



Transition Settings

Prediction Filter Library Instrument Full-Scan Ion Mobility

MS1 filtering

Isotope peaks included: Precursor mass analyzer:

Peaks: Resolving power:

Isotope labeling enrichment: Ignore SIM scans

MS/MS filtering

Acquisition method: Product mass analyzer:

Isolation scheme: Resolving power:

Use high-selectivity extraction

Retention time filtering

Use only scans within minutes of MS/MS IDs

Use only scans within minutes of predicted RT

Include all matching scans

OK Cancel

Transition Settings

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Min m/z: m/z Max m/z: m/z

Dynamic min product m/z

Method match tolerance m/z: m/z

Firmware transition limit: Firmware inclusion limit:

Min time: min Max time: min

Triggered chromatogram acquisition

OK Cancel

Import Transition List: Identify Columns

Molecule Name	Precursor Formula	Precursor Adduct	Precursor Charge	Explicit Retention time	Product m/z	Product Charge	Precursor CE
A	C10H13N5O4	[M+H]	1	8.2	136.062	1	26
C	C9H13N3O5	[M+H]	1	2.8	112.051	1	19
G	C10H13N5O5	[M+H]	1	5.8	152.057	1	20
ho5C	C9H13N3O6	[M+H]	1	2.7	128.046	1	19
m3U	C10H14N2O6	[M+H]	1	8.1	127.051	1	20
mo5U	C10H14N2O7	[M+H]	1	7.8	143.046	1	18
m5U	C10H14N2O6	[M+H]	1	7.9	127.051	1	17
U	C9H12N2O6	[M+H]	1	3.5	113.035	1	17
m3U-1	C10H14N2O6	[M+H]	1	8.1	96.008	1	50
m5U-1	C10H14N2O6	[M+H]	1	7.9	110.024	1	41
m3U-2	C10H14N2O6	[M+H]	1	8.1	133.049	1	16
m5U-2	C10H14N2O6	[M+H]	1	7.9	54.033	1	59

Peptides Molecules Show unused columns

Check For Errors OK Cancel