

## Columns

### Meta information

Num	ID of the detected feature pair. Arbitrary. Only valid in this column and cannot be used to reference the feature pair in the different chromatograms
MZ	The m/z value of the monoisotopic, native feature
L_MZ	The m/z value of the labeled feature. Theoretical
D_MZ	The m/z difference between MZ and L_MZ. Theoretical
RT	The retention time of the feature pair. It is determined as the most abundant scan for the chromatographic peak of the monoisotopic, native feature
Xn	The number of labeling atoms
Charge	The number of charges of this feature pair. Determined by the difference between the native and the labeled feature
ScanEvent	The HRMS scan event in which this feature pair was detected
Ionisation_Mode	The ionization mode this feature pair was detected in
Tracer	The tracer used for the experiment.
OGroup	ID of the feature group this feature pairs was assigned to. All rows (i.e. feature pairs) with the same ID in the column OGroup are ions of the same metabolite.

### Sample information

<SampleName>_Area_N	For each sample the following 4 columns are saved The peak area of the monoisotopic, native feature
<SampleName>_Area_L	The peak area of the labeled feature
<SampleName>_FID	The ID of the feature pair in the respective file. They are only unique in this file and cannot be referenced to the Num column in the meta information
<SampleName>_GroupID	The feature group ID of the feature pair in the respective file. They are only unique in this file and cannot be referenced to the OGroup column in the meta information

At the bottom of the list of the detected feature pairs the most important data processing parameters are saved as comments starting in the column Num with a #-symbol.