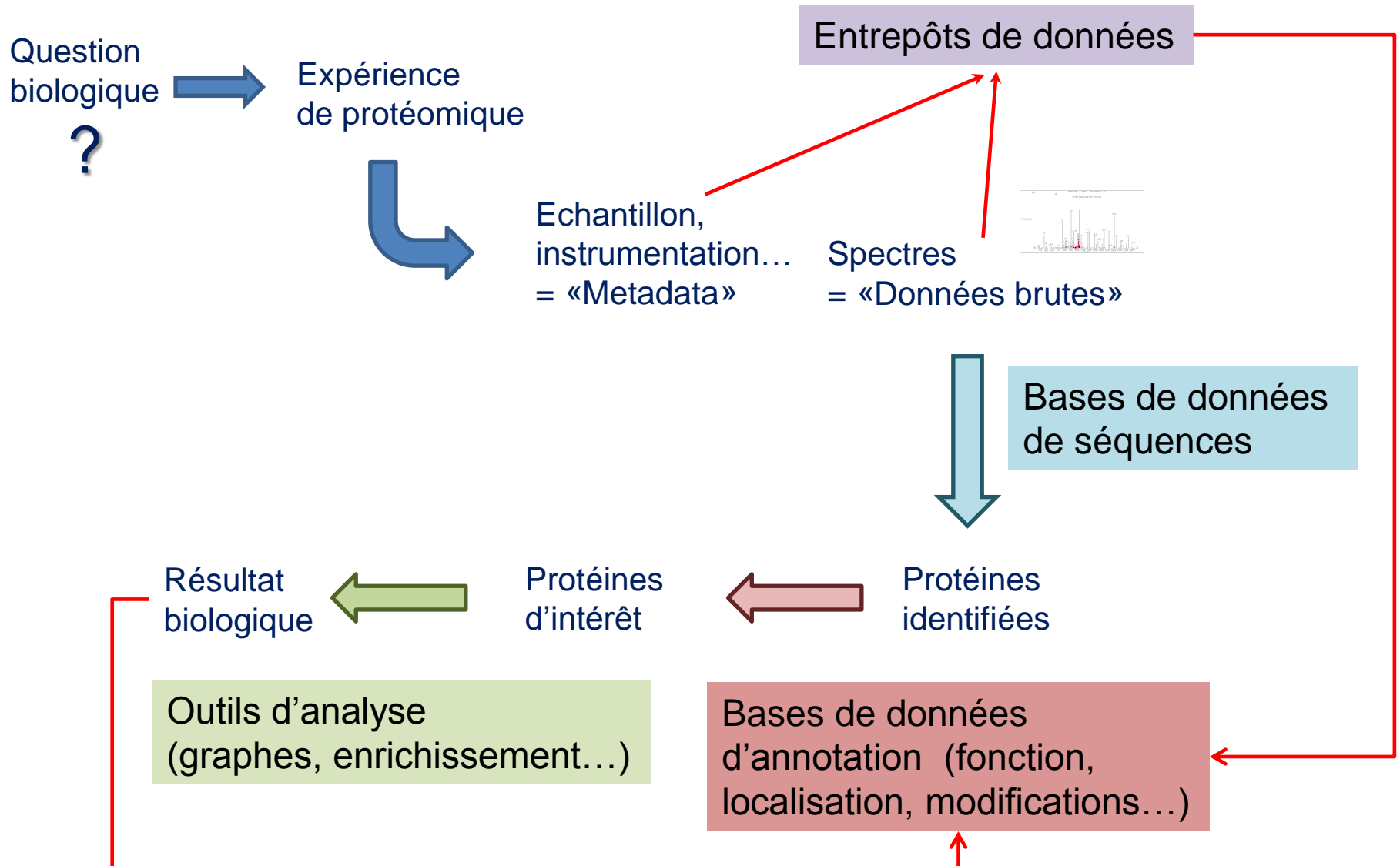


# **Bases de données et ressources pour la protéomique**

**Lydie LANE,**  
*Swiss Institute of Bioinformatics (SIB),  
CALIPHO Group*

**25 septembre 2012 , Workshop « Protéomique et Maladies Rares»**

# Bases de données et protéomique sont indissociables





# <http://www.ebi.ac.uk/pride/>



Username:  Password:

[Register](#) or [Retrieve lost password](#)

## Search Summary View

Select an Experiment (The results will remain restricted according to your original search)

Search filtered on: identificationAccession number , with parameters P29375

[View Instructions](#)

This Table Describes 96 Experiments.

To sort by any of the first seven columns, click the heading.  
(Repeated clicking changes the direction of the sort.)

?

Accession	Title	Species	Tissue	Cell Type	GO Term	Disease	Protein Count	Peptide Count	Spectra Count	Retrieve Details (View in web browser or download as XML file)	Experiment Selection	Select Reference Experiment
5	HUPO Plasma Proteome Project, Lab # 1 Expt # 37	Homo sapiens (Human)	blood plasma	-	-	Disease free	1	3	0	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
11	HUPO Plasma Proteome Project, Lab # 1 Expt # 43	Homo sapiens (Human)	blood serum	-	-	Disease free	1	1	0	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
69	HUPO Plasma Proteome Project, Lab # 29 Expt # 47	Homo sapiens (Human)	blood serum	-	-	Disease free	1	1	0	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
72	HUPO Plasma Proteome Project, Lab # 29 Expt # 50	Homo sapiens (Human)	blood plasma	-	-	Disease free	1	1	0	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
79	HUPO Plasma Proteome Project, Lab # 34 Expt # 15	Homo sapiens (Human)	blood serum	-	-	Disease free	1	2	0	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
1635	Differential COFRADIC N-terminal proteomic analysis of Fas-induced apoptotic protein cleavage in Jurkat cells (1/4)	Homo sapiens (Human)	JURKAT cell	-	apoptosis	-	1	1	1	<a href="#">Web View</a> <a href="#">PRIDE Inspector</a> <a href="#">Download</a>	<input type="checkbox"/>	
		Homo								<a href="#">Web View</a>		

PRIDE core version: 2.8.16

PRIDE web version: 2.8.17

- Search
  - Advanced Search
  - Browse
  - PRIDE BioMart
- Submission Guidelines
- Documentation
- Tools
- Log in
- Acknowledgements
- Contact PRIDE Support

# <http://www.peptideatlas.org/>

ISB Home



PEPTIDEATLAS HOME

Search **All Builds** Current Build Queries SRMAtlas PTPAtlas Submission

Seattle Proteome Center

Select Build Stats & Lists Peps & Prots for Default Builds Summarize Peptide

PEPTIDEATLAS:  
Overview  
Contacts  
Data Contributors  
Publications  
Software  
Database Schema  
Feedback  
FAQ

[show row descriptions](#)

**Build Overview**

Build Name	Human Brain PeptideAtlas 2011-12 Ens64
Build Description	The Human Brain Proteome Project data sets are provided by Young Mok Park from KBSI, Korea and Steve Stein from NIST. The data was searched using Xltandem, and processed using TPP.
Reference Database	Ensembl Human Protein Set v64.37g+ IPI v3.71 + Swiss-Prot 201109+ cRAP + decoys
Build Date	2011-12-06
# Samples	19
PSM FDR threshold (applied to each experiment)	0.0035000
Probability threshold	N/A
Canonical Proteins	2466
Distinct Peptides	15890
Total Observations	253253

ATLAS DATA:  
Data Repository  
Human Plasma (Farrah, et al.)  
HPPP Data Central  
PeptideAtlas Builds  
Search Database

[show column descriptions](#)

**Sample Contribution**

ID	Sample_Name	#_Spectra_Searched	#_Spectra_ID'd	#_Distinct	#_Unique	#_Progressive	#_Cumulative	#_Proteins	#_Cum_Prots	FDR_(%)	Sample_Date
4872	HsBrain1_PE	147751	28087	5444	472	6375	6375	1389	1389	ND	2010-11-19
4875	HsBrain1_PS	66470	1969	380	25	113	6488	140	1399	ND	2010-11-19
4870	HsBrain1_S12	139693	24310	2881	276	1334	7822	718	1539	ND	2010-11-19
4874	HsBrain2_PE	133089	31862	5774	339	2481	10303	1404	1857	ND	2010-11-19
4873	HsBrain2_PS	118060	10581	1750	31	246	10549	552	1883	ND	2010-11-19
4871	HsBrain2_S12	88102	12847	3066	126	799	11348	744	1952	ND	2010-11-19
5160	bpp_lab_12_epilepsy_bn_1149_96_200mcg_cam	14557	1681	163	10	45	11393	46	1957	ND	2011-05-26
5161	bpp_lab_12_epilepsy_bn_1149_96_2d-1c_cam	24591	5622	670	116	268	11661	244	2006	ND	2011-05-26
5166	bpp_lab_12_epilepsy_bn_1149_96_300mcg_cam	10161	1903	174	23	34	11695	48	2007	ND	2011-05-26
5167	bpp_lab_12_epilepsy_bn_1149_96_4mcg_cam	12609	2162	262	9	27	11722	64	2009	ND	2011-05-26
5165	bpp_lab_12_post_mortem_bn_rz104_200mcg_cam	18425	2627	271	55	64	11786	81	2016	ND	2011-05-26
5172	bpp_lab_12_post_mortem_bn_rz104_2d-1c_cam	19144	5544	536	39	87	11873	194	2026	ND	2011-05-26
5170	bpp_lab_12_post_mortem_bn_rz104_300mcg_cam	25485	3484	257	50	61	11934	66	2028	ND	2011-05-26
5163	bpp_lab_12_post_mortem_bn_rz104_4mcg_cam	14382	2881	316	14	19	11953	84	2030	ND	2011-05-26

Contribute Data  
Genome Browser Setup

RELATED:  
SRMAtlas  
Phosphopep  
Unipep  
mspecLINE

SPECTRAL LIBS:  
Libraries + Info  
SpectraST Search

GLOSSARY/TERMS:  
Atlas nomenclature  
SGD nomenclature  
Protein ID terms

<http://www.proteomexchange.org/>

## Mission

The ProteomeXchange consortium has been set up to provide a single point of submission of MS proteomics data to the main existing proteomics repositories, and to encourage the data exchange between them for optimal data dissemination.

The ProteomeXchange consortium is supported by the European Commission 'ProteomeXchange' grant.

Submit Data

Access Data

## News

### New ProteomeXchange dataset PXD000005

POST DATE: SATURDAY, SEPTEMBER 22, 2012 - 00:45

Dear ProteomeXchange subscriber, a new ProteomeXchange dataset is being...

## Upcoming Events

### Basic course: Bioinformatics for MS analysis

MONDAY, 15TH OCT, 2012

Basic course: Bioinformatics for MS analysis

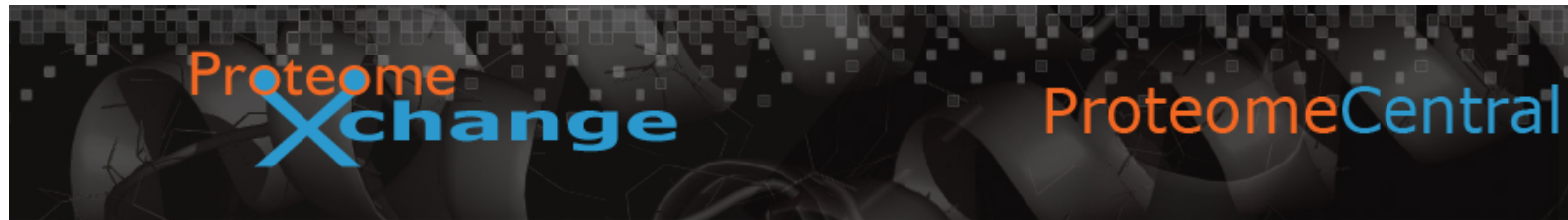
Organiser: EuPA...

### Wellcome Trust Proteomics Bioinformatics Course 2012

MONDAY, 5TH NOV, 2012

The yearly Wellcome Trust Advanced Course in Proteomics

# ProteomeCentral for ProteomeXchange



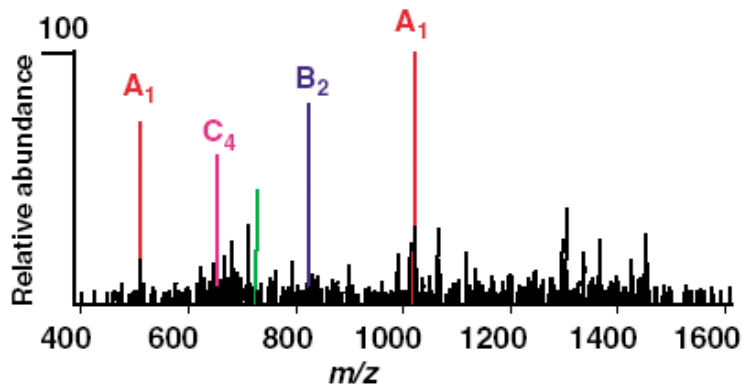
Search:

<a href="#">Dataset Identifier</a>	<a href="#">Repository</a>	<a href="#">Primary Submitter</a>	<a href="#">Title</a>	<a href="#">Species</a>	<a href="#">Instrument</a>	<a href="#">Publication</a>	<a href="#">Announcement Date</a>
<a href="#">PXD000001</a>	PRIDE	Laurent Gatto	TMT spikes	Erwinia carotovora	orbitrap	no publication	2012-05-11
<a href="#">PXD000002</a>	PRIDE	Attila Csordas	Combined personal saliva proteome and microbioproteome	Homo sapiens	linear ion trap	no publication	2012-05-11
<a href="#">PXD000003</a>	PeptideAtlas	Ruth Huettnerhain	Human CAP ovarian cancer plasma (Huettnerhain et al.)	Homo sapiens	AB SCIEX 5500 QTrap	<a href="#">Huettnerhain et al. 2012</a>	2012-05-11
<a href="#">PXD000005</a>	PRIDE	Rui Branca	Proteomic screen reveals Fbw7 as a modulator of the NF-kB pathway	Homo sapiens	LTQ Orbitrap Velos		
<a href="#">PXD000012</a>	PRIDE	Jean-Paul Noben	Resveratrol-induced changes of the human adipocyte secretion profile.	Homo sapiens	Ion Trap		
<a href="#">PXD000013</a>	PRIDE	Lennart Martens	iQUARI	Homo sapiens Pyrococcus furiosus	LTQ Orbitrap	<a href="#">Vauder et al. 2012</a>	2012-08-13
<a href="#">PXD000014</a>	PRIDE	Yuri Obukhov	human 293 cells PEDF LC-MS/MS	Homo sapiens	LTQ Orbitrap	no publication	2012-08-08
<a href="#">PXD000017</a>	PRIDE	Viktoria	Analysis of the rat hypothalamus proteome by data independent	Rattus	Q-ToF		2012-08-08

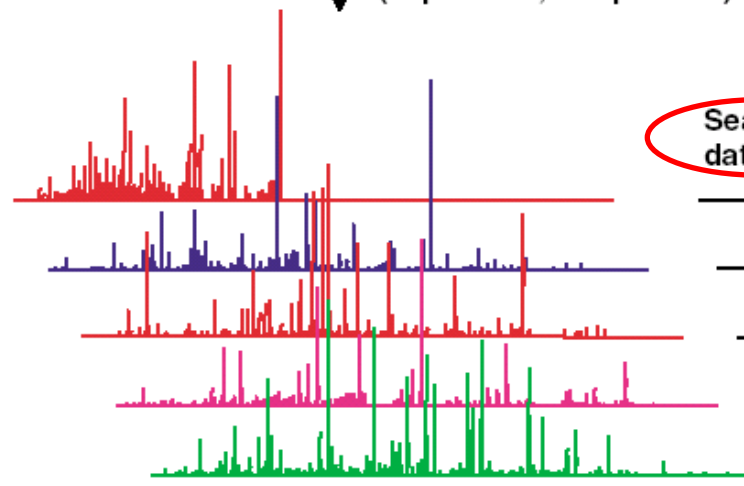
- 8 datasets released and announced
- 16 identifiers reserved for datasets in process







Analyze by MS/MS  
(Top 5 ions, see panel B)



Identification of proteins:  
A, B, C and .....

Sequences of all peptides:

A<sub>1</sub>, A<sub>2</sub>,  
B<sub>1</sub>, B<sub>2</sub>, B<sub>3</sub>,  
C<sub>1</sub>, C<sub>2</sub>, C<sub>4</sub>, and .....

Output all data

5 peptide sequences:

LLTTIADAAK

EFNDPSNAGLQNGFK

LLTTIADAAK

SAGGNYVVFGEAK

EDDVEEAVQAADR

La base de données de séquences utilisée pour l'identification des peptides à partir des spectres doit être « complète » pour un organisme donné

# The human proteomics initiative (HPI)



8<sup>TH</sup> SIENA MEETING

FROM GENOME TO PROTEOME:

INTEGRATION AND PROTEOME COMPLETION

*Siena, Italy, August 31st- September 4th, 2008*

Auditorium Giurisprudenza e Scienze Politiche

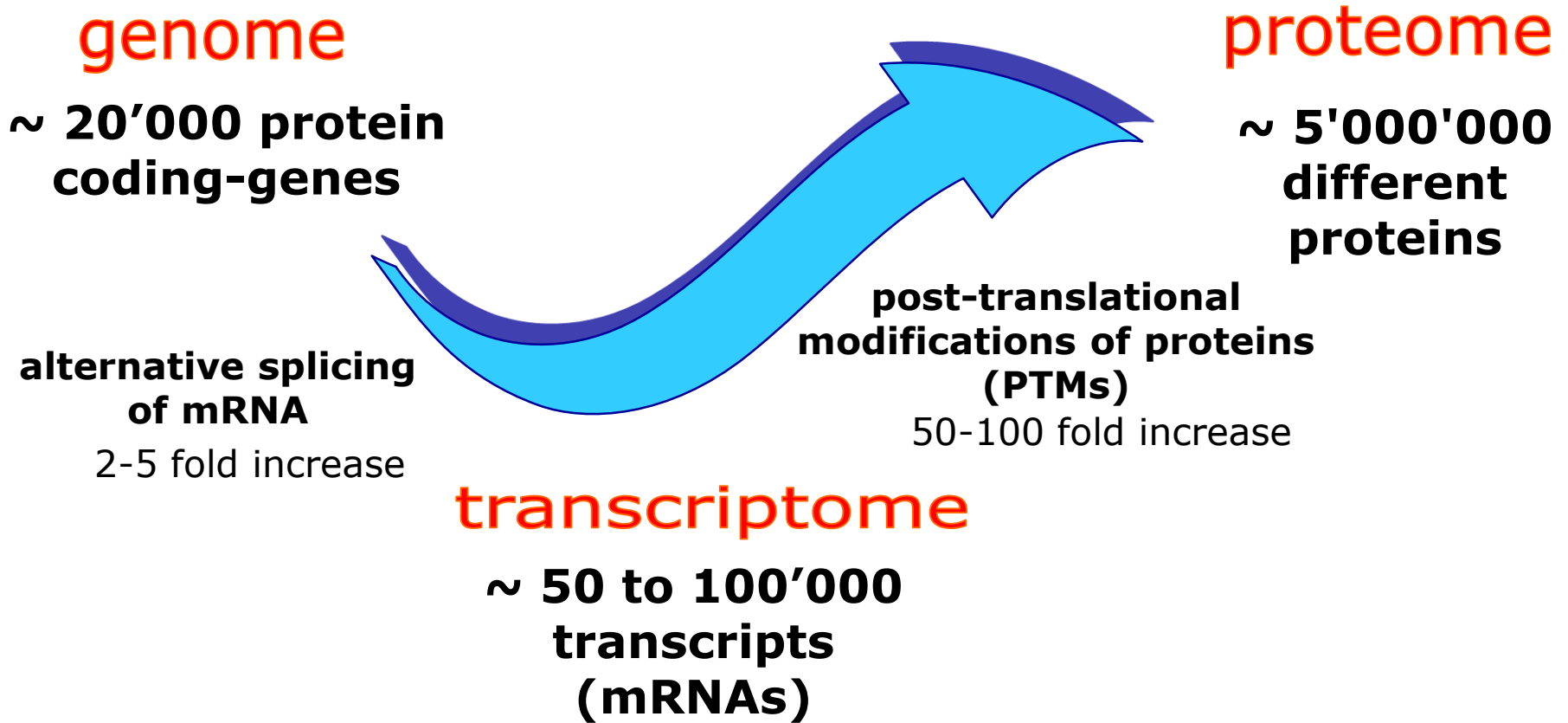


**UniProt Releases 'Complete' Set of  
20K Human Proteins at Siena Meeting**

[September 4, 2008]



# Comment définir un “protéome humain” complet?



# Le protéome humain dans



- **20'225** entrées ★ (~gènes codants);
- **16'000** isoformes d'épissage dans **8'100** entrées: **50'000** séquences protéiques;
- **65'000** variants; **22'500** liés à des maladies; les autres sont des polymorphismes
- **80'000** PTMs (50% prouvées expérimentalement).

- Une ressource spécifique pour les protéines humaines
- Ne remplace pas UniProtKB/Swiss-prot qui reste la base de référence pour les séquences humaines
- Vise à intégrer des résultats d'expériences à haut débit en transcriptomique, protéomique etc...
- Avec un souci constant de qualité





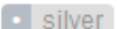


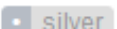




*Nucleic Acids Research*, 2011, 1–8  
doi:10.1093/nar/gkr1179

### neXtProt: a knowledge platform for human proteins

Lydie Lane<sup>1,2</sup>, Ghislaine Argoud-Puy<sup>1</sup>, Aurore Britan<sup>1</sup>, Isabelle Cusin<sup>1</sup>, Paula D. Duek<sup>1</sup>, Olivier Evalet<sup>1</sup>, Alain Gateau<sup>1</sup>, Pascale Gaudet<sup>1,\*</sup>, Anne Gleizes<sup>1</sup>, Alexandre Masselot<sup>3</sup>, Catherine Zwahlen<sup>1</sup> and Amos Bairoch<sup>1,2</sup>

<sup>1</sup>CALIPHO group, Swiss Institute of Bioinformatics, CMU - 1, rue Michel Servet 1211 Geneva 4, Switzerland,  
<sup>2</sup>Department of Human Protein Sciences, Faculty of Medicine, University of Geneva and <sup>3</sup>GeneBio, c/o Swiss Institute of Bioinformatics, CMU - 1, rue Michel Servet 1211 Geneva 4, Switzerland

- 83'600 PTMs
- > 320'000 variants [= UniProtKB (65'000) + dbSNP + COSMIC]

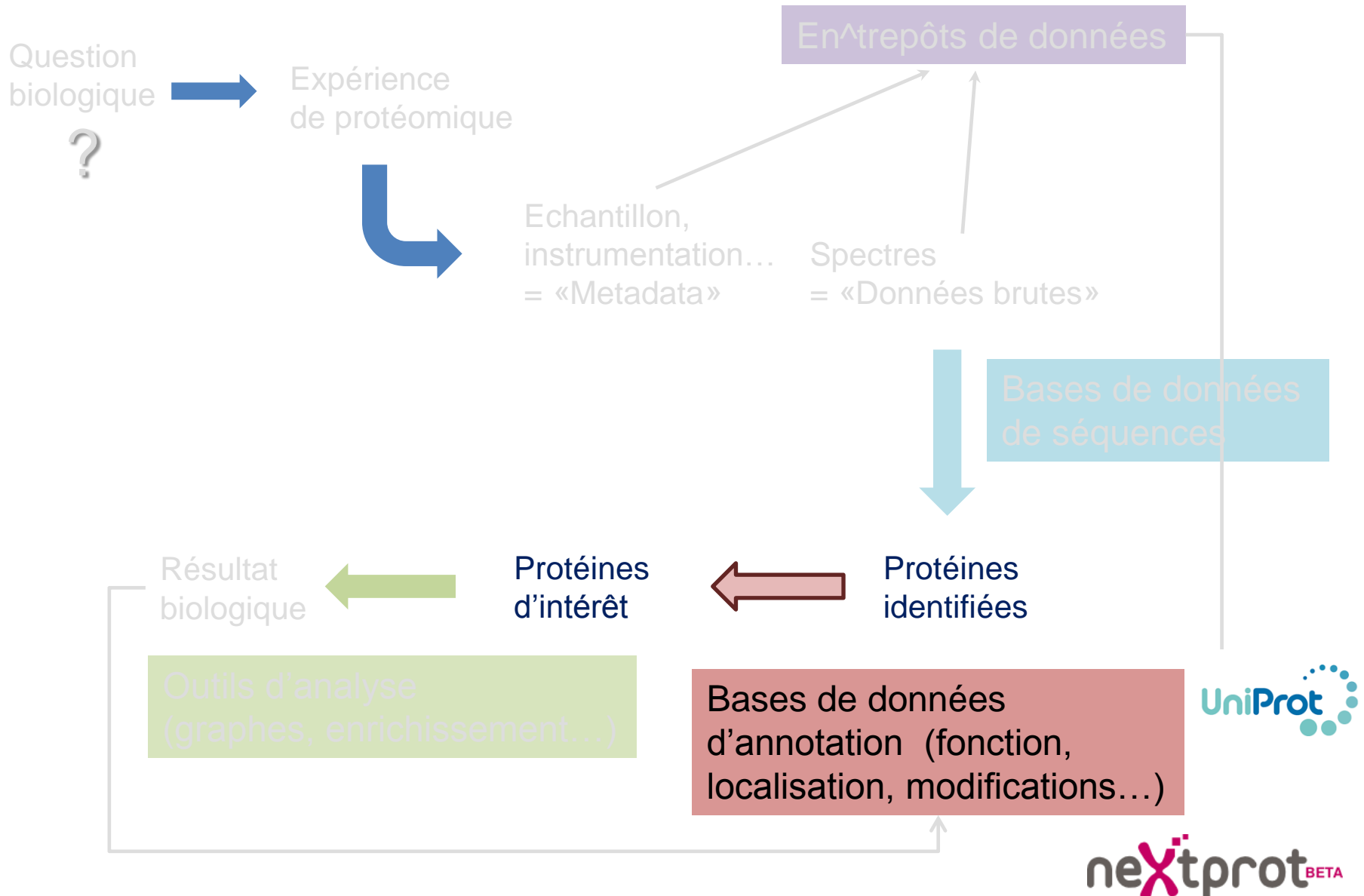
Variant	<a href="#">172</a>	1	I → N ; dbSNP: <a href="#">rs147233169</a> 	 dbSNP
				
Variant	<a href="#">192</a>	1	G → D ; dbSNP: <a href="#">rs143919163</a> 	 dbSNP
				
Variant	<a href="#">220</a>	1	P → L : In Ins resistance; severe.	 UniProtKB
Variant	<a href="#">228</a>	1	C → R : In a gastric adenocarcinoma sample; somatic mutation.	 UniProtKB
Variant	<a href="#">236</a>	1	H → R : In <a href="#">LEPRCH</a> ; Winnipeg; in one patient with in RMS heterozygous compound with S-386; may impair receptor processing. ; dbSNP: <a href="#">rs121913145</a> 	 dbSNP UniProtKB

# neXtProt est la première ressource à avoir implémenté le format PEFF

= “Proteomics-enriched FASTA format”, ce qui devrait permettre aux outils d’identification un accès plus facile aux informations de variants et de PTM.

```
>nxp:Q9HCU4 \NcbiTaxId=9606 \Pname=Cadherin EGF LAG seven-pass G-type  
receptor 2 \Gname=CELSR2 \Processed=(1|31|SIGNAL) (32|2923|CHAIN)  
\ModRes=(1591|MOD:00035) (1810|MOD:00035)  
\Variant=(1066|1066|Q) (1639|1639|H) (1992|1992|R) (2387|2387|A)  
MRSPATGVPL PTPPPPLLLL LLLLLPPPLL GDQVGPCRSL GSRGRGSSGA CAPMGWLCPS  
SASNLWLYTS RCRDAGTELT GHLVPHHDGL RVWCPESEAH IPLPPAPEGC PWSCRLLGIG  
GHLSPQGKLT LPEEHPCLKA PRLRCQSCKL AQAPGLRAGE RSPEESLGGR RKRNVNTAPQ  
FQPPSYQATV PENQPAGTPV ASLRAIDPDE GEAGRLEYTM DALFDSRSNQ FFSLDPVTGA  
VTTAEELDRE TKSTHVFRVT AQDHGMPRRS ALATLTILVT DTNDHDPVFE QQEYKESLRE  
NLEVGYEVLV VRATDGDAPP NANILYRLL E GSGGSPSEVF EIDPRSGVIR TRGPVDREEV  
ESYQLTVEAS DQGRDPGPRS TTA AVFLSVE DDNDNAPQFS EKRYVVQVRE DVT PGAPVLR  
VTASDRDKGS NAVVHYSIMS GNARGQFYLD AQTGALDVVS PLDYETTKEY TLRVRAQDGG  
RPPLSNVSGL VTVQVLDIND NAPIFVSTPF QATVLESVPL GYLVLHVQAI DADAGDNARL  
EYRLAGVGHD FPFTINNGTG WISVAAELDR EEVDFYSFGV EARDHGTPAL TASASVSVTV  
LDVNDNNPTF TQPEYTVRLN EDAAVGTSVV TVSAVDRDAH SVITYQITSG NTRNRFSITS
```

# 3- Filtrage des résultats d'identification





# Différentes vues pour une même protéine

## Protein

Function

Medical

Expression

Interactions

Localisation

Sequence annot.

Structures

Identifiers

Gene

Exons

Identifiers

References

Publications

Patents

Submissions

Web resources

### INS » Insulin

☆ favorize label

Cleaved into: Insulin A chain ; Insulin B chain .

[extend overview](#)

1 69 1

GENE REF ISO

Gene name: INS .

Family name: [Insulin](#)

This protein has been shown to exist at protein level

#### Positional Annotations referenced on Iso 1

Isoform Iso 1

[show graphical display](#)

Category	Names	Positions	Length	Description	Evidences	Also present in isoforms
VARIANTS	Variant	34	1	H → D : In familial hyperproinsulinemia ; Providence.	1	
	Variant	48	1	F → S : Associated with diabetes mellitus type-II; Los-Angeles.	3	
	Variant	80	1	R → I : In familial hyperproinsulinemia ; Kyoto.	1	

#### Medical

[show evidences](#)

DISEASE Defects in INS are the cause of familial hyperproinsulinemia [ MIM:176730 [↗](#)]. Curated UniProtKB

PHARMACEUTICAL Available under the names Humulin or Humalog (Eli Lilly) and Novolin (Novo Nordisk). Used in the treatment of diabetes. Humalog is an insulin analog with 52-Lys-Pro-53 instead of 52-Pro-Lys-53. Curated UniProtKB

According to Orphanet, this protein is involved in the following diseases:

Diabetes mellitus, neonatal [224](#) [↗](#)

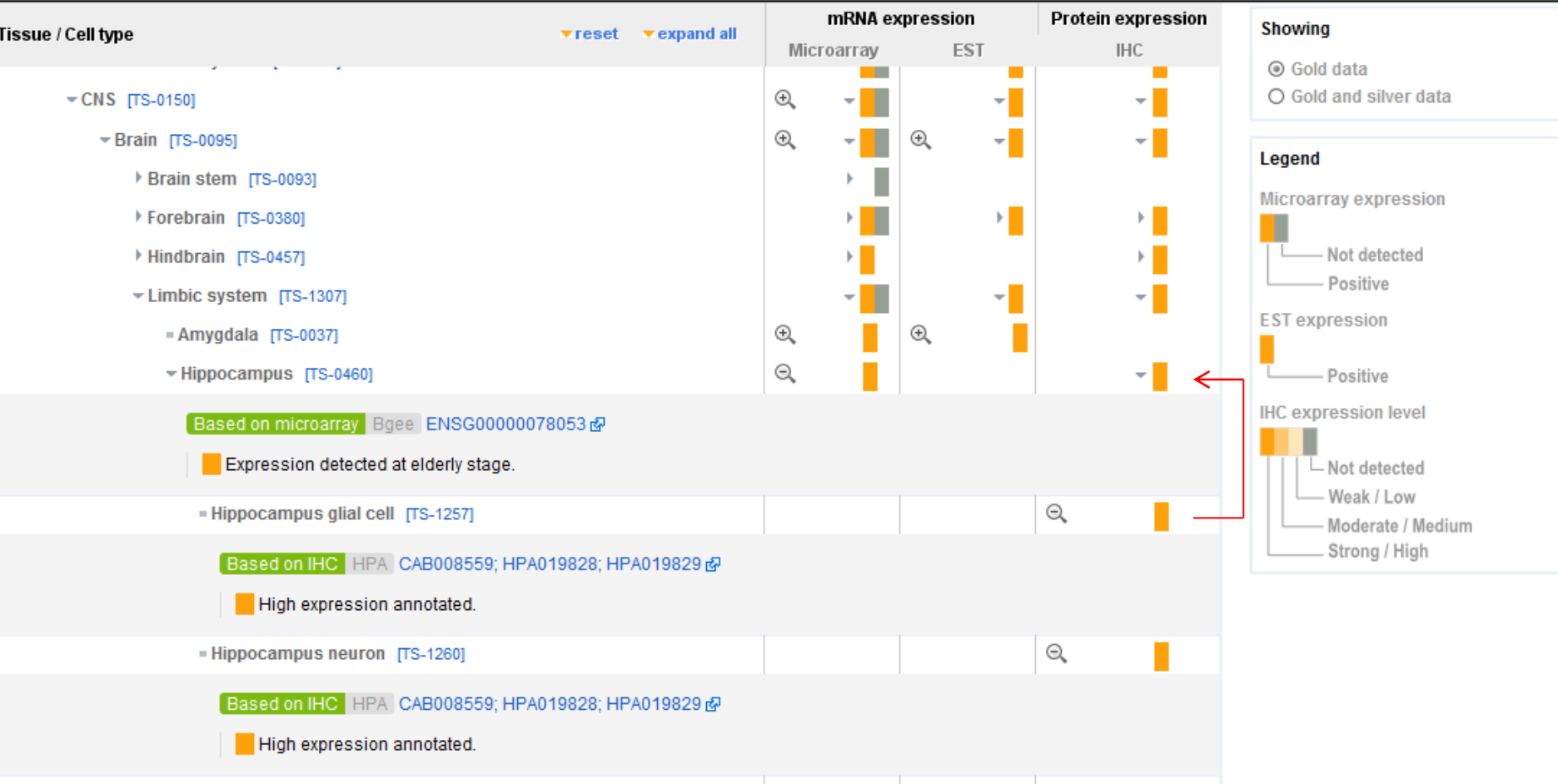
Diabetes mellitus, neonatal, permanent [99885](#) [↗](#)

#### Keywords

DISEASE Diabetes mellitus [definition](#) [KW-0219]

Disease mutation [definition](#) [KW-0225]

# Exemple : dans la vue «Expression», les données obtenues au niveau mRNA et protéine ont été intégrées et unifiées

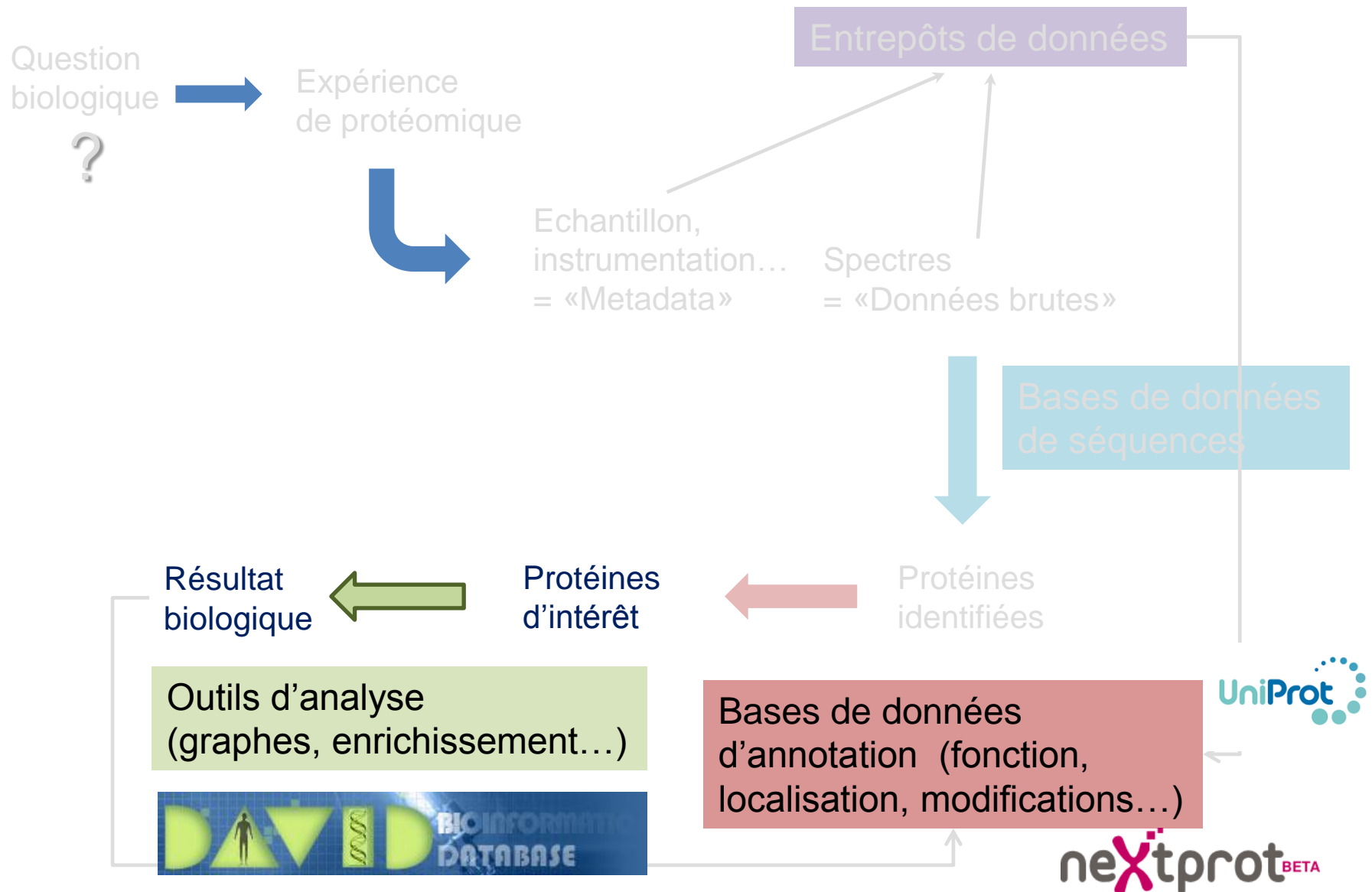


# Accès par programme

- Toutes les données incluses dans neXtProt (expression, localisation subcellulaire, variants et PTM) peuvent être explorées par une application dédiée

[www.nextprot.org/rest/](http://www.nextprot.org/rest/)

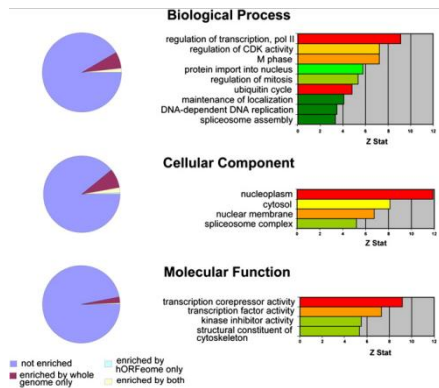
# 3- Analyse des résultats d'identification



# Outils d'analyse de listes de protéines

De nombreux outils bioinformatiques proposent une analyse statistique du contenu en annotation.

La plupart analysent les **termes GO** présents dans les entrées (*DAVID, AmiGO etc..*) <http://david.abcc.ncifcrf.gov>



*neXtProt va proposer prochainement un outil mesurant l'enrichissement de tout type d'annotation*

# Outil d'enrichissement (beta test)

- Exemple : Liste de 49 partenaires de Lyn
- Enrichissement en UniProt KWs :

UniProt keyword Hide table

Name	nb in list	nb in db	Fisher	Fisher ease	Benjamini	Genes
KW-0597: Phosphoprotein	46	7909	1,03E-14	2,33E-14	1,28E-12	FCGR2B EGFR BTK PTPN6 PSMC5 JAK2 SYK FAM82A2 FCGR1A STAT5A LILRB3 CD5 NDFIP2 SCIMP PDE4A PXN HCLS1 ARAP3 CSK KHDRBS1 CDKN1B PAG1 INPP5D DOK1 ANKRD54 KIT TOM1L1 TGFB11H PTPN11 ADAM15 MUC1 LPXN PPP1R15A CD72 FER CDK4 GAB2 LIME1 CBL PTPRC EPOR SH2B2 CD79A MS4A2 SIRPA CD19
KW-0727: SH2 domain	10	108	3,61E-13	1,20E-11	3,29E-10	STAT5A INPP5D PTPN11 BTK PTPN6 SH2B2 JAK2 SYK CSK FER
KW-1064: Adaptive immunity	8					
KW-0472: Membrane	39					
KW-0002: 3D-structure	32					
KW-0829: Tyrosine-protein kinase	7					
KW-1003: Cell membrane	23					
KW-0391: Immunity	10					
KW-0963: Cytoplasm	27					
KW-0729: SH3-binding	5					
KW-0656: Proto-oncogene	6					
KW-0418: Kinase	8					
KW-0393: Immunoglobulin domain	7					
KW-0677: Repeat	24	4862	3,42E-4	6,70E-4	3,07E-3	INPP5D ANKRD54 KIT TGFB11H FCGR2B PTPN11 EGFR PTPN6 JAK2 MUC1 SYK LPXN PPP1R15A FCGR1A LILRB3 CD5 CBL NDFIP2 PTPRC PXN HCLS1 ARAP3 SIRPA CD19
KW-0399: Innate immunity	4	143	5,41E-4	5,85E-3	1,89E-2	BTK JAK2 SYK FCGR1A
KW-0564: Palmitate	5	258	5,48E-4	4,16E-3	1,43E-2	PAG1 CD36 LIME1 SCIMP MUC1
KW-0832: Ubl conjugation	12	1598	5,88E-4	1,76E-3	6,45E-3	INPP5D KIT CBL NDFIP2 EGFR PDE4A EPOR PSMC5 SYK FASLG KHDRBS1 CDKN1B
KW-0440: LIM domain	3	71	8,99E-4	1,44E-2	3,97E-2	TGFB11H PXN LPXN
KW-0966: Cell projection	5	402	3,75E-3	1,86E-2	4,88E-2	PDE4A ADAM15 ARAP3 LPXN FER
KW-1133: Transmembrane helix	22	5166	5,55E-3	9,47E-3	2,89E-2	PAG1 CD36 KIT FCGR2B EGFR ADAM15 MUC1 FASLG FAM82A2 FCGR1A CD72 LILRB3 LIME1 CD5 NDFIP2 PTPRC SCIMP EPOR CD79A MS4A2 SIRPA CD19
KW-0067: ATP-binding	9	1355	7,08E-3	1,91E-2	4,76E-2	CDK4 KIT EGFR BTK PSMC5 JAK2 SYK CSK FER

Proteins 1 to 10 of 120 show  summary | details export

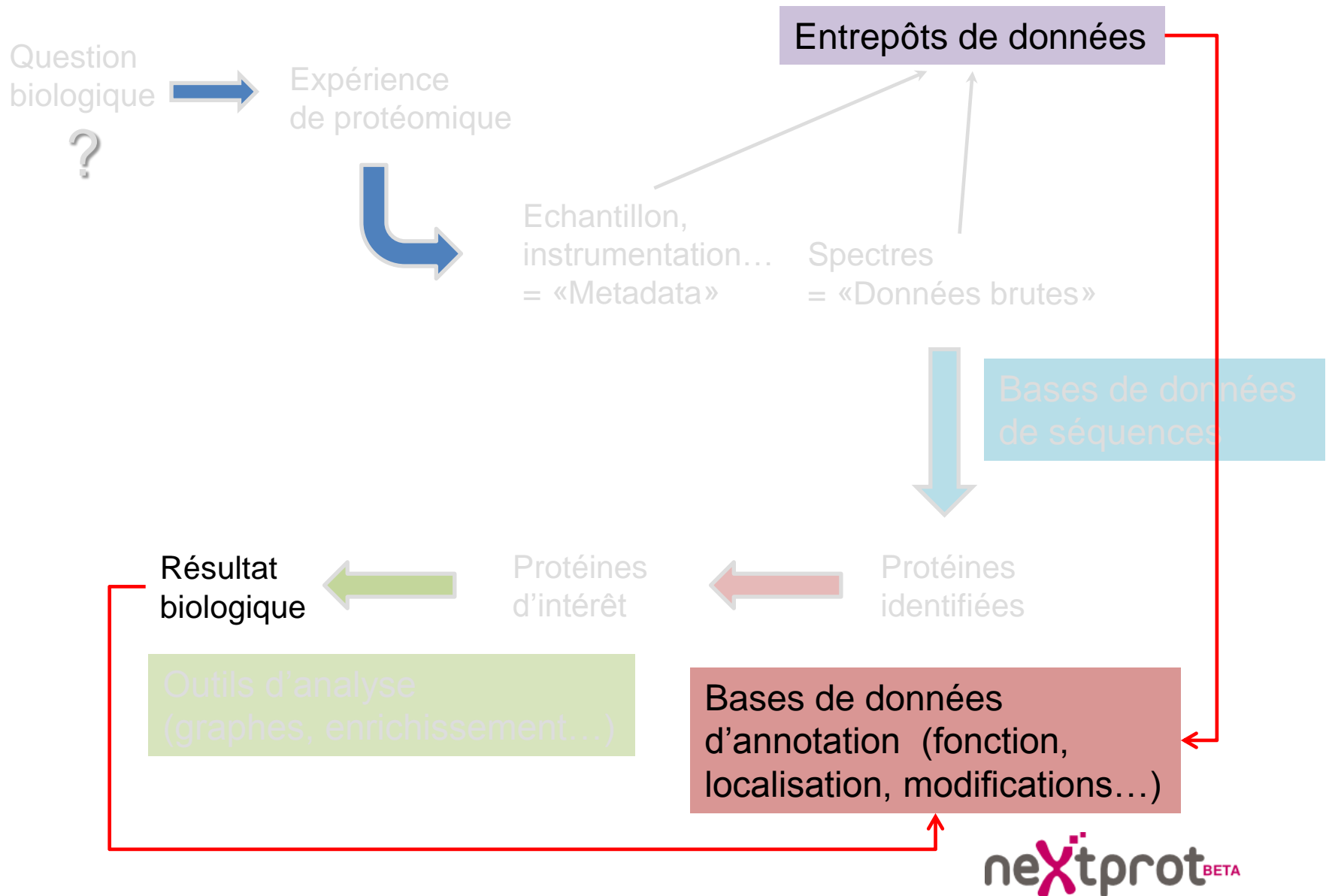
☆ **Tyrosine-protein kinase Lyn (*LYN*) [NX\_P07948]**

Non-receptor tyrosine-protein kinase that transmits signals from cell surface receptors and plays an important role in the regulation of innate and adaptive immune responses, hematopoiesis, responses to growth factors and cytokines, integrin signaling, [more]

Gene location: [8q12.1](#) Isoforms: [2](#) Variants: [14](#) PTMs: [20](#) Sequence length: [512](#)

Disease: [yes](#) 3D structure: [yes](#) Proteomics: [yes](#) Tissue expression: [yes](#) Mutagenesis: [yes](#)

# 4- Intégration des données de protéomique



- Function
- Medical
- Expression
- Interactions
- Localisation
- Sequence
- Proteomics**
- Structures
- Identifiers
- Gene
- Exons
- Identifiers
- References
- Curated publications (35)
- Additional publications (43)
- Patents (0)
- Submissions (6)
- Web resources (0)

## YWHAE » 14-3-3 protein epsilon (14-3-3E)

Gene name: YWHAE  
Family name: 14-3-3

[☆ favorite](#) [🏷 label](#)  
[▶ extend overview](#)

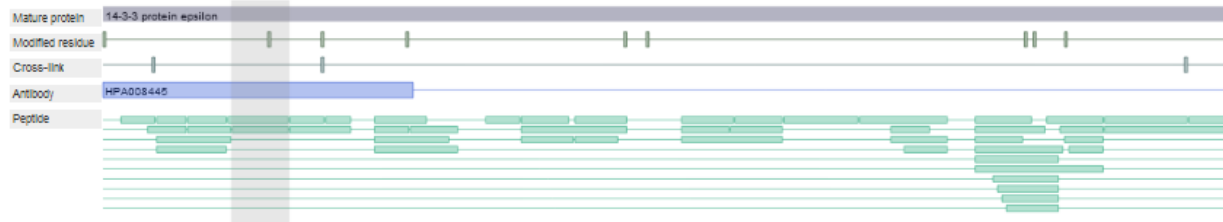
1 84 2  
GENE REF ISO



One or more isoforms of this protein have been shown to exist at protein level

Displayed isoform: **Iso 1** [change isoform](#)

Processing 
  Modified residue 
 [All/None](#)



Name	Position	Length	Description	Evidence
Peptide	29 - 42	14	PAP00035462	1 neXtProt
Peptide	30 - 42	13	PAP00079784	2 neXtProt PeptideAtlas human brain

↑ Evidence 1: **EXP** neXtProt

**Mass spectrometric analysis of lysine ubiquitylation reveals promiscuity at site level.**  
 Danielsen J.M., Sylvestersen K.B., Bekker-Jensen S., Szklarczyk D., Poulsen J.W., Horn H., Jensen L.J., Mailand N., Nielsen M.L.  
*Mol. Cell Proteomics* 10, M110.003590-M110.003590 (2011) [Full text:[10.1074/mcp.M110.003590](https://doi.org/10.1074/mcp.M110.003590)] [PubMed:[21139048](https://pubmed.ncbi.nlm.nih.gov/21139048/)]

[Show abstract](#)

Lysine ubiquitination sites in U2OS and HEK293T cells

[Hide experimental details](#)

**Detection method**

Mass spectrometry nano LC-MS/MS.

**Cell line**

U2OS [[CVCL\\_0042](#)]; HEK293T [[CVCL\\_0083](#)].

**Sample preparation**

Strep-HA-tagged ubiquitin conjugated proteins pull down with Strep-Tactin Sepharose. Separation by SDS-PAGE, reduction and alkylation. Trypsin digestion, resulting in diglycine remnant of ubiquitin attached to Lys.

**Instrument/platform**

Nanoscale C18 HPLC coupled to LTQ Orbitrap Velos (fragmentation by HCD) mass

Isoform **Iso 1** 255 aa, Mass: 29174 Da, pI: 4.63

[View FASTA](#) [BLAST sequence](#) [BLAST selection](#)

```

1  MDDREDLVYQ AKLAPQAERY DEMVESMKRY AGMDVVELTVE ERNLLSVAYK
51  NVIGARRASW RIISSEIQKE ENKGGEDKLE MIREYRQMVE TELKLICCDI
101 LDVLDKHLIP AANTGESKVF YYMKGGDYHR YLAEFATGND RKEAAENSLV
151 AYKAASDIAM TELPPTHPIR LGLALNFSVF YYEILNSPDR ACRLAKAAFD
201 DAIAELDTLS EESYKDSTLI MQLLRDNLTL WISDMQGDGE EQNKEALQDV
251 EDENQ
    
```



# Infrastructures bioinformatiques pour le HUPO Human Proteome Project



## Mission:

The Human Proteome Project, by characterizing all 21 000 genes of the known genome, will generate the map of the protein based molecular architecture of the human body and become a resource to help elucidate biological and molecular function and advance diagnosis and treatment of diseases.

## Overview:

The Human Proteome Project is an international project organized by the Human Proteome Organization (HUPO) that aims to revolutionize our understanding of the human proteome via a coordinated effort by many research laboratories around the world...  
[Read more...]

## Latest News:

- HPP Draft web site is in progress

## Documents:

- Article on HPP Launch in Sydney 2010
- White paper
- document 3

Ab/IHC data

# THE HUMAN PROTEIN ATLAS

MS data

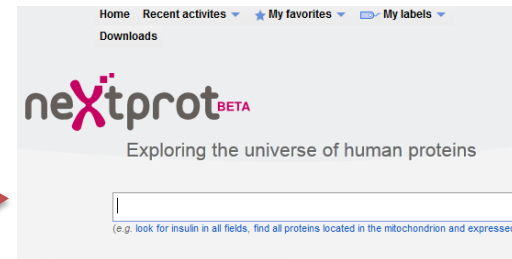
## ProteomeXchange

EBI PRIDE  
(MS/MS)

ISB PASSEL  
(SRM)

PeptideAtlas  
reprocessing

Raw  
storage



# Remerciements

- ProteomExchange consortium
- UniProtKB consortium
- The Human Protein Atlas
- GO consortium
- neXtProt

... et tous les biocurateurs qui maintiennent ces ressources utilisables gratuitement par la communauté

**ISB** International Society  
for Biocuration