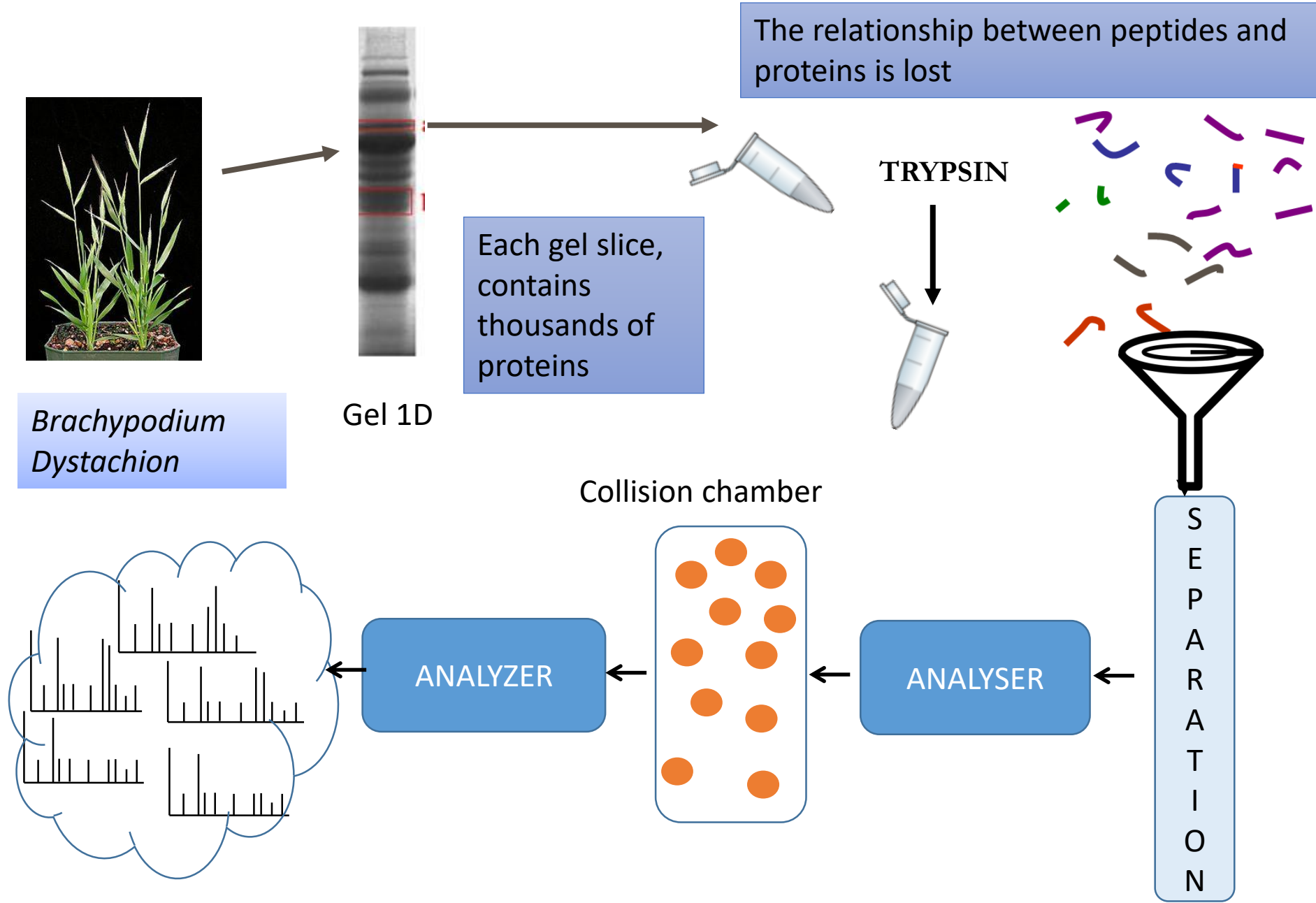
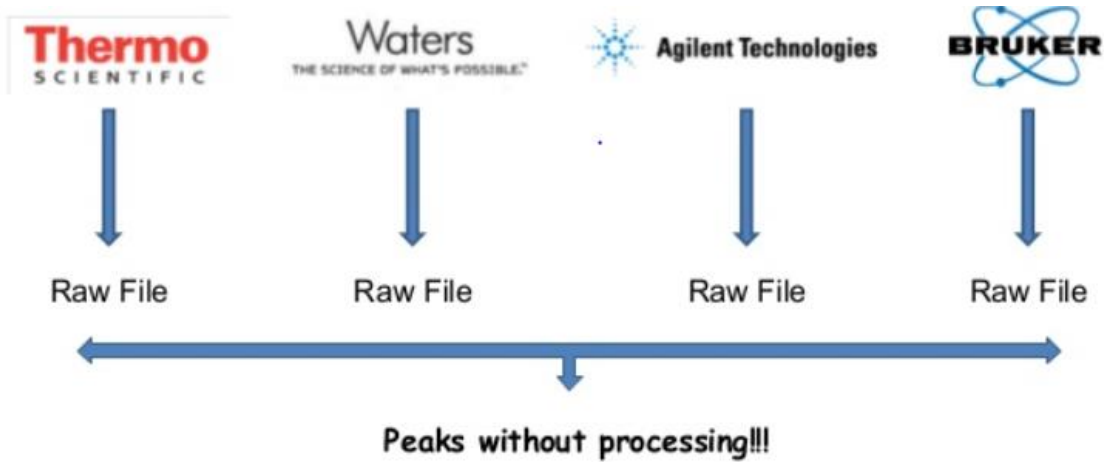




WorkShop inter-CATI SysMics-eMPrEInTE (Jeudi 17 Octobre)

Classical approach in MS/MS: bottom-up





Etape de peak picking

des outils (msConvert, rawConverter,...) pour obtenir les formats utilisés par les moteurs d'interprétation
Plusieurs formats : mgf, mzML, etc....

Interprétation des spectres : PSM, puis protéines

De très nombreux logiciels disponibles. Des 'guidelines' pour pouvoir publier dans les journaux de protéomique

Un format « standard » mzIdentML

Required Manuscript Content and Publication Guidelines for *Molecular & Cellular Proteomics*

1. Information That Must Be Provided in the Experimental Procedures Section

- Experimental Design and Statistical Rationale
- Database Search Parameters And Acceptance Criteria For Identifications

2. Information That Must Be Provided in the Results Section or in Supplemental Material

- Protein And Peptide Identification
- Posttranslational Modifications
- Protein Inference From Peptide Assignments
- Peptide and Protein Quantification
- Quantification of Peptides, Modified Peptides and Proteins Using Targeted MS Approaches

3. Submission of Raw Data to a Repository

Providing Access to Annotated Spectra

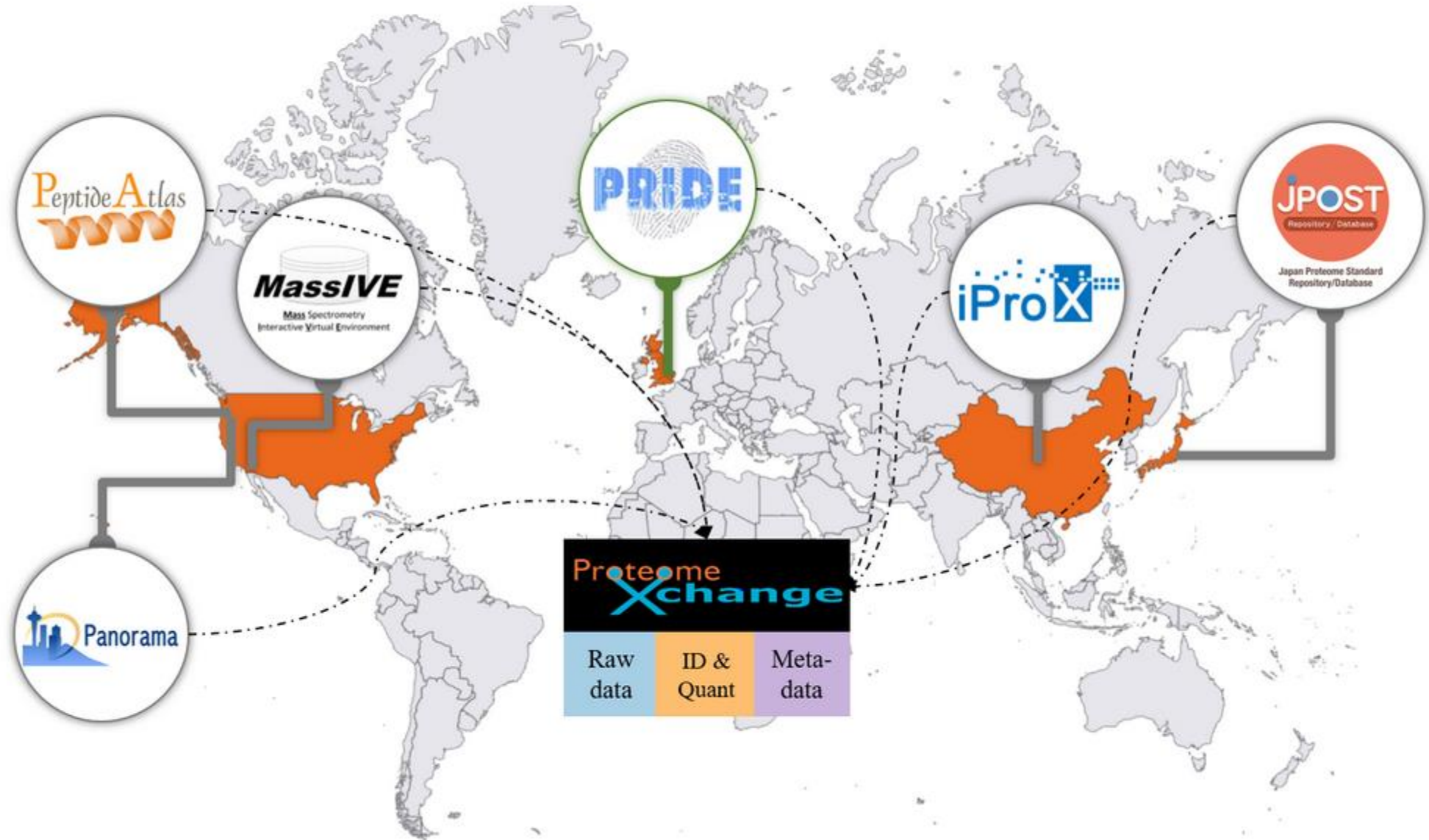
Currently, the [guidelines for MCP](#) require that annotated spectra be provided in these two cases:

- proteins identified on the basis of single peptide
- post-translationally modified peptides

Guidelines for the Publication of Glycomic Studies

- Création de ProteomeXChange, 2016. Soumission partielle ou totale
- . Spectres en format RAW ou mzML + Quelques métadonnées
 - . Résultats d'identification si soumission « totale »

Embed



PRIDE Controlled Vocabulary

The PRIDE PRoteomics IDentifications (PRIDE) database is a centralized, structured proteomics data, including protein and peptide identifications, post-translational evidence.

[Terms](#) [Download](#) [Ontology Homepage](#) [Contact](#)

[Browse Terms](#) [Browse Properties](#) [Ontology history](#)

- [Cv Label](#)
- [Experiment Type](#)
- [Experiment additional parameter](#)
- [File Properties](#)
- [Gel additional parameter](#)
- [Identification additional parameter](#)
- [ModificationItem additional parameter](#)
- [Peptide item additional parameter](#)
- [Processing method additional parameter](#)
- [Protocol step description additional parameter](#)
- [Quantification parameter](#)
- [Reference additional parameter](#)
- [Sample description additional parameter](#)
- [Search algorithm](#)
- [UO_0000235](#)



ELSEVIER

EuPA Open Proteomics

Volume 8, September 2015, Pages 28-35



Ten years of public proteomics data: How things have evolved, and where the next ten years should lead us

Kenneth Verheggen ^{a, b, c}, Lennart Martens ^{a, b, c}  

[Show more](#)

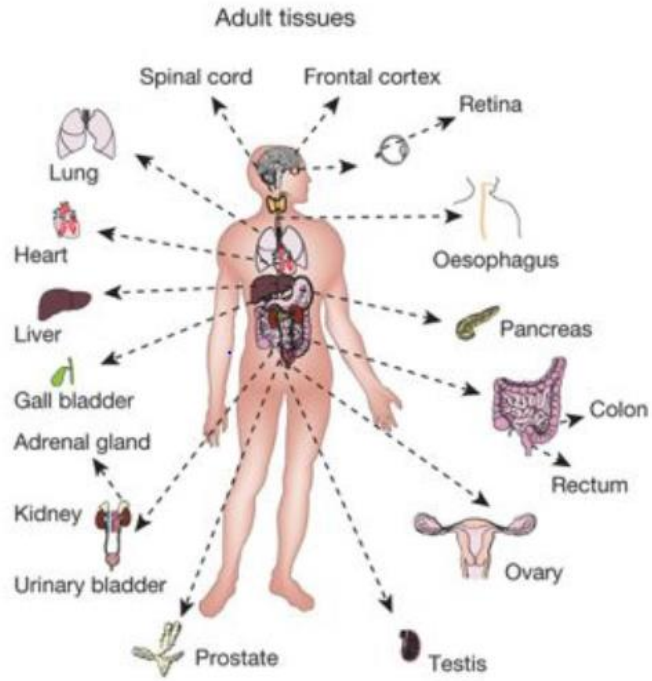
<https://doi.org/10.1016/j.euprot.2015.07.014>

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a



HPP PROGRESS TO DATE (PHASE I)

19,587

PREDICTED PROTEINS



2,579

MISSING PROTEINS (neXtProt PE2,3,4)



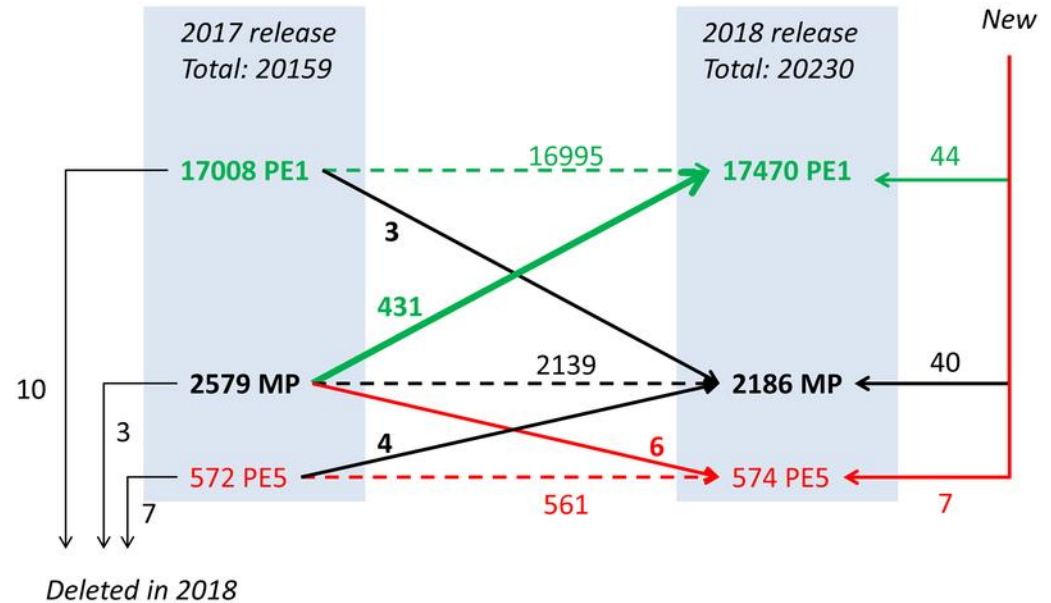
87%

COMPLETE



Evidence of the human proteome

The Human Proteome Project (HPP) is an international project organized by the Human Proteome Organization (HUPO) : 50 research teams worldwide organized by chromosome, mitochondria, biological processes, and disease categories plus resource pillar groups for affinity-based protein capture, mass spectrometry, knowledge bases, and, most recently, pathology.



Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Omenn GS et al., JPR, 2018

NextProt s'appuie sur une ontologie décrite en RDFS : contient l'état des connaissances actuelles sur le protéome humain (Swiss Institute of Bioinformatics)



Exploring the universe of human proteins

proteins ▾ Simple search Advanced search (SPARQL)

Gold only ▾

e.g.: Search for MSH6 in proteins, Search for author Doolittle in publications, Search for liver in terms

▶ Getting started

- » The human proteome
- » Simple search
- » Advanced search (SPARQL)
- » Analyze
BLAST, list management, peptide uniqueness checker
- » Download
XML, FASTA, PEFF
- » Technical corner
Viewers, API, SPARQL

📄 Data sources



Release contents

📰 News

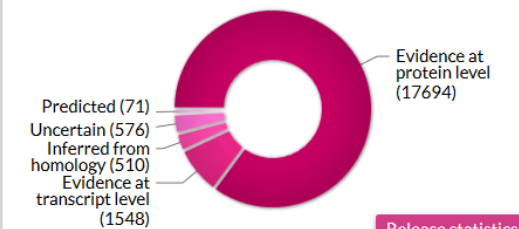


- » New release with variant frequency da...
Sep 04, 2019
- » New Publication: A Critical Guide to ...
Jun 11, 2019
- » PEFF publication and usability improv...
May 29, 2019

News archive

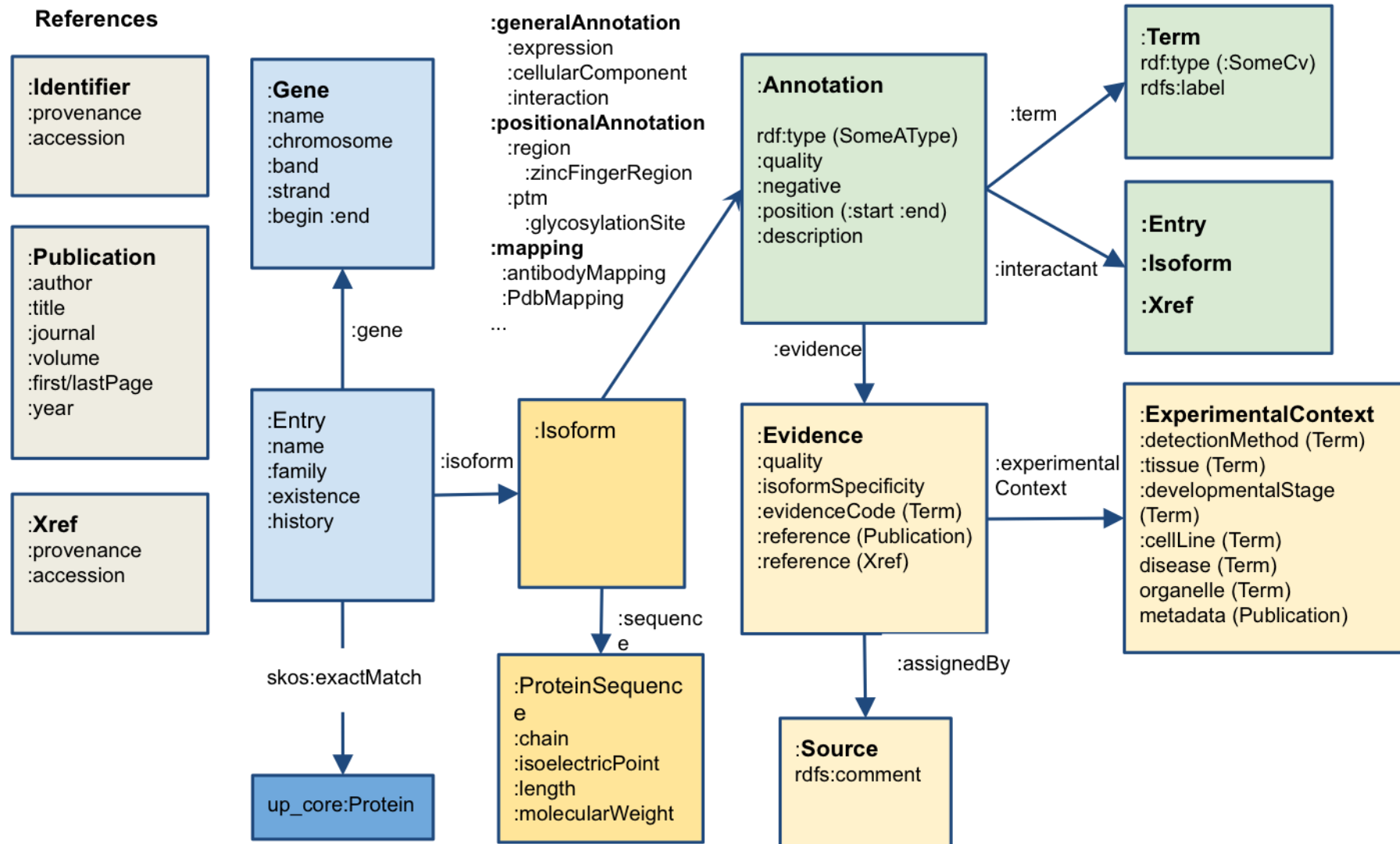
📅 Release 2019-08-22

Protein existence in neXtProt



Release statistics

Un modèle simplifié de NextProt



End point SparQL

neXtProt SNORQL Services Help About Contact us

SPARQL endpoint: <https://api.nextprot.org/sparql>

PREFIX...

```
SELECT DISTINCT * WHERE {  
  ?s ?p ?o  
}  
LIMIT 10
```

Query title

Here you can write your SPARQL queries

html Go Reset

eg. peroxisome, liver

Tags Filter sparql examples

- NXQ_00001 - Proteins phosphorylated
cellular component phosphorylation PTM su
- NXQ_00002 - Proteins that are located
cellular component subcellular location tutorial
- NXQ_00003 - Proteins with 7 transmembrane
domain region topology transmembrane ti
- NXQ_00004 - Proteins highly expressed
expression tutorial
- NXQ_00005 - Proteins located in mitochondria
cellular component subcellular location tutorial
- NXQ_00006 - Proteins whose genes are located on chromosomes
chromosomal location disease tutorial
- NXQ_00007 - Proteins associated with diseases
disease tutorial
- NXQ_00008 - Proteins whose genes are p53
chromosomal location gene tutorial
- NXQ_00009 - Proteins with 3 disulfide bonds
function PTM tutorial
- NXQ_00010 - Proteins that are glycosylated
carbohydrate cellular component glycosylation
- NXQ_00011 - Proteins that are expressed
expression function tutorial
- NXQ_00012 - Proteins that interact with other proteins
function interaction PPI tutorial
- NXQ_00013 - Proteins that have a protein domain

How to write your query ?

- Select your query from the examples on the right side
- Find terms appropriate to your query using the term finder (e.g. peroxisome, liver)
- You can save your queries on the [search interface](#) or directly using the [api](#) and access them in SNORQL using the `My Queries` tag.