Tools to search, explore and interrogate your proteomics data with UniProt.

Explore key protein features

UniProt protein feature viewer

Integrating proteomics and genomics data with the variant viewer

3D protein structure viewer

- Based on canonical protein sequences.
- Can view protein domains, PTM sites, structural features, proteomic peptides, experimental mutagenesis sites, and natural variants.
- Cross references to publications and mapped databases.
- Selected features are highlighted on protein 3D structure, when available.

Proteins API

www.ebi.ac.uk/proteins/api/doc/

- No programming experience required!
- Structured, multiple query search functionality.
- Example request code in Curl, Perl, Python, Java, and R.
- Programmatic interface for accessing genomic coordinates of UniProt sequences, including isoforms – full genomic coordinates for proteins, exons (including exon sequences), and protein features.
- Downloadable formats; XML, JSON, FASTA, and GFF. Variation data also returns PEFF formatted results (HUPO Proteomics Standards Initiative).

Variation data output

- "wildType": "P",
  "polyphenPrediction": "benign",
  "siftPrediction": "tolerated",
  "siftScore": 0.12625,
  "cytogeneticBand": "3p22.1",
  "consequenceType": "missense",
  "genomicLocation": "NC_000003.12:g.41224558C>A",
  "sourceType": "large_scale_study"

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  "type": "VARIANT",
  "description": ["LSS_COSMIC"]: primary tissue(s): thyroid, large_intestine",
  "alternativeSequence": "V",
  "begin": "20",
  "end": "20",

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