

## Use of template for data import in HCPprofiler software

### Template\_Proteins.txt

- **Accession** – Column A: Enter 1 protein accession number per line in this column
- **Description** – Column B: Enter the protein description
- **MW [kDa]** – Column C: Enter the molecular weight in kilodalton
- **Calc. pI** – Column D: Enter the calculated isoelectric point of the protein (if possible, if not it can be empty)

*This file is for the protein information allowing the quantity calculations and chart representations.*

*Please note that the HCPprofiler protein nomenclature must be as follows:  
"sp|ANAQUANT-1|ANAQUANT-1" in the Accession column.*

### Template\_PeptideGroups.txt

- **Sequence** - Column A: Enter one peptide sequence per line
- **Modifications** - Column B: Modification information (1 per line, so a same peptide sequence can be in several lines with or without different modification)
- **Master Protein Accessions** - Column C: Enter the accession number of the protein. If there are several proteins in the same sequence, follow this nomenclature: Protein1; Protein2
- Column D: Empty
- Column E: Empty
- Column F: Empty (the information is already in the Template\_Proteins file)
- Column G: Empty
- **Abundance** – Column H: Peptide raw abundance

*If fractionation, enter each abundance in column H, I, J...*

*Please note that the HCPprofiler protein nomenclature must be as follows:  
"sp|ANAQUANT-1|ANAQUANT-1" in the Master Protein Accessions column.*

### HCPprofiler software

1. Create a **New project**
2. Click on **Import new sample**
3. Select **Proteom Discoverer** software
4. Click on **Select "\_PeptideGroups.txt" and "\_Proteins.txt"**
5. Select your data files **"\_PeptideGroups.txt"** and **"\_Proteins.txt"**
6. Click on **Next**
7. Enter your sample information

**Import New Sample**

Sample name  
Sample 1\_HCPprofiler

Fractionnement ☐ BEADS diluted into sample ☒

Final Sample volume: 150 µL Injected volume: 2 µL

Quality control accession - opt: CQ-1 Injected QC quantity - opt: X fmol

Drug substance (Accession) - opt: DS Isoelectric Point - opt:  Injected drug substance quantity - opt: 266 ng

**Import Sample →**

Possibility of adding a quality control before the digestion step  
**Example with BSA:**  
- Proline: sp|P02769|ALBU\_BOVIN  
- Proteome Discoverer: P02769

Not necessary with proteome discoverer

8. Click on **Import Sample**