http://imgt.cines.fr

Systèmes d'information
-
Ontologies
Bases de connaissances

1
Système d'information (SI)

Ensemble des moyens

organisation (CNRS,…),
acteurs,
systèmes informatiques

nécessaires au traitement et à l'exploitation des informations dans le cadre d'objectifs définis

IMGT®,
the international ImMunoGeneTics information system

http://imgt.cines.fr

IMGT Home page - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
IMGT databases
IMGT/LIGM-DB (IG and TR from 150 species) (LIGM, Montpellier, France) (106 340 entries - 01/10/2006)
IMGT/MHC-DB (IMGT/MHC-HLA, -NHP, -DLA, -FLA) (ANRI, BPRC, hosted at EBI)
IMGT/PRIMER-DB (IG and TR from 11 species) (LIGM, Montpellier, France) (1 864 entries - 01/10/2006)
IMGT/GENE-DB (IG and TR genes from human and mouse) (LIGM, Montpellier, France) (1 512 genes, 2 458 alleles - 01/10/2006)
IMGT/3Dstructure-DB (IG and TR, MHC and RPI gene and allele identification and IMGT Colliers de Perles) (1 055 entries - 10/07/2006)
IMGT Web resources
IMGT Repertoire (IG and TR, MHC and RPI)
IMGT Index (FactsBook)
IMGT Scientific chart (Sequence description, Numbering, Nomenclature, Representation rules)
IMGT Bloc-notes (Interesting links, PubMed, Meeting announcements, Postdoctoral positions and jobs, Search engines...)
IMGT Education (IMGT Lexique, Aide-mémoire, Tutorials, Questions and answers, Enseignements...)
IMGT Medical page, IMGT Veterinary page, IMGT Biotechnology page
IMGT Posters and diaporama
The IMGT Immunoinformatics page
IMGT tools
IMGT/V-QUEST (sequence alignment software for IG, TR and HLA)
IMGT/JunctionAnalysis (for human and mouse IG and TR)
IMGT/Allele-Align
IMGT/DomainDisplay (Amino acid sequences) NEW!
IMGT/PhyloGene
IMGT/LocusView, IMGT/GeneView, IMGT/GeneSearch, IMGT/CloneSearch (for human IGK, IGL, IGH, TRA/TRD, TRB, TRG, mouse TRA/TRD and human MHC)
IMGT/GeneInfo (TIMC and ICH, Grenoble; LIGM, Montpellier)
IMGT/GeneFrequency NEW!
IMGT/DomainGapAlign NEW!
IMGT/Collier-de-Perles NEW!
IMGT/DomainSuperimpose NEW!
IMGT/StructuralQuery
IMGT other accesses
IMGT Other accesses (SRS, FTP...)
Compare your sequence against IMGT (BLAST, FASTA)
IMGT/LIGM-DB Sequence submission
IMGT flat file release information
Search
Google
www
IMGT domain

Système informatique

Partie automatisée d'un système d'information.

Le **système informatique** regroupe :

- le matériel physique et câblage (PC, réseau,….)
- Le réseau (adresse IP, noms, …)
- Le(s) système(s) d'exploitation (Windows, Linux, …)
- Sauvegardes

- **L'application et ses éléments d'accompagnement:**
  bases de données,
  logiciels de développement,
  interfaces d'exploitation, …

Les objectifs de IMGT/LIGM-DB

- Contenir toutes les séquences Ig et TcR des bases EMBL/GenBank/DDBJ

  de 106.000 séquences de 150 espèces

- Expertiser les séquences en fonction des connaissances en immunogénétique

  - description des motifs,
  - identification des gènes, …

- Suivi et intégration des nouvelles connaissances

Particularités des séquences IG et TR

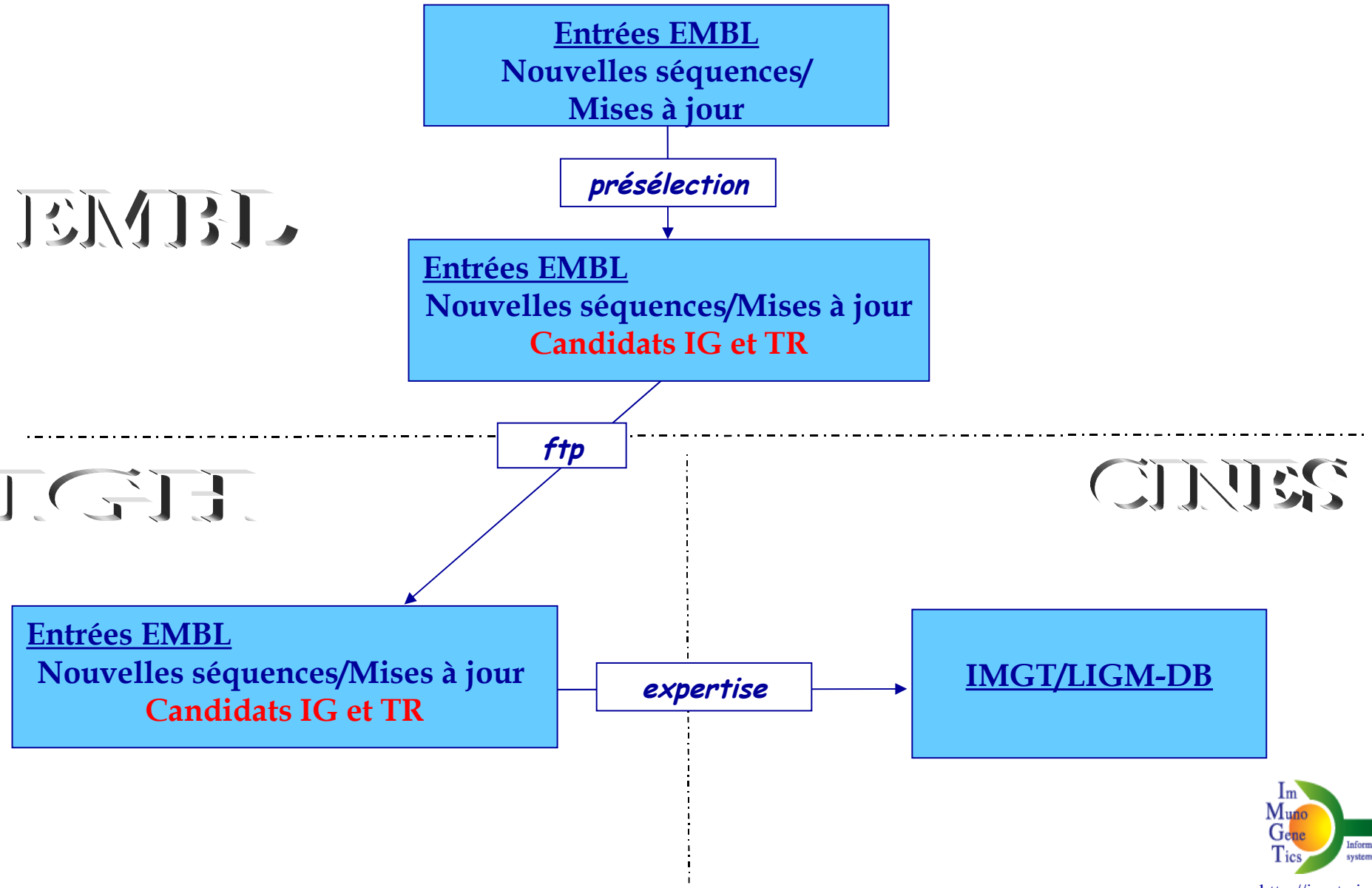
- Elles sont nombreuses
- Une forte similitude
- De petites différences très significatives
- Des nomenclatures hétérogènes

Administration et contrôle de données dans un système d'information: exemple de IMGT/LIGM-DB

1- Contrôler et coordonner les flux des données de différentes sources dans la base: comment coordonner l'entrée des séquences (700 arrivées par semaine) , des annotations et la distribution?

2- Gérer les accès aux données : qui annote les séquences, quelles informations peuvent être consultées, extraites et modifiées, et par qui?

IMGT/LIGM-DB: application distribuée



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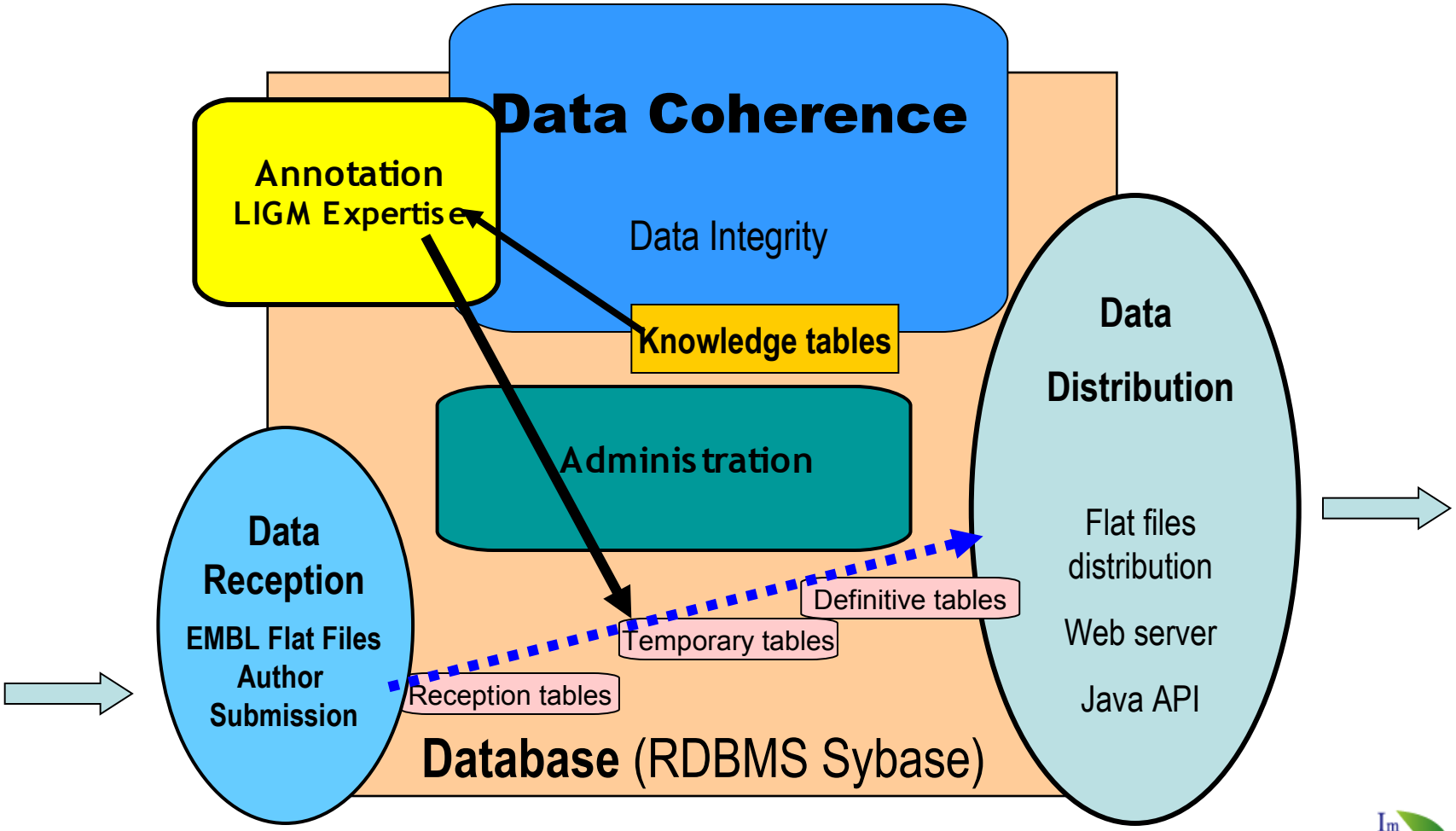
Une application informatique distribuée

utilise plusieurs machines

L'architecture d'une application distribuée est donnée par:

- la description des machines utilisées,
- les fonctions de ces machines pour l'application:
  - fonction stockage des données
  - fonction traitements des données
  - fonction interface utilisateur

Contrôler et coordonner les flux de données



A l'arrivée dans IMGT

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

EMBL FLAT-FILE

```
ID   AY998750   standard; mRNA; HUM; 366 BP.
XX
AC   AY998750;
XX
SV   AY998750.1
XX
DT   25-APR-2005 (Rel. 83, Created)
DT   25-APR-2005 (Rel. 83, Last updated, Version 1)
XX
DE   Homo sapiens isolate 4H immunoglobulin heavy chain variable region (IGHV1)
DE   mRNA, IGHV1-2*04 allele, partial cds.
XX
KW   .
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-366
RX   PUBMED; 15706403.
RA   Stamatopoulos K., Belessi C., Papadaki T., Kalagiakou E., Stavroyianni N.,
RA   Douka V., Afendaki S., Saloum R., Parasi A., Anagnostou D., Laoutaris N.,
RA   Fassas A., Anagnostopoulos A.;
RT   "Immunoglobulin Heavy- And Light-chain Repertoire in Splenic Marginal Zone
RT   Lymphoma";
RL   (er) Mol. Med. (2005) In press
XX
```

Après expertise dans IMGT

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

IMGT FLAT-FILE

```
ID   AY998750 IMGT/LIGM annotation : automatic; mRNA; HUM; 366 BP.
XX
AC   AY998750;
XX
DT   25-MAY-2005 (Rel. 200521-3, arrived in LIGM-DB )
DT   25-AUG-2005 (Rel. 200534-4, Last updated, Version 3)
XX
DE   Homo sapiens isolate 4H immunoglobulin heavy chain variable region (IGHV1)
DE   mRNA, IGHV1-2*04 allele, partial cds.  ;
DE   mRNA; rearranged configuration; Ig-Heavy; regular; functionality
DE   productive; group IGHV; subgroup HV1.
XX
KW   antigen receptor; immunoglobulin superfamily; Ig; Ig-Heavy; variable;
KW   diversity; joining; immunoglobulin.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-366
RX   PUBMED; 15706403.
RA   Stamatopoulos K., Belessi C., Papadaki T., Kalagiakou E., Stavroyianni N.,
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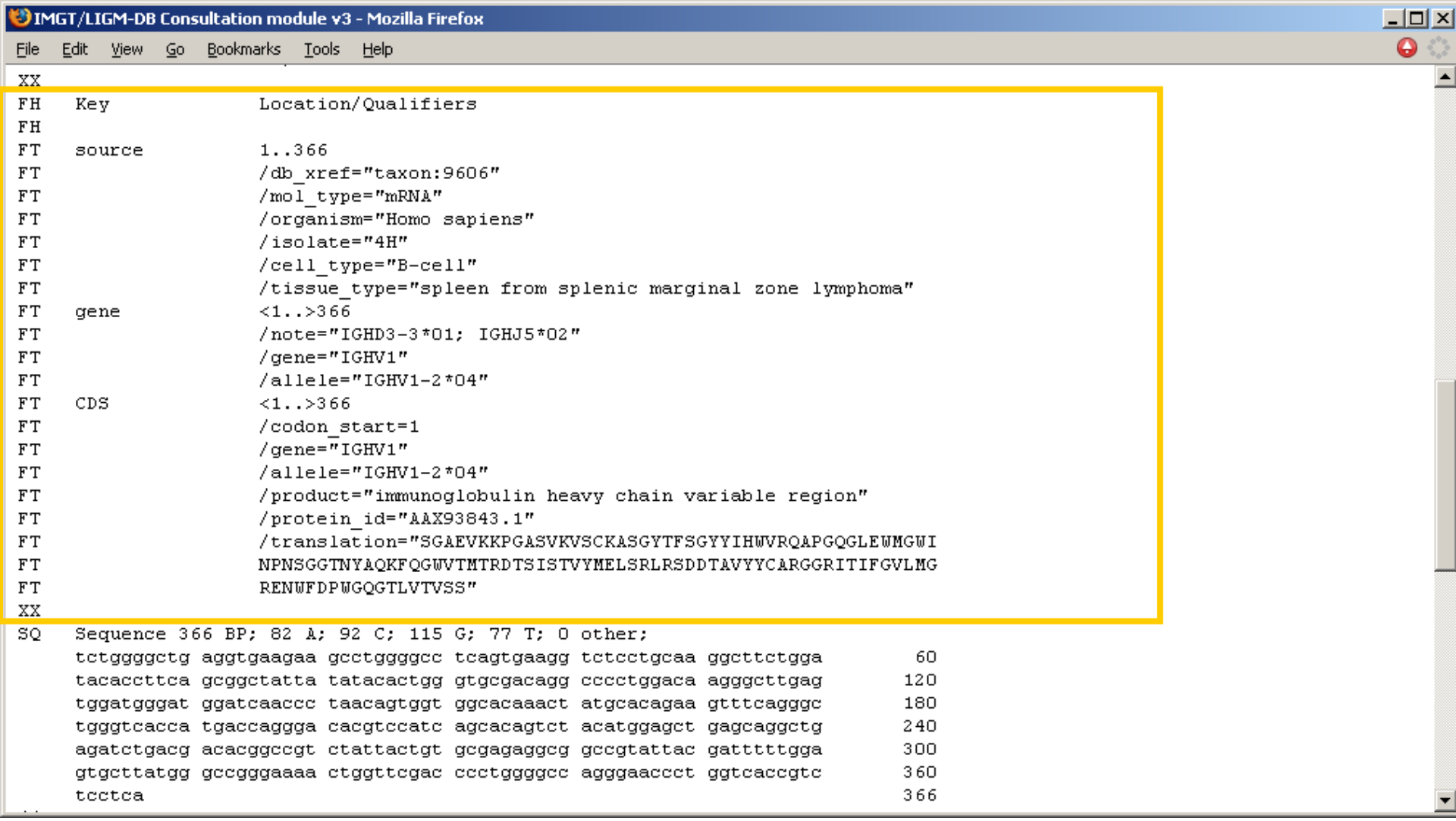
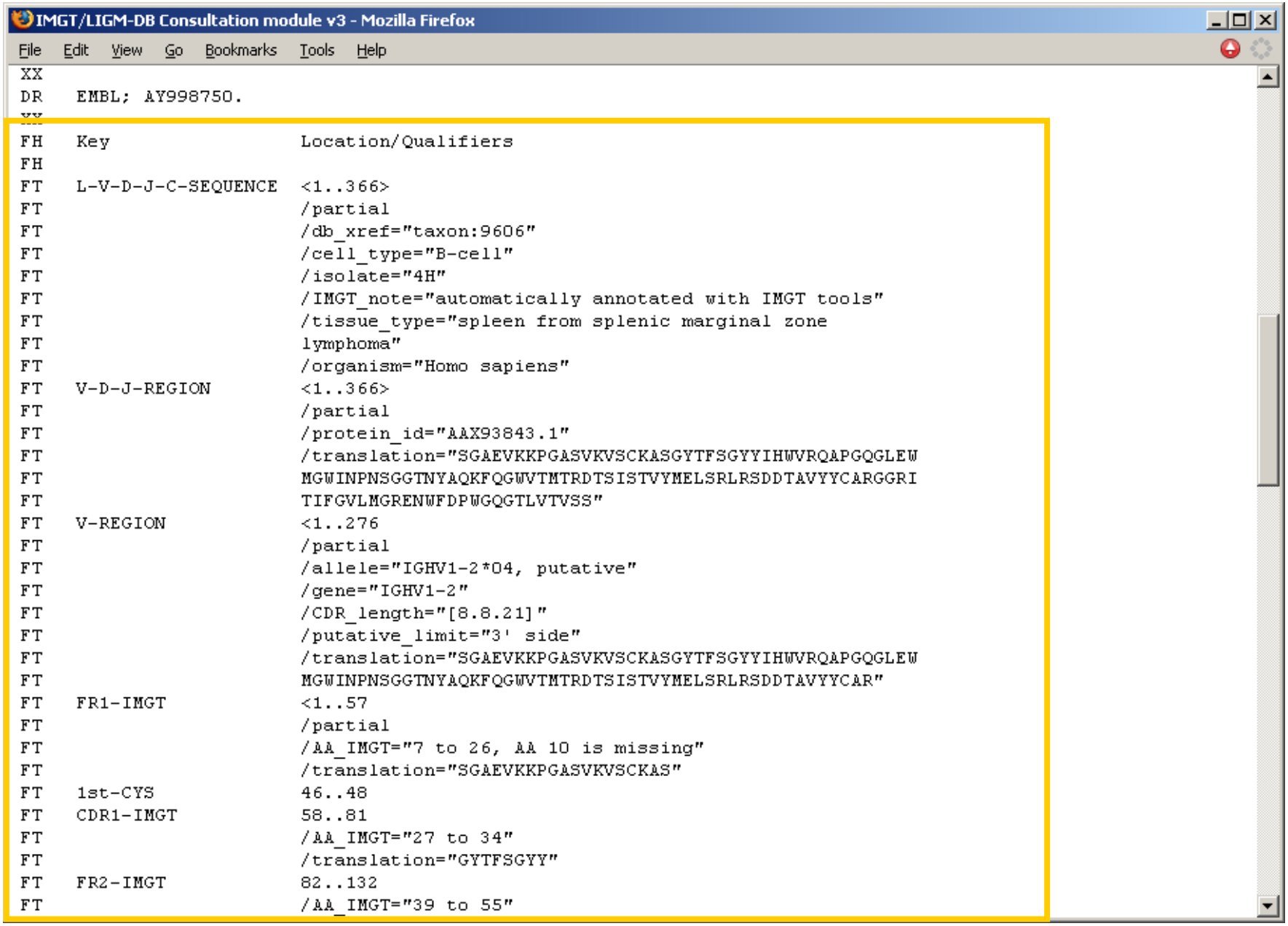
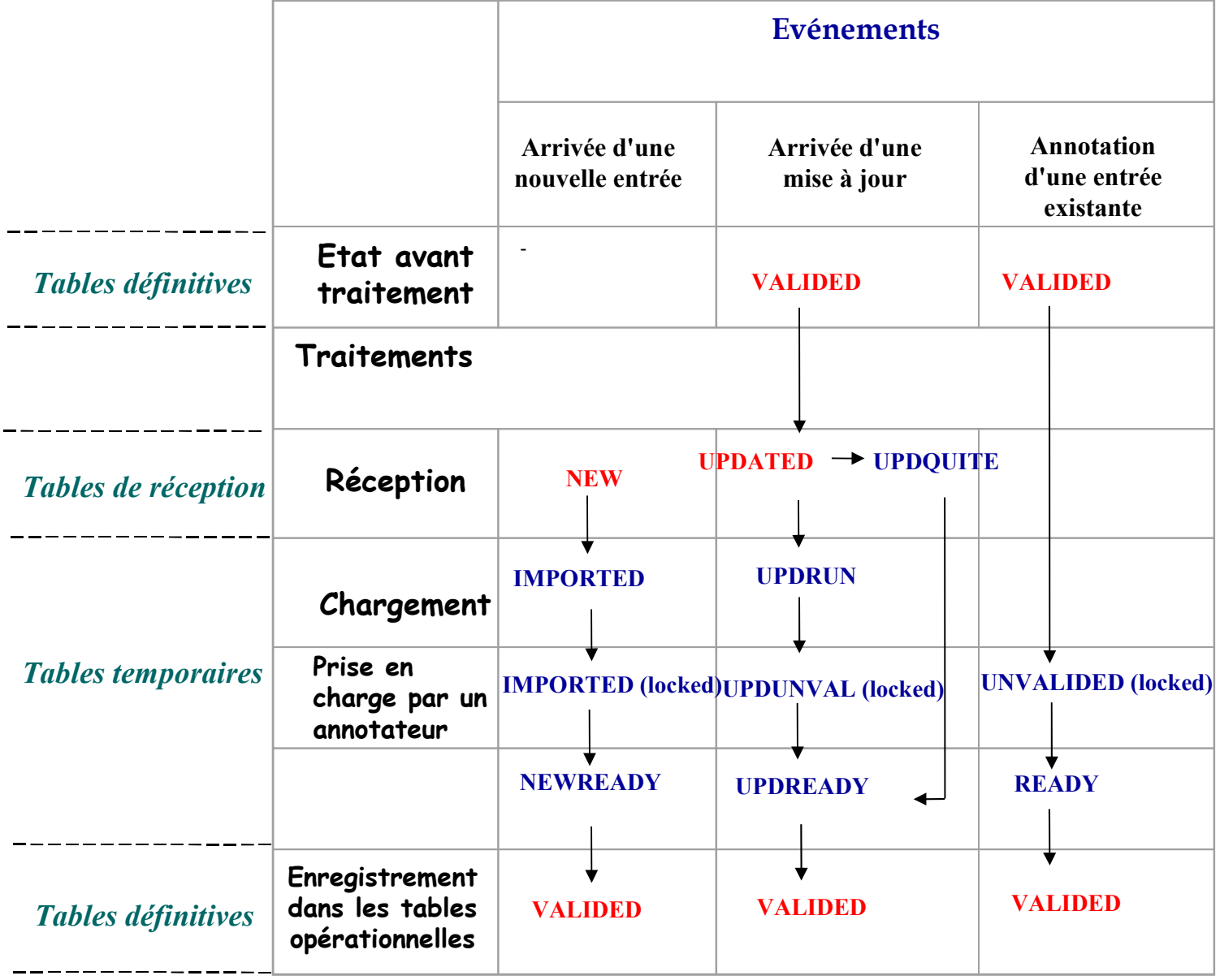
RA   Fassas A., Anagnostopoulos A.;
RT   "Immunoglobulin Heavy- And Light-chain Repertoire in Splenic Marginal Zone
```

A l'arrivée dans IMGT



Après expertise dans IMGT





(locked) : indique que l'entrée est prise en charge par un annotateur

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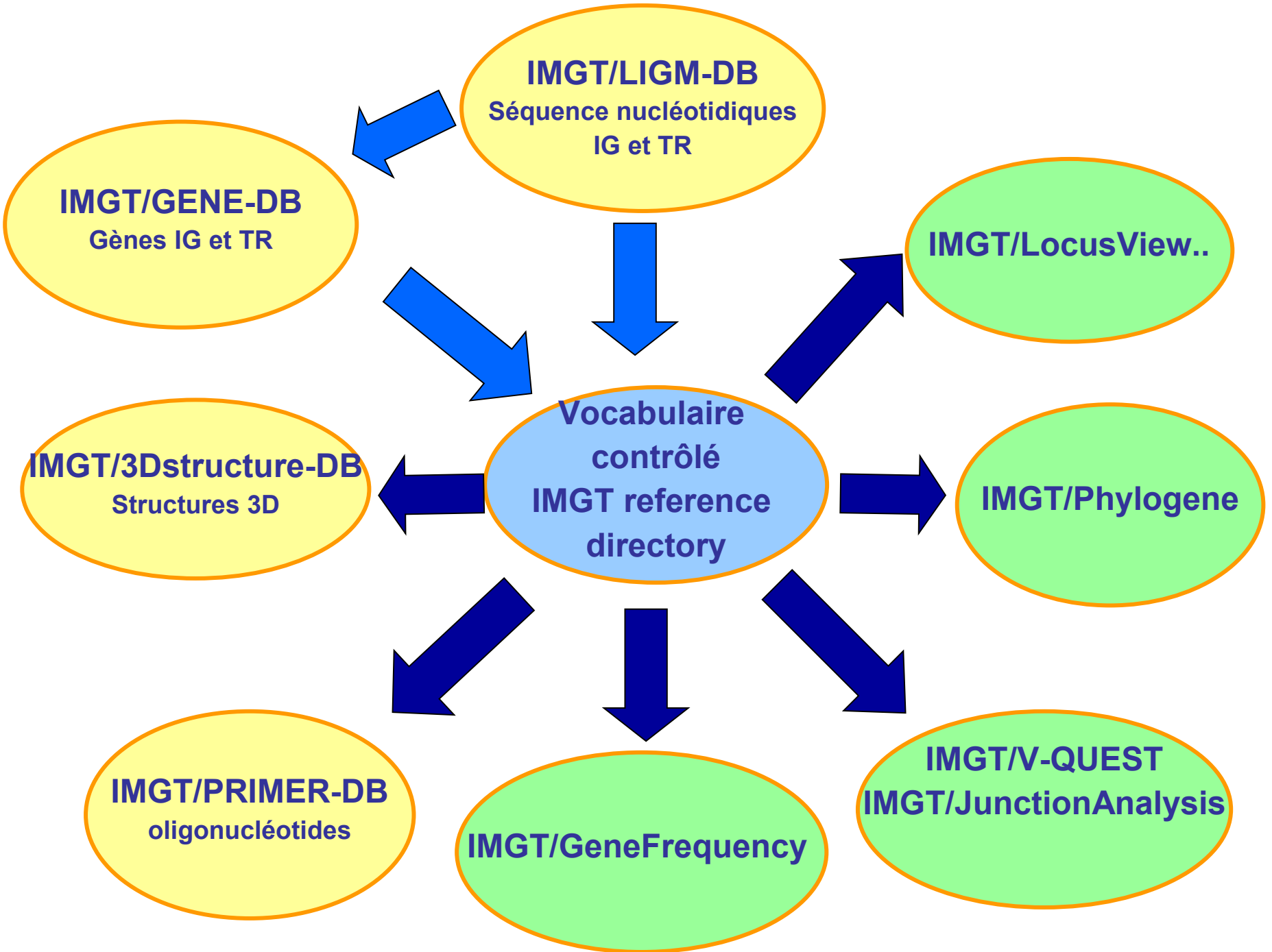

IMGT/LIGM-DB
Séquence nucléotidiques
IG et TR
IMGT/GENE-DB
Gènes IG et TR
IMGT/LocusView..
Vocabulaire
contrôlé
IMGT reference
directory
IMGT/3Dstructure-DB
Structures 3D
IMGT/Phylogene
IMGT/PRIMER-DB
oligonucléotides
IMGT/GeneFrequency
IMGT/V-QUEST
IMGT/JunctionAnalysis

Rôles des responsables de SI

Assurer la cohérence d'un ensemble d'informations qui comprend des données (dans une base de données...), des applications, interfaces pour un ensemble d'utilisateurs

On demande en plus:

- la disponibilité de l'information le plus rapidement possible
- simultanément sous différents formats
- à travers diverses interfaces
- "tout le monde" veut offrir des services

Les utilisateurs ont des demandes difficiles à anticiper, qui évoluent rapidement

Complexité des SI

- Les systèmes d'information n'ont jamais été conçus pour durer si longtemps ou pour être résistant au temps qui passe (bug de l'an 2000)
- Il faudrait adapter de certaines méthodes, standards, protocoles dépassés / oubliés.
- Les versions des outils, standards, middleware changent plusieurs fois au cours d'un même projet.
- "la toute dernière release, (ou la version beta)" des outils disponibles comprend souvent de noumbreux bugs.

Quand c'est enfin mature, c'est déjà obsolète !

La durée de vie d'un SI dépend de

- Portabilité il existe plusieurs plateformes alternatives qui peuvent faire tourner le système

- Evolutivité : un système est évolutif, on peut:
  - ajouter des fonctionnalités
  - augmenter ses capacités maximum
  - l'adapter à des besoins différents / nouveaux
  - corriger des dysfonctionnements

- Réutilisation Un système est réutilisable s'il peut être intégré (en totalité ou en partie) dans un nouveau projet.

- Standardisation: **ensemble de propriétés décrites dans une norme, supportée ou certifiée par un organisme officiel.**

Information et connaissance

•**Une Information** comprend des données primaires issues l'expérimentation (mesures, images, séquences) ainsi que les données secondaires qui comprennent aussi ce qu'il est nécessaire de connaître pour leur analyse.

(résultats + matériels & méthodes).

•**La connaissance** inclut tout ce qu'il est nécessaire pour réaliser l'annotation des données, telle qu'elle peut être réalisée par des experts dans un domaine particulier.

=> vocabulaire contrôlé, standardisé,
règles d'annotation, dépendance entre les termes

2

Ontologies

Bases de connaissance

-

IMGT-ONTOLOGY

Quelques exemples de questions

Qu'est-ce qu'un gène?

=> plusieurs définitions

Dans une base de données:

établissement d'un dictionnaire des données

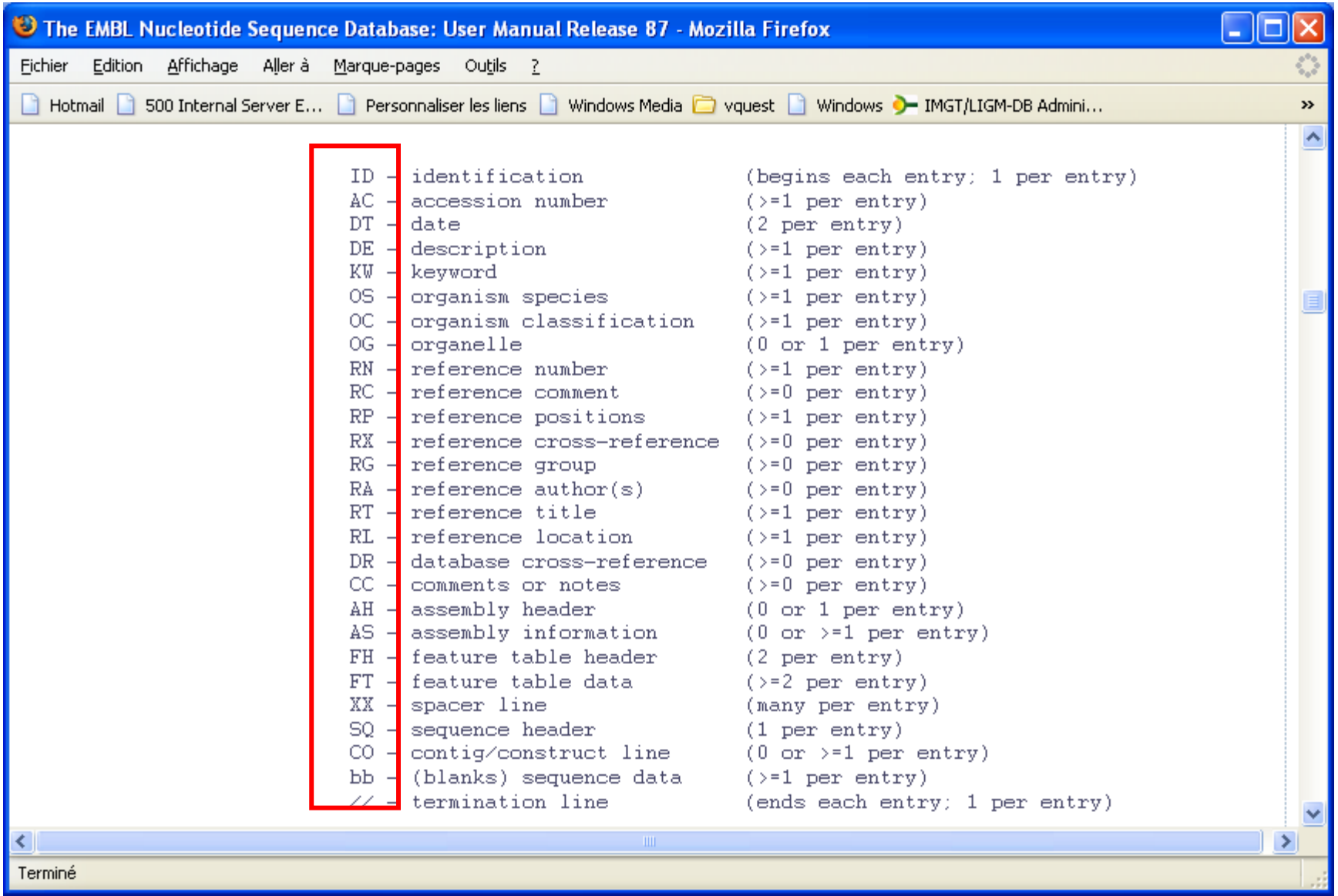
mises en place de contraintes à travers un vocabulaire contrôlé

Recherches bibliographique à travers des thesaurus de mots clés

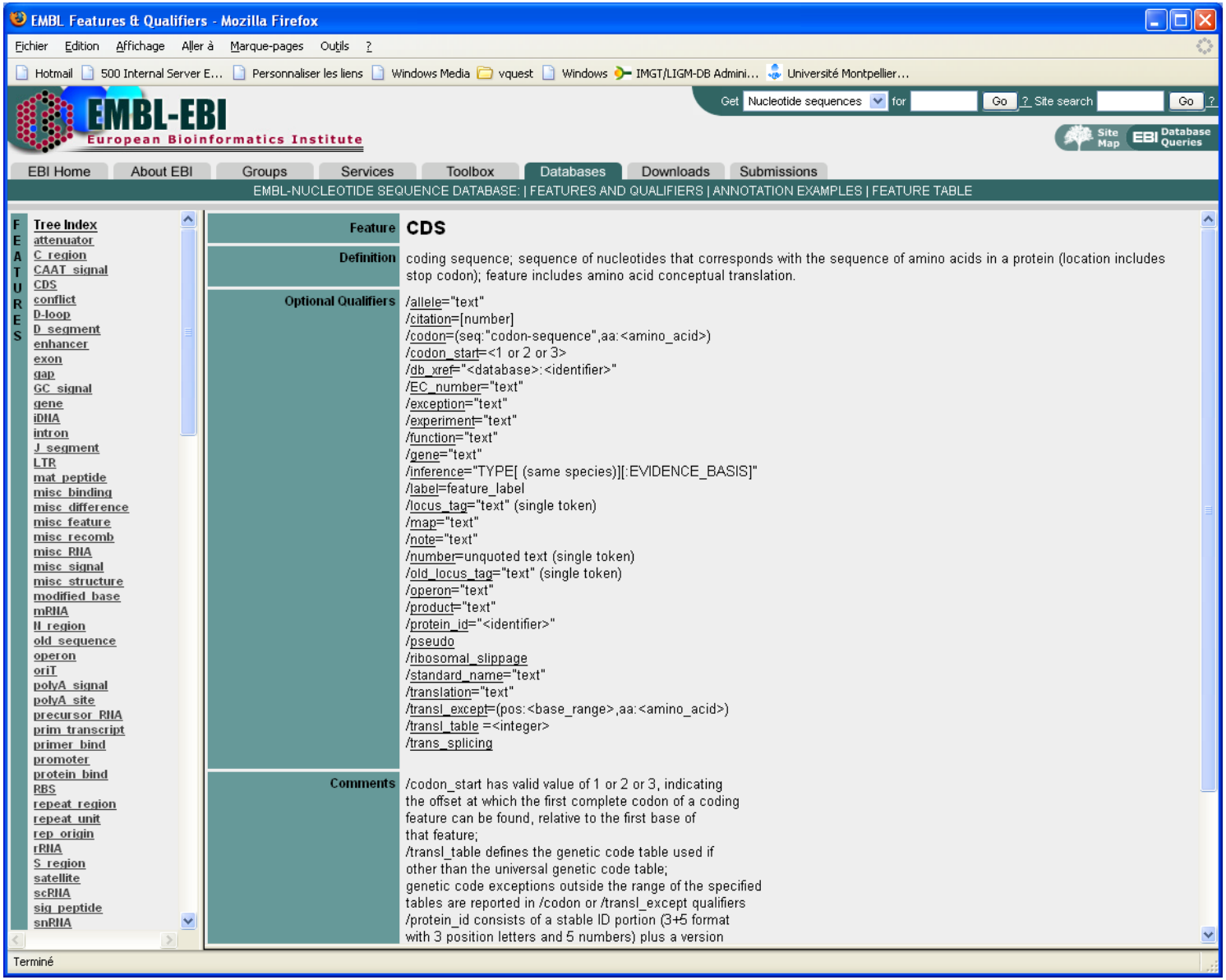
Comment ces termes sont –ils reliés?

Le vocabulaire contrôlé des bases de données généralistes DDBJ/EMBL/GenBank

Des codes pour indiquer les types d'information

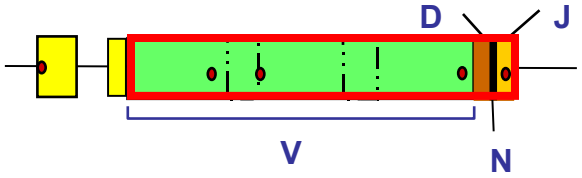


EMBL Feature labels



http://www3.ebi.ac.uk/Services/WebFeat/

EMBL Feature labels



The DDBJ/EMBL/GenBank Feature Table: Definition - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

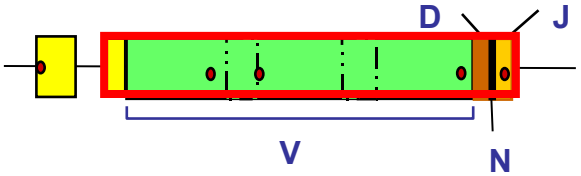
Hotmail 500 Internal Server E... Personnaliser les liens Windows Media vquest Windows IMGT/LIGM-DB Admini...

Feature Key	V_region
Definition	variable region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for the variable amino terminal portion; can be composed of V_segments, D_segments, N_regions, and J_segments;
Optional qualifiers	/allele="text" /citation=[number] /db_xref="<database>:<identifier>" /experiment="text" /gene="text" /inference="TYPE[(same species)][:EVIDENCE_BASIS]" /label=feature_label /locus_tag="text" (single token) /map="text" /note="text" /old_locus_tag="text" (single token) /product="text" /pseudo /standard_name="text"
Parent Key	CDS
Organism scope	eukaryotes

Terminé

http://www.ebi.ac.uk/embl/Documentation/FT_definitions/feature_table.html

EMBL Feature labels



The DDBJ/EMBL/GenBank Feature Table: Definition - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

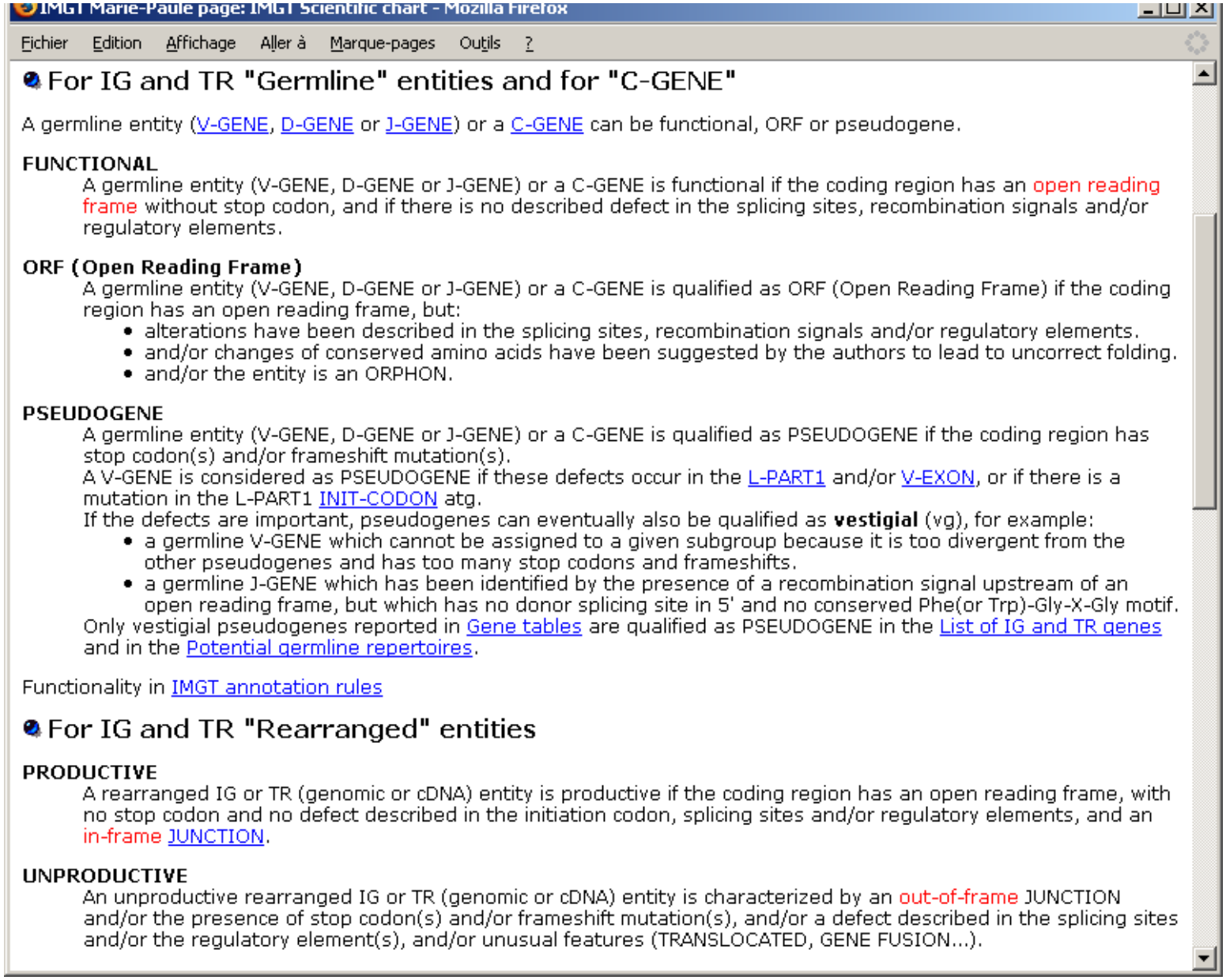
Hotmail 500 Internal Server E... Personnaliser les liens Windows Media vquest Windows IMGT/LIGM-DB Admini...

Feature Key	V_segment
Definition	variable segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for most of the variable region (V_region) and the last few amino acids of the leader peptide;
Optional qualifiers	/allele="text" /citation=[number] /db_xref="<database>:<identifier>" /experiment="text" /gene="text" /inference="TYPE[(same species)][:EVIDENCE_BASIS]" /label=feature_label /locus_tag="text" (single token) /map="text" /note="text" /old_locus_tag="text" (single token) /product="text" /pseudo /standard_name="text"
Parent Key	CDS
Organism scope	eukaryotes

Terminé

http://www.ebi.ac.uk/embl/Documentation/FT_definitions/feature_table.html

Définition de la fonctionalité dans IMGT



IMGT Marie-Paule page: IMGT Scientific chart - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

For IG and TR "Germline" entities and for "C-GENE"

A germline entity (V-GENE, D-GENE or J-GENE) or a C-GENE can be functional, ORF or pseudogene.

FUNCTIONAL

A germline entity (V-GENE, D-GENE or J-GENE) or a C-GENE is functional if the coding region has an open reading frame without stop codon, and if there is no described defect in the splicing sites, recombination signals and/or regulatory elements.

ORF (Open Reading Frame)

A germline entity (V-GENE, D-GENE or J-GENE) or a C-GENE is qualified as ORF (Open Reading Frame) if the coding region has an open reading frame, but:

- alterations have been described in the splicing sites, recombination signals and/or regulatory elements.
- and/or changes of conserved amino acids have been suggested by the authors to lead to uncorrect folding.
- and/or the entity is an ORPHON.

PSEUDOGENE

A germline entity (V-GENE, D-GENE or J-GENE) or a C-GENE is qualified as PSEUDOGENE if the coding region has stop codon(s) and/or frameshift mutation(s).
A V-GENE is considered as PSEUDOGENE if these defects occur in the L-PART1 and/or V-EXON, or if there is a mutation in the L-PART1 INIT-CODON atg.
If the defects are important, pseudogenes can eventually also be qualified as **vestigial** (vg), for example:

- a germline V-GENE which cannot be assigned to a given subgroup because it is too divergent from the other pseudogenes and has too many stop codons and frameshifts.
- a germline J-GENE which has been identified by the presence of a recombination signal upstream of an open reading frame, but which has no donor splicing site in 5' and no conserved Phe(or Trp)-Gly-X-Gly motif.

Only vestigial pseudogenes reported in Gene tables are qualified as PSEUDOGENE in the List of IG and TR genes and in the Potential germline repertoires.

Functionality in IMGT annotation rules

For IG and TR "Rearranged" entities

PRODUCTIVE

A rearranged IG or TR (genomic or cDNA) entity is productive if the coding region has an open reading frame, with no stop codon and no defect described in the initiation codon, splicing sites and/or regulatory elements, and an in-frame JUNCTION.

UNPRODUCTIVE

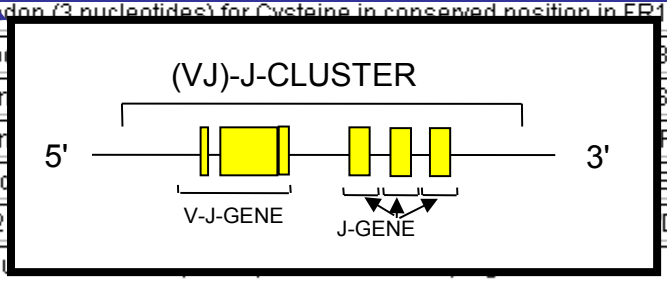
An unproductive rearranged IG or TR (genomic or cDNA) entity is characterized by an out-of-frame JUNCTION and/or the presence of stop codon(s) and/or frameshift mutation(s), and/or a defect described in the splicing sites and/or the regulatory element(s), and/or unusual features (TRANSLOCATED, GENE FUSION...).

List and definition of IMGT standardized labels

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

Label name	Definition
(DJ)-C-CLUSTER	genomic DNA in rearranged configuration including at least one D-J-GENE and one C-GENE
(DJ)-J-C-CLUSTER	genomic DNA in rearranged configuration including at least one D-J-GENE, one J-GENE and one C-GENE
(DJ)-J-CLUSTER	genomic DNA in rearranged configuration including at least one D-J-GENE, and one J-GENE
(VDJ)-C-CLUSTER	genomic DNA in rearranged configuration including at least one V-D-J-GENE and one C-GENE
(VDJ)-J-C-CLUSTER	genomic DNA in rearranged configuration including at least one V-D-J-GENE, one J-GENE and one C-GENE
(VDJ)-J-CLUSTER	genomic DNA in rearranged configuration including at least one V-D-J-GENE and one J-GENE
(VJ)-C-CLUSTER	genomic DNA in rearranged configuration including at least one V-J-GENE and one C-GENE
(VJ)-J-C-CLUSTER	genomic DNA in rearranged configuration including at least one V-J-GENE, one J-GENE and one C-GENE
(VJ)-J-CLUSTER	genomic DNA in rearranged configuration including at least one V-J-GENE and one J-GENE
1st-CYS	Codon (3 nucleotides) for Cysteine in conserved position in FR1
2nd-CYS	co…
3'D-HEPTAMER	7 r…
3'D-NONAMER	9 r… RS
3'D-RS	rec… ER, and 3'D-NONAMER in 3'of the D-REGION of a D-GENE
3'D-SPACER	12 … D-NONAMER of a 3'D-RS
3'UTR	3' …
3'V-REGION	region from 2nd-CYS to the 3' end of the V-REGION (for germline and rearranged)
5'D-HEPTAMER	7 nucleotide recombination site like CACTGTG, part of a 5'D-RS
5'D-NONAMER	9 nucleotide recombination site like GGTTTTTGT, part of a 5'D-RS
5'D-RS	recombination signal including the 5'D-NONAMER, 5'D-SPACER and 5'D-HEPTAMER in 5' of the D-REGION of a D-GENE, or in 5' of the D-REGION of D-J-GENE
5'D-SPACER	12 or 23 nucleotide spacer between the 5'D-HEPTAMER and 5'D-NONAMER of a 5'D-RS



http://imgt.cines.fr/cgi-bin/IMGTlect.jv?query=7#

Ontologies

Une **ontologie** définit formellement les **termes** employés pour **décrire et représenter** un **domaine de connaissance**.

Les ontologies sont destinées à être utilisées par:

- des personnes
- des bases de données
- des applications

ayant besoin de partager des informations.

Ontologies

Au sein d'une ontologie, les termes sont regroupés sous forme de **concepts** (ou classes) sémantiques.

Les ontologies incluent les **définitions**, informatiquement exploitables, des **concepts** élémentaires et de leurs **relations**.

Les ontologies doivent permettre le **partage** et la **réutilisation des connaissances**.

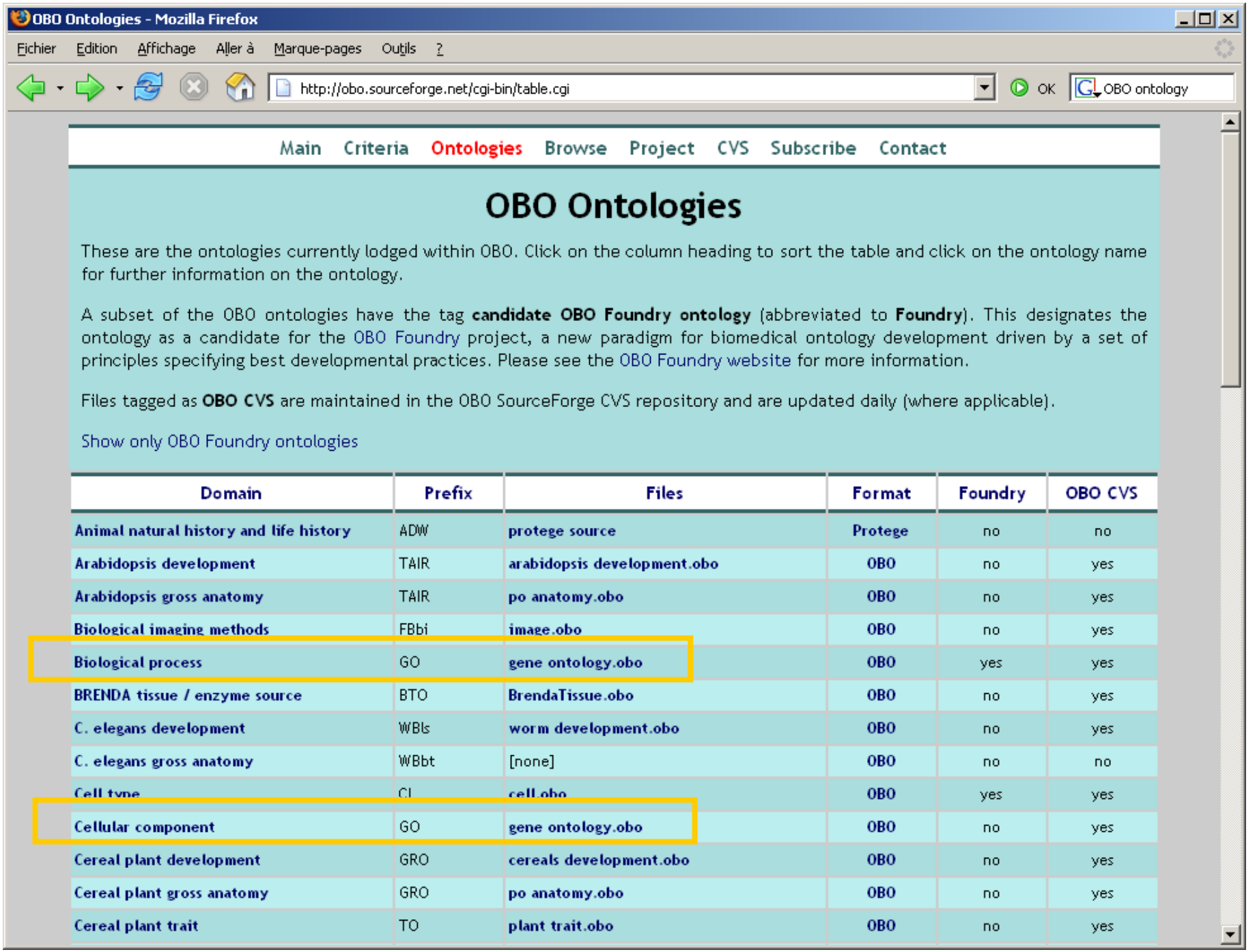
Bases de connaissances:

Une ontologie ainsi que l'ensemble des **instances** individuelles des **concepts** constituent une base de connaissances. Une frontière subtile marque la fin d'une ontologie et le début d'une base de connaissances._

Les ontologies en Biologie

- On s'interresse aux ontologies qui sont du domaine publique.
- Leur nombre augmente régulièrement (besoin de définir de partager).
- Elles couvrent des sujets et domaines différents.

OBO (Open Biological Ontologies) recense les ontologies en biologie. (http://obo.sourceforge.net/)



Main Criteria Ontologies Browse Project CVS Subscribe Contact

OBO Ontologies

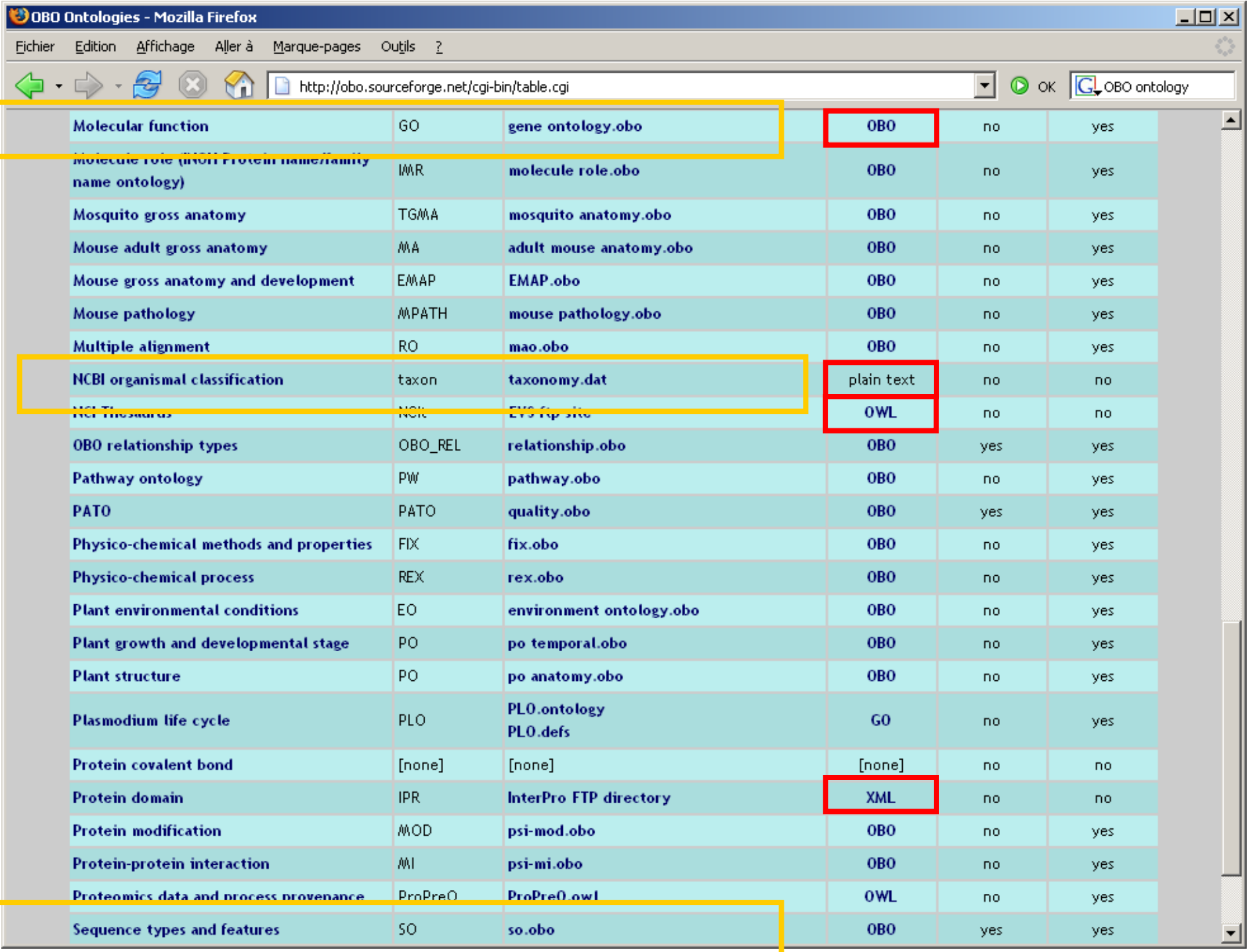
These are the ontologies currently lodged within OBO. Click on the column heading to sort the table and click on the ontology name for further information on the ontology.

A subset of the OBO ontologies have the tag **candidate OBO Foundry ontology** (abbreviated to **Foundry**). This designates the ontology as a candidate for the OBO Foundry project, a new paradigm for biomedical ontology development driven by a set of principles specifying best developmental practices. Please see the OBO Foundry website for more information.

Files tagged as **OBO CVS** are maintained in the OBO SourceForge CVS repository and are updated daily (where applicable).

Show only OBO Foundry ontologies

Domain	Prefix	Files	Format	Foundry	OBO CVS
Animal natural history and life history	ADW	protege source	Protege	no	no
Arabidopsis development	TAIR	arabidopsis development.obo	OBO	no	yes
Arabidopsis gross anatomy	TAIR	po anatomy.obo	OBO	no	yes
Biological imaging methods	FBbi	image.obo	OBO	no	yes
Biological process	GO	gene ontology.obo	OBO	yes	yes
BRENDA tissue / enzyme source	BTO	BrendaTissue.obo	OBO	no	yes
C. elegans development	WBls	worm development.obo	OBO	no	yes
C. elegans gross anatomy	WBbt	[none]	OBO	no	no
Cell type	CL	cell.obo	OBO	yes	yes
Cellular component	GO	gene ontology.obo	OBO	no	yes
Cereal plant development	GRO	cereals development.obo	OBO	no	yes
Cereal plant gross anatomy	GRO	po anatomy.obo	OBO	no	yes
Cereal plant trait	TO	plant trait.obo	OBO	no	yes



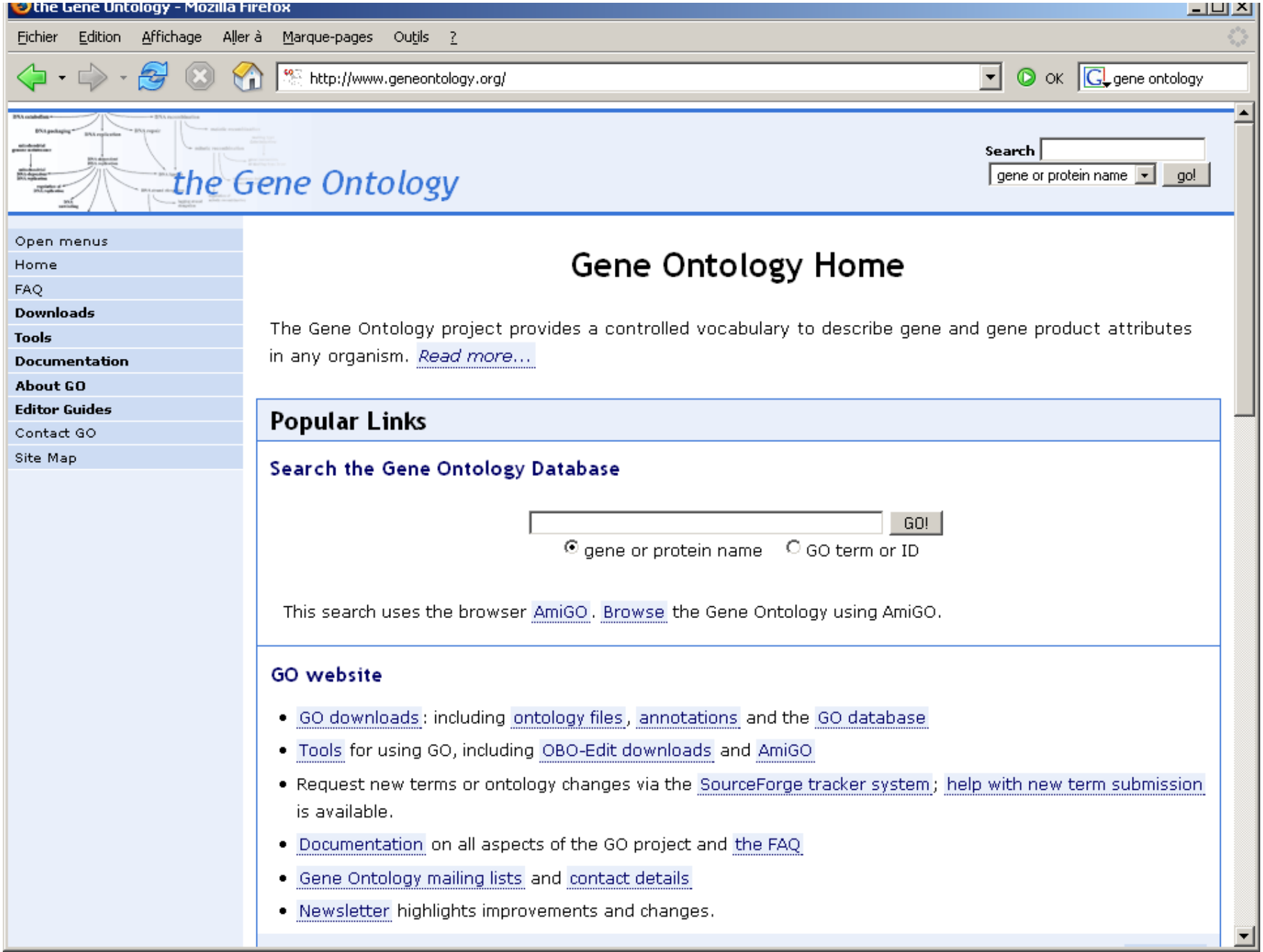
Molecular function	GO	gene ontology.obo	OBO	no	yes
name ontology)	MR	molecule role.obo	OBO	no	yes
Mosquito gross anatomy	TGMA	mosquito anatomy.obo	OBO	no	yes
Mouse adult gross anatomy	MA	adult mouse anatomy.obo	OBO	no	yes
Mouse gross anatomy and development	EMAP	EMAP.obo	OBO	no	yes
Mouse pathology	MPATH	mouse pathology.obo	OBO	no	yes
Multiple alignment	RO	mao.obo	OBO	no	yes
NCBI organismal classification	taxon	taxonomy.dat	plain text	no	no
			OWL	no	no
OBO relationship types	OBO_REL	relationship.obo	OBO	yes	yes
Pathway ontology	PW	pathway.obo	OBO	no	yes
PATO	PATO	quality.obo	OBO	yes	yes
Physico-chemical methods and properties	FIX	fix.obo	OBO	no	yes
Physico-chemical process	REX	rex.obo	OBO	no	yes
Plant environmental conditions	EO	environment ontology.obo	OBO	no	yes
Plant growth and developmental stage	PO	po temporal.obo	OBO	no	yes
Plant structure	PO	po anatomy.obo	OBO	no	yes
Plasmodium life cycle	PLO	PLO.ontology PLO.defs	GO	no	yes
Protein covalent bond	[none]	[none]	[none]	no	no
Protein domain	IPR	InterPro FTP directory	XML	no	no
Protein modification	MOD	psi-mod.obo	OBO	no	yes
Protein-protein interaction	MI	psi-mi.obo	OBO	no	yes
Proteomics data and process provenance	ProPreO	ProPreO.owl	OWL	no	yes
Sequence types and features	SO	so.obo	OBO	yes	yes

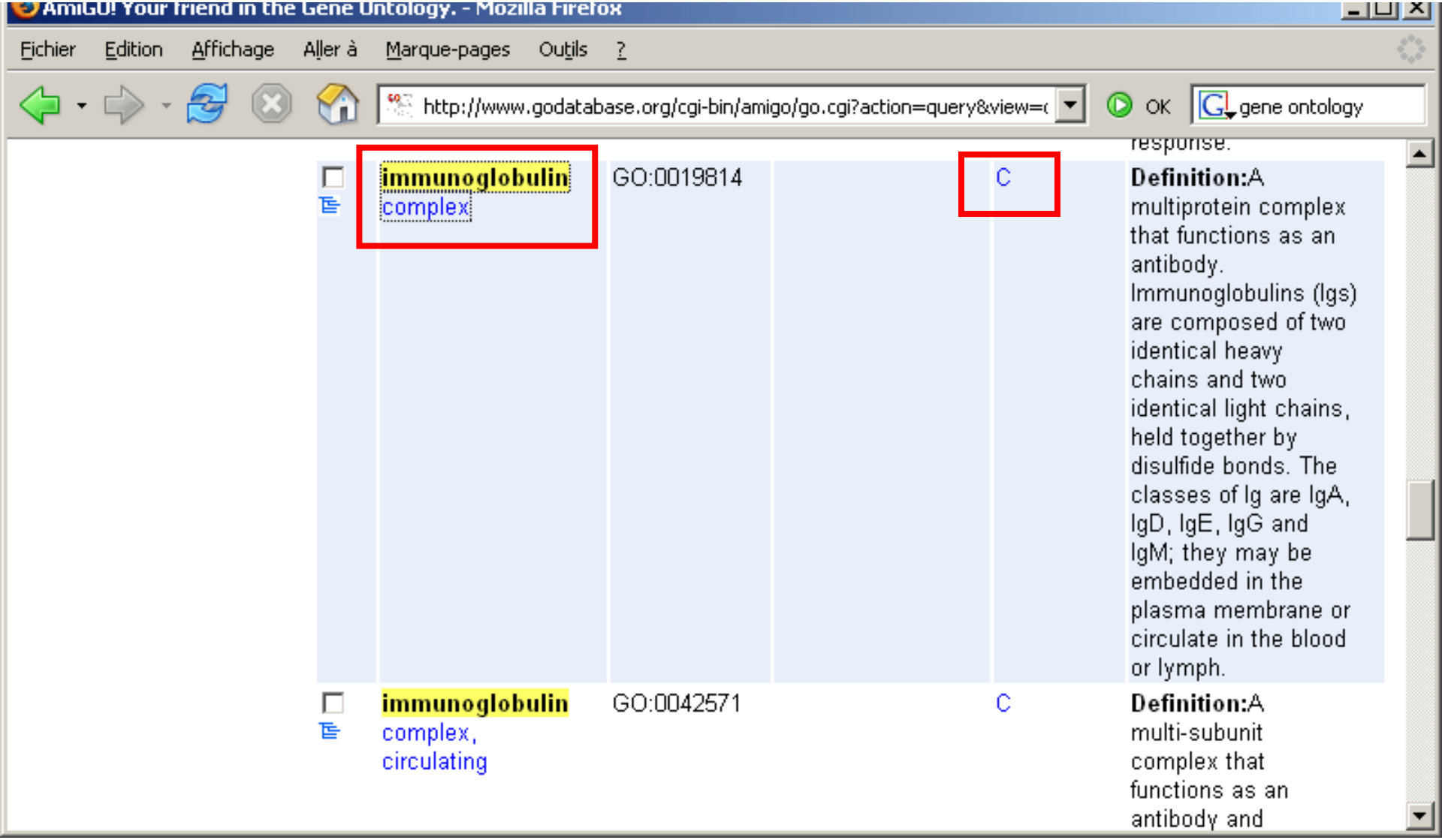
Gene **O**ntology.

•GO a été créée en 1998. GO résulte d'une collaboration entre plusieurs bases de données (FlyBase ,drosophile, the Saccharomyces Genome Database, et des base de données de génomes (homme et souris), etc.

•GO comprend 3 parties axées sur :

- **la fonction moléculaire** (fonction des gènes exprimés ex: ATPase activity.
- **le processus biologique** (rôles biologique généraux de fonctions moléculaire complexes ex: la mitose).
- **les composants cellulaires** (structures subcellulaires, localisation des complexes macromoleculaires ex: le noyau, le télomère).


the Gene Ontology - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
http://www.geneontology.org/
OK
gene ontology
the Gene Ontology
Search
gene or protein name
go!
Open menus
Home
FAQ
Downloads
Tools
Documentation
About GO
Editor Guides
Contact GO
Site Map
Gene Ontology Home
The Gene Ontology project provides a controlled vocabulary to describe gene and gene product attributes in any organism. Read more...
Popular Links
Search the Gene Ontology Database
GO!
gene or protein name
GO term or ID
This search uses the browser AmiGO. Browse the Gene Ontology using AmiGO.
GO website
GO downloads: including ontology files, annotations and the GO database
Tools for using GO, including OBO-Edit downloads and AmiGO
Request new terms or ontology changes via the SourceForge tracker system; help with new term submission is available.
Documentation on all aspects of the GO project and the FAQ
Gene Ontology mailing lists and contact details
Newsletter highlights improvements and changes.


AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
http://www.godatabase.org/cgi-bin/amigo/go.cgi?action=query&view=
OK
gene ontology
response.
immunoglobulin complex
GO:0019814
C
Definition:A multiprotein complex that functions as an antibody. Immunoglobulins (Igs) are composed of two identical heavy chains and two identical light chains, held together by disulfide bonds. The classes of Ig are IgA, IgD, IgE, IgG and IgM; they may be embedded in the plasma membrane or circulate in the blood or lymph.
immunoglobulin complex, circulating
GO:0042571
C
Definition:A multi-subunit complex that functions as an antibody and

AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
http://www.godatabase.org/cgi-bin/amigo/go.cgi?view=details&search_constraint=terms&depth
OK
AmiGO
immunoglobulin complex
Accession: GO:0019814
Ontology: cellular_component
Synonyms: None
Definition:
A multiprotein complex that functions as an antibody. Immunoglobulins (Igs) are composed of two identical heavy chains and two identical light chains, held together by disulfide bonds. The classes of Ig are IgA, IgD, IgE, IgG and IgM; they may be embedded in the plasma membrane or circulate in the blood or lymph.
Definition Source:
GOC:jl
ISBN:0140512713
Comment: None
Term Context:
Term Ancestors
Term Siblings
Submit
Term Lineage
all : all
GO:0005575 : cellular_component
GO:0043234 : protein complex
GO:0019814 : immunoglobulin complex
Graphical View

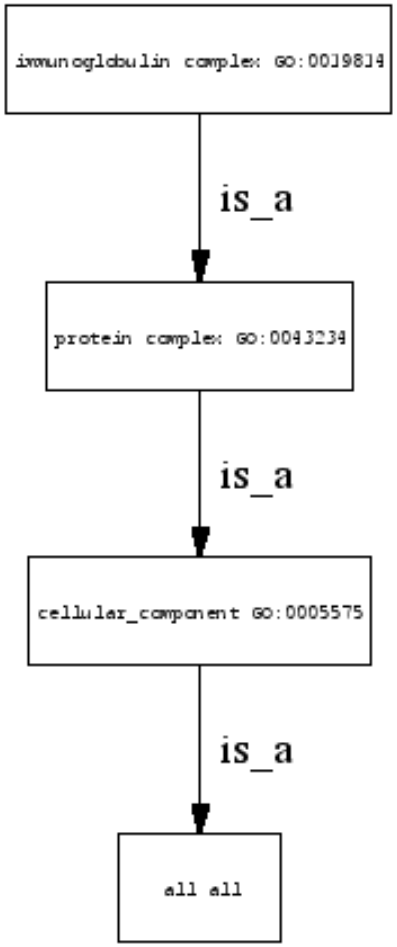
AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox

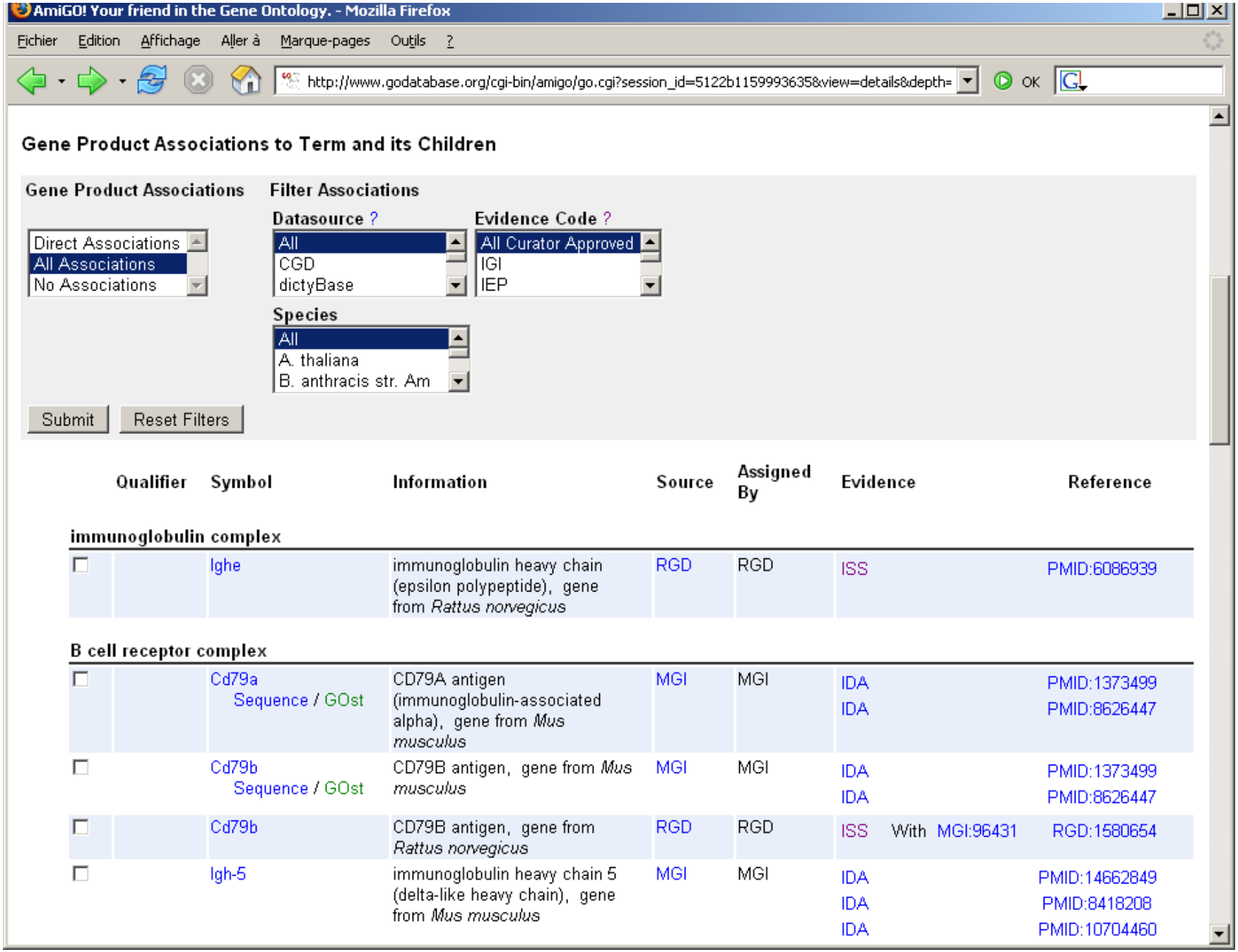
Fichier Edition Affichage Aller à Marque-pages Outils ?

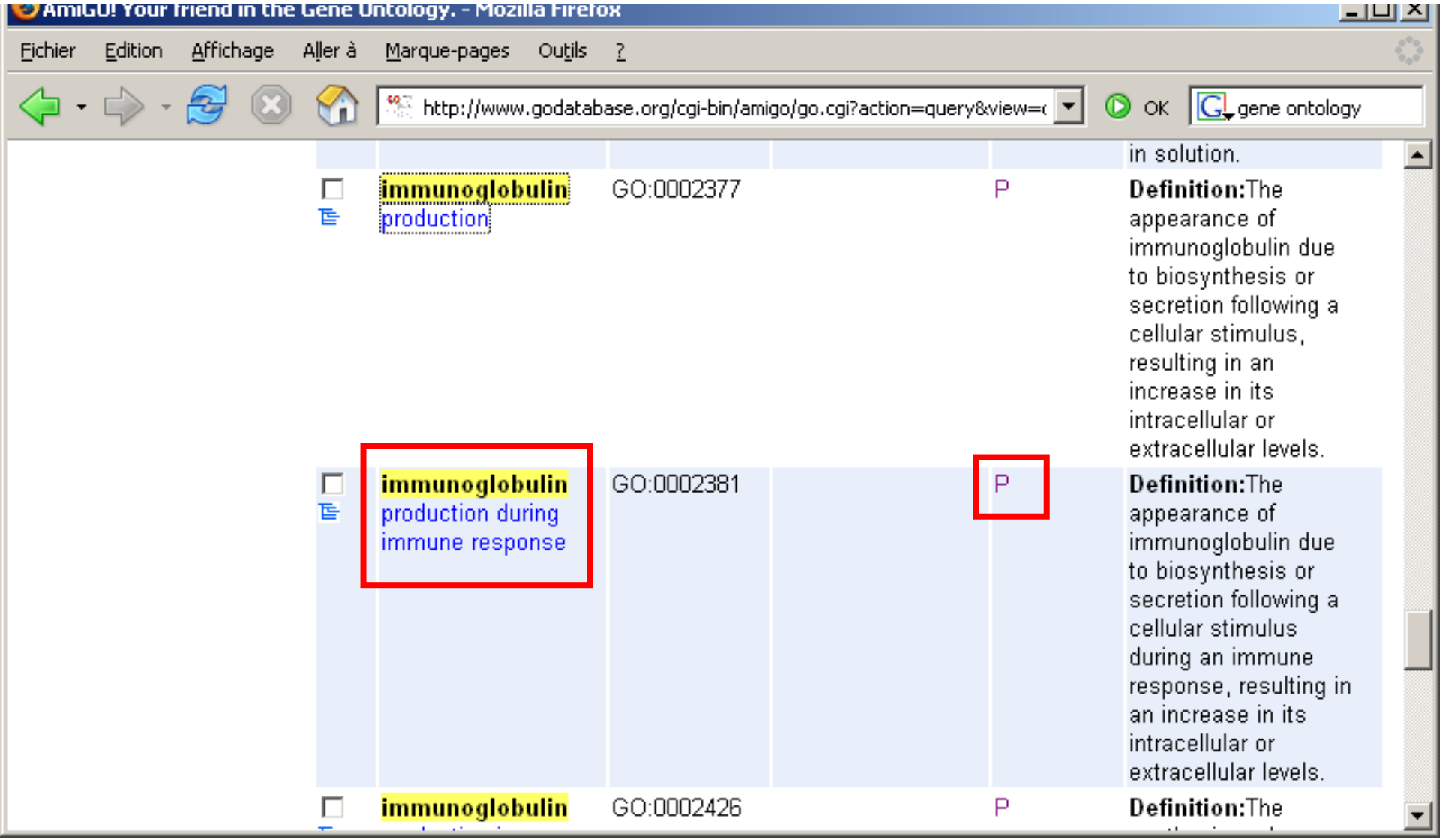
immunoglobulin complex Graphical View

Layout: Vertical | Box Color: White | Text Color: Black | Format: Graphic View

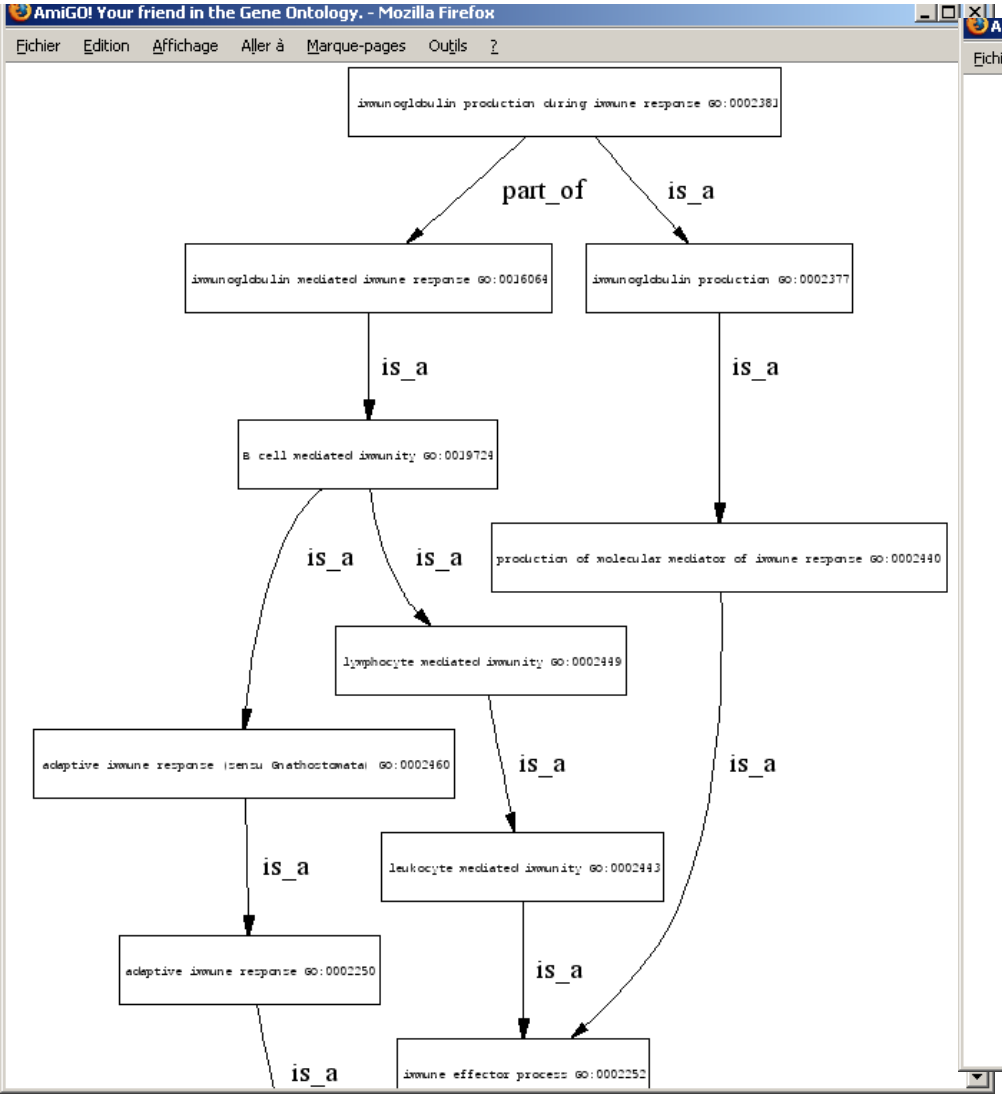
Envoyer

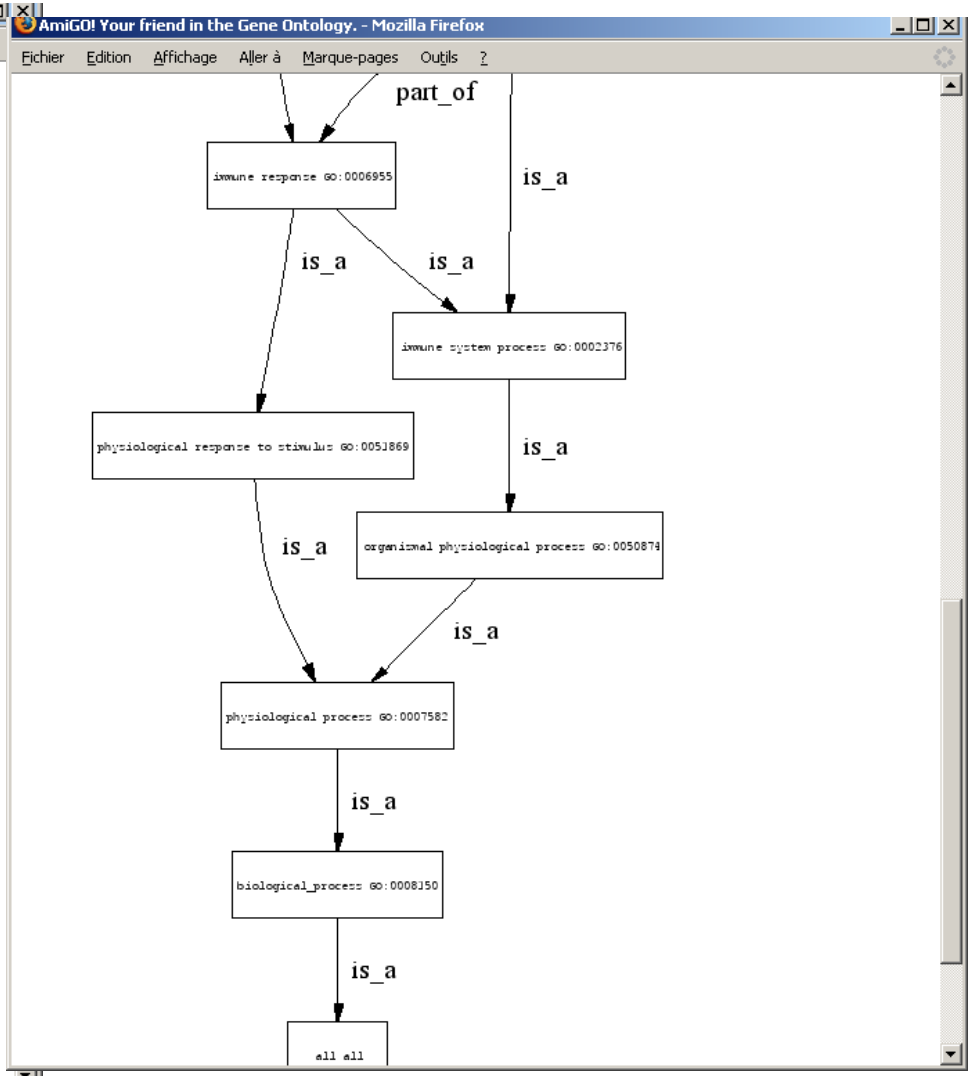


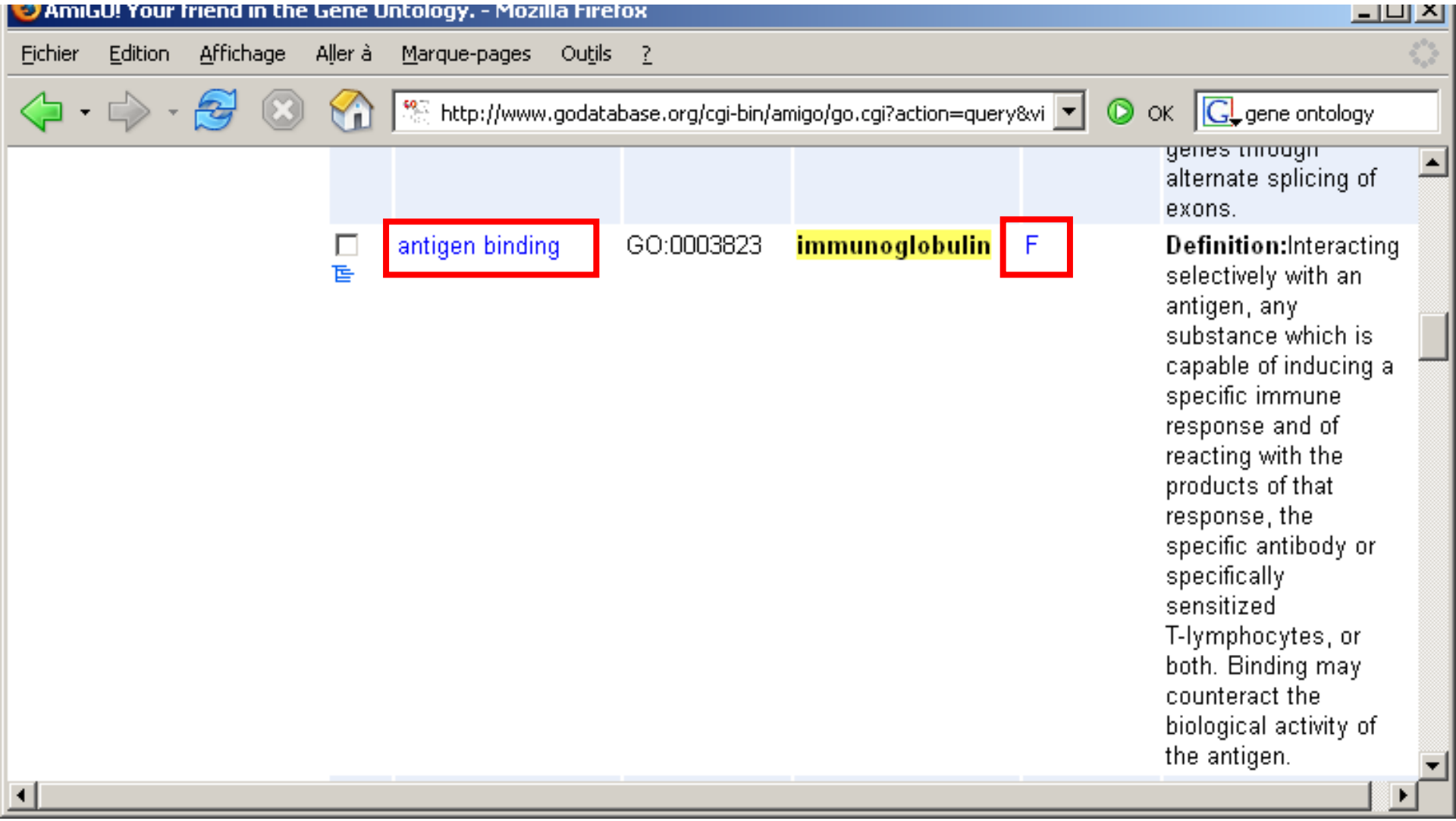

AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
http://www.godatabase.org/cgi-bin/amigo/go.cgi?session_id=5122b1159993635&view=details&depth=
OK
Gene Product Associations to Term and its Children
Gene Product Associations
Direct Associations
All Associations
No Associations
Filter Associations
Datasource ?
All
CGD
dictyBase
Evidence Code ?
All Curator Approved
IGI
IEP
Species
All
A. thaliana
B. anthracis str. Am
Submit
Reset Filters
Qualifier
Symbol
Information
Source
Assigned By
Evidence
Reference
immunoglobulin complex
Ighe
immunoglobulin heavy chain (epsilon polypeptide), gene from Rattus norvegicus
RGD
RGD
ISS
PMID:6086939
B cell receptor complex
Cd79a
Sequence / GOst
CD79A antigen (immunoglobulin-associated alpha), gene from Mus musculus
MGI
MGI
IDA
IDA
PMID:1373499
PMID:8626447
Cd79b
Sequence / GOst
CD79B antigen, gene from Mus musculus
MGI
MGI
IDA
IDA
PMID:1373499
PMID:8626447
Cd79b
CD79B antigen, gene from Rattus norvegicus
RGD
RGD
ISS
With MGI:96431
RGD:1580654
Igh-5
immunoglobulin heavy chain 5 (delta-like heavy chain), gene from Mus musculus
MGI
MGI
IDA
IDA
IDA
PMID:14662849
PMID:8418208
PMID:10704460


AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
http://www.godatabase.org/cgi-bin/amigo/go.cgi?action=query&view=
OK
gene ontology
in solution.
immunoglobulin production
GO:0002377
P
Definition:The appearance of immunoglobulin due to biosynthesis or secretion following a cellular stimulus, resulting in an increase in its intracellular or extracellular levels.
immunoglobulin production during immune response
GO:0002381
P
Definition:The appearance of immunoglobulin due to biosynthesis or secretion following a cellular stimulus during an immune response, resulting in an increase in its intracellular or extracellular levels.
immunoglobulin
GO:0002426
P
Definition:The

immunoglobulin production during immune response graphical View






AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox
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http://www.godatabase.org/cgi-bin/amigo/go.cgi?action=query&vi
OK
gene ontology
alternate splicing of exons.
antigen binding
GO:0003823
immunoglobulin
F
Definition:Interacting selectively with an antigen, any substance which is capable of inducing a specific immune response and of reacting with the products of that response, the specific antibody or specifically sensitized T-lymphocytes, or both. Binding may counteract the biological activity of the antigen.

AmiGO! Your friend in the Gene Ontology. - Mozilla Firefox

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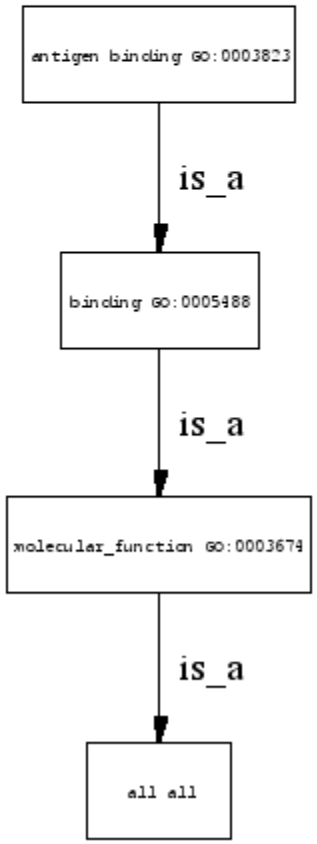
AmiGO

antigen binding Graphical View

Layout: Vertical | Box Color: White | Text Color: Black | Format: Graphic View

Envoyer



Dans le domaine de l'immunogénétique

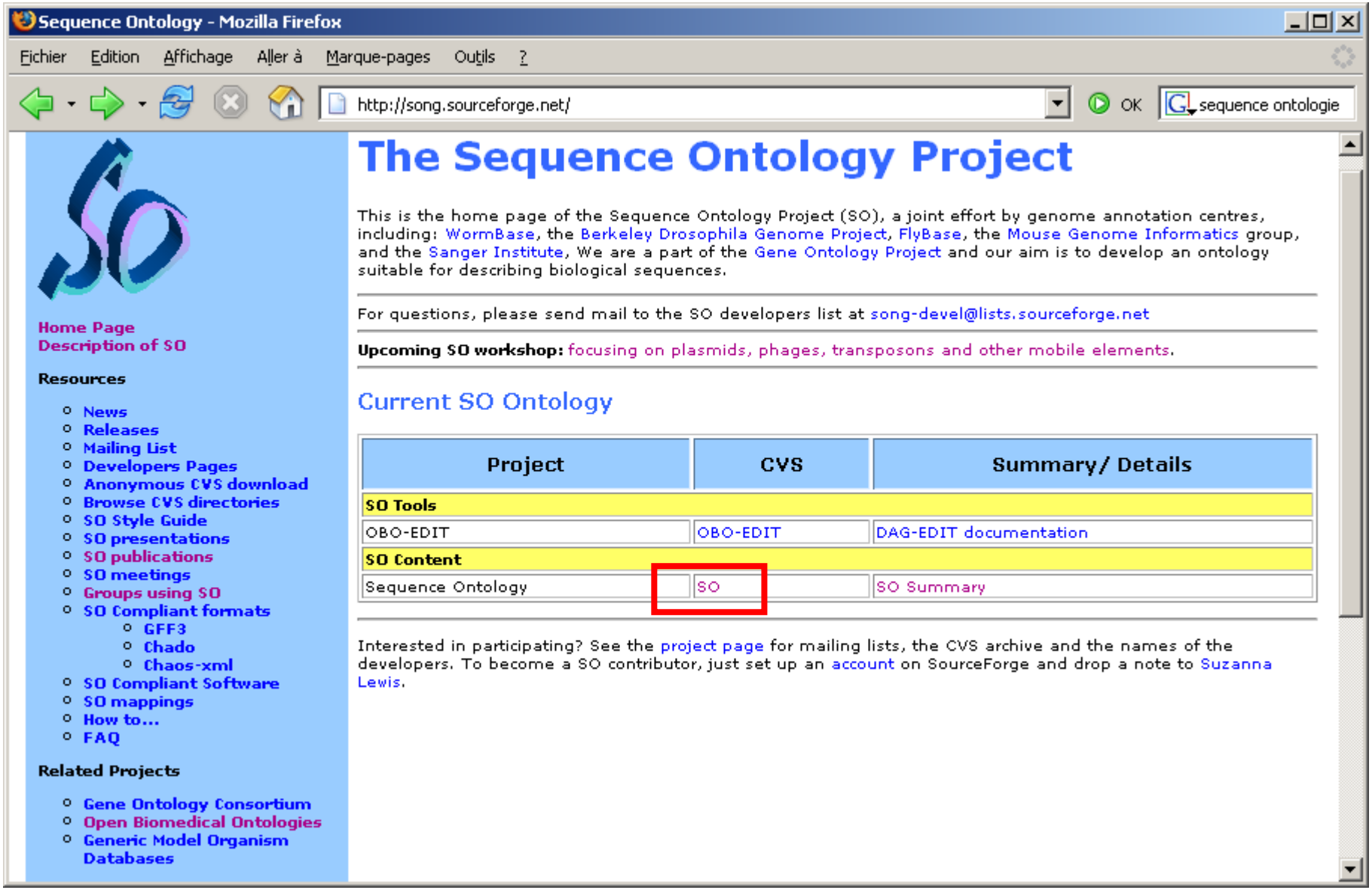
Problèmes et limites de GO:

- Comment se compose le site de reconnaissance d'un anticorps?

- Quels sont les motifs constitutifs importants?

- Comment caractériser précisément des séquences d'IG (.. et des TR): identification, classification des gènes, description, numérotation des acides aminés, obtention ?

Sequence Ontology:
une ontologie pour décrire les séquences biologiques

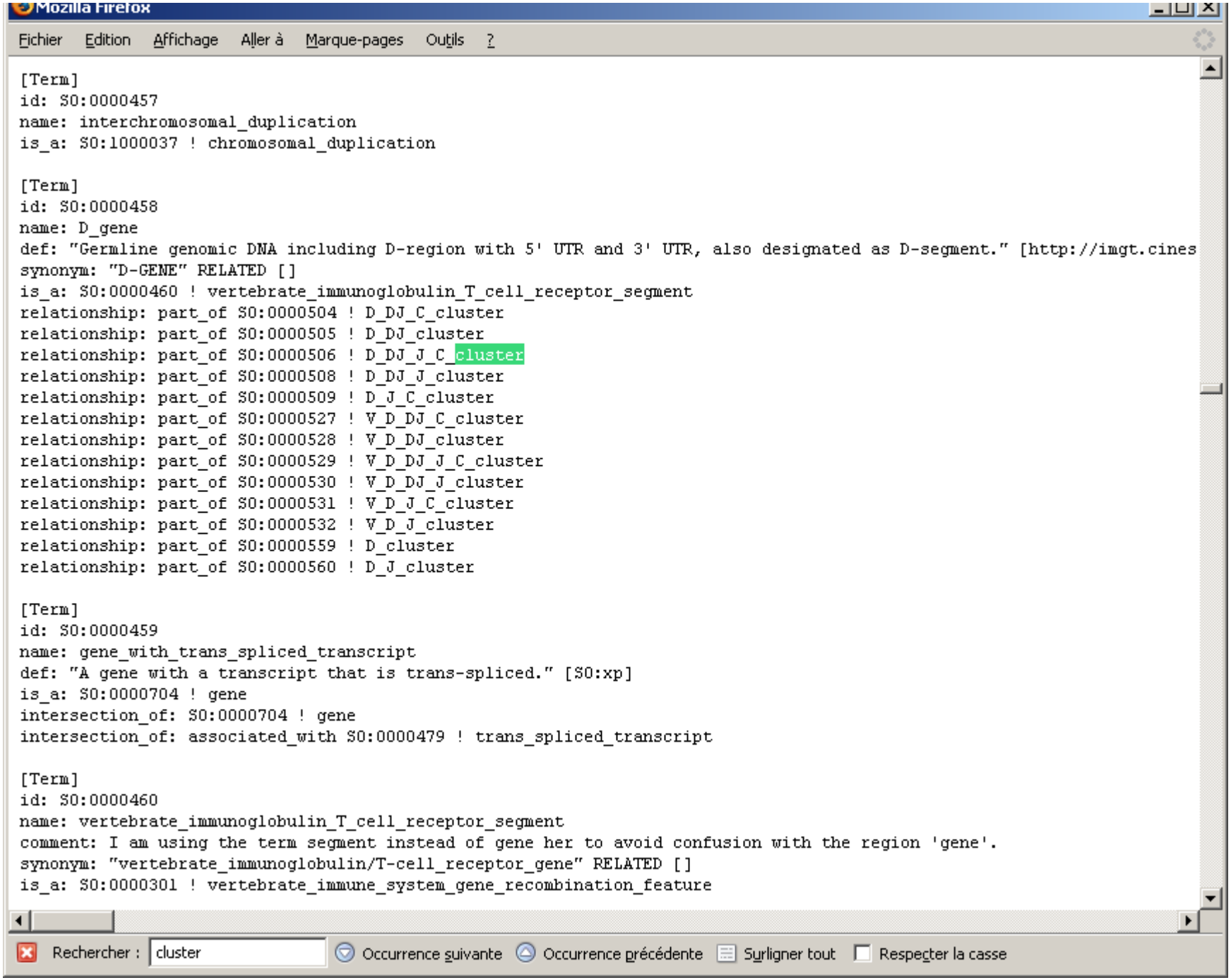


Sequence Ontology:

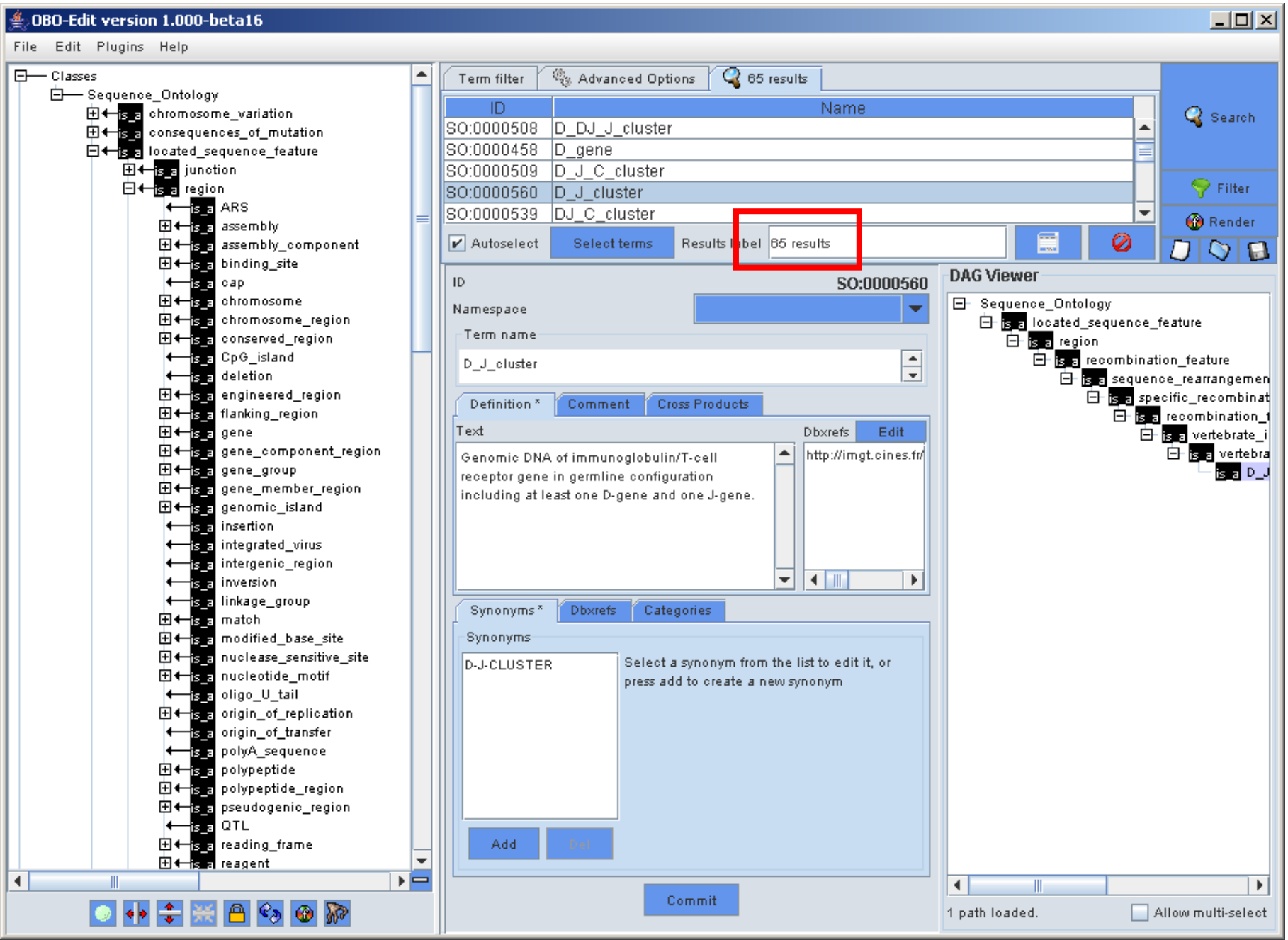
- Vocabulaire controlé pour l'annotation des séquences nucléotidiques

- proposer une representation structurée des annotations

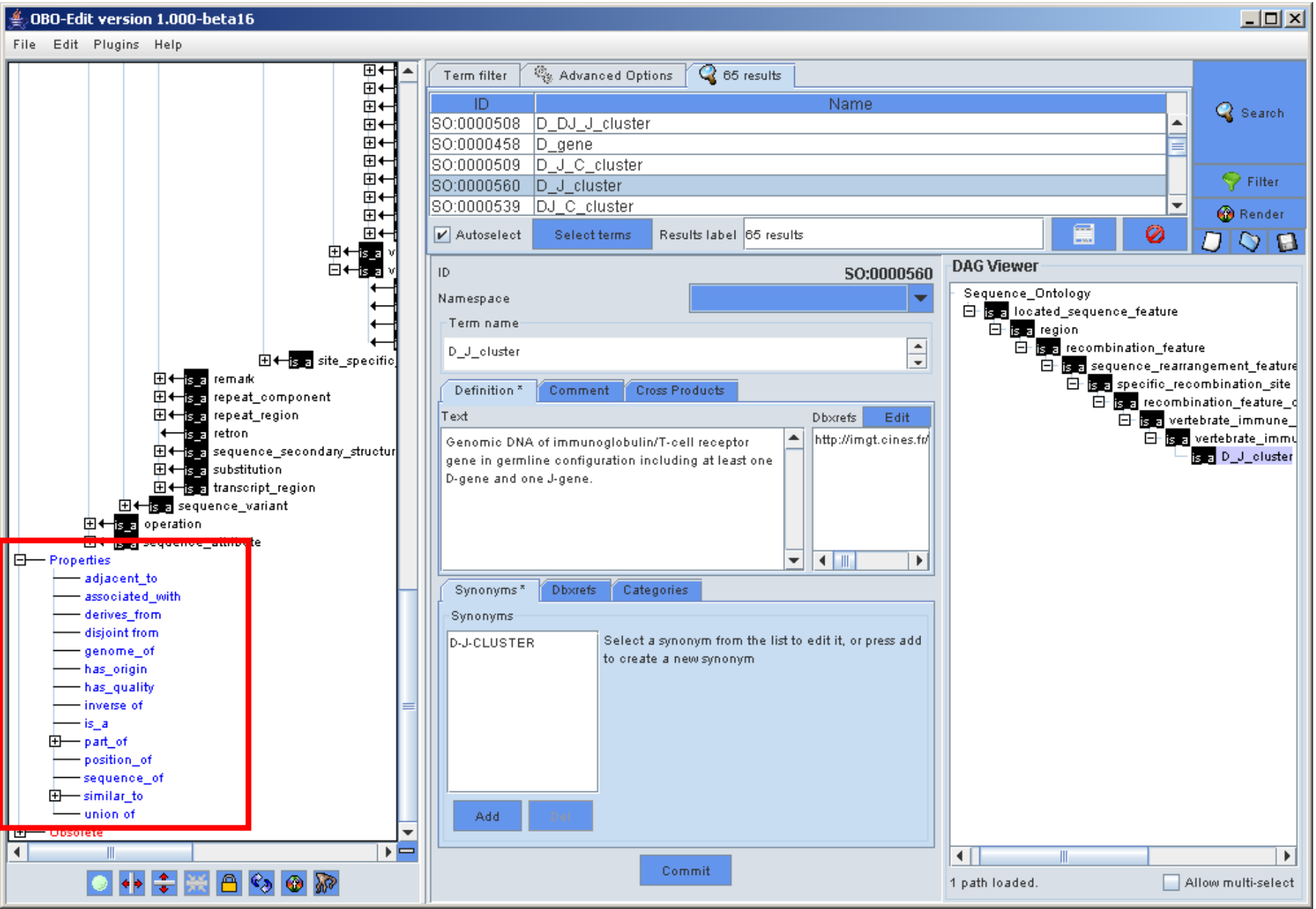
- vocabulaire pour la description des mutations


Mozilla Firefox
Fichier Edition Affichage Aller à Marque-pages Outils ?
[Term]
id: SO:0000457
name: interchromosomal_duplication
is_a: SO:1000037 ! chromosomal_duplication
[Term]
id: SO:0000458
name: D_gene
def: "Germline genomic DNA including D-region with 5' UTR and 3' UTR, also designated as D-segment." [http://imgt.cines
synonym: "D-GENE" RELATED []
is_a: SO:0000460 ! vertebrate_immunoglobulin_T_cell_receptor_segment
relationship: part_of SO:0000504 ! D_DJ_C_cluster
relationship: part_of SO:0000505 ! D_DJ_cluster
relationship: part_of SO:0000506 ! D_DJ_J_C_cluster
relationship: part_of SO:0000508 ! D_DJ_J_cluster
relationship: part_of SO:0000509 ! D_J_C_cluster
relationship: part_of SO:0000527 ! V_D_DJ_C_cluster
relationship: part_of SO:0000528 ! V_D_DJ_cluster
relationship: part_of SO:0000529 ! V_D_DJ_J_C_cluster
relationship: part_of SO:0000530 ! V_D_DJ_J_cluster
relationship: part_of SO:0000531 ! V_D_J_C_cluster
relationship: part_of SO:0000532 ! V_D_J_cluster
relationship: part_of SO:0000559 ! D_cluster
relationship: part_of SO:0000560 ! D_J_cluster
[Term]
id: SO:0000459
name: gene_with_trans_spliced_transcript
def: "A gene with a transcript that is trans-spliced." [SO:xp]
is_a: SO:0000704 ! gene
intersection_of: SO:0000704 ! gene
intersection_of: associated_with SO:0000479 ! trans_spliced_transcript
[Term]
id: SO:0000460
name: vertebrate_immunoglobulin_T_cell_receptor_segment
comment: I am using the term segment instead of gene her to avoid confusion with the region 'gene'.
synonym: "vertebrate_immunoglobulin/T-cell_receptor_gene" RELATED []
is_a: SO:0000301 ! vertebrate_immune_system_gene_recombination_feature
Rechercher : cluster
Occurrence suivante
Occurrence précédente
Surligner tout
Respecter la casse

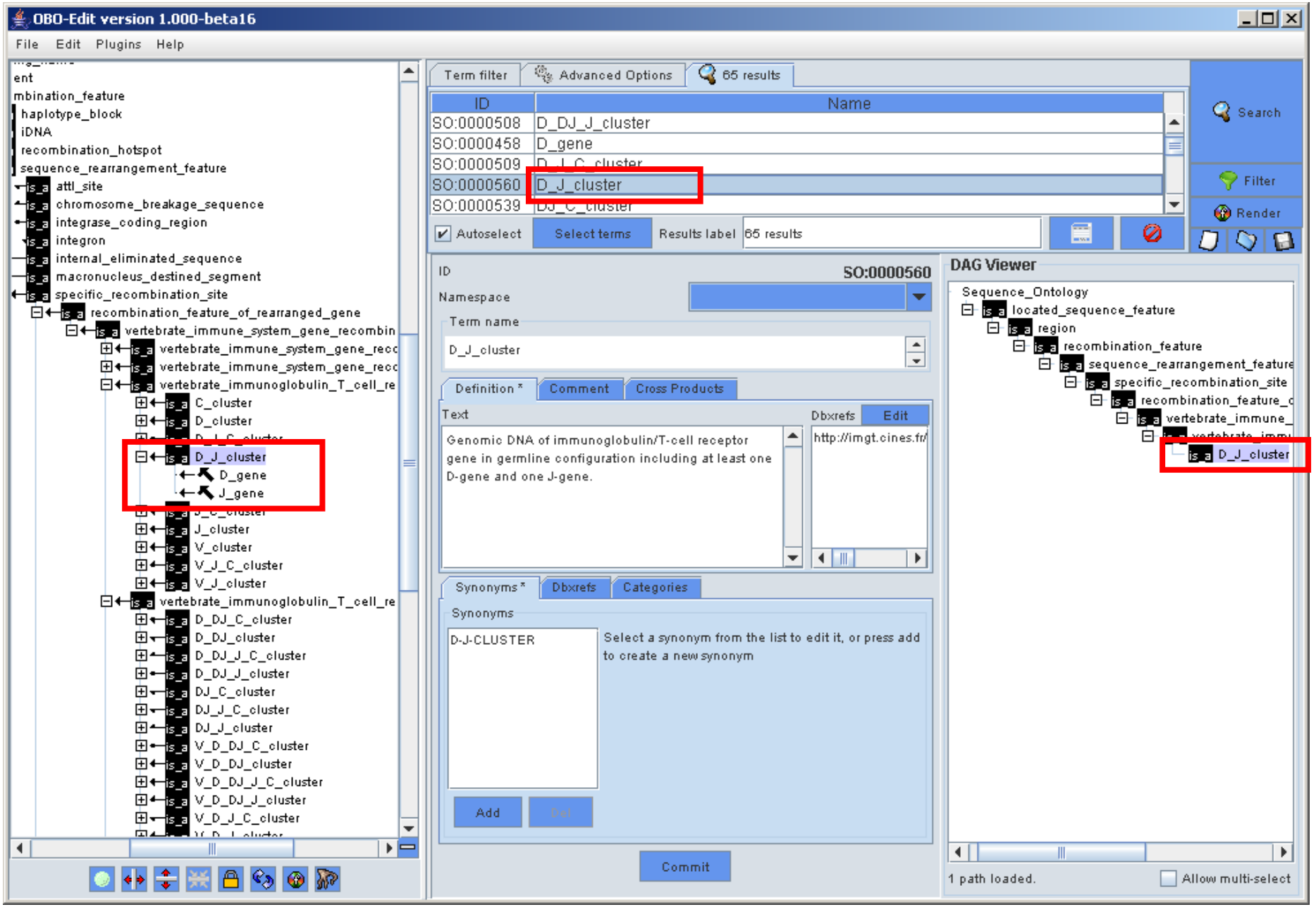
Sequence Ontology dans OBO-edit



Sequence Ontology dans OBO-edit



Sequence Ontology dans OBO-edit



Dans le domaine de l'immunogénétique

Limites de SO:

- Il est nécessaire de prendre en compte d'autres informations
  type de gènes, type de chaîne, …

- Il faut des relations plus précises que « part_of »
  entre les motifs

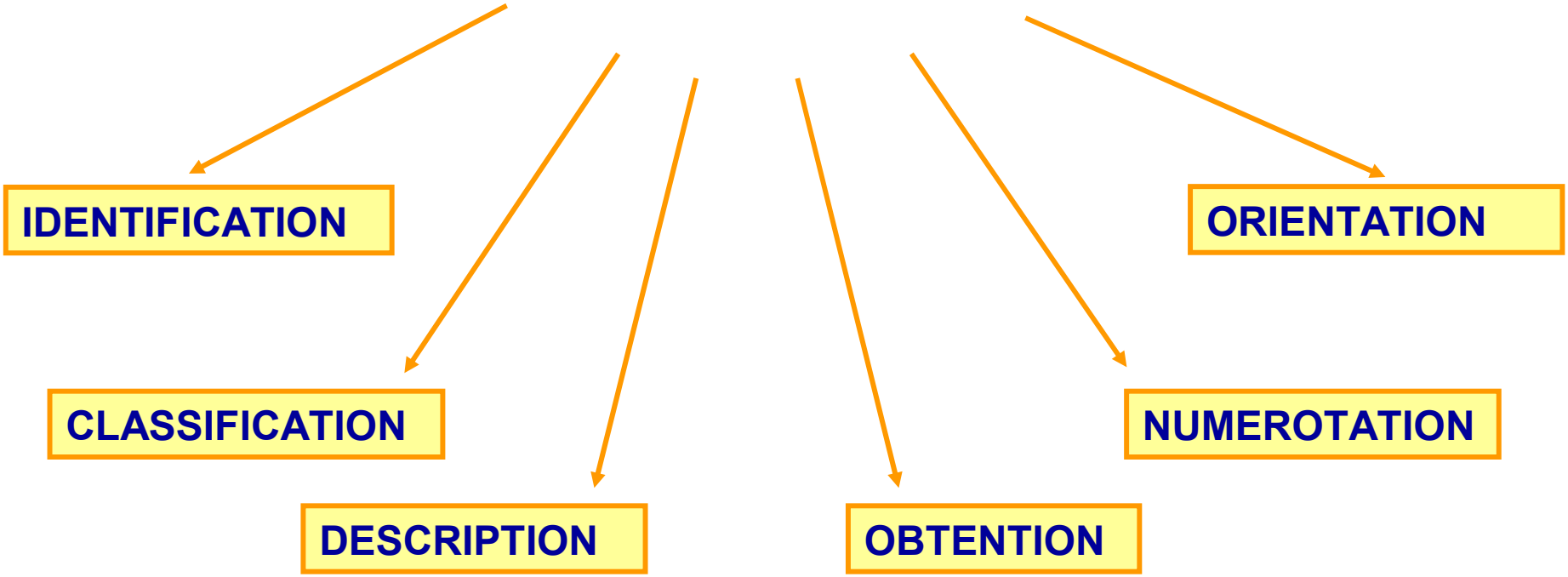
- Comment caractériser précisément des séquences d'IG
  (.. et des TR): identification, classification des gènes,
  description, numérotation des acides aminés, obtention ?

=> nécessité d'une ontologie spécifique

IMGT-ONTOLOGY

Pour standardiser, partager, réutiliser et représenter les connaissances en immunogénétique

IMGT-ONTOLOGY regroupe 6 concepts:



IMGT-ONTOLOGY

IMGT Scientific chart :
IMGT-ONTOLOGY en *langage naturel* pour les biologistes

IMGT-ML :
formalisation en XML à des fins de programmation

En cours : édition avec Protégé
pour faciliter la représentation et le partage
(agents humains et logiciels)

The Protégé Ontology Editor and Knowledge Acquisition System - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://protege.stanford.edu/

OK protege

protégé

Search:

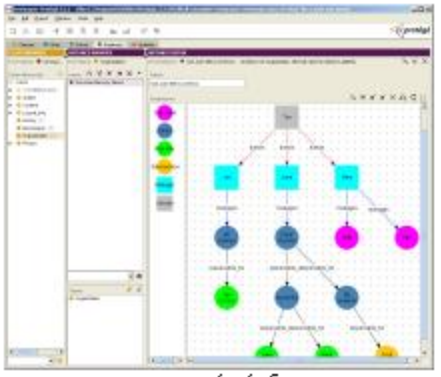
HOME | OVERVIEW | DOCUMENTATION | DOWNLOADS | SUPPORT | COMMUNITY | WIKI | ABOUT US

welcome to protégé

Protégé is a free, open source ontology editor and knowledge-base framework.

The Protégé platform supports two main ways of modeling ontologies via the Protégé-Frames and Protégé-OWL editors. Protégé ontologies can be exported into a variety of formats including RDF(S), OWL, and XML Schema. (more)

Protégé is based on Java, is extensible, and provides a plug-and-play environment that makes it a flexible base for rapid prototyping and application development. (more)



go to protégé-frames

go to protégé-owl

Protégé is supported by a strong community of developers and academic, government and corporate users, who are using Protégé for knowledge solutions in areas as diverse as biomedicine, intelligence gathering, and corporate modeling.

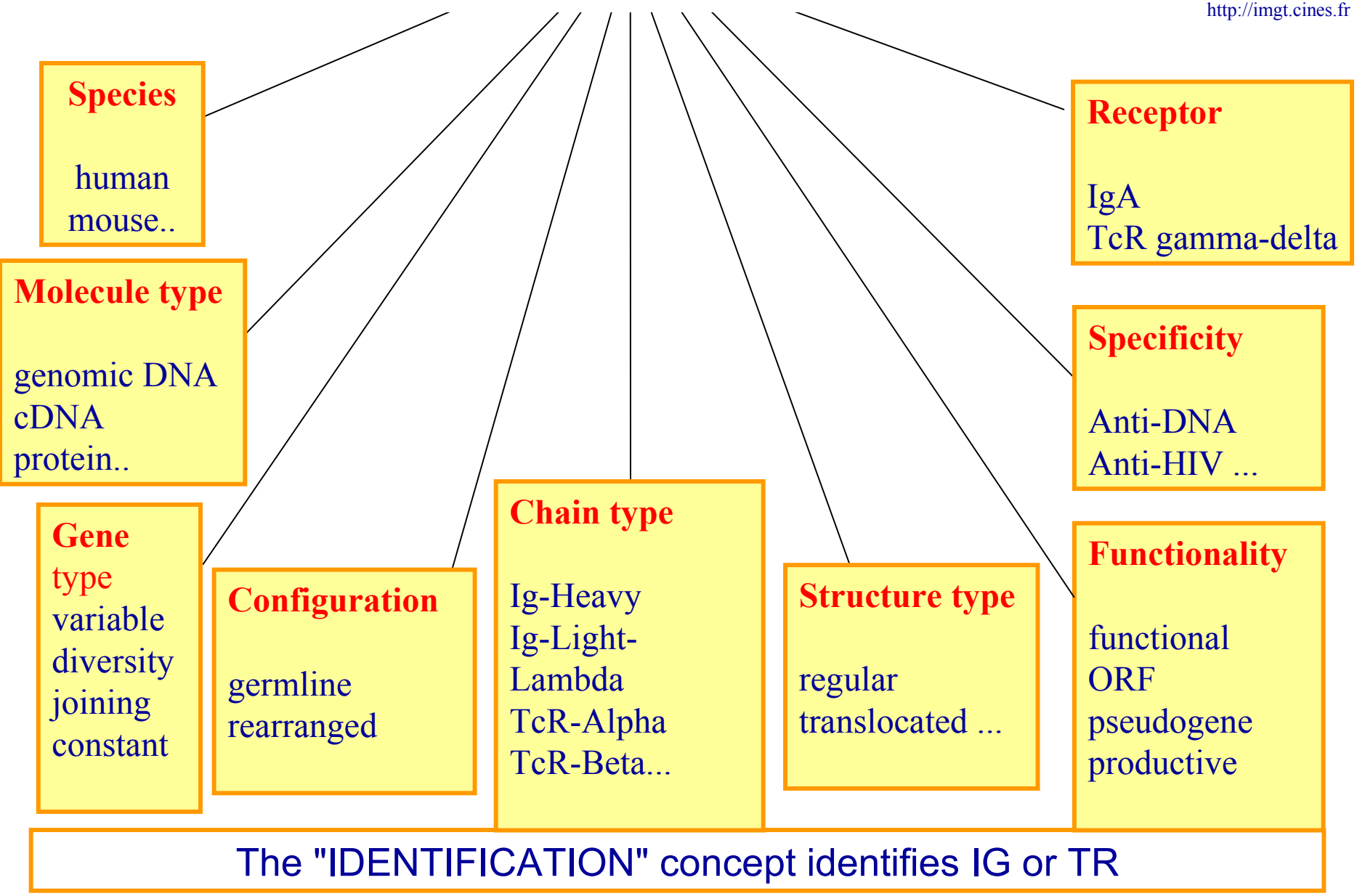
community	
Registered Users	56,404
protege-users list members	17,552
protege-discussion list members	5,579
protege-owl list members	2,422

Protégé is available from this site as a free download

Rechercher : cluster Occurrence suivante Occurrence précédente Surligner tout Respecter la casse

"IDENTIFICATION"

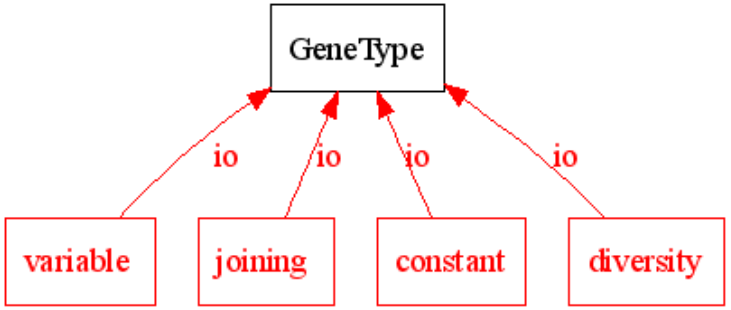
http://imgt.cines.fr



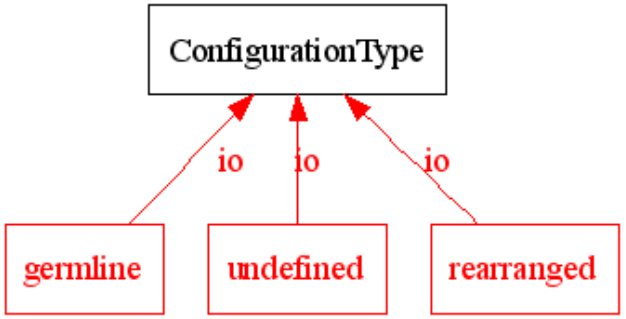
The "IDENTIFICATION" concept identifies IG or TR

Exemple de representation avec Protégé

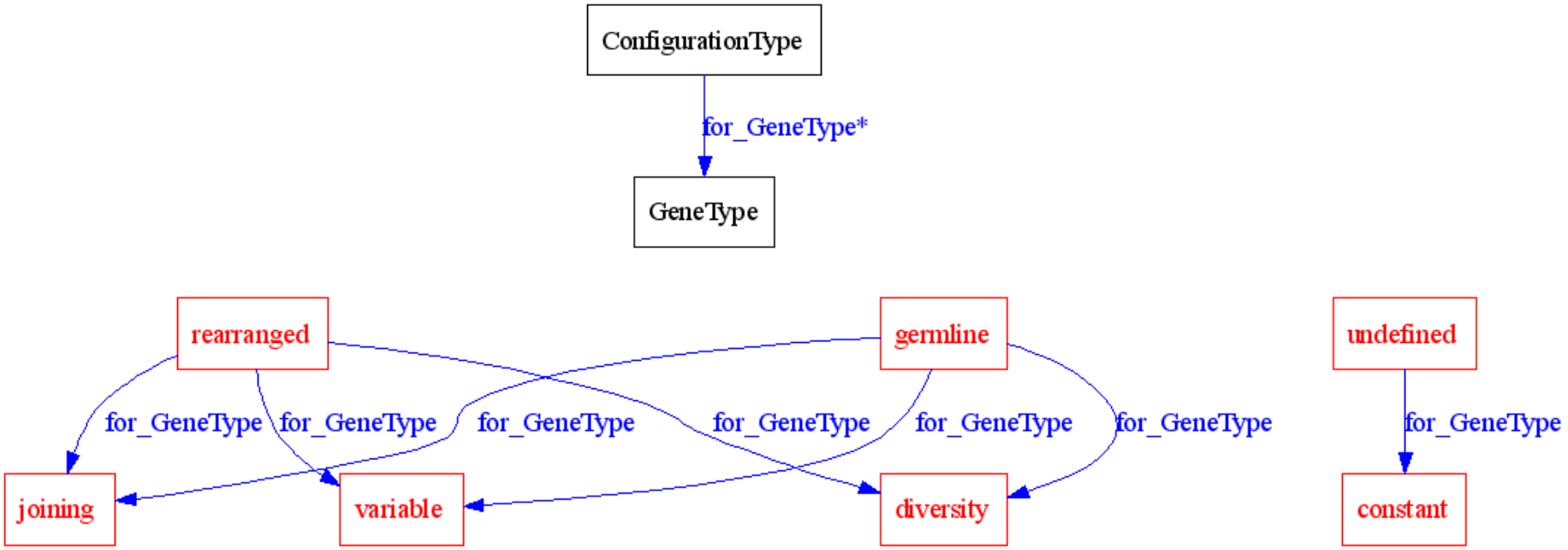
Instances de Gene Type



Instances de Configuration Type

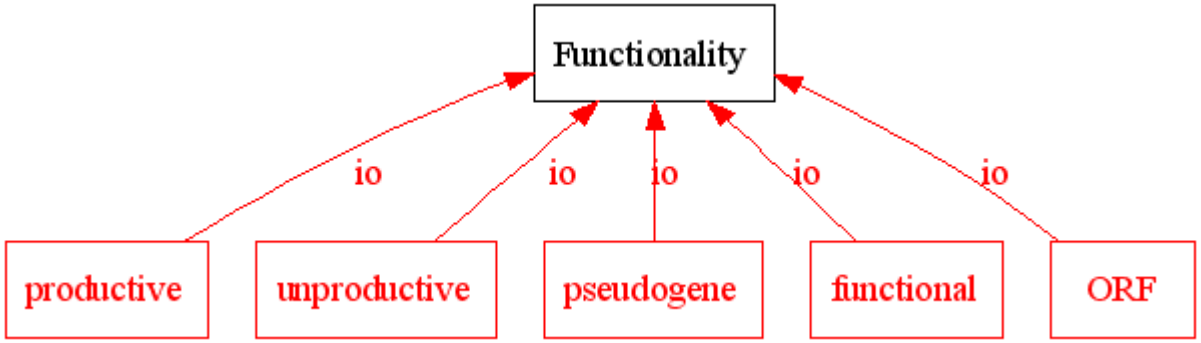


Relation entre Gene Type et Configuration Type

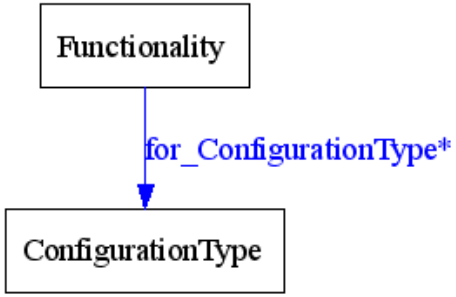


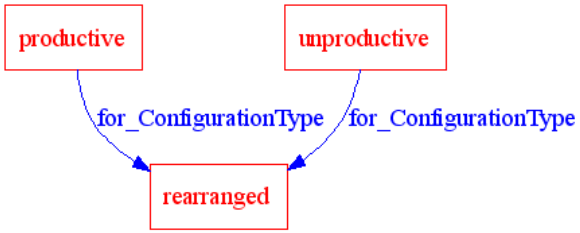
Exemple de representation avec Protégé

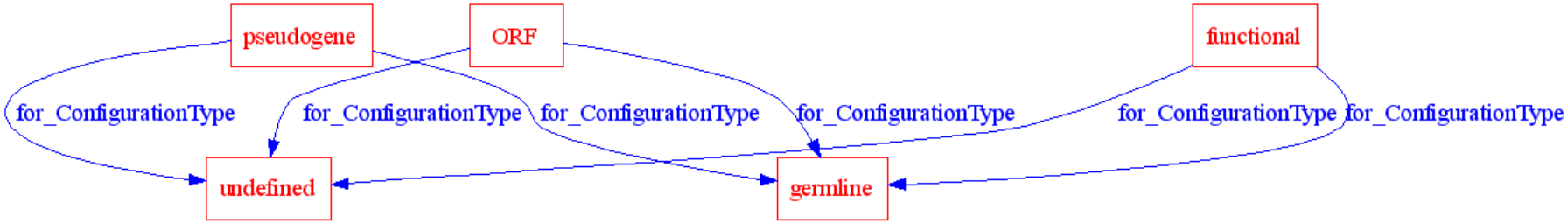
Instances de Functionality

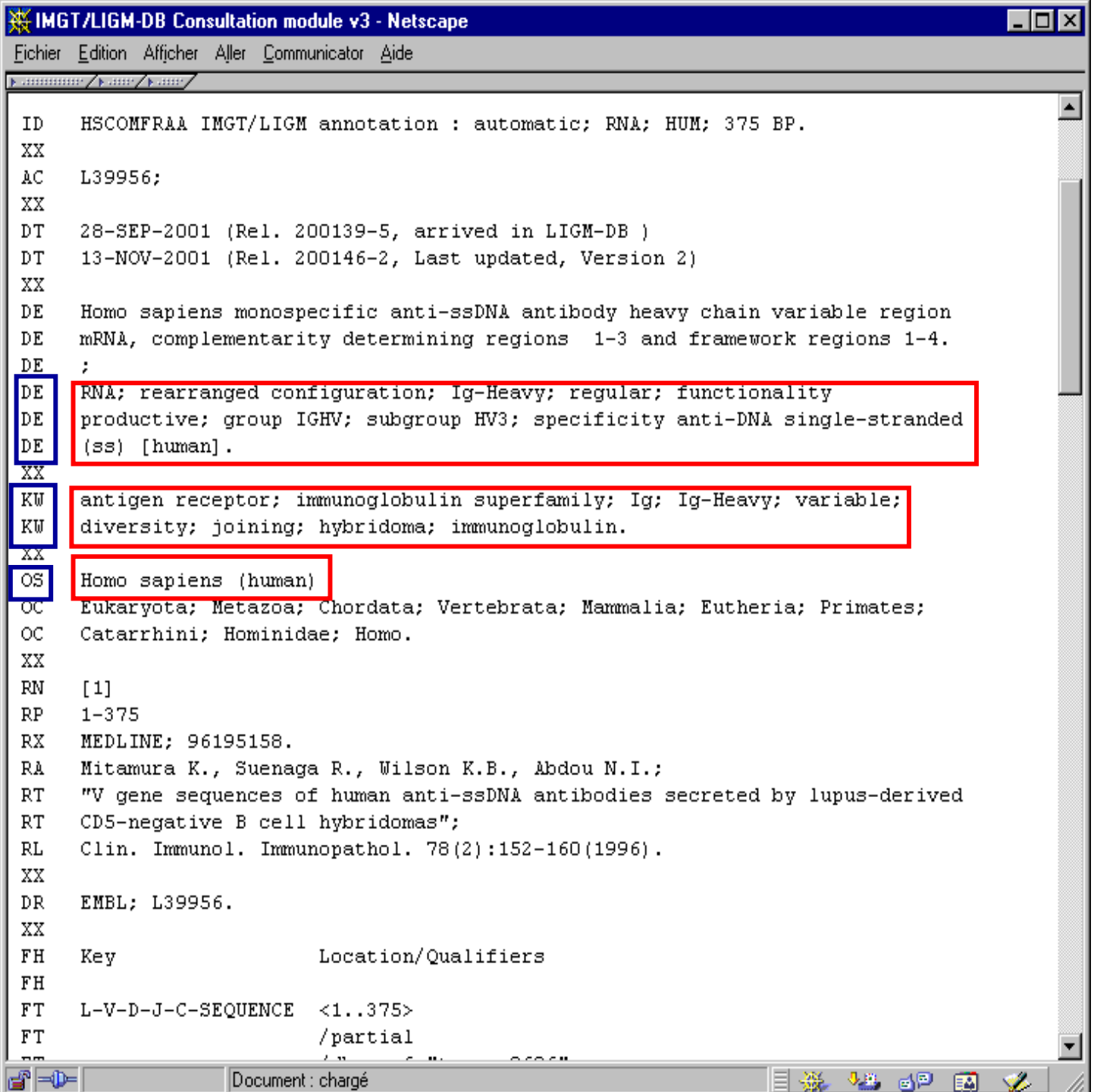


Relation entre Functionality et Configuration Type







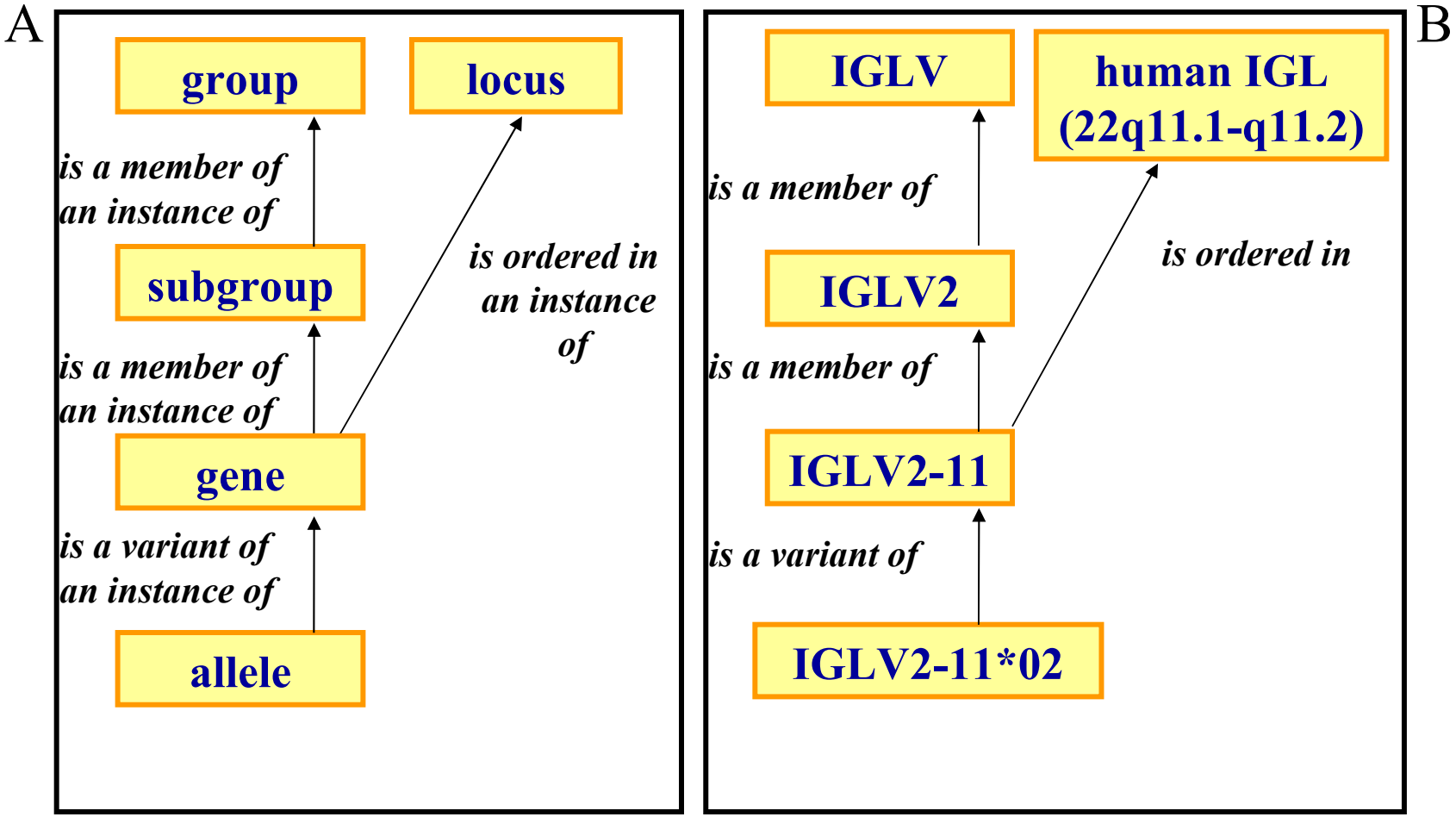


Im Muno Gene Tics Information system®

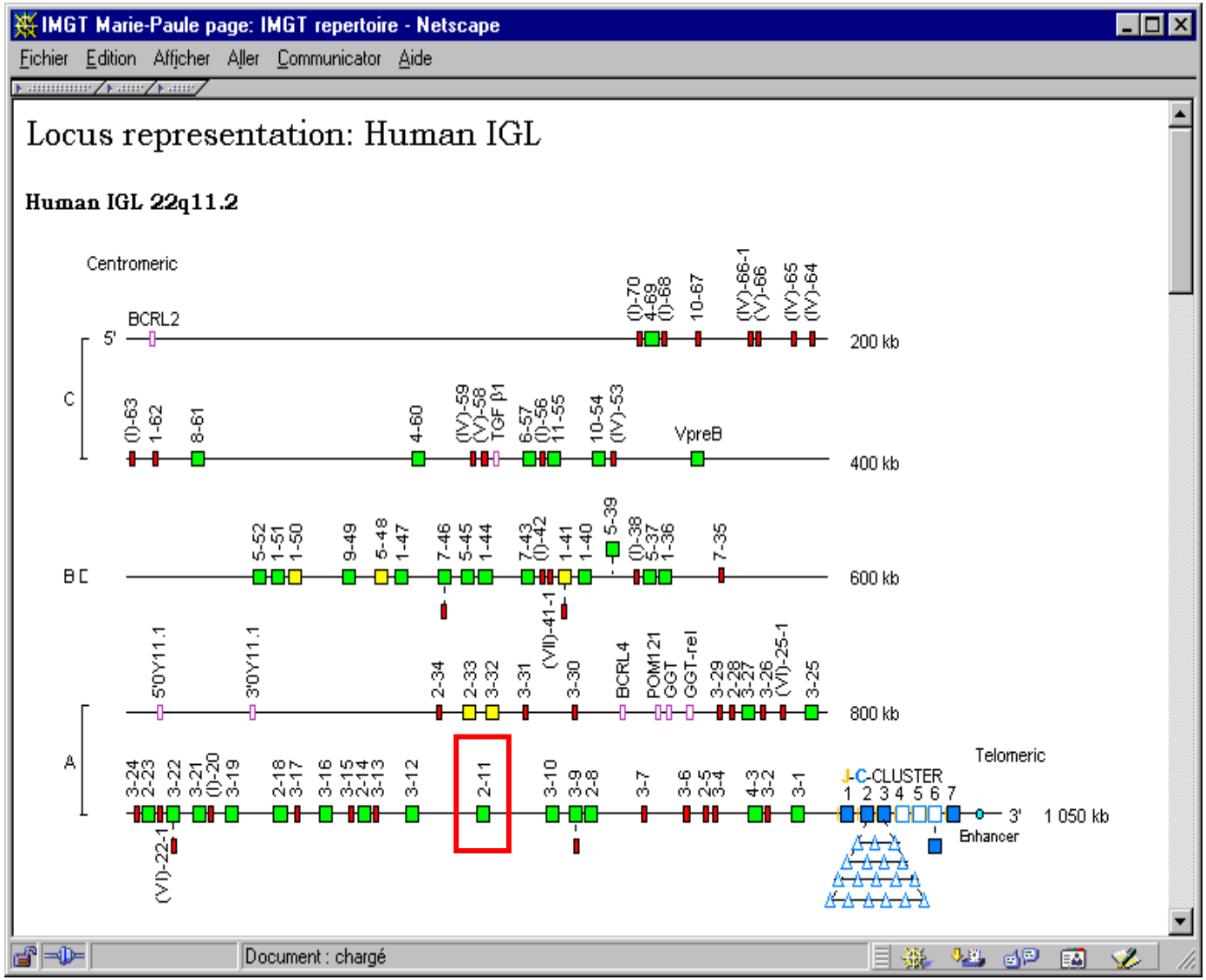
http://imgt.cines.fr

"CLASSIFICATION"

http://imgt.cines.fr



The "CLASSIFICATION" concept organizes the immunogenetics knowledge useful to name and classify IG and TR genes in IMGT.


IMGT Marie-Paule page: IMGT repertoire - Netscape
Fichier Edition Afficher Aller Communicator Aide
Locus representation: Human IGL
Human IGL 22q11.2
Centromeric
BCRL2
5'
200 kb
C
VpreB
400 kb
B
600 kb
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Enhancer
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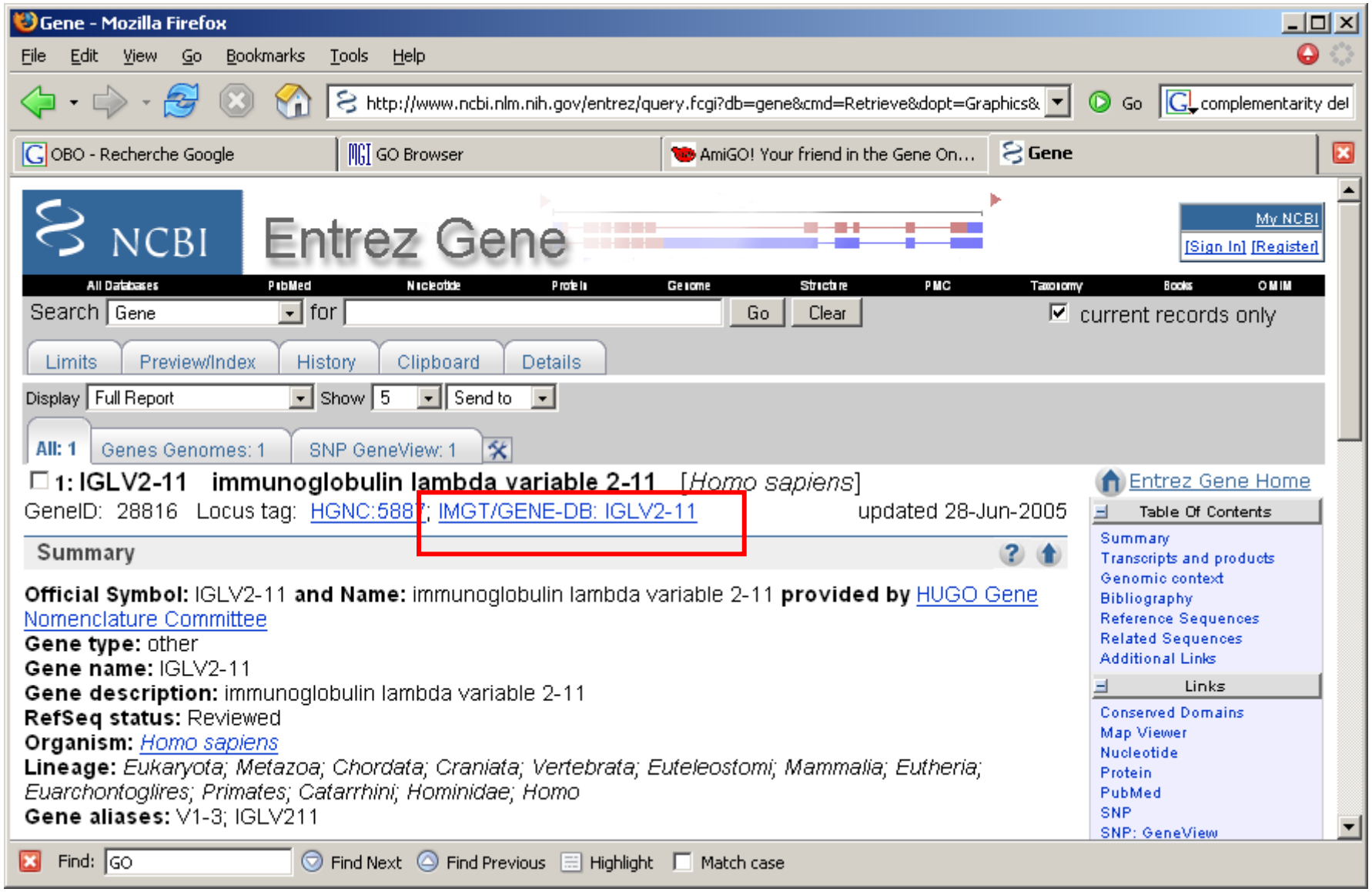
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Display Full Report Show 5 Send to
All: 1 Genes Genomes: 1 SNP GeneView: 1
1: IGLV2-11 immunoglobulin lambda variable 2-11 [Homo sapiens]
GeneID: 28816 Locus tag: HGNC:5887; IMGT/GENE-DB: IGLV2-11 updated 28-Jun-2005
Summary
Official Symbol: IGLV2-11 and Name: immunoglobulin lambda variable 2-11 provided by HUGO Gene Nomenclature Committee
Gene type: other
Gene name: IGLV2-11
Gene description: immunoglobulin lambda variable 2-11
RefSeq status: Reviewed
Organism: Homo sapiens
Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
Gene aliases: V1-3; IGLV211
Entrez Gene Home
Table Of Contents
Summary
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Genomic context
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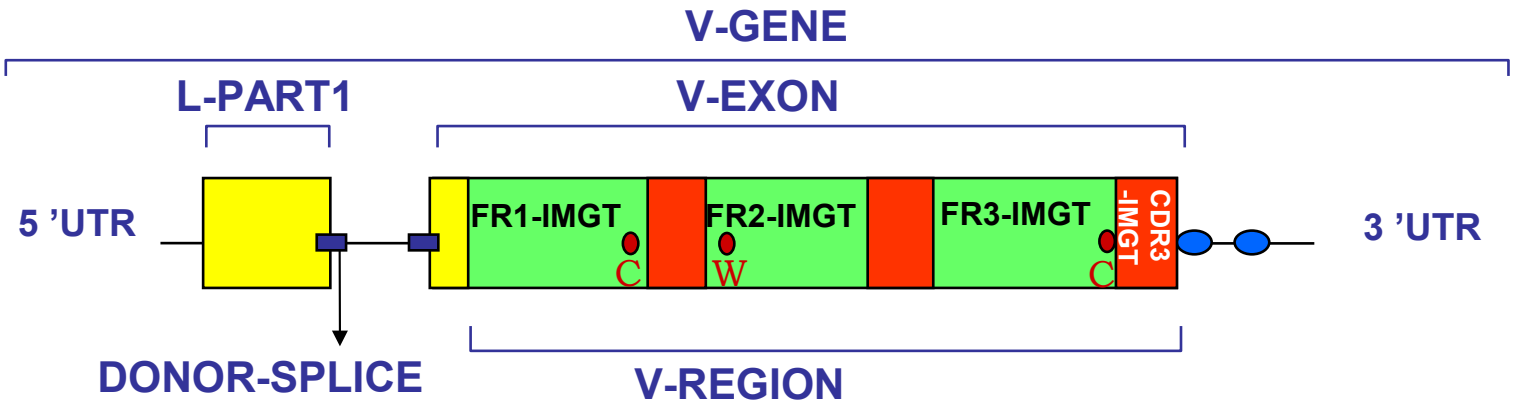
Reference Sequences
Related Sequences
Additional Links
Links
Conserved Domains
Map Viewer
Nucleotide
Protein
PubMed
SNP
SNP: GeneView
Find: GO
Find Next
Find Previous
Highlight
Match case

"DESCRIPTION"



Label 1	Label	Label relations
V-GENE	V-EXON	
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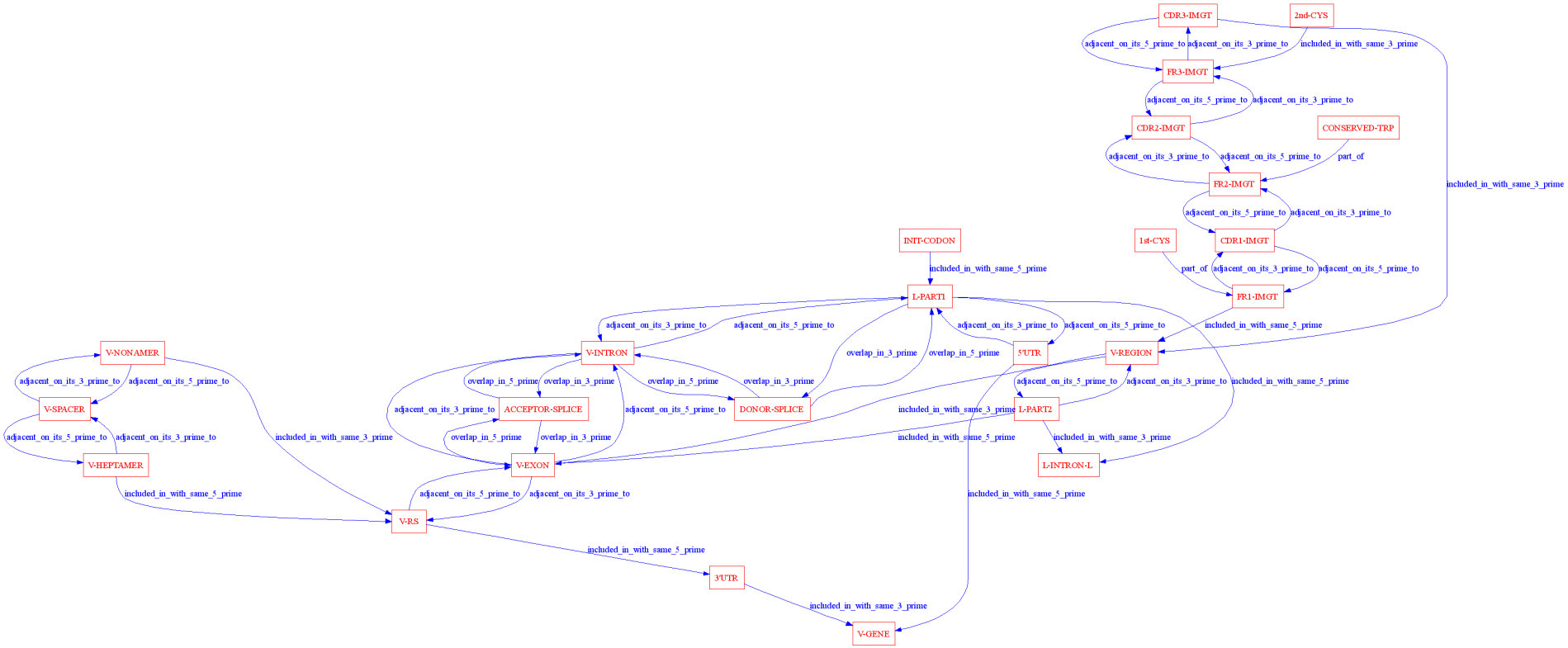
L-PART1	DONOR-SPLICE	
V-REGION	FR1-IMGT	
V-REGION	CDR3-IMGT	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2nd-CYS
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included_in_with_same_3_prime
FR3-IMGT
adjacent_on_its_5_prime_to
adjacent_on_its_3_prime_to
CDR2-IMGT
CONSERVED-TRP
adjacent_on_its_3_prime_to
adjacent_on_its_5_prime_to
part_of
FR2-IMGT
included_in_with_same_3_prime
adjacent_on_its_5_prime_to
adjacent_on_its_3_prime_to
CDR1-IMGT
1st-CYS
part_of
adjacent_on_its_3_prime_to
adjacent_on_its_5_prime_to
FR1-IMGT
included_in_with_same_5_prime
INIT-CODON
included_in_with_same_5_prime
L-PART1
adjacent_on_its_3_prime_to
adjacent_on_its_5_prime_to
V-INTRON
adjacent_on_its_3_prime_to
adjacent_on_its_5_prime_to
5'UTR
V-REGION
overlap_in_3_prime
overlap_in_5_prime
V-NONAMER
adjacent_on_its_3_prime_to
adjacent_on_its_5_prime_to
overlap_in_5_prime
overlap_in_3_prime
overlap_in_5_prime
overlap_in_3_prime
adjacent_on_its_5_prime_to
adjacent_on_its_3_prime_to
included_in_with_same_5_prime
V-SPACER
adjacent_on_its_3_prime_to
ACCEPTOR-SPLICE
DONOR-SPLICE
L-PART2
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adjacent_on_its_5_prime_to
adjacent_on_its_3_prime_to
included_in_with_same_3_prime
overlap_in_5_prime
overlap_in_3_prime
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included_in_with_same_3_prime
V-HEPTAMER
V-EXON
L-INTRON-L
included_in_with_same_5_prime
adjacent_on_its_5_prime_to
adjacent_on_its_3_prime_to
included_in_with_same_5_prime
V-RS
included_in_with_same_5_prime
3'UTR
included_in_with_same_3_prime
V-GENE

IMGT/LIGM-DB Consultation module v3 - Netscape
Fichier Edition Affichar Aller Communicator Aide
Signets Adresse : http://ligm.igh.cnrs.fr:8104/cgi-bin/IMGTlect.jv Infos connexes
Im Muno Gene Tics Information system®
http://imgt.cines.fr

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FT   CDR2-IMGT           154..162
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FT   FR3-IMGT            163..270
FT                       /AA_IMGT="66 to 104, AA 73, 81, 82 missing"
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FT   CDR3-IMGT           271..297
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XX
SQ   Sequence 297 BP; 60 A; 93 C; 71 G; 73 T; 0 other;
     cagtctgccc tgactcagcc tcgctcagtg tccgggtctc ctggacagtc agtcaccatc        60
     tcctgcactg gaaccagcag tgatattggt ggttataact atgtctcctg gtaccaacag       120
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"NUMEROTATION"

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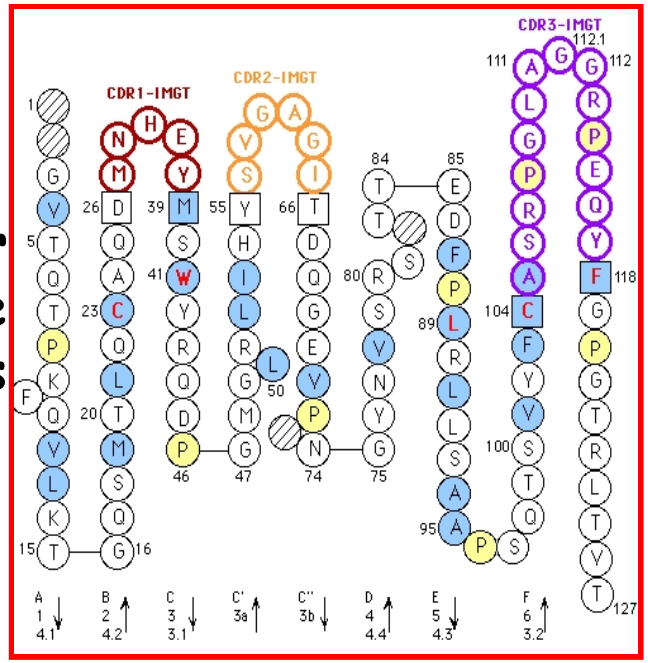
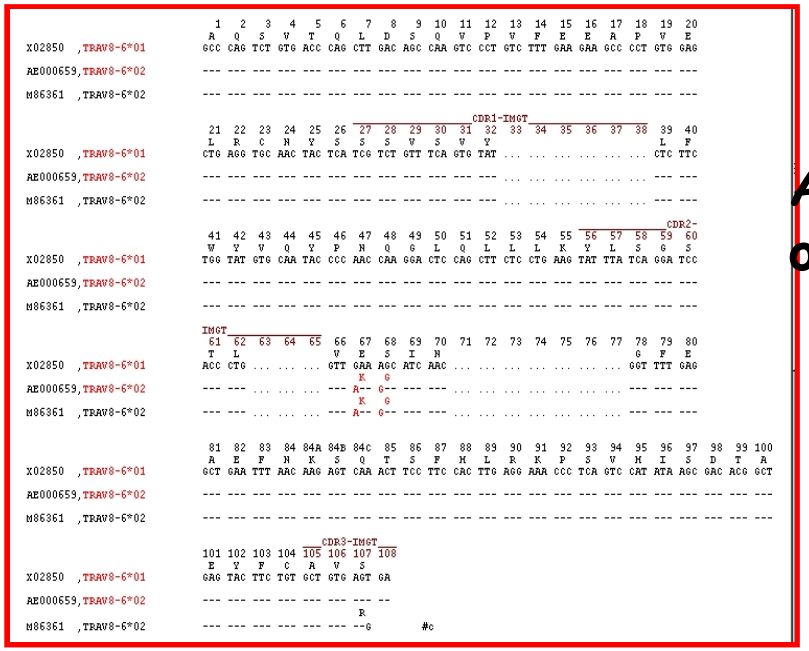
Collier De Perles





Alignment of alleles

Protein Display

TRAV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
	1 10 20	30	40 50	60	70 80 84ABC 90 100	110
AE000658, TRAV1-1	GQSLEQ.PSEVTAVEGAIVQINCTYQ	TSGFYG.....	LSWYQQHDGGAPTFLSY	NALDG.....	LEETG.....RFSSFLSRSDSYGYLLLQELQMKDSASYFC	AVR.....
AE000658, TRAV1-2	GQNIDQ.PTEMTATEGAIVQINCTYQ	TSGFNG.....	LFWYQQHAGEAPTFLSY	NVLDG.....	LEEKG.....RFSSFLSRSKGYSYLLLKELQMKDSASYLC	AVR.....
AE000658, TRAV2	KDQVFQ.PSTVASSEGAVVEIFCNHS	VSNAYN.....	FFWYLHFPGCAPRLLVK	GSK.....	PSQQG.....RYNMTYER..FSSSLLILQVREADAAVYYC	AVE.....
AE000658, TRAV3	AQSVAQPEDQVNVAEGNPLTVKCTYS	VSGNPY.....	LFWYVQYPNRGLQFLLK	YITGDNL...	VKGSY.....GFEAEFNKSQTSFHLKKPSALVSDSALYFC	AVRD.....
AE000658, TRAV4	LAKTTQ.PISMDSYEGQEVNITCSHN	NIATNDY.....	ITWYQQFPSQGPRFIIQ	GYKT.....	KVTNE.....VASLFIPADRKSSTLSLPRVSLSDTAVYYC	LVGD.....
AE000659, TRAV5	GEDVEQS.LFLSVREGDSSVINCTYT	DSSSTY.....	LYWYKQEPGAGLQLLTY	IFSNMD.....	MKQDQ.....RLTVLLNKKDKHLSLRIADTQTGDSAIYFC	AES.....
AE000659, TRAV6	SQKIEQNSEALNIQEGKTATLTCNYT	NYSPAY.....	LQWYRQDPGRGPVFLLL	IRENEK.....	EKRKE.....RLKVTFDTTLKQSLFHITASQPADSATYLC	ALD.....
AE000659, TRAV7	ENQVEHSPHFLGPQQGDVASMSCTYS	VSRFNN.....	LQWYRQNTGMGPKHLLS	MYSAGY.....	EKQKG.....RLNATLLK..NGSSLYITAVQPEDSATYFC	AVD.....
AE000659, TRAV8-1	AQSVSQHNHHVILSEAASLELGCNYS	YGGTVN.....	LFWYVQYPGQHLQLLLK	YFSGDPL...	VKGIK.....GFEAEFIKSKFSFNLRKPSVQWSDTAEYFC	AVN.....
AE000659, TRAV8-2	AQSVTQLDSHVSVSEGTPVLLRCNYS	SSYSPS.....	LFWYVQHPNKGLQLLLK	YTSAATL...	VKGIN.....GFEAEFKKSETSFHLTKPSAHMSDAAEYFC	VVS.....
AE000659, TRAV8-3	AQSVTQPDIHITVSEGASLELRCNYS	YGATPY.....	LFWYVQSPGQGLQLLLK	YFSGDTL...	VQGIK.....GFEAEFKRSQSSFNLRKPSVHWSDAAEYFC	AVG.....
AE000659, TRAV8-4	AQSVTQLGSHVSVSEGALVLLRCNYS	SSVPPY.....	LFWYVQYPNQGLQLLLK	YTSAATL...	VKGIN.....GFEAEFKKSETSFHLTKPSAHMSDAAEYFC	AVS.....
X02850 , TRAV8-6	AQSVTQLDSQVPVFEEAPVELRCNYS	SSVSVY.....	LFWYVQYPNQGLQLLLK	YLSGSTL...	VESIN.....GFEAEFNKSQTSFHLRKPSVHISDTAEYFC	AVS.....
AE000660, TRAV8-7	TQSVTQLDGHITVSEEAPLELKCNYS	YSGVPS.....	LFWYVQYSSQSLQLLLK	DLTEATQ...	VKGIR.....GFEAEFKKSETSFYLRKPSTHVSDAAEYFC	AVGDR.....
AE000659, TRAV9-1	GDSVWQTEGQVLPSEGDSLIVNCSYE	TTQYPS.....	LFWYVQYPGEGPQLHLK	AMKAND.....	KGRNK.....GFEAMYRKETTSFHLEKDSVQFSDSAVYFC	ALS.....

"OBTENTION"

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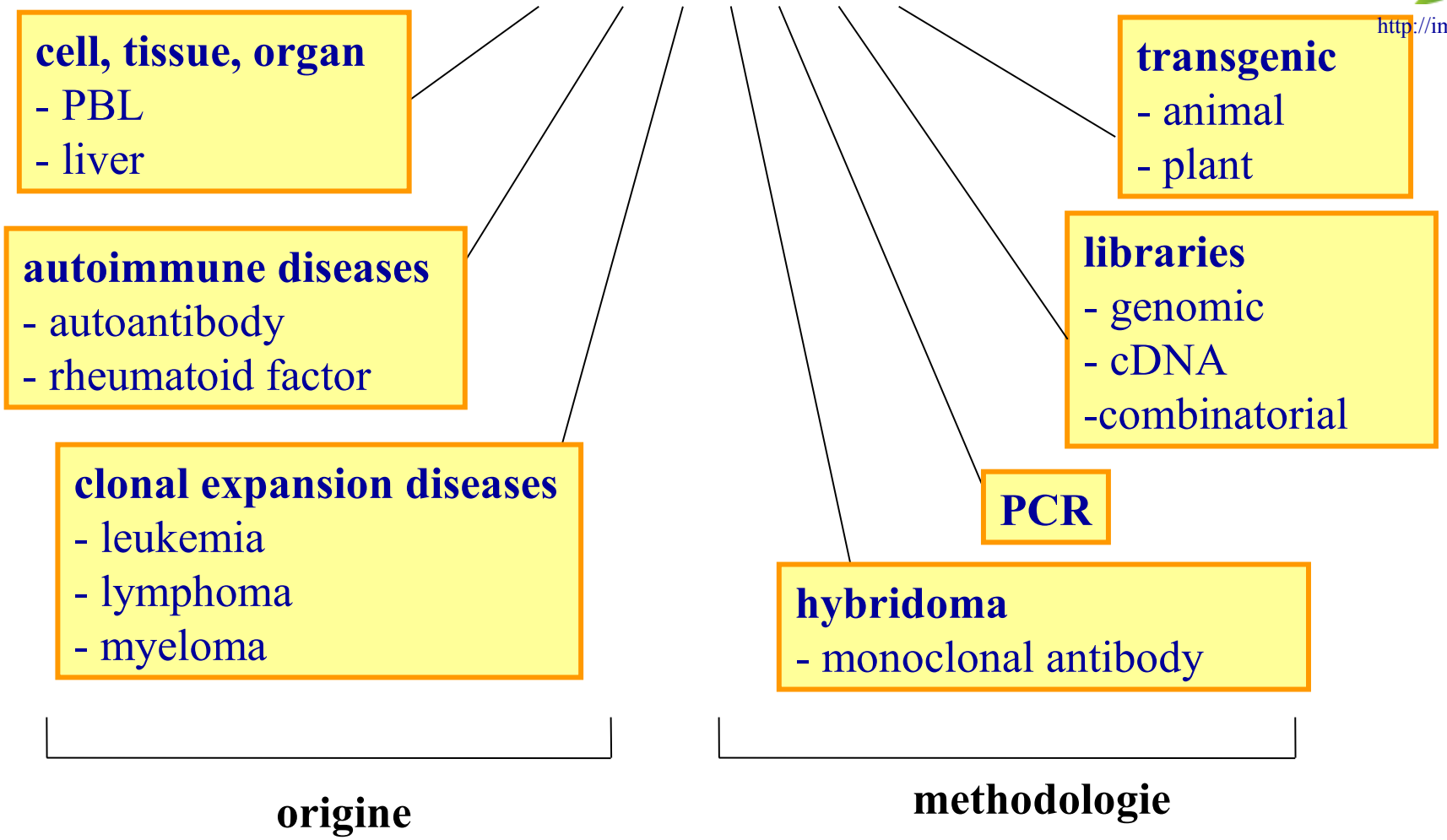

The "OBTENTION" concept specifies the origin and methodology

« ORIENTATION »

ttp://imgt.cines.fr

IMGT Repertoire (RPI) - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

IMGT									
Gene	Chromosomal localization	Gene orientation on chromosome	Gene in locus			Gene in sequence			
			Locus	Positions	Orientation	IMGT/LIGM-DB accession number	IMGT labels	Positions	Orientation
IGKC_C-REGION	2q11.2	REV	IGK			V00557	C-REGION	334..653	sense
IGKJ5	2q11.2	REV	IGK	1714417..AP001215		J00242	J-RS+J-REGION	1536..1612	sense
IGKJ4	2q11.2	REV	IGK	1714102..AP001215		J00242	J-RS+J-REGION	1221..1297	sense
IGKJ3	2q11.2	REV	IGK	1713760..AP001215		J00242	J-RS+J-REGION	880..955	sense
IGKJ2	2q11.2	REV	IGK	1713455..AP001215		J00242	J-RS+J-REGION	573..650	sense
IGKJ1	2q11.2	REV	IGK	1713093..AP001215		J00242	J-RS+J-REGION	212..288	sense
IGKV4-1	2q11.2	FWD	IGK	1689406..AP001211		Z00023	L-PART1+V-INTRON+V-EXON+V-RS	98..709	sense
IGKV5-2	2q11.2	FWD	IGK	1677682..AP001211		X02485	L-PART1+V-INTRON+V-EXON+V-RS	304..822	sense
IGKV7-3	2q11.2	REV	IGK	1659929..AP001211		X12682	L-PART1+V-INTRON+V-EXON	683..1281	sense
IGKV2-4	2q11.2	REV	IGK	1643349..AP001240		X72814	L-PART1+V-INTRON+V-EXON	569..1296	sense
IGKV1-5	2q11.2	REV	IGK	1627697..AP001241		Z00001	L-PART1+V-INTRON+V-EXON+V-RS	297..802	sense
IGKV1-6	2q11.2	REV	IGK	1608734..AP001230		M64858	L-PART1+V-INTRON+V-EXON+V-RS	131..637	sense
IGKV3-7	2q11.2	REV	IGK	1596528..AP001230		X02725	L-PART1+V-INTRON+V-EXON+V-RS	134..680	sense
IGKV1-8	2q11.2	REV	IGK	1582586..AP001209		K02097	L-PART1+V-INTRON+V-EXON	950..1427	sense
IGKV1-9	2q11.2	REV	IGK	1565034..AP001209		K02096	L-PART1+V-INTRON+V-EXON	691..1168	sense
IGKV2-10	2q11.2	REV	IGK	1555022..AP001209		Z00012	L-PART1+V-INTRON+V-EXON	121..814	sense
IGKV3-11	2q11.2	REV	IGK	1547845..AP001231		X01668	L-PART1+V-INTRON+V-EXON+V-RS	134..677	sense
IGKV1-12	2q11.2	REV	IGK	1534792..AP001231		V01577	L-PART1+V-INTRON+V-EXON+V-RS	1170..1674	sense
IGKV1-13	2q11.2	REV	IGK	1529026..AP001231		K02093	L-PART1+V-INTRON+V-EXON	427..903	sense
IGKV2-14	2q11.2	REV	IGK	1496996..AP001228		X72810	L-PART1+V-INTRON+V-EXON	191..956	sense
IGKV3-15	2q11.2	REV	IGK	1489840..AP001228		M23090	L-PART1+V-INTRON+V-EXON+V-RS	676..1219	sense
IGKV1-16	2q11.2	REV	IGK	1475162..AP001243		J00248	L-PART1+V-INTRON+V-EXON+V-RS	131..636	sense

Rechercher : cluster Occurrence suivante Occurrence précédente Surligner tout Respecter la casse

Annotation and IMGT-ONTOLOGY concepts

IDENTIFICATION

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

```
ID   AY998750 IMGT/LIGM annotation : automatic; mRNA; HUM; 366 BP.
XX
AC   AY998750;
XX
DT   25-MAY-2005 (Rel. 200521-3, arrived in LIGM-DB )
DT   25-AUG-2005 (Rel. 200534-4, Last updated, Version 3)
XX
DE   Homo sapiens isolate 4H immunoglobulin heavy chain variable region (IGHV1)
DE   mRNA, IGHV1-2*04 allele, partial cds.
DE   mRNA; rearranged configuration; Ig-Heavy; regular; functionality
DE   productive; group IGHV; subgroup HV1.
XX
KW   antigen receptor; immunoglobulin superfamily; Ig; Ig-Heavy; variable;
KW   diversity; joining; immunoglobulin.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC   Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-366
RX   PUBMED; 15706403.
RA   Stamatopoulos K., Belessi C., Papadaki T., Kalagiakou E., Stavroyianni N.,
RA   Douka V., Afendaki S., Saloum R., Parasi A., Anagnostou D., Laoutaris N.,
RA   Fassas A., Anagnostopoulos A.;
RT   "Immunoglobulin Heavy- And Light-chain Repertoire in Splenic Marginal Zone
RT   Lymphoma";
RL   (er) Mol. Med. (2005) In press
XX
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RA   Douka V., Afendaki S., Saloum R., Parasi A., Anagnostou D., Laoutaris N.,
RA   Fassas A., Anagnostopoulos A.;
RT   ;
RL   Submitted (30-MAR-2005) to the EMBL/GenBank/DDBJ databases.
RL   Hematology Department and HCT Unit, Papanikolaou General Hospital,
RL   Thessaloniki 57010, Greece
XX
DR   EMBL; AY998750.
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FH   Key                 Location/Qualifiers
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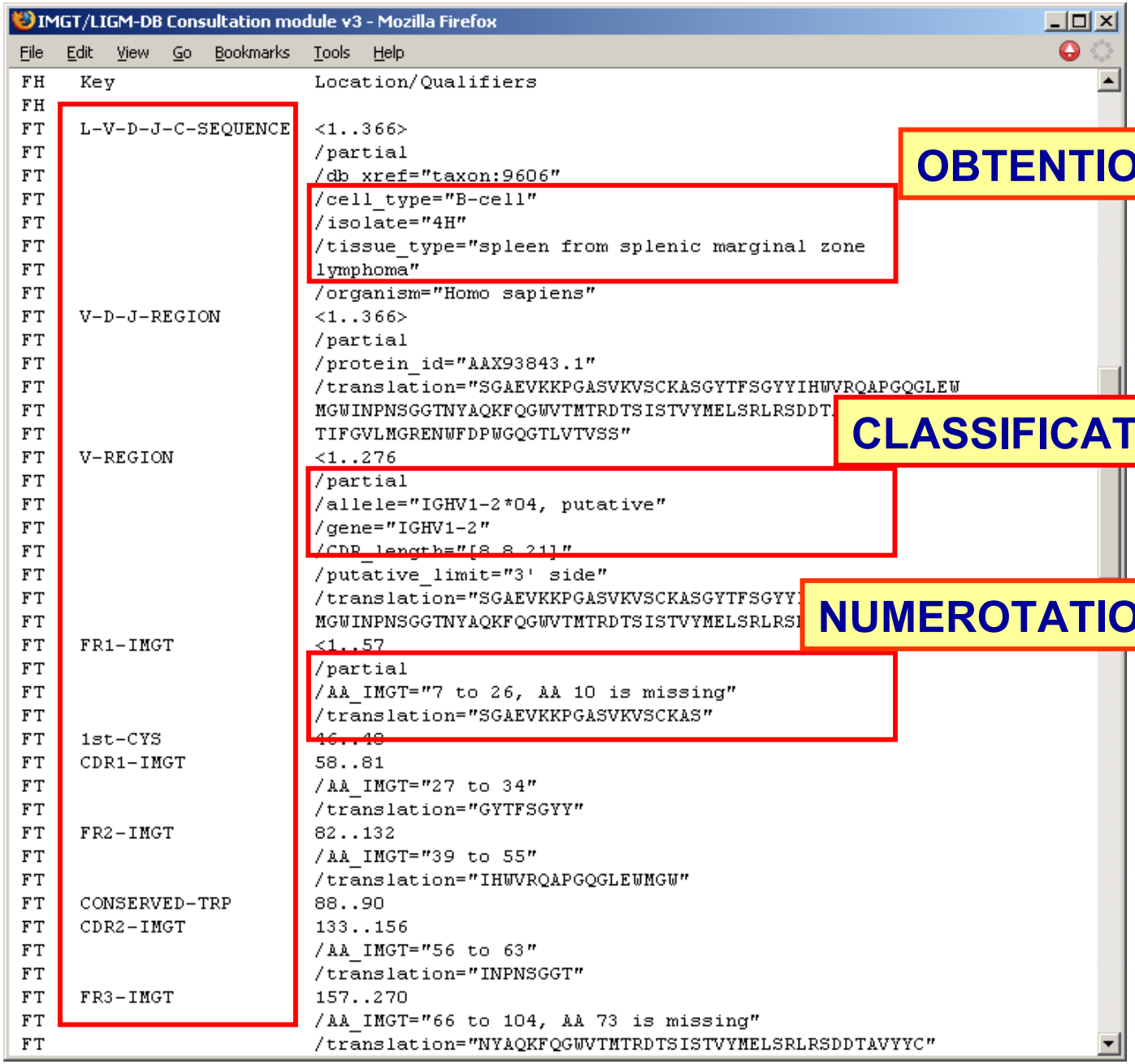
Annotation and IMGT-ONTOLOGY concepts



Im Muno Gene Tics Information system®

Les atouts de IMGT-ONTOLOGY

1 - Pour les utilisateurs:

- Définir un vocabulaire précis et spécifique du domaine qui permette de décrire en détail toutes les caractéristiques des IG et des TR
- Proposer ce vocabulaire standardisé comme critères de sélection dans la base

Les atouts de IMGT-ONTOLOGY

2 - Pour les annotateurs du laboratoire:

- Faciliter la communication au sein de l'équipe
- Faciliter la formation du nouveau personnel
- Etablir les règles d'annotation qui expriment les dépendances entre les termes du vocabulaire

Les atouts de IMGT-ONTOLOGY

3 - Automatisation des procédures:

- Alléger le travail des annotateurs
- Développer des outil d'annotation

Les atouts de IMGT-ONTOLOGY

4 – Intégration des nouvelles connaissances en immunogénétique

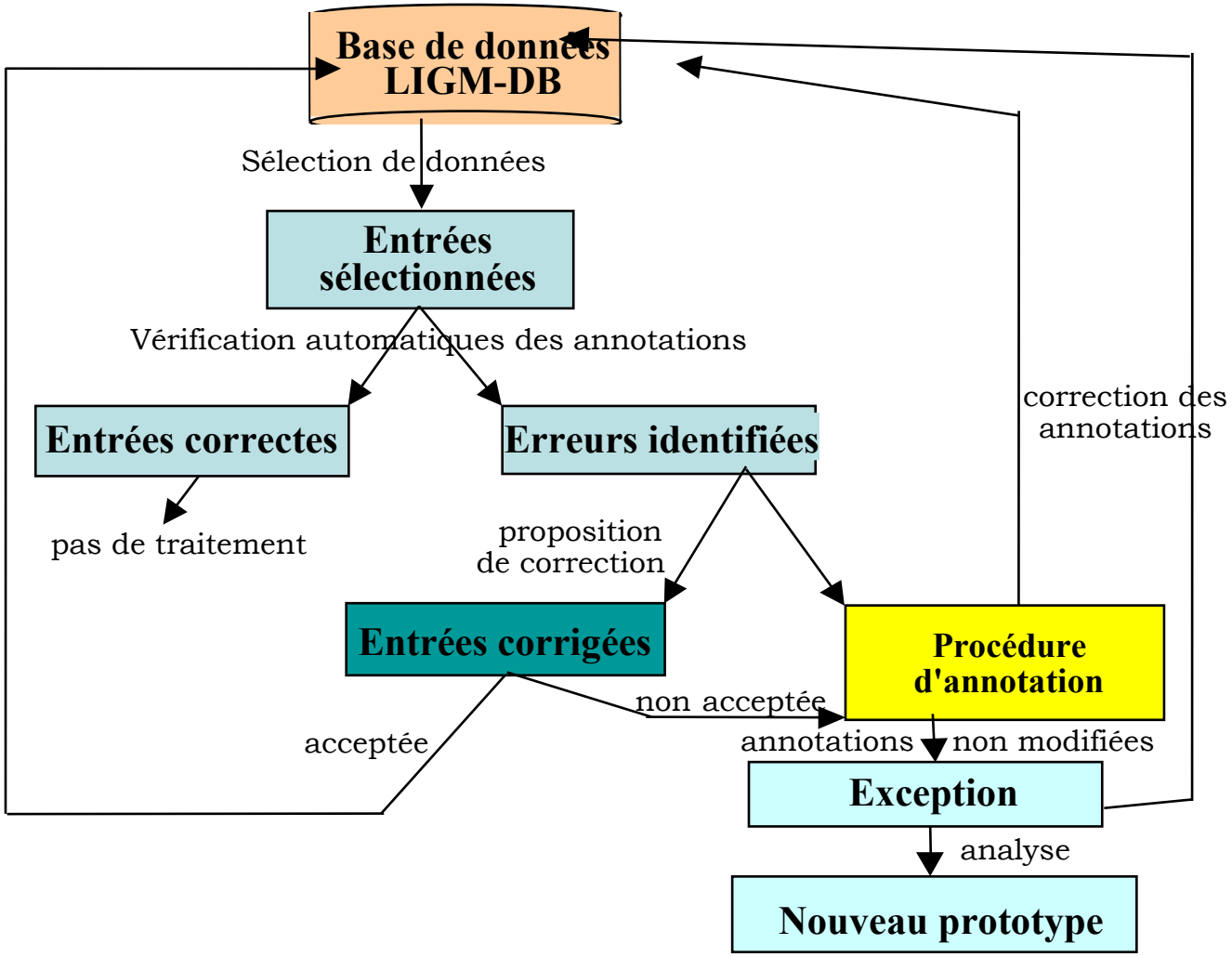
- Modifier les règles existantes
- Appliquer les modifications aux données préexistantes

Exemple d'aplication:
la mise à jour/contrôle des annotations

1 – Nouvelle nomenclature des gènes

2 – Nouveaux gènes

Contrôle des annotations des gènes germline TRAV chez la souris



Exemple :la stratégie d'IMGT pour l'annotation des séquences en immunogénétique sur Basée IMGT-ONTOLOGY

➔ Annotation manuelle (séquences d'ADN génomique)

- la plus précise
- la plus fiable
- indispensable pour la caractérisation de nouveaux gènes et génomes

➔ Annotation automatique (sequences d'ADNc)

- efficace quand les règles sont connues
- indispensable compte tenu du volume de données publiées
  - Contrôles de cohérence
  - Qualité très proche de l'annotation manuelle
  - plus de 9000 ADNc annotés automatiquement

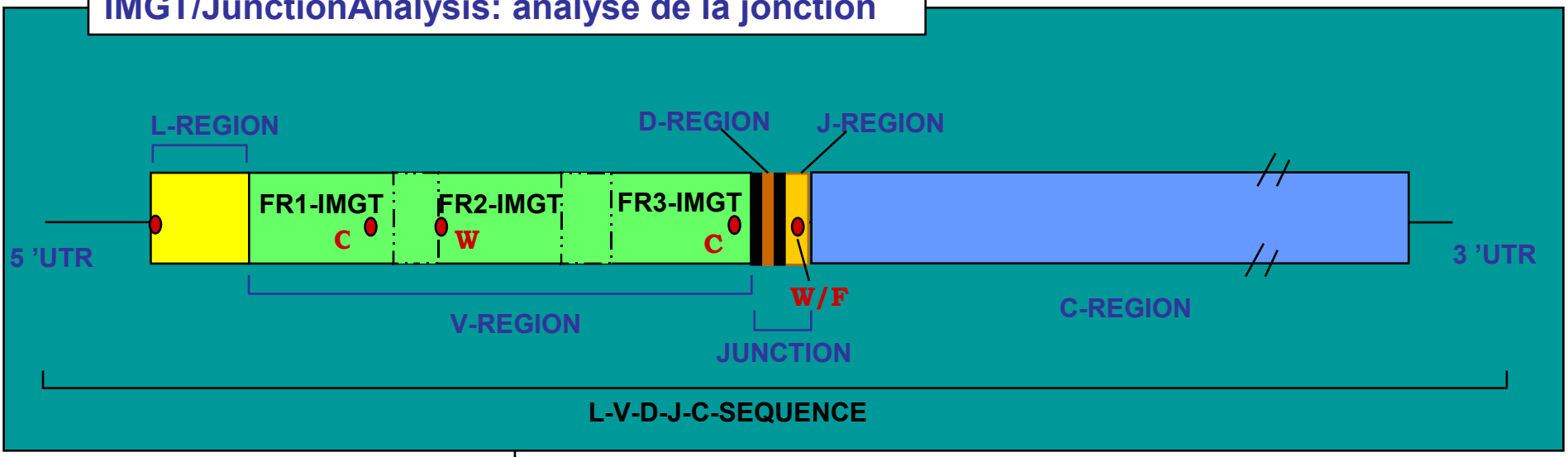
Im Muno Gene Tics Information system®

Automat, programme Java

IMGT/LIGM-DB: sélection de séquences cDNA

IMGT/V-QUEST: identification des gènes V, D, J ou V, J

IMGT/JunctionAnalysis: analyse de la jonction

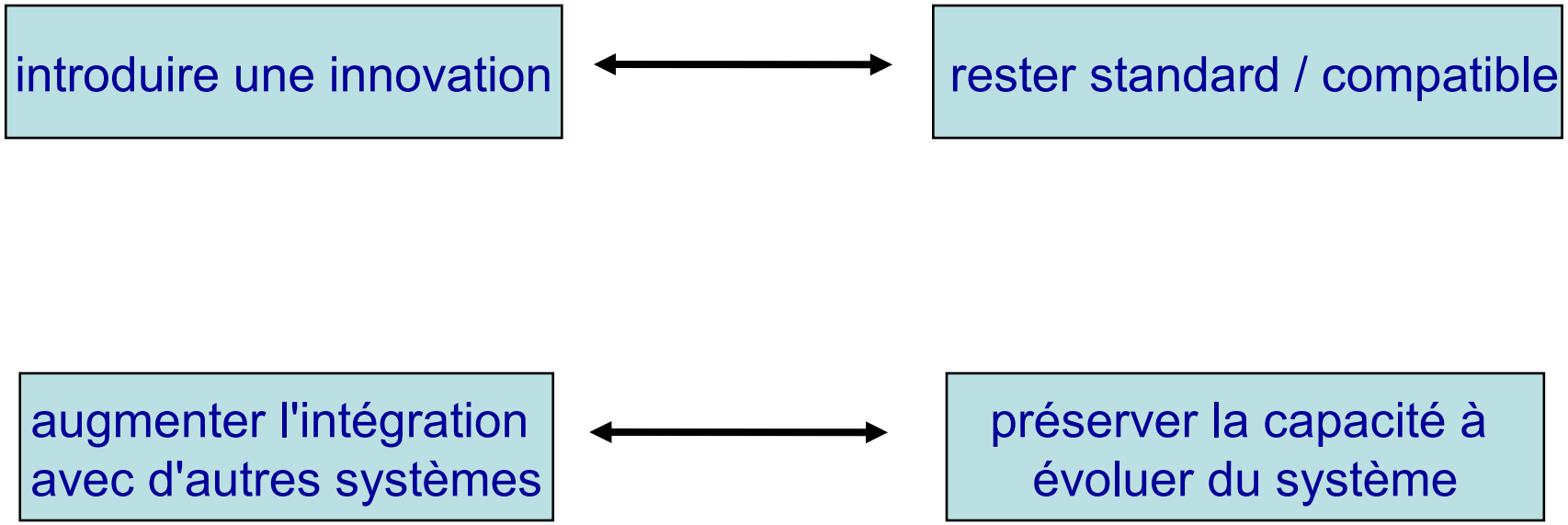


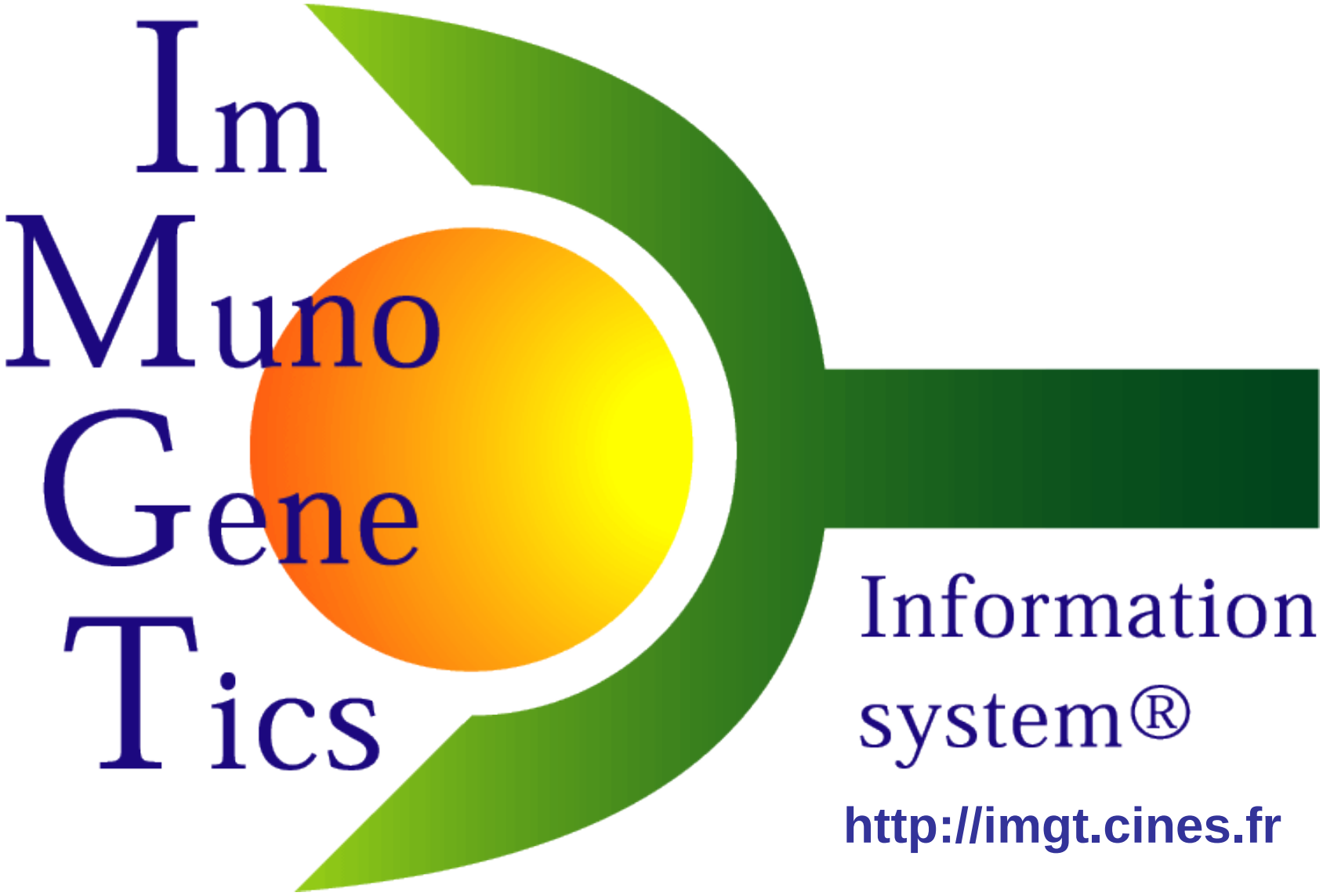
Evaluation de la fonctionnalité

Contrôle des critères d'identification de la séquence

Procédure d'annotation (comme les annotateurs)

L’équilibre des SI

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