

Bovine-CSF_1_50uL-01
LTQ Orbitrap Velos MS

Creator: iOrbitrap
Last modified: 05/09/2012 by iOrbitrap

MS Run Time (min): 130.00

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: nanoLC+434

Scan Event Details:

- 1: FTMS + p norm !corona !pi o(380.0-2000.0)
CV = 0.0V
- 2: FTMS + c norm Dep Wideband MS/MS Most intense ion from (1)
Activation Type: HCD
Min. Signal Required: 500.0
Isolation Width: 1.00
Normalized Coll. Energy: 40.0
Default Charge State: 4
Activation Time: 0.200
FT first mass mode: fixed at m/z
FT first mass value: 100.00
CV = 0.0V

Scan Event 2 repeated for top 20 peaks.

Lock Masses:

Pos List Name:	445
Source:	API Source
Mass List:	445.119800
Neg List Name:	N/A
Source:	API Source
Mass List:	(none)

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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 enabled
Add/subtract mass not enabled
FT master scan preview mode enabled
Charge state screening enabled
Charge state dependent ETD time not enabled
Monoisotopic precursor selection enabled
Non-peptide monoisotopic recognition not 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): 5.000
Exclusion mass width relative to high (ppm): 5.000
Parent mass width relative to mass
Parent mass width relative to low (ppm): 3.000
Parent mass width relative to high (ppm): 3.000
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

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Dynamic exclusion enabled
Repeat Count: 1
Repeat Duration: 15.00
Exclusion List Size: 500
Exclusion Duration: 15.00
Exclusion mass width relative to mass
Exclusion mass width relative to low (ppm): 5.000
Exclusion mass width relative to high (ppm): 5.000
Expiration: disabled
Isotopic data dependence not enabled

Custom Data Dependent Settings:
Not enabled