

# UniProt SPARQL: A small tutorial



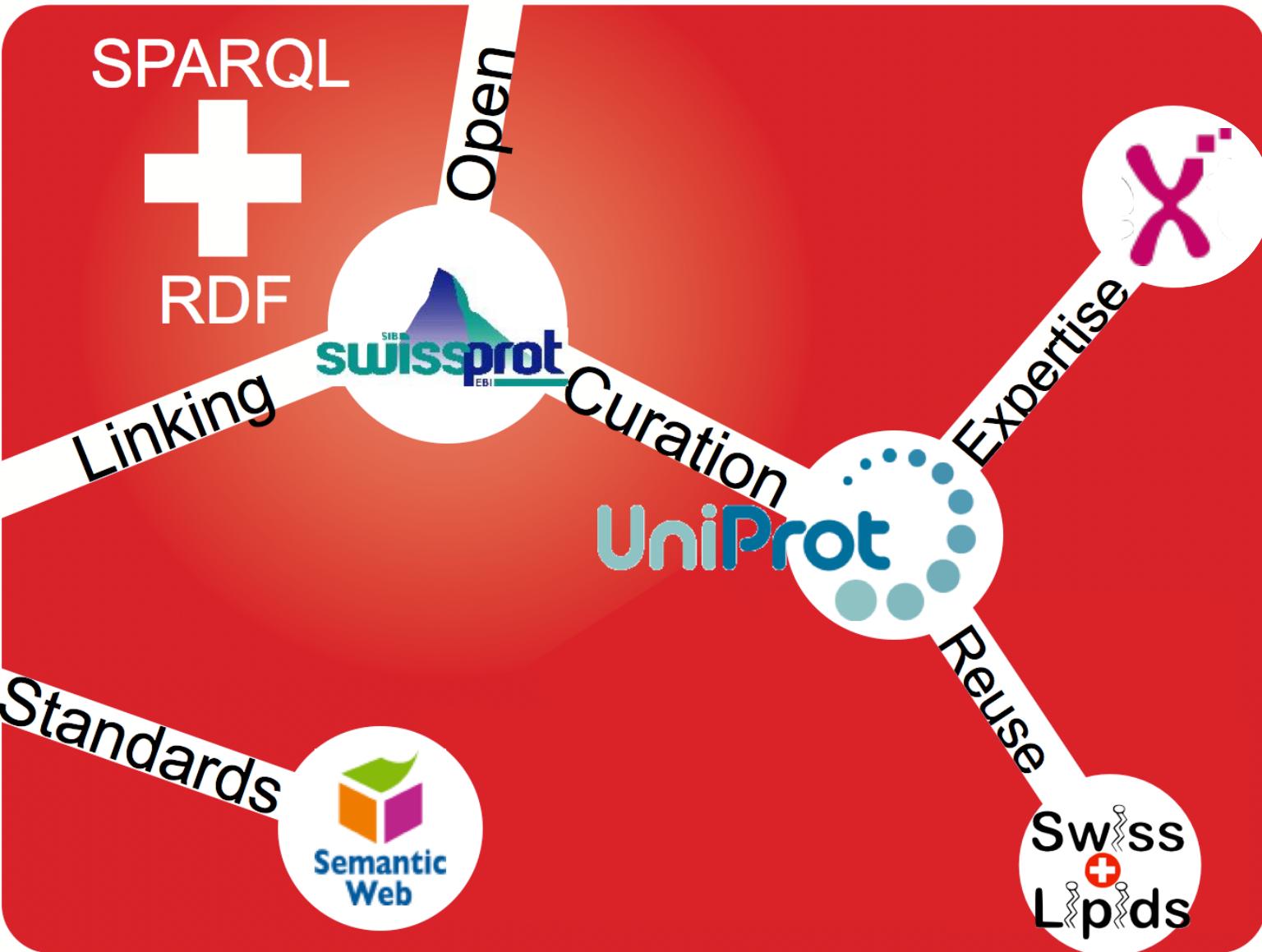
Jerven Bolleman  
Swiss-Prot



Swiss Institute of  
Bioinformatics

# UniProt SPARQL

- Next to [www.uniprot.org](http://www.uniprot.org)
  - for analytics
  - answering questions
    - not aimed at keyword search
  - your UniProt Data Base in the cloud
- 14 billion triples
  - in 17 graphs
- [help@uniprot.org](mailto:help@uniprot.org)
  - interested in your queries/questions/comments
  - we want you to use our data!
    - all questions are welcome



## Your SPARQL query

[Add common prefixes](#)

1

[Submit Query](#)

## About

This SPARQL endpoint contains all UniProt data. It is free to access and supports the [SPARQL 1.1 Standard](#).

There are 13,948,325,880 triples in this release (2015\_06). All triples are available in the default graph. There are 17 named graphs.

## Documentation

The documentation about UniProt RDF is spread into 2 parts

1. [Classes and predicates defined by the UniProt consortium](#)
2. [Statistics and diagrams](#)

## News



POLQ, a new target for cancer therapy?

[UniProt release 2015\\_06](#)

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[UniProt release 2015\\_05](#)

Of CAT tails and protein translation by-products | Reducing redundancy in proteomes | Changes to the controlled vocabulary of human diseases

[UniProt release 2015\\_04](#)

[News archive](#)

## Examples

1. Select all taxa from the [UniProt taxonomy](#): ([show](#))
2. Select all bacterial taxa, and their scientific name, from the [UniProt taxonomy](#): ([show](#))
3. Select all E-Coli K12 (including strains) UniProt entries and their amino acid sequence: ([show](#))
4. Select the UniProt entry with the mnemonic 'A4\_HUMAN': ([show](#))
5. Select a mapping of UniProt to PDB entries using the UniProt cross-references to the [PDB database](#): ([show](#))
6. Select all cross-references to external databases of the category '3D structure databases' of UniProt entries that are classified with the keyword '3Fe-4S': ([show](#))
7. Select all UniProt entries, and their recommended protein name, that have a preferred gene name that contains the text 'DNA': ([show](#))
8. Select the preferred gene name and disease annotation of all human UniProt entries that are known to be involved in a disease: ([show](#))
9. Select all human UniProt entries with a sequence variant that leads to a 'loss of function': ([show](#))
10. Select all human UniProt entries with a sequence variant that leads to a tyrosine to phenylalanine substitution: ([show](#))
11. Select all UniProt entries with annotated transmembrane regions and the regions' begin and end coordinates on the canonical sequence: ([show](#))
12. Select all UniProt entries that were integrated on the 30th of November 2010: ([show](#))
13. Was any UniProt entry integrated on the 9th of January 2013? ([show](#))
14. Construct new triples of the type 'HumanProtein' from all human UniProt entries: ([show](#))
15. Select all triples that relate to the EMBL CDS entry AA089367.1: ([show](#))
16. Select all triples that relate to the taxon that describes *Homo sapiens*: ([show](#))
17. Select the average number of cross-references to the [PDB database](#) of UniProt entries that have at least one cross-reference to the PDB database: ([show](#))
18. Select the number of UniProt entries for each of the EC (Enzyme Commission) second level categories: ([show](#))

UniProt

SPARQL Downloads Documentation/Help Contact

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1
```

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# <http://www.uniprot.org/core/>

## Core

### Navigation Panel

Classes ( 167 )	Absorption_Annotation
Properties ( 138 )	
Object properties ( 57 )	alternativeName
Datatype properties ( 81 )	abstract

### Ontology description

<http://purl.uniprot.org/core/> (rdf:type owl:Ontology )

rdfs:comment Properties and classes used for protein annotation. xsd:string

### Classes

**Absorption\_Annotation** (rdf:type owl:Class )

rdfs:label	Absorption xsd:string
rdfs:subClassOf	Biophysicochemical_Annotation
rdfs:comment	Indicates the wavelength in nm at which photoreactive proteins such as opsins and DNA photolyases show maximal absorption. xsd:string

**Active\_Site\_Annotation** (rdf:type owl:Class )

rdfs:label	Active Site xsd:string
rdfs:subClassOf	Site_Annotation
rdfs:comment	Amino acid(s) involved in the activity of an enzyme. xsd:string

<http://www.uniprot.org/format/>

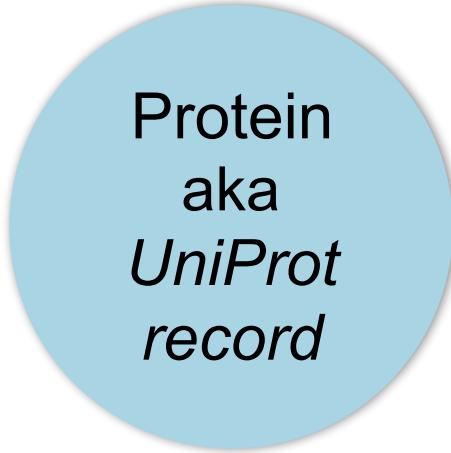
!! work in progress !!

- Description of the different formats
  - Examples in Turtle and JSON-LD
- Bug reports very welcome
- Focuses on UniProtKB

RDF can be downloaded from [uniprot.org](http://uniprot.org)

[Download](#)[Add to basket](#)[Columns](#) Download selected (0) Download all (49293307)**Format:**  Compressed  Uncompressed[Preview first 10](#)[Go](#)

UniProtKB



UniRef

Cluster  
aka  
*UniRef record*

50%

90%

100%

UniParc

Sequence  
aka  
*UniParc*

Taxonomy

UniProtKB

Protein  
aka  
*UniProt*  
*record*

Taxonomy

UniRef

Cluster  
aka  
*UniRef record*

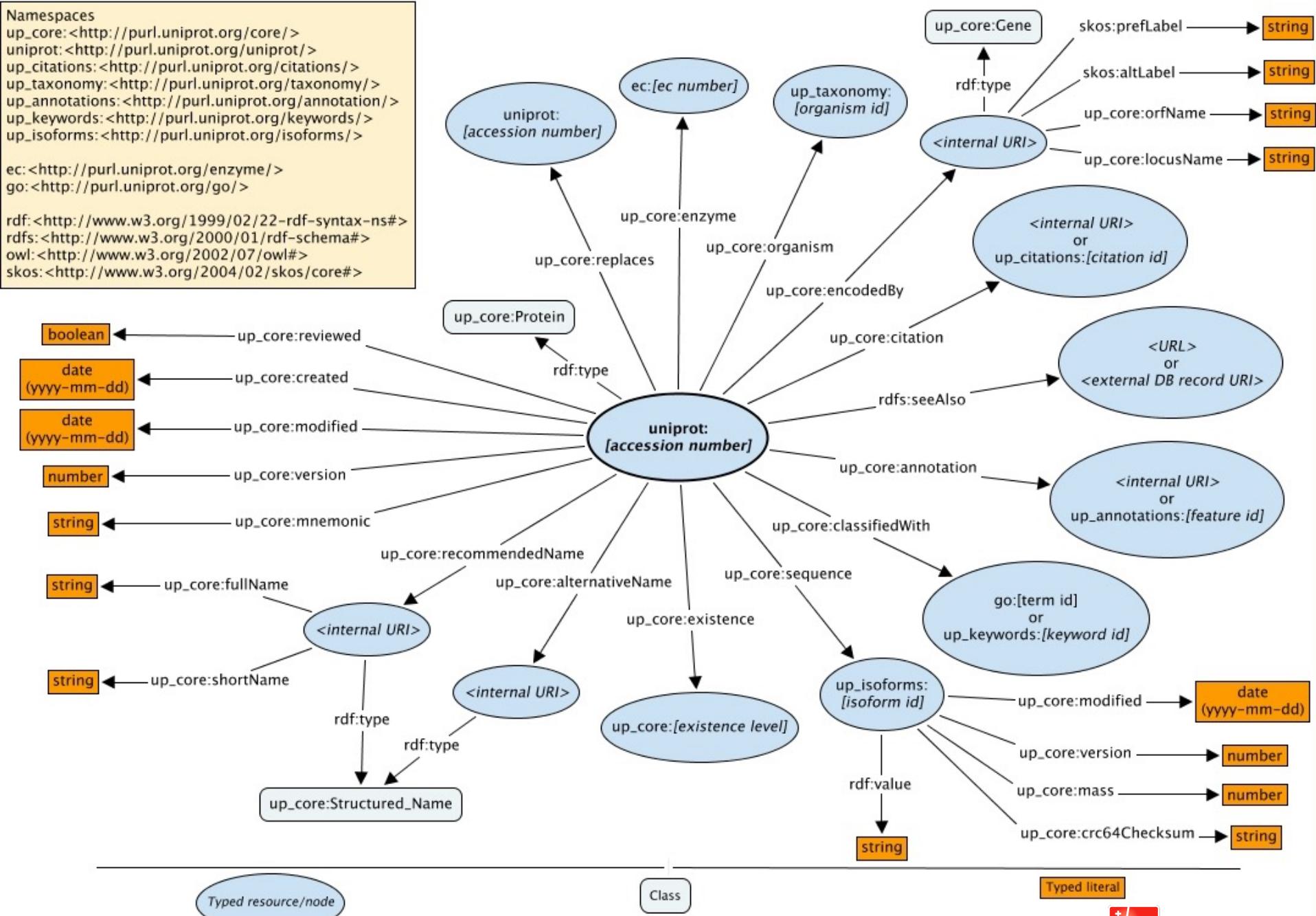
50%

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UniParc

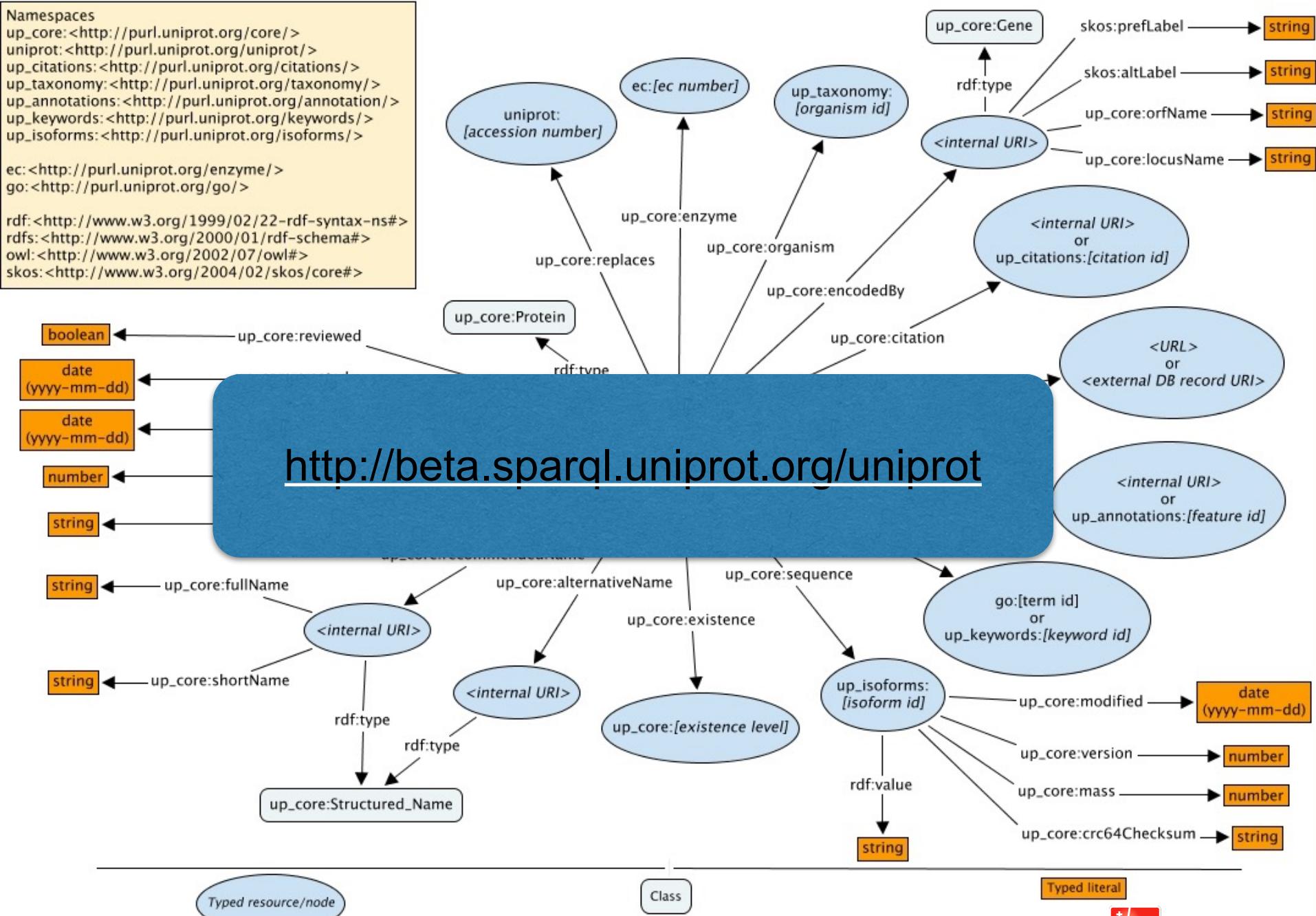
Sequence  
aka  
*UniParc*

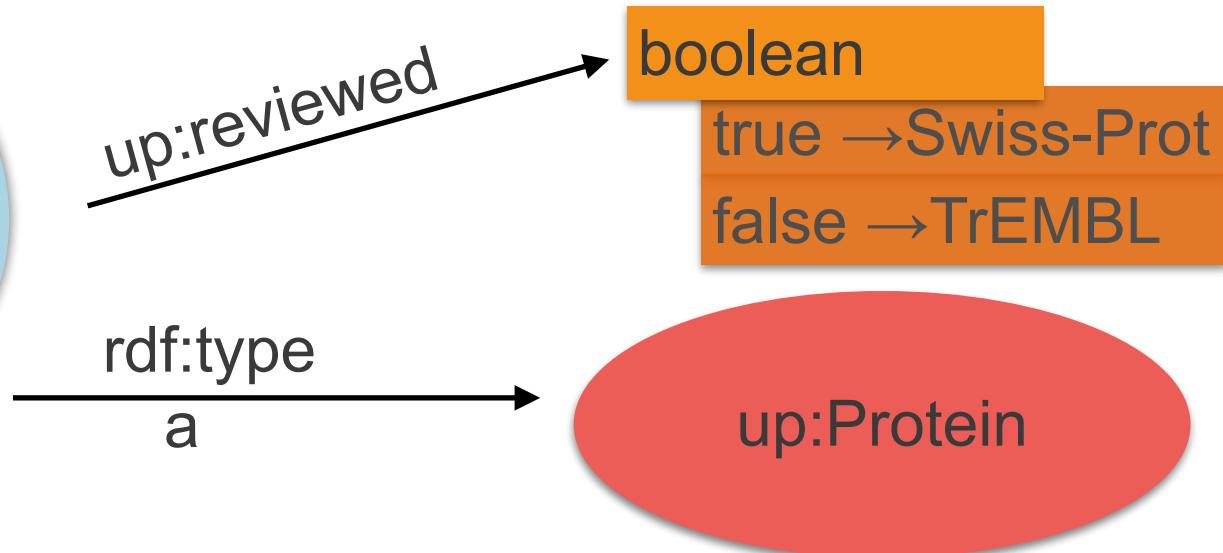
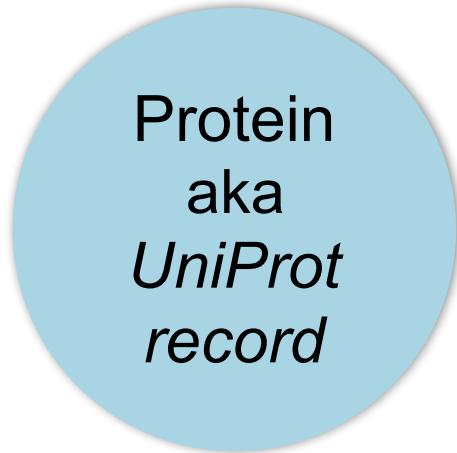


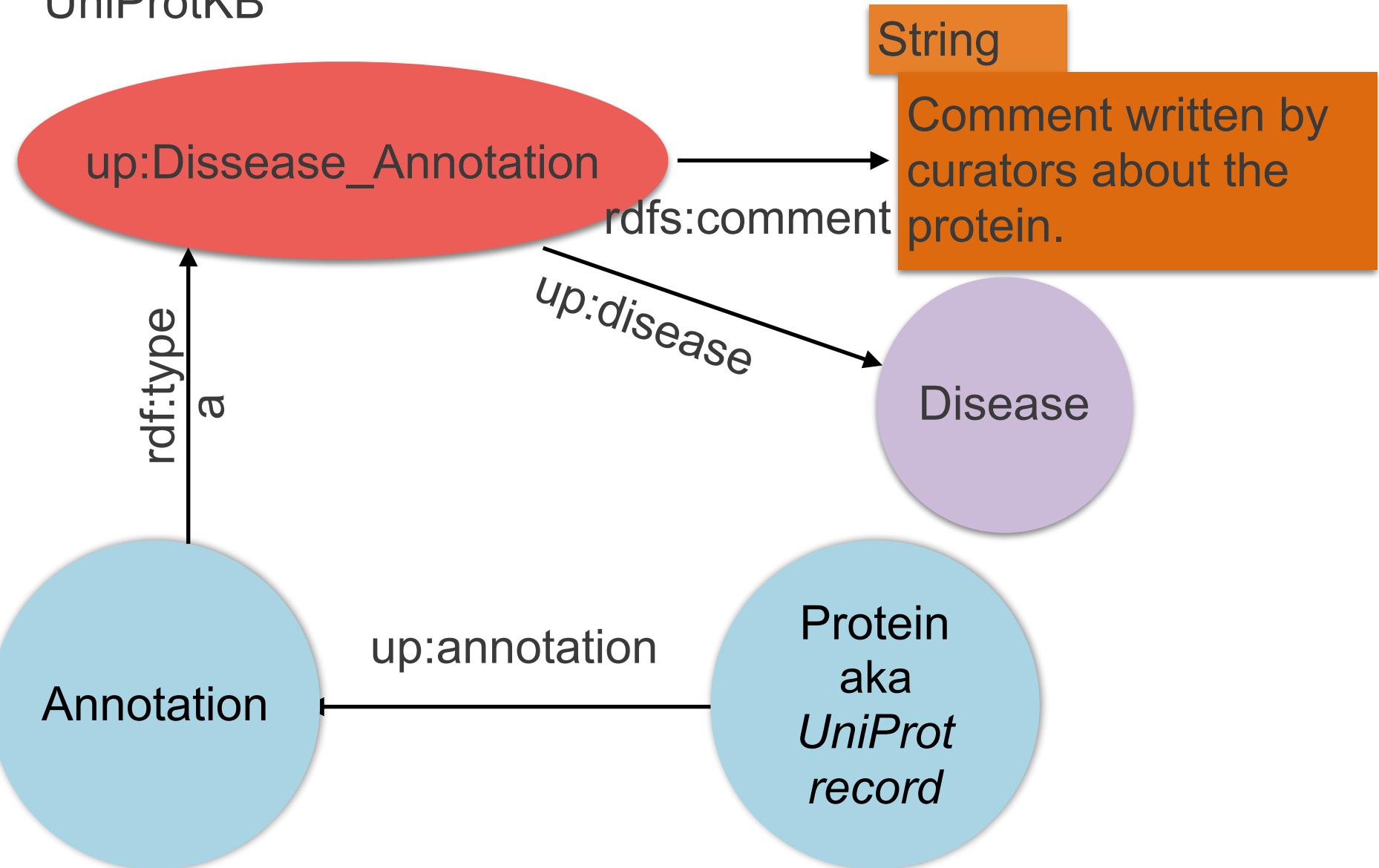
```
Namespaces
up_core:<http://purl.uniprot.org/core/>
uniprot:<http://purl.uniprot.org/uniprot/>
up_citations:<http://purl.uniprot.org/citations/>
up_taxonomy:<http://purl.uniprot.org/taxonomy/>
up_annotations:<http://purl.uniprot.org/annotation/>
up_keywords:<http://purl.uniprot.org/keywords/>
up_isoforms:<http://purl.uniprot.org/isoforms/>

ec:<http://purl.uniprot.org/enzyme/>
go:<http://purl.uniprot.org/go/>

rdf:<http://www.w3.org/1999/02/22-rdf-syntax-ns#>
rdfs:<http://www.w3.org/2000/01/rdf-schema#>
owl:<http://www.w3.org/2002/07/owl#>
skos:<http://www.w3.org/2004/02/skos/core#>
```







# UniProtKB

Protein  
aka  
*UniProt*  
*record*

Taxonomy

Locations

Keywords

Controlled vocabularies  
to help you find information

ChEBI

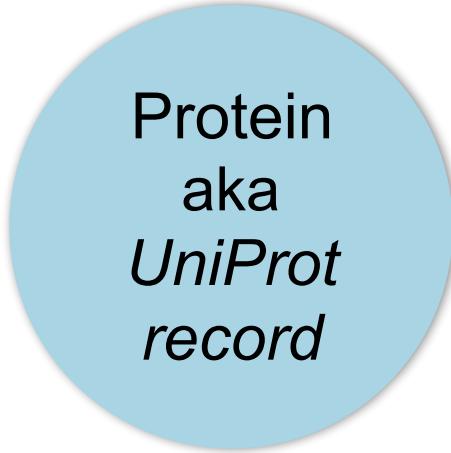
GO

FALDO

BIBO

Reusing ontologies  
for ease of integration

UniProtKB



UniRef

Cluster  
aka  
*UniRef record*

50%

90%

100%

UniParc

Sequence  
aka  
*UniParc*

Taxonomy

UniProtKB

Protein  
aka  
*UniProt record*

Taxonomy

Taxon

UniRef

Cluster  
aka  
*UniRef record*

50%

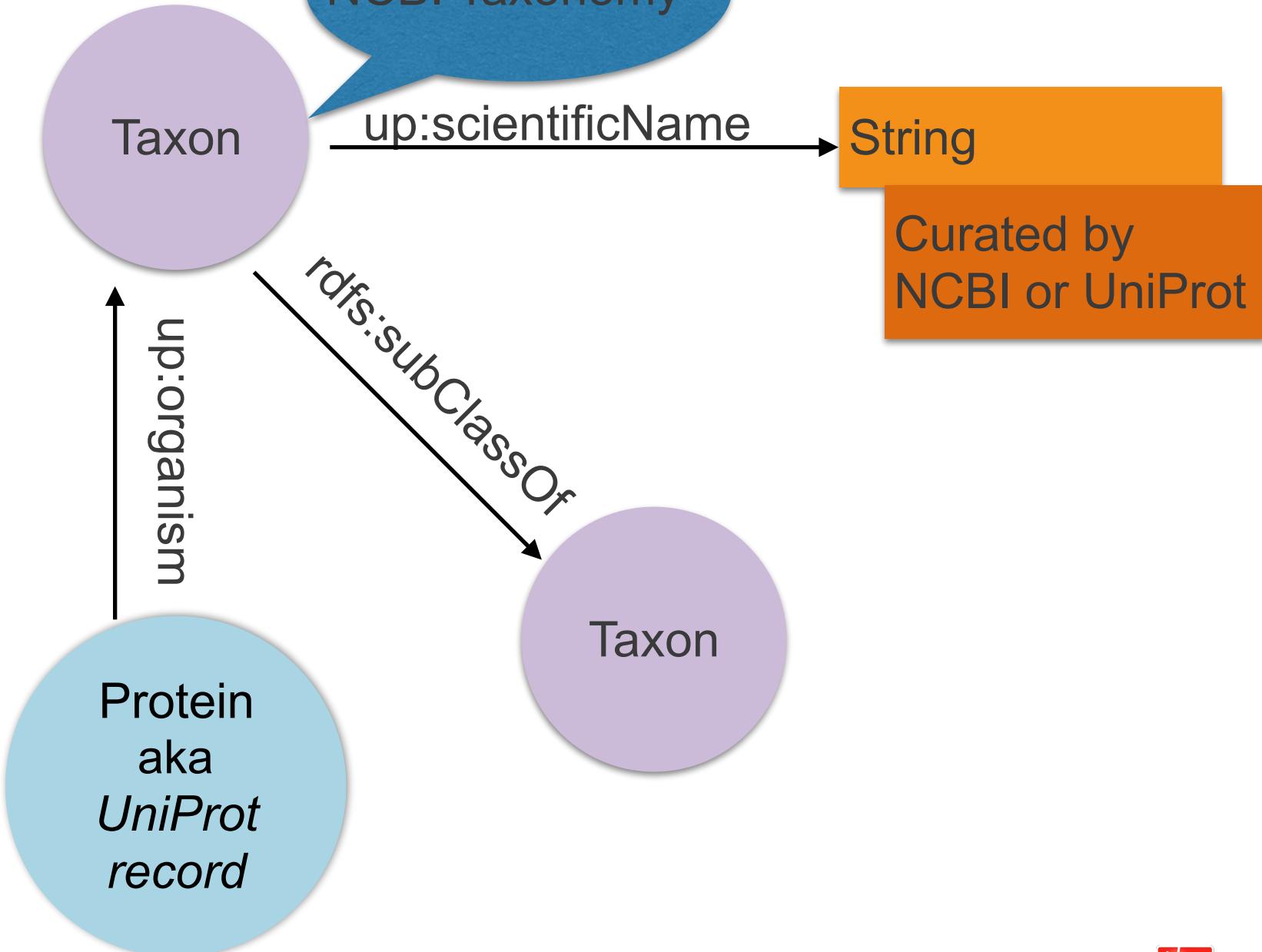
90%

100%

UniParc

Sequence  
aka  
*UniParc*

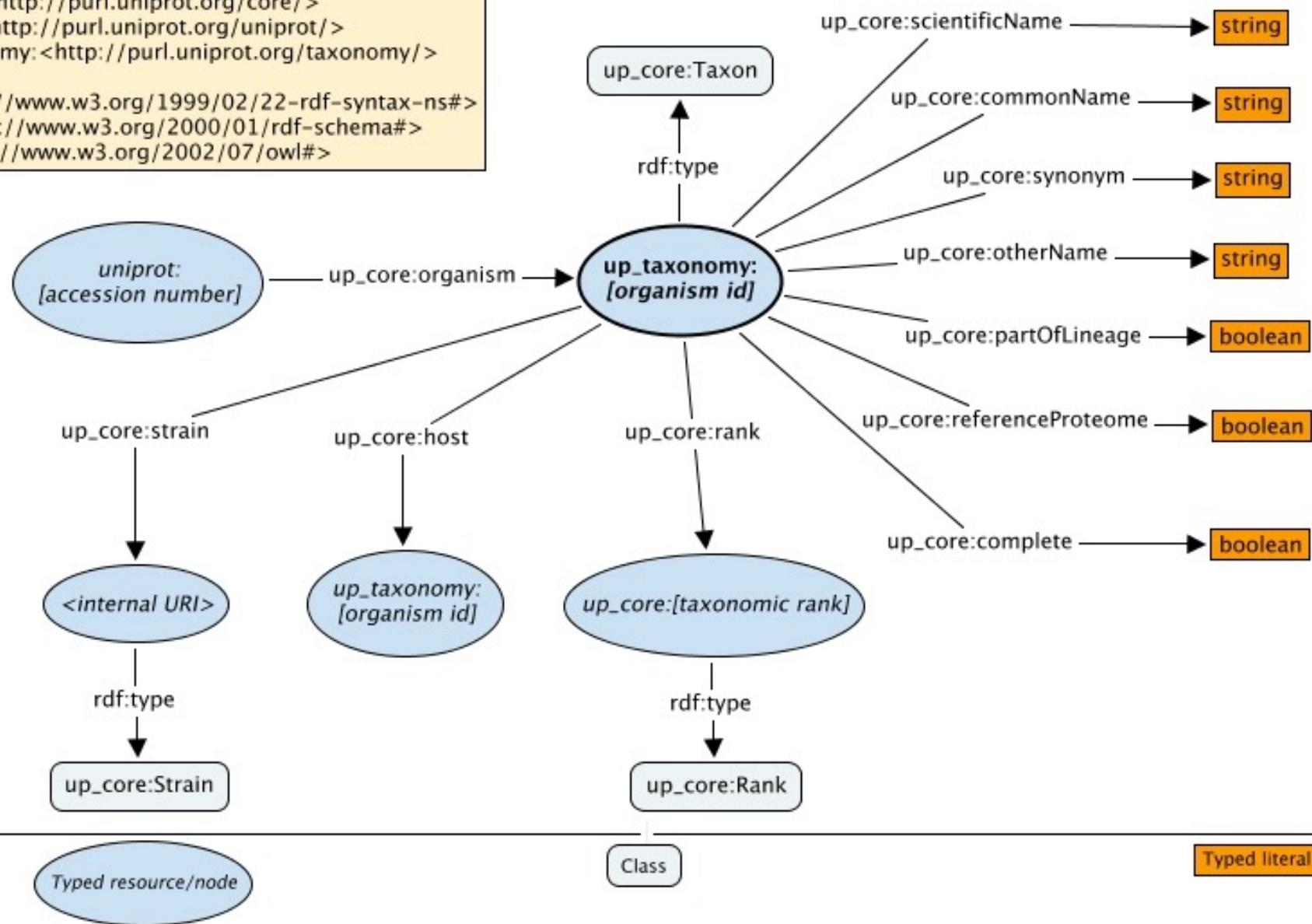
# Taxonomy



## Namespaces

up\_core:<<http://purl.uniprot.org/core/>>  
 uniprot:<<http://purl.uniprot.org/uniprot/>>  
 up\_taxonomy:<<http://purl.uniprot.org/taxonomy/>>

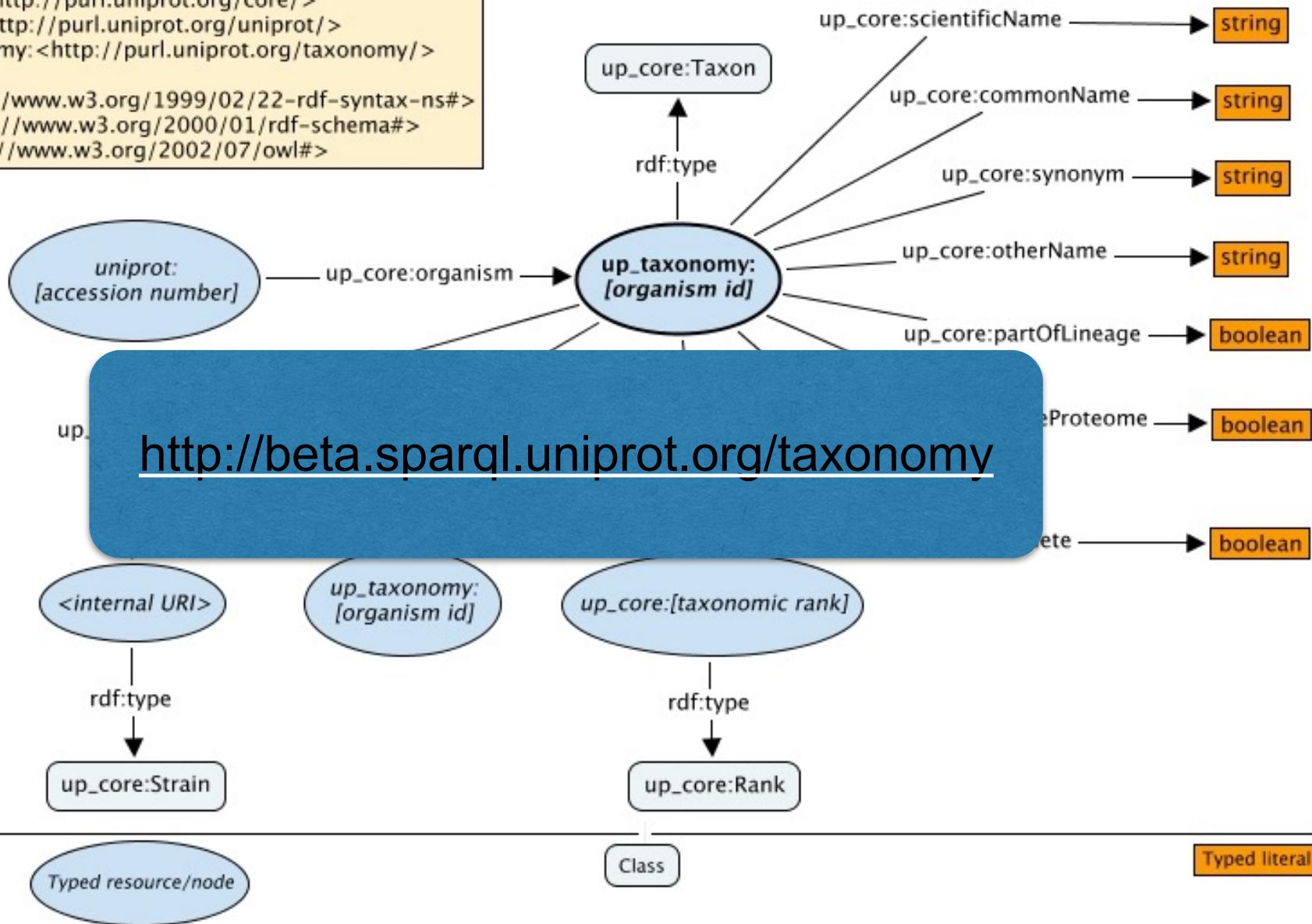
rdf:<<http://www.w3.org/1999/02/22-rdf-syntax-ns#>>  
 rdfs:<<http://www.w3.org/2000/01/rdf-schema#>>  
 owl:<<http://www.w3.org/2002/07/owl#>>



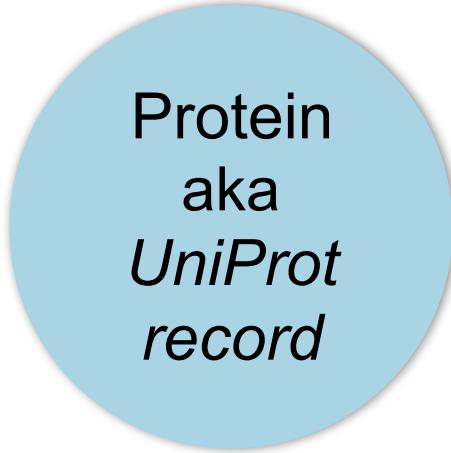
## Namespaces

up\_core:<<http://purl.uniprot.org/core/>>  
uniprot:<<http://purl.uniprot.org/uniprot/>>  
up\_taxonomy:<<http://purl.uniprot.org/taxonomy/>>

rdf:<<http://www.w3.org/1999/02/22-rdf-syntax-ns#>>  
rdfs:<<http://www.w3.org/2000/01/rdf-schema#>>  
owl:<<http://www.w3.org/2002/07/owl#>>



UniProtKB



UniRef

Cluster  
aka  
*UniRef record*

50%

90%

100%

UniParc

Sequence  
aka  
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Taxonomy

UniProtKB

UniRef

50%

Cluster  
aka  
*UniRef record*

90%

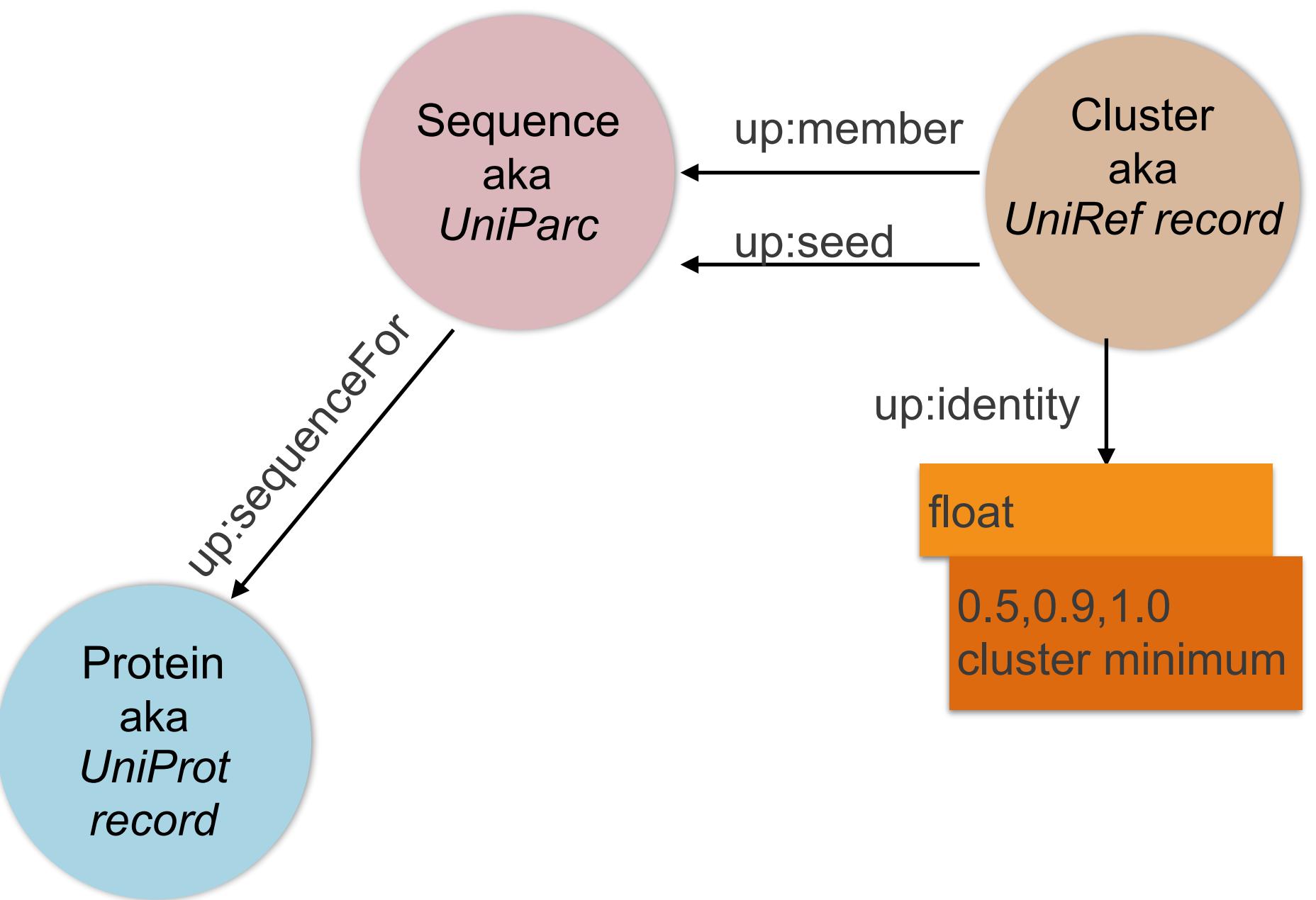
100%

Protein  
aka  
*UniProt record*

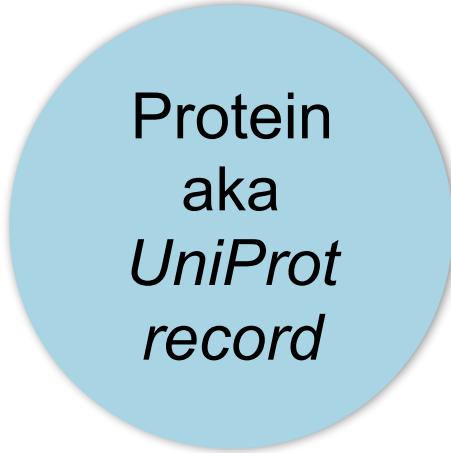
UniParc

Sequence  
aka  
*UniParc*

Taxonomy



UniProtKB



UniRef

Cluster  
aka  
*UniRef record*

50%

90%

100%

UniParc

Sequence  
aka  
*UniParc*

Taxonomy

**UniProtKB**

Protein  
aka  
*UniProt*  
*record*

Taxonomy

**UniRef**

Cluster  
aka  
*UniRef record*

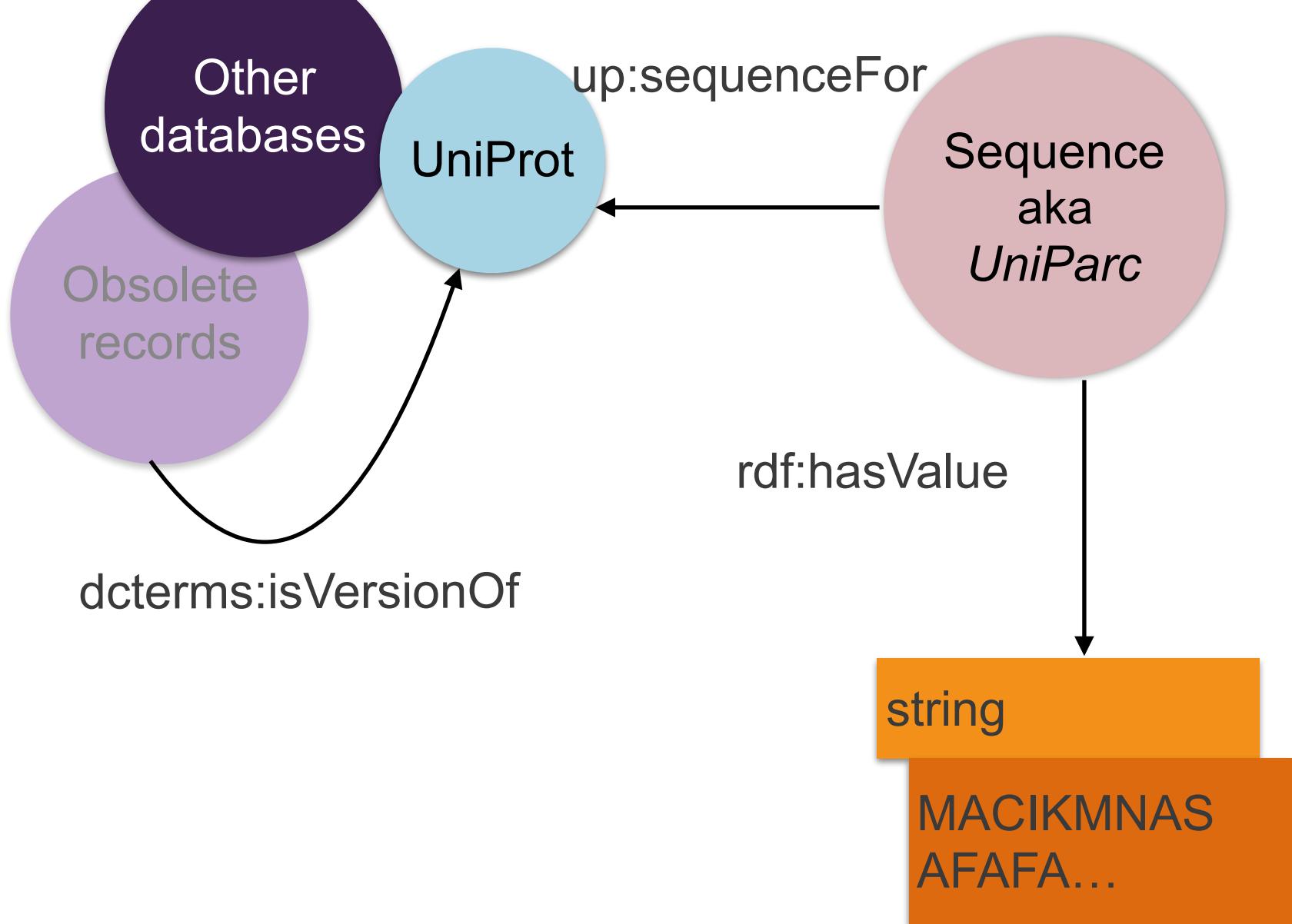
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**UniParc**

Sequence  
aka  
*UniParc*



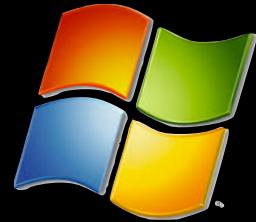
# We are using EPO and EPO receptors as training data

- <http://www.uniprot.org/uniprot/P19235>
  - EPO\_HUMAN
- <http://www.uniprot.org/uniprot/P01588>
  - EPOR\_HUMAN
- <http://www.uniprot.org/uniparc/UPI000012A0AD>
- [http://www.uniprot.org/uniref/UniRef100\\_P19235](http://www.uniprot.org/uniref/UniRef100_P19235)
- etc...

`./start-uniprot.sh`

or

`./start-uniprot.bat`



<http://localhost:9999>

<http://bc2-2015.sparql.uniprot.org/>

► SPARQL playground Documentation FAQs Data About

Resources ▾



#### 6) Select Proteins similar to Human EPO isform 3

Show prefixes ...

endpoint: <http://localhost:9999/sparql>

```
SELECT ?epoLike
WHERE {?cluster up:identity "0.9"^^xsd:float;
          up:member ?member, ?member2 .
          ?member up:sequenceFor ?epoLike .
          ?member2 up:sequenceFor uniprot:P19235-3 .
          FILTER(?epoLike != uniprot:P19235-3)
}
```

html Go Reset

Query time is 0.188[s] for 9 rows

#### epoLike

```
<http://purl.uniprot.org/EPO/JA684580.1>
<http://purl.uniprot.org/USPTO/ADA04868.1>
```

© 2015 SIB

Tags ▾ Filter sparql examples

1) Select all taxa from the UniProt taxonomy

2) Select all taxa, and their scientific name, from the UniProt taxonomy

3) All Swiss-Prot entries

4) Select UniProt records with a related disease

4) Select UniProt records with a related disease and a comment

4) Select UniProt records with a related disease plus more information about the disease

5) Proteins that are in the genus Hominidae

6) Select Proteins similar to Human EPO isform 3



Swiss Institute of  
Bioinformatics

File Edit View History Bookmarks Dots Help

http://www.google.com/search?hl=fr&sa=X&ei=260f304a9f02d8d076301

# Google Error

## We're sorry...

... but your query looks similar to automated requests from a computer virus or spyware application. To protect our users, we can't process your request right now.

We'll restore your access as quickly as possible, so try again soon. In the meantime, if you suspect that your computer or network has been infected, you might want to run a [virus checker](#) or [spyware remover](#) to make sure that your systems are free of viruses and other spurious software.

If you're continually receiving this error, you may be able to resolve the problem by deleting your Google cookies and revisiting Google. For browser-specific instructions, please consult your browser's online support center.

We apologize for the inconvenience, and hope we'll see you again on Google.

To continue searching, please type the characters you see below:



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Date: [redacted] | Tor Disabled: [redacted] | IP: 69.239.181.129:43 | Proxy/Proxy-Disabled: [redacted] | Profile: [redacted] | NW: [redacted]