Link <http://www.uniprot.org/manual/sequence_annotation>

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| **Subsection** | **Content** |
| **Molecule processing** |  |
| [Initiator methionine](http://www.uniprot.org/manual/init_met) | Cleavage of the initiator methionine |
| [Signal](http://www.uniprot.org/manual/signal) | Sequence targeting proteins to the secretory pathway or periplasmic space |
| [Transit peptide](http://www.uniprot.org/manual/transit) | Extent of a transit peptide for organelle targeting |
| [Propeptide](http://www.uniprot.org/manual/propep) | Part of a protein that is cleaved during maturation or activation |
| [Chain](http://www.uniprot.org/manual/chain) | Extent of a polypeptide chain in the mature protein |
| [Peptide](http://www.uniprot.org/manual/peptide) | Extent of an active peptide in the mature protein |
| **Regions** |  |
| [Topological domain](http://www.uniprot.org/manual/topo_dom) | Location of non-membrane regions of membrane-spanning proteins |
| [Transmembrane](http://www.uniprot.org/manual/transmem) | Extent of a membrane-spanning region |
| [Intramembrane](http://www.uniprot.org/manual/intramem) | Extent of a region located in a membrane without crossing it |
| [Domain](http://www.uniprot.org/manual/domain) | Position and type of each modular protein domain |
| [Repeat](http://www.uniprot.org/manual/repeat) | Positions of repeated sequence motifs or repeated domains |
| [Calcium binding](http://www.uniprot.org/manual/ca_bind) | Position(s) of calcium binding region(s) within the protein |
| [Zinc finger](http://www.uniprot.org/manual/zn_fing) | Position(s) and type(s) of zinc fingers within the protein |
| [DNA binding](http://www.uniprot.org/manual/dna_bind) | Position and type of a DNA-binding domain |
| [Nucleotide binding](http://www.uniprot.org/manual/np_bind) | Nucleotide phosphate binding region |
| [Region](http://www.uniprot.org/manual/region) | Region of interest in the sequence |
| [Coiled coil](http://www.uniprot.org/manual/coiled) | Positions of regions of coiled coil within the protein |
| [Motif](http://www.uniprot.org/manual/motif) | Short (up to 20 amino acids) sequence motif of biological interest |
| [Compositional bias](http://www.uniprot.org/manual/compbias) | Region of compositional bias in the protein |
| **Sites** |  |
| [Active site](http://www.uniprot.org/manual/act_site) | Amino acid(s) directly involved in the activity of an enzyme |
| [Metal binding](http://www.uniprot.org/manual/metal) | Binding site for a metal ion |
| [Binding site](http://www.uniprot.org/manual/binding) | Binding site for any chemical group (co-enzyme, prosthetic group, etc.) |
| [Site](http://www.uniprot.org/manual/site) | Any interesting single amino acid site on the sequence |
| **Amino acid modifications** |  |
| [Non-standard residue](http://www.uniprot.org/manual/non_std) | Occurence of non-standard amino acids (selenocysteine and pyrrolysine) in the protein sequence |
| [Modified residue](http://www.uniprot.org/manual/mod_res) | Modified residues excluding lipids, glycans and protein cross-links |
| [Lipidation](http://www.uniprot.org/manual/lipid) | Covalently attached lipid group(s) |
| [Glycosylation](http://www.uniprot.org/manual/carbohyd) | Covalently attached glycan group(s) |
| [Disulfide bond](http://www.uniprot.org/manual/disulfid) | Cysteine residues participating in disulfide bonds |
| [Cross-link](http://www.uniprot.org/manual/crosslnk) | Residues participating in covalent linkage(s) between proteins |
| **Natural variations** |  |
| [Alternative sequence](http://www.uniprot.org/manual/var_seq) | Amino acid change(s) producing alternate protein isoforms |
| [Natural variant](http://www.uniprot.org/manual/variant) | Description of a natural variant of the protein |
| **Experimental info** |  |
| [Mutagenesis](http://www.uniprot.org/manual/mutagen) | Site which has been experimentally altered by mutagenesis |
| [Sequence uncertainty](http://www.uniprot.org/manual/unsure) | Regions of uncertainty in the sequence |
| [Sequence conflict](http://www.uniprot.org/manual/conflict) | Description of sequence discrepancies of unknown origin |
| [Non-adjacent residues](http://www.uniprot.org/manual/non_cons) | Indicates that two residues in a sequence are not consecutive |
| [Non-terminal residue](http://www.uniprot.org/manual/non_ter) | The sequence is incomplete. Indicate that a residue is not the terminal residue of the complete protein |
| **Secondary structure** |  |
| [Helix](http://www.uniprot.org/manual/helix) | Helical regions within the experimentally determined protein structure |
| [Turn](http://www.uniprot.org/manual/turn) | Turns within the experimentally determined protein structure |
| [Beta strand](http://www.uniprot.org/manual/strand) | Beta strand regions within the experimentally determined protein structure |