Protein groups

The Protein Groups table contains information on the identified proteins in the processed raw-files. Each single row contains the group of proteins that could be reconstructed from a set of peptides.

Name	Separator	Description
Protein IDs		Identifier(s) of protein(s) contained in the protein group. They are sorted by number of identified peptides in descending order.
Majority protein IDs		These are the IDs of those proteins that have at least half of the peptides that the leading protein has.
Peptide counts (all)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Peptide counts (razor+unique)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Peptide counts (unique)		Number of peptides associated with each protein in protein group, occuring in the order as the protein IDs occur in the 'Protein IDs' column. Here distinct peptide sequences are counted. Modified forms or different charges are counted as one peptide.
Protein names		Name(s) of protein(s) contained within the group.
Gene names		Name(s) of the gene(s) associated to the protein(s) contained within the group.
Fasta headers		Fasta headers(s) of protein(s) contained within the group.
Proteins		Number of proteins contained within the group. This corresponds to the number of entries in the colum 'Protein IDs'.
Peptides		The total number of peptide sequences associated with the protein group (i.e. for all the proteins in the group).
Razor + unique peptides		The total number of razor + unique peptides associated with the protein group (i.e. these peptides are shared with another protein group).
Unique peptides		The total number of unique peptides associated with the protein group (i.e. these peptides are not shared with another protein group).
Peptides 0h_1		
Peptides 0h_2		
Peptides 0h_3		
Peptides BSA_1		
Peptides BSA_2		
Peptides BSA_3		
Peptides FN_1		
Peptides FN_2		
Peptides FN_3		
Peptides GFR_1		
Peptides GFR_2		
Peptides GFR_3		
Peptides LAM_1		
Peptides LAM_2		
Peptides LAM_3		
Peptides Matr 12h_1		
Peptides Matr 12h_2		
Peptides Matr 12h_3		
Peptides Matr 24h_1		
Peptides Matr 24h_2		
Peptides Matr 24h_3		
Peptides Matr 30h_1		
Peptides Matr 30h_2		
Peptides Matr 30h_3		
Peptides Matr dil_1		
Peptides Matr dil_2		
Peptides Matr dil_3		
Razor + unique peptides 0h_1		

Razor + unique peptides 0h_2		
Razor + unique peptides 0h_3		
Razor + unique peptides BSA_1		
Razor + unique peptides BSA_2		
Razor + unique peptides BSA_3		
Razor + unique peptides FN_1		
Razor + unique peptides FN_2		
Razor + unique peptides FN_3		
Razor + unique peptides GFR_1		
Razor + unique peptides GFR_2		
Razor + unique peptides GFR_3		
Razor + unique peptides LAM_1		
Razor + unique peptides LAM_2		
Razor + unique peptides LAM_3		
Razor + unique peptides Matr 12h_1		
Razor + unique peptides Matr 12h_2		
Razor + unique peptides Matr 12h_3		
Razor + unique peptides Matr 24h_1		
Razor + unique peptides Matr 24h_2		
Razor + unique peptides Matr 24h_3		
Razor + unique peptides Matr 30h_1		
Razor + unique peptides Matr 30h_2		
Razor + unique peptides Matr 30h_3		
Razor + unique peptides Matr dil_1		
Razor + unique peptides Matr dil_2		
Razor + unique peptides Matr dil_3		
Unique peptides 0h_1		
Unique peptides 0h_2		
Unique peptides 0h_3		
Unique peptides BSA_1		
Unique peptides BSA_2		
Unique peptides BSA_3		
Unique peptides FN_1		
Unique peptides FN_2		
Unique peptides FN_3		
Unique peptides GFR_1		
Unique peptides GFR_2		
Unique peptides GFR_3		
Unique peptides LAM_1		
Unique peptides LAM_2		
Unique peptides LAM_3		
Unique peptides Matr 12h_1		
Unique peptides Matr 12h_2		
Unique peptides Matr 12h_3		
Unique peptides Matr 24h_1		
Unique peptides Matr 24h_2		
Unique peptides Matr 24h_3		
Unique peptides Matr 30h_1		
Unique peptides Matr 30h_2		
Unique peptides Matr 30h_3		
Unique peptides Matr dil_1		
Unique peptides Matr dil_2		
Unique peptides Matr dil_3		
Sequence coverage [%]		Percentage of the sequence that is covered by the identified peptides of the best protein sequence contained in the group.
Unique + razor sequence coverage [%]		Percentage of the sequence that is covered by the identified unique and razor peptides of the best protein sequence contained in the group.

Unique sequence coverage [%]		Percentage of the sequence that is covered by the identified unique peptides of the best protein sequence contained in the group.
Mol. weight [kDa]		Molecular weight of the leading protein sequence contained in the protein group.
Sequence length		The length of the leading protein sequence contained in the group.
Sequence lengths		The length of all sequences of the proteins contained in the group.
Slice average		
Slice 1		
Slice 2		
Slice 3		
Slice 4		
Slice 5		
Slice 6		
Slice 7		
Slice 8		
Slice 9		
Slice 10		
Slice 11		
Slice 12		
Slice 13		
Slice 14		
Slice 15		
Slice 16		
Slice 17		
Slice 18		
Slice 31		
Slice 32		
Slice 33		
Slice 34		
Slice 35		
Slice 36		
Slice 37		
Slice 38		
Slice 39		
Slice 40		
Slice 41		
Slice 42		
Slice 43		
Slice 44		
Slice 45		
Slice 46		
Slice 47		
Slice 48		
Slice 61		
Slice 62		
Slice 63		
Slice 64		
Slice 65		
Slice 66		
Slice 67		
Slice 68		
Slice 69		
Slice 70		
Slice 71		
Slice 72		
Slice 73		
Slice 74		
Slice 75		
Slice 76		
Slice 77		
Slice 78		
Experiment 0h_1		

Experiment 0h_2		
Experiment 0h_3		
Experiment BSA_1		
Experiment BSA_2		
Experiment BSA_3		
Experiment FN_1		
Experiment FN_2		
Experiment FN_3		
Experiment GFR_1		
Experiment GFR_2		
Experiment GFR_3		
Experiment LAM_1		
Experiment LAM_2		
Experiment LAM_3		
Experiment Matr 12h_1		
Experiment Matr 12h_2		
Experiment Matr 12h_3		
Experiment Matr 24h_1		
Experiment Matr 24h_2		
Experiment Matr 24h_3		
Experiment Matr 30h_1		
Experiment Matr 30h_2		
Experiment Matr 30h_3		
Experiment Matr dil_1		
Experiment Matr dil_2		
Experiment Matr dil_3		
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Ratio H/L		The ratio between two heavy and light label partners.
Ratio H/L normalized		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%]		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count		Number of redundant peptides used for quantitation.
Ratio H/L 0h_1		The ratio between two heavy and light label partners.
Ratio H/L normalized 0h_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] 0h_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count 0h_1		Number of redundant peptides used for quantitation.
Ratio H/L 0h_2		The ratio between two heavy and light label partners.
Ratio H/L normalized 0h_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] 0h_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count 0h_2		Number of redundant peptides used for quantitation.
Ratio H/L 0h_3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0h_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] 0h_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count 0h_3		Number of redundant peptides used for quantitation.
Ratio H/L BSA_1		The ratio between two heavy and light label partners.
Ratio H/L normalized BSA_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] BSA_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count BSA_1		Number of redundant peptides used for quantitation.
Ratio H/L BSA_2		The ratio between two heavy and light label partners.
Ratio H/L normalized BSA_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] BSA_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.

Ratio H/L count BSA_2		Number of redundant peptides used for quantitation.
Ratio H/L BSA_3		The ratio between two heavy and light label partners.
Ratio H/L normalized BSA_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] BSA_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count BSA_3		Number of redundant peptides used for quantitation.
Ratio H/L FN_1		The ratio between two heavy and light label partners.
Ratio H/L normalized FN_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] FN_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count FN_1		Number of redundant peptides used for quantitation.
Ratio H/L FN_2		The ratio between two heavy and light label partners.
Ratio H/L normalized FN_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] FN_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count FN_2		Number of redundant peptides used for quantitation.
Ratio H/L FN_3		The ratio between two heavy and light label partners.
Ratio H/L normalized FN_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] FN_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count FN_3		Number of redundant peptides used for quantitation.
Ratio H/L GFR_1		The ratio between two heavy and light label partners.
Ratio H/L normalized GFR_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] GFR_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count GFR_1		Number of redundant peptides used for quantitation.
Ratio H/L GFR_2		The ratio between two heavy and light label partners.
Ratio H/L normalized GFR_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] GFR_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count GFR_2		Number of redundant peptides used for quantitation.
Ratio H/L GFR_3		The ratio between two heavy and light label partners.
Ratio H/L normalized GFR_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] GFR_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count GFR_3		Number of redundant peptides used for quantitation.
Ratio H/L LAM_1		The ratio between two heavy and light label partners.
Ratio H/L normalized LAM_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] LAM_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count LAM_1		Number of redundant peptides used for quantitation.
Ratio H/L LAM_2		The ratio between two heavy and light label partners.
Ratio H/L normalized LAM_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] LAM_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count LAM_2		Number of redundant peptides used for quantitation.
Ratio H/L LAM_3		The ratio between two heavy and light label partners.
Ratio H/L normalized LAM_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] LAM_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count LAM_3		Number of redundant peptides used for quantitation.
Ratio H/L Matr 12h_1		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 12h_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.

Ratio H/L variability [%] Matr 12h_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 12h_1		Number of redundant peptides used for quantitation.
Ratio H/L Matr 12h_2		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 12h_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 12h_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 12h_2		Number of redundant peptides used for quantitation.
Ratio H/L Matr 12h_3		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 12h_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 12h_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 12h_3		Number of redundant peptides used for quantitation.
Ratio H/L Matr 24h_1		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 24h_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 24h_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 24h_1		Number of redundant peptides used for quantitation.
Ratio H/L Matr 24h_2		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 24h_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 24h_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 24h_2		Number of redundant peptides used for quantitation.
Ratio H/L Matr 24h_3		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 24h_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 24h_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 24h_3		Number of redundant peptides used for quantitation.
Ratio H/L Matr 30h_1		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 30h_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 30h_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 30h_1		Number of redundant peptides used for quantitation.
Ratio H/L Matr 30h_2		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 30h_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 30h_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 30h_2		Number of redundant peptides used for quantitation.
Ratio H/L Matr 30h_3		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr 30h_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr 30h_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr 30h_3		Number of redundant peptides used for quantitation.
Ratio H/L Matr dil_1		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr dil_1		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr dil_1		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr dil_1		Number of redundant peptides used for quantitation.
Ratio H/L Matr dil_2		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr dil_2		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr dil_2		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr dil_2		Number of redundant peptides used for quantitation.

Ratio H/L Matr dil_3		The ratio between two heavy and light label partners.
Ratio H/L normalized Matr dil_3		Normalized ratio between two medium and light label partners. The median of the total ratio population was shifted to 1.
Ratio H/L variability [%] Matr dil_3		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the naturally logarithmized ratios times 100.
Ratio H/L count Matr dil_3		Number of redundant peptides used for quantitation.
Sequence coverage 0h_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage 0h_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage 0h_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage BSA_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage BSA_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage BSA_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage FN_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage FN_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage FN_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage GFR_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage GFR_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage GFR_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage LAM_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage LAM_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage LAM_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 12h_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 12h_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 12h_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 24h_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 24h_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 24h_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 30h_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 30h_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr 30h_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.

Sequence coverage Matr dil_1 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr dil_2 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Sequence coverage Matr dil_3 [%]		Percentage of the sequence that is covered by the identified peptides in this sample of the longest protein sequence contained within the group.
Intensity		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity 0h_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L 0h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H 0h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity 0h_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L 0h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H 0h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity 0h_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L 0h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H 0h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity BSA_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L BSA_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H BSA_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity BSA_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L BSA_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H BSA_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity BSA_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L BSA_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H BSA_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity FN_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L FN_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H FN_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity FN_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L FN_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H FN_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity FN_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L FN_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H FN_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity GFR_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L GFR_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H GFR_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity GFR_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L GFR_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H GFR_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity GFR_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L GFR_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H GFR_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity LAM_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L LAM_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H LAM_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity LAM_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L LAM_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H LAM_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity LAM_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L LAM_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H LAM_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 12h_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 12h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 12h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 12h_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 12h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 12h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 12h_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 12h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 12h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.

Intensity Matr 24h_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 24h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 24h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 24h_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 24h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 24h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 24h_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 24h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 24h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 30h_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 30h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 30h_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 30h_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 30h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 30h_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr 30h_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr 30h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr 30h_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr dil_1		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr dil_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr dil_1		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr dil_2		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr dil_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr dil_2		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Intensity Matr dil_3		Summed up eXtracted Ion Current (XIC) of all isotopic clusters associated with the identified AA sequence. In case of a labeled experiment this is the total intensity of all the isotopic patterns in the label cluster.
Intensity L Matr dil_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the light label partner.
Intensity H Matr dil_3		Summed up eXtracted Ion Current (XIC) of the isotopic cluster linked to the heavy label partner.
Only identified by site		When marked with '+', this particular protein group was identified only by a modification site.
Reverse		When marked with '+', this particular protein group contains no protein, made up of at least 50% of the peptides of the leading protein, with a peptide derived from the reversed part of the decoy database. These should be removed for further data analysis. The 50% rule is in place to prevent spurious protein hits to erroneously flag the protein group as reverse.

Contaminant		When marked with '+', this particular protein group was found to be a commonly occurring contaminant. These should be removed for further data analysis.
id		A unique (consecutive) identifier for each row in the proteinGroups table, which is used to cross-link the information in this file with the information stored in the other files.
Peptide IDs		Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'peptides.txt'.
Peptide is razor		Indicates for each peptide ID if it is a razor or group unique peptide (true) or a non unique non razor peptide (false).
Mod. peptide IDs		
Evidence IDs		
MS/MS IDs		
Best MS/MS		The identifier of the best (in terms of quality) MS/MS scans identifying the peptides of this protein, referenced against the msms table.
Oxidation (M) site IDs		Identifier(s) for site(s) associated with the protein group, which show(s) evidence of the modification, referenced against the appropriate modification site file.
Oxidation (M) site positions		Positions of the sites in the leading protein of this group.