http://www.imgt.org

Systèmes d'information
-
Ontologies
Bases de connaissances

UE FMBS312 Bioinformatique (TC3 du MR2 BioMed)

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28 septembre 2011

Système d'information

Ensemble des moyens

organisation (CNRS,…),
acteurs,
systèmes informatiques

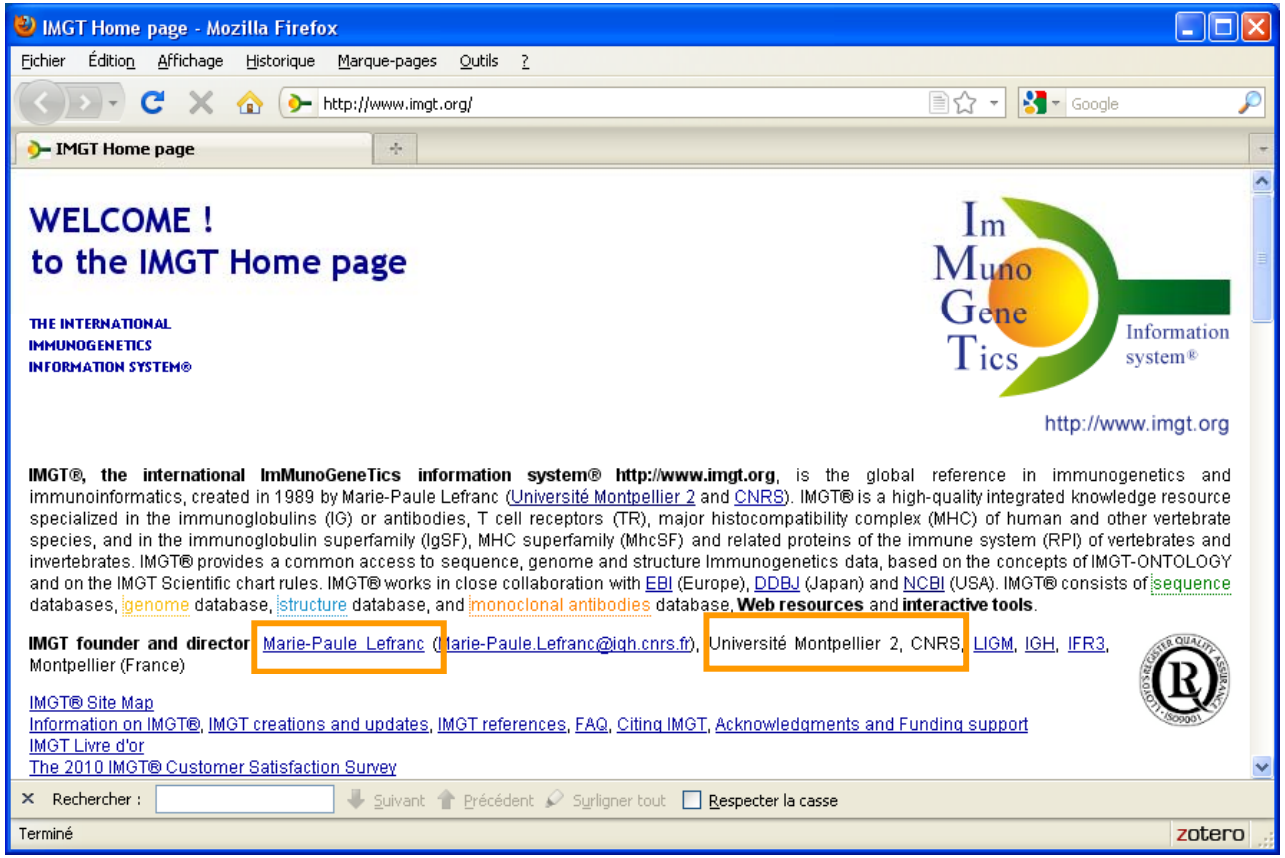
.

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

IMGT®, the international ImMunoGeneTics information system® (http://www.imgt.org)

Source unique de connaissances en immunogénétique et immunoinformatique, au niveau international.

IMGT® est spécialisé dans les séquences, structures et données génétiques des immunoglobulines (IG), des récepteurs T (TR), du complexe majeur d'histocompatibilité (MHC) des vertébrés, des protéines des superfamilles IgSF et MhcSF, et des protéines apparentées du système immunitaire.



Synthèse des immunoglobulines

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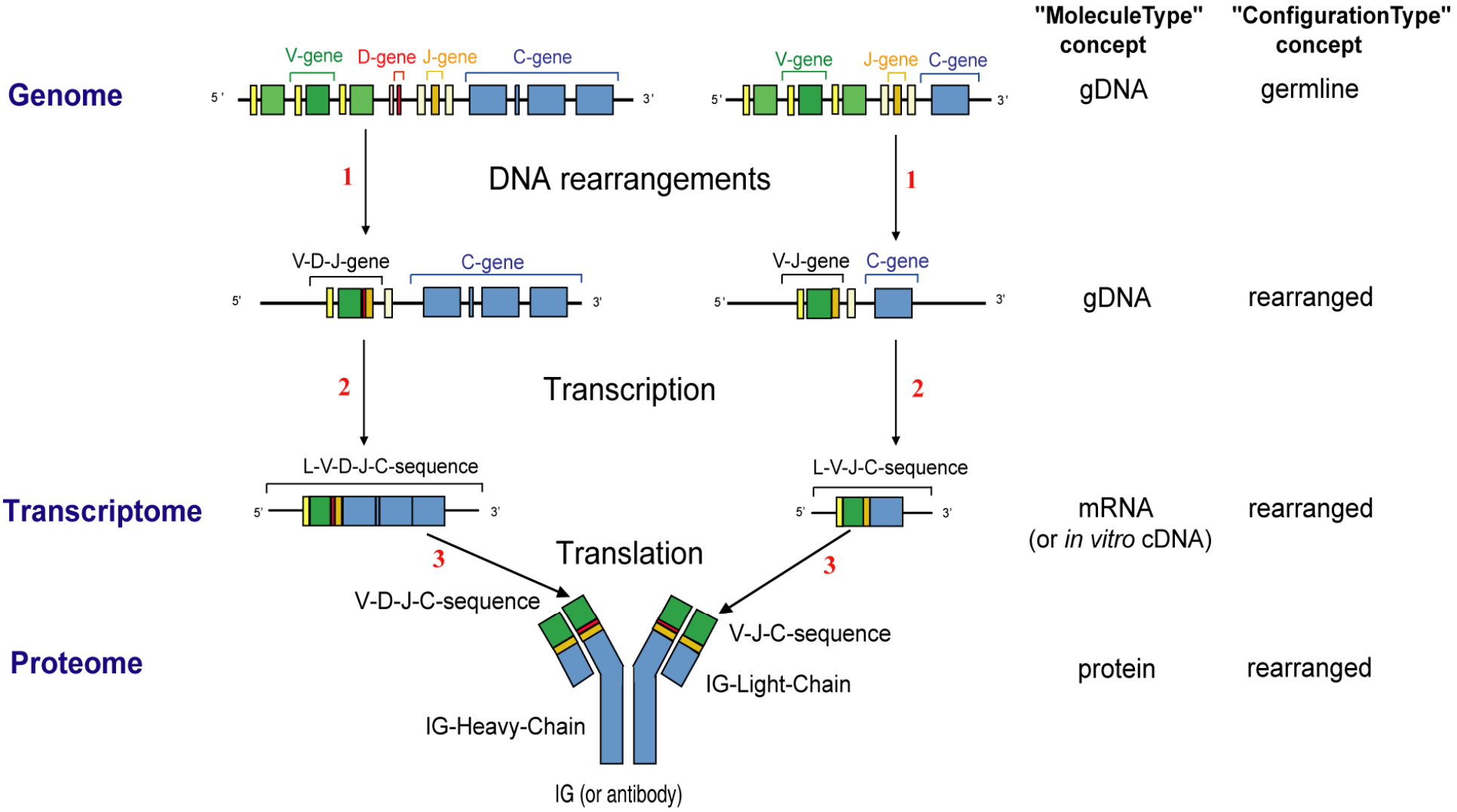


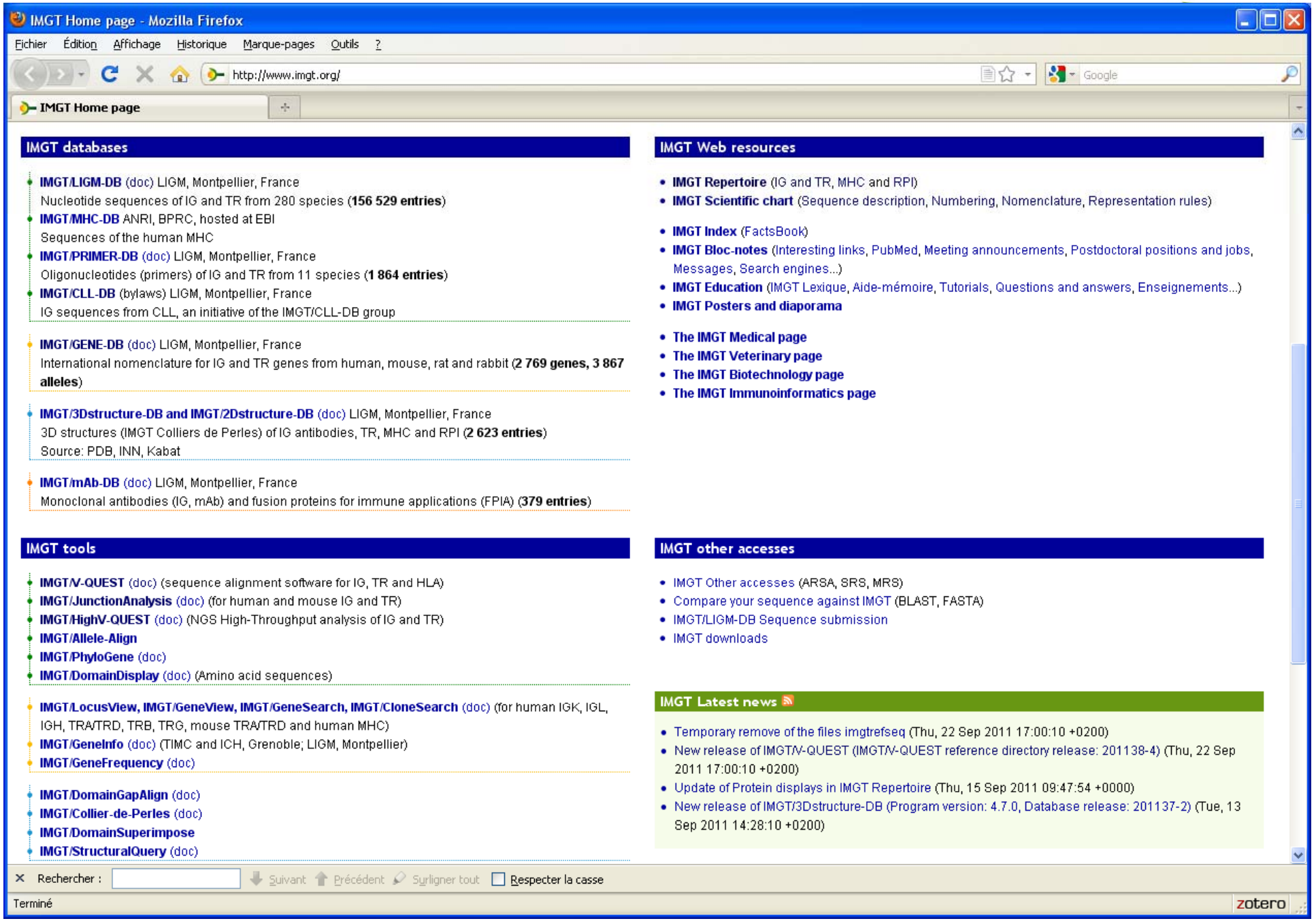
Système informatique (SI)

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

- **Les applications :**
  bases de données,
  logiciels de développement,
  interfaces d'exploitation, …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IMGT databases
IMGT/LIGM-DB (doc) LIGM, Montpellier, France
Nucleotide sequences of IG and TR from 280 species (156 529 entries)
IMGT/MHC-DB ANRI, BPRC, hosted at EBI
Sequences of the human MHC
IMGT/PRIMER-DB (doc) LIGM, Montpellier, France
Oligonucleotides (primers) of IG and TR from 11 species (1 864 entries)
IMGT/CLL-DB (bylaws) LIGM, Montpellier, France
IG sequences from CLL, an initiative of the IMGT/CLL-DB group
IMGT/GENE-DB (doc) LIGM, Montpellier, France
International nomenclature for IG and TR genes from human, mouse, rat and rabbit (2 769 genes, 3 867 alleles)
IMGT/3Dstructure-DB and IMGT/2Dstructure-DB (doc) LIGM, Montpellier, France
3D structures (IMGT Colliers de Perles) of IG antibodies, TR, MHC and RPI (2 623 entries)
Source: PDB, INN, Kabat
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Monoclonal antibodies (IG, mAb) and fusion proteins for immune applications (FPIA) (379 entries)
IMGT Web resources
IMGT Repertoire (IG and TR, MHC and RPI)
IMGT Scientific chart (Sequence description, Numbering, Nomenclature, Representation rules)
IMGT Index (FactsBook)
IMGT Bloc-notes (Interesting links, PubMed, Meeting announcements, Postdoctoral positions and jobs, Messages, Search engines...)
IMGT Education (IMGT Lexique, Aide-mémoire, Tutorials, Questions and answers, Enseignements...)
IMGT Posters and diaporama
The IMGT Medical page
The IMGT Veterinary page
The IMGT Biotechnology page
The IMGT Immunoinformatics page
IMGT tools
IMGT/V-QUEST (doc) (sequence alignment software for IG, TR and HLA)
IMGT/JunctionAnalysis (doc) (for human and mouse IG and TR)
IMGT/HighV-QUEST (doc) (NGS High-Throughput analysis of IG and TR)
IMGT/Allele-Align
IMGT/PhyloGene (doc)
IMGT/DomainDisplay (doc) (Amino acid sequences)
IMGT/LocusView, IMGT/GeneView, IMGT/GeneSearch, IMGT/CloneSearch (doc) (for human IGK, IGL, IGH, TRA/TRD, TRB, TRG, mouse TRA/TRD and human MHC)
IMGT/GeneInfo (doc) (TIMC and ICH, Grenoble; LIGM, Montpellier)
IMGT/GeneFrequency (doc)
IMGT/DomainGapAlign (doc)
IMGT/Collier-de-Perles (doc)
IMGT/DomainSuperimpose
IMGT/StructuralQuery (doc)
IMGT other accesses
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Compare your sequence against IMGT (BLAST, FASTA)
IMGT/LIGM-DB Sequence submission
IMGT downloads
IMGT Latest news
Temporary remove of the files imgtrefseq (Thu, 22 Sep 2011 17:00:10 +0200)
New release of IMGT/V-QUEST (IMGT/V-QUEST reference directory release: 201138-4) (Thu, 22 Sep 2011 17:00:10 +0200)
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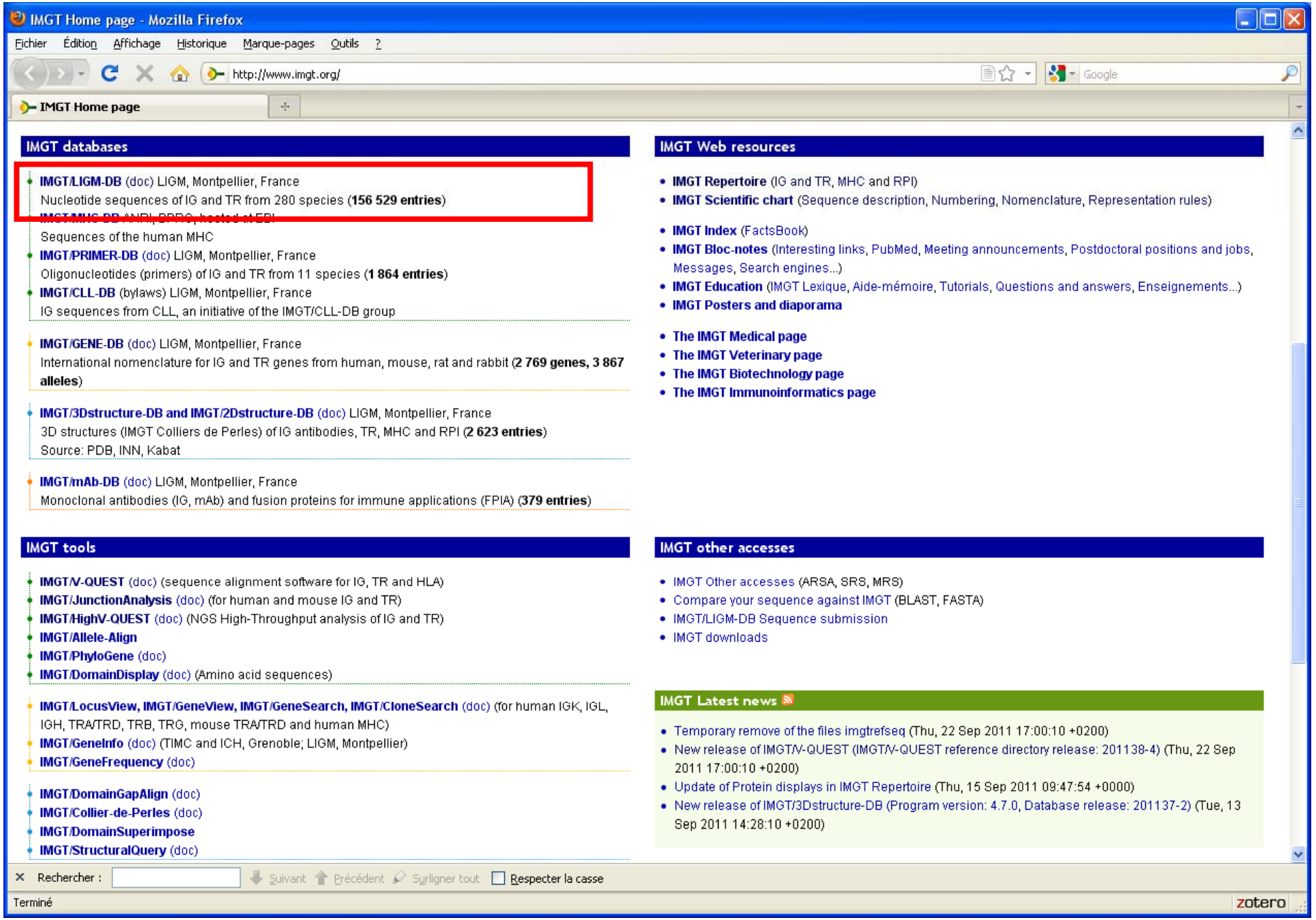
New release of IMGT/3Dstructure-DB (Program version: 4.7.0, Database release: 201137-2) (Tue, 13 Sep 2011 14:28:10 +0200)
Rechercher :
Suivant Précédent Surligner tout Respecter la casse
Terminé
zotero

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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Les objectifs de IMGT/LIGM-DB

http://www.imgt.org

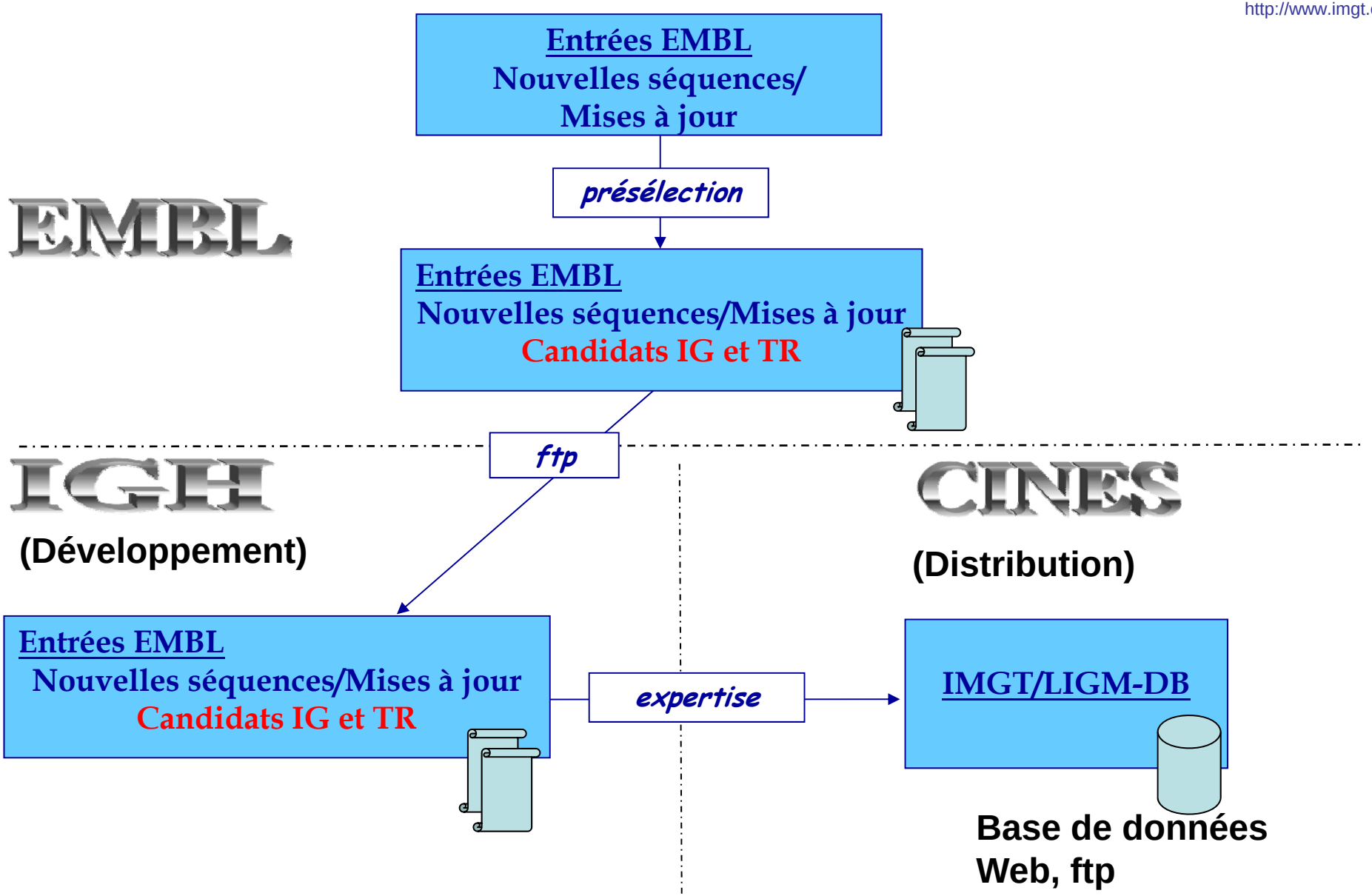
- Contenir toutes les séquences IG et TR des bases EMBL/GenBank/DDBJ
  + de 149.500 séquences de 235 espèces

- Expertiser les séquences en fonction des connaissances en immunogénétique
  - identification des gènes,
  - description des motifs (régions codantes, ...)

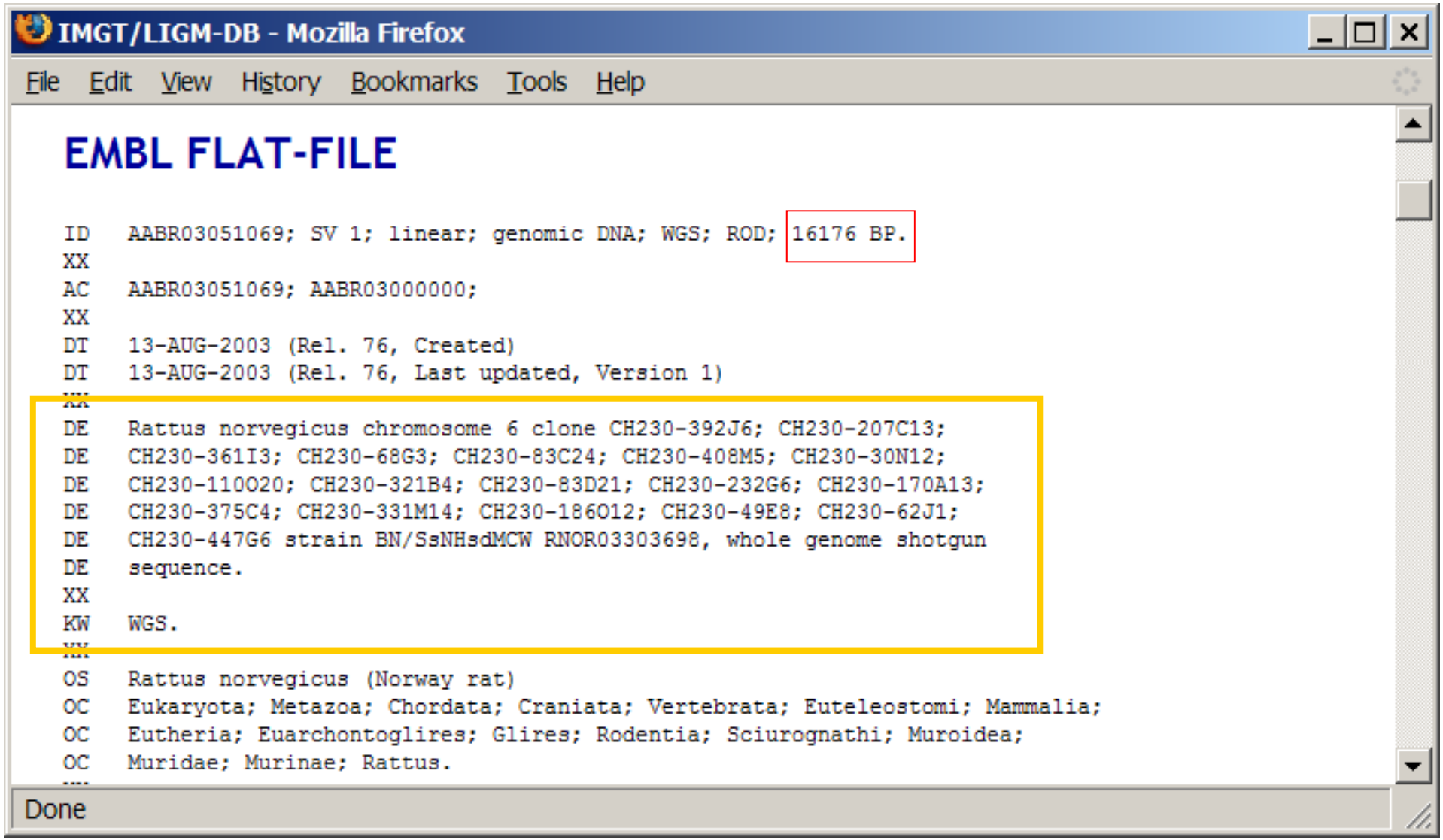
- Suivi et intégration des nouvelles connaissances dans le système d'information IMGT®

IMGT/LIGM-DB: application distribuée

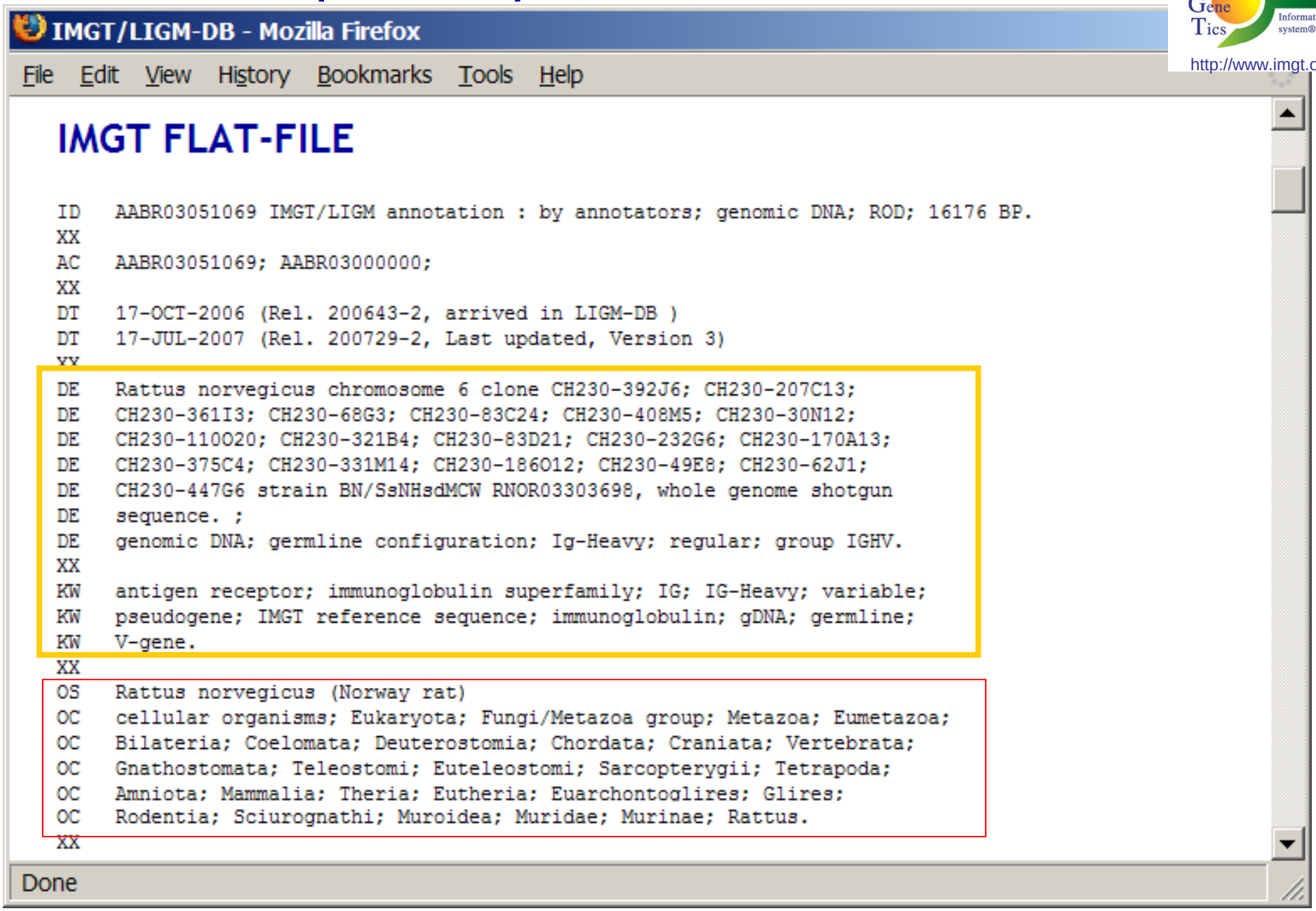
http://www.imgt.org



A l'arrivée dans IMGT®



Après expertise dans IMGT®



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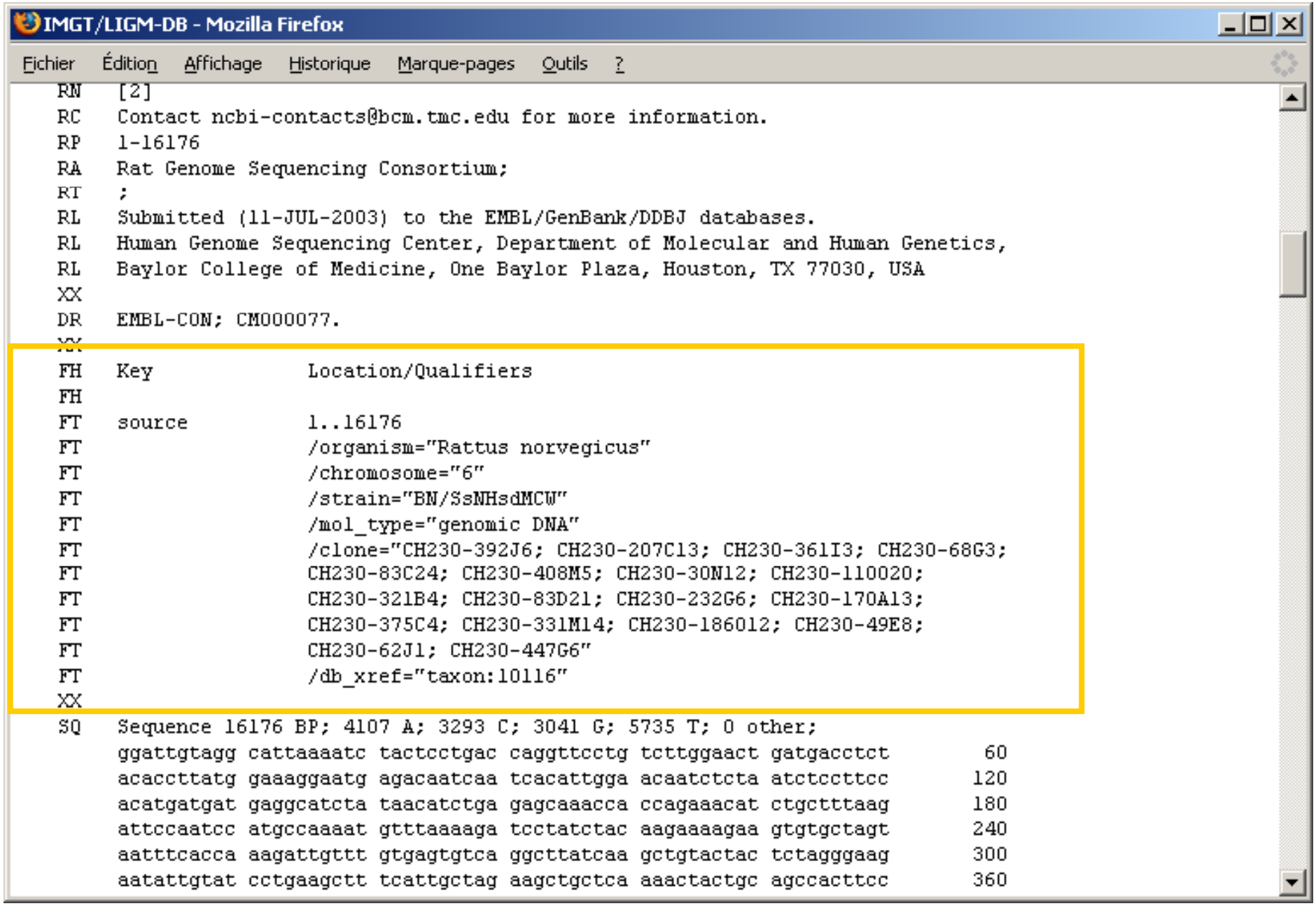

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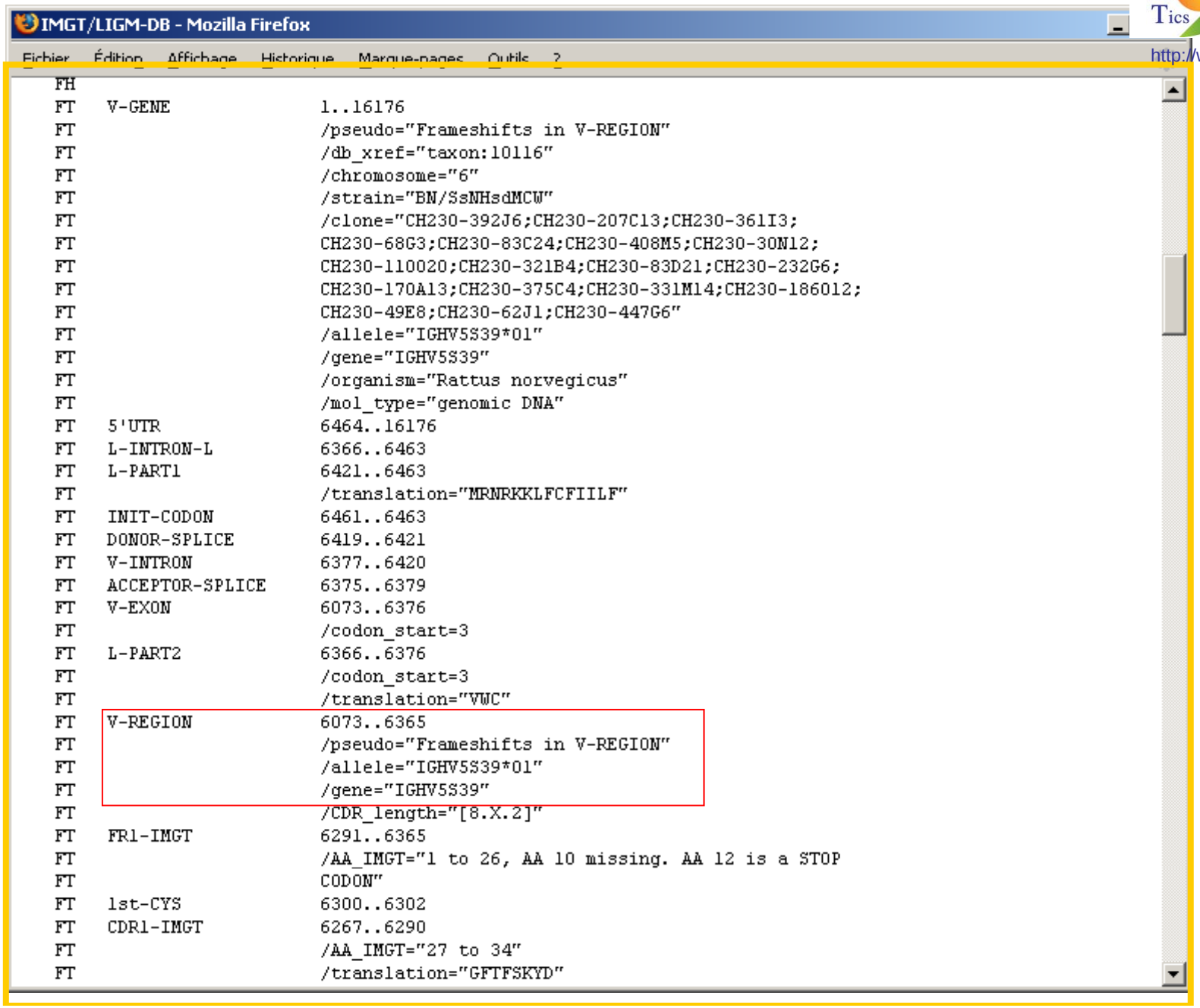


http://www.imgt.org

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

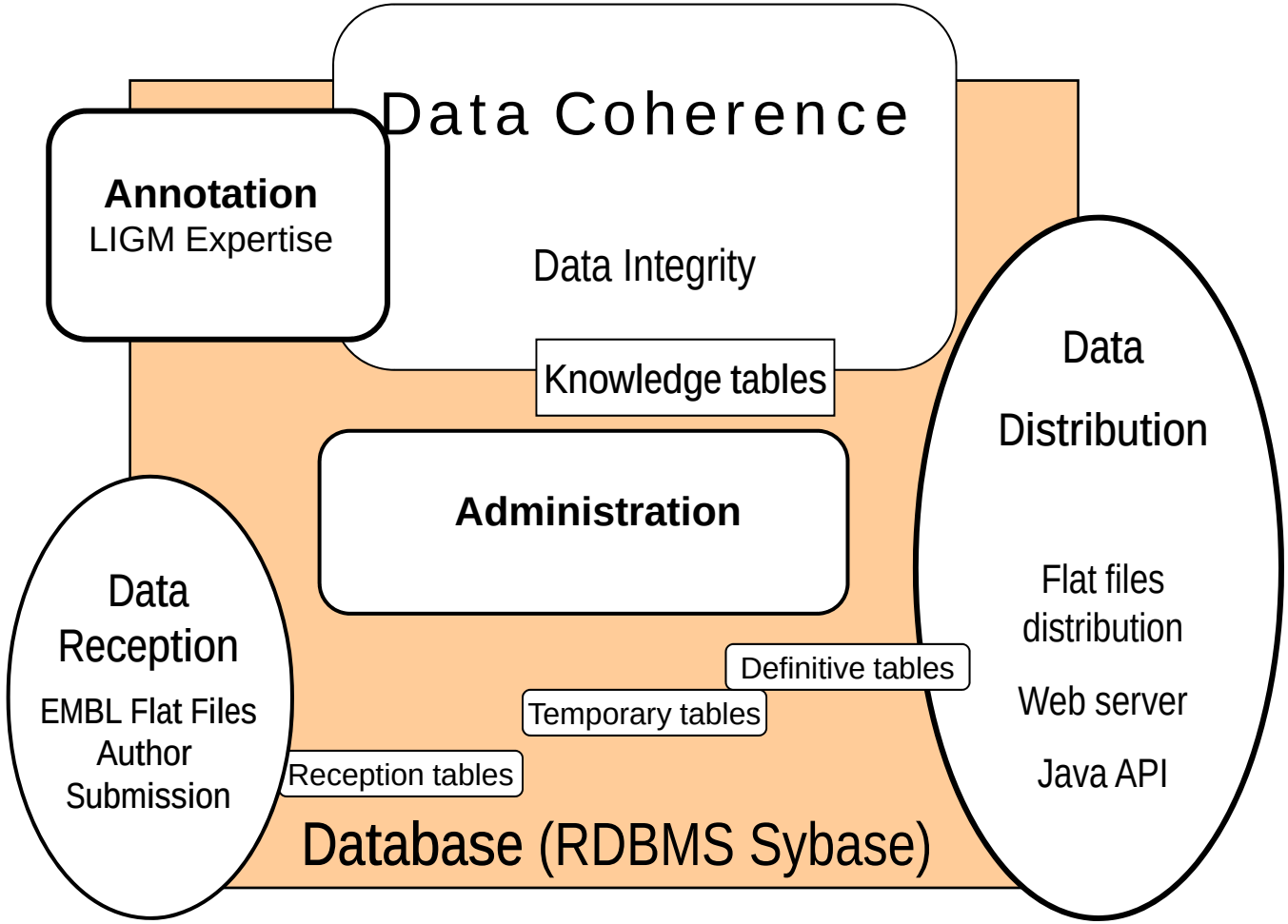
http://www.imgt.org

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

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

1- Coordination des flux de données

http://www.imgt.org



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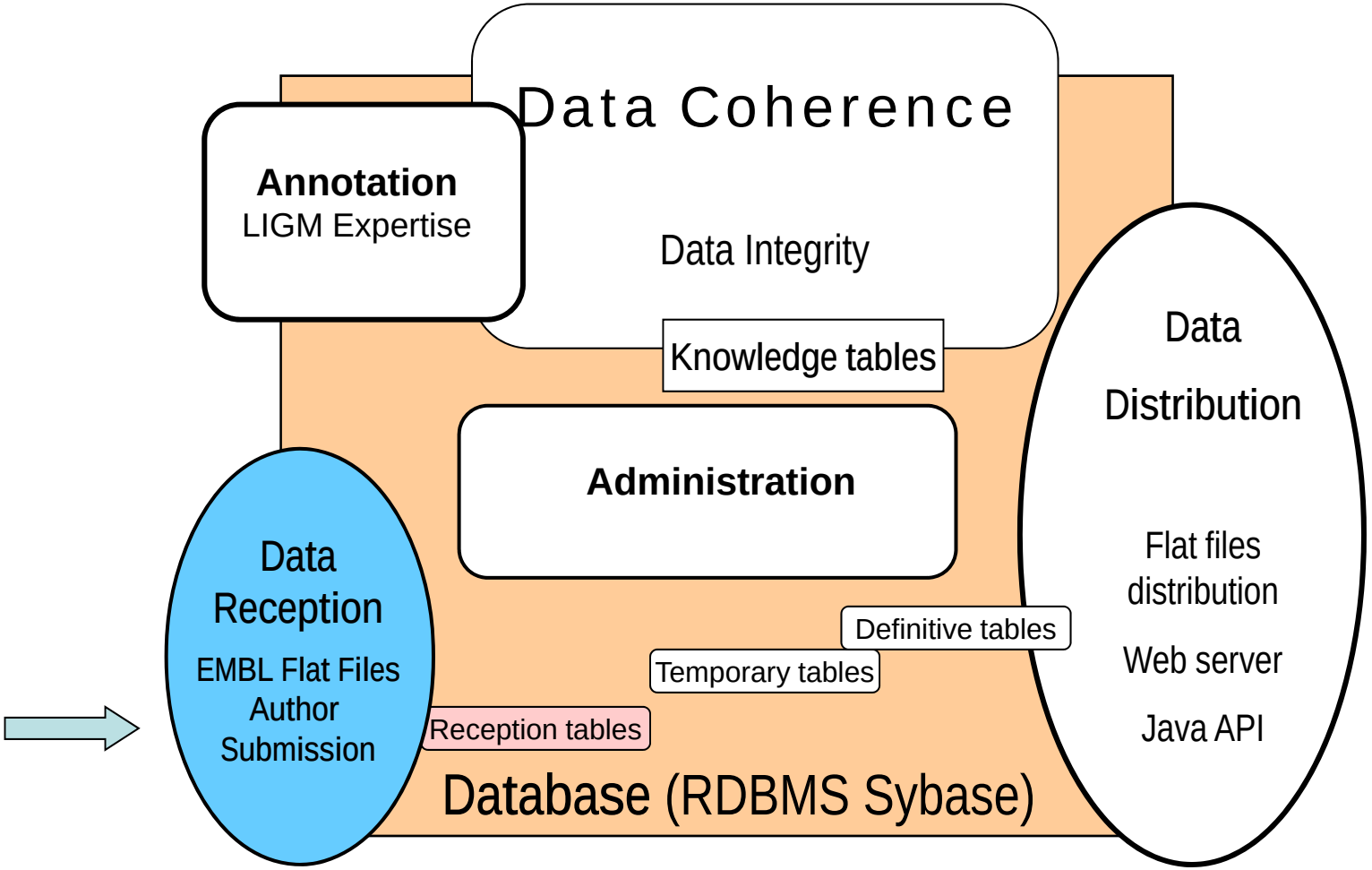

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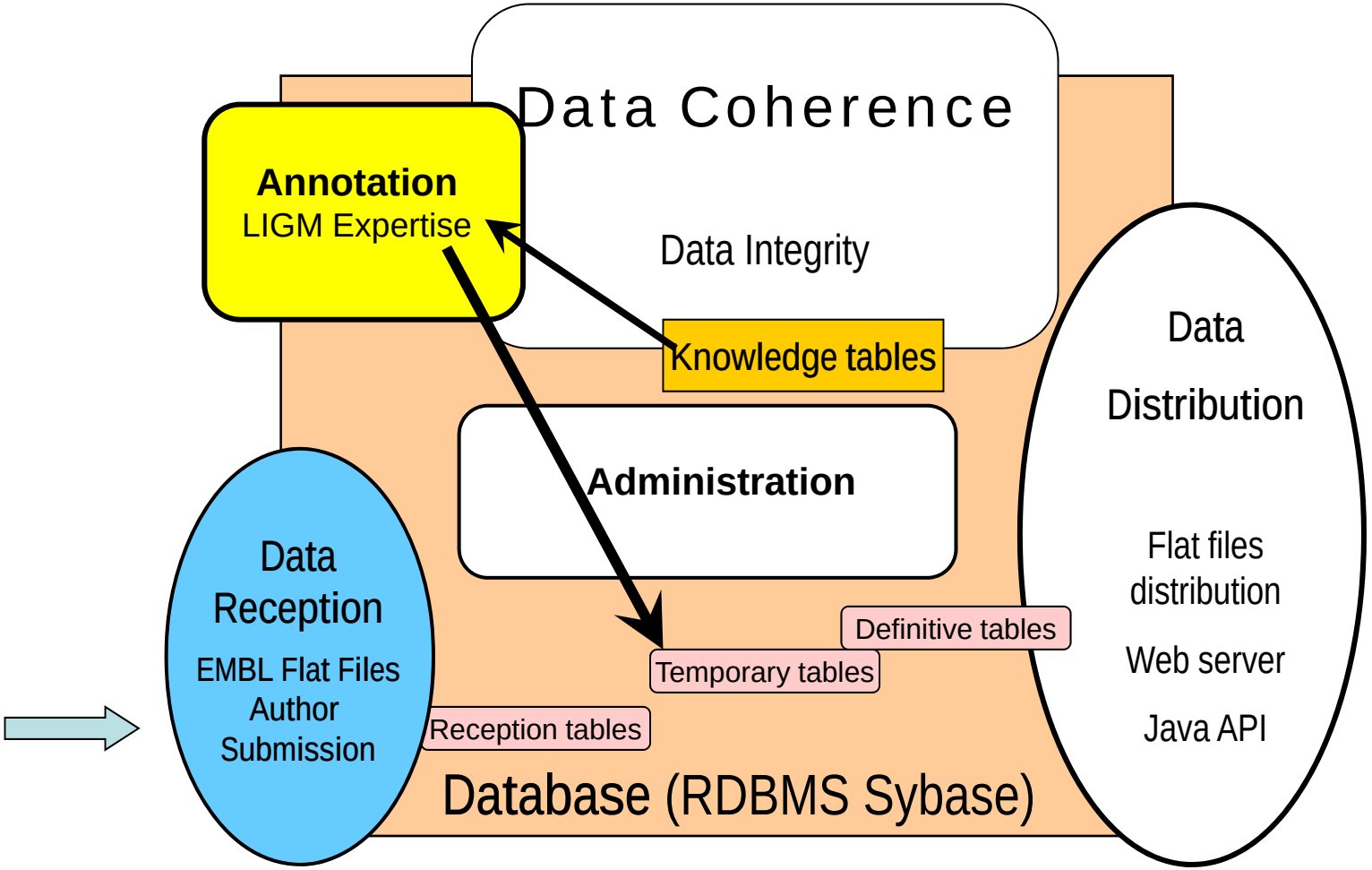

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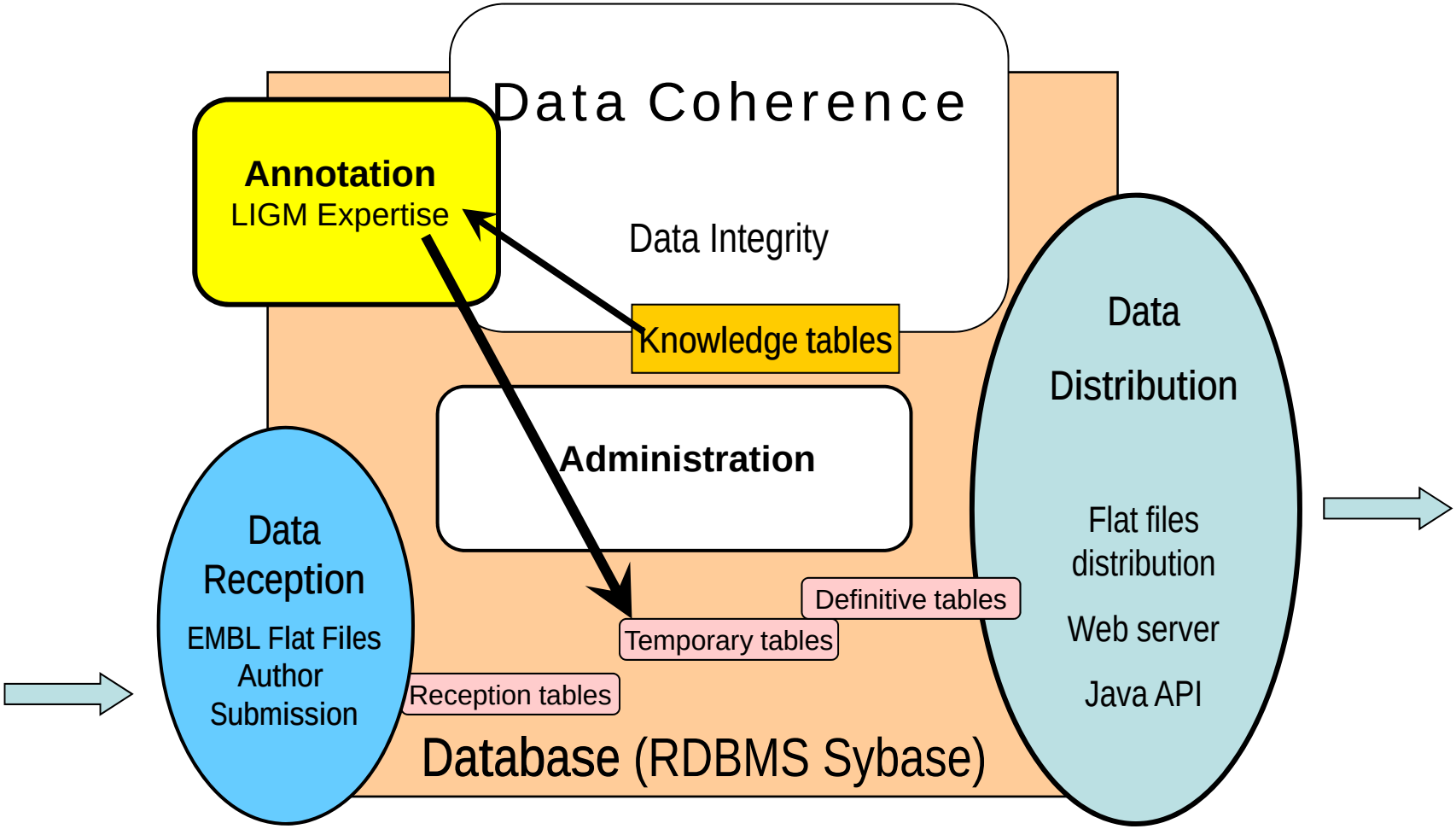

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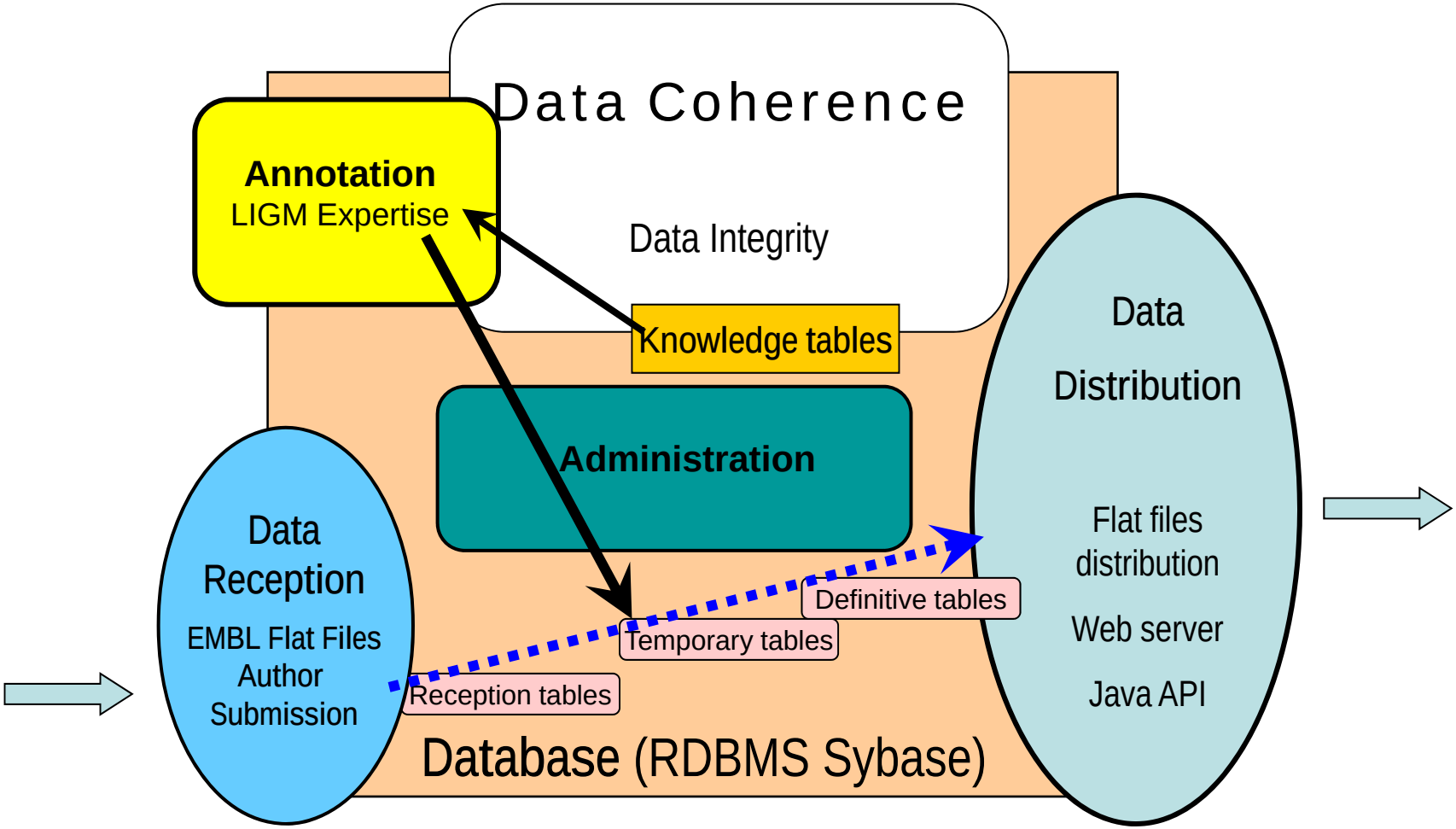

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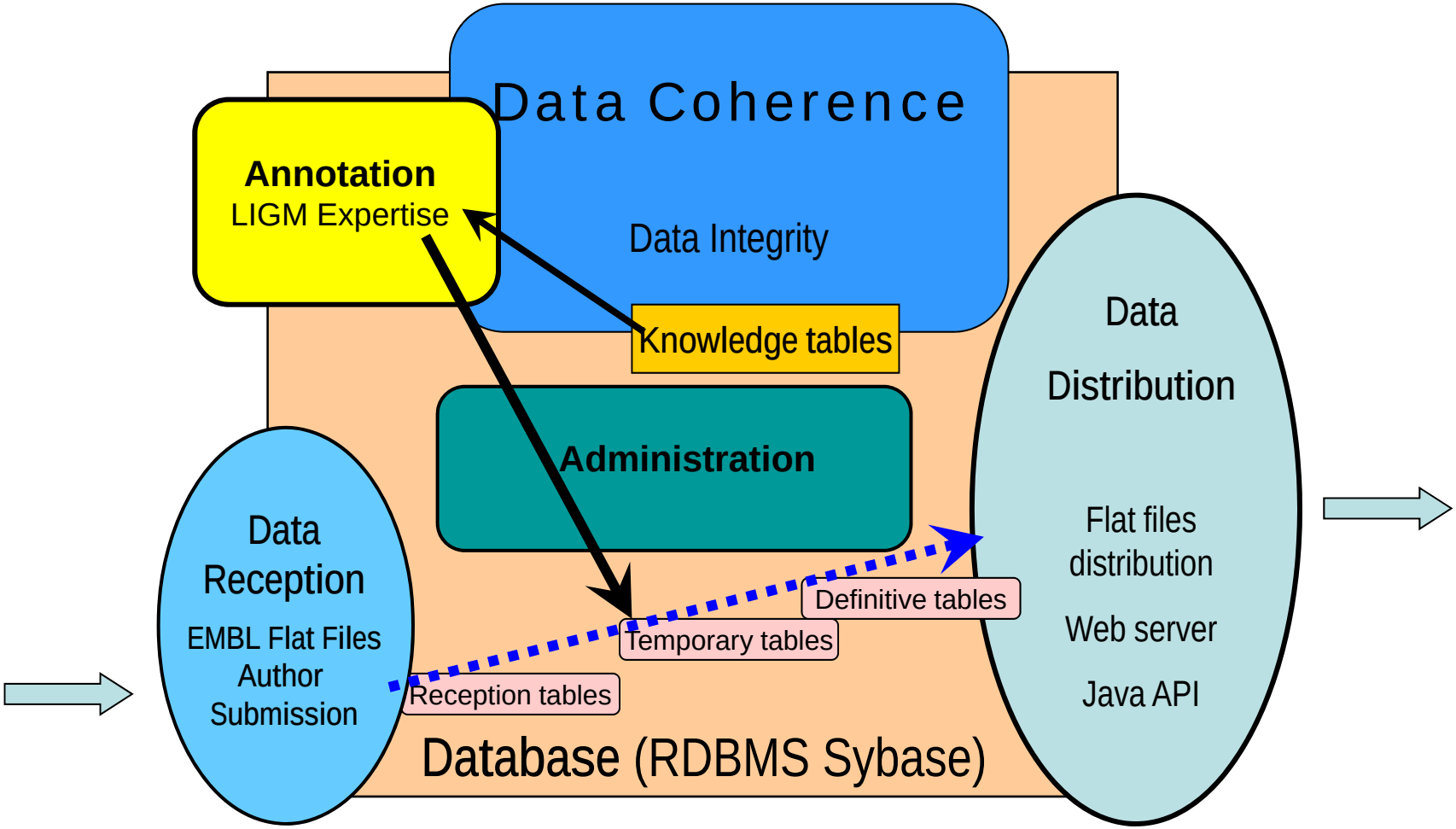
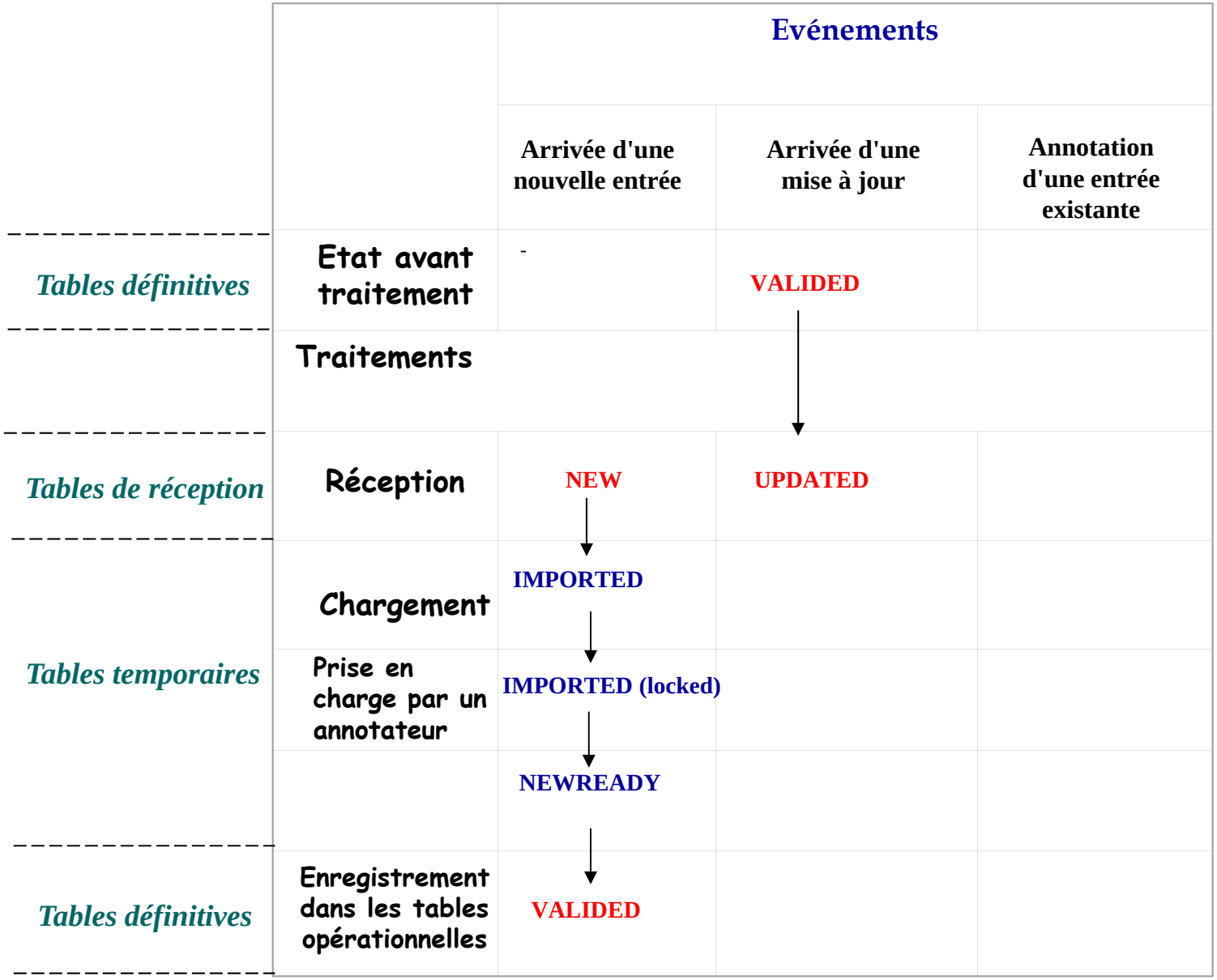


2 - Gestion accès aux données



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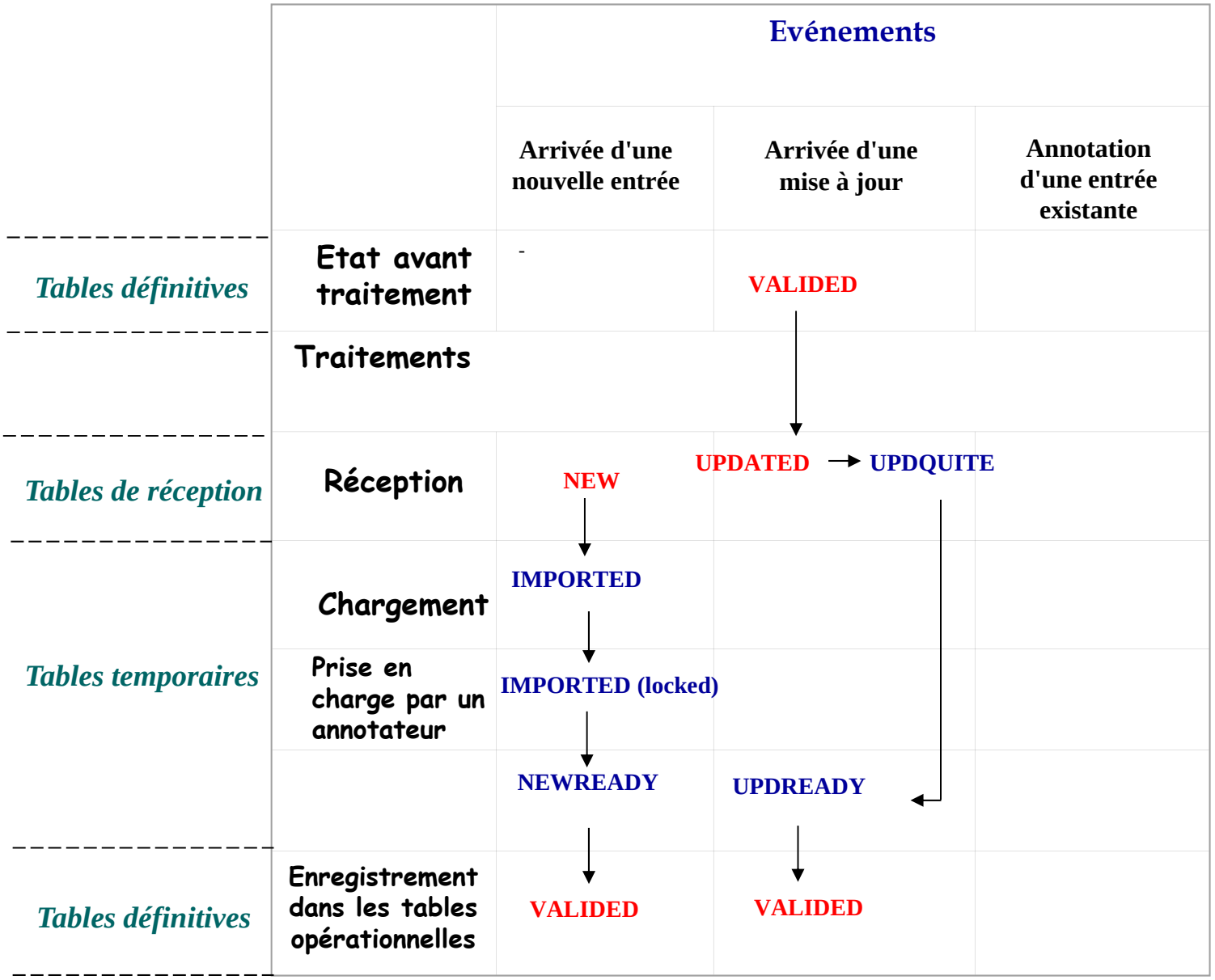

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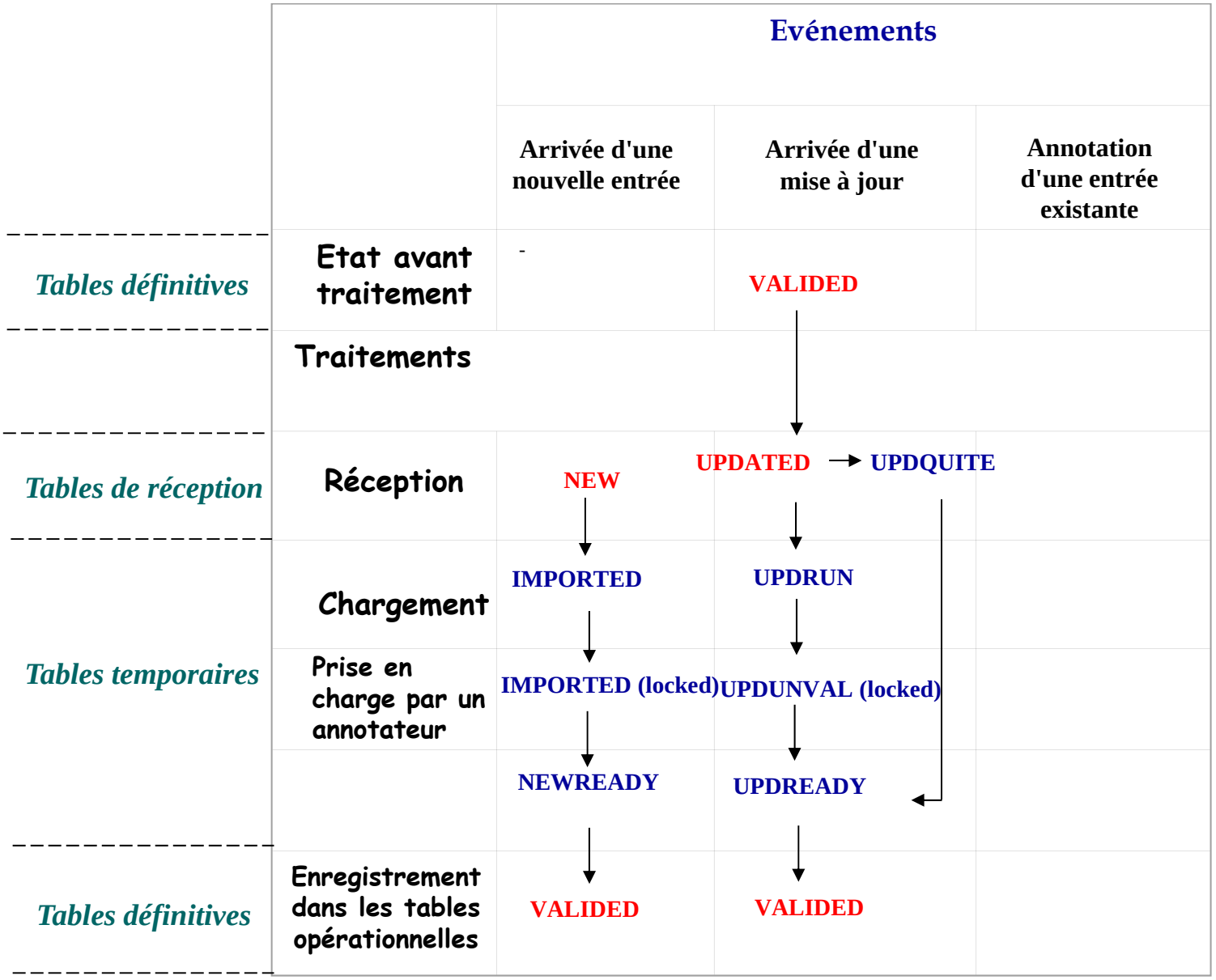

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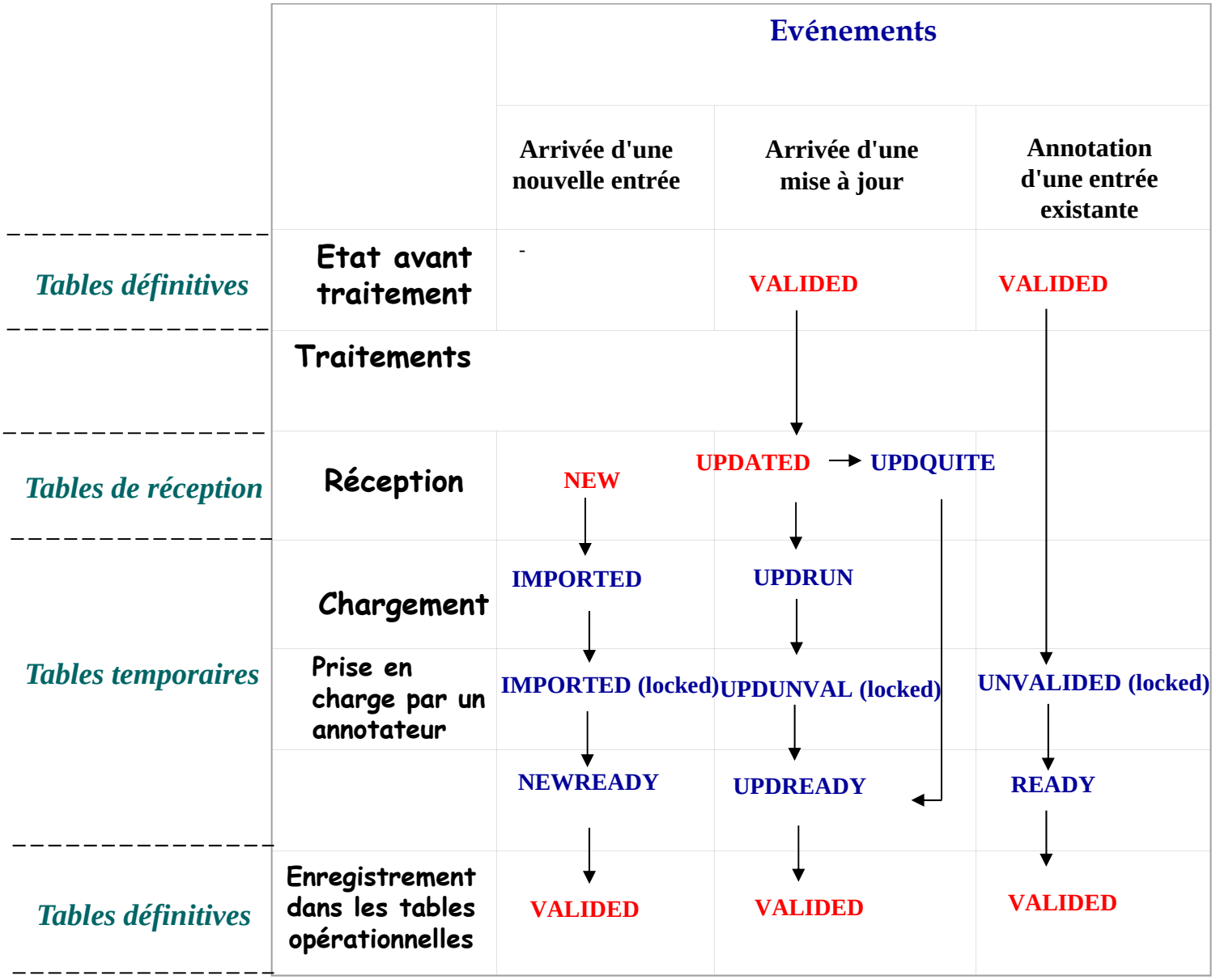

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Information et connaissance

- **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'expertise de données réalisée par des spécialistes dans un domaine scientifique particulier.

=> Nécessité d'utiliser le même vocabulaire standardisé, contrôlé (terminologie)

=> Nécessité de définir les dépendances entre les termes (ontologie)

Un exemple de question

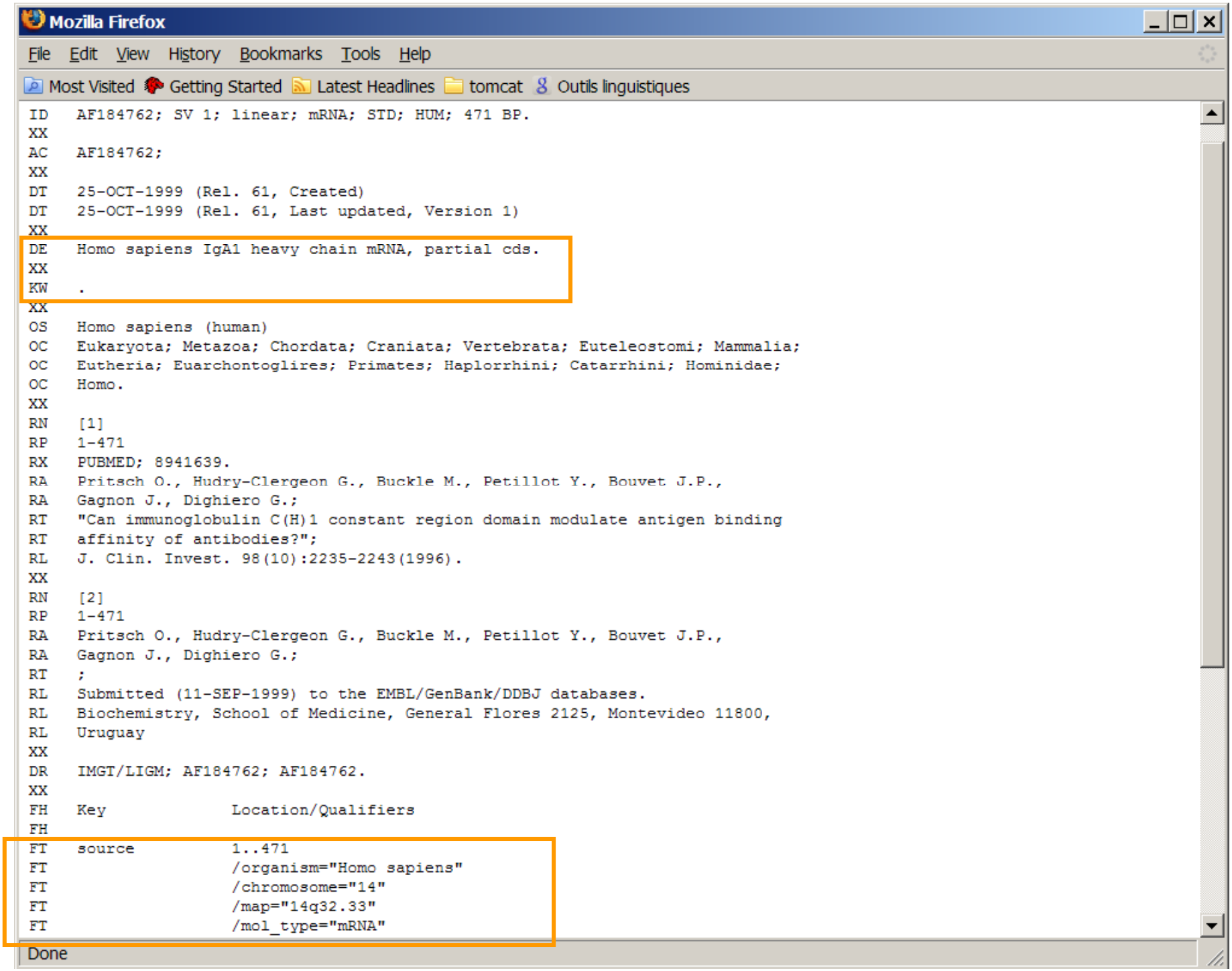
Qu'est-ce qu'un gène?

=> plusieurs définitions

Dans une base de données:

- établissement d'un dictionnaire des données
- mise en place de contraintes à travers un vocabulaire contrôlé

Recherches bibliographiques à travers des thesaurus de mots clés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ID AF184762; SV 1; linear; mRNA; STD; HUM; 471 BP.
XX
AC AF184762;
XX
DT 25-OCT-1999 (Rel. 61, Created)
DT 25-OCT-1999 (Rel. 61, Last updated, Version 1)
XX
DE Homo sapiens IgA1 heavy chain mRNA, partial cds.
XX
KW .
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae;
OC Homo.
XX
RN [1]
RP 1-471
RX PUBMED; 8941639.
RA Pritsch O., Hudry-Clergeon G., Buckle M., Petillot Y., Bouvet J.P.,
RA Gagnon J., Dighiero G.;
RT "Can immunoglobulin C(H)1 constant region domain modulate antigen binding
RT affinity of antibodies?";
RL J. Clin. Invest. 98(10):2235-2243(1996).
XX
RN [2]
RP 1-471
RA Pritsch O., Hudry-Clergeon G., Buckle M., Petillot Y., Bouvet J.P.,
RA Gagnon J., Dighiero G.;
RT ;
RL Submitted (11-SEP-1999) to the EMBL/GenBank/DDBJ databases.
RL Biochemistry, School of Medicine, General Flores 2125, Montevideo 11800,
RL Uruguay
XX
DR IMGT/LIGM; AF184762; AF184762.
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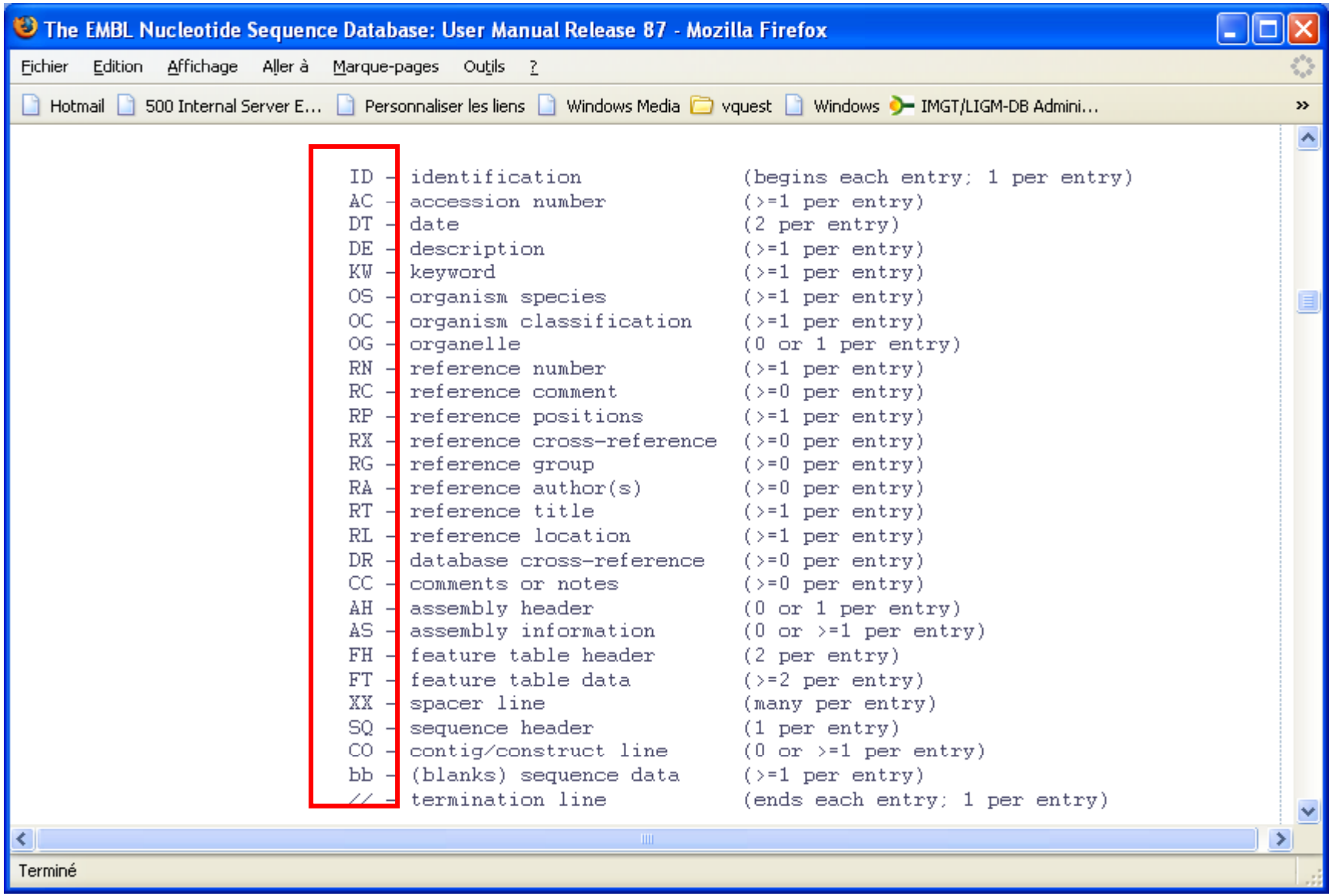
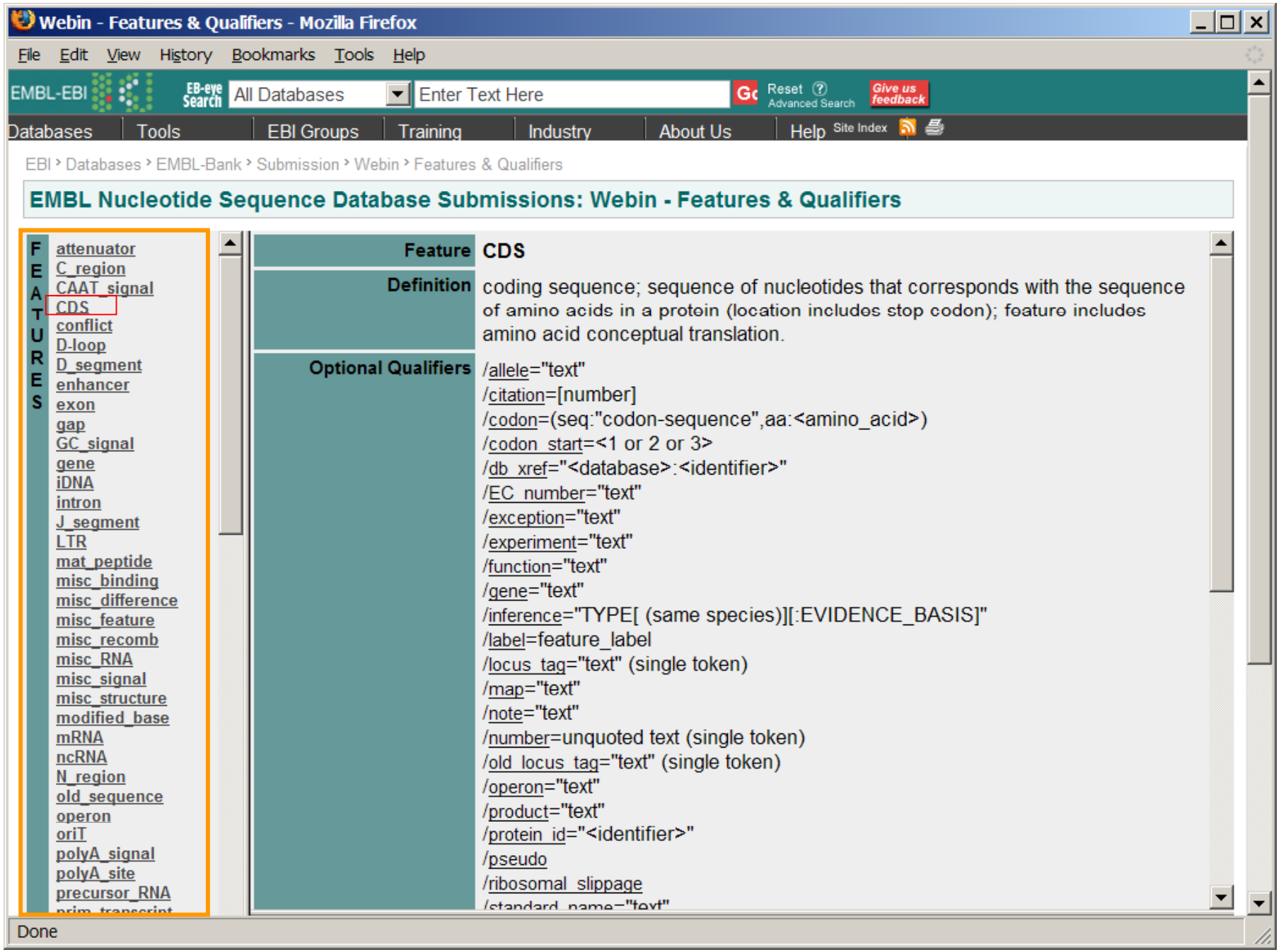
Done

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

Des codes pour indiquer les types d'information



EMBL Feature labels (http://www.ebi.ac.uk/embl/WebFeat/index.html)



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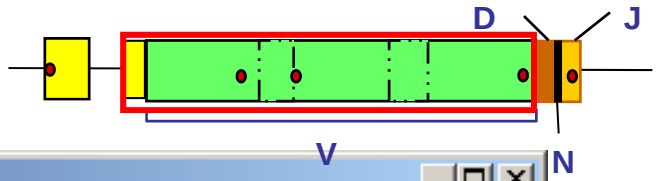

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EBI > Databases > EMBL-Bank > Submission > Webin > Features & Qualifiers

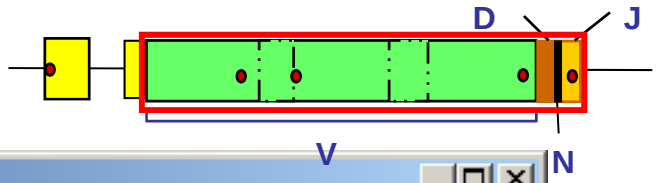
EMBL Nucleotide Sequence Database Submissions: Webin - Features & Qualifiers

Feature	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="<databas /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"

code la majeur partie de la région variable (V_region) et les quelques acides aminés du peptide signal

?

EMBL Feature labels



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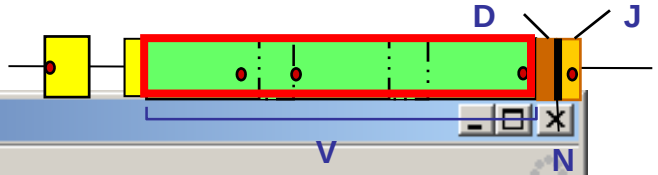
EMBL Nucleotide Sequence Database Submissions: Webin - Features & Qualifiers

Feature	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"

peut être composé de V_segments, D_segments, N_regions, et J_segments

?

List and definition of IMGT standardized labels



IMGT/LIGM-DB - Mozilla Firefox

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	corresponding region in cDNA
V-EXON	germline genomic DNA including L-PART2 and V-REGION
V-GENE	germline genomic DNA including L-PART1, V-INTRON and V-EXON, with the 5'UTR and 3'UTR
V-GENE-MODULE	germline genomic DNA including L-PART1, V-INTRON, V-EXON and V-RS
V-HEPTAMER	7 nucleotide recombination site, like CACAGTG, part of V-RS
V-INTRON	non coding sequence between L-PART1 and V-EXON, in genomic DNA, or corresponding sequence in unspliced cDNA
V-J-C-CLUSTER	genomic DNA in germline configuration including at least one V-GENE, one J-GENE and one C-GENE
V-J-C-REGION	coding region including V-, J- and C- REGION, in cDNA
V-J-CLUSTER	genomic DNA in germline configuration including at least one V-GENE and one J-GENE
V-J-EXON	rearranged genomic DNA including L-PART2, V- and J- REGION
V-J-GENE	rearranged genomic DNA including L-PART1, V-INTRON and V-J-EXON, with the 5'UTR and 3'UTR
V-J-REGION	coding region including V- and J-REGION, in rearranged genomic DNA, or corresponding region in cDNA
V-LIKE-DOMAIN	coding region of non-IG and non-TR similar to an IG or TR V-DOMAIN
V-NONAMER	9 nucleotide recombination site, like ACAAAAACC, part of V-RS
V-REGION	coding region of V-GENE without the leader peptide (plus 1 or 2 nucleotide(s) before the V-HEPTAMER, if present), or corresponding region in cDNA
V-RS	recombination signal including V-HEPTAMER, V-SPACER and V-NONAMER in 3' of V-REGION of a V-GENE or V-SEQUENCE
V-SPACER	12 or 23 nucleotide spacer between the V-HEPTAMER and the V-NONAMER of a V-RS

OK

OK

Quelle est la signification des ces termes dans le contexte de la biologie?

Comment ces termes sont-ils organisés?

Comment sont-il reliés?

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: ils définissent un groupe d'individus possédant des propriétés similaires.

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.

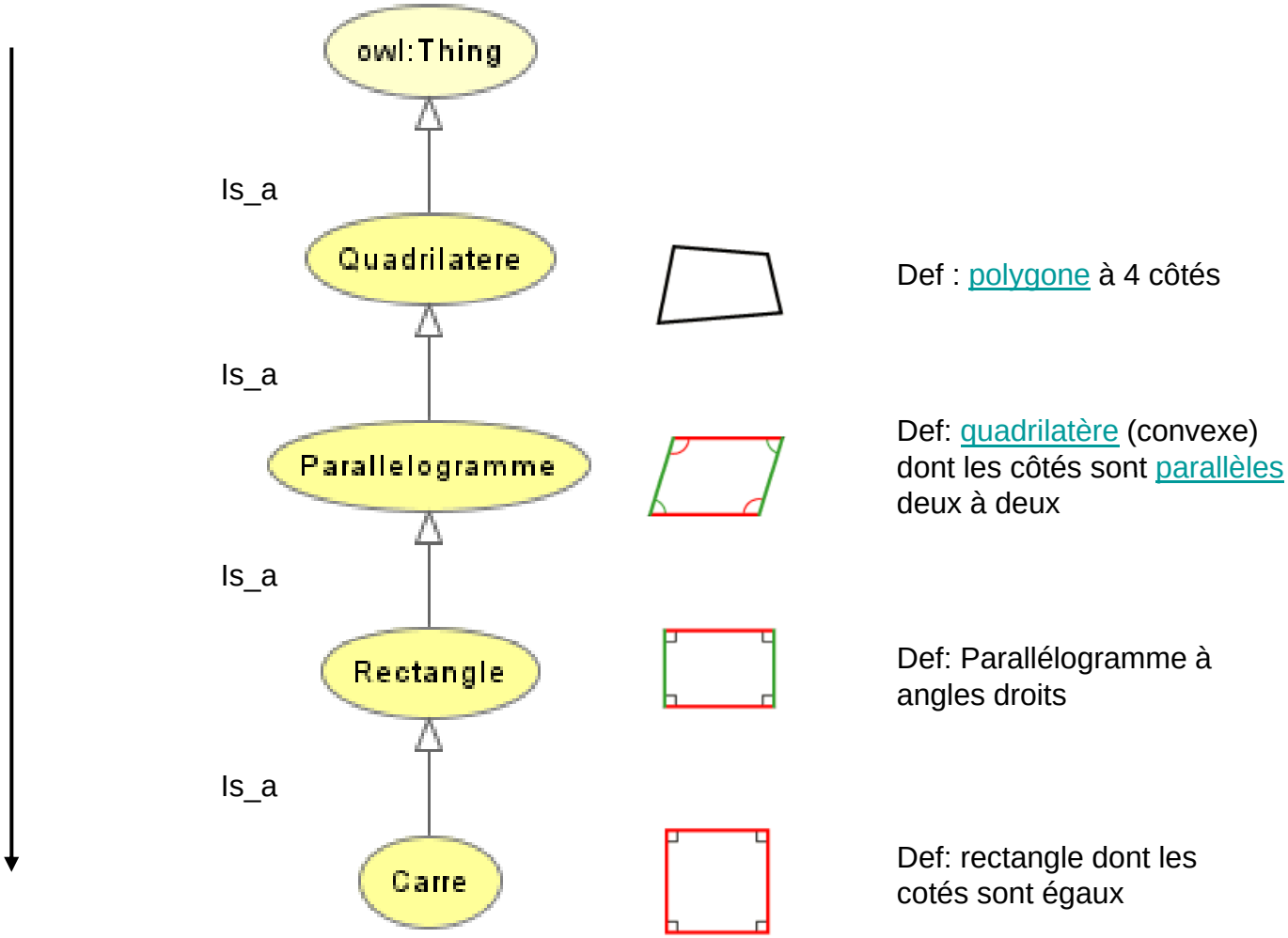
Exemple simple: les formes géométriques
représentation hiérarchique de concepts avec la relation « is_a »
(OWL, Web Ontology Language)

Notion de Classe :

Définit un groupe d'individus possédant des propriétés similaires.

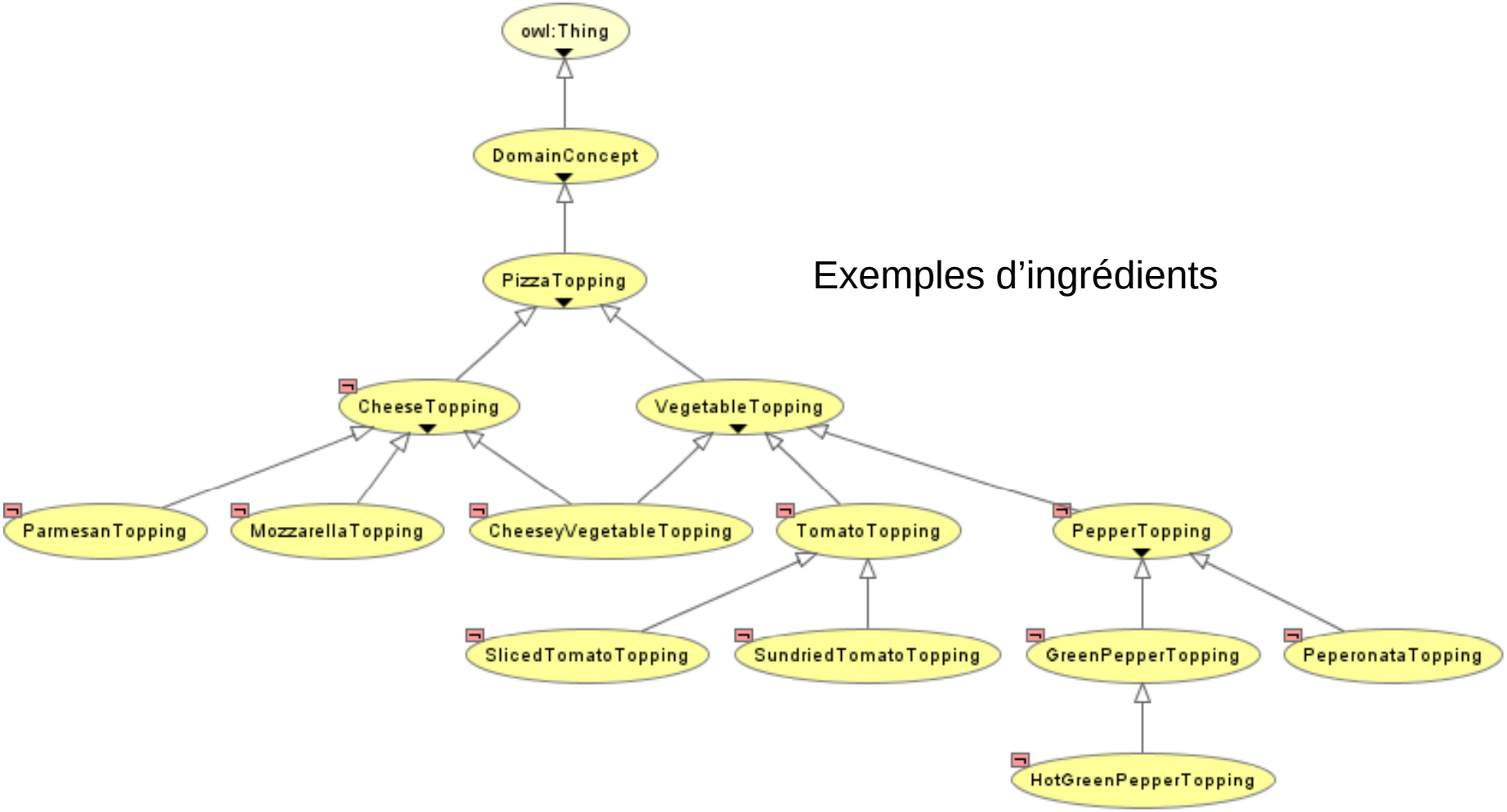
Thing est la classe mère.

spécialisation



Exemple de hiérarchie : ontologie des pizzas

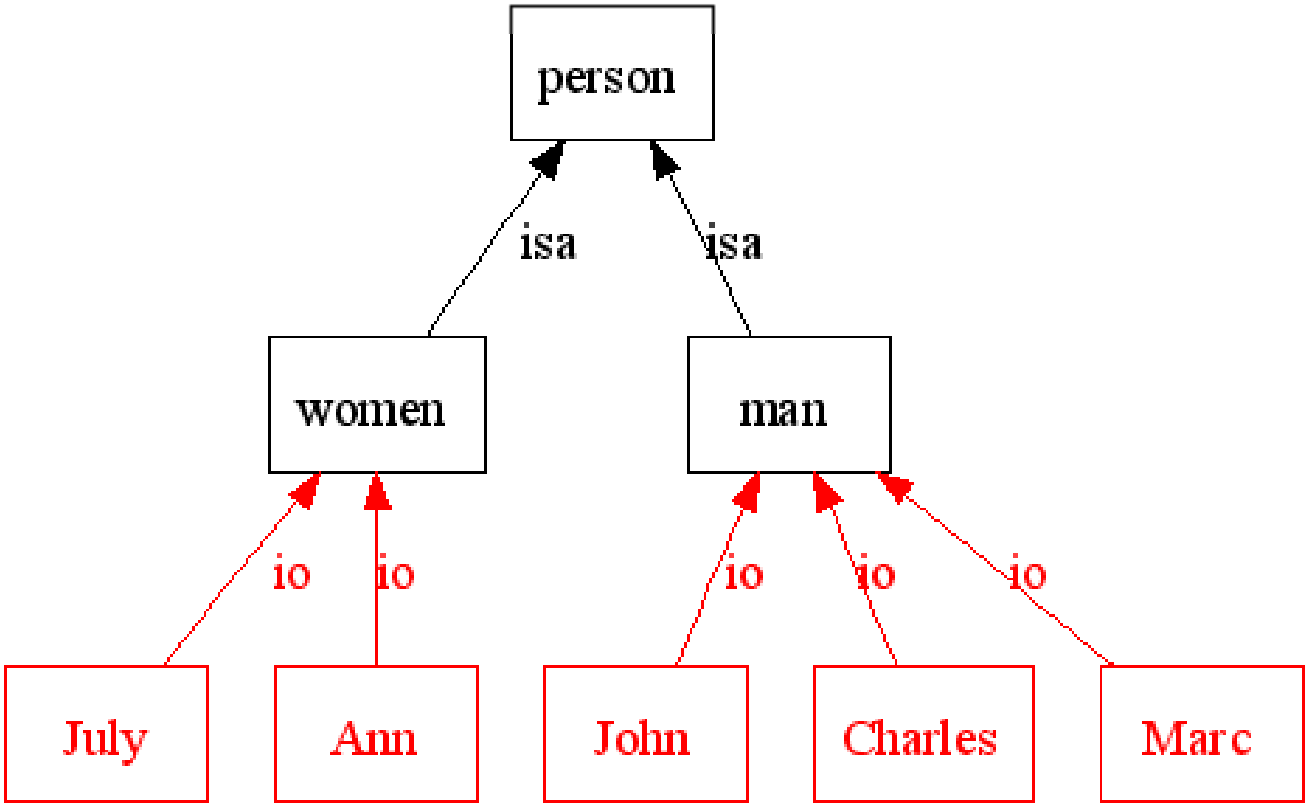
(exemple fournit avec l'éditeur d'ontologies Protégé http://protege.stanford.edu/)



Exemples d'ingrédients

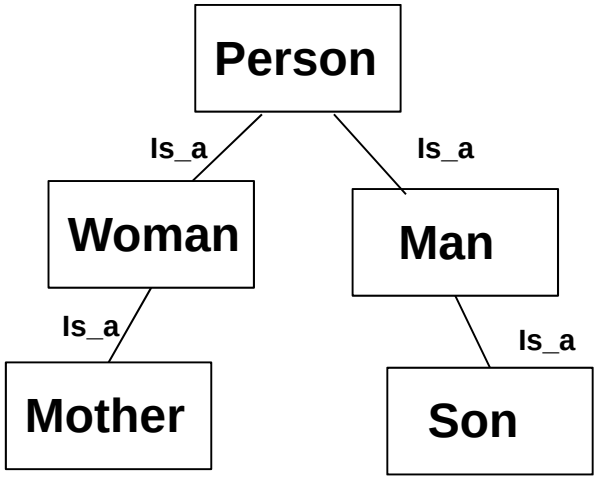
Instances

Ce sont les « individus » qui peuplent les classes



Propriétés/Relations
(OWL, Web Ontology Language)

- **Propriété d'objet** : relie une instance à une autre instance

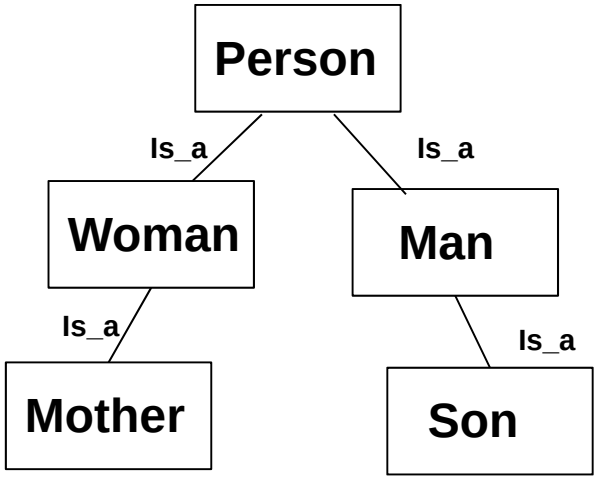


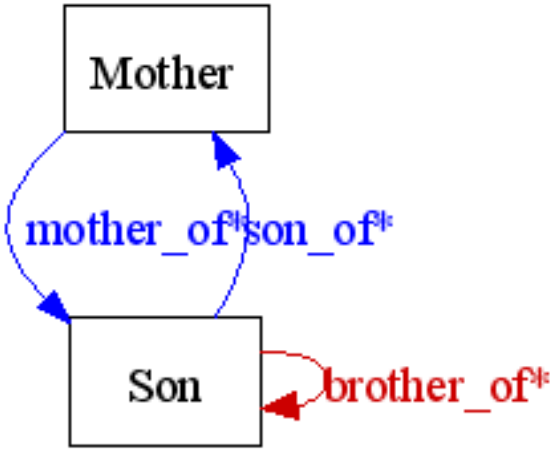
- **Propriété de type de données**: relie une instance à des valeurs:

  - Birth date
  - …

Propriétés/Relations
(OWL, Web Ontology Language)

- **Propriété d'objet** : relie une instance à une autre instance





- **Propriété de type de données**: relie une instance à des valeurs:

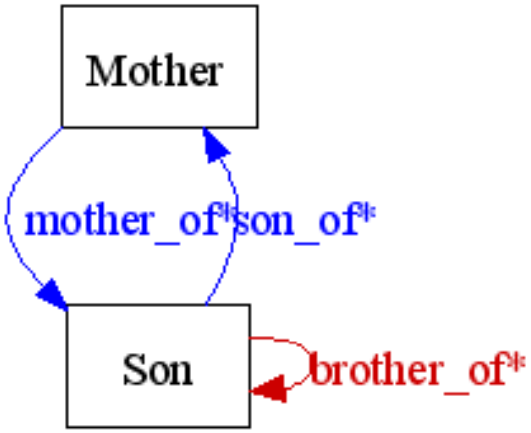
  - Birth date
  - …

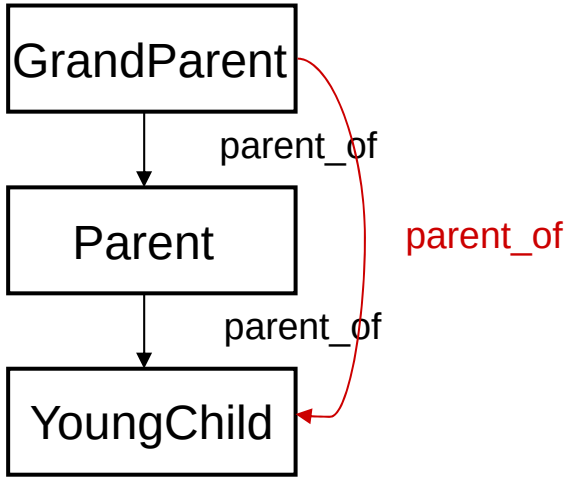
Caractérisation des Propriétés/Relations
(OWL, Web Ontology Language)

domain : classes pour lesquelles est définie la propriété,
range : classes reliées par la propriété au domain.

domain	relation	range
Person	birth date	Integer
Son	brother_of	Son
Mother	mother_of	Son
Son	son_of	Mother

Caractérisation des Propriétés/relations: symétriques, transitives, inverses et fonctionnelles

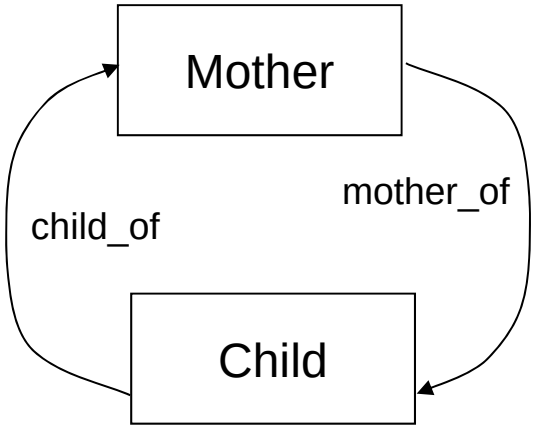




(familles de 3 générations avec de jeunes enfants)

Symétrique: brother_of
Transitive: parent_of
Inverse: son_of / mother_of
Fonctionnelle : son_of

Caractérisation des Propriétés/Relations : cardinalités



Ex de familles nombreuses de moins de 10 enfants

- Une mère a au moins 3 enfants
- Une mère a au plus 10 enfants
- Un enfant a une et une seule mère

minCardinality: toute instance de la classe sera relié par la propriété à au moins x individus Exemple: propriété mother_of de la classe Mother : minCardinality=3

maxCardinality: toute instance de la classe sera relié par la propriété à au plus x individus Exemple: propriété mother_of de la classe Mother : maxCardinality=10

cardinality: toute instance de la classe sera relié par la propriété à exactement x individus Exemple: propriété son_of de la classe Mother : cardinality=1

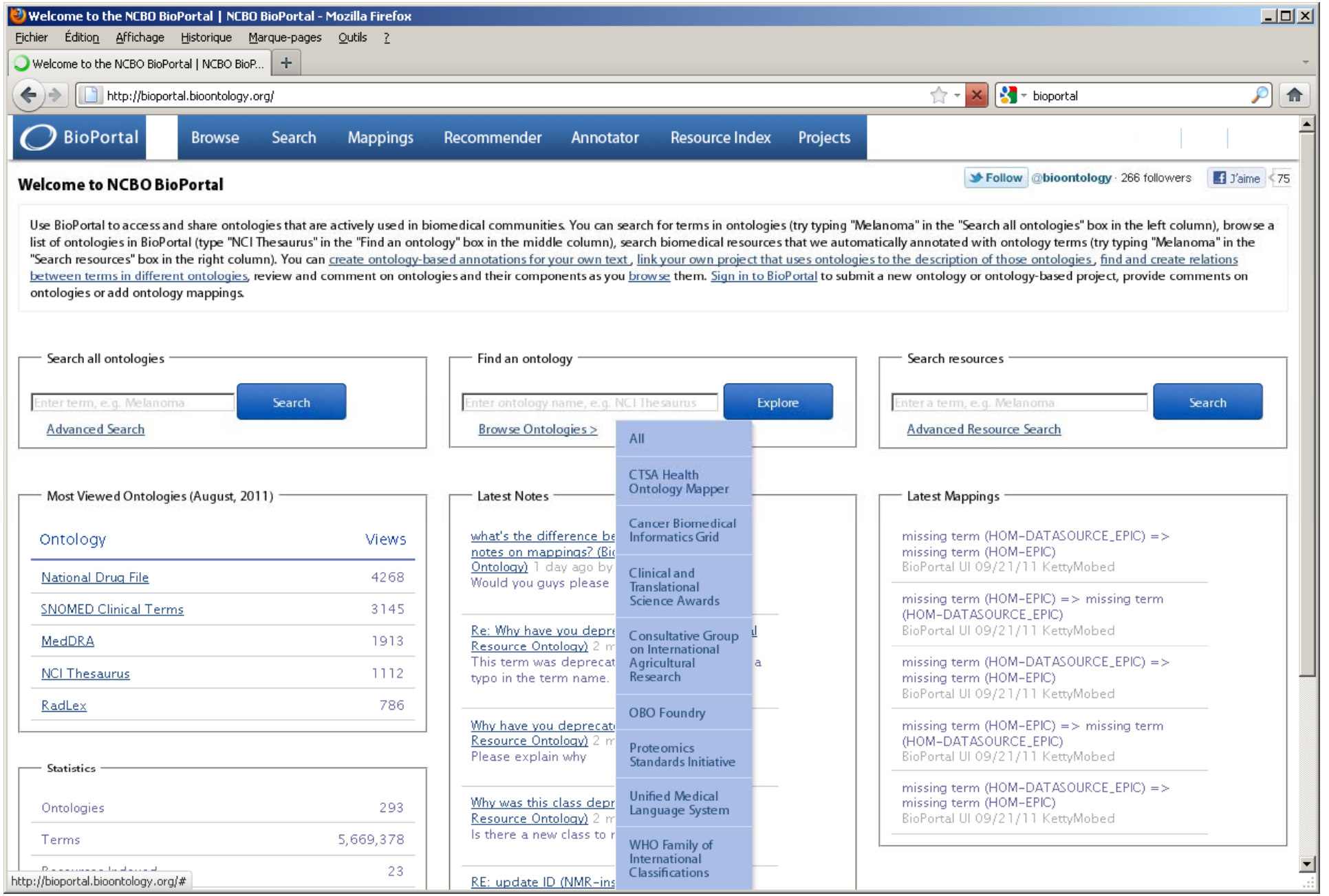
Les ontologies en Biologie

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

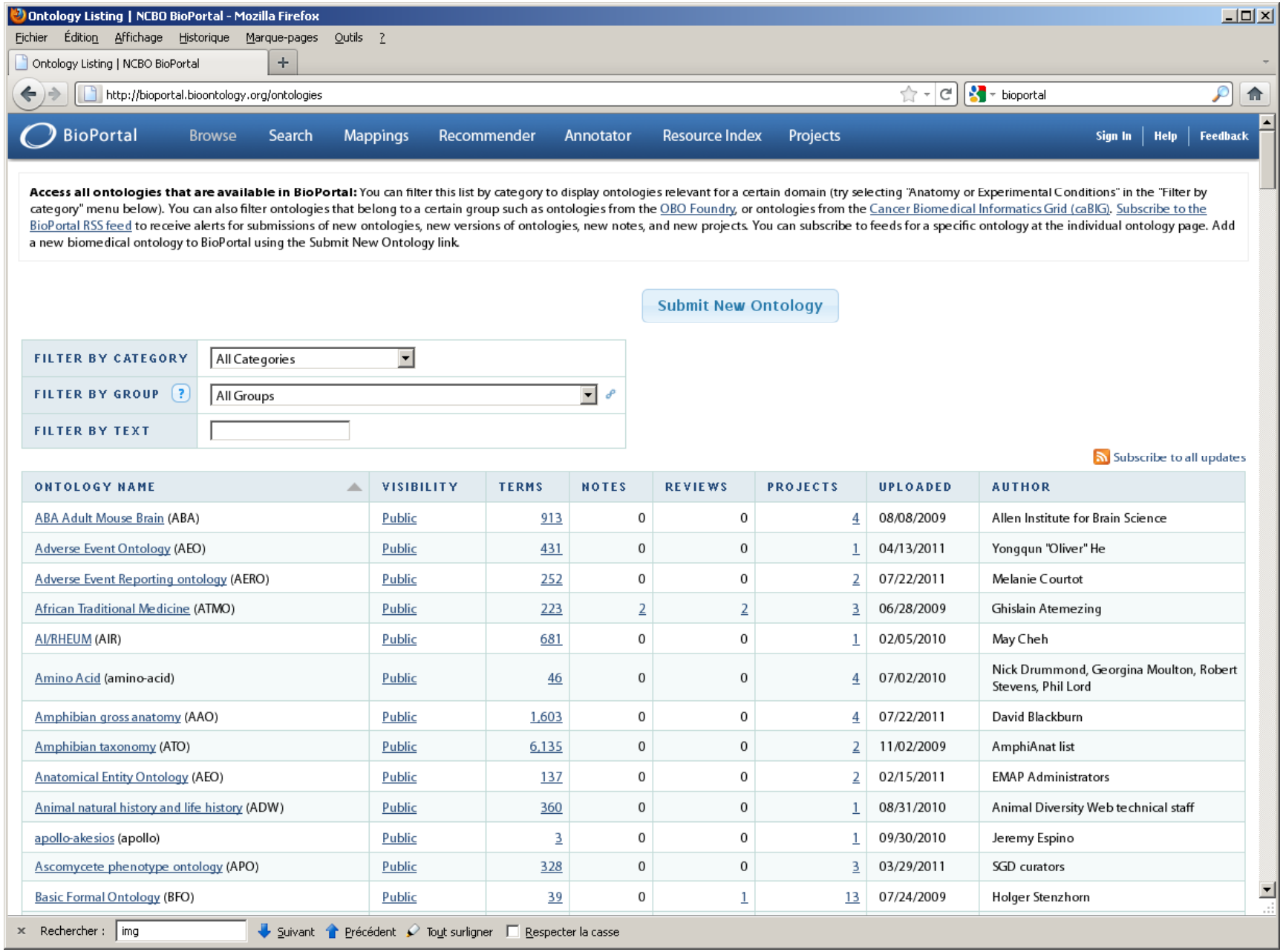
NCBO Bioportal (http://bioportal.bioontology.org/)
OBO (Open Biological Ontologies) (http://www.obofoundry.org/)

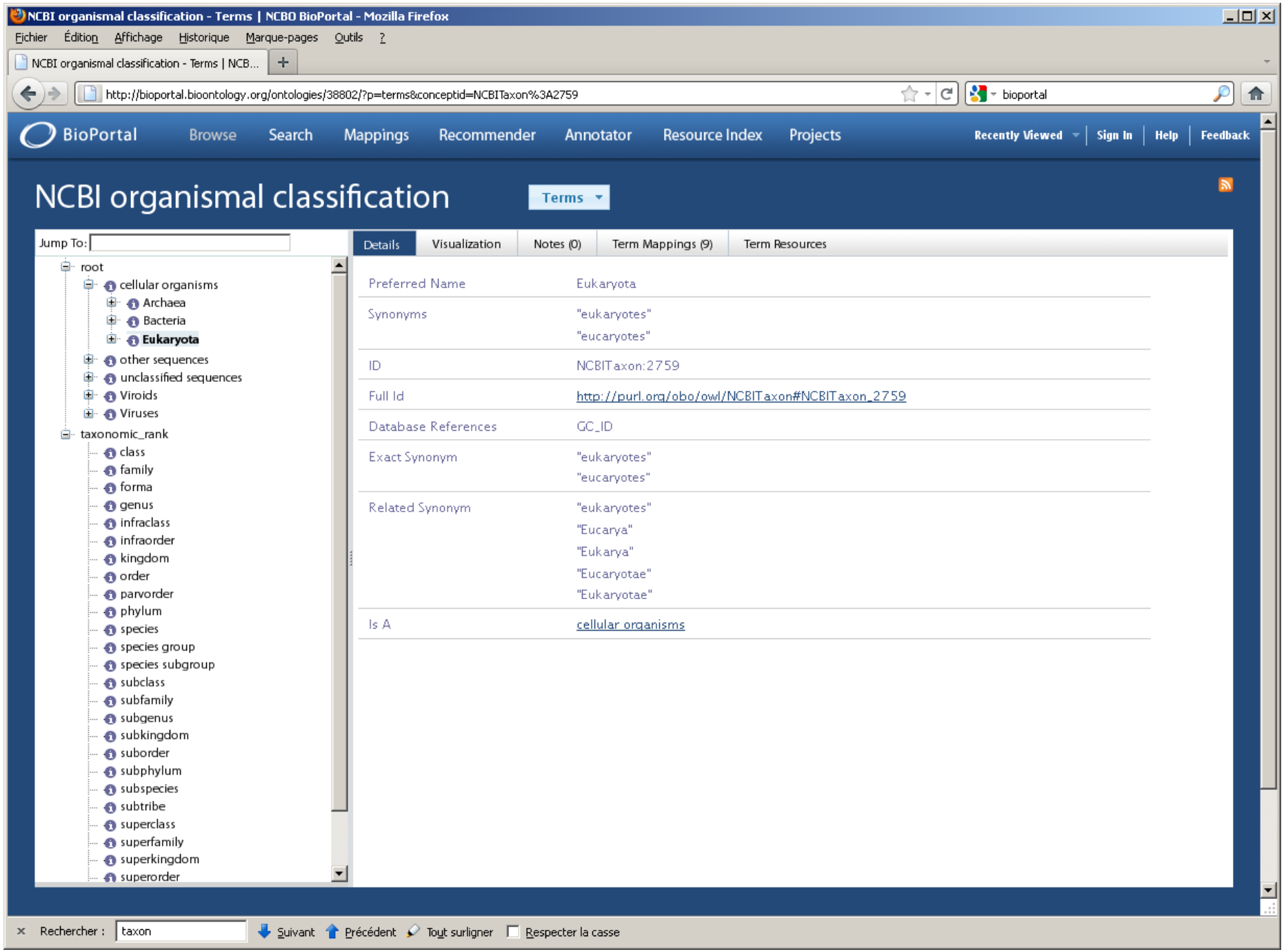
recensent les ontologies en biologie.

NCBO Bioportal (http://bioportal.bioontology.org/)



NCBO Bioportal




NCBI organismal classification - Terms | NCBO BioPortal - Mozilla Firefox
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NCBI organismal classification - Terms | NCB...
http://bioportal.bioontology.org/ontologies/38802/?p=terms&conceptid=NCBITaxon%3A2759
bioportal
BioPortal
Browse
Search
Mappings
Recommender
Annotator
Resource Index
Projects
Recently Viewed
Sign In
Help
Feedback
NCBI organismal classification
Terms
Jump To:
root
cellular organisms
Archaea
Bacteria
Eukaryota
other sequences
unclassified sequences
Viroids
Viruses
taxonomic_rank
class
family
forma
genus
infraclass
infraorder
kingdom
order
parvorder
phylum
species
species group
species subgroup
subclass
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subphylum
subspecies
subtribe
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superkingdom
superorder
Details
Visualization
Notes (0)
Term Mappings (9)
Term Resources
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Synonyms
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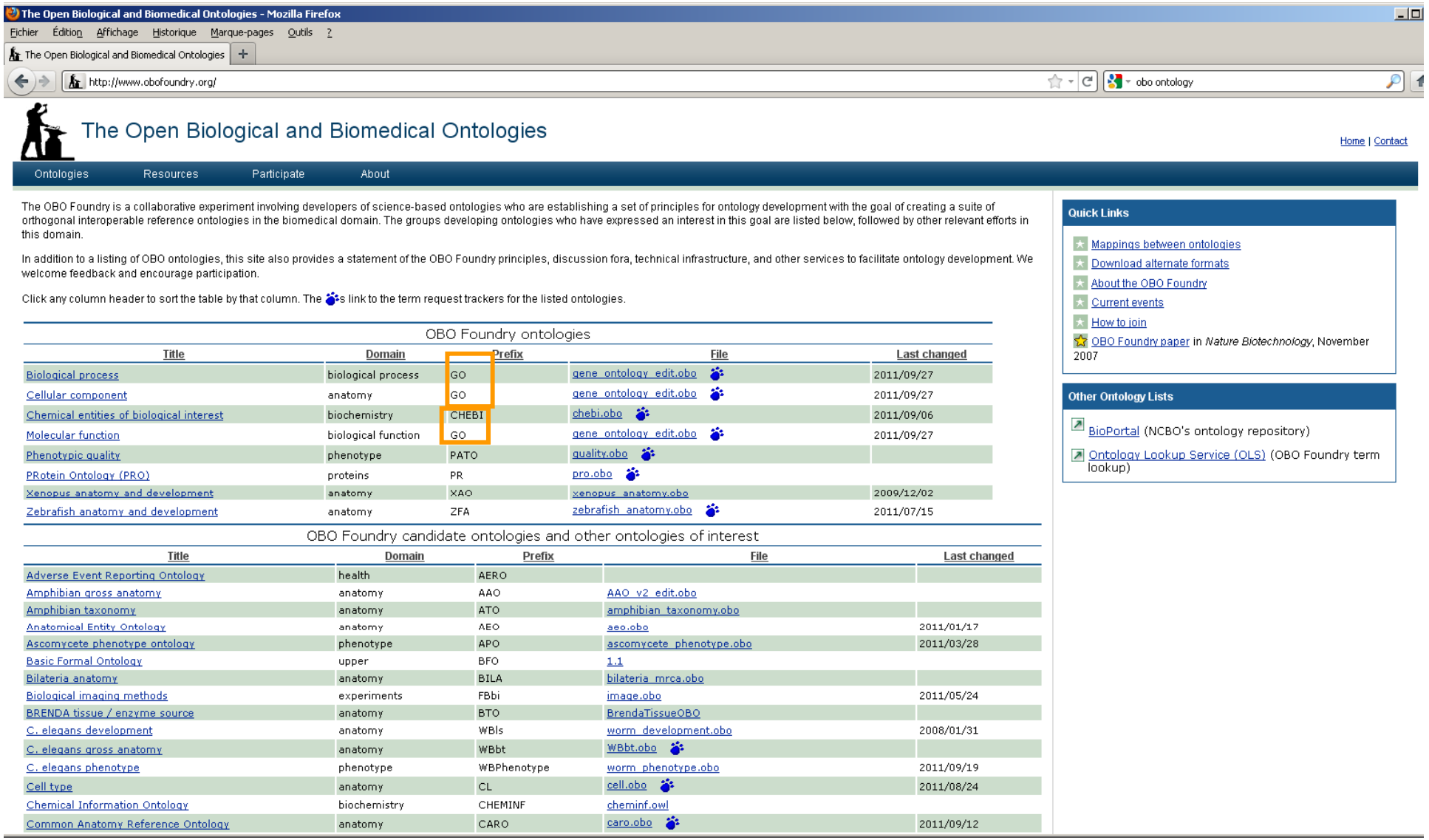
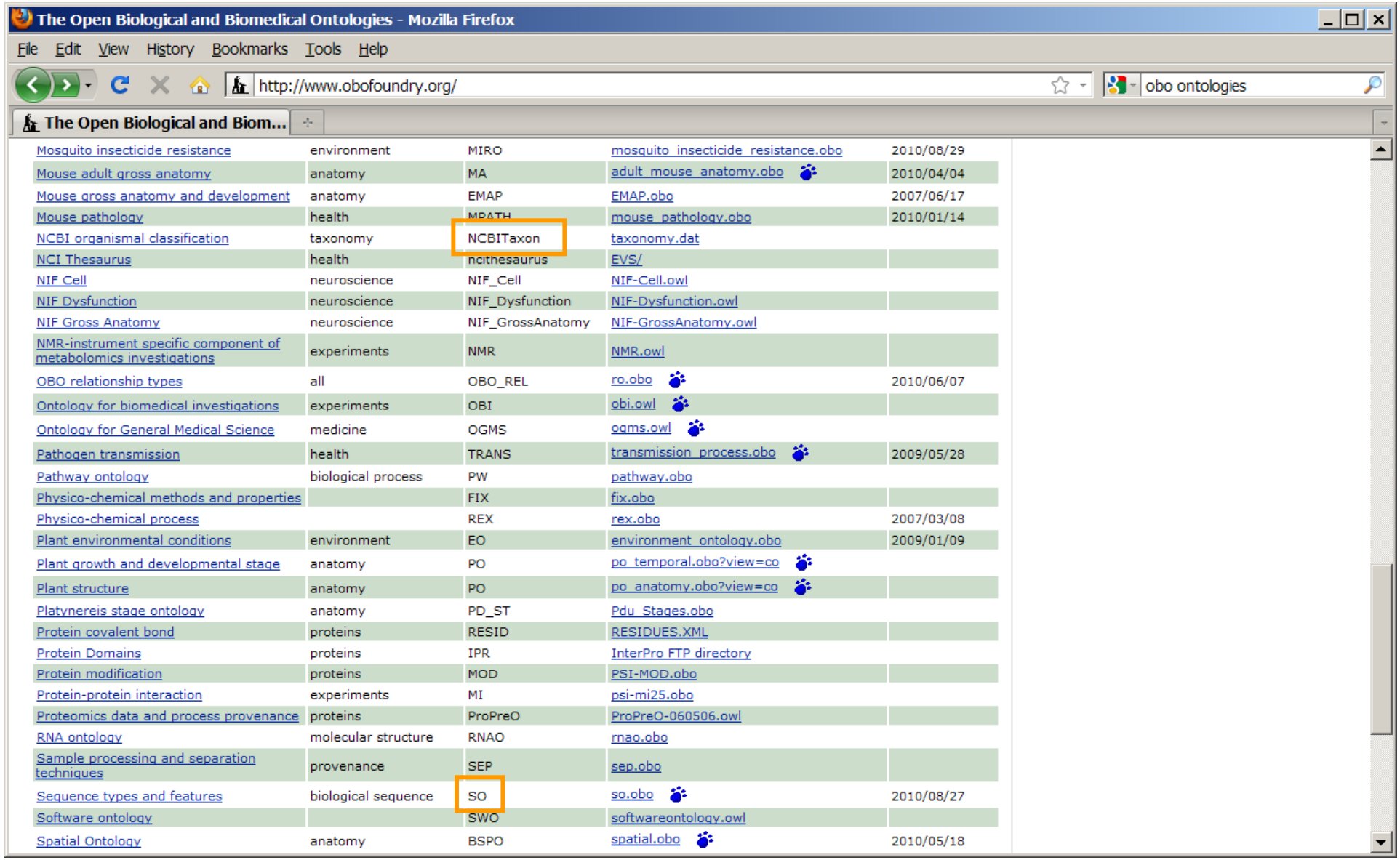
"eucaryotes"
ID
NCBITaxon:2759
Full Id
http://purl.org/obo/owl/NCBITaxon#NCBITaxon_2759
Database References
GC_ID
Exact Synonym
"eukaryotes"
"eucaryotes"
Related Synonym
"eukaryotes"
"Eucarya"
"Eukarya"
"Eucaryotae"
"Eukaryotae"
Is A
cellular organisms
Rechercher :
taxon
Suivant
Précédent
Tout surligner
Respecter la casse

OBO (http://www.obofoundry.org/)



OBO (http://www.obofoundry.org/)



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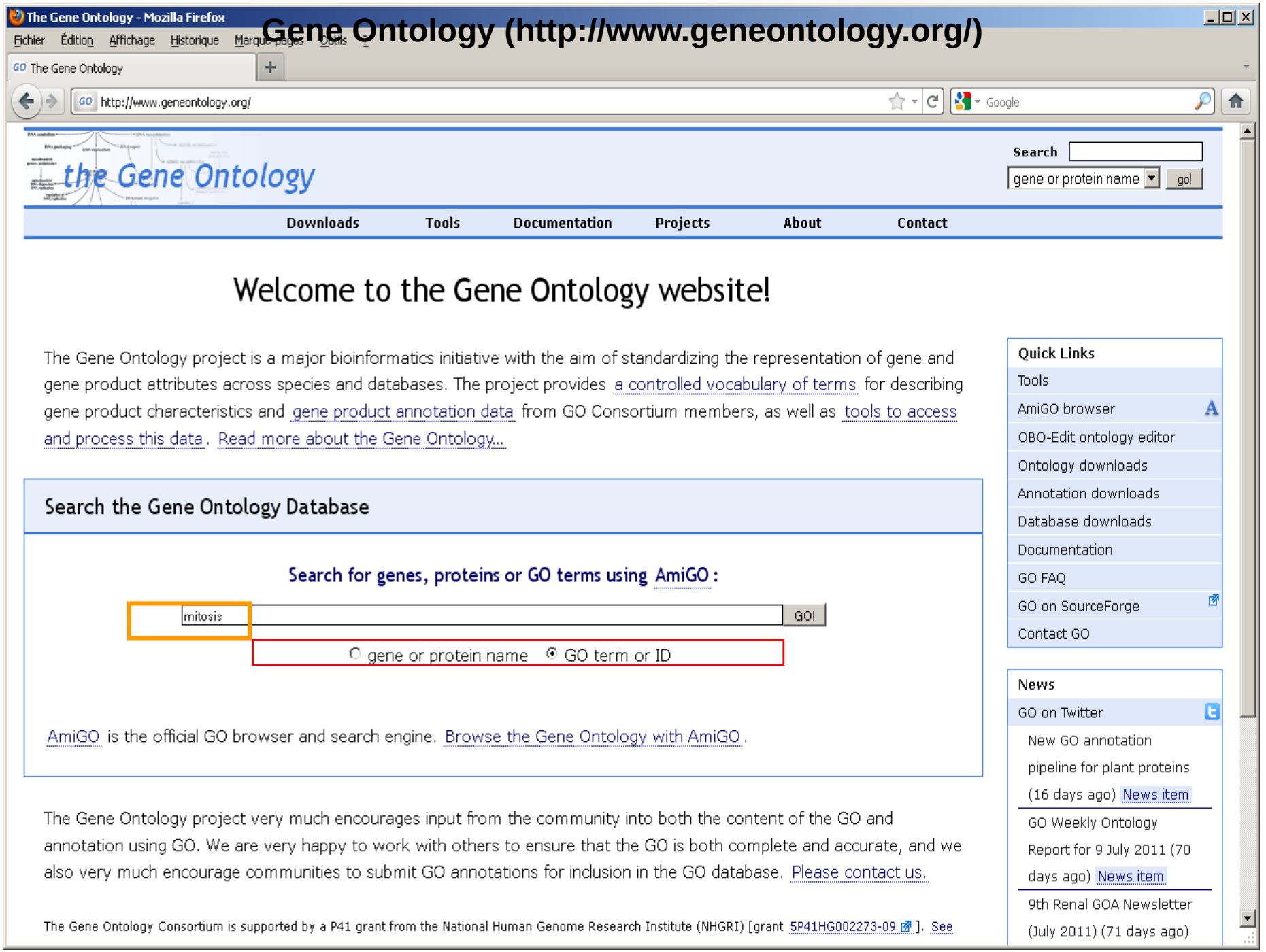
Mouse adult gross anatomy	anatomy	MA	adult_mouse_anatomy.obo	2010/04/04
Mouse gross anatomy and development	anatomy	EMAP	EMAP.obo	2007/06/17
Mouse pathology	health	MPATH	mouse_pathology.obo	2010/01/14
NCBI organismal classification	taxonomy	NCBITaxon	taxonomy.dat	
NCI Thesaurus	health	ncithesaurus	EVS/	
NIF Cell	neuroscience	NIF_Cell	NIF-Cell.owl	
NIF Dysfunction	neuroscience	NIF_Dysfunction	NIF-Dysfunction.owl	
NIF Gross Anatomy	neuroscience	NIF_GrossAnatomy	NIF-GrossAnatomy.owl	
NMR-instrument specific component of metabolomics investigations	experiments	NMR	NMR.owl	
OBO relationship types	all	OBO_REL	ro.obo	2010/06/07
Ontology for biomedical investigations	experiments	OBI	obi.owl	
Ontology for General Medical Science	medicine	OGMS	ogms.owl	
Pathogen transmission	health	TRANS	transmission_process.obo	2009/05/28
Pathway ontology	biological process	PW	pathway.obo	
Physico-chemical methods and properties		FIX	fix.obo	
Physico-chemical process		REX	rex.obo	2007/03/08
Plant environmental conditions	environment	EO	environment_ontology.obo	2009/01/09
Plant growth and developmental stage	anatomy	PO	po_temporal.obo?view=co	
Plant structure	anatomy	PO	po_anatomy.obo?view=co	
Platynereis stage ontology	anatomy	PD_ST	Pdu_Stages.obo	
Protein covalent bond	proteins	RESID	RESIDUES.XML	
Protein Domains	proteins	IPR	InterPro FTP directory	
Protein modification	proteins	MOD	PSI-MOD.obo	
Protein-protein interaction	experiments	MI	psi-mi25.obo	
Proteomics data and process provenance	proteins	ProPreO	ProPreO-060506.owl	
RNA ontology	molecular structure	RNAO	rnao.obo	
Sample processing and separation techniques	provenance	SEP	sep.obo	
Sequence types and features	biological sequence	SO	so.obo	2010/08/27
Software ontology		SWO	softwareontology.owl	
Spatial Ontology	anatomy	BSPO	spatial.obo	2010/05/18

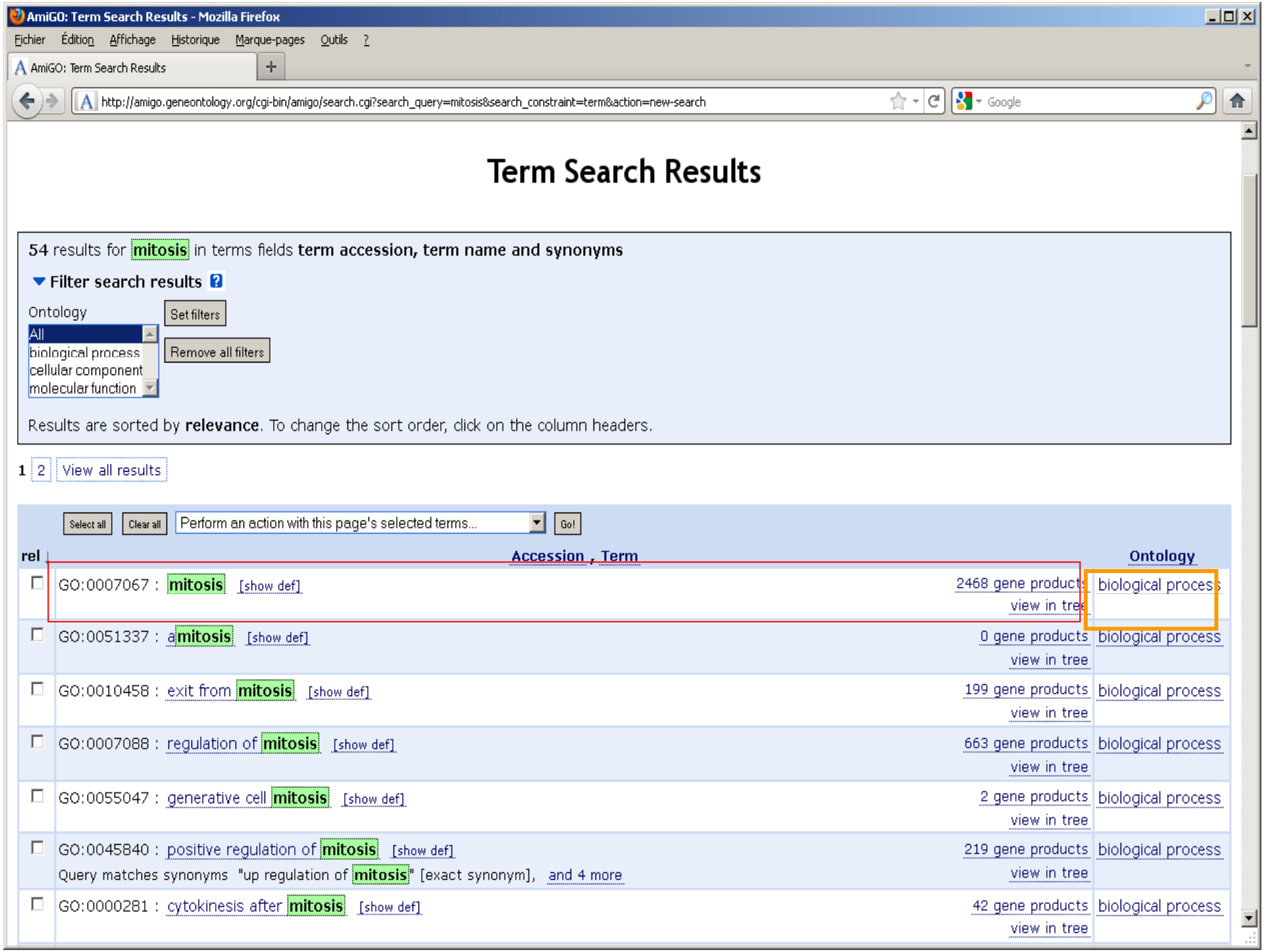
Gene Ontology.

- GO a été créée en 1998. GO résulte d'une collaboration entre plusieurs bases de données: FlyBase (drosophile), the Saccharomyces Genome Database, et des bases 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).

Gene Ontology (http://www.geneontology.org/)




AmiGO: Term Search Results - Mozilla Firefox
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AmiGO: Term Search Results
http://amigo.geneontology.org/cgi-bin/amigo/search.cgi?search_query=mitosis&search_constraint=term&action=new-search
Google
Term Search Results
54 results for mitosis in terms fields term accession, term name and synonyms
Filter search results
Ontology
All
biological process
cellular component
molecular function
Set filters
Remove all filters
Results are sorted by relevance. To change the sort order, click on the column headers.
1 2 View all results
Select all
Clear all
Perform an action with this page's selected terms...
Go!
rel
Accession , Term
Ontology
GO:0007067 : mitosis [show def]
2468 gene products
view in tree
biological process
GO:0051337 : amitosis [show def]
0 gene products
view in tree
biological process
GO:0010458 : exit from mitosis [show def]
199 gene products
view in tree
biological process
GO:0007088 : regulation of mitosis [show def]
663 gene products
view in tree
biological process
GO:0055047 : generative cell mitosis [show def]
2 gene products
view in tree
biological process
GO:0045840 : positive regulation of mitosis [show def]
Query matches synonyms "up regulation of mitosis" [exact synonym], and 4 more
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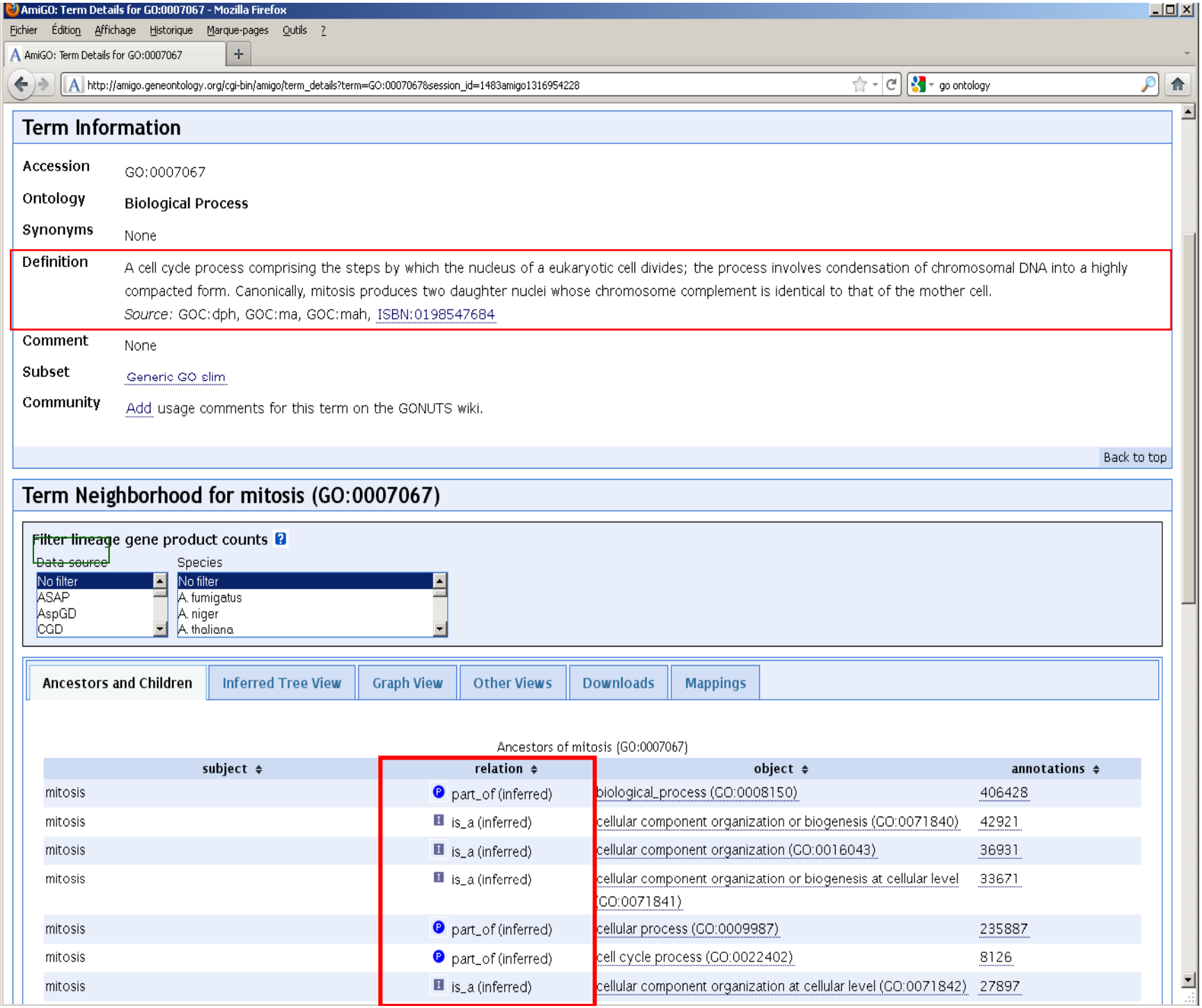
biological process
GO:0000281 : cytokinesis after mitosis [show def]
42 gene products
view in tree
biological process


AmiGO: Term Details for GO:0007067 - Mozilla Firefox
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AmiGO: Term Details for GO:0007067
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go ontology
Term Information
Accession GO:0007067
Ontology Biological Process
Synonyms None
Definition A cell cycle process comprising the steps by which the nucleus of a eukaryotic cell divides; the process involves condensation of chromosomal DNA into a highly compacted form. Canonically, mitosis produces two daughter nuclei whose chromosome complement is identical to that of the mother cell.
Source: GOC:dph, GOC:ma, GOC:mah, ISBN:0198547684
Comment None
Subset Generic GO slim
Community Add usage comments for this term on the GONUTS wiki.
Back to top
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Filter lineage gene product counts
Data source
Species
No filter
ASAP
AspGD
CGD
No filter
A. fumigatus
A. niger
A. thaliana
Ancestors and Children
Inferred Tree View
Graph View
Other Views
Downloads
Mappings
Ancestors of mitosis (GO:0007067)
subject
relation
object
annotations
mitosis
part_of (inferred)
biological_process (GO:0008150)
406428
mitosis
is_a (inferred)
cellular component organization or biogenesis (GO:0071840)
42921
mitosis
is_a (inferred)
cellular component organization (GO:0016043)
36931
mitosis
is_a (inferred)
cellular component organization or biogenesis at cellular level (GO:0071841)
33671
mitosis
part_of (inferred)
cellular process (GO:0009987)
235887
mitosis
part_of (inferred)
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8126
mitosis
is_a (inferred)
cellular component organization at cellular level (GO:0071842)
27897

AmiGO: Term Details for GO:0007067 - Mozilla Firefox

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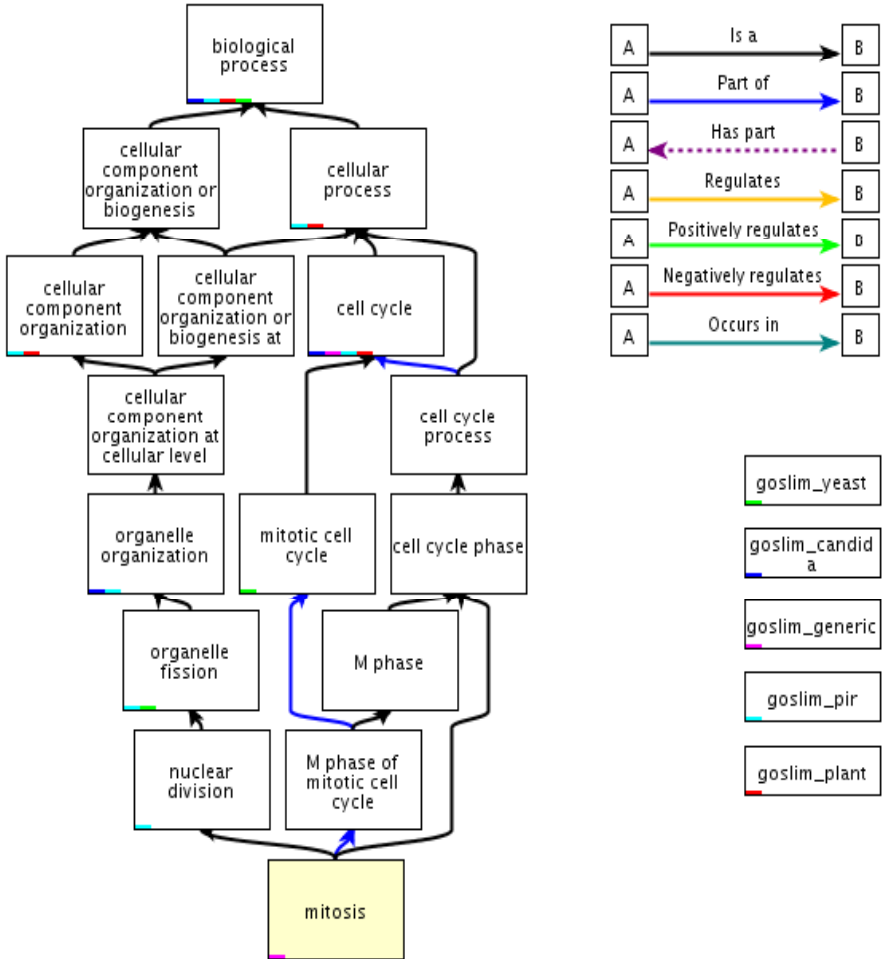
AmiGO: Term Details for GO:0007067

http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0007067&session_id=1483amigo1316954228

go ontology

View this term in QuickGO.



goslim_yeast

goslim_candida

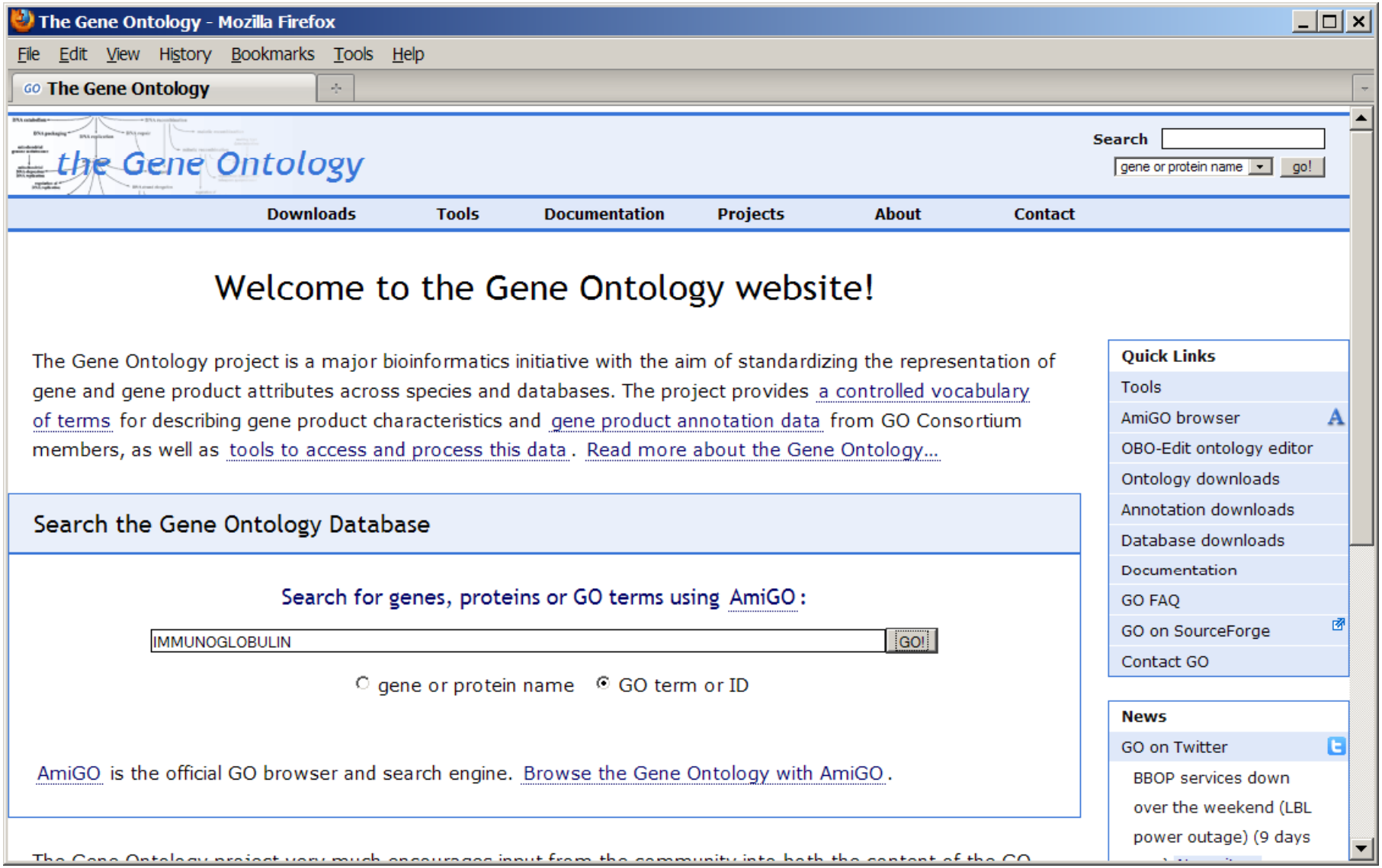
goslim_generic

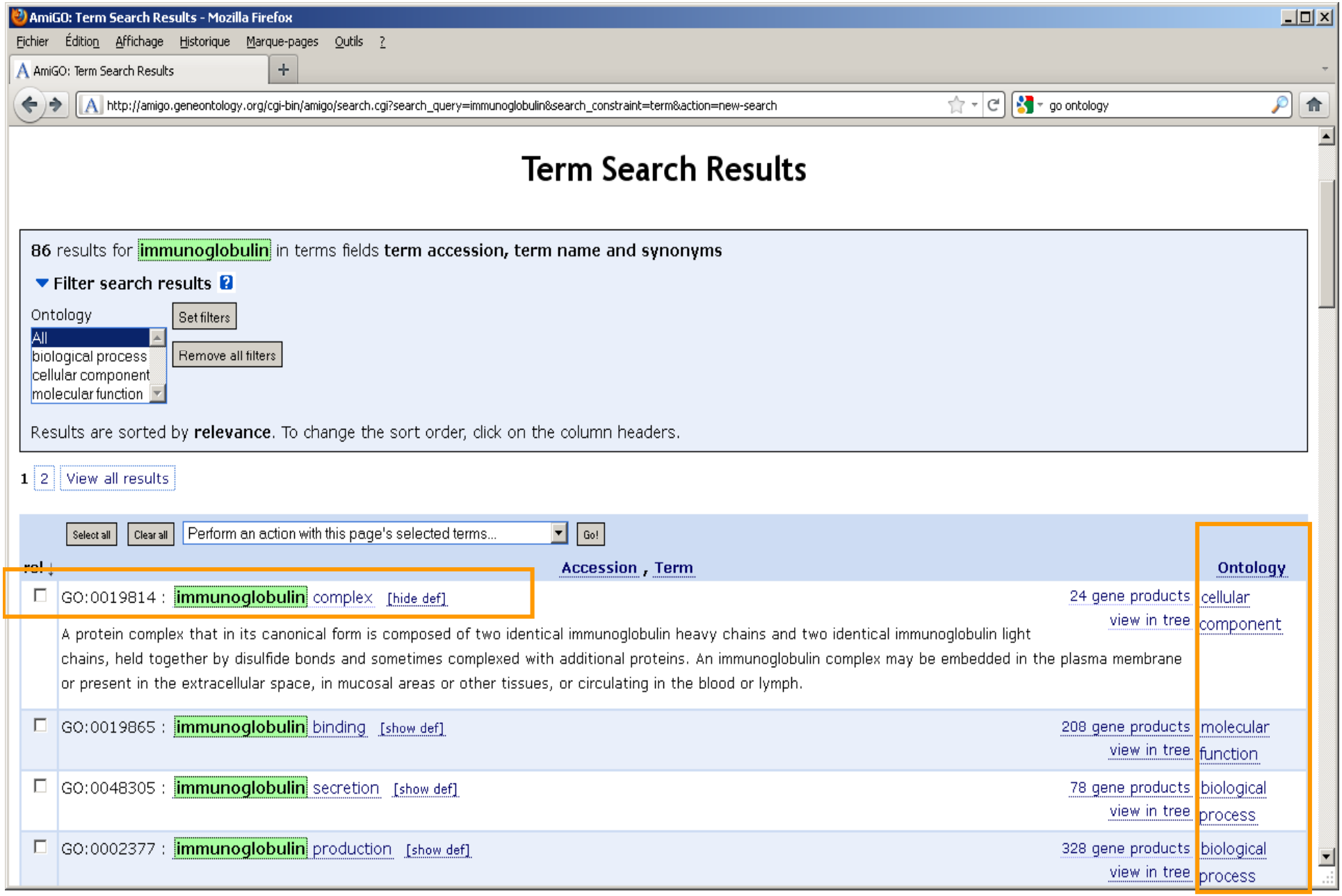
goslim_pir

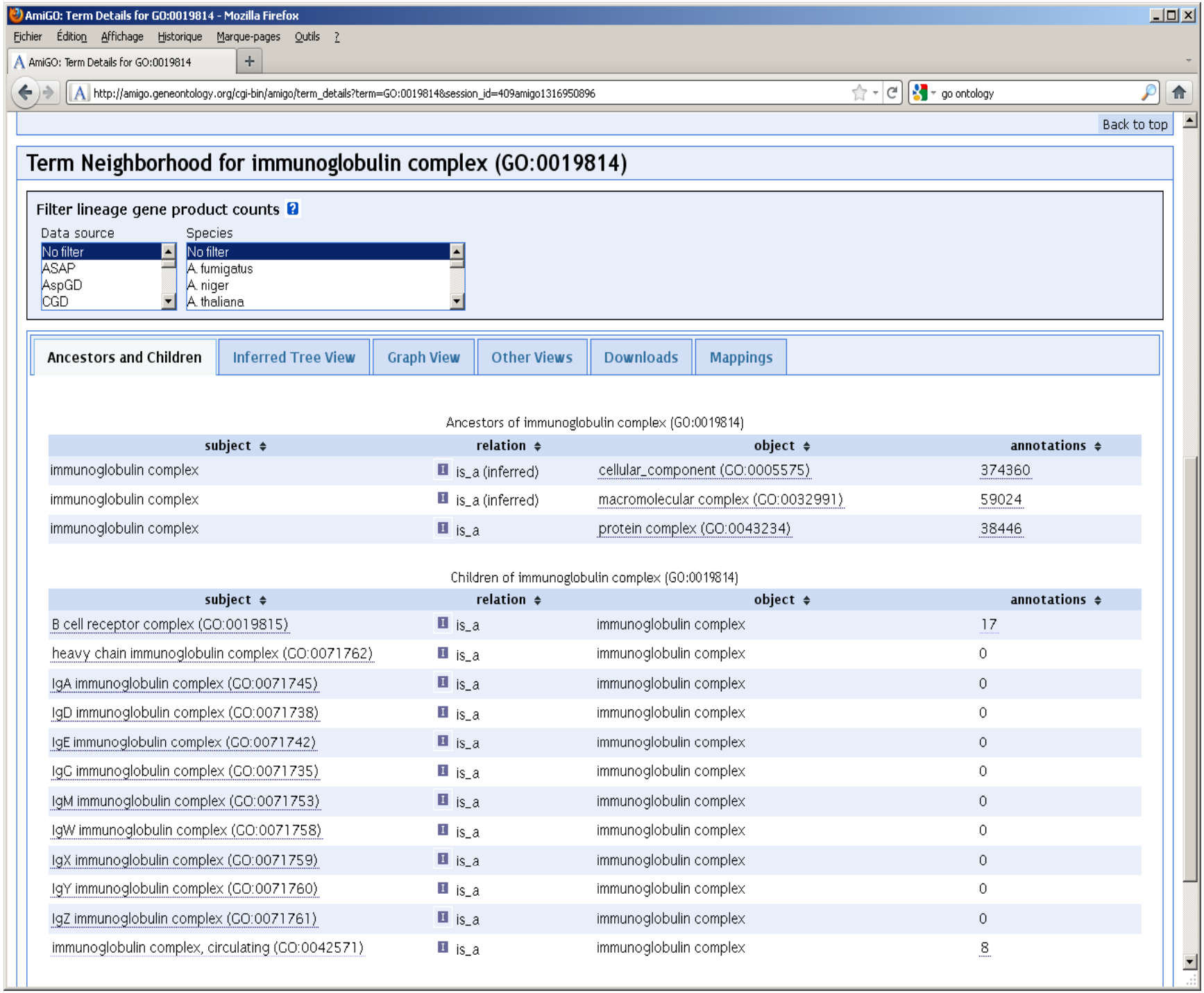
goslim_plant

QuickGO - http://www.ebi.ac.uk/QuickGO

Back to top


The Gene Ontology - Mozilla Firefox
File Edit View History Bookmarks Tools Help
The Gene Ontology
the Gene Ontology
Search
gene or protein name
go!
Downloads
Tools
Documentation
Projects
About
Contact
Welcome to the Gene Ontology website!
The Gene Ontology project is a major bioinformatics initiative with the aim of standardizing the representation of gene and gene product attributes across species and databases. The project provides a controlled vocabulary of terms for describing gene product characteristics and gene product annotation data from GO Consortium members, as well as tools to access and process this data. Read more about the Gene Ontology...
Search the Gene Ontology Database
Search for genes, proteins or GO terms using AmiGO:
IMMUNOGLOBULIN
GO!
gene or protein name
GO term or ID
AmiGO is the official GO browser and search engine. Browse the Gene Ontology with AmiGO.
Quick Links
Tools
AmiGO browser
OBO-Edit ontology editor
Ontology downloads
Annotation downloads
Database downloads
Documentation
GO FAQ
GO on SourceForge
Contact GO
News
GO on Twitter
BBOP services down over the weekend (LBL power outage) (9 days


AmiGO: Term Search Results - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
AmiGO: Term Search Results
http://amigo.geneontology.org/cgi-bin/amigo/search.cgi?search_query=immunoglobulin&search_constraint=term&action=new-search
go ontology
Term Search Results
86 results for immunoglobulin in terms fields term accession, term name and synonyms
Filter search results
Ontology
All
biological process
cellular component
molecular function
Set filters
Remove all filters
Results are sorted by relevance. To change the sort order, click on the column headers.
1 2 View all results
Select all
Clear all
Perform an action with this page's selected terms...
Go!
Accession , Term
Ontology
GO:0019814 : immunoglobulin complex [hide def]
24 gene products
view in tree
cellular component
A protein complex that in its canonical form is composed of two identical immunoglobulin heavy chains and two identical immunoglobulin light chains, held together by disulfide bonds and sometimes complexed with additional proteins. An immunoglobulin complex may be embedded in the plasma membrane or present in the extracellular space, in mucosal areas or other tissues, or circulating in the blood or lymph.
GO:0019865 : immunoglobulin binding [show def]
208 gene products
view in tree
molecular function
GO:0048305 : immunoglobulin secretion [show def]
78 gene products
view in tree
biological process
GO:0002377 : immunoglobulin production [show def]
328 gene products
view in tree
biological process


AmiGO: Term Details for GO:0019814 - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
AmiGO: Term Details for GO:0019814
http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0019814&session_id=409amigo1316950896
go ontology
Back to top
Term Neighborhood for immunoglobulin complex (GO:0019814)
Filter lineage gene product counts
Data source
No filter
ASAP
AspGD
CGD
Species
No filter
A. fumigatus
A. niger
A. thaliana
Ancestors and Children
Inferred Tree View
Graph View
Other Views
Downloads
Mappings
Ancestors of immunoglobulin complex (GO:0019814)
subject
relation
object
annotations
immunoglobulin complex
is_a (inferred)
cellular_component (GO:0005575)
374360
immunoglobulin complex
is_a (inferred)
macromolecular complex (GO:0032991)
59024
immunoglobulin complex
is_a
protein complex (GO:0043234)
38446
Children of immunoglobulin complex (GO:0019814)
subject
relation
object
annotations
B cell receptor complex (GO:0019815)
is_a
immunoglobulin complex
17
heavy chain immunoglobulin complex (GO:0071762)
is_a
immunoglobulin complex
0
IgA immunoglobulin complex (GO:0071745)
is_a
immunoglobulin complex
0
IgD immunoglobulin complex (GO:0071738)
is_a
immunoglobulin complex
0
IgE immunoglobulin complex (GO:0071742)
is_a
immunoglobulin complex
0
IgG immunoglobulin complex (GO:0071735)
is_a
immunoglobulin complex
0
IgM immunoglobulin complex (GO:0071753)
is_a
immunoglobulin complex
0
IgW immunoglobulin complex (GO:0071758)
is_a
immunoglobulin complex
0
IgX immunoglobulin complex (GO:0071759)
is_a
immunoglobulin complex
0
IgY immunoglobulin complex (GO:0071760)
is_a
immunoglobulin complex
0
IgZ immunoglobulin complex (GO:0071761)
is_a
immunoglobulin complex
0
immunoglobulin complex, circulating (GO:0042571)
is_a
immunoglobulin complex
8

AmiGO: Term Details for GO:0019814 - Mozilla Firefox

Fichier Édition Affichage Historique Marque-pages Outils ?

AmiGO: Term Details for GO:0019814

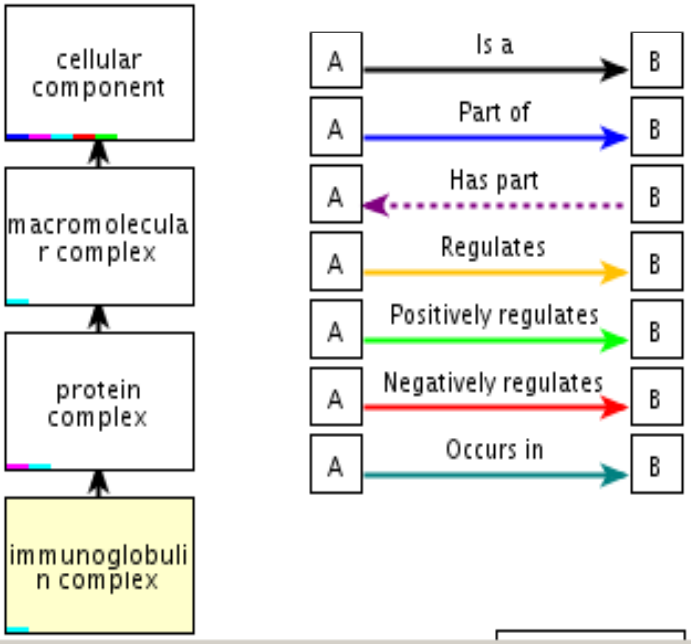
http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0019814&sessic

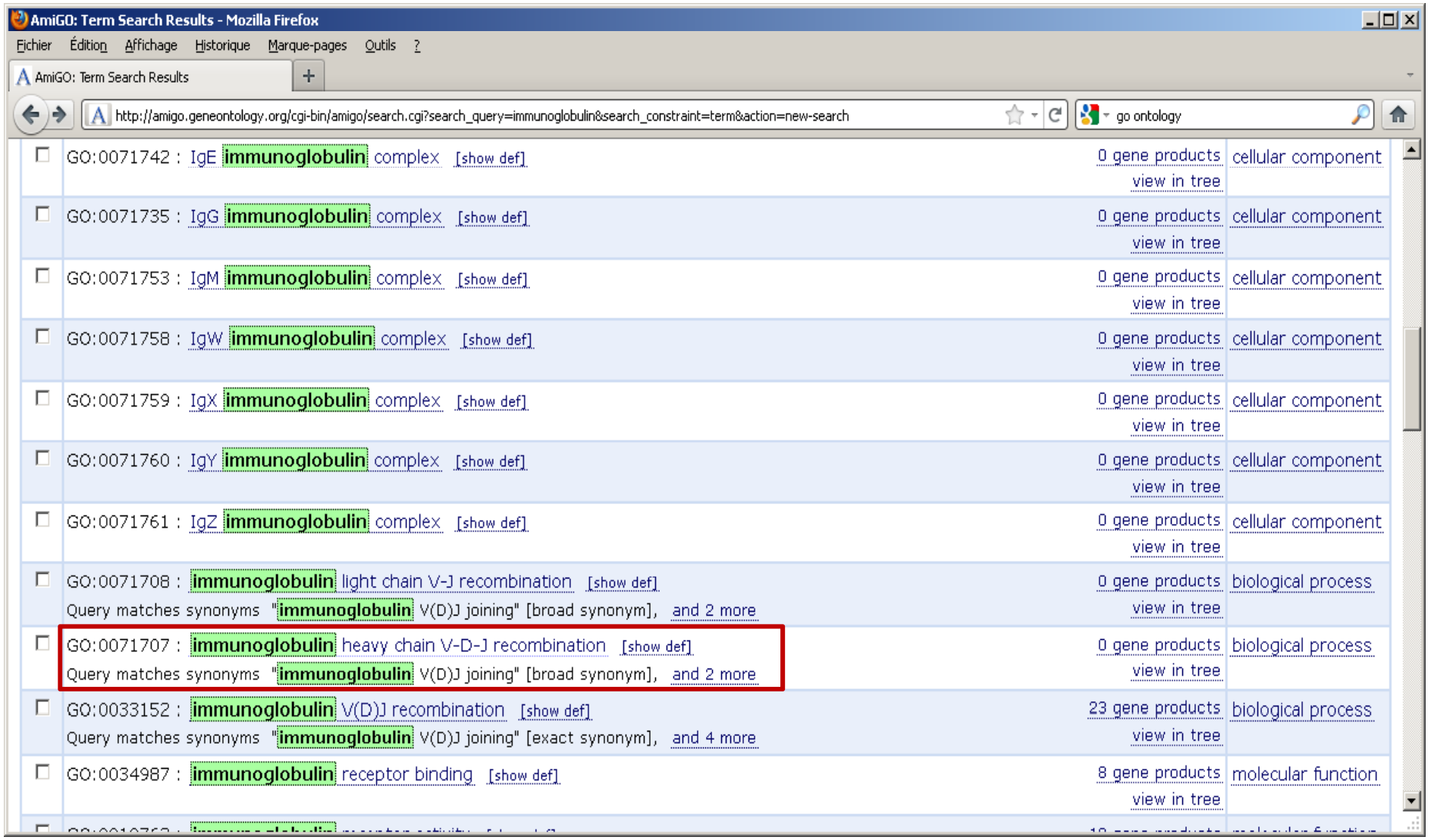
go ontology

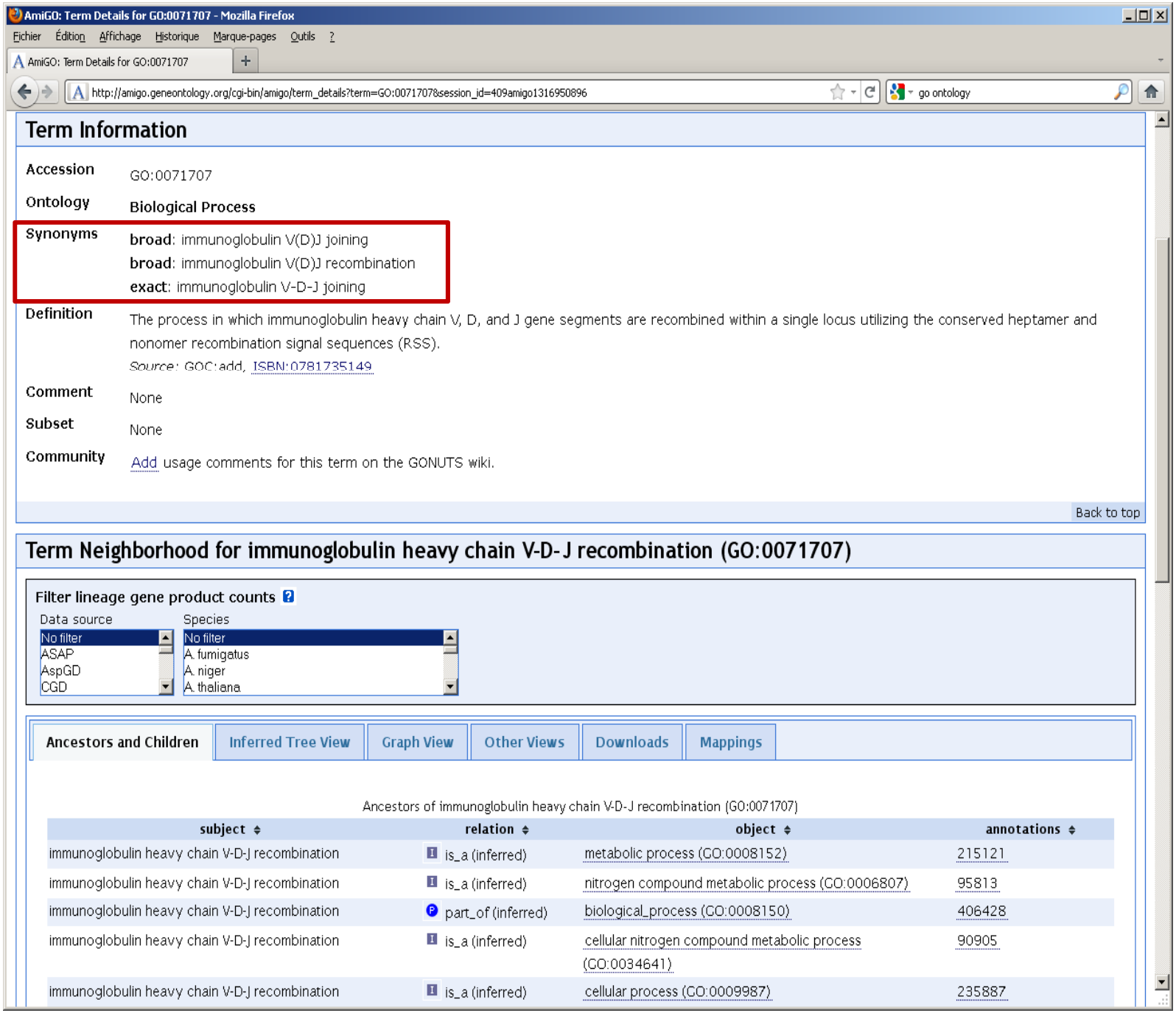
Ancestors and Children | Inferred Tree View | **Graph View** | Other Views

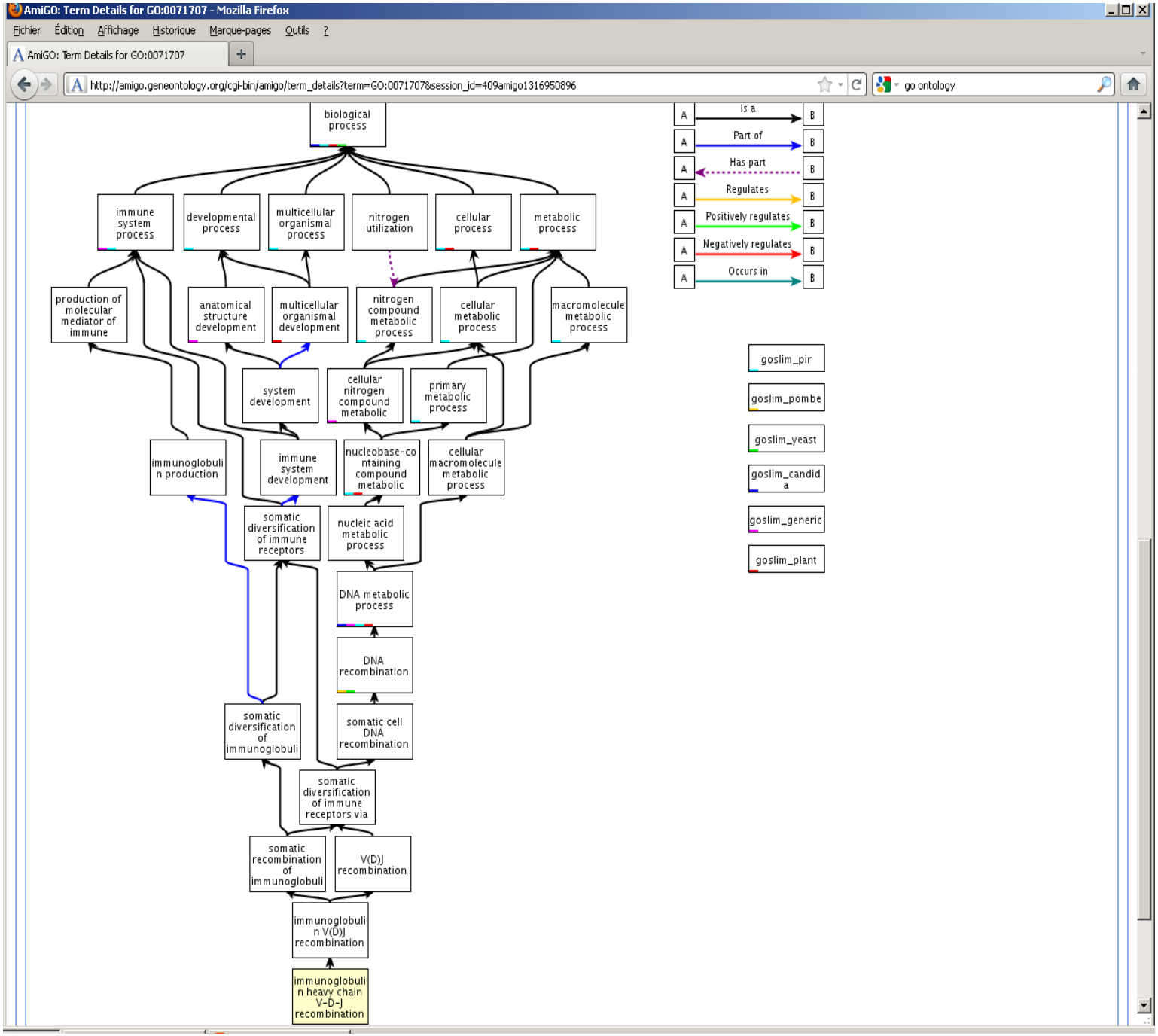
Downloads | Mappings

View this term in QuickGO.




AmiGO: Term Search Results - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
AmiGO: Term Search Results
http://amigo.geneontology.org/cgi-bin/amigo/search.cgi?search_query=immunoglobulin&search_constraint=term&action=new-search
go ontology
GO:0071742 : IgE immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071735 : IgG immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071753 : IgM immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071758 : IgW immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071759 : IgX immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071760 : IgY immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071761 : IgZ immunoglobulin complex [show def]
0 gene products
view in tree
cellular component
GO:0071708 : immunoglobulin light chain V-J recombination [show def]
Query matches synonyms "immunoglobulin V(D)J joining" [broad synonym], and 2 more
0 gene products
view in tree
biological process
GO:0071707 : immunoglobulin heavy chain V-D-J recombination [show def]
Query matches synonyms "immunoglobulin V(D)J joining" [broad synonym], and 2 more
0 gene products
view in tree
biological process
GO:0033152 : immunoglobulin V(D)J recombination [show def]
Query matches synonyms "immunoglobulin V(D)J joining" [exact synonym], and 4 more
23 gene products
view in tree
biological process
GO:0034987 : immunoglobulin receptor binding [show def]
8 gene products
view in tree
molecular function


AmiGO: Term Details for GO:0071707 - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
AmiGO: Term Details for GO:0071707
http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0071707&session_id=409amigo1316950896
go ontology
Term Information
Accession GO:0071707
Ontology Biological Process
Synonyms broad: immunoglobulin V(D)J joining
broad: immunoglobulin V(D)J recombination
exact: immunoglobulin V-D-J joining
Definition The process in which immunoglobulin heavy chain V, D, and J gene segments are recombined within a single locus utilizing the conserved heptamer and nonomer recombination signal sequences (RSS).
Source: GOC:add, ISBN:0781735149
Comment None
Subset None
Community Add usage comments for this term on the GONUTS wiki.
Back to top
Term Neighborhood for immunoglobulin heavy chain V-D-J recombination (GO:0071707)
Filter lineage gene product counts
Data source
No filter
ASAP
AspGD
CGD
Species
No filter
A. fumigatus
A. niger
A. thaliana
Ancestors and Children
Inferred Tree View
Graph View
Other Views
Downloads
Mappings
Ancestors of immunoglobulin heavy chain V-D-J recombination (GO:0071707)
subject
relation
object
annotations
immunoglobulin heavy chain V-D-J recombination
is_a (inferred)
metabolic process (GO:0008152)
215121
immunoglobulin heavy chain V-D-J recombination
is_a (inferred)
nitrogen compound metabolic process (GO:0006807)
95813
immunoglobulin heavy chain V-D-J recombination
part_of (inferred)
biological_process (GO:0008150)
406428
immunoglobulin heavy chain V-D-J recombination
is_a (inferred)
cellular nitrogen compound metabolic process (GO:0034641)
90905
immunoglobulin heavy chain V-D-J recombination
is_a (inferred)
cellular process (GO:0009987)
235887


AmiGO: Term Details for GO:0071707 - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
AmiGO: Term Details for GO:0071707
http://amigo.geneontology.org/cgi-bin/amigo/term_details?term=GO:0071707&session_id=409amigo1316950896
go ontology
biological process
immune system process
developmental process
multicellular organismal process
nitrogen utilization
cellular process
metabolic process
production of molecular mediator of immune
anatomical structure development
multicellular organismal development
nitrogen compound metabolic process
cellular metabolic process
macromolecule metabolic process
system development
cellular nitrogen compound metabolic
primary metabolic process
immunoglobuli n production
immune system development
nucleobase-co ntaining compound metabolic
cellular macromolecule metabolic process
somatic diversification of immune receptors
nucleic acid metabolic process
DNA metabolic process
DNA recombination
somatic diversification of immunoglobuli
somatic cell DNA recombination
somatic diversification of immune receptors via
somatic recombination of immunoglobuli
V(D)J recombination
immunoglobuli n V(D)J recombination
immunoglobuli n heavy chain V-D-J recombination
A Is a B
A Part of B
A Has part B
A Regulates B
A Positively regulates B
A Negatively regulates B
A Occurs in B
goslim_pir
goslim_pombe
goslim_yeast
goslim_candid a
goslim_generic
goslim_plant

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

(http://www.sequenceontology.org/)

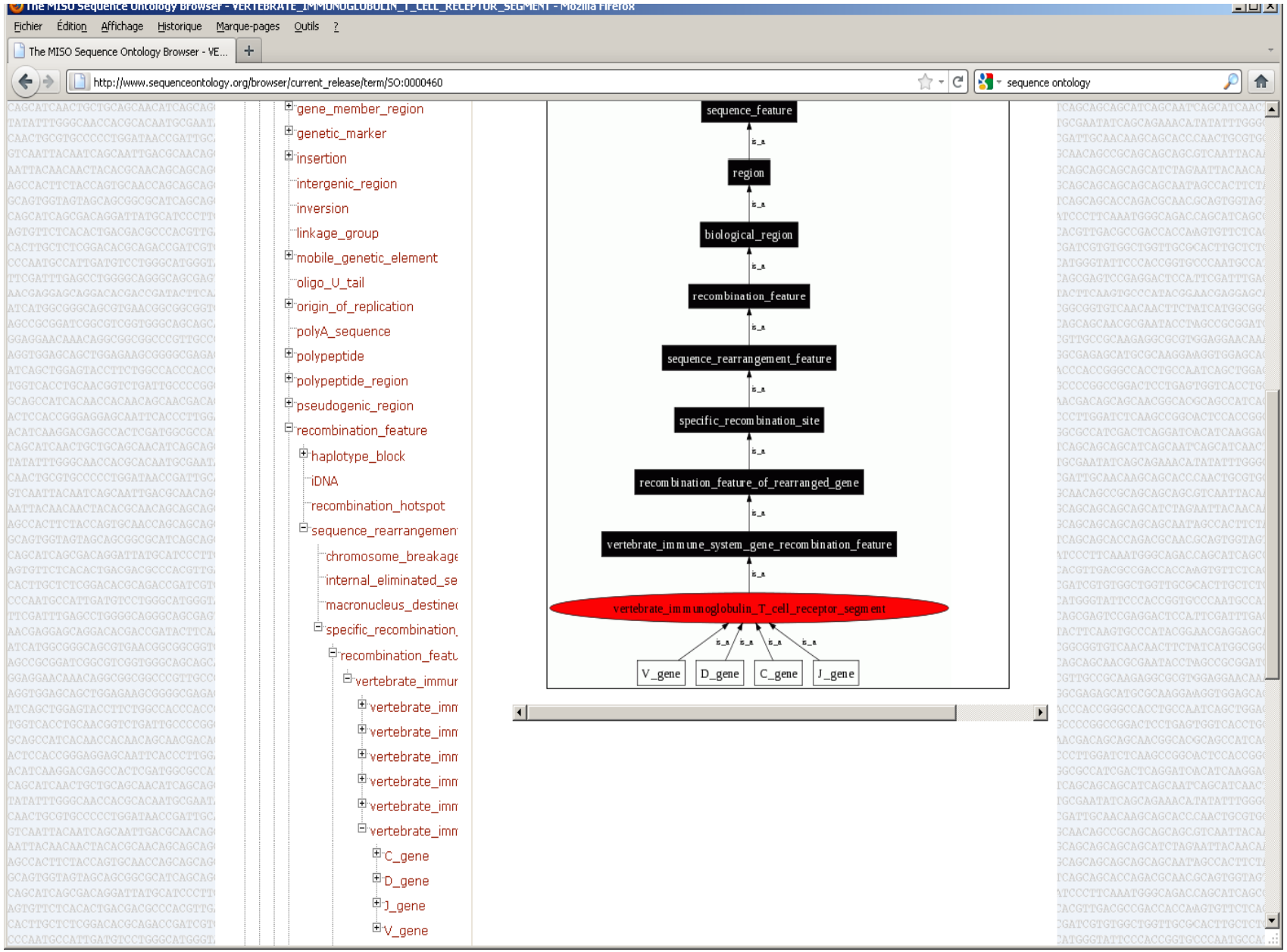
- Vocabulaire contrôlé pour l'annotation des séquences et l'annotation des génomes

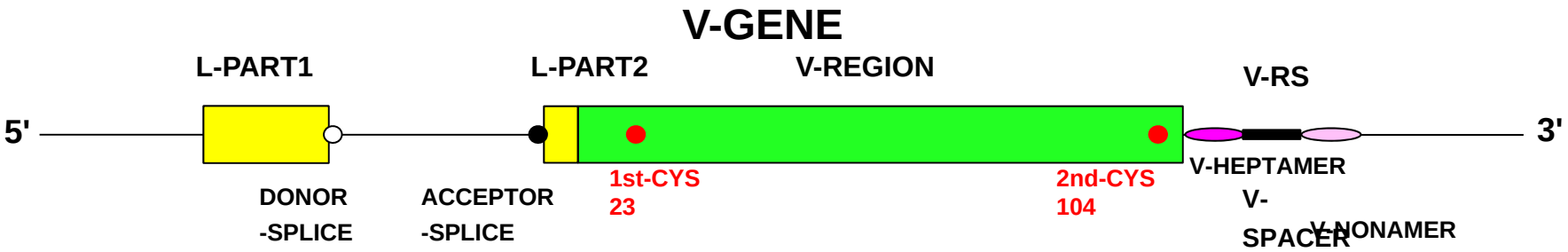
- proposer une représentation structurée des annotations

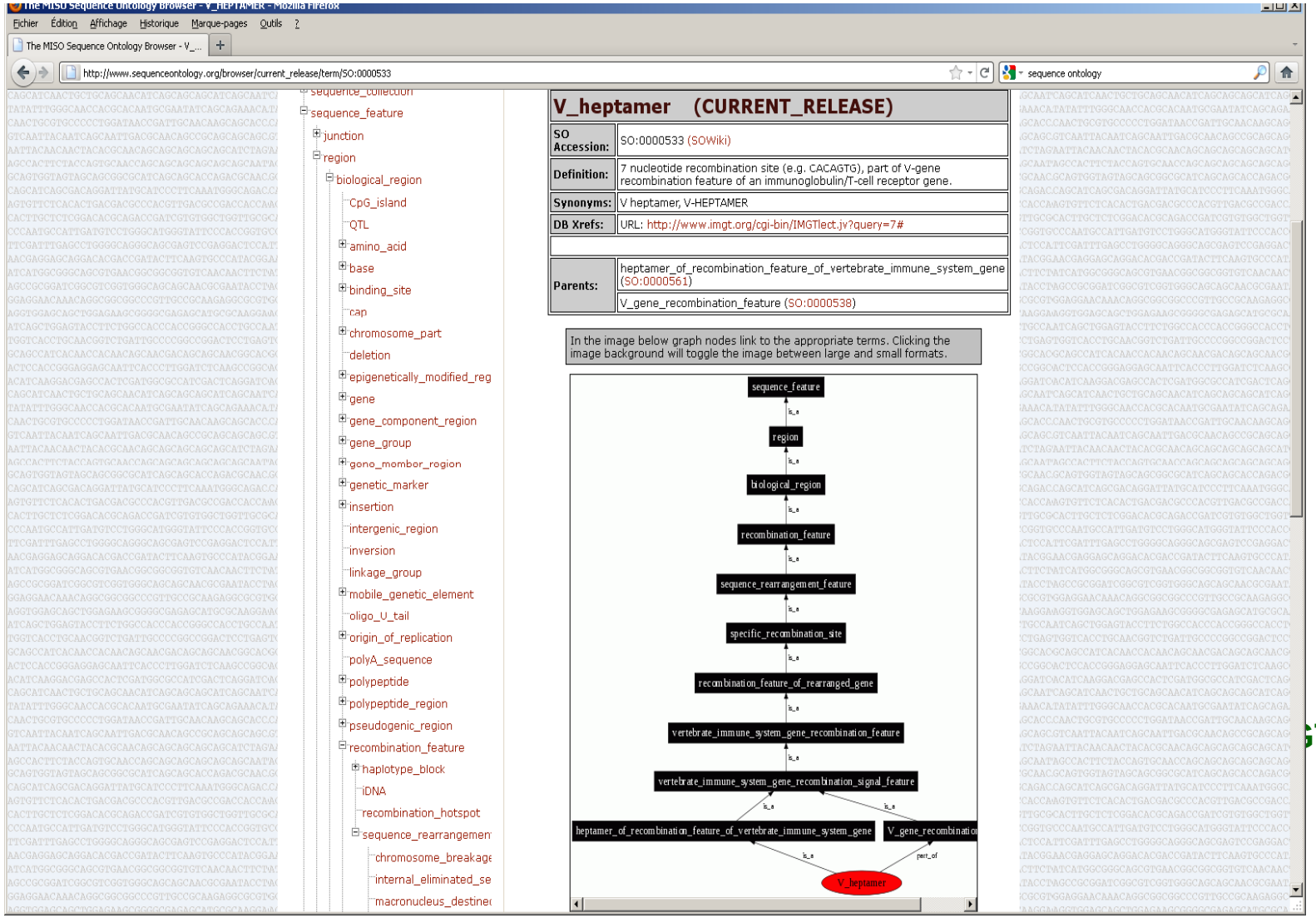
- vocabulaire pour la description des mutations

Sequence Ontology:
une ontologie pour décrire les séquences biologiques

The MISO Sequence Ontology Browser - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
The MISO Sequence Ontology Browser
http://www.sequenceontology.org/browser/obob.cgi
sequence ontology
MISO
The Sequence Ontology Browser
Home Browser Wiki GFF3 Resources About Request A Term Site Map
Search for Terms: immmunoglobulin
Search
Select Release: CURRENT RELEASE
sequence_attribute
sequence_collection
sequence_feature
sequence_variant
Obsolete Terms
Relationship
Welcome to MISO, the Sequence Ontology Browser
Search for a SO term by entering a SO term name or synonym in the query box above;
Explore the structure of SO and browse for SO terms using the expandable, cascading tree on the left;
Go to the detail page for a term where you can:
Get details about a term, it's definition and relationships;
See graphical views of a term's place in the ontology and link to it's neighbors;
Export details about a term in a variety of formats;
And access and contribute detailed documentation about a term and it's history by linking through to the SO wiki
Copyright © 2008 Sequence Ontology. All rights reserved.
Valid XHTML 1.0 Strict


The MISO Sequence Ontology Browser - VERTEBRATE_IMMUNOGLOBULIN_T_CELL_RECEPTOR_SEGMENT - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
The MISO Sequence Ontology Browser - VE...
http://www.sequenceontology.org/browser/current_release/term/SO:0000460
sequence ontology
gene_member_region
genetic_marker
insertion
intergenic_region
inversion
linkage_group
mobile_genetic_element
oligo_U_tail
origin_of_replication
polyA_sequence
polypeptide
polypeptide_region
pseudogenic_region
recombination_feature
haplotype_block
iDNA
recombination_hotspot
sequence_rearrangemen
chromosome_breakage
internal_eliminated_se
macronucleus_destine
specific_recombination_
recombination_featu
vertebrate_immur
vertebrate_imm
vertebrate_imm
vertebrate_imm
vertebrate_imm
vertebrate_imm
vertebrate_imm
C_gene
D_gene
J_gene
V_gene
sequence_feature
is_a
region
biological_region
recombination_feature
sequence_rearrangement_feature
specific_recombination_site
recombination_feature_of_rearranged_gene
vertebrate_immune_system_gene_recombination_feature
vertebrate_immunoglobulin_T_cell_receptor_segment
V_gene
D_gene
C_gene
J_gene


V-GENE
L-PART1
L-PART2
V-REGION
V-RS
5'
3'
DONOR
-SPLICE
ACCEPTOR
-SPLICE
1st-CYS
23
2nd-CYS
104
V-HEPTAMER
V-
SPACER
V-NONAMER


The MISO Sequence Ontology Browser - V_HEPTAMER - Mozilla Firefox
Fichier Édition Affichage Historique Marque-pages Outils ?
The MISO Sequence Ontology Browser - V_...
http://www.sequenceontology.org/browser/current_release/term/SO:0000533
sequence ontology
sequence_collection
sequence_feature
junction
region
biological_region
CpG_island
QTL
amino_acid
base
binding_site
cap
chromosome_part
deletion
epigenetically_modified_reg
gene
gene_component_region
gene_group
gene_member_region
genetic_marker
insertion
intergenic_region
inversion
linkage_group
mobile_genetic_element
oligo_U_tail
origin_of_replication
polyA_sequence
polypeptide
polypeptide_region
pseudogenic_region
recombination_feature
haplotype_block
iDNA
recombination_hotspot
sequence_rearrangemen
chromosome_breakag
internal_eliminated_se
macronucleus_destine
V_heptamer (CURRENT_RELEASE)
SO Accession: SO:0000533 (SOWiki)
Definition: 7 nucleotide recombination site (e.g. CACAGTG), part of V-gene recombination feature of an immunoglobulin/T-cell receptor gene.
Synonyms: V heptamer, V-HEPTAMER
DB Xrefs: URL: http://www.imgt.org/cgi-bin/IMGTlect.jv?query=7#
Parents: heptamer_of_recombination_feature_of_vertebrate_immune_system_gene (SO:0000561)
V_gene_recombination_feature (SO:0000538)
In the image below graph nodes link to the appropriate terms. Clicking the image background will toggle the image between large and small formats.
sequence_feature
region
biological_region
recombination_feature
sequence_rearrangement_feature
specific_recombination_site
recombination_feature_of_rearranged_gene
vertebrate_immune_system_gene_recombination_feature
vertebrate_immune_system_gene_recombination_signal_feature
heptamer_of_recombination_feature_of_vertebrate_immune_system_gene
V_gene_recombinatio
is_a
part_of
V_heptamer

Dans le domaine de l'immunogénétique

Limites de SO:

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

- 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 ?

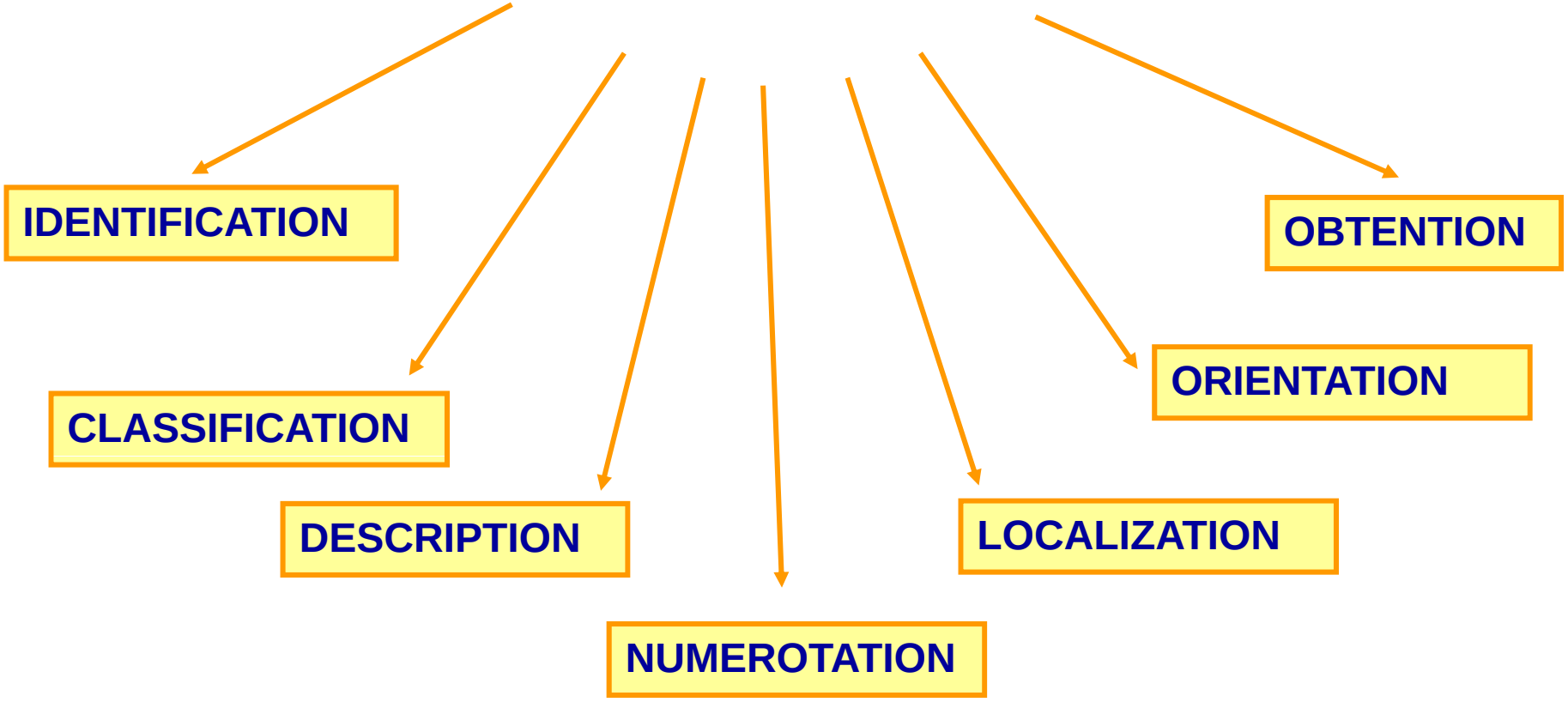
=> nécessité d'une ontologie spécifique

IMGT-ONTOLOGY

http://www.imgt.org

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

IMGT-ONTOLOGY repose sur 7 axiomes:



IMGT-ONTOLOGY

http://www.imgt.org

IMGT Scientific chart :

IMGT-ONTOLOGY en *langage naturel* pour les biologistes

http://imgt.cines.fr/textes/IMGTScientificChart/

En cours : édition en langage OWL

Version v1.0.0 sur le site BioPortal

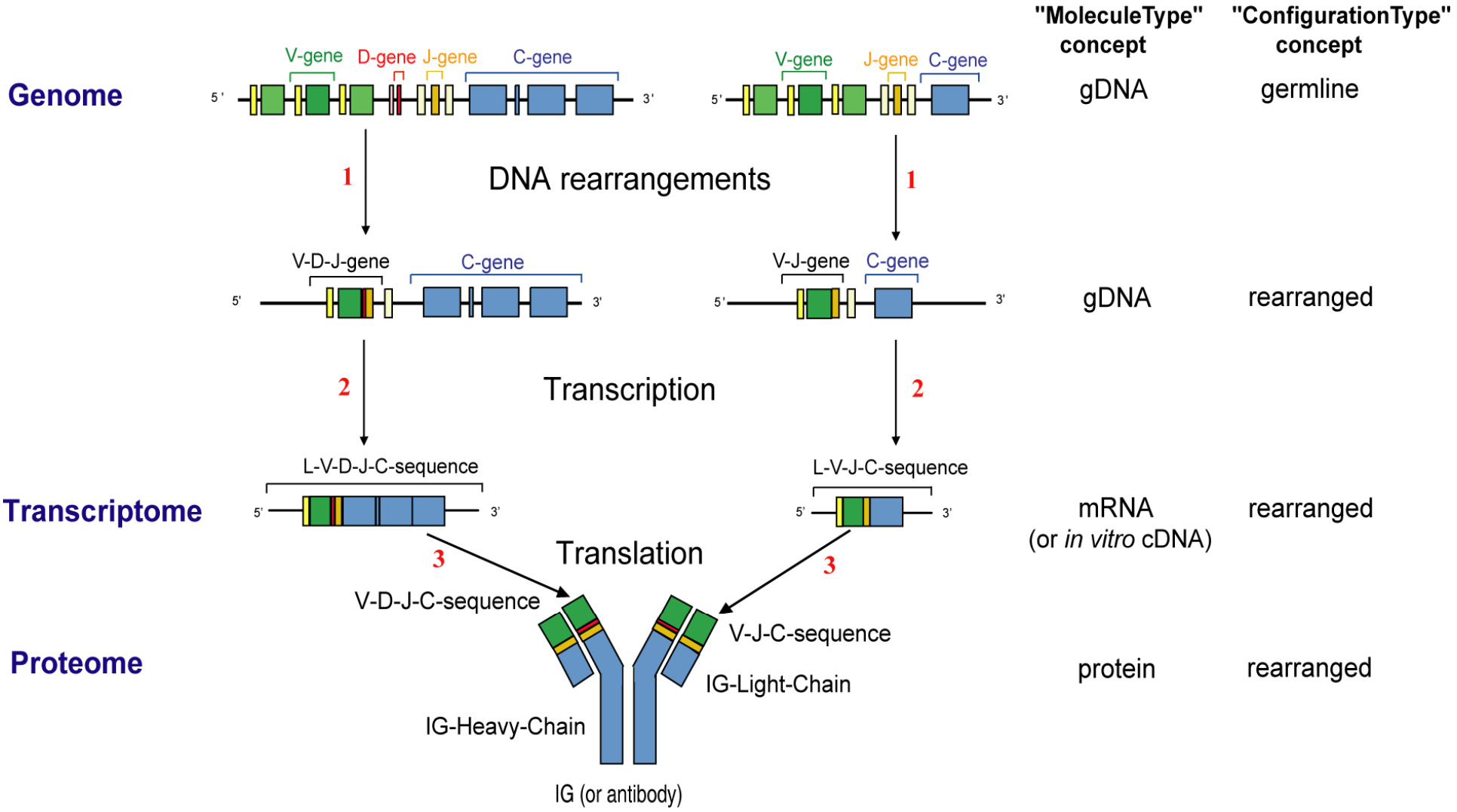
(http://bioportal.bioontology.org/visualize/42685)

Concepts d'Indentification

http://www.imgt.org

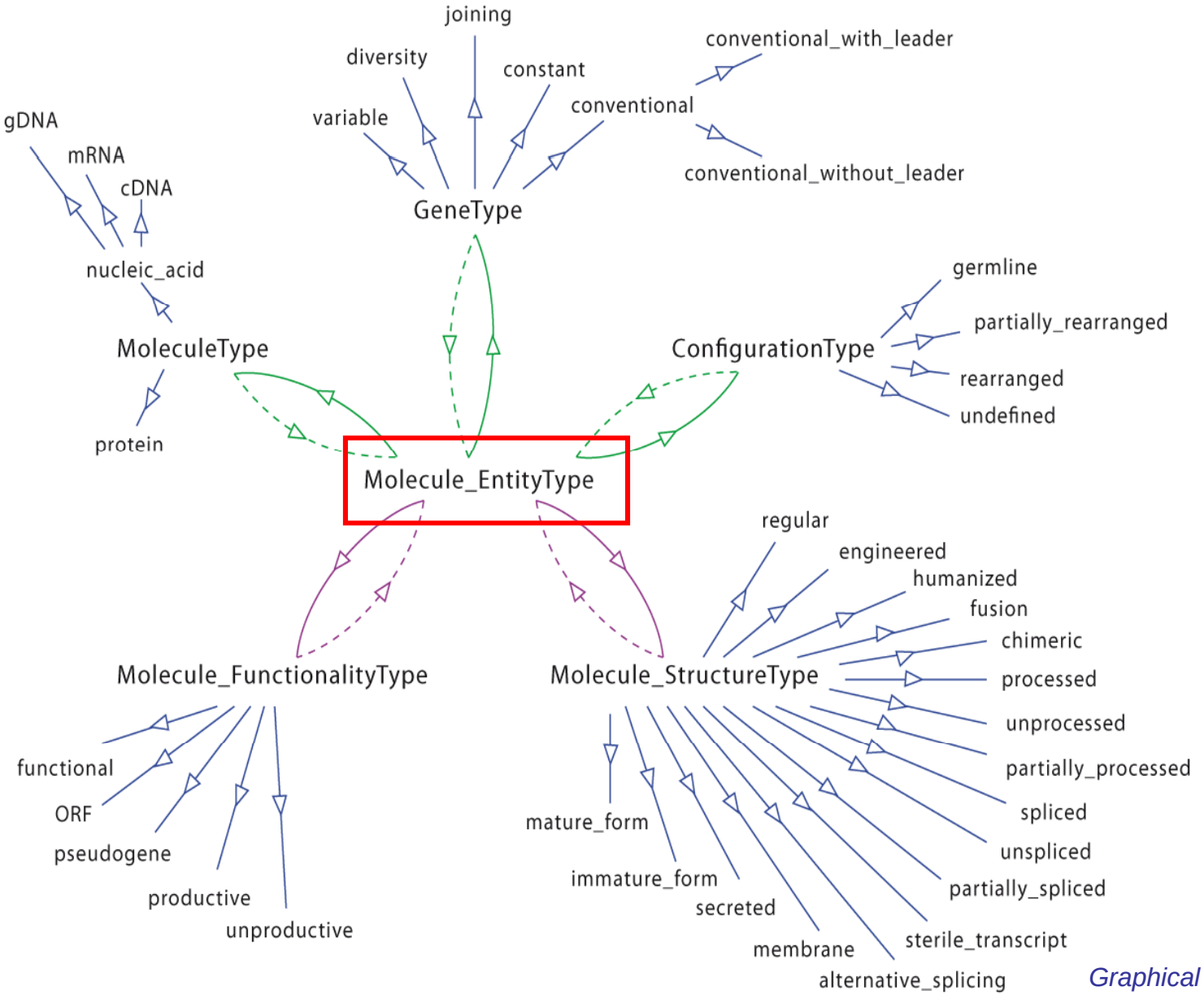
Synthèse des immunoglobulines

http://www.imgt.org



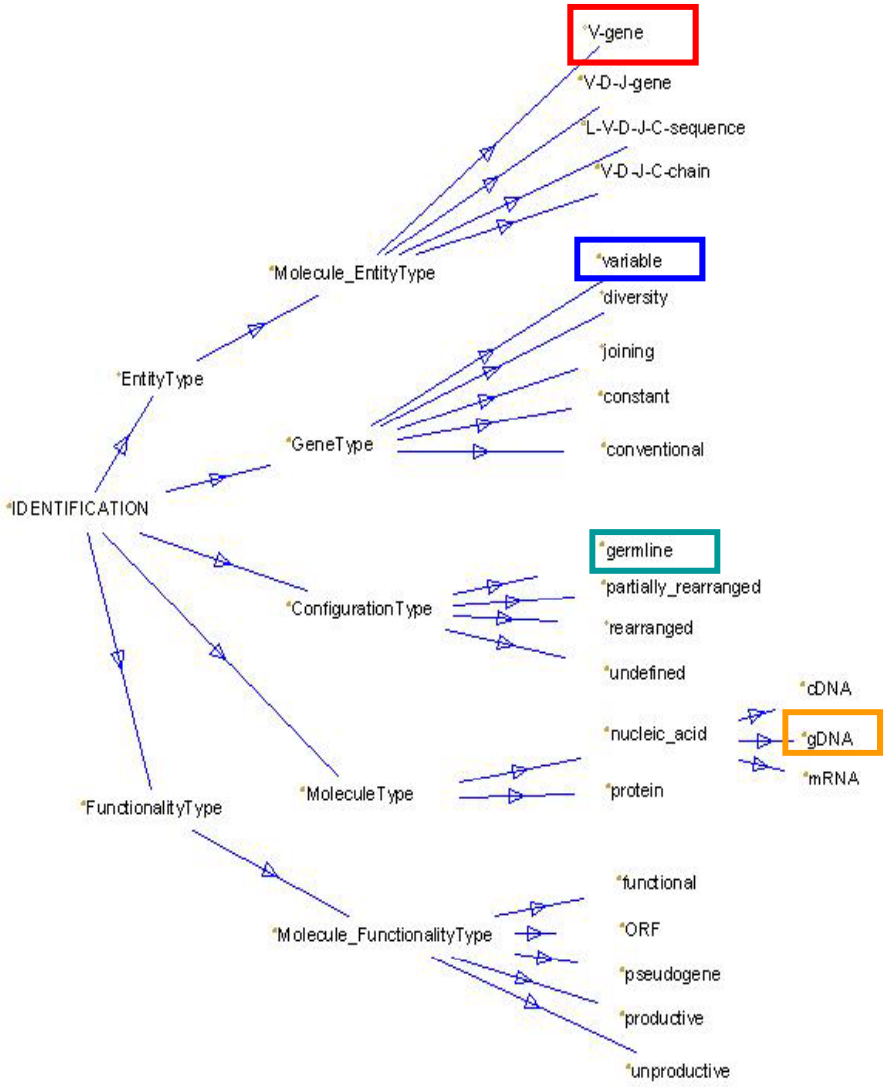
Relationships between Molecule_EntityType and the other IDENTIFICATION concepts

http://www.imgt.org



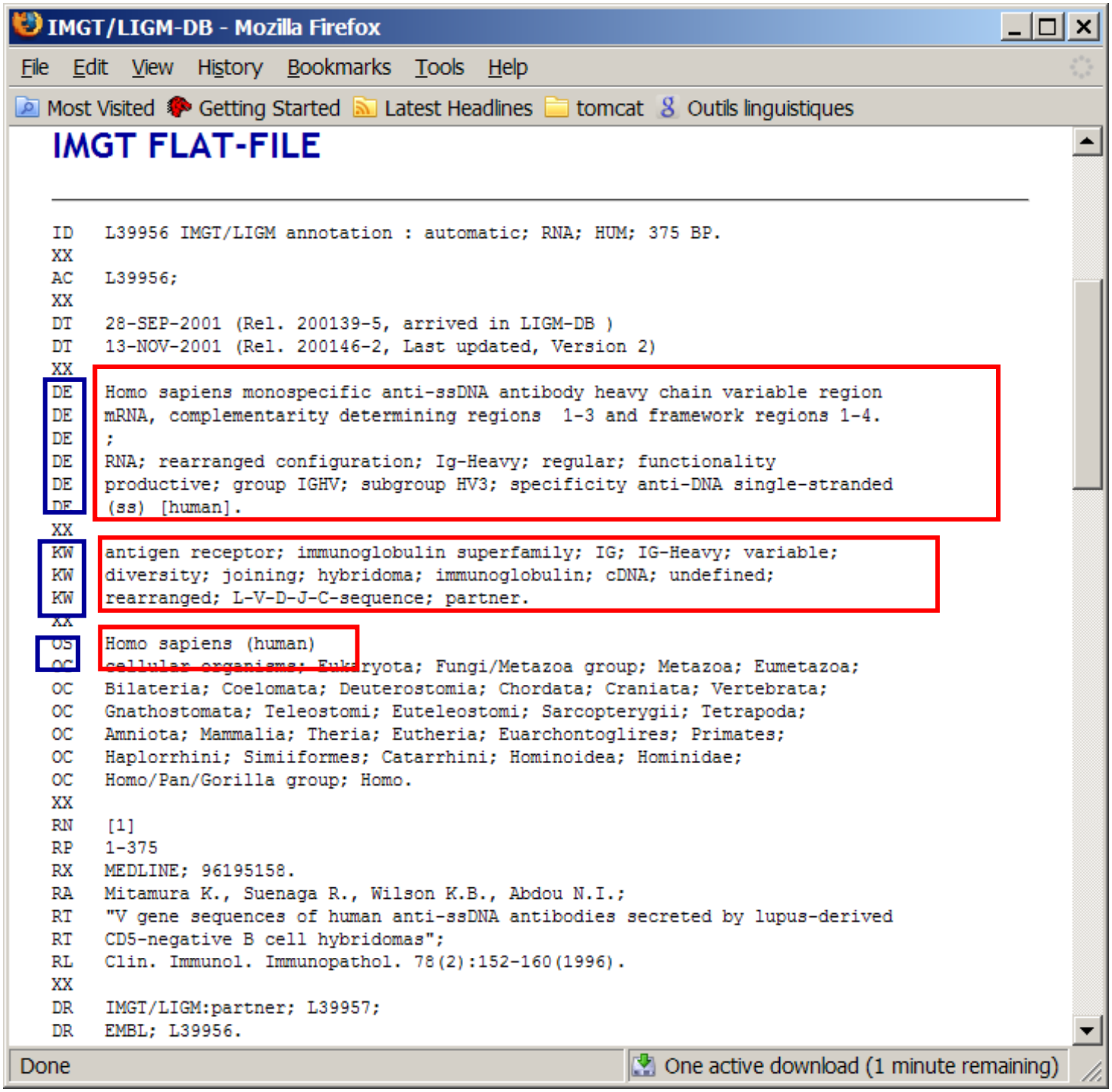
Graphical representation generated with

Result: the formalization of the relationships between concepts of IDENTIFICATION allows to represent the rules of the dependency between keywords used in IMGT® databases



IMGT/LIGM-DB flatfile

```
ID   X07448 IMGT/LIGM annotation : by annotators; genomic DNA; HUM; 618 BP.
XX
AC   X07448;
XX
DT   15-MAY-1995 (Rel. 2, arrived in LIGM-DB )
DT   20-OCT-2008 (Rel. 200843-1, Last updated, Version 10)
XX
DE   Human V35 gene for Ig heavy chain  ;
DE   genomic DNA; germline configuration; Ig-Heavy; regular; functionality
DE   functional; group IGHV; subgroup HV1.
XX
KW   antigen receptor; Immunoglobulin superfamily (IgSF);
KW   immunoglobulin (IG); IG-Heavy; variable; IMGT reference sequence; gDNA;
KW   germline; functional; V-gene.
XX
OS   Homo sapiens (human)
OC   cellular organisms; Eukaryota; Fungi/Metazoa group; Metazoa; Eumetazoa;
OC   Bilateria; Coelomata; Deuterostomia; Chordata; Craniata; Vertebrata;
OC   Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Tetrapoda;
OC   Amniota; Mammalia; Theria; Eutheria; Euarchontoglires; Primates;
OC   Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae;
OC   Homo/Pan/Gorilla group; Homo.
XX
RN   [1]
RP   1-618
RX   PUBMED; 2841108.
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno
H.,
RA   Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus";
RL   EMBO J. 7(4):1047-1051(1988).
XX
```



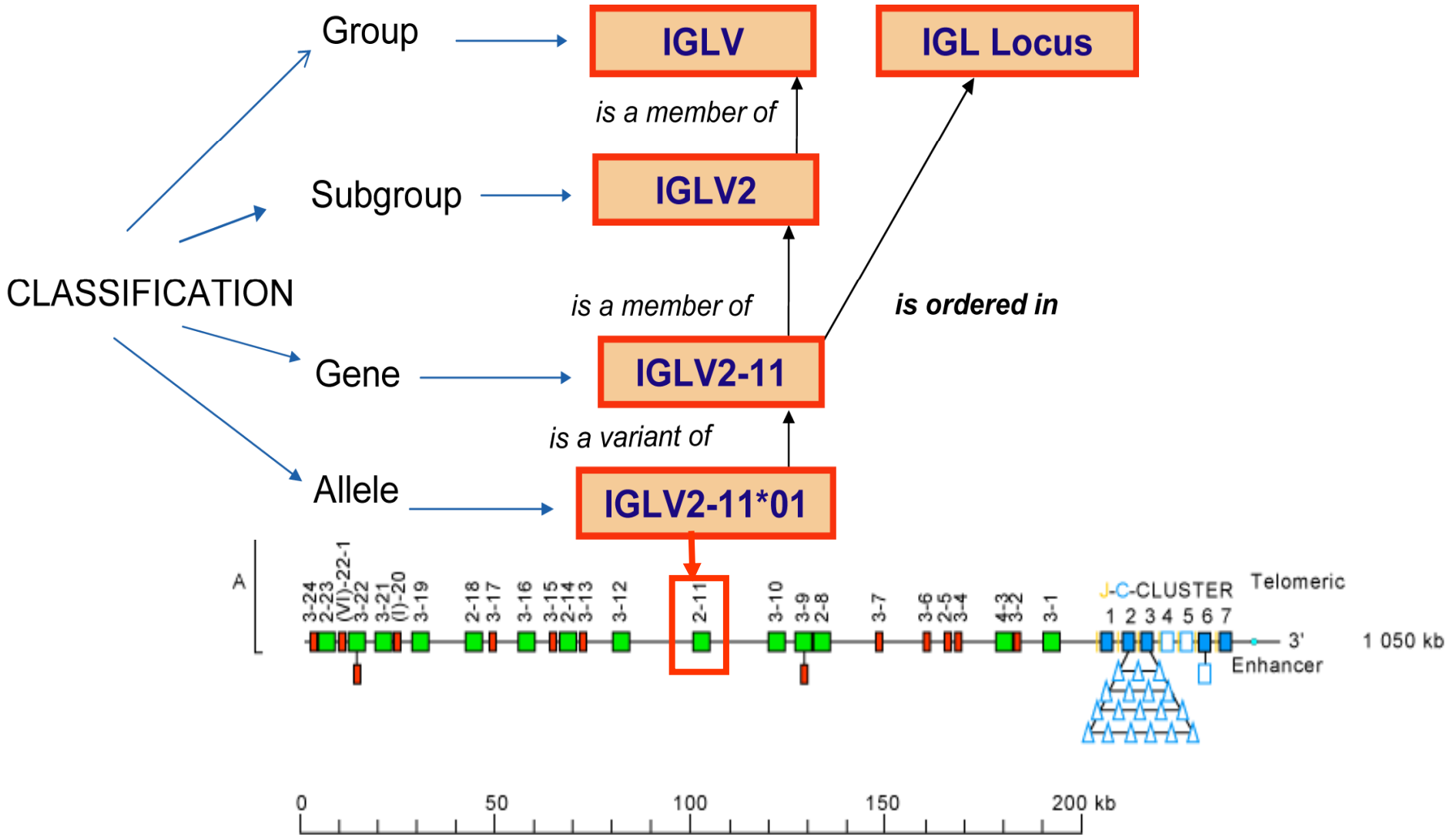
Im Muno Gene Tics Information system®

http://www.imgt.org

Concepts of CLASSIFICATION: IMGT® gene nomenclature

http://www.imgt.org

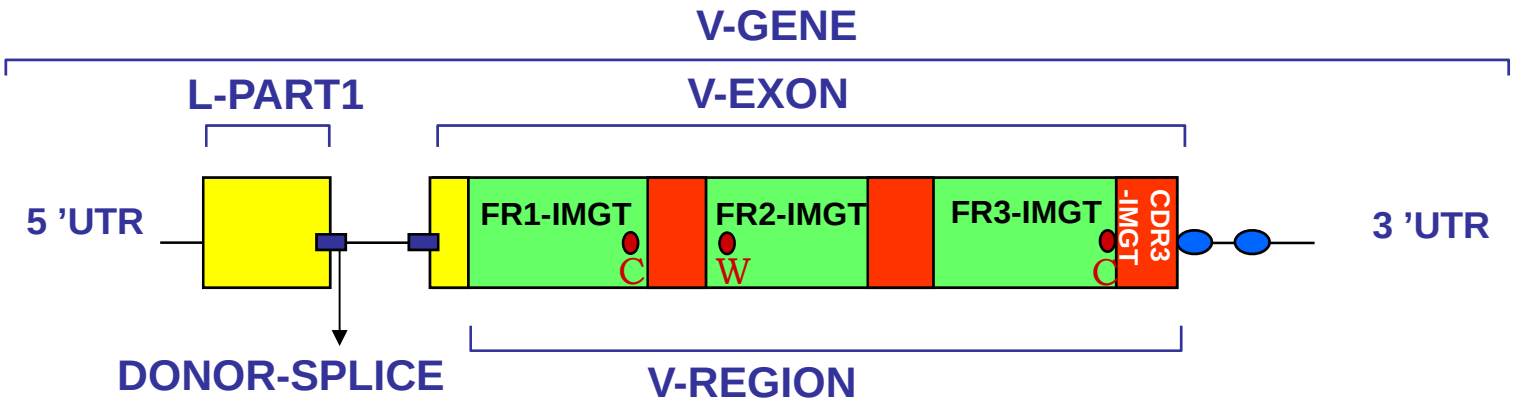
Human IGL locus (22q11.2)



IGHV1-2 immunoglobulin heavy variable 1-2 [Homo sapiens] - Gene result - Mozilla Firefox
File Edit View History Bookmarks Tools Help
http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Retrieve&dopt=Graphics&list_uids=28474
bioportal NCBO
IGHV1-2 immunoglobulin he...
NCBI Resources How To
My NCBI Sign In
Entrez Gene
Genes and mapped phenotypes
Search: Gene
Limits Advanced search Help
Search Clear
Display Settings: Full Report
Send to:
IGHV1-2 immunoglobulin heavy variable 1-2 [Homo sapiens]
Gene ID: 28474, updated on 4-Sep-2009
Summary
Official Symbol IGHV1-2 provided by HGNC
Official Full Name immunoglobulin heavy variable 1-2 provided by HGNC
Primary source HGNC:5550
See related IMGT/GENE-DB:IGHV1-2
Gene type other
RefSeq status REVIEWED
Organism Homo sapiens
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as IGHV12; IGHV1-2
Genomic regions, transcripts, and products
Table of contents
Summary
Genomic regions, transcripts, and products
Genomic context
Bibliography
General gene info
Reference sequences
Related sequences
Additional links
Links
Conserved Domains
Full text in PMC
Genome
Map Viewer
Nucleotide

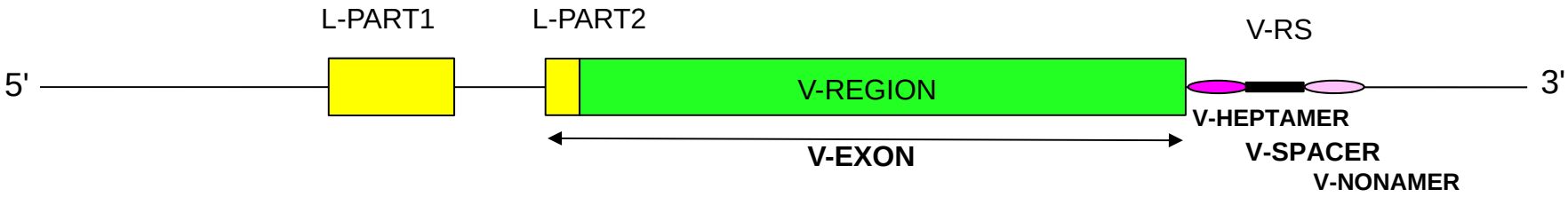
"DESCRIPTION"

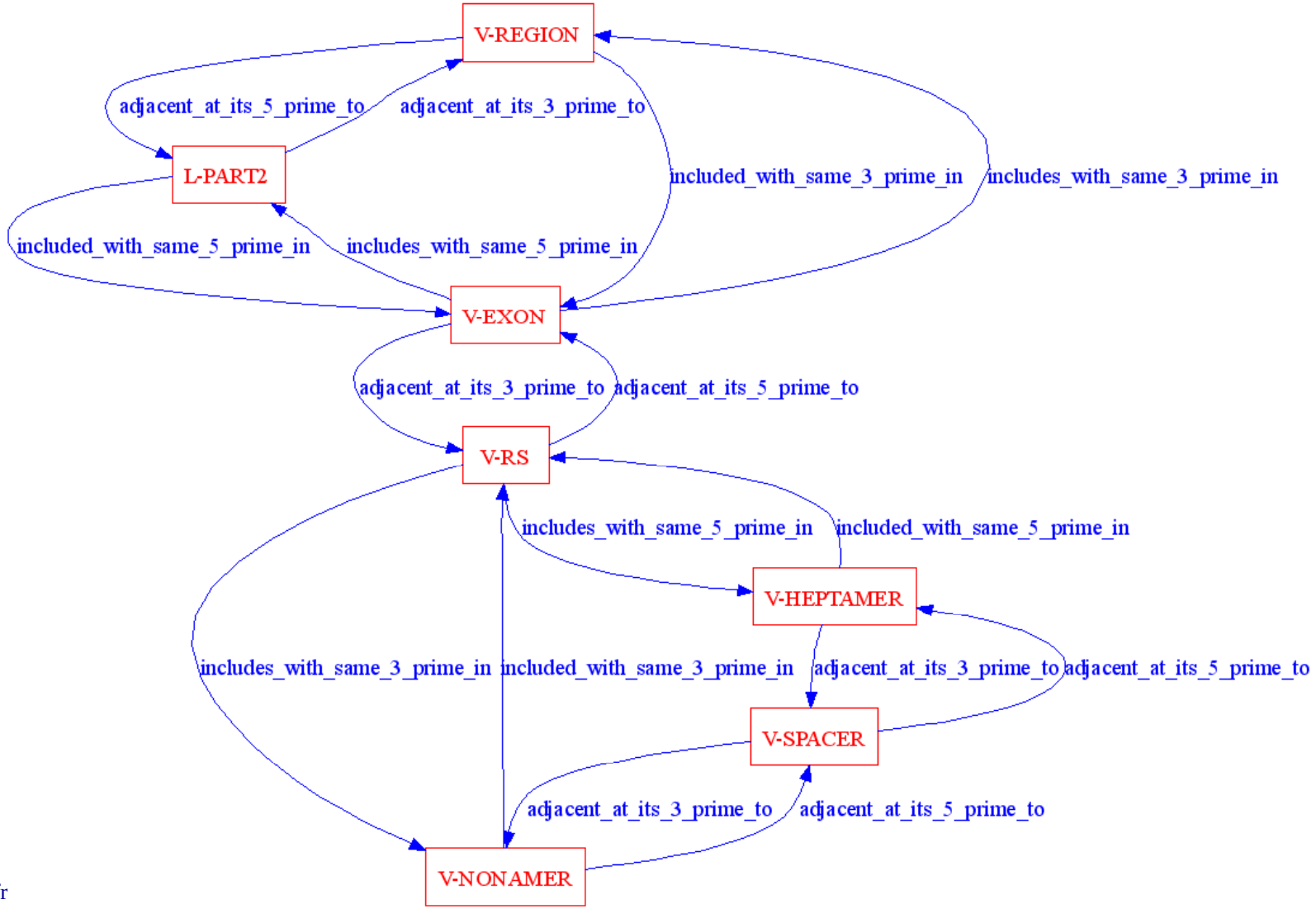
http://www.imgt.org



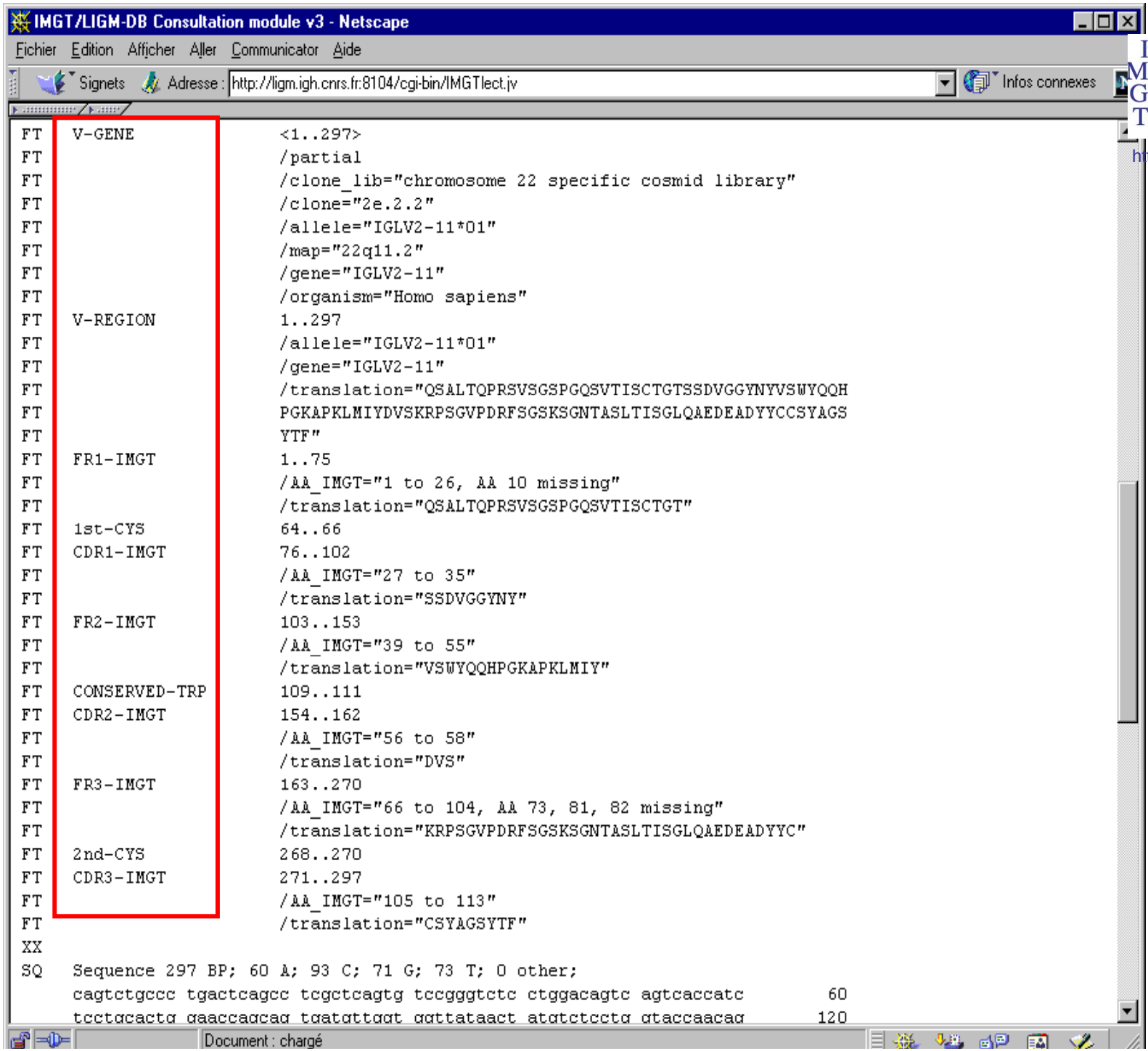
Label 1	Label	Label relations
V-GENE	V-EXON	
FR3-IMGT	CDR3-IMGT	
L-PART1	DONOR-SPLICE	
V-REGION	FR1-IMGT	
V-REGION	CDR3-IMGT	

V-GENE





http://imgt.cines.fr



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"NUMEROTATION"

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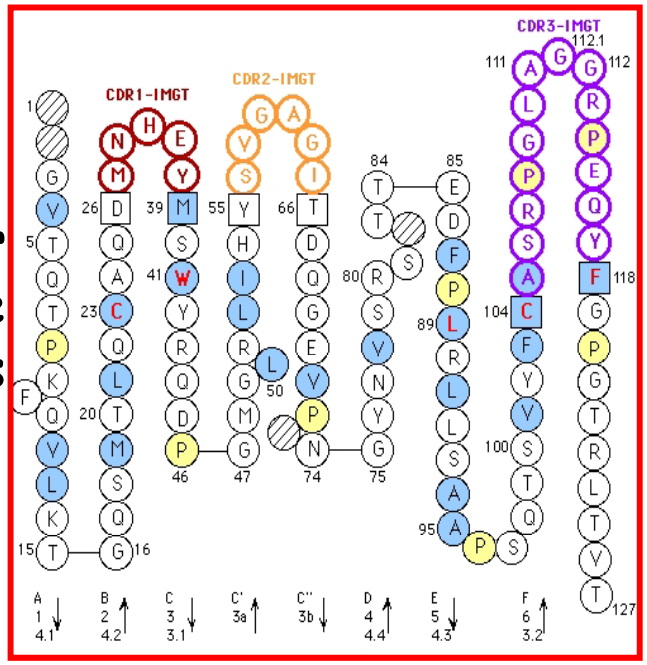
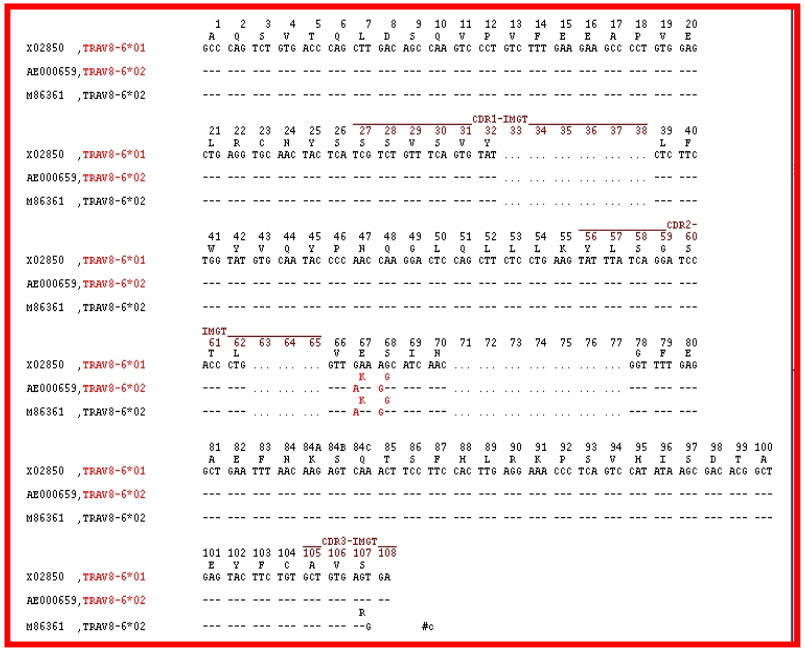
Collier De Perles





Alignment of alleles

Protein Display

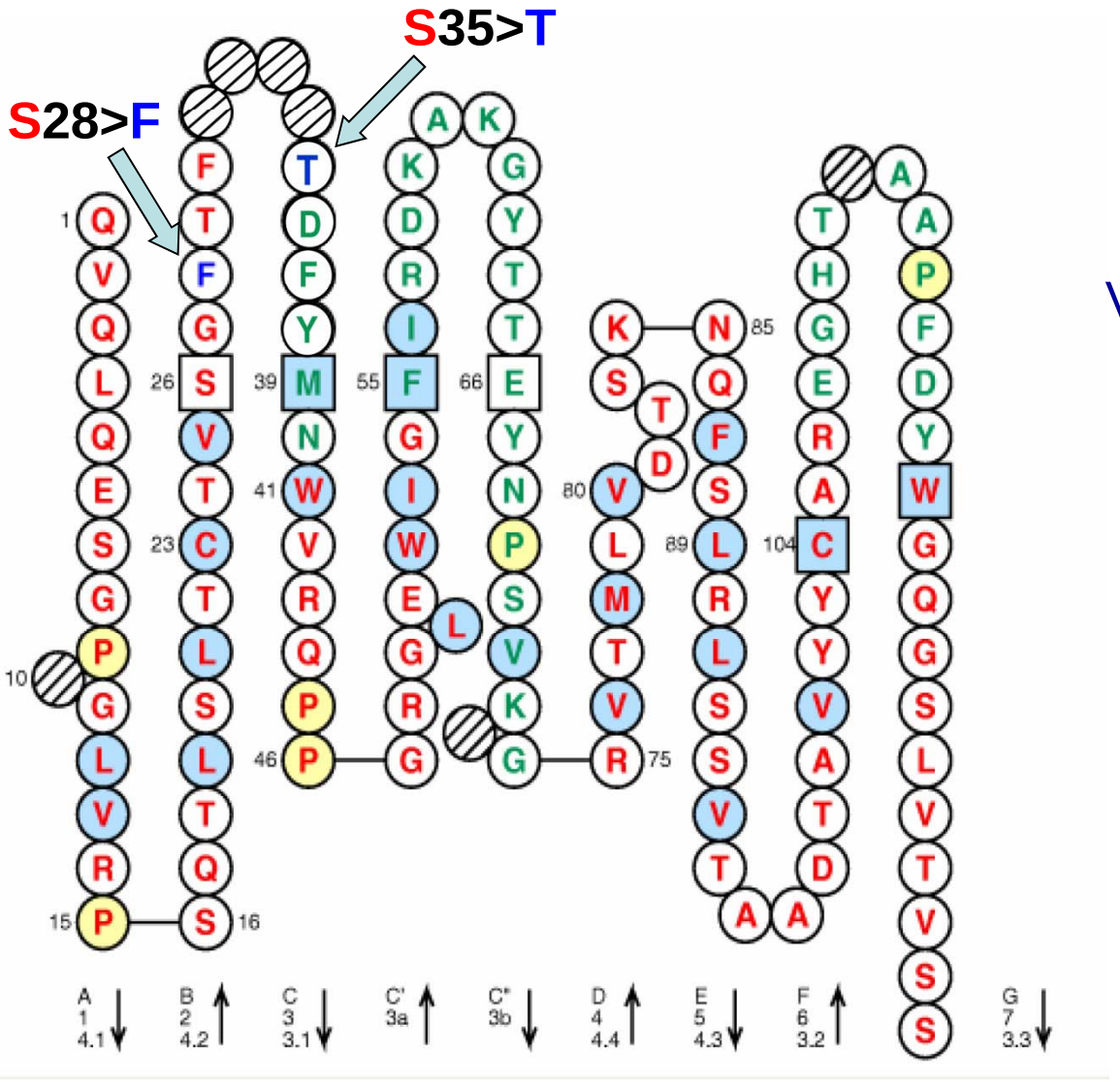
TRAV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
AE000658,TRAV1-1	GQSLEQ.PSEVTAVEGAIVQINCTYQ	TSGFYG	LSWYQQHDGGAPTFLSY	NALDG	LEETG.RFSSFLSRSDSYGYLLLQELQMKDSASYFC	AVR
AE000658,TRAV1-2	GQNIDQ.PTEMTATEGAIVQINCTYQ	TSGFNG	LFWYQQHAGEAPTFLSY	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	GDSVWQTEGQWLPSEGDSLIWNCSYE	TTQYPS	LFWYVQYPGEGPQLHLK	AMKAND	KGRNK.GFEAMYRKETTSFHLEKDSVQESDSAWYFC	ALS

Antibody humanization and engineering

Alemtuzumab (CAMPATH®)

http://www.imgt.org

2 mutations:



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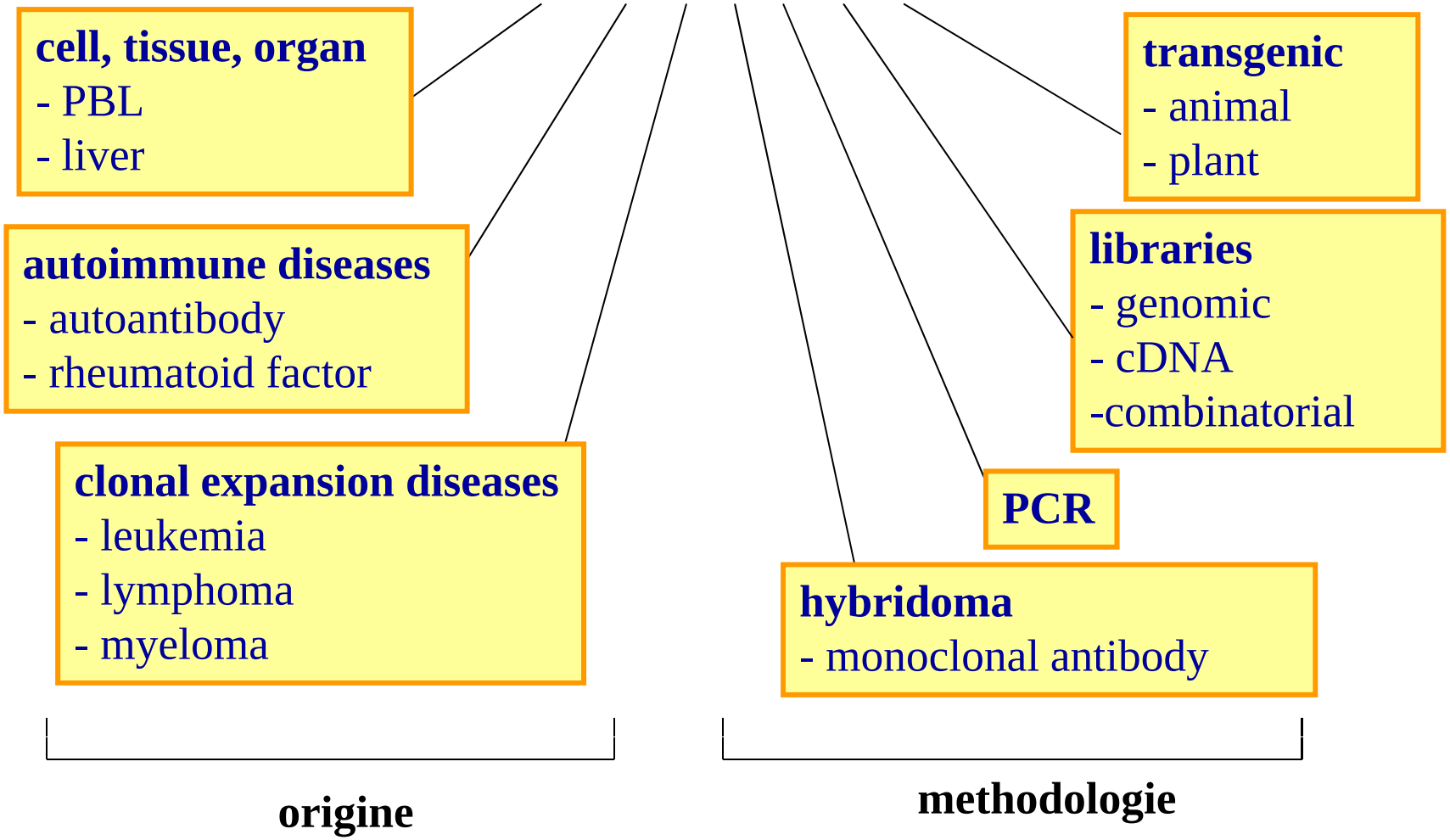
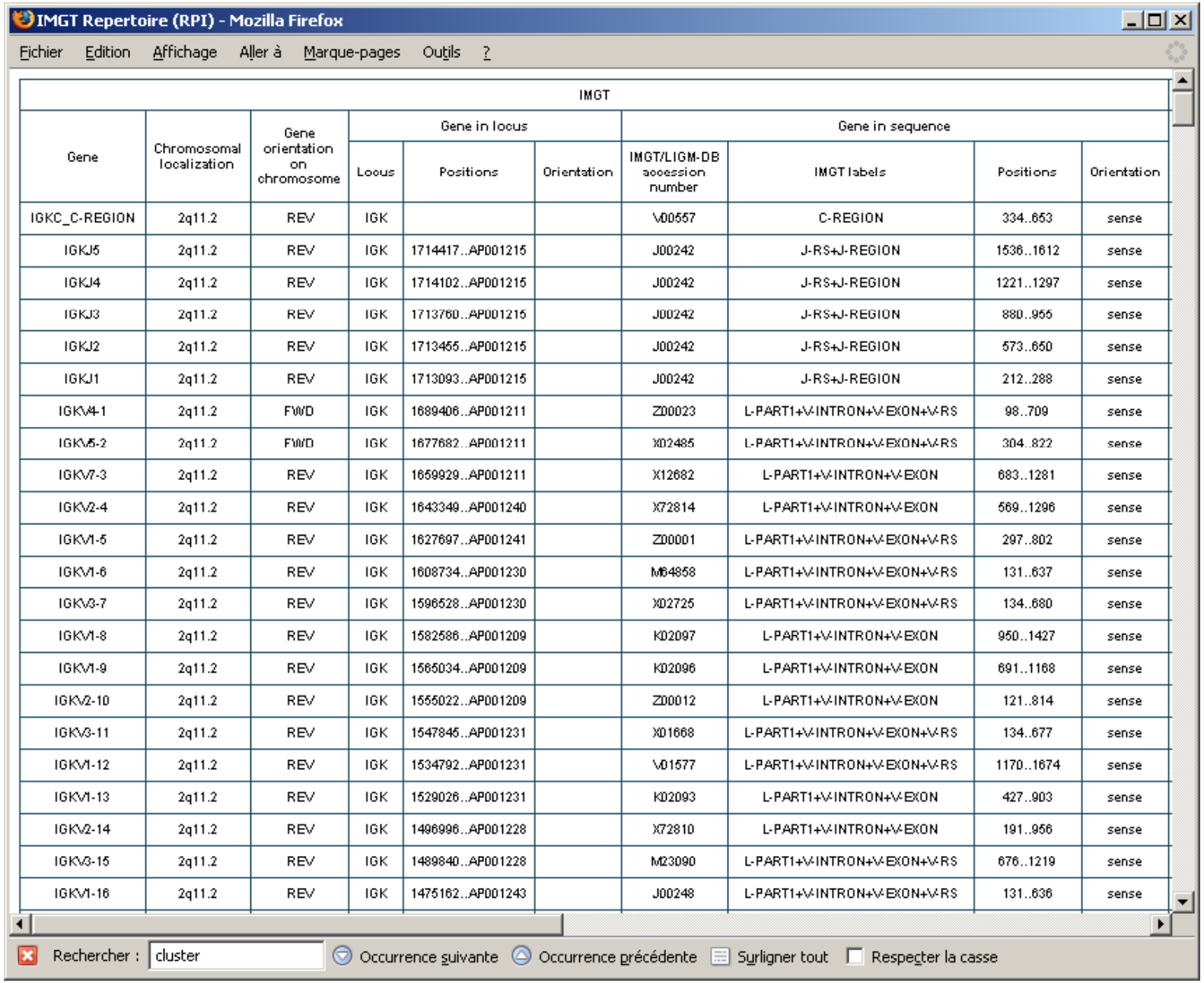
"OBTENTION"



The "OBTENTION" concepts specify the origin and methodology

"ORIENTATION"



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

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Annotation and IMGT-ONTOLOGY concepts

IDENTIFICATION

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

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```
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
RN   [2]
RP   1-366
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   ;
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.
XX
FH   Key                 Location/Qualifiers
FH
FT   L-V-D-J-C-SEQUENCE  <1..366>
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Annotation and IMGT-ONTOLOGY concepts

http://www.imgt.org

DESCRIPTION

IMGT/LIGM-DB Consultation module v3 - Mozilla Firefox

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FT                       /AA_IMGT="39 to 55"
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FT   CDR2-IMGT           133..156
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OBTENTION

CLASSIFICATION

NUMEROTATION

Les atouts de IMGT-ONTOLOGY

http://www.imgt.org

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

http://www.imgt.org

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

http://www.imgt.org

3 - Automatisation des procédures:

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

Les atouts de IMGT-ONTOLOGY

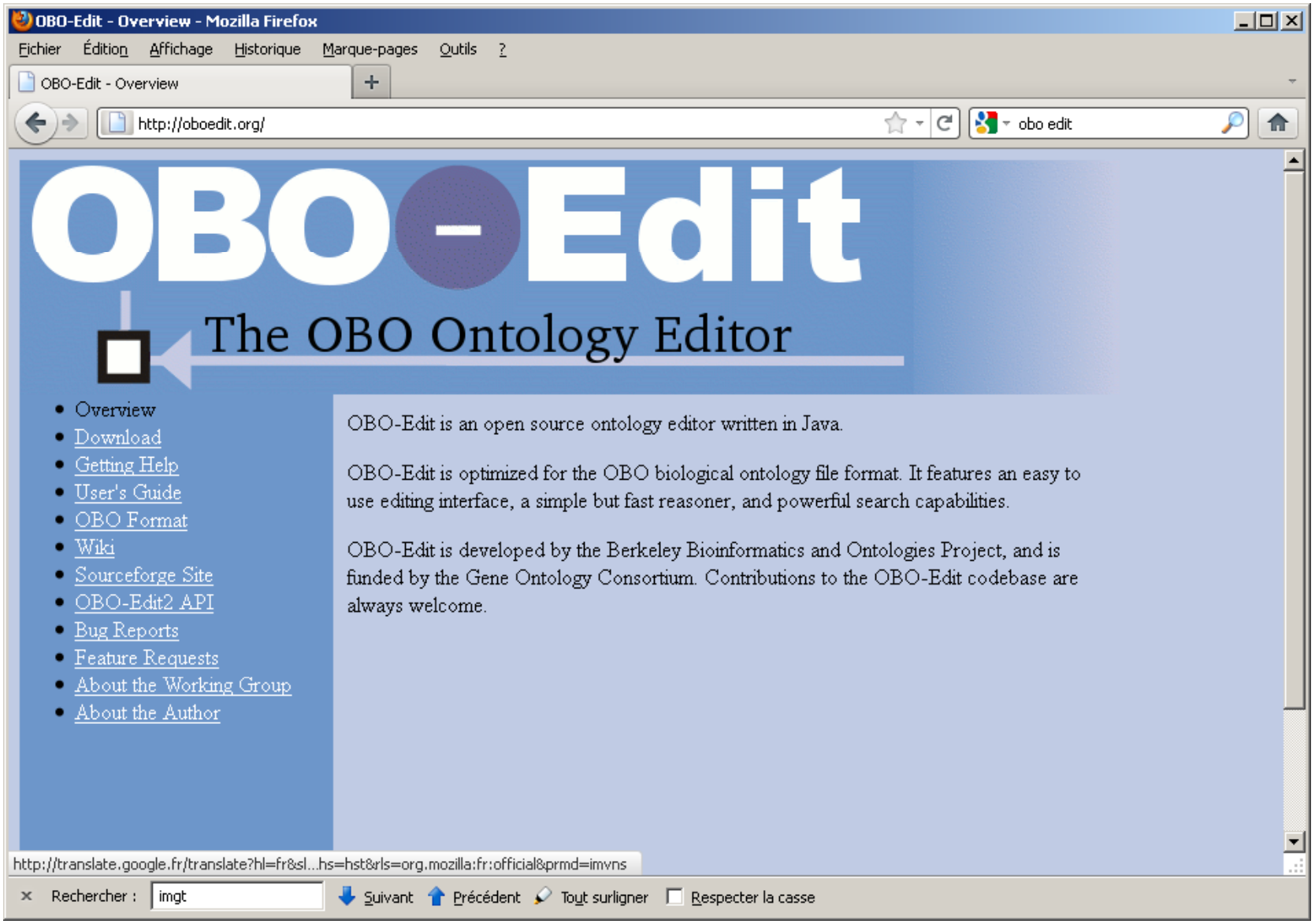
http://www.imgt.org

4 – Intégration des nouvelles connaissances en immunogénétique

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

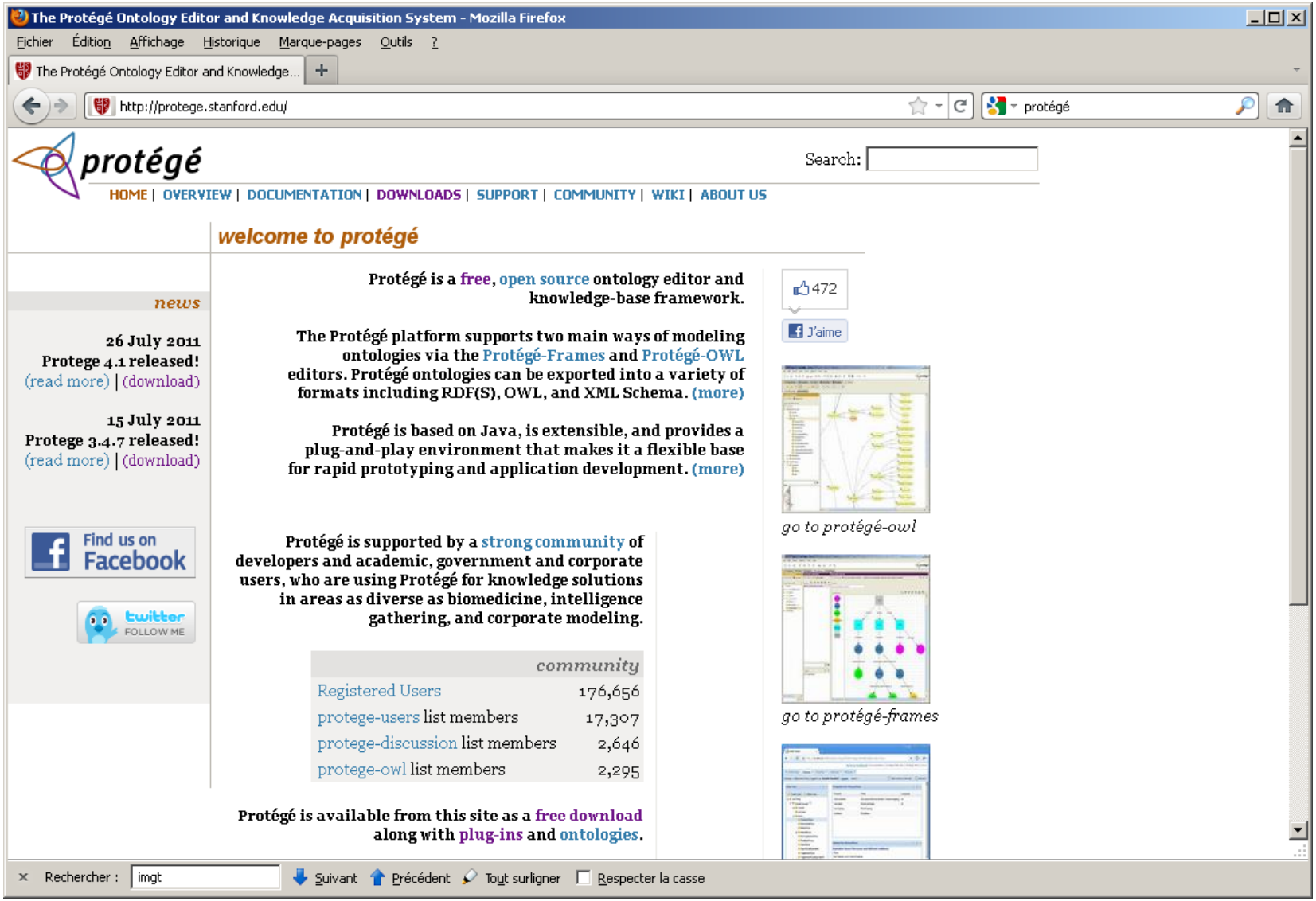
Exemple d'éditeur d'ontologie: OBO-Edit (GO, SO, …)

http://oboedit.org/



Exemple d'éditeur d'ontologie: Protégé

http://protege.stanford.edu/



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

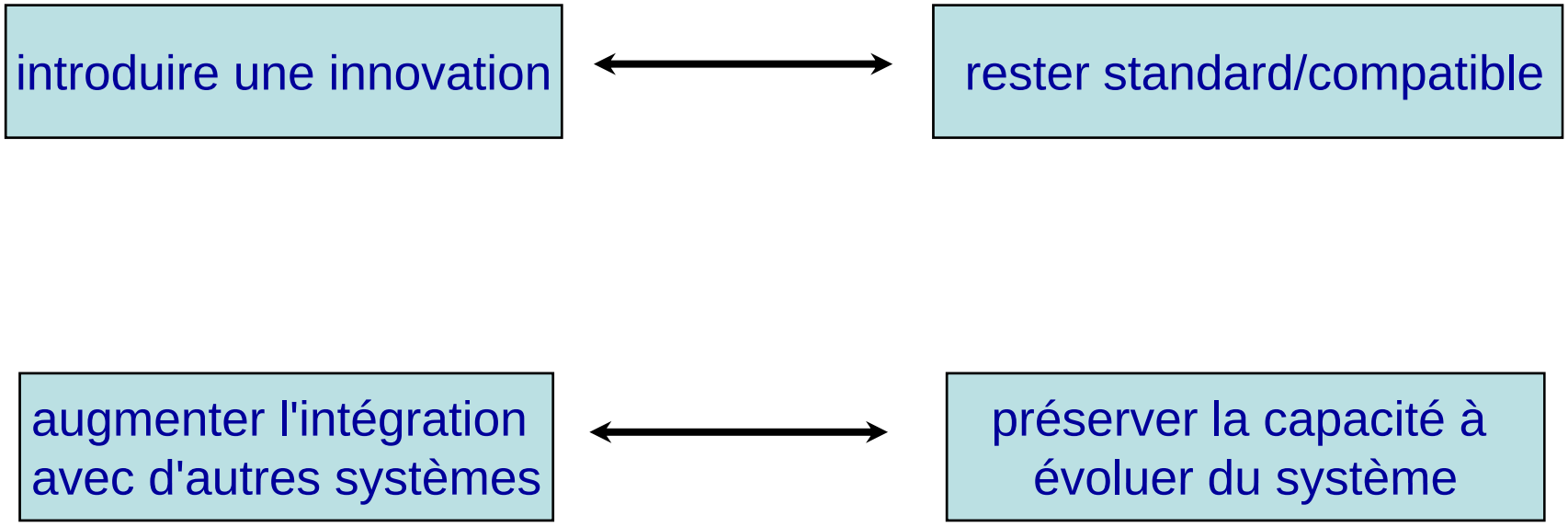
- Les systèmes d'information n'ont jamais été conçus pour durer si longtemps ou pour être résistants au temps qui passe (bug de l'an 2000)
- Il faudrait adapter certaines méthodes, standards, protocoles dépassés/oubliés.
- Les versions des outils, standards, changent plusieurs fois au cours d'un même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

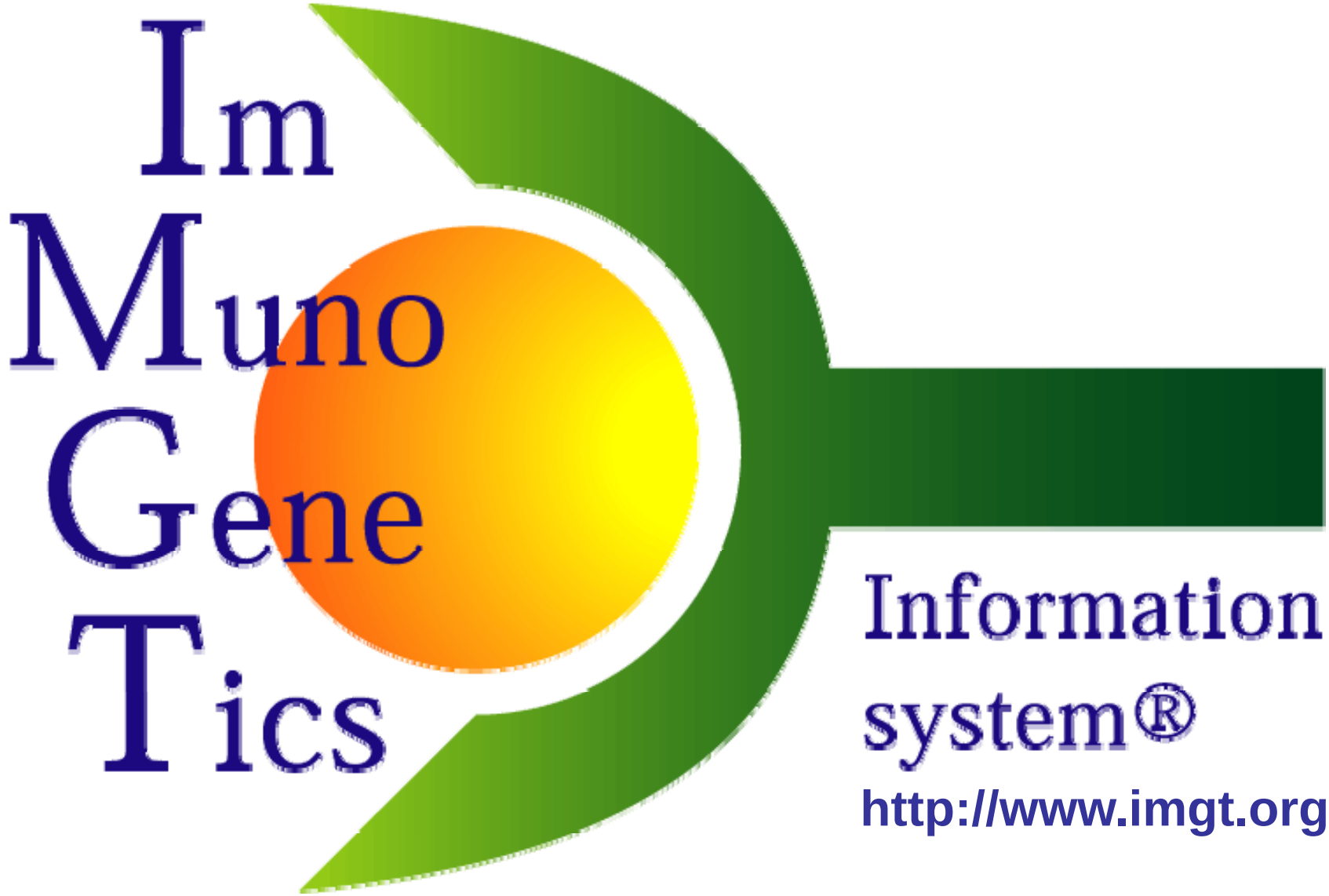
Quand c'est enfin mature, c'est déjà obsolète !

La durée de vie d'un SI dépend de

- Portabilité: il existe plusieurs plate-formes 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.**

L’équilibre des SI

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