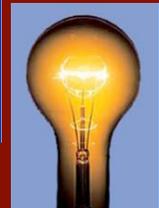
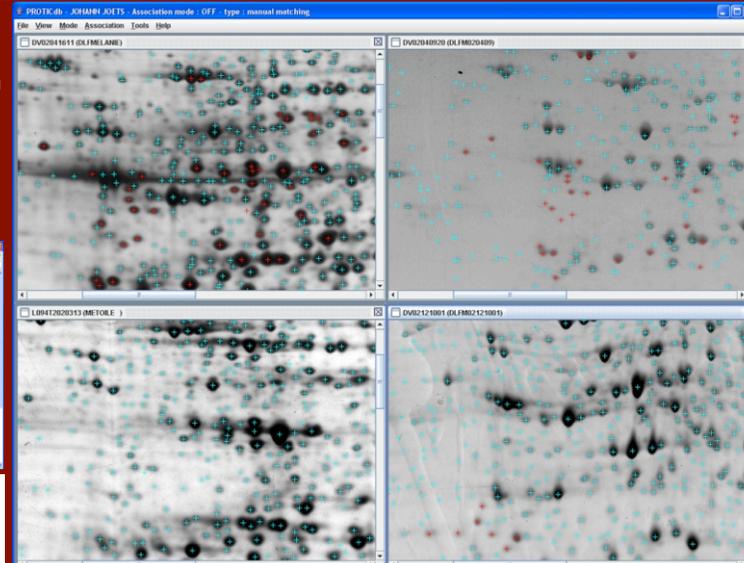
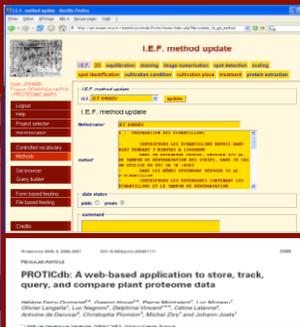
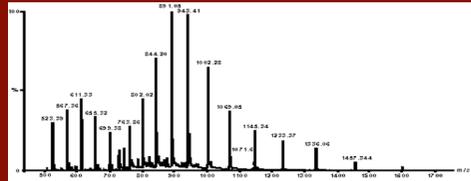
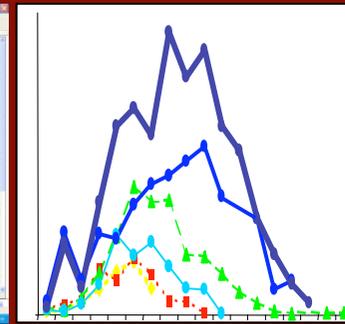
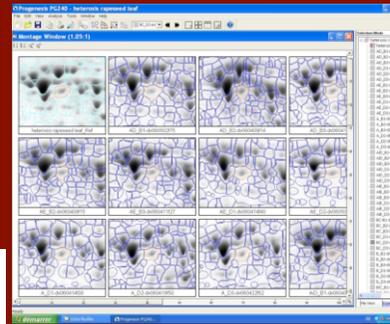


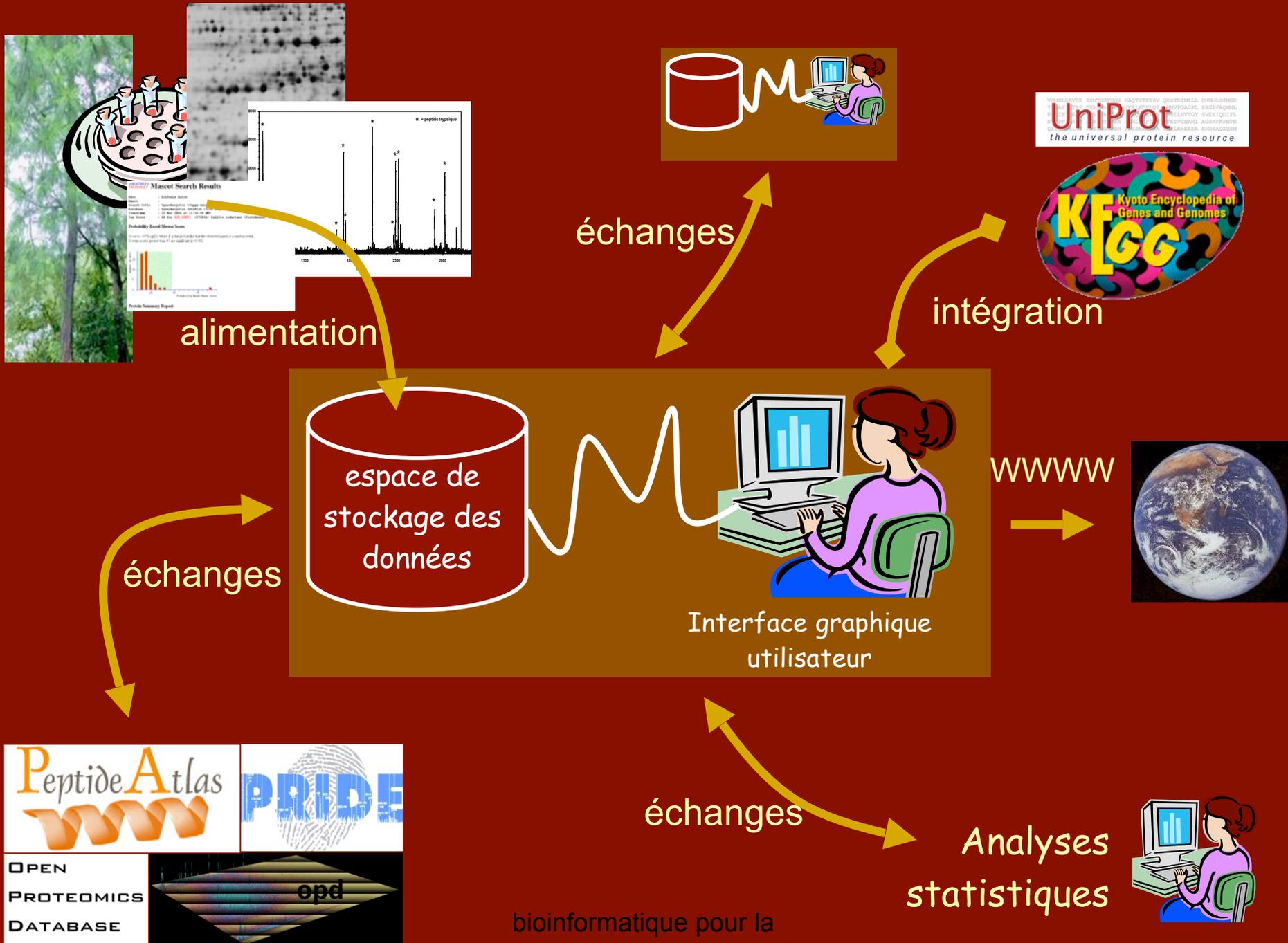
# La gestion des données des programmes de protéomique



UniProt  
the universal protein resource



bioinformatique pour la  
protéomique - Juin 2006 - INRIA  
Grenoble



# Chargement des données

# Chargement des données

Quelles données conserver ?

Toutes : LIMS

traçabilité complète (normalisation)

complexe, presque spécifique à chaque laboratoire

Données directement utiles à l'interprétation des expériences

traçabilité incomplète

moins complexe et donc plus facile à faire évoluer, moins dépendant de l'environnement technique

Comment les soumettre ?

Via une personne spécialisée (administrateur)

Par l'utilisateur lui-même

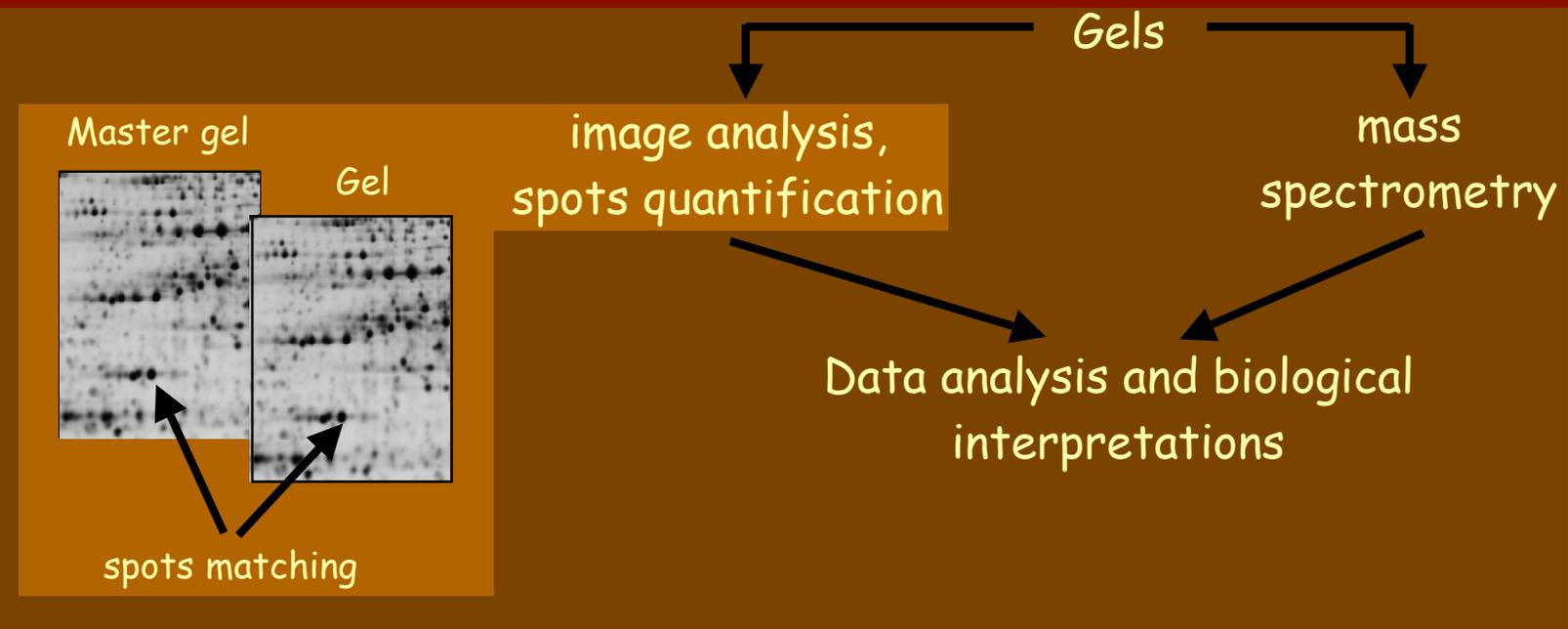
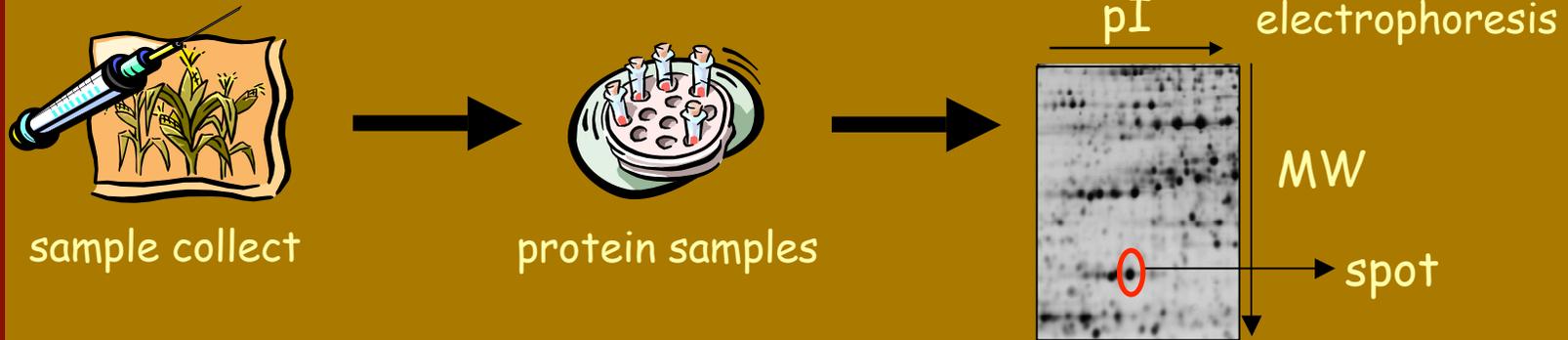
-adapté à la plupart des laboratoires.

-pas besoin d'un environnement informatique important

-l'utilisateur est aussi le meilleur expert de ses données

# inventaire

Données non-électroniques



Données électroniques

# Les problèmes liés au chargement des données

## 1) les données non -électroniques

Saisie manuelle par les utilisateurs  
fastidieux

-> risques d'erreurs

=> vérifications automatiques

=> vocabulaire contrôlé obligatoire

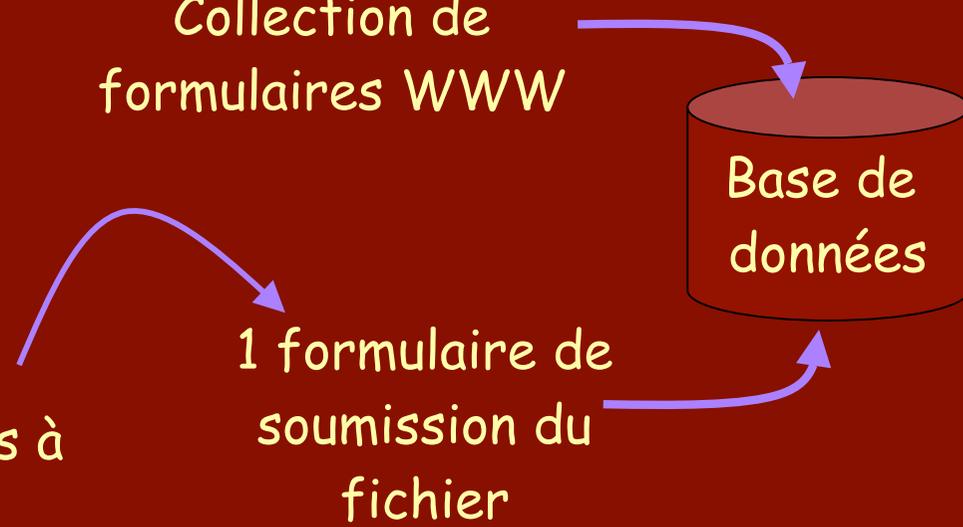
-Petits jeux de données

Collection de  
formulaires WWW

-Jeux de données volumineux

Un fichier tableur unique  
rassemblant toutes les données à  
saisir de la plante à l'image

1 formulaire de  
soumission du  
fichier



Base de  
données

# Les problèmes liés au chargement des données

## 1) les données non -électroniques

Les vocabulaires contrôlés (~ontologie)

Il s'agit de dictionnaires propres à une thématique et à un ensemble d'acteurs qui les ont adopté (labo, communauté) associant un nom (unique) à un objet (biologique).

Les noms déjà en usage dans la communauté doivent être pris en compte (gestion des synonymes).

- \*Permettent d'éviter les erreurs de saisie (orthographe)

- \*Facilitent l'interrogation des bases de données et aident à obtenir des réponses exhaustives

- \*Indispensables à l'intégration semie-automatisée des données

- \*Tous les champs de la protéomique ne sont pas encore couverts

- \*A partir d'un certain niveau de détail, les experts divergent sur les choix des termes et de leurs définitions (caractères phénotypiques et leurs mesures)

# Les problèmes liés au chargement des données

## 1) les données non -électroniques

Les vocabulaires contrôlés (~ontologie)

The screenshot shows the Ontology Lookup Service (OLS) homepage in a Mozilla Firefox browser. The browser's address bar shows the URL <http://www.ebi.ac.uk/ontology-lookup/>. The page features the EMBL-EBI logo and navigation menus for 'Services', 'Toolbox', 'Databases', and 'Downloads'. The main content area is titled 'OLS Ontology Lookup Service' and contains a search interface. The search term 'Mass Spectroscopy CV (PSI-MS) [PSI]' is entered in the 'Search Ontology' field. A dropdown menu displays a list of ontologies, with 'Mass Spectroscopy CV (PSI-MS) [PSI]' selected. The 'Term Name' field is empty, and the 'Additional Information' field contains a partial search instruction: 'Enter a partial search entering in the form. If the form. If you see ". redirected to a page v box while the Gene C'. Below the search interface, there is a 'Project description' section.

OLS Ontology Lookup Service

Enter Ontology Term

Search Ontology:

Term Name:

Additional Information:

Enter a partial search entering in the form. If the form. If you see ". redirected to a page v box while the Gene C

For better search resu 4'-(L-tryptophan), try

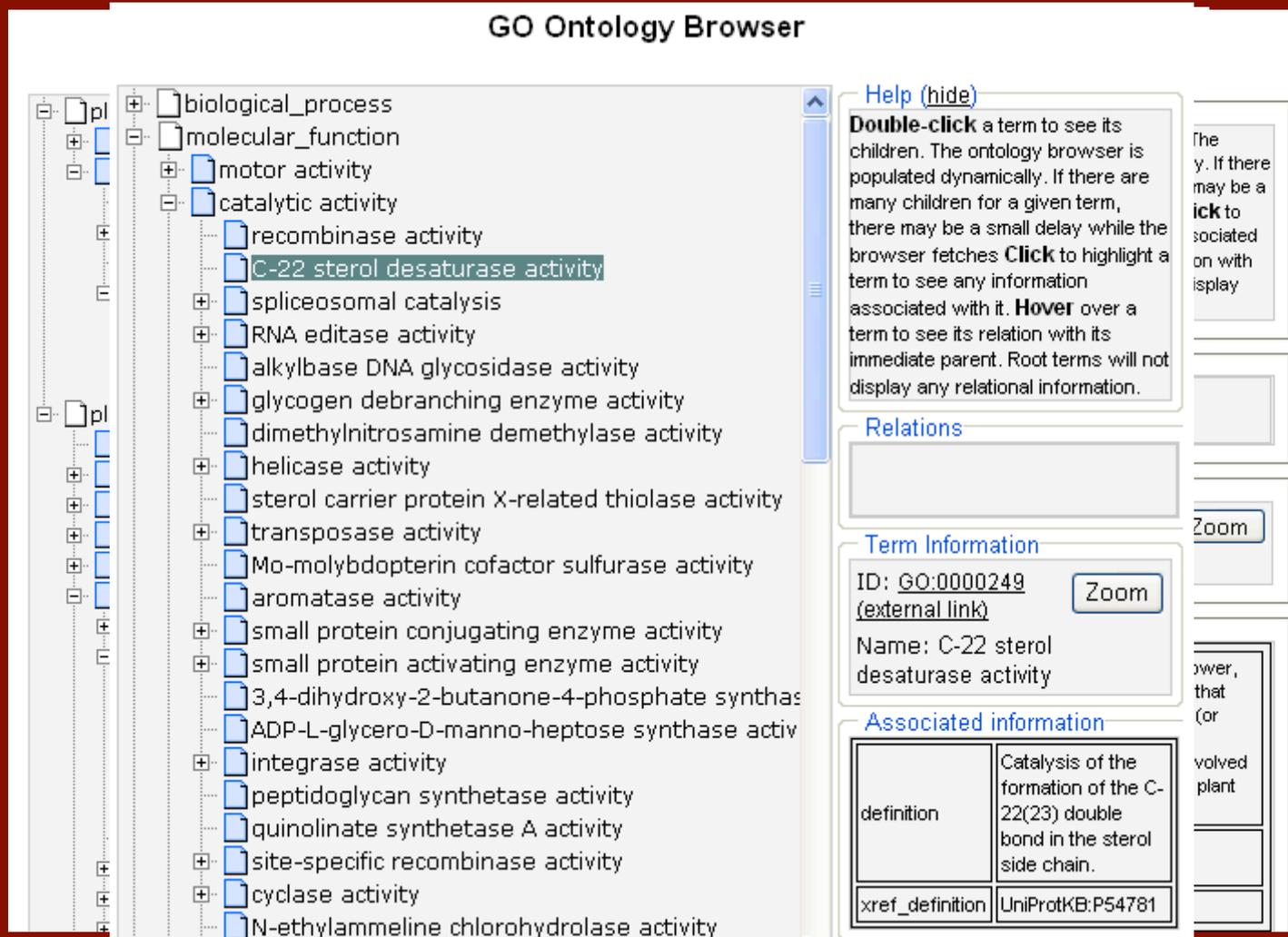
You can browse an o the complete ontology from which the onto

Project description

# Les problèmes liés au chargement des données

## 1) les données non -électroniques

Les vocabulaires contrôlés (~ontologie)



GO Ontology Browser

biological\_process  
molecular\_function  
motor activity  
catalytic activity  
recombinase activity  
**C-22 sterol desaturase activity**  
spliceosomal catalysis  
RNA editase activity  
alkylbase DNA glycosidase activity  
glycogen debranching enzyme activity  
dimethylnitrosamine demethylase activity  
helicase activity  
sterol carrier protein X-related thiolase activity  
transposase activity  
Mo-molybdopterin cofactor sulfurase activity  
aromatase activity  
small protein conjugating enzyme activity  
small protein activating enzyme activity  
3,4-dihydroxy-2-butanone-4-phosphate synthase activity  
ADP-L-glycero-D-manno-heptose synthase activity  
integrase activity  
peptidoglycan synthetase activity  
quinolinate synthetase A activity  
site-specific recombinase activity  
cyclase activity  
N-ethylammeline chlorohydrolase activity

**Help (hide)**  
Double-click a term to see its children. The ontology browser is populated dynamically. If there are many children for a given term, there may be a small delay while the browser fetches. Click to highlight a term to see any information associated with it. Hover over a term to see its relation with its immediate parent. Root terms will not display any relational information.

**Relations**

**Term Information**  
ID: [GO:0000249](#) (external link)   
Name: C-22 sterol desaturase activity

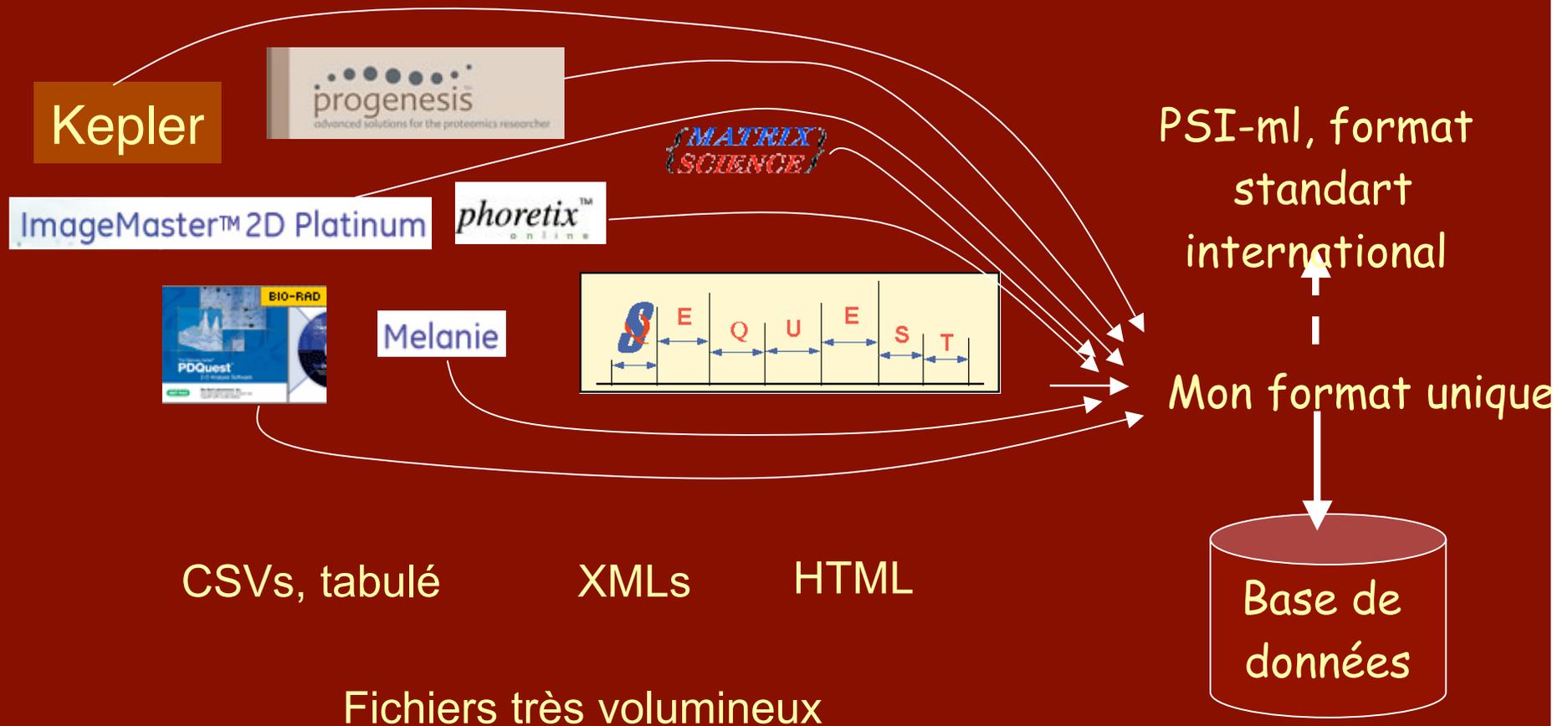
**Associated information**

definition	Catalysis of the formation of the C-22(23) double bond in the sterol side chain.
xref_definition	UniProtKB:P54781

# Les problèmes liés au chargement des données

## 2) les données électroniques

Formats et types de données très hétérogènes



# PROTICdb

## Interface de chargement des données

**PROTICdb**

Protic login - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/

**PROTICdb**

Protic  
a plant proteomic Database

Login  
Help  
Credits

**Login**

*Login form to Protic*

login   
password   
submit

PROTICdb is a new web-based application designed for large-scale plant proteomic programs. This software allows to store and query data related to: (i) the experimental design (including plant, protein sample description and 2D-PAGE protocol), (ii) the behaviour of individual spots (in respect to qualitative and quantitative protein expression), and (iii) the identification of the proteins. Database feeding can be achieved by uploading different formatted files or using web forms. The query of data proceeds from a graphical tool that uses a clickable annotated image of the 2D-gel. Links to external databases are available. The biological relationship between spots (e.g. allelic variants, identical function, post-translational modification) is defined, controlled and stored; eventually a network of the connected spots is made available. Furthermore, to allow different experiments to be jointly analyzed (e.g. to obtain the correlation between protein expressions), different types of objects (plants, samples, gels, spots) can be aggregated. PROTICdb is based on the Oracle or the PostgreSQL DBMS and is available upon request.

[Support](#)

PROTICdb 1.2.1beta, mar 2006

# Interface de chargement des données

PROTICdb homepage - Mozilla Firefox

Eichier Edition Affichage Aller à Marque-pages Outils ?

← → ↻ × 🏠 P http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?session=login&file=proti OK



**PROTICdb homepage**

User: JOHANN

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Credits

### Protic overview

<b>Projects :</b>	15
<b>Experiments :</b>	18
<b>Plants :</b>	81
<b>Plant samples :</b>	135
<b>Protein samples :</b>	157
<b>Gels :</b>	149
<b>Detection experiments :</b>	143
<b>Spots (detected) :</b>	174731
<b>Spots (identified) :</b>	1739

[Support](#)

PROTICdb 1.2.1beta, mar 2006

Terminé

# Interface de chargement des données

Protic project selector - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

← → ↻ × 🏠 P http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=&file=project\_sel



## Protic project selector

User: JOHANN

- Logout
- Help
- Project selector**
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Credits

### Project

Please select a project : **BRASSICA NAPUS - PROTEOMIC MAPS** ▼

[Support](#)

PROTICdb 1.2.1beta, mar 2006

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=&file=project\_selector

# Interface de chargement des données

PROTICdb homepage - Mozilla Firefox

Echier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=project\_overview



**PROTICdb homepage**

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

### Project overview

<b>Experiments :</b>	1
<b>Plants :</b>	3
<b>Plant samples :</b>	3
<b>Protein samples :</b>	3
<b>Gels :</b>	3
<b>Detection experiments :</b>	3
<b>Spots (detected) :</b>	5458
<b>Spots (identified) :</b>	576

[get a report file for an identification order](#)

Terminé

# Interface de chargement des données

New Plant - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=form&file=create



## New Plant

[Plant](#) [Plant sample](#) [Protein sample](#) [Gel](#) [Gel image](#)

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

### Plant update

plant/experiment  
1802/BRASSICA NAPUS - PROTEOMIC MAPS  
[update](#)

### New plant

Plant name\*

### Experiment

experiment name   
[update](#) [new](#)

### Genetics

Population/line :  [update](#) [new](#)  
genotype  [update](#) [new](#)  
test  [update](#) [new](#)

### Cultivation

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=form&file=create\_plant

# Interface de chargement des données

PROTICdb homepage - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=cv&file=view\_reference



## PROTICdb homepage

**Controlled vocabulary**

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary**
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

Plant		Plant sample harvesting and protein sample							
<u>genotype</u>	<u>plant test</u>	<u>plant population</u>	<u>sample organ</u>	<u>rank definition</u>	<u>subcellular compartment</u>	<u>tissue</u>	<u>harvesting stage</u>	<u>protein sample quality</u>	<u>concentration unit</u>
Arabidopsis thaliana	N.A.	A188	5TH LEAF	0-10CM	N.A.	LEAF	3J APRES ARRET CROISSANCE F6	EXCELLENT	MG/ML
Brassica napus SYNTHETIC AMPHIDIPOID	N.R.	B73	6TH LEAF	0-2 CM	N.R.	N.A.	3J APRES CROISSANCE CONSTANTE DE LA FEUILLE 6	N.A.	N.A.
Brassica napus SYNTHETIC AMPHIHAPLOID	RC VS HDEM	BRAIN 97	8TH LEAF	10-20CM		N.R.	3J APRÈS CROISSANCE CONSTANTE DE LA FEUILLE 6	N.R.	
Brassica oleracea HDEM		SMOOTH F2	ADULT LEAF	12-14 CM		ROOT	3J+18H		
Brassica oleracea RC		F252	ADULT ROOT	20-22 CM		STEM	ADULT PLANT		
Brassica rapa Z1		F2LIGNEE	ADULT STEM	6-8 CM		WHOLE KERNEL	FEUILLE 4		
Saccharomyces cerevisiae		MBS	EAR LEAF	7-12 CM			FEUILLE 5 ADULTE		

# Interface de chargement des données

Plant to image form - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=chargement\_plant\_image\_fr



## Plant to image form

[plant2image \(txt file\)](#) [virtual spot detection \(update\)](#) [spot detection \(new/update\)](#)  
[MS identification request \(in\)](#) [MS identification request \(out\)](#) [identification results \(txt file\)](#)

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

### Plant to image file upload

[here is the excel template file](#)

Choose your experiment : **BRASSICA NAPUS - PROTEOMIC MAPS** [update](#) [new](#)

Select your file :

[Submit](#)

### Gel image file upload

Only jpg file can be viewed in the gel browser.  
Do not submit image file from PDQUEST here.

image file format

Select your gel image file :

[Submit](#)

# Consultation, interrogation et export des données

# Le navigateur de gels

The image displays a complex software interface for navigating 2D gel electrophoresis data. It features several overlapping windows:

- Spot Information Panel (Top Left):** A hierarchical tree showing the structure of the data. It includes:
  - Spot n° 1279**
    - General
    - Relations
      - 1279 (DV02041611) - 3592 (GEL7DAPBLEU)
      - 3592 (GEL7DAPBLEU) - 1386 (DV02121001)
      - Type: match
      - Comment: Manual matching
      - Author: JOHANN JOETS
      - Creation date: 2004-08-16 15:41:17.0
    - Identification
      - validated
    - MS details
      - Match 0(3)
        - gi|1346501|sp|P37228| MDHG\_SOYBN MALATE
          - MDHG\_SOYBN MALATE DEHYDROGENASE,
          - Match score: 20.22
          - 1346501|entrez (link)
        - Swiss Prot Keywords / GO
          - P37228|swiss prot (link)
        - Swiss Prot Keywords / GO
          - TRANSIT PEPTIDE
          - GLYOXYLATE BYPASS
          - GLYOXYISOME
          - NAD
          - OXIDOREDUCTASE
          - TRICARBOXYLIC ACID CYCLE
            - PROTEIN INVOLVED IN THE TRICAR...
            - GO:0006099|GO (link)
        - Peptid (DDLFINAGVIK)
          - MH+: 1318.7
          - Z: 2
          - XC: 4.44
          - Delta CN: 0.24
          - SP: 1733.4
          - RSP: 1
          - Count: 21
        - Peptid (DDLFINAGVIK)
      - gi|126896|sp|P17783| MDHM\_CITLA MALATE DE...
    - Quantification
      - Area: 7.49
      - Area unit:
      - Volume: 381889
      - Volume unit:
      - Pic height:
      - Pic height unit:
      - Sx:
      - Sy:
      - Sx sy unit:
      - Method scaling name: NO

- NCBI Sequence Viewer (Bottom Left):** A window showing the protein sequence for P37228. The search criteria are "Protein" and "P37228". The results show:
- LOCUS: P37228, 353 aa
- DEFINITION: Malate dehydrogenase, glyoxysomal precursor
- ACCESSION: P37228
- VERSION: P37228 GI:1346501
- DBSOURCE: swissprot: locus MDHG\_SOYBN, accession P37228
- class: standard.
- created: Oct 1, 1994.
- sequence updated: Feb 1, 1996.
- annotation updated: Jun 15, 2004.
- xrefs: gi: 169976, gi: 169977
- xrefs (non-sequence databases): HSSPP00346, InterProIPR001252, PfamPF02866, PfamPF00051, PROSITEPS00068
- KEYWORDS: Oxidoreductase; Tricarboxylic acid cycle; (
- 2D Gel Image (Center):** A grayscale image of a 2D gel with a zoom level of 5. A red arrow points to a specific spot labeled "1279".
- Project Information (Top Right):** Project: PLANT RESPONSE... Comment: Zea mays F2 Plant: P T 3 3 J Organ: 6TH LEAF Spots: 9 (ident.) 1817 (det.)
- Project Information (Bottom Right):** Project: Comment: Organism: Plant: Organ: Spots: 0 (ident.) 0 (det.)



# Le navigateur de gels

Protica - jjoets - Association mode : ON - type : multigenic family

File View Mode Association Tools Help

20D050101

Zoom level  
1

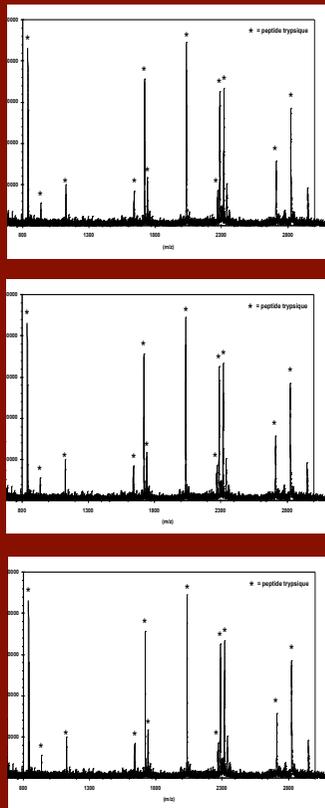
Exported data

spot_num:spot_soft_num (volume)	11D17D101:PROCBILLESEGM:NO	17D3D
991:194	4267	0
145:1168	35716	0
396:1216	15536	0
484:702	12077	0
1571:14	0	42
231:705	0	2615
380:1014	0	81762
174:827	17604	0
1164:1008	9625	0
231:1340	30295	0
359:386	8069	0
1199:513	1918	0
164:326	7660	0
1689:507	0	72
977:1323	2244	0
676:772	0	3197
87:770	73313	0
525:312	4894	0
112:902	62745	0
1580:539	0	591
139:1290	25343	0
557:979	5239	0
244:404	0	596
343:684	0	33880
704:679	24156	0
800:257	4524	0
1685:761	0	505
133:117	0	1856
1533:1017	8255	0
962:196	0	669
671:552	0	3582
673:1626	12384	0
828:1638	10002	0
399:1628	28840	0
892:1309	6993	0
370:414	10830	0
1245:409	1307	0
1009:576	0	3888
132:356	28085	0

General informations .  
Plant name : F2  
Organ name : 6TH LEAF  
Project name : PROTICDE...  
Number of identified spot : 0  
Number of detected spot : 2046

protica - jjoets - Association mode : ON - type : multigenic family  
Grenoble

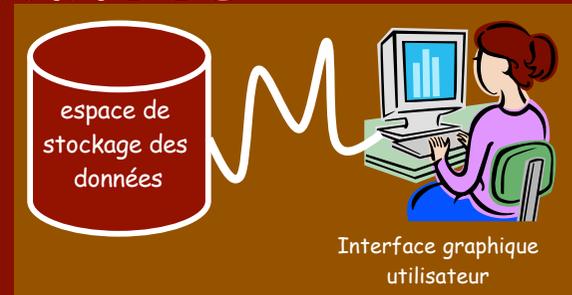
# Consultation, interrogation et exportation des données



BioWorks

ProteinLynx GS

LaunchPad



MzData

Mascot

Phenyx

Dépôts publics de données

# Le Query Builder

PROTICdb query builder - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?menu=&file=query



**PROTICdb query builder**

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

[open query builder tutorial](#)

You are searching for :

- spots
- gels**
- protein samples
- plant samples
- plants

# Le Query Builder

PROTICdb query builder - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=query



## PROTICdb query builder

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
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- Controlled vocabulary
- Methods
- Gel browser
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- Form based feeding
- File based feeding

[open query builder tutorial](#)

You are searching for spots meeting following criteria :

Select criterium **MS identification**

**add to query**

- MS identification
- Spot properties
- Master spot properties
- Project
- Gel
- Gene Ontology
- Gel image
- Protein sample
- Plant sample
- Plant

# Le Query Builder

PROTICdb query builder - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=query



## PROTICdb query builder

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

[open query builder tutorial](#)  
You are searching for spots meeting following criteria :

**MS identification**

Protein/gene name (PFK):

Protein/gene description (Phospho-Fructo Kinase):  MS method:

Include identification from manual matching :

number of matching spots :

Additional criterium  Operator

Terminé

# Le Query Builder

PROTICdb query builder-report settings - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=query



## PROTICdb query builder-report settings

User: JOHANN  
Project: BRASSICA NAPUS  
- PROTEOMIC MAPS

- Logout
- Help
- Project selector
- Administration
- Controlled vocabulary
- Methods
- Gel browser
- Query builder
- Form based feeding
- File based feeding

**report format**

master spot report  spot report

**choose data to display**

master spot number  numbering system  spot software number  spot manual number

spot coordinates x  y

MW (obs)  pl (obs)

volume  normalized volume  area  peak height

protein/gene name  protein/gene description

display in

# le Query Builder

PROTICdb spot report - Mozilla Firefox

Fichier Edition Affichage Aller à Marque-pages Outils ?

http://uln.moulon.inra.fr/~bioinfo/proticdb/Protic/home/index.php?file=results\_spot

## PROTICdb spot report

[back to report settings](#)

[back to query builder](#)

spots 1-25 of 25

[next](#)

30

[previous](#)

spot software number	spot manual number	master spot number	gel name	image name	x	y	MW (obs)	pl (obs)	numbering system	volume	normalized volume	area	peak height	protein/gene name
1193	L1147	1193	LEAF - SYNTHETIC BRASSICA NAPUS	LEAF - SYNTHETIC BRASSICA NAPUS	890	1014	41021	4.88417	LEAF - SYNTHETIC BRASSICA NAPUS	115433	0.199629	7.87		• AT1G32060 PHOSPHORIBULOKINASE (EC 2.7.1.19) PRECURSOR LIKE PROTEIN
1904	L1996	1904	LEAF - SYNTHETIC BRASSICA NAPUS	LEAF - SYNTHETIC BRASSICA NAPUS	2395	2393	14619	6.36375	LEAF - SYNTHETIC BRASSICA NAPUS	31190.7	0.0539407	22.49		• AT4G09320 NUCLEOSIDE-DIPHOSPHATE KINASE
426	R367	426	ROOT - SYNTHETIC BRASSICA NAPUS	ROOT - SYNTHETIC BRASSICA NAPUS	2650	452	65216	6.60795	ROOT - SYNTHETIC BRASSICA NAPUS	3182.83	0.01282	3.24		• AT1G20950 PUTATIVE PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE ALPHA SUBUNIT
582	R547	582	ROOT - SYNTHETIC BRASSICA NAPUS	ROOT - SYNTHETIC BRASSICA NAPUS	1759	535	61294	5.80645	ROOT - SYNTHETIC BRASSICA NAPUS	9419.92	0.0379422	2.44		• AT5G08570 PYRUVATE KINASE
1224	R1057	1224	ROOT - SYNTHETIC BRASSICA NAPUS	ROOT - SYNTHETIC BRASSICA NAPUS	1256	902	42367	5.28539	ROOT - SYNTHETIC BRASSICA NAPUS	31891.1	0.128453	4.39		• AT3G09820 ADENOSINE KINASE LIKE PROTEIN

Terminé

# Prochaines versions de PROTIcDb

Correction de bugs

Formulaire unique pour la soumission de tous les types de données

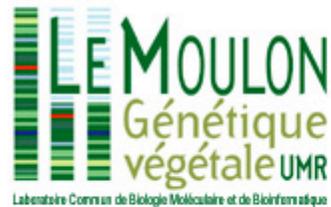
Outil de consultation des spectres de masse annotés

Amélioration des outils d'édition et de suppression des données

## futures versions de PROTIcDb

Stockage des résultats d'analyses statistiques

Elargissement de l'intégration de données



# PROTICdb est disponible gratuitement

PROTICdb

Tuesday, 25 April 2006

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## PROTICdb: a plant 2-D PAGE database

Project leader	Johann Joets ( <a href="#">contact</a> )
Project team	Olivier Langella, H�el�ene Denos, Thomas Leboucher, Pierre Montalent, Guy Decoux, Thierry Balliau, Michel Ziwy
Project previous staff members	Gwenn Houel, Luc Moreau, Luc Negrone, Delphine Vincent, Johan Bordeaux
Project collaborators	H�el�ene Ferry-Dumazet, Antoine de Daruvar (CBIB, Bordeaux, France) C�eline Lalanne, Christophe Plomion (INRA, BIOGECO, Cestas, France)

PROTICdb is a web-based application mainly designed to store and analyse plant proteome data obtained by two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) and mass spectrometry (MS). The objectives of PROTICdb are twofold: 1/ to store, track and query information related to a proteomic experiment, i.e. from tissue sampling to protein identification via the quantitative measurement of protein accumulation by image analysis, 2/ to integrate information from the user own expertise or other sources into a knowledge base, and support the interpretation of the data (e.g. function, post-translational modification, allelic variant determination...). The insertion of data into the relational database of PROTICdb is achieved either by direct upload of output of widely used image analysis and MS identification or by filling web forms. 2-D PAGE annotated maps can be displayed, queried and compared through a graphical interface. Links to external databases are available. Quantitative data can be easily exported into a tabulated format for statistical analyses. PROTICdb is based on the Oracle or the PostgreSQL DataBase Management System (DBMS).

### News

PROTICdb 1.2 is now available.  
 This new version includes an advanced query builder tool. It is now possible to search for protein, sample, gel, ... according to a large number of criteria. A flash tutorial is provided, describing the main functionalities of this new tool.  
 The gel browser was improved (faster gel image loading).  
 PROTICdb 1.2 will be presented at the [Swiss Proteomics Society 2005 Congress](#), Zurich, Switzerland.  
 The PROTICdb poster is available [here](#).

### The PROTICdb newsletter

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