



ProteoMe  
Informatics  
group SIB

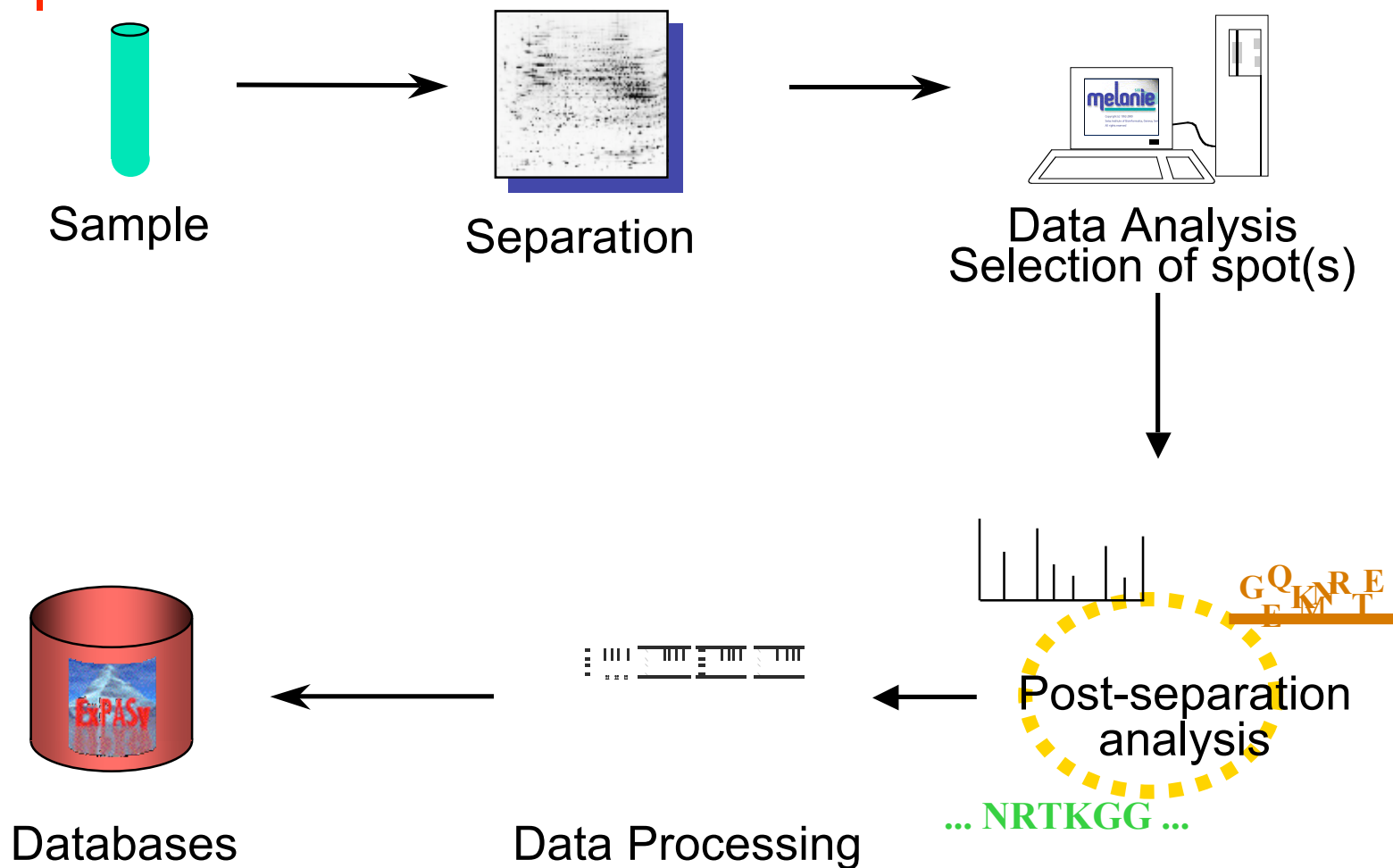
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- Marc Tuloup
- Daniel Walther
- Nadine Zangger



# Proteomics pathway





# LIMS

- Close collaboration with BPRG
- Applied Biosystems
  - SQL\*LIMS, v4.0 (sample plans, projects, samples)
  - RIS (Proteomics module: Melanie image logging for 1-DE, 2-DE, spot logging, MS peaklists uploads, identification launches, validation of protein identification, ELISA, immunoblots)
  - SQL GT (plate management)



# Logical Principle

- Projects/submissions contain
- Samples to which one can assess
- Tasks/Methods that produce
- Results



**Data Browser** [Icons: Home, Print, Refresh, Save]

**S. aureus**

- N315
  - N315/Total extract
  - N315/Total membrane extracts
    - CENTRIFUGE METHOD
    - N315/Membrane Soluble
      - CENTRIFUGE METHOD
      - N315/Soluble-2D02-0757
      - N315/Soluble 1D Gel Aliquot
    - N315/Membrane Pellet
      - CENTRIFUGE METHOD
      - CENTRIFUGE
    - N315/Membrane Chlorophorme
      - CENTRIFUGE METHOD

**Attributes** | **Gel Image** | **MS Data & Proteins**

Version: 2/2 | Status: ON\_GOING\_VALIDATION | User: PENLIMS | Date: 11/26/2003

Rank	Accession No.	Mass	Score	Protein Name	Masses M...	Validate
1	Q895Z1	46.456	18	(Q895Z1) Cell division protein ftsA.	4 / 20	<input checked="" type="checkbox"/>
2	Q8P5I6	25.896	10	(Q8P5I6) Acetoacetyl-coA reductase.	3 / 20	<input checked="" type="checkbox"/>
3	Q92FA3	63.221	6	(Q92FA3) Putative peptidoglycan bound protein (LPXTG motif).	2 / 20	<input checked="" type="checkbox"/>
4	Q883Y7	43.193	6	(Q883Y7) 3-oxoacyl-(acyl-carrier-protein) synthase I.	3 / 20	<input checked="" type="checkbox"/>
5	Q87V26	46.976	6	(Q87V26) Gluconate transporter family protein.	1 / 20	<input type="checkbox"/>
6	Q8UIQ7	10.969	5	(Q8UIQ7) Hypothetical protein Atu0236.	2 / 20	<input type="checkbox"/>
7	Q10884	53.457	4	(Q10884) Probable formate hydrogenlyase CY251.05.	1 / 20	<input type="checkbox"/>
8	Q50119	6.551	3	(Q50119) U650y.	2 / 20	<input type="checkbox"/>

**Peptide Data**

Chec...	Mass Matched	Mass Ca...	Delta	St...	End	Sequence	Modifica...	Miss	Score	Validate
<input type="checkbox"/>	1.079,47	2.155,11	1,81	2	22	TLRIAYVTSGMGVSGTAICQK		1	8	<input checked="" type="checkbox"/>
<input type="checkbox"/>	1.079,63	2.157,09	0,15	103	121	DDWNAVIASNLHSLFNITK		0	0	<input type="checkbox"/>
<input type="checkbox"/>	1.531,49	3.062,37	-1,40	47	74	EQRELGFDFVASEGNAADWDSTMAA...		1	1	<input checked="" type="checkbox"/>

**Gel Viewer**

**Gel Image**

**MS Data**

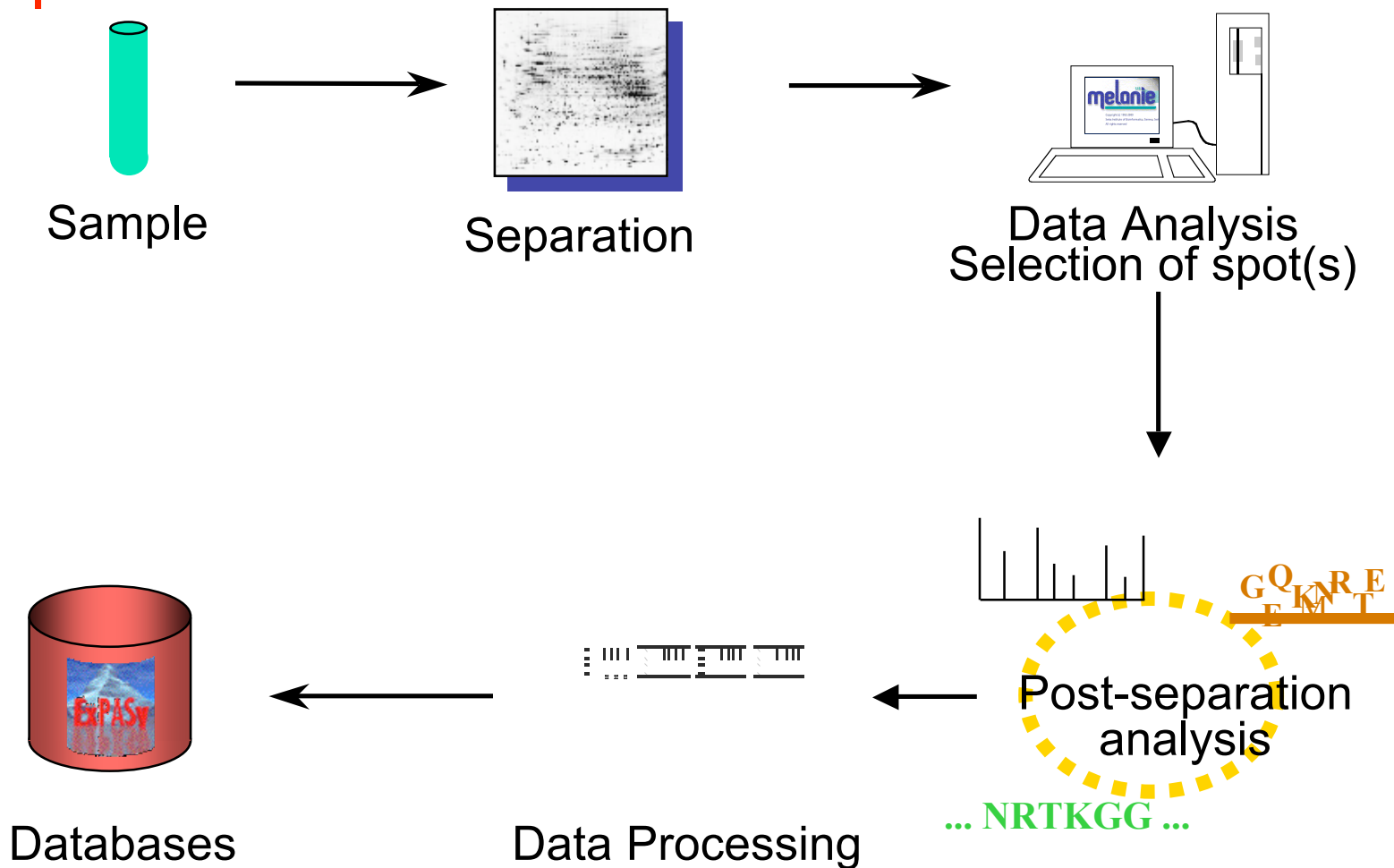
Peak	Ion Mass	Intensity	Area	Charge
1	876,90	870	980,1	0
2	1.079,47	3.026	844,5	0
3	1.079,63	3.238	696,4	0
4	1.379,40	1.610	704,3	0
5	1.379,60	1.313	181,1	0
6	1.395,60	521	240,0	0
7	1.531,49	1.668	261,0	0
8	1.531,71	2.223	784,9	0

**MSMS Data**

Ion Mass	Intensity	Area	Charge
70,06	1.320	093,4	1
84,08	199	904,2	1
86,09	1.612	847,2	1
101,06	508	104,7	1
104,03	567	132,6	1
110,05	206	962,9	1
120,09	225	913,4	1
129,11	474	032,9	1



# Proteomics pathway



# The MELANIE 2D gel analysis software

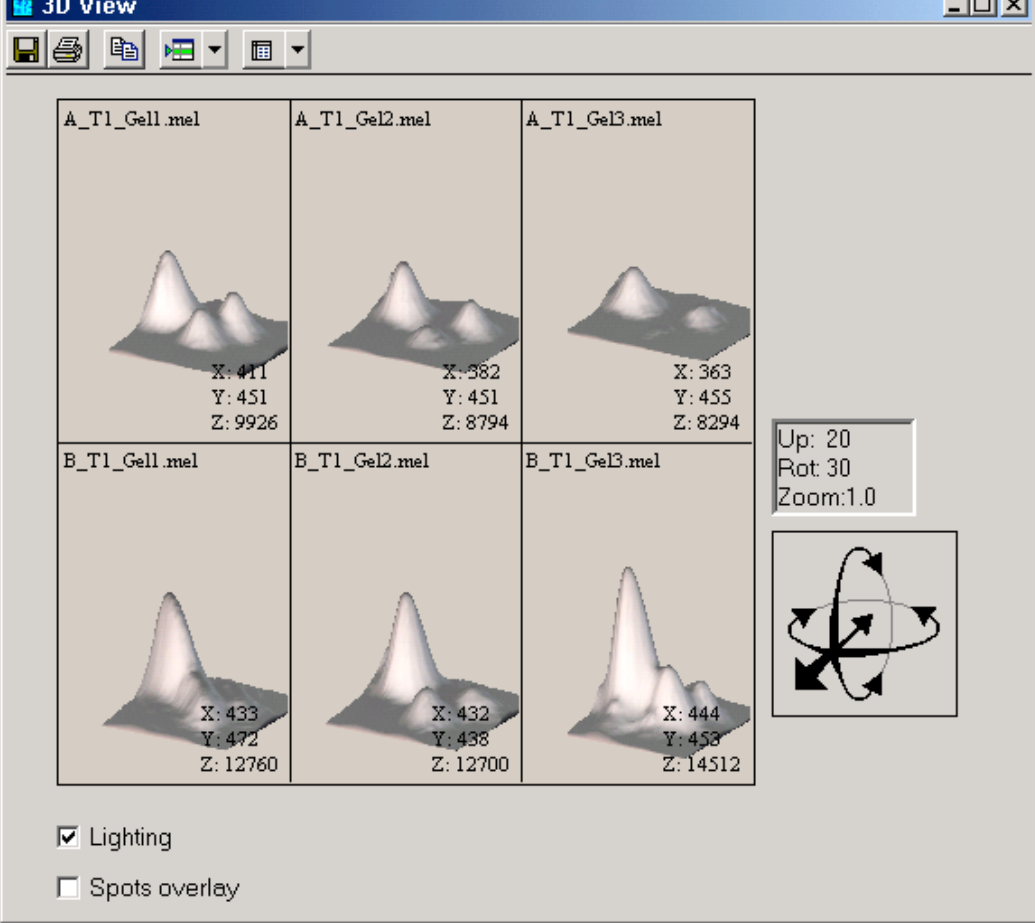
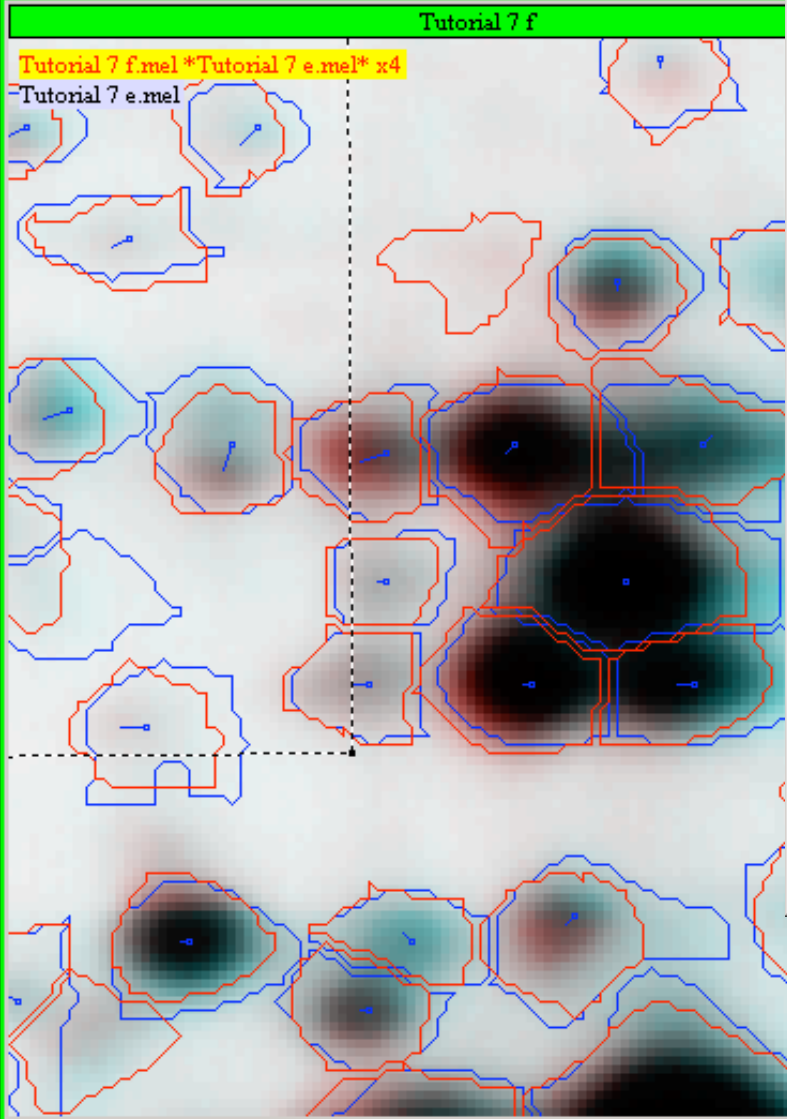


## Benefits:

Accurately and rapidly identifies and quantifies your spots, matches your gel images, and finds significant protein expression changes.

Offers numerous filtering, querying, reporting, statistical and graphing options so that you can easily view, compare, analyse and present your results.





Melanie

File View Edit Show Select Analyze Reports Tools Window Help

Ref: Master Hidden: Master

930018c-w 930033c 93013ne-w

930018c-w.mel (NEWBORN) x2 930033c.mel (NEWBORN) x2 93013ne-w.mel (NEWBORN) x2

Classes+Groups Histograms

Factor Projection Plot

Heuristic Clustering Plot

Factor Projection Report

Projection onto axes 1-2  
The chosen statistics are

Copy to Clipboard

Heuristic Clustering Plot (%Vol)

Factor 2

930013\_newborn  
930033\_newborn  
930018\_newborn

5743 + 6654 +  
6723 + 6680 +

6466 + 6853 +  
6413 + 6965 +  
93006\_old 7098 +

93007\_old

6485 +

93008\_old

93006ve-w.mel (0

93000003 - old  
93000007 - old  
93000006 - old  
93000013 - newborn  
93000033 - newborn  
93000018 - newborn

Axe2	Quality
313753	0.197446
102084	0.351920
654757	0.265397
633853	0.600895
260273	0.310865
214721	0.425813
172333	0.663190
164736	0.427793
161601	0.485403
158286	0.614625
154975	0.969795
150053	0.181428
147637	0.559598
104379	0.559944
102051	0.483470
970537	0.270215
967343	0.465411
943742	0.907673
443277	0.508044
413340	0.508645
255479	0.656571
170787	0.933898
121733	0.791583
341e-4	0.589941
166e-4	0.772060

Gels: 6 Spots: 6

Groups+Gels

# Integration into the laboratory workflow

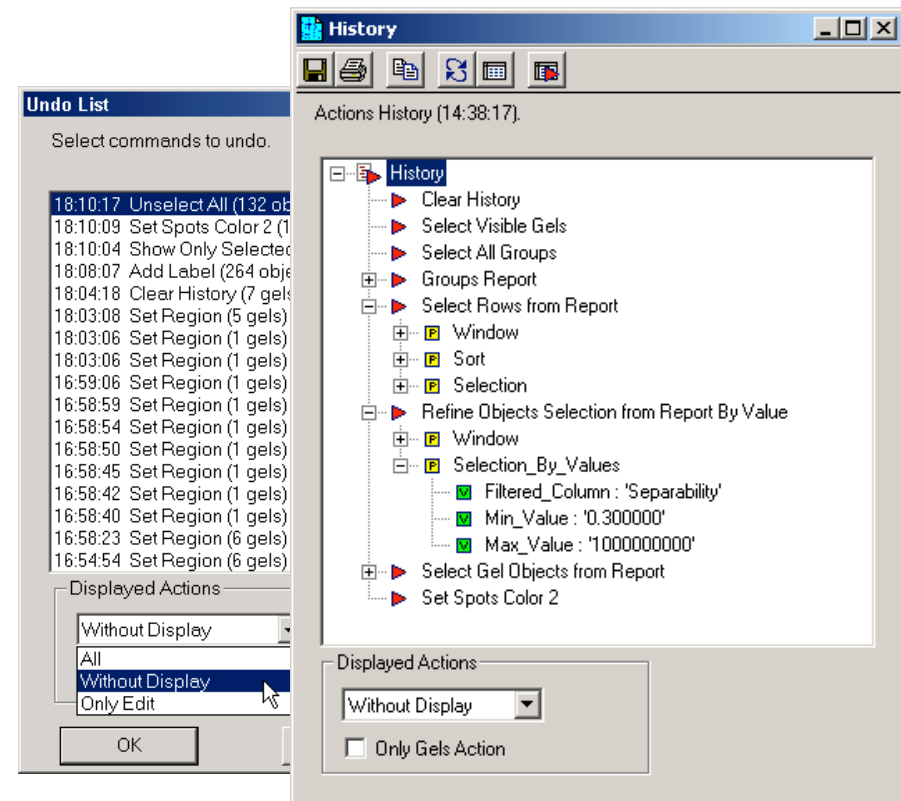


- Integration with Amersham Biosciences' ImageScanner™ via LabScan™ 5.0, also developed by the SIB team
- Direct image acquisition from Twain compatible scanners
- Support of multiple file formats (.tif, .gel, .img, .png)
- Unrivalled annotation capabilities with the possibility to link gel objects to external query engines or data sources of any format (text, html, spreadsheet, multimedia, 2DE database entry, etc.), located locally or on the Internet
- Fully automated integration with spot-picking robots
- Clipboard support to copy images, graphics and tables to other programs

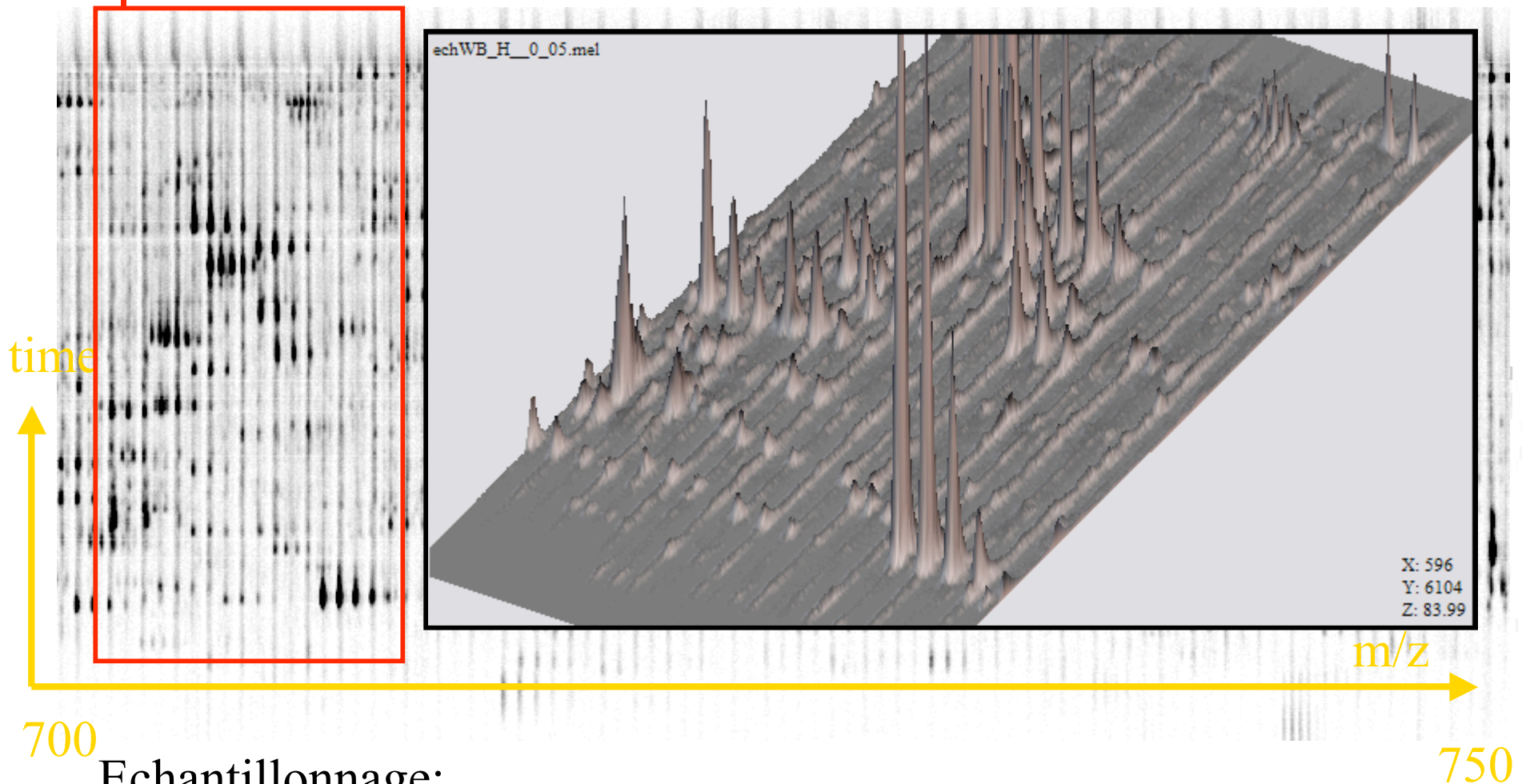
# Facilities to secure data and assure quality



- Unique identifier for each spot, gel, and report to ensure data integrity and consistency
- Backup and restore functions
- Sophisticated Undo/Redo function
- History function tracks all operations for control and quality assurance



# HPLC-ESI/QTOF



700

750

Echantillonnage:

3s – 44 min

0.05 – [400-1200] m/z

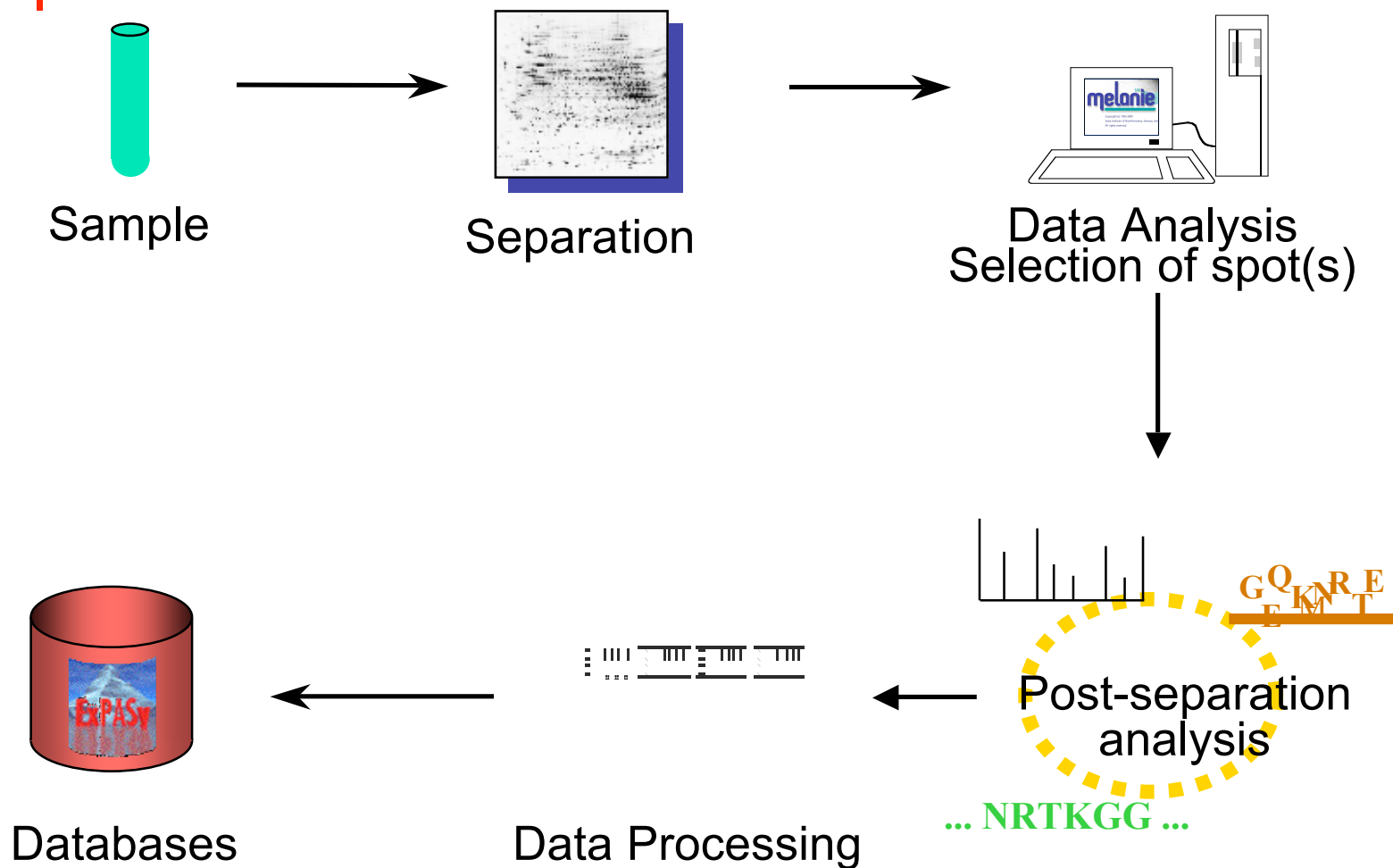
→ 900 spectres MS

→ 16000 mesures

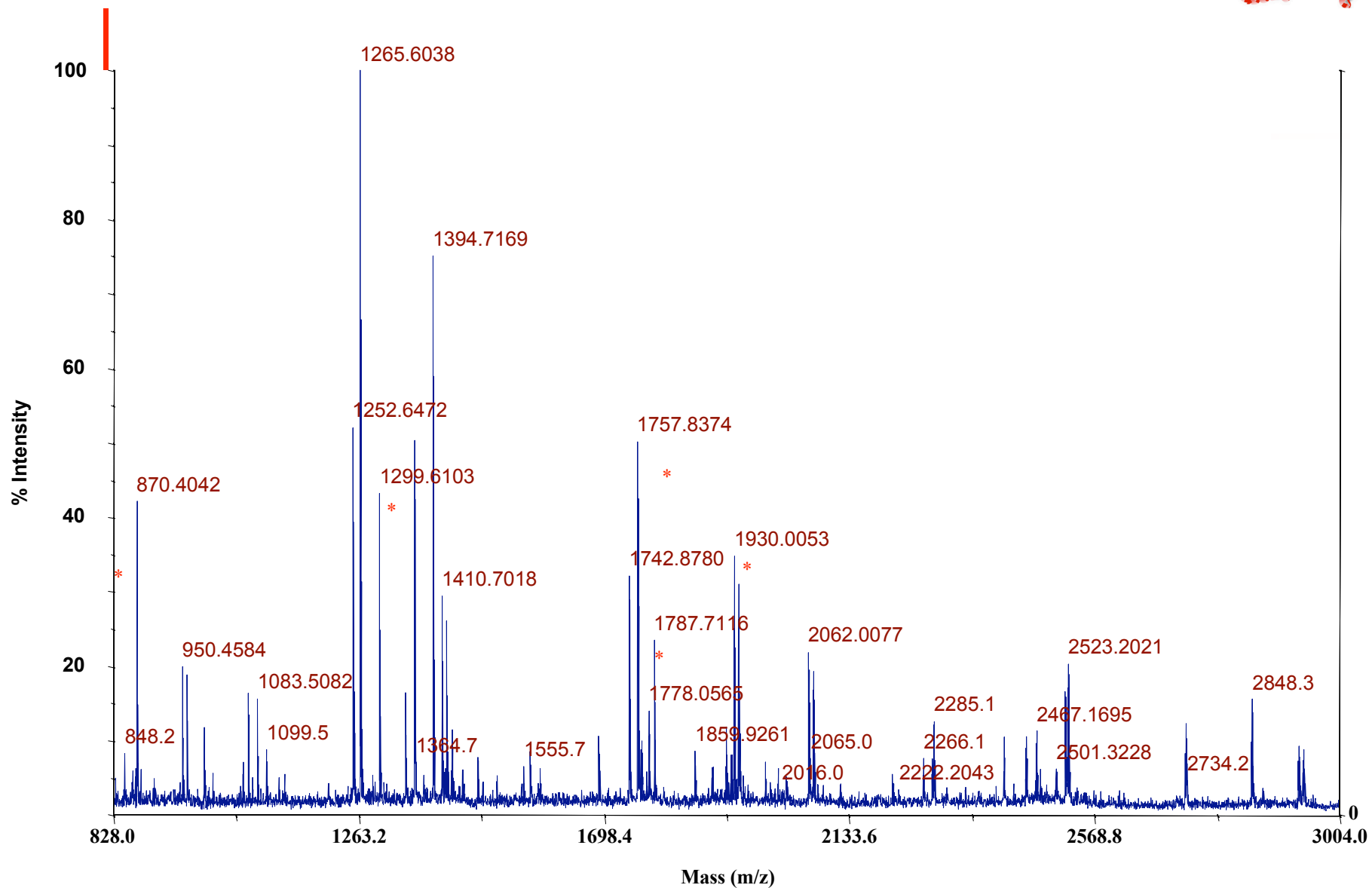
→ ~29



# Proteomics pathway



# MS Interpretation









Aldente version Beta 02/09/2003 feedback is welcome : sample\_name - Mozilla

Aldente version Beta 02/09/2003 feedback is welcome [Documentation](#) [Input summary](#) [Printable page](#)

Date 20/11/2003 10:59:38 UTC

Release Swiss-Prot Release 41.26 of 04-Oct-2003: 135090 entries

Proteins Scanned 149801 / In mass range 141860 / Enough hits 49789 / Enough hits after alignment 30723 / Displayed 20

Peptides Generated 7833156 / Matching 436003 / Average of 55 peptides per protein

Aldente version Beta 02/09/2003 feedback is welcome : sample\_name - Mozilla

Rank	Score	Hits	Taxon
1	4.08	20	Homo sapiens
2	3.94	13	Homo sapiens
3	3.55	17	Mus musculus
4	3.29	9	Rattus norvegicus
5	2.82	6	other Streptophyta
6	2.80	6	other Bacteria
7	2.44	5	Archaea
8	2.38	8	other Firmicutes
9	2.38	10	Schizosaccharomycetes
10	2.34	7	
11	2.33	3	
12	2.32	7	
13	2.31	9	
14	2.28	4	
15	2.24	7	
16	2.14	6	
17	1.58	7	
18	0.92	5	
19	0.71	5	
20	0.71	5	

2) [Q9Y2X3](#) NOP5\_HUMAN Swiss-Prot: Homo sapiens Nucleolar protein NOP5 (Nucleolar protein 5) (NOP58) (HSPC120). [Up](#)

Score : 3.94 Hits : 13 Mw : 59577 pI : 9.03 Coverage : 28% Shift : -0.026667 dalton Slope : 47 ppm

Exp	Theo	Intensity	Delta	Dev	Cont	MC	CAM	MSO	PTM	Position	Sequence
Da	Da	UI	% rank	Da	ppm	ppm					
975.502	975.504004	1795	13	51	-0.00	-2	-21	-	1	1/1	

Aldente version Beta 02/09/2003 feedback is welcome : sample\_name / NOP5\_HUMAN - Mozilla

Score : 3.94 Hits : 13 Mw : 59577 pI : 9.03 Coverage : 28% Shift : -0.026667 Slope : 47

**ALDENTE results for: sample\_name 19.11.03 14:06**

Score	Matches	AC	ID
2.62	20	P17844	DDX5_HUMAN
2.39	13	Q9Y2X3	NOP5_HUMAN
2.11	17	Q61656	DDX5_MOUSE
1.62	9	Q90Z86	NOP5_RAT
1.20	9	O14254	IDHP_SCHPO
1.18	6	P03346	GAG_HTLV2_C3
1.16	8	P51962	RIBB_PHOPO
1.10	5	Q8PTU1	PSMA_METMA
1.07	6	P23139	YPE2_RHORU
1.07	7	P54214	SFAS_DUNBI
1.04	4	P09168	OGT_ECOLI
1.04	4	P09168	OGT_ECOLI
1.00	3	P10396	REP1_ECOLI
0.96	6	Q43854	UGS2_WHEAT
0.95	9	Q08426	ECHP_HUMAN
0.93	4	Q9KYP1	PAAD_STRCO
0.90	9	Q92719	THIC_RHIME
0.87	3	G9A259	FFG_CAUCR
0.83	5	P09428	ILT1_BOVIN_C1
0.60	3	P06112	PHAA_SYNPF

Graphical visualisation of

Selected:  Last Selected:

Create mass list for

Selected

Unselected

Intensity	Delta	Dev	Score	Cont	MC	CAM	MSO	PTM	Position	Sequence	
% rank	Da	ppm	ppm						start end		
13	51	-0.00	-2	-21	0.07	-	1	1/1	-	207 - 214	CLQKVGDR
15	43	-0.08	-66	-91	0.08	-	1	-	0/1	361 - 371	MLAAKTVLAIR
21	24	0.12	97	72	0.21	-	-	1/1	-	197 - 206	ISDNLTYCK
100	1	0.09	65	38	0.20	-	1	0/1	1/1	175 - 184	ELNRYMRCR
100	1	0.05	36	9	1.50	-	-	-	-	269 - 278	TQLYELQNR
36	6	0.11	83	56	0.18	-	1	1/1	0/1	175 - 184	ELNRYMRCR
60	3	0.05	35	7	0.91	-	-	-	0/1	121 - 133	SQMDGLIPVEPR
18	28	0.04	28	0	0.17	-	-	-	1/1	121 - 133	SQMDGLIPVEPR
18	33	0.04	24	-5	0.18	-	-	-	-	222 - 235	LSELLPEVEAEVK
10	67	0.02	13	-17	0.10	-	-	-	1/1	1 - 15	MLVLFETSQVYAIK
10	67	0.02	11	-20	0.11	-	-	-	-	338 - 353	YGLIYHSLVQQTSPK
18	30	0.15	86	54	0.09	-	1	2/2	-	197 - 210	IISDNLTYCKKQLQK
34	8	0.06	34	2	0.34	-	-	-	0/1	372 - 388	YDAFQEDSSAMGVENR
11	62	-0.04	-23	-56	0.03	-	-	0/1	1/1	102 - 117	LNLSCHSPVNVLMR
11	65	0.06	34	2	0.10	-	-	-	1/1	372 - 388	YDAFQEDSSAMGVENR
29	12	0.05	27	-4	0.30	-	-	-	1/1	102 - 117	LNLSCHSPVNVLMR
10	69	-0.20	-106	-139	0.11	-	-	-	0/1	50 - 67	FQDTAEALAAFTALMEGK
15	40	0.05	24	-9	0.16	-	-	-	0/3	279 - 297	MMAIAPNVTVMVGLVGAR
9	83	0.02	10	-23	0.05	-	1	-	-	22 - 37	LQEVDSLWKEFETPEK
6	100	0.09	41	6	0.03	-	1	-	-	468 - 485	VEEEEEKVAEEETSQK
6	97	0.08	36	1	0.03	-	1	1/1	0/1	100 - 117	EKLNLSCHSPVNVLMR
5	102	-0.09	-41	-75	0.01	-	1	0/1	1/1	102 - 120	LNLSCHSPVNVLMRGR

the calculation of the score  
 calculation of the score  
 some identical masses but the alignment can discriminate between them  
 some identical masses but the alignment only cannot discriminate between them, discrimination is done on the score

Peak description area



The screenshot displays the Aldente software interface (version 02/09/2003) with three main panels:

- Left Panel (Project Tree):** Shows a 'NewParamProject' with a 'Global view' containing 'Z119\_A03\_b\_0001'. It is further divided into 'Param', 'Sample', and 'Result' sub-views.
- Middle Panel (Search Results):** Displays the 'Result of submission (19/11/2003 13:20:20 UTC)'. It lists search statistics: 'Found 20 result(s) in : Swiss-Prot Release 41.25 of 26-Sep-2003: 134803 entries'. Below this, it shows 'Number of scanned proteins : 142534', 'Number of proteins in mass range : 135951', 'Number of proteins compatible : 46634', 'Number of proteins scored : 28607', 'Number of peptides generated : 7371693', and 'Number of peptides compatible : 410460'. A table lists search results with columns for Score, AC, ID, and Taxon.
- Right Panel (Protein Sequence):** Shows the sequence for 'DDX5\_HUMAN (P17844)'. The sequence is: `MSGYSDDRDRGRDGRGFGAPRFGGSRAGI  
LVKKKMINLDELPKFEKQFYQEHFDLRF  
EITVGRHNCPKPLNMFYANFPANVIDV  
QAQGWVALSGLDMVGYAQTGSGRTLSI  
FLERDGPICLVLPATRELAQQVQVVAJ  
IYGGAPKGPQIRLDRGVEICLATPGRV  
RITVILVDEADRLDNGFEPQIRKIVDG  
IUPKEVRLAEDFLRQYIHIMGALELS  
HDVEKDEKIRLMEEMSEKKNLIVFI  
MRDGGPANGIHGDKSQEERAVVNEFF  
ASRGLDVEDYKFLINVDYVNSSEDIYHE  
AYTFTPNINIKQVSDLSVLRFAWQAIN  
GRSRGRGQKDDDRDRYSAGHREGFNTH  
LIRKDFGARTQNCWYSAAHITNGSFGSI  
GWPTGTQYQNGDSTQYGGSNVPHNNGC  
APHIQTVPNPTGYSQ`
- Bottom Right Panel (Mass Spectrum):** Shows a mass spectrum plot with 'Available filters' set to 'Same peak and same peptide'. It displays 'Selected matches' with a table of AC, m/z, and Mass values. The plot shows several peaks, with a prominent one at m/z 868.606. Below the plot, there are input fields for 'Min X', 'Max X', 'Min Y', 'Max Y', 'Min Z', and 'Max Z'.

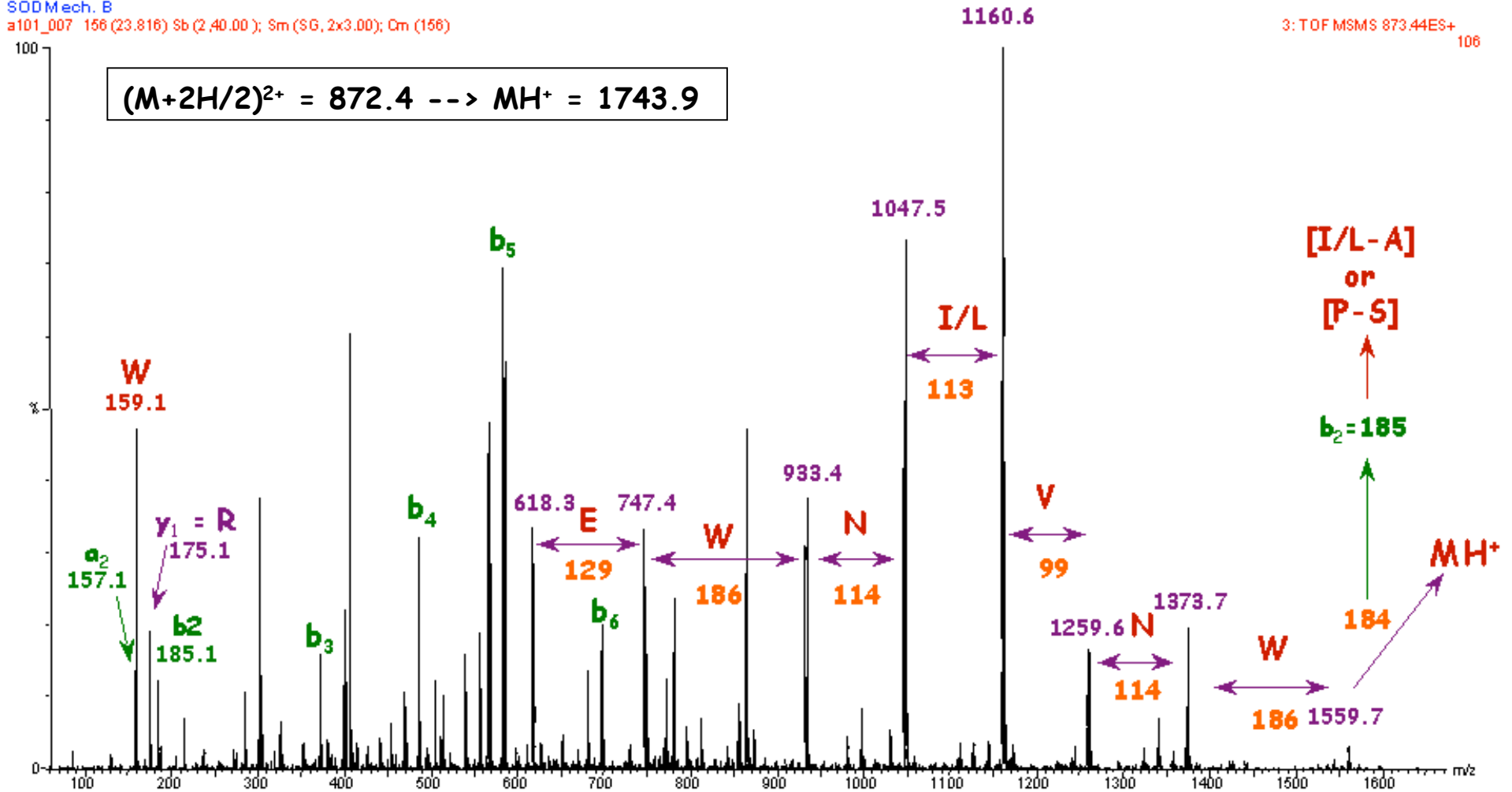
- Java interface (standalone)
  - Creation and management of projects
  - Batch process capabilities
  - Various possibilities of result visualization
  - Spectra manipulation features

# MS-MS Interpretation

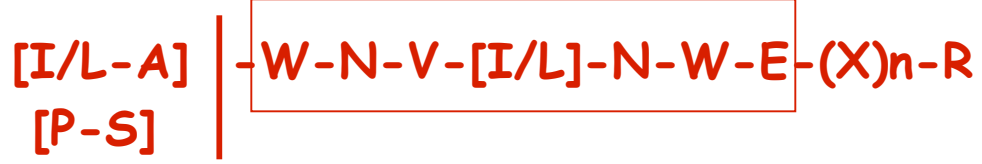
SODMech. B

a101\_007 156 (23.816) Sb (2.40.00); Sm (SG, 2x3.00); Cm (156)

3: TOF MSMS 873.44ES+  
106



$$(M+2H/2)^{2+} = 872.4 \rightarrow MH^+ = 1743.9$$



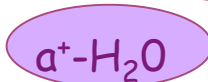
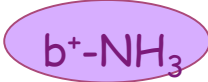
# MS-MS: Popitam



SOURCE MS/MS PEAK LIST

## 1) INTERPRETING

ionic hypothesis



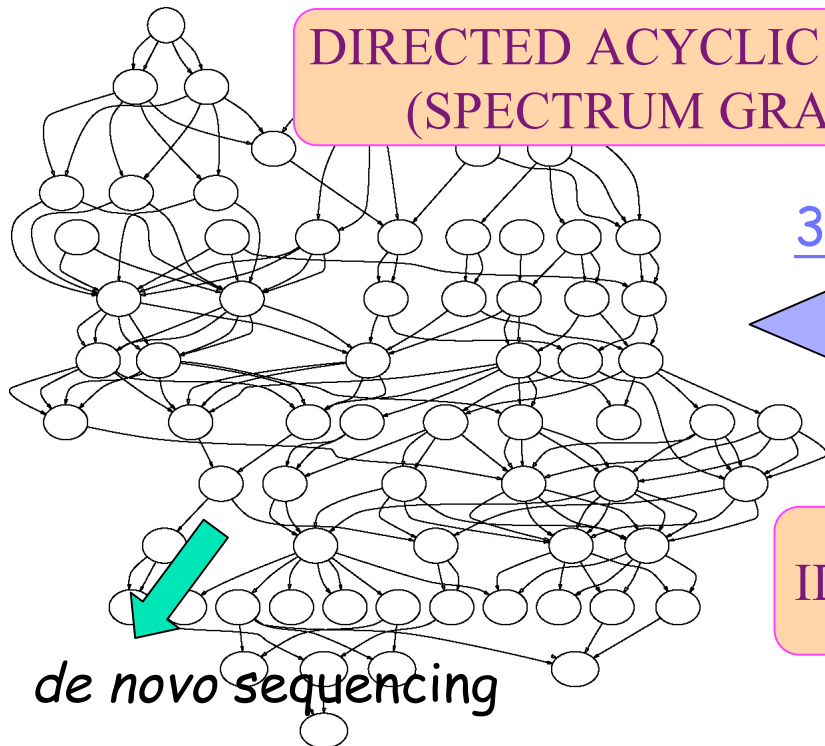
ionic m/z

singly charged b-ions

INTERPRETED PEAK LIST

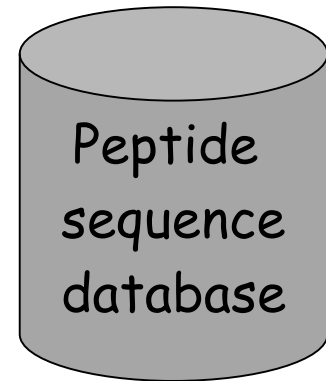
## 2) STRUCTURING

DIRECTED ACYCLIC GRAPH (SPECTRUM GRAPH)



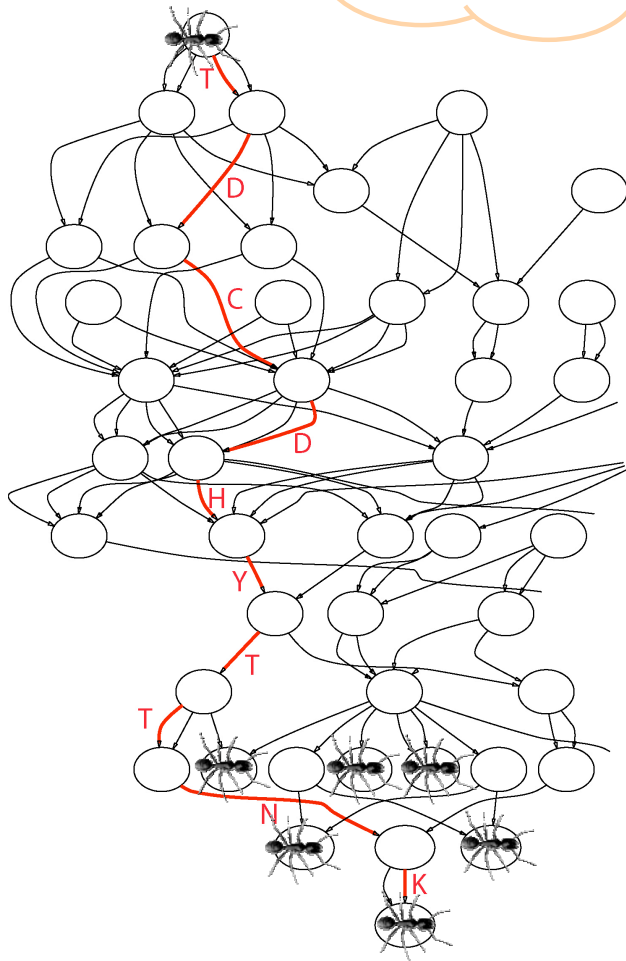
## 3) COMPARING

IDENTIFICATION

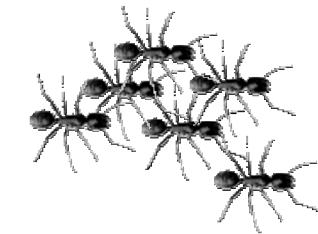


TDCDHYTTNK

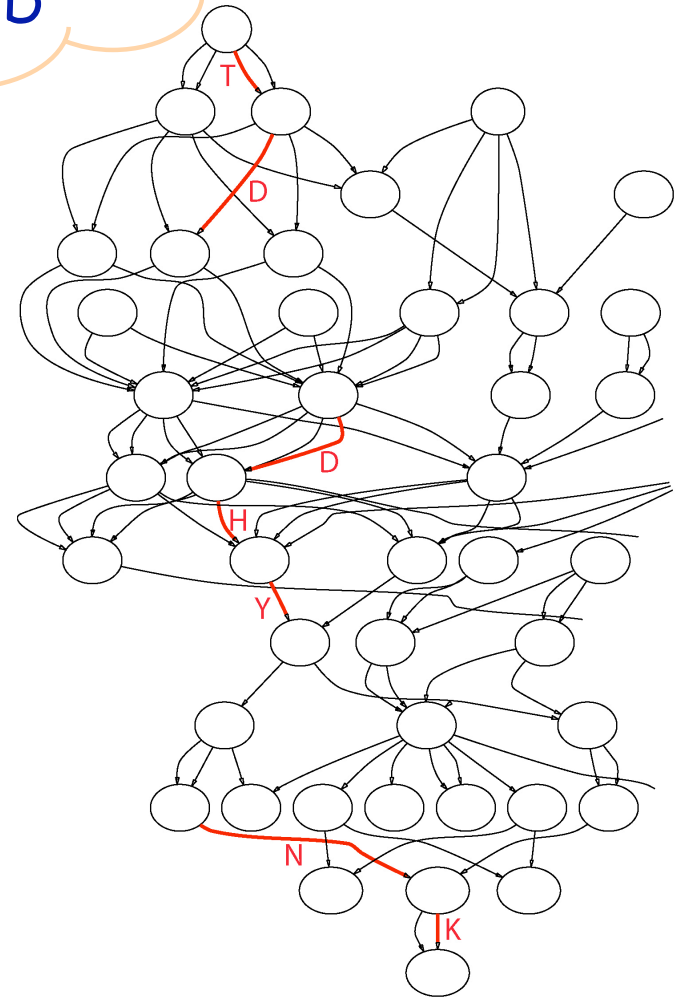
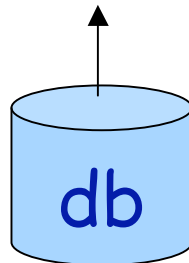
YTTN NK YTT  
CDH TDCD ...



full path algorithm



TDCDHYTTNK



tag algorithm



# ExPASy Proteomics tools

- Take into account Swiss-Prot annotations concerning PTMs and splice variants.
- Closely integrated and hyperlinked with Swiss-Prot and TrEMBL entries on ExPASy, and among each other.
- <http://www.expasy.org/tools/>

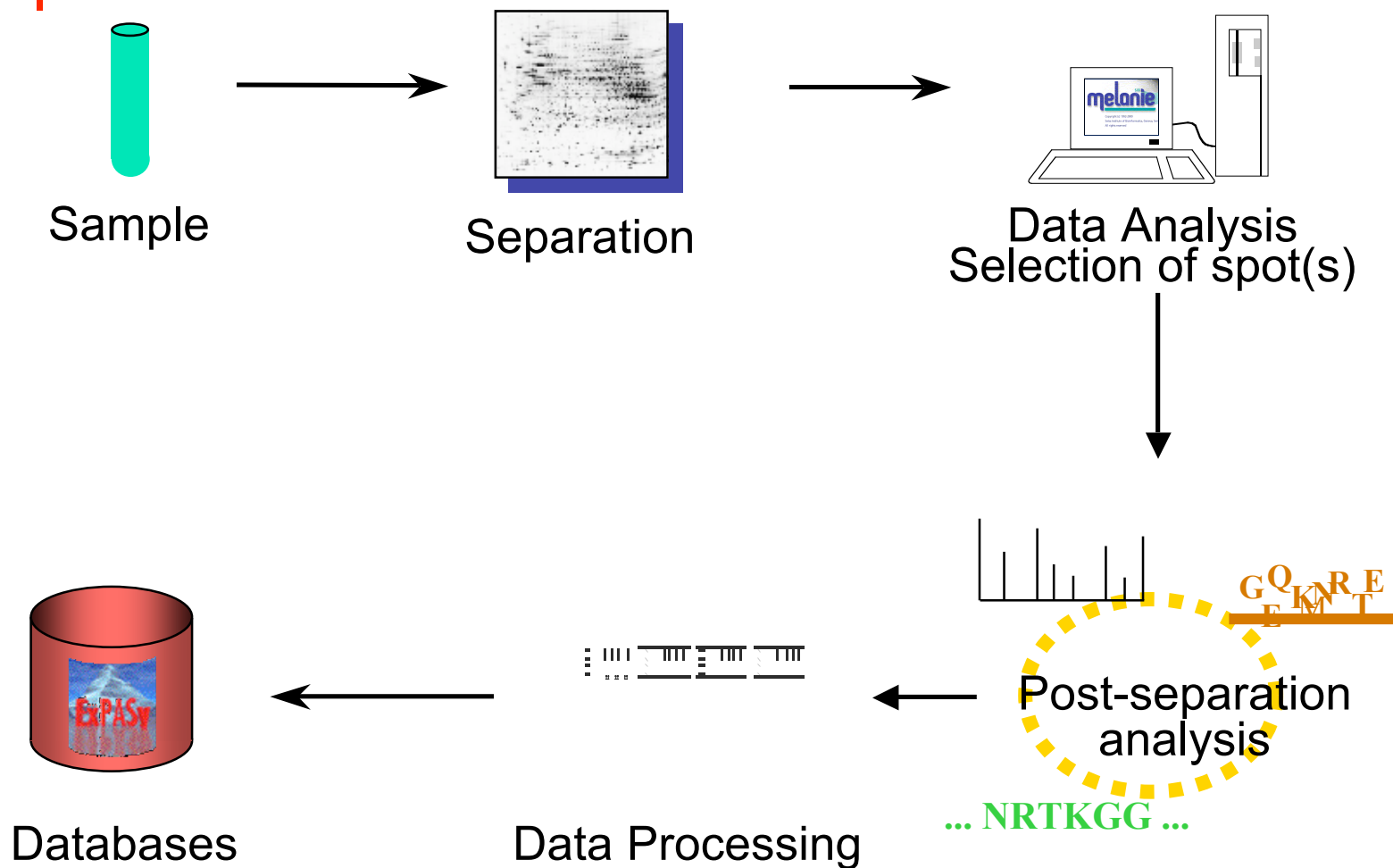


# ExPASy Proteomics tools

- Protein identification
  - AACompIdent, AACompSim, MultiIdent, Peptident/Aldente, TagIdent
- Protein characterization
  - FindMod, GlycoMod, FindPept, Myristoylator, Sulfinator
- Primary structure analysis
  - Protparam, Compute pI/Mw, ProtScale
- Tertiary structure
  - SWISS-MODEL



# Proteomics pathway





# SWISS-2DPAGE

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Release 17.0 (Mar 2004) : 1265 entries (3971 spots)  
in 36 reference maps:

- *Human*: 18 maps (Liver, Plasma, Red blood cells, ...),
- *Mus musculus* : 6 maps (Liver, Islets, ...),
- *Arabidopsis thaliana*, *Dictyostellium discoideum*,  
*Saccharomyces cerevisiae*, *Staphylococcus aureus*
- *Escherichia coli*: 8 maps (for several pI ranges)

# Structure of SWISS-2DPAGE



## Nice2DPage View of SWISS-2DPAGE:

P02679

### General information about the entry

<a href="#">View entry in original SWISS-2DPAGE format</a>	
Entry name	FIBG_HUMAN
Primary accession number	P02679
Entered in SWISS-2DPAGE in	Release 00, August
Last modified in	Release 08, Novem

### Name and origin of the protein

Description	FIBRINOGEN GA
From	HOMO SAPIENS
Taxonomy	EUKARYOTA; M MAMMALIA; EU

### References

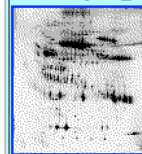
- [1]  
MAPPING ON GEL.  
MEDLINE, 96007934. [NCBI, ExPASy, Israel, SANCHEZ J.-C., APPEL R.D., GOLAZ O.G., P.D.F.;  
ELECTROPHORESIS 16:1131-1151(1995).
- [2]  
MAPPING ON GEL.  
MEDLINE, 78094420. [NCBI, ExPASy, Israel, ANDERSON N.L., ANDERSON N.G.:

PROC. NATL. ACAD. SCI. U.S.A. 74:5421-5425(1977).

### 2D PAGE maps for identified proteins

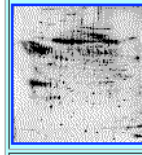
[Compute the theoretical pI/Mw](#)

#### Cerebrospinal\_Fluid



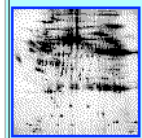
- MAP LOCATIONS: • SPOT [2D-000BYX](#): p
- SPOT [2D-000BY](#): pI=5.53, Mw=51657
  - SPOT [2D-000BZ6](#): pI=5.59, Mw=51526
- MAPPING: MATCHING WITH THE PLAS

#### HepG2\_Secreted\_Proteins



- MAP LOCATIONS: • SPOT [2D-000](#)
- SPOT [2D-00091T](#): pI=5.37, Mw=46
  - SPOT [2D-00091V](#): pI=5.45, Mw=46
- MAPPING: MATCHING WITH TH

#### Plasma



- MAP LOCATIONS: • SPOT [2D-000](#)
- SPOT [2D-0004VU](#): pI=5.03, Mw=51
  - SPOT [2D-0004VY](#): pI=5.13, Mw=51
  - SPOT [2D-0004VZ](#): pI=5.16, Mw=50
  - SPOT [2D-0004WN](#): pI=5.44, Mw=4
  - SPOT [2D-0004WQ](#): pI=5.34, Mw=4
  - SPOT [2D-0004WR](#): pI=5.56, Mw=4
  - SPOT [2D-0004WT](#): pI=5.24, Mw=4
  - SPOT [2D-0004WU](#): pI=5.65, Mw=4
  - SPOT [2D-0004XS](#): pI=5.44, Mw=48
  - SPOT [2D-0004XV](#): pI=5.56, Mw=48
  - SPOT [2D-0004ZZ](#): pI=5.56, Mw=44
  - SPOT [2D-000500](#): pI=5.62, Mw=44
- MAPPING: MATCHING WITH TH

### Copyright

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## NiceProt View of SWISS-PROT: [P02679](#)

Quick BLAST search [new](#)

[\[General\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

### General information about the entry

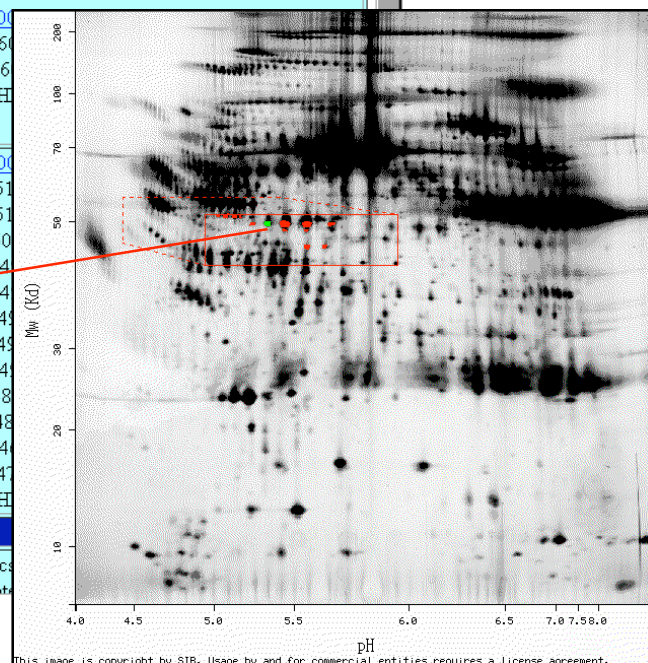
Entry name	FIBG_HUMAN
Primary accession number	P02679
Secondary accession number(s)	None
Entered in SWISS-PROT in	Release 01, July 1986
Sequence was last modified in	Release 05, August 1987
Annotations were last modified in	Release 40, October 2000

### Name and origin of the protein

Protein name	FIBRINOGEN GAMMA-A CHAIN [Precursor]
Synonym(s)	None
Gene name(s)	FGG
From	<a href="#">Homo sapiens (Human)</a>
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI TaxID	9606

### References

- [1]  
SEQUENCE FROM N.A.  
MEDLINE=85252774 [NCBI, ExPASy, Israel, Japan], PubMed=2990550.  
[Rixon M.W., Chung D.W., Davie E.W.](#)  
"Nucleotide sequence of the gene for the gamma chain of human fibrinogen."



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# Make 2D-DB II

- Relational format structure (PostgreSQL)
- Conversion of already existing federated 2-DE databases or creation of new ones
- Automatic updates related to external data



## Make 2D-DB II

- Facilitate the maintenance through Web interfaces (queries, updates)
- Flexible structure (facilitate extension to new information types)
- Interconnect remote databases in order to build a virtual global one
- Generation of flat file and XML formats



# 2D-PAGE Test DB

## 2D-PAGE Test Database

*This is a fictive database to test the Make2D-DB II tool*

### Search by:

- accession number
- description, ID or gene
- author
- spot ID / serial number
- ▶ **pl/Mw range**

-----  
[combined fields](#)

-----  
[proteins in a map](#)

-----  
[navigate the maps](#)

## Search proteins by pI/Mw range

### pI Range:

min. =>  max. =>

### Mw Range (K.Daltons):

min. =>  max. =>

-- Limit to Map:

Sorted by:  protein ID  Map

Please give a **pI** range for your spots. For example, you may type *7.25* or *just 7*. Give also a range for **Mw** in **Kilo Daltons**. You may type, for example, *90.550* or *110*. The search will include all maps, except when you limit your search to a particular map.



2D-PAGE Test Database

### Gateways to other related servers

- [SWISS-2DPAGE](#) - The two-dimensional polyacrylamide gel electrophoresis database of the [Swiss Institute of Bioinformatics](#) in Geneva
- [WORLD-2DPAGE](#) - Index to other Federated 2-D PAGE databases
- [ExPASy](#) - The proteomics web server of the [Swiss Institute of Bioinformatics](#), in Geneva

*This database was constructed using the [Make2D-DB II](#) package (ver. 0.39) from the [WORLD-2DPAGE](#) of the [ExPASy](#) web server*



## Search entries by combining different search keywords

Search by:

- accession number
- description, ID or gene
- author
- spot ID / serial number
- pI/Mw range

combined fields

proteins in a map

navigate the maps

Enter keywords in the form below. Keywords may be any word or partial word of at least 2 characters long. Use of wildcards ("\*" or "?") is authorized. For each separate field, you can choose to interpret spaces as 'or' or 'and' operators. When using more than one field, you have the choice to define 'or' or 'and' operators relative to the other fields.

Execute query    Reset

**Field 1** Interpret spaces between keywords as:  OR  AND  adjacent

1.5. Keywords  field contains: plasma and not:

-----  OR  AND -----

**Field 2** Interpret spaces between keywords as:  OR  AND  adjacent

2.1. Organism Name / Classification  field contains: human and not:

Searching in '2D-PAGE Test Database' for entries matching your query.

**Query result:** 4 entries matching criteria

Accession number	Description
P02760	ALPHA-1-MICROGLOBULIN / INTER-ALPHA-TRYPSIN INHIBITOR LIGHT CHAIN (PROTEIN HC) (HI30)
P02741	C-REACTIVE PROTEIN PRECURSOR
P05090	APOLIPOPROTEIN D
P13693	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23)



2D-PAGE Test Database (Combined)

Save -- To save the table in a file, give a file name here:  file type:  Unix  Windows/DOS

*If you choose to save your file in **text** format, make sure you check the right file type for your system. Otherwise, to keep a copy in **HTML** format, you will simply need to save the result page directly from your browser.*

Execute query    Reset

EBP federated 2D-PAGE Viewer: [Swiss-2DPAGE ECOLI](#)  
ECOLI-DIGE4.5-6.5 (All spots)

*This is an EBP internal server to query 'EBP federated 2D-PAGE' in relational (PostgreSQL) format*



Switch to Gel:

ECOLI-DIGE4.5-6.5 { Escherichia coli DIGE (4.5-6.5) }

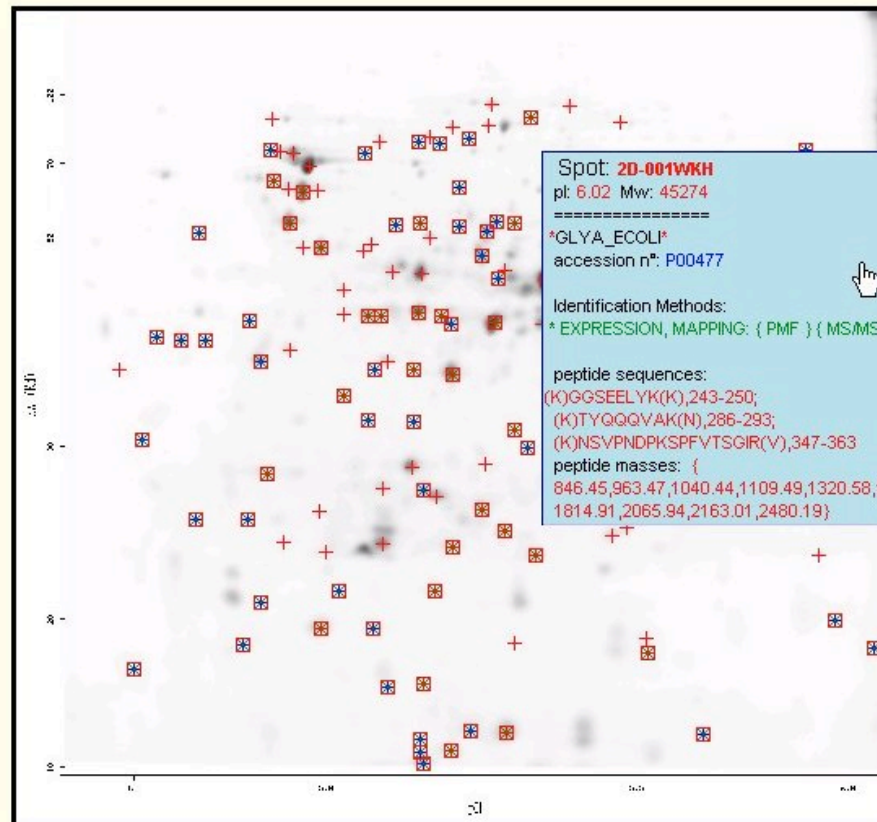
Re-scale Gel to: 50% View: all identified proteins Refresh

Display:  + Identified spots

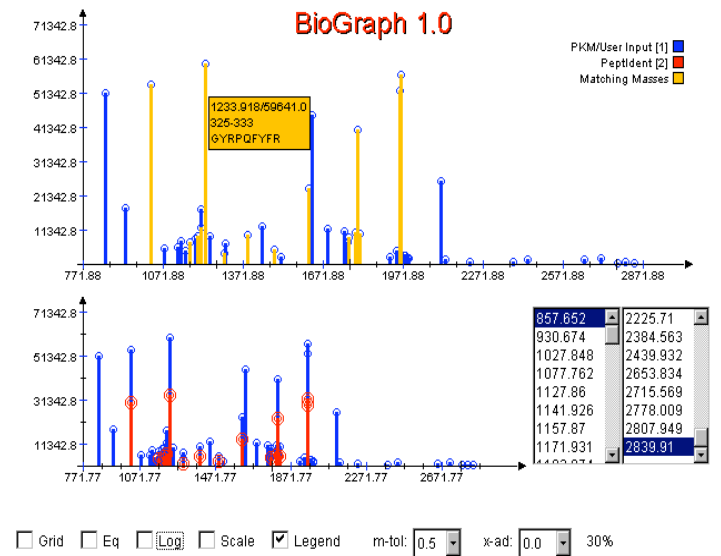
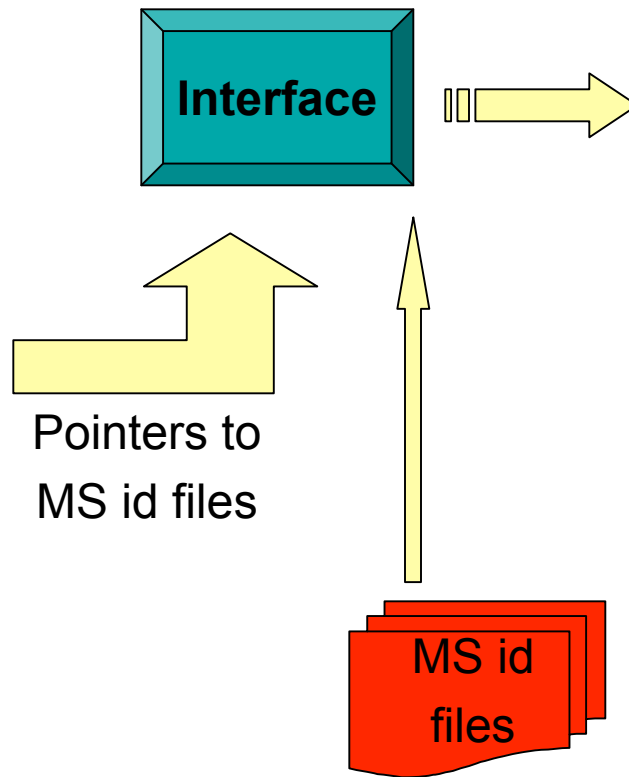
Experimental results for:  X Peptide Sequencing (MS/MS)  + AA composition  + PMF (+ PMF and AA comp.)

Other identification/mapping technics:

(   Tandem MS   Micro-Sequencing   Tagging   Gel Matching   Comigration   Immunoblotting )



# Integration of various experimental annotations



Visual representation



Thank you for your  
attention



ProteoMe  
Informatics  
group SIB

