Creator: Elite super user

Last modified: 10/4/2011 by Elite Super user

MS Run Time (min): 120.00

Sequence override of method parameters not enabled.

Divert Valve: not used during run

Contact Closure: not used during run

Syringe Pump: not used during run

MS Detector Settings:

Real-time modifications to method disabled

Stepped collision energy not enabled

Additional Microscans:

MS2 0 0

MS3 0 0

MS4 0 0

MS5 0 0

MS6 0 0

MS7 0 0

MS8 0 0

MS9 0 0

MS10 0 0

Experiment Type: Nth Order Double Play

Tune Method: nanoESI\_03082011\_1us

Scan Event Details:

1: FTMS + p norm o(300.0-1650.0)

CV = 0.0V

2: FTMS + p norm Dep MS/MS Most intense ion from (1)

Activation Type: HCD

Min. Signal Required: 5000.0

Isolation Width: 2.00

Normalized Coll. Energy: 35.0

Default Charge State: 2

Activation Time: 0.100

FT first mass mode: fixed at m/z

FT first mass value: 120.00

CV = 0.0V

Scan Event 2 repeated for top 15 peaks.

Lock Masses:

Pos List Name: N/A

Source: API Source

Mass List: (none)

Neg List Name: N/A

Source: API Source

Mass List: (none)

Data Dependent Settings:

Use separate polarity settings disabled

Parent Mass List: (none)

Reject Mass List: (none)

Neutral Loss Mass List: (none)

Product Mass List: (none)

Neutral loss in top: 3

Product in top: 3

Most intense if no parent masses found not enabled

Add/subtract mass not enabled

FT master scan preview mode not enabled

Charge state screening enabled

Charge state dependent ETD time not enabled

Monoisotopic precursor selection enabled

Non-peptide monoisotopic recognition enabled

Charge state rejection enabled

Unassigned charge states : rejected

Charge state 1 : rejected

Charge state 2 : not rejected

Charge state 3 : not rejected

Charge states 4+ : not rejected

Chromatography mode is disabled

Global Data Dependent Settings:

Predict ion injection time enabled

Use global parent and reject mass lists not enabled

Exclude parent mass from data dependent selection not enabled

Exclusion mass width relative to mass

Exclusion mass width relative to low (ppm): 10.000

Exclusion mass width relative to high (ppm): 10.000

Parent mass width by mass

Parent mass width low: 0.50000

Parent mass width high: 0.50000

Reject mass width relative to mass

Reject mass width relative to low (ppm): 10.000

Reject mass width relative to high (ppm): 10.000

Zoom/UltraZoom scan mass width by mass

Zoom/UltraZoom scan mass width low: 5.00

Zoom/UltraZoom scan mass width high: 5.00

FT SIM scan mass width low: 5.00

FT SIM scan mass width high: 5.00

Neutral Loss candidates processed by decreasing intensity

Neutral Loss mass width by mass

Neutral Loss mass width low: 0.50000

Neutral Loss mass width high: 0.50000

Product candidates processed by decreasing intensity

Product mass width by mass

Product mass width low: 0.50000

Product mass width high: 0.50000

MS mass range: 0.00-1000000.00

MSn mass range by mass

MSn mass range: 0.00-1000000.00

Use m/z values as masses not enabled

Analog UV data dep. not enabled

Dynamic exclusion enabled

Repeat Count: 1

Repeat Duration: 30.00

Exclusion List Size: 500

Exclusion Duration: 60.00

Exclusion mass width relative to mass

Exclusion mass width relative to low (ppm): 10.000

Exclusion mass width relative to high (ppm): 10.000

Expiration: disabled

Isotopic data dependence not enabled

Custom Data Dependent Settings:

Not enabled