PAF guidelines

The file format comprises 19 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	Qualifier	GOA source: flags that modify the interpretation of an annotation one (or more) of **NOT**, contributes_to, colocalizes_with 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 2 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	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)
9	Evidence_source	Pubmed ID or database source for the evidence. Mandatory, cardinality 1. (or >1?)	PMID:17227845 PIRSF:PIRSF03791
10	Taxon	Taxon identifier for the species that the annotation is extracted from. Related to column 9. Not mandatory, cardinality 0 or 1.	TaxID:10090
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	Inferred_from	This field is used only for certain types of evidence	If Evidence code IPI

		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 EXP is used then	UniProtKB:Q80W99-1| PRO:000000693
13	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.	UniProtKB:VAR_017607 UniProtKB:Q80W99-1
14	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
15	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
16	Date	From GOA source: Date on which the annotation was made; format is YYYYMMDD this field is mandatory, cardinality 1.	20080808
17	Assigned_by	The database which made the annotation. This field is mandatory, cardinality 1. Format: Source DB:curator initials.	PRO:CNA or MGI:HJD
18	Equivalent forms	List the equivalent form in other organisms. Not mandatory, cardinality 0 or 1.	UniProtKB:P47928-1, P41139-1
19	Comments	Curator comment for some annotations	Free text

Table 2. 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