Banques et bases de données

- Banques de données généralistes
- Banques et/ou bases de données spécialisées
- Banques de « connaissances » et autres ressources

Banques généralistes

Banques de séquences d'acides nucléiques (créées dans les années 1980):

Contiennent **toutes** les séquences d'acides nucléiques produites dans les laboratoires publiques (>100 milliards de bp, >100 millions de séquences)

Pour qu'une publication faisant référence à une ou des séquences soit acceptée, il faut que la (les) séquences ait(ent) été déposée(s) au préalable dans une de ces banques et ait(ent) obtenu un **numéro d'accession**

EMBL : la banque européenne maintenue à l'EBI (European Bioinformatics Institut) à Cambridge (UK)

GenBank : la banque américaine maintenue au NCBI (National Center for Biotechnology Information) à Bethesda (USA)

DDBJ : la banque japonaise (DNA Data Bank of Japan)

Synchronisation régulière entre ces 3 banques : INSD (International Nucleotide Sequence Database collaboration)

Exemple d'entrée dans la banque EMBL

```
ID   AY115493; SV 1; linear; genomic DNA; STD; MUS; 48787 BP.
XX
AC   AY115493;
XX
DT   03-JUL-2002 (Rel. 72, Created)
DT   03-JUL-2002 (Rel. 72, Last updated, Version 1)
XX
DE   Mus musculus transmembrane glycoprotein E11 (E11) gene, promoter region,
DE   exons 1 through 6 and complete cds.
XX
KW   .
XX
OS   Mus musculus (house mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea;
OC   Muridae; Murinae; Mus.
XX
RN   [1]
RP   1-48787
RA   Lu Y., Zhang J., Harris M.A., Harris S.E., Bonewald L., Feng J.;
RT   "Cloning and characterization studies of mouse E11 gene and its spatial and
RT   temporal expression pattern during development";
RL   Unpublished.
XX
RN   [2]
RP   1-48787
RA   Lu Y., Zhang J., Harris M.A., Harris S.E., Bonewald L., Feng J.;
RT   ;
RL   Submitted (28-MAY-2002) to the EMBL/GenBank/DDBJ databases.
RL   Oral Biology, School of Dentistry, University of Missouri-Kansas City, 650
RL   E. 25th Street, Kansas City, MO 64108, USA
XX
```

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FH   Key             Location/Qualifiers
FH
FT   source          1..48787
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FT                   /strain="129/SV"
FT                   /mol_type="genomic DNA"
FT                   /db_xref="taxon:10090"
FT   promoter        1..9640
FT                   /gene="E11"
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FT                   40324..40435,41199..42193)
FT                   /gene="E11"
FT                   /product="transmembrane glycoprotein E11"
FT   exon            9641..9915
FT                   /gene="E11"
FT                   /number=1
FT   CDS             join(9849..9915,33318..33454,35464..35620,39063..39101,
FT                   40324..40435,41199..41205)
FT                   /codon_start=1
FT                   /gene="E11"
FT                   /product="transmembrane glycoprotein E11"
FT                   /note="gp38; PA2.26; OTS8"
FT                   /db_xref="GOA:Q62011"
FT                   /db_xref="InterPro:IPR008783"
FT                   /db_xref="MGI:103098"
FT                   /db_xref="UniProtKB/Swiss-Prot:Q62011"
FT                   /protein_id="AAM66761.1"
FT                   /translation="MWTVPVLFWVLGSVWFWDSAQGGTIGVNEDDIVTPGTGDGMVPPG
FT                   IEDKITTTGATGGLNESTGKAPLVPTQRERGTKPPLEELSTSATSDHDHREHESTTTVK
FT                   VVTSHSVDKKTSHPNRDNAGDETQTTDKKDGLPVVTLVGIIVGVLLAIGFVGGIFIVVM
FT                   KKISGRFSP"
FT   exon            33318..33454
FT                   /gene="E11"
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FT                   /number=3
FT   exon            39063..39101
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FT                   /number=5
FT   exon            41199..42193
FT                   /gene="E11"
FT                   /number=6
FT   polyA_signal    42172..42177
FT                   /gene="E11"
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Exemple d'entrée dans la banque EMBL (suite)

Exemple d'entrée dans la banque EMBL

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SQ   Sequence 48787 BP; 12689 A; 11292 C; 11677 G; 13094 T; 35 other;
     tatagtcact cttgccaatt gcactaagga taacccaacc ttggtttaaa aaaaaaaatc        60
     ctgactcaaa gatgaatttc acacttagca gagacattta cctgccaaga aagacacaat       120
     gcacccccat gtcagctccc ctccacctca ccccatgaca ccccaaagcc tgtggtgctt       180
     tcttaagaga ggctgttcga acaccgtgtc ctactgcttt ccactgccag gacgacaggc       240
     aattcttcag cctaggtaaa cttcaggaaa ataaagttta atcaagagct gtgtctggtg       300
     acggctttct taacatgaga atccaaaggg gtagctatat gacctggaaa aagacagtga       360
     ttcaggggtg tacacgtggt tgtgtacttg cctctgtgtg catctgcgtg tgtgtatgtc       420
     tctctgtgtg tgcacacccg agtggcgaat gtttgtatgt agtgtgtgta tgtatgtgtg       480
     tgtgtctgtg tgctgtgtgg tatatgtgtg tgcgcgcgtg agagtgtgta atgtgtctgg       540
     gctctccttg ttataaaatc accaggatcc cactatgaca cgcacatacg aactgccttc       600
     caaaggtccc acctctgaat gacacaaccc cgtcgcttat cctctcagca cctcaaagag       660
     aagattaatt tttcaacaca ggaatccttt ggggacgact tccaaaccgc agcacacagc       720
     aaccctgaat gaaatctgca cgtctggggg caacgctcca ccttaggagc aagcatagct       780
     gagggctttg tgtttctgta tcaaagtcca aagtggaaaa agaacagagg acgggggaag       840
     ..............
     gcaaagctct aggtcaatga gaaaccctgt ctcaaacaaa agggagaagc ccctaaggcc     48600
     tgacagctgg ggtttgtctt ctgatttcca tgcgcatgag cacggatatg cacacatata     48660
     cctgcataca cacacacaca cacacacaca cacacacaca agcatactcg tgcacatatg     48720
     tgcattcata taaacacata cacacaaaaa tgaaccttat cttatttaat tacttttttt     48780
     ggcacag                                                              48787
//
```

Exemple d'entrée dans la banque GenBank

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LOCUS       AY115493               48787 bp    DNA     linear   ROD 05-JUN-2006
DEFINITION  Mus musculus transmembrane glycoprotein E11 (E11) gene, promoter
            region, exons 1 through 6 and complete cds.
ACCESSION   AY115493
VERSION     AY115493.1  GI:21684686
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48787)
  AUTHORS   Zhang,K., Barragan-Adjemian,C., Ye,L., Kotha,S., Dallas,M., Lu,Y.,
            Zhao,S., Harris,M., Harris,S.E., Feng,J.Q. and Bonewald,L.F.
  TITLE     E11/gp38 Selective Expression in Osteocytes: Regulation by
            Mechanical Strain and Role in Dendrite Elongation
  JOURNAL   Mol. Cell. Biol. 26 (12), 4539-4552 (2006)
   PUBMED   16738320
REFERENCE   2  (bases 1 to 48787)
  AUTHORS   Lu,Y., Zhang,J., Harris,M.A., Harris,S.E., Bonewald,L. and Feng,J.
  TITLE     Cloning and characterization studies of mouse E11 gene and its
            spatial and temporal expression pattern during development
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 48787)
  AUTHORS   Lu,Y., Zhang,J., Harris,M.A., Harris,S.E., Bonewald,L. and Feng,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAY-2002) Oral Biology, School of Dentistry,
            University of Missouri-Kansas City, 650 E. 25th Street, Kansas
            City, MO 64108, USA
```

```
FEATURES             Location/Qualifiers
     source          1..48787
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129/Sv"
                     /db_xref="taxon:10090"
     gene            1..42193
                     /gene="E11"
     promoter        1..9640
                     /gene="E11"
     mRNA            join(9641..9915,33318..33454,35464..35620,39063..39101,
                     40324..40435,41199..42193)
                     /gene="E11"
                     /product="transmembrane glycoprotein E11"
     exon            9641..9915
                     /gene="E11"
                     /number=1
     CDS             join(9849..9915,33318..33454,35464..35620,39063..39101,
                     40324..40435,41199..41205)
                     /gene="E11"
                     /note="gp38; PA2.26; OTS8"
                     /codon_start=1
                     /product="transmembrane glycoprotein E11"
                     /protein_id="AAM66761.1"
                     /db_xref="GI:21684687"
                     /translation="MWTVPVLFWVLGSVWFWDSAQGGTIGVNEDDIVTPGTGDGMVPP
                     GIEDKITTTGATGGLNESTGKAPLVPTQRERGTKPPLEELSTSATSDHDHREHESTTT
                     VKVVTSHSVDKKTSHPNRDNAGDETQTTDKKDGLPVVTLVGIIVGVLLAIGFVGGIFI
                     VVMKKISGRFSP"
     exon            33318..33454
                     /gene="E11"
                     /number=2
     exon            35464..35620
                     /gene="E11"
                     /number=3
     exon            39063..39101
                     /gene="E11"
                     /number=4
     exon            40324..40435
                     /gene="E11"
                     /number=5
     exon            41199..42193
                     /gene="E11"
                     /number=6
     polyA_signal    42172..42177
                     /gene="E11"
```

Exemple d'entrée dans la banque GenBank (suite)

Banques généralistes

Banques de séquences protéiques :

Les deux plus importantes :

SwissProt (1986) : banque manuellement annotée et « nettoyée »

PIR/NBRF (1984) : banque américaine fournissant une classification des protéines basée sur la similarité entre les séquences.

TrEMBL : traduction automatique des CDS d'EMBL
GenPept : traduction automatique des CDS de GenBank

En 2002, création du consortium **UniProt** (Universal Protein Resource) constitué par le groupe SwissProt-TrEMBL et le groupe PIR

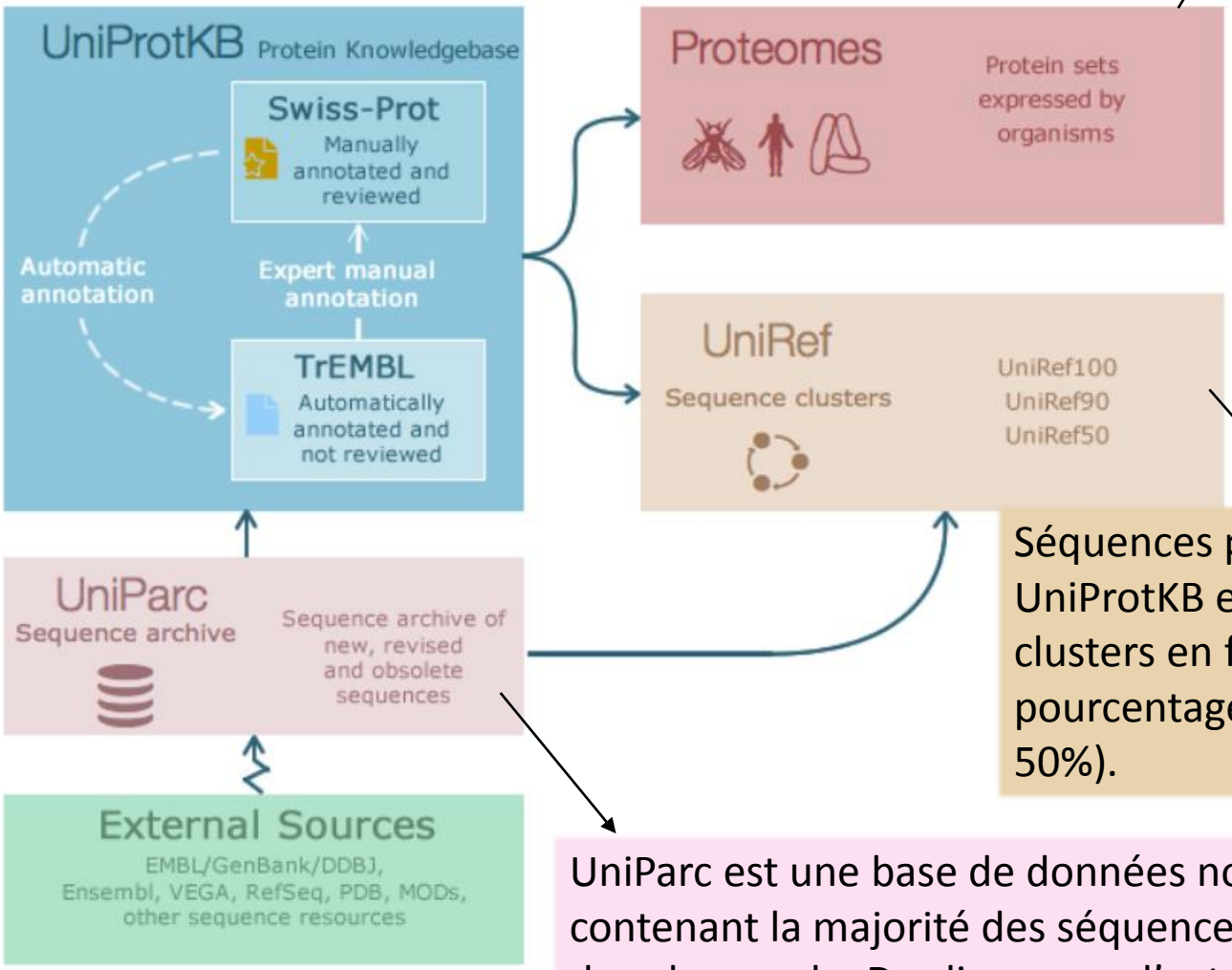
But : fournir une seule ressource centralisée pour les séquences protéiques et les annotations fonctionnelles

Maintien de deux sections enrichies de la classification automatique de PIR : **UniProt/SwissProt** (annotée et « nettoyée »)
UniProt/TrEMBL

UniProt aujourd'hui: > 71 millions de séquences

UniProtKB

Séquences protéiques des génomes complétement séquencés



Séquences protéiques provenant de UniProtKB et UniParc regroupées en clusters en fonction de leur pourcentage d'identité (100%, 90%, 50%).

UniParc est une base de données non redondante contenant la majorité des séquences protéiques disponibles dans le monde. Des liens vers d'autres bases de données permettent d'accéder à des informations complémentaires.

Exemple d'entrée dans la banque SwissProt

```
ID   PDPN_MOUSE     STANDARD;      PRT;   172 AA.
AC   Q62011; Q546R8; Q61612;
DT   01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 2.
DT   19-SEP-2006, entry version 45.
DE   Podoplanin precursor (Glycoprotein 38) (Gp38) (OTS-8) (PA2.26 antigen)
DE   (Aggrus) (T1A) (T1-alpha) (Transmembrane glycoprotein E11).
GN   Name=Pdpn; Synonyms=Gp38, Ots8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91207913; PubMed=2088477;
RA   Nose K., Saito H., Kuroki T.;
RT   "Isolation of a gene sequence induced later by tumor-promoting 12-O-
RT   tetradecanoylphorbol-13-acetate in mouse osteoblastic cells (MC3T3-E1)
RT   and expressed constitutively in ras-transformed cells.";
RL   Cell Growth Differ. 1:511-518(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=BALB/c;
RX   MEDLINE=93018879; PubMed=1402691; DOI=10.1084/jem.176.5.1477;
RA   Farr A.G., Berry M.L., Kim A., Nelson A.J., Welch M.P., Aruffo A.;
RT   "Characterization and cloning of a novel glycoprotein expressed by
RT   stromal cells in T-dependent areas of peripheral lymphoid tissues.";
RL   J. Exp. Med. 176:1477-1482(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 24-30 AND 66-73,
RP   FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND GLYCOSYLATION.
RX   MEDLINE=20044810; PubMed=10574709;
RA   Scholl F.G., Gamallo C., Vilaro S., Quintanilla M.;
RT   "Identification of PA2.26 antigen as a novel cell-surface mucin-type
RT   glycoprotein that induces plasma membrane extensions and increased
RT   motility in keratinocytes.";
RL   J. Cell Sci. 112:4601-4613(1999)
```

Exemple d'entrée dans la banque SwissProt (suite)

```
CC   -!- FUNCTION: May be involved in cell migration and/or actin
CC       cytoskeleton organization. When expressed in keratinocytes,
CC       induces changes in cell morphology with transfected cells showing
CC       an elongated shape, numerous membrane protrusions, major
CC       reorganization of the actin cytoskeleton, increased motility and
CC       decreased cell adhesion. Required for normal lung cell
CC       proliferation and alveolus formation at birth. Induces platelet
CC       aggregation. Does not have any effect on folic acid or amino acid
CC       transport. Does not function as a water channel or as a regulator
CC       of aquaporin-type water channels.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein. Localized to actin-rich microvilli and plasma membrane
CC       projections such as filopodia, lamellipodia and ruffles.
CC   -!- TISSUE SPECIFICITY: Detected at high levels in lung and brain, at
CC       lower levels in kidney, stomach, liver, spleen and esophagus, and
CC       not detected in skin and small intestine. Expressed in epithelial
CC       cells of choroid plexus, ependyma, glomerulus and alveolus, in
CC       mesothelial cells and in endothelia of lymphatic vessels. Also
CC       expressed in stromal cells of peripheral lymphoid tissue and
CC       thymic epithelial cells. Detected in carcinoma cell lines and
CC       cultured fibroblasts. Expressed at higher levels in colon
CC       carcinomas than in normal colon tissue.
CC   -!- INDUCTION: Down-regulated by treatment with puromycin
CC       aminonucleoside.
CC   -!- PTM: Extensively O-glycosylated. Contains sialic acid residues. O-
CC       glycosylation is necessary for platelet aggregation activity.
CC   -!- PTM: The N-terminus is blocked (By similarity).
CC   -!- MISCELLANEOUS: Mice lacking Pdpn die at birth of respiratory
CC       failure due to a low number of attenuated type I cells, narrow and
CC       irregular air spaces, and defective formation of alveolar
CC       saccules.
CC   -!- SIMILARITY: Belongs to the podoplanin family.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
```

Exemple d'entrée dans la banque SwissProt (suite)

```
DR   EMBL; M73748; AAA39866.1; -; mRNA.
DR   EMBL; M96645; AAA37724.1; -; mRNA.
DR   EMBL; AJ250246; CAB58997.1; -; mRNA.
DR   EMBL; AJ297944; CAC16152.1; -; mRNA.
DR   EMBL; AY115493; AAM66761.1; -; Genomic_DNA.
DR   EMBL; AK158855; BAE34695.1; -; mRNA.
DR   EMBL; BC026551; AAH26551.1; -; mRNA.
DR   Ensembl; ENSMUSG00000028583; Mus musculus.
DR   KEGG; mmu:14726; -.
DR   MGI; MGI:103098; Pdpn.
DR   ArrayExpress; Q62011; -.
DR   RZPD-ProtExp; IOM20239; -.
DR   GO; GO:0030175; C:filopodium; IDA.
DR   GO; GO:0030027; C:lamellipodium; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0001726; C:ruffle; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0001946; P:lymphangiogenesis; IMP.
DR   GO; GO:0051272; P:positive regulation of cell motility; IDA.
DR   InterPro; IPR008783; Podoplanin.
DR   PANTHER; PTHR16861; Podoplanin; 1.
DR   Pfam; PF05808; Podoplanin; 1.
KW   Cell shape; Developmental protein; Direct protein sequencing;
KW   Glycoprotein; Membrane; Sialic acid; Signal; Transmembrane.
FT   SIGNAL        1     22       Potential.
FT   CHAIN        23    172       Podoplanin.
FT                                 /FTId=PRO_0000021352.
FT   TOPO_DOM     23    141       Extracellular (Potential).
FT   TRANSMEM    142    162       Potential.
FT   TOPO_DOM    163    172       Cytoplasmic.
.....................
FT   CONFLICT     29     31       EDD -> KNN (in Ref. 2).
FT   CONFLICT     38     39       GD -> EN (in Ref. 1).
SQ   SEQUENCE   172 AA;  18233 MW;  C035ED251918CE6F CRC64;
     MWTVPVLFWV LGSVWFWDSA QGGTIGVNED DIVTPGTGDG MVPPGIEDKI TTTGATGGLN
     ESTGKAPLVP TQRERGTKPP LEELSTSATS DHDHREHEST TTVKVVTSHS VDKKTSHPNR
     DNAGDETQTT DKKDGLPVVT LVGIIVGVLL AIGFVGGIFI VVMKKISGRF SP
//
```

Banques généralistes

Banques de structures :

La Protein Database (PDB) stockent les structures protéiques obtenues par RMN ou cristallographie

Une entrée contient donc les coordonnées de tous les atomes de la structure

Exemple d'entrée dans la banque PDB

```
HEADER    PERIPLASMIC BINDING PROTEIN            17-AUG-97   4MBP
TITLE     MALTODEXTRIN BINDING PROTEIN WITH BOUND MALTETROSE
COMPND    MOL_ID: 1;
COMPND   2 MOLECULE: MALTODEXTRIN BINDING PROTEIN;
COMPND   3 CHAIN: NULL
SOURCE    MOL_ID: 1;
SOURCE   2 ORGANISM_SCIENTIFIC: ESCHERICHIA COLI;
SOURCE   3 STRAIN: K12;
SOURCE   4 CELLULAR_LOCATION: PERIPLASM;
SOURCE   5 GENE: MALE
KEYWDS    PERIPLASMIC BINDING PROTEIN, TRANSPORT, SUGAR TRANSPORT
EXPDTA    X-RAY DIFFRACTION
AUTHOR    J.C.SPURLINO,F.A.QUIOCHO
REVDAT   1   25-FEB-98 4MBP    0
JRNL        AUTH   F.A.QUIOCHO,J.C.SPURLINO,L.E.RODSETH
JRNL        TITL   EXTENSIVE FEATURES OF TIGHT OLIGOSACCHARIDE BINDING
JRNL        TITL 2 REVEALED IN HIGH-RESOLUTION STRUCTURES OF THE
JRNL        TITL 3 MALTODEXTRIN TRANSPORT/CHEMOSENSORY RECEPTOR
JRNL        REF    STRUCTURE (LONDON)            V.   5   997 1997
JRNL        REFN   ASTM STRUE6  UK ISSN 0969-2126                2005
REMARK   1
REMARK   1 REFERENCE 1
REMARK   1  AUTH   A.J.SHARFF,L.E.RODSETH,F.A.QUIOCHO
REMARK   1  TITL   REFINED 1.8-A STRUCTURE REVEALS THE MODE OF BINDING
REMARK   1  TITL 2 OF BETA-CYCLODEXTRIN TO THE MALTODEXTRIN BINDING
REMARK   1  TITL 3 PROTEIN
REMARK   1  REF    BIOCHEMISTRY                  V.  32 10553 1993
REMARK   1  REFN   ASTM BICHAW  US ISSN 0006-2960                0033
REMARK   2 RESOLUTION. 1.7  ANGSTROMS.
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : PROLSQ
REMARK   3   AUTHORS     : KONNERT,HENDRICKSON
REMARK   3
REMARK   3  DATA USED IN REFINEMENT.
REMARK   3   RESOLUTION RANGE HIGH (ANGSTROMS) : 1.7
REMARK   3   RESOLUTION RANGE LOW  (ANGSTROMS) : 10.0
REMARK   3   DATA CUTOFF            (SIGMA(F)) : 2.0
REMARK   3   COMPLETENESS FOR RANGE        (%) : 89.
REMARK   3   NUMBER OF REFLECTIONS             : 29814
REMARK   3
REMARK   3  FIT TO DATA USED IN REFINEMENT.
REMARK   3   CROSS-VALIDATION METHOD          : NULL
REMARK   3   FREE R VALUE TEST SET SELECTION  : NULL
REMARK   3   R VALUE     (WORKING + TEST SET) : NULL
```

Exemple d'entrée dans la banque PDB (suite)

```
DBREF  4MBP      1   370  SWS    P02928   MALE_ECOLI      27    396
SEQRES   1    370  LYS ILE GLU GLU GLY LYS LEU VAL ILE TRP ILE ASN GLY
.............
SEQRES  27    370  PHE TRP TYR ALA VAL ARG THR ALA VAL ILE ASN ALA ALA
SEQRES  28    370  SER GLY ARG GLN THR VAL ASP GLU ALA LEU LYS ASP ALA
SEQRES  29    370  GLN THR ARG ILE THR LYS
..............
ATOM      1  N   LYS     1     -14.189  28.577  49.986  1.00 59.37           N
ATOM      2  CA  LYS     1     -14.427  27.969  48.643  1.00 60.26           C
ATOM      3  C   LYS     1     -14.388  26.456  48.756  1.00 60.10           C
ATOM      4  O   LYS     1     -14.139  25.752  47.779  1.00 60.59           O
ATOM      5  CB  LYS     1     -13.396  28.459  47.636  1.00 60.34           C
ATOM      6  N   ILE     2     -14.546  25.990  49.995  1.00 60.57           N
ATOM      7  CA  ILE     2     -14.875  24.597  50.323  1.00 59.62           C
ATOM      8  C   ILE     2     -15.574  23.742  49.238  1.00 59.40           C
ATOM      9  O   ILE     2     -15.081  22.687  48.873  1.00 60.19           O
ATOM     10  CB  ILE     2     -15.681  24.585  51.659  1.00 58.28           C
ATOM     11  CG1 ILE     2     -14.724  24.301  52.826  1.00 59.82           C
ATOM     12  CG2 ILE     2     -16.838  23.622  51.603  1.00 57.23           C
ATOM     13  CD1 ILE     2     -15.337  24.388  54.226  1.00 59.04           C
ATOM     14  N   GLU     3     -16.602  24.290  48.599  1.00 61.26           N
ATOM     15  CA  GLU     3     -17.646  23.482  47.944  1.00 61.93           C
ATOM     16  C   GLU     3     -18.288  22.453  48.893  1.00 62.35           C
ATOM     17  O   GLU     3     -19.019  22.844  49.814  1.00 62.86           O
ATOM     18  CB  GLU     3     -17.108  22.769  46.711  1.00 61.59           C
ATOM     19  CG  GLU     3     -18.212  22.251  45.809  1.00 60.99           C
ATOM     20  CD  GLU     3     -18.778  23.313  44.867  1.00 63.62           C
ATOM     21  OE1 GLU     3     -18.216  24.442  44.804  1.00 63.52           O
ATOM     22  OE2 GLU     3     -19.806  23.016  44.199  1.00 64.93           O
ATOM     23  N   GLU     4     -17.924  21.178  48.713  1.00 60.97           N
ATOM     24  CA  GLU     4     -18.411  20.010  49.472  1.00 59.71           C
ATOM     25  C   GLU     4     -19.240  19.084  48.606  1.00 57.65           C
ATOM     26  O   GLU     4     -19.990  19.524  47.740  1.00 58.14           O
ATOM     27  CB  GLU     4     -19.222  20.381  50.704  1.00 60.49           C
ATOM     28  CG  GLU     4     -20.145  19.273  51.192  1.00 66.79           C
ATOM     29  CD  GLU     4     -19.416  17.960  51.537  1.00 71.32           C
ATOM     30  OE1 GLU     4     -18.345  18.014  52.202  1.00 74.47           O
ATOM     31  OE2 GLU     4     -19.941  16.873  51.166  1.00 71.40           O
ATOM     32  N   GLY     5     -19.052  17.787  48.793  1.00 56.22           N
ATOM     33  CA  GLY     5     -19.860  16.837  48.055  1.00 56.05           C
ATOM     34  C   GLY     5     -19.171  16.369  46.800  1.00 54.46           C
ATOM     35  O   GLY     5     -19.574  15.345  46.223  1.00 54.62           O
.............
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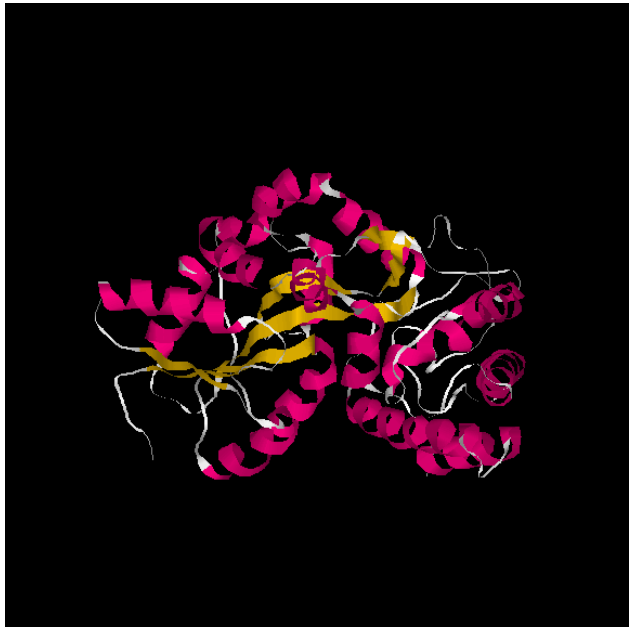


Banques/bases de données spécialisées

Chaque année, en janvier, le journal Nucleic Acids Research publie un numéro spécial dédié aux bases de données

The 2015 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection

Michael Y. Galperin, Daniel J. Rigden and Xosé M. Fernández-Suárez.

The 2015 *Nucleic Acids Research* Database Issue contains 172 papers that include descriptions of 56 new molecular biology databases, and updates on 115 databases whose descriptions have been previously published in *NAR* or other journals. Following the classification that has been introduced last year in order to simplify navigation of the entire issue, these articles are divided into eight subject categories. This year's highlights include RNAcentral, an international community portal to various databases on noncoding RNA; ValidatorDB, a validation database for protein structures and their ligands; SASBDB, a primary repository for small-angle scattering data of various macromolecular complexes; MoonProt, a database of 'moonlighting' proteins, and two new databases of protein–protein and other macromolecular complexes, ComPPI and the Complex Portal. This issue also includes an unusually high number of cancer-related databases and other databases dedicated to genomic basics of disease and potential drugs and drug targets. The size of *NAR* online Molecular Biology Database Collection, http://www.oxfordjournals.org/nar/database/a/, remained approximately the same, following the addition of 74 new resources and removal of 77 obsolete web sites. The entire Database Issue is freely available online on the *Nucleic Acids Research* web site (http://nar.oxfordjournals.org/).

En 2014, **1552** bases de données étaient répertoriées dans cette collection

Banques/bases de données spécialisées

Certaines modélisent des chemins métaboliques ou des processus de régulation :

- Regulondb (regulation) et EcoCyc (métabolisme) pour *E. coli*
- Extension de EcoCyc à MetaCyc (multiorganismes, surtout microorganismes et plantes) et AraCyc (Arabidopsis thaliana)

- KEGG : Kyoto Encyclopedia of Genes and Genomes

  Quatre parties :

  - **Pathway** database
  - Genes database
  - Genome database
  - Orthology database
  - …

KEGG Search Help

» Japanese

KEGG Home
Release notes
Current statistics
Plea from KEGG

KEGG Database
KEGG overview
Searching KEGG
KEGG mapping
Color codes

KEGG Objects
Pathway maps
Brite hierarchies

KEGG Software
KegTools
KEGG API
KGML

KEGG FTP
Subscription

GenomeNet

DBGET/LinkDB

Feedback

Kanehisa Labs

KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (See Release notes for new and updated features).

Main entry point to the KEGG web service

KEGG2	KEGG Table of Contents	Update notes

Data-oriented entry points

KEGG PATHWAY	KEGG pathway maps	[Pathway list]
KEGG BRITE	BRITE functional hierarchies	[Brite list]
KEGG MODULE	KEGG modules	[Module list | Statistics]
KEGG ORTHOLOGY	Ortholog groups	[KO system]
KEGG GENOME	Genomes	[KEGG organisms]
KEGG GENES	Genes and proteins	[Release history]
KEGG COMPOUND	Small molecules	[Compound classification]
KEGG REACTION	Biochemical reactions	[Reaction modules]
KEGG DISEASE	Human diseases	[Cancer | Infectious disease]
KEGG DRUG	Drugs	[ATC drug classification]
KEGG MEDICUS	Health information resource	[Drug labels search]

Organism-specific entry points

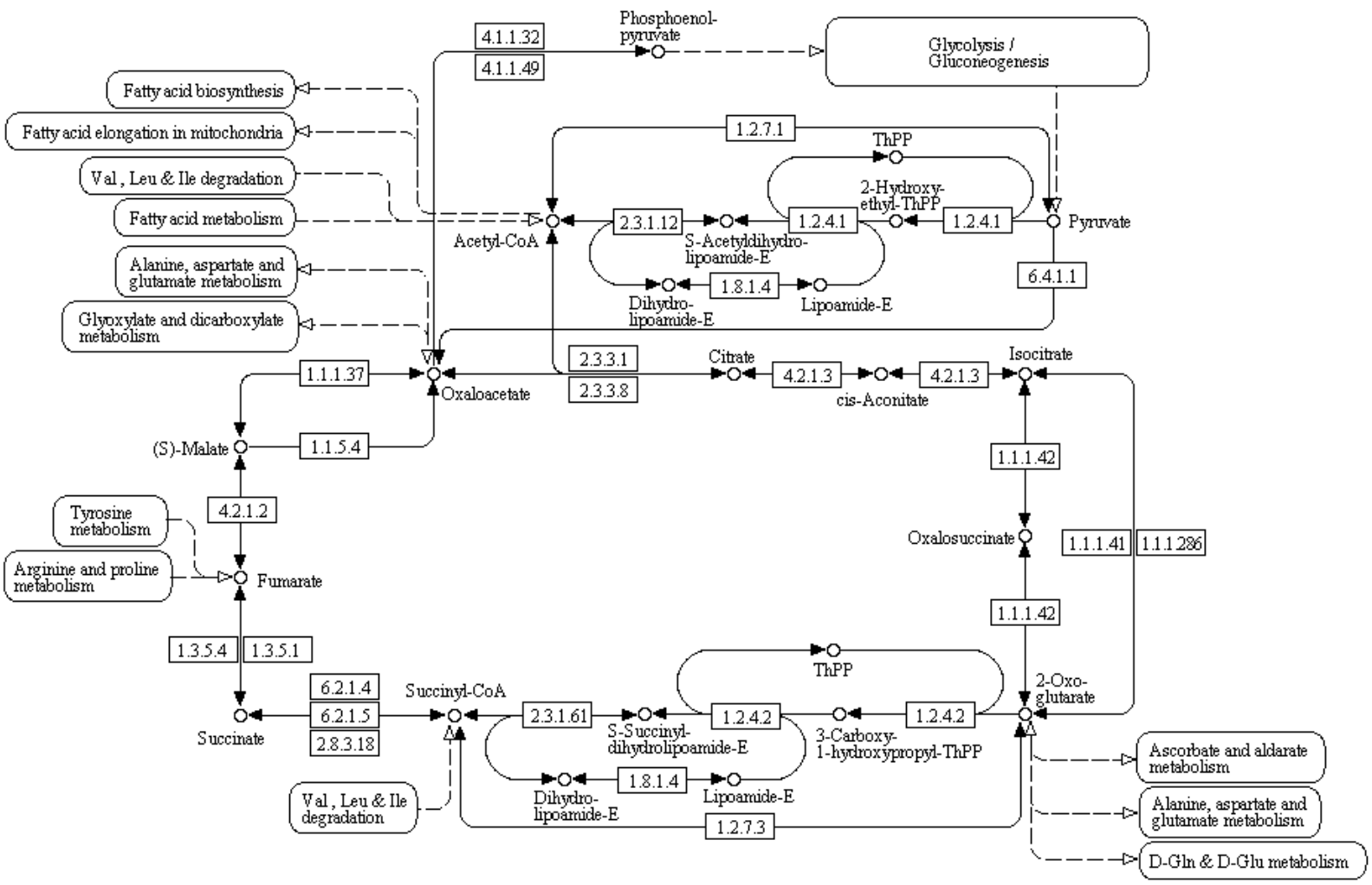
KEGG Organisms Enter org code(s) Go hsa hsa eco

Annotation and analysis tools

KEGG Annotation	KEGG Orthology (KO) based annotation *New!*
BlastKOALA	Automatic KO annotation service
KEGG Mapper	KEGG PATHWAY/BRITE/MODULE mapping tools
KEGG Atlas	Navigation tool to explore KEGG global maps
BLAST/FASTA	Sequence similarity search
SIMCOMP	Chemical structure similarity search

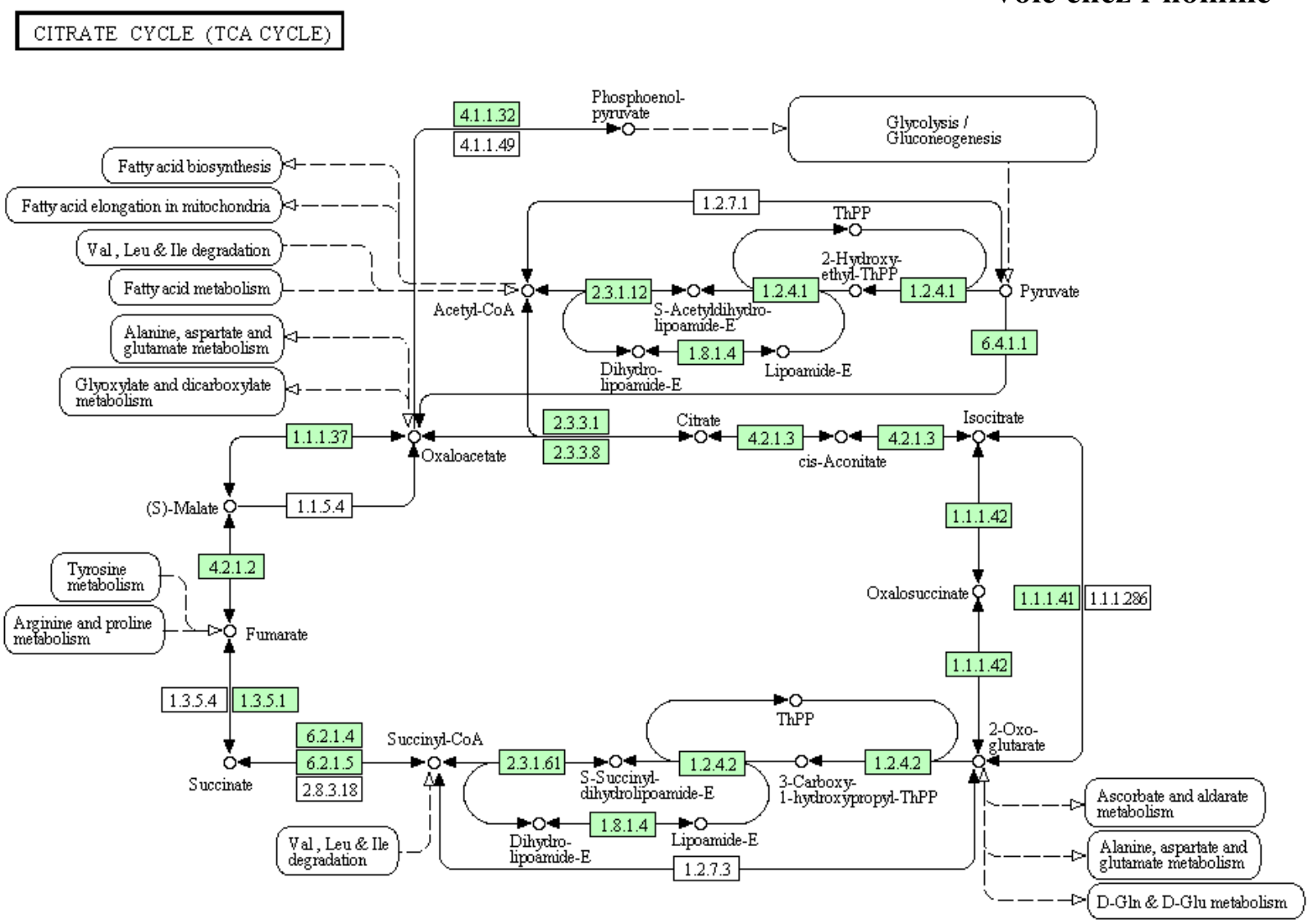
Exemple de voie métabolique

Voie de référence



Exemple de voie métabolique

Voie chez l'homme

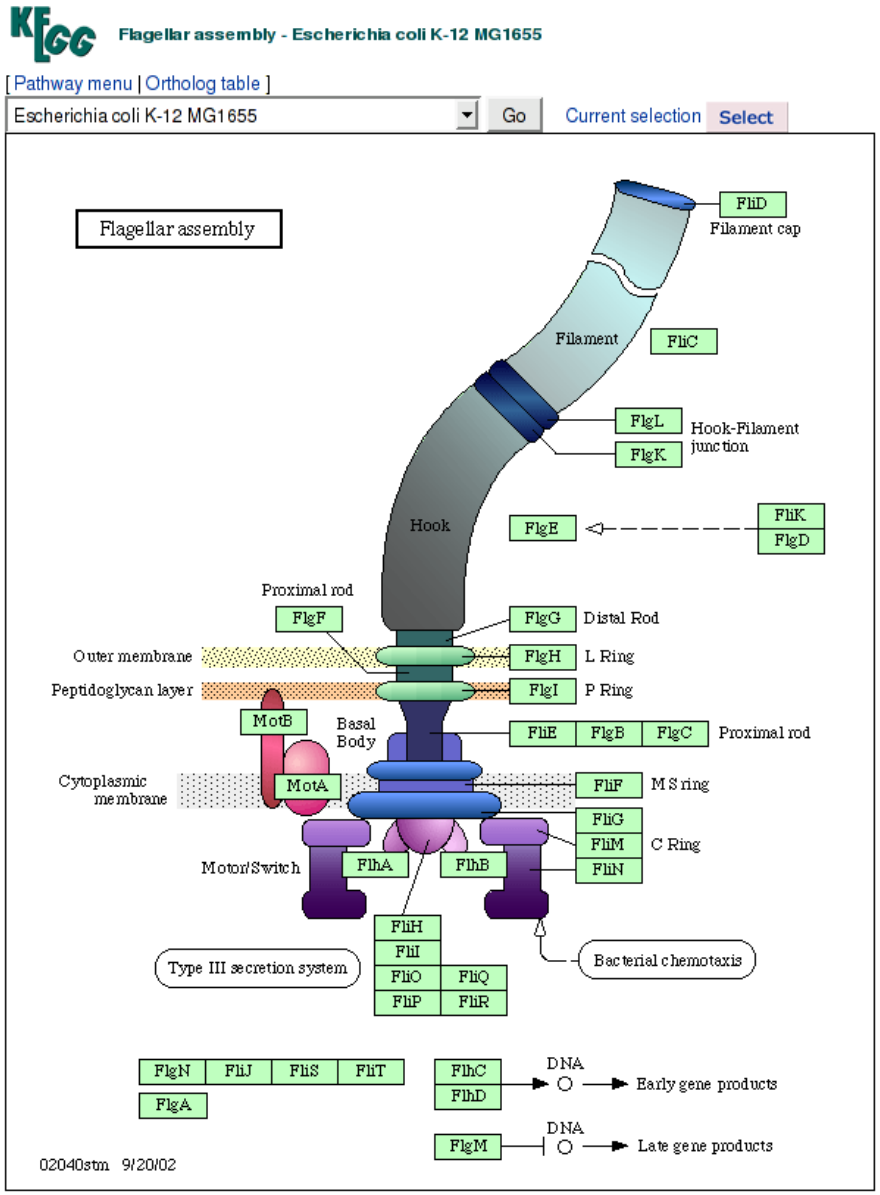


Nomenclature des enzymes

- Classification hiérarchique (4 niveaux) des activités enzymatiques
- Une réaction est référencée par un code : EC number

```
1   Oxidoreductases
2   Transferases
   2.1   Transferring one-carbon groups
     2.1.1   Methyltransferases
       2.1.1.1   nicotinamide N-methyltransferase
       2.1.1.2   guanidinoacetate N-methyltransferase
       2.1.1.3   thetin—homocysteine S-methyltransferase
       2.1.1.4   acetylserotonin O-methyltransferase
       2.1.1.5   betaine—homocysteine S-methyltransferase
         …
    2.8   Transferring sulfur-containing groups
    2.9   Transferring selenium-containing groups
3   Hydrolases
4   Lyases
5   Isomerases
6   Ligases
```

Exemple de processus cellulaire : assemblage du flagelle



Autres ressources

PubMed : banque bibliographique (>20 millions de références)

OMIM : Online Mendelian Inheritance in Man : base de connaissances sur les maladies génétiques humaines

Gene Ontology : Vocabulaire structuré pour décrire les produits des gènes des différents organismes (PAS une banque mais un modèle des connaissances)

Gene Ontology

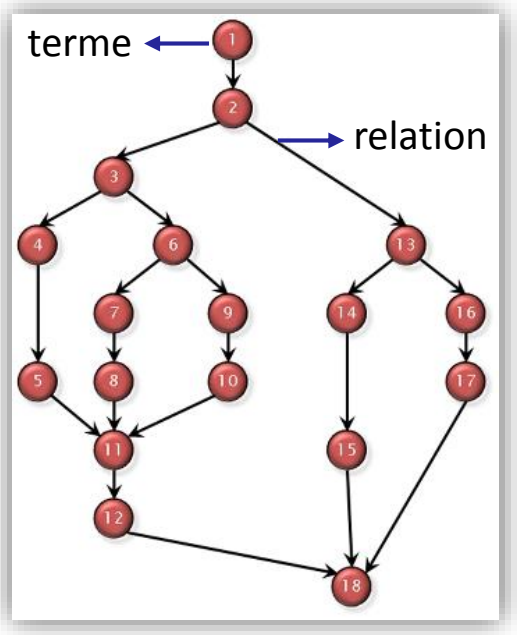
Gene Ontology est un projet destiné à structurer la description des gènes et des produits géniques en utilisant un vocabulaire contrôlé (un même terme pour décrire un même concept) et structuré commun à toutes les espèces. Cette structuration s'appelle une ontologie. Ce projet bio-informatique poursuit trois objectifs :

- gérer et enrichir le vocabulaire contrôlé décrivant les gènes et leurs produits,
- gérer les *annotations*, c'est-à-dire les informations rattachées aux gènes et à leurs produits,
- fournir les outils permettant d'accéder aux informations structurées dans le cadre du projet.

Gene ontology a été intialement créée en 1998 par un consortium de chercheurs étudiants le génome de trois organisme modèles : *Drosophila melanogaster*, *Mus musculus* et *Saccharomyces cerevisiae*. Depuis, d'autres bases de données sur des organismes modèles ont rejoint le consortium pour contribuer au développement du projet.

Gene Ontology

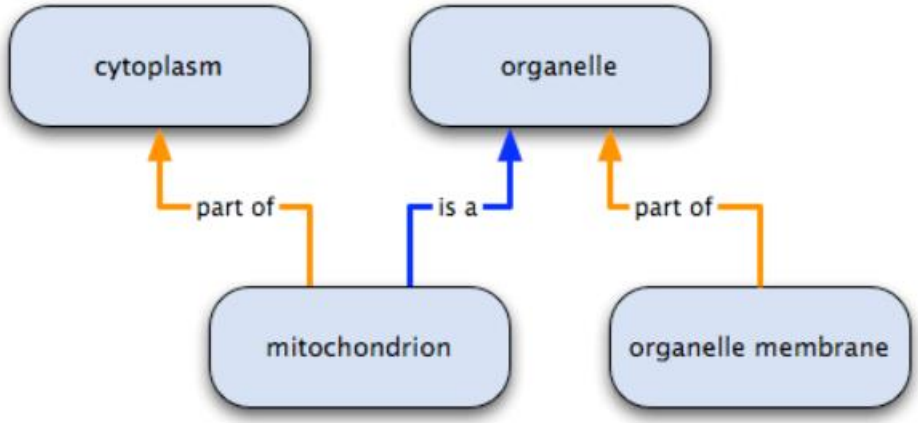
La base GO est conçue comme un graphe orienté acyclique, ce qui permet de représenter une hiérarchie. Chaque nœud du graphe représente un terme et les arêtes les relations entre les termes. Chaque terme est en relation avec un ou plusieurs termes du même domaine, et parfois d'autres domaines. Le vocabulaire GO est construit pour être indépendant des espèces considérées, avec des termes applicables à la fois aux organismes multicellulaires et unicellulaires, aux eucaryotes et aux procaryotes.



graphe acyclique orienté

Deux types de relation :

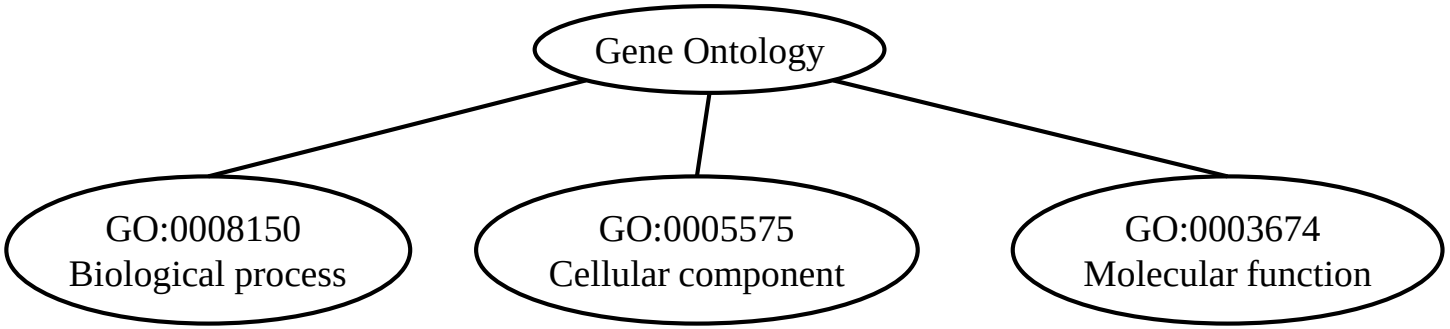
- *is a* : exemple la mitochondrie est un sous-type d'organelle (permet la spécification)
- *part of* : la membrane de l'organelle est une partie de l'organelle



Gene Ontology

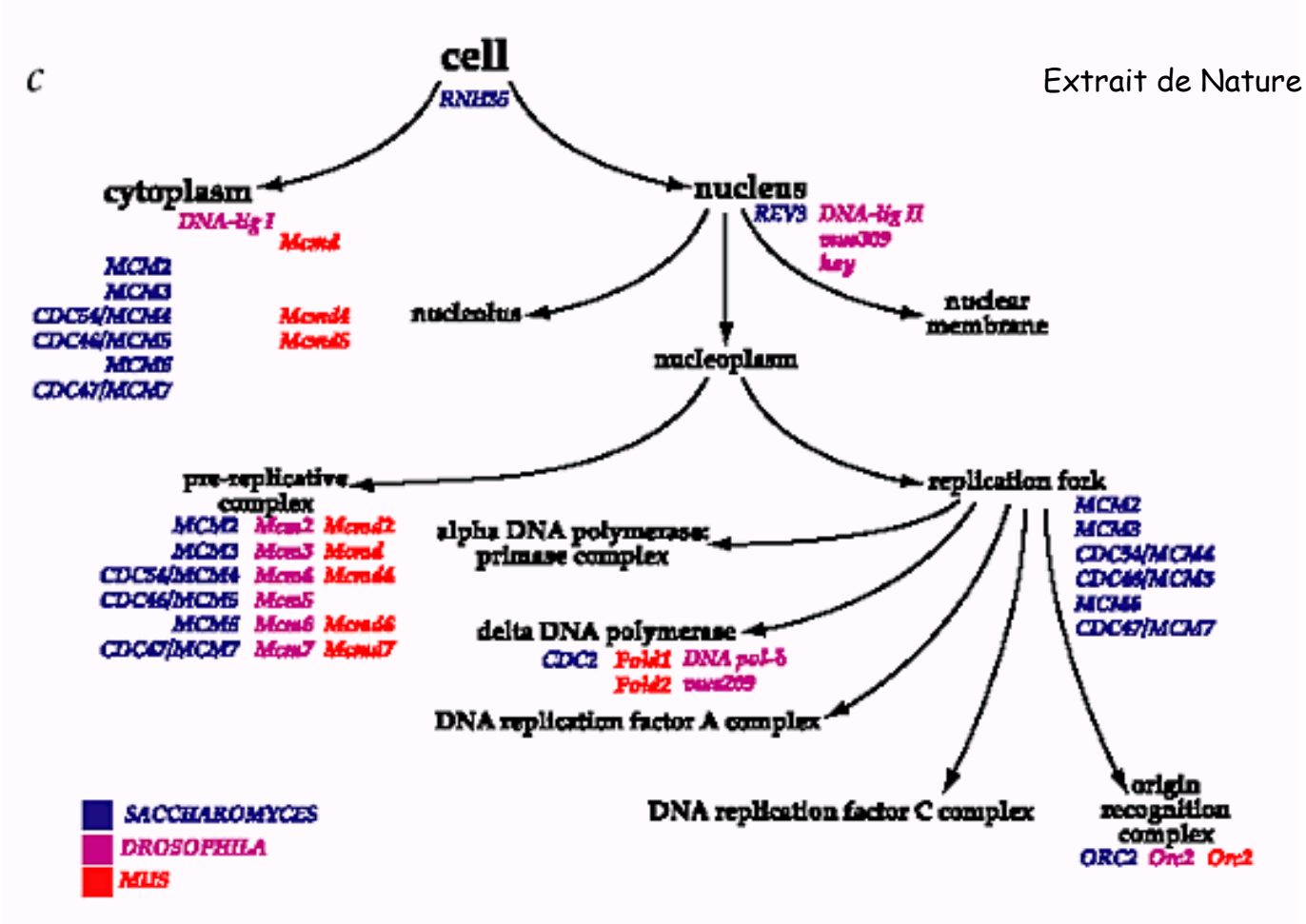
En fait trois ontogies :

- Cellular component
- Biological process
- Molecular function



Gene Ontology : Cellular component ontology

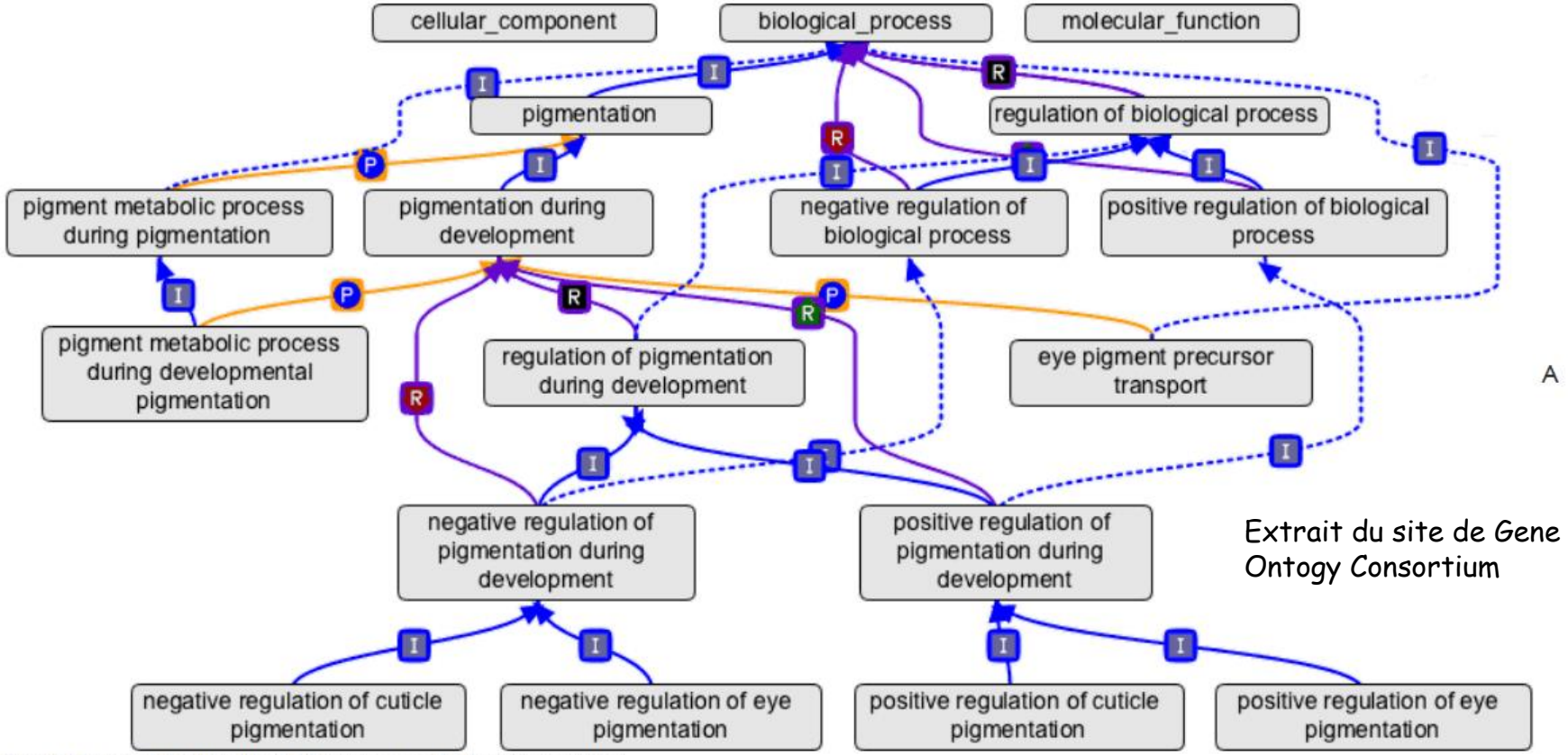
Ces termes décrivent un composant d'une cellule qui fait partie d'un objet plus grand, tel qu'une structure anatomique (par exemple le réticulum endoplasmique rugueux ou le noyau mais aussi un groupe de produit de gènes (par exemple le ribosome, le protéasome ou un dimère de protéine)



Extrait de Nature genetics (2000) 25, 25-29

Gene Ontology : Biological process ontology

Ces termes décrivent une série d'évènements accomplie par un ou plusieurs ensembles organisés de fonctions moléculaires. Pas équivalent à un « pathway » car n'essaie pas de représenter la dynamique ou les dépendances nécessaires pour décrire un « pathway ». Exemple de termes généraux « transduction de signal ». Exemple de termes plus spécifiques « processus métabolique de la pyrimidine ». Distinction entre processus biologique et fonction moléculaire : un processus doit avoir plus d'une étapes distinctes.



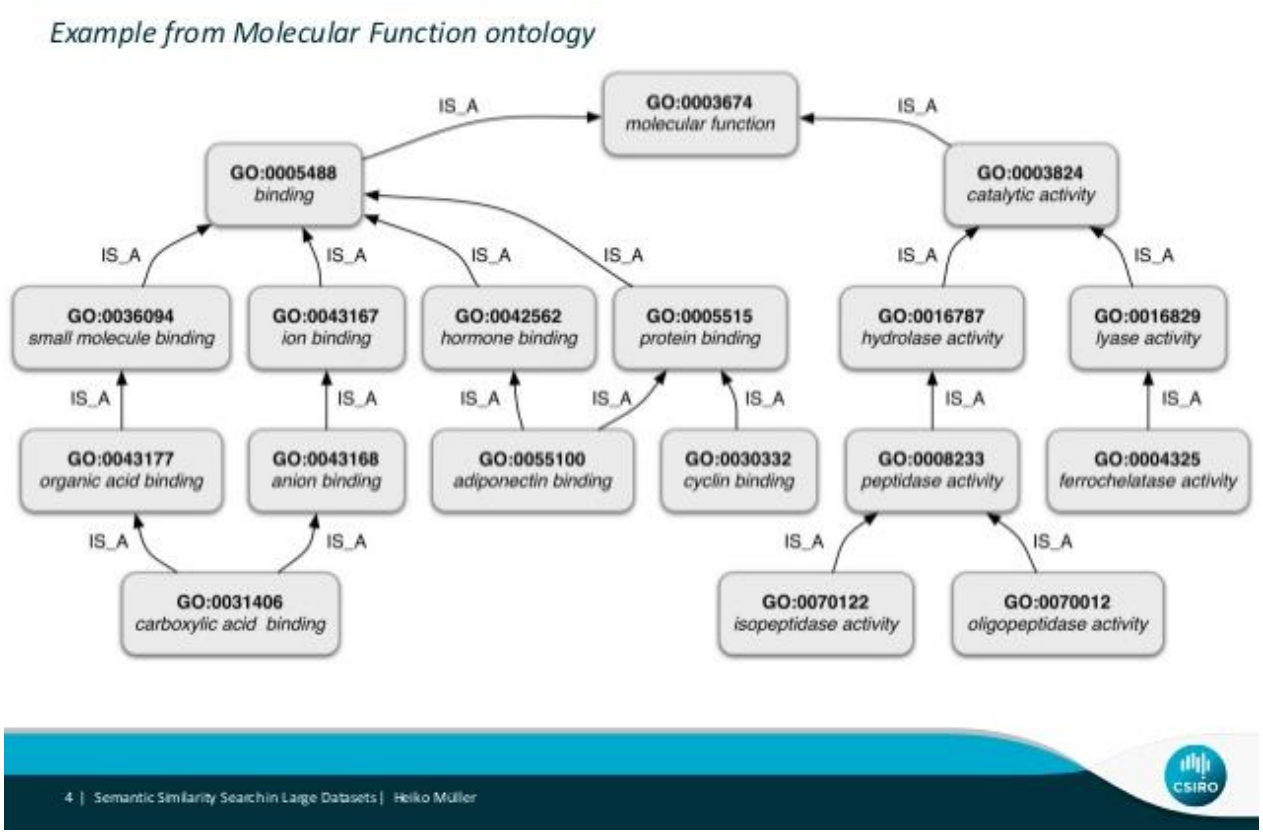
A

Extrait du site de Gene Ontogy Consortium

set of terms under the biological process node pigmentation.

Gene Ontology : Molecular function ontology

Ces termes décrivent des activités qui se produisent au niveau moléculaire, telles que "activité catalytique" ou "activité de liaison". Les fonctions moléculaires correspondent généralement à des activités pouvant être réalisées par des produits géniques individuels, mais certaines activités sont réalisées par des complexes. Exemples de termes fonctionnels généraux « activité catalytique » et « activité transporteur »; Exemples de termes fonctionnels plus étroits « activité adénylate cyclase » ou « la liaison au récepteur Toll ».



Annotation Gene Ontology

- Un numéro unique représentant le terme
- L'ontologie (P pour Biological Process, C pour Cellular component et F pour Molecular Function
- Une description

```
DR   GO; GO:0030175; C:filopodium; IDA.
DR   GO; GO:0030027; C:lamellipodium; IDA.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0001726; C:ruffle; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   GO; GO:0030324; P:lung development; IMP.
DR   GO; GO:0001946; P:lymphangiogenesis; IMP.
DR   GO; GO:0051272; P:positive regulation of cell motility; IDA.
```

Interrogation des bases de données

Les banques de données sont maintenues par divers instituts et organismes. Elles sont mises à disposition, le plus généralement, via un site Web (serveurs) proposant une interface de consultation et d'interrogation. De plus, ces serveurs proposent parfois des interfaces pour l'utilisation de logiciels en ligne.

Principaux sites :

- Serveur de l'EBI : European Bioinformatics Institute (Europe)

- Serveur du NCBI : National Center for Biotechnology Information (US)
    - **Entrez** (http://www.ncbi.nlm.nih.gov/gquery/)

Interrogation banques protéiques uniquement :

- Serveur Uniprot: http://www.uniprot.org/

Entrez

NCBI Resources How To Sign in to NCBI

Search NCBI databases

Help

topoisomerase [keyword] AND streptococcus pneumoniae [organism] Search

Literature

Books	books and reports
MeSH	ontology used for PubMed indexing
NLM Catalog	books, journals and more in the NLM Collections
PubMed	scientific & medical abstracts/citations
PubMed Central	full-text journal articles

Health

ClinVar	human variations of clinical significance
dbGaP	genotype/phenotype interaction studies
GTR	genetic testing registry
MedGen	medical genetics literature and links
OMIM	online mendelian inheritance in man
PubMed Health	clinical effectiveness, disease and drug reports

Genomes

Assembly	genomic assembly information
BioProject	biological projects providing data to NCBI
BioSample	descriptions of biological source materials
Clone	genomic and cDNA clones
dbVar	genome structural variation studies
Epigenomics	epigenomic studies and display tools
Genome	genome sequencing projects by organism
GSS	genome survey sequences
Nucleotide	DNA and RNA sequences
Probe	sequence-based probes and primers
SNP	short genetic variations
SRA	high-throughput DNA and RNA sequence read archive
Taxonomy	taxonomic classification and nomenclature catalog

Genes

EST	expressed sequence tag sequences
Gene	collected information about gene loci
GEO DataSets	functional genomics studies
GEO Profiles	gene expression and molecular abundance profiles
HomoloGene	homologous gene sets for selected organisms
PopSet	sequence sets from phylogenetic and population studies
UniGene	clusters of expressed transcripts

Proteins

Conserved Domains	conserved protein domains
Protein	protein sequences
Protein Clusters	sequence similarity-based protein clusters
Structure	experimentally-determined biomolecular structures

Chemicals

BioSystems	molecular pathways with links to genes, proteins and chemicals
PubChem BioAssay	bioactivity screening studies
PubChem Compound	chemical information with structures, information and links
PubChem Substance	deposited substance and chemical information

Résultat de la requête

NCBI Resources How To Sign in to NCBI

Search NCBI databases

Help

topoisomerase [keyword] AND streptococcus pneumoniae [organism] Search

About 608 search results for "topoisomerase [keyword] AND streptococcus pneumoniae [organism]"

Literature

Books	1	books and reports
MeSH	0	ontology used for PubMed indexing
NLM Catalog	0	books, journals and more in the NLM Collections
PubMed	0	scientific & medical abstracts/citations
PubMed Central	346	full-text journal articles

Health

ClinVar	0	human variations of clinical significance
dbGaP	0	genotype/phenotype interaction studies
GTR	0	genetic testing registry
MedGen	0	medical genetics literature and links
OMIM	0	online mendelian inheritance in man
PubMed Health	0	clinical effectiveness, disease and drug reports

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PopSet	0	sequence sets from phylogenetic and population studies
UniGene	0	clusters of expressed transcripts

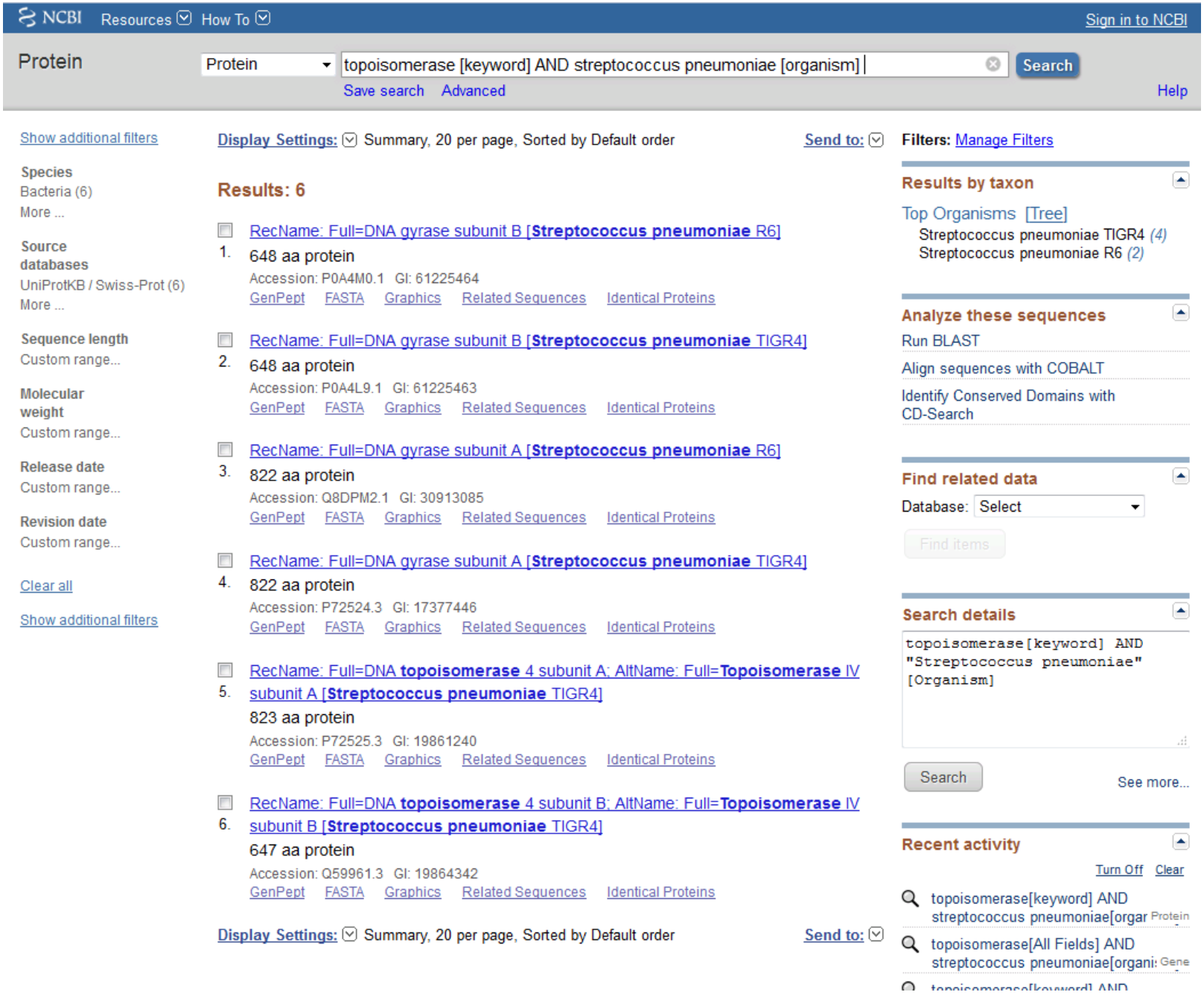
Proteins

Conserved Domains	0	conserved protein domains
Protein	6	protein sequences
Protein Clusters	12	sequence similarity-based protein clusters
Structure	23	experimentally-determined biomolecular structures

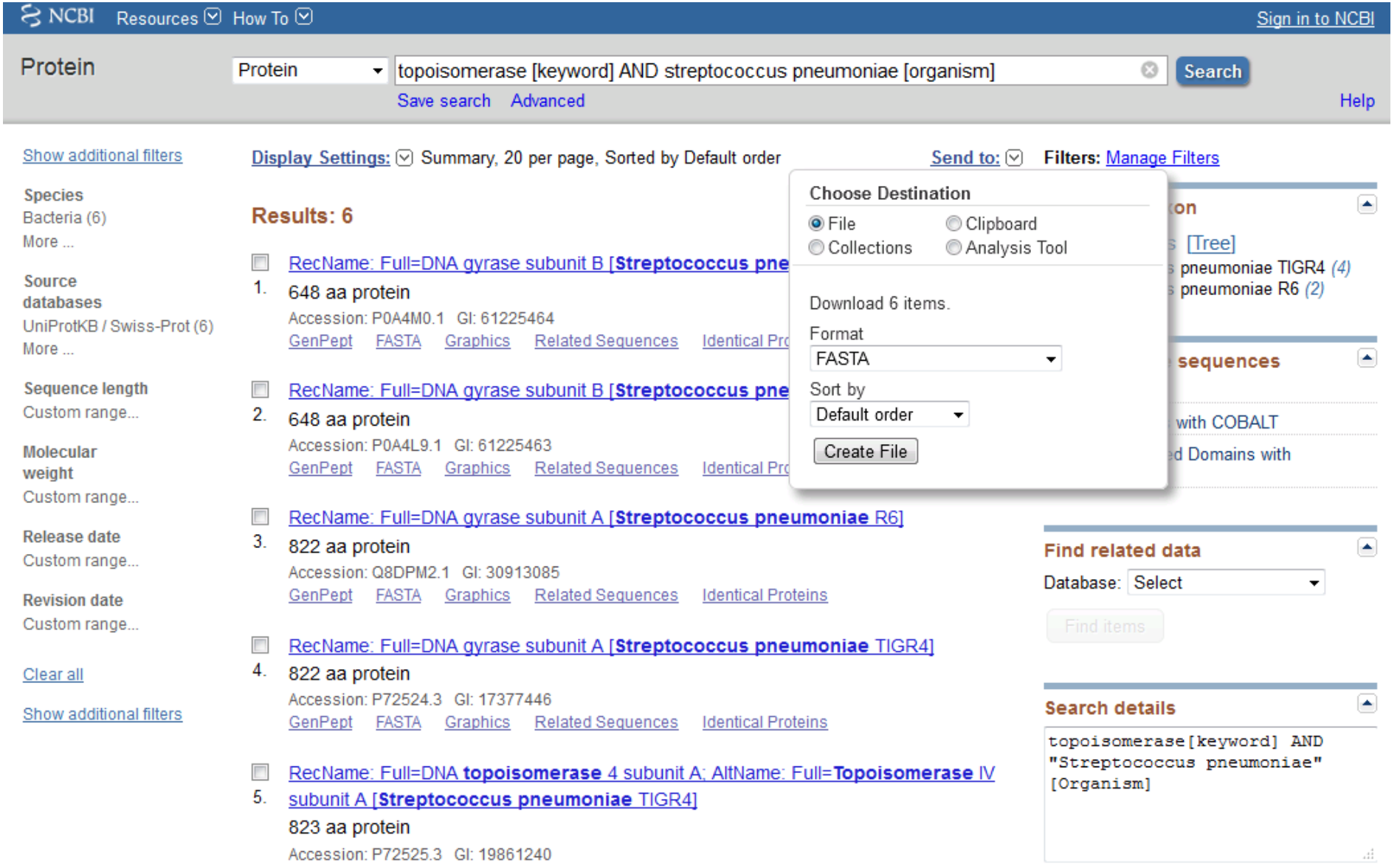
Chemicals

BioSystems	0	molecular pathways with links to genes, proteins and chemicals
PubChem BioAssay	0	bioactivity screening studies
PubChem Compound	0	chemical information with structures, information and links
PubChem Substance	0	deposited substance and chemical information

Résultat de la requête dans la banque Protein



Récupération des séquences dans un fichier



Séquences récupérées
Format Fasta

```
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EPDDSITVVDDGRGIPVDIQEKTGRPAVETVFTVLHAGGKFGGGGYKVSGGLHGVGSSVVNALSTQLDVH
VHKNGKIHYQEYRRGHVVADLEIVGDTDKTGTTVHFTPDPKIFTETTIFDFDKLNKRIQELAFLNRGLQI
SITDKRQGLEQTKHYHYEGGIASYVEYINENKDVIFDTPIYTDGEMDDITVEVAMQYTTGYHENVMSFAN
NIHTHEGGTHEQGFRTALTRVINDYARKNKLLKDNEDNLTGEDVREGLTAVISVKHPNPQFEGQTKTKLG
NSEVVKITNRLFSEAFSDFLMENPQIAKRIVEKGILAAKARVAAKRAREVTRKKSGLEISNLPGKLADCS
SNNPAETELFIVEGDSAGGSAKSGRNREFQAILPIRGKILNVEKASMDKILANEEIRSLFTAMGTGFGAE
FDVSKARYQKLVLMTDADVDGAHIRTLLLTLIYRYMKPILEAGYVYIAQPPIYGVKVGSEIKEYIQPGAD
QEIKLQEALARYSEGRTKPTIQRYKGLGEMDDHQLWETTMDPEHRLMARVSVDDAAEADKIFDMLMGDRV
EPRREFIEENAVYSTLDV

>gi|61225463|sp|P0A4L9.1|GYRB_STRPN RecName: Full=DNA gyrase subunit B
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EPDDSITVVDDGRGIPVDIQEKTGRPAVETVFTVLHAGGKFGGGGYKVSGGLHGVGSSVVNALSTQLDVH
VHKNGKIHYQEYRRGHVVADLEIVGDTDKTGTTVHFTPDPKIFTETTIFDFDKLNKRIQELAFLNRGLQI
SITDKRQGLEQTKHYHYEGGIASYVEYINENKDVIFDTPIYTDGEMDDITVEVAMQYTTGYHENVMSFAN
NIHTHEGGTHEQGFRTALTRVINDYARKNKLLKDNEDNLTGEDVREGLTAVISVKHPNPQFEGQTKTKLG
NSEVVKITNRLFSEAFSDFLMENPQIAKRIVEKGILAAKARVAAKRAREVTRKKSGLEISNLPGKLADCS
SNNPAETELFIVEGDSAGGSAKSGRNREFQAILPIRGKILNVEKASMDKILANEEIRSLFTAMGTGFGAE
FDVSKARYQKLVLMTDADVDGAHIRTLLLTLIYRYMKPILEAGYVYIAQPPIYGVKVGSEIKEYIQPGAD
QEIKLQEALARYSEGRTKPTIQRYKGLGEMDDHQLWETTMDPEHRLMARVSVDDAAEADKIFDMLMGDRV
EPRREFIEENAVYSTLDV

>gi|30913085|sp|Q8DPM2.1|GYRA_STRR6 RecName: Full=DNA gyrase subunit A
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VMGKYHPHGDSSIYEAMVRMAQWWSYRYMLVDGHGNFGSMDGDSAAAQRYTEARMSKIALEMLRDINKNT
VDFVDNYDANEREPLVLPARFPNLLVNGATGIAVGMATNIPPHNLGETIDAVKLVMDNPEVTTKDLMEVL
PGPDFPTGALVMGKSGIHKAYETGKGSIVLRSRTEIETTKTGRERIVVTEFPYMVNKTKVHEHIVRLVQE
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ILDMRLRRLTGLERDKIQSEYDDLLALIADLADILAKPERVSQIIKDELDEVKRKFSDKRRTELMVGQVL
SLEDEDLIEESDVLITLSNRGYIKRLDQDEFTAQKRGGRGVQGTGVKDDDFVRELVSTSTHDHLLFFTNK
GRVYRLKGYEIPEYGRTAKGLPVVNLLKLDEDESIQTVINVESDRSDDAYLFFTTRHGIVKRTSVKEFAN
IRQNGLKALNLKDEDELINVLLAEGDMDIIIGTKFGYAVRFNQSAVRGMSRIATGVKGVNLREGDTVVGA
SLITDQDEVLIITEKGYGKRTVATEYPTKGRGGKGMQTAKITEKNGLLAGLMTVQGDEDLMIITDTGVMI
RTNLANISQTGRATMGVKVMRLDQDAQIVTFTTVAVAEKEEVGTENETEGEA

>gi|17377446|sp|P72524.3|GYRA_STRPN RecName: Full=DNA gyrase subunit A
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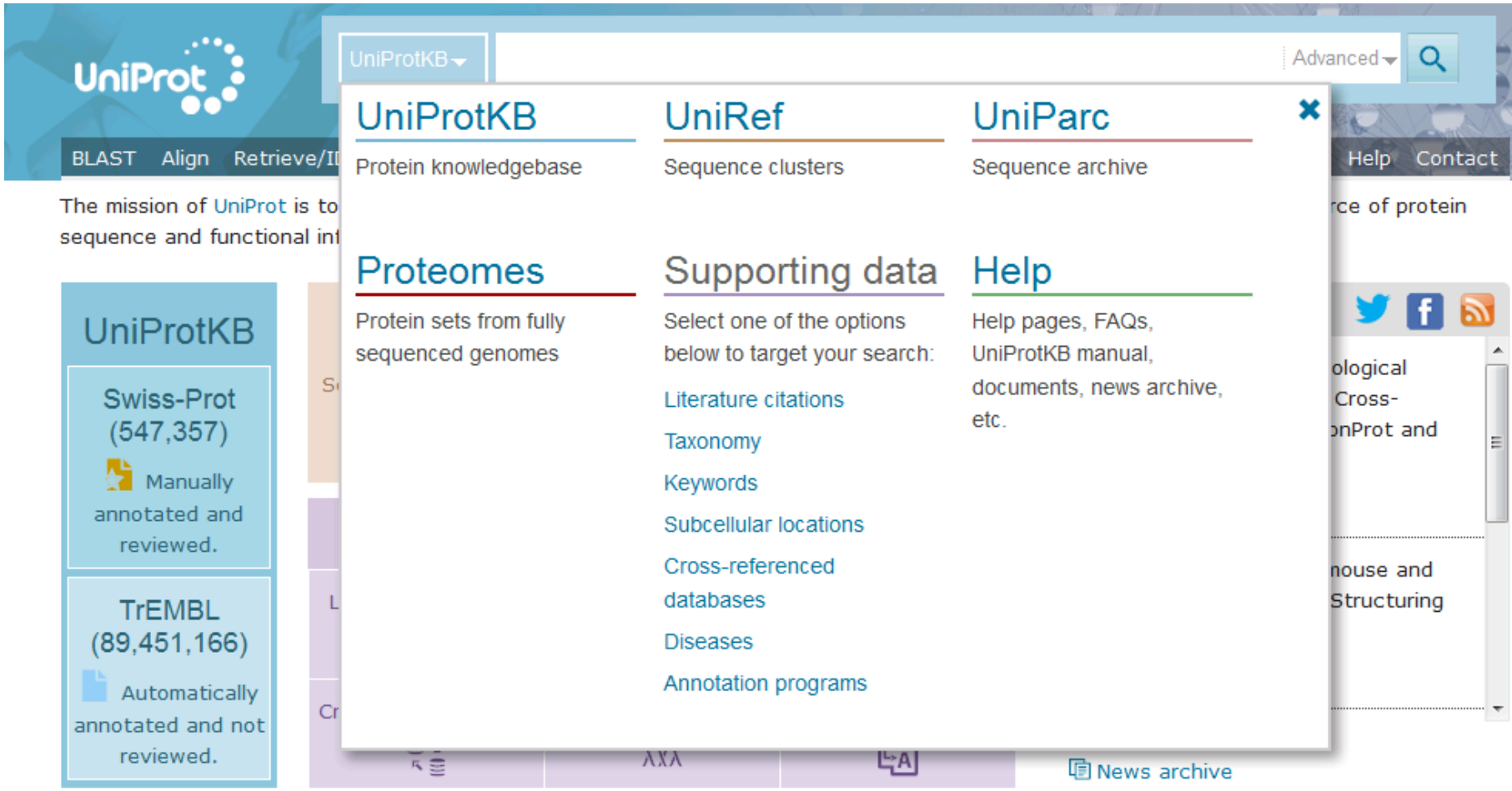
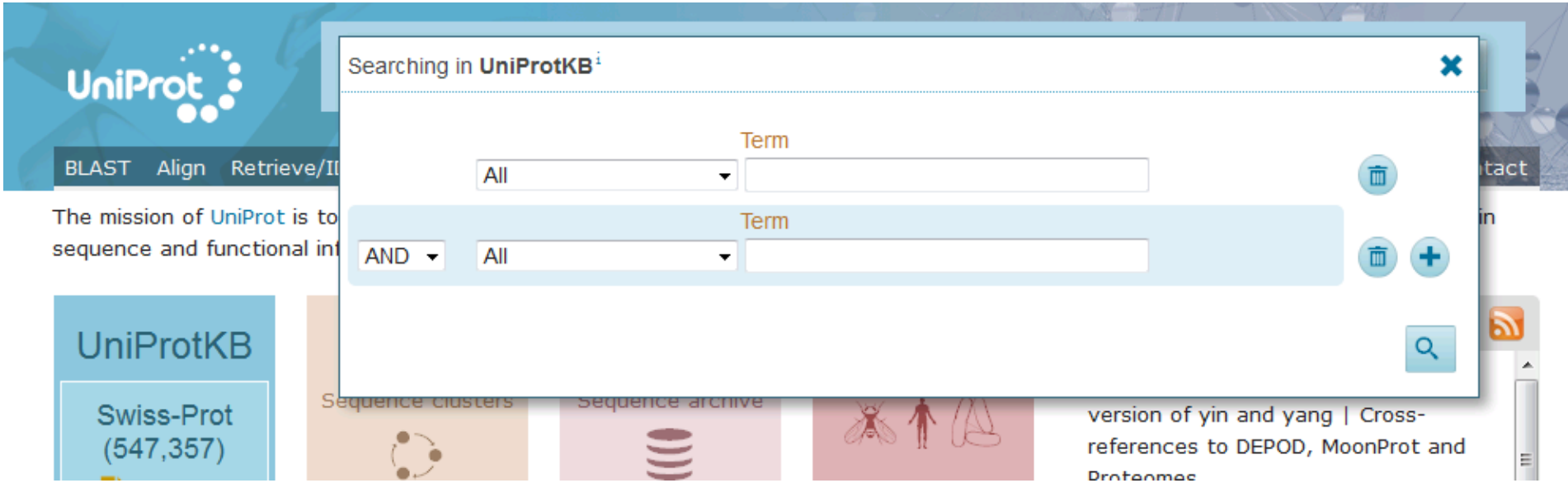
```

Interrogation sur le site d'UniProtKB : choix de la base de données

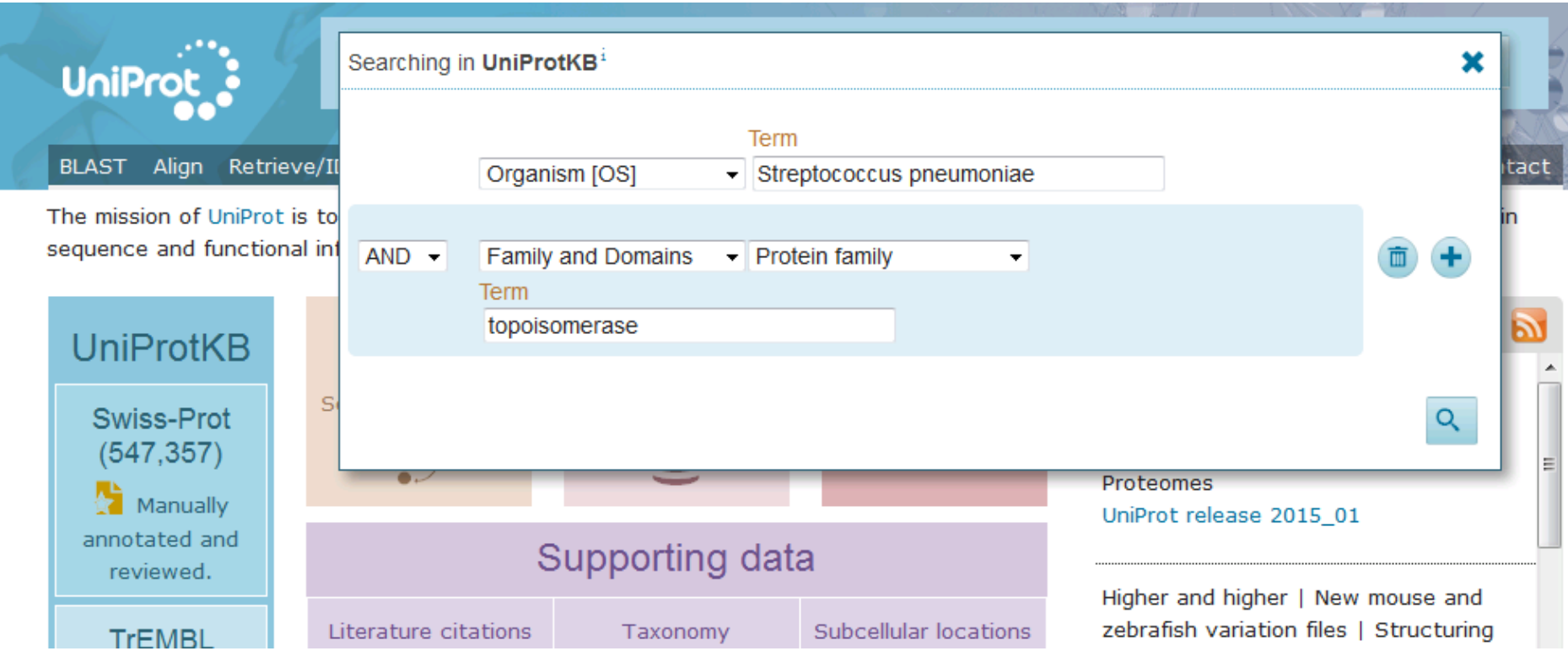


Interrogation sur le site d'UniProtKB : construction de la requête



Dans le menu déroulant, choisir le champ de la fiche dans lequel on veut rechercher le terme.
All signifie que la recherche du terme se fera dans toute la fiche

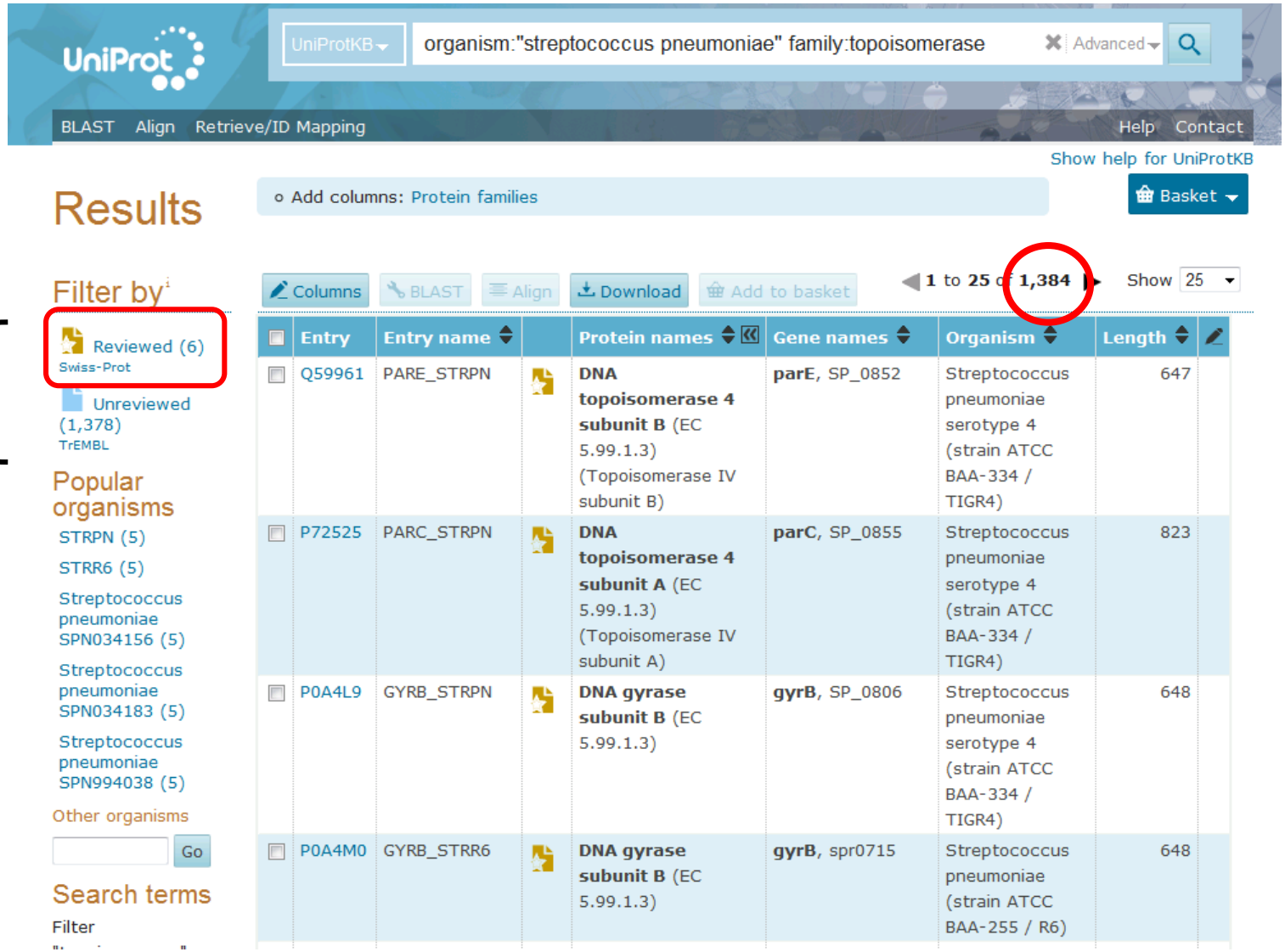
Interrogation sur le site d'UniProtKB : construction de la requête



La recherche de *Streptococcus pneumoniae* restreint au champ Organism
La recherche du terme topoisomerase dans le champ Protein Family

Interrogation sur le site d'UniProtKB : resultat de la requête

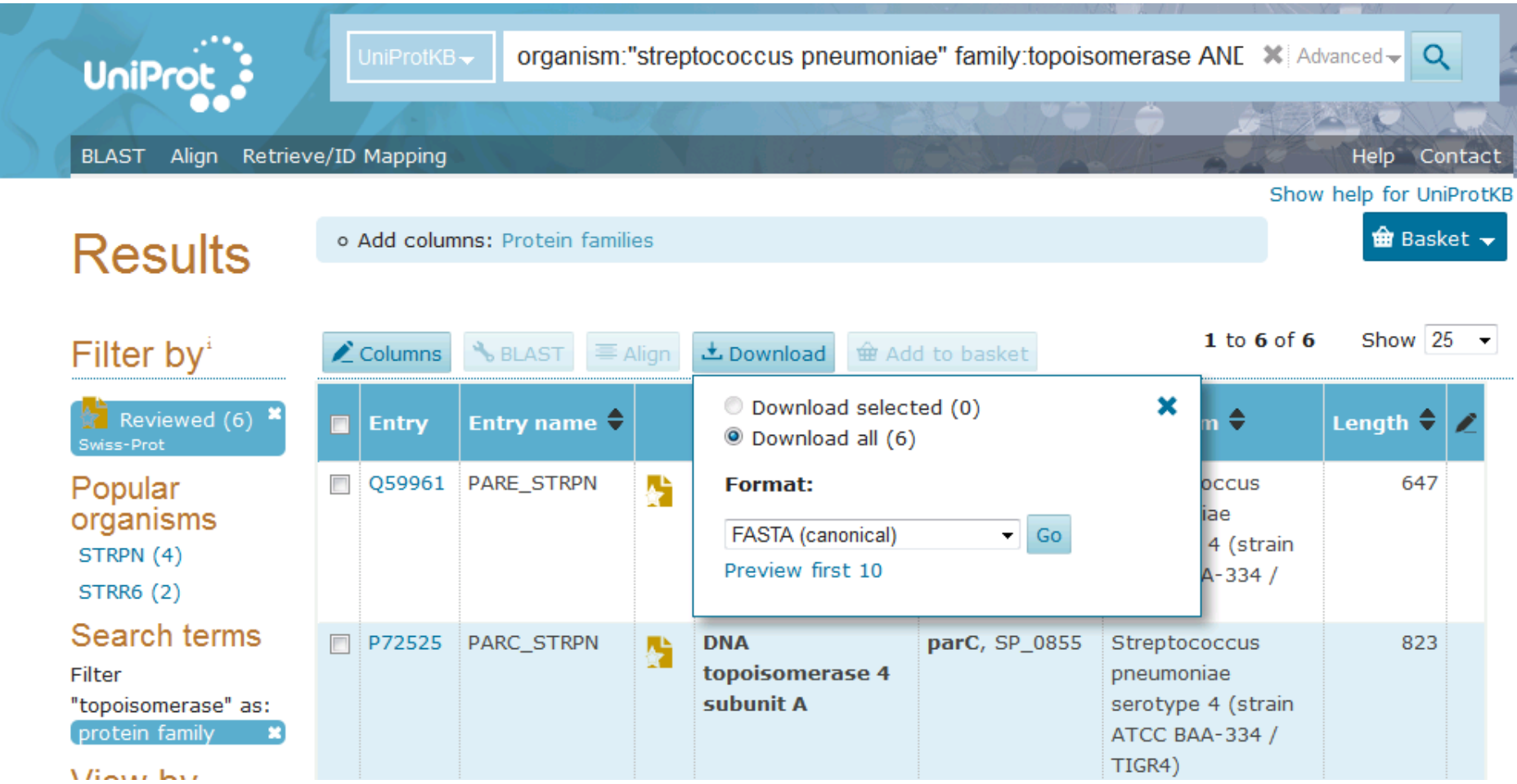
Distribution des séquences en fonction de la banque de données



1384 séquences versus 6 sur le site du NCBI

6 dans la banque SwissProt expertisée

Récupération des séquences dans un fichier



Séquences récupérées
Format Fasta

```
>sp|Q59961|PARE_STRPN DNA topoisomerase 4 subunit B OS=Streptococcus pneumoniae serotype 4 |(
MSKKEININNYNDDAIQVLEGLDAVRKRPGMYIGSTDGAGLHHLVWEIVDNAVDEALSGF
GDRIDVTINKDGSLTVQDHGRGMPTGMHAMGIPTVEVIFTILHAGGKFGQGGYKTSGGLH
GVGSSVVNALSSWLEVEITRDGAVYKQRFENGGKPVTTLKKIGTAPKSKTGTKVTFMPDA
TIFSTTDFKYNTISERLNESAFLLKNVTLSLTDKRTNEAIEFHYENGVQDFVSYLNEDKE
ILTPVLYFEGEDNGFQVEVALQYNDGFSDNILSFVNNVRTKDGGTHETGLKSAITKVMND
YARKTGLLKEKDKNLEGSDYREGLAAVLSILVPEEHLQFEGQTKDKLGSPLARPVVDGIV
ADKLTFFLMENGELASNLIRKAIKARDAREAARKARDESRNGKKNKKDKGLLSGKLTPAQ
SKNPAKNELYLVEGDSAGGSAKQGRDRKFQAILPLRGKVVNTAKAKMADILKNEEINTMI
YTIGAGVGADFSIEDANYDKIIIMTDADTDGAHIQTLLLTFFYRYMRPLVEAGHVYIALP
PLYKMSKGKGKKEEVAYAWTDGELEELRKQFGKGATLQRYKGLGEMNADQLWETTMNPET
RTLIRVTIEDLARAERRVNVLMGDKVEPRRKWIEDNVKFTLEETTVF
>sp|P72525|PARC_STRPN DNA topoisomerase 4 subunit A OS=Streptococcus pneumoniae serotype 4 (
MSNIQNMSLEDIMGERFGRYSKYIIQDRALPDIRDGLKPVQRRILYSMNKDSNTFDKSYR
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ARLSEIAGYLLQDIEKKTVPFAWNFDDTEKEPTVLPAAFPNLLVNGSTGISAGYATDIPP
HNLAEVIDAAVYMIDHPTAKIDKLMEFLPGPDFPTGAIIQGRDEIKKAYETGKGRVVVRS
KTEIEKLKGGKEQIVIIEIPYEINKANLVKKIDDVRVNNKVAGIAEVRDESDRDGLRIAI
ELKKDANTELVLNYLFKYTDLQINYNFNMVAIDNFTPRQVGIVPILSSYIAHRREVILAR
SRFDKEKAEKRLHIVEGLIRVISILDEVIALIRASENKADAKENLKVSYDFTEEQAEAIV
TLQLYRLTNTDVVVLQEEEAELREKIAMLAAIIGDERTMYNLMKKELREVKKKFATPRLS
SLEDTAKAIEIDTASLIAEEDTYVSVTKAGYIKRTSPRSFAASTLEEIGKRDDDRLIFVQ
SAKTTQHLLMFTSLGNVIYRPIHELADIRWKDIGEHLSQTITNFETNEEILYVEVLDQFD
DATTYFAVTRLGQIKRVERKEFTPWRTYRSKSVKYAKLKDDTDQIVAVAPIKLDDVVLVS
QNGYALRFNIEEVPVVGAKAAGVKAMNLKEDDVLQSGFICNTSSFYLLTQRGSLKRVSIE
EILATSRAKRGLQVLRELKNKPHRVFLAGAVAEQGFVGDFFSTEVDVNDQTLLVQSNKGT
IYESRLQDLNLSERTSNGSFISDTISDEEVFDAYLQEVVTEDK
>sp|P0A4L9|GYRB_STRPN DNA gyrase subunit B OS=Streptococcus pneumoniae serotype 4 (strain AT
MTEEIKNLQAQDYDASQIQVLEGLEAVRMRPGMYIGSTSKEGLHHLVWEIVDNSIDEALA
GFASHIQVFIEPDDSITVVDDGRGIPVDIQEKTGRPAVETVFTVLHAGGKFGGGGYKVSG
GLHGVGSSVVNALSTQLDVHVHKNGKIHYQEYRRGHVVADLEIVGDTDKTGTTVHFTPDP
KIFTETTIFDFDKLNKRIQELAFLNRGLQISITDKRQGLEQTKHYHYEGGIASYVEYINE
NKDVIFDTPIYTDGEMDDITVEVAMQYTTGYHENVMSFANNIHTHEGGTHEQGFRTALTR
VINDYARKNKLLKDNEDNLTGEDVREGLTAVISVKHPNPQFEGQTKTKLGNSEVVKITNR
LFSEAFSDFLMENPQIAKRIVEKGILAAKARVAAKRAREVTRKKSGLEISNLPGKLADCS
SNNPAETELFIVEGDSAGGSAKSGRNREFQAILPIRGKILNVEKASMDKILANEEIRSLF
TAMGTGFGAEFDVSKARYQKLVLMTDADVDGAHIRTLLLTLIYRYMKPILEAGYVYIAQP
PIYGVKVGSEIKEYIQPGADQEIKLQEALARYSEGRTKPTIQRYKGLGEMDDHQLWETTM
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>sp|P0A4M0|GYRB_STRR6 DNA gyrase subunit B OS=Streptococcus pneumoniae (strain ATCC BAA-255
MTEEIKNLQAQDYDASQIQVLEGLEAVRMRPGMYIGSTSKEGLHHLVWEIVDNSIDEALA
```

Interconnexion des banques de données : références croisées

Définition : Lien (référence) d'une entrée d'une banque vers une entrée d'une (autre) banque.

```
LOCUS       CAA65843                 268 aa            linear   PLN 19-DEC-1997
DEFINITION  CBEL protein, formerly GP34 [Phytophthora parasitica].
ACCESSION   CAA65843
VERSION     CAA65843.1  GI:2706495
DBSOURCE    embl accession X97205.1
KEYWORDS    .
SOURCE      Phytophthora parasitica
  ORGANISM  Phytophthora parasitic
            Eukaryota; stramenopil
REFERENCE   1
  AUTHORS   Mateos,F.V., Rickauer,
  TITLE     Cloning and characteri
            Phytophthora parasitic
            cellulose-binding and
  JOURNAL   Mol. Plant Microbe Int
   PUBMED   9390419
REFERENCE   2
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FEATURES             Location/Qualifiers
     source          1..268
                     /organism="Phytophthora parasitica"
                     /cultivar="nicotianae"
                     /db_xref="taxon:4792"
                     /clone="B_311.2"
                     /tissue_type="mycelium"
                     /clone_lib="lambda Zap II"
     Protein         1..268
                     /product="CBEL protein, formerly GP34"
                     /function="elicits defense reactions in host"
     sig peptide     1..18
     Region          23..55
                     /region_name="CBM_1"
                     /note="Fungal cellulose binding domain; cl02521"
                     /db_xref="CDD:154956"
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     CDS             1..268
                     /gene="cbel1"
                     /coded_by="X97205.1:53..859"
                     /note="localized in cell wall;
                     lectin-like and cellulose-binding properties"
                     /db_xref="GOA:O42830"
                     /db_xref="InterPro:IPR000177"
                     /db_xref="InterPro:IPR000254"
                     /db_xref="InterPro:IPR003014"
                     /db_xref="InterPro:IPR003609"
                     /db_xref="UniProtKB/TrEMBL:O42830"
ORIGIN
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