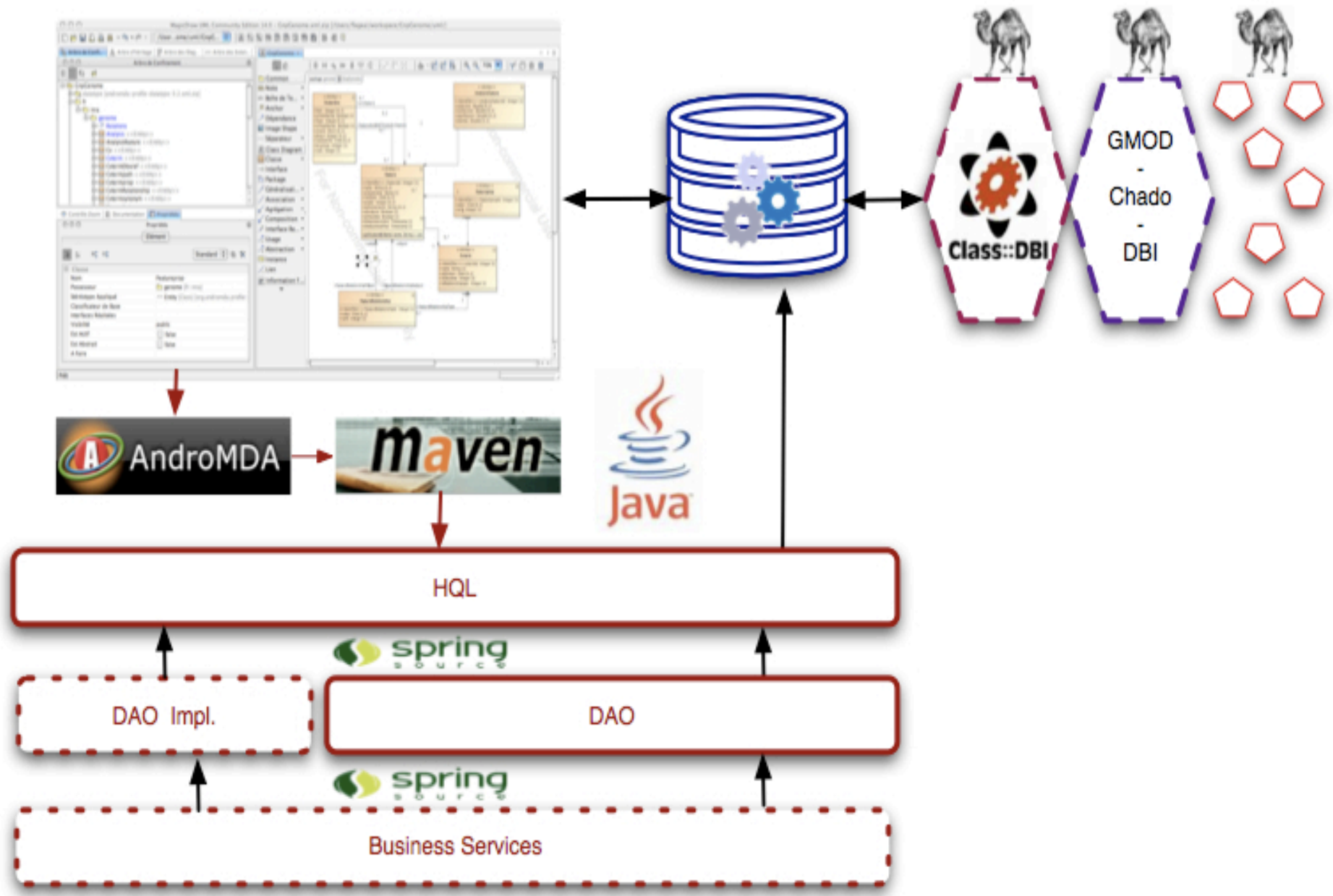
Catégorie C

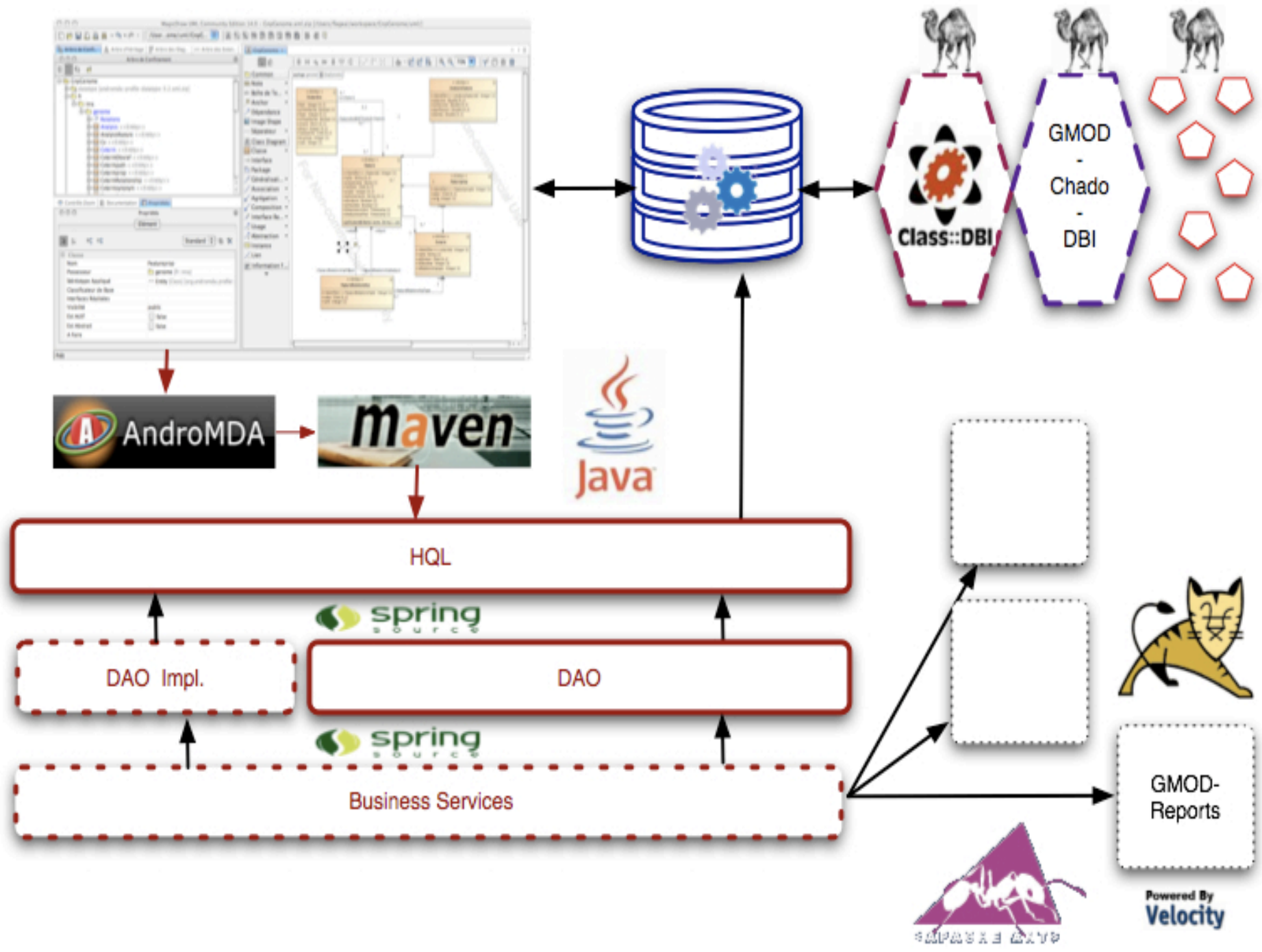
Catégorie D













Gene Report

ACYPI009445-RA_1

Description

Genomic Position

Transcripts

Similarity

OtherProperties

Gmod Report System - copyright INRA 2009

http://webapps1.genouest.org/grs-1.6/grs?reportID=aphidbase_genome_report&objectID=ACYPI006415-RA#



Gene Report

ACYPI006147-RA_1

Description

ID ApisOBP2-transcript

Name ApisOBP2-transcript

Synonym ACYPI006147-RA_1

Synonym ApisOBP2-transcript

Synonym ACYPIG179180-jjzhou-RA

owner Name : Jing-Jiang Zhou
Institute : Rothamsted Research

comments putative odorant-binding protein 2.

Genomic Position

Transcripts

Similarity

OtherProperties

Gene Report

ACYPI006147-RA_1

Description

ID ApisOBP2-transcript

Name ApisOBP2-transcript

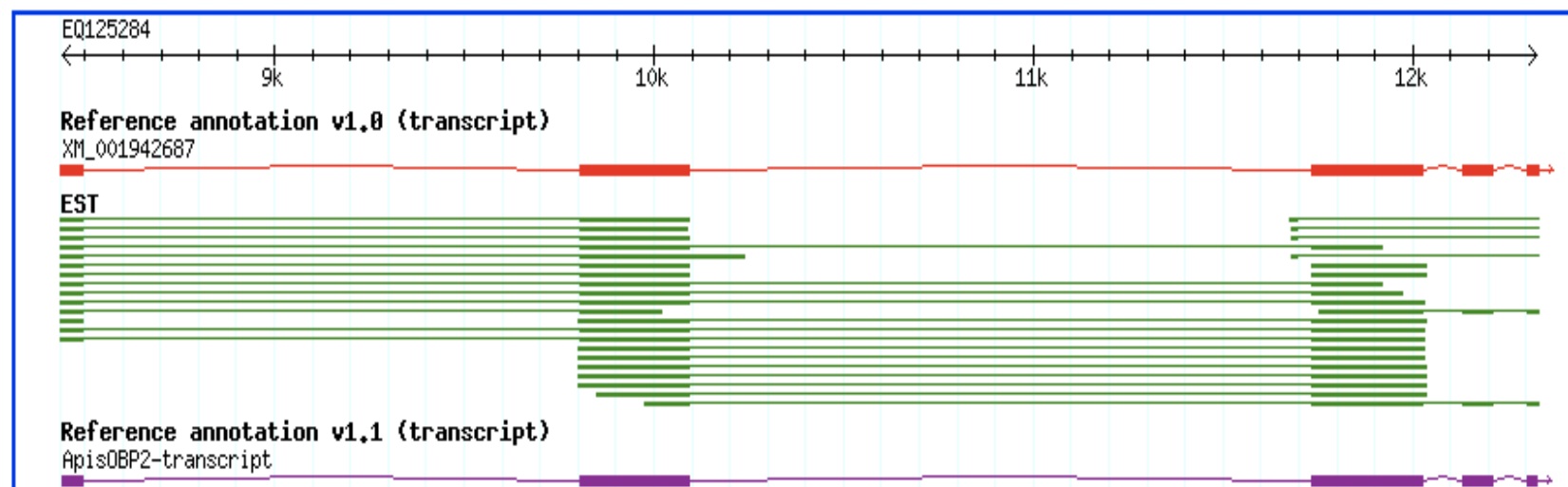
Synonym ACYPIG179180-jjzhou-RA

Synonym ApisOBP2-transcript

Synonym ACYPI006147-RA_1

+ Genomic Position

Gbrowse



+ Transcripts

+ Similarity

Description

ID ApisOBP2-transcript**Name** ApisOBP2-transcript**Synonym** ACYPI006147-RA_1**Synonym** ApisOBP2-transcript**Synonym** ACYPIG179180-jjzhou-RA**owner** Name : Jing-Jiang Zhou
Institute : Rothamsted Research**comments** putative odorant-binding protein 2.

Genomic Position

Start **Stop** **Strand**

8440 12325 PLUS

Scaffold

EQ125284

Transcripts

mRNA Name **Scaffold** **Start** **Stop** **Strand**

ApisOBP2-transcript EQ125284 8440 12325 PLUS

>ApisOBP2-transcript_mRNA

ATGAAGGTATCTGCAGCGACCGCGTCTGGTCGCTCTGGTCGCCACCGTGCAGAGCTCGGACCCATGTAACATATCTACTTGCTACAAGAGCGGCACGA
 CGAAGCCGCAATGGCCGTACGCCCACTCACCTGCCGGTACAGTCATCGTCCACCCAGACCACCCACAGACCAGTACGCCAAGGATCACGTGCA
 CGGTTCAACCACCACCAAGTCCGGTGTCAATGCTACGGTCACGACAGCCAGCGGAGCGTCCGTCAACGGCACTGAACCGCCGGCCGTCAAGTCTTCC
 GCCGGAGTAACCGGAACTCCACCACGCCCAAGCCTACAATGACCGAAGGACATGTGGCTCTGAAACAGAAGTTGAACACAATTGCGGTGAAGTCAAGG
 ACGAGCTGCACGCGCCCAAGAGATCATGGCACTGGTCAGTAAACACGGTAGTACCGCAGAACGAGCAACAAAGGTGCTACTTAGAGTGCCTGTACAAAA
 TCTTAATTTGATCAAAAATAACAAGTTCAGTGTGGAAGACGGCAAGGCGATGGCTAGAATACGCTTCGCAAATCAACCAGAAGGCACAAAGGAGCAGTA
 ACCATAATAGAAACTTGCGAAAAAGAAGCTGTTATCGATCCGAAACCACCTGAAAAATGCGCAGCTGGACGAGTAATCAGAACTGCTTCGTCAAAAACG
 GAGAAAAATAAATTTCTTCCCTAAAGCATAA

>ApisOBP2-transcript_prot

MKVSAATAVLVALVATVQSSDPCNISTCYKSGTTKPPMAVTPHLPVQSSSTQTSHPQTTYAKDHVHGSTTTKSGVNATVTTASGASVNGTEPPAVVKSS
 AGVTGNSTTPKPTMTBGHVALKQKLNLTIAVKCKDELHAPQEIMALVNSNTVVPQNEQQRCYLECVYKNLNLIKNNKFSVEDGKAMARIRFANQPPEHKKAV
 TIIETCEKEAVIDPKTTEKCAAGRVI RNCVFKNGEKINFFPKA

Exon **Start** **Stop** **Strand**

ACYPIE9001-jjzhou 8440 8494 PLUS

ACYPIE9002-jjzhou 9804 10089 PLUS

ACYPIE9003-jjzhou 11734 12023 PLUS

ACYPIE9004-jjzhou 12130 12210 PLUS

ACYPIE9005-jjzhou 12301 12325 PLUS

Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	12456	13152	+	FF308174
Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	9976	12465	-	EX631171
Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	8221	11917	+	EX645090
Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	11754	12677	-	EX645235
Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	8246	10019	+	EX646992
Acyrtosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	12335	12465	-	EX648195
Acyrtosiphon pisum	head	ApHL3SD	12696	13007	-	DY228241
Acyrtosiphon pisum	whole body, nymphs and adults	Acyrtosiphon pisum, Pea Aphid	9801	12032	+	CN582915
Acyrtosiphon pisum	whole body, nymphs and adults	Acyrtosiphon pisum, Pea Aphid	8283	8494	+	CN583930
Acyrtosiphon pisum	whole insect	ApMS	9801	12030	+	CN754376
Acyrtosiphon pisum	whole insect	ApMS	9801	12030	+	CN758381
Acyrtosiphon pisum	whole insect	ApMS	9801	12032	+	CN760196
Acyrtosiphon pisum	whole insect	ApMS	9801	12032	+	CN764432
Acyrtosiphon pisum	whole insect	ApMS	8231	12030	+	CN764449
Acyrtosiphon pisum	whole insect	ApMS	8283	12030	+	CN764329
Acyrtosiphon pisum	whole insect	ApMS	8283	12030	+	CN754121
Acyrtosiphon pisum	whole insect	ApMS	8231	11969	+	CN758303
Acyrtosiphon pisum	whole insect	ApMS	9801	12032	+	CN759740

Summary of organism

value	Number	frequency
Acyrtosiphon pisum	24	1.0

Summary of tissue_type

value	Number	frequency
whole insect	9	0.375
Whole body, nymphs and adults, winged and wingless	12	0.5
head	1	0.041666668
whole body, nymphs and adults	2	0.083333336

Summary of clone_lib

value	Number	frequency
Pea aphid whole body normalized full length cDNA library	12	0.5
ApHL3SD	1	0.041666668
Acyrtosiphon pisum, Pea Aphid	2	0.083333336
ApMS	9	0.375

Protein Similarities

query_name	analysis	hit_name	description	interpro_id	go	positions
XP_001942722	Gene3D	G3DSA:1.10.238.20	no description	IPR006170	Molecular Function: odorant binding (GO:0005549), Biological Process: transport (GO:0006810)	120-241
XP_001942722	HMMPfam	PF01395	PBP_GOBP	IPR006170	Molecular Function: odorant binding (GO:0005549), Biological Process: transport (GO:0006810)	113-235
XP_001942722	HMMSmart	SM00708	no description	IPR006625		127-234
XP_001942722	Seg	seg	seg			2-17,47-60
XP_001942722	superfamily	SSF47565	Insect pheromone/odorant-binding proteins	IPR006170	Molecular Function: odorant binding (GO:0005549), Biological Process: transport (GO:0006810)	113-241

OtherProperties

New services and perspectives

- More graphics and more statistics
- Cross reference towards paralogous and orthologous genes
- Gene ontology trees
- Publication References
- Add annotation by authorised curators
- Versionning

http://webapps1.genouest.org/grs-1.6/grs?reportID=aphidbase_genome_report&objectID=ACYPI006415-RA#.



GNPAnnot project
www.gnpannot.org



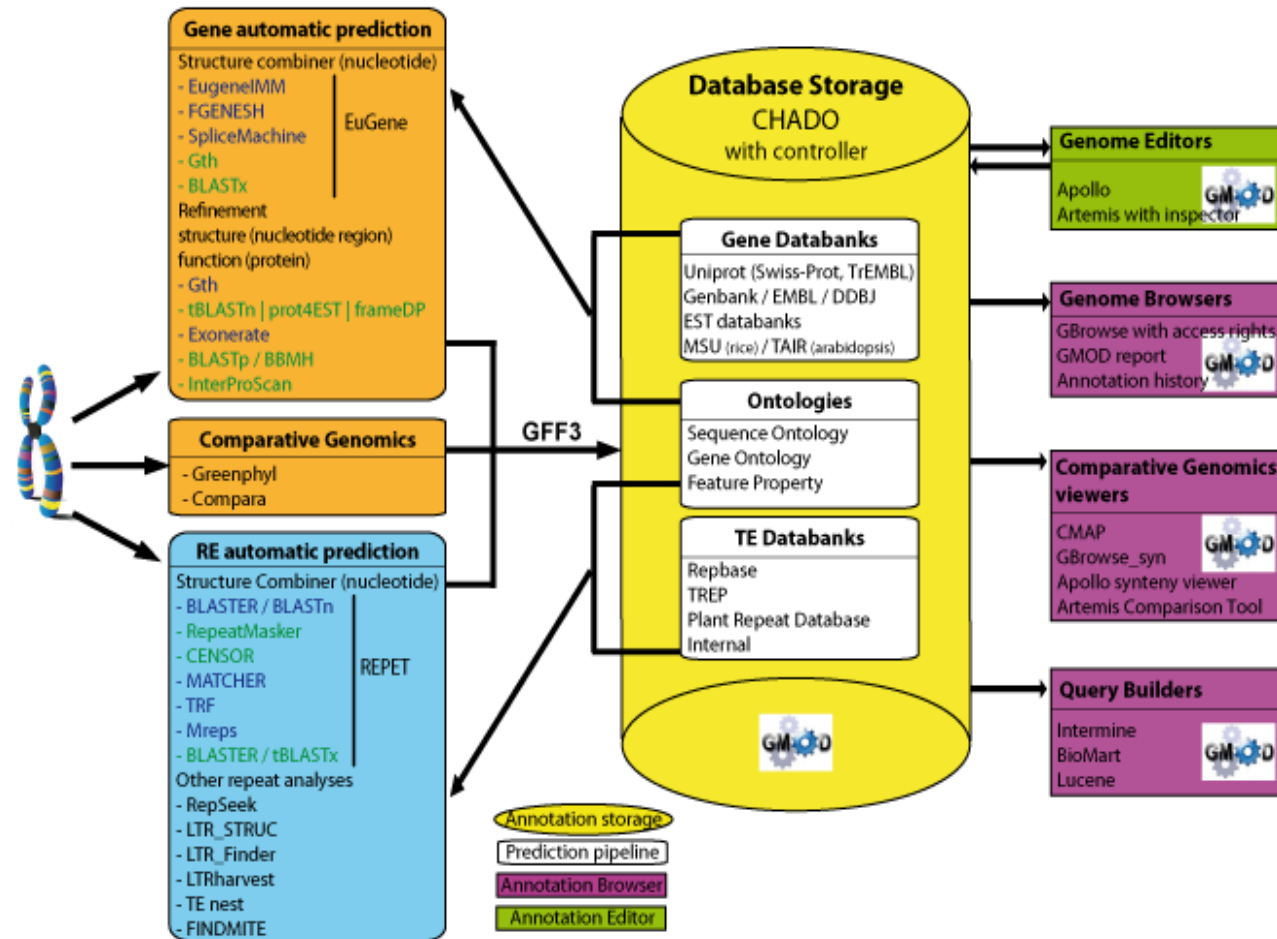
GMOD Community



Valentin Guignon (CIRAD, UMR DAP)

Presentation by Michael Alaux (INRA, URGI)

1. Context
2. Annotator Access Restriction on Biological Features
 1. Architecture
 2. PostgreSQL Embedded Part
 3. Genome Browser Integration
3. History of Manual Annotations
 1. Architecture
 2. PostgreSQL Embedded Part
 3. Genome Browser Integration
4. Inspector of Manual Annotations
 1. Architecture
 2. PostgreSQL Embedded Part
 3. Genome Browser Integration
5. Conclusion

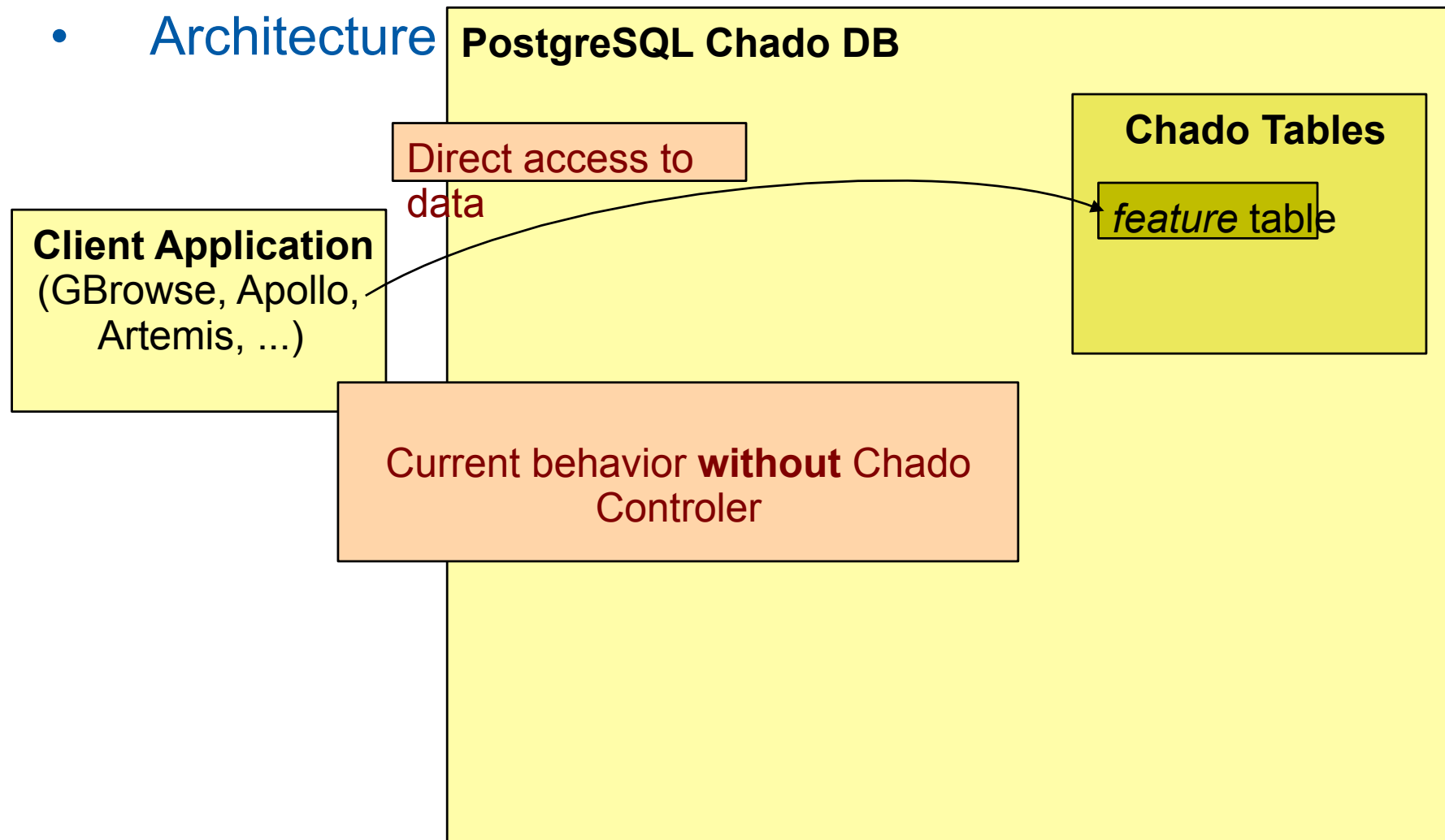


- Needs
 - Restrict access to specific contigs
 - contig visibility and write access
 - manage access by groups
 - Help manual annotation process
 - Auto-fill properties
 - Improve quality
 - Keep track of annotations
 - old records with date and author

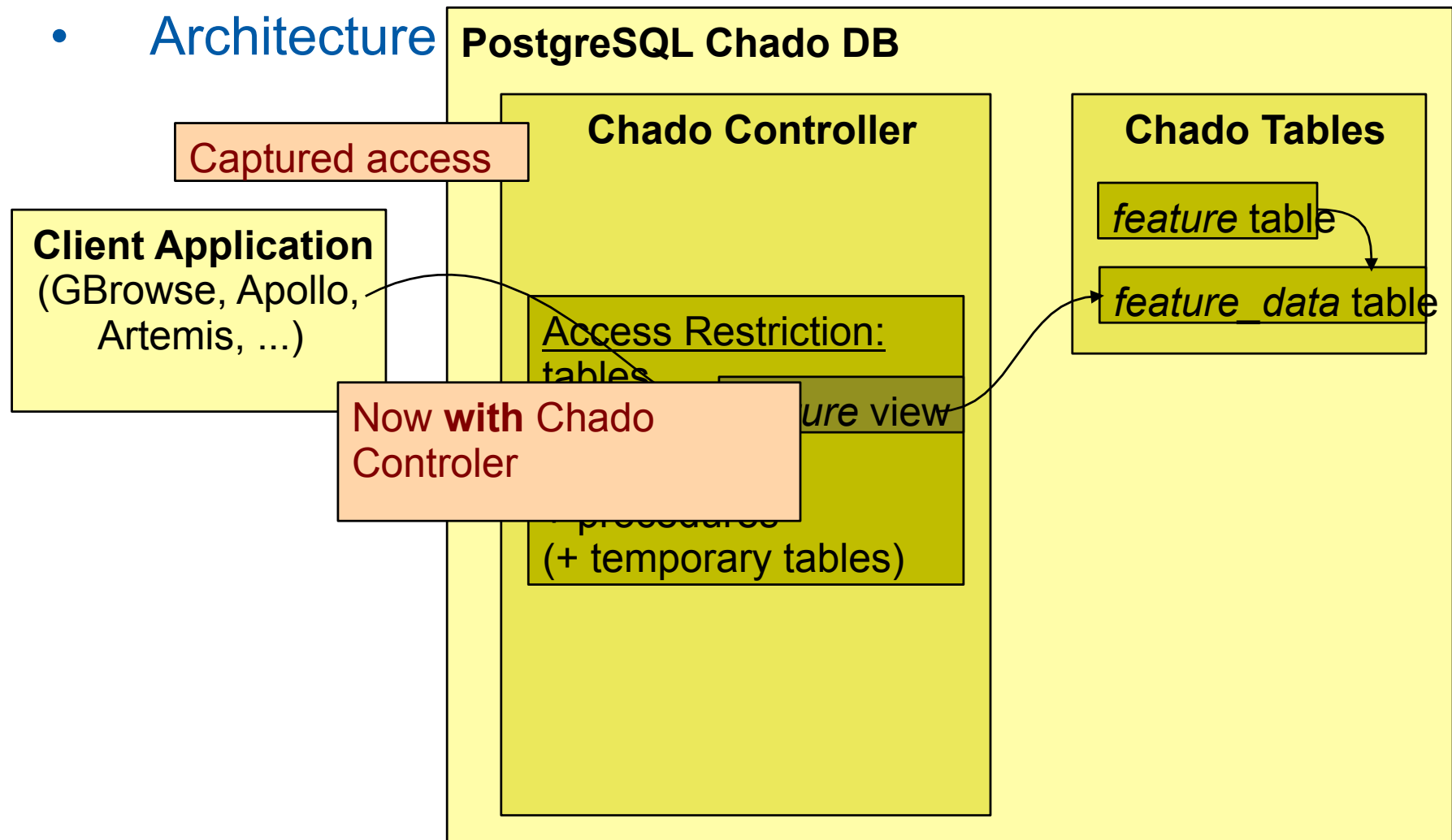
Goals

- Manage access right to Chado features
- Inspect manual annotations
- Manage history of manual annotations

- Architecture



- Architecture



• PostgreSQL Embedded Part

- Access to feature table through a view with rules (for *insert/update/delete*)
- Restrictions using a table of users/groups and a table to associate an access level for each feature to a user or a group
- To improve queries speed, a temporary access table is created for each PostgreSQL session (for softwares with persistent connexion like Artemis or Apollo)

•Genome Browser Integration

- ◆ Web access → each page = a new PostgreSQL session
- ◆ Temporary access tables init. slows down GBrowse too much
→ solution: integrate access restriction to GBrowse queries using a special account (with read access on everything)

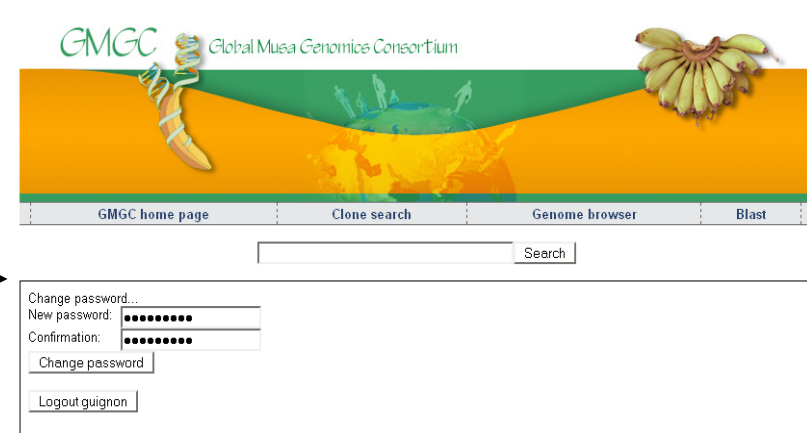


The landmark named *scaffold_0009:1..20000* is not recognized. See the help pages for suggestions.

■ Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.

Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

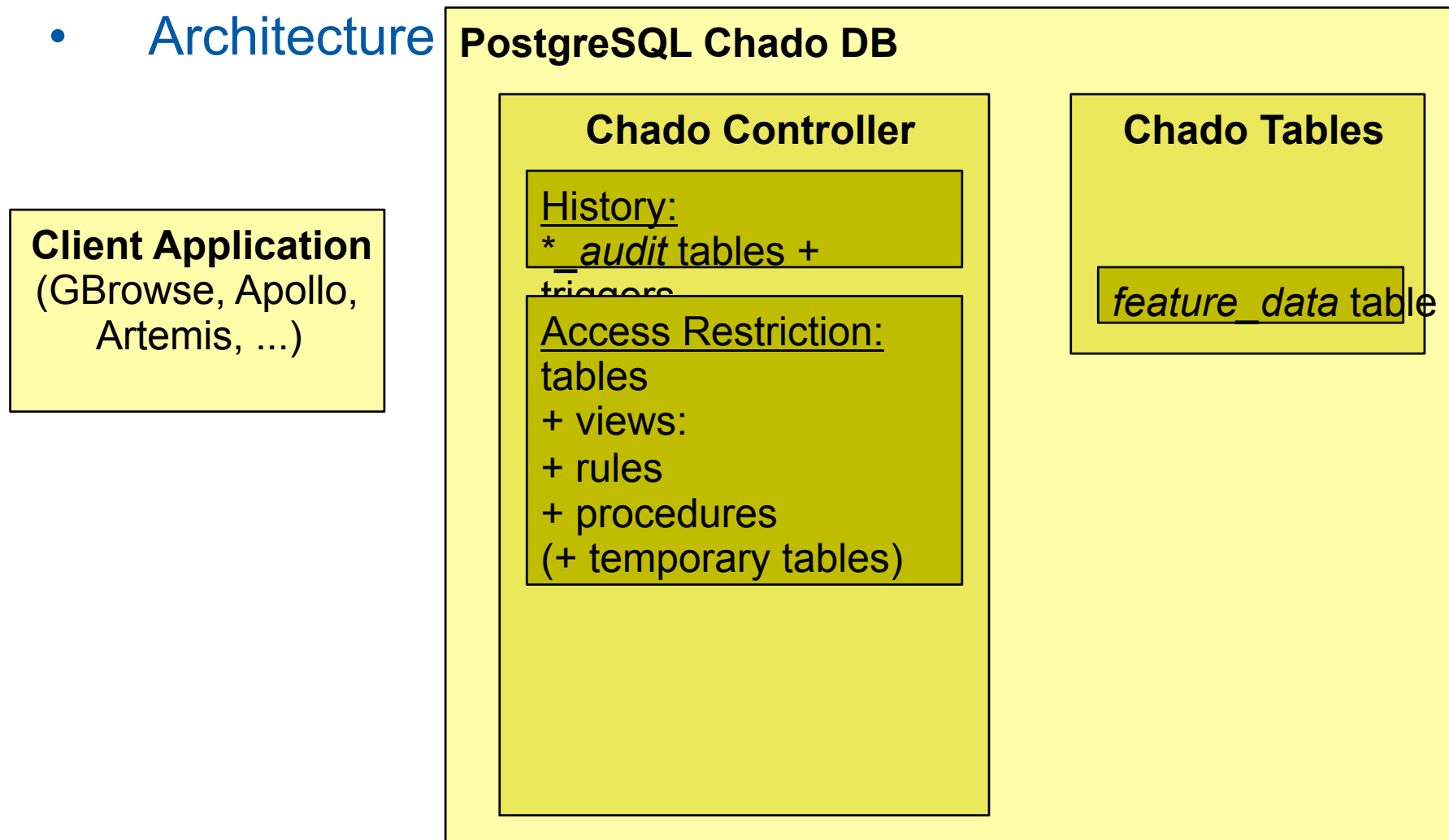


Showing 20 kbp from *scaffold_0009*, positions 1 to 20,000

■ Instructions

Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.

- Architecture



- PostgreSQL Embedded Part
- based on Chado audit module with some adds:
 - Author of the modification
 - Group of transaction identifier

•Genome Browser Integration: a *gbrowse details*-like script

Curated annotation
(modifications in
bold)

Previous
annotation of
MaC088K20_g
300

```

Date: 20:42 06/01/2010
Author: sidibebocs

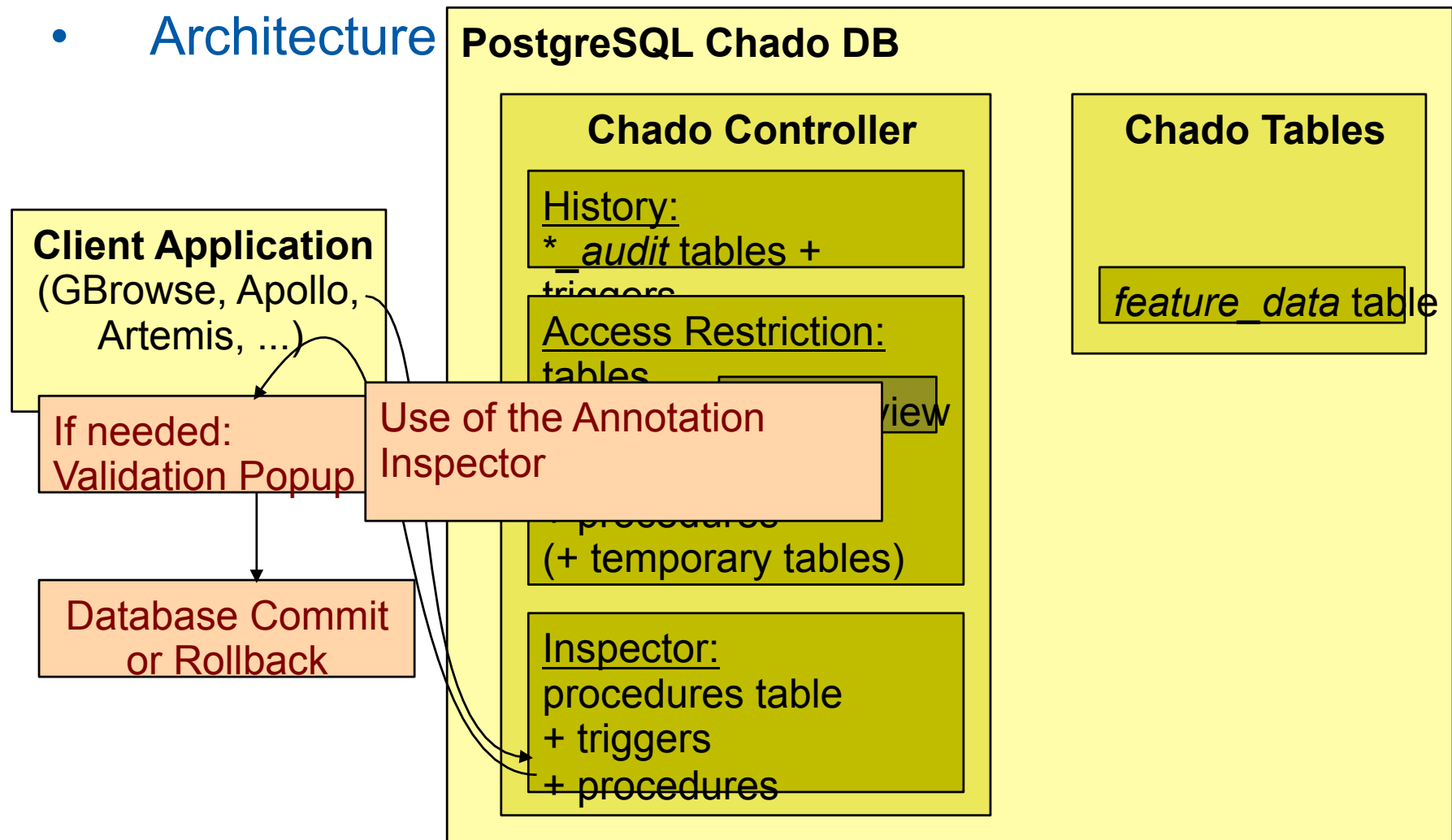
Gene: [+]132826..138435 - 19:47 06/01/2010
mRNA: [+]132826..138435 - 19:47 06/01/2010
Exon: [-]Join(132826..133731, 136131..136499, 136606..136872, 137384..137511, 138198..138436) - 19:47 06/01/2010
      Join(132826..133731, 136131..136499, 136606..136872, 137384..137511, 138198..138435) - 19:47 06/01/2010
/owner="sidibebocs"
/annotator_comment="The two first exons have been merged due to similarity results (Scov was < 0.8)"
/inference="{EuGene rice 3.2; uniprot_sprot:O82436; uniprot_trembl:A1I1Y2}"
/length="635 aa"
Product "Ethylene receptor protein"
/completeness="complete"
/evidence_code="IC 1"
/gene="ERS3"
/eC_number="2.7.13.3"
/locus_tag="MaC088K20_g300"
PMID="19357434"
    
```

```

Date: 18:21 06/01/2010
Author: gnpannot

Gene: 132826..138435
mRNA: 132826..138435
Exon: Join(132826..133731, 136131..136499, 136606..136872, 137384..137511, 138198..138435)
/owner="fcb"
/annotator_comment="to fill"
/inference="{EuGene rice 3.2; uniprot_sprot:O82436; uniprot_trembl:A1I1Y2}"
/length="635 aa"
Product [+]"Ethylene receptor protein" - 11:57 06/01/2010
/completeness="complete"
/evidence_code="2"
/locus_tag=[+]"MaC088K20_g300" - 18:21 06/01/2010
    
```

- Architecture



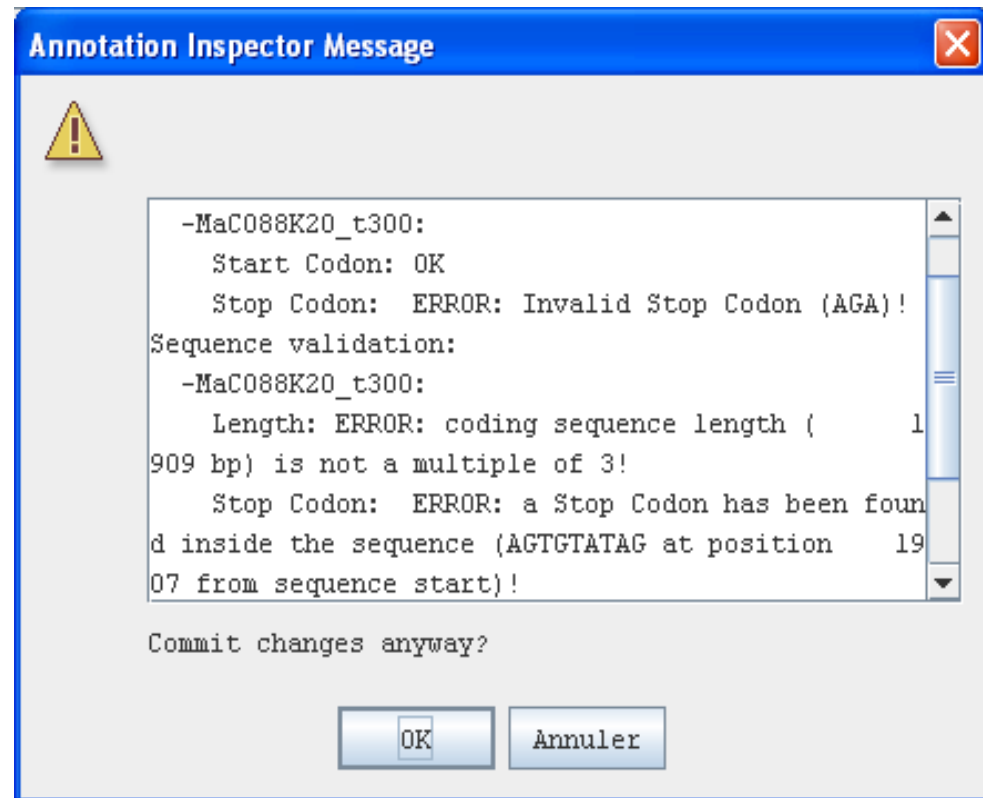
• PostgreSQL Embedded Part

- Based on triggers to auto-fill some feature properties (e.g. “/owner”, “/color”, TE structure,...)
- Additional procedures for inspection of the structure and the function of curated genes to be called by the genome editor (e.g. start/stop codon, CDS length, splicing sites,...)

- Genome Editor Integration
- Artemis calls the **initialization** procedure once connecting to Chado.
- Then, before each set of transactions to commit, it calls a procedure to get a new **group of transaction identifier**.
- Then, all the queries are executed and just before the commit, an **inspection procedure** is called with the identifier obtained earlier.
- Finally, the procedure returns the **inspection status** and Artemis can either **commit or rollback**.

- Genome Editor Integration

Example of error message of invalid structural curation of MaC088K20_g300



•Features

•Annotator Access Restriction

- Feature-level access control
- User and group management
- Administration interface
- Backward compatibility

•History of Manual Annotations

- Keeps track of user actions

•Inspector of Manual Annotations

- Many checks and annotation automation

•Extra-features

- install/update/uninstall script
- Chado Controller versions tracking
- compatibility mode script (for *COPY FROM* queries)
- annotation inspector is extensible
- some parts of the Chado Controller can be enabled/disabled “live”

• Perspectives

- Include Annotation History into GMOD Report
- “chado_undo.pl” script
- Improve administration interface
- Access restriction for Bio::Seq::Feature and JBrowse
- Annotation inspector for Apollo

- GMOD report:

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- Chado controller:

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- ◆ Sebastien Reboux
- ◆ Delphine Steinbach
- ◆ Daphné Verdelet
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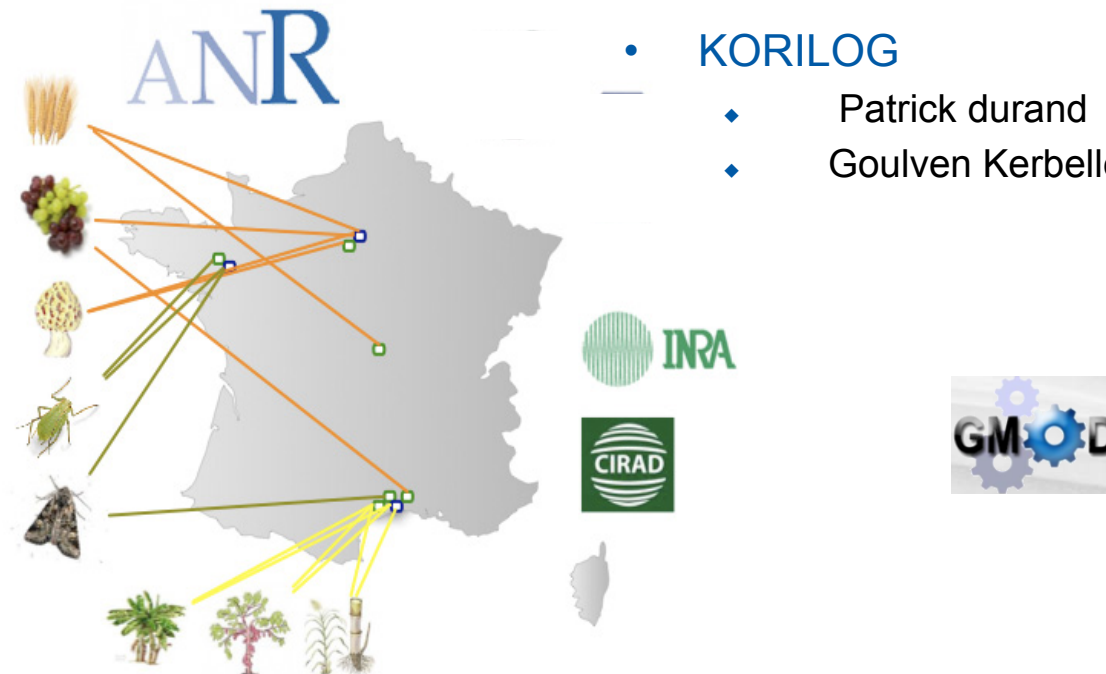
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