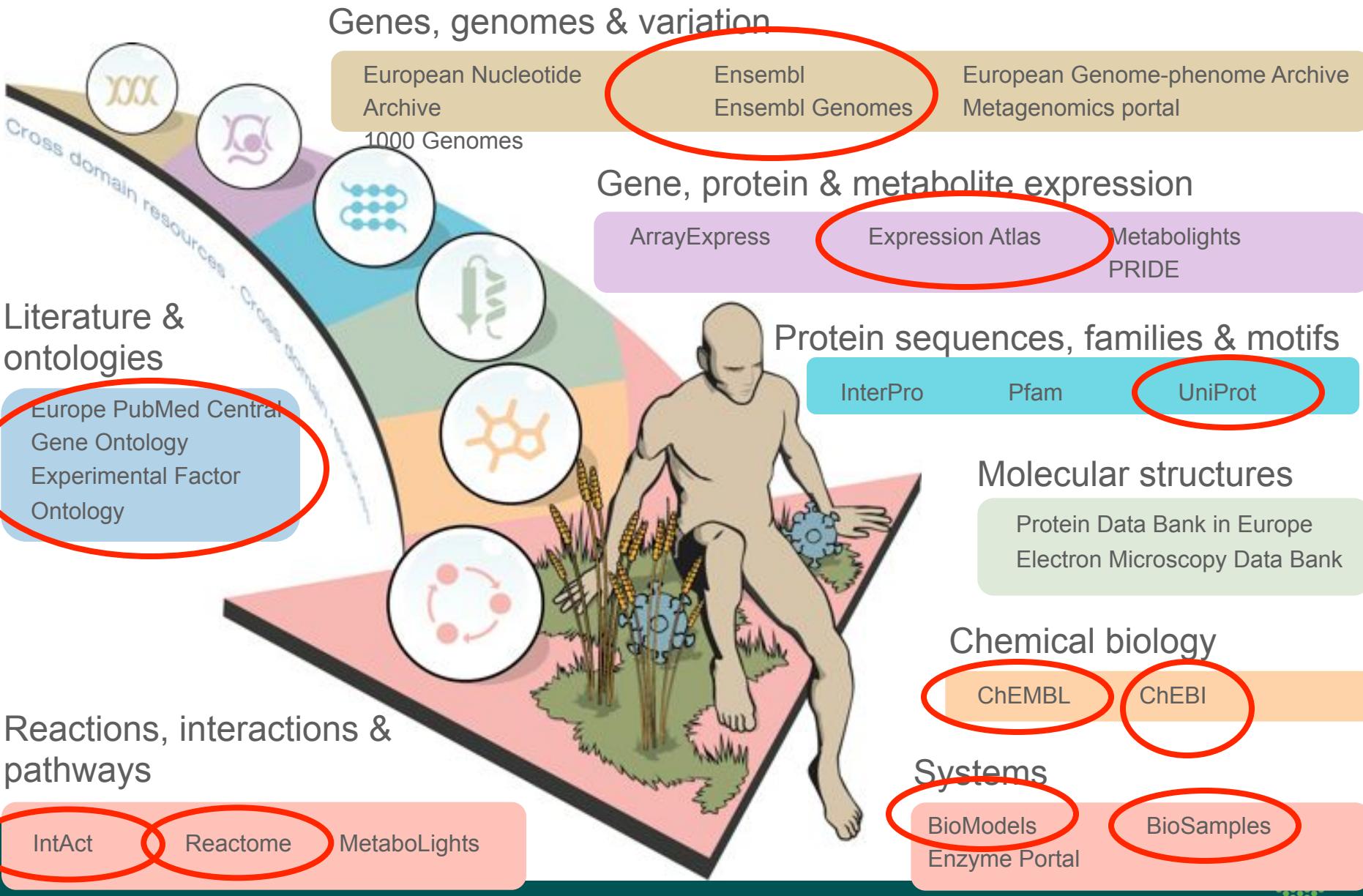


# *Capturing Provenance for a Linkset of Convenience*

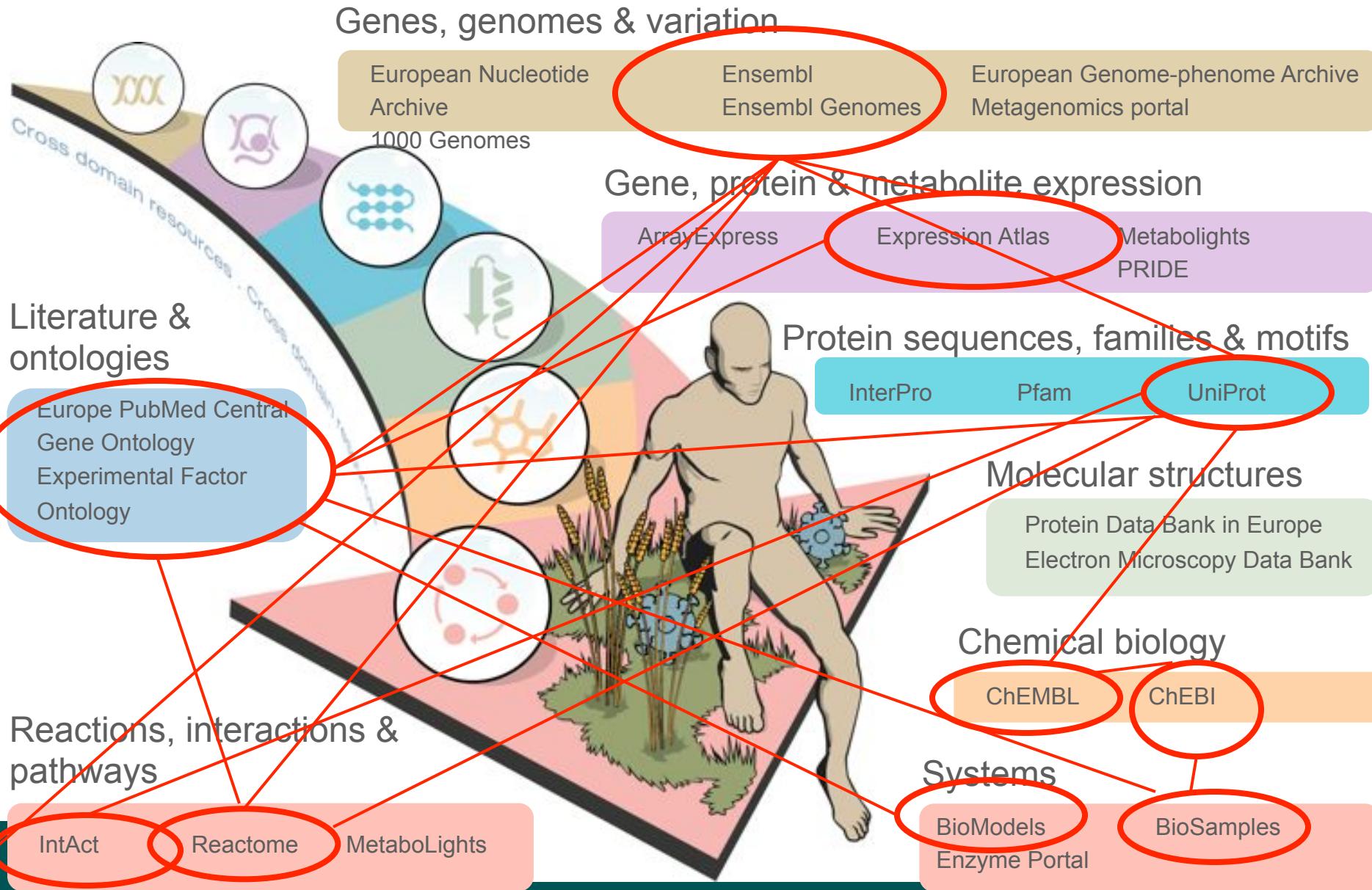
Simon Jupp [jupp@ebi.ac.uk](mailto:jupp@ebi.ac.uk)

Samples, Phenotypes and Ontologies  
European Bioinformatics Institute

# RDF data resources at EMBL-EBI



# Lots of links, but what are the integration points?



# Integration points

- Most common integration point gene or protein id
  - UniProt or Ensembl id
  - Ontology terms (GO, EFO)
- Most databases include db cross references to support hyperlinking and search
  - Mappings come from multiple source
  - Mappings get imported from other resources



```
Q6GZ4 UniProtKB-ID 001R_FRG3G
Q6GZ4 GI 81941549
Q6GZ4 GI 47868116
Q6GZ4 GI 49237298
Q6GZ4 UniRef100 UniRef100_Q6GZ4
Q6GZ4 UniRef98 UniRef98_Q6GZ4
Q6GZ4 UniRef50 UniRef50_Q6GZ4
Q6GZ4 UniParc UP18000380FD4
Q6GZ4 EMBL AYS48484
Q6GZ4 EMBL-CDS AT099668..1
Q6GZ4 NCBI_TaxID 654924
Q6GZ4 RefSeq YP_031579..1
Q6GZ4 RefSeq_NT NC_085946..1
Q6GZ4 GenID 2947773
Q6GZ3 UniProtKB-ID 002L_FRG3G
Q6GZ3 GI 49237299
Q6GZ3 GI 47868117
Q6GZ3 GI 81941548
Q6GZ3 UniRef100 UniRef100_Q6GZ3
Q6GZ3 UniRef98 UniRef98_Q6GZ3
Q6GZ3 UniRef50 UniRef50_Q6GZ3
Q6GZ3 UniParc UP18000380FD5
Q6GZ3 EMBL AYS48484
Q6GZ3 EMBL-CDS AT099661..1
Q6GZ3 NCBI_TaxID 654924
Q6GZ3 RefSeq YP_031588..1
Q6GZ3 RefSeq_NT NC_085946..1
Q6GZ3 GenID 2947774
Q197F UniProtKB-ID 002R_IIV3
Q197F GI 186073583
Q197F GI 109287888
Q197F GI 123888694
Q197F UniRef100 UniRef100_Q197F
Q197F UniRef98 UniRef98_Q197F
Q197F UniRef50 UniRef50_Q197F
Q197F UniParc UP18000383464
Q197F EMBL DQ643392
Q197F EMBL-CDS ABF82032..1
Q197F NCBI_TaxID 345281
Q197F RefSeq YP_654574..1
Q197F RefSeq_NT NC_088187..1
Q197F GenID 4156251
Q197F UniProtKB-ID 003L_IIV3
Q197F GI 186073584
Q197F GI 109287881
Q197F GI 123888693
Q197F UniRef100 UniRef100_Q197F
Q197F UniRef98 UniRef98_Q197F
```

# Ensembl 2 UniProt example – BRAF gene



Ensembl gene ENSG00000157764

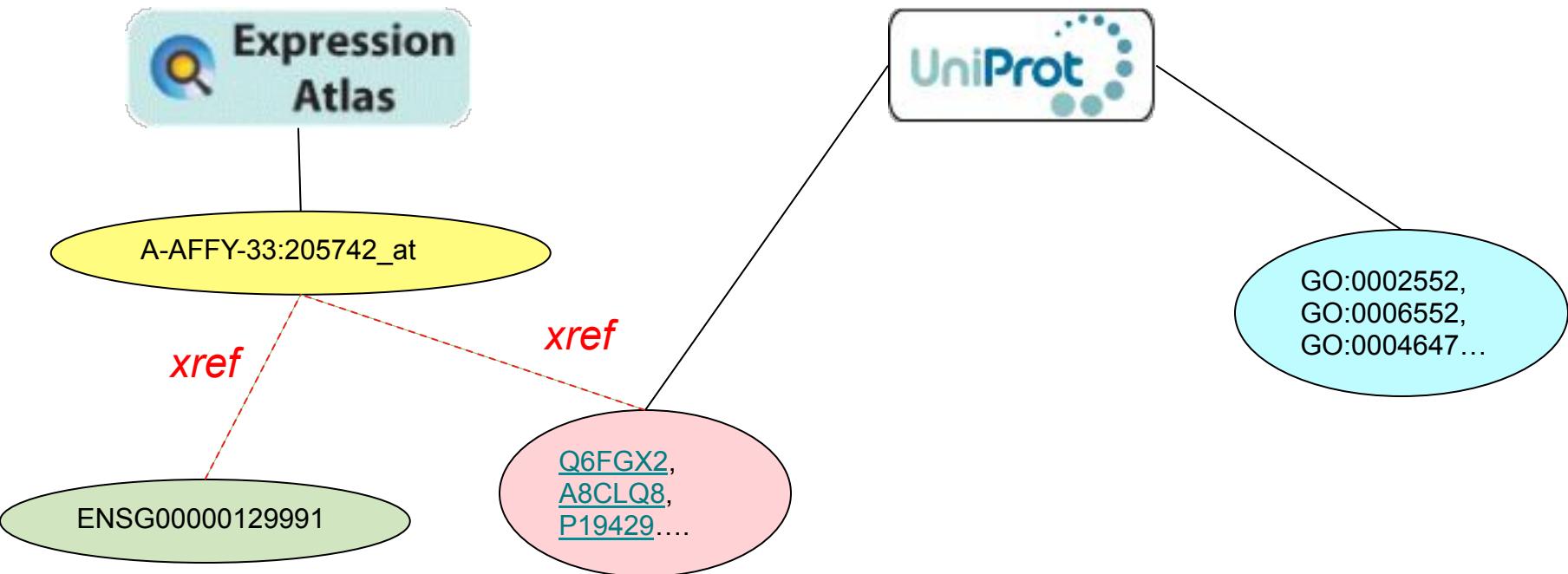
transcriptid	peptide	uniprotacc
BRAF-001	ensemblprotein:ENSP00000288622	ESFF37
BRAF-001	ensemblprotein:ENSP00000288622	Q7SMQ8
BRAF-001	ensemblprotein:ENSP00000288622	D7PB64
BRAF-001	ensemblprotein:ENSP00000288622	P15056
BRAF-002	ensemblprotein:ENSP00000418039	H7C5K3
BRAF-003	ensemblprotein:ENSP00000418039	ESFF37
BRAF-005	ensemblprotein:ENSP00000418033	H7C4S5
BRAF-005	ensemblprotein:ENSP00000418033	ESFF37



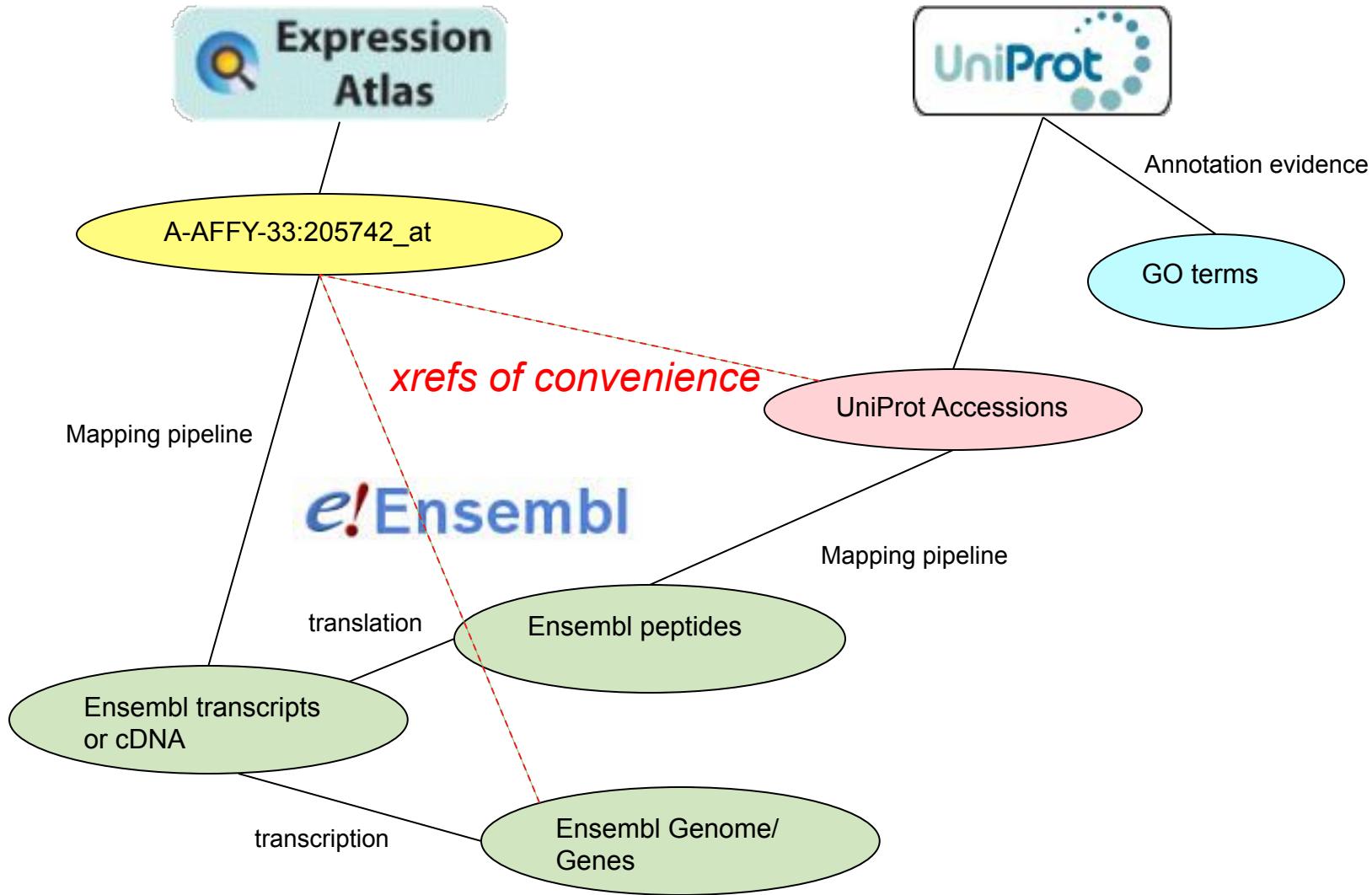
#	Entry	Entry name	Protein names	Gene names	Organism	Length	
□	H7C560	H7C560_HUMAN	Serine/threonine-protein kinase B-r...	BRAF	Homo sapiens (Human)	375	
□	P15056	BRAF_HUMAN	Serine/threonine-protein kinase B-r...	BRAF, BRAF1, RAFB1	Homo sapiens (Human)	766	
□	H7C4S5	H7C4S5_HUMAN	Serine/threonine-protein kinase B-r...	BRAF	Homo sapiens (Human)	102	
□	H7C5K3	H7C5K3_HUMAN	Serine/threonine-protein kinase B-r...	BRAF	Homo sapiens (Human)	194	

# Querying across resources

*“Show expression for ENSG00000129991 (TNNI3) with its GO annotations from Uniprot”*

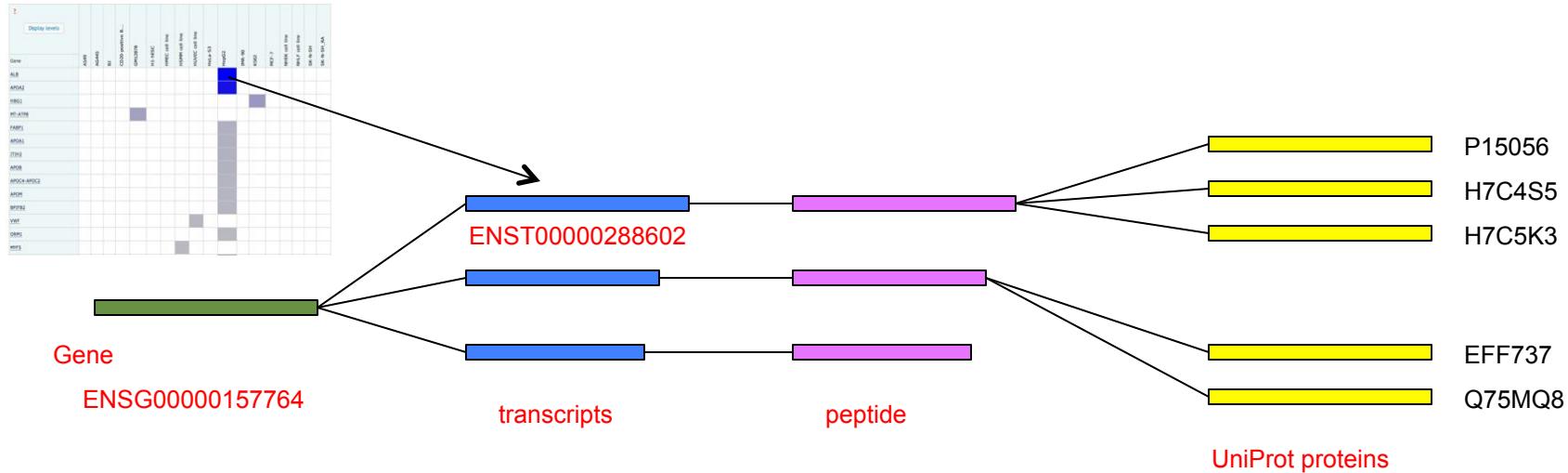


# Convenience links derived from stronger links



# Need to be careful with Xrefs

RNASeq experiment shows expression of transcript ENST00000288602



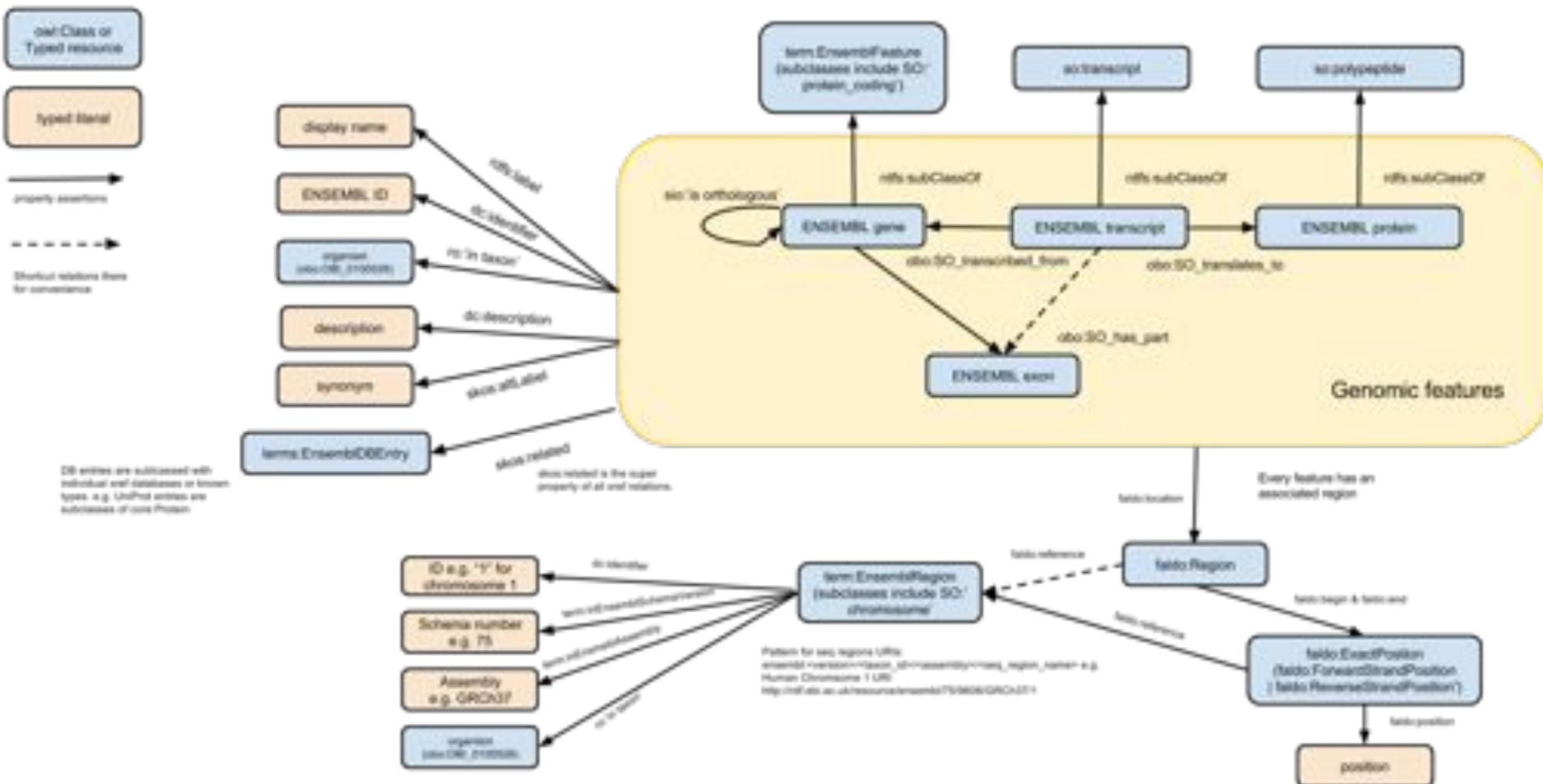
Would you expect this experiments to be returned in a search for Q75MQ8?

- probably yes

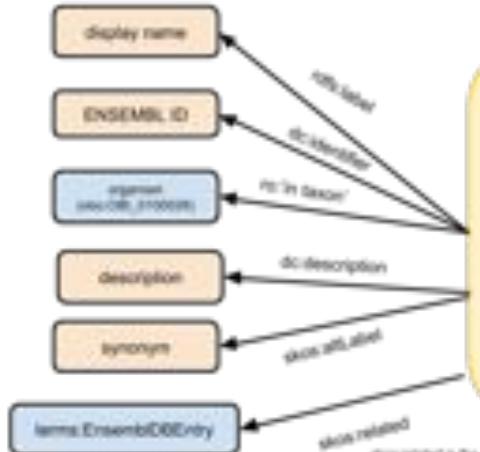
Is there evidence for the expression on this protein?

- possibly not

# Ensembl core RDF schema



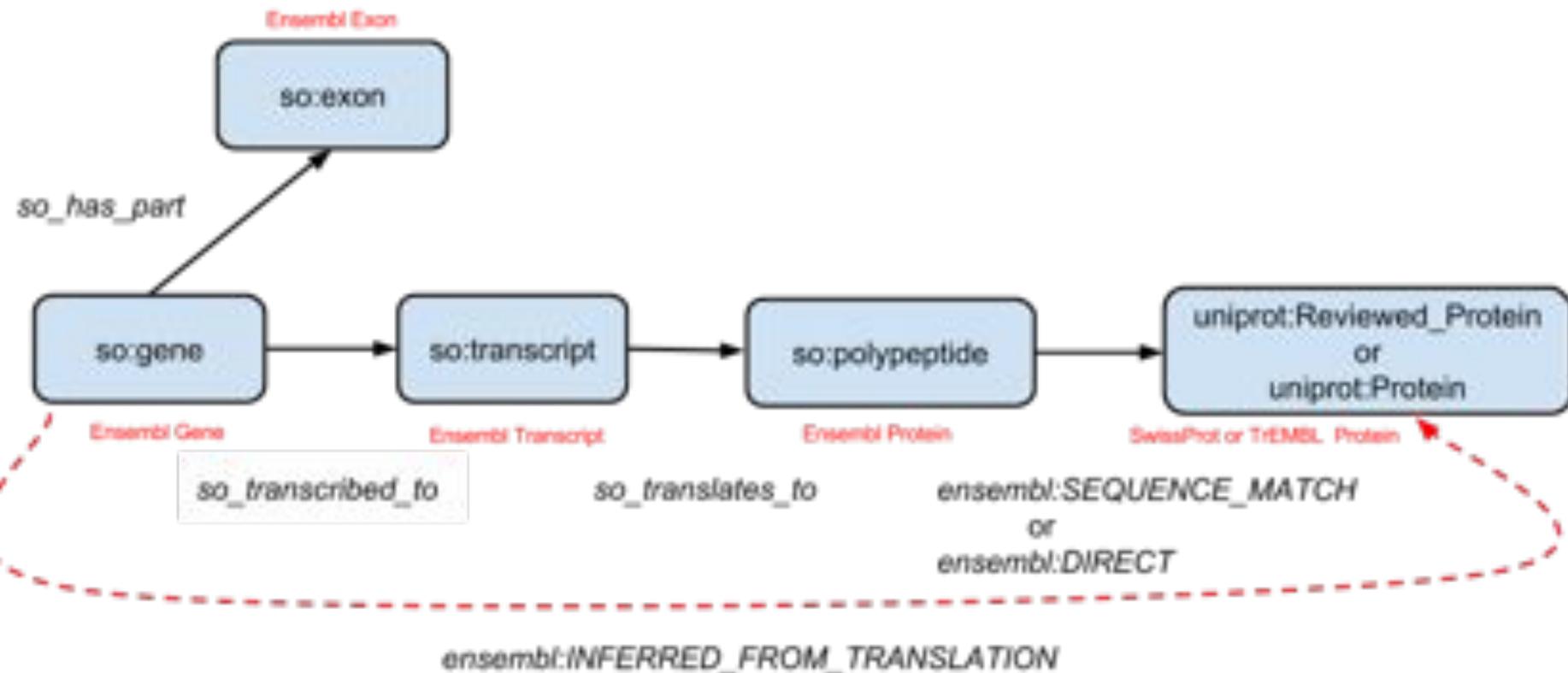
DB entries are subcategorised with individual ensembl databases or known genes, e.g. UniProt entries are subclasses of core Protein



Pattern for seq\_regions (URIs:  
 ensembl>ensembl>region\_id>assembly>seq\_region\_name>Human Chromosome 1 URI  
[http://identifiers.org/resource/ensembl/7/assembly/seq\\_region\\_name/HumanChromosome1](http://identifiers.org/resource/ensembl/7/assembly/seq_region_name/HumanChromosome1))



# Ensembl Gene to UniProt protein

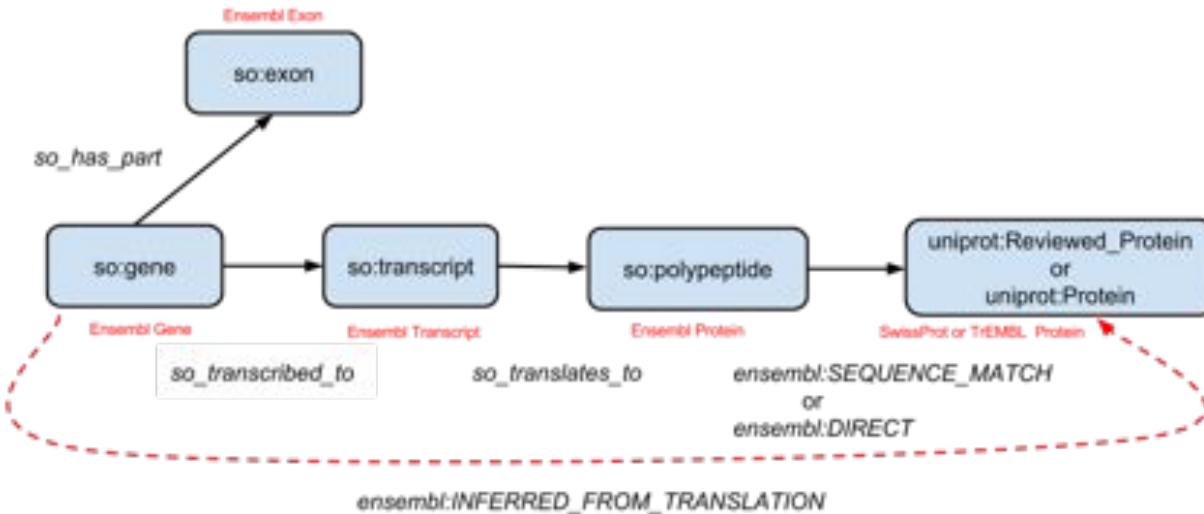


*How can we capture that the link of convenience is derived from the longer chain of links above?*

# VoID

- Vocabulary for describing linked datasets
- Describe partitions/subsets in a dataset
  - Class partitions e.g. all triples where subject of a given type
  - Property partitions e.g. all triples where a given property is used
- VoID linksets
  - Description of links between datasets (or partitions)
  - We can use VoID to cut a large dataset like ensembl into smaller datasets based on partitions
  - We can use linksets to describe how these subsets relate to each within Ensembl, and to external datasets like UniProt

# Describing subsets and linksets with VoID



## Subsets

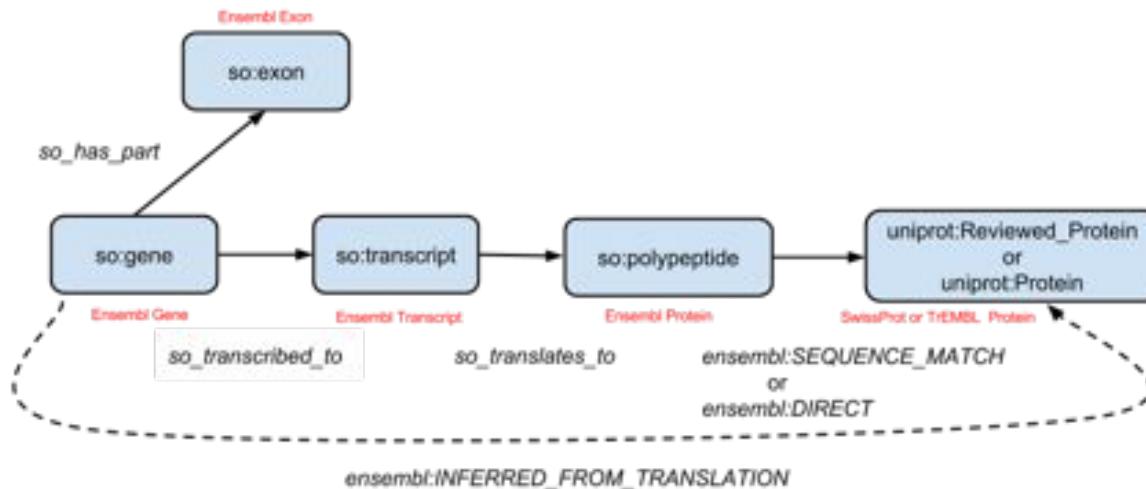
- **All Ensembl gene subset:** :gene\_partition *void:class* ensembl:Gene
- **All Ensembl transcript subset:** :transcript\_partition *void:class* ensembl:Transcript
- **All Ensembl protein subset:** :protein\_partition *void:class* ensembl:Protein
- **All UniProt reviewed protein subset:** :uniprot\_reviewed\_partition *void:class* uniprot:Reviewed\_Protein

## Example Linkset

- **Gene Transcript linkset:**

```
:gene_transcript_partition a void:Linkset ;  
    void:linkPredicate so:transcribed_to ;  
    void:subjectTarget :gene_partition ;  
    void:objectTarget :transcript_partition
```
- **Repeat for transcript-protein, protein-uniprot, gene-uniprot**

# Derived Linksets



## Linkset of convenience

- A linkset derived from other linksets

:gene\_to\_uniprot\_protein\_linkset *prov:wasDerivedFrom*

```
:gene_to_transcript, :transcript_to_peptide, :peptide_to_uniprot ;  
void:subjectTarget :gene_partition ;  
void:objectTarget :reviewed_uniprot_partition
```

***prov:wasDerivedFrom*** - “A derivation is a transformation of an entity into another, an update of an entity resulting in a new one, or the construction of a new entity based on a pre-existing entity.”

# Implementation – 1013 linksets defined

<http://tinyurl.com/pswgo8l>

About: protein\_coding INFERRED\_FROM\_TRANSLATION Uniprot/SWISSPROT linkset



<http://rdf.ebi.ac.uk/dataset/ensembl/76/linkset-3d94016/ef4d6626d4540a5eae81d5e8>

Type: [Linkset](#)

[more types...](#)

## Related to

### **wasDerivedFrom** (Linkset)

- protein NONE Uniprot/SWISSPROT linkset
- protein CHECKSUM Uniprot/SWISSPROT linkset
- protein DEPENDENT Uniprot/SWISSPROT linkset
- protein DIRECT Uniprot/SWISSPROT linkset
- protein SEQUENCE\_MATCH Uniprot/SWISSPROT linkset
- [linkset-transcript-SO\\_translates\\_to\\_protein](#)
- [linkset-transcript-SO\\_transcribed\\_from\\_protein\\_coding](#)

### **linkPredicate** (ObjectProperty)

- [Inferred mapping from translation](#)

### **objectTarget**

- [SWISSPROT-dataset-partition](#)

### **subjectTarget**

- [protein\\_coding-dataset-partition](#)

# Generic query to explore a dataset

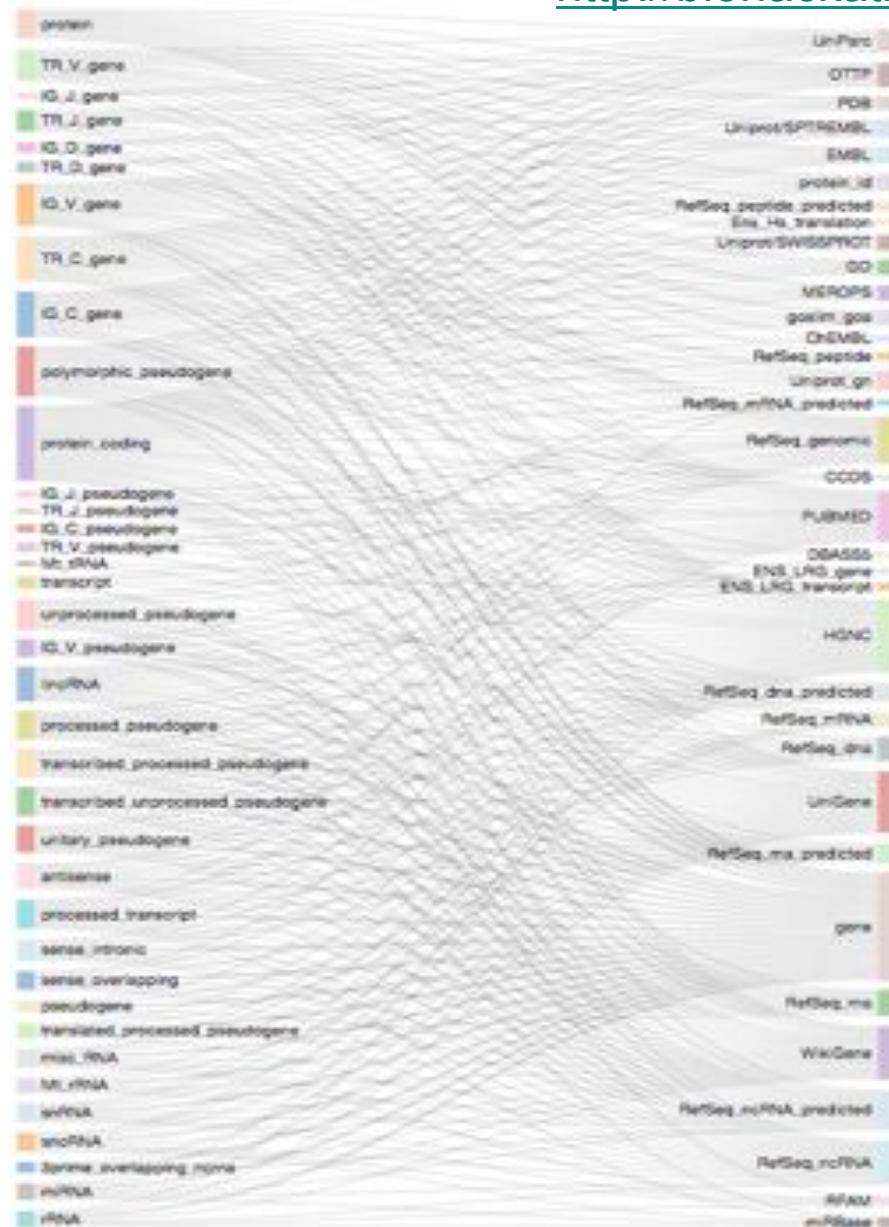
```
PREFIX void:<http://rdfs.org/ns/void#>
PREFIX rdfs:<http://www.w3.org/2000/01/rdf-schema#>

SELECT DISTINCT ?subject ?subject_name ?object ?object_name
WHERE {
    ?linkset a void:Linkset ;
    void:objectTarget [void:class ?object] ;
    void:subjectTarget [void:class ?subject] .
    ?subject rdfs:label ?subject_name .
    ?object rdfs:label ?object_name .
}
```

# Visualising Linksets

<http://tinyurl.com/p3gw7of>

<http://biohackathon.org/d3sparql/>



# Querying convenience links

```
PREFIX void:<http://rdfs.org/ns/void#>
```

```
PREFIX prov:<http://www.w3.org/ns/prov#>
```

```
PREFIX ensemblterms: <http://rdf.ebi.ac.uk/terms/ensembl/>
```

```
PREFIX core: <http://purl.uniprot.org/core/>
```

```
SELECT ?subject ?rel ?object ?derivedLinksetRelation WHERE
```

```
{
```

```
?subject ?rel ?object .
```

```
?subject a ?subjectType .
```

```
?object a ?objectType .
```

```
?linkset void:linkPredicate ?rel .
```

```
?linkset prov:wasDerivedFrom ?derivedLinkset .
```

```
?derivedLinkset void:linkPredicate ?derivedLinksetRelation .
```

```
VALUES ?subjectType {ensemblterms:protein_coding}
```

```
VALUES ?objectType {core:Reviewed_Protein core:Protein}
```

Ensembl gene

UniProt Protein

```
}
```

# Querying convenience links

subject	rel	object	derivedLinksetRelation
ensembl:ENSCAG00000000004	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G367>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001545	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G5C3>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001545	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G5C3>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001305	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G4X0>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001305	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G4X0>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000002395	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G672>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000002395	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G672>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001095	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G4J3>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001095	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G4J3>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000001908	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G5P3>	ensemblTerms:SEQUENCE_MATCH
ensembl:ENSCAG00000000004	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G367>	ensemblTerms:DIRECT
ensembl:ENSCAG00000001545	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G5C3>	ensemblTerms:DIRECT
ensembl:ENSCAG00000001545	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G5C3>	ensemblTerms:DIRECT
ensembl:ENSCAG00000001305	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://purl.uniprot.org/uniprot/H9G4X0>	ensemblTerms:DIRECT
ensembl:ENSCAG00000001305	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G4X0>	ensemblTerms:DIRECT
ensembl:ENSCAG00000002395	ensemblTerms:INFERRED_FROM_TRANSLATION	<http://identifiers.org/uniprot/H9G672>	ensemblTerms:DIRECT

# Utility of the linksets

- Provenance based schema for publishing and sharing linksets across resources
- Tune query precision (scientific lenses)
- Used to assist SPARQL autocomplete widgets
- Potential for use by query optimizers to improve query plans for federated querying

# Is VoID+PROV the right vocabulary for this?

- It's possible that linksets are still over generalisations
  - Semantics aren't well defined
  - Some cases require more fine grained solution (consider % sequence similarity)
- Alternative approaches
  - Nanopublications, Open Biological Associations (OBAN)
  - Property singleton pattern
  - OWL modeling
- Open to other ideas???

# Acknowledgement

- Alasdair Gray and James Malone
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  - Andy Jenkinson, Mark Davies, Marco Brandizi, Sarala Wimalaratne, Leyla Garcia, Jerven Bolleman