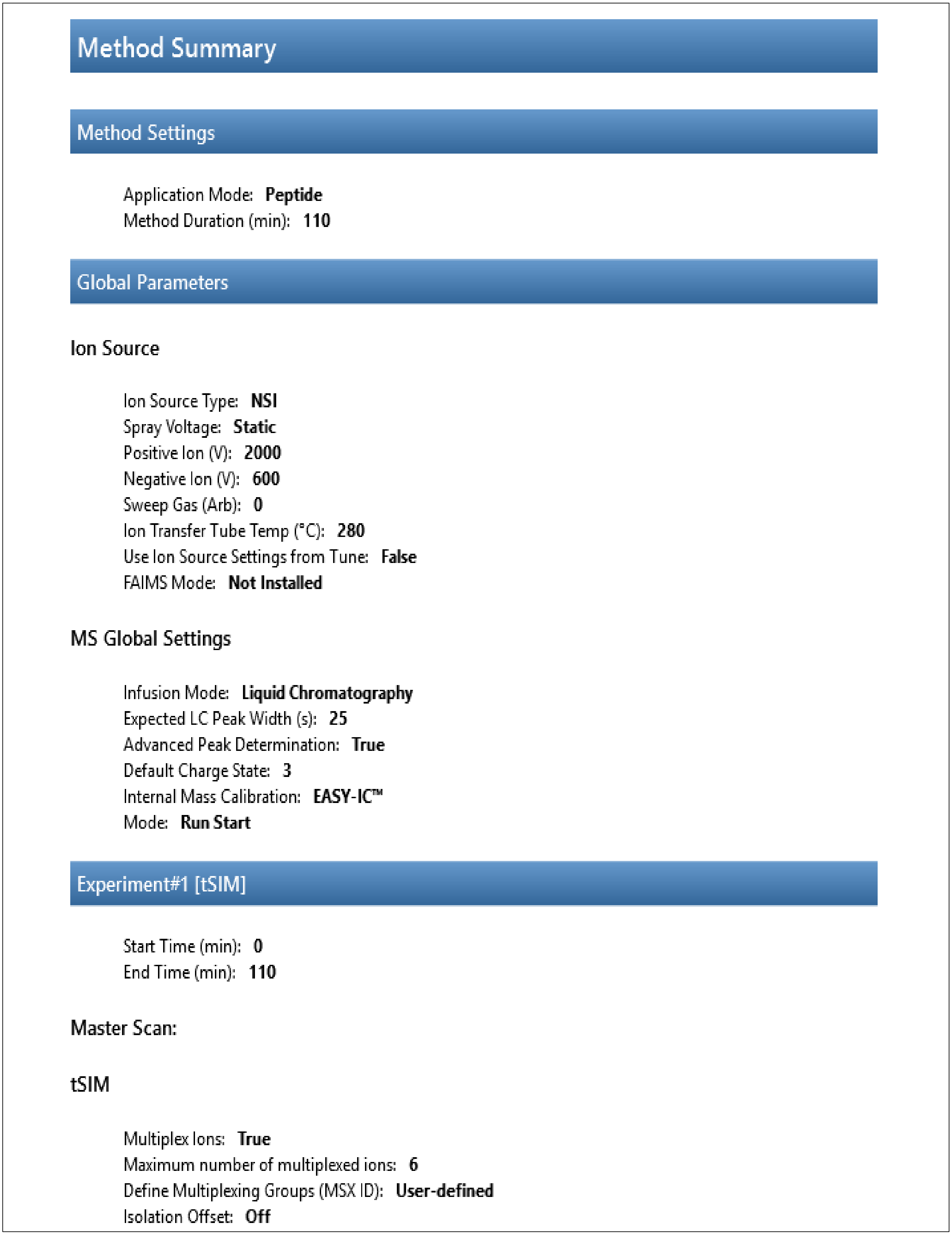
```
Thermo EASY-LC method print for Thermo


 Sample pickup:

   Volume [µl]          : 4.00
   Flow [µl / min]      : 20.00


 Sample loading:

   Volume [µl]          : 10.00
   Flow [µl / min]      : (unspecified)
   Max. pressure [Bar]  : 750.00


 Gradient:

       Time [mm:ss]      Duration [mm:ss]      Flow [nl/min]     Mixture [%B]
              00:00                 00:00             250.00             2.00
              05:00                 05:00             250.00             2.00
              80:00                 75:00             250.00            28.00
              90:00                 10:00             250.00            44.00
              95:00                 05:00             250.00           100.00
              98:00                 03:00             300.00           100.00
             101:00                 03:00             300.00             2.00
             104:00                 03:00             300.00             2.00
             107:00                 03:00             300.00           100.00
             110:00                 03:00             300.00           100.00


 Pre-column equilibration:

   Volume [µl]          : 0.00
   Flow [µl / min]      : (unspecified)
   Max. pressure [Bar]  : 750.00


 Analytical column equilibration:

   Volume [µl]          : 3.00
   Flow [µl / min]      : (unspecified)
   Max. pressure [Bar]  : 750.00


 Autosampler wash:

   Flush volume [µl]    : 100.00
```



Method Summary

Method Settings

Application Mode: **Peptide**
Method Duration (min): **110**

Global Parameters

Ion Source

Ion Source Type: **NSI**
Spray Voltage: **Static**
Positive Ion (V): **2000**
Negative Ion (V): **600**
Sweep Gas (Arb): **0**
Ion Transfer Tube Temp (°C): **280**
Use Ion Source Settings from Tune: **False**
FAIMS Mode: **Not Installed**

MS Global Settings

Infusion Mode: **Liquid Chromatography**
Expected LC Peak Width (s): **25**
Advanced Peak Determination: **True**
Default Charge State: **3**
Internal Mass Calibration: **EASY-IC™**
Mode: **Run Start**

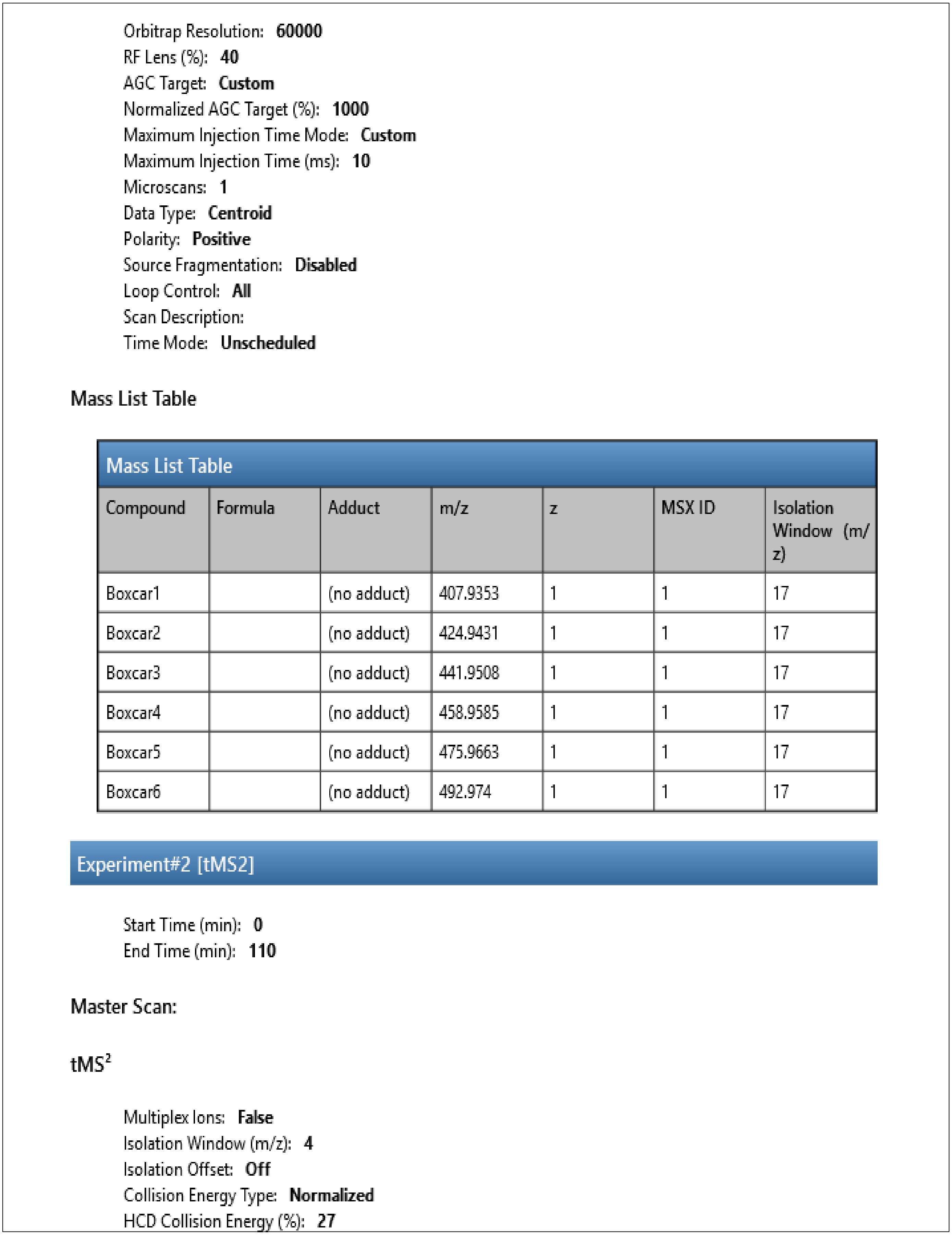
Experiment#1 [tSIM]

Start Time (min): **0**
End Time (min): **110**

Master Scan:

tSIM

Multiplex Ions: **True**
Maximum number of multiplexed ions: **6**
Define Multiplexing Groups (MSX ID): **User-defined**
Isolation Offset: **Off**



Orbitrap Resolution: **60000**
RF Lens (%): **40**
AGC Target: **Custom**
Normalized AGC Target (%): **1000**
Maximum Injection Time Mode: **Custom**
Maximum Injection Time (ms): **10**
Microscans: **1**
Data Type: **Centroid**
Polarity: **Positive**
Source Fragmentation: **Disabled**
Loop Control: **All**
Scan Description:
Time Mode: **Unscheduled**

Mass List Table

Mass List Table

Compound	Formula	Adduct	m/z	z	MSX ID	Isolation Window (m/z)
Boxcar1		(no adduct)	407.9353	1	1	17
Boxcar2		(no adduct)	424.9431	1	1	17
Boxcar3		(no adduct)	441.9508	1	1	17
Boxcar4		(no adduct)	458.9585	1	1	17
Boxcar5		(no adduct)	475.9663	1	1	17
Boxcar6		(no adduct)	492.974	1	1	17

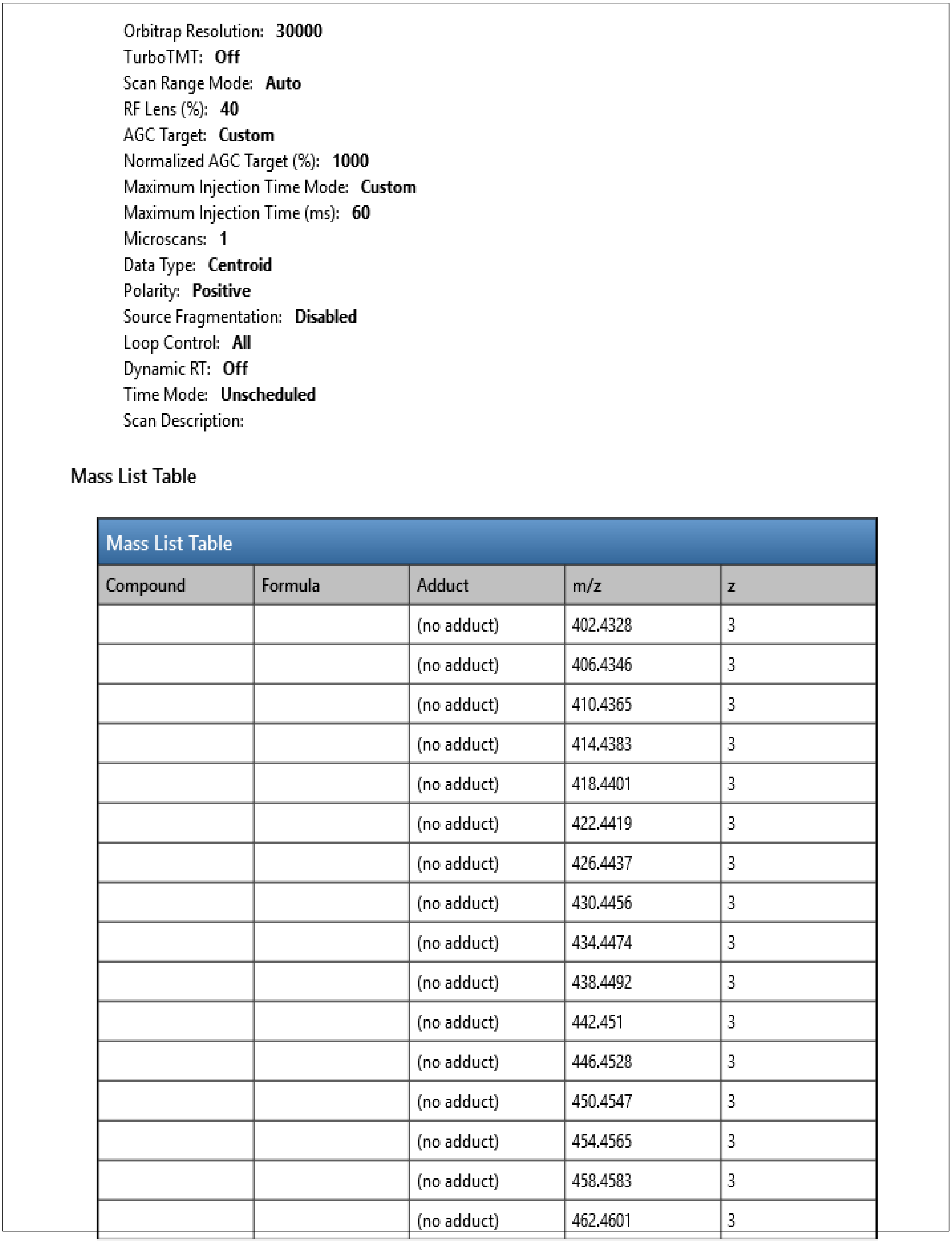
Experiment#2 [tMS2]

Start Time (min): **0**
End Time (min): **110**

Master Scan:

tMS^2

Multiplex Ions: **False**
Isolation Window (m/z): **4**
Isolation Offset: **Off**
Collision Energy Type: **Normalized**
HCD Collision Energy (%): **27**

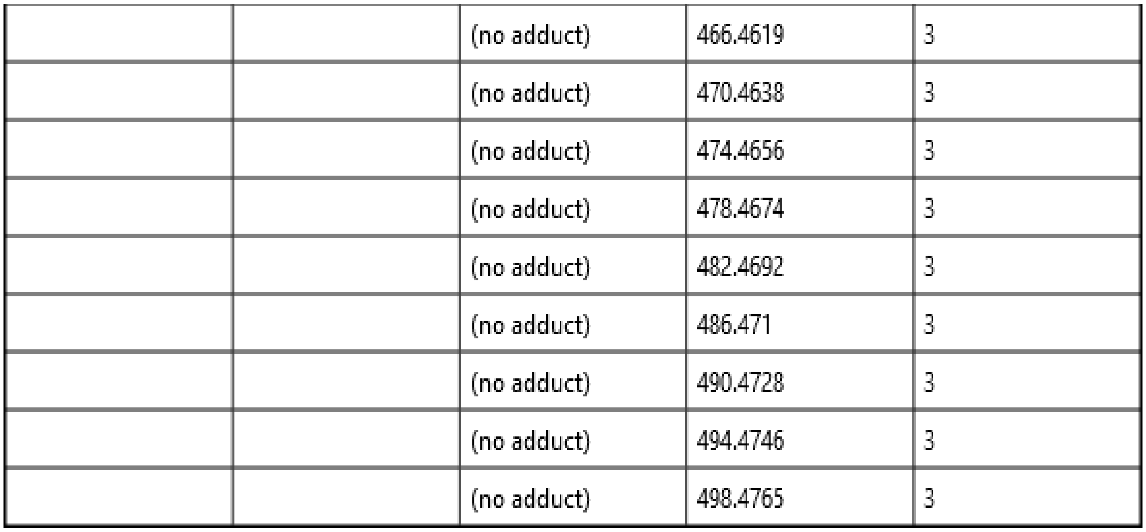


Orbitrap Resolution: **30000**
TurboTMT: **Off**
Scan Range Mode: **Auto**
RF Lens (%): **40**
AGC Target: **Custom**
Normalized AGC Target (%): **1000**
Maximum Injection Time Mode: **Custom**
Maximum Injection Time (ms): **60**
Microscans: **1**
Data Type: **Centroid**
Polarity: **Positive**
Source Fragmentation: **Disabled**
Loop Control: **All**
Dynamic RT: **Off**
Time Mode: **Unscheduled**
Scan Description:

Mass List Table

Mass List Table

Compound	Formula	Adduct	m/z	z
		(no adduct)	402.4328	3
		(no adduct)	406.4346	3
		(no adduct)	410.4365	3
		(no adduct)	414.4383	3
		(no adduct)	418.4401	3
		(no adduct)	422.4419	3
		(no adduct)	426.4437	3
		(no adduct)	430.4456	3
		(no adduct)	434.4474	3
		(no adduct)	438.4492	3
		(no adduct)	442.451	3
		(no adduct)	446.4528	3
		(no adduct)	450.4547	3
		(no adduct)	454.4565	3
		(no adduct)	458.4583	3
		(no adduct)	462.4601	3



		(no adduct)	466.4619	3
		(no adduct)	470.4638	3
		(no adduct)	474.4656	3
		(no adduct)	478.4674	3
		(no adduct)	482.4692	3
		(no adduct)	486.471	3
		(no adduct)	490.4728	3
		(no adduct)	494.4746	3
		(no adduct)	498.4765	3