

Method Summary

Method Settings

Application Mode: **Peptide**
Method Duration (min): **53**

Global Parameters

Ion Source

Ion Source Type: **NSI**
Spray Voltage: **Static**
Positive Ion (V): **1500**
Negative Ion (V): **1500**
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): **10**
Advanced Peak Determination: **True**
Default Charge State: **2**
Enable Xcalibur AcquireX Ab method modifications: **False**
Internal Mass Calibration: **Off**

Experiment #1 [MS]

Start Time (min): **0**
End Time (min): **53**

Master Scan:

Full Scan

Orbitrap Resolution: **120000**
Scan Range (m/z): **200-1500**
RF Lens (%): **60**
AGC Target: **Custom**
Normalized AGC Target (%): **100**
Maximum Injection Time Mode: **Auto**
Microscans: **1**
Data Type: **Centroid**
Polarity: **Positive**
Source Fragmentation: **Disabled**
Scan Description:

Experiment #2 [Product Ion Scan]

Start Time (min): **0**
End Time (min): **53**

Master Scan:

Product Ion

Multiplex Ions: **False**
 Q1 Resolution (m/z): **2**
 Q1 Offset: **m/z Offset**
 Q1 Offset (m/z): **0.1**
 Reported Mass: **Offset Mass**
 Collision Energy Type: **Normalized**
 Orbitrap Resolution: **30000**
 TurboTMT: **Off**
 Scan Range Mode: **Auto**
 RF Lens (%): **60**
 AGC Target: **Custom**
 Normalized AGC Target (%): **100**
 Maximum Injection Time Mode: **Auto**
 Microscans: **1**
 Data Type: **Centroid**
 Source Fragmentation: **Disabled**
 Loop Control: **N**
 N (Number of Spectra): **30**
 Dynamic RT: **Off**
 Scan Description: **SST**
 Time Mode: **Unscheduled**

Product Ion Scan

Product Ion Scan						
Compound	Formula	Adduct	Precursor (m/z)	Precursor Charge (z)	Collision Energies (%)	Polarity
SSAAPPPPPR (heavy)		(no adduct)	493.7683	2	28	Positive
SSAAPPPPPR (heavy)		(no adduct)	329.5146	3	28	Positive
GISNEGQNASIK (heavy)		(no adduct)	613.3168	2	28	Positive
GISNEGQNASIK (heavy)		(no adduct)	409.2136	3	28	Positive
HVLTSIGEK (heavy)		(no adduct)	496.2867	2	28	Positive
HVLTSIGEK (heavy)		(no adduct)	331.1936	3	28	Positive
DIPVPKPK (heavy)		(no adduct)	451.2835	2	28	Positive
DIPVPKPK (heavy)		(no adduct)	301.1914	3	28	Positive
IGDYAGIK (heavy)		(no adduct)	422.7364	2	28	Positive
IGDYAGIK (heavy)		(no adduct)	282.16	3	28	Positive
TASEFDSAIAQDK (heavy)		(no adduct)	695.8324	2	28	Positive
TASEFDSAIAQDK (heavy)		(no adduct)	464.2241	3	28	Positive
SAAGAFGPESLR (heavy)		(no adduct)	586.8003	2	28	Positive
SAAGAFGPESLR (heavy)		(no adduct)	391.536	3	28	Positive
ELQSGVDTYLQ TK (heavy)		(no adduct)	773.8956	2	28	Positive
ELQSGVDTYLQ TK (heavy)		(no adduct)	516.2661	3	28	Positive
GLILVGGYGTR (heavy)		(no adduct)	558.326	2	28	Positive
GLILVGGYGTR (heavy)		(no adduct)	372.5531	3	28	Positive

GILFVSGVSGGE EGAR (heavy)	(no adduct)	801.4115	2	28	Positive
GILFVSGVSGGE EGAR (heavy)	(no adduct)	534.6101	3	28	Positive
SFANQPLEVVYS K (heavy)	(no adduct)	745.3925	2	28	Positive
SFANQPLEVVYS K (heavy)	(no adduct)	497.2641	3	28	Positive
LTILEELR (heavy)	(no adduct)	498.8018	2	28	Positive
LTILEELR (heavy)	(no adduct)	332.8703	3	28	Positive
NGFILDGFPR (heavy)	(no adduct)	573.3025	2	28	Positive
NGFILDGFPR (heavy)	(no adduct)	382.5374	3	28	Positive
ELASGLSFPVGFK (heavy)	(no adduct)	680.3736	2	28	Positive
ELASGLSFPVGFK (heavy)	(no adduct)	453.9181	3	28	Positive
LSSEAPALFQFDL K (heavy)	(no adduct)	787.4212	2	28	Positive
LSSEAPALFQFDL K (heavy)	(no adduct)	525.2832	3	28	Positive