PAF guidelines

The file format comprises 19 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)	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.	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)

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12	**Taxon**	Taxon identifier for the species that the annotation is extracted from. Related to column 9. Not mandatory, cardinality 0 or 1.	NCBITaxon:10090
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	**Protein_region**	For proteolytic products the amino acid region span is added. The residue span region is in reference 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 that 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 TLR=AMM
19	**Comments**	Curator comment for some annotations	Free text

Modifiers:

Table 2. Modifiers used for ontology annotation: column 4

Modifier	Definition
NOT	*negation of the relation indicated*. Can be used with: participates_in (a biological process) part_of (a complex) located_in (a cellular component) has_function (a molecular function) has_part (a domain) Comment: This is used when a PRO term is known to not have the quality indicated by the relation. Example: PR:000000652
contributes_to	*enables in some (possibly unknown) way*.

	Can be used with: has_function 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: PR:000000682

decreased	*less able relative to normal*.
	  Can be used with:
	     has_function
	     participates_in
	
	Comment 1: Indicates that the protein performs the function less efficiently that 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.
	
	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

increased	*more able relative to normal*.
	  Can be used with:
	     has_function
	     participates_in
	
	Comment1: For has_function indicates that the protein performs the function more efficiently that the form indicated in the Relative_to column. For participates_in indicates that involvement of the protein or complex in the process is favored.
	
	Comment 2: It is mandatory to fill the column Relative_to with the PRO ID corresponding to the protein of reference.
	Example: PR:000000563 relative_to PR:000002529

altered	*different from the indicated entity, but not in a more-or-less-able way*.
	  Can be used with:
	     has_function
	
	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:000000760 relative_to PR:000002604

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	http://www.obofoundry.org/ro/#OBO_REL:located_in

	location	
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
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_modification	PSI-MOD	Relation between an independent continuant and a modification