

PAF guidelines

The file format comprises 17 tab-delimited fields.

Column	Column Title	Description	Example
1	PRO_ID	PRO identifier, mandatory	PR: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)	smad5 beta (for PR:000000478)
4	Modifier	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 (for GO:0007368)
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.	PR: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	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 (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.	IDA (inferred from direct assay)
12	Taxon	Taxon identifier for the species that the annotation is extracted from. Related to column 9. Not mandatory,	NCBITaxon:10090

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		cardinality 0 or 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:PIRSF500500).	If Evidence code IPI UniProtKB:Q80W99-1 PR: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	Date	From GOA source: Date on which the annotation was made; format is YYYYMMDD this field is mandatory, cardinality 1.	20080808
16	Assigned_by	The database which made the annotation. This field is mandatory, cardinality 1. Format: Source DB:curator initials.	PRO:CNA or TLR=AMM
17	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 border="0"> <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>capable_of</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: PR:000025936</p>	participates_in	(a biological process)	part_of	(a complex)	located_in	(a cellular component)	capable_of	(a molecular function)	has_part	(a domain)
participates_in	(a biological process)										
part_of	(a complex)										
located_in	(a cellular component)										
capable_of	(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>capable_of</p> <p>Comment: Only applies to a protein when describing the function of a complex in which it is found. See http://purl.obolibrary.org/obo/RO_0002326 Example: PR:Q9WVC5-1</p>										
decreased	<p><i>less able relative to normal.</i></p> <p>Can be used with:</p> <p>capable_of participates_in</p> <p>Comment 1: Indicates that the protein performs the function less efficiently than the form indicated in the Relative_to column. For participates_in indicates that involvement of the protein or complex in the process is less favored relative to normal.</p> <p>Comment 2: It is mandatory to fill the column Relative_to with the PRO ID corresponding to the protein of reference. Example: PR:000002609 relative_to PR:000002605</p>										
increased	<p><i>more able relative to normal.</i></p> <p>Can be used with:</p> <p>capable_of participates_in</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>capable_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. 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). Example: PR:000000854 relative_to PR:000002622</p>										

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Relations:

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

Relation	Ontology	Definition
expressed_in	CL cell type	http://purl.obolibrary.org/obo/RO_0002206
located_in	GO component subcellular location	http://purl.obolibrary.org/obo/RO_0001025
has_part	Domain/modifications	http://purl.obolibrary.org/obo/BFO_0000051
has_function	GO molecular function	http://purl.obolibrary.org/obo/RO_0000085
participates_in	GO biological process	http://purl.obolibrary.org/obo/RO_0000056
associated_with_disease_progression associated_with_disease_suppression	Disease (DO)	Relation between protein or protein complex and disease. Relation could be direct or indirect.
has_role	ChEBI biomarker	http://purl.obolibrary.org/obo/RO_0000087
part_of	GO complex	http://purl.obolibrary.org/obo/BFO_0000050