1. CHROM – Protein chromosome/scaffold.
2. POS within Protein – Position of the variation.
3. ID – Variation ID. Each variation has an unique id (within one proVcf file)
4. REF – Reference amino acid.
5. ALT – ORF amino acid.
6. QUAL – Average q-value of the peptides supporting the variation or ‘-1’ if there is no peptide evidence.
7. FILTER – TRANS or PASS. TRANS means the variation only has transcript level evidence. ‘PASS’ means it has peptide evidence as well.
8. INFO – Info column has several values. If vcf file is for peptide evidence, it will have four extra field.

INFO fields:

1. SubjectID - Protein/reference sequence ID.
2. QueryID – ORF ID.
3. Alignment – Alignment tells us about the mapping between the Reference and the ORF. It has six sub fields.
   1. QueryLength – Length of the ORF.
   2. QueryStart – Start location of the alignment within the ORF.
   3. QueryEnd – End location of the alignment within the ORF.
   4. SubjectLength – Length of the reference sequence.
   5. SubjectStart – Start location of the alignment within the reference/protein sequence
   6. SubjectEnd – End location of the alignment within the reference/protein sequence.
4. Type – Variation type, six possible values. i.e. SAP, SSAP, ALT, SALT, INS, DEL
5. QPOS – Position of the variation in respect to the ORF sequence.
6. PeptideCount – Number of peptide supports this
7. UniquePeptideCount - Number of unique peptide
8. Peptides – unique peptide sequence
9. Score – score represents the quality/reliability of the variation