

# UniProt, a FAIRness assessment

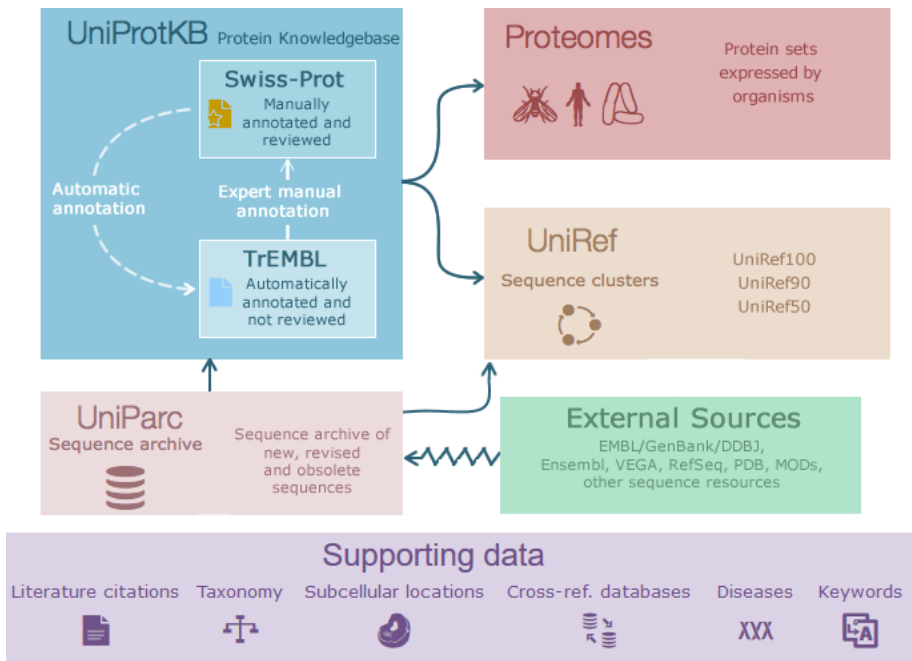
UniProt datasets

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Protein Function Development Team

EMBL-EBI

# UniProt at a glance



## Universal Protein Resource

- Comprehensive resource for protein sequence and annotation data.
- Datasets: UniProt Knowledgebase (UniProtKB), UniProt Reference Clusters (UniRef), UniProt Archive (UniParc) and Proteomes
- Supporting data: Diseases, taxonomy, keywords, subcellular location, citations, cross-references

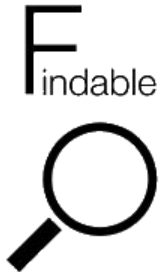
Our FAIR story starts from the website

[schema.org](https://schema.org)



Bioschemas

# UniProt datasets, nearly 100% FAIR



Metric	Assessment
FM-F1A Identifier uniqueness	Stable and unique identifiers → accessions
FM-F1B Identifier persistence	PURL identifiers
FM-F2 Machine readability of metadata	RDF format + VOID file FASTA files + headers XSD for XML
FM-F3 Resource identifier in metadata	PURL included in RDF Accession always provided
FM-F4 Indexed in a searchable resource	Indexed by Google, FAIRsharing, identifiers.org



Metric	Assessment
FM-A1.1 Access protocol	HTTPS for webpages & FTP for downloads
FM-A1.2 Access authorization	Public datasets, not authorization required
FM-A2 Metadata longevity	Entry history always available Archive specialized dataset

# UniProt datasets, nearly 100% FAIR

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Metric	Assessment
FM-I1 Use a knowledge representation language	UniProt ontology for RDF
FM-I2 Use FAIR vocabularies	Uses well-known ontologies whenever possible
FM-I3 Use qualified references	“seeAlso” or “cross-reference” is commonly used

R  
eusable

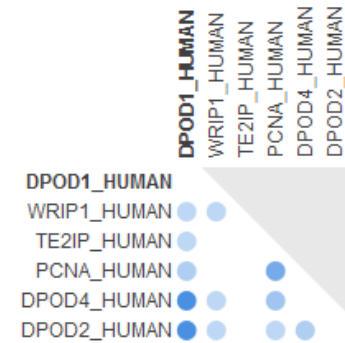
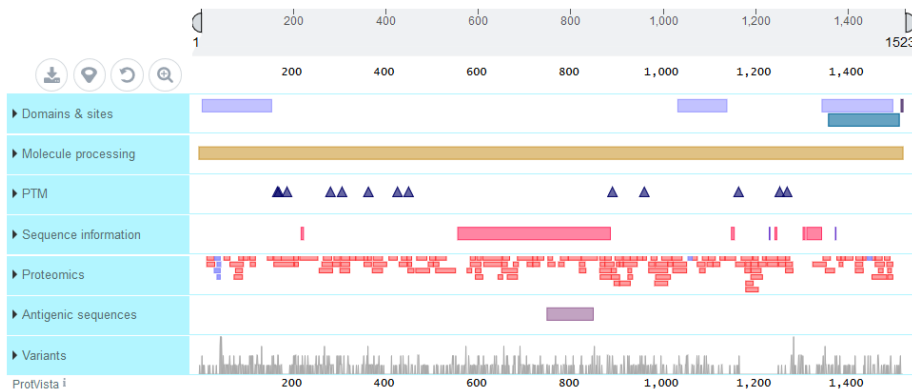


Metric	Assessment
FM-R1.1 Accessible usage license	Creative commons attribution (CC BY 4.0)
FM-R1.2 Detailed provenance	Provided on help pages Machine-readable via VOID for RDF On entries via Evidence Codes
FM-R1.3 Meets community standard	<b>What certification body should be used?</b>

# Tools, looking for FAIRness



ebi-webcomponents & ebi-uniprot



Protein API → <https://www.ebi.ac.uk/protiens/api/doc/>

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## Proteins

The Proteins service provides an interface for accessing UniProtKB entries and UniProtKB isoform entries. The features service provides protein functional annotations from UniProt Knowledgebase (UniProtKB) protein entries. The variation, proteomics and antigen services provide annotations imported and mapped from large scale data sources, such as 1000 Genomes, ExAC (Exome Aggregation Consortium), COSMIC (Catalogue Of Somatic Mutations In Cancer), PeptideAtlas, MaxQB (MaxQuant DataBase), EPD (Encyclopedia of Proteome Dynamics) and HPA, along with UniProtKB annotations for these feature types (if applicable).

The proteins service returns XML, JSON and FASTA formatted results. Features, variation, proteomics and antigen all return XML, JSON and GFF formatted results, with variation also returning PEFF formatted results.

**proteins** [Show/Hide](#) [List Operations](#) [Expand Operations](#)

GET	<a href="/proteins">/proteins</a>	<a href="#">Search UniProt entries</a>
GET	<a href="/proteins/interaction/{accession}">/proteins/interaction/{accession}</a>	<a href="#">Get UniProt interactions by accession</a>
GET	<a href="/proteins/{accession}">/proteins/{accession}</a>	<a href="#">Get UniProt entry by accession</a>
GET	<a href="/proteins/{accession}/isoforms">/proteins/{accession}/isoforms</a>	<a href="#">Get UniProt isoform entries from parent entry accession</a>
GET	<a href="/proteins/{dbtype}:{dbid}">/proteins/{dbtype}:{dbid}</a>	<a href="#">Get UniProt entries by UniProt cross reference and its ID</a>

**features** [Show/Hide](#) [List Operations](#) [Expand Operations](#)

# Conclusions

- FAIRness assessment is not easy
  - Principles are broad
  - Metrics help but are not always clear
  - Certification/validation mechanisms could help but where are they?



# UniProt Team

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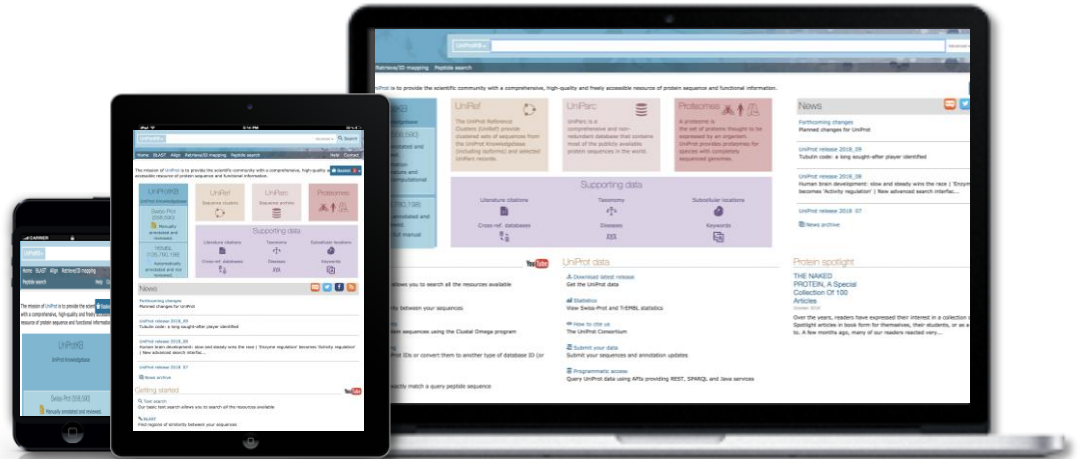
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# Your Feedback Matters!

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