
Projet ABC
Analyse et Base de Connaissance

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Journées de l'institut IDBC, novembre 2002

Ontologie

- *Contexte : partage de connaissance*
- *Rôle : production d'un vocabulaire contrôlé pouvant s'appliquer à la connaissance du rôle des transcrits et protéines*

Buts

- I. Visualisation des transcrits liés aux termes de l'ontologie*
- II. Évolutions internes de l'ontologie pour une meilleure adéquation au sujet de recherche, knowledge management (projet)*

Gene Ontology (GO)

GO

Biological process

Objectif biologique du gène

Cellular component

*Localisation intracellulaire
où le produit du gène est actif*

Molecular function

Activité biochimique du produit

The screenshot shows the DAG-Edit version 1.311 software interface. On the left is a hierarchical tree of Gene Ontology terms, including biological processes, cellular components, and molecular functions. The main window is titled 'Find terms' and shows search options. Below that, the 'DAG Viewer' displays the selected term 'GO:0003673' with its definition, synonyms, and general DbXrefs. The interface includes a 'Commit' button and a 'Cancel to New Term' button.

DAG-Edit version 1.311

File Edit Plugins Filters

Gene_Ontology

- biological_process
 - behavior
 - biological_process unknown
 - cell communication
 - cell growth and/or maintenance
 - death
 - developmental processes
 - obsolete
 - physiological processes
 - viral life cycle
- cellular_component
 - cell
 - cellular_component unknown
 - external protective structure
 - extracellular
 - obsolete
 - unlocalized
- molecular_function
 - anti-toxin
 - anticoagulant
 - antifreeze
 - antioxidant
 - apoptosis regulator
 - cell adhesion molecule
 - chaperone
 - chaperone regulator
 - cytoskeletal regulator
 - defense/immunity protein
 - enzyme
 - enzyme regulator
 - ice nucleation
 - ligand binding or carrier
 - lysin
 - molecular_function unknown
 - motor
 - obsolete
 - protein stabilization
 - protein tagging
 - signal transducer
 - small nuclear RNA
 - storage protein
 - structural molecule
 - surfactant
 - toxin
 - transcription regulator
 - translation regulator
 - transporter
 - triplet codon-amino acid adaptor

Find terms

ID equals Find

Search all terms Search children of selection Search selection Case sensitive search

No search performed

ID: **GO:0003673**

Term name: Gene_Ontology

Definition:

Text: Dbxrefs: Edit

Synonyms:

Select a synonym from the list to edit it, or press add to create a new synonym

Add Del

General DbXrefs:

Select a dbxref from the list to edit it, or press add to create a new dbxref

Add Del

Comment:

Commit Cancel to New Term

Exemples de concepts et relations

- Exemples

GO:0003673 : Gene Ontology (30674)

GO:0008150 : biological process (23487)

GO:0008151 : cell growth and/or maintenance (15526)

GO:0008152 : metabolism (10826)

GO:0009058 : biosynthesis (2327)

GO:0009059 : macromolecule biosynthesis (1684)

GO:0006412 : protein biosynthesis (1572)

GO:0006411 : protein metabolism and modification (4159)

GO:0006412 : protein biosynthesis (1572)

GO:0006461 : protein complex assembly (111)

GO:0007582 : physiological processes (695)

GO:0007585 : respiration (26)

GO:0005575 : cellular component (14402)

GO:0005623 : cell (11523)

GO:0005622 : intracellular (10239)

GO:0005737 : cytoplasm (5373)

GO:0005739 : mitochondrion (1433)

GO:0003674 : molecular function (21459)

GO:0005215 : transporter (1920)

GO:0005372 : water transporter (5)

- 2 types de relations

Protéine

is a
Enzyme

is a
ATP synthase

part of
Domaine F0

part of
Domaine F1

I. Visualisation des transcrits liés aux termes de l'ontologie

Associations termes - transcrits

- *Evidences* : codes pour juger de la qualité de l'annotation
Exemples :
 - *IEA* : inferred from electronic annotation
 - *TAS* : traceable author statement
- *Bases de données* pour les transcrits (*Swiss-Prot, TrEMBL, SGD...*)
- *Articles* justifiant l'annotation (*Pubmed*)

Visualisation termes - transcrits

The screenshot displays the DAG-Edit version 1.311 interface. On the left, a tree view of Gene Ontology terms is shown, with 'cell growth' circled in red. A red arrow points from this term to a central window titled 'DAG Viewer'. Above this window is a 'Find terms' search bar with a dropdown menu set to 'equals' and a 'Find' button. Below the search bar, there are radio buttons for 'Search all terms', 'Search children of selection', and 'Search selection', along with a 'Case sensitive search' checkbox. The 'DAG Viewer' window shows a list of genes associated with the 'cell growth' term, with a 'database filter : ALL' label. The list includes various gene identifiers and descriptions, such as 'fb:FBgn0011217: IMP fb fb#0093291 id:3966 no full_name eff [gene]' and 'sp:O00257: TAS : pubmed 9315667 id:7137 Chromobox protein homolog 4 CBX4_HUMAN [IPI000108]'. At the bottom of the interface, there is an 'InterPro:IPR003939' dropdown menu, 'Add' and 'Remove' buttons, a 'Comment' text area, and 'Commit' and 'Commit As New Term' buttons.

Gene_Ontology

- biological_process
 - behavior
 - biological_process unkn
 - cell communication
 - cell growth and/or maint
 - autophagy
 - budding
 - cell cycle
 - cell growth**
 - cell motility
 - cell organization and biogenesis
 - cell proliferation
 - cell shape and cell size control
 - cell-cell fusion
 - chemi-mechanical coupling
 - homeostasis
 - membrane fusion
 - metabolism
 - sporulation
 - stress response
 - transport
 - death
 - developmental processes
 - obsolete
 - physiological processes
 - viral life cycle
- cellular_component
- molecular_function

Find terms

Find

Search all terms Search children of selection Search selection Case sensitive search

No search performed

GO:0016049 DAG Viewer

cell growth

database filter : ALL

- fb:FBgn0011217: IMP fb fb#0093291 id:3966 no full_name eff [gene]
- fb:FBgn0003612: IMP fb fb#0136940 id:6422 no full_name Su(var)2-10 [gene]
- sp:O00257: TAS : pubmed 9315667 id:7137 Chromobox protein homolog 4 CBX4_HUMAN [IPI000108]
- sp:O14646: TAS : pubmed 9326634 id:7263 Chromodomain-helicase-DNA-binding protein 1 CHD1_HUMAN [IPI00025316]
- sp:O14647: TAS : pubmed 9326634 id:7264 Chromodomain-helicase-DNA-binding protein 2 CHD2_HUMAN [IPI00025316]
- sp:O75367: IEA goa interpre id:7833 Core histone macro-H2A.1 H2AY_HUMAN [IPI00025316]
- sp:O95985: TAS : pubmed 9786843 id:8164 DNA topoisomerase III beta-1 TP3B_HUMAN [IPI0000150]
- sp:P01133: TAS : pubmed 10436156 id:8257 Pro-epidermal growth factor precursor EGF_HUMAN [IPI00020085]
- sp:P02261: NAS sp NOREFERENCE id:8438 Histone H2A.c/d/i/n/p H2AC_HUMAN [IPI00020085]
- sp:P02278: IEA goa interpre id:8439 Histone H2B.a/g/k H2BA_HUMAN [IPI00020101]
- sp:P02304: IEA goa interpre id:8440 Histone H4 H4_HUMAN [IPI00020463]
- sp:P04553: IEA goa interpre id:8596 Sperm protamine P1 HSP1_HUMAN [IPI00024682]
- sp:P04554: IEA goa interpre id:8597 Sperm histone P2 precursor HSP2_HUMAN [IPI00024683]
- sp:P04908: NAS sp NOREFERENCE id:8624 Histone H2A.m H2AM_HUMAN [IPI00026272]
- sp:P06351: NAS sp NOREFERENCE id:8730 Histone H3.3 H33_HUMAN [IPI00026258]
- sp:P06899: IEA goa interpre id:8767 Histone H2B.r H2BR_HUMAN [IPI00027861]
- sp:P07199: IEA goa splaw id:8779 Major centromere autoantigen B CENB_HUMAN [IPI00010388]
- sp:P07305: IEA goa interpre id:8788 Histone H1' H10_HUMAN [IPI00011153]
- sp:P09429: IEA goa splaw id:8959 High mobility group protein HMG1 HMG1_HUMAN [IPI00014459]
- sp:P09430: IEA goa interpre id:8960 Spermatid nuclear transition protein 1 STP1_HUMAN [IPI00014460]
- sp:P10412: NAS sp NOREFERENCE id:9045 Histone H1B H14_HUMAN [IPI00020958]
- sp:P16104: NAS sp NOREFERENCE id:9425 Histone H2A.x H2AX_HUMAN [IPI00027366]
- sp:P16106: NAS sp NOREFERENCE id:9426 Histone H3.1 H31_HUMAN [IPI00027367]
- sp:P16401: NAS sp NOREFERENCE id:9446 Histone H1A H15_HUMAN [IPI00028533]
- sp:P16402: NAS sp NOREFERENCE id:9447 Histone H1C H13_HUMAN [IPI00028534]
- sp:P16403: NAS sp NOREFERENCE id:9448 Histone H1D H16_HUMAN [IPI00028535]

InterPro:IPR003939

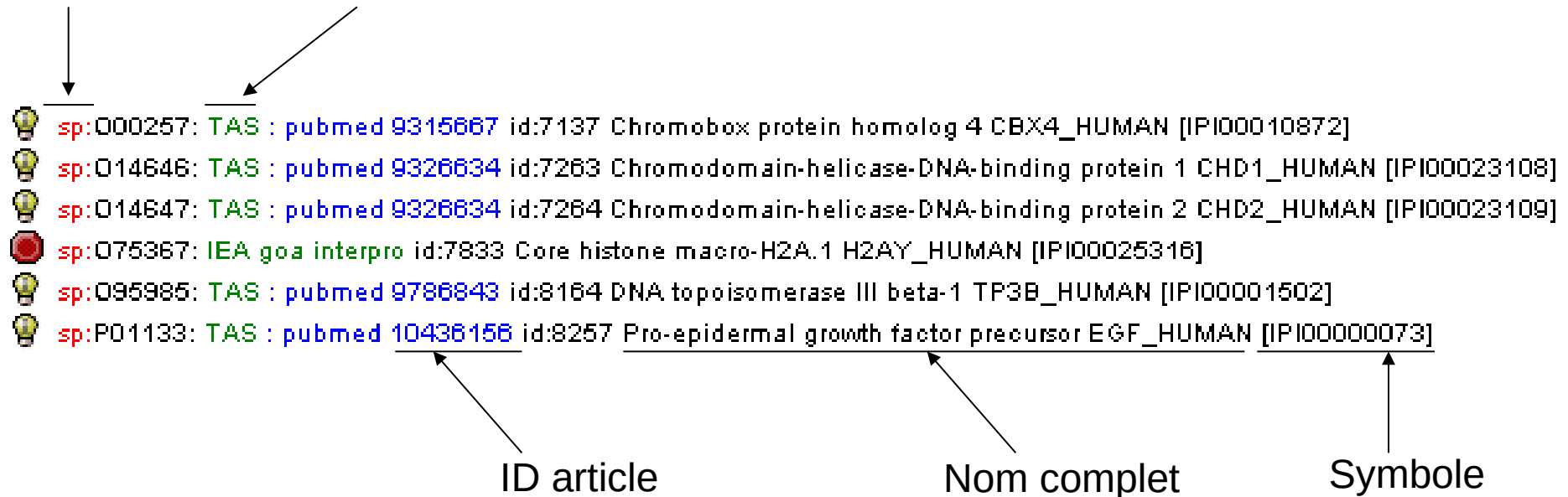
Add Remove

Comment

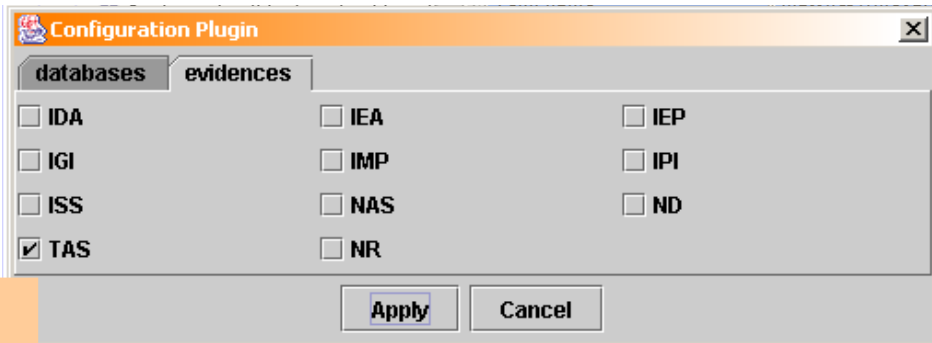
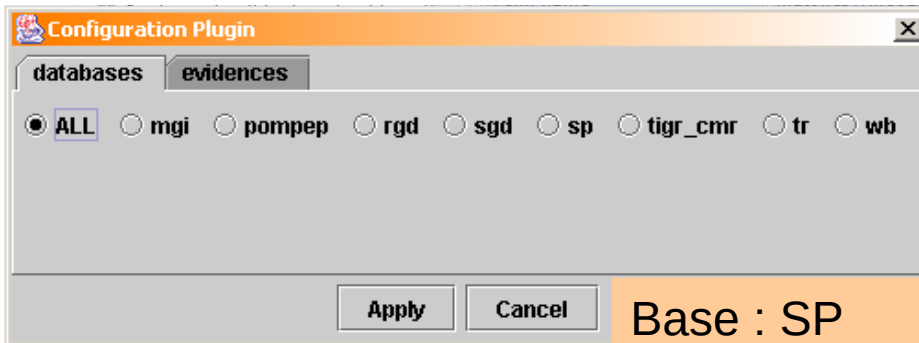
Commit Commit As New Term

Informations présentées

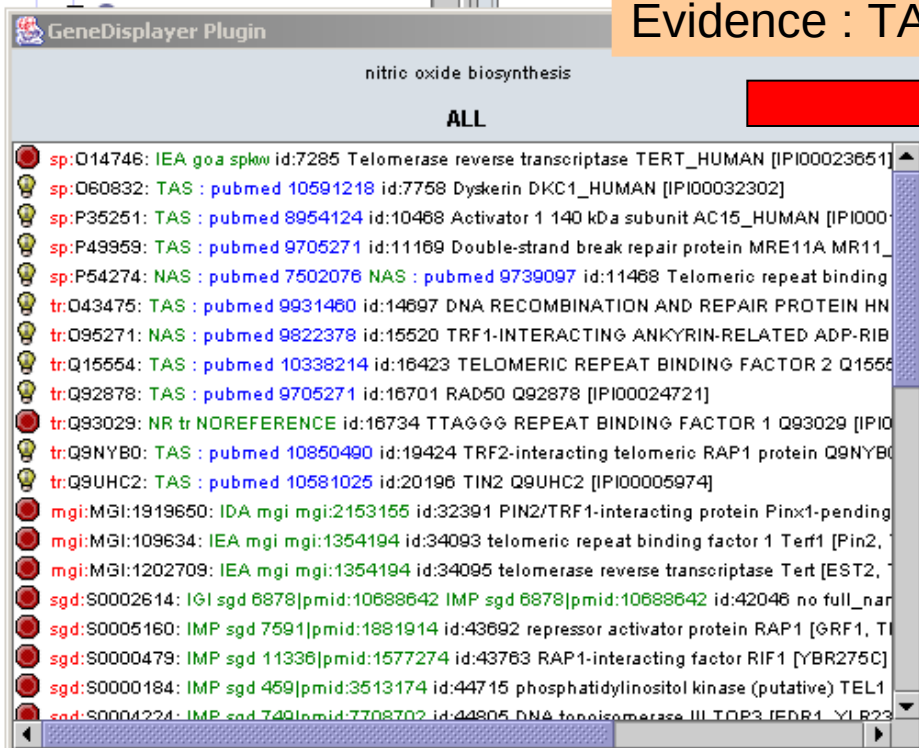
Base de données Evidence



Filtre des résultats



Base : SP
Evidence : TAS



Liens aux bases de données

The image shows a screenshot of the DAG-Edit software interface (version 1.311) with several windows and annotations. The main window displays a Gene Ontology tree on the left, with 'defense/immunity protein' highlighted in red. A red arrow points from this term to a 'GeneDisplayer Plugin' window showing a list of genes associated with this term. Another red arrow points from the 'GeneDisplayer Plugin' window to a 'NiceProt View of SWISS-PROT: P12882' window, which displays protein information for MYH1_HUMAN.

Gene Ontology Tree (Left):

- biological_process
- cellular_component
- molecular_function
 - anti-toxin
 - anticoagulant
 - antifreeze
 - antioxidant
 - apoptosis regulator
 - cell adhesion molecule
 - chaperone
 - chaperone regulator
 - cytoskeletal regulator
 - defense/immunity protein** (circled in red)
 - enzyme
 - ice nucleation
 - ligand binding
 - lysin
 - molecular function
 - motor
 - obsolete
 - protein structure
 - protein transport
 - signal transduction
 - small nucleic acid
 - storage
 - structural molecule
 - surfactant
 - toxin
 - transcription
 - translation
 - transport
 - triplet codon

Find terms (Top):

ID equals [] Find

Search all terms Search children of selection Search selection Case sensitive search

No search performed

DAG Viewer (Right):

Gene Ontology

- molecular_function
 - defense/immunity protein

GeneDisplayer Plugin (Middle):

defense/immunity protein

ALL

- fb:FBgn0002741: ISS fb fbr0105495 id:4992 no full_name Mhc [gene]
- fb:FBgn0002772: NAS fb fbr0105495 id:5010 no full_name Mlc1 [gene]
- fb:FBgn0002773: NAS fb fbr0105495 id:5011 no full_name Mlc2 [gene]
- sp:P12882: NR sp NOREFERENCE id:9208 Myosin heavy chain, skeletal muscle, adult 1 MYH1_HUMAN
- sp:P13533: NAS sp NOREFERENCE id:9237 Myosin heavy chain, cardiac muscle alpha isoform MYH7
- sp:Q9UKX2: TAS : pubmed 10388558 id:13818 Myosin heavy chain, skeletal muscle, adult 2 MYH2
- sp:Q9UKX3: TAS : pubmed 10388558 id:13819 Myosin heavy chain, skeletal muscle, extraocular muscle 1 MYH10
- sp:Q9Y623: NR sp NOREFERENCE id:14128 Myosin heavy chain, skeletal muscle, fetal MYH4_HUMAN
- tr:Q92679: NAS : pubmed 3021460 id:16668 BETA-MYOSIN HEAVY CHAIN Q92679 [PII000226]
- tgi:THC730406: IEA sp P13533 id:80276 no full_name THC730406 []
- tgi:TC39783: IEA sp P12882 id:125710 no full_name TC39783 []
- fb:FBgn0029776: ISS fb fbr0132100 id:1512 no full_name CG15780 [gene]
- fb:FBgn0040034: ISS fb fbr0132100 id:1520 no full_name CG15831 [gene]
- fb:FBgn0031410: ISS fb fbr0132100 id:1639 no full_name CG17237 [gene]
- fb:FBgn0000317: ISS fb fbr0132100 id:3516 no full_name ok [gene]
- fb:FBgn0013765: ISS fb fbr0105495 id:3539 no full_name onn [gene]
- fb:FBgn0000410: ISS fb fbr0132100 id:3729 no full_name d [gene]
- fb:FBgn0015933: ISS fb fbr0132100 id:3809 no full_name didum [gene]
- fb:FBgn0011225: ISS fb fbr0132100 id:4696 no full_name jar [gene]
- fb:FBgn0002741: ISS fb fbr0132100 id:4992 no full_name Mhc [gene]

NiceProt View of SWISS-PROT: P12882 (Right):

SWISS-PROT: P12882

Printer-friendly view Quick BlastP search

[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

General information about the entry

| | |
|--------------------------|------------|
| Entry name | MYH1_HUMAN |
| Primary accession number | P12882 |

Internet

Annotations:

- Orange box: Gènes liés (points to 'defense/immunity protein')
- Orange box: Base de données (points to 'NiceProt View of SWISS-PROT: P12882')
- Red arrows: Connect 'defense/immunity protein' to the gene list and the gene list to the protein view.

Liens aux articles

The image shows a screenshot of the Gene Ontology (GO) software interface. The main window displays a hierarchical tree of biological processes on the left, with 'circulation' highlighted in red. A search bar at the top right contains the term 'GO:0008015'. Below the search bar, a 'GeneDisplayer Plugin' window shows a list of associated genes, including 'sp:P53396: TAS : pubmed 1371749 id:11419 ATP-citrate ACLY_HUMAN [IPI00021290]'. A red arrow points from the 'circulation' term in the tree to the 'GeneDisplayer Plugin' window. Another red arrow points from the 'GeneDisplayer Plugin' window to a 'PubMed' window. The PubMed window shows a search for '1371749' and a list of results, including the article 'Elshourbagy NA, Near JC, Kmetz PJ, Wells TN, Groot PH, Saxty BA, Hughes SA, Franklin M, Gloger IS. Cloning and expression of a human ATP-citrate lyase cDNA. Eur J Biochem. 1993 Mar;199(2):401-9'.

Gene Ontology

biological_process

- cell growth and/or maintenance
- death
- developmental processes
- obsolete
- physiological processes
- circulation
- digestion
- diuresis
- excreti
- extrace
- fat bod
- gallsto
- germin
- hemost
- host ce
- immun
- lactati
- molting
- natriur
- nodula
- nutritio
- parturit
- pathog
- peristal
- physiol
- pollina
- respirat
- sleep
- thermo
- water h
- viral life cy
- cellular_compc
- molecular_func
- anti-toxin
- anticoagul
- antifreeze
- antioxidant
- apoptosis regulator
- cell adhesion molecule
- chaperone
 - HSC70-interacting
 - HSP70/HSP90 organizing protein
 - chaperonin ATPase
 - fimbrial chaperone
 - heat shock protein
 - lectin-binding chaperone
 - metallochaperone
 - nucleosome assembly chaperone
 - ribosomal chaperone
 - tubulin folding
- chaperone regulator

Find terms

ID equals

Search all terms Search children of selection Search selection Case sensitive search

search performed

GO:0008015

DAG Viewer

Gene_Ontology

- biological_process
- physiological processes
- circulation

GeneDisplayer Plugin

circulation

ALL

- sp:P53396: TAS : pubmed 1371749 id:11419 ATP-citrate ACLY_HUMAN [IPI00021290]
- tgi:THC832139: IEA sp P53396 id:88464 no full_name THC832139 []
- tgi:THC832142: IEA sp P53396 id:88465 no full_name THC832142 []
- tgi:TC91603: IEA sp P53396 id:113441 no full_name TC91603 []
- tgi:TC89971: IEA sp P53396 id:115095 no full_name TC89971 []
- tgi:TC12576: IEA sp P53396 id:116063 no full_name TC12576 []

Entrez-PubMed - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

Précédente Recherche Favoris Média

Adresse http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=&DB=

PubMed

Nucleotide Protein Genome Structure PopSet Taxono

ed for 1371749 Go Clear

Limits Preview/Index History Clipboa

Display Summary Sort Save Text Clip

1: Elshourbagy NA, Near JC, Kmetz PJ, Wells TN, Groot PH, Saxty BA, Hughes SA, Franklin M, Gloger IS. Cloning and expression of a human ATP-citrate lyase cDNA. Eur J Biochem. 1993 Mar;199(2):401-9

Commit Commit As New Term

II. Évolutions internes de l'ontologie pour une meilleure adéquation au sujet de recherche (projet)

Prise en charge de l'ontologie

DAG-Edit version 1.311

File Edit Plugins Filters

Gene_Ontology

- biological_process
 - behavior
 - adult behavior
 - behavioral fear response
 - chemosensory behavior
 - feeding behavior
 - grooming behavior
 - larval behavior
 - learning and memory
 - locomotory behavior
 - mechanosensory behavior
 - reproductive behavior
 - rhythmic behavior
 - circadian rhythm
 - eclosion rhythm
 - entrainment of circadian c
 - ultradian rhythm
 - thermosensory behavior
 - visual behavior
 - biological_process unknown
 - cell communication
 - cell growth and/or maintenance
 - death
 - developmental processes
 - obsolete
 - physiological processes
 - viral life cycle
- cellular_component
- molecular_function



DAG-Edit version 1.311

File Edit Plugins Filters

Gene_Ontology

- biological_process
 - behavior
 - adult behavior
 - behavioral fear response
 - chemosensory behavior
 - feeding behavior
 - grooming behavior
 - larval behavior
 - learning and memory
 - locomotory behavior
 - mechanosensory behavior
 - reproductive behavior
 - rhythmic behavior
 - circadian rhythm
 - cell communication
 - eclosion rhythm
 - entrainment of circadian clock
 - luteinizing hormon release
 - pregnancy
 - ultradian rhythm
 - thermosensory behavior
 - visual behavior
 - biological_process unknown
 - cell communication
 - cell growth and/or maintenance
 - death
 - developmental processes
 - obsolete

Partage de connaissances

- *Différentes « vues » de l'ontologie correspondant aux informations entrées par les différents utilisateurs de l'ontologie :*
 - *L'administrateur*
 - *L'expert*
 - *Le post-doctorant*
 - *L'étudiant*
- *Confronter ces différentes vues*

Conclusion

- *Permet d'obtenir toutes les informations recherchées nécessaire à la compréhension et à l'analyse*
- *Manque l'aspect développement de données propres à la thématique du laboratoire (qui permet à l'expert d'enrichir l'ontologie existante) : phase que nous démarrons...*