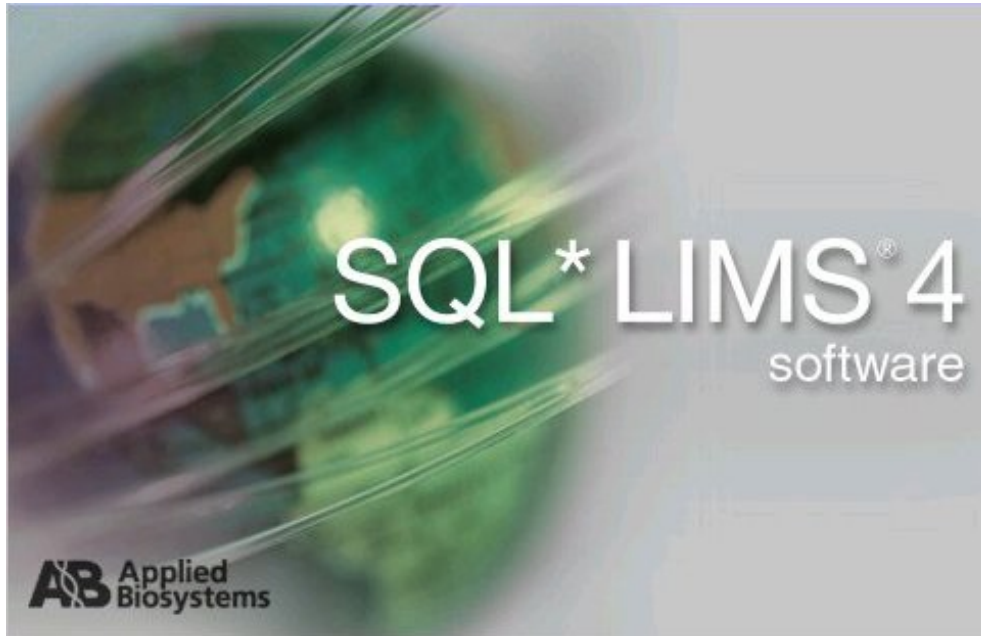


# La solution SQL\*LIMS appliquée à la plate-forme Protéomique du Génopôle Toulouse Midi-Pyrénées



**LIMS : Laboratory Information Management System**

# Consortium ASG

CIPF - Saint Julien



Pierre Fabre

J-F Haeuw CIPF  
A V. Dorselaer LSMBO  
J-C Michalski LGSM  
B. Monsarrat IPBS

LSMBO - Strasbourg



LGSM - Lille



IPBS - Toulouse



Cancer  
biomarkers

## Programme Protéomique et Cancer

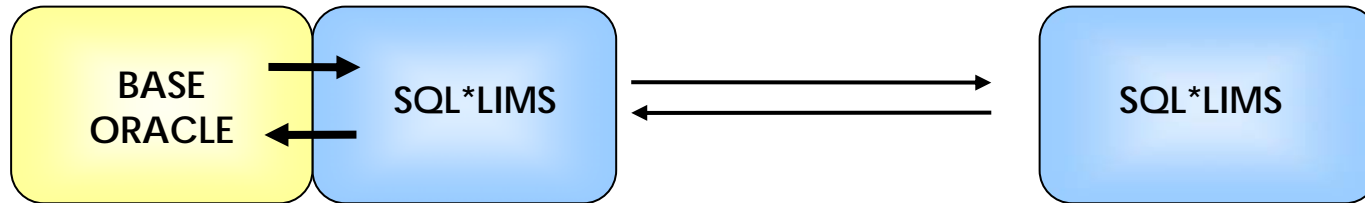
### BESOINS :

- ❑ Gérer et exploiter l'ensemble des données
- ❑ Permettre le partage d'informations entre les partenaires du projet
- ❑ Création d'une base de données commune
  - Collecte d'information
  - Stockage et organisation
  - Mise à disposition

### MISE EN PLACE SQL\* LIMS:

- ❑ Décembre 2001 – juin 2002 : évaluation de solutions
- ❑ Juillet 2002 : version commerciale installée au CIPF, début des développements spécifiques
- ❑ Juin 2003 : déploiement et formation

# Architecture du LIMS de la plate-forme protéomique de Toulouse



## **SERVEURS :**

Oracle 8i, contenant les données  
Application serveur SQL\*LIMS

## **CLIENT :**

Application cliente SQL\*LIMS

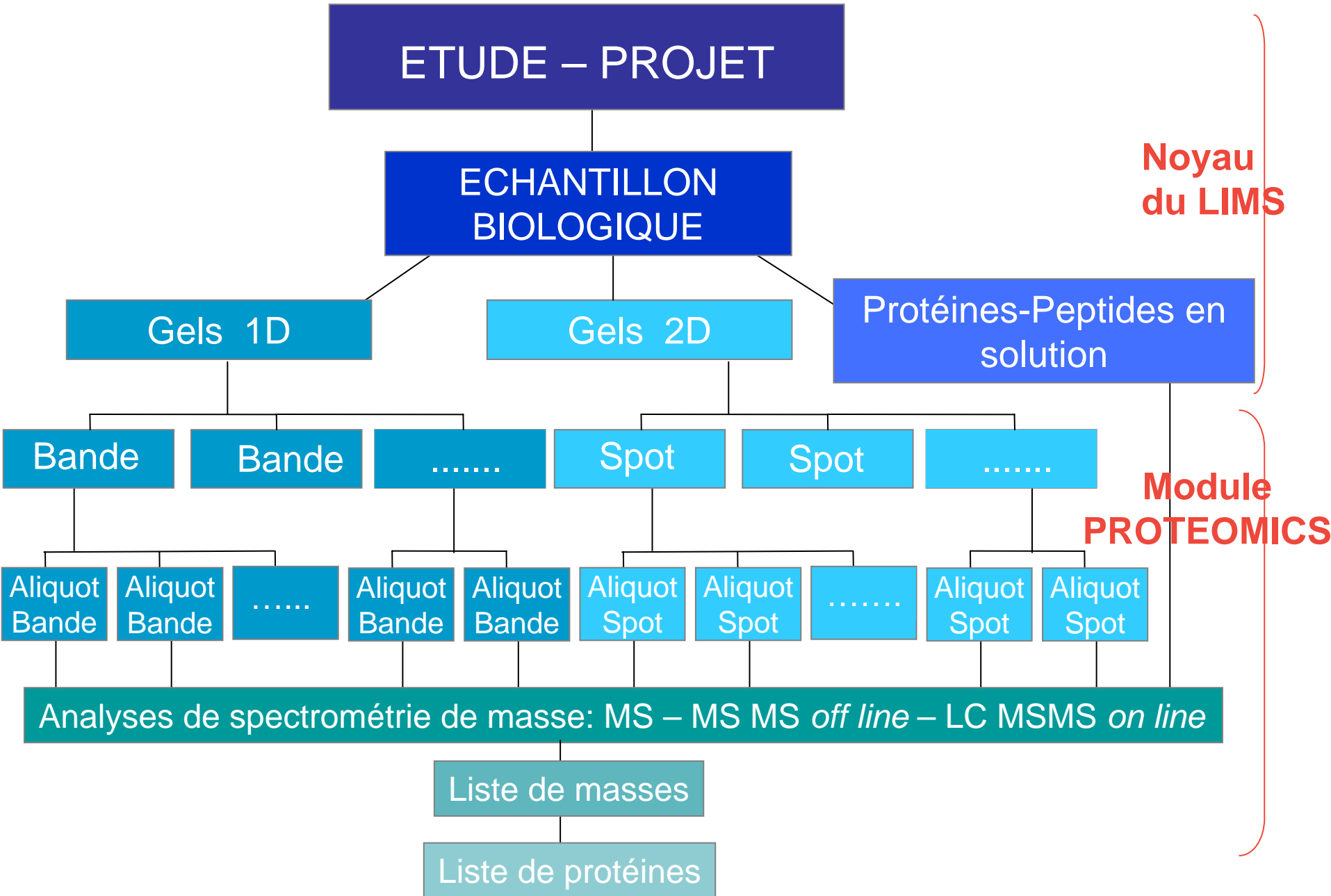
- ❑ Le client communique avec le serveur SQL\*LIMS via le réseau.
- ❑ SQL\*LIMS interagit avec la base Oracle (requêtes ou entrées de résultats).
- ❑ SQL\*LIMS renvoie les résultats au client.

## **Installation en cours :**

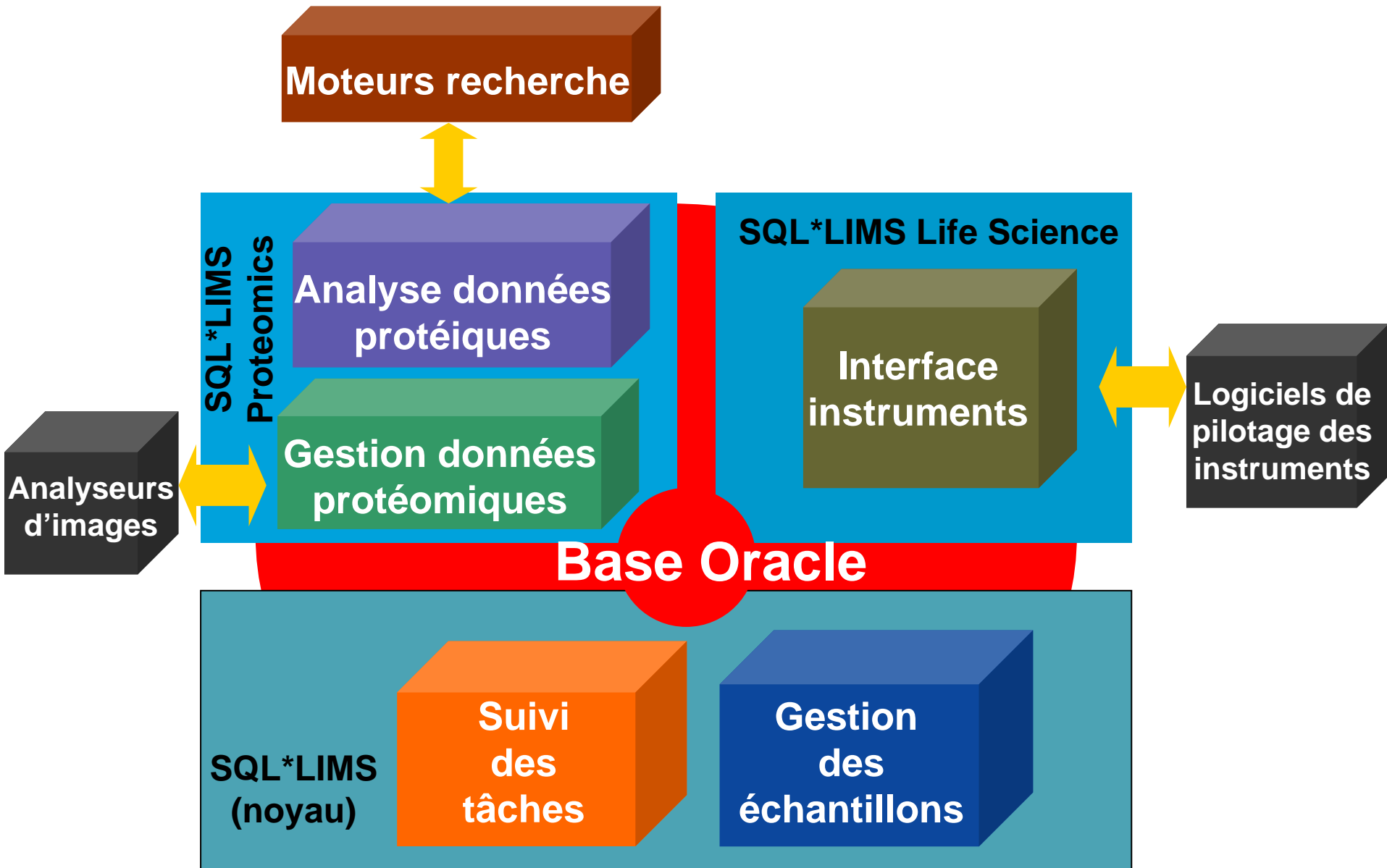
- première phase fin avril
- deuxième phase 8-11 juin



# Flux d'analyses sur la plate-forme



# Composants du logiciel



# Connexion LIMS - Instruments

QSTAR



Analyst QS

MALDI-TOF TOF



4700 Explorer

MALDI-TOF

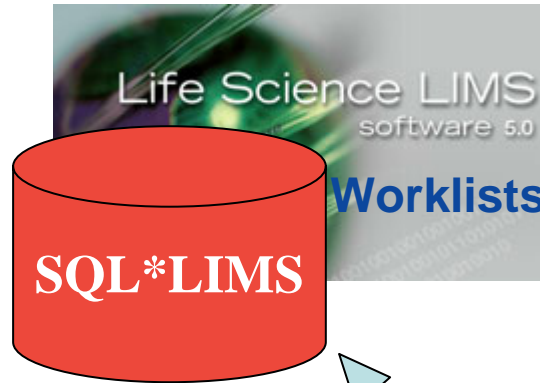


Voyager

QTRAP



Analyst QT



Xcalibur



TRAPPE IONIQUE

# Création d'une feuille de travail (*Worklist*)

The screenshot shows the SQL\*GT application window. On the left, a tree view displays a hierarchy of containers under 'Main'. The 'Containers' folder is expanded, showing several sub-folders and containers. A context menu is open over the container '20011020-001-S01-G001-C01-900000043', with the 'Create Sample Sheet' option highlighted. The main area of the window contains a search interface with 'Containers' selected in the 'Search For' dropdown and 'Standard' in the 'Type' dropdown. Below the search fields are input boxes for 'Container ID', 'Parent Container ID', 'Name', 'Datagroup', 'Description', 'Class', 'Status', 'Userstamp', and 'Timestamp'. A 'Find' button is located to the right. Below the search area is a section for the 'SQL Script' with a table header '20011020-001-S01-G001-C01-900000043' and an 'Action' column. The table has 4 columns and 8 rows (A-H).

|   | 1                        | 2                        | 3                        | 4                        |
|---|--------------------------|--------------------------|--------------------------|--------------------------|
| A | 20011020-001-S01-G001#1  | 20011020-001-S01-G001#2  | 20011020-001-S01-G001#3  | 20011020-001-S01-G001#4  |
| B | 20011020-001-S01-G001#11 | 20011020-001-S01-G001#12 | 20011020-001-S01-G001#13 | 20011020-001-S01-G001#14 |
| C | 20011020-001-S01-G001#21 | 20011020-001-S01-G001#22 | 20011020-001-S01-G001#23 | 20011020-001-S01-G001#24 |
| D | 20011020-001-S01-G001#31 | 20011020-001-S01-G001#32 | 20011020-001-S01-G001#33 | 20011020-001-S01-G001#34 |
| E | 20011020-001-S01-G001#41 | 20011020-001-S01-G001#42 | 20011020-001-S01-G001#43 | 20011020-001-S01-G001#44 |
| F |                          |                          |                          |                          |
| G |                          |                          |                          |                          |
| H |                          |                          |                          |                          |

QStar Worklist Preview

| Sampl... | Sample ID | Com... | Acquisition ... | Processing ... | Rack ... | Plate Code | Vial P... | Dilutio... | Weight t... | Type         | Rack ... | Plate ... | Set Name | Output File Name                   |
|----------|-----------|--------|-----------------|----------------|----------|------------|-----------|------------|-------------|--------------|----------|-----------|----------|------------------------------------|
|          | 200000064 |        | ACQ Method      | Proc Method    | Rack1    | 900000006  | 1         | 9.9        | 99.9        | API QSTAR... | 99       | 1         | Name     | C:\QStarResults\200000064\20000... |
|          | 200000065 |        | ACQ Method      | Proc Method    | Rack1    | 900000006  | 2         | 9.9        | 99.9        | API QSTAR... | 99       | 2         | Name     | C:\QStarResults\200000065\20000... |
|          | 200000066 |        | ACQ Method      | Proc Method    | Rack1    | 900000006  | 3         | 9.9        | 99.9        | API QSTAR... | 99       | 3         | Name     | C:\QStarResults\200000066\20000... |
|          | 200000072 |        | ACQ Method      | Proc Method    | Rack1    | 900000006  | 4         | 9.9        | 99.9        | API QSTAR... | 99       | 4         | Name     | C:\QStarResults\200000072\20000... |



# Connexion LIMS – Moteurs de recherche

{MATRIX}  
{SCIENCE}

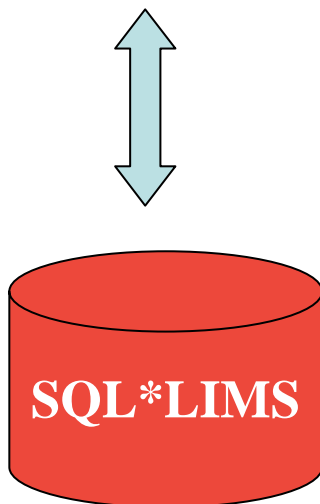
## Mascot Search

- **Peptide Mass Fingerprint:** The experimental data are a list of peptide mass values from an enzymatic digest of a protein.
  - [Search form](#)
  - [Example of results report](#)
  - [More information](#)
- **Sequence Query:** One or more peptide mass values associated with information such as partial or ambiguous sequence strings, amino acid composition information, MS/MS fragment ion masses, etc. A super-set of a sequence tag query.
  - [Search form](#)
  - [Example of results report](#)
  - [More information](#)
- **MS/MS Ion Search:** Identification based on raw MS/MS data from one or more peptides.
  - [Search form](#)
  - [Example of results report](#)
  - [More information](#)

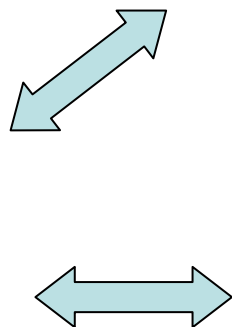
**Search Form Defaults:** You can save your preferred search form defaults as a browser cookie by following [this link](#).

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## Mascot 1.9



## Protein Prospector 3.2.1.



## Bioworks 2.1

# Soumission d'une recherche

**Protein Search Settings**

Sample ID:  Result ID:

Search engine:   Show Obsolete Records

| Name                             | Description                              | URL  | User          |
|----------------------------------|--|--|---------------|
| Mascot MS/MS Ion Search v1.8/1.9 | Mascot MS/MS Ion Search v1.8/1.9 Default | http://frodon/mascot/cgi/nph-mascot.exe... | OPS\$LIMSTEST |

**Protein Identification Searching**

Name:

Description:

URL:

Proxy Proxy:  Port:

Login:  Password:

Private

Obsolete

| Text                         | Value                         |
|------------------------------|-------------------------------|
| MS/MS tol. +/-               | 0.8                           |
| MS/MS tol. unit              | Da                            |
| Peptide charge               | 2+                            |
| Monoisotopic/Average         | Monoisotopic                  |
| Data format                  | Mascot generic [NOT EDITABLE] |
| Precursor (m/z)              |                               |
| Instrument                   | Default                       |
| Overview                     | False [NOT EDITABLE]          |
| Report top hits              | 20                            |
| MS PEAK FILTER               | -----                         |
| . Peak Density: Max peaks(s) | 50                            |
| . Min Mass Range (Da)        | 500                           |
| . Max Mass Range (Da)        | 4000                          |
| . Min S/N                    | 10                            |
| . Min Intensity              | 100                           |
| . Max Peak/Spot              | 200                           |
| MS/MS PEAK FILTER            | -----                         |
| .. Peak Density: Max peak(s) | 50                            |
| .. Min Mass Range (Da)       | 500                           |
| .. Max Mass Range (Da)       | 4000                          |

Compatible avec les moteurs de recherche locaux (Mascot – Protein Prospector – Sequest) ou accessibles par Internet.

# Résultat d'une recherche et enregistrement

**Protein Identification Loader**

**File Edit**

**Search Data**

Sample ID: 200000207

User Sample ID: 1LV2DB0924-11

Search Engine: Mascot MS/MS Ion Search v1.8

Results File Name: ion\LOCALS~1\Temp\Mascot MS MS Ion Search v1.838065.html

Create New Result in LIMS?

Result ID:

Store Results File in LIMS?

**Search Params**

| Property | Value |
|----------|-------|
|----------|-------|

| Rank | Accession No. | Mass   | Score | Protein Name   | Masses Match... | Load                                |
|------|---------------|--------|-------|--|-----------------|-------------------------------------|
| 1    | H11_BOVIN     | 10 359 | 320   | (P02253) Histone H1.1 (Fragment)   | 8 / 331         | <input checked="" type="checkbox"/> |
| 1    | H12_HUMAN     | 21 221 | 320   | (P16403) Histone H1.2 (Histone H1d)  | 8 / 331         | <input checked="" type="checkbox"/> |
| 2    | H12_RAT       | 21 843 | 315   | (P15865) Histone H1.2 (H1d)  | 8 / 331         | <input checked="" type="checkbox"/> |
| 2    | H14_HUMAN     | 21 721 | 311   | (P10412) Histone H1.4 (Histone H1b)  | 8 / 331         | <input checked="" type="checkbox"/> |
| 3    | H13_HUMAN     | 22 205 | 295   | (P16402) Histone H1.3 (Histone H1c)  | 6 / 331         | <input checked="" type="checkbox"/> |
| 4    | RS3_HUMAN     | 26 671 | 294   | (P23396) 40S ribosomal protein S3  | 7 / 331         | <input type="checkbox"/>            |
| 5    | LDHB_HUMAN    | 36 484 | 289   | (P07195) L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart sub...)        | 6 / 331         | <input type="checkbox"/>            |
| 6    | GBLP_HUMAN    | 35 055 | 287   | (P25388) Guanine nucleotide-binding protein beta subunit-like protein 12.3 (P205)...     | 6 / 331         | <input type="checkbox"/>            |
| 7    | LDHA_HUMAN    | 36 534 | 286   | (P00338) L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A) (LDH muscle su...)        | 8 / 331         | <input type="checkbox"/>            |
| 8    | ANX2_HUMAN    | 38 449 | 279   | (P07355) Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobi...) | 6 / 331         | <input type="checkbox"/>            |
| 9    | RL7A_HUMAN    | 29 846 | 271   | (P11518) 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)         | 4 / 331         | <input type="checkbox"/>            |
| 9    | RL7A_MOUSE    | 29 827 | 271   | (P12970) 60S ribosomal protein L7a (Surfeit locus protein 3)                             | 4 / 331         | <input type="checkbox"/>            |

Select All

Deselect All

**Peptide Data**

| Checked                  | Mass Match... | Mass Calc. | Delta | Start | End | Sequence      | Modification | Miss | Score | Load                                |
|--------------------------|---------------|------------|-------|-------|-----|---------------|--------------|------|-------|-------------------------------------|
| <input type="checkbox"/> | 421,75        | 0,00       | 0,00  | 0     | 0   | VAGAATPKK     |              | 0    | 17    | <input checked="" type="checkbox"/> |
| <input type="checkbox"/> | 423,25        | 0,00       | 0,00  | 0     | 0   | SGVSLAALK     |              | 0    | 75    | <input checked="" type="checkbox"/> |
| <input type="checkbox"/> | 486,94        | 0,00       | 0,00  | 0     | 0   | SGVSLAALKK    |              | 0    | 24    | <input checked="" type="checkbox"/> |
| <input type="checkbox"/> | 554,28        | 0,00       | 0,00  | 0     | 0   | ALAAAGYDVEK   |              | 0    | 74    | <input checked="" type="checkbox"/> |
| <input type="checkbox"/> | 599,83        | 0,00       | 0,00  | 0     | 0   | ASGPPVSELITK  |              | 0    | 37    | <input checked="" type="checkbox"/> |
| <input type="checkbox"/> | 663,87        | 0,00       | 0,00  | 0     | 0   | KASGPPVSELITK |              | 0    | 83    | <input checked="" type="checkbox"/> |

# Présentation

The screenshot displays the SQL\*LIMS Client V4.0 for Windows NT interface. The main window title is "SQL\*LIMS Client V4.0 for Windows NT - Denethor@limstest". The menu bar includes "File", "Log", "Results", "View", "Approve", "Edit", "Events", "Utilities", "Help", and "Window". The "Utilities" menu is open, showing options: "Memos", "Oracle Tools", "User", "Translation", "Template Menu", "System Menu", "Life Science LIMS", "Proteomics Module" (highlighted), "Show Application Toolbar", and "Show User Toolbar". A "Proteomics Menu" dialog box is open, showing "File", "Edit", "Search", and "Help" menus. The main window has a sidebar with icons for "Enter Studies", "Enter Samples", "View Samples", "Add Tasks", "View Tasks", and "Enter Results". A splash screen for "SQL\*LIMS 4 software" by "Applied Biosystems" is overlaid on the main window. The status bar at the bottom shows "Record: 1/1".

# Chargement des données “Gel” et “Spots”

**Gel&Spot Loader**

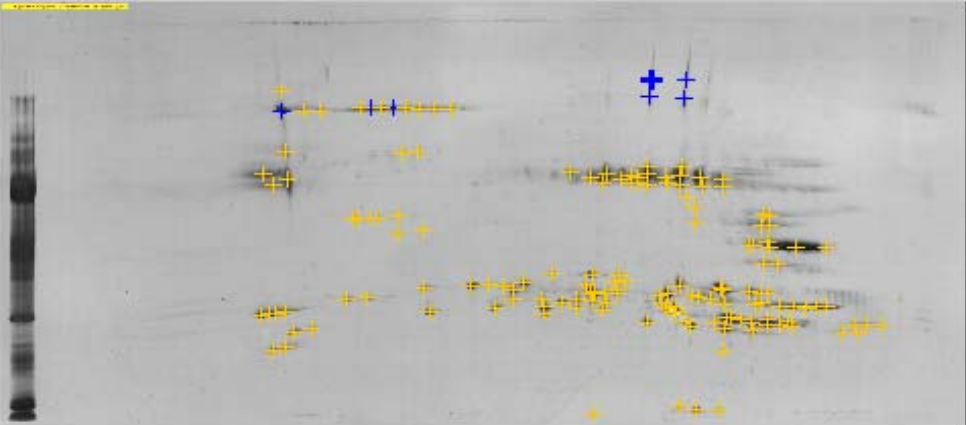
**Sample Data**  
 Sample ID: 200000178  
 User Sample ID: Src1/CARM1-01-2LV2DB0306-2DG02

**Gel Data**  
 Gel Type: Melanie 2D  
 Gel Image: 1-(09+10+11+12)-Sypro+Ag-sansspots.jpg  
 Spot Report File: \\Mel3 Biops.0010\2LV2DB0306\_030504.txt  
 Cut Report: U:\Cut report\2LV2DB0306\_030504.txt

**Container Data**

| Available                | Name          | Template       | Wells | Free ... |
|--------------------------|---------------|----------------|-------|----------|
| <input type="checkbox"/> | SpotSETCarine | 96 WELL PLA... | 96    | 89       |
| <input type="checkbox"/> | test2         | 96 WELL PLA... | 96    | 93       |

**Gel Image**  
 Contrast:   Edge Detection  Invert



**Spot Data**

| Logged                              | Spot Id       | Spot Status | XCoord | YCoord | PI    | MW [kDa] | OD  | Area     | Vol.    | % OD      | % Vol.    |
|-------------------------------------|---------------|-------------|--------|--------|-------|----------|-----|----------|---------|-----------|-----------|
| <input checked="" type="checkbox"/> | 2LV2DB0306-1  | LOADED      | 1 557  | 204    | -1,00 | -0,0     | 130 | 0,093925 | 11,589  | 0,4957290 | 0,0498768 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-2  | LOADED      | 1 640  | 206    | -1,00 | -0,0     | 147 | 0,166175 | 23,163  | 0,5605560 | 0,0996913 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-4  | LOADED      | 1 553  | 251    | -1,00 | -0,0     | 115 | 0,079475 | 8,641   | 0,4385290 | 0,0371899 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-5  | LOADED      | 1 635  | 257    | -1,00 | -0,0     | 136 | 0,137275 | 18,106  | 0,5186090 | 0,0779248 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-7  | LOADED      | 940    | 280    | -1,00 | -0,0     | 176 | 0,708050 | 115,434 | 0,6711410 | 0,4968100 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-9  | LOADED      | 672    | 288    | -1,00 | -0,0     | 209 | 1,372750 | 270,230 | 0,7969800 | 1,1630300 |
| <input checked="" type="checkbox"/> | 2LV2DB0306-11 | LOADED      | 887    | 281    | -1,00 | -0,0     | 178 | 0,628575 | 107,154 | 0,6787670 | 0,4611750 |
| <input type="checkbox"/>            | 2LV2DB0306-3  | LOADED      | 672    | 236    | -1,00 | -0,0     | 129 | 0,093925 | 11,733  | 0,4919150 | 0,0504988 |
| <input type="checkbox"/>            | 2LV2DB0306-6  | LOADED      | 912    | 280    | -1,00 | -0,0     | 180 | 0,729725 | 122,731 | 0,6863940 | 0,5282160 |
| <input type="checkbox"/>            | 2LV2DB0306-8  | LOADED      | 970    | 280    | -1,00 | -0,0     | 167 | 0,556325 | 85,558  | 0,6368210 | 0,3682310 |
| <input type="checkbox"/>            | 2LV2DB0306-10 | LOADED      | 861    | 281    | -1,00 | -0,0     | 163 | 0,397375 | 60,062  | 0,6215680 | 0,2584960 |
| <input type="checkbox"/>            | 2LV2DB0306-12 | LOADED      | 1 002  | 282    | -1,00 | -0,0     | 147 | 0,281775 | 39,636  | 0,5605560 | 0,1705890 |
| <input type="checkbox"/>            | 2LV2DB0306-13 | LOADED      | 1 075  | 283    | -1,00 | -0,0     | 162 | 0,252875 | 38,531  | 0,6177550 | 0,1658310 |
| <input type="checkbox"/>            | 2LV2DB0306-14 | LOADED      | 1 038  | 284    | -1,00 | -0,0     | 148 | 0,339575 | 47,779  | 0,5643680 | 0,2056330 |
| <input type="checkbox"/>            | 2LV2DB0306-15 | LOADED      | 726    | 287    | 1,00  | 0,0      | 160 | 0,222075 | 32,452  | 0,6062140 | 0,1420210 |

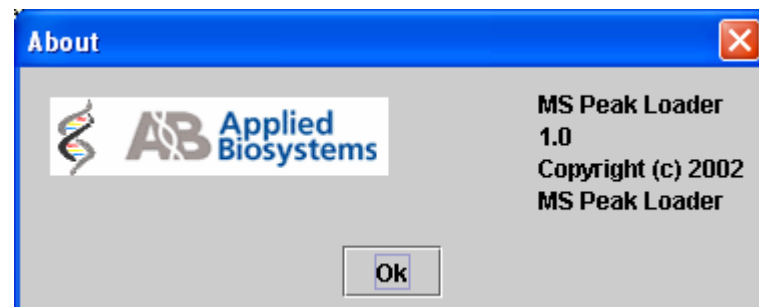
# Chargement des listes de masses - *Peaklists*

| Name                      | Description                      | Mass Spectrometer         | Post Process Sw       | Freq.(sec.) | Scheduled                           | Manual                              |
|---------------------------|----------------------------------|---------------------------|-----------------------|-------------|-------------------------------------|-------------------------------------|
| QSTAR                     | Applied Biosystems QSTAR PUL...  | MS/MS AB QSTAR PULSA...   | Analyst 1.0           | 20          | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> |
| TOF-TOF MANUAL            | Applied Biosystems TOF TOF       | MALDI-TOF                 |                       | 300         | <input type="checkbox"/>            | <input checked="" type="checkbox"/> |
| AUTOFLEX                  | Bruker Daltonics AUTOFLEX        | MS Bruker AUTOFLEX        | Xmass 5.1.1           | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |
| BIFLEX                    | Bruker Daltonics BIFLEX          | MS Bruker BIFLEX          | Xmass 5.0             | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |
| ULTRAFLEX                 | Bruker Daltonics ULTRAFLEX       | MS Bruker ULTRAFLEX       | Xmass 5.0             | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |
| ESQUIRE 3000+ (MS run)    | Bruker Daltonics ESQUIRE 3000... | MS/MS Bruker ESQUIRE 3... | Data Analysis 2.1/2.2 | 0           | <input type="checkbox"/>            | <input type="checkbox"/>            |
| ESQUIRE 3000+ (MS/MS run) | Bruker Daltonics ESQUIRE 3000... | MS/MS Bruker ESQUIRE 3... | Data Analysis 2.1/2.2 | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |
| QTOF                      | Micromass QTOF II (MS run)       | Micromass QTOF            |                       | 0           | <input type="checkbox"/>            | <input type="checkbox"/>            |
| QTOF II (MS run)          | Micromass QTOF II (MS run)       | MS Micromass QTOF II      | MassLynx 3.5          | 0           | <input type="checkbox"/>            | <input type="checkbox"/>            |
| QTOF II (MS/MS run)       | Micromass QTOF II (MS/MS run)    | MS Micromass QTOF II      | MassLynx 3.5          | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |
| LCQ DECA                  | Thermo Finnigan LCQ DECA         | MS Thermo Finnigan LCQ... | Xcalibur 1.2          | 300         | <input type="checkbox"/>            | <input type="checkbox"/>            |

**Description** Applied Biosystems QSTAR PULSAR I  
**Mass Spectrometer** MS/MS AB QSTAR PULSAR I  
**Post Process Sw** Analyst 1.0  
**Input File Dir.** U:\LIMS\_peakliststestpeakloader **Ext.** tmp  
**Processed File Dir.** U:\LIMS\_peakliststestpeakloader **Ext.** DON  
**Error File Dir.** U:\LIMS\_peakliststestpeakloader **Ext.** BAD  
**Frequency (sec.)** 20  
**Precursor**  
**Attached Files**

| Description | File | Attached of |
|-------------|------|-------------|
|             |      |             |

Un programme externe  
PeakLoader.exe récupère  
automatiquement les *peaklists*



# Visualisation des données à travers le Module Proteomics

Src1/CARM1

Src1/CARM1-01

Src1/CARM1-01-1LV2DB0924-2D601

- 1LV2DB0924-1
- 1LV2DB0924-2
- 1LV2DB0924-4

PROTEIN ANALYSIS METHOD

PROTEIN ANALYSIS

PROTEIN ANALYSIS

TOF-TOF MANUAL

Mascot PMF v1.8

1LV2DB0924-5

1LV2DB0924-7

1LV2DB0924-9

1LV2DB0924-11

Src1/CARM1-01-1LV2DB0924-11-1

Src1/CARM1-01-1LV2DB0924-11-2

Src1/CARM1-01-1LV2DB0924-11-3

Src1/CARM1-01-1LV2DB0924-11-4

Src1/CARM1-01-1LV2DB0924-11-5

Container MS Data & Proteins

Version: 1/1 Status: NOT\_YET\_VALIDATED User: LIMSTEST Date: 05/03/2004

| Rank | Accession No. | Mass   | Score | Protein Name   | Masses Mat... | Validate                 |
|------|---------------|--------|-------|--|---------------|--------------------------|
| 1    | PSA2_HUMAN    | 25 865 | 63    | Proteasome subunit alpha type 2 (EC 3.4.99.46) (Proteasome compon... | 8 / 49        | <input type="checkbox"/> |

Peptide Data

| Chec...                  | Mass Mat... | Mass Ca... | Del... | Start | End | Sequence              | Modification  | Miss | Score | Validate                 |
|--------------------------|-------------|------------|--------|-------|-----|-----------------------|---------------|------|-------|--------------------------|
| <input type="checkbox"/> | 787,45      | 786,45     | -0,01  | 220   | 226 | LTPTEVK               |               | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 895,45      | 894,44     | -0,01  | 53    | 59  | SILYDER               |               | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 943,56      | 942,55     | 0,00   | 219   | 226 | RLTPTEVK              |               | 1    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 1 072,59    | 1 071,59   | -0,01  | 39    | 49  | AAN...                |               | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 1 478,71    | 1 477,71   | -0,01  | 4     | 17  | GYSFSLTTFSPSGK        |               | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 1 580,75    | 1 579,75   | 0,00   | 70    | 83  | HIGLVYSGMGPDYR        | Oxidation (M) | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 1 627,77    | 1 626,77   | 0,00   | 113   | 127 | VASVMQEYTGSGGVR       | Oxidation (M) | 0    | 0     | <input type="checkbox"/> |
| <input type="checkbox"/> | 2 521,37    | 2 520,34   | 0,03   | 92    | 112 | LAQQYYLVYQEPIPTAQLVQR |               | 0    | 0     | <input type="checkbox"/> |

**Zoom graphique pour naviguer de l'étude aux données protéiques**

**Protéines et peptides validés**

Peak Viewer

MS Data

| Peak | Ion Mass | Intensity | Area | Charge |
|------|----------|-----------|------|--------|
| 61   | 1 462,11 | 657       | 0,0  | 0      |
| 62   | 1 466,12 | 762       | 0,0  | 0      |
| 63   | 1 476,09 | 1 087     | 0,0  | 0      |
| 64   | 1 478,71 | 4 834     | 0,0  | 0      |
| 65   | 1 482,10 | 1 475     | 0,0  | 0      |
| 66   | 1 498,07 | 299       | 0,0  | 0      |
| 67   | 1 500,71 | 281       | 0,0  | 0      |
| 68   | 1 545,73 | 5 951     | 0,0  | 0      |
| 69   | 1 565,63 | 2 145     | 0,0  | 0      |
| 70   | 1 570,70 | 1 003     | 0,0  | 0      |
| 71   | 1 580,75 | 1 131     | 0,0  | 0      |
| 72   | 1 627,77 | 7 134     | 0,0  | 0      |
| 73   | 1 643,75 | 1 032     | 0,0  | 0      |
| 74   | 1 667,81 | 1 895     | 0,0  | 0      |

Visualisation des données de MS ou MS/MS

Attributes

| Property         | Value                |
|------------------|----------------------|
| Result ID        | 40000265             |
| Component        | Mascot PMF v1.8      |
| Text Value       | PROTEIN DATA ENTERED |
| Number Value     |                      |
| Units            | NONE                 |
| Value Type       | TEXT                 |
| Result Version   | 1                    |
| Limits           |                      |
| Status/Condition |                      |
| Information      |                      |
| System IDs       |                      |
| Attributes       |                      |

Bloc détaillé pour toute information additionnelle

Gel Image

Contrast:  Edge Detection  Invert

Filters

- All Spots
- Samples
- MS
- MS MS
- Identified

Visualisation du gel

# Conclusions

## SQL\*LIMS répond aux exigences de la plate-forme Protéomique :

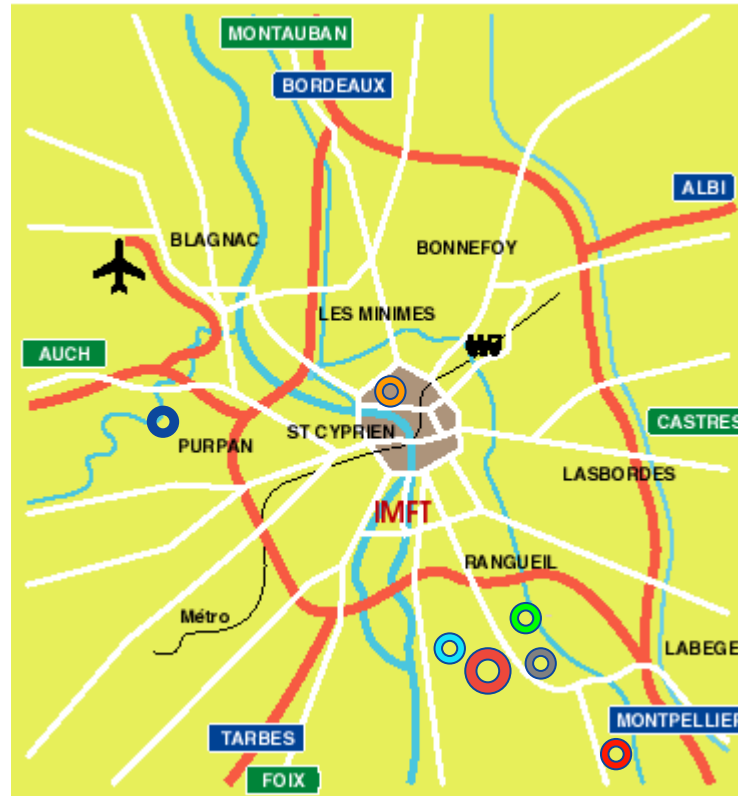
- Sécurité des données
- Traçabilité des échantillons
- Audit
- Intégrations des instruments et des moteurs de recherche
- Codes barres et leur lecture optique
- Rapports Oracle automatiques personnalisables
- Intégration de tous les types de données d'une plate-forme protéomique



# Perspectives

Centre  
Claudius Régaud

IFR30 Purpan



Partager des informations  
sur des projets communs  
avec nos partenaires  
toulousains.

INSA

IFR31 Rangueil

IFR109 UPS

**IPBS** IFR40

Plate-forme Protéomique