Summary

The summary file contains summary information for all the raw files processed with a single MaxQuant run. The summary information consists of some MaxQuant parameters, information of the raw file contents, and statistics on the peak detection. Based on this file a quick overview can be gathered on the quality of the data in the raw file.

The last row in this file contains the summary information for each column on each of the processed files.

Name	**Separator**	**Description**
Raw file		The raw file processed.
Experiment		Experiment name assigned to this LC-MS run in the experimental design.
Enzyme		The protease used to digest the protein sample.
Enzyme mode		The protease used to digest the protein sample.
Enzyme first search		The protease used for the first search.
Enzyme mode first search		The protease used for the first search.
Use enzyme first search		Marked with '+' when a different protease setup was used for the first search.
Variable modifications		The variable modification(s) used during the identification of peptides.
Fixed modifications		The fixed modification(s) used during the identification of peptides.
Multi modifications		The multi modification(s) used during the identification of peptides.
Variable modifications first search		The variable modification(s) used during the first search.
Use variable modifications first search		Marked with '+' when different variable modifications were used for the first search.
Requantify		The number of labels used.
Multiplicity		The number of labels used.
Max. missed cleavages		The maximum allowed number of missed cleavages.
Max. labeled AAs		The maximum allowed of labeled amino acids in a peptide amino acid sequence.
Labels0		The labels used in the labeling experiment. Allowed values for X: 0=light; 1=medium; 2=heavy label partner.
Labels1		The labels used in the labeling experiment. Allowed values for X: 0=light; 1=medium; 2=heavy label partner.
LC-MS run type		The type of LC-MS run. Usually it will be 'Standard' which refers to a conventional shotgun proteomics run with data-dependent MS/MS.
Time-dependent recalibration		When marked with '+', time-dependent recalibration was applied to improve the data quality.
MS		The number of MS spectra recorded in this raw file.
MS/MS		The number of MS/MS spectra recorded in this raw file.
MS3		The number of MS3 spectra recorded in this raw file.
MS/MS submitted		The number of tandem MS spectra submitted for analysis.
MS/MS submitted (SIL)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as part of a labeling cluster.
MS/MS submitted (ISO)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as an isotopic pattern.
MS/MS submitted (PEAK)		The number of tandem MS spectra submitted for analysis, where the precursor ion was detected as a single peak.
MS/MS identified		The total number of identified tandem MS spectra.
MS/MS identified (SIL)		The total number of identified tandem MS spectra, where the precursor ion was detected as part of a labeling cluster.
MS/MS identified (ISO)		The total number of identified tandem MS spectra, where the precursor ion was detected as an isotopic pattern.
MS/MS identified (PEAK)		The total number of identified tandem MS spectra, where the precursor ion was detected as a single peak.
MS/MS identified [%]		The percentage of identified tandem MS spectra.
MS/MS identified (SIL) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as part of a labeling cluster.
MS/MS identified (ISO) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as an isotopic pattern.
MS/MS identified (PEAK) [%]		The percentage of identified tandem MS spectra, where the precursor ion was detected as a single peak.

Peptide sequences identified		The total number of unique peptide amino acid sequences identified from the recorded tandem mass spectra.
Peaks		The total number of peaks detected in the full scans.
Peaks sequenced		The total number of peaks sequenced by tandem MS.
Peaks sequenced [%]		The percentage of peaks sequenced by tandem MS.
Peaks repeatedly sequenced		The total number of peaks repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Peaks repeatedly sequenced [%]		The percentage of peaks repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Isotope patterns		The total number of detected isotope patterns.
Isotope patterns sequenced		The total number of isotope patterns sequenced by tandem MS.
Isotope patterns sequenced (z>1)		The total number of isotope patterns sequenced by tandem MS with a charge state of 2 or more.
Isotope patterns sequenced [%]		The percentage of isotope patterns sequenced by tandem MS.
Isotope patterns sequenced (z>1) [%]		The percentage of isotope patterns sequenced by tandem MS with a charge state of 2 or more.
Isotope patterns repeatedly sequenced		The total number of isotope patterns repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Isotope patterns repeatedly sequenced [%]		The percentage of isotope patterns repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets		The total number of detected labeling pairs.
Multiplets z=1		The total number of detected labeling pairs with a charge state of 1.
Multiplets z=2		The total number of detected labeling pairs with a charge state of 2.
Multiplets z=3		The total number of detected labeling pairs with a charge state of 3.
Multiplets z=4		The total number of detected labeling pairs with a charge state of 4.
Multiplets z=5		The total number of detected labeling pairs with a charge state of 5.
Multiplets z=6		The total number of detected labeling pairs with a charge state of 6.
Multiplets z=7		The total number of detected labeling pairs with a charge state of 7.
Multiplets sequenced		The total number of labeling pairs sequenced by tandem MS.
Multiplets sequenced [%]		The percentage of labeling pairs sequenced by tandem MS.
Multiplets repeatedly sequenced		The total number of labeling pairs repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets repeatedly sequenced [%]		The percentage of labeling pairs repeatedly sequenced (i.e. 1 or more times) by tandem MS.
Multiplets identified		The total number of labeling pairs identified.
Multiplets identified [%]		The percentage of labeling pairs identified.
Recalibrated		When marked with '+', the masses taken from the raw file were recalibrated.
Av. absolute mass deviation [ppm]		The average absolute mass deviation found comparing to the identification mass in parts per million.
Mass standard deviation [ppm]		The standard deviation of the mass deviation found comparing to the identification mass in parts per million.
Av. absolute mass deviation [mDa]		The average absolute mass deviation found comparing to the identification mass in milli-Dalton.
Mass standard deviation [mDa]		The standard deviation of the mass deviation found comparing to the identification mass in milli-Dalton.

Evidence

The evidence file combines all the information about the identified peptides and normally is the only file required for processing the results. Additional information about the peptides, modifications, proteins, etc. can be found in the other files by unique identifier linkage.

Name	**Separator**	**Description**
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column 'Sequence'.
C Count		The number of instances of C contained within the sequence. The value for this can reliably be determined in the case of labeling partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
Modifications		Post-translational modifications contained within the identified peptide sequence.
Modified sequence		Sequence representation including the post-translational modifications (abbreviation of the modification in brackets before the modified AA). The sequence is always surrounded by underscore characters ('_').
Oxidation (M) Probabilities		Sequence representation of the peptide including PTM positioning probabilities ([0..1], where 1 is best match) for 'Oxidation (M)'.
Oxidation (M) Score Diffs		Sequence representation for each of the possible PTM positions in each possible configuration, the difference is calculated between the identification score with the PTM added to that position and the best scoring identification where no PTM is added to that position. When this value is negative, it is unlikely that the particular modification is located at this position.
Acetyl (Protein N-term)		The number of occurrences of the modification 'Acetyl (Protein N-term)'.
Oxidation (M)		The number of occurrences of the modification 'Oxidation (M)'.
Missed cleavages		Number of missed enzymatic cleavages.
Proteins		The identifiers of the proteins this particular peptide is associated with.
Leading proteins		The identifiers of the proteins in the proteinGroups file, with this protein as best match, this particular peptide is associated with. When multiple matches are found here, the best scoring protein can be found in the 'Leading Razor Protein' column.
Leading razor protein		The identifier of the best scoring protein, from the proteinGroups file this, this peptide is associated to.
Type		The type of the feature. 'MSMS' for an MS/MS spectrum without an MS1 isotope pattern assigned. 'ISO-MSMS' MS1 isotope cluster identified by MS/MS. 'MULTI-MSMS' MS1 labeling cluster identified by MS/MS. 'MULTI-SECPEP' MS1 labeling cluster identified by MS/MS as second peptide. 'MULTI-MATCH' MS1 labeling cluster identified by matching between runs. In case of label-free data there is no difference between 'MULTI' and 'ISO'.
Labeling State		Labeling state of the precursor isotope pattern used to identify the peptide.
Raw file		The name of the RAW-file the mass spectral data was derived from.
Experiment		
MS/MS m/z		The m/z used for fragmentation (not necessarily the mono-isotopic m/z).
Charge		The charge-state of the precursor ion.
m/z		The recalibrated mass-over-charge value of the precursor ion.
Mass		The predicted monoisotopic mass of the identified peptide sequence.
Uncalibrated - Calibrated m/z [ppm]		The difference between the uncalibrated and recalibrated mass-over-charge value of the precursor ion measured in parts-per-million. This gives an indication of the mass drift in the original data, which was automatically corrected by MaxQuant.
Uncalibrated - Calibrated m/z [Da]		The difference between the uncalibrated and recalibrated mass-over-charge value of the precursor ion measured in parts-per-million. This gives an indication of the mass drift in the original data, which was automatically corrected by MaxQuant.
Mass error [ppm]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence in parts per million.

Mass error [Da]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence in milli-Dalton.
Uncalibrated mass error [ppm]		Mass error of the uncalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence. Note: This column can contain missing values (denoted as NaN).
Uncalibrated mass error [Da]		Mass error of the uncalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence. Note: This column can contain missing values (denoted as NaN).
Max intensity m/z 0		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.
Max intensity m/z 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.
Retention time		The uncalibrated retention time in minutes in the elution profile of the precursor ion.
Retention length		The total retention time length of the peak (last time point first time point).
Calibrated retention time		The recalibrated retention time in minutes in the elution profile of the precursor ion.
Calibrated retention time start		The recalibrated retention start in minutes in the elution profile of the precursor ion.
Calibrated retention time finish		The recalibrated retention finish in minutes in the elution profile of the precursor ion.
Retention time calibration		The difference in minutes between the uncalibrated and recalibrated retention time. This gives an indication of the retention time drift in the original data, which was automatically corrected by MaxQuant. Note: This column can contain missing values (NaN).
Match time difference		When the option match between runs is used in MaxQuant, this value indicates the time difference between the feature from the raw file it was taken from and the feature from the raw file it was matched to.
Match m/z difference		When the option match between runs is used in MaxQuant, this value indicates the m/z difference between the feature from the raw file it was taken from and the feature from the raw file it was matched to.
Match q-value		This is the q-value for features that have been identified by 'matching between runs'.
Match score		The andromeda score of the MS/MS identification that is the source of this identification by 'matching between runs'.
Number of data points		The number of data points (peak centroids) collected for this peptide feature.
Number of scans		The number of MS scans that the 3d peaks of this peptide feature are overlapping with.
Number of isotopic peaks		The number of isotopic peaks contained in this peptide feature.
PIF		Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Fraction of total spectrum		The percentage the ion intensity makes up of the total intensity of the whole spectrum.
Base peak fraction		The percentage the parent ion intensity in comparison to the highest peak in the MS spectrum.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
MS/MS count		The number of sequencing events for this sequence, which matches the number of identifiers stored in the column MS/MS IDs.
MS/MS scan number		The RAW-file derived scan number of the MS/MS with the highest peptide identification score (the highest score is stored in the column 'Score').
Score		Andromeda score for the best associated MS/MS spectrum.
Delta score		Score difference to the second best identified peptide.
Combinatorics		Number of possible distributions of the modifications over the peptide sequence.
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 ratio sub-populations was shifted to 1.
Ratio H/L shift		

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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
Potential contaminant		When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id		A unique (consecutive) identifier for each row in the evidence table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs		The identifier of the protein-group this redundant peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple ids can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Peptide ID		The identifier of the non-redundant peptide sequence.
Mod. peptide ID		Identifier of the associated modification summary stored in the file 'modificationSpecificPeptides.txt'.
MS/MS IDs		Identifier(s) of the associated MS/MS summary(s) stored in the file 'msms.txt'.
Best MS/MS		Identifier(s) of the best MS/MS associated spectrum stored in the file 'msms.txt'.
Oxidation (M) site IDs		Identifier(s) of the modification summary stored in the file 'Oxidation (M)Sites.txt'.
Taxonomy IDs		Taxonomy identifiers.

Peptides

The peptides table contains information on the identified peptides in the processed raw-files.

Name	**Separator**	**Description**
Sequence		The amino acid sequence of the identified peptide.
N-term cleavage window		Sequence window from -15 to 15 around the N-terminal cleavage site of this peptide.
C-term cleavage window		Sequence window from -15 to 15 around the C-terminal cleavage site of this peptide.
Amino acid before		The amino acid in the protein sequence before the peptide.
First amino acid		The amino acid in the first position of the peptide sequence.
Second amino acid		The amino acid in the first position of the peptide sequence.
Second last amino acid		The amino acid in the last position of the peptide sequence.
Last amino acid		The amino acid in the last position of the peptide sequence.
Amino acid after		The amino acid in the protein sequence after the peptide.
A Count		The number of instances of the 'A' amino acid contained within the sequence.
R Count		The number of instances of the 'R' amino acid contained within the sequence.
N Count		The number of instances of the 'N' amino acid contained within the sequence.
D Count		The number of instances of the 'D' amino acid contained within the sequence.
C Count		The number of instances of the 'C' amino acid contained within the sequence.
Q Count		The number of instances of the 'Q' amino acid contained within the sequence.
E Count		The number of instances of the 'E' amino acid contained within the sequence.
G Count		The number of instances of the 'G' amino acid contained within the sequence.
H Count		The number of instances of the 'H' amino acid contained within the sequence.
I Count		The number of instances of the 'I' amino acid contained within the sequence.
L Count		The number of instances of the 'L' amino acid contained within the sequence.
K Count		The number of instances of the 'K' amino acid contained within the sequence.
M Count		The number of instances of the 'M' amino acid contained within the sequence.
F Count		The number of instances of the 'F' amino acid contained within the sequence.
P Count		The number of instances of the 'P' amino acid contained within the sequence.
S Count		The number of instances of the 'S' amino acid contained within the sequence.
T Count		The number of instances of the 'T' amino acid contained within the sequence.
W Count		The number of instances of the 'W' amino acid contained within the sequence.
Y Count		The number of instances of the 'Y' amino acid contained within the sequence.
V Count		The number of instances of the 'V' amino acid contained within the sequence.
U Count		The number of instances of the 'U' amino acid contained within the sequence.
O Count		The number of instances of the 'O' amino acid contained within the sequence.
Length		The length of the sequence stored in the column "Sequence".
Missed cleavages		Number of missed enzymatic cleavages.
Mass		Monoisotopic mass of the peptide.
Proteins		Identifiers of proteins this peptide is associated with.
Leading razor protein		Identifier of the leading protein in the protein group which uses this peptide for quantification. (Either unique or razor.)
Start position		Position of the first amino acid of this peptide in the protein sequence. (one-based)
End position		Position of the last amino acid of this peptide in the protein sequence. (one-based)

Unique (Groups)		When marked with '+', this particular peptide is unique to a single protein group in the proteinGroups file.
Unique (Proteins)		When marked with '+', this particular peptide is unique to a single protein sequence in the fasta file(s).
Charges		All charge states that have been observed.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Score		Highest Andromeda score for the associated MS/MS spectra.
Identification type 0,02_B001		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B002		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B003		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B004		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B005		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B006		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B007		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B008		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B009		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B010		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B011		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B012		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B013		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B014		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B015		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B016		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B017		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B018		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B019		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B020		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B021		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B022		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B023		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B024		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B025		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B026		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B027		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B028		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B029		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B030		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B031		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B032		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B033		Indicates whether this experiment was identified by MS/MS or only by matching between runs.

Identification type 0,02_B034		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B035		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B036		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B037		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B038		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B039		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B040		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B041		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B042		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B043		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B044		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B045		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B046		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B047		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B048		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B049		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B050		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B051		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B052		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B053		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B054		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B055		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B056		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Experiment 0,02_B001		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B002		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B003		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B004		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B005		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B006		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B007		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B008		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B009		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B010		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B011		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B012		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B013		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B014		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B015		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B016		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B017		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B018		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B019		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B020		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B021		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B022		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B023		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B024		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B025		Number of evidence entries for this 'Experiment'.

Experiment 0,02_B026		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B027		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B028		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B029		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B030		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B031		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B032		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B033		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B034		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B035		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B036		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B037		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B038		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B039		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B040		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B041		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B042		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B043		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B044		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B045		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B046		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B047		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B048		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B049		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B050		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B051		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B052		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B053		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B054		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B055		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B056		Number of evidence entries for this 'Experiment'.
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 ratio sub-populations 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 natural logarithm of ratios times 100.
Ratio H/L count		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type		
Ratio H/L 0,02_B001		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B001		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B001		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B001		
Ratio H/L 0,02_B002		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B002		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B002		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B002		
Ratio H/L 0,02_B003		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B003		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B003		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B003		
Ratio H/L 0,02_B004		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B004		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B004		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B004		
Ratio H/L 0,02_B005		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B005		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B005		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B005		
Ratio H/L 0,02_B006		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B006		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B006		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B006		
Ratio H/L 0,02_B007		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B007		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B007		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B007		
Ratio H/L 0,02_B008		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B008		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B008		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B008		
Ratio H/L 0,02_B009		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B009		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B009		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B009		
Ratio H/L 0,02_B010		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B010		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L variability [%] 0,02_B010		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B010		
Ratio H/L 0,02_B011		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B011		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B011		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B011		
Ratio H/L 0,02_B012		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B012		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B012		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B012		
Ratio H/L 0,02_B013		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B013		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B013		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B013		
Ratio H/L 0,02_B014		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B014		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B014		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B014		
Ratio H/L 0,02_B015		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B015		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B015		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B015		
Ratio H/L 0,02_B016		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B016		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B016		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B016		
Ratio H/L 0,02_B017		The ratio between two heavy and light label partners.

Ratio H/L normalized 0,02_B017		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B017		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B017		
Ratio H/L 0,02_B018		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B018		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B018		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B018		
Ratio H/L 0,02_B019		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B019		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B019		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B019		
Ratio H/L 0,02_B020		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B020		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B020		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B020		
Ratio H/L 0,02_B021		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B021		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B021		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B021		
Ratio H/L 0,02_B022		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B022		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B022		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B022		
Ratio H/L 0,02_B023		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B023		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B023		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type 0,02_B023		
Ratio H/L 0,02_B024		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B024		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B024		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B024		
Ratio H/L 0,02_B025		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B025		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B025		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B025		
Ratio H/L 0,02_B026		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B026		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B026		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B026		
Ratio H/L 0,02_B027		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B027		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B027		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B027		
Ratio H/L 0,02_B028		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B028		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B028		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B028		
Ratio H/L 0,02_B029		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B029		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B029		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B029		
Ratio H/L 0,02_B030		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B030		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B030		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B030		
Ratio H/L 0,02_B031		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B031		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B031		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B031		
Ratio H/L 0,02_B032		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B032		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B032		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B032		
Ratio H/L 0,02_B033		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B033		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B033		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B033		
Ratio H/L 0,02_B034		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B034		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B034		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B034		
Ratio H/L 0,02_B035		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B035		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B035		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B035		
Ratio H/L 0,02_B036		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B036		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B036		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B036		
Ratio H/L 0,02_B037		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B037		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B037		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B037		
Ratio H/L 0,02_B038		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B038		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B038		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B038		
Ratio H/L 0,02_B039		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B039		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B039		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B039		
Ratio H/L 0,02_B040		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B040		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B040		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B040		
Ratio H/L 0,02_B041		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B041		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B041		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B041		
Ratio H/L 0,02_B042		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B042		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B042		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B042		
Ratio H/L 0,02_B043		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B043		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B043		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B043		
Ratio H/L 0,02_B044		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B044		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L variability [%] 0,02_B044		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B044		
Ratio H/L 0,02_B045		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B045		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B045		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B045		
Ratio H/L 0,02_B046		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B046		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B046		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B046		
Ratio H/L 0,02_B047		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B047		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B047		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B047		
Ratio H/L 0,02_B048		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B048		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B048		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B048		
Ratio H/L 0,02_B049		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B049		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B049		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B049		
Ratio H/L 0,02_B050		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B050		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B050		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B050		
Ratio H/L 0,02_B051		The ratio between two heavy and light label partners.

Ratio H/L normalized 0,02_B051		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B051		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B051		
Ratio H/L 0,02_B052		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B052		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B052		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B052		
Ratio H/L 0,02_B053		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B053		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B053		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B053		
Ratio H/L 0,02_B054		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B054		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B054		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B054		
Ratio H/L 0,02_B055		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B055		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B055		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B055		
Ratio H/L 0,02_B056		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B056		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B056		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B056		
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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B001		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 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B002		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 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B003		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 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B004		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 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B005		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 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B006		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 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B007		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 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B008		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 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B009		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 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B010		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 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B011		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 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B012		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 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B013		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 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B014		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 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B015		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 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B016		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 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B017		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 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B018		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 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B019		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 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B020		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 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B021		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 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B022		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 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B023		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 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B024		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 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B025		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 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B026		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 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B027		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 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B028		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 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B029		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 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B030		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 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B031		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 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B032		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 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B033		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 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B034		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 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B035		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 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B036		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 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B037		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 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B038		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 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B039		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 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B040		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 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B041		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 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B042		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 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B043		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 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B044		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 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B045		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 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B046		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 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B047		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 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B048		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 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B049		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 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B050		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 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B051		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 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B052		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 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B053		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 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B054		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 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B055		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 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B056		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 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
Potential contaminant		When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id		A unique (consecutive) identifier for each row in the peptides table, which is used to cross-link the information in this table with the information stored in the other tables.
Protein group IDs		The identifiers of the protein groups this peptide was linked to, referenced against the proteinGroups table.
Mod. peptide IDs		Identifier(s) for peptide sequence(s), associated with the peptide, referenced against the corresponding modified peptides table.
Evidence IDs		Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidence table.
MS/MS IDs		The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best MS/MS		The identifier of the best (in terms of quality) MS/MS scan identifying this peptide, 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.
Taxonomy IDs		Taxonomy identifiers.
MS/MS Count		

Modification-specific peptides

Name	Separator	Description
Sequence		The identified AA sequence of the peptide.
C Count		The number of instances of the 'C' AA contained within the sequence. The value for this can reliably be determined in the case of SILAC partners based on the distance between the partners. These counts are used to solidify the peptide identification process.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to 'unmodified'.
Mass		Charge corrected mass of the precursor ion.
Mass Fractional Part		The values after the decimal point (ie value - floor(value)).
Protein Groups		IDs of the protein groups to which this peptide belongs.
Proteins		The identifiers of the proteins this particular peptide is associated with.
Unique (Groups)		When marked with '+', this particular peptide is unique to a single protein group in the proteinGroups file.
Unique (Proteins)		When marked with '+', this particular peptide is unique to a single protein sequence in the fasta file(s).
Acetyl (Protein N-term)		Number of Acetyl (Protein N-term) on this peptide.
Oxidation (M)		Number of Oxidation (M) on this peptide.
Missed cleavages		Number of missed enzymatic cleavages.
Identification type 0,02_B001		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B002		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B003		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B004		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B005		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B006		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B007		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B008		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B009		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B010		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B011		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B012		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B013		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B014		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B015		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B016		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B017		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B018		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B019		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B020		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B021		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B022		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B023		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B024		Indicates whether this experiment was identified by MS/MS or only by matching between runs.

Identification type 0,02_B025		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B026		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B027		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B028		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B029		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B030		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B031		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B032		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B033		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B034		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B035		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B036		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B037		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B038		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B039		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B040		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B041		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B042		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B043		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B044		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B045		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B046		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B047		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B048		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B049		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B050		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B051		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B052		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B053		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B054		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B055		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B056		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Experiment 0,02_B001		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B002		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B003		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B004		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B005		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B006		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B007		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B008		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B009		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B010		Number of evidence entries for this 'Experiment'.

Experiment 0,02_B011		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B012		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B013		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B014		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B015		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B016		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B017		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B018		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B019		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B020		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B021		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B022		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B023		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B024		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B025		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B026		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B027		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B028		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B029		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B030		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B031		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B032		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B033		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B034		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B035		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B036		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B037		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B038		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B039		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B040		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B041		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B042		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B043		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B044		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B045		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B046		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B047		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B048		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B049		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B050		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B051		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B052		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B053		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B054		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B055		Number of evidence entries for this 'Experiment'.
Experiment 0,02_B056		Number of evidence entries for this 'Experiment'.
Retention time		Retention time in minutes averaged over the evidence entries belonging to this modification-specific peptide.
Calibrated retention time		Calibrated retention time averaged over the evidence entries belonging to this modification-specific peptide. Obviously this only makes sense if retention time recalibration has been performed which is the case when matching between run is selected.
Charges		All charge states that have been observed.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
MS/MS scan number		The RAW-file derived scan number of the MS/MS with the highest peptide identification score (the highest score is stored in the column 'Score').
Raw file		The name of the RAW-file the mass spectral data was derived from.
Score		Andromeda score for the best identified among the associated MS/MS spectra.
Delta score		Score difference to the second best identified peptide.
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.

Potential contaminant		When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
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 ratio sub-populations 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 natural logarithm of ratios times 100.
Ratio H/L count		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type		
Ratio H/L 0,02_B001		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B001		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B001		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B001		
Ratio H/L 0,02_B002		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B002		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B002		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B002		
Ratio H/L 0,02_B003		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B003		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B003		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B003		
Ratio H/L 0,02_B004		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B004		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B004		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B004		
Ratio H/L 0,02_B005		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B005		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B005		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B005		
Ratio H/L 0,02_B006		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B006		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B006		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B006		
Ratio H/L 0,02_B007		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B007		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B007		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B007		
Ratio H/L 0,02_B008		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B008		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B008		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B008		
Ratio H/L 0,02_B009		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B009		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B009		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B009		
Ratio H/L 0,02_B010		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B010		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B010		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B010		
Ratio H/L 0,02_B011		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B011		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B011		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B011		
Ratio H/L 0,02_B012		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B012		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B012		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B012		
Ratio H/L 0,02_B013		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B013		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L variability [%] 0,02_B013		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B013		
Ratio H/L 0,02_B014		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B014		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B014		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B014		
Ratio H/L 0,02_B015		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B015		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B015		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B015		
Ratio H/L 0,02_B016		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B016		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B016		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B016		
Ratio H/L 0,02_B017		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B017		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B017		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B017		
Ratio H/L 0,02_B018		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B018		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B018		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B018		
Ratio H/L 0,02_B019		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B019		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B019		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B019		
Ratio H/L 0,02_B020		The ratio between two heavy and light label partners.

Ratio H/L normalized 0,02_B020		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B020		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B020		
Ratio H/L 0,02_B021		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B021		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B021		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B021		
Ratio H/L 0,02_B022		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B022		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B022		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B022		
Ratio H/L 0,02_B023		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B023		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B023		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B023		
Ratio H/L 0,02_B024		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B024		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B024		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B024		
Ratio H/L 0,02_B025		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B025		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B025		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B025		
Ratio H/L 0,02_B026		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B026		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B026		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L type 0,02_B026		
Ratio H/L 0,02_B027		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B027		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B027		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B027		
Ratio H/L 0,02_B028		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B028		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B028		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B028		
Ratio H/L 0,02_B029		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B029		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B029		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B029		
Ratio H/L 0,02_B030		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B030		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B030		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B030		
Ratio H/L 0,02_B031		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B031		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B031		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B031		
Ratio H/L 0,02_B032		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B032		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B032		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B032		
Ratio H/L 0,02_B033		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B033		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B033		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B033		
Ratio H/L 0,02_B034		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B034		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B034		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B034		
Ratio H/L 0,02_B035		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B035		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B035		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B035		
Ratio H/L 0,02_B036		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B036		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B036		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B036		
Ratio H/L 0,02_B037		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B037		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B037		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B037		
Ratio H/L 0,02_B038		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B038		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B038		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B038		
Ratio H/L 0,02_B039		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B039		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B039		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B039		
Ratio H/L 0,02_B040		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B040		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B040		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B040		
Ratio H/L 0,02_B041		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B041		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B041		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B041		
Ratio H/L 0,02_B042		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B042		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B042		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B042		
Ratio H/L 0,02_B043		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B043		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B043		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B043		
Ratio H/L 0,02_B044		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B044		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B044		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B044		
Ratio H/L 0,02_B045		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B045		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B045		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B045		
Ratio H/L 0,02_B046		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B046		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B046		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B046		
Ratio H/L 0,02_B047		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B047		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L variability [%] 0,02_B047		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B047		
Ratio H/L 0,02_B048		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B048		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B048		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B048		
Ratio H/L 0,02_B049		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B049		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B049		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B049		
Ratio H/L 0,02_B050		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B050		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B050		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B050		
Ratio H/L 0,02_B051		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B051		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B051		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B051		
Ratio H/L 0,02_B052		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B052		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B052		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B052		
Ratio H/L 0,02_B053		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B053		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B053		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B053		
Ratio H/L 0,02_B054		The ratio between two heavy and light label partners.

Ratio H/L normalized 0,02_B054		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B054		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B054		
Ratio H/L 0,02_B055		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B055		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B055		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B055		
Ratio H/L 0,02_B056		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B056		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B056		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B056		
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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B001		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 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B002		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 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B003		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 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B004		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 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B005		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 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B006		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 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B007		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 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B008		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 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B009		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 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B010		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 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B011		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 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B012		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 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B013		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 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B014		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 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B015		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 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B016		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 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B017		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 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B018		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 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B019		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 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B020		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 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B021		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 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B022		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 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B023		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 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B024		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 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B025		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 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B026		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 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B027		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 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B028		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 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B029		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 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B030		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 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B031		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 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B032		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 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B033		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 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B034		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 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B035		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 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B036		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 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B037		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 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B038		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 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B039		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 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B040		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 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B041		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 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B042		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 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B043		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 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B044		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 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B045		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 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B046		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 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B047		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 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B048		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 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B049		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 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B050		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 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B051		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 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B052		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 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B053		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 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B054		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 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B055		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 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B056		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 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
id		A unique (consecutive) identifier for each row in the peptides table, which is used to cross-link the information in this table with the information stored in the other tables.
Protein group IDs		The identifiers of the protein groups this peptide was linked to, referenced against the proteinGroups table.
Peptide ID		Identifier of the associated peptide sequence summary, which can be found in the file 'peptides.txt'.
Evidence IDs		Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidence table.
MS/MS IDs		The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best MS/MS		The identifier of the best (in terms of quality) MS/MS scan identifying this peptide, referenced against the msms table.
Oxidation (M) site IDs		Identifier(s) for site(s) associated with this peptide, which show(s) evidence of the modification, referenced against the appropriate modification site file.
MS/MS Count		
Taxonomy IDs		Taxonomy identifiers.

Oxidation (M)Sites

Name	**Separator**	**Description**
Proteins		Identifiers of proteins this site is associated with.
Positions within proteins		For each protein identifier in the 'Proteins' column you find here the position of the site in the respective protein sequence. The index of the first amino acid in the sequence is 1.
Leading proteins		
Protein		Identifier of the protein this peptide is associated with.
Fasta headers		Descriptions of proteins this peptide is associated with.
Localization prob		
Score diff		
PEP		The posterior error probability (PEP) of the best identified modified peptide containing this site.
Score		The Andromeda score of the best identified modified peptide containing this site.
Delta score		The Andromeda delta score of the best identified modified peptide containing this site.
Score for localization		The Andromeda score of the MS/MS spectrum used for calculating the localization score for this site.
Localization prob 0,02_B001		
Score diff 0,02_B001		
PEP 0,02_B001		
Score 0,02_B001		
Localization prob 0,02_B002		
Score diff 0,02_B002		
PEP 0,02_B002		
Score 0,02_B002		
Localization prob 0,02_B003		
Score diff 0,02_B003		
PEP 0,02_B003		
Score 0,02_B003		
Localization prob 0,02_B004		
Score diff 0,02_B004		
PEP 0,02_B004		
Score 0,02_B004		
Localization prob 0,02_B005		
Score diff 0,02_B005		
PEP 0,02_B005		
Score 0,02_B005		
Localization prob 0,02_B006		
Score diff 0,02_B006		
PEP 0,02_B006		
Score 0,02_B006		
Localization prob 0,02_B007		
Score diff 0,02_B007		
PEP 0,02_B007		
Score 0,02_B007		
Localization prob 0,02_B008		
Score diff 0,02_B008		
PEP 0,02_B008		
Score 0,02_B008		
Localization prob 0,02_B009		
Score diff 0,02_B009		
PEP 0,02_B009		
Score 0,02_B009		
Localization prob 0,02_B010		
Score diff 0,02_B010		
PEP 0,02_B010		
Score 0,02_B010		
Localization prob 0,02_B011		
Score diff 0,02_B011		

PEP 0,02_B011		
Score 0,02_B011		
Localization prob 0,02_B012		
Score diff 0,02_B012		
PEP 0,02_B012		
Score 0,02_B012		
Localization prob 0,02_B013		
Score diff 0,02_B013		
PEP 0,02_B013		
Score 0,02_B013		
Localization prob 0,02_B014		
Score diff 0,02_B014		
PEP 0,02_B014		
Score 0,02_B014		
Localization prob 0,02_B015		
Score diff 0,02_B015		
PEP 0,02_B015		
Score 0,02_B015		
Localization prob 0,02_B016		
Score diff 0,02_B016		
PEP 0,02_B016		
Score 0,02_B016		
Localization prob 0,02_B017		
Score diff 0,02_B017		
PEP 0,02_B017		
Score 0,02_B017		
Localization prob 0,02_B018		
Score diff 0,02_B018		
PEP 0,02_B018		
Score 0,02_B018		
Localization prob 0,02_B019		
Score diff 0,02_B019		
PEP 0,02_B019		
Score 0,02_B019		
Localization prob 0,02_B020		
Score diff 0,02_B020		
PEP 0,02_B020		
Score 0,02_B020		
Localization prob 0,02_B021		
Score diff 0,02_B021		
PEP 0,02_B021		
Score 0,02_B021		
Localization prob 0,02_B022		
Score diff 0,02_B022		
PEP 0,02_B022		
Score 0,02_B022		
Localization prob 0,02_B023		
Score diff 0,02_B023		
PEP 0,02_B023		
Score 0,02_B023		
Localization prob 0,02_B024		
Score diff 0,02_B024		
PEP 0,02_B024		
Score 0,02_B024		
Localization prob 0,02_B025		
Score diff 0,02_B025		
PEP 0,02_B025		
Score 0,02_B025		
Localization prob 0,02_B026		
Score diff 0,02_B026		
PEP 0,02_B026		
Score 0,02_B026		
Localization prob 0,02_B027		
Score diff 0,02_B027		

PEP 0,02_B027		
Score 0,02_B027		
Localization prob 0,02_B028		
Score diff 0,02_B028		
PEP 0,02_B028		
Score 0,02_B028		
Localization prob 0,02_B029		
Score diff 0,02_B029		
PEP 0,02_B029		
Score 0,02_B029		
Localization prob 0,02_B030		
Score diff 0,02_B030		
PEP 0,02_B030		
Score 0,02_B030		
Localization prob 0,02_B031		
Score diff 0,02_B031		
PEP 0,02_B031		
Score 0,02_B031		
Localization prob 0,02_B032		
Score diff 0,02_B032		
PEP 0,02_B032		
Score 0,02_B032		
Localization prob 0,02_B033		
Score diff 0,02_B033		
PEP 0,02_B033		
Score 0,02_B033		
Localization prob 0,02_B034		
Score diff 0,02_B034		
PEP 0,02_B034		
Score 0,02_B034		
Localization prob 0,02_B035		
Score diff 0,02_B035		
PEP 0,02_B035		
Score 0,02_B035		
Localization prob 0,02_B036		
Score diff 0,02_B036		
PEP 0,02_B036		
Score 0,02_B036		
Localization prob 0,02_B037		
Score diff 0,02_B037		
PEP 0,02_B037		
Score 0,02_B037		
Localization prob 0,02_B038		
Score diff 0,02_B038		
PEP 0,02_B038		
Score 0,02_B038		
Localization prob 0,02_B039		
Score diff 0,02_B039		
PEP 0,02_B039		
Score 0,02_B039		
Localization prob 0,02_B040		
Score diff 0,02_B040		
PEP 0,02_B040		
Score 0,02_B040		
Localization prob 0,02_B041		
Score diff 0,02_B041		
PEP 0,02_B041		
Score 0,02_B041		
Localization prob 0,02_B042		
Score diff 0,02_B042		
PEP 0,02_B042		
Score 0,02_B042		
Localization prob 0,02_B043		
Score diff 0,02_B043		

PEP 0,02_B043		
Score 0,02_B043		
Localization prob 0,02_B044		
Score diff 0,02_B044		
PEP 0,02_B044		
Score 0,02_B044		
Localization prob 0,02_B045		
Score diff 0,02_B045		
PEP 0,02_B045		
Score 0,02_B045		
Localization prob 0,02_B046		
Score diff 0,02_B046		
PEP 0,02_B046		
Score 0,02_B046		
Localization prob 0,02_B047		
Score diff 0,02_B047		
PEP 0,02_B047		
Score 0,02_B047		
Localization prob 0,02_B048		
Score diff 0,02_B048		
PEP 0,02_B048		
Score 0,02_B048		
Localization prob 0,02_B049		
Score diff 0,02_B049		
PEP 0,02_B049		
Score 0,02_B049		
Localization prob 0,02_B050		
Score diff 0,02_B050		
PEP 0,02_B050		
Score 0,02_B050		
Localization prob 0,02_B051		
Score diff 0,02_B051		
PEP 0,02_B051		
Score 0,02_B051		
Localization prob 0,02_B052		
Score diff 0,02_B052		
PEP 0,02_B052		
Score 0,02_B052		
Localization prob 0,02_B053		
Score diff 0,02_B053		
PEP 0,02_B053		
Score 0,02_B053		
Localization prob 0,02_B054		
Score diff 0,02_B054		
PEP 0,02_B054		
Score 0,02_B054		
Localization prob 0,02_B055		
Score diff 0,02_B055		
PEP 0,02_B055		
Score 0,02_B055		
Localization prob 0,02_B056		
Score diff 0,02_B056		
PEP 0,02_B056		
Score 0,02_B056		
Diagnostic peak		
Number of Oxidation (M)		Different numbers of Oxidation (M) on peptides that this site is involved in.
Amino acid		
Sequence window		
Modification window		
Peptide window coverage		
Oxidation (M) Probabilities		
Oxidation (M) Score diffs		
Position in peptide		

Charge		Charge state of the precursor ion.
Mass error [ppm]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence.
Identification type 0,02_B001		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B002		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B003		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B004		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B005		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B006		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B007		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B008		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B009		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B010		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B011		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B012		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B013		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B014		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B015		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B016		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B017		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B018		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B019		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B020		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B021		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B022		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B023		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B024		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B025		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B026		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B027		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B028		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B029		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B030		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B031		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B032		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B033		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B034		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B035		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B036		Indicates whether this experiment was identified by MS/MS or only by matching between runs.

Identification type 0,02_B037		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B038		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B039		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B040		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B041		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B042		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B043		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B044		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B045		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B046		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B047		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B048		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B049		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B050		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B051		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B052		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B053		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B054		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B055		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B056		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Ratio H/L		The ratio between two heavy and light label partners.
Ratio H/L___1		The ratio between two heavy and light label partners.
Ratio H/L___2		The ratio between two heavy and light label partners.
Ratio H/L___3		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 ratio sub-populations was shifted to 1.
Ratio H/L normalized___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep.		
Ratio H/L localized		
Ratio H/L variability [%]		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type		
Occupancy L		
Occupancy H		
Ratio H/L 0,02_B001		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B001___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B001___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B001___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B001		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B001___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B001___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B001___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B001		
Ratio H/L localized 0,02_B001		
Ratio H/L variability [%] 0,02_B001		
Ratio H/L count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B001		
Occupancy L 0,02_B001		
Occupancy H 0,02_B001		
Ratio H/L 0,02_B002		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B002___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B002___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B002___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B002		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B002___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B002___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B002___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B002		
Ratio H/L localized 0,02_B002		
Ratio H/L variability [%] 0,02_B002		
Ratio H/L count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B002		
Occupancy L 0,02_B002		
Occupancy H 0,02_B002		
Ratio H/L 0,02_B003		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B003___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B003___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B003___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B003		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B003___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B003___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B003___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B003		
Ratio H/L localized 0,02_B003		
Ratio H/L variability [%] 0,02_B003		
Ratio H/L count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B003		
Occupancy L 0,02_B003		
Occupancy H 0,02_B003		
Ratio H/L 0,02_B004		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B004___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B004___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B004___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B004		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B004___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B004___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B004___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B004		
Ratio H/L localized 0,02_B004		

Ratio H/L variability [%] 0,02_B004		
Ratio H/L count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B004		
Occupancy L 0,02_B004		
Occupancy H 0,02_B004		
Ratio H/L 0,02_B005		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B005___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B005___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B005___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B005		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B005___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B005___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B005___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B005		
Ratio H/L localized 0,02_B005		
Ratio H/L variability [%] 0,02_B005		
Ratio H/L count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B005		
Occupancy L 0,02_B005		
Occupancy H 0,02_B005		
Ratio H/L 0,02_B006		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B006___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B006___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B006___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B006		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B006___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B006___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B006___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B006		
Ratio H/L localized 0,02_B006		
Ratio H/L variability [%] 0,02_B006		
Ratio H/L count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B006		
Occupancy L 0,02_B006		
Occupancy H 0,02_B006		
Ratio H/L 0,02_B007		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B007___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B007___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B007___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B007		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B007___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B007___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B007___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B007		
Ratio H/L localized 0,02_B007		
Ratio H/L variability [%] 0,02_B007		
Ratio H/L count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B007		
Occupancy L 0,02_B007		
Occupancy H 0,02_B007		
Ratio H/L 0,02_B008		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B008___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B008___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B008___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B008		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B008___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B008___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B008___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B008		
Ratio H/L localized 0,02_B008		
Ratio H/L variability [%] 0,02_B008		
Ratio H/L count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B008		
Occupancy L 0,02_B008		
Occupancy H 0,02_B008		
Ratio H/L 0,02_B009		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B009___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B009___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B009___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B009		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B009___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B009___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B009___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B009		
Ratio H/L localized 0,02_B009		
Ratio H/L variability [%] 0,02_B009		
Ratio H/L count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B009		
Occupancy L 0,02_B009		
Occupancy H 0,02_B009		
Ratio H/L 0,02_B010		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B010___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B010___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B010___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B010		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B010___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B010___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B010___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B010		
Ratio H/L localized 0,02_B010		
Ratio H/L variability [%] 0,02_B010		
Ratio H/L count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B010		
Occupancy L 0,02_B010		

Occupancy H 0,02_B010		
Ratio H/L 0,02_B011		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B011___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B011___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B011___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B011		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B011___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B011___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B011___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B011		
Ratio H/L localized 0,02_B011		
Ratio H/L variability [%] 0,02_B011		
Ratio H/L count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B011		
Occupancy L 0,02_B011		
Occupancy H 0,02_B011		
Ratio H/L 0,02_B012		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B012___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B012___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B012___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B012		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B012___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B012___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B012___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B012		
Ratio H/L localized 0,02_B012		
Ratio H/L variability [%] 0,02_B012		
Ratio H/L count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B012		
Occupancy L 0,02_B012		
Occupancy H 0,02_B012		
Ratio H/L 0,02_B013		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B013___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B013___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B013___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B013		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B013___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B013___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B013___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B013		
Ratio H/L localized 0,02_B013		
Ratio H/L variability [%] 0,02_B013		
Ratio H/L count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B013		
Occupancy L 0,02_B013		
Occupancy H 0,02_B013		
Ratio H/L 0,02_B014		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B014___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B014___2		The ratio between two heavy and light label partners.

Ratio H/L 0,02_B014___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B014		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B014___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B014___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B014___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B014		
Ratio H/L localized 0,02_B014		
Ratio H/L variability [%] 0,02_B014		
Ratio H/L count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B014		
Occupancy L 0,02_B014		
Occupancy H 0,02_B014		
Ratio H/L 0,02_B015		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B015___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B015___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B015___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B015		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B015___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B015___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B015___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B015		
Ratio H/L localized 0,02_B015		
Ratio H/L variability [%] 0,02_B015		
Ratio H/L count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B015		
Occupancy L 0,02_B015		
Occupancy H 0,02_B015		
Ratio H/L 0,02_B016		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B016___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B016___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B016___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B016		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B016___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B016___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B016___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B016		
Ratio H/L localized 0,02_B016		
Ratio H/L variability [%] 0,02_B016		
Ratio H/L count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B016		
Occupancy L 0,02_B016		
Occupancy H 0,02_B016		
Ratio H/L 0,02_B017		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B017___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B017___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B017___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B017		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B017___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B017___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B017___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B017		
Ratio H/L localized 0,02_B017		
Ratio H/L variability [%] 0,02_B017		
Ratio H/L count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B017		
Occupancy L 0,02_B017		
Occupancy H 0,02_B017		
Ratio H/L 0,02_B018		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B018___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B018___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B018___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B018		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B018___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B018___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B018___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B018		
Ratio H/L localized 0,02_B018		
Ratio H/L variability [%] 0,02_B018		
Ratio H/L count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B018		
Occupancy L 0,02_B018		
Occupancy H 0,02_B018		
Ratio H/L 0,02_B019		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B019___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B019___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B019___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B019		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B019___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B019___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B019___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B019		
Ratio H/L localized 0,02_B019		
Ratio H/L variability [%] 0,02_B019		
Ratio H/L count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B019		
Occupancy L 0,02_B019		
Occupancy H 0,02_B019		
Ratio H/L 0,02_B020		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B020___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B020___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B020___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B020		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B020___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B020___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B020___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B020		
Ratio H/L localized 0,02_B020		
Ratio H/L variability [%] 0,02_B020		
Ratio H/L count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B020		
Occupancy L 0,02_B020		
Occupancy H 0,02_B020		
Ratio H/L 0,02_B021		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B021___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B021___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B021___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B021		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B021___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B021___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B021___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B021		
Ratio H/L localized 0,02_B021		
Ratio H/L variability [%] 0,02_B021		
Ratio H/L count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B021		
Occupancy L 0,02_B021		
Occupancy H 0,02_B021		
Ratio H/L 0,02_B022		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B022___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B022___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B022___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B022		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B022___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B022___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B022___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B022		
Ratio H/L localized 0,02_B022		
Ratio H/L variability [%] 0,02_B022		
Ratio H/L count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B022		
Occupancy L 0,02_B022		
Occupancy H 0,02_B022		
Ratio H/L 0,02_B023		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B023___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B023___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B023___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B023		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B023___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B023___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B023___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B023		
Ratio H/L localized 0,02_B023		

Ratio H/L variability [%] 0,02_B023		
Ratio H/L count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B023		
Occupancy L 0,02_B023		
Occupancy H 0,02_B023		
Ratio H/L 0,02_B024		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B024___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B024___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B024___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B024		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B024___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B024___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B024___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B024		
Ratio H/L localized 0,02_B024		
Ratio H/L variability [%] 0,02_B024		
Ratio H/L count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B024		
Occupancy L 0,02_B024		
Occupancy H 0,02_B024		
Ratio H/L 0,02_B025		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B025___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B025___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B025___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B025		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B025___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B025___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B025___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B025		
Ratio H/L localized 0,02_B025		
Ratio H/L variability [%] 0,02_B025		
Ratio H/L count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B025		
Occupancy L 0,02_B025		
Occupancy H 0,02_B025		
Ratio H/L 0,02_B026		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B026___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B026___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B026___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B026		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B026___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B026___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B026___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B026		
Ratio H/L localized 0,02_B026		
Ratio H/L variability [%] 0,02_B026		
Ratio H/L count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B026		
Occupancy L 0,02_B026		
Occupancy H 0,02_B026		
Ratio H/L 0,02_B027		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B027___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B027___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B027___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B027		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B027___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B027___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B027___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B027		
Ratio H/L localized 0,02_B027		
Ratio H/L variability [%] 0,02_B027		
Ratio H/L count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B027		
Occupancy L 0,02_B027		
Occupancy H 0,02_B027		
Ratio H/L 0,02_B028		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B028___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B028___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B028___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B028		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B028___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B028___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B028___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B028		
Ratio H/L localized 0,02_B028		
Ratio H/L variability [%] 0,02_B028		
Ratio H/L count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B028		
Occupancy L 0,02_B028		
Occupancy H 0,02_B028		
Ratio H/L 0,02_B029		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B029___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B029___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B029___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B029		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B029___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B029___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B029___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B029		
Ratio H/L localized 0,02_B029		
Ratio H/L variability [%] 0,02_B029		
Ratio H/L count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B029		
Occupancy L 0,02_B029		

Occupancy H 0,02_B029		
Ratio H/L 0,02_B030		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B030___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B030___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B030___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B030		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B030___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B030___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B030___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B030		
Ratio H/L localized 0,02_B030		
Ratio H/L variability [%] 0,02_B030		
Ratio H/L count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B030		
Occupancy L 0,02_B030		
Occupancy H 0,02_B030		
Ratio H/L 0,02_B031		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B031___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B031___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B031___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B031		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B031___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B031___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B031___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B031		
Ratio H/L localized 0,02_B031		
Ratio H/L variability [%] 0,02_B031		
Ratio H/L count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B031		
Occupancy L 0,02_B031		
Occupancy H 0,02_B031		
Ratio H/L 0,02_B032		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B032___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B032___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B032___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B032		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B032___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B032___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B032___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B032		
Ratio H/L localized 0,02_B032		
Ratio H/L variability [%] 0,02_B032		
Ratio H/L count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B032		
Occupancy L 0,02_B032		
Occupancy H 0,02_B032		
Ratio H/L 0,02_B033		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B033___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B033___2		The ratio between two heavy and light label partners.

Ratio H/L 0,02_B033___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B033		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B033___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B033___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B033___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B033		
Ratio H/L localized 0,02_B033		
Ratio H/L variability [%] 0,02_B033		
Ratio H/L count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B033		
Occupancy L 0,02_B033		
Occupancy H 0,02_B033		
Ratio H/L 0,02_B034		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B034___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B034___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B034___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B034		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B034___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B034___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B034___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B034		
Ratio H/L localized 0,02_B034		
Ratio H/L variability [%] 0,02_B034		
Ratio H/L count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B034		
Occupancy L 0,02_B034		
Occupancy H 0,02_B034		
Ratio H/L 0,02_B035		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B035___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B035___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B035___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B035		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B035___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B035___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B035___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B035		
Ratio H/L localized 0,02_B035		
Ratio H/L variability [%] 0,02_B035		
Ratio H/L count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B035		
Occupancy L 0,02_B035		
Occupancy H 0,02_B035		
Ratio H/L 0,02_B036		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B036___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B036___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B036___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B036		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B036___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B036___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B036___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B036		
Ratio H/L localized 0,02_B036		
Ratio H/L variability [%] 0,02_B036		
Ratio H/L count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B036		
Occupancy L 0,02_B036		
Occupancy H 0,02_B036		
Ratio H/L 0,02_B037		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B037___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B037___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B037___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B037		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B037___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B037___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B037___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B037		
Ratio H/L localized 0,02_B037		
Ratio H/L variability [%] 0,02_B037		
Ratio H/L count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B037		
Occupancy L 0,02_B037		
Occupancy H 0,02_B037		
Ratio H/L 0,02_B038		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B038___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B038___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B038___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B038		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B038___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B038___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B038___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B038		
Ratio H/L localized 0,02_B038		
Ratio H/L variability [%] 0,02_B038		
Ratio H/L count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B038		
Occupancy L 0,02_B038		
Occupancy H 0,02_B038		
Ratio H/L 0,02_B039		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B039___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B039___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B039___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B039		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B039___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B039___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B039___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B039		
Ratio H/L localized 0,02_B039		
Ratio H/L variability [%] 0,02_B039		
Ratio H/L count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B039		
Occupancy L 0,02_B039		
Occupancy H 0,02_B039		
Ratio H/L 0,02_B040		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B040___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B040___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B040___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B040		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B040___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B040___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B040___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B040		
Ratio H/L localized 0,02_B040		
Ratio H/L variability [%] 0,02_B040		
Ratio H/L count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B040		
Occupancy L 0,02_B040		
Occupancy H 0,02_B040		
Ratio H/L 0,02_B041		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B041___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B041___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B041___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B041		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B041___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B041___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B041___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B041		
Ratio H/L localized 0,02_B041		
Ratio H/L variability [%] 0,02_B041		
Ratio H/L count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B041		
Occupancy L 0,02_B041		
Occupancy H 0,02_B041		
Ratio H/L 0,02_B042		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B042___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B042___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B042___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B042		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B042___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B042___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B042___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B042		
Ratio H/L localized 0,02_B042		

Ratio H/L variability [%] 0,02_B042		
Ratio H/L count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B042		
Occupancy L 0,02_B042		
Occupancy H 0,02_B042		
Ratio H/L 0,02_B043		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B043___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B043___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B043___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B043		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B043___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B043___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B043___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B043		
Ratio H/L localized 0,02_B043		
Ratio H/L variability [%] 0,02_B043		
Ratio H/L count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B043		
Occupancy L 0,02_B043		
Occupancy H 0,02_B043		
Ratio H/L 0,02_B044		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B044___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B044___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B044___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B044		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B044___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B044___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B044___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B044		
Ratio H/L localized 0,02_B044		
Ratio H/L variability [%] 0,02_B044		
Ratio H/L count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B044		
Occupancy L 0,02_B044		
Occupancy H 0,02_B044		
Ratio H/L 0,02_B045		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B045___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B045___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B045___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B045		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B045___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B045___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B045___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B045		
Ratio H/L localized 0,02_B045		
Ratio H/L variability [%] 0,02_B045		
Ratio H/L count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L iso-count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B045		
Occupancy L 0,02_B045		
Occupancy H 0,02_B045		
Ratio H/L 0,02_B046		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B046___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B046___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B046___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B046		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B046___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B046___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B046___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B046		
Ratio H/L localized 0,02_B046		
Ratio H/L variability [%] 0,02_B046		
Ratio H/L count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B046		
Occupancy L 0,02_B046		
Occupancy H 0,02_B046		
Ratio H/L 0,02_B047		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B047___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B047___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B047___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B047		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B047___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B047___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B047___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B047		
Ratio H/L localized 0,02_B047		
Ratio H/L variability [%] 0,02_B047		
Ratio H/L count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B047		
Occupancy L 0,02_B047		
Occupancy H 0,02_B047		
Ratio H/L 0,02_B048		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B048___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B048___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B048___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B048		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B048___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B048___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B048___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B048		
Ratio H/L localized 0,02_B048		
Ratio H/L variability [%] 0,02_B048		
Ratio H/L count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B048		
Occupancy L 0,02_B048		

Occupancy H 0,02_B048		
Ratio H/L 0,02_B049		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B049___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B049___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B049___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B049		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B049___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B049___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B049___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B049		
Ratio H/L localized 0,02_B049		
Ratio H/L variability [%] 0,02_B049		
Ratio H/L count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B049		
Occupancy L 0,02_B049		
Occupancy H 0,02_B049		
Ratio H/L 0,02_B050		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B050___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B050___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B050___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B050		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B050___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B050___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B050___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B050		
Ratio H/L localized 0,02_B050		
Ratio H/L variability [%] 0,02_B050		
Ratio H/L count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B050		
Occupancy L 0,02_B050		
Occupancy H 0,02_B050		
Ratio H/L 0,02_B051		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B051___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B051___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B051___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B051		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B051___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B051___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B051___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B051		
Ratio H/L localized 0,02_B051		
Ratio H/L variability [%] 0,02_B051		
Ratio H/L count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B051		
Occupancy L 0,02_B051		
Occupancy H 0,02_B051		
Ratio H/L 0,02_B052		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B052___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B052___2		The ratio between two heavy and light label partners.

Ratio H/L 0,02_B052___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B052		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B052___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B052___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B052___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B052		
Ratio H/L localized 0,02_B052		
Ratio H/L variability [%] 0,02_B052		
Ratio H/L count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B052		
Occupancy L 0,02_B052		
Occupancy H 0,02_B052		
Ratio H/L 0,02_B053		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B053___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B053___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B053___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B053		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B053___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B053___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B053___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B053		
Ratio H/L localized 0,02_B053		
Ratio H/L variability [%] 0,02_B053		
Ratio H/L count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B053		
Occupancy L 0,02_B053		
Occupancy H 0,02_B053		
Ratio H/L 0,02_B054		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B054___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B054___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B054___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B054		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B054___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B054___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B054___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B054		
Ratio H/L localized 0,02_B054		
Ratio H/L variability [%] 0,02_B054		
Ratio H/L count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B054		
Occupancy L 0,02_B054		
Occupancy H 0,02_B054		
Ratio H/L 0,02_B055		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B055___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B055___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B055___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B055		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B055___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B055___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B055___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B055		
Ratio H/L localized 0,02_B055		
Ratio H/L variability [%] 0,02_B055		
Ratio H/L count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B055		
Occupancy L 0,02_B055		
Occupancy H 0,02_B055		
Ratio H/L 0,02_B056		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B056___1		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B056___2		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B056___3		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B056		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B056___1		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B056___2		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B056___3		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L unmod. pep. 0,02_B056		
Ratio H/L localized 0,02_B056		
Ratio H/L variability [%] 0,02_B056		
Ratio H/L count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B056		
Occupancy L 0,02_B056		
Occupancy H 0,02_B056		
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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L		
Ratio mod/base H		
Intensity 0,02_B001		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 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B001		
Ratio mod/base H 0,02_B001		
Intensity 0,02_B002		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 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B002		
Ratio mod/base H 0,02_B002		
Intensity 0,02_B003		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 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B003		
Ratio mod/base H 0,02_B003		
Intensity 0,02_B004		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 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B004		
Ratio mod/base H 0,02_B004		
Intensity 0,02_B005		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 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B005		
Ratio mod/base H 0,02_B005		
Intensity 0,02_B006		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 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B006		
Ratio mod/base H 0,02_B006		
Intensity 0,02_B007		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 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B007		
Ratio mod/base H 0,02_B007		
Intensity 0,02_B008		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 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B008		
Ratio mod/base H 0,02_B008		
Intensity 0,02_B009		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 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B009		
Ratio mod/base H 0,02_B009		
Intensity 0,02_B010		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 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B010		
Ratio mod/base H 0,02_B010		

Intensity 0,02_B011		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 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B011		
Ratio mod/base H 0,02_B011		
Intensity 0,02_B012		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 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B012		
Ratio mod/base H 0,02_B012		
Intensity 0,02_B013		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 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B013		
Ratio mod/base H 0,02_B013		
Intensity 0,02_B014		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 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B014		
Ratio mod/base H 0,02_B014		
Intensity 0,02_B015		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 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B015		
Ratio mod/base H 0,02_B015		
Intensity 0,02_B016		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 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B016		
Ratio mod/base H 0,02_B016		
Intensity 0,02_B017		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 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B017		
Ratio mod/base H 0,02_B017		
Intensity 0,02_B018		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 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B018		
Ratio mod/base H 0,02_B018		
Intensity 0,02_B019		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 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B019		
Ratio mod/base H 0,02_B019		
Intensity 0,02_B020		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 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B020		
Ratio mod/base H 0,02_B020		
Intensity 0,02_B021		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 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B021		
Ratio mod/base H 0,02_B021		
Intensity 0,02_B022		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 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B022		
Ratio mod/base H 0,02_B022		
Intensity 0,02_B023		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 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B023		
Ratio mod/base H 0,02_B023		
Intensity 0,02_B024		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 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B024		
Ratio mod/base H 0,02_B024		
Intensity 0,02_B025		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 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B025		
Ratio mod/base H 0,02_B025		

Intensity 0,02_B026		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 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B026		
Ratio mod/base H 0,02_B026		
Intensity 0,02_B027		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 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B027		
Ratio mod/base H 0,02_B027		
Intensity 0,02_B028		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 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B028		
Ratio mod/base H 0,02_B028		
Intensity 0,02_B029		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 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B029		
Ratio mod/base H 0,02_B029		
Intensity 0,02_B030		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 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B030		
Ratio mod/base H 0,02_B030		
Intensity 0,02_B031		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 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B031		
Ratio mod/base H 0,02_B031		
Intensity 0,02_B032		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 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B032		
Ratio mod/base H 0,02_B032		
Intensity 0,02_B033		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 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B033		
Ratio mod/base H 0,02_B033		
Intensity 0,02_B034		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 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B034		
Ratio mod/base H 0,02_B034		
Intensity 0,02_B035		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 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B035		
Ratio mod/base H 0,02_B035		
Intensity 0,02_B036		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 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B036		
Ratio mod/base H 0,02_B036		
Intensity 0,02_B037		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 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B037		
Ratio mod/base H 0,02_B037		
Intensity 0,02_B038		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 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B038		
Ratio mod/base H 0,02_B038		
Intensity 0,02_B039		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 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B039		
Ratio mod/base H 0,02_B039		
Intensity 0,02_B040		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 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B040		
Ratio mod/base H 0,02_B040		

Intensity 0,02_B041		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 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B041		
Ratio mod/base H 0,02_B041		
Intensity 0,02_B042		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 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B042		
Ratio mod/base H 0,02_B042		
Intensity 0,02_B043		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 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B043		
Ratio mod/base H 0,02_B043		
Intensity 0,02_B044		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 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B044		
Ratio mod/base H 0,02_B044		
Intensity 0,02_B045		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 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B045		
Ratio mod/base H 0,02_B045		
Intensity 0,02_B046		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 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B046		
Ratio mod/base H 0,02_B046		
Intensity 0,02_B047		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 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B047		
Ratio mod/base H 0,02_B047		
Intensity 0,02_B048		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 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.

Intensity H 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B048		
Ratio mod/base H 0,02_B048		
Intensity 0,02_B049		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 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B049		
Ratio mod/base H 0,02_B049		
Intensity 0,02_B050		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 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B050		
Ratio mod/base H 0,02_B050		
Intensity 0,02_B051		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 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B051		
Ratio mod/base H 0,02_B051		
Intensity 0,02_B052		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 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B052		
Ratio mod/base H 0,02_B052		
Intensity 0,02_B053		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 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B053		
Ratio mod/base H 0,02_B053		
Intensity 0,02_B054		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 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B054		
Ratio mod/base H 0,02_B054		
Intensity 0,02_B055		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 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B055		
Ratio mod/base H 0,02_B055		

Intensity 0,02_B056		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 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Ratio mod/base L 0,02_B056		
Ratio mod/base H 0,02_B056		
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the protein sequence database. These should be removed for further data analysis.
Potential contaminant		When marked with '+', this particular peptide was found to be part of a commonly occurring contaminant. These should be removed for further data analysis.
id		A unique (consecutive) identifier for each row in the site table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs		The identifier of the protein-group this peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id’s can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Positions		The positions of the modifications in the protein amino acid sequence.
Position		The position of the modification in the protein amino acid sequence.
Peptide IDs		Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'peptides.txt'.
Mod. peptide IDs		Identifier(s) of the associated peptide sequence(s) summary, which can be found in the file 'modificationSpecificPeptides.txt'.
Evidence IDs		Identifier(s) for analyzed peptide evidence associated with the protein group referenced against the evidence table.
MS/MS IDs		The identifiers of the MS/MS scans identifying this peptide, referenced against the msms table.
Best localization evidence ID		
Best localization MS/MS ID		
Best localization raw file		
Best localization scan number		
Best score evidence ID		
Best score MS/MS ID		
Best score raw file		
Best score scan number		
Best PEP evidence ID		
Best PEP MS/MS ID		
Best PEP raw file		
Best PEP scan number		

Protein groups

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

Name	**Separator**	**Description**
Protein IDs		Identifiers of proteins 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, occurring 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, occurring 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, occurring 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.
Fasta headers		Fasta headers(s) of protein(s) contained in the group.
Number of proteins		Number of proteins contained within the group. This corresponds to the number of entries in the column '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 0,02_B001		Number of peptides (distinct peptide sequences) in experiment 0,02_B001
Peptides 0,02_B002		Number of peptides (distinct peptide sequences) in experiment 0,02_B002
Peptides 0,02_B003		Number of peptides (distinct peptide sequences) in experiment 0,02_B003
Peptides 0,02_B004		Number of peptides (distinct peptide sequences) in experiment 0,02_B004
Peptides 0,02_B005		Number of peptides (distinct peptide sequences) in experiment 0,02_B005
Peptides 0,02_B006		Number of peptides (distinct peptide sequences) in experiment 0,02_B006
Peptides 0,02_B007		Number of peptides (distinct peptide sequences) in experiment 0,02_B007
Peptides 0,02_B008		Number of peptides (distinct peptide sequences) in experiment 0,02_B008
Peptides 0,02_B009		Number of peptides (distinct peptide sequences) in experiment 0,02_B009
Peptides 0,02_B010		Number of peptides (distinct peptide sequences) in experiment 0,02_B010
Peptides 0,02_B011		Number of peptides (distinct peptide sequences) in experiment 0,02_B011
Peptides 0,02_B012		Number of peptides (distinct peptide sequences) in experiment 0,02_B012
Peptides 0,02_B013		Number of peptides (distinct peptide sequences) in experiment 0,02_B013
Peptides 0,02_B014		Number of peptides (distinct peptide sequences) in experiment 0,02_B014
Peptides 0,02_B015		Number of peptides (distinct peptide sequences) in experiment 0,02_B015
Peptides 0,02_B016		Number of peptides (distinct peptide sequences) in experiment 0,02_B016
Peptides 0,02_B017		Number of peptides (distinct peptide sequences) in experiment 0,02_B017
Peptides 0,02_B018		Number of peptides (distinct peptide sequences) in experiment 0,02_B018

Peptides 0,02_B019		Number of peptides (distinct peptide sequences) in experiment 0,02_B019
Peptides 0,02_B020		Number of peptides (distinct peptide sequences) in experiment 0,02_B020
Peptides 0,02_B021		Number of peptides (distinct peptide sequences) in experiment 0,02_B021
Peptides 0,02_B022		Number of peptides (distinct peptide sequences) in experiment 0,02_B022
Peptides 0,02_B023		Number of peptides (distinct peptide sequences) in experiment 0,02_B023
Peptides 0,02_B024		Number of peptides (distinct peptide sequences) in experiment 0,02_B024
Peptides 0,02_B025		Number of peptides (distinct peptide sequences) in experiment 0,02_B025
Peptides 0,02_B026		Number of peptides (distinct peptide sequences) in experiment 0,02_B026
Peptides 0,02_B027		Number of peptides (distinct peptide sequences) in experiment 0,02_B027
Peptides 0,02_B028		Number of peptides (distinct peptide sequences) in experiment 0,02_B028
Peptides 0,02_B029		Number of peptides (distinct peptide sequences) in experiment 0,02_B029
Peptides 0,02_B030		Number of peptides (distinct peptide sequences) in experiment 0,02_B030
Peptides 0,02_B031		Number of peptides (distinct peptide sequences) in experiment 0,02_B031
Peptides 0,02_B032		Number of peptides (distinct peptide sequences) in experiment 0,02_B032
Peptides 0,02_B033		Number of peptides (distinct peptide sequences) in experiment 0,02_B033
Peptides 0,02_B034		Number of peptides (distinct peptide sequences) in experiment 0,02_B034
Peptides 0,02_B035		Number of peptides (distinct peptide sequences) in experiment 0,02_B035
Peptides 0,02_B036		Number of peptides (distinct peptide sequences) in experiment 0,02_B036
Peptides 0,02_B037		Number of peptides (distinct peptide sequences) in experiment 0,02_B037
Peptides 0,02_B038		Number of peptides (distinct peptide sequences) in experiment 0,02_B038
Peptides 0,02_B039		Number of peptides (distinct peptide sequences) in experiment 0,02_B039
Peptides 0,02_B040		Number of peptides (distinct peptide sequences) in experiment 0,02_B040
Peptides 0,02_B041		Number of peptides (distinct peptide sequences) in experiment 0,02_B041
Peptides 0,02_B042		Number of peptides (distinct peptide sequences) in experiment 0,02_B042
Peptides 0,02_B043		Number of peptides (distinct peptide sequences) in experiment 0,02_B043
Peptides 0,02_B044		Number of peptides (distinct peptide sequences) in experiment 0,02_B044
Peptides 0,02_B045		Number of peptides (distinct peptide sequences) in experiment 0,02_B045
Peptides 0,02_B046		Number of peptides (distinct peptide sequences) in experiment 0,02_B046
Peptides 0,02_B047		Number of peptides (distinct peptide sequences) in experiment 0,02_B047
Peptides 0,02_B048		Number of peptides (distinct peptide sequences) in experiment 0,02_B048
Peptides 0,02_B049		Number of peptides (distinct peptide sequences) in experiment 0,02_B049
Peptides 0,02_B050		Number of peptides (distinct peptide sequences) in experiment 0,02_B050
Peptides 0,02_B051		Number of peptides (distinct peptide sequences) in experiment 0,02_B051
Peptides 0,02_B052		Number of peptides (distinct peptide sequences) in experiment 0,02_B052
Peptides 0,02_B053		Number of peptides (distinct peptide sequences) in experiment 0,02_B053
Peptides 0,02_B054		Number of peptides (distinct peptide sequences) in experiment 0,02_B054
Peptides 0,02_B055		Number of peptides (distinct peptide sequences) in experiment 0,02_B055
Peptides 0,02_B056		Number of peptides (distinct peptide sequences) in experiment 0,02_B056

Razor + unique peptides 0,02_B001		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B001
Razor + unique peptides 0,02_B002		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B002
Razor + unique peptides 0,02_B003		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B003
Razor + unique peptides 0,02_B004		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B004
Razor + unique peptides 0,02_B005		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B005
Razor + unique peptides 0,02_B006		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B006
Razor + unique peptides 0,02_B007		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B007
Razor + unique peptides 0,02_B008		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B008
Razor + unique peptides 0,02_B009		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B009
Razor + unique peptides 0,02_B010		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B010
Razor + unique peptides 0,02_B011		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B011
Razor + unique peptides 0,02_B012		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B012
Razor + unique peptides 0,02_B013		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B013
Razor + unique peptides 0,02_B014		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B014
Razor + unique peptides 0,02_B015		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B015
Razor + unique peptides 0,02_B016		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B016
Razor + unique peptides 0,02_B017		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B017
Razor + unique peptides 0,02_B018		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B018
Razor + unique peptides 0,02_B019		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B019
Razor + unique peptides 0,02_B020		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B020
Razor + unique peptides 0,02_B021		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B021
Razor + unique peptides 0,02_B022		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B022
Razor + unique peptides 0,02_B023		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B023
Razor + unique peptides 0,02_B024		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B024
Razor + unique peptides 0,02_B025		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B025
Razor + unique peptides 0,02_B026		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B026
Razor + unique peptides 0,02_B027		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B027
Razor + unique peptides 0,02_B028		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B028
Razor + unique peptides 0,02_B029		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B029
Razor + unique peptides 0,02_B030		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B030
Razor + unique peptides 0,02_B031		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B031
Razor + unique peptides 0,02_B032		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B032
Razor + unique peptides 0,02_B033		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B033
Razor + unique peptides 0,02_B034		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B034
Razor + unique peptides 0,02_B035		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B035
Razor + unique peptides 0,02_B036		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B036
Razor + unique peptides 0,02_B037		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B037
Razor + unique peptides 0,02_B038		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B038

Razor + unique peptides 0,02_B039		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B039
Razor + unique peptides 0,02_B040		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B040
Razor + unique peptides 0,02_B041		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B041
Razor + unique peptides 0,02_B042		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B042
Razor + unique peptides 0,02_B043		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B043
Razor + unique peptides 0,02_B044		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B044
Razor + unique peptides 0,02_B045		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B045
Razor + unique peptides 0,02_B046		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B046
Razor + unique peptides 0,02_B047		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B047
Razor + unique peptides 0,02_B048		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B048
Razor + unique peptides 0,02_B049		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B049
Razor + unique peptides 0,02_B050		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B050
Razor + unique peptides 0,02_B051		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B051
Razor + unique peptides 0,02_B052		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B052
Razor + unique peptides 0,02_B053		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B053
Razor + unique peptides 0,02_B054		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B054
Razor + unique peptides 0,02_B055		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B055
Razor + unique peptides 0,02_B056		Number of razor + unique peptides (distinct peptide sequences) in experiment 0,02_B056
Unique peptides 0,02_B001		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B001
Unique peptides 0,02_B002		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B002
Unique peptides 0,02_B003		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B003
Unique peptides 0,02_B004		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B004
Unique peptides 0,02_B005		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B005
Unique peptides 0,02_B006		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B006
Unique peptides 0,02_B007		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B007
Unique peptides 0,02_B008		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B008
Unique peptides 0,02_B009		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B009
Unique peptides 0,02_B010		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B010
Unique peptides 0,02_B011		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B011
Unique peptides 0,02_B012		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B012
Unique peptides 0,02_B013		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B013
Unique peptides 0,02_B014		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B014
Unique peptides 0,02_B015		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B015
Unique peptides 0,02_B016		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B016
Unique peptides 0,02_B017		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B017
Unique peptides 0,02_B018		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B018
Unique peptides 0,02_B019		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B019
Unique peptides 0,02_B020		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B020

Unique peptides 0,02_B021		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B021
Unique peptides 0,02_B022		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B022
Unique peptides 0,02_B023		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B023
Unique peptides 0,02_B024		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B024
Unique peptides 0,02_B025		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B025
Unique peptides 0,02_B026		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B026
Unique peptides 0,02_B027		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B027
Unique peptides 0,02_B028		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B028
Unique peptides 0,02_B029		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B029
Unique peptides 0,02_B030		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B030
Unique peptides 0,02_B031		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B031
Unique peptides 0,02_B032		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B032
Unique peptides 0,02_B033		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B033
Unique peptides 0,02_B034		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B034
Unique peptides 0,02_B035		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B035
Unique peptides 0,02_B036		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B036
Unique peptides 0,02_B037		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B037
Unique peptides 0,02_B038		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B038
Unique peptides 0,02_B039		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B039
Unique peptides 0,02_B040		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B040
Unique peptides 0,02_B041		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B041
Unique peptides 0,02_B042		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B042
Unique peptides 0,02_B043		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B043
Unique peptides 0,02_B044		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B044
Unique peptides 0,02_B045		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B045
Unique peptides 0,02_B046		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B046
Unique peptides 0,02_B047		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B047
Unique peptides 0,02_B048		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B048
Unique peptides 0,02_B049		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B049
Unique peptides 0,02_B050		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B050
Unique peptides 0,02_B051		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B051
Unique peptides 0,02_B052		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B052
Unique peptides 0,02_B053		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B053
Unique peptides 0,02_B054		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B054
Unique peptides 0,02_B055		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B055
Unique peptides 0,02_B056		Number of unique peptides (distinct peptide sequences) in experiment 0,02_B056
Sequence coverage [%]		Percentage of the sequence that is covered by the identified peptides of the first 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.
Q-value		This is the ratio of reverse to forward protein groups.
Score		Protein score which is derived from peptide posterior error probabilities.
Identification type 0,02_B001		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B002		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B003		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B004		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B005		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B006		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B007		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B008		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B009		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B010		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B011		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B012		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B013		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B014		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B015		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B016		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B017		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B018		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B019		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B020		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B021		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B022		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B023		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B024		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B025		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B026		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B027		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B028		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B029		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B030		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B031		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B032		Indicates whether this experiment was identified by MS/MS or only by matching between runs.

Identification type 0,02_B033		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B034		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B035		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B036		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B037		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B038		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B039		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B040		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B041		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B042		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B043		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B044		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B045		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B046		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B047		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B048		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B049		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B050		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B051		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B052		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B053		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B054		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B055		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
Identification type 0,02_B056		Indicates whether this experiment was identified by MS/MS or only by matching between runs.
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 ratio sub-populations 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 natural logarithm of ratios times 100.
Ratio H/L count		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type		
Ratio H/L 0,02_B001		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B002		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B003		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B004		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B005		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B006		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B007		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B008		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B009		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B010		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B011		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B012		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B013		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B014		The ratio between two heavy and light label partners.

Ratio H/L 0,02_B015		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B016		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B017		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B018		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B019		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B020		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B021		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B022		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B023		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B024		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B025		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B026		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B027		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B028		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B029		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B030		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B031		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B032		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B033		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B034		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B035		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B036		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B037		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B038		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B039		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B040		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B041		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B042		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B043		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B044		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B045		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B046		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B047		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B048		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B049		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B050		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B051		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B052		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B053		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B054		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B055		The ratio between two heavy and light label partners.
Ratio H/L 0,02_B056		The ratio between two heavy and light label partners.
Ratio H/L normalized 0,02_B001		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B002		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B003		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B004		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B005		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B006		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B007		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B008		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B009		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B010		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B011		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B012		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B013		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B014		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B015		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B016		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B017		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B018		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B019		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B020		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B021		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B022		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B023		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B024		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B025		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B026		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B027		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B028		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B029		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B030		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B031		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B032		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B033		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B034		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B035		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B036		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B037		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B038		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B039		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B040		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B041		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B042		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B043		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B044		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B045		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B046		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B047		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B048		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B049		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B050		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B051		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.

Ratio H/L normalized 0,02_B052		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B053		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B054		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B055		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L normalized 0,02_B056		Normalized ratio between two medium and light label partners. The median of ratio sub-populations was shifted to 1.
Ratio H/L variability [%] 0,02_B001		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B002		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B003		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B004		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B005		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B006		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B007		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B008		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B009		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B010		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B011		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B012		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B013		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B014		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B015		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B016		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B017		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B018		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B019		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B020		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B021		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B022		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B023		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L variability [%] 0,02_B024		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B025		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B026		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B027		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B028		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B029		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B030		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B031		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B032		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B033		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B034		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B035		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B036		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B037		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B038		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B039		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B040		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B041		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B042		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B043		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B044		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B045		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B046		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B047		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B048		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B049		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B050		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.

Ratio H/L variability [%] 0,02_B051		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B052		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B053		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B054		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B055		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L variability [%] 0,02_B056		Coefficient of variability over all redundant quantifiable peptides. It is calculated as the standard deviation of the natural logarithm of ratios times 100.
Ratio H/L count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation.

Ratio H/L count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation.
Ratio H/L iso-count 0,02_B001		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B002		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B003		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B004		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B005		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B006		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B007		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B008		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B009		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B010		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B011		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B012		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L iso-count 0,02_B013		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B014		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B015		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B016		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B017		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B018		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B019		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B020		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B021		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B022		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B023		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B024		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B025		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B026		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B027		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B028		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B029		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B030		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B031		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B032		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B033		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B034		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B035		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B036		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B037		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B038		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B039		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B040		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B041		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B042		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B043		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B044		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B045		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B046		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B047		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B048		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B049		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B050		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.

Ratio H/L iso-count 0,02_B051		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B052		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B053		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B054		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B055		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L iso-count 0,02_B056		Number of redundant peptides (MS1 features) used for quantitation that are quantified with the re-quantify method.
Ratio H/L type 0,02_B001		
Ratio H/L type 0,02_B002		
Ratio H/L type 0,02_B003		
Ratio H/L type 0,02_B004		
Ratio H/L type 0,02_B005		
Ratio H/L type 0,02_B006		
Ratio H/L type 0,02_B007		
Ratio H/L type 0,02_B008		
Ratio H/L type 0,02_B009		
Ratio H/L type 0,02_B010		
Ratio H/L type 0,02_B011		
Ratio H/L type 0,02_B012		
Ratio H/L type 0,02_B013		
Ratio H/L type 0,02_B014		
Ratio H/L type 0,02_B015		
Ratio H/L type 0,02_B016		
Ratio H/L type 0,02_B017		
Ratio H/L type 0,02_B018		
Ratio H/L type 0,02_B019		
Ratio H/L type 0,02_B020		
Ratio H/L type 0,02_B021		
Ratio H/L type 0,02_B022		
Ratio H/L type 0,02_B023		
Ratio H/L type 0,02_B024		
Ratio H/L type 0,02_B025		
Ratio H/L type 0,02_B026		
Ratio H/L type 0,02_B027		
Ratio H/L type 0,02_B028		
Ratio H/L type 0,02_B029		
Ratio H/L type 0,02_B030		
Ratio H/L type 0,02_B031		
Ratio H/L type 0,02_B032		
Ratio H/L type 0,02_B033		
Ratio H/L type 0,02_B034		
Ratio H/L type 0,02_B035		
Ratio H/L type 0,02_B036		
Ratio H/L type 0,02_B037		
Ratio H/L type 0,02_B038		
Ratio H/L type 0,02_B039		
Ratio H/L type 0,02_B040		
Ratio H/L type 0,02_B041		
Ratio H/L type 0,02_B042		
Ratio H/L type 0,02_B043		
Ratio H/L type 0,02_B044		
Ratio H/L type 0,02_B045		
Ratio H/L type 0,02_B046		
Ratio H/L type 0,02_B047		
Ratio H/L type 0,02_B048		
Ratio H/L type 0,02_B049		
Ratio H/L type 0,02_B050		
Ratio H/L type 0,02_B051		
Ratio H/L type 0,02_B052		
Ratio H/L type 0,02_B053		
Ratio H/L type 0,02_B054		

Ratio H/L type 0,02_B055		
Ratio H/L type 0,02_B056		
Sequence coverage 0,02_B001 [%]		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 0,02_B002 [%]		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 0,02_B003 [%]		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 0,02_B004 [%]		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 0,02_B005 [%]		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 0,02_B006 [%]		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 0,02_B007 [%]		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 0,02_B008 [%]		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 0,02_B009 [%]		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 0,02_B010 [%]		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 0,02_B011 [%]		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 0,02_B012 [%]		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 0,02_B013 [%]		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 0,02_B014 [%]		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 0,02_B015 [%]		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 0,02_B016 [%]		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 0,02_B017 [%]		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 0,02_B018 [%]		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 0,02_B019 [%]		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 0,02_B020 [%]		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 0,02_B021 [%]		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 0,02_B022 [%]		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 0,02_B023 [%]		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 0,02_B024 [%]		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 0,02_B025 [%]		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 0,02_B026 [%]		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 0,02_B027 [%]		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 0,02_B028 [%]		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 0,02_B029 [%]		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 0,02_B030 [%]		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 0,02_B031 [%]		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 0,02_B032 [%]		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 0,02_B033 [%]		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 0,02_B034 [%]		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 0,02_B035 [%]		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 0,02_B036 [%]		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 0,02_B037 [%]		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 0,02_B038 [%]		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 0,02_B039 [%]		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 0,02_B040 [%]		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 0,02_B041 [%]		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 0,02_B042 [%]		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 0,02_B043 [%]		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 0,02_B044 [%]		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 0,02_B045 [%]		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 0,02_B046 [%]		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 0,02_B047 [%]		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 0,02_B048 [%]		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 0,02_B049 [%]		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 0,02_B050 [%]		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 0,02_B051 [%]		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 0,02_B052 [%]		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 0,02_B053 [%]		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 0,02_B054 [%]		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 0,02_B055 [%]		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 0,02_B056 [%]		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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B001		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 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B001		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B002		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 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B002		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B003		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 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B003		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B004		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 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B004		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B005		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 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B005		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B006		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 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B006		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B007		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 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B007		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B008		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 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B008		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B009		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 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B009		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B010		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 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B010		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B011		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 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B011		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B012		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 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B012		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B013		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 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B013		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B014		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 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B014		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B015		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 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B015		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B016		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 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B016		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B017		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 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B017		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B018		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 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B018		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B019		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 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B019		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B020		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 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B020		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B021		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 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B021		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B022		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 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B022		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B023		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 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B023		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B024		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 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B024		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B025		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 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B025		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B026		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 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B026		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B027		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 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B027		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B028		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 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B028		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B029		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 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B029		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B030		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 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B030		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B031		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 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B031		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B032		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 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B032		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B033		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 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B033		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B034		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 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B034		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B035		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 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B035		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B036		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 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B036		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B037		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 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B037		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B038		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 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B038		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B039		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 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B039		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B040		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 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B040		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B041		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 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B041		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B042		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 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B042		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B043		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 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B043		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B044		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 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B044		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B045		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 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B045		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B046		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 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B046		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B047		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 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B047		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B048		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 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B048		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.

Intensity 0,02_B049		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 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B049		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B050		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 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B050		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B051		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 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B051		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B052		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 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B052		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B053		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 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B053		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B054		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 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B054		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B055		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 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B055		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensity 0,02_B056		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 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the light label partner.
Intensity H 0,02_B056		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
iBAQ peptides		
iBAQ		
iBAQ L		
iBAQ H		
iBAQ 0,02_B001		
iBAQ L 0,02_B001		
iBAQ H 0,02_B001		
iBAQ 0,02_B002		
iBAQ L 0,02_B002		
iBAQ H 0,02_B002		
iBAQ 0,02_B003		
iBAQ L 0,02_B003		
iBAQ H 0,02_B003		

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iBAQ L 0,02_B004		
iBAQ H 0,02_B004		
iBAQ 0,02_B005		
iBAQ L 0,02_B005		
iBAQ H 0,02_B005		
iBAQ 0,02_B006		
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iBAQ H 0,02_B006		
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Peptide sequences		Peptide sequences belonging to this protein group.
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.
Potential contaminant		When marked with '+', this particular protein group was found to be a commonly occurring contaminant. It is recommended to remove them 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		Identifiers of the associated peptides, which correspond to rows in the peptides table.
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.
Taxonomy IDs		Taxonomy identifiers.

All peptides

Name	Separator	Description
Raw file		Name of the raw file the spectral data was extracted from.
Type		The type of detection for the peptide. MULTI – A labeling multiplet was detected. ISO – An isotope pattern was detected.
Charge		The charge state of the peptide.
m/z		The mass divided by the charge of the charged peptide.
Mass		The mass of the neutral peptide ((m/z-proton) * charge).
Uncalibrated m/z		m/z before re-calibrations have been applied.
Number of data points		The number of data points (peak centroids) collected for this peptide feature.
Number of scans		The number of MS scans that the 3d peaks of this peptide feature are overlapping with.
Number of isotopic peaks		The number of isotopic peaks contained in this peptide feature.
PIF		Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Mass fractional part		The values after the radix point (ie value - floor(value)).
Mass deficit		Empirically derived deviation measure to the next nearest integer scaled to center around 0. Can be used to visually detect contaminants in a plot setting Mass against this value. m*a+b – round(m*a+b) m: the peptide mass a: 0.99954 b: -0.04
Mass precision [ppm]		The precision of the mass detection of the peptide in parts-per-million.
Max intensity m/z 0		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.
Max intensity m/z 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.
Retention time		The retention time of the peak detected for the peptide measured in minutes.
Retention length		The total retention time width of the peak (last time point – first time point) in seconds.
Retention length (FWHM)		The full width at half maximum value retention time width of the peak in seconds.
Min scan number		The first scan number at which the peak was encountered.
Max scan number		The last scan number at which the peak was encountered.
Identified		When marked with '+' this particular MS/MS scan was identified as a peptide; when marked with ‘-‘ no identification was made.
Reverse		When marked with '+' this particular MS/MS scan was assigned to a decoy sequence.
MS/MS IDs		Unique identifier linking this identification to the MS/MS scans.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column “Sequence”.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to ‘unmodified’. Note: This column only set when this MS/MS spectrum has been identified.
Modified sequence		Sequence representation of the peptide including location(s) of modified AAs. Note: This column only set when this MS/MS spectrum has been identified.
Proteins		Identifiers of proteins this peptide is associated with. Note: This column only set when this MS/MS spectrum has been identified.
Score		The score of the identification (higher is better).
PEP		The posterior error probability of the identification (smaller is better).

Cys Count		The number of instances of Cys contained within the sequence. The value for this can reliably be determined in the case of label partners, based on the distance between the partners. These counts are used to solidify the peptide identification process.
Ratio H/L		The ratio between two heavy and light multiplet members.
Ratio H/L normalized		Normalized ratio between two heavy and light multiplet members. The median of the total ratio population was shifted to 1.
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 belonging to the light label partner.
Intensity H		Summed up eXtracted Ion Current (XIC) of the isotopic cluster belonging to the heavy label partner.
Intensities L		Elution profile of the light peptide.
Intensities H		Elution profile of the heavy peptide.
Isotope pattern L		Isotope pattern of the light peptide.
Isotope pattern H		Isotope pattern of the heavy peptide.
MS/MS Count		The number of MS/MS spectra recorded for the peptide.
MSMS Scan Numbers		The scan numbers where the MS/MS spectra were recorded.
MSMS label States		The label partner detected for the peptide. The value 0 is always the light partner. In the case of double label labeling 1 is the heavy partner. In the case of triple label labeling 1 is the medium and 2 the heavy partner.
MSMS Isotope Indices		Indices of the isotopic peaks that the MS/MS spectra reside on. A value of 0 corresponds to the monoisotopic peak.

MS scans

The msScans table contains information about the full scans, which can be used to verify data quality and generated useful statistics about the interaction between the samples and LC.

Name	Separator	Description
Raw file		The name of the RAW-file the mass spectral data originates from.
Scan number		The scan number (defined in the raw-file) at which the full scan was made.
Scan index		The consecutive index of this full scan.
Retention time		The retention time at which the full scan was made.
Cycle time		The total time (full scan including the tandem MS scans) this full scan has taken up.
Ion injection time		The total injection time that was required to capture the specified amount of ions. This value is limited by a maximum, which can be used to determine whether the time has maxed out (indicative of a bad acquisition).
Base peak intensity		The intensity of the most intense ion in the spectrum.
Total ion current		The total intensity acquired in the full scan.
MS/MS count		The number of tandem MS scans that were made based on this full scan (e.g. a top 10 method selects the top 10 most intense ions in the scan and fragments those).
Mass calibration		The applied mass correction in Th to the full scan.
Experiment		
Peak length		The average time between the start and the end of the peaks detected in the full scan.
Isotope pattern length		The average time between the start and the end of the isotope patterns detected in the full scan.
Multiplet length		The average time between the start and the end of the isotope patterns of the labeling multiplets detected in the full scan.
Peaks / s		The average number of peaks detected per second of chromatography.
Single peaks / s		The average number of single peaks detected per second of chromatography.
Isotope patterns / s		The average number of isotope patterns detected per second of chromatography.
Single isotope patterns / s		The average number of single isotope patterns detected per of second chromatography.
Multiplets / s		The average number of labeling multiplets detected per of second chromatography.
Identified multiplets / s		The percentage of labeling multiplets actually identified.
Multiplet identification rate [%]		The percentage of the detected labeling multiplets that were identified.
MS/MS / s		The average number of MS/MS events per second of chromatography.
Identified MS/MS / s		The average number of identified MS/MS events per second of chromatography.
MS/MS identification rate [%]		The percentage of tandem MS scans that were identified.
Intens Comp Factor		Taken from the Thermo RAW file.
CTCD Comp		Taken from the Thermo RAW file.
RawOvFtT		For Thermo Fisher only. TIC estimation done with the orbitrap cell.
AGC Fill		Taken from the Thermo RAW file.

MZ range

Name	**Separator**	**Description**
Raw file		The name of the RAW-file the mass spectral data was derived from.
m/z		The mass-over-charge value.
Peaks / Da		The average number of peaks detected per Dalton.
Single peaks / Da		The average number of single peaks detected per Dalton.
Isotope patterns / Da		The average number of isotope patterns detected per Dalton.
Single isotope patterns / Da		The average number of single isotope patterns detected per Dalton.
SILAC pairs / Da		The average number of SILAC pairs detected per Dalton.
Identified SILAC pairs / Da		The percentage of SILAC pairs actually identified.
SILAC identification rate [%]		The percentage of the detected SILAC pairs that were identified.
MS/MS / Da		The average number of MS/MS events per Dalton.
Identified MS/MS / Da		The average number of identified MS/MS events per Dalton.
Identification rate [%]		The percentage of tandem MS scans that were identified.

MS/MS scans

Name	Separator	Description
Raw file		Name of the RAW file the spectral MS/MS data was extracted from.
Scan number		RAW file derived scan number for the MS/MS spectrum.
Retention time		Time point along the elution profile at which the MS/MS data was recorded.
Ion injection time		The ion inject time for the MS/MS scan. This can be used to determine if this time equals to the maximum ion inject time, general indicative of a lower quality spectrum.
Total ion current		The total ion current of the MS/MS scan. For Thermo data this value is calculated by summing all the intensity values found in the mass spectral data, which is different from the Xcalibur reported TIC (Xcalibur TIC is about 25% of the value reported here).
Collision energy		The collision energy used for the fragmentation that resulted in this MS/MS scan.
Summations		For time of flight instruments only.
Base peak intensity		The intensity of the most intense ion in the spectrum.
Elapsed time		The time the MS/MS scan took to complete.
Identified		When marked with '+' this particular MS/MS scan was identified as a peptide; when marked with ‘-‘ no identification was made.
Matched		When marked with '+' this particular MS/MS scan was retrieved by matching between runs.
Reverse		When marked with '+' this particular MS/MS scan was assigned to a decoy sequence.
MS/MS IDs		Unique identifier linking this identification to the MS/MS scans.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column “Sequence”.
Filtered peaks		Number of peaks after the 'top X per 100 Da' filtering.
m/z		Recalibrated m/z of the precursor ion.
Mass		Charge corrected mass of the precursor ion.
Charge		Charge state of the precursor ion.
Type		The type of precursor ion as identified by MaxQuant. ISO – isotopic cluster. PEAK – single peak. MULTI – labeling cluster.
Fragmentation		The type of fragmentation used to create the MS/MS spectrum. CID – Collision Induced Dissociation. HCD – High energy Collision induced Dissociation. ETD – Electron Transfer Dissociation.
Mass analyzer		The mass analyzer used to record the MS/MS spectrum. ITMS – Ion trap. FTMS – Fourier transform ICR or orbitrap cell. TOF – Time of flight.
Parent intensity fraction		The percentage the parent ion intensity makes up of the total intensity in the selection window.
Fraction of total spectrum		The percentage the parent ion intensity makes up of the total intensity of the whole MS spectrum.
Base peak fraction		The percentage the parent ion intensity in comparison to the highest peak in he MS spectrum.
Precursor full scan number		The full scan number where the precursor ion was selected for fragmentation.
Precursor intensity		The intensity of the precursor ion at the scan number it was selected.
Precursor apex fraction		The fraction the intensity of the precursor ion makes up of the peak (apex) intensity.
Precursor apex offset		How many full scans the precursor ion is offset from the peak (apex) position.
Precursor apex offset time		How much time the precursor ion is offset from the peak (apex) position.
Scan event number		This number indicates which MS/MS scan this one is in the consecutive order of the MS/MS scans that are acquired after an MS scan.
Modifications		Post-translational modifications contained within the sequence. When no modifications exist, this is set to ‘unmodified’. Note: This column only set when this MS/MS spectrum has been identified.

Modified sequence		Sequence representation of the peptide including location(s) of modified AAs. Note: This column only set when this MS/MS spectrum has been identified.
Proteins		Identifiers of proteins this peptide is associated with. Note: This column only set when this MS/MS spectrum has been identified.
Score		The score of the identification (higher is better).
PEP		The posterior error probability of the identification (smaller is better).
Experiment		
Reporter PIF		
Reporter fraction		
Intens Comp Factor		Taken from the Thermo RAW file.
CTCD Comp		Taken from the Thermo RAW file.
RawOvFtT		For Thermo Fisher only. TIC estimation done with the orbitrap cell.
AGC Fill		Taken from the Thermo RAW file.
Scan index		Consecutive index of the MS/MS spectrum.
MS scan index		Consecutive index of the MS spectrum prior to this MS/MS spectrum.
MS scan number		Scan number of the MS spectrum prior to this MS/MS spectrum.

MS/MS

Name	**Separator**	**Description**
Raw file		The name of the RAW file the mass spectral data was read from.
Scan number		The RAW-file derived scan number of the MS/MS spectrum.
Scan index		The consecutive index of the MS/MS spectrum.
Sequence		The identified AA sequence of the peptide.
Length		The length of the sequence stored in the column "Sequence".
Missed cleavages		Number of missed enzymatic cleavages.
Modifications		Post-translational modifications contained within the identified peptide sequence.
Modified sequence		Sequence representation including the post-translational modifications (abbreviation of the modification in brackets before the modified AA). The sequence is always surrounded by underscore characters ('_').
Oxidation (M) Probabilities		Sequence representation of the peptide including PTM positioning probabilities ([0..1], where 1 is best match) for 'Oxidation (M)'.
Oxidation (M) Score diffs		
Acetyl (Protein N-term)		
Oxidation (M)		
Proteins		The identifiers of the proteins the identified peptide is associated with.
Charge		The charge state of the precursor ion.
Fragmentation		The type of fragmentation used to create the MS/MS spectrum. CID – Collision Induced Dissociation. HCD – High energy Collision induced Dissociation. ETD – Electron Transfer Dissociation.
Mass analyzer		The mass analyzer used to record the MS/MS spectrum. ITMS – Ion trap. FTMS – Fourier transform ICR or orbitrap cell. TOF – Time of flight.
Type		The type of precursor ion as identified by MaxQuant. ISO – isotopic cluster. PEAK – single peak. MULTI – labeling cluster.
Scan event number		
Isotope index		
m/z		The mass-over-charge of the precursor ion.
Mass		The charge corrected mass of the precursor ion.
Mass error [ppm]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence expressed in parts per million.
Mass error [Da]		Mass error of the recalibrated mass-over-charge value of the precursor ion in comparison to the predicted monoisotopic mass of the identified peptide sequence expressed in atomic mass units.
Simple mass error [ppm]		
Retention time		The uncalibrated retention time in minutes where the MS/MS spectrum has been acquired.
PEP		Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
Score		Andromeda score for the best associated MS/MS spectrum.
Delta score		Score difference to the second best identified peptide with a different amino acid sequence.
Score diff		Score difference to the second best positioning of modifications identified peptide with the same amino acid sequence.
Localization prob		
Combinatorics		Number of possible distributions of the modifications over the peptide sequence.
Labeling state		Labeling state of the precursor isotope pattern used to identify the peptide.
PIF		Short for Parent Ion Fraction; indicates the fraction the target peak makes up of the total intensity in the inclusion window.
Fraction of total spectrum		The percentage the parent ion intensity makes up of the total intensity of the whole spectrum.
Base peak fraction		The percentage the parent ion intensity in comparison to the highest peak in he MS spectrum.

Precursor full scan number		The full scan number where the precursor ion was selected for fragmentation.
Precursor Intensity		The intensity of the precursor ion at the scan number it was selected.
Precursor apex fraction		The fraction the intensity of the precursor ion makes up of the peak (apex) intensity.
Precursor apex offset		How many full scans the precursor ion is offset from the peak (apex) position.
Precursor apex offset time		How much time the precursor ion is offset from the peak (apex) position.
Matches		The species of the peaks in the fragmentation spectrum after TopN filtering.
Intensities		The intensities of the peaks in the fragmentation spectrum after TopN filtering.
Mass deviations [Da]		The mass deviation of each peak in the fragmentation spectrum in absolute mass units.
Mass deviations [ppm]		The mass deviation of each peak in the fragmentation spectrum in parts per million.
Masses		The masses-over-charge of the peaks in the fragmentation spectrum.
Number of matches		The number of peaks matching to the predicted fragmentation spectrum.
Intensity coverage		The fraction of intensity in the MS/MS spectrum that is annotated.
Peak coverage		The fraction of peaks in the MS/MS spectrum that are annotated.
Neutral loss level		How many neutral losses were applied to each fragment in the Andromeda scoring.
ETD identification type		For ETD spectra several different combinations of ion series are scored. Here the highest scoring combination is indicated
Reverse		When marked with '+', this particular peptide was found to be part of a protein derived from the reversed part of the decoy database. These should be removed for further data analysis.
All scores		
All sequences		
All modified sequences		
Reporter PIF		
Reporter fraction		
id		A unique (consecutive) identifier for each row in the msms table, which is used to cross-link the information in this file with the information stored in the other files.
Protein group IDs		The identifier of the protein-group this redundant peptide sequence is associated with, which can be used to look up the extended protein information in the file 'proteinGroups.txt'. As a single peptide can be linked to multiple proteins (e.g. in the case of razor-proteins), multiple id's can be stored here separated by a semicolon. As a protein can be identified by multiple peptides, the same id can be found in different rows.
Peptide ID		The identifier of the non-redundant peptide sequence.
Mod. peptide ID		Identifier of the associated modification summary stored in the file 'modificationSpecificPeptides.txt'.
Evidence ID		Identifier of the associated evidence stored in the file 'evidence.txt'.
Oxidation (M) site IDs		Identifier of the associated entry stored in the file 'Oxidation (M)Sites.txt'.