

PAG 1

PDH 1.1

accession = Prot A.1
name="interaction FDR" value="1001.a:256:0.001:TRUE
name="interaction FDR" value="1002.a:478:0.07:FALSE

PDH 1.2

accession = Prot A.2
name="interaction FDR" value="1001.a:258:0.001:TRUE
name="interaction FDR" value="1002.a:480:0.07:TRUE

PAG 2

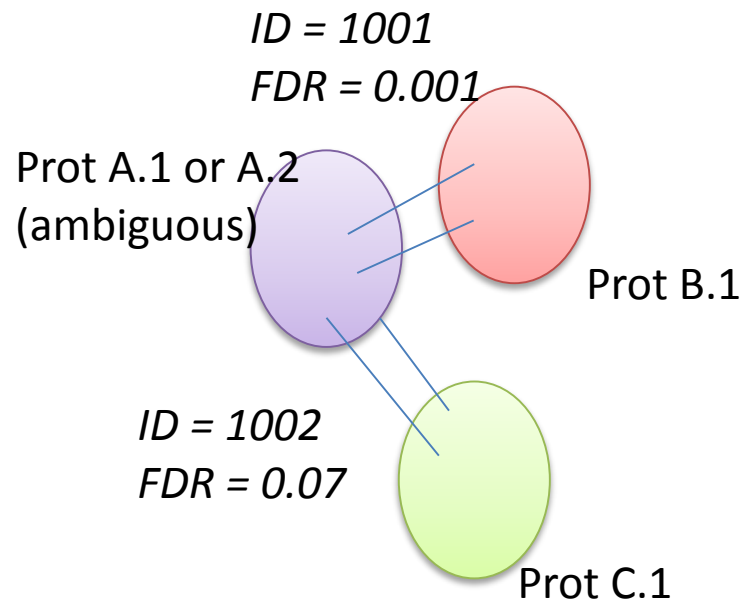
PDH 2.1

accession = Prot B.1
name="interaction FDR" value="1001.b:135:0.001:TRUE

PAG 3

PDH 1.1

accession = Prot A.1
name="interaction FDR" value="1002.b:135:0.07:FALSE



Explanation

IDs on Proteins are to name and describe the overall interaction evidence (potentially based off multiple peptides) for the pairwise interaction.

In mzIdentML, they will be represented by different ProteinDetectionHypothesis (PDH) elements within different ProteinAmbiguityGroup (PAG) elements, sharing the same ID and score.

These CV terms must have a paired structure of
int_ID.a | b:POS | null:SCORE_OR_VALUE:PASS_THRESHOLD



1)



2)



3)



4)

- 1) The two partners in the interaction share the same *integer* value for ID followed by *a* or *b*. If there is ambiguity in protein identification, two different ProteinDetectionHypothesis (PDH) elements, within the same ProteinAmbiguityGroup (PAG), MAY share the same ID and suffix (a or b). A given identifier (integer and suffix) value MUST NOT be used in more than PAG.
- 2) The export software MAY indicate the general position of the interaction (potentially taking on board multiple pairs of cross-linked peptides), with respect to the protein sequence – using a 1-based counting system. A “null” MAY be used if the export software does not wish to include a value.
- 3) The score or statistical value for the interaction.
- 4) “true” or “false” to indicate whether the score or value has passed a reported threshold in the file.