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

Classical approach in MS/MS: bottom-up

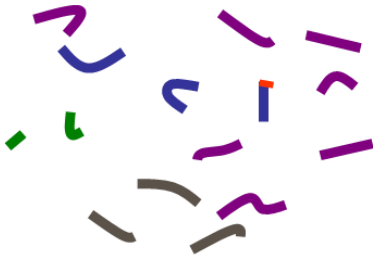
Brachypodium Dystachion

Gel 1D

Each gel slice, contains thousands of proteins

The relationship between peptides and proteins is lost

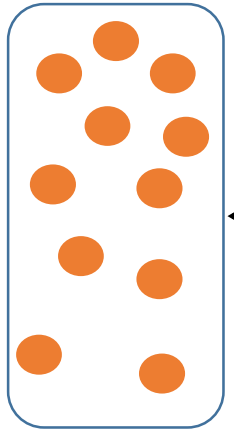
TRYPSIN



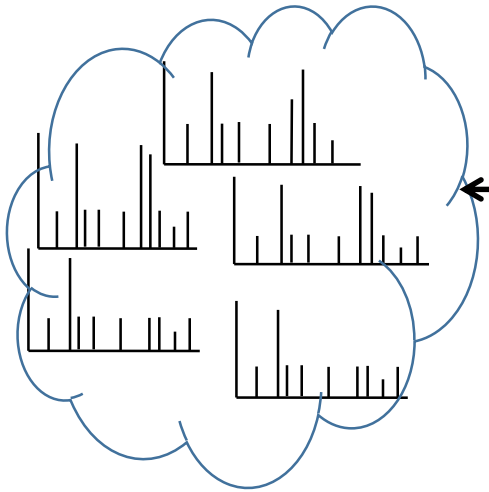
SEPARATION

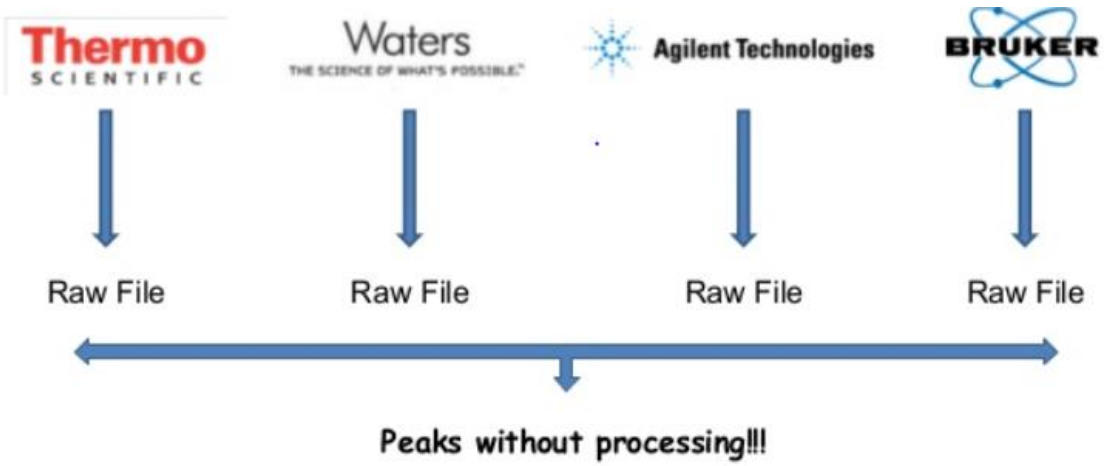
ANALYSER

Collision chamber



ANALYZER





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:

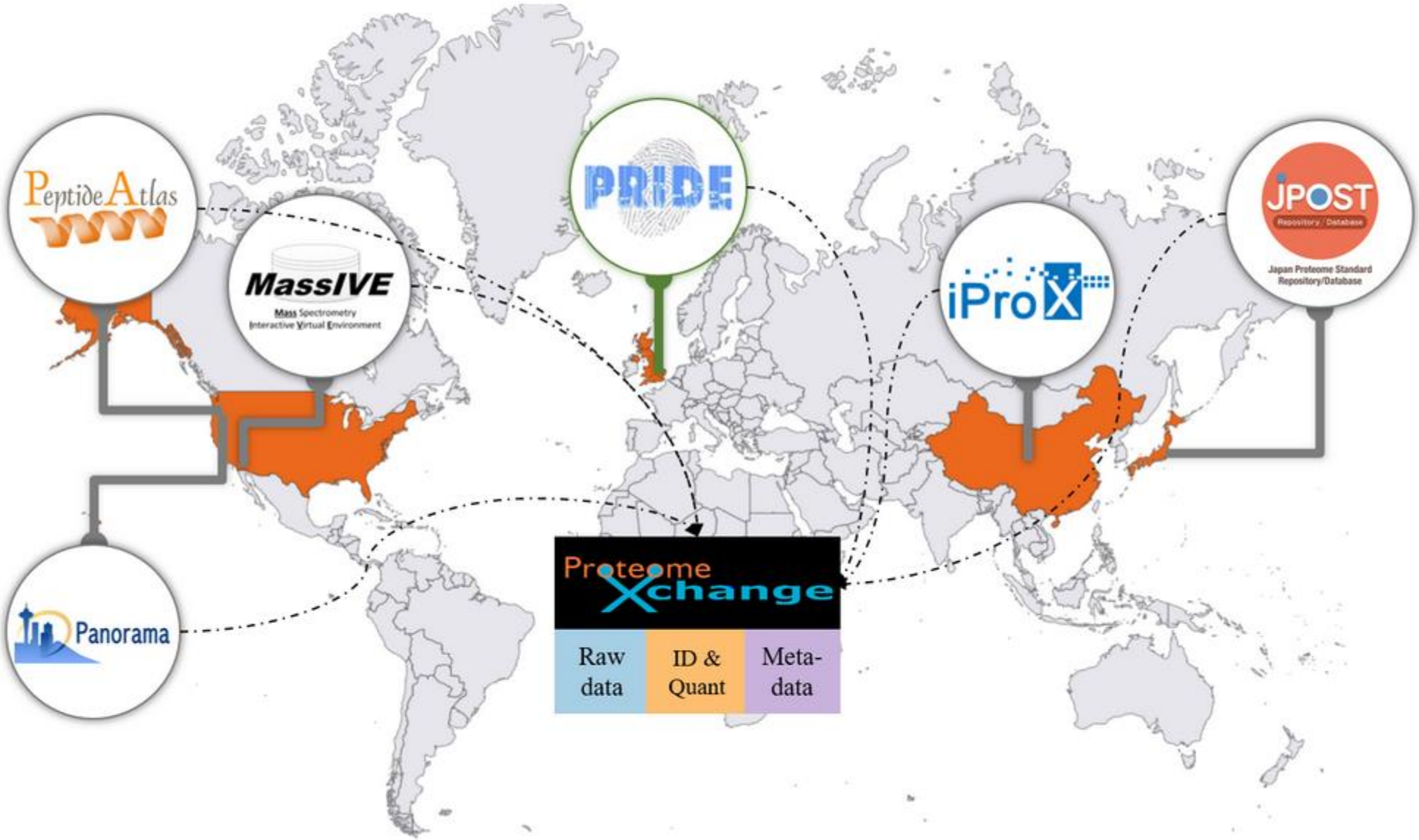
- proteins identified on the basis of single peptide
- post-translationally modified peptides

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 »



PRIDE Controlled Vocabulary

The PRIDE PRoteomics IDEntifications (PRIDE) database is a centralized, st
proteomics data, including protein and peptide identifications, post-translat
evidence.

Search PRIDE

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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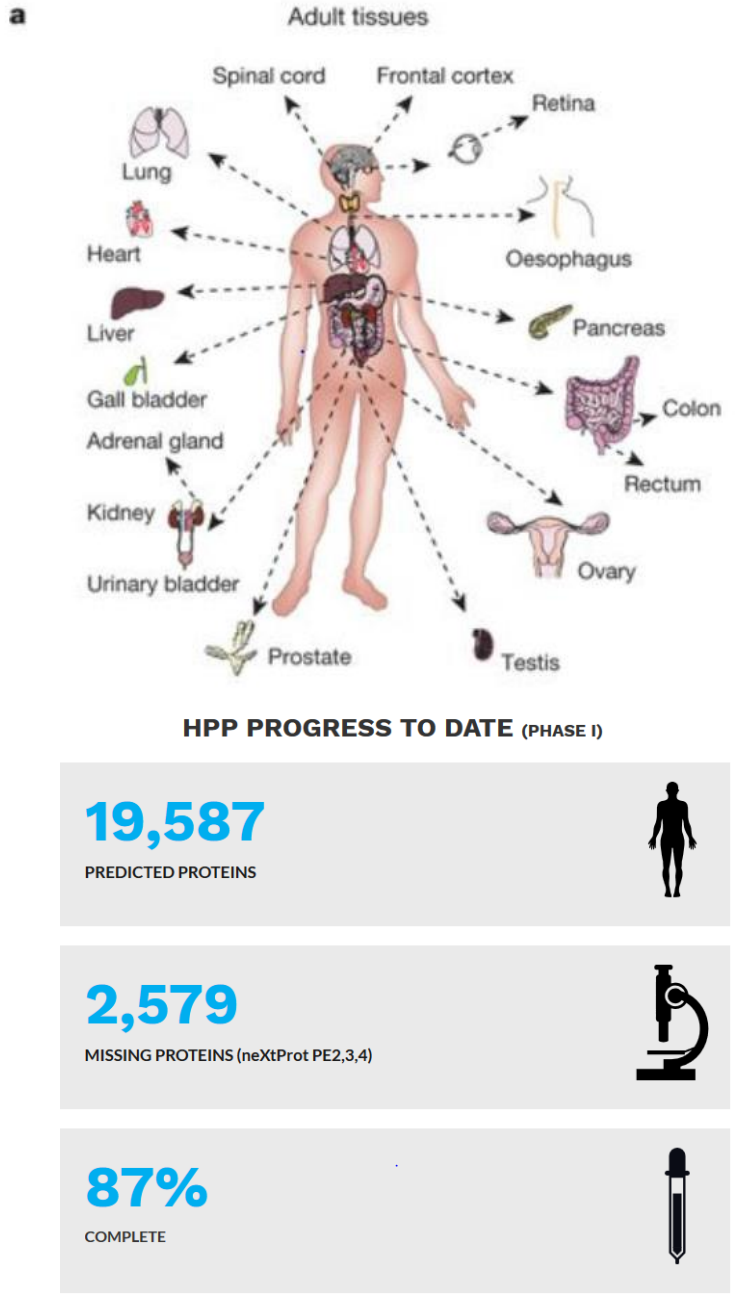
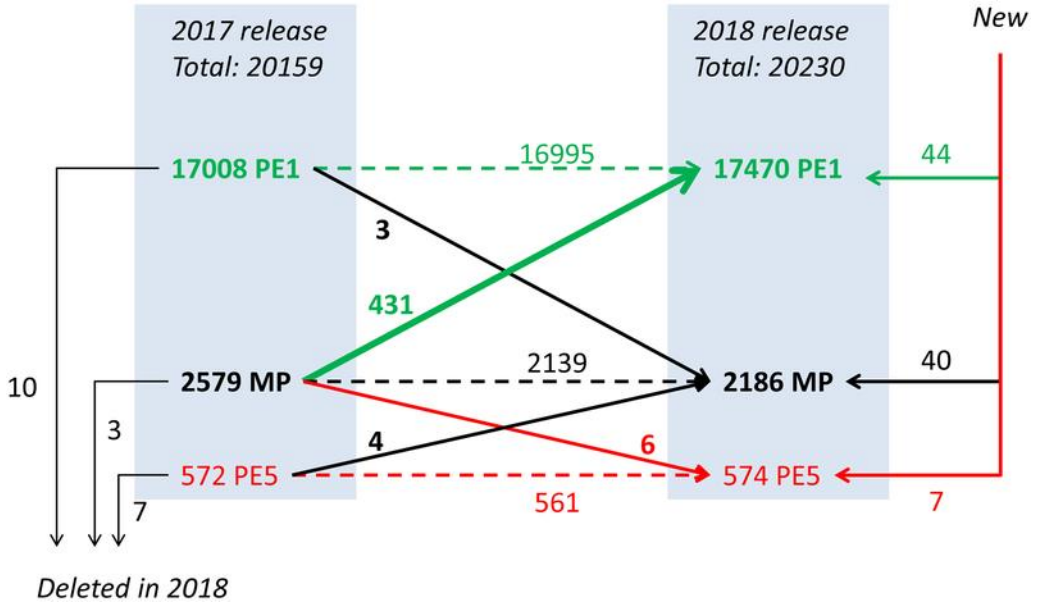
Evidence of the human proteome

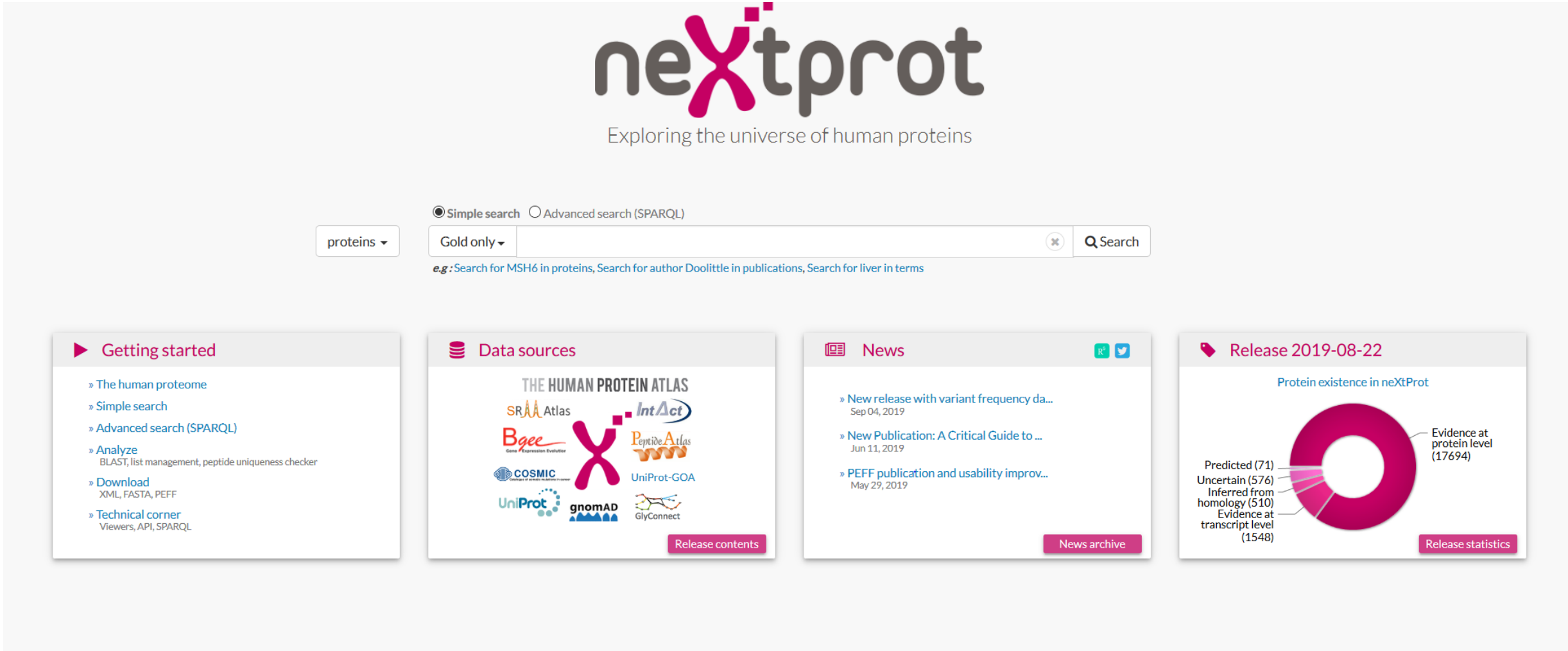
The Human Proteome Project (HPP) is an international project organized by the Human Proteome Organization (HUPO) : 50 research teams worldwide organized by chromosome, mitochondria, biological processes, and disease categories plus resource pillar groups for affinity-based protein capture, mass spectrometry,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



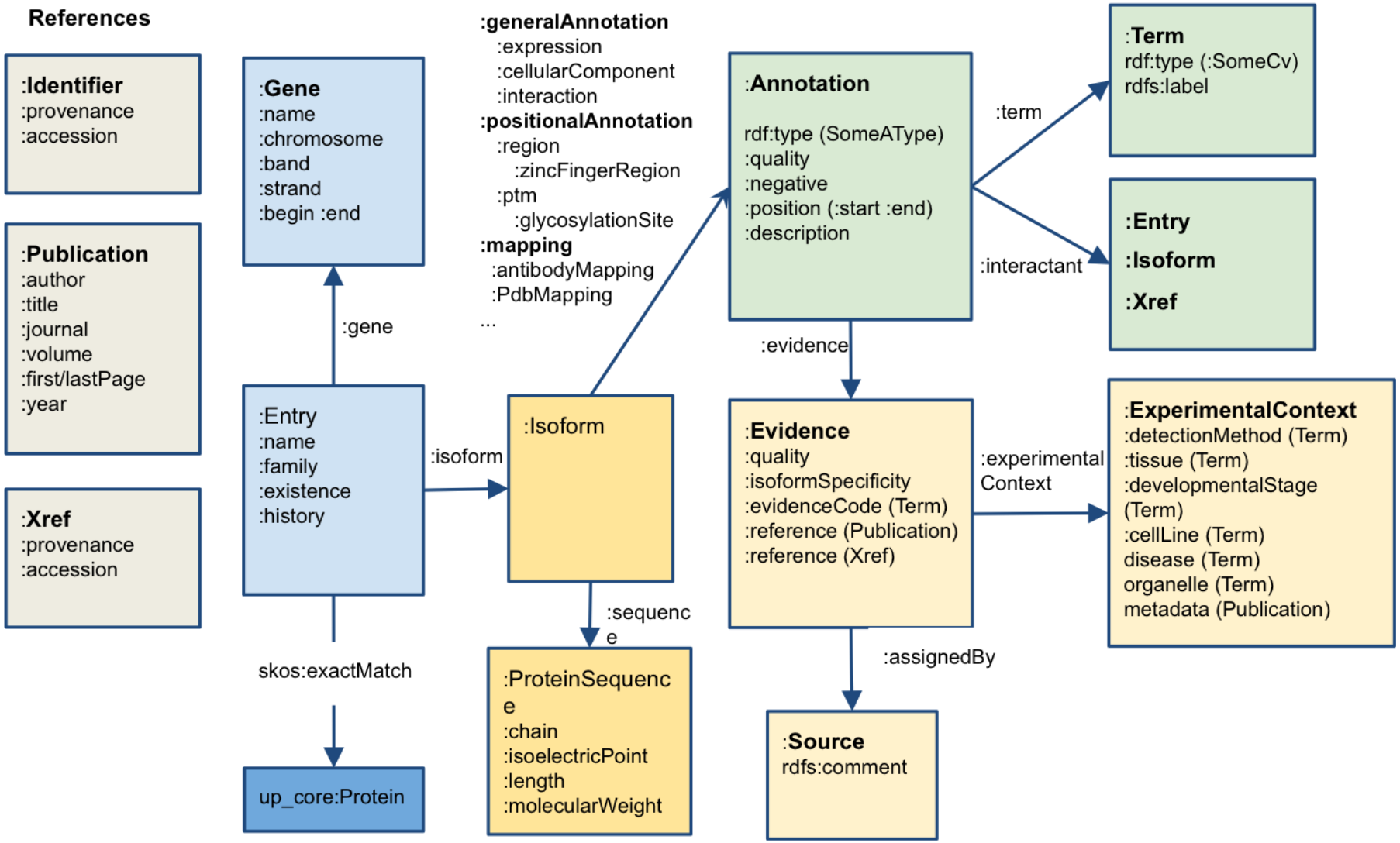


Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Omenn GS et al., JPR, 2018

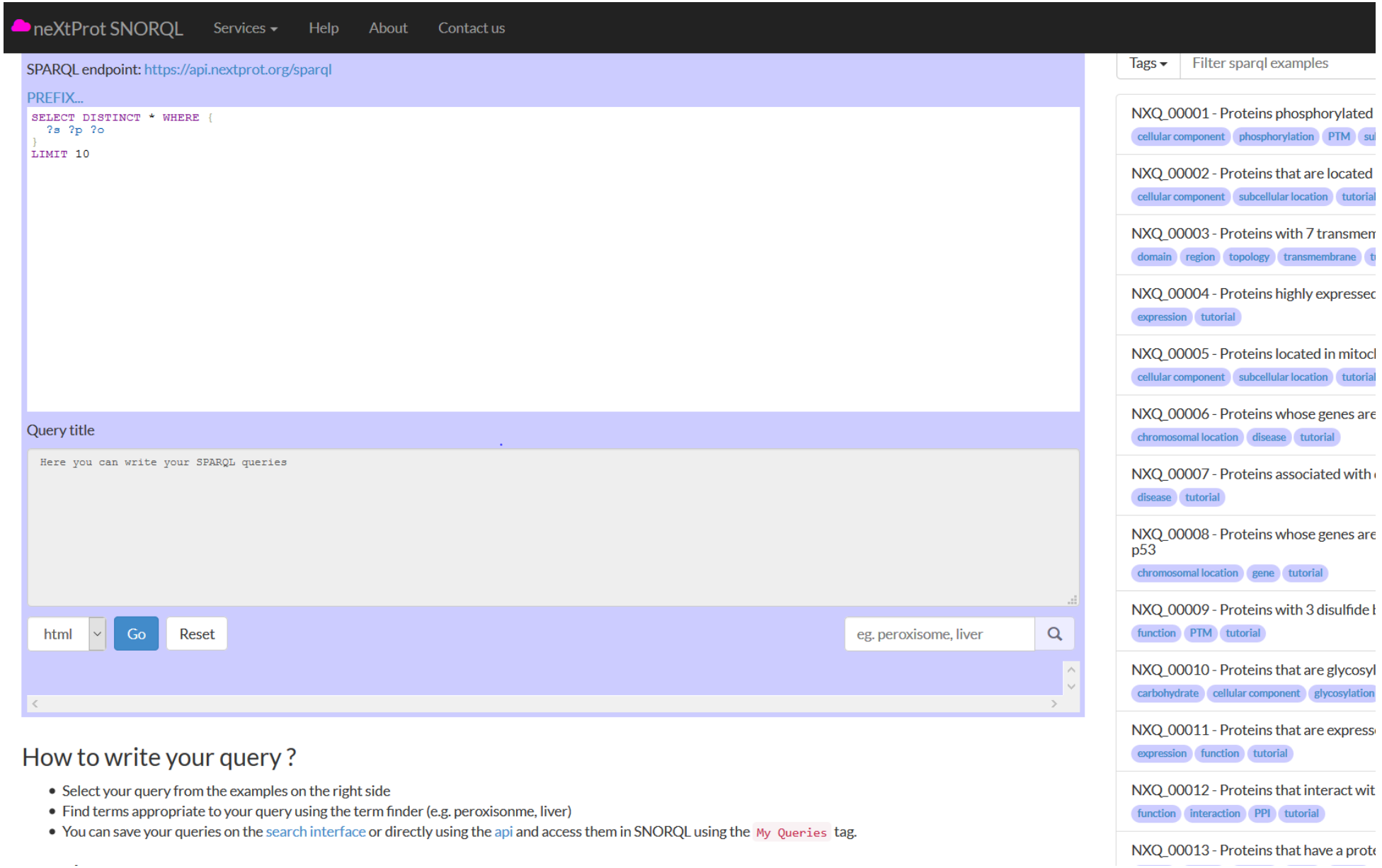
NextProt s ’appuie sur une ontologie décrite en RDFS : contient l’état des connaissances actuelles sur le protéome humain (Swiss Institute of Bioinformatics)



Un modèle simplifié de NextProt



End point SparQL



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. peroxisonme, 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.