

# *Une solution LIMS pour la protéomique haut-débit*



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# Plate-forme protéomique haut-débit

- Regroupement majeur d'équipements (~3 M€)
- Automatisation et robotisation accrue
- Laboratory Instrument Management System+ workflow (LWS)
- Exploitation par la société **Innova Proteomics**
- Savoir-faire protégé
- Stages de formation en protéomique

## Objectifs 2005

Vrai haut-débit: > 1000 protéines identifiées/24h

Accréditation Assurance Qualité (norme ISO 9001)



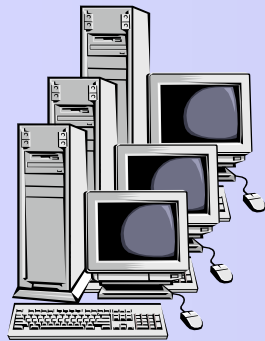
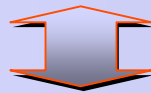
# Plate-forme Protéomique Haut-débit



2D-PAGE

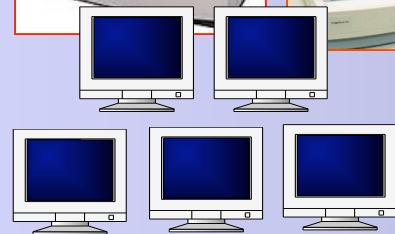


Ettan Workstation (prototype)  
(Amersham Biosciences)

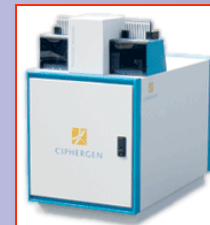
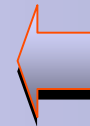


Serveurs NT, Linux &  
BDD Oracle

LWS



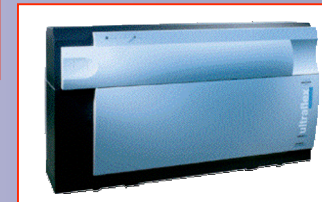
Analyse d'image et traitement  
des données



SELDI/TOF  
Ciphergen



Q-TOF Micro  
Micromass



MALDI TOF/TOF  
Ultraflex Bruker



MALDI-TOF  
Autoflex Bruker

## Besoins

### ● Suivi et Traçabilité:

- Echantillons
- Process
- Résultats

**Confidentialité !**

### ● Gestion:

- Procédures et Modes Opératoires
- Réactifs
- Personnel de la plate-forme

# Ettan Spot Handling Workstation (Amersham Biosciences)





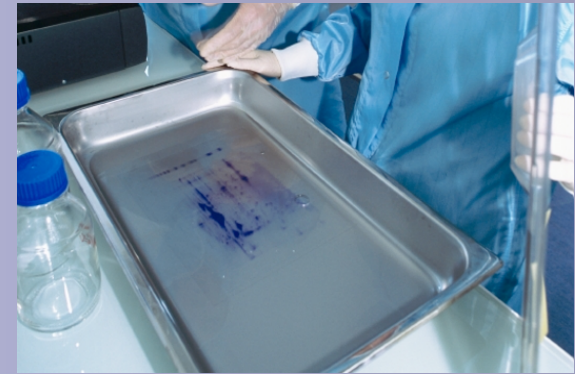
# The 2D-MS workflow...



**Sample Preparation**



**2D Gel electrophoresis**



**Gel staining**



**Introducing gel into SHW**



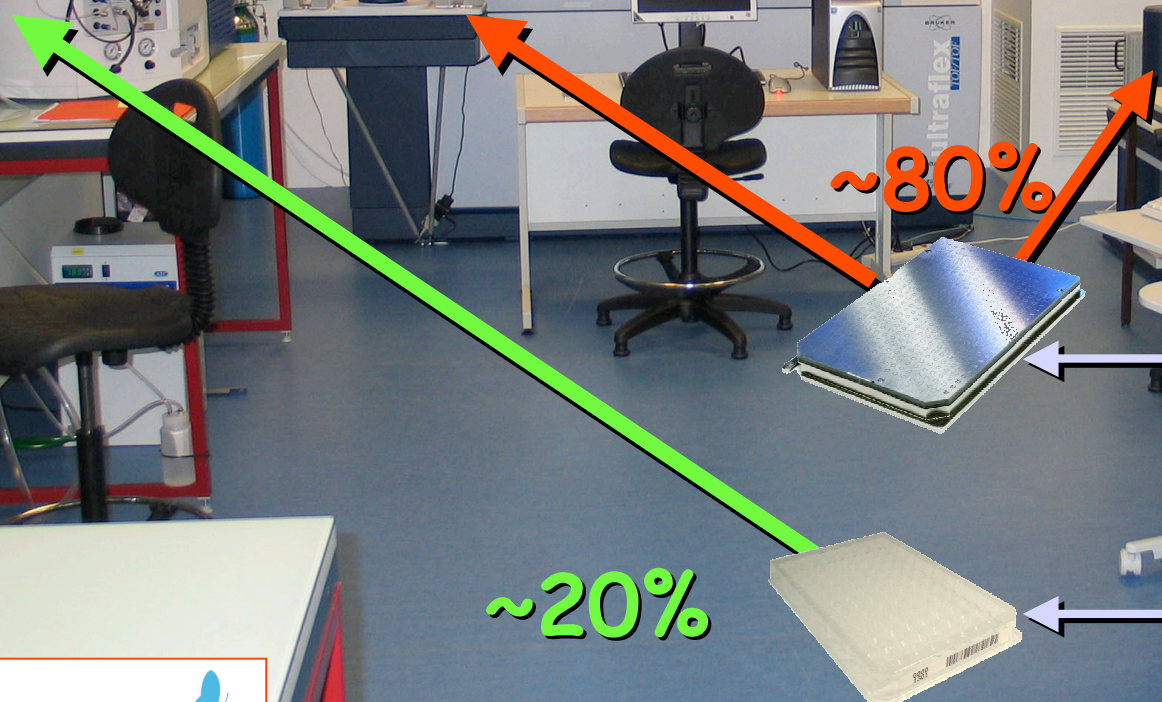
**General checking ahead of run**



**Run in progress...**



# 2D-MS workflow...



# Scierra Web - Log in

The screenshot shows a Microsoft Internet Explorer browser window titled "Login - Microsoft Internet Explorer". The address bar contains the URL "01977028/180817925/6/7001/7001/7002/7002/7001/-1". The browser's menu bar includes "File", "Edit", "View", "Favorites", "Tools", and "Help". The toolbar shows "Back", "Forward", "Home", "Search", "Favorites", "History", "Print", and "W". The address bar also includes "Go", "Links", "Passagen", "Google", "Hotmail", "Login", and "xynet".

The main content area features a header with the "Amersham Biosciences" logo on the left and the "Scierra" logo on the right. Below the header is a login form with the following elements:

- Username:** A text input field containing the text "sara".
- Password:** A password input field with masked characters "XXXXXXXXXX".
- Login:** A button labeled "Login".

To the right of the login form is the "CIMARRON" logo, which consists of a blue stylized leaf or drop shape above the word "CIMARRON".

Below the login form is a large, light-colored rectangular box containing the text "Welcome to Scierra!".

At the bottom of the page, there is a footer with the following text:

Copyright © Amersham Biosciences 2001-2002 - All rights reserved. Copyright © Cimarron Software, Inc. 1995-2002 - All rights reserved. Contact Mikael Lundgren (tel: 21272, mobil 070-3400105) worldwide.

The browser's status bar at the bottom shows "Done" and "Local intranet".

# Edition de permissions

**Edit Permissions**

Projects | Reports | Applications

Name

Ettan 2D-MS

**Edit Permissions**

Users

Name

Lab Managers

Research Associates

System Administrators

Add

Browse

Remove

**Permissions**

Permission	Allow
Create Ad Hoc Reports	<input checked="" type="checkbox"/>
Results Browsing	<input checked="" type="checkbox"/>
View All Work Requests	<input checked="" type="checkbox"/>

Save

OK Help

# Management de projet

The screenshot shows a web application interface for project management. At the top left is the Amersham Biosciences logo, and at the top right is the Sierra logo. Below the logos is a navigation bar with a "LOGOUT" link and a "GO:" dropdown menu. The main content area is divided into two columns. The left column is titled "Project: go" and includes a subtitle "projets Genopole Ouest". Underneath, there is a "Project Details" section with two links: "Edit Permissions" and "Edit Project". Below that is a "Subprojects" section with a list of 15 subproject links, including "go : CHUBrest Abgrall Thrombose chpin", "go : Gauducheau cancersein chpin", "go : genopole profilprot nagui", "go : germ cellgerm nagui", "go : Germ Evrard spermatogenese chpin", "go : Germ Staub endocrinedisruptor chpin", "go : go germ cellulesgerm nagui", "go : go germ zzzz essais aglan", "go : IFR26 LePendu lait nagui", "go : IFR26 Valette Mitochondries nagui", "go : test", "go : testisrob", "go : U456 Gilot macrophages nagui", "go : UMR6061 Chesnel Xenopuslaevis chpin", "go : UMR6061 Galibert USF1 chpin", and "Create a New Subproject". The right column is titled "Applications" and includes a section for "Etan 2D-MS" with five links: "Request Work", "View Past Work Requests", "Edit Methods", "Define Samples", "Edit Samples", and "Reports". At the bottom of the page, there is a "View by Task" link and a status bar showing the URL "http://lws-app:7001/sampledef/projectview.jsp?projId=817619263" and an "Intranet local" icon.

Amersham Biosciences

Sierra

LOGOUT GO:

## Project: go

*projets Genopole Ouest*

### Project Details

- [Edit Permissions](#)
- [Edit Project](#)

### Subprojects

- [go : CHUBrest Abgrall Thrombose chpin](#)
- [go : Gauducheau cancersein chpin](#)
- [go : genopole profilprot nagui](#)
- [go : germ cellgerm nagui](#)
- [go : Germ Evrard spermatogenese chpin](#)
- [go : Germ Staub endocrinedisruptor chpin](#)
- [go : go germ cellulesgerm nagui](#)
- [go : go germ zzzz essais aglan](#)
- [go : IFR26 LePendu lait nagui](#)
- [go : IFR26 Valette Mitochondries nagui](#)
- [go : test](#)
- [go : testisrob](#)
- [go : U456 Gilot macrophages nagui](#)
- [go : UMR6061 Chesnel Xenopuslaevis chpin](#)
- [go : UMR6061 Galibert USF1 chpin](#)
- [Create a New Subproject](#)

### Applications

#### Etan 2D-MS

- [Request Work](#)
- [View Past Work Requests](#)
- [Edit Methods](#)
- [Define Samples](#)
- [Edit Samples](#)
- [Reports](#)

[View by Task](#)

http://lws-app:7001/sampledef/projectview.jsp?projId=817619263

Intranet local



# Réception d'échantillon

Sierra - Ettan 2D-MS: Sample Receiving

File Window Tools View Help

Start Work: <scan>

Navigator

Workflow Graph

- Sample Receiving
- 1D Electrophoresis
- 2D Electrophoresis
- Gel Staining
- Image Analysis
- Spot Handling
- MALDI-MS

Sample Receiving

Filter: Active Is Active

	Work Request ID	Requestor	Request Date	Project	Queue Time
	1063	Helena	Aug 15, 2002	Violet	04:54
	1066	helena	Aug 15, 2002	Scarlet	01:31
✓	1067	sara	Aug 15, 2002	Diabetes project	00:04

Use External ID as Internal ID

Work Request or Sample ID: <scan>

External ID: <scan> Internal ID: <scan>

Work Request	Ext. ID	Int. ID	Type	Container	Received	Condition
1067	tube-101		Protein Sample	Tube	<input type="checkbox"/>	

Finish Activity Clear Window Close Window

sara

**Attribution d'un code-barre lors de la réception de l'échantillon**

**Echantillon: Gel 2D, protéine dans un tube, microplaque**

# Sample Request & Request sheet




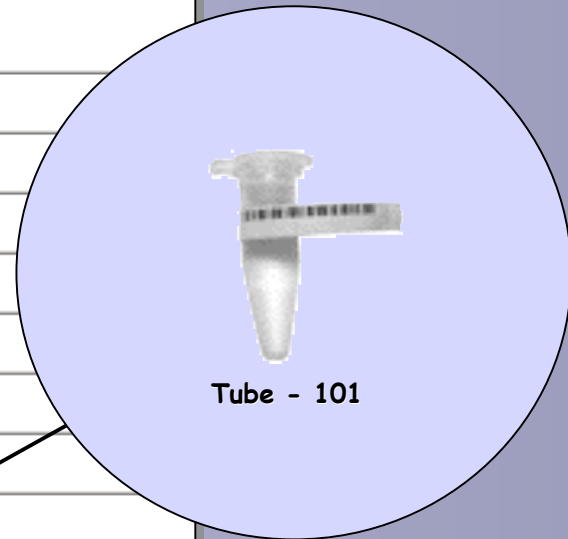
1067

Ettan 2D-MS Work Request

<b>Request ID:</b>	1067
<b>Request Date:</b>	Aug 15, 2002 03:11 PM
<b>Requestor:</b>	sara
<b>Project:</b>	Diabetes project
<b>Request Description:</b>	Mouse sample
<b>Request Instructions:</b>	Identify the 50 strongest spots in the basic interval.
<b>Status:</b>	Pending

Sample Work:

Request Item ID	Type	Instructions	Spot Pick List	Digest	Status
1	 tube-101				
	Protein Tube			true	Pending



Tube - 101

# Electrophorèse 1D

Sierra - Ettan 2D-MS: 1D Electrophoresis

File Window Tools View Help

Start Work: <scan>

**Navigator**

Workflow Graph

- Sample Receiving
- 1D Electrophoresis**
- 2D Electrophoresis
- Gel Staining
- Image Analysis
- Spot Handling
- MALDI-MS

**Ettan 2D-MS: 1D Electrophoresis**

Batch Definition | Batch Selection | Batch Processing

Sample application: Rehyd.+Sep., Standard holder | Batch name: SS 020815 | Batch ID: 817789238 | Scan order:  row  column  Keep batch intact

Tube: tube-100 | Strip: <scan> | Rehydration solution:

#	Tube ID	IPG strip	Strip ID	Rehydration solution	Rehyd. Solution ID	Sample amount	Cup position	Archive
1	✓ tube-1...	IPG 18 3...		Rehydration solution, st...			N/A	<input type="checkbox"/>

**Rehydration** | **Separation**

Duration: 2 h | Instrument: Multiphor

Method: 18cm:NI:C/R (1.0) | Total kilovolt hours [kVh]:

Instrument ID: <scan>

Power supply ID: <scan>

Buttons: Save, Finish, Close window

Windows taskbar: sara

**Fournir les informations relatives au traitement de l'échantillon**

# Electrophorèse 2D

Sierra - Ettan 2D-MS: 2D Electrophoresis

File Window Tools View Help

Start Work: <scan>

**Navigator**

Workflow Graph

- Sample Receiving
- 1D Electrophoresis
- 2D Electrophoresis**
- Gel Staining
- Image Analysis
- Spot Handling
- MALDI-MS

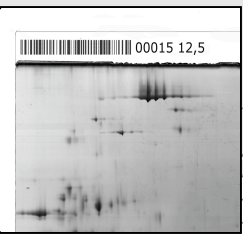
**Ettan 2D-MS: 2D Electrophoresis**

Batch Definition | Batch Selection | Batch Processing

Batch name: reh+sep    Batch ID: 817988648    Scan order:  row  column     Keep batch intact

Strip: <scan>    Gel: <scan>

#	Strip ID	Gel ID
1	✓ 91	✓ kl2
2	✓ 92	✓ kl1
3	✓ 93	✓ kl3
4	✓ 90	✓ kl4



**Liaison des ID  
IEF strip et Gel 2e dimension**

**Equilibration**

Method: Basic equilibration (1)

Equilibration buffer 1: <scan>    Duration 1: \_\_\_\_\_

Equilibration buffer 2: <scan>    Duration 2: \_\_\_\_\_

**Separation**

Method: DALT II std (1)    Instrument ID: <scan>

Gel type: Ettan DALT II Gel 12.5%    Buffer kit: dfsafdsaf

Anode buffer: <scan>    Cathode buffer: <scan>

Save    Finish    Close window

sara



# Method Editor

**Method Editor**

**Methods**

- IPGphor
  - 18cm:3-10,3-10NL,4-7:C (1.0)
  - 18cm:3-10,3-10NL,4-7:P (1.0)
  - 18cm:3-10,3-10NL,4-7:R (1.0)
  - 18cm:6-11:C (1.0)
  - 18cm:6-11:P (1.0)
  - 18cm:6-9:C (1.0)
  - 18cm:6-9:P (1.0)
  - 18cm:NI:C (1.0)
  - 18cm:NI:P (1.0)
  - 18cm:NI:R (1.0)
  - 24cm:3-10,3-10NL,4-7,3-7:C (1.0)
  - 24cm:3-10,3-10NL,4-7,3-7:C (1.0)
  - 24cm:3-10,3-10NL,4-7,3-7:P (1.0)
  - 24cm:3-10,3-10NL,4-7,3-7:R (1.0)
  - 24cm:6-9:C (1.0)
  - 24cm:6-9:C\_Alt (1.0)
  - 24cm:6-9:P (1.0)
  - 24cm:NI:C (1.0)
  - 24cm:NI:C\_Alt (1.0)
  - 24cm:NI:P (1.0)
  - 24cm:NI:R (1.0)
  - metod (1)
- Multiphor
- Equilibration
- Dalt II
- Staining
- Spot Handling Workstation
- MALDI

**Methods**

Name: 18cm:3-10,3-10NL,4-7:C  
Version: 1.0  
Description: Step 2 and 3 voltage may not be reached within the suggested step duration. C, cup loading  
Status: Approved

#	Gradient Type	Duration	Current (mA/strip)	Voltage (V)	Voltage hour (kVh)
1	Gradient	0:01		500.0	0.01
2	Gradient	1:30		4000.0	3.4
3	Step & Hold	3:10		8000.0	24.6

New step Delete step

? New Save Delete Close window

# Coloration de gels: Batch Processing

The screenshot shows the 'Scierra - Ettan 2D-MS: Gel Staining' software interface. On the left, a 'Navigator' panel shows a 'Workflow Graph' with steps: Sample Receiving, 1D Electrophoresis, 2D Electrophoresis, Gel Staining (circled in red), Image Analysis, Spot Handling, and MALDI-MS. The main window is titled 'Ettan 2D-MS: Gel Staining' and has tabs for 'Batch Definition', 'Batch Selection', and 'Batch Processing'. Under 'Batch Definition', 'Batch name' is 'Batch ID' and 'Batch ID' is '817912471'. Below this, 'Gel:' is '<scan>' and 'Method' is 'Coomassie Staining (1.0)'. A table lists four gels with their IDs. An arrow points from a green text box at the bottom to the fourth gel ID. The table of method steps is as follows:

Method step	Method step duration	Method step solution	Solution ID	Duration
1	1-2 h	Ethanol/Acetic Acid (4...	<scan>	
2	1h -	CBB Staining	<scan>	
3	? -	Ethanol/Acetic Acid (2...	<scan>	

Choix du protocole de coloration de gel

Buttons at the bottom right: Save, Finish, Close window. Username 'sara' is visible at the bottom left.

# Staining method

The screenshot shows the 'Method Editor' window. On the left is a 'Methods' tree view with folders for IPGphor, Multiphor, Equilibration, Dalt II, Staining, Spot Handling Workstation, and MALDI. Under 'Staining', several methods are listed, with 'Silver Staining (1.0)' selected. The main area displays the configuration for this method:

Methods  
Name: Silver Staining  
Version: 1.0  
Description: \* The first fixation may be prolonged up to 3 days if desired for the sake of convenience. \*\* By omitting glutardialdehyde from the sensitizer and formaldehyde from the silver nitrate solution and skipping the "preservative step", the method  
Status: Approved

#	Step	Duration	Reagent
1	Fixing	2 x 60 min*	Ethanol/Acetic Acid (40/10)
2	Sensitizing**	60 min	Silver Sensitizer
3	Washing	5 x 8 min	water-wash
4	Silver Reaction**	60 min	Silver Stain
5	Washing	4 x 1 min	water-wash
6	Developing***	5 min****	Silver Developer
7	Stop	45 min	Silver Stop
8	Washing	2 x 30 min	water-wash
9	Preserving**	20 min	Silver Preserver

Buttons: New step, Delete step, New, Save, Delete, Close window

# Analyse d'image - Importation d'un fichier image

Sierra - Ettan 2D-MS: Image Analysis

File Window Tools View Help

Start Work: <scan>

**Navigator**

Workflow Graph

- Sample Receiving
- 1D Electrophoresis
- 2D Electrophoresis
- Gel Staining
- Image Analysis**
- Spot Handling
- MALDI-MS

**Ettan 2D-MS: Image Analysis**

Image Acquisition | Image Selection | Image Results

Select gels to scan

Gel: <scan> Filter: Active Is Active

	Gel ID	Staining method	Instrument	Spot Handling me...	Staining date	Insertion date
	g4-5_1	Silver Staining (1.0)	ImageScanner		Aug 5, 20	
	g5_1	Silver Staining (1.0)	ImageScanner		Aug 5, 20	
	bo-gel2	Silver Staining (1.0)	ImageScanner	PDS fast (1.0)	Aug 6, 20	
	2002-08-12-A	Silver Staining (1.0)	ImageScanner		Aug 12, 2	
	sara-gel-1	Colloidal Coomas...	ImageScanner	SilverPDS_1.4 (1.0)	Aug 13, 2	
	g3.5_2	Silver Staining (1.0)	ImageScanner		Aug 14, 2	
	demo020819	Coomassie Staini...			Aug 16, 2	
!	gel123	SYPRO ruby (1.0)	Typhoon	SilverPDS_1.4 (1.0)	Aug 20, 2	
	Gel4-7;2	SYPRO ruby (1.0)	Typhoon	PDS superfast (1.0)	Aug 22, 2	
!	Gel4-7;4	SYPRO ruby (1.0)	Typhoon	PDS superfast (1.0)	Aug 22, 2	
	Gel4-7;1	SYPRO ruby (1.0)	Typhoon	PDS superfast (1.0)	Aug 22, 2	

Instrument: ImageScanner

Instrument ID: <scan>

**Select image**

Look in: ss03074

- .java
- Application Data
- Cookies
- Desktop
- Favorites
- Local Settings
- My Documents

File name:

Files of type: TIFF (.tiff, tif)

Select image Cancel

Finish Close window

**Importation du fichier image généré par le logiciel d'analyse**



# Spot Handling

Sierra - Ettan 2D-MS: Spot Handling

File Window Tools View Help

Start Work: <scan>

**Navigator**

Workflow Graph

- Sample Receiving
- 1D Electrophoresis
- 2D Electrophoresis
- Gel Staining
- Image Analysis
- Spot Handling**
- MALDI-MS

**Ettan 2D-MS: Spot Handling**

Batch Definition

Batch name:      Batch ID: 817664569

**Gel - Tray mapping/Plate scanning**

Filter: Approved

Gel: 100064700098450003      Tray: 701073722098580001

Method: IP - Ag Pro v 2.0

Target type: Bruker AnchorChip 600 µm

Target definition: Scout MTP 384

#	Item ID
1	ss2003

Target - Sample Tray mapping

Target ID: <scan>      MS sample tray ID: <scan>      Num

#	Target ID	MS s
---	-----------	------

Entrée des informations pour le process d'un gel 2D

# Spot Handling Method Management

Spot Handling Method Management

Method Overview | Spot Picking Details | Digestion Details | Spotting Details | Close

Name	Diameter	Status	Path
Black	1.4	Tested	D
Blue	1.4	Approved	PDS
Dark green PDS	1.4	Approved	PDS
<b>DS-orange</b>	<b>1.4</b>	<b>Approved</b>	<b>DS</b>
Gray	1.4	Approved	P
light green	1.4	Approved	PDS
LWS 20020910	1.4	Draft	PDS
P fast	1.4	Approved	P
P-orange	1.4	Tested	P
PD-darkgreen	1.4	Approved	PD
PD-winered	1.4	Approved	PD
PD-yellow	1.4	Tested	PD
PDS fast	1.4	Approved	PDS
PDS superfast	1.4	Approved	PDS
Pink	1.4	Approved	DS
Red	1.4	Tested	PDS
S-winered	1.4	Approved	S
ss-test	1.4	Draft	PDS
Stresstest 020904	1.4	Tested	S
BasicPDS_1.4	1.4	Standard	PDS
BasicPDS_2.0	2.0	Standard	PDS
SilverPDS_1.4	1.4	Standard	PDS
SilverPDS_2.0	2.0	Standard	PDS

**Method**

Name: DS-orange  
Status: Approved  
Picker head  $\varnothing$ : 1.4 mm

**Path**

Picking:   
Digestion:   
Spotting:

**Description**

Basic method for a digesting spotting.  
Suitable to use for Coomassie and SYPRO Ruby stained gels.  
Spotting by "Dissolve in matrix" method.

Copy Save

# Spot Handling: Réglages

**Spot Handling Method Management** [Close]

Method Overview | Spot Picking Details | **Digestion Details** | Spotting Details

---

**MP1 preparation**

Number of steps:

	1	2	3
<b>Dispense reagent</b>		Ambic 50 mM/MeOH 50%	100 µl
<input type="checkbox"/> <b>Add second reagent</b>		Na2S2O3 100 mM	50 µl
Mix	<input type="text" value="1"/> Strokes		50 µl
<b>Incubate</b>	<input type="radio"/> Incubator <input checked="" type="radio"/> Hotel		20 min
<b>Aspirate reagent</b>			110 µl

---

**MP1 drying**  min

---

**Enzyme addition**

**Transfer Enzyme** Priming:

Enzyme:   µl

**Buffer addition**

**Incubate**  Incubator     Hotel  min

**Dispense buffer**   µl

---

**Digestion**

**Incubate**  Incubator     Hotel  min

---

**Extraction**

Number of steps:

	1	2
<b>Dispense liquid in MP1</b>	ACN 50%/TFA 0.1%	60 µl
<b>Incubate</b>	<input type="radio"/> Incubator <input checked="" type="radio"/> Hotel	
<input type="checkbox"/> <b>Add second liquid</b>	ACN 50%/TFA 0.1%	0 µl
Mix	<input type="text" value="0"/> Strokes	0 µl
<b>Incubate</b>	<input checked="" type="radio"/> Incubator <input type="radio"/> Hotel	
<input checked="" type="checkbox"/> <b>Transfer from MP1 to MP2</b>		60 µl

---

**MP2 drying**  min

# Spot Handling: Liquid Mapping

Scierra - Ettan 2D-MS: Spot Handling

File Window Tools View Help

Start Work: <scan>

**Navigator**

Workflow Graph

- Sample Receiving
- 1D Electrophoresis
- 2D Electrophoresis
- Gel Staining
- Image Analysis
- Spot Handling
- MALDI-MS

**Ettan 2D-MS: Spot Handling**

Batch Definition | Batch Selection | Batch Processing

Batch name: Batch ID

**Spot Handling Batch Processing**

Batch Id: 817915726  
Method Name: SilverPDS\_1.4  
Remaining Time: 0h 38min

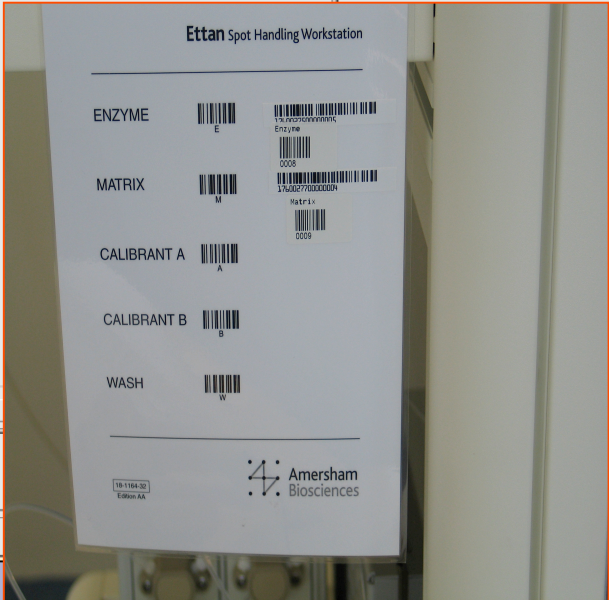
Filter: Sta  
Metho: Silv  
Target: Wit

**Batch data received**

Liquid Mapping | Batch Data Confirmation | Carrier Identification | Batch Monitoring | Close

Connected Liquids				Not Connected Liquids		
Location	Type	Required Amount	Loc	Type	Amount	
(P) Picker	Water	2.3 ml	(n)	K3Fe(CN) <sub>6</sub> 30 mM	24.8 ml	
(1) Valve 1	Ambic 50 mM/MeOH 50%	59.2 ml	(n)	Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub> 100 mM	64.0 ml	
(2) Valve 2	ACN 75%	59.2 ml	(E)	Trypsin/Ambic 20 mM	1.2 ml	
(3) Valve 3	Ambic 20 mM	20.0 ml	(M)	4-HCCA mix	288 µl	
(4) Valve 4	ACN 50%/TFA 0.1%	108.8 ml				
(5) Valve 5	Water	207.2 ml				
(6) Valve 6		0.0 ml				
(7) Valve 7		0.0 ml				
(8) Valve 8		0.0 ml				
(E) Enzyme		0.0 ml				
(S) Spotter	ACN 50%/TFA 0.5%	22.3 ml				
(M) Matrix		0 µl				
(A) Calibrant A		0 µl				
(B) Calibrant B		0 µl				
(W) Wash Liquid		0 µl				

Enter Barcode (Loc, Identity)



Ettan Spot Handling Workstation

ENZYME E  
MATRIX M  
CALIBRANT A A  
CALIBRANT B B  
WASH W

Amersham Biosciences

# Spot Handling: Batch Completed

**Spot Handling Batch Processing** [X]

**Batch Completed**

**Batch Id** 817915726  
**Method Name** SilverPDS\_1.4  
**Remaining Time** 0h 0min

Liquid Mapping | Batch Data Confirmation | Carrier Identification | **Batch Monitoring** | Close

**Gel Carriers** 1  
Spot Picking from Gel to MP1  
Gel out

**Micro Plates (MP1)** 1  
Spot Picking from Gel to MP1  
MP1 Aspiration after Spot P...  
MP1 Digestion Preparation  
Dry MP1 before Digestion  
Add Enzyme  
Digest  
Extract  
MP out after extraction

**Micro Plates (MP2)** 1  
Extract  
Dry MP1/MP2  
Dissolve in matrix  
MP out after spotting

**Slide Plates** 1  
Dissolve in matrix  
SP out

Confirm Batch Completion | Pause



# Gestion des réactifs

Reagent Inventory

File Edit View Sort Filter Help

Reagent Inventory

- AutoSeq96
- Chemicals
- Deionized water
- dNTP Mix
- Dye
- Electrophoresis
  - Agarose sealing solution
  - Ammonium persulphate 10%
  - Anode/Cathode Buffer
  - Bind-Silane working solution
  - Bromophenol blue stock, 1%
  - Buffer Kit 2D
  - Cleaning solution, IPGphor Strip Holder
  - Equilibration Solution
  - Gel storage solution
  - IPG Buffer
  - IPG Cover Fluid
  - Laemmli SDS electrophoresis buffer
  - Monomer stock solution
  - Rehydration Solution
  - SDS 10%
  - SDS equilibration stock
  - Thioreaa rehydration stock
  - Tris-HCl, pH 8.8, 1.5 M**
  - Urea rehydration stock
- Exonuclease I
- ExoSAP-IT
- Gel 1D
- Gel 2D
- Genotyping Markers
- Genotyping Size Standard
- Loading Solution
- Long Read Matrix
- Marker
- MegaBACE LPA Buffer
- MS Sample Tray
- PCR Nucleotide Mix

<scan> Find

View Reagent:

Name: Tris-HCl, pH 8.8, 1.5 M

Part Number:

Parent: Electrophoresis

Vendor: in-house

Description:

Recipe

Reagent	Quantity
water to 1000 ml	750.0 ml
Tris base	181.7 g
HCl*	20.0 ml

Attributes

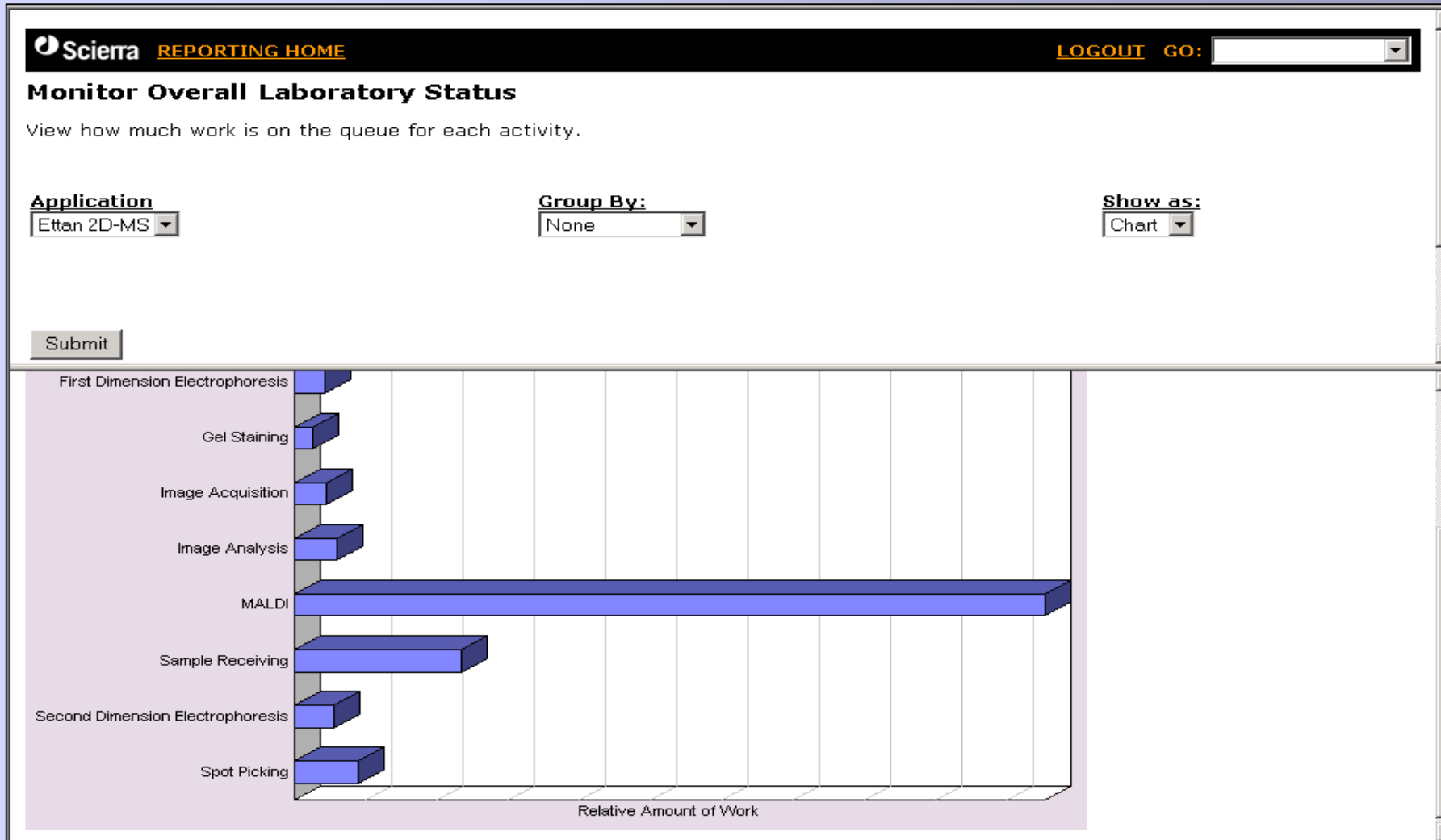
Name	Value
------	-------

Attribute Definitions

Name	Type	Default
------	------	---------

New Inventory Item Modify Delete

# Etat d'utilisation du plateau technique



# Rapport d'analyse

The screenshot shows a web application interface for Amersham Biosciences. At the top left is the Amersham Biosciences logo, and at the top right is the Sierra logo. Below the logos is a navigation bar with a "LOGOUT" link and a "GO:" dropdown menu. The main content area is titled "Select a Report" and is divided into two columns: "Standard Reports" and "Ad hoc Reports".

**Standard Reports**

- [Contents Layout per Barcode](#)
- [Contents per Barcode](#)
- [Monitor Overall Laboratory Status](#)
- [Monitor Work Requests](#)
- [Normalize and Aliquot Plate Contents](#)
- [Project Components](#)
- [Protocol Summary](#)
- [Sample Condition Summary](#)
- [Compare Protein Hit Lists](#)
- [Detected proteins in gel](#)
- [Proteins to Samples](#)
- [Samples to Proteins](#)

**Ad hoc Reports**

- **[New Adhoc Query](#)**
  - [Protein Tube MD](#)
  - [Protein Tube MDgel](#)

A large green box with black text is overlaid on the page, containing the text: "Edition d'un rapport d'analyse selon modèle standard ou Ad Hoc".

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Local intranet

# Rapport d'analyse standard

Scierra **REPORTING HOME** LOGOUT GO:

## Detected proteins in gel

Showing which proteins are represented in a gel.

Gel ID:  Include sub-rankings:

Yes  
 No

N° Spot, ID protéine (accession number) et score

---

Home
Separate Window
All Results
No Grouping
Excel
XML
Comma Separated
Tab Separated
◀ ▶

Total number of spots in gel: 213

### Summary of Gel ID 1760023611111300052

#### Upstream gel information

Title	Value
Gel ID	1760023611111300052
Created	2002.08.06-17:57
1D Strip	-

#### Spots for Gel 1760023611111300052

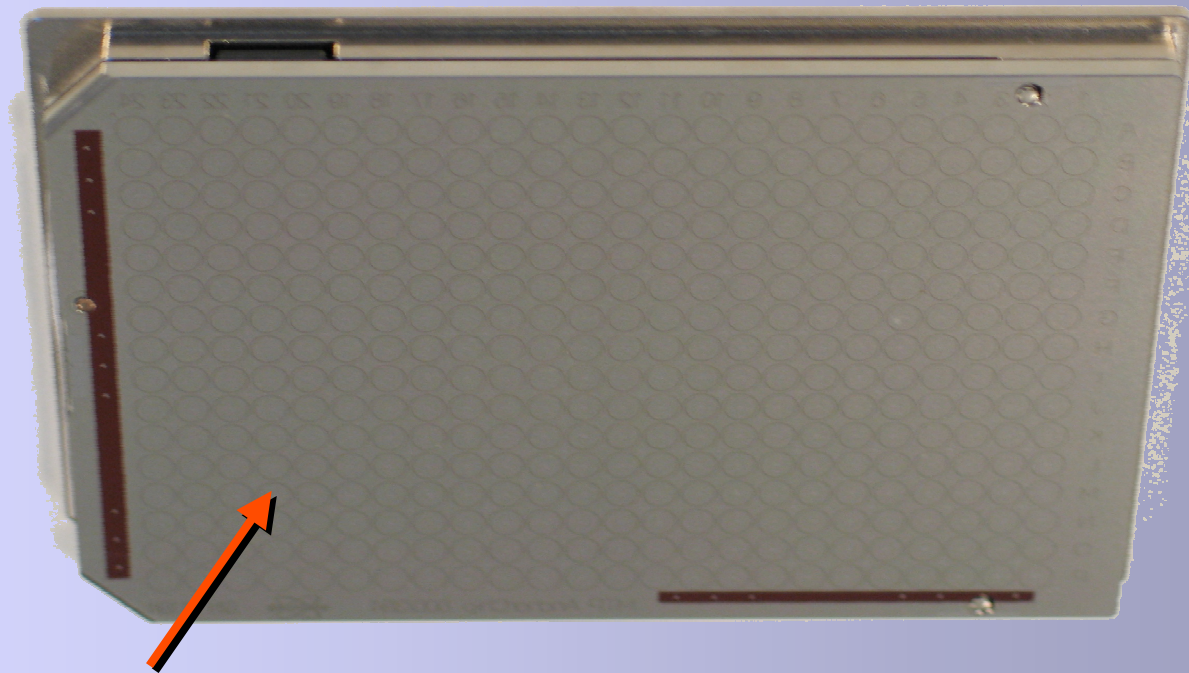
Pick list	Gel Spot#	MALDI Run	Ranking	Expectation value	Protein ID	Protein name	Coverage
<a href="#">1760023611111300052-1</a>	1	2002.08.22-15:11	1	0.679	gi 285957 dbj BAA03515.1	(D14689) KIAA0023 [Homo sapiens]	5.7
<a href="#">1760023611111300052-1</a>	2	2002.08.22-15:11	1	0.110	gi 5102894 emb CAB45280.1	(AL079314) hypothetical protein, similar to (U06944) PRAJA1 [Mus musculus] [Homo sapiens]	19.8
<a href="#">1760023611111300052-1</a>	3	2002.08.22-15:11	1	0.512	gi 5102894 emb CAB45280.1	(AL079314) hypothetical protein, similar to (U06944) PRAJA1 [Mus musculus] [Homo sapiens]	19.4
<a href="#">1760023611111300052-1</a>	4	2002.08.22-15:11	1	0.725	gi 16126790 ref NP_421354.1	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Caulobacter crescentus]	26.3
<a href="#">1760023611111300052-1</a>	5	2002.08.22-15:11	1	0.205	gi 15600753 ref NP_254247.1	ATP synthase A chain [Pseudomonas aeruginosa]	20.4

Local intranet





Ground steel 384 MTP AnchorChip 600  $\mu\text{m}$   
(Bruker Daltonics)



Transponder



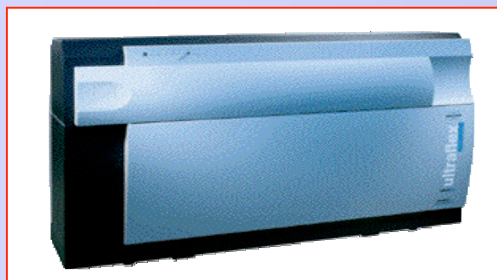
# Fichiers de résultats MS



SELDI/TOF  
*Ciphergen*



MALDI-TOF  
*Autoflex Bruker*



MALDI-TOF/TOF



Q-TOF Micro  
*Micromass*

**LWS**  
Version 2.0