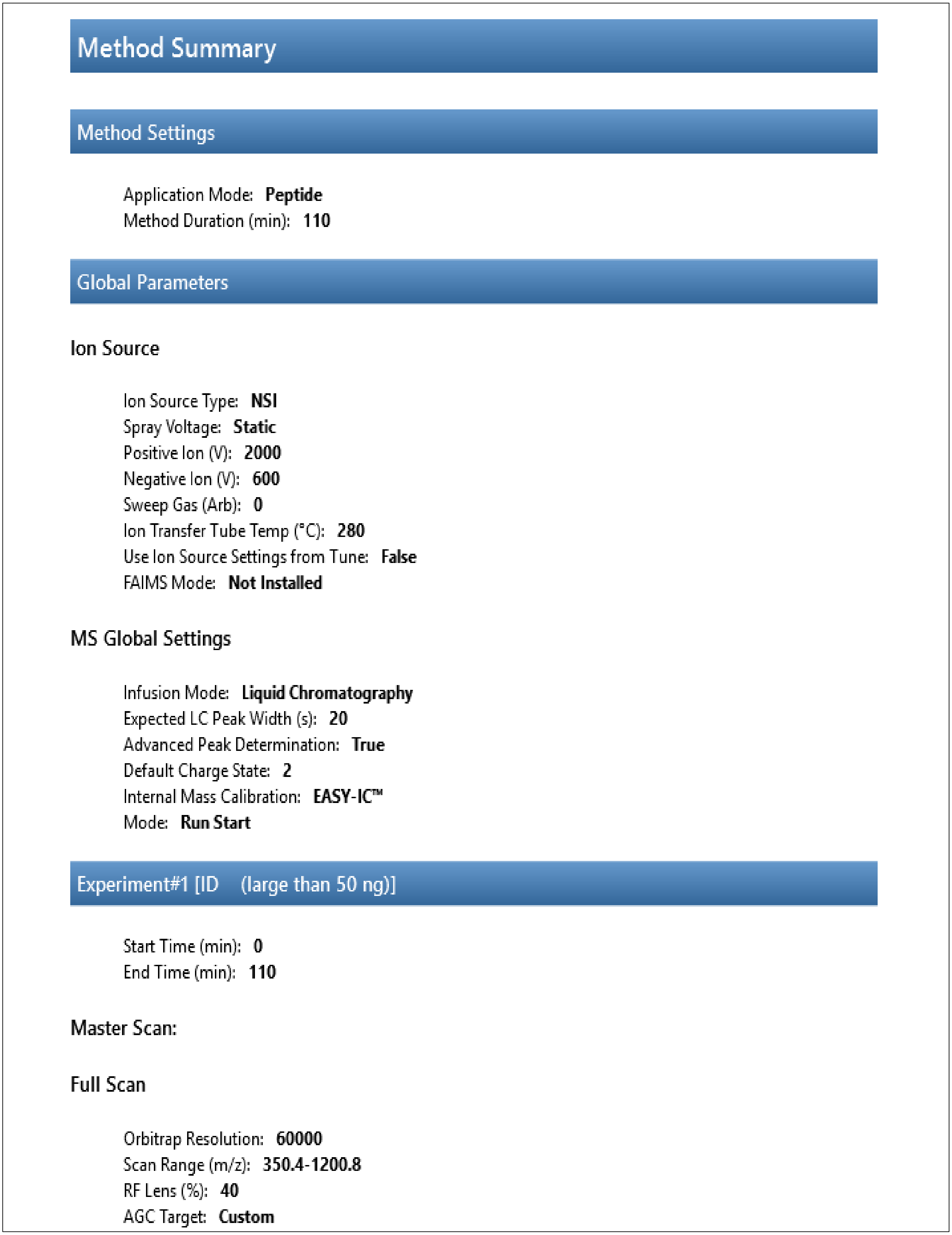
```
Thermo EASY-LC method print for Thermo


 Sample pickup:

   Volume [µl]         : 4.00
   Flow [µl / min]     : 10.00


 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             8.00
              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): **20**
Advanced Peak Determination: **True**
Default Charge State: **2**
Internal Mass Calibration: **EASY-IC™**
Mode: **Run Start**

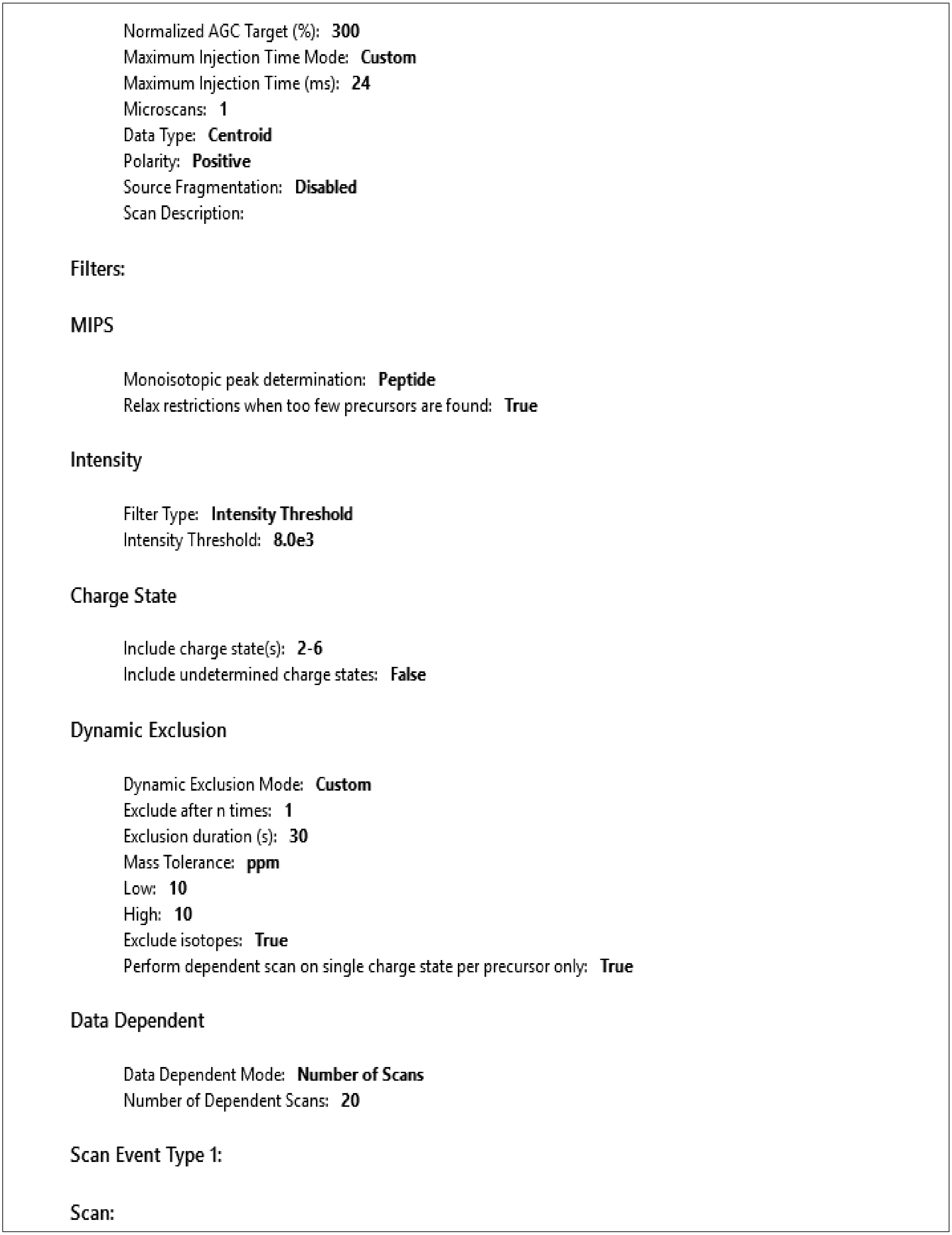
Experiment#1 [ID (large than 50 ng)]

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

Master Scan:

Full Scan

Orbitrap Resolution: **60000**
Scan Range (m/z): **350.4-1200.8**
RF Lens (%): **40**
AGC Target: **Custom**



Normalized AGC Target (%): **300**
Maximum Injection Time Mode: **Custom**
Maximum Injection Time (ms): **24**
Microscans: **1**
Data Type: **Centroid**
Polarity: **Positive**
Source Fragmentation: **Disabled**
Scan Description:

Filters:

MIPS

Monoisotopic peak determination: **Peptide**
Relax restrictions when too few precursors are found: **True**

Intensity

Filter Type: **Intensity Threshold**
Intensity Threshold: **8.0e3**

Charge State

Include charge state(s): **2-6**
Include undetermined charge states: **False**

Dynamic Exclusion

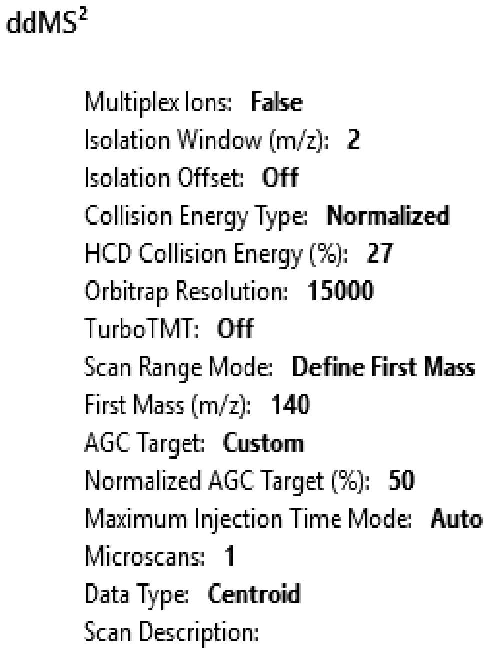
Dynamic Exclusion Mode: **Custom**
Exclude after n times: **1**
Exclusion duration (s): **30**
Mass Tolerance: **ppm**
Low: **10**
High: **10**
Exclude isotopes: **True**
Perform dependent scan on single charge state per precursor only: **True**

Data Dependent

Data Dependent Mode: **Number of Scans**
Number of Dependent Scans: **20**

Scan Event Type 1:

Scan:



ddMS^2

Multiplex Ions: **False**
Isolation Window (m/z): **2**
Isolation Offset: **Off**
Collision Energy Type: **Normalized**
HCD Collision Energy (%): **27**
Orbitrap Resolution: **15000**
TurboTMT: **Off**
Scan Range Mode: **Define First Mass**
First Mass (m/z): **140**
AGC Target: **Custom**
Normalized AGC Target (%): **50**
Maximum Injection Time Mode: **Auto**
Microscans: **1**
Data Type: **Centroid**
Scan Description: