

PAF guidelines

The file format comprises 20 tab-delimited fields

Column	Column Title	Description	Example
1	PRO_ID	PRO identifier, mandatory	PRO:000000971
2	Object_term	Name of the PRO term, Mandatory, cardinality 1	voltage-gated potassium channel subunit KCNA10 isoform 1
3	Object_synonym	Other names by which the described object is known, Optional field. Cardinality 0, 1 or >1. Separated by (e.g. smad5beta smad5b)	smad5beta (for smad5 isoform 2)
4	Modifier (ex Qualifier)	Modifiers are used within an annotation to modify a relation between a PRO term (protein) and another term (which can be internal or external to PRO). It includes the qualifiers used by GO: NOT , and contributes_to . And also includes decreased , increased and altered (see table 2 below for more information). This field is not mandatory; cardinality 0, 1, >1; for cardinality >1 use a pipe to separate entries (e.g. NOT contributes_to).	NOT
5	Relation	Relation to the corresponding annotation. For the list of relations used in PRO see table 3 below. Mandatory, cardinality 1.	participates_in
6	Ontology_ID	ID for the corresponding annotation. Mandatory, cardinality 1.	GO:0007368
7	Ontology_term	Term name for the corresponding ontology ID (linked to column 6). Mandatory, cardinality 1.	determination of left/right symmetry
8	Relative_to	The column contains a PRO identifier. Modifiers increased, decreased and altered require an entry in this column to indicate what the change is relative to.	PRO:000000074
9	Interaction_with	To indicate binding partner. For GO component complex and GO function protein binding. If possible indicate the most exact protein object by using PRO ID. If part of a complex please add the GO ID for the corresponding one. Not mandatory, cardinality 0 or 1.	PRO ID UniProtKB Ac GO ID (complex)
10	Evidence_source	Pubmed ID or database source for the evidence. Mandatory, cardinality 1. (or >1?)	PMID:17227845 PIRSF:PIRSF03791
11	Taxon	Taxon identifier for the species that the annotation is extracted from. Related to column 9. Not mandatory, cardinality 0 or 1.	TaxID:10090
12	Evidence_code	At the ProEvo level, the evidence code is ISS (inferred by sequence and/or structural similarity) At the protein form level only experimental evidence codes are allowed. If no expertise in evidence code assignation please use EXP	IDA (inferred from direct assay)

		(experimental evidence) as a general code. For GO term protein binding, the evidence code should be IPI. From GOA source: see the GO evidence code guide for the list of valid evidence codes for GO annotations. This field is mandatory for GO terms, cardinality 1.	
13	Inferred_from	This field is used only for certain types of evidence code: IPI and ISS for PRO. Cardinality 0, 1, >1; for cardinality >1 use a pipe to separate entries (e.g. PANTHER:PTHR13703:SF17 PIRSF:PIRSF50050). If EXP is used then	If Evidence code IPI UniProtKB:Q80W99-1 PRO:000000693
14	DB_ID	GOA Source:one or more unique identifiers for a single source cited as an authority for the attribution of the ontology ID to the DB_Object_ID . This may be a literature reference or a database record. The syntax is DB:accession_number.	UniProt_VAR:VAR_017607 UniProtKB:Q80W99-1
15	Protein_region	When the protein object is not the full sequence the amino acid region span is added. The residue span region refers to the sequence displayed in column 13. Not mandatory, cardinality 0 or 1.	154-861
16	Modified_residue(s), MOD_ID	To indicate the residue(s) that has undergone a post-translational modification and the type of modification. Format: 3 letter code residue-#, MOD_ID. The residue number refers to the sequence displayed in column 13. Not mandatory, cardinality 0,1 or >1. If more than one residue modified with same modification then separate residues using / . If more than one type of modification then separate them by pipes .	Cys-190, MOD:00113 Cys-20/Cys-190, MOD:00113 Cys-190, MOD:00113 Ser-200, MOD:00046
17	Date	From GOA source: Date on which the annotation was made; format is YYYYMMDD this field is mandatory, cardinality 1.	20080808
18	Assigned_by	The database which made the annotation. This field is mandatory, cardinality 1. Format: Source DB:curator initials.	PRO:CNA or MGI:HJD
19	Equivalent_forms	List the equivalent form in other organisms. Not mandatory, cardinality 0 or 1.	UniProtKB:P47928-1, P41139-1
20	Comments	Curator comment for some annotations	Free text

Modifiers:

Table 2. Modifiers used for ontology annotation: column 4

Modifier	Definition										
NOT	<p><i>negation of the relation indicated.</i></p> <p>Can be used with:</p> <table><tr><td>participates_in</td><td>(a biological process)</td></tr><tr><td>part_of</td><td>(a complex)</td></tr><tr><td>located_in</td><td>(a cellular component)</td></tr><tr><td>has_function</td><td>(a molecular function)</td></tr><tr><td>has_part</td><td>(a domain)</td></tr></table> <p>Comment: This is used when a PRO term is known to not have the quality indicated by the relation. Example: PRO:000000652</p>	participates_in	(a biological process)	part_of	(a complex)	located_in	(a cellular component)	has_function	(a molecular function)	has_part	(a domain)
participates_in	(a biological process)										
part_of	(a complex)										
located_in	(a cellular component)										
has_function	(a molecular function)										
has_part	(a domain)										
contributes_to	<p><i>enables in some (possibly unknown) way.</i></p> <p>Can be used with:</p> <p>has_function</p> <p>Comment: Only applies to a protein when describing the function of a complex in which it is found. See http://www.geneontology.org/GO.annotation.conventions.shtml#contributes_to. Example: PRO:000000682</p>										
decreased	<p><i>less able relative to normal.</i></p> <p>Can be used with:</p> <p>has_function</p> <p>Comment 1: Indicates that the protein performs the function less efficiently than the form indicated in the Relative_to column.</p> <p>Comment 2: It is mandatory to fill the column Relative_to with the PRO ID corresponding to the protein of reference. Example: PRO:000002609 relative_to PRO:000002605</p>										
increased	<p><i>more able relative to normal.</i></p> <p>Can be used with:</p> <p>has_function</p> <p>Comment 1: Indicates that the protein performs the function more efficiently than the form indicated in the Relative_to column.</p> <p>Comment 2: It is mandatory to fill the column Relative_to with the PRO ID corresponding to the protein of reference. Example: PRO:00000563 relative_to PRO:000002529</p>										
altered	<p><i>different from the indicated entity, but not in a more-or-less-able way.</i></p> <p>Can be used with:</p> <p>has_function part_of</p> <p>Comment: Indicates that the indicated quality differs in some way from the form indicated in the Relative_to column, but “some way” does not include ability.</p>										

	<p>When used with part_of, it indicates that the association of the protein with the complex is unusual in some way (or the complex itself is unusual). Like contributes_to (see below), “altered part_of” is a place holder combination that will disappear once annotations are made directly to the complex (the unusual complex will become an entity directly).</p> <p>Example: PRO:000000760 relative_to PRO:000002604</p>
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Relations:

Table 3. Relations used for ontology annotation: for column 5

Relation	Ontology	Definition
part_of	GO Component complexes	http://www.obofoundry.org/ro/#OBO_REL:part_of
located_in	GO component subcellular location	http://www.obofoundry.org/ro/#OBO_REL:located_in
has_part	Domain (interpro/pfam)	Inverse of part_of
has_agent	SO mutation causing....	http://www.obofoundry.org/ro/#OBO_REL:has_agent
has_function	GO molecular function	RO_proposed (alt_id OBO_REL:0000031)
participates_in	GO biological process	Inverse relation of has_participant http://www.obofoundry.org/ro/#OBO_REL:has_participant
agent_in	Disease (MIM)	Inverse of has_agent
has_modification	PSI-MOD	Relation between an independent continuant and a modification