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 [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): **4**
Microscans: **1**
Data Type: **Centroid**
Polarity: **Positive**
Source Fragmentation: **Disabled**
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)	413.4378	1	1	126
Boxcar2		(no adduct)	521.4869	1	1	90
Boxcar3		(no adduct)	611.0276	1	1	89
Boxcar4		(no adduct)	705.5706	1	1	100
Boxcar5		(no adduct)	823.124	1	1	135.1
Boxcar6		(no adduct)	1045.7252	1	1	310.1

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: