



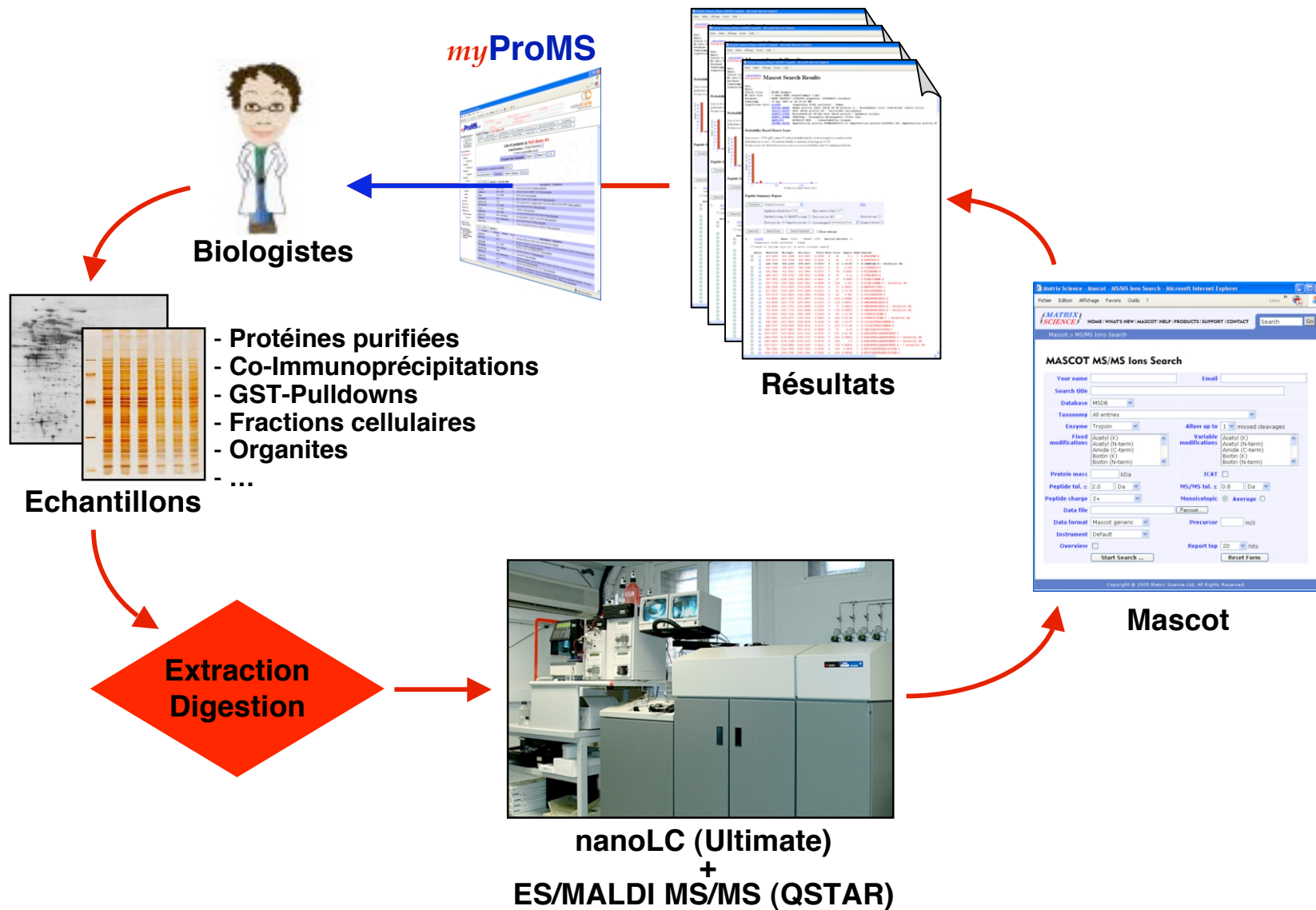
institut**Curie**

# *my*ProMS

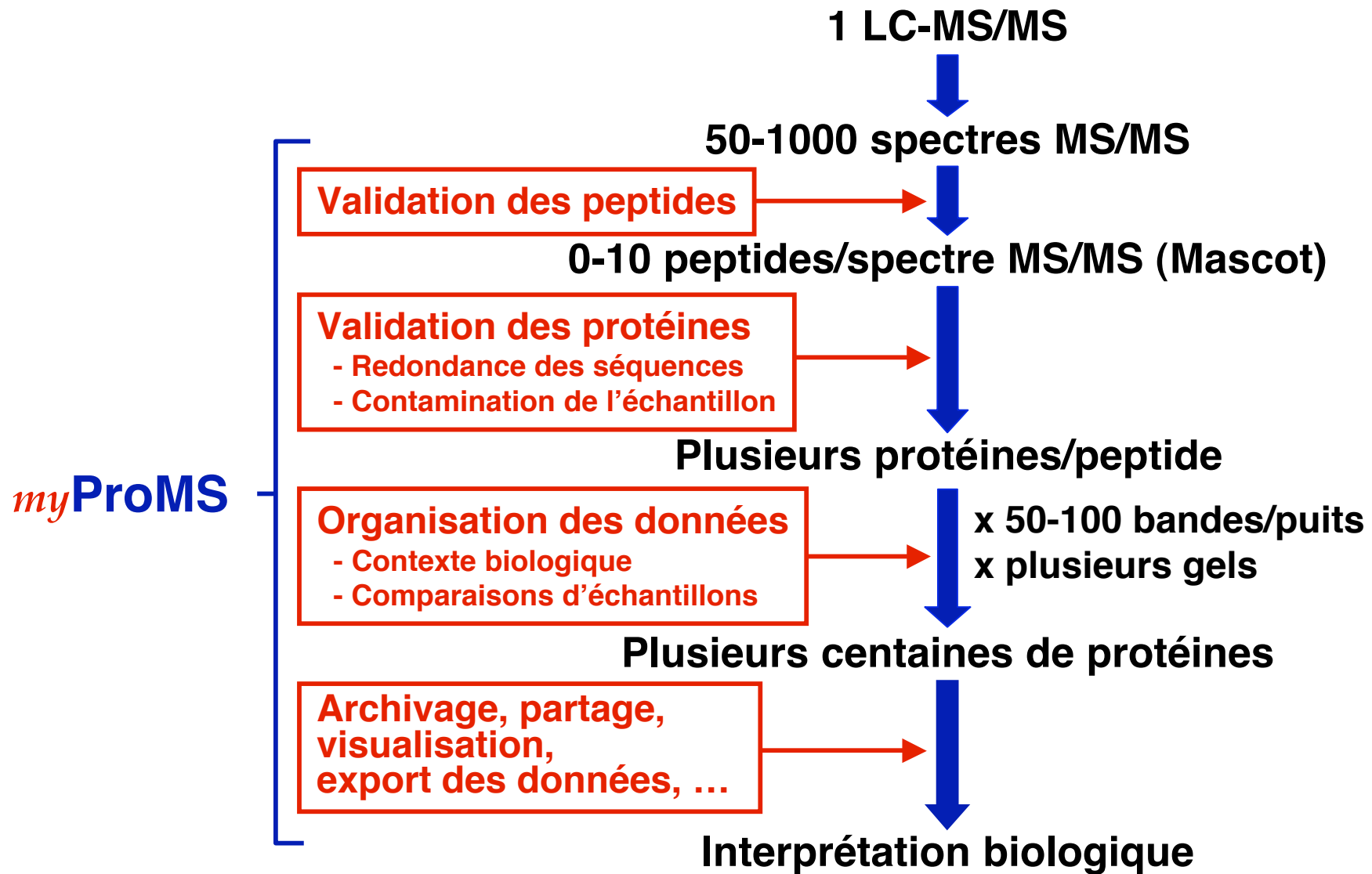
**Un serveur web pour la gestion et la validation  
des données protéomiques issues de la  
Spectrométrie de Masse**

**Patrick Poulet, Service de Bioinformatique, Institut Curie, Paris.**

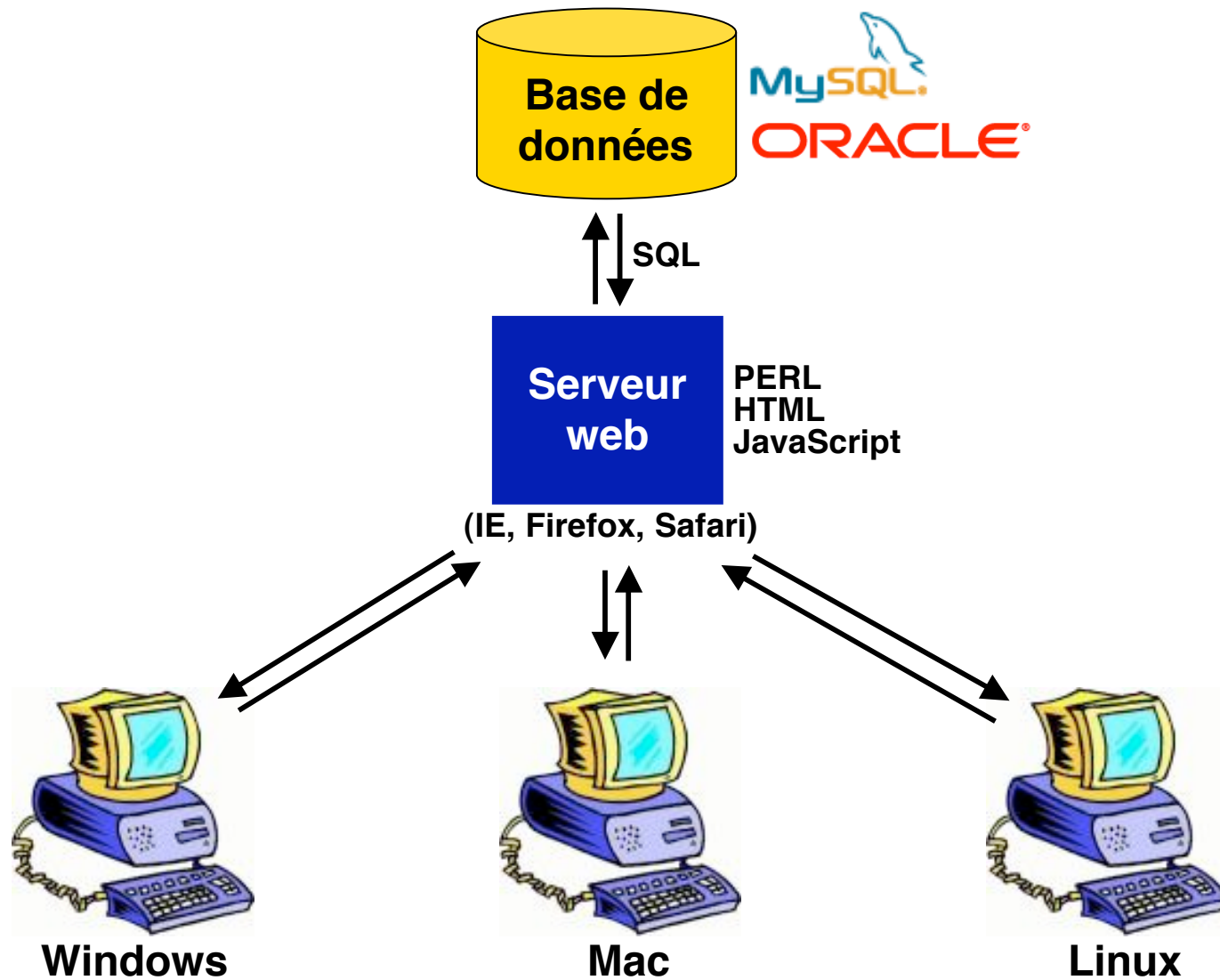
# Le service MS de l'Institut Curie



# Les problèmes rencontrés



# Architecture du serveur *my*ProMS

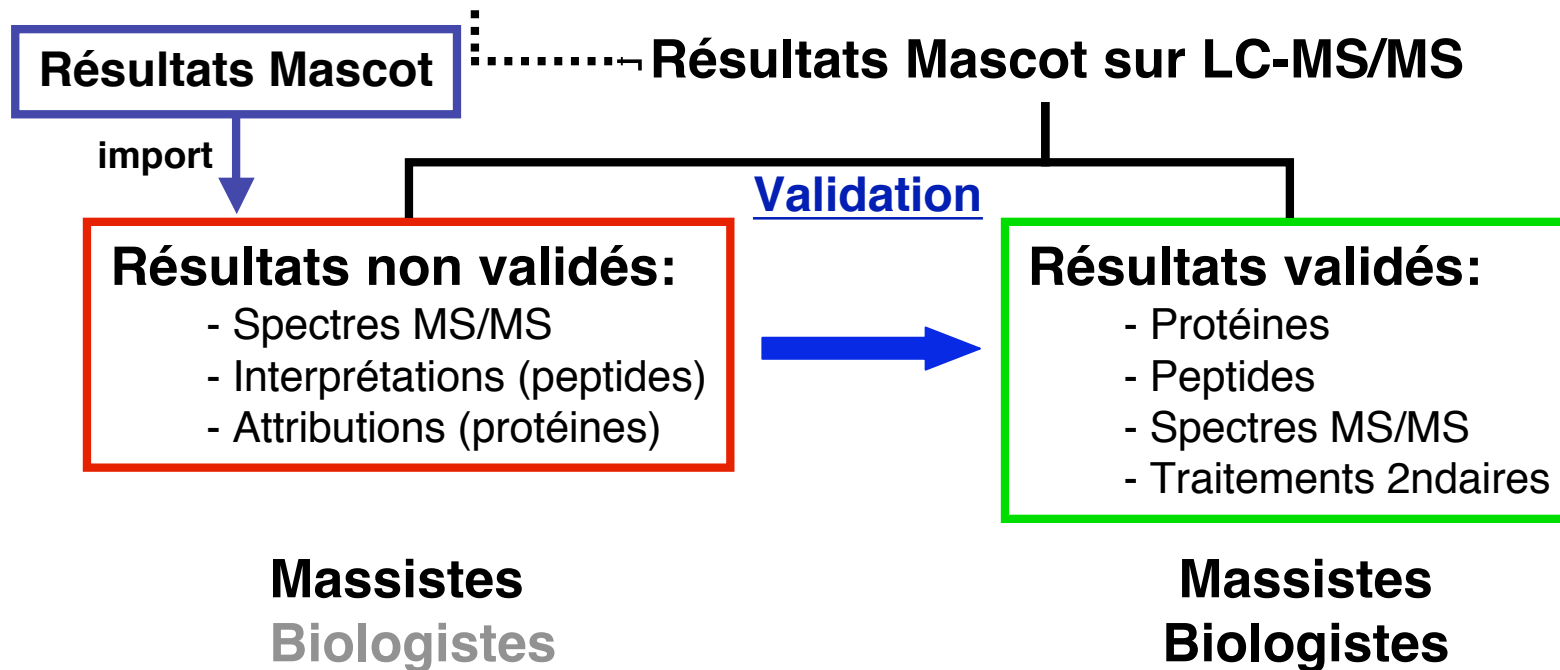


# Organisation des données dans *myProMS*

→ **Projets:** (ex: gels 1D / 2D)

⋮  
→ **Expériences:** (ex: 1 puits de gel 1D / 1 gel 2D)

⋮  
→ **Echantillons:** (ex: 1 bande 1D / 1 spot 2D)



# Exemple de projet

**Validation automatique**

Small GTPases > Pull-down #1

Summary Add Sample(s) **AutoValidation** Filter / Duplicate Protein List Search for Proteins Clustering  
Edit Combine Analyses Clear Validation Remove Filter Export List Compare 2 Items Cluster List

**Automated Validation of all MS/MS Analyses in Experiment Pull-down #1.**

**Résultats Mascot partiellement validés**

**Résultats Mascot non-validés**

**Actions possibles**

**Résultats**

Expand Item  
Expand All  
Close Project

Small GTPases  
Pull-down #1  
Band 1  
Analysis 1  
Band 2  
analysis 2  
Band 2  
analysis 3  
Band 4  
Ana 4c  
Band 5  
Pull-down #2  
Control  
Control 2  
Mascot 2.1  
Moved Exp

MS/MS Analysis :  
○ : data not imported.  
○ : not validated.  
○ : partially validated.  
● : validated.

Overwrite previous validations/rejections.  
*All proteins matched by validated peptides will be validated unless Protein Validation Rules are applied.*

**Protein Validation Rules**

Validate only proteins meeting the following criteria.  
- containing at least 3 peptide(s).  
- and with score  $\geq 200$   
- and with peptide coverage  $\geq$  %.

Keep only best matching protein(s) for each match group.  
 Overwrite previous exclusions.

Auto-Validate

# Validation automatique des résultats de Mascot

myProMS v1.7

Small GTPases > Pull-down #1

Automated Validation of all MS/MS Analyses in Experiment Pull-down #1.

**Interpretation Validation Rules**

- Validate interpretations meeting the following criteria.
- Reject interpretations that do not meet these criteria.
  - minimum score if 1: 90, 2: 80, ≥3: 70 peptides/protein.
  - Exclude already rejected interpretations (if any) from count.
  - and size from 10 aa to aa.
  - and mass error ≤ 0.1 Da.
  - and Rank ≤ 2
- Select only 1 (best) interpretation/query.
- Overwrite previous validations/rejections.

*All proteins matched by validated peptides will be validated unless Protein Validation Rules are applied.*

**Protein Validation Rules**

- Validate only proteins meeting the following criteria.
  - containing at least 3 peptide(s).
  - and with score ≥ 200
  - and with peptide coverage ≥ %.
- Keep only best matching protein(s) for each match group.
- Overwrite previous exclusions.

Auto-Validate

**Validation des peptides**

**Validation des protéines**

# Validation manuelle

**Peptides matching protein gi|189617** Mass: 36057 Da Score: 395.2

Description: protein PP4-X, *unknown organism*

Select	Reject	Query	Rank	Score	Mr(obs)	Delta	Miss	Proteins	Analyses	Peptide
<input checked="" type="checkbox"/>	<input type="checkbox"/>	188	1	93.2	791.39	0.05	0	4	2	K.AASGFNAMEDAQTLR.K
<input checked="" type="checkbox"/>	<input type="checkbox"/>	196	1	(91.9)	799.42	0.11	0	-	-	K.AASGFNAMEDAQTLR.K + Oxidation (M)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	193	1	(79.0)	799.39	0.05	0	-	-	K.AASGFNAMEDAQTLR.K + Oxidation (M)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	216	1	(76.5)	820.38	0.01	0	-	-	K.AASGFNAMEDAQTLR.K + Acetyl (N-term) + Oxidation (M)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	189	1	(60.0)	791.41	0.07	0	-	-	K.AASGFNAMEDAQTLR.K
<input checked="" type="checkbox"/>	<input type="checkbox"/>	187	1	(48.6)	791.38	0.02	0	-	-	K.AASGFNAMEDAQTLR.K
<input checked="" type="checkbox"/>	<input type="checkbox"/>	198	1	(42.2)	799.46	0.18	0	-	-	K.AASGFNAMEDAQTLR.K + Oxidation (M)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	195	1	(26.2)	799.41	0.08	0	-	-	K.AASGFNAMEDAQTLR.K + Oxidation (M)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	212	1	(24.0)	812.39	0.02	0	-	-	K.AASGFNAMEDAQTLR.K + Acetyl (N-term)
<input checked="" type="checkbox"/>	<input type="checkbox"/>	101	1	77.5	597.92	0.02	0	6	6	K.AASGFNAMEDAQTLR.K

#	b	b <sup>++</sup>	b <sup>+</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>+</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	58.03	29.52					G							11
2	171.11	86.06					L	1117.59	559.30	1100.56	550.78	1099.57	550.29	10
3	228.13	114.57					G	1004.50	502.75	987.47	494.24	986.49	493.75	9
4	329.18	165.10			311.17	156.09	T	947.48	474.24	930.45	465.73	929.47	465.24	8
5	444.21	222.61			426.20	213.60	D	846.43	423.72	829.41	415.21	828.42	414.71	7
6	559.24	280.12			541.23	271.12	D	731.41	366.21	714.38	357.69	713.39	357.20	6
7	673.28	337.14	656.25	328.63	655.27	328.14	N	616.38	308.69	599.35	300.18	598.37	299.69	5
8	774.33	387.67	757.30	379.15	756.32	378.66	T	502.34	251.67	485.31	243.16	484.32	242.67	4
9	887.41	444.21	870.38	435.70	869.40	435.20	L	401.29	201.15	384.26	192.63			3
10	1000.50	500.75	983.47	492.24	982.48	491.75	I	288.20	144.61	271.18	136.09			2
11							R	175.12	88.06	158.09	79.55			1

monoisotopic mass of neutral peptide (Mr): 1173.60  
 modified modifications: Carbamidomethyl (C)



# Validation manuelle

**Peptides matching protein gi|189617** Mass: 36057 Da Score: 395.2

Description: protein PP4-X, *unknown organism*

Select	Reject	Query	Rank	Score	Mr(obs)	Delta	Miss	Proteins	Analyses	Peptide
<input checked="" type="checkbox"/>	<input type="checkbox"/>	188	1	93.2	791.39	0.05	0	4	2	MASGNNMEEACTLQK
<input checked="" type="checkbox"/>	<input type="checkbox"/>	101	1	77.5	587.82	0.03	0	6	2	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	230	1	76.7	570.64	0.09	1	4	2	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	112	1	74.4	594.84	0.04	1	6	2	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	152	1	73.5	690.35	0.04	0	5	2	R.DEGNYLDDALVR.Q
<input type="checkbox"/>	<input type="checkbox"/>	67	1	69.3	559.77	0.05	0	5	2	R.SDTSFMFQR.V
<input type="checkbox"/>	<input type="checkbox"/>	52	1	59.7	538.30	0.04	0	6	2	R.AEIDMLDIR.A
<input type="checkbox"/>	<input type="checkbox"/>	171	1	51.5	507.60	0.03	1	6	2	K.SMKGLGTDNTLIR.V
<input type="checkbox"/>	<input type="checkbox"/>	31	1	50.6	498.28	0.02	0	5	2	K.FLTVLCR.N

Confidence level: Good Save selection / Next >> or Validate Match Group for interpretations  $\geq 20$  or Clear Match Group

Match to Query 101 (587.82,2+) File: Q4911BL.wiff, Sample: MBE 14 001 (sample number 1), Elution: 21.75 to 21.82 min, Period: 1, Cycle(s): 1036 (Experiment 2), 1036 (Experiment 3)

**Sélectionner/rejeter les peptides**

**Transfert des résultats validés aux biologistes**

**Exclude la protéine**

#	b	y	b <sup>+</sup>	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>+</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
							G							11
							L	1117.59	559.30	1100.56	550.78	1099.57	550.29	10
							G	1004.50	502.75	987.47	494.24	986.49	493.75	9
4	329.18	165.10			311.17	156.09	T	947.48	474.24	930.45	465.73	929.47	465.24	8
5	444.21	222.61			426.20	213.60	D	846.43	423.72	829.41	415.21	828.42	414.71	7
					541.23	271.12	D	731.41	366.21	714.38	357.69	713.39	357.20	6
					663.65	328.14	N	616.38	308.69	599.35	300.18	598.37	299.69	5
					1575.63	378.66	T	502.34	251.67	485.31	243.16	484.32	242.67	4
9	887.41	444.21	870.38	435.70	869.40	435.20	L	401.29	201.15	384.26	192.63			3
10	1000.50	500.75	983.47	492.24	982.48	491.75	I	288.20	144.61	271.18	136.09			2
11							R	175.12	88.06	158.09	79.55			1

Monoisotopic mass of neutral peptide (Mr): 1173.60  
Fixed modifications: Carbamidomethyl (C)

# Filtrage des protéines avant la validation

myProMS - Microsoft Internet Explorer

myProMS v1.7

Small GTPases > Pull-down #1 > Band 4 > Ana 4c

Summary Validation Filter / Duplicate Search for Proteins Edit Delete Compare 2 Items

**Apply Filter(s) on a Non-validated MS/MS Analysis Ana 4c**

Use proteins from items selected on the right >>>

Select filter

If partially validated MS/MS Analyses are set as filter: Only validated proteins will be used.  
If unvalidated MS/MS Analyses are set as filter:  
 Ignore already rejected proteins.  
 Ignore proteins matched by a single peptide with score below : 20

Keep proteins  unique to Ana 4c.  
 common to filter and Ana 4c.

**and / or**  
**Use proteins from selected species**

Choose from List :  Homo sapiens (382)  human, Peptide Mutant,... (1)  
 human, skeletal muscle... (1)  Mus musculus (1)  
 unknown organism (206)

Proteins from selected species must be  kept.  
 excluded.

**and / or**  
**Use a list of proteins from a local file**

Choose file : D:\myProMS\contaminants.txt Percourir...

Keep proteins  unique to Ana 4c.  
 common to file and Ana 4c.

**Filtered MS/MS Analyses**

Duplicate MS/MS Analysis before applying filter.  
(Validated proteins from partially validated MS/MS Analyses will not be duplicated)

Filter Name : filter#1 (Will be added to filtered MS/MS Analysis name)

Comments : (Will be added to filtered MS/MS Analysis comments)

Apply Filter Clear Cancel

Autres éléments du projet

Organismes

Liste de protéines

Renommer Dupliquer

Expand Item Expand All Close Project

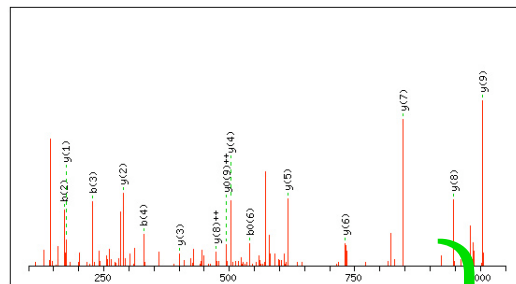
Small GTPases Pull-down #1 Band 1 Analysis 1 Band 2 analysis 2 Band 3 analysis 3 Band 4 Ana 4c Band 5 Pull-down #2 Band 1b Band 2 Band 3 Control Control 2 Mascot 2.1 Moved Exp

MS/MS Analysis :  
● : data not imported.  
● : not validated.  
● : partially validated.  
● : validated.

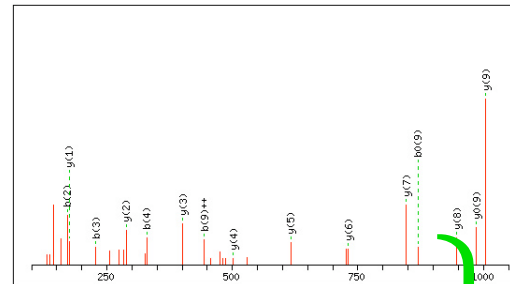
# Autres fonctionnalités pour la validation

Validation d'un même peptide dans plusieurs échantillons.

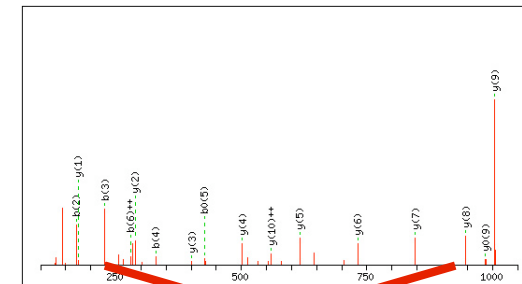
**GLGTDDNTLIR** (2+, sans mod.)



Echantillon #1



Echantillon #2



Echantillon #3

Sauvegarde de spectres de références.

## Autres fonctionnalités pour la validation

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- } **Validation d'un même peptide dans plusieurs échantillons.**
- } **Sauvegarde de spectres de références.**
- } **Commentaire pour chaque peptide validé.**
- } **Fusion des résultats Mascot de plusieurs LC-MS/MS.**
- } **Combinaison:  
    Filtre(s) +  
    Validation(s) automatique(s) +  
    Validation manuelle.**

# Visualisation des résultats validés – 1

myProMS - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

Précédente < > Rec

<< Back

## Graphical View - Match Group of cathepsin S

<< Back

### Edit Match Group **cathepsin S** (MS/MS Analysis **Analysis 1**)

Graphical View

Alias	Visible	Proteins	Cluster	Peptide	Score	Description - Organism
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	cathepsin S	Cat S	5	420	cathepsin S preproprotein; Cat S <i>Mus musculus</i>
<input type="checkbox"/>	<input type="checkbox"/>	Cat S pre	Cat S	5	420	Cathepsin S precursor <i>unknown organism</i>
<input type="checkbox"/>	<input type="checkbox"/>	gi 12805315	Cat S	5	420	Ctss protein <i>Mus musculus</i>
<input type="checkbox"/>	<input type="checkbox"/>	gi 3850787	Cat S	5	420	cathepsin S <i>Mus musculus</i>
<input type="checkbox"/>	<input type="checkbox"/>	gi 3929823	Cat S	4	325	cathepsin S <i>Mus musculus</i>
<input type="checkbox"/>	<input type="checkbox"/>	gi 4138250	Cat S	1	94	cathepsin S <i>Mus musculus</i>

gi|3850787 (score: 419.58, coverage: 20.0 %): cathepsin S (330 aa) *Mus musculus*

gi|3929823 (score: 325.08, coverage: 31.9 %): cathepsin S (163 aa) *Mus musculus*

gi|4138250 (score: 94.5, coverage: 31.1 %): cathepsin S (45 aa) *Mus musculus*

Alias	Score	Protein	Peptide	Description - Organism
gi 4138250	5.2	Cat S	1	cathepsin S <i>Mus musculus</i>
Rab5c	23.4	RAB5	3	Rab5c protein <i>Mus musculus</i>
gi 18390323	23.9	-	3	RAB14, member RAS oncogene family <i>Mus musculus</i>
gi 34147513	23.5	-	3	RAB7, member RAS oncogene family; Ras-associated protein RAB7 <i>Homo sapiens</i>
gi 12832758	23.6	RAB5	2	unnamed protein product <i>Mus musculus</i>
gi 9837556	28.8	IP30	1	lysosomal thiol reductase IP30 precursor <i>Mus musculus</i>
gi 6754124	28.9	Cat S pneu...	1	histocompatibility 2, class II, locus Mb2 <i>Mus musculus</i>
Unnamed	114.6	mannosidase	1	unnamed protein product <i>Mus musculus</i>

Graphical View Edit Match Group

MS/MS Analysis :

- ⊙ : data not imported.
- ⊙ : not validated.
- ⊙ : partially validated.
- ⊙ : validated.

# Visualisation des résultats validés – 1

myProMS - Microsoft Internet Explorer

Fichier Edition Affichage Favoris Outils ?

Précédente Rechercher Favoris Média Liens

myProMS v1.7

MPKPROTEOME CUBI SMFAIOPANALYSIS ATNTTGKQLFDQVVKUSING INSTITUTGL  
PTWLKLDKKVSAQ MASS CURIEESGYL SPECTROMETRY PARI SEVRKENY PEDVAEELI  
QDITQKIMYSQL FRANCEQVKEGILS DATABASE VDNKGFTAVLLGSAVVRDQWEDRI \*

institutCurie  
Together, let's beat cancer.

ppoullet (Bioinformatician)

Expand Item  
Expand All  
Close Project

Small GTPases

Pull-down #1

Band 1  
Analysis 1  
Band 2  
analysis 2  
Band 3  
analysis 3  
Band 4  
Ana 4c  
Band 5

Pull-down #2

Band 1b  
Band 2  
Band 3

Control  
Control 2  
Mascot 2.1  
Moved Exp

Move item up.  
Move item down.

MS/MS Analysis :

- data not imported.
- not validated.
- partially validated.
- validated.

Small GTPases > Pull-down #1

Summary Add Sample(s) AutoValidation Filter / Duplicate Protein List Search for Proteins Clustering  
Edit Combine Analyses Clear Validation Remove Filter Export List Compare 2 Items Cluster List

List of proteins in Pull-down #1

Classification : Protein families  
 Show unclassified  
 Raw list  
 Project hierarchy  
 Confirmed proteins  
 Item comparison  
 My classification  
 Protein families

Graphical view of peptide matches Display

Add selected proteins to Category: --Select a Category--

Check / Uncheck All GTPases : Hydrolyse GTP

Proteins	MW (kDa)	Cluster	Pept.	Description - Organism
<input type="checkbox"/> Rab5c x2	23.4	RAB5	4	Rab5c protein <i>Mus musculus</i>
<input type="checkbox"/> gi 18390323	23.9	-	3	RAB14, member RAS oncogene family <i>Mus musculus</i>
<input type="checkbox"/> gi 12832758 x2	23.6	RAB5	3	RAB5, member RAS oncogene family <i>Mus musculus</i>
<input type="checkbox"/> gi 34147513	23.5	-	1	guanine nucleotide-binding protein (G protein) <i>Homo sapiens</i>
<input type="checkbox"/> gi 1730229	40.5	Gi2 al	1	guanine nucleotide-binding protein (G protein) <i>Homo sapiens</i>
<input type="checkbox"/> gi 22203744	21.5	-	1	c-K-ras2 protein <i>Mus musculus</i>
<input type="checkbox"/> gi 6677819 x2	23.8	-	1	Harvey rat sarcoma oncogene, subgroup R <i>Mus musculus</i>
<input type="checkbox"/> Sec22b	24.7	-	1	vesicle trafficking protein sec22b <i>Homo sapiens</i>

Check / Uncheck All Cathepsins : cathepsin

Proteins	MW (kDa)	Cluster	Pept.	Description - Organism
<input type="checkbox"/> cathepsin S	38.5	Cat S	5	cathepsin S preproprotein; Cat S <i>Mus musculus</i>
<input type="checkbox"/> Cat S pre	38.4	Cat S	4	Cathepsin S precursor <i>unknown organism</i>
<input type="checkbox"/> gi 6681083	29.1	-	1	cathepsin G preproprotein <i>Mus musculus</i>

Check / Uncheck All ATP : ATP-binding proteins

Proteins	MW (kDa)	Cluster	Pept.	Description - Organism
<input type="checkbox"/> gi 4757810	59.8	-	2	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle; ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 2, <i>Mus musculus</i>

Réorganisation des protéines

# Visualisation des résultats validés – 2

**MS/MS Fragmentation of LISLSAQNLVDCSNEEK**

Store Spectrum as Reference

Match to Query 672 (960.44,2+) Elution from: 48.08 to 48.08 period: 0 experiment: 1 cycles: 1  
From data file F:\PE ScieX Data\Projects\API Instrument\Data\Q1516DL.wiff

Click mouse within plot area to zoom in by factor of two about that point  
Or, Plot from 0 to 1700 Da

Monoisotopic mass of neutral peptide (Mr): 1918.93  
Fixed modifications: Carbamidomethyl (C)  
Ions Score: 81 Matches (Bold Red): 29/168 Fragment ions using 36 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>++</sup>	#
1	MRAP													
61	EKNI	86.10	43.55		114.09	57.55			L					17
121	RTLE	199.18	100.09		227.18	114.09			I	1806.85	903.93	1789.83	895.42	16
181	EEKY	286.21	143.61		314.21	157.61			S	1693.77	847.39	1676.74	838.88	15
241	FGDE	399.30	200.15		427.29	214.15			L	1606.74	803.87	1589.71	795.36	14
301	DYWI	486.33	243.67		514.32	257.67			S	1493.65	747.33	1476.63	738.82	13
		557.37	279.19		585.36	293.18			A	1406.62	703.82	1389.60	695.30	12
		685.42	343.22	668.40	334.70	713.42	357.21	696.39	Q	1335.59	668.30	1318.56	659.78	11
		799.47	400.24	782.44	391.72	827.46	414.24	810.44	N	1207.53	604.27	1190.50	595.75	10
		912.55	456.78	895.53	448.27	940.55	470.78	923.52	L	1093.48	547.25	1076.46	538.73	9
		1011.62	506.31	994.59	497.80	1039.62	520.31	1022.59	V	980.40	490.70	963.37	482.19	8
		1126.65	563.83	1109.62	555.31	1154.64	577.82	1137.62	D	881.33	441.17	864.30	432.66	7
		1286.68	643.84	1269.65	635.33	1314.67	657.84	1297.65	C	766.30	383.66	749.28	375.14	6
		1373.71	687.36	1356.68	678.85	1401.70	701.36	1384.68	S	606.27	303.64	589.25	295.13	5
		1487.75	744.38	1470.73	735.87	1515.75	758.38	1498.72	N	519.24	260.12	502.21	251.61	4
		1516.80	808.90	1599.77	800.39	1644.79	822.90	1627.76	E	405.20	203.10	388.17	194.59	3
		1617.84	873.42	1728.81	864.91	1773.83	887.42	1756.81	E	276.16	138.58	259.13	130.07	2
									K	147.11	74.06	130.09	65.55	1

External Protein SeqHour Recorder BLAST F

BLAST Covered Sequence BLAST peptide-covered sequence only at NCBI.

## Edit Protein cathepsin S

Identifiant : gi|10946582

ProMoS : cathepsin S

Description : cathepsin S preproprotein; Cat S

Comments :

listes des échantillons dans lesquels la protéine a été identifiée

## Graphical View - cathepsin S

View: Standard Expanded

Peptides identifiés

Light all its occurrences.

preproprotein; Cat S (340.697 kDa, monomer)  
L > Analysis 1 (score: 419.58, coverage: 19.4 %)

Exp	Mr(calc)	Delta	Miss	Sequence
18.98	968.11	-0.87	0	LISLSAQNLVDCSNEEK
31.15	794.70	-0.07	1	LISLSAQNLVDCSNEEKYGHK
07.76	754.86	-0.05	0	YIQLPFGDEDALK
43.94	648.97	-0.06	0	GPVSVGIDASHSSFFFYK
25.76	813.86	-0.05	0	NSWGLNFGDQGYIR

# Visualisation des résultats validés – 2

The screenshots illustrate the workflow from protein identification to BLAST search. The left window shows the NCBI protein viewer for cathepsin S (NP\_067256), including its definition, accession number, and a list of references. The middle window shows the BLAST search results, displaying 200 hits to 62 unique species, with a detailed view of the top hit (BAC25906). The right window shows the BLAST search form with the protein sequence: NPAPGHLIIPFLVHFLVCSVAMEQLQRPDPLDYHVDLWETHEKVEKDENEEFVPLIWEKMLKFIIMHINLEYSHGMYQVGHNDMGDMTNEEISCRGALRISRGSPKVTFRSYSNRTLPDVTWREKQCVTEVKYGGSCGACWAFSAVGLGQLKTKLISLSAQNLVDCSNEEKYMGGGGVMTAEFQVLIIDGGLEADASYPKAMDEKCHYNSHNRAATCSRYIQLPFGDEALREAVATKGPVSVGIDASHSSFFFRKSGVYDPSCTGNVHGLVTVGGY.

**Peptide list:**

#	Start	End	Sequence
1	167	183	LISLSAQNLVDCSNEEK
2	167	187	LISLSAQNLVDCSNEEKYGNK
3	236	248	YIQLFFGDEEDALK
4	255	272	GPVSVGIDASHSSFFFYK
5	307	320	NSWGLNFGDQGYIR

**External links for cathepsin S:**

Link	Description
<a href="#">Protein Entry at NCBI</a>	Protein Entry at NCBI
<a href="#">SeqHound</a>	Various biological annotations (GO, Medline, etc...)
<a href="#">Recorded BLAST hits</a>	Pre-processed BLAST results
<a href="#">BLAST Full Sequence</a>	BLAST entire protein sequence at NCBI.
<a href="#">BLAST Covered Sequence</a>	BLAST peptide-covered sequence only at NCBI.

**Liens vers serveurs externes**



## Autres fonctionnalités

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- } **Comparaison d'échantillons, de puits ou de gels entiers.**
- } **Regroupement des protéines similaires en clusters.**
- } **Recherche de protéines par mot-clés ou par séquence.**
- } **Export des résultats validés dans Excel.**

# Bilan - Perspectives

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## } **myProMS** à l'Institut Curie :

- Mis en service en Avril 2004.
- 2381 résultats Mascot importés (LC-MS/MS).
- 7311 spectres MS/MS de référence.
- 78975 peptides validés.
- 62262 protéines identifiées.

## } **Améliorations prévues :**

- Intégration de 'Gene Ontology' (GO) pour l'annotation des protéines.
- Fonctions de recherche avancées et statistiques sur protéines et peptides.
- Intégration des résultats d'autres moteurs de recherche: Phenyx, SEQUEST, ...
- Gestion des données issues de la protéomique quantitative.

## } **Disponibilité :**

- Gratuit pour les laboratoires publics
- Version locale de Mascot non indispensable

# Remerciements

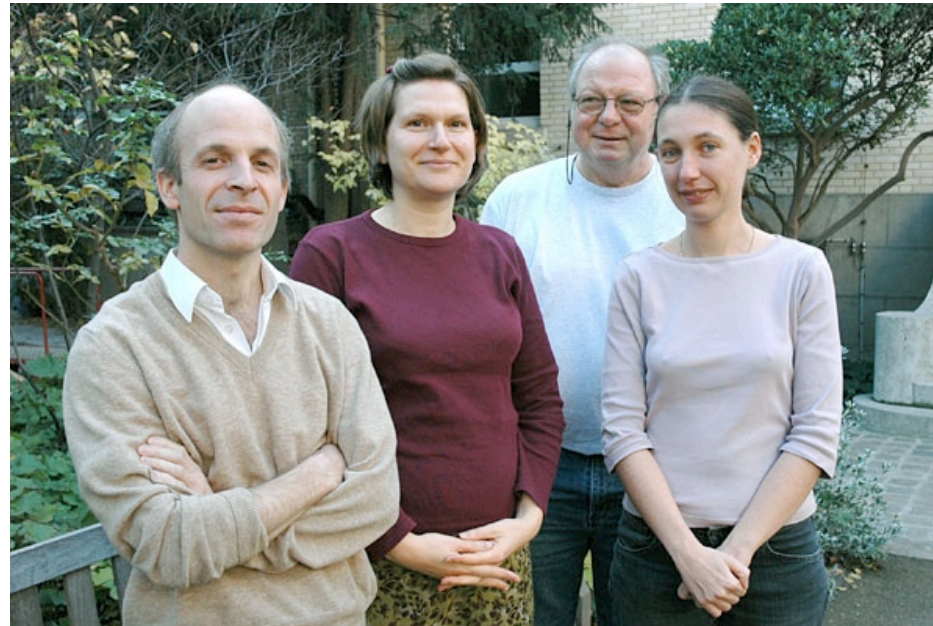
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**Emmanuel Barillot**



**Le service de Spectrométrie de Masse  
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