

Additional Data File 5: MS/MS spectra and fragment assignments of single peptide-based identifications (Part 2)

Gene symbol: EG238662

Protein name: similar to vitamin A-deficient testicular protein 11-like

Protein accession numbers: IPI00553346,IPI00664742

Peptide sequence: APEETQGLTASPALTEPK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.95 SEQUEST DCn score: 0.483

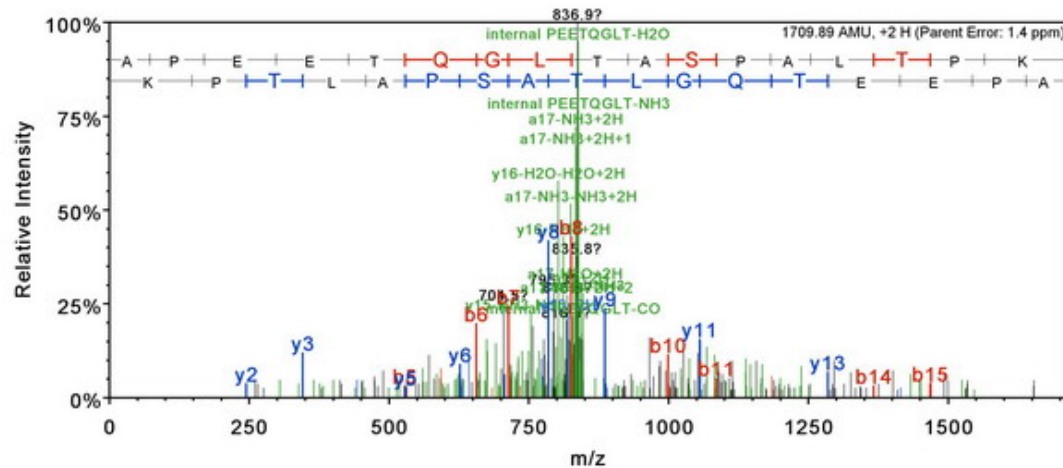
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 855.951

Actual minus calculated peptide mass (AMU): 0.002319



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1710.9	856.0	1693.9	1692.9	17
2	169.1				P	1639.9	820.4	1622.8	1621.8	16
3	298.1			280.1	E	1542.8	771.9	1525.8	1524.8	15
4	427.2			409.2	E	1413.8	707.4	1396.7	1395.8	14
5	528.2			510.2	T	1284.7	642.9	1267.7	1266.7	13
6	656.3	328.7	639.3	638.3	Q	1183.7	592.3	1166.6	1165.7	12
7	713.3	357.2	696.3	695.3	G	1055.6	528.3	1038.6	1037.6	11
8	826.4	413.7	809.4	808.4	L	998.6	499.8	981.6	980.6	10
9	927.4	464.2	910.4	909.4	T	885.5	443.3	868.5	867.5	9
10	998.5	499.7	981.5	980.5	A	784.5	392.7	767.4	766.5	8
11	1085.5	543.3	1068.5	1067.5	S	713.4	357.2	696.4	695.4	7
12	1182.6	591.8	1165.5	1164.5	P	626.4	313.7	609.4	608.4	6
13	1253.6	627.3	1236.6	1235.6	A	529.3		512.3	511.3	5
14	1366.7	683.9	1349.7	1348.7	L	458.3		441.3	440.3	4
15	1467.7	734.4	1450.7	1449.7	T	345.2		328.2	327.2	3
16	1564.8	782.9	1547.8	1546.8	P	244.2		227.1		2
17	1710.9	856.0	1693.9	1692.9	K	147.1		130.1		1

Gene symbol: EG432825

Protein name: Predicted

Protein accession numbers: IPI00420449

Peptide sequence: NTSTQNSNITNQISNINK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.47 SEQUEST DCn score: 0.594

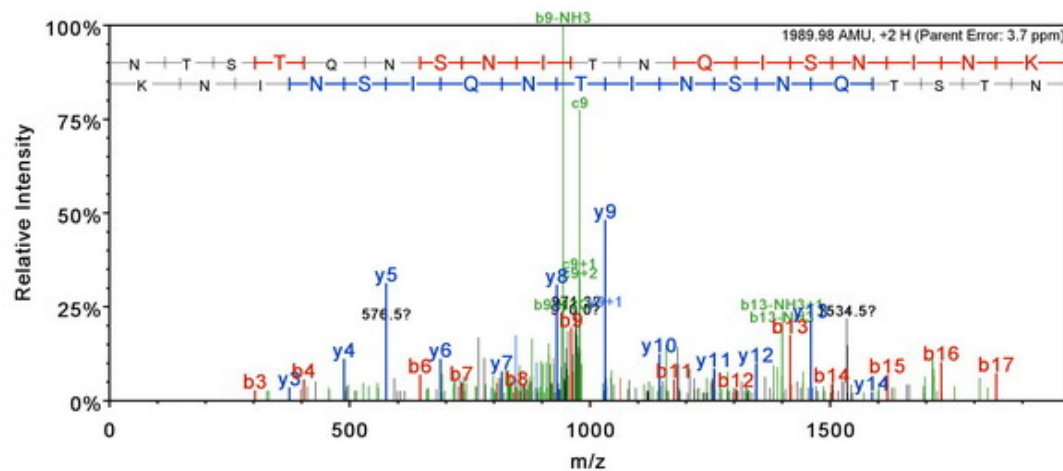
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 995.9972

Actual minus calculated peptide mass (AMU): 0.007324



Peptide sequence: TLTTVQGIADDYDK

Exclusive (unique to this protein): TRUE

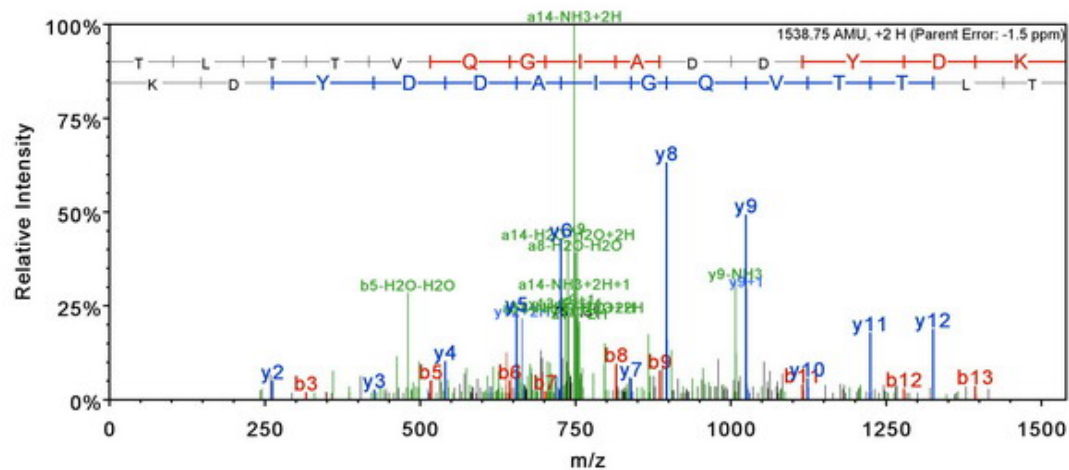
SEQUEST XCorr score: 2.81 SEQUEST DCn score: 0.643

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 770.3801

Actual minus calculated peptide mass (AMU): -0.002319



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1539.8	770.4	1522.7	1521.7	14
2	215.1			197.1	L	1438.7	719.9	1421.7	1420.7	13
3	316.2			298.2	T	1325.6	663.3	1308.6	1307.6	12
4	417.2			399.2	T	1224.6	612.8	1207.5	1206.6	11
5	516.3			498.3	V	1123.5	562.3	1106.5	1105.5	10
6	644.4	322.7	627.3	626.4	Q	1024.5	512.7	1007.4	1006.5	9
7	701.4	351.2	684.4	683.4	G	896.4	448.7	879.4	878.4	8
8	814.5	407.7	797.4	796.5	I	839.4	420.2	822.4	821.4	7
9	885.5	443.3	868.5	867.5	A	726.3	363.7	709.3	708.3	6
10	1000.5	500.8	983.5	982.5	D	655.3		638.2	637.3	5
11	1115.6	558.3	1098.5	1097.5	D	540.2		523.2	522.2	4
12	1278.6	639.8	1261.6	1260.6	Y	425.2		408.2	407.2	3
13	1393.7	697.3	1376.6	1375.6	D	262.1		245.1	244.1	2
14	1539.8	770.4	1522.7	1521.7	K	147.1		130.1		1

Gene symbol: EG436081

Protein name: similar to ribosomal protein L36

Protein accession numbers: IPI00463297,IPI00474487,IPI00555019,IPI00853670

Peptide sequence: EELSNVLAAMR

Exclusive (unique to this protein): TRUE

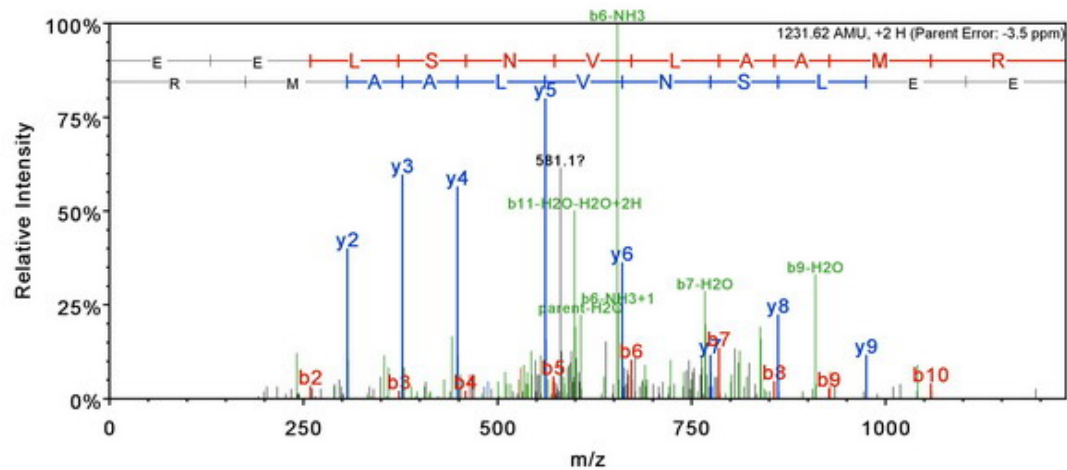
SEQUEST XCorr score: 2.84 SEQUEST DCn score: 0.636

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 616.8173

Actual minus calculated peptide mass (AMU): -0.004273



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1232.6	616.8	1215.6	1214.6	11
2	259.1			241.1	E	1103.6	552.3	1086.6	1085.6	10
3	372.2			354.2	L	974.6	487.8	957.5	956.5	9
4	459.2			441.2	S	861.5	431.2	844.4	843.5	8
5	573.3		556.2	555.2	N	774.4	387.7	757.4		7
6	672.3	336.7	655.3	654.3	V	660.4	330.7	643.4		6
7	785.4	393.2	768.4	767.4	L	561.3		544.3		5
8	856.4	428.7	839.4	838.4	A	448.2		431.2		4
9	927.5	464.2	910.5	909.5	A	377.2		360.2		3
10	1058.5	529.8	1041.5	1040.5	M	306.2		289.1		2
11	1232.6	616.8	1215.6	1214.6	R	175.1		158.1		1

Gene symbol: EG545013

Protein name: Predicted

Protein accession numbers: IPI00474846

Peptide sequence: NTSTQNYNITNQILNINK

Exclusive (unique to this protein): TRUE

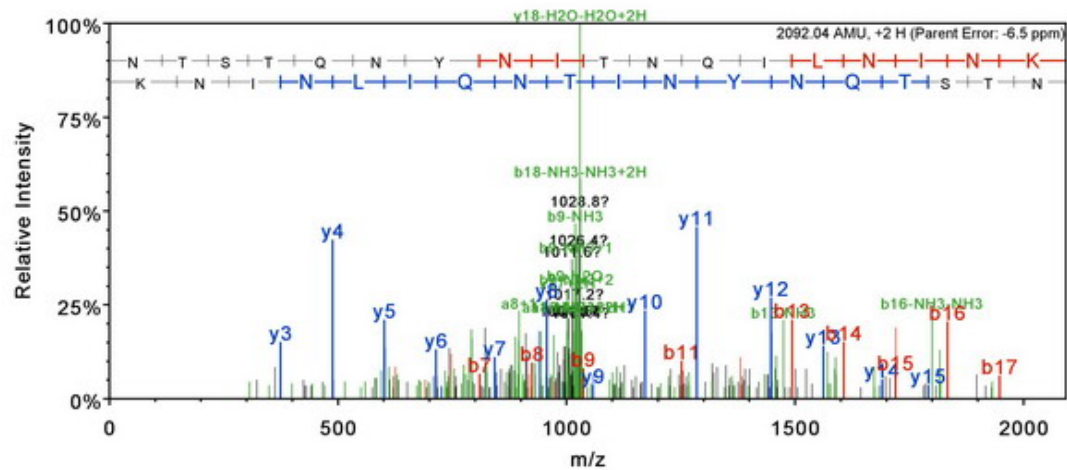
SEQUEST XCorr score: 4.03 SEQUEST DCn score: 0.653

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1047.0283

Actual minus calculated peptide mass (AMU): -0.013655



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	2093.1	1047.0	2076.0	2075.1	18
2	216.1		199.1	198.1	T	1979.0	990.0	1962.0	1961.0	17
3	303.1		286.1	285.1	S	1878.0	939.5	1861.0	1860.0	16
4	404.2		387.2	386.2	T	1790.9	896.0	1773.9	1772.9	15
5	532.2		515.2	514.2	Q	1689.9	845.5	1672.9	1671.9	14
6	646.3	323.6	629.3	628.3	N	1561.8	781.4	1544.8	1543.8	13
7	809.3	405.2	792.3	791.3	Y	1447.8	724.4	1430.8	1429.8	12
8	923.4	462.2	906.4	905.4	N	1284.7	642.9	1267.7	1266.7	11
9	1036.5	518.7	1019.4	1018.5	I	1170.7	585.9	1153.7	1152.7	10
10	1137.5	569.3	1120.5	1119.5	T	1057.6	529.3	1040.6	1039.6	9
11	1251.6	626.3	1234.5	1233.5	N	956.6	478.8	939.5		8
12	1379.6	690.3	1362.6	1361.6	Q	842.5	421.8	825.5		7
13	1492.7	746.9	1475.7	1474.7	I	714.5	357.7	697.4		6
14	1605.8	803.4	1588.8	1587.8	L	601.4		584.3		5
15	1719.8	860.4	1702.8	1701.8	N	488.3		471.3		4
16	1832.9	917.0	1815.9	1814.9	I	374.2		357.2		3
17	1947.0	974.0	1929.9	1929.0	N	261.2		244.1		2
18	2093.1	1047.0	2076.0	2075.1	K	147.1		130.1		1

Gene symbol: EG546265

Protein name: similar to Ubiquitin-conjugating enzyme E2 I

Protein accession numbers: IPI00462940

Peptide sequence: MLFKDDYPSSPPK

Exclusive (unique to this protein): TRUE

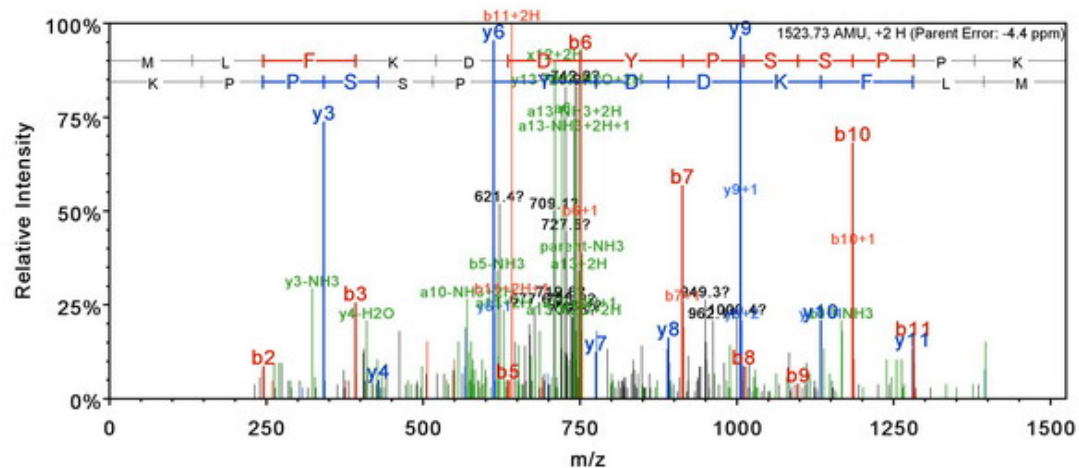
SEQUEST XCorr score: 3.46 SEQUEST DCn score: 0.597

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 762.8711

Actual minus calculated peptide mass (AMU): -0.0067152



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1524.7	762.9	1507.7	1506.7	13
2	245.1				L	1393.7	697.4	1376.7	1375.7	12
3	392.2				F	1280.6	640.8	1263.6	1262.6	11
4	520.3	260.6	503.3		K	1133.5	567.3	1116.5	1115.5	10
5	635.3	318.2	618.3	617.3	D	1005.5	503.2	988.4	987.4	9
6	750.4	375.7	733.3	732.3	D	890.4	445.7	873.4	872.4	8
7	913.4	457.2	896.4	895.4	Y	775.4	388.2	758.4	757.4	7
8	1010.5	505.7	993.4	992.5	P	612.3	306.7	595.3	594.3	6
9	1097.5	549.3	1080.5	1079.5	S	515.3		498.3	497.3	5
10	1184.5	592.8	1167.5	1166.5	S	428.3		411.2	410.2	4
11	1281.6	641.3	1264.6	1263.6	P	341.2		324.2		3
12	1378.6	689.8	1361.6	1360.6	P	244.2		227.1		2
13	1524.7	762.9	1507.7	1506.7	K	147.1		130.1		1

Gene symbol: EG622236

Protein name: similar to ribosomal protein L27 isoform 1

Protein accession numbers: IPI00623893

Peptide sequence: YSVDIPLDK

Exclusive (unique to this protein): TRUE

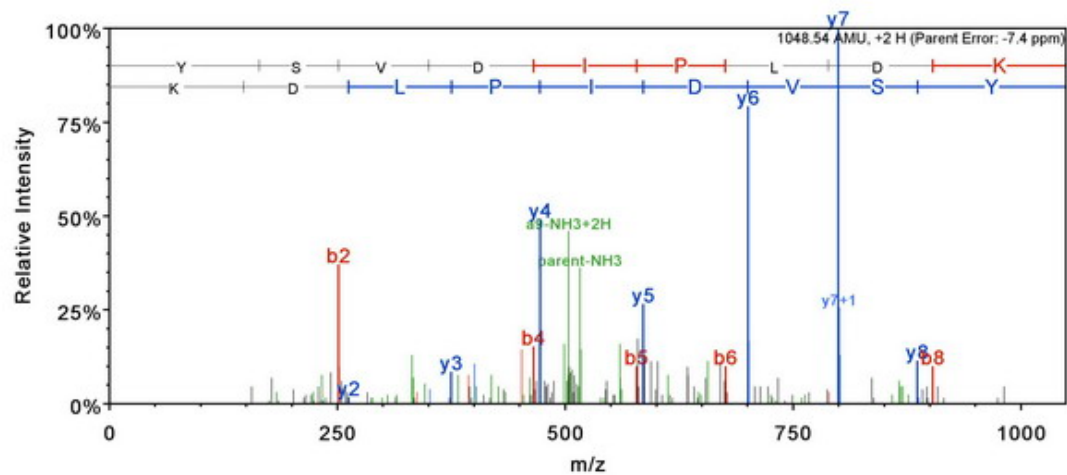
SEQUEST XCorr score: 2.57 SEQUEST DCn score: 0.513

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 525.2761

Actual minus calculated peptide mass (AMU): -0.007813



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1049.5	525.3	1032.5	1031.5	9
2	251.1			233.1	S	886.5	443.8	869.5	868.5	8
3	350.2			332.2	V	799.5	400.2	782.4	781.5	7
4	465.2			447.2	D	700.4	350.7	683.4	682.4	6
5	578.3			560.3	I	585.4		568.3	567.4	5
6	675.3	338.2		657.3	P	472.3		455.3	454.3	4
7	788.4	394.7		770.4	L	375.2		358.2	357.2	3
8	903.5	452.2		885.4	D	262.1		245.1	244.1	2
9	1049.5	525.3	1032.5	1031.5	K	147.1		130.1		1

Gene symbol: EG622589

Protein name: similar to 60S ribosomal protein L12

Protein accession numbers: IPI00457862

Peptide sequence: QAQIEVVPSASALIIK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.42 SEQUEST DCn score: 0.644

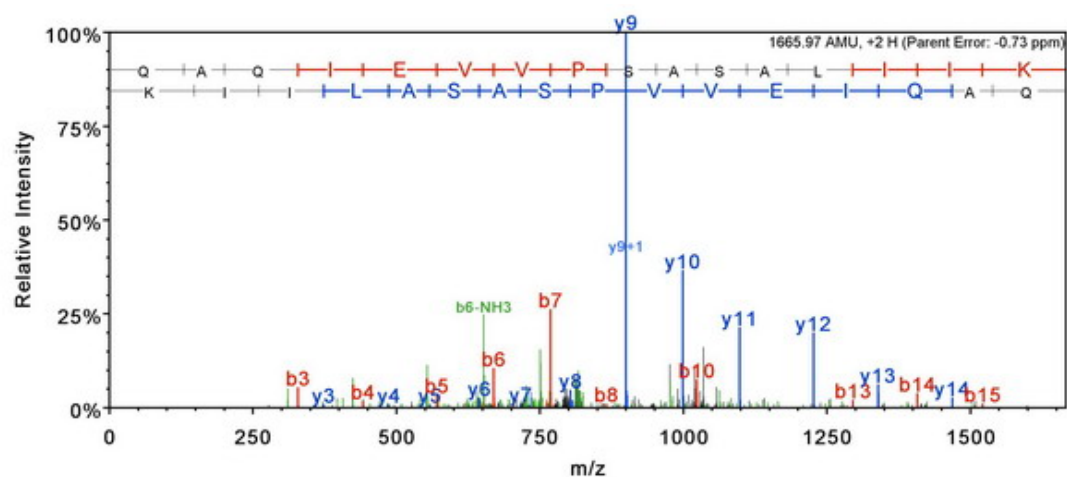
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 833.9906

Actual minus calculated peptide mass (AMU): -0.0012249



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	1667.0	834.0	1650.0	1649.0	16
2	200.1		183.1		A	1538.9	770.0	1521.9	1520.9	15
3	328.2		311.1		Q	1467.9	734.4	1450.9	1449.9	14
4	441.3		424.2		I	1339.8	670.4	1322.8	1321.8	13
5	570.3		553.3	552.3	E	1226.7	613.9	1209.7	1208.7	12
6	669.4	335.2	652.3	651.4	V	1097.7	549.4	1080.7	1079.7	11
7	768.4	384.7	751.4	750.4	V	998.6	499.8	981.6	980.6	10
8	865.5	433.2	848.5	847.5	P	899.6	450.3	882.5	881.6	9
9	952.5	476.8	935.5	934.5	S	802.5	401.8	785.5	784.5	8
10	1023.6	512.3	1006.5	1005.5	A	715.5	358.2	698.5	697.5	7
11	1110.6	555.8	1093.5	1092.6	S	644.4	322.7	627.4	626.4	6
12	1181.6	591.3	1164.6	1163.6	A	557.4		540.4		5
13	1294.7	647.9	1277.7	1276.7	L	486.4		469.3		4
14	1407.8	704.4	1390.8	1389.8	I	373.3		356.3		3
15	1520.9	760.9	1503.8	1502.9	I	260.2		243.2		2
16	1667.0	834.0	1650.0	1649.0	K	147.1		130.1		1

Gene symbol: EG625716

Protein name: similar to organic anion transporting polypeptide 3 isoform 1

Protein accession numbers: IPI00659001,IPI00673552

Peptide sequence: VFGGIPAPVYIGALLDR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.56 SEQUEST DCn score: 0.403

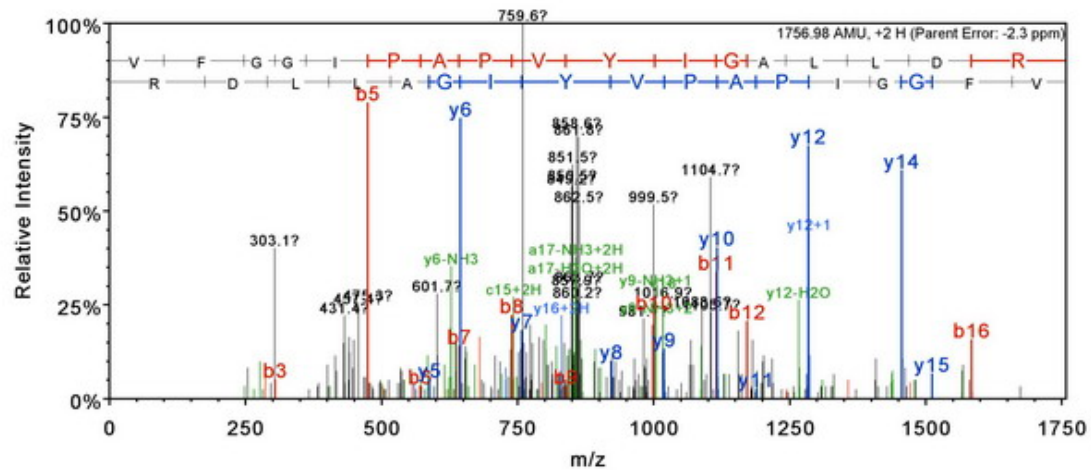
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 879.4998

Actual minus calculated peptide mass (AMU): -0.0040256



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1758.0	879.5	1741.0	1740.0	17
2	247.1				F	1658.9	830.0	1641.9	1640.9	16
3	304.2				G	1511.9	756.4	1494.8	1493.9	15
4	361.2				G	1454.8	727.9	1437.8	1436.8	14
5	474.3				I	1397.8	699.4	1380.8	1379.8	13
6	571.3	286.2			P	1284.7	642.9	1267.7	1266.7	12
7	642.4	321.7			A	1187.7	594.3	1170.7	1169.7	11
8	739.4	370.2			P	1116.6	558.8	1099.6	1098.6	10
9	838.5	419.8			V	1019.6	510.3	1002.6	1001.6	9
10	1001.6	501.3			Y	920.5	460.8	903.5	902.5	8
11	1114.6	557.8			I	757.5	379.2	740.4	739.5	7
12	1171.7	586.3			G	644.4	322.7	627.4	626.4	6
13	1242.7	621.9			A	587.4		570.3	569.3	5
14	1355.8	678.4			L	516.3		499.3	498.3	4
15	1468.9	734.9			L	403.2		386.2	385.2	3
16	1583.9	792.5		1565.9	D	290.2		273.1	272.1	2
17	1758.0	879.5	1741.0	1740.0	R	175.1		158.1		1

Gene symbol: EG667525;LOC676948;LOC100043269

Protein name: similar to 40S ribosomal protein S19

Protein accession numbers: IPI00665513

Peptide sequence: ELAPYDENWFYTR

Exclusive (unique to this protein): TRUE

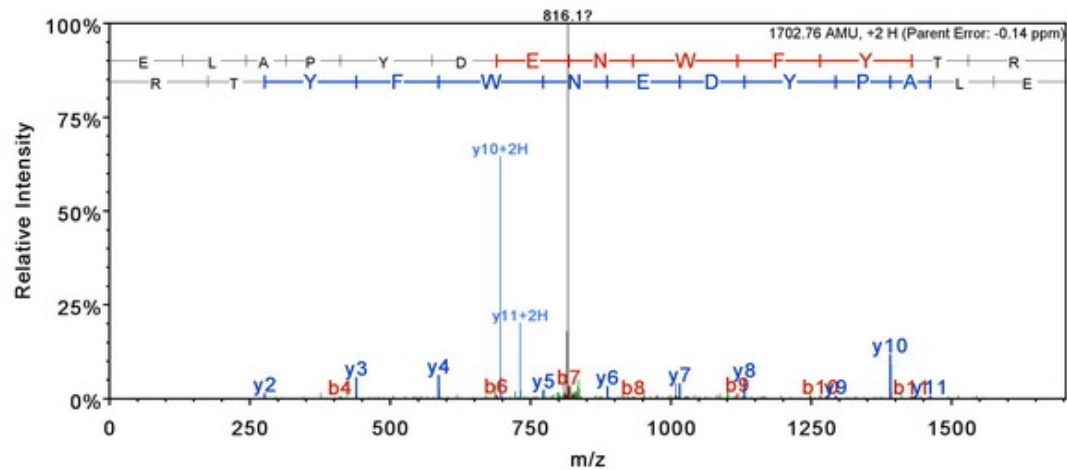
SEQUEST XCorr score: 3.08 SEQUEST DCn score: 0.684

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 852.389

Actual minus calculated peptide mass (AMU): -0.0002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1703.8	852.4	1686.7	1685.8	13
2	243.1			225.1	L	1574.7	787.9	1557.7	1556.7	12
3	314.2			296.2	A	1461.6	731.3	1444.6	1443.6	11
4	411.2			393.2	P	1390.6	695.8	1373.6	1372.6	10
5	574.3			556.3	Y	1293.5	647.3	1276.5	1275.5	9
6	689.3	345.2		671.3	D	1130.5	565.8	1113.5	1112.5	8
7	818.4	409.7		800.4	E	1015.5	508.2	998.4	997.5	7
8	932.4	466.7	915.4	914.4	N	886.4	443.7	869.4	868.4	6
9	1118.5	559.7	1101.5	1100.5	W	772.4		755.4	754.4	5
10	1265.5	633.3	1248.5	1247.5	F	586.3		569.3	568.3	4
11	1428.6	714.8	1411.6	1410.6	Y	439.2		422.2	421.2	3
12	1529.7	765.3	1512.6	1511.7	T	276.2		259.1	258.2	2
13	1703.8	852.4	1686.7	1685.8	R	175.1		158.1		1

Gene symbol: Eif2b1

Protein name: Translation initiation factor eIF-2B subunit alpha

Protein accession numbers: IPI00116761

Peptide sequence: FISLTSLEYSDYSK

Exclusive (unique to this protein): TRUE

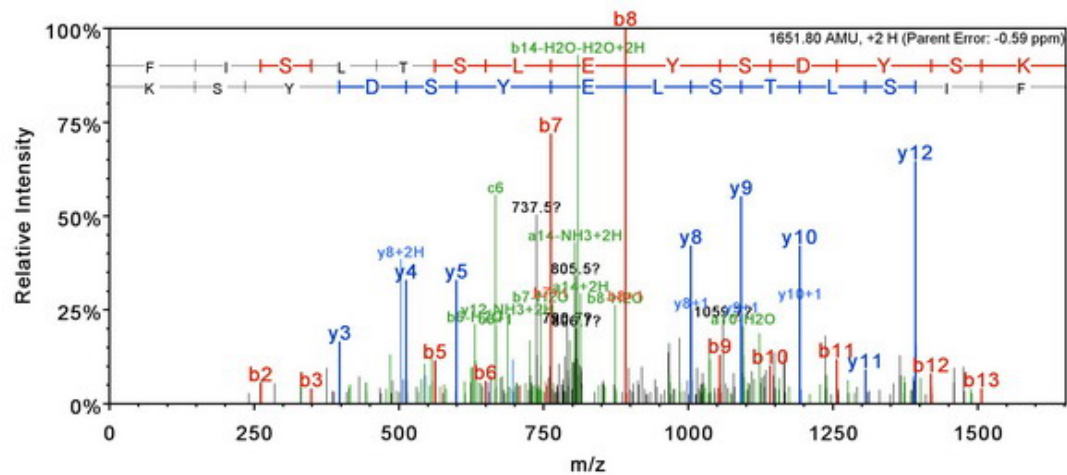
SEQUEST XCorr score: 4.1 SEQUEST DCn score: 0.57

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 826.9064

Actual minus calculated peptide mass (AMU): -0.0009766



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1652.8	826.9	1635.8	1634.8	14
2	261.2				I	1505.7	753.4	1488.7	1487.7	13
3	348.2			330.2	S	1392.7	696.8	1375.6	1374.6	12
4	461.3			443.3	L	1305.6	653.3	1288.6	1287.6	11
5	562.3			544.3	T	1192.5	596.8	1175.5	1174.5	10
6	649.4	325.2		631.4	S	1091.5	546.3	1074.5	1073.5	9
7	762.4	381.7		744.4	L	1004.5	502.7	987.4	986.5	8
8	891.5	446.3		873.5	E	891.4	446.2	874.4	873.4	7
9	1054.5	527.8		1036.5	Y	762.3	381.7	745.3	744.3	6
10	1141.6	571.3		1123.6	S	599.3		582.2	581.3	5
11	1256.6	628.8		1238.6	D	512.2		495.2	494.2	4
12	1419.7	710.3		1401.7	Y	397.2		380.2	379.2	3
13	1506.7	753.9		1488.7	S	234.2		217.1	216.1	2
14	1652.8	826.9	1635.8	1634.8	K	147.1		130.1		1

Gene symbol: Eif2b3

Protein name: Eukaryotic translation initiation factor 2B, subunit 3

Protein accession numbers: IPI00126069,IPI00648960

Peptide sequence: YVVDLFMENR

Exclusive (unique to this protein): TRUE

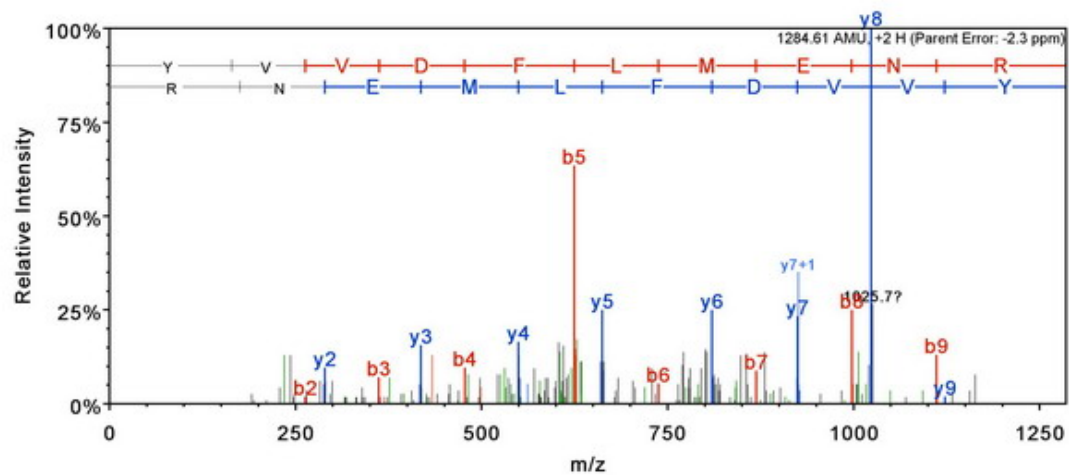
SEQUEST XCorr score: 3.41 SEQUEST DCn score: 0.498

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 643.3149

Actual minus calculated peptide mass (AMU): -0.00293



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1285.6	643.3	1268.6	1267.6	10
2	263.1				V	1122.6	561.8	1105.5	1104.5	9
3	362.2				V	1023.5	512.3	1006.5	1005.5	8
4	477.2			459.2	D	924.4	462.7	907.4	906.4	7
5	624.3			606.3	F	809.4	405.2	792.4	791.4	6
6	737.4	369.2		719.4	L	662.3		645.3	644.3	5
7	868.4	434.7		850.4	M	549.3		532.2	531.2	4
8	997.5	499.2		979.5	E	418.2		401.2	400.2	3
9	1111.5	556.3	1094.5	1093.5	N	289.2		272.1		2
10	1285.6	643.3	1268.6	1267.6	R	175.1		158.1		1

Gene symbol: Eif3s3

Protein name: Eukaryotic translation initiation factor 3 subunit 3

Protein accession numbers: IPI00128202

Peptide sequence: VDEMSQDIK

Exclusive (unique to this protein): TRUE

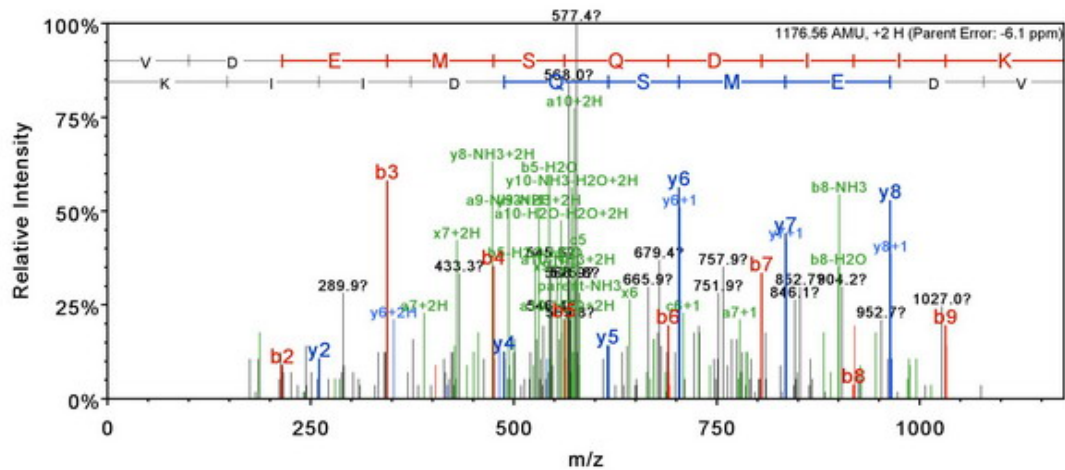
SEQUEST XCorr score: 2.55 SEQUEST DCn score: 0.447

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 589.2891

Actual minus calculated peptide mass (AMU): -0.007202



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1177.6	589.3	1160.5	1159.6	10
2	215.1			197.1	D	1078.5	539.8	1061.5	1060.5	9
3	344.2			326.1	E	963.5	482.3	946.5	945.5	8
4	475.2			457.2	M	834.4	417.7	817.4	816.4	7
5	562.2			544.2	S	703.4	352.2	686.4	685.4	6
6	690.3	345.6	673.3	672.3	Q	616.4		599.3	598.4	5
7	805.3	403.2	788.3	787.3	D	488.3		471.3	470.3	4
8	918.4	459.7	901.4	900.4	I	373.3		356.3		3
9	1031.5	516.2	1014.5	1013.5	I	260.2		243.2		2
10	1177.6	589.3	1160.5	1159.6	K	147.1		130.1		1

Gene symbol: Eif3s4

Protein name: Eukaryotic translation initiation factor 3 subunit 4

Protein accession numbers: IPI00622371

Peptide sequence: ELAEQLGLSTGEK

Exclusive (unique to this protein): TRUE

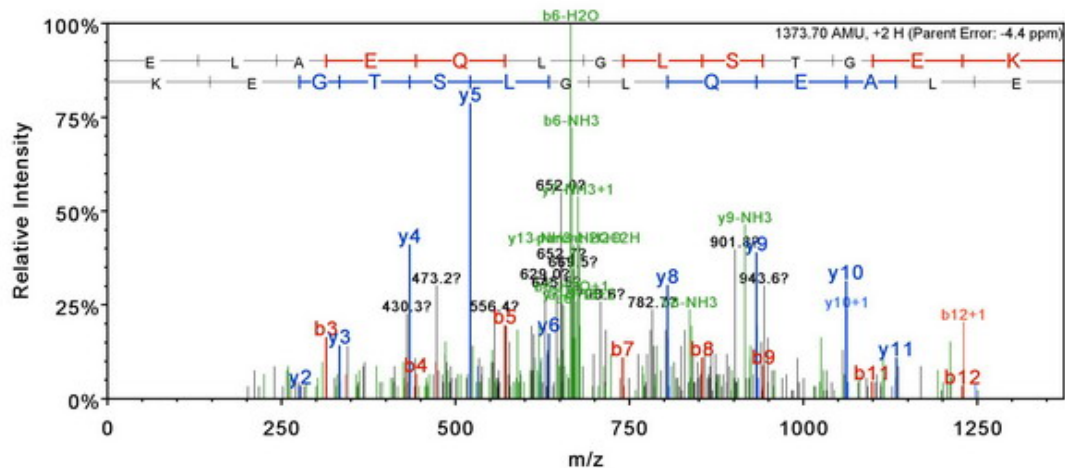
SEQUEST XCorr score: 2.56 SEQUEST DCn score: 0.441

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 687.8569

Actual minus calculated peptide mass (AMU): -0.0059849



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1374.7	687.9	1357.7	1356.7	13
2	243.1			225.1	L	1245.7	623.3	1228.6	1227.7	12
3	314.2			296.2	A	1132.6	566.8	1115.6	1114.6	11
4	443.2			425.2	E	1061.5	531.3	1044.5	1043.5	10
5	571.3		554.3	553.3	Q	932.5	466.8	915.5	914.5	9
6	684.4	342.7	667.3	666.4	L	804.5	402.7	787.4	786.4	8
7	741.4	371.2	724.4	723.4	G	691.4	346.2	674.3	673.4	7
8	854.5	427.7	837.4	836.5	L	634.3	317.7	617.3	616.3	6
9	941.5	471.3	924.5	923.5	S	521.3		504.2	503.3	5
10	1042.5	521.8	1025.5	1024.5	T	434.2		417.2	416.2	4
11	1099.6	550.3	1082.5	1081.5	G	333.2		316.2	315.2	3
12	1228.6	614.8	1211.6	1210.6	E	276.2		259.1	258.1	2
13	1374.7	687.9	1357.7	1356.7	K	147.1		130.1		1

Gene symbol: ENSMUSG00000074356;Cdkn2aip

Protein name: 16 days embryo head cDNA, RIKEN full-length enriched library,
clone:C130060J12 product:similar to PUTATIVE SERINE-RICH PROTEIN

Protein accession numbers: IPI00263028

Peptide sequence: NAGDLVPATDETADAESGAR

Exclusive (unique to this protein): TRUE

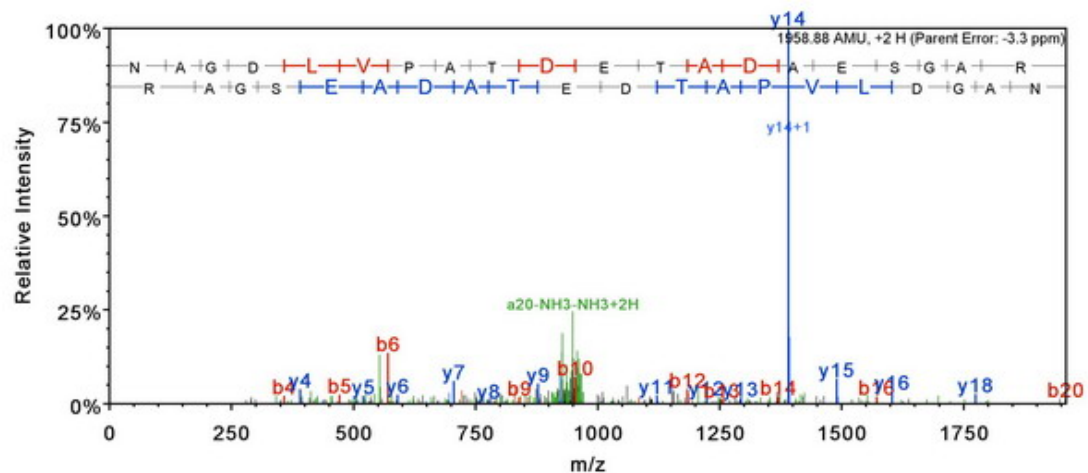
SEQUEST XCorr score: 3.33 SEQUEST DCn score: 0.61

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 980.4456

Actual minus calculated peptide mass (AMU): -0.00647



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1959.9	980.5	1942.9	1941.9	20
2	186.1		169.1		A	1845.9	923.4	1828.8	1827.8	19
3	243.1		226.1		G	1774.8	887.9	1757.8	1756.8	18
4	358.1		341.1	340.1	D	1717.8	859.4	1700.8	1699.8	17
5	471.2		454.2	453.2	L	1602.8	801.9	1585.7	1584.8	16
6	570.3	285.7	553.3	552.3	V	1489.7	745.3	1472.7	1471.7	15
7	667.3	334.2	650.3	649.3	P	1390.6	695.8	1373.6	1372.6	14
8	738.4	369.7	721.4	720.4	A	1293.6	647.3	1276.5	1275.5	13
9	839.4	420.2	822.4	821.4	T	1222.5	611.8	1205.5	1204.5	12
10	954.5	477.7	937.4	936.4	D	1121.5	561.2	1104.4	1103.5	11
11	1083.5	542.3	1066.5	1065.5	E	1006.4	503.7	989.4	988.4	10
12	1184.5	592.8	1167.5	1166.5	T	877.4	439.2	860.4	859.4	9
13	1255.6	628.3	1238.5	1237.6	A	776.4	388.7	759.3	758.3	8
14	1370.6	685.8	1353.6	1352.6	D	705.3	353.2	688.3	687.3	7
15	1441.6	721.3	1424.6	1423.6	A	590.3	295.7	573.3	572.3	6
16	1570.7	785.9	1553.7	1552.7	E	519.3		502.2	501.2	5
17	1657.7	829.4	1640.7	1639.7	S	390.2		373.2	372.2	4
18	1714.7	857.9	1697.7	1696.7	G	303.2		286.2		3
19	1785.8	893.4	1768.8	1767.8	A	246.2		229.1		2
20	1959.9	980.5	1942.9	1941.9	R	175.1		158.1		1

Gene symbol: Epb4.1l3

Protein name: 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110001B22 product:erythrocyte protein band 4.1-like 3, full insert sequence

Protein accession numbers: IPI00404739

Peptide sequence: GEEVDQSAPEQEQPATVSHEEEQASTIR

Exclusive (unique to this protein): TRUE

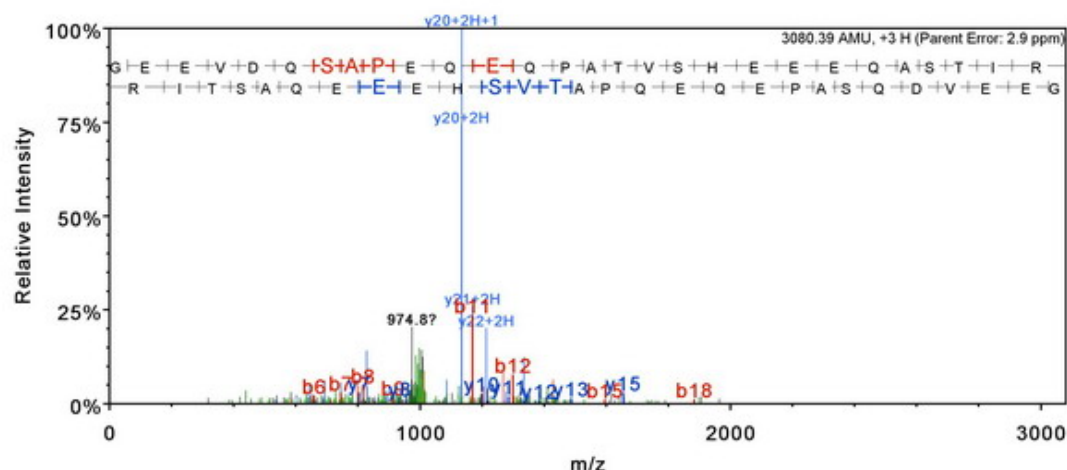
SEQUEST XCorr score: 3.18 SEQUEST DCn score: 0.394

Fix modifications: None

Variable modifications: None

Charge: 3 Observed m/z: 1027.8042

Actual minus calculated peptide mass (AMU): 0.009033



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	3081.4	1541.2	3064.4	3063.4	28
2	187.1			169.1	E	3024.4	1512.7	3007.3	3006.4	27
3	316.1			298.1	E	2895.3	1448.2	2878.3	2877.3	26
4	415.2			397.2	V	2766.3	1383.6	2749.3	2748.3	25
5	530.2			512.2	D	2667.2	1334.1	2650.2	2649.2	24
6	658.3	329.6	641.2	640.3	Q	2552.2	1276.6	2535.2	2534.2	23
7	745.3	373.2	728.3	727.3	S	2424.1	1212.6	2407.1	2406.1	22
8	816.3	408.7	799.3	798.3	A	2337.1	1169.0	2320.1	2319.1	21
9	913.4	457.2	896.4	895.4	P	2266.1	1133.5	2249.0	2248.1	20
10	1042.4	521.7	1025.4	1024.4	E	2169.0	1085.0	2152.0	2151.0	19
11	1170.5	585.8	1153.5	1152.5	Q	2040.0	1020.5	2022.9	2022.0	18
12	1299.5	650.3	1282.5	1281.5	E	1911.9	956.5	1894.9	1893.9	17
13	1427.6	714.3	1410.6	1409.6	Q	1782.9	891.9	1765.8	1764.9	16
14	1524.7	762.8	1507.6	1506.6	P	1654.8	827.9	1637.8	1636.8	15
15	1595.7	798.4	1578.7	1577.7	A	1557.8	779.4	1540.7	1539.7	14
16	1696.7	848.9	1679.7	1678.7	T	1486.7	743.9	1469.7	1468.7	13
17	1795.8	898.4	1778.8	1777.8	V	1385.7	693.3	1368.6	1367.7	12
18	1882.8	941.9	1865.8	1864.8	S	1286.6	643.8	1269.6	1268.6	11
19	2019.9	1010.5	2002.9	2001.9	H	1199.6	600.3	1182.5	1181.6	10
20	2148.9	1075.0	2131.9	2130.9	E	1062.5	531.8	1045.5	1044.5	9
21	2278.0	1139.5	2261.0	2260.0	E	933.5	467.2	916.4	915.5	8
22	2407.0	1204.0	2390.0	2389.0	E	804.4	402.7	787.4	786.4	7
23	2535.1	1268.0	2518.1	2517.1	Q	675.4	338.2	658.4	657.4	6
24	2606.1	1303.6	2589.1	2588.1	A	547.3		530.3	529.3	5
25	2693.1	1347.1	2676.1	2675.1	S	476.3		459.3	458.3	4
26	2794.2	1397.6	2777.2	2776.2	T	389.3		372.2	371.2	3
27	2907.3	1454.1	2890.3	2889.3	I	288.2		271.2		2
28	3081.4	1541.2	3064.4	3063.4	R	175.1		158.1		1

Gene symbol: Epn2

Protein name: Isoform 1 of Epsin-2

Protein accession numbers: IPI00336844

Peptide sequence: MAQVATGVGSNQITFGR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.27 SEQUEST DCn score: 0.611

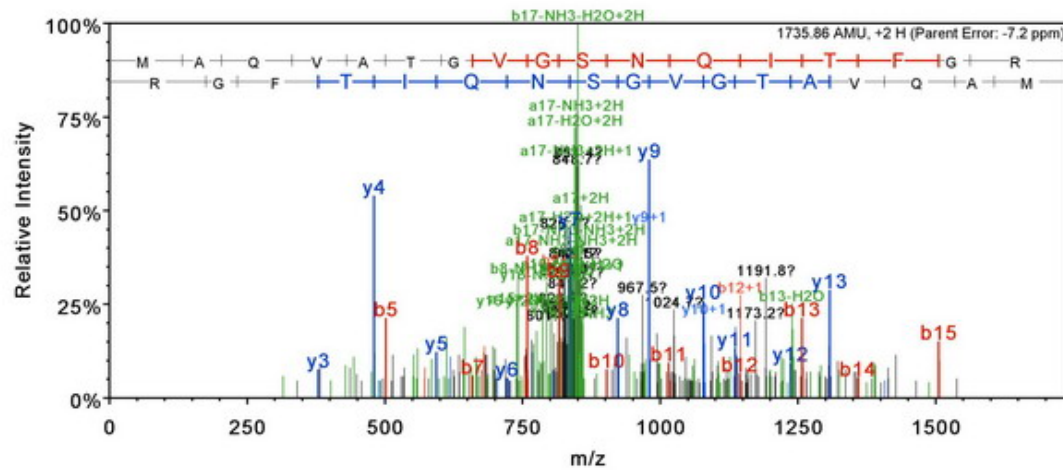
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 868.9354

Actual minus calculated peptide mass (AMU): -0.01245



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1736.9	868.9	1719.9	1718.9	17
2	203.1				A	1605.8	803.4	1588.8	1587.8	16
3	331.1		314.1		Q	1534.8	767.9	1517.8	1516.8	15
4	430.2		413.2		V	1406.7	703.9	1389.7	1388.7	14
5	501.3		484.2		A	1307.7	654.3	1290.6	1289.7	13
6	602.3	301.7	585.3	584.3	T	1236.6	618.8	1219.6	1218.6	12
7	659.3	330.2	642.3	641.3	G	1135.6	568.3	1118.6	1117.6	11
8	758.4	379.7	741.4	740.4	V	1078.6	539.8	1061.5	1060.5	10
9	815.4	408.2	798.4	797.4	G	979.5	490.3	962.5	961.5	9
10	902.4	451.7	885.4	884.4	S	922.5	461.7	905.5	904.5	8
11	1016.5	508.8	999.5	998.5	N	835.4	418.2	818.4	817.4	7
12	1144.5	572.8	1127.5	1126.5	Q	721.4	361.2	704.4	703.4	6
13	1257.6	629.3	1240.6	1239.6	I	593.3		576.3	575.3	5
14	1358.7	679.8	1341.7	1340.7	T	480.3		463.2	462.3	4
15	1505.7	753.4	1488.7	1487.7	F	379.2		362.2		3
16	1562.8	781.9	1545.7	1544.8	G	232.1		215.1		2
17	1736.9	868.9	1719.9	1718.9	R	175.1		158.1		1

Gene symbol: Ercc2

Protein name: TFIIF basal transcription factor complex helicase subunit

Protein accession numbers: IPI00310721,IPI00621522

Peptide sequence: FYEEFDIHGR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.73 SEQUEST DCn score: 0.63

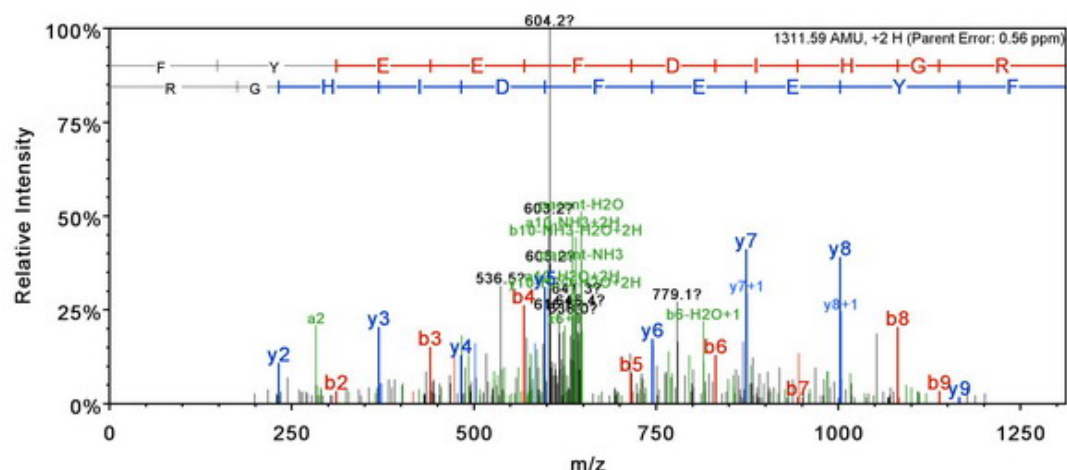
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 656.8024

Actual minus calculated peptide mass (AMU): 0.0007324



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1312.6	656.8	1295.6	1294.6	10
2	311.1				Y	1165.5	583.3	1148.5	1147.5	9
3	440.2			422.2	E	1002.5	501.7	985.4	984.5	8
4	569.2			551.2	E	873.4	437.2	856.4	855.4	7
5	716.3			698.3	F	744.4	372.7	727.4	726.4	6
6	831.3	416.2		813.3	D	597.3	299.2	580.3	579.3	5
7	944.4	472.7		926.4	I	482.3	241.7	465.3		4
8	1081.5	541.2		1063.5	H	369.2	185.1	352.2		3
9	1138.5	569.8		1120.5	G	232.1		215.1		2
10	1312.6	656.8	1295.6	1294.6	R	175.1		158.1		1

Gene symbol: Ergic3

Protein name: Isoform 2 of Endoplasmic reticulum-Golgi intermediate compartment protein 3

Protein accession numbers: IPI00132454,IPI00626555

Peptide sequence: VEVTVFDPNSLDPNR

Exclusive (unique to this protein): TRUE

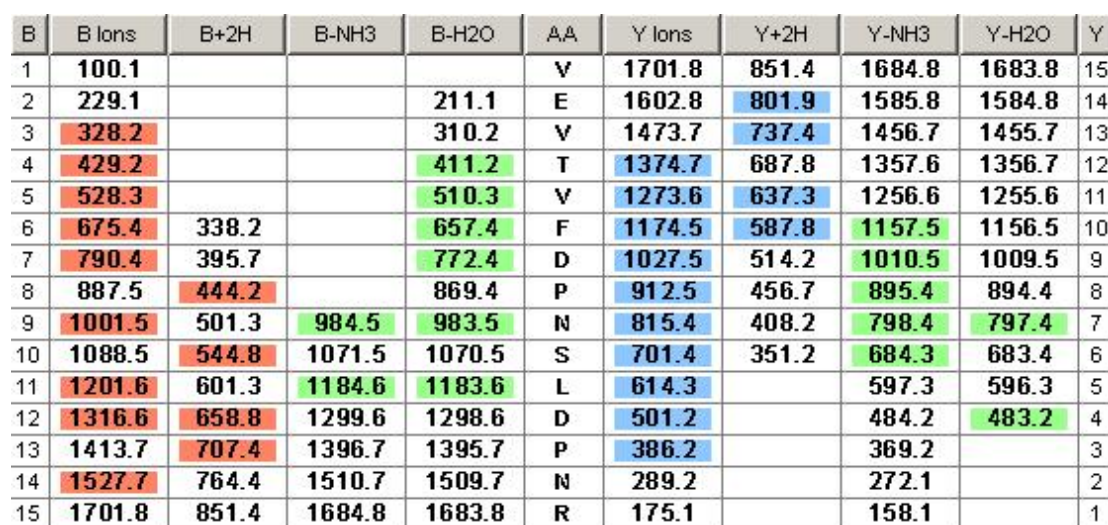
SEQUEST XCorr score: 3.6 SEQUEST DCn score: 0.615

Fix modifications: None

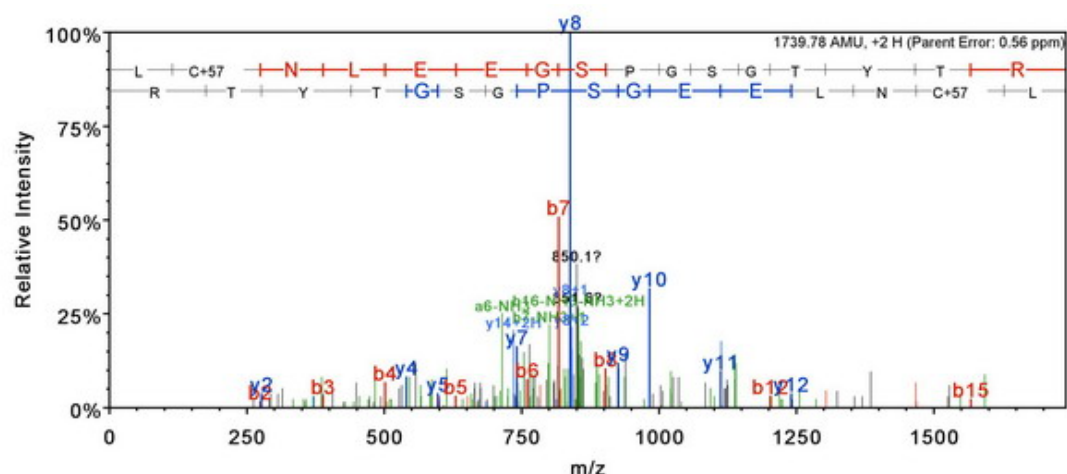
Variable modifications: None

Charge: 2 Observed m/z: 851.4275

Actual minus calculated peptide mass (AMU): 0.002319



Actual minus calculated peptide mass (AMU): 0.0009766



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1740.8	870.9	1723.8	1722.8	16
2	274.1				C+57	1627.7	814.4	1610.7	1609.7	15
3	388.2		371.1		N	1467.7	734.3	1450.7	1449.7	14
4	501.3		484.2		L	1353.6	677.3	1336.6	1335.6	13
5	630.3		613.3	612.3	E	1240.5	620.8	1223.5	1222.5	12
6	759.3	380.2	742.3	741.3	E	1111.5	556.3	1094.5	1093.5	11
7	816.4	408.7	799.3	798.4	G	982.5	491.7	965.4	964.5	10
8	903.4	452.2	886.4	885.4	S	925.4	463.2	908.4	907.4	9
9	1000.4	500.7	983.4	982.4	P	838.4	419.7	821.4	820.4	8
10	1057.5	529.2	1040.4	1039.5	G	741.4	371.2	724.3	723.3	7
11	1144.5	572.8	1127.5	1126.5	S	684.3	342.7	667.3	666.3	6
12	1201.5	601.3	1184.5	1183.5	G	597.3		580.3	579.3	5
13	1302.6	651.8	1285.5	1284.5	T	540.3		523.3	522.3	4
14	1465.6	733.3	1448.6	1447.6	Y	439.2		422.2	421.2	3
15	1566.7	783.8	1549.7	1548.7	T	276.2		259.1	258.2	2
16	1740.8	870.9	1723.8	1722.8	R	175.1		158.1		1

Gene symbol: F8

Protein name: Coagulation factor VIII precursor

Protein accession numbers: IPI00111807

Peptide sequence: SSRIQESNNFLKETK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.55 SEQUEST DCn score: 0.298

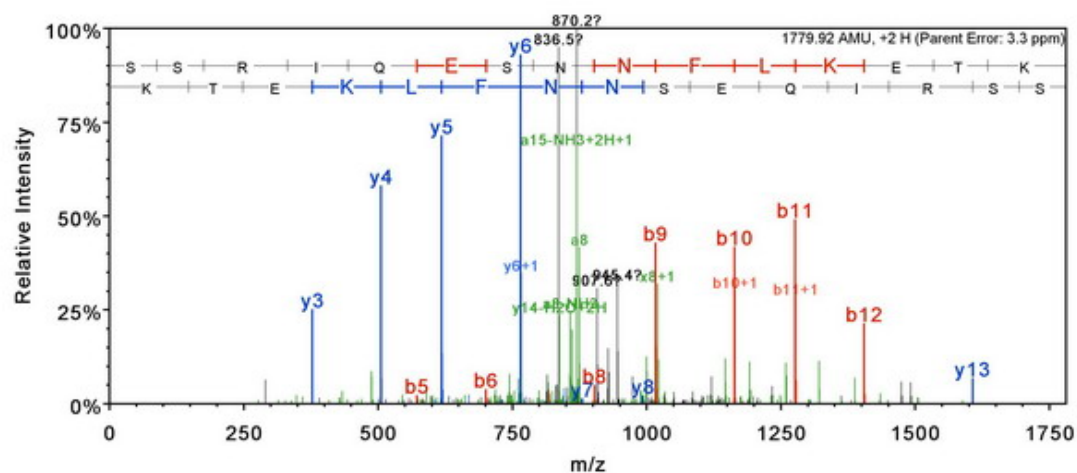
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 890.9665

Actual minus calculated peptide mass (AMU): 0.005859



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1780.9	891.0	1763.9	1762.9	15
2	175.1			157.1	S	1693.9	847.5	1676.9	1675.9	14
3	331.2	166.1	314.2	313.2	R	1606.9	803.9	1589.8	1588.8	13
4	444.3	222.6	427.2	426.3	I	1450.8	725.9	1433.7	1432.7	12
5	572.3	286.7	555.3	554.3	Q	1337.7	669.3	1320.6	1319.7	11
6	701.4	351.2	684.3	683.4	E	1209.6	605.3	1192.6	1191.6	10
7	788.4	394.7	771.4	770.4	S	1080.6	540.8	1063.5	1062.6	9
8	902.4	451.7	885.4	884.4	N	993.5	497.3	976.5	975.5	8
9	1016.5	508.7	999.5	998.5	N	879.5	440.3	862.5	861.5	7
10	1163.5	582.3	1146.5	1145.5	F	765.5	383.2	748.4	747.4	6
11	1276.6	638.8	1259.6	1258.6	L	618.4	309.7	601.4	600.4	5
12	1404.7	702.9	1387.7	1386.7	K	505.3	253.2	488.3	487.3	4
13	1533.8	767.4	1516.7	1515.8	E	377.2		360.2	359.2	3
14	1634.8	817.9	1617.8	1616.8	T	248.2		231.1	230.2	2
15	1780.9	891.0	1763.9	1762.9	K	147.1		130.1		1

Gene symbol: Faf1

Protein name: Fas-associated factor 1

Protein accession numbers: IPI00420245

Peptide sequence: NVYDLTSIPVR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.01 SEQUEST DCn score: 0.641

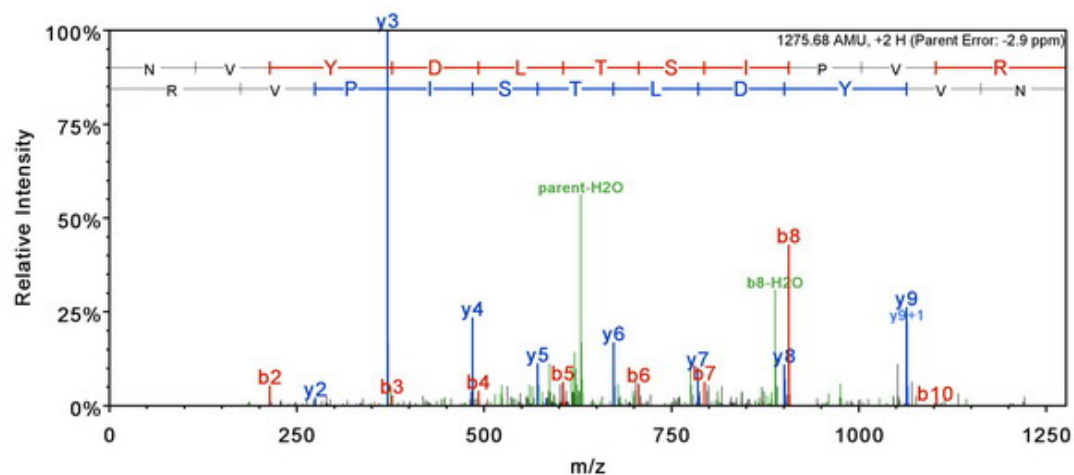
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 638.8472

Actual minus calculated peptide mass (AMU): -0.003662



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1276.7	638.9	1259.7	1258.7	11
2	214.1		197.1		V	1162.7	581.8	1145.6	1144.6	10
3	377.2		360.2		Y	1063.6	532.3	1046.5	1045.6	9
4	492.2		475.2	474.2	D	900.5	450.8	883.5	882.5	8
5	605.3		588.3	587.3	L	785.5	393.3	768.5	767.5	7
6	706.3	353.7	689.3	688.3	T	672.4	336.7	655.4	654.4	6
7	793.4	397.2	776.4	775.4	S	571.4		554.3	553.4	5
8	906.5	453.7	889.4	888.5	I	484.3		467.3		4
9	1003.5	502.3	986.5	985.5	P	371.2		354.2		3
10	1102.6	551.8	1085.5	1084.6	V	274.2		257.2		2
11	1276.7	638.9	1259.7	1258.7	R	175.1		158.1		1

Gene symbol: Fbl;LOC100044829

Protein name: rRNA 2'-O-methyltransferase fibrillarin

Protein accession numbers: IPI00119581

Peptide sequence: TNIIPVIEDAR

Exclusive (unique to this protein): TRUE

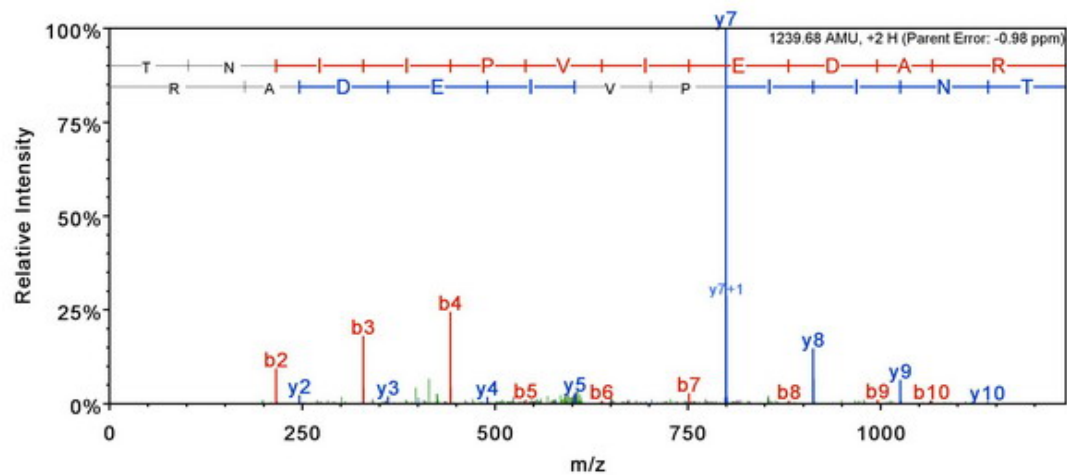
SEQUEST XCorr score: 2.74 SEQUEST DCn score: 0.576

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 620.8484

Actual minus calculated peptide mass (AMU): -0.0012249



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1240.7	620.9	1223.7	1222.7	11
2	216.1		199.1	198.1	N	1139.6	570.3	1122.6	1121.6	10
3	329.2		312.2	311.2	I	1025.6	513.3	1008.6	1007.6	9
4	442.3		425.2	424.3	I	912.5	456.8	895.5	894.5	8
5	539.3		522.3	521.3	P	799.4	400.2	782.4	781.4	7
6	638.4	319.7	621.4	620.4	V	702.4	351.7	685.4	684.4	6
7	751.5	376.2	734.5	733.5	I	603.3		586.3	585.3	5
8	880.5	440.8	863.5	862.5	E	490.2		473.2	472.2	4
9	995.5	498.3	978.5	977.5	D	361.2		344.2	343.2	3
10	1066.6	533.8	1049.5	1048.6	A	246.2		229.1		2
11	1240.7	620.9	1223.7	1222.7	R	175.1		158.1		1

Gene symbol: Fbxo45

Protein name: F-box/SPRY domain-containing protein 1

Protein accession numbers: IPI00170059

Peptide sequence: GYEFLGVAFR

Exclusive (unique to this protein): TRUE

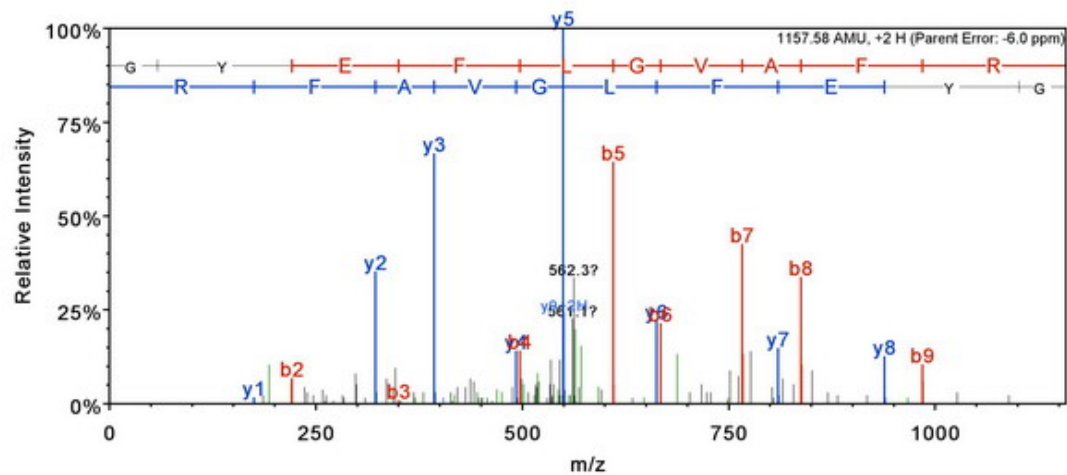
SEQUEST XCorr score: 3.4 SEQUEST DCn score: 0.551

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 579.7978

Actual minus calculated peptide mass (AMU): -0.006958



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1158.6	579.8	1141.6	1140.6	10
2	221.1				Y	1101.6	551.3	1084.5	1083.6	9
3	350.1			332.1	E	938.5	469.8	921.5	920.5	8
4	497.2			479.2	F	809.5	405.2	792.4		7
5	610.3			592.3	L	662.4	331.7	645.4		6
6	667.3	334.2		649.3	G	549.3		532.3		5
7	766.4	383.7		748.4	V	492.3		475.3		4
8	837.4	419.2		819.4	A	393.2		376.2		3
9	984.5	492.8		966.5	F	322.2		305.2		2
10	1158.6	579.8	1141.6	1140.6	R	175.1		158.1		1

Gene symbol: Fech

Protein name: Ferrochelatase

Protein accession numbers: IPI00228343

Peptide sequence: YVHPLTEEAIEEMER

Exclusive (unique to this protein): TRUE

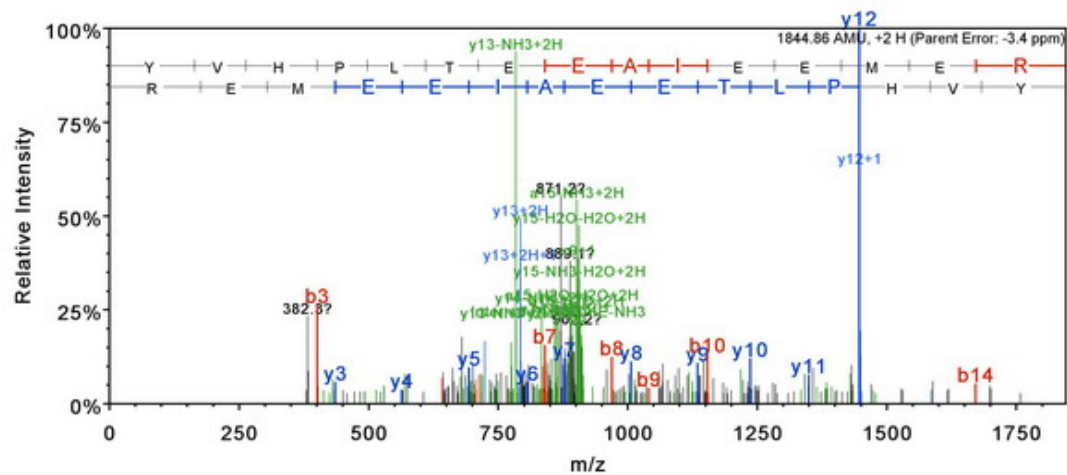
SEQUEST XCorr score: 3.03 SEQUEST DCn score: 0.361

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 923.4354

Actual minus calculated peptide mass (AMU): -0.0063456



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1845.9	923.4	1828.8	1827.9	15
2	263.1				V	1682.8	841.9	1665.8	1664.8	14
3	400.2	200.6			H	1583.7	792.4	1566.7	1565.7	13
4	497.3	249.1			P	1446.7	723.8	1429.7	1428.7	12
5	610.3	305.7			L	1349.6	675.3	1332.6	1331.6	11
6	711.4	356.2		693.4	T	1236.5	618.8	1219.5	1218.5	10
7	840.4	420.7		822.4	E	1135.5	568.3	1118.5	1117.5	9
8	969.5	485.2		951.5	E	1006.5	503.7	989.4	988.4	8
9	1040.5	520.8		1022.5	A	877.4	439.2	860.4	859.4	7
10	1153.6	577.3		1135.6	I	806.4	403.7	789.4	788.4	6
11	1282.6	641.8		1264.6	E	693.3		676.3	675.3	5
12	1411.7	706.3		1393.7	E	564.3		547.2	546.2	4
13	1542.7	771.9		1524.7	M	435.2		418.2	417.2	3
14	1671.8	836.4		1653.8	E	304.2		287.1	286.2	2
15	1845.9	923.4	1828.8	1827.9	R	175.1		158.1		1

Gene symbol: Fgfr1op2

Protein name: CDNA, RIKEN full-length enriched library, clone:I920193N03
product:HSPC123-like protein homolog

Protein accession numbers: IPI00110657,IPI00133534

Peptide sequence: PRSTLVMGIQQENR

Exclusive (unique to this protein): TRUE

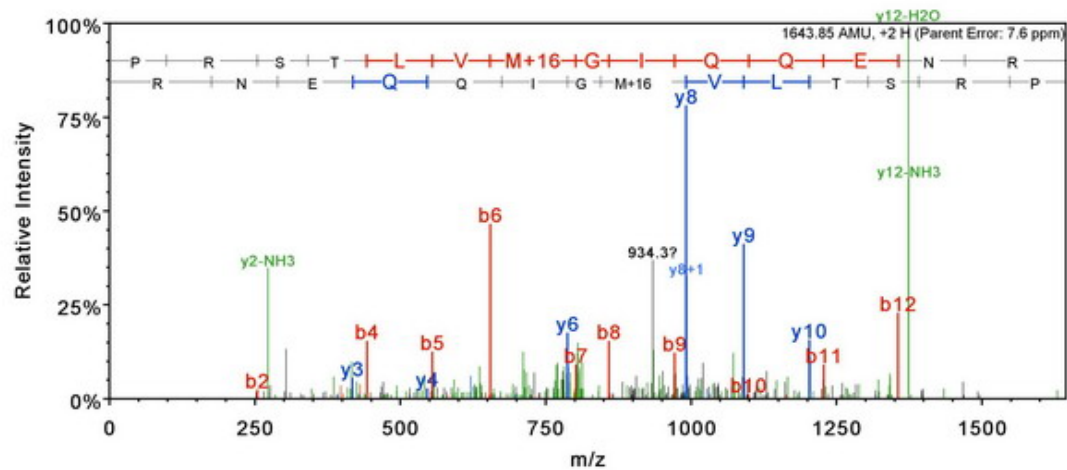
SEQUEST XCorr score: 2.77 SEQUEST DCn score: 0.495

Fix modifications: None

Variable modifications: M7: Oxidation (+16.00)

Charge: 2 Observed m/z: 822.9348

Actual minus calculated peptide mass (AMU): 0.01257



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	98.1				P	1644.9	822.9	1627.8	1626.8	14
2	254.2	127.6	237.1		R	1547.8	774.4	1530.8	1529.8	13
3	341.2	171.1	324.2	323.2	S	1391.7	696.4	1374.7	1373.7	12
4	442.2	221.6	425.2	424.2	T	1304.7	652.8	1287.6	1286.7	11
5	555.3	278.2	538.3	537.3	L	1203.6	602.3	1186.6	1185.6	10
6	654.4	327.7	637.4	636.4	V	1090.5	545.8	1073.5	1072.5	9
7	801.4	401.2	784.4	783.4	M+16	991.5	496.2	974.4	973.5	8
8	858.5	429.7	841.4	840.4	G	844.4	422.7	827.4	826.4	7
9	971.5	486.3	954.5	953.5	I	787.4	394.2	770.4	769.4	6
10	1099.6	550.3	1082.6	1081.6	Q	674.3		657.3	656.3	5
11	1227.7	614.3	1210.6	1209.6	Q	546.3		529.2	528.3	4
12	1356.7	678.9	1339.7	1338.7	E	418.2		401.2	400.2	3
13	1470.7	735.9	1453.7	1452.7	N	289.2		272.1		2
14	1644.9	822.9	1627.8	1626.8	R	175.1		158.1		1

Gene symbol: Fis1

Protein name: Mitochondrial fission 1 protein

Protein accession numbers: IPI00132217

Peptide sequence: GIVLLELLPK

Exclusive (unique to this protein): TRUE

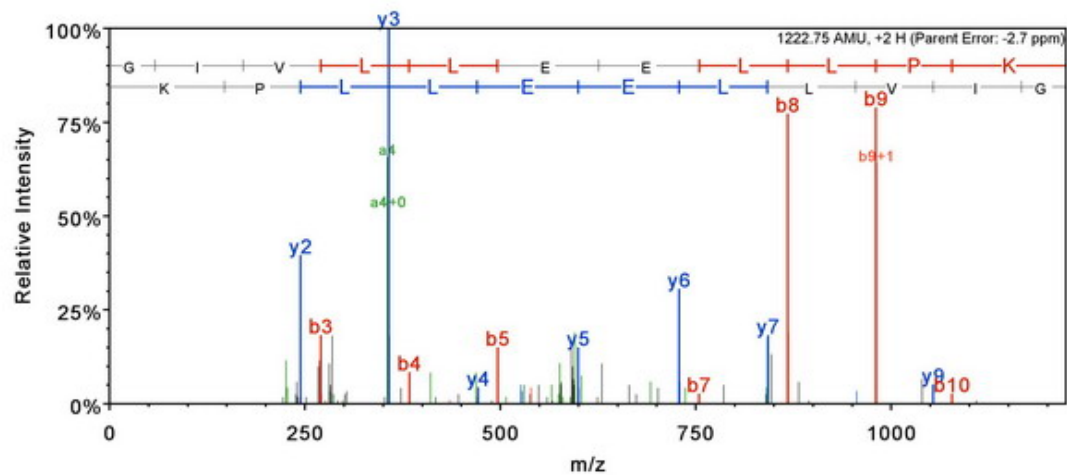
SEQUEST XCorr score: 3.18 SEQUEST DCn score: 0.445

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 612.3832

Actual minus calculated peptide mass (AMU): -0.003296



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1223.8	612.4	1206.7	1205.8	11
2	171.1				I	1166.7	583.9	1149.7	1148.7	10
3	270.2				V	1053.7	527.3	1036.6	1035.7	9
4	383.3				L	954.6	477.8	937.6	936.6	8
5	496.4				L	841.5	421.3	824.5	823.5	7
6	625.4	313.2		607.4	E	728.4	364.7	711.4	710.4	6
7	754.4	377.7		736.4	E	599.4		582.4	581.4	5
8	867.5	434.3		849.5	L	470.3		453.3		4
9	980.6	490.8		962.6	L	357.3		340.2		3
10	1077.7	539.3		1059.7	P	244.2		227.1		2
11	1223.8	612.4	1206.7	1205.8	K	147.1		130.1		1

Gene symbol: Fkbpl

Protein name: FK506-binding protein-like

Protein accession numbers: IPI00130791

Peptide sequence: EENAQQILNTAIPFR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.67 SEQUEST DCn score: 0.413

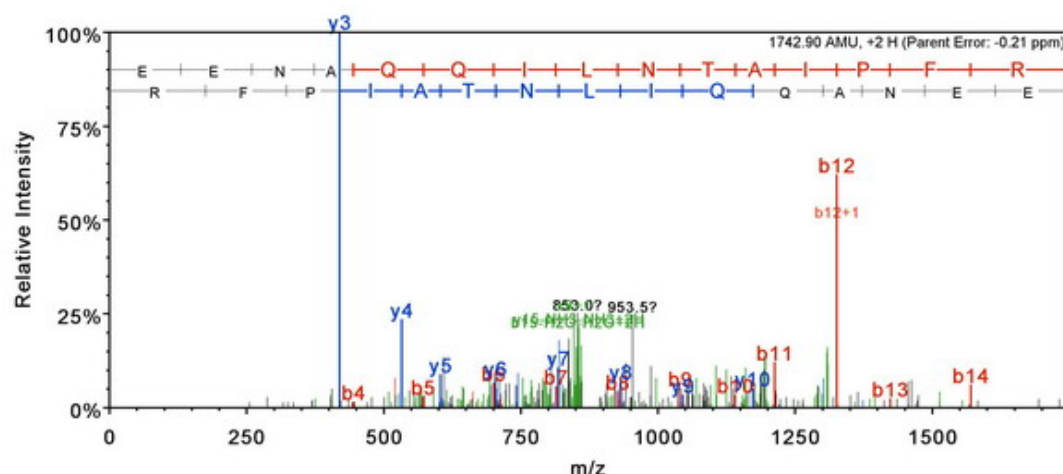
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 872.4553

Actual minus calculated peptide mass (AMU): -0.0003662



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1743.9	872.5	1726.9	1725.9	15
2	259.1			241.1	E	1614.9	807.9	1597.8	1596.9	14
3	373.1		356.1	355.1	N	1485.8	743.4	1468.8	1467.8	13
4	444.2		427.2	426.2	A	1371.8	686.4	1354.8	1353.8	12
5	572.2		555.2	554.2	Q	1300.7	650.9	1283.7	1282.7	11
6	700.3	350.7	683.3	682.3	Q	1172.7	586.8	1155.7	1154.7	10
7	813.4	407.2	796.4	795.4	I	1044.6	522.8	1027.6	1026.6	9
8	926.5	463.7	909.4	908.5	L	931.5	466.3	914.5	913.5	8
9	1040.5	520.8	1023.5	1022.5	N	818.5	409.7	801.4	800.4	7
10	1141.5	571.3	1124.5	1123.5	T	704.4	352.7	687.4	686.4	6
11	1212.6	606.8	1195.6	1194.6	A	603.4		586.3		5
12	1325.7	663.3	1308.6	1307.7	I	532.3		515.3		4
13	1422.7	711.9	1405.7	1404.7	P	419.2		402.2		3
14	1569.8	785.4	1552.8	1551.8	F	322.2		305.2		2
15	1743.9	872.5	1726.9	1725.9	R	175.1		158.1		1

Gene symbol: Fnta

Protein name: Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit

Protein accession numbers: IPI00118904,IPI00757762

Peptide sequence: LWDNELQYVDQLLK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.88 SEQUEST DCn score: 0.491

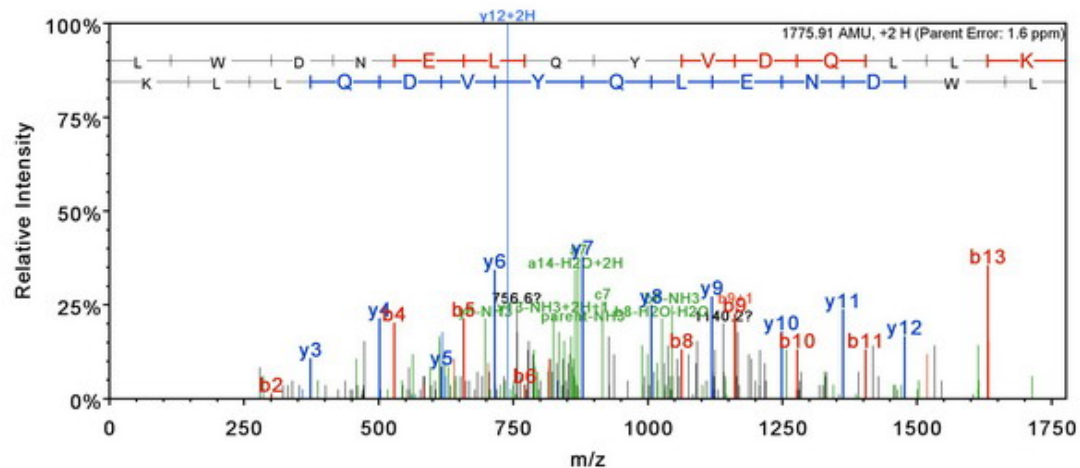
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 888.964

Actual minus calculated peptide mass (AMU): 0.0028056



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1776.9	889.0	1759.9	1758.9	14
2	300.2				W	1663.8	832.4	1646.8	1645.8	13
3	415.2			397.2	D	1477.8	739.4	1460.7	1459.7	12
4	529.2		512.2	511.2	N	1362.7	681.9	1345.7	1344.7	11
5	658.3		641.3	640.3	E	1248.7	624.9	1231.7	1230.7	10
6	771.4	386.2	754.3	753.4	L	1119.6	560.3	1102.6	1101.6	9
7	899.4	450.2	882.4	881.4	Q	1006.6	503.8	989.5	988.6	8
8	1062.5	531.8	1045.5	1044.5	Y	878.5	439.8	861.5	860.5	7
9	1161.6	581.3	1144.5	1143.5	V	715.4	358.2	698.4	697.4	6
10	1276.6	638.8	1259.6	1258.6	D	616.4		599.3	598.4	5
11	1404.6	702.8	1387.6	1386.6	Q	501.3		484.3		4
12	1517.7	759.4	1500.7	1499.7	L	373.3		356.3		3
13	1630.8	815.9	1613.8	1612.8	L	260.2		243.2		2
14	1776.9	889.0	1759.9	1758.9	K	147.1		130.1		1

Gene symbol: Fsip2

Protein name: similar to FLJ44048 protein

Protein accession numbers: IPI00352763,IPI00750014

Peptide sequence: VFRPEKEDEVQAAK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.75 SEQUEST DCn score: 0.303

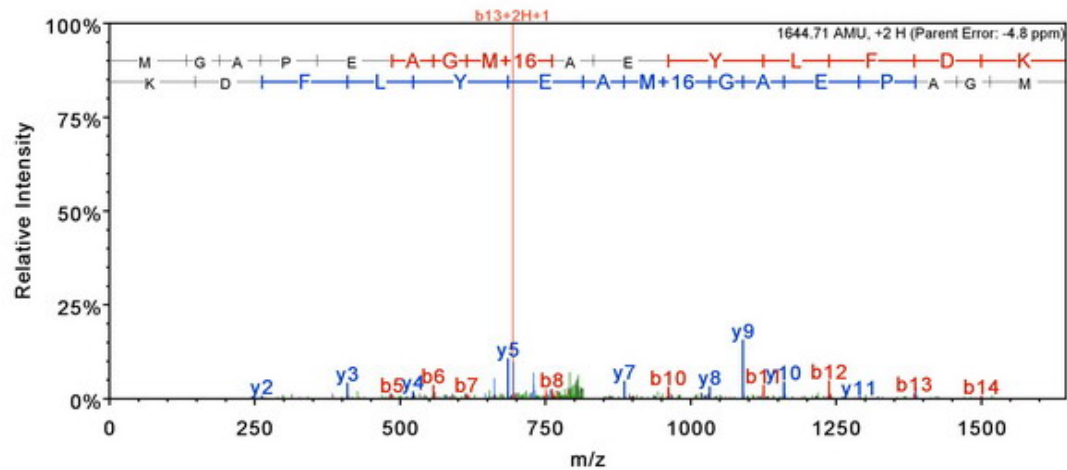
Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 823.4279

Actual minus calculated peptide mass (AMU): -0.007202

B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1645.9	823.4	1628.8	1627.8	14
2	247.1				F	1546.8	773.9	1529.8	1528.8	13
3	403.3	202.1	386.2		R	1399.7	700.4	1382.7	1381.7	12
4	500.3	250.7	483.3		P	1243.6	622.3	1226.6	1225.6	11
5	629.3	315.2	612.3	611.3	E	1146.6	573.8	1129.5	1128.5	10
6	757.4	379.2	740.4	739.4	K	1017.5	509.3	1000.5	999.5	9
7	886.5	443.7	869.5	868.5	E	889.4	445.2	872.4	871.4	8
8	1001.5	501.3	984.5	983.5	D	760.4	380.7	743.4	742.4	7
9	1130.5	565.8	1113.5	1112.5	E	645.4	323.2	628.3	627.4	6
10	1229.6	615.3	1212.6	1211.6	V	516.3		499.3		5
11	1357.7	679.3	1340.7	1339.7	Q	417.3		400.2		4
12	1428.7	714.9	1411.7	1410.7	A	289.2		272.2		3
13	1499.8	750.4	1482.7	1481.7	A	218.2		201.1		2
14	1645.9	823.4	1628.8	1627.8	K	147.1		130.1		1



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1645.7	823.4	1628.7	1627.7	15
2	189.1				G	1514.7	757.9	1497.7	1496.7	14
3	260.1				A	1457.7	729.3	1440.6	1439.7	13
4	357.2				P	1386.6	693.8	1369.6	1368.6	12
5	486.2			468.2	E	1289.6	645.3	1272.5	1271.6	11
6	557.2	279.1		539.2	A	1160.5	580.8	1143.5	1142.5	10
7	614.3	307.6		596.3	G	1089.5	545.3	1072.5	1071.5	9
8	761.3	381.2		743.3	M+16	1032.5	516.7	1015.4	1014.5	8
9	832.3	416.7		814.3	A	885.4	443.2	868.4	867.4	7
10	961.4	481.2		943.4	E	814.4	407.7	797.4	796.4	6
11	1124.4	562.7		1106.4	Y	685.4		668.3	667.4	5
12	1237.5	619.3		1219.5	L	522.3		505.3	504.3	4
13	1384.6	692.8		1366.6	F	409.2		392.2	391.2	3
14	1499.6	750.3		1481.6	D	262.1		245.1	244.1	2
15	1645.7	823.4	1628.7	1627.7	K	147.1		130.1		1

Gene symbol: Gale

Protein name: UDP-glucose 4-epimerase

Protein accession numbers: IPI00153129

Peptide sequence: ADTAWNALLR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.79 SEQUEST DCn score: 0.281

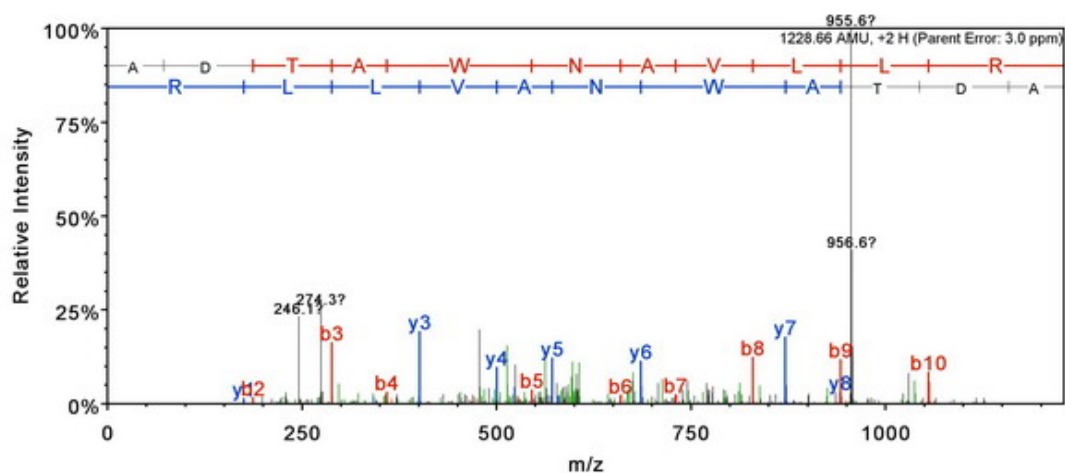
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 615.3379

Actual minus calculated peptide mass (AMU): 0.003662



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1229.7	615.3	1212.6	1211.7	11
2	187.1			169.1	D	1158.6	579.8	1141.6	1140.6	10
3	288.1			270.1	T	1043.6	522.3	1026.6	1025.6	9
4	359.2			341.2	A	942.6	471.8	925.5		8
5	545.2			527.2	W	871.5	436.3	854.5		7
6	659.3	330.1	642.3	641.3	N	685.4	343.2	668.4		6
7	730.3	365.7	713.3	712.3	A	571.4		554.4		5
8	829.4	415.2	812.4	811.4	V	500.4		483.3		4
9	942.5	471.7	925.4	924.5	L	401.3		384.3		3
10	1055.5	528.3	1038.5	1037.5	L	288.2		271.2		2
11	1229.7	615.3	1212.6	1211.7	R	175.1		158.1		1

Gene symbol: Galnt3

Protein name: Polypeptide N-acetylgalactosaminyltransferase 3

Protein accession numbers: IPI00330383,IPI00652440

Peptide sequence: TVHSVLYSSPAILLK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.17 SEQUEST DCn score: 0.649

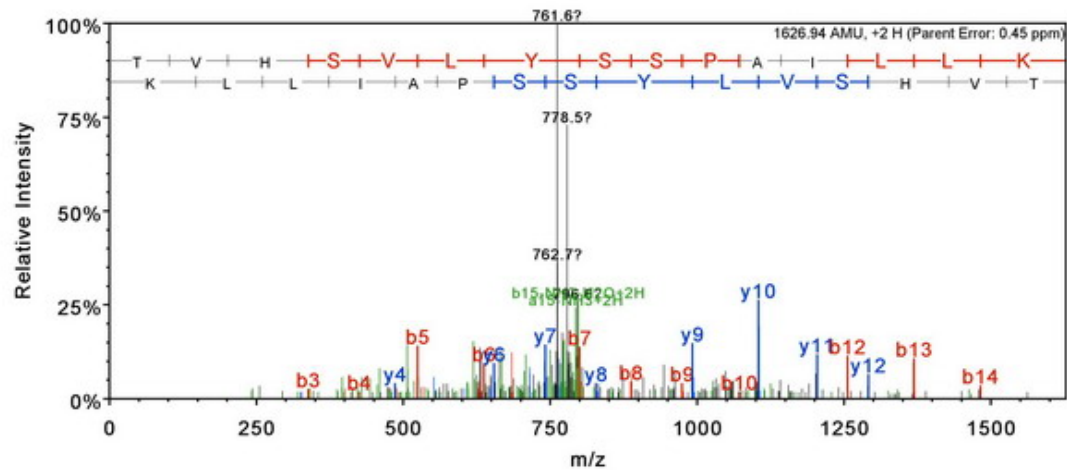
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 814.4755

Actual minus calculated peptide mass (AMU): 0.0007324



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1627.9	814.5	1610.9	1609.9	15
2	201.1			183.1	V	1526.9	764.0	1509.9	1508.9	14
3	338.2	169.6		320.2	H	1427.8	714.4	1410.8	1409.8	13
4	425.2	213.1		407.2	S	1290.8	645.9	1273.7	1272.8	12
5	524.3	262.6		506.3	V	1203.7	602.4	1186.7	1185.7	11
6	637.4	319.2		619.4	L	1104.7	552.8	1087.6	1086.7	10
7	800.4	400.7		782.4	Y	991.6	496.3	974.6	973.6	9
8	887.5	444.2		869.5	S	828.5	414.8	811.5	810.5	8
9	974.5	487.8		956.5	S	741.5	371.3	724.5	723.5	7
10	1071.5	536.3		1053.5	P	654.5	327.7	637.4		6
11	1142.6	571.8		1124.6	A	557.4		540.4		5
12	1255.7	628.3		1237.7	I	486.4		469.3		4
13	1368.8	684.9		1350.7	L	373.3		356.3		3
14	1481.8	741.4		1463.8	L	260.2		243.2		2
15	1627.9	814.5	1610.9	1609.9	K	147.1		130.1		1

Gene symbol: Garnl1

Protein name: Isoform 1 of GTPase-activating RapGAP domain-like 1

Protein accession numbers: IPI00454161,IPI00460042

Peptide sequence: SNVNFVTEIFR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.55 SEQUEST DCn score: 0.407

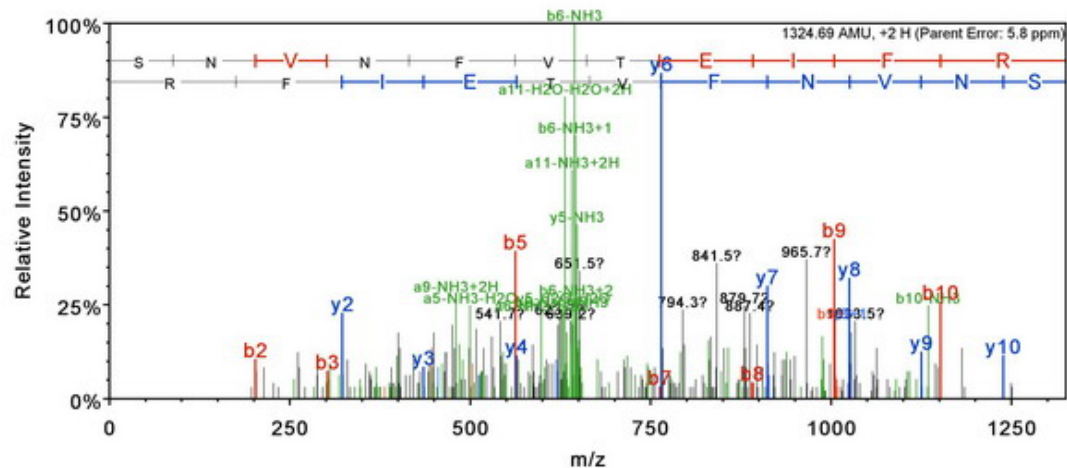
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 663.3504

Actual minus calculated peptide mass (AMU): 0.00769



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1325.7	663.4	1308.7	1307.7	11
2	202.1		185.1	184.1	N	1238.7	619.8	1221.6	1220.6	10
3	301.2		284.1	283.1	V	1124.6	562.8	1107.6	1106.6	9
4	415.2		398.2	397.2	N	1025.5	513.3	1008.5	1007.5	8
5	562.3		545.2	544.3	F	911.5	456.3	894.5	893.5	7
6	661.3	331.2	644.3	643.3	V	764.4	382.7	747.4	746.4	6
7	762.4	381.7	745.4	744.4	T	665.4		648.3	647.4	5
8	891.4	446.2	874.4	873.4	E	564.3		547.3	546.3	4
9	1004.5	502.8	987.5	986.5	I	435.3		418.3		3
10	1151.6	576.3	1134.5	1133.6	F	322.2		305.2		2
11	1325.7	663.4	1308.7	1307.7	R	175.1		158.1		1

Gene symbol: Gbas

Protein name: NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630048H15 product:glioblastoma amplified sequence, full insert sequence

Protein accession numbers: IPI00651782

Peptide sequence: PGPNIYELR

Exclusive (unique to this protein): TRUE

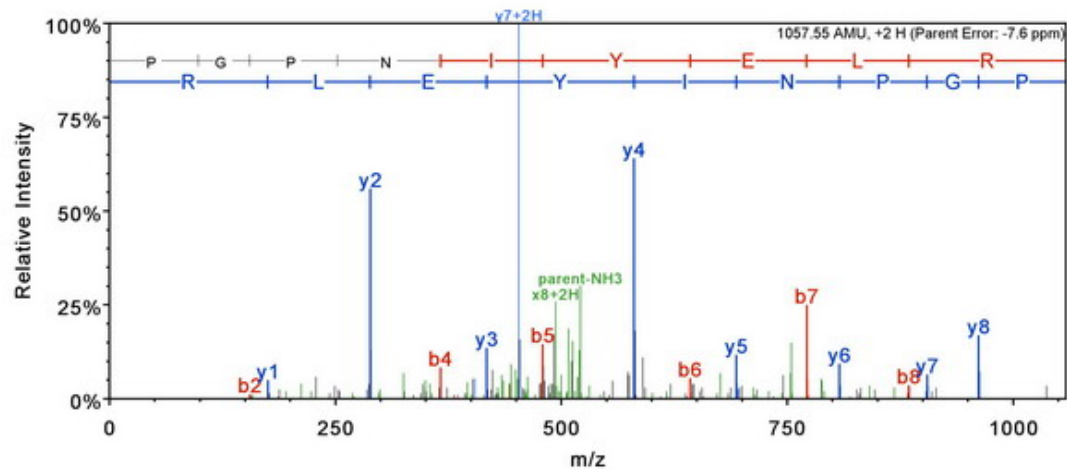
SEQUEST XCorr score: 3.28 SEQUEST DCn score: 0.241

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 529.7817

Actual minus calculated peptide mass (AMU): -0.008057



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	98.1				P	1058.6	529.8	1041.5	1040.5	9
2	155.1				G	961.5	481.3	944.5	943.5	8
3	252.1				P	904.5	452.8	887.5	886.5	7
4	366.2		349.2		N	807.4	404.2	790.4	789.4	6
5	479.3		462.2		I	693.4		676.4	675.4	5
6	642.3	321.7	625.3		Y	580.3		563.3	562.3	4
7	771.4	386.2	754.3	753.4	E	417.3		400.2	399.2	3
8	884.5	442.7	867.4	866.4	L	288.2		271.2		2
9	1058.6	529.8	1041.5	1040.5	R	175.1		158.1		1

Gene symbol: Gemin5

Protein name: Gem-associated protein 5

Protein accession numbers: IPI00226397,IPI00649659

Peptide sequence: VGPGAGASPGAPPFR

Exclusive (unique to this protein): TRUE

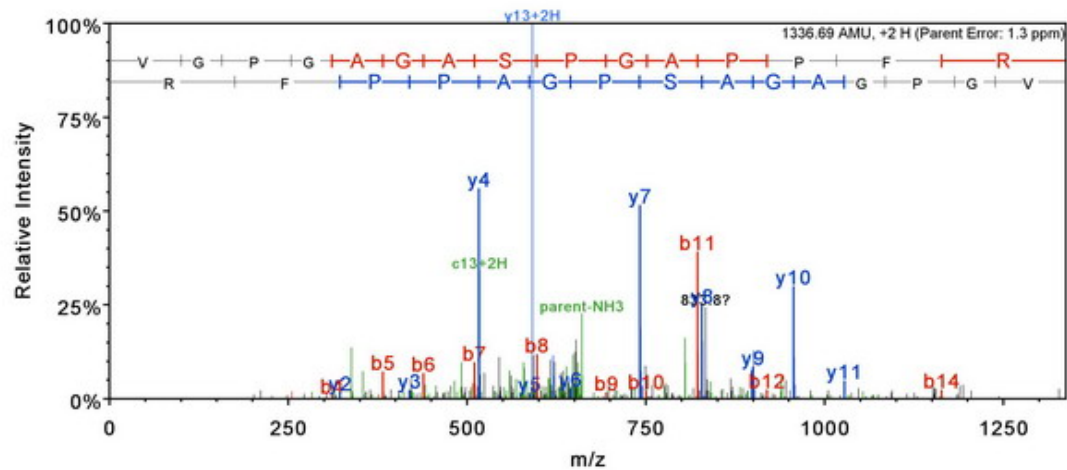
SEQUEST XCorr score: 2.66 SEQUEST DCn score: 0.656

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 669.3531

Actual minus calculated peptide mass (AMU): 0.001709



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1337.7	669.4	1320.7	1319.7	15
2	157.1				G	1238.6	619.8	1221.6	1220.6	14
3	254.2				P	1181.6	591.3	1164.6	1163.6	13
4	311.2				G	1084.5	542.8	1067.5	1066.5	12
5	382.2				A	1027.5	514.3	1010.5	1009.5	11
6	439.2	220.1			G	956.5	478.8	939.5	938.5	10
7	510.3	255.6			A	899.5	450.2	882.5	881.5	9
8	597.3	299.2		579.3	S	828.4	414.7	811.4	810.4	8
9	694.4	347.7		676.3	P	741.4	371.2	724.4		7
10	751.4	376.2		733.4	G	644.4	322.7	627.3		6
11	822.4	411.7		804.4	A	587.3		570.3		5
12	919.5	460.2		901.5	P	516.3		499.3		4
13	1016.5	508.8		998.5	P	419.2		402.2		3
14	1163.6	582.3		1145.6	F	322.2		305.2		2
15	1337.7	669.4	1320.7	1319.7	R	175.1		158.1		1

Gene symbol: Ggn

Protein name: gametogenetin isoform 1

Protein accession numbers: IPI00330597

Peptide sequence: ITLASSATSPTESQVR

Exclusive (unique to this protein): TRUE

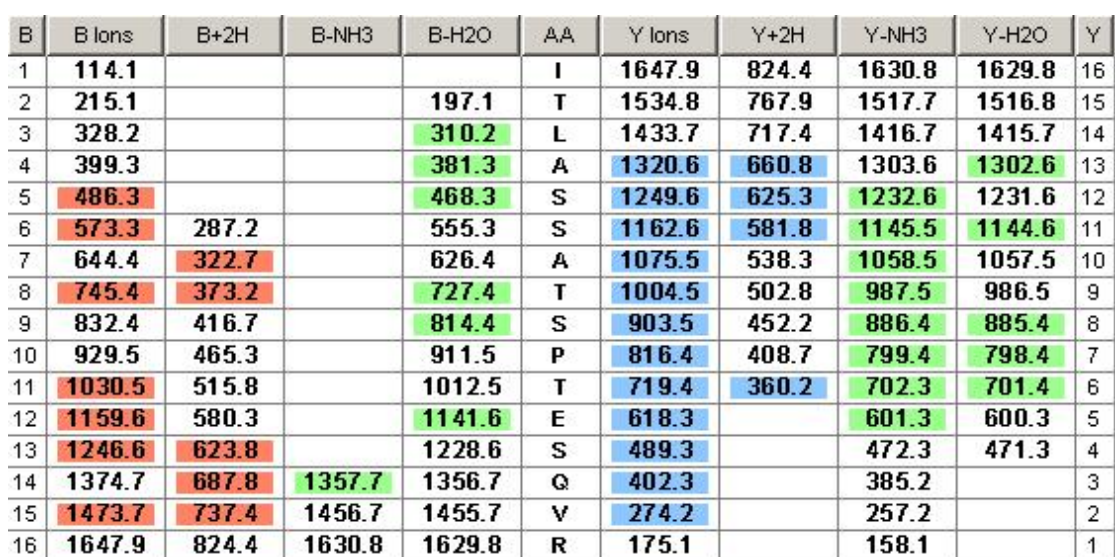
SEQUEST XCorr score: 2.69 SEQUEST DCn score: 0.528

Fix modifications: None

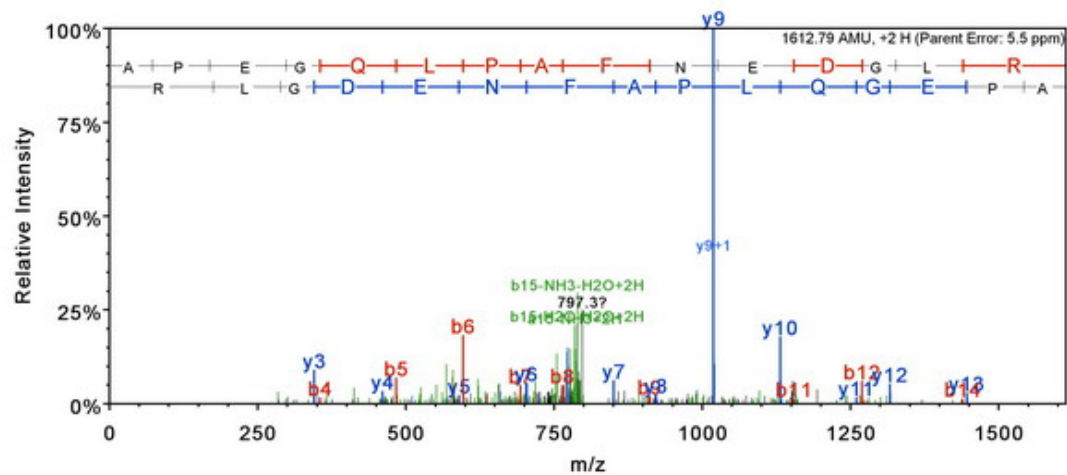
Variable modifications: None

Charge: 2 Observed m/z: 824.4247

Actual minus calculated peptide mass (AMU): -0.013757



Actual minus calculated peptide mass (AMU): 0.008789



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1613.8	807.4	1596.8	1595.8	15
2	169.1				P	1542.8	771.9	1525.7	1524.7	14
3	298.1			280.1	E	1445.7	723.4	1428.7	1427.7	13
4	355.2			337.2	G	1316.7	658.8	1299.6	1298.7	12
5	483.2		466.2	465.2	Q	1259.6	630.3	1242.6	1241.6	11
6	596.3	298.7	579.3	578.3	L	1131.6	566.3	1114.5	1113.6	10
7	693.4	347.2	676.3	675.4	P	1018.5	509.8	1001.5	1000.5	9
8	764.4	382.7	747.4	746.4	A	921.4	461.2	904.4	903.4	8
9	911.5	456.2	894.4	893.5	F	850.4	425.7	833.4	832.4	7
10	1025.5	513.3	1008.5	1007.5	N	703.3	352.2	686.3	685.3	6
11	1154.5	577.8	1137.5	1136.5	E	589.3		572.3	571.3	5
12	1269.6	635.3	1252.5	1251.6	D	460.3		443.2	442.2	4
13	1326.6	663.8	1309.6	1308.6	G	345.2		328.2		3
14	1439.7	720.3	1422.7	1421.7	L	288.2		271.2		2
15	1613.8	807.4	1596.8	1595.8	R	175.1		158.1		1

Gene symbol: Git1

Protein name: ARF GTPase-activating protein GIT1

Protein accession numbers: IPI00470095,IPI00649373

Peptide sequence: SLSSPTDNLELSAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.49 SEQUEST DCn score: 0.439

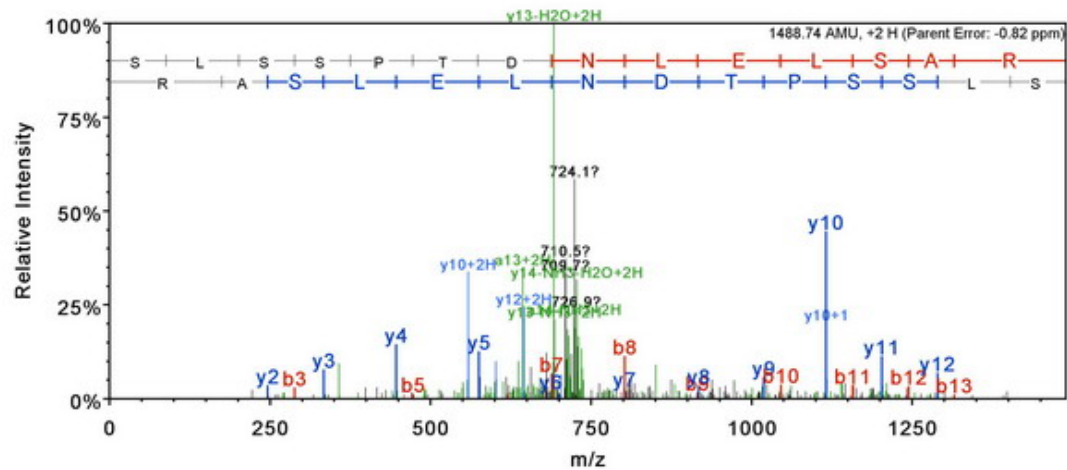
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 745.3782

Actual minus calculated peptide mass (AMU): -0.0012249



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1489.8	745.4	1472.7	1471.7	14
2	201.1			183.1	L	1402.7	701.9	1385.7	1384.7	13
3	288.2			270.1	S	1289.6	645.3	1272.6	1271.6	12
4	375.2			357.2	S	1202.6	601.8	1185.6	1184.6	11
5	472.2			454.2	P	1115.6	558.3	1098.5	1097.6	10
6	573.3	287.2		555.3	T	1018.5	509.8	1001.5	1000.5	9
7	688.3	344.7		670.3	D	917.5	459.2	900.4	899.5	8
8	802.4	401.7	785.3	784.4	N	802.4	401.7	785.4	784.4	7
9	915.4	458.2	898.4	897.4	L	688.4	344.7	671.4	670.4	6
10	1044.5	522.8	1027.5	1026.5	E	575.3		558.3	557.3	5
11	1157.6	579.3	1140.5	1139.6	L	446.3		429.3	428.3	4
12	1244.6	622.8	1227.6	1226.6	S	333.2		316.2	315.2	3
13	1315.6	658.3	1298.6	1297.6	A	246.2		229.1		2
14	1489.8	745.4	1472.7	1471.7	R	175.1		158.1		1

Gene symbol: Glt8d1

Protein name: Isoform 1 of Glycosyltransferase 8 domain-containing protein 1

Protein accession numbers: IPI00467883

Peptide sequence: LGGTIAAINSVHQNTR

Exclusive (unique to this protein): TRUE

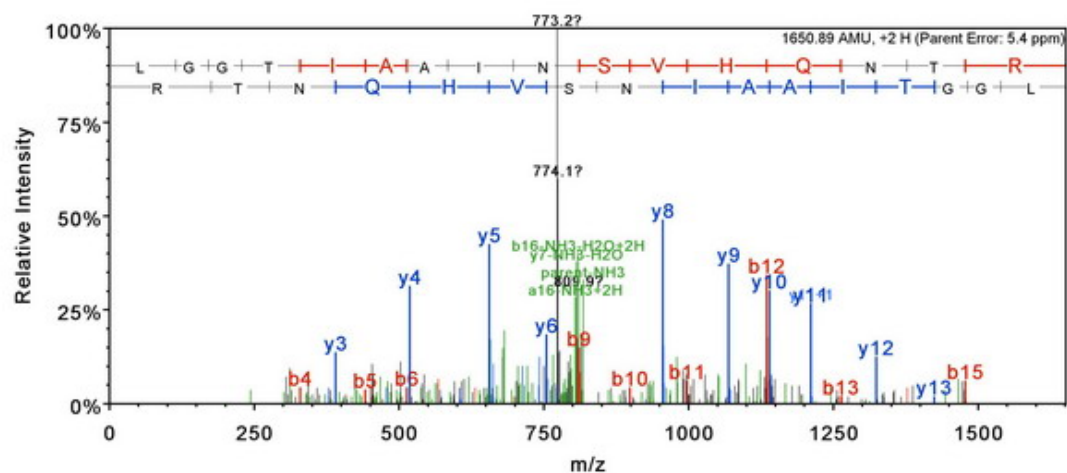
SEQUEST XCorr score: 2.92 SEQUEST DCn score: 0.623

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 826.4524

Actual minus calculated peptide mass (AMU): 0.0089149



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1651.9	826.5	1634.9	1633.9	16
2	171.1				G	1538.8	769.9	1521.8	1520.8	15
3	228.1				G	1481.8	741.4	1464.8	1463.8	14
4	329.2			311.2	T	1424.8	712.9	1407.7	1406.8	13
5	442.3			424.3	I	1323.7	662.4	1306.7	1305.7	12
6	513.3	257.2		495.3	A	1210.6	605.8	1193.6	1192.6	11
7	584.3	292.7		566.3	A	1139.6	570.3	1122.6	1121.6	10
8	697.4	349.2		679.4	I	1068.5	534.8	1051.5	1050.5	9
9	811.5	406.2	794.4	793.5	N	955.5	478.2	938.4	937.5	8
10	898.5	449.8	881.5	880.5	S	841.4	421.2	824.4	823.4	7
11	997.6	499.3	980.5	979.6	V	754.4	377.7	737.4	736.4	6
12	1134.6	567.8	1117.6	1116.6	H	655.3	328.2	638.3	637.3	5
13	1262.7	631.9	1245.7	1244.7	Q	518.3		501.2	500.3	4
14	1376.7	688.9	1359.7	1358.7	N	390.2		373.2	372.2	3
15	1477.8	739.4	1460.8	1459.8	T	276.2		259.1	258.2	2
16	1651.9	826.5	1634.9	1633.9	R	175.1		158.1		1

Gene symbol: Gm1141

Protein name: Novel protein

Protein accession numbers: IPI00775963

Peptide sequence: IQTNVIAVESNPIR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.03 SEQUEST DCn score: 0.678

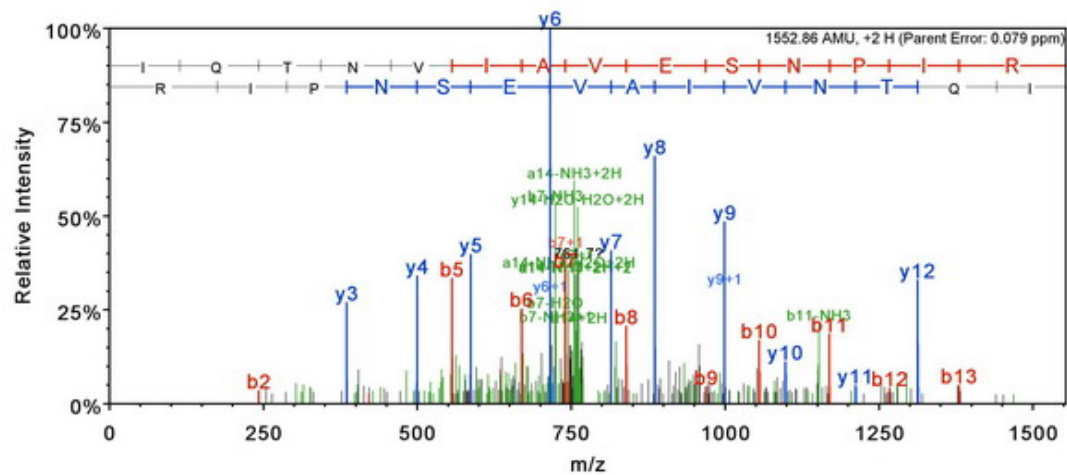
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 777.4366

Actual minus calculated peptide mass (AMU): 0.0001221



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1553.9	777.4	1536.8	1535.9	14
2	242.2		225.1		Q	1440.8	720.9	1423.8	1422.8	13
3	343.2		326.2	325.2	T	1312.7	656.9	1295.7	1294.7	12
4	457.2		440.2	439.2	N	1211.7	606.3	1194.7	1193.7	11
5	556.3		539.3	538.3	V	1097.6	549.3	1080.6	1079.6	10
6	669.4	335.2	652.4	651.4	I	998.6	499.8	981.5	980.6	9
7	740.4	370.7	723.4	722.4	A	885.5	443.2	868.5	867.5	8
8	839.5	420.3	822.5	821.5	V	814.4	407.7	797.4	796.4	7
9	968.5	484.8	951.5	950.5	E	715.4	358.2	698.4	697.4	6
10	1055.6	528.3	1038.5	1037.6	S	586.3		569.3	568.3	5
11	1169.6	585.3	1152.6	1151.6	N	499.3		482.3		4
12	1266.7	633.8	1249.6	1248.7	P	385.3		368.2		3
13	1379.8	690.4	1362.7	1361.7	I	288.2		271.2		2
14	1553.9	777.4	1536.8	1535.9	R	175.1		158.1		1

Gene symbol: Gm234

Protein name: hypothetical protein

Protein accession numbers: IPI00348144

Peptide sequence: LQGTEEMTDIIDTEELFR

Exclusive (unique to this protein): TRUE

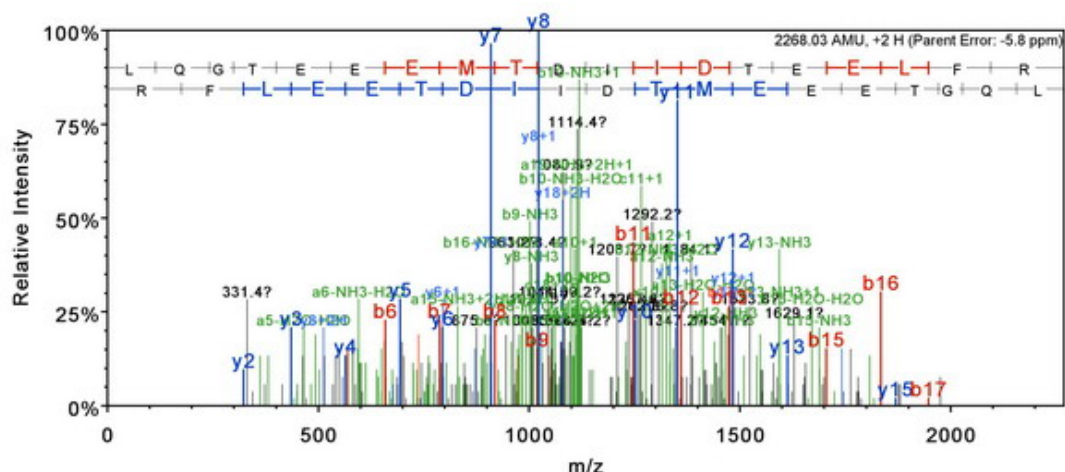
SEQUEST XCorr score: 4.36 SEQUEST DCn score: 0.787

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1135.0248

Actual minus calculated peptide mass (AMU): -0.013156



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	2269.1	1135.0	2252.0	2251.0	19
2	242.2		225.1		Q	2156.0	1078.5	2138.9	2138.0	18
3	299.2		282.2		G	2027.9	1014.5	2010.9	2009.9	17
4	400.2		383.2	382.2	T	1970.9	986.0	1953.9	1952.9	16
5	529.3		512.2	511.3	E	1869.8	935.4	1852.8	1851.8	15
6	658.3	329.7	641.3	640.3	E	1740.8	870.9	1723.8	1722.8	14
7	787.4	394.2	770.3	769.3	E	1611.8	806.4	1594.7	1593.8	13
8	918.4	459.7	901.4	900.4	M	1482.7	741.9	1465.7	1464.7	12
9	1019.4	510.2	1002.4	1001.4	T	1351.7	676.3	1334.7	1333.7	11
10	1134.5	567.7	1117.4	1116.5	D	1250.6	625.8	1233.6	1232.6	10
11	1247.5	624.3	1230.5	1229.5	I	1135.6	568.3	1118.6	1117.6	9
12	1360.6	680.8	1343.6	1342.6	I	1022.5	511.8	1005.5	1004.5	8
13	1475.7	738.3	1458.6	1457.7	D	909.4	455.2	892.4	891.4	7
14	1576.7	788.9	1559.7	1558.7	T	794.4	397.7	777.4	776.4	6
15	1705.8	853.4	1688.7	1687.7	E	693.4		676.3	675.4	5
16	1834.8	917.9	1817.8	1816.8	E	564.3		547.3	546.3	4
17	1947.9	974.4	1930.9	1929.9	L	435.3		418.3		3
18	2094.9	1048.0	2077.9	2076.9	F	322.2		305.2		2
19	2269.1	1135.0	2252.0	2251.0	R	175.1		158.1		1

Gene symbol: Golga5

Protein name: Golgin subfamily A member 5

Protein accession numbers: IPI00316682

Peptide sequence: APVSPSSPSGVSSVNTSVTTTK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.58 SEQUEST DCn score: 0.588

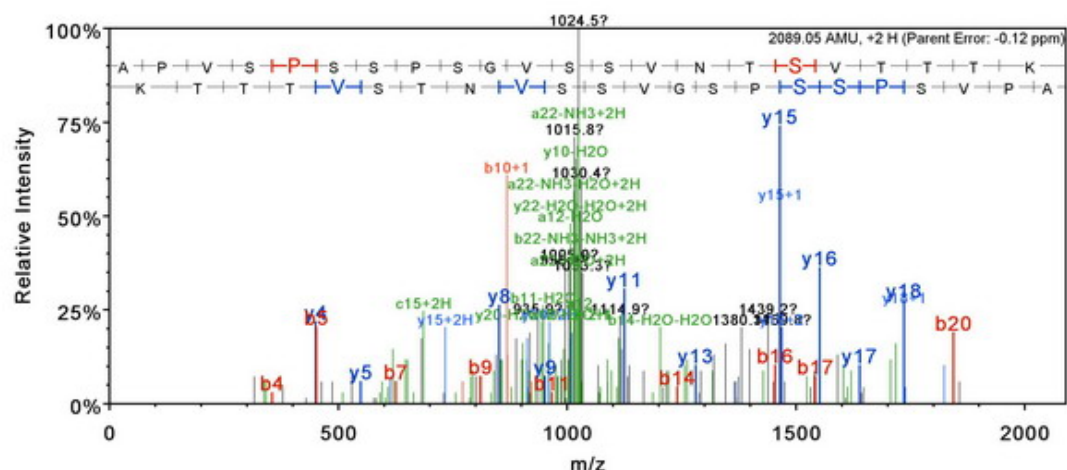
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1045.5345

Actual minus calculated peptide mass (AMU): -0.0002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2090.1	1045.5	2073.0	2072.1	22
2	169.1				P	2019.0	1010.0	2002.0	2001.0	21
3	268.2				V	1922.0	961.5	1905.0	1904.0	20
4	355.2			337.2	S	1822.9	912.0	1805.9	1804.9	19
5	452.3			434.2	P	1735.9	868.4	1718.8	1717.9	18
6	539.3	270.1		521.3	S	1638.8	819.9	1621.8	1620.8	17
7	626.3	313.7		608.3	S	1551.8	776.4	1534.8	1533.8	16
8	723.4	362.2		705.4	P	1464.8	732.9	1447.7	1446.7	15
9	810.4	405.7		792.4	S	1367.7	684.4	1350.7	1349.7	14
10	867.4	434.2		849.4	G	1280.7	640.8	1263.6	1262.7	13
11	966.5	483.8		948.5	V	1223.7	612.3	1206.6	1205.6	12
12	1053.5	527.3		1035.5	S	1124.6	562.8	1107.5	1106.6	11
13	1140.5	570.8		1122.5	S	1037.5	519.3	1020.5	1019.5	10
14	1239.6	620.3		1221.6	V	950.5	475.8	933.5	932.5	9
15	1353.7	677.3	1336.6	1335.7	N	851.5	426.2	834.4	833.4	8
16	1454.7	727.9	1437.7	1436.7	T	737.4	369.2	720.4	719.4	7
17	1541.7	771.4	1524.7	1523.7	S	636.4	318.7	619.3	618.4	6
18	1640.8	820.9	1623.8	1622.8	V	549.3		532.3	531.3	5
19	1741.9	871.4	1724.8	1723.9	T	450.3		433.2	432.3	4
20	1842.9	922.0	1825.9	1824.9	T	349.2		332.2	331.2	3
21	1944.0	972.5	1926.9	1926.0	T	248.2		231.1	230.2	2
22	2090.1	1045.5	2073.0	2072.1	K	147.1		130.1		1

Gene symbol: Grhpr

Protein name: Glyoxylate reductase/hydroxypyruvate reductase

Protein accession numbers: IPI00130530

Peptide sequence: NTMSLLAANNLLAGLR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.05 SEQUEST DCn score: 0.401

Fix modifications: None

Variable modifications: None

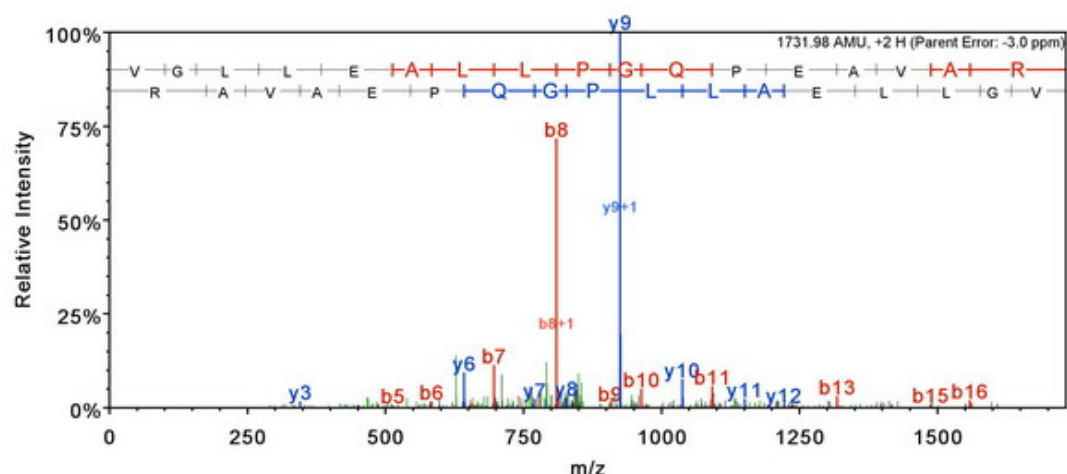
Charge: 2

Observed m/z: 836.4659

Actual minus calculated peptide mass (AMU): 0.002319



Actual minus calculated peptide mass (AMU): -0.005127



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1733.0	867.0	1716.0	1715.0	17
2	157.1				G	1633.9	817.5	1616.9	1615.9	16
3	270.2				L	1576.9	789.0	1559.9	1558.9	15
4	383.3				L	1463.8	732.4	1446.8	1445.8	14
5	512.3			494.3	E	1350.7	675.9	1333.7	1332.7	13
6	583.4	292.2		565.3	A	1221.7	611.4	1204.7	1203.7	12
7	696.4	348.7		678.4	L	1150.7	575.8	1133.6	1132.7	11
8	809.5	405.3		791.5	L	1037.6	519.3	1020.6	1019.6	10
9	906.6	453.8		888.6	P	924.5	462.8	907.5	906.5	9
10	963.6	482.3		945.6	G	827.4	414.2	810.4	809.4	8
11	1091.7	546.3	1074.6	1073.6	Q	770.4	385.7	753.4	752.4	7
12	1188.7	594.9	1171.7	1170.7	P	642.4	321.7	625.3	624.4	6
13	1317.7	659.4	1300.7	1299.7	E	545.3		528.3	527.3	5
14	1388.8	694.9	1371.8	1370.8	A	416.3		399.2		4
15	1487.9	744.4	1470.8	1469.8	V	345.2		328.2		3
16	1558.9	780.0	1541.9	1540.9	A	246.2		229.1		2
17	1733.0	867.0	1716.0	1715.0	R	175.1		158.1		1

Gene symbol: Gstm4

Protein name: Adult male testis cDNA, RIKEN full-length enriched library, clone:4930583C14

product: hypothetical Glutathione S-transferase N terminus containing protein, full insert sequence

Protein accession numbers: IPI00137528

Peptide sequence: EYIEINPLR

Exclusive (unique to this protein): TRUE

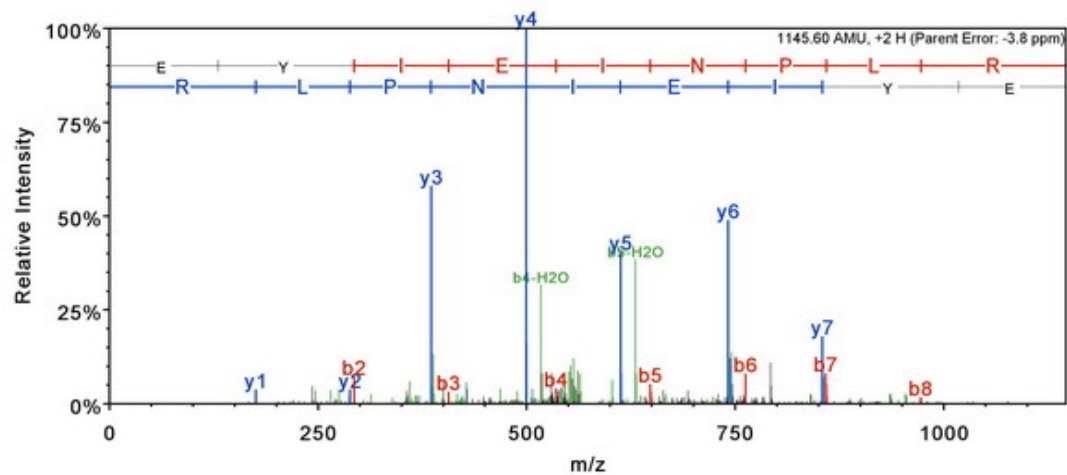
SEQUEST XCorr score: 2.96 SEQUEST DCn score: 0.41

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 573.8097

Actual minus calculated peptide mass (AMU): -0.004395



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1146.6	573.8	1129.6	1128.6	9
2	293.1			275.1	Y	1017.6	509.3	1000.6	999.6	8
3	406.2			388.2	I	854.5	427.8	837.5	836.5	7
4	535.2			517.2	E	741.4	371.2	724.4	723.4	6
5	648.3			630.3	I	612.4		595.4		5
6	762.4	381.7	745.3	744.4	N	499.3		482.3		4
7	859.4	430.2	842.4	841.4	P	385.3		368.2		3
8	972.5	486.8	955.5	954.5	L	288.2		271.2		2
9	1146.6	573.8	1129.6	1128.6	R	175.1		158.1		1

Gene symbol: Gtf2h3

Protein name: TFIIH basal transcription factor complex p34 subunit

Protein accession numbers: IPI00122664

Peptide sequence: SNQLAVIASHIQESR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.53 SEQUEST DCn score: 0.548

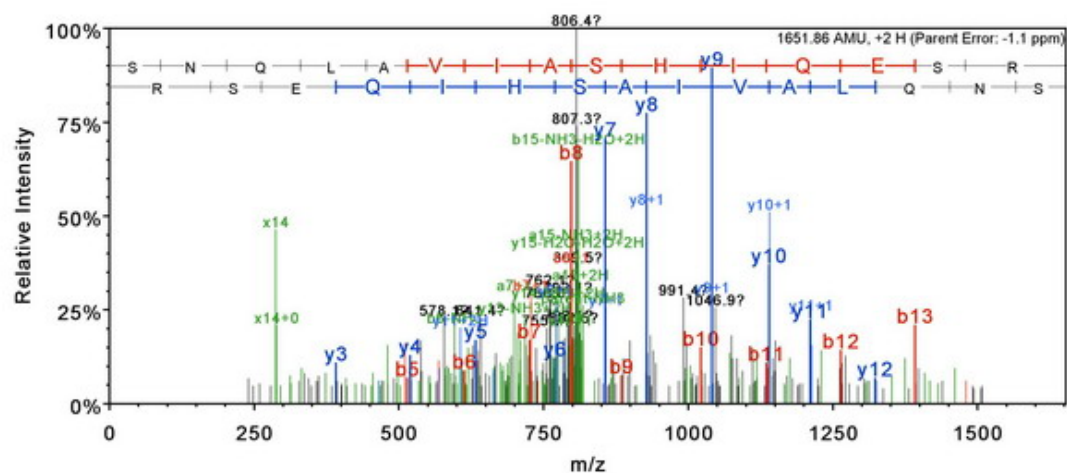
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 826.939

Actual minus calculated peptide mass (AMU): -0.001831



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1652.9	826.9	1635.9	1634.9	15
2	202.1		185.1	184.1	N	1565.8	783.4	1548.8	1547.8	14
3	330.1		313.1	312.1	Q	1451.8	726.4	1434.8	1433.8	13
4	443.2		426.2	425.2	L	1323.7	662.4	1306.7	1305.7	12
5	514.3		497.2	496.3	A	1210.7	605.8	1193.6	1192.6	11
6	613.3	307.2	596.3	595.3	V	1139.6	570.3	1122.6	1121.6	10
7	726.4	363.7	709.4	708.4	I	1040.5	520.8	1023.5	1022.5	9
8	797.5	399.2	780.4	779.4	A	927.5	464.2	910.4	909.5	8
9	884.5	442.8	867.5	866.5	S	856.4	428.7	839.4	838.4	7
10	1021.5	511.3	1004.5	1003.5	H	769.4	385.2	752.4	751.4	6
11	1134.6	567.8	1117.6	1116.6	I	632.3		615.3	614.3	5
12	1262.7	631.9	1245.7	1244.7	Q	519.3		502.2	501.2	4
13	1391.7	696.4	1374.7	1373.7	E	391.2		374.2	373.2	3
14	1478.8	739.9	1461.7	1460.8	S	262.1		245.1	244.1	2
15	1652.9	826.9	1635.9	1634.9	R	175.1		158.1		1

Gene symbol: H47

Protein name: Selenoprotein S

Protein accession numbers: IPI00114477

Peptide sequence: QLDQAETVLEPDVVVK

Exclusive (unique to this protein): TRUE

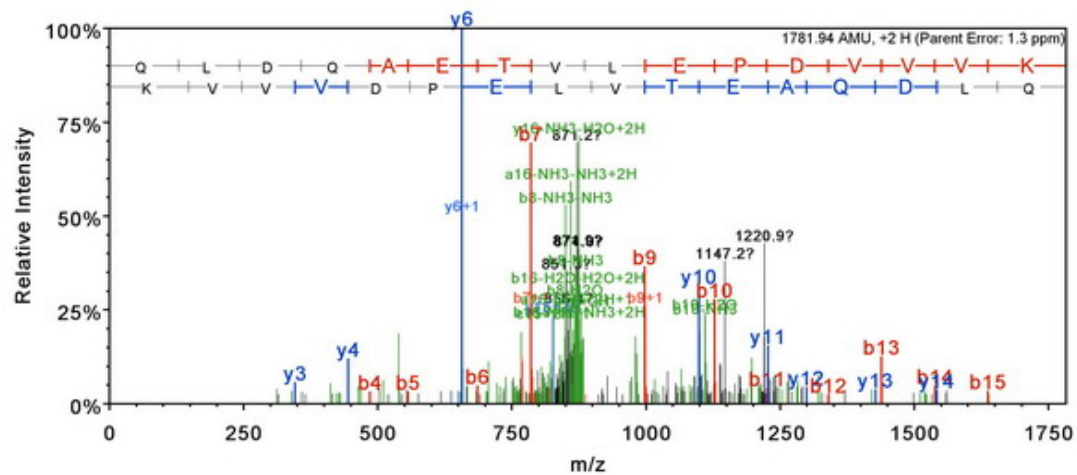
SEQUEST XCorr score: 3.5 SEQUEST DCn score: 0.474

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 891.9796

Actual minus calculated peptide mass (AMU): 0.002319



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	1783.0	892.0	1765.9	1764.9	16
2	242.2		225.1		L	1654.9	828.0	1637.9	1636.9	15
3	357.2		340.2	339.2	D	1541.8	771.4	1524.8	1523.8	14
4	485.2		468.2	467.2	Q	1426.8	713.9	1409.8	1408.8	13
5	556.3		539.3	538.3	A	1298.7	649.9	1281.7	1280.7	12
6	685.3	343.2	668.3	667.3	E	1227.7	614.4	1210.7	1209.7	11
7	786.4	393.7	769.3	768.4	T	1098.6	549.8	1081.6	1080.6	10
8	885.4	443.2	868.4	867.4	V	997.6	499.3	980.6	979.6	9
9	998.5	499.8	981.5	980.5	L	898.5	449.8	881.5	880.5	8
10	1127.6	564.3	1110.5	1109.5	E	785.4	393.2	768.4	767.4	7
11	1224.6	612.8	1207.6	1206.6	P	656.4	328.7	639.4	638.4	6
12	1339.6	670.3	1322.6	1321.6	D	559.4		542.3	541.3	5
13	1438.7	719.9	1421.7	1420.7	V	444.3		427.3		4
14	1537.8	769.4	1520.8	1519.8	V	345.3		328.2		3
15	1636.8	818.9	1619.8	1618.8	V	246.2		229.2		2
16	1783.0	892.0	1765.9	1764.9	K	147.1		130.1		1

Gene symbol: Habp4

Protein name: Isoform 1 of Intracellular hyaluronan-binding protein 4

Protein accession numbers: IPI00123374

Peptide sequence: FHQLLDDESDPFDILR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.33 SEQUEST DCn score: 0.652

Fix modifications: None

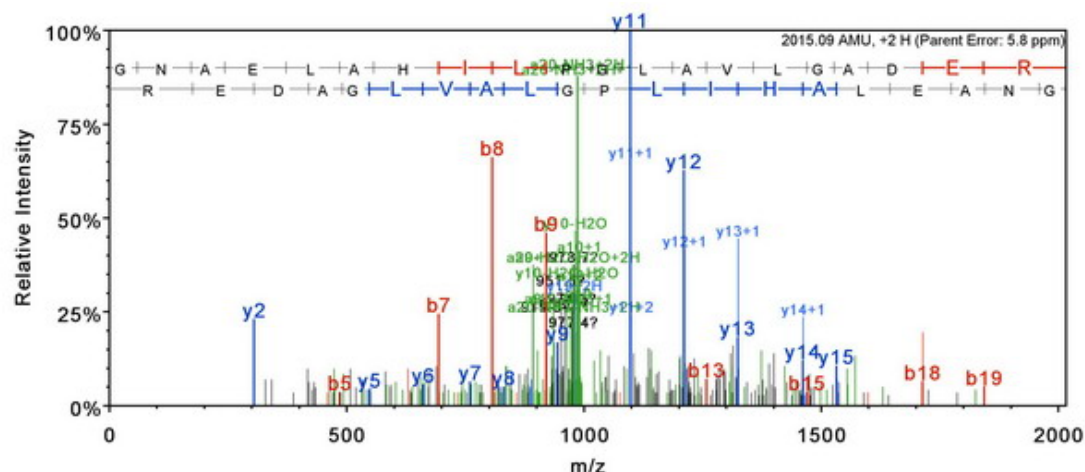
Variable modifications: None

Charge: 2

Observed m/z: 980.4676

Actual minus calculated peptide mass (AMU): -0.018157

B	B-ions	B+2H	B-NH3	B-H2O	AA	Y-ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1960.0	980.5	1942.9	1941.9	16
2	285.1	143.1			H	1812.9	906.9	1795.9	1794.9	15
3	413.2	207.1	396.2		Q	1675.8	838.4	1658.8	1657.8	14
4	526.3	263.6	509.3		L	1547.8	774.4	1530.7	1529.8	13
5	639.4	320.2	622.3		L	1434.7	717.8	1417.7	1416.7	12
6	754.4	377.7	737.4	736.4	D	1321.6	661.3	1304.6	1303.6	11
7	869.4	435.2	852.4	851.4	D	1206.6	603.8	1189.5	1188.5	10
8	998.5	499.7	981.4	980.5	E	1091.5	546.3	1074.5	1073.5	9
9	1085.5	543.3	1068.5	1067.5	S	962.5	481.8	945.5	944.5	8
10	1200.5	600.8	1183.5	1182.5	D	875.5	438.2	858.4	857.5	7
11	1297.6	649.3	1280.5	1279.6	P	760.4	380.7	743.4	742.4	6
12	1444.6	722.8	1427.6	1426.6	F	663.4		646.4	645.4	5
13	1559.7	780.3	1542.6	1541.7	D	516.3		499.3	498.3	4
14	1672.8	836.9	1655.7	1654.7	I	401.3		384.3		3
15	1785.8	893.4	1768.8	1767.8	L	288.2		271.2		2
16	1960.0	980.5	1942.9	1941.9	R	175.1		158.1		1



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	2016.1	1008.6	1999.1	1998.1	20
2	172.1		155.1		N	1959.1	980.0	1942.0	1941.1	19
3	243.1		226.1		A	1845.0	923.0	1828.0	1827.0	18
4	372.2		355.1	354.1	E	1774.0	887.5	1757.0	1756.0	17
5	485.2		468.2	467.2	L	1644.9	823.0	1627.9	1626.9	16
6	556.3	278.6	539.3	538.3	A	1531.9	766.4	1514.8	1513.9	15
7	693.3	347.2	676.3	675.3	H	1460.8	730.9	1443.8	1442.8	14
8	806.4	403.7	789.4	788.4	I	1323.8	662.4	1306.7	1305.8	13
9	919.5	460.3	902.5	901.5	L	1210.7	605.8	1193.7	1192.7	12
10	1016.6	508.8	999.5	998.5	P	1097.6	549.3	1080.6	1079.6	11
11	1073.6	537.3	1056.5	1055.6	G	1000.5	500.8	983.5	982.5	10
12	1186.7	593.8	1169.6	1168.7	L	943.5	472.3	926.5	925.5	9
13	1257.7	629.4	1240.7	1239.7	A	830.4	415.7	813.4	812.4	8
14	1356.8	678.9	1339.7	1338.8	V	759.4	380.2	742.4	741.4	7
15	1469.9	735.4	1452.8	1451.8	L	660.3	330.7	643.3	642.3	6
16	1526.9	763.9	1509.8	1508.9	G	547.3		530.2	529.2	5
17	1597.9	799.5	1580.9	1579.9	A	490.2		473.2	472.2	4
18	1712.9	857.0	1695.9	1694.9	D	419.2		402.2	401.2	3
19	1842.0	921.5	1825.0	1824.0	E	304.2		287.1	286.2	2
20	2016.1	1008.6	1999.1	1998.1	R	175.1		158.1		1

Gene symbol: Hars

Protein name: Histidyl-tRNA synthetase, cytoplasmic

Protein accession numbers: IPI00116991,IPI00331327

Peptide sequence: IGDYVQQHGGVSLVEQLLQDPK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.29 SEQUEST DCn score: 0.253

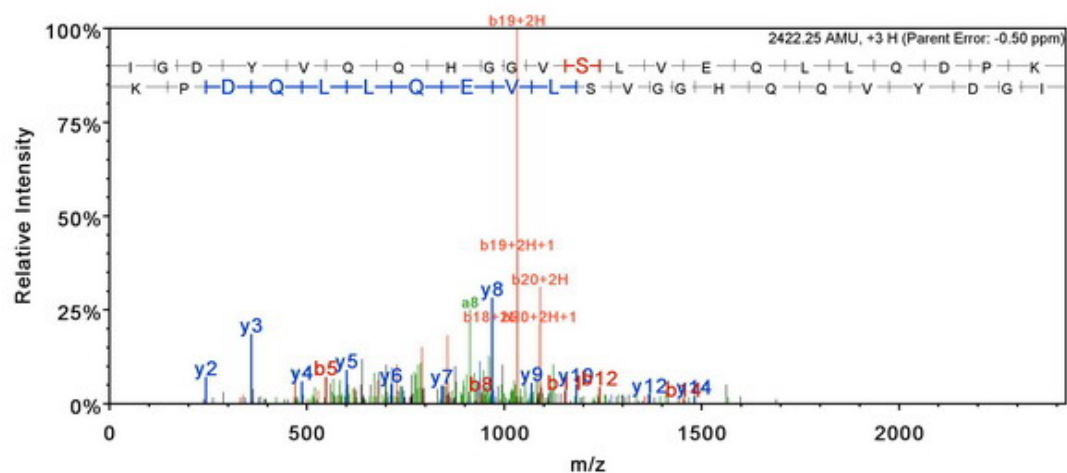
Fix modifications: None

Variable modifications: None

Charge: 3

Observed m/z: 808.4239

Actual minus calculated peptide mass (AMU): -0.0012249



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	2423.3	1212.1	2406.2	2405.3	22
2	171.1				G	2310.2	1155.6	2293.2	2292.2	21
3	286.1			268.1	D	2253.2	1127.1	2236.1	2235.1	20
4	449.2			431.2	Y	2138.1	1069.6	2121.1	2120.1	19
5	548.3			530.3	V	1975.1	988.0	1958.0	1957.1	18
6	676.3	338.7	659.3	658.3	Q	1876.0	938.5	1859.0	1858.0	17
7	804.4	402.7	787.4	786.4	Q	1747.9	874.5	1730.9	1729.9	16
8	941.5	471.2	924.4	923.4	H	1619.9	810.4	1602.9	1601.9	15
9	998.5	499.7	981.4	980.5	G	1482.8	741.9	1465.8	1464.8	14
10	1055.5	528.3	1038.5	1037.5	G	1425.8	713.4	1408.8	1407.8	13
11	1154.6	577.8	1137.5	1136.5	V	1368.8	684.9	1351.8	1350.8	12
12	1241.6	621.3	1224.6	1223.6	S	1269.7	635.4	1252.7	1251.7	11
13	1354.7	677.8	1337.7	1336.7	L	1182.7	591.8	1165.7	1164.7	10
14	1453.7	727.4	1436.7	1435.7	V	1069.6	535.3	1052.6	1051.6	9
15	1582.8	791.9	1565.8	1564.8	E	970.5	485.8	953.5	952.5	8
16	1710.9	855.9	1693.8	1692.8	Q	841.5	421.2	824.5	823.5	7
17	1823.9	912.5	1806.9	1805.9	L	713.4	357.2	696.4	695.4	6
18	1937.0	969.0	1920.0	1919.0	L	600.3		583.3	582.3	5
19	2065.1	1033.0	2048.1	2047.1	Q	487.3		470.2	469.2	4
20	2180.1	1090.5	2163.1	2162.1	D	359.2		342.2	341.2	3
21	2277.2	1139.1	2260.1	2259.1	P	244.2		227.1		2
22	2423.3	1212.1	2406.2	2405.3	K	147.1		130.1		1

Gene symbol: Hdgfrp3

Protein name: Isoform 1 of Hepatoma-derived growth factor-related protein 3

Protein accession numbers: IPI00224067,IPI00608040,IPI00654313

Peptide sequence: GFNEGLWEIENNPQVK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.76 SEQUEST DCn score: 0.503

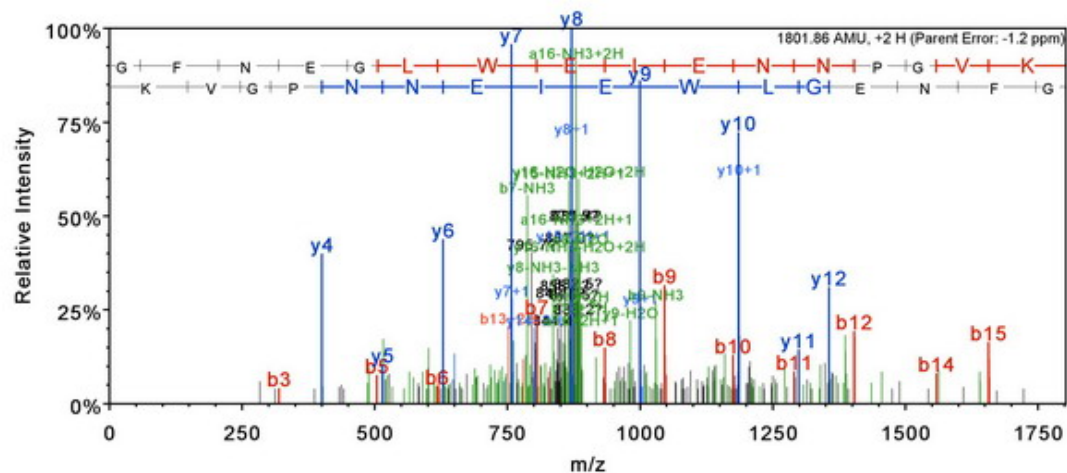
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 901.9385

Actual minus calculated peptide mass (AMU): -0.0021955



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1802.9	901.9	1785.8	1784.9	16
2	205.1				F	1745.9	873.4	1728.8	1727.8	15
3	319.1		302.1		N	1598.8	799.9	1581.8	1580.8	14
4	448.2		431.2	430.2	E	1484.7	742.9	1467.7	1466.7	13
5	505.2		488.2	487.2	G	1355.7	678.4	1338.7	1337.7	12
6	618.3	309.7	601.3	600.3	L	1298.7	649.8	1281.7	1280.7	11
7	804.4	402.7	787.3	786.4	W	1185.6	593.3	1168.6	1167.6	10
8	933.4	467.2	916.4	915.4	E	999.5	500.3	982.5	981.5	9
9	1046.5	523.8	1029.5	1028.5	I	870.5	435.7	853.4	852.5	8
10	1175.5	588.3	1158.5	1157.5	E	757.4	379.2	740.4	739.4	7
11	1289.6	645.3	1272.5	1271.6	N	628.3	314.7	611.3		6
12	1403.6	702.3	1386.6	1385.6	N	514.3		497.3		5
13	1500.7	750.8	1483.7	1482.7	P	400.3		383.2		4
14	1557.7	779.4	1540.7	1539.7	G	303.2		286.2		3
15	1656.8	828.9	1639.7	1638.8	V	246.2		229.2		2
16	1802.9	901.9	1785.8	1784.9	K	147.1		130.1		1

Gene symbol: HdIbp

Protein name: Vigilin

Protein accession numbers: IPI00123379

Peptide sequence: LVGEIMQETGTR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.79 SEQUEST DCn score: 0.466

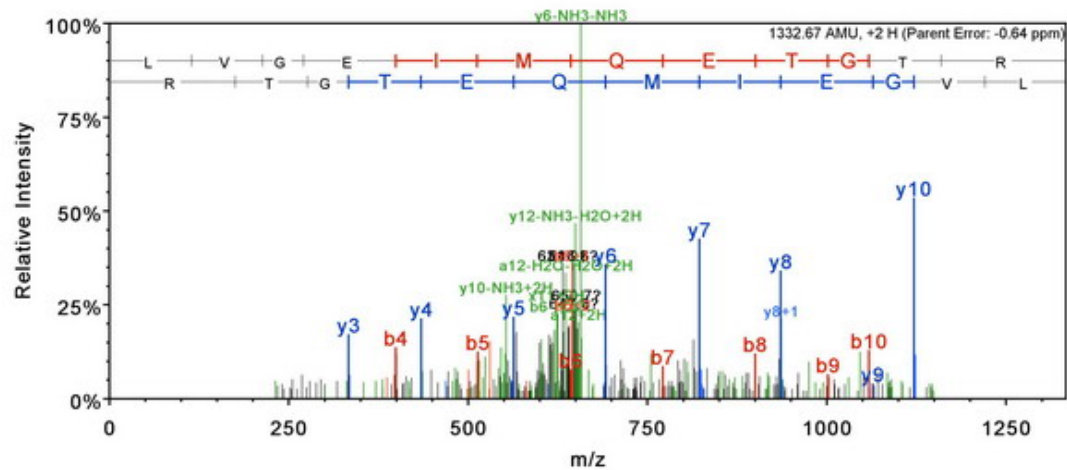
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 667.3429

Actual minus calculated peptide mass (AMU): -0.0008545



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1333.7	667.3	1316.7	1315.7	12
2	213.2				V	1220.6	610.8	1203.6	1202.6	11
3	270.2				G	1121.5	561.3	1104.5	1103.5	10
4	399.2			381.2	E	1064.5	532.8	1047.5	1046.5	9
5	512.3			494.3	I	935.5	468.2	918.4	917.5	8
6	643.4	322.2		625.3	M	822.4	411.7	805.4	804.4	7
7	771.4	386.2	754.4	753.4	Q	691.3	346.2	674.3	673.3	6
8	900.5	450.7	883.4	882.4	E	563.3		546.3	545.3	5
9	1001.5	501.3	984.5	983.5	T	434.2		417.2	416.2	4
10	1058.5	529.8	1041.5	1040.5	G	333.2		316.2	315.2	3
11	1159.6	580.3	1142.5	1141.6	T	276.2		259.1	258.2	2
12	1333.7	667.3	1316.7	1315.7	R	175.1		158.1		1

Gene symbol: Heatr5b

Protein name: HEAT repeat containing 5B

Protein accession numbers: IPI00762140

Peptide sequence: MAGLQALEDIIK

Exclusive (unique to this protein): TRUE

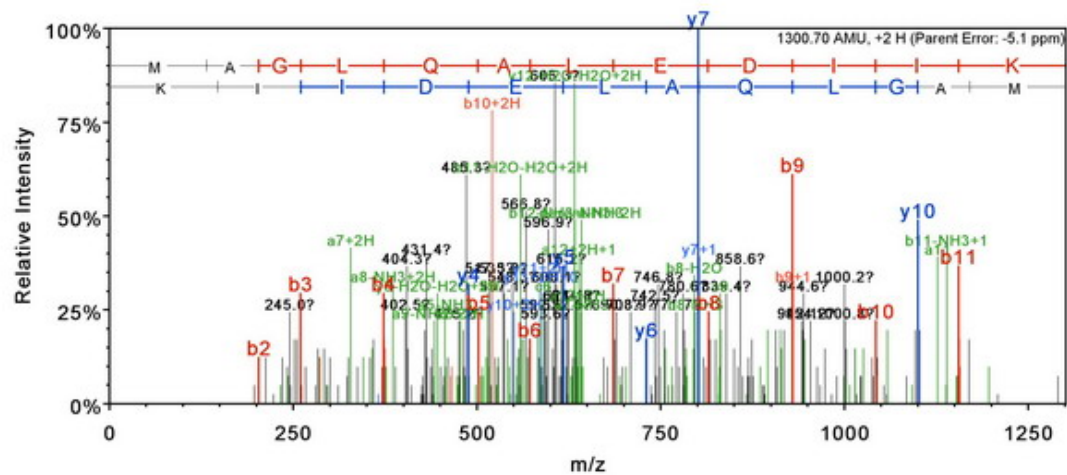
SEQUEST XCorr score: 2.59 SEQUEST DCn score: 0.198

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 651.3577

Actual minus calculated peptide mass (AMU): -0.006592



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1301.7	651.4	1284.7	1283.7	12
2	203.1				A	1170.7	585.8	1153.7	1152.7	11
3	260.1				G	1099.6	550.3	1082.6	1081.6	10
4	373.2				L	1042.6	521.8	1025.6	1024.6	9
5	501.3		484.2		Q	929.5	465.3	912.5	911.5	8
6	572.3	286.7	555.3		A	801.5	401.2	784.5	783.5	7
7	685.4	343.2	668.3		L	730.4	365.7	713.4	712.4	6
8	814.4	407.7	797.4	796.4	E	617.4		600.3	599.3	5
9	929.4	465.2	912.4	911.4	D	488.3		471.3	470.3	4
10	1042.5	521.8	1025.5	1024.5	I	373.3		356.3		3
11	1155.6	578.3	1138.6	1137.6	I	260.2		243.2		2
12	1301.7	651.4	1284.7	1283.7	K	147.1		130.1		1

Gene symbol: Herc4

Protein name: Isoform 1 of Probable E3 ubiquitin-protein ligase HERC4

Protein accession numbers: IPI00453903,IPI00554980

Peptide sequence: ENIVGDAMEVLR

Exclusive (unique to this protein): TRUE

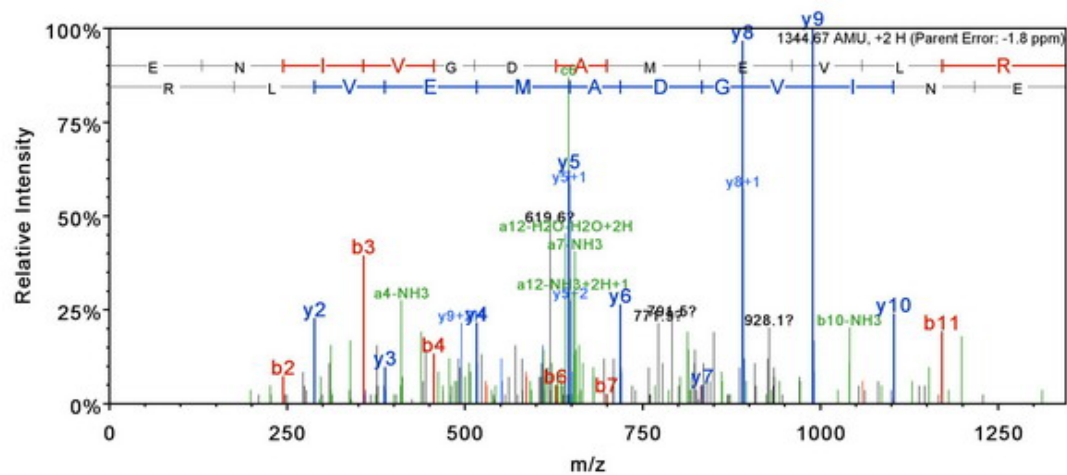
SEQUEST XCorr score: 2.87 SEQUEST DCn score: 0.422

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 673.342

Actual minus calculated peptide mass (AMU): -0.002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1345.7	673.3	1328.7	1327.7	12
2	244.1		227.1	226.1	N	1216.6	608.8	1199.6	1198.6	11
3	357.2		340.2	339.2	I	1102.6	551.8	1085.6	1084.6	10
4	456.3		439.2	438.2	V	989.5	495.3	972.5	971.5	9
5	513.3		496.2	495.3	G	890.4	445.7	873.4	872.4	8
6	628.3	314.7	611.3	610.3	D	833.4	417.2	816.4	815.4	7
7	699.3	350.2	682.3	681.3	A	718.4	359.7	701.4	700.4	6
8	830.4	415.7	813.4	812.4	M	647.4		630.3	629.3	5
9	959.4	480.2	942.4	941.4	E	516.3		499.3	498.3	4
10	1058.5	529.8	1041.5	1040.5	V	387.3		370.3		3
11	1171.6	586.3	1154.5	1153.6	L	288.2		271.2		2
12	1345.7	673.3	1328.7	1327.7	R	175.1		158.1		1

Gene symbol: Hif1an

Protein name: Isoform 1 of Hypoxia-inducible factor 1 alpha inhibitor

Protein accession numbers: IPI00652254

Peptide sequence: EEAEAPGPAWDESQLR

Exclusive (unique to this protein): TRUE

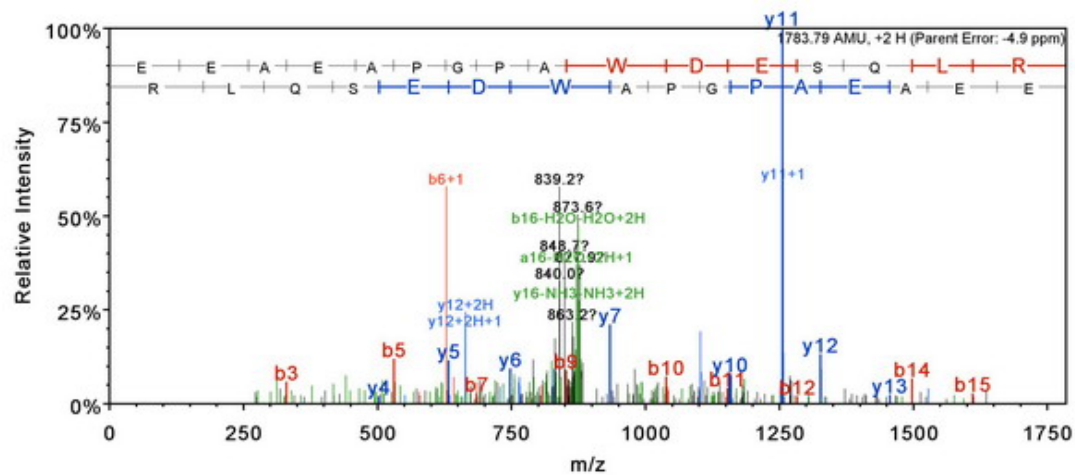
SEQUEST XCorr score: 2.65 SEQUEST DCn score: 0.53

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 892.9042

Actual minus calculated peptide mass (AMU): -0.008789



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1784.8	892.9	1767.8	1766.8	16
2	259.1			241.1	E	1655.8	828.4	1638.7	1637.8	15
3	330.1			312.1	A	1526.7	763.9	1509.7	1508.7	14
4	459.2			441.2	E	1455.7	728.4	1438.7	1437.7	13
5	530.2			512.2	A	1326.6	663.8	1309.6	1308.6	12
6	627.3	314.1		609.3	P	1255.6	628.3	1238.6	1237.6	11
7	684.3	342.7		666.3	G	1158.5	579.8	1141.5	1140.5	10
8	781.3	391.2		763.3	P	1101.5	551.3	1084.5	1083.5	9
9	852.4	426.7		834.4	A	1004.5	502.7	987.5	986.5	8
10	1038.5	519.7		1020.4	W	933.4	467.2	916.4	915.4	7
11	1153.5	577.2		1135.5	D	747.4	374.2	730.3	729.4	6
12	1282.5	641.8		1264.5	E	632.3		615.3	614.3	5
13	1369.5	685.3		1351.5	S	503.3		486.3	485.3	4
14	1497.6	749.3	1480.6	1479.6	Q	416.3		399.2		3
15	1610.7	805.9	1593.7	1592.7	L	288.2		271.2		2
16	1784.8	892.9	1767.8	1766.8	R	175.1		158.1		1

Gene symbol: Hist1h2ba

Protein name: Histone H2B type 1-A

Protein accession numbers: IPI00111957

Peptide sequence: AMSIMNSFVTDIFER

Exclusive (unique to this protein): TRUE

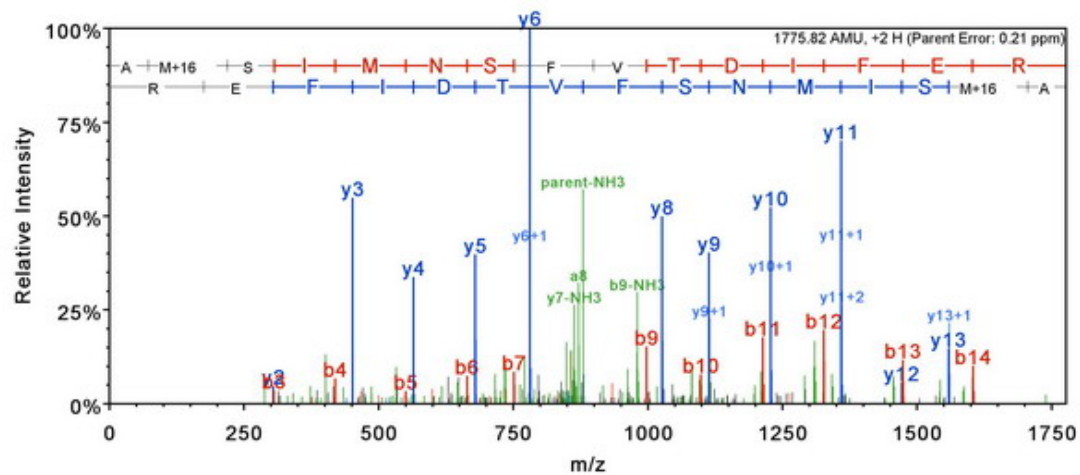
SEQUEST XCorr score: 5.14 SEQUEST DCn score: 0.634

Fix modifications: None

Variable modifications: M2: Oxidation (+16.00)

Charge: 2 Observed m/z: 888.9191

Actual minus calculated peptide mass (AMU): 0.0003662



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1776.8	888.9	1759.8	1758.8	15
2	219.1				M+16	1705.8	853.4	1688.8	1687.8	14
3	306.1			288.1	S	1558.8	779.9	1541.7	1540.8	13
4	419.2			401.2	I	1471.7	736.4	1454.7	1453.7	12
5	550.2			532.2	M	1358.6	679.8	1341.6	1340.6	11
6	664.3	332.6	647.3	646.3	N	1227.6	614.3	1210.6	1209.6	10
7	751.3	376.2	734.3	733.3	S	1113.6	557.3	1096.5	1095.5	9
8	898.4	449.7	881.4	880.4	F	1026.5	513.8	1009.5	1008.5	8
9	997.5	499.2	980.4	979.4	V	879.5	440.2	862.4	861.5	7
10	1098.5	549.8	1081.5	1080.5	T	780.4	390.7	763.4	762.4	6
11	1213.5	607.3	1196.5	1195.5	D	679.3		662.3	661.3	5
12	1326.6	663.8	1309.6	1308.6	I	564.3		547.3	546.3	4
13	1473.7	737.3	1456.7	1455.7	F	451.2		434.2	433.2	3
14	1602.7	801.9	1585.7	1584.7	E	304.2		287.1	286.2	2
15	1776.8	888.9	1759.8	1758.8	R	175.1		158.1		1

Gene symbol: Hist1h2bp

Protein name: Isoform 1 of Histone H2B type 1-P

Protein accession numbers: IPI00648991,IPI00761713

Peptide sequence: AMGIMNSFVNDIFER

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 5.08 SEQUEST DCn score: 0.658

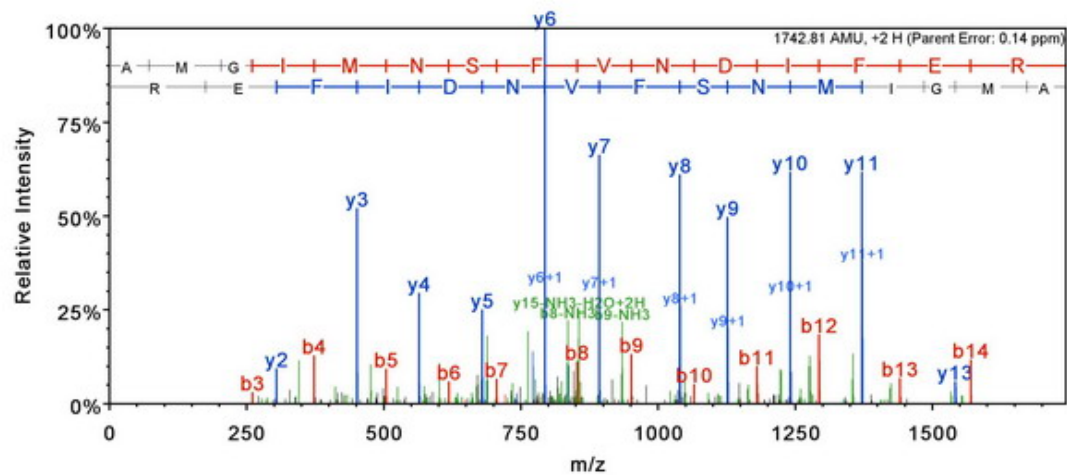
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 872.4139

Actual minus calculated peptide mass (AMU): 0.0002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1743.8	872.4	1726.8	1725.8	15
2	203.1				M	1672.8	836.9	1655.8	1654.8	14
3	260.1				G	1541.7	771.4	1524.7	1523.7	13
4	373.2				I	1484.7	742.9	1467.7	1466.7	12
5	504.2				M	1371.6	686.3	1354.6	1353.6	11
6	618.3	309.6	601.3		N	1240.6	620.8	1223.6	1222.6	10
7	705.3	353.2	688.3	687.3	S	1126.5	563.8	1109.5	1108.5	9
8	852.4	426.7	835.4	834.4	F	1039.5	520.3	1022.5	1021.5	8
9	951.4	476.2	934.4	933.4	V	892.5	446.7	875.4	874.4	7
10	1065.5	533.3	1048.5	1047.5	N	793.4	397.2	776.4	775.4	6
11	1180.5	590.8	1163.5	1162.5	D	679.3		662.3	661.3	5
12	1293.6	647.3	1276.6	1275.6	I	564.3		547.3	546.3	4
13	1440.7	720.8	1423.6	1422.7	F	451.2		434.2	433.2	3
14	1569.7	785.4	1552.7	1551.7	E	304.2		287.1	286.2	2
15	1743.8	872.4	1726.8	1725.8	R	175.1		158.1		1

Gene symbol: Hmgcl

Protein name: Lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730031H02 product:3-hydroxy-3-methylglutaryl- Coenzyme A lyase, full insert sequence

Protein accession numbers: IPI00379694

Peptide sequence: LIDMLSEAGLPVIEATSFVSPK

Exclusive (unique to this protein): TRUE

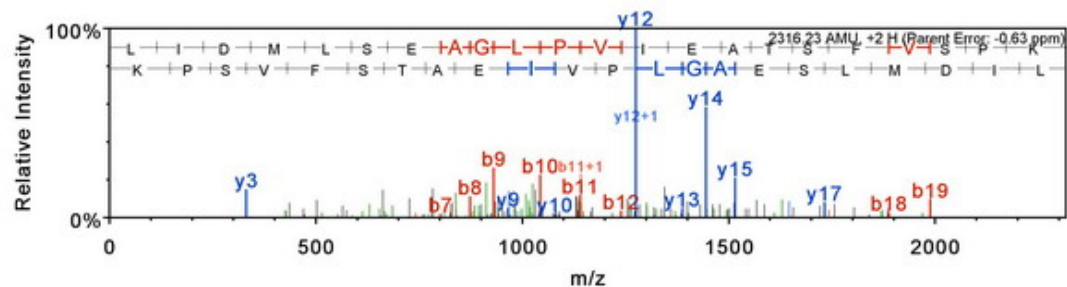
SEQUEST XCorr score: 2.71 SEQUEST DCn score: 0.407

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1159.1215

Actual minus calculated peptide mass (AMU): -0.001465



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	2317.2	1159.1	2300.2	2299.2	22
2	227.2				I	2204.2	1102.6	2187.1	2186.1	21
3	342.2			324.2	D	2091.1	1046.0	2074.0	2073.1	20
4	473.2			455.2	M	1976.0	988.5	1959.0	1958.0	19
5	586.3			568.3	L	1845.0	923.0	1828.0	1827.0	18
6	673.4	337.2		655.4	S	1731.9	866.5	1714.9	1713.9	17
7	802.4	401.7		784.4	E	1644.9	823.0	1627.9	1626.9	16
8	873.4	437.2		855.4	A	1515.8	758.4	1498.8	1497.8	15
9	930.5	465.7		912.5	G	1444.8	722.9	1427.8	1426.8	14
10	1043.5	522.3		1025.5	L	1387.8	694.4	1370.8	1369.8	13
11	1140.6	570.8		1122.6	P	1274.7	637.9	1257.7	1256.7	12
12	1239.7	620.3		1221.7	V	1177.7	589.3	1160.6	1159.6	11
13	1352.8	676.9		1334.7	I	1078.6	539.8	1061.5	1060.6	10
14	1481.8	741.4		1463.8	E	965.5	483.3	948.5	947.5	9
15	1552.8	776.9		1534.8	A	836.5	418.7	819.4	818.4	8
16	1653.9	827.4		1635.9	T	765.4	383.2	748.4	747.4	7
17	1740.9	871.0		1722.9	S	664.4	332.7	647.3	646.4	6
18	1888.0	944.5		1870.0	F	577.3		560.3	559.3	5
19	1987.1	994.0		1969.0	V	430.3		413.2	412.3	4
20	2074.1	1037.5		2056.1	S	331.2		314.2	313.2	3
21	2171.1	1086.1		2153.1	P	244.2		227.1		2
22	2317.2	1159.1	2300.2	2299.2	K	147.1		130.1		1

Gene symbol: Hnrph2

Protein name: Heterogeneous nuclear ribonucleoprotein H'

Protein accession numbers: IPI00108143

Peptide sequence: ATENDIYNFFSPLNPMR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.44 SEQUEST DCn score: 0.518

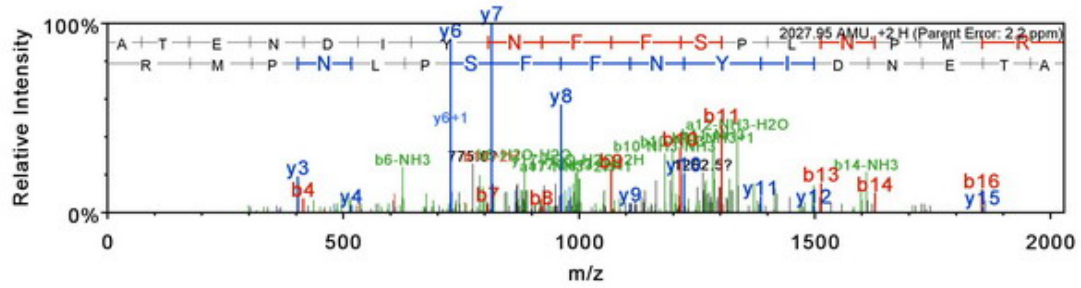
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1014.9806

Actual minus calculated peptide mass (AMU): 0.004395



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2029.0	1015.0	2011.9	2010.9	17
2	173.1			155.1	T	1957.9	979.5	1940.9	1939.9	16
3	302.1			284.1	E	1856.9	928.9	1839.8	1838.9	15
4	416.2		399.2	398.2	N	1727.8	864.4	1710.8	1709.8	14
5	531.2		514.2	513.2	D	1613.8	807.4	1596.8	1595.8	13
6	644.3	322.7	627.3	626.3	I	1498.8	749.9	1481.7	1480.7	12
7	807.4	404.2	790.3	789.3	Y	1385.7	693.3	1368.6	1367.7	11
8	921.4	461.2	904.4	903.4	N	1222.6	611.8	1205.6	1204.6	10
9	1068.5	534.7	1051.4	1050.5	F	1108.6	554.8	1091.5	1090.5	9
10	1215.5	608.3	1198.5	1197.5	F	961.5	481.3	944.5	943.5	8
11	1302.6	651.8	1285.5	1284.5	S	814.4	407.7	797.4	796.4	7
12	1399.6	700.3	1382.6	1381.6	P	727.4	364.2	710.4		6
13	1512.7	756.9	1495.7	1494.7	L	630.3		613.3		5
14	1626.7	813.9	1609.7	1608.7	N	517.3		500.2		4
15	1723.8	862.4	1706.8	1705.8	P	403.2		386.2		3
16	1854.8	927.9	1837.8	1836.8	M	306.2		289.1		2
17	2029.0	1015.0	2011.9	2010.9	R	175.1		158.1		1

Peptide sequence: DLNYCFSGMSDHR

Exclusive (unique to this protein): FALSE

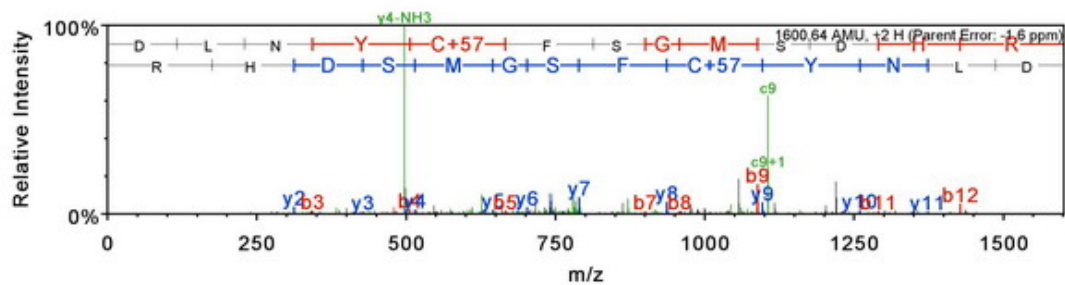
SEQUEST XCorr score: 2.64 SEQUEST DCn score: 0.844

Fix modifications: C5: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2 Observed m/z: 801.3265

Actual minus calculated peptide mass (AMU): -0.002564



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	116.0			98.0	D	1601.7	801.3	1584.6	1583.6	13
2	229.1			211.1	L	1486.6	743.8	1469.6	1468.6	12
3	343.2		326.1	325.2	N	1373.5	687.3	1356.5	1355.5	11
4	506.2		489.2	488.2	Y	1259.5	630.3	1242.5	1241.5	10
5	666.3		649.2	648.3	C+57	1096.4	548.7	1079.4	1078.4	9
6	813.3	407.2	796.3	795.3	F	936.4	468.7	919.4	918.4	8
7	900.4	450.7	883.3	882.4	S	789.3	395.2	772.3	771.3	7
8	957.4	479.2	940.4	939.4	G	702.3	351.7	685.3	684.3	6
9	1088.4	544.7	1071.4	1070.4	M	645.3	323.1	628.3	627.3	5
10	1175.5	588.2	1158.4	1157.4	S	514.2	257.6	497.2	496.2	4
11	1290.5	645.7	1273.5	1272.5	D	427.2	214.1	410.2	409.2	3
12	1427.5	714.3	1410.5	1409.5	H	312.2	156.6	295.2		2
13	1601.7	801.3	1584.6	1583.6	R	175.1		158.1		1

Peptide sequence: PSGEAFVELESEDEVK

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 4.49 SEQUEST DCn score: 0.598

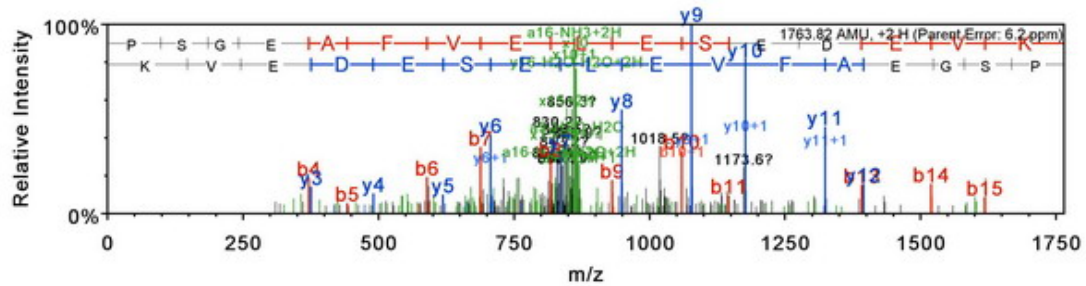
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 882.9184

Actual minus calculated peptide mass (AMU): 0.01086



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	98.1				P	1764.8	882.9	1747.8	1746.8	16
2	185.1			167.1	S	1667.8	834.4	1650.7	1649.8	15
3	242.1			224.1	G	1580.7	790.9	1563.7	1562.7	14
4	371.2			353.2	E	1523.7	762.4	1506.7	1505.7	13
5	442.2			424.2	A	1394.7	697.8	1377.6	1376.7	12
6	589.3	295.1		571.3	F	1323.6	662.3	1306.6	1305.6	11
7	688.3	344.7		670.3	V	1176.6	588.8	1159.5	1158.5	10
8	817.4	409.2		799.4	E	1077.5	539.3	1060.5	1059.5	9
9	930.5	465.7		912.5	L	948.5	474.7	931.4	930.4	8
10	1059.5	530.3		1041.5	E	835.4	418.2	818.3	817.4	7
11	1146.5	573.8		1128.5	S	706.3	353.7	689.3	688.3	6
12	1275.6	638.3		1257.6	E	619.3		602.3	601.3	5
13	1390.6	695.8		1372.6	D	490.3		473.2	472.2	4
14	1519.6	760.3		1501.6	E	375.2		358.2	357.2	3
15	1618.7	809.9		1600.7	V	246.2		229.2		2
16	1764.8	882.9	1747.8	1746.8	K	147.1		130.1		1

Peptide sequence: STGEAFVQFASQEIAEK

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 4.91 SEQUEST DCn score: 0.656

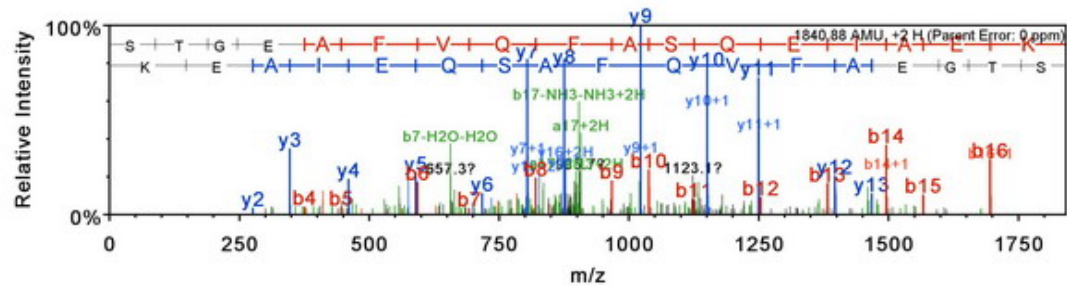
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 921.45

Actual minus calculated peptide mass (AMU): 0



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1841.9	921.5	1824.9	1823.9	17
2	189.1			171.1	T	1754.9	877.9	1737.8	1736.9	16
3	246.1			228.1	G	1653.8	827.4	1636.8	1635.8	15
4	375.2			357.1	E	1596.8	798.9	1579.8	1578.8	14
5	446.2			428.2	A	1467.8	734.4	1450.7	1449.7	13
6	593.3	297.1		575.3	F	1396.7	698.9	1379.7	1378.7	12
7	692.3	346.7		674.3	V	1249.6	625.3	1232.6	1231.6	11
8	820.4	410.7	803.4	802.4	Q	1150.6	575.8	1133.5	1132.6	10
9	967.5	484.2	950.4	949.4	F	1022.5	511.8	1005.5	1004.5	9
10	1038.5	519.8	1021.5	1020.5	A	875.5	438.2	858.4	857.4	8
11	1125.5	563.3	1108.5	1107.5	S	804.4	402.7	787.4	786.4	7
12	1253.6	627.3	1236.5	1235.6	Q	717.4	359.2	700.4	699.4	6
13	1382.6	691.8	1365.6	1364.6	E	589.3		572.3	571.3	5
14	1495.7	748.4	1478.7	1477.7	I	460.3		443.3	442.3	4
15	1566.7	783.9	1549.7	1548.7	A	347.2		330.2	329.2	3
16	1695.8	848.4	1678.8	1677.8	E	276.2		259.1	258.1	2
17	1841.9	921.5	1824.9	1823.9	K	147.1		130.1		1

Gene symbol: Hook2

Protein name: Hook homolog 2

Protein accession numbers: IPI00381165

Peptide sequence: EYIEELEPPTDSSTAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.98 SEQUEST DCn score: 0.614

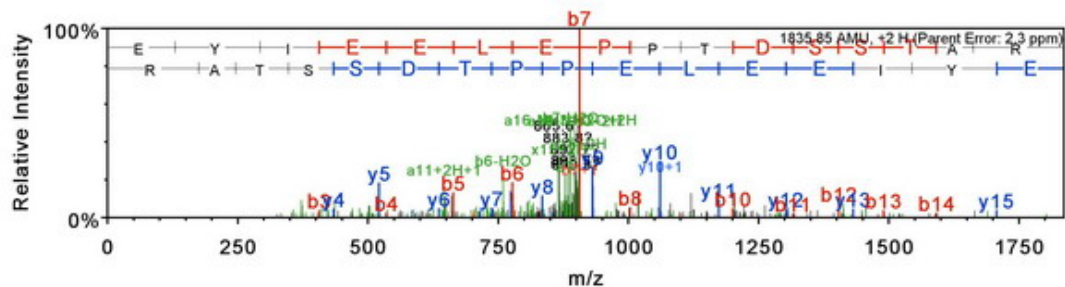
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 918.9313

Actual minus calculated peptide mass (AMU): 0.00415



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1836.9	918.9	1819.8	1818.8	16
2	293.1			275.1	Y	1707.8	854.4	1690.8	1689.8	15
3	406.2			388.2	I	1544.7	772.9	1527.7	1526.7	14
4	535.2			517.2	E	1431.7	716.3	1414.6	1413.7	13
5	664.3			646.3	E	1302.6	651.8	1285.6	1284.6	12
6	777.4	389.2		759.4	L	1173.6	587.3	1156.5	1155.6	11
7	906.4	453.7		888.4	E	1060.5	530.8	1043.5	1042.5	10
8	1003.5	502.2		985.5	P	931.5	466.2	914.4	913.4	9
9	1100.5	550.8		1082.5	P	834.4	417.7	817.4	816.4	8
10	1201.6	601.3		1183.5	T	737.3	369.2	720.3	719.3	7
11	1316.6	658.8		1298.6	D	636.3	318.7	619.3	618.3	6
12	1403.6	702.3		1385.6	S	521.3		504.2	503.3	5
13	1490.7	745.8		1472.6	S	434.2		417.2	416.2	4
14	1591.7	796.4		1573.7	T	347.2		330.2	329.2	3
15	1662.7	831.9		1644.7	A	246.2		229.1		2
16	1836.9	918.9	1819.8	1818.8	R	175.1		158.1		1

Gene symbol: Hspe1

Protein name: 10 kDa heat shock protein, mitochondrial

Protein accession numbers: IPI00263863

Peptide sequence: VLQATVVAVGSGGK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.06 SEQUEST DCn score: 0.686

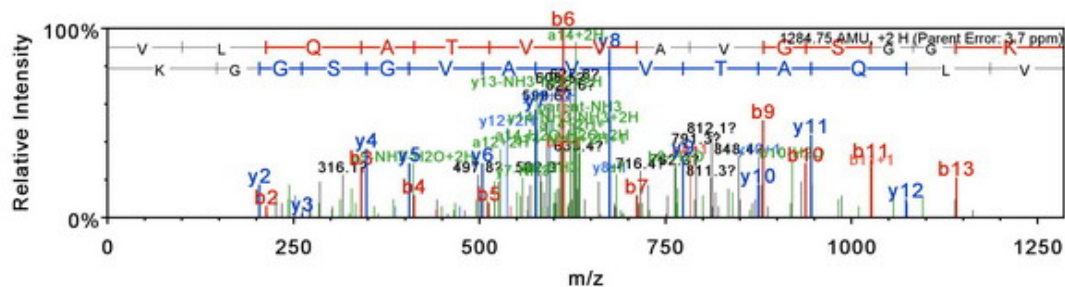
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 643.3804

Actual minus calculated peptide mass (AMU): 0.004761



clone:B930036N12 product:HUNTINGTIN-INTERACTING PROTEIN-1 PROTEIN
INTERACTOR, full insert sequence

Protein accession numbers: IPI00312710

Peptide sequence: YINNQLEHLVQEYR

Exclusive (unique to this protein): TRUE

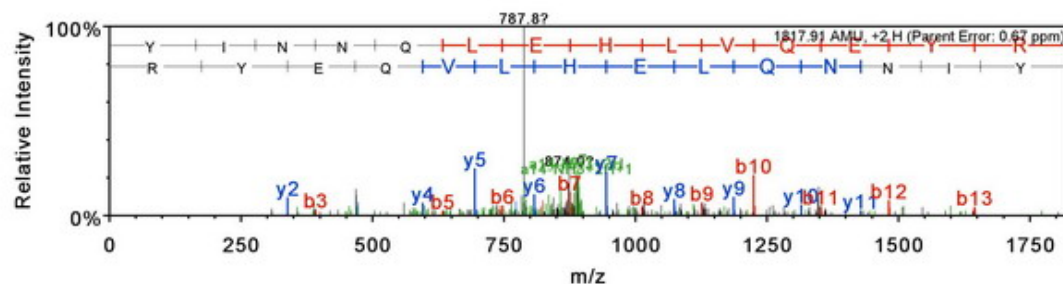
SEQUEST XCorr score: 3.01 SEQUEST DCn score: 0.597

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 909.9615

Actual minus calculated peptide mass (AMU): 0.0012249



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1818.9	910.0	1801.9	1800.9	14
2	277.2				I	1655.9	828.4	1638.8	1637.8	13
3	391.2		374.2		N	1542.8	771.9	1525.7	1524.8	12
4	505.2		488.2		N	1428.7	714.9	1411.7	1410.7	11
5	633.3		616.3		Q	1314.7	657.8	1297.7	1296.7	10
6	746.4	373.7	729.4		L	1186.6	593.8	1169.6	1168.6	9
7	875.4	438.2	858.4	857.4	E	1073.5	537.3	1056.5	1055.5	8
8	1012.5	506.8	995.5	994.5	H	944.5	472.8	927.5	926.5	7
9	1125.6	563.3	1108.5	1107.6	L	807.4	404.2	790.4	789.4	6
10	1224.6	612.8	1207.6	1206.6	V	694.4		677.3	676.3	5
11	1352.7	676.9	1335.7	1334.7	Q	595.3		578.3	577.3	4
12	1481.7	741.4	1464.7	1463.7	E	467.2		450.2	449.2	3
13	1644.8	822.9	1627.8	1626.8	Y	338.2		321.2		2
14	1818.9	910.0	1801.9	1800.9	R	175.1		158.1		1

Gene symbol: Ift81

Protein name: Isoform CDV-1R of Intraflagellar transport 81

Protein accession numbers: IPI00153942

Peptide sequence: LEVPSEFLQDETVDATNK

Exclusive (unique to this protein): TRUE

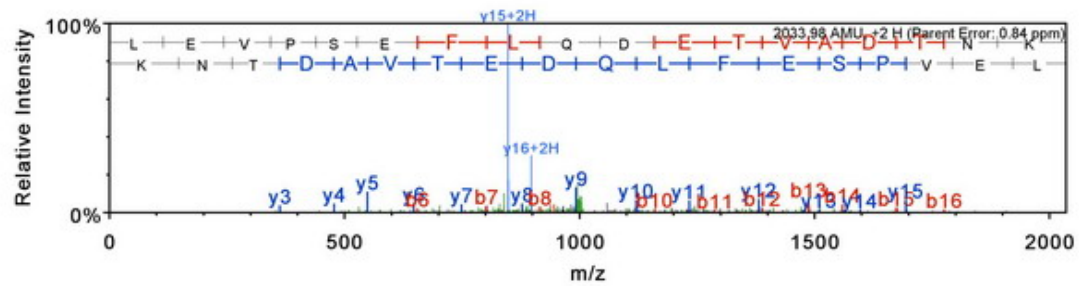
SEQUEST XCorr score: 4.06 SEQUEST DCn score: 0.632

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1017.9985

Actual minus calculated peptide mass (AMU): 0.001709



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	2035.0	1018.0	2018.0	2017.0	18
2	243.1			225.1	E	1921.9	961.5	1904.9	1903.9	17
3	342.2			324.2	V	1792.9	896.9	1775.8	1774.9	16
4	439.3			421.3	P	1693.8	847.4	1676.8	1675.8	15
5	526.3			508.3	S	1596.7	798.9	1579.7	1578.7	14
6	655.3	328.2		637.3	E	1509.7	755.4	1492.7	1491.7	13
7	802.4	401.7		784.4	F	1380.7	690.8	1363.6	1362.7	12
8	915.5	458.3		897.5	L	1233.6	617.3	1216.6	1215.6	11
9	1043.5	522.3	1026.5	1025.5	Q	1120.5	560.8	1103.5	1102.5	10
10	1158.6	579.8	1141.5	1140.6	D	992.5	496.7	975.4	974.4	9
11	1287.6	644.3	1270.6	1269.6	E	877.4	439.2	860.4	859.4	8
12	1388.7	694.8	1371.6	1370.7	T	748.4	374.7	731.4	730.4	7
13	1487.7	744.4	1470.7	1469.7	V	647.3	324.2	630.3	629.3	6
14	1558.8	779.9	1541.7	1540.8	A	548.3		531.2	530.3	5
15	1673.8	837.4	1656.8	1655.8	D	477.2		460.2	459.2	4
16	1774.8	887.9	1757.8	1756.8	T	362.2		345.2	344.2	3
17	1888.9	944.9	1871.9	1870.9	N	261.2		244.1		2
18	2035.0	1018.0	2018.0	2017.0	K	147.1		130.1		1

Gene symbol: Impad1

Protein name: Inositol monophosphatase 3

Protein accession numbers: IPI00228719

Peptide sequence: FSLFGLGSEPAAGEAEVASDGGTVDLR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.52 SEQUEST DCn score: 0.663

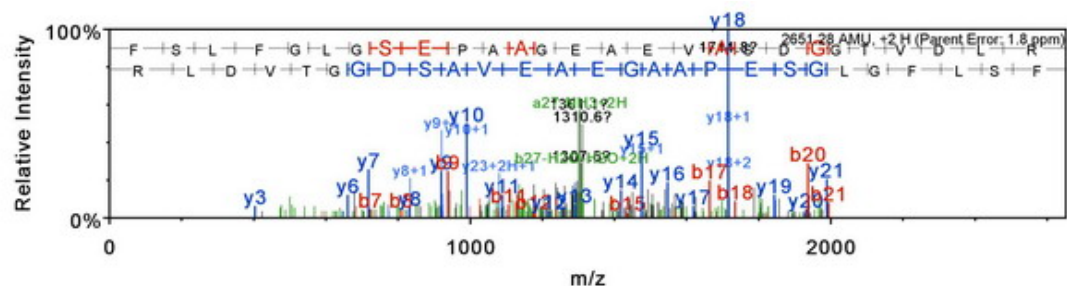
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1326.646

Actual minus calculated peptide mass (AMU): 0.004883



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	2652.3	1326.6	2635.3	2634.3	27
2	235.1			217.1	S	2505.2	1253.1	2488.2	2487.2	26
3	348.2			330.2	L	2418.2	1209.6	2401.2	2400.2	25
4	495.3			477.3	F	2305.1	1153.0	2288.1	2287.1	24
5	552.3			534.3	G	2158.0	1079.5	2141.0	2140.0	23
6	665.4	333.2		647.4	L	2101.0	1051.0	2084.0	2083.0	22
7	722.4	361.7		704.4	G	1987.9	994.5	1970.9	1969.9	21
8	809.4	405.2		791.4	S	1930.9	966.0	1913.9	1912.9	20
9	938.5	469.7		920.5	E	1843.9	922.4	1826.8	1825.9	19
10	1035.5	518.3		1017.5	P	1714.8	857.9	1697.8	1696.8	18
11	1106.5	553.8		1088.5	A	1617.8	809.4	1600.8	1599.8	17
12	1177.6	589.3		1159.6	A	1546.7	773.9	1529.7	1528.7	16
13	1234.6	617.8		1216.6	G	1475.7	738.4	1458.7	1457.7	15
14	1363.7	682.3		1345.6	E	1418.7	709.8	1401.7	1400.7	14
15	1434.7	717.9		1416.7	A	1289.6	645.3	1272.6	1271.6	13
16	1563.7	782.4		1545.7	E	1218.6	609.8	1201.6	1200.6	12
17	1662.8	831.9		1644.8	V	1089.5	545.3	1072.5	1071.5	11
18	1733.8	867.4		1715.8	A	990.5	495.8	973.5	972.5	10
19	1820.9	910.9		1802.9	S	919.5	460.2	902.4	901.4	9
20	1935.9	968.5		1917.9	D	832.4	416.7	815.4	814.4	8
21	1992.9	997.0		1974.9	G	717.4	359.2	700.4	699.4	7
22	2049.9	1025.5		2031.9	G	660.4	330.7	643.3	642.4	6
23	2151.0	1076.0		2133.0	T	603.4		586.3	585.3	5
24	2250.1	1125.5		2232.1	V	502.3		485.3	484.3	4
25	2365.1	1183.0		2347.1	D	403.2		386.2	385.2	3
26	2478.2	1239.6		2460.2	L	288.2		271.2		2
27	2652.3	1326.6	2635.3	2634.3	R	175.1		158.1		1

Gene symbol: Ipo11

Protein name: Isoform 1 of Importin-11

Protein accession numbers: IPI00280252,IPI00720099

Peptide sequence: IFQNMSPLLELSSENLR

Exclusive (unique to this protein): TRUE

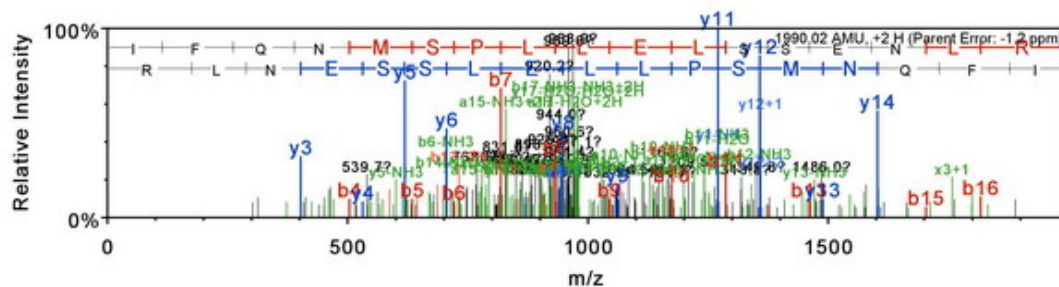
SEQUEST XCorr score: 3.78 SEQUEST DCn score: 0.516

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 996.0163

Actual minus calculated peptide mass (AMU): -0.002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1991.0	996.0	1974.0	1973.0	17
2	261.2				F	1877.9	939.5	1860.9	1859.9	16
3	389.2		372.2		Q	1730.9	865.9	1713.9	1712.9	15
4	503.3		486.2		N	1602.8	801.9	1585.8	1584.8	14
5	634.3		617.3		M	1488.8	744.9	1471.8	1470.8	13
6	721.3	361.2	704.3	703.3	S	1357.7	679.4	1340.7	1339.7	12
7	818.4	409.7	801.4	800.4	P	1270.7	635.9	1253.7	1252.7	11
8	931.5	466.2	914.4	913.5	L	1173.7	587.3	1156.6	1155.6	10
9	1044.6	522.8	1027.5	1026.5	L	1060.6	530.8	1043.5	1042.5	9
10	1173.6	587.3	1156.6	1155.6	E	947.5	474.2	930.5	929.5	8
11	1286.7	643.8	1269.7	1268.7	L	818.4	409.7	801.4	800.4	7
12	1373.7	687.4	1356.7	1355.7	S	705.4	353.2	688.3	687.3	6
13	1460.8	730.9	1443.7	1442.7	S	618.3		601.3	600.3	5
14	1589.8	795.4	1572.8	1571.8	E	531.3		514.3	513.3	4
15	1703.8	852.4	1686.8	1685.8	N	402.3		385.2		3
16	1816.9	909.0	1799.9	1798.9	L	288.2		271.2		2
17	1991.0	996.0	1974.0	1973.0	R	175.1		158.1		1

Gene symbol: Ipo13

Protein name: Isoform 1 of Importin-13

Protein accession numbers: IPI00169541,IPI00453577

Peptide sequence: LFQAEDSPVDSQGR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.83 SEQUEST DCn score: 0.565

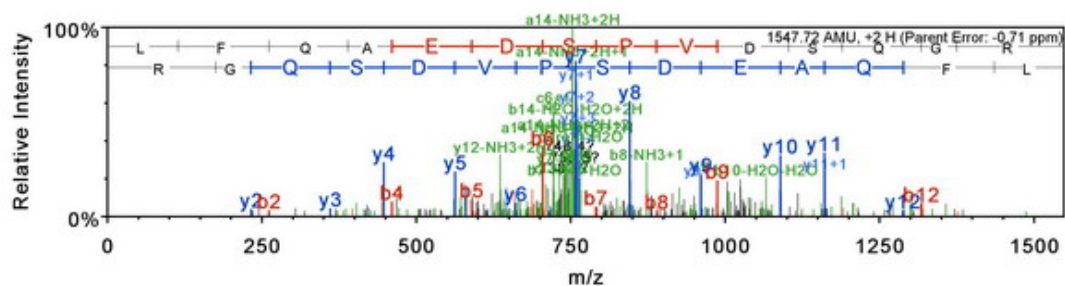
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 774.8681

Actual minus calculated peptide mass (AMU): -0.001099



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1548.7	774.9	1531.7	1530.7	14
2	261.2				F	1435.7	718.3	1418.6	1417.6	13
3	389.2		372.2		Q	1288.6	644.8	1271.5	1270.6	12
4	460.3		443.2		A	1160.5	580.8	1143.5	1142.5	11
5	589.3		572.3	571.3	E	1089.5	545.2	1072.5	1071.5	10
6	704.3	352.7	687.3	686.3	D	960.4	480.7	943.4	942.4	9
7	791.4	396.2	774.3	773.4	S	845.4	423.2	828.4	827.4	8
8	888.4	444.7	871.4	870.4	P	758.4	379.7	741.4	740.4	7
9	987.5	494.2	970.5	969.5	V	661.3	331.2	644.3	643.3	6
10	1102.5	551.8	1085.5	1084.5	D	562.3		545.2	544.3	5
11	1189.5	595.3	1172.5	1171.5	S	447.2		430.2	429.2	4
12	1317.6	659.3	1300.6	1299.6	Q	360.2		343.2		3
13	1374.6	687.8	1357.6	1356.6	G	232.1		215.1		2
14	1548.7	774.9	1531.7	1530.7	R	175.1		158.1		1

Gene symbol: Iqcg

Protein name: IQ domain-containing protein G

Protein accession numbers: IPI00265356,IPI00753342

Peptide sequence: AEELLLEEIEK

Exclusive (unique to this protein): TRUE

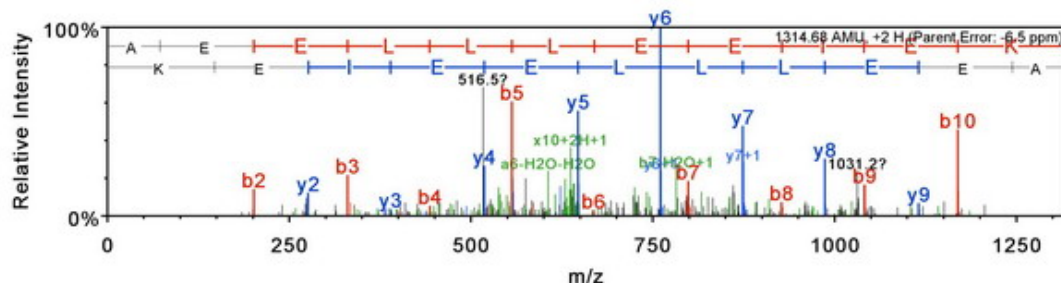
SEQUEST XCorr score: 3.34 SEQUEST DCn score: 0.32

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 658.3496

Actual minus calculated peptide mass (AMU): -0.0085453



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1315.7	658.4	1298.7	1297.7	11
2	201.1			183.1	E	1244.7	622.8	1227.6	1226.7	10
3	330.1			312.1	E	1115.6	558.3	1098.6	1097.6	9
4	443.2			425.2	L	986.6	493.8	969.6	968.6	8
5	556.3			538.3	L	873.5	437.3	856.5	855.5	7
6	669.4	335.2		651.4	L	760.4	380.7	743.4	742.4	6
7	798.4	399.7		780.4	E	647.3		630.3	629.3	5
8	927.5	464.2		909.5	E	518.3		501.3	500.3	4
9	1040.5	520.8		1022.5	I	389.2		372.2	371.2	3
10	1169.6	585.3		1151.6	E	276.2		259.1	258.1	2
11	1315.7	658.4	1298.7	1297.7	K	147.1		130.1		1

Gene symbol: Ivd

Protein name: Isovaleryl-CoA dehydrogenase, mitochondrial precursor

Protein accession numbers: IPI00471246

Peptide sequence: LYEIGAGTSEVR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.03 SEQUEST DCn score: 0.552

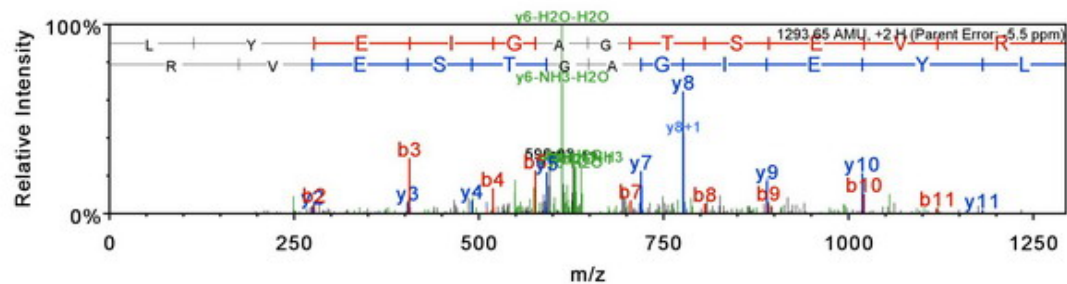
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 647.8325

Actual minus calculated peptide mass (AMU): -0.0070758



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1294.7	647.8	1277.6	1276.7	12
2	277.2				Y	1181.6	591.3	1164.5	1163.6	11
3	406.2			388.2	E	1018.5	509.8	1001.5	1000.5	10
4	519.3			501.3	I	889.5	445.2	872.5	871.5	9
5	576.3			558.3	G	776.4	388.7	759.4	758.4	8
6	647.3	324.2		629.3	A	719.4	360.2	702.3	701.4	7
7	704.4	352.7		686.4	G	648.3	324.7	631.3	630.3	6
8	805.4	403.2		787.4	T	591.3		574.3	573.3	5
9	892.4	446.7		874.4	S	490.3		473.2	472.3	4
10	1021.5	511.3		1003.5	E	403.2		386.2	385.2	3
11	1120.5	560.8		1102.5	V	274.2		257.2		2
12	1294.7	647.8	1277.6	1276.7	R	175.1		158.1		1

Gene symbol: Jmjd1a

Protein name: Isoform 1 of JmjC domain-containing histone demethylation protein 2A

Protein accession numbers: IPI00460716

Peptide sequence: FDDLMANIPLPEYTR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.11 SEQUEST DCn score: 0.606

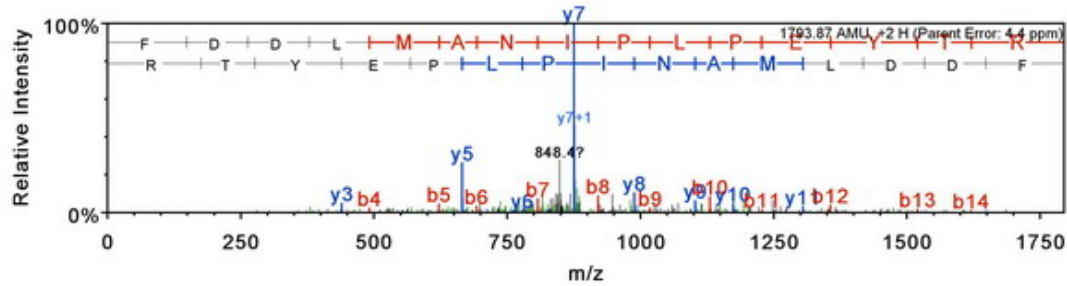
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 897.9448

Actual minus calculated peptide mass (AMU): 0.007813



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1794.9	897.9	1777.9	1776.9	15
2	263.1			245.1	D	1647.8	824.4	1630.8	1629.8	14
3	378.1			360.1	D	1532.8	766.9	1515.8	1514.8	13
4	491.2			473.2	L	1417.8	709.4	1400.7	1399.7	12
5	622.3			604.2	M	1304.7	652.8	1287.6	1286.7	11
6	693.3	347.2		675.3	A	1173.6	587.3	1156.6	1155.6	10
7	807.3	404.2	790.3	789.3	N	1102.6	551.8	1085.6	1084.6	9
8	920.4	460.7	903.4	902.4	I	988.6	494.8	971.5	970.5	8
9	1017.5	509.2	1000.5	999.5	P	875.5	438.2	858.4	857.5	7
10	1130.6	565.8	1113.5	1112.5	L	778.4	389.7	761.4	760.4	6
11	1227.6	614.3	1210.6	1209.6	P	665.3		648.3	647.3	5
12	1356.7	678.8	1339.6	1338.6	E	568.3		551.3	550.3	4
13	1519.7	760.4	1502.7	1501.7	Y	439.2		422.2	421.2	3
14	1620.8	810.9	1603.7	1602.8	T	276.2		259.1	258.2	2
15	1794.9	897.9	1777.9	1776.9	R	175.1		158.1		1

Gene symbol: Katnal1

Protein name: 45 kDa protein

Protein accession numbers: IPI00830971

Peptide sequence: FYAPTTIFIDEIDSICSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.48 SEQUEST DCn score: 0.693

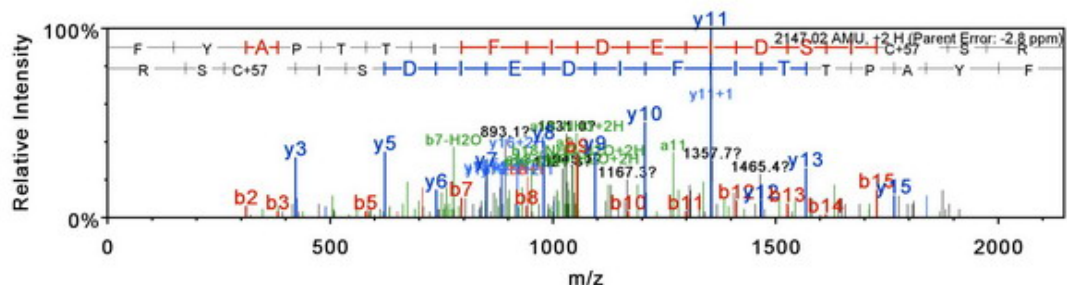
Fix modifications: C16: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2

Observed m/z: 1074.5171

Actual minus calculated peptide mass (AMU): -0.006104



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	2148.0	1074.5	2131.0	2130.0	18
2	311.1				Y	2001.0	1001.0	1983.9	1983.0	17
3	382.2				A	1837.9	919.5	1820.9	1819.9	16
4	479.2				P	1766.9	883.9	1749.8	1748.9	15
5	580.3			562.3	T	1669.8	835.4	1652.8	1651.8	14
6	681.3	341.2		663.3	T	1568.8	784.9	1551.7	1550.8	13
7	794.4	397.7		776.4	I	1467.7	734.4	1450.7	1449.7	12
8	941.5	471.2		923.5	F	1354.6	677.8	1337.6	1336.6	11
9	1054.6	527.8		1036.5	I	1207.6	604.3	1190.5	1189.5	10
10	1169.6	585.3		1151.6	D	1094.5	547.7	1077.5	1076.5	9
11	1298.6	649.8		1280.6	E	979.5	490.2	962.4	961.4	8
12	1411.7	706.4		1393.7	I	850.4	425.7	833.4	832.4	7
13	1526.7	763.9		1508.7	D	737.3	369.2	720.3	719.3	6
14	1613.8	807.4		1595.8	S	622.3		605.3	604.3	5
15	1726.9	863.9		1708.9	I	535.3		518.2	517.3	4
16	1886.9	944.0		1868.9	C+57	422.2		405.2	404.2	3
17	1973.9	987.5		1955.9	S	262.1		245.1	244.1	2
18	2148.0	1074.5	2131.0	2130.0	R	175.1		158.1		1

Gene symbol: Khdrbs1

Protein name: KH domain-containing, RNA-binding, signal transduction-associated protein 1

Protein accession numbers: IPI00458765

Peptide sequence: KDDEENYLDLFSHK

Exclusive (unique to this protein): TRUE

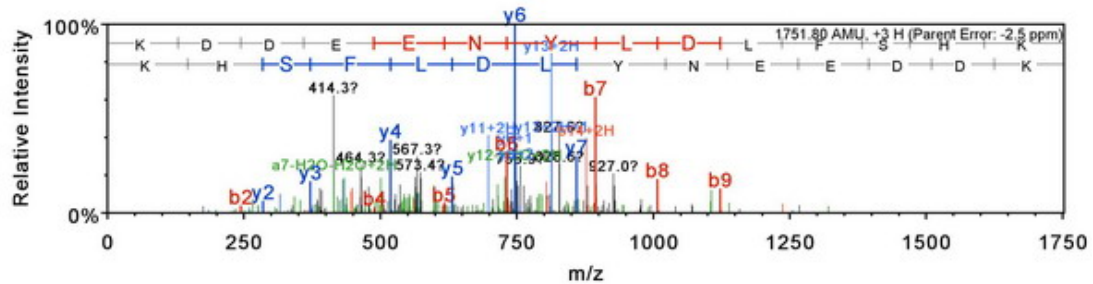
SEQUEST XCorr score: 3.04 SEQUEST DCn score: 0.569

Fix modifications: None

Variable modifications: None

Charge: 3 Observed m/z: 584.9398

Actual minus calculated peptide mass (AMU): -0.004395



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1	65.1	112.1		K	1752.8	876.9	1735.8	1734.8	14
2	244.1	122.6	227.1	226.1	D	1624.7	812.9	1607.7	1606.7	13
3	359.2	180.1	342.1	341.2	D	1509.7	755.4	1492.7	1491.7	12
4	488.2	244.6	471.2	470.2	E	1394.7	697.8	1377.6	1376.7	11
5	617.2	309.1	600.2	599.2	E	1265.6	633.3	1248.6	1247.6	10
6	731.3	366.2	714.3	713.3	N	1136.6	568.8	1119.5	1118.6	9
7	894.4	447.7	877.3	876.3	Y	1022.5	511.8	1005.5	1004.5	8
8	1007.4	504.2	990.4	989.4	L	859.5	430.2	842.4	841.5	7
9	1122.5	561.7	1105.4	1104.5	D	746.4	373.7	729.4	728.4	6
10	1235.5	618.3	1218.5	1217.5	L	631.4	316.2	614.3	613.4	5
11	1382.6	691.8	1365.6	1364.6	F	518.3	259.6	501.3	500.3	4
12	1469.6	735.3	1452.6	1451.6	S	371.2	186.1	354.2	353.2	3
13	1606.7	803.9	1589.7	1588.7	H	284.2	142.6	267.1		2
14	1752.8	876.9	1735.8	1734.8	K	147.1		130.1		1

Gene symbol: Kif15

Protein name: Kinesin family member 15

Protein accession numbers: IPI00115366

Peptide sequence: TSLLNLVDLAGSER

Exclusive (unique to this protein): TRUE

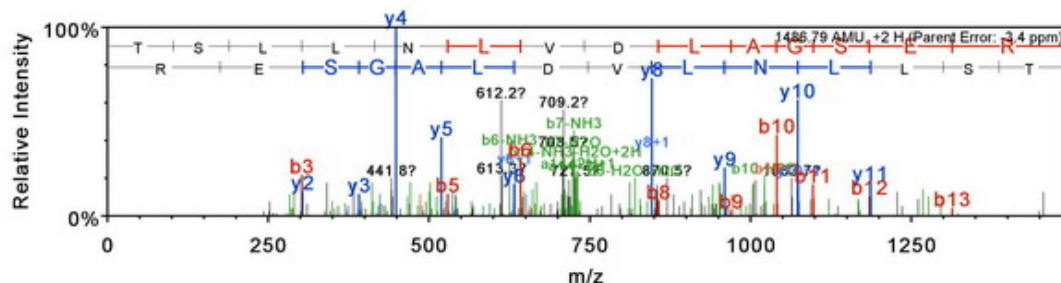
SEQUEST XCorr score: 3.46 SEQUEST DCn score: 0.565

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 744.4049

Actual minus calculated peptide mass (AMU): -0.005005



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1487.8	744.4	1470.8	1469.8	14
2	189.1			171.1	S	1386.8	693.9	1369.7	1368.8	13
3	302.2			284.2	L	1299.7	650.4	1282.7	1281.7	12
4	415.3			397.3	L	1186.6	593.8	1169.6	1168.6	11
5	529.3		512.3	511.3	N	1073.6	537.3	1056.5	1055.5	10
6	642.4	321.7	625.4	624.4	L	959.5	480.3	942.5	941.5	9
7	741.5	371.2	724.4	723.4	V	846.4	423.7	829.4	828.4	8
8	856.5	428.7	839.5	838.5	D	747.4	374.2	730.3	729.4	7
9	969.6	485.3	952.5	951.6	L	632.3	316.7	615.3	614.3	6
10	1040.6	520.8	1023.6	1022.6	A	519.3		502.2	501.2	5
11	1097.6	549.3	1080.6	1079.6	G	448.2		431.2	430.2	4
12	1184.7	592.8	1167.6	1166.6	S	391.2		374.2	373.2	3
13	1313.7	657.4	1296.7	1295.7	E	304.2		287.1	286.2	2
14	1487.8	744.4	1470.8	1469.8	R	175.1		158.1		1

Gene symbol: Kif1b

Protein name: Isoform 2 of Kinesin-like protein KIF1B

Protein accession numbers: IPI00407144,IPI00411082

Peptide sequence: ISLVDLAGSER

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 2.83 SEQUEST DCn score: 0.456

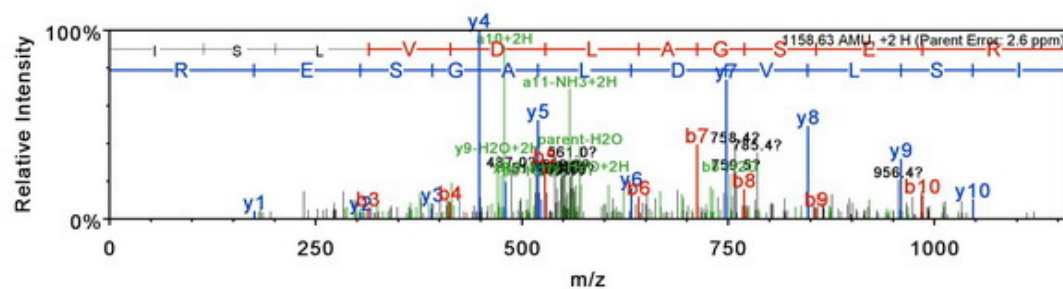
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 580.3217

Actual minus calculated peptide mass (AMU): 0.003052



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1159.6	580.3	1142.6	1141.6	11
2	201.1			183.1	S	1046.5	523.8	1029.5	1028.5	10
3	314.2			296.2	L	959.5	480.3	942.5	941.5	9
4	413.3			395.3	V	846.4	423.7	829.4	828.4	8
5	528.3			510.3	D	747.4	374.2	730.3	729.4	7
6	641.4	321.2		623.4	L	632.3	316.7	615.3	614.3	6
7	712.4	356.7		694.4	A	519.3		502.2	501.2	5
8	769.5	385.2		751.4	G	448.2		431.2	430.2	4
9	856.5	428.7		838.5	S	391.2		374.2	373.2	3
10	985.5	493.3		967.5	E	304.2		287.1	286.2	2
11	1159.6	580.3	1142.6	1141.6	R	175.1		158.1		1

Peptide sequence: IVEGQGSSEVISPPPEEVNR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.58 SEQUEST DCn score: 0.586

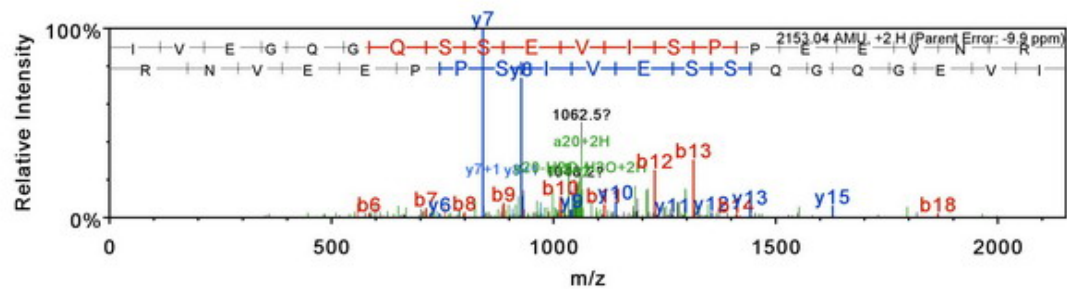
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1077.5272

Actual minus calculated peptide mass (AMU): -0.02124



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	2154.1	1077.5	2137.0	2136.1	20
2	213.2				V	2041.0	1021.0	2024.0	2023.0	19
3	342.2			324.2	E	1941.9	971.5	1924.9	1923.9	18
4	399.2			381.2	G	1812.9	906.9	1795.9	1794.9	17
5	527.3		510.3	509.3	Q	1755.9	878.4	1738.8	1737.8	16
6	584.3	292.7	567.3	566.3	G	1627.8	814.4	1610.8	1609.8	15
7	712.4	356.7	695.3	694.4	Q	1570.8	785.9	1553.7	1552.8	14
8	799.4	400.2	782.4	781.4	S	1442.7	721.9	1425.7	1424.7	13
9	886.4	443.7	869.4	868.4	S	1355.7	678.3	1338.7	1337.7	12
10	1015.5	508.2	998.4	997.5	E	1268.7	634.8	1251.6	1250.6	11
11	1114.5	557.8	1097.5	1096.5	V	1139.6	570.3	1122.6	1121.6	10
12	1227.6	614.3	1210.6	1209.6	I	1040.5	520.8	1023.5	1022.5	9
13	1314.7	657.8	1297.6	1296.6	S	927.5	464.2	910.4	909.4	8
14	1411.7	706.4	1394.7	1393.7	P	840.4	420.7	823.4	822.4	7
15	1508.8	754.9	1491.7	1490.8	P	743.4	372.2	726.3	725.4	6
16	1637.8	819.4	1620.8	1619.8	E	646.3		629.3	628.3	5
17	1766.9	883.9	1749.8	1748.8	E	517.3		500.3	499.3	4
18	1865.9	933.5	1848.9	1847.9	V	388.2		371.2		3
19	1980.0	990.5	1962.9	1962.0	N	289.2		272.1		2
20	2154.1	1077.5	2137.0	2136.1	R	175.1		158.1		1

Gene symbol: Kif2b

Protein name: Kinesin-like protein KIF2B

Protein accession numbers: IPI00350032

Peptide sequence: ALDINTGNPNFETMR

Exclusive (unique to this protein): TRUE

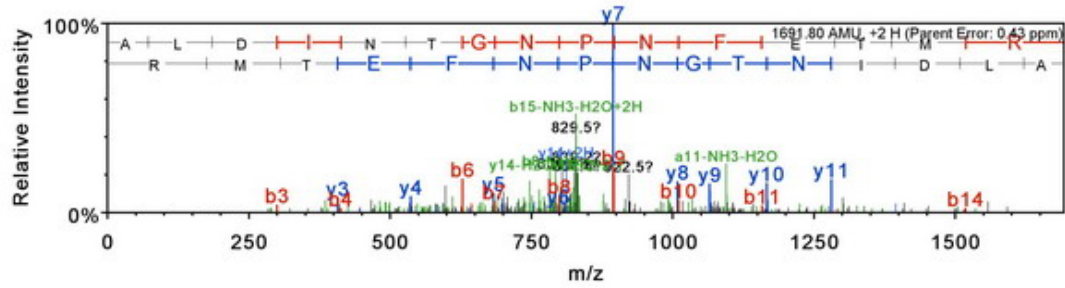
SEQUEST XCorr score: 2.64 SEQUEST DCn score: 0.622

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 846.9051

Actual minus calculated peptide mass (AMU): 0.0007324



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1692.8	846.9	1675.8	1674.8	15
2	185.1				L	1621.8	811.4	1604.7	1603.8	14
3	300.2			282.2	D	1508.7	754.8	1491.7	1490.7	13
4	413.2			395.2	I	1393.7	697.3	1376.6	1375.6	12
5	527.3		510.3	509.3	N	1280.6	640.8	1263.5	1262.6	11
6	628.3	314.7	611.3	610.3	T	1166.5	583.8	1149.5	1148.5	10
7	685.4	343.2	668.3	667.3	G	1065.5	533.2	1048.5	1047.5	9
8	799.4	400.2	782.4	781.4	N	1008.5	504.7	991.4	990.5	8
9	896.5	448.7	879.4	878.4	P	894.4	447.7	877.4	876.4	7
10	1010.5	505.8	993.5	992.5	N	797.4	399.2	780.3	779.4	6
11	1157.6	579.3	1140.5	1139.5	F	683.3		666.3	665.3	5
12	1286.6	643.8	1269.6	1268.6	E	536.3		519.2	518.2	4
13	1387.7	694.3	1370.6	1369.6	T	407.2		390.2	389.2	3
14	1518.7	759.9	1501.7	1500.7	M	306.2		289.1		2
15	1692.8	846.9	1675.8	1674.8	R	175.1		158.1		1

Gene symbol: Kpna4

Protein name: Importin subunit alpha-4

Protein accession numbers: IPI00129792

Peptide sequence: VQNTSLEAIVQNASSDNQGIQLSAVQAAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.56 SEQUEST DCn score: 0.455

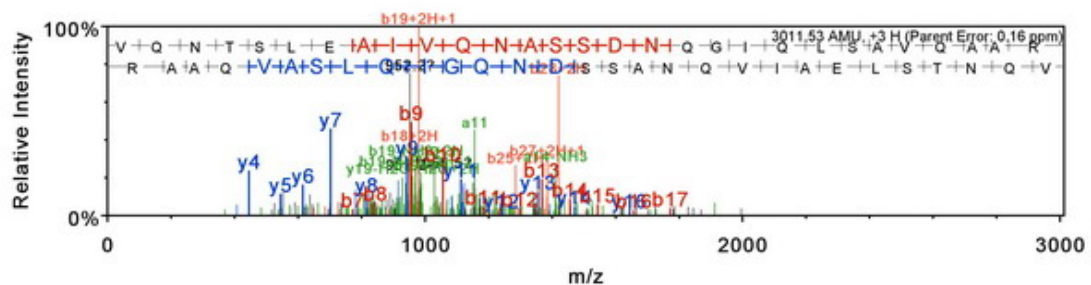
Fix modifications: None

Variable modifications: None

Charge: 3

Observed m/z: 1004.8503

Actual minus calculated peptide mass (AMU): 0.0004883



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	3012.5	1506.8	2995.5	2994.5	29
2	228.1		211.1		Q	2913.5	1457.2	2896.4	2895.5	28
3	342.2		325.2		N	2785.4	1393.2	2768.4	2767.4	27
4	443.2		426.2	425.2	T	2671.4	1336.2	2654.3	2653.3	26
5	530.3		513.2	512.3	S	2570.3	1285.7	2553.3	2552.3	25
6	643.3	322.2	626.3	625.3	L	2483.3	1242.2	2466.3	2465.3	24
7	772.4	386.7	755.4	754.4	E	2370.2	1185.6	2353.2	2352.2	23
8	843.4	422.2	826.4	825.4	A	2241.2	1121.1	2224.1	2223.2	22
9	956.5	478.8	939.5	938.5	I	2170.1	1085.6	2153.1	2152.1	21
10	1055.6	528.3	1038.5	1037.6	V	2057.0	1029.0	2040.0	2039.0	20
11	1183.6	592.3	1166.6	1165.6	Q	1958.0	979.5	1940.9	1940.0	19
12	1297.7	649.3	1280.7	1279.7	N	1829.9	915.5	1812.9	1811.9	18
13	1368.7	684.9	1351.7	1350.7	A	1715.9	858.4	1698.8	1697.9	17
14	1455.7	728.4	1438.7	1437.7	S	1644.8	822.9	1627.8	1626.8	16
15	1542.8	771.9	1525.8	1524.8	S	1557.8	779.4	1540.8	1539.8	15
16	1657.8	829.4	1640.8	1639.8	D	1470.8	735.9	1453.7	1452.8	14
17	1771.9	886.4	1754.8	1753.8	N	1355.7	678.4	1338.7	1337.7	13
18	1899.9	950.5	1882.9	1881.9	Q	1241.7	621.4	1224.7	1223.7	12
19	1956.9	979.0	1939.9	1938.9	G	1113.6	557.3	1096.6	1095.6	11
20	2070.0	1035.5	2053.0	2052.0	I	1056.6	528.8	1039.6	1038.6	10
21	2198.1	1099.5	2181.0	2180.1	Q	943.5	472.3	926.5	925.5	9
22	2311.2	1156.1	2294.1	2293.1	L	815.5	408.2	798.5	797.5	8
23	2398.2	1199.6	2381.2	2380.2	S	702.4	351.7	685.4	684.4	7
24	2469.2	1235.1	2452.2	2451.2	A	615.4	308.2	598.3		6
25	2568.3	1284.7	2551.3	2550.3	V	544.3		527.3		5
26	2696.3	1348.7	2679.3	2678.3	Q	445.3		428.2		4
27	2767.4	1384.2	2750.4	2749.4	A	317.2		300.2		3
28	2838.4	1419.7	2821.4	2820.4	A	246.2		229.1		2
29	3012.5	1506.8	2995.5	2994.5	R	175.1		158.1		1

Gene symbol: Krt16

Protein name: Keratin intermediate filament 16a

Protein accession numbers: IPI00131209

Peptide sequence: GQTGGDVNVEMDAAPGVDLNR

Exclusive (unique to this protein): TRUE

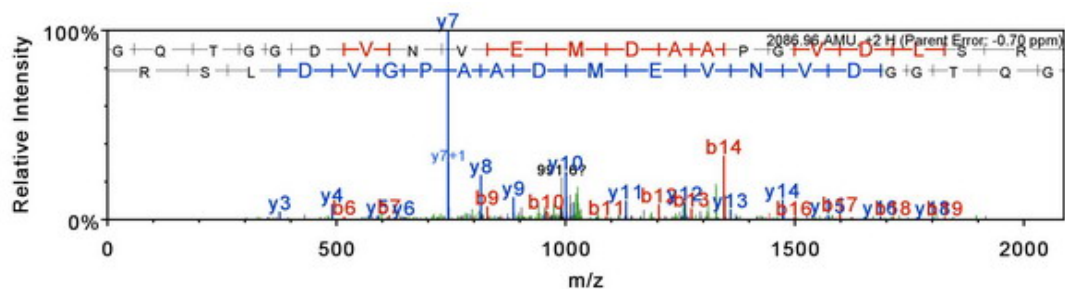
SEQUEST XCorr score: 4.33 SEQUEST DCn score: 0.684

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1044.4867

Actual minus calculated peptide mass (AMU): -0.001465



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	2088.0	1044.5	2070.9	2070.0	21
2	186.1		169.1		Q	2031.0	1016.0	2013.9	2012.9	20
3	287.1		270.1	269.1	T	1902.9	952.0	1885.9	1884.9	19
4	344.2		327.1	326.2	G	1801.8	901.4	1784.8	1783.8	18
5	401.2		384.2	383.2	G	1744.8	872.9	1727.8	1726.8	17
6	516.2	258.6	499.2	498.2	D	1687.8	844.4	1670.8	1669.8	16
7	615.3	308.1	598.3	597.3	V	1572.8	786.9	1555.7	1554.8	15
8	729.3	365.2	712.3	711.3	N	1473.7	737.4	1456.7	1455.7	14
9	828.4	414.7	811.4	810.4	V	1359.7	680.3	1342.6	1341.7	13
10	957.4	479.2	940.4	939.4	E	1260.6	630.8	1243.6	1242.6	12
11	1088.5	544.7	1071.4	1070.5	M	1131.5	566.3	1114.5	1113.5	11
12	1203.5	602.3	1186.5	1185.5	D	1000.5	500.8	983.5	982.5	10
13	1274.5	637.8	1257.5	1256.5	A	885.5	443.2	868.5	867.5	9
14	1345.6	673.3	1328.5	1327.6	A	814.4	407.7	797.4	796.4	8
15	1442.6	721.8	1425.6	1424.6	P	743.4	372.2	726.4	725.4	7
16	1499.6	750.3	1482.6	1481.6	G	646.4	323.7	629.3	628.3	6
17	1598.7	799.9	1581.7	1580.7	V	589.3		572.3	571.3	5
18	1713.7	857.4	1696.7	1695.7	D	490.3		473.2	472.3	4
19	1826.8	913.9	1809.8	1808.8	L	375.2		358.2	357.2	3
20	1913.9	957.4	1896.8	1895.8	S	262.1		245.1	244.1	2
21	2088.0	1044.5	2070.9	2070.0	R	175.1		158.1		1

Peptide sequence: TRLEQEIATYR

Exclusive (unique to this protein): FALSE

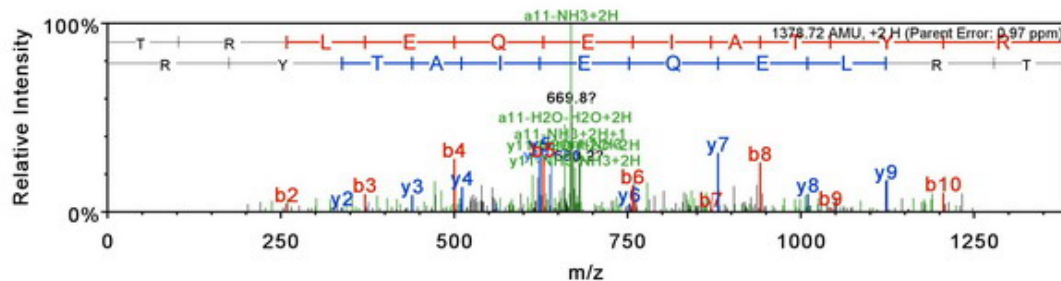
SEQUEST XCorr score: 3.19 SEQUEST DCn score: 0.417

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 690.3688

Actual minus calculated peptide mass (AMU): 0.001343



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1379.7	690.4	1362.7	1361.7	11
2	258.2	129.6	241.1	240.2	R	1278.7	639.8	1261.7	1260.7	10
3	371.2	186.1	354.2	353.2	L	1122.6	561.8	1105.5	1104.6	9
4	500.3	250.7	483.3	482.3	E	1009.5	505.3	992.5	991.5	8
5	628.3	314.7	611.3	610.3	Q	880.5	440.7	863.4	862.4	7
6	757.4	379.2	740.4	739.4	E	752.4	376.7	735.4	734.4	6
7	870.5	435.7	853.4	852.5	I	623.4		606.3	605.3	5
8	941.5	471.3	924.5	923.5	A	510.3		493.2	492.3	4
9	1042.5	521.8	1025.5	1024.5	T	439.2		422.2	421.2	3
10	1205.6	603.3	1188.6	1187.6	Y	338.2		321.2		2
11	1379.7	690.4	1362.7	1361.7	R	175.1		158.1		1

Gene symbol: Krt7

Protein name: Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610009O09

product:similar to keratin K7, type II, epithelial, 55K

Protein accession numbers: IPI00406377

Peptide sequence: LALDIEIATYR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.93 SEQUEST DCn score: 0.616

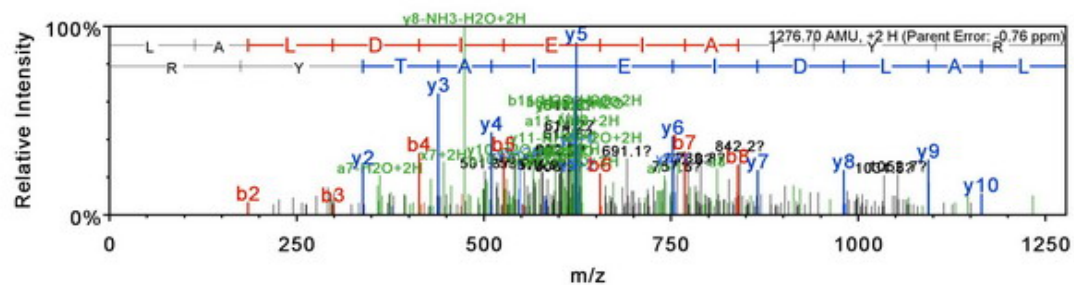
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 639.3588

Actual minus calculated peptide mass (AMU): -0.0009766



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1277.7	639.4	1260.7	1259.7	11
2	185.1				A	1164.6	582.8	1147.6	1146.6	10
3	298.2				L	1093.6	547.3	1076.6	1075.6	9
4	413.2			395.2	D	980.5	490.8	963.5	962.5	8
5	526.3			508.3	I	865.5	433.2	848.5	847.5	7
6	655.4	328.2		637.4	E	752.4	376.7	735.4	734.4	6
7	768.5	384.7		750.4	I	623.4		606.3	605.3	5
8	839.5	420.3		821.5	A	510.3		493.2	492.3	4
9	940.5	470.8		922.5	T	439.2		422.2	421.2	3
10	1103.6	552.3		1085.6	Y	338.2		321.2		2
11	1277.7	639.4	1260.7	1259.7	R	175.1		158.1		1

Gene symbol: Lasp1

Protein name: LIM and SH3 domain protein 1

Protein accession numbers: IPI00125091,IPI00648086,IPI00649913

Peptide sequence: GFSVVADTPELQR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.82 SEQUEST DCn score: 0.294

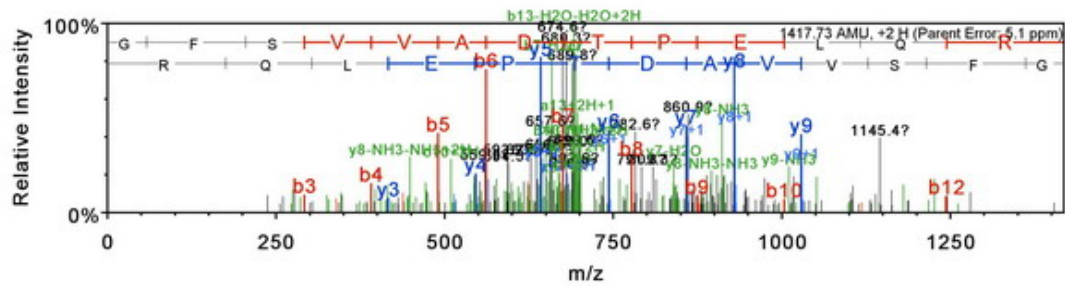
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 709.8715

Actual minus calculated peptide mass (AMU): 0.007202



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1418.7	709.9	1401.7	1400.7	13
2	205.1				F	1361.7	681.4	1344.7	1343.7	12
3	292.1			274.1	S	1214.6	607.8	1197.6	1196.6	11
4	391.2			373.2	V	1127.6	564.3	1110.6	1109.6	10
5	490.3			472.3	V	1028.5	514.8	1011.5	1010.5	9
6	561.3	281.2		543.3	A	929.5	465.2	912.4	911.5	8
7	676.3	338.7		658.3	D	858.4	429.7	841.4	840.4	7
8	777.4	389.2		759.4	T	743.4	372.2	726.4	725.4	6
9	874.4	437.7		856.4	P	642.4		625.3	624.4	5
10	1003.5	502.2		985.5	E	545.3		528.3	527.3	4
11	1116.6	558.8		1098.5	L	416.3		399.2		3
12	1244.6	622.8	1227.6	1226.6	Q	303.2		286.2		2
13	1418.7	709.9	1401.7	1400.7	R	175.1		158.1		1

Gene symbol: LOC100039695

Protein name: hypothetical protein

Protein accession numbers: IPI00354889

Peptide sequence: VWLDPNETNEIANANSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.78 SEQUEST DCn score: 0.727

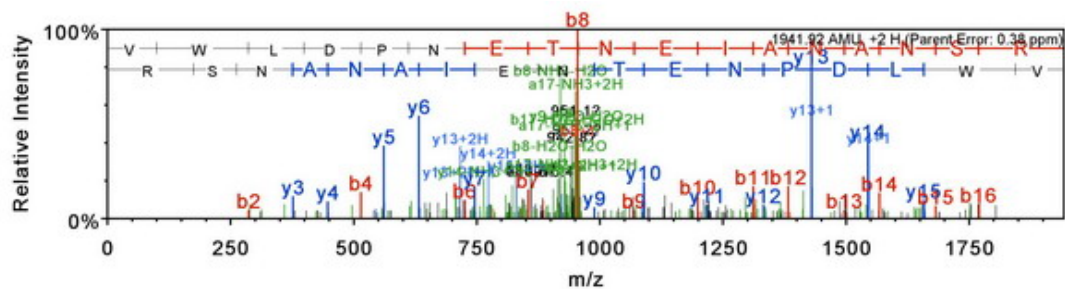
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 971.9672

Actual minus calculated peptide mass (AMU): 0.0007324



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1942.9	972.0	1925.9	1924.9	17
2	286.2				W	1843.9	922.4	1826.8	1825.9	16
3	399.2				L	1657.8	829.4	1640.8	1639.8	15
4	514.3			496.3	D	1544.7	772.9	1527.7	1526.7	14
5	611.3			593.3	P	1429.7	715.3	1412.6	1411.7	13
6	725.4	363.2	708.3	707.4	N	1332.6	666.8	1315.6	1314.6	12
7	854.4	427.7	837.4	836.4	E	1218.6	609.8	1201.5	1200.6	11
8	955.5	478.2	938.4	937.4	T	1089.5	545.3	1072.5	1071.5	10
9	1069.5	535.3	1052.5	1051.5	N	988.5	494.7	971.5	970.5	9
10	1198.5	599.8	1181.5	1180.5	E	874.4	437.7	857.4	856.4	8
11	1311.6	656.3	1294.6	1293.6	I	745.4	373.2	728.4	727.4	7
12	1382.7	691.8	1365.6	1364.7	A	632.3	316.7	615.3	614.3	6
13	1496.7	748.9	1479.7	1478.7	N	561.3		544.3	543.3	5
14	1567.7	784.4	1550.7	1549.7	A	447.2		430.2	429.2	4
15	1681.8	841.4	1664.8	1663.8	N	376.2		359.2	358.2	3
16	1768.8	884.9	1751.8	1750.8	S	262.1		245.1	244.1	2
17	1942.9	972.0	1925.9	1924.9	R	175.1		158.1		1

Gene symbol: LOC100041766;Ube2d2

Protein name: Ubiquitin-conjugating enzyme E2 D2

Protein accession numbers: IPI00125135,IPI00411116

Peptide sequence: VLLSICSLLCDPNPDDPLVPEIAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.61 SEQUEST DCn score: 0.701

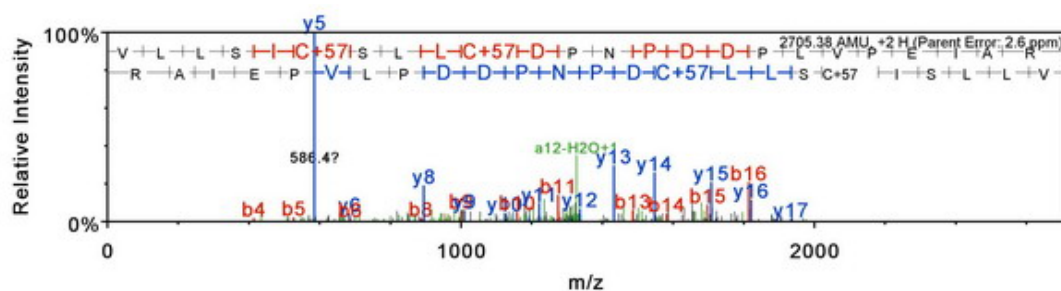
Fix modifications: C6: Carbamidomethyl (+57.02), C10: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2

Observed m/z: 1353.6999

Actual minus calculated peptide mass (AMU): 0.0070758



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	2706.4	1353.7	2689.4	2688.4	24
2	213.2				L	2607.3	1304.2	2590.3	2589.3	23
3	326.2				L	2494.2	1247.6	2477.2	2476.2	22
4	413.3			395.3	S	2381.2	1191.1	2364.1	2363.1	21
5	526.4			508.4	I	2294.1	1147.6	2277.1	2276.1	20
6	686.4	343.7		668.4	C+57	2181.0	1091.0	2164.0	2163.0	19
7	773.4	387.2		755.4	S	2021.0	1011.0	2004.0	2003.0	18
8	886.5	443.8		868.5	L	1934.0	967.5	1916.9	1916.0	17
9	999.6	500.3		981.6	L	1820.9	911.0	1803.9	1802.9	16
10	1159.6	580.3		1141.6	C+57	1707.8	854.4	1690.8	1689.8	15
11	1274.7	637.8		1256.6	D	1547.8	774.4	1530.7	1529.8	14
12	1371.7	686.4		1353.7	P	1432.7	716.9	1415.7	1414.7	13
13	1485.7	743.4	1468.7	1467.7	N	1335.7	668.4	1318.7	1317.7	12
14	1582.8	791.9	1565.8	1564.8	P	1221.7	611.3	1204.6	1203.6	11
15	1697.8	849.4	1680.8	1679.8	D	1124.6	562.8	1107.6	1106.6	10
16	1812.9	906.9	1795.8	1794.8	D	1009.6	505.3	992.5	991.6	9
17	1909.9	955.5	1892.9	1891.9	P	894.5	447.8	877.5	876.5	8
18	2023.0	1012.0	2006.0	2005.0	L	797.5	399.3	780.5	779.5	7
19	2122.1	1061.5	2105.0	2104.1	V	684.4	342.7	667.4	666.4	6
20	2219.1	1110.1	2202.1	2201.1	P	585.3		568.3	567.3	5
21	2348.2	1174.6	2331.1	2330.1	E	488.3		471.3	470.3	4
22	2461.2	1231.1	2444.2	2443.2	I	359.2		342.2		3
23	2532.3	1266.6	2515.3	2514.3	A	246.2		229.1		2
24	2706.4	1353.7	2689.4	2688.4	R	175.1		158.1		1

Gene symbol: LOC100042927

Protein name: Novel protein similar to Histone H2A

Protein accession numbers: IPI00752099

Peptide sequence: GELPLSLVDR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.66 SEQUEST DCn score: 0.32

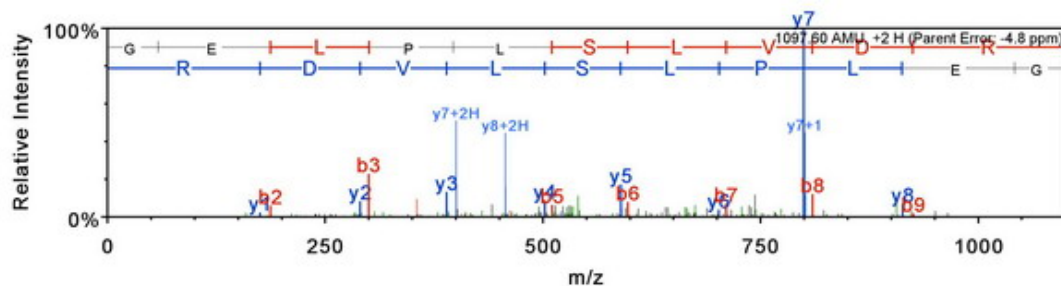
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 549.8093

Actual minus calculated peptide mass (AMU): -0.005249



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1098.6	549.8	1081.6	1080.6	10
2	187.1			169.1	E	1041.6	521.3	1024.6	1023.6	9
3	300.2			282.2	L	912.6	456.8	895.5	894.5	8
4	397.2			379.2	P	799.5	400.2	782.4	781.5	7
5	510.3			492.3	L	702.4	351.7	685.4	684.4	6
6	597.3	299.2		579.3	S	589.3		572.3	571.3	5
7	710.4	355.7		692.4	L	502.3		485.3	484.3	4
8	809.5	405.2		791.5	V	389.2		372.2	371.2	3
9	924.5	462.8		906.5	D	290.2		273.1	272.1	2
10	1098.6	549.8	1081.6	1080.6	R	175.1		158.1		1

Gene symbol: LOC100043681

Protein name: similar to Chain A, Crystal Structure Of Human Rangap1-Ubc9

Protein accession numbers: IPI00850259

Peptide sequence: DHPFGFVAVPTK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.77 SEQUEST DCn score: 0.629

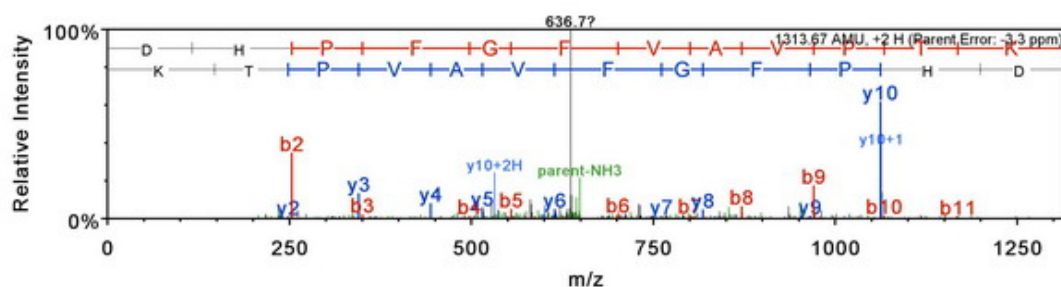
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 657.8442

Actual minus calculated peptide mass (AMU): -0.004395



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	116.0			98.0	D	1314.7	657.9	1297.7	1296.7	12
2	253.1	127.1		235.1	H	1199.7	600.3	1182.6	1181.7	11
3	350.2	175.6		332.1	P	1062.6	531.8	1045.6	1044.6	10
4	497.2	249.1		479.2	F	965.6	483.3	948.5	947.5	9
5	554.2	277.6		536.2	G	818.5	409.7	801.5	800.5	8
6	701.3	351.2		683.3	F	761.5	381.2	744.4	743.5	7
7	800.4	400.7		782.4	V	614.4	307.7	597.4	596.4	6
8	871.4	436.2		853.4	A	515.3		498.3	497.3	5
9	970.5	485.7		952.5	V	444.3		427.3	426.3	4
10	1067.5	534.3		1049.5	P	345.2		328.2	327.2	3
11	1168.6	584.8		1150.6	T	248.2		231.1	230.2	2
12	1314.7	657.9	1297.7	1296.7	K	147.1		130.1		1

Peptide sequence: MLFKDDYPSSPPK

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 3.46 SEQUEST DCn score: 0.597

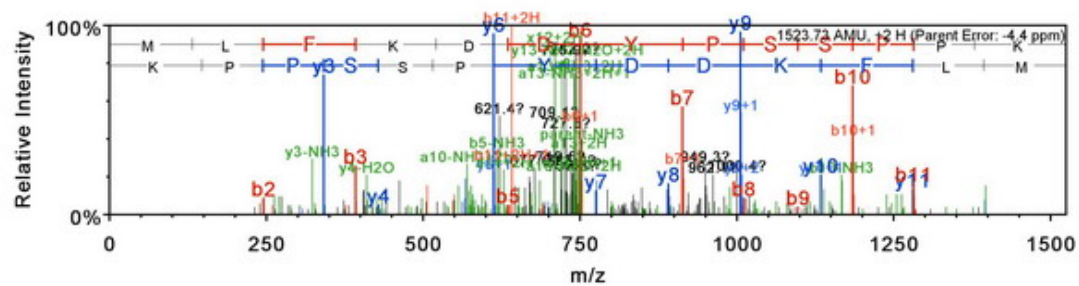
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 762.8711

Actual minus calculated peptide mass (AMU): -0.0067152



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1524.7	762.9	1507.7	1506.7	13
2	245.1				L	1393.7	697.4	1376.7	1375.7	12
3	392.2				F	1280.6	640.8	1263.6	1262.6	11
4	520.3	260.6	503.3		K	1133.5	567.3	1116.5	1115.5	10
5	635.3	318.2	618.3	617.3	D	1005.5	503.2	988.4	987.4	9
6	750.4	375.7	733.3	732.3	D	890.4	445.7	873.4	872.4	8
7	913.4	457.2	896.4	895.4	Y	775.4	388.2	758.4	757.4	7
8	1010.5	505.7	993.4	992.5	P	612.3	306.7	595.3	594.3	6
9	1097.5	549.3	1080.5	1079.5	S	515.3		498.3	497.3	5
10	1184.5	592.8	1167.5	1166.5	S	428.3		411.2	410.2	4
11	1281.6	641.3	1264.6	1263.6	P	341.2		324.2		3
12	1378.6	689.8	1361.6	1360.6	P	244.2		227.1		2
13	1524.7	762.9	1507.7	1506.7	K	147.1		130.1		1

Gene symbol: LOC100045629;Wdr26

Protein name: WD repeat protein 26

Protein accession numbers: IPI00226275,IPI00755422,IPI00756773

Peptide sequence: GQFYQCDLDGNLLDSWEGVR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.54 SEQUEST DCn score: 0.249

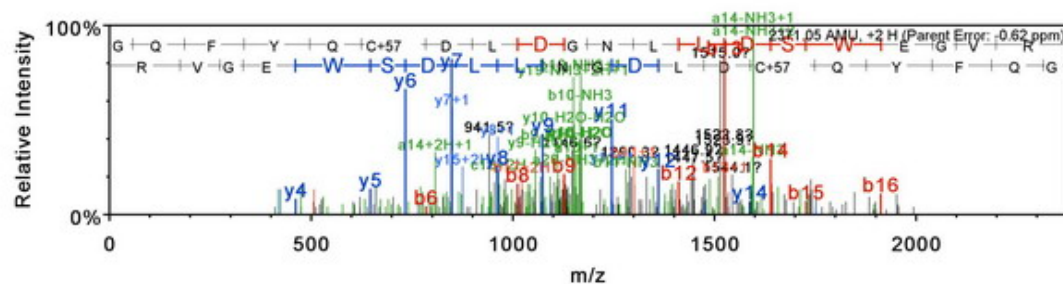
Fix modifications: C6: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2

Observed m/z: 1186.5342

Actual minus calculated peptide mass (AMU): -0.001465



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	2372.1	1186.5	2355.0	2354.1	20
2	186.1		169.1		Q	2315.0	1158.0	2298.0	2297.0	19
3	333.2		316.1		F	2187.0	1094.0	2170.0	2169.0	18
4	496.2		479.2		Y	2039.9	1020.5	2022.9	2021.9	17
5	624.3		607.3		Q	1876.9	938.9	1859.8	1858.8	16
6	784.3	392.7	767.3		C+57	1748.8	874.9	1731.8	1730.8	15
7	899.3	450.2	882.3	881.3	D	1588.8	794.9	1571.7	1570.8	14
8	1012.4	506.7	995.4	994.4	L	1473.7	737.4	1456.7	1455.7	13
9	1127.5	564.2	1110.4	1109.4	D	1360.7	680.8	1343.6	1342.6	12
10	1184.5	592.7	1167.4	1166.5	G	1245.6	623.3	1228.6	1227.6	11
11	1298.5	649.8	1281.5	1280.5	N	1188.6	594.8	1171.6	1170.6	10
12	1411.6	706.3	1394.6	1393.6	L	1074.6	537.8	1057.5	1056.5	9
13	1524.7	762.8	1507.7	1506.7	L	961.5	481.2	944.5	943.5	8
14	1639.7	820.4	1622.7	1621.7	D	848.4	424.7	831.4	830.4	7
15	1726.7	863.9	1709.7	1708.7	S	733.4	367.2	716.3	715.4	6
16	1912.8	956.9	1895.8	1894.8	W	646.3		629.3	628.3	5
17	2041.9	1021.4	2024.8	2023.9	E	460.3		443.2	442.2	4
18	2098.9	1049.9	2081.9	2080.9	G	331.2		314.2		3
19	2198.0	1099.5	2180.9	2179.9	V	274.2		257.2		2
20	2372.1	1186.5	2355.0	2354.1	R	175.1		158.1		1

Gene symbol: LOC100046038;LOC100041269

Protein name: hypothetical protein

Protein accession numbers: IPI00754460

Peptide sequence: AEAVGAALLDSLQSSQYR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.34 SEQUEST DCn score: 0.632

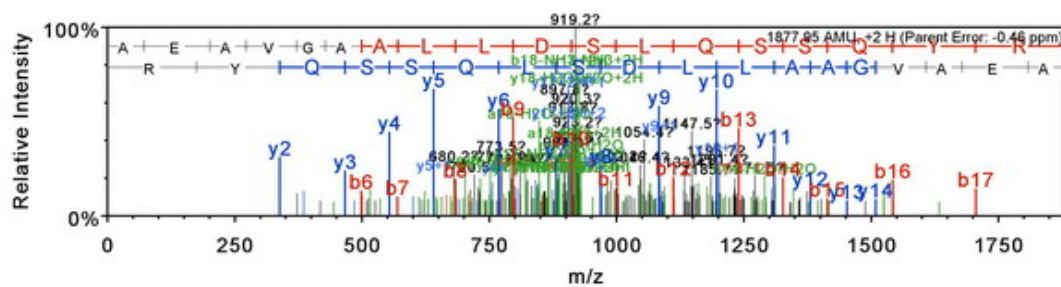
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 939.9816

Actual minus calculated peptide mass (AMU): -0.0008545



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1879.0	940.0	1861.9	1861.0	18
2	201.1			183.1	E	1807.9	904.5	1790.9	1789.9	17
3	272.1			254.1	A	1678.9	839.9	1661.9	1660.9	16
4	371.2			353.2	V	1607.8	804.4	1590.8	1589.8	15
5	428.2			410.2	G	1508.8	754.9	1491.7	1490.8	14
6	499.3	250.1		481.2	A	1451.8	726.4	1434.7	1433.7	13
7	570.3	285.7		552.3	A	1380.7	690.9	1363.7	1362.7	12
8	683.4	342.2		665.4	L	1309.7	655.3	1292.7	1291.7	11
9	796.5	398.7		778.5	L	1196.6	598.8	1179.6	1178.6	10
10	911.5	456.3		893.5	D	1083.5	542.3	1066.5	1065.5	9
11	998.5	499.8		980.5	S	968.5	484.7	951.5	950.5	8
12	1111.6	556.3		1093.6	L	881.5	441.2	864.4	863.4	7
13	1239.7	620.3	1222.6	1221.7	Q	768.4	384.7	751.3	750.4	6
14	1326.7	663.9	1309.7	1308.7	S	640.3		623.3	622.3	5
15	1413.7	707.4	1396.7	1395.7	S	553.3		536.3	535.3	4
16	1541.8	771.4	1524.8	1523.8	Q	466.2		449.2		3
17	1704.8	852.9	1687.8	1686.8	Y	338.2		321.2		2
18	1879.0	940.0	1861.9	1861.0	R	175.1		158.1		1

Gene symbol: LOC100046904;LOC100039888;OTTMUSG00000000267

Protein name: Stathmin 1 (Stmn1) pseudogene

Protein accession numbers: IPI00475138

Peptide sequence: ASGQAFELILSPR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.04 SEQUEST DCn score: 0.459

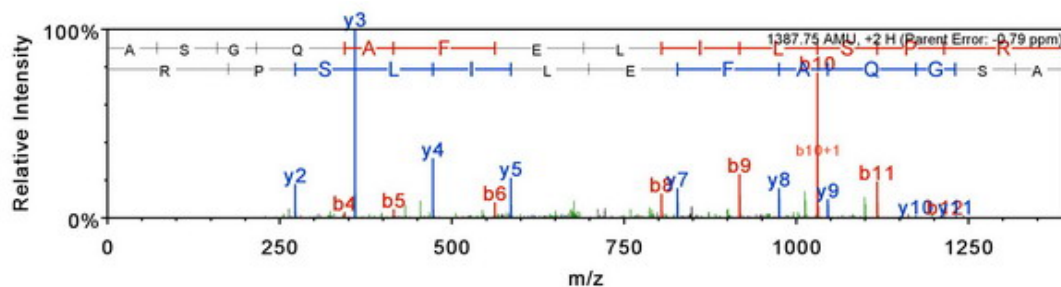
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 694.8803

Actual minus calculated peptide mass (AMU): -0.001099



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1388.8	694.9	1371.7	1370.7	13
2	159.1			141.1	S	1317.7	659.4	1300.7	1299.7	12
3	216.1			198.1	G	1230.7	615.9	1213.7	1212.7	11
4	344.2		327.1	326.2	Q	1173.7	587.3	1156.6	1155.7	10
5	415.2		398.2	397.2	A	1045.6	523.3	1028.6	1027.6	9
6	562.3	281.6	545.2	544.3	F	974.6	487.8	957.5	956.6	8
7	691.3	346.2	674.3	673.3	E	827.5	414.3	810.5	809.5	7
8	804.4	402.7	787.4	786.4	L	698.5	349.7	681.4	680.5	6
9	917.5	459.2	900.5	899.5	I	585.4		568.4	567.4	5
10	1030.6	515.8	1013.5	1012.6	L	472.3		455.3	454.3	4
11	1117.6	559.3	1100.6	1099.6	S	359.2		342.2	341.2	3
12	1214.6	607.8	1197.6	1196.6	P	272.2		255.2		2
13	1388.8	694.9	1371.7	1370.7	R	175.1		158.1		1

Gene symbol: LOC100048062;LOC665931;Wdr89;Rplp2

Protein name: LOC665931 protein

Protein accession numbers: IPI00742383

Peptide sequence: YVASYLLAALGGNSSPSAK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.12 SEQUEST DCn score: 0.466

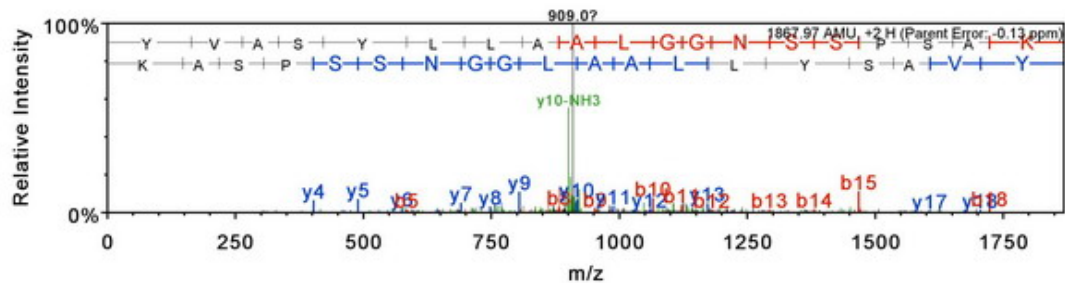
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 934.9916

Actual minus calculated peptide mass (AMU): -0.0002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1869.0	935.0	1852.0	1851.0	19
2	263.1				V	1705.9	853.5	1688.9	1687.9	18
3	334.2				A	1606.8	803.9	1589.8	1588.8	17
4	421.2			403.2	S	1535.8	768.4	1518.8	1517.8	16
5	584.3			566.3	Y	1448.8	724.9	1431.8	1430.8	15
6	697.4	349.2		679.4	L	1285.7	643.4	1268.7	1267.7	14
7	810.4	405.7		792.4	L	1172.6	586.8	1155.6	1154.6	13
8	881.5	441.2		863.5	A	1059.5	530.3	1042.5	1041.5	12
9	952.5	476.8		934.5	A	988.5	494.8	971.5	970.5	11
10	1065.6	533.3		1047.6	L	917.5	459.2	900.4	899.5	10
11	1122.6	561.8		1104.6	G	804.4	402.7	787.4	786.4	9
12	1179.6	590.3		1161.6	G	747.4	374.2	730.3	729.4	8
13	1293.7	647.4	1276.7	1275.7	N	690.3	345.7	673.3	672.3	7
14	1380.7	690.9	1363.7	1362.7	S	576.3	288.7	559.3	558.3	6
15	1467.8	734.4	1450.7	1449.7	S	489.3		472.2	471.3	5
16	1564.8	782.9	1547.8	1546.8	P	402.2		385.2	384.2	4
17	1651.8	826.4	1634.8	1633.8	S	305.2		288.2	287.2	3
18	1722.9	861.9	1705.8	1704.9	A	218.2		201.1		2
19	1869.0	935.0	1852.0	1851.0	K	147.1		130.1		1

Gene symbol: LOC100048815

Protein name: similar to PF6

Protein accession numbers: IPI00848491

Peptide sequence: APPVVVEIENTER

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 3.02 SEQUEST DCn score: 0.432

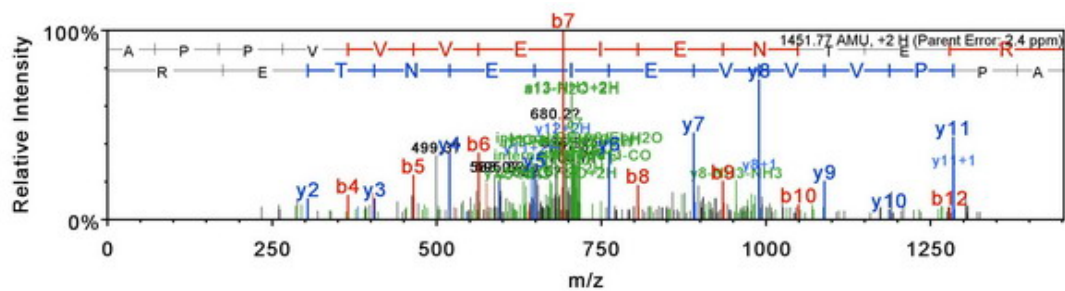
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 726.8906

Actual minus calculated peptide mass (AMU): 0.0035358



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1452.8	726.9	1435.7	1434.8	13
2	169.1				P	1381.7	691.4	1364.7	1363.7	12
3	266.1				P	1284.7	642.8	1267.7	1266.7	11
4	365.2				V	1187.6	594.3	1170.6	1169.6	10
5	464.3				V	1088.6	544.8	1071.5	1070.5	9
6	563.4	282.2			V	989.5	495.3	972.5	971.5	8
7	692.4	346.7		674.4	E	890.4	445.7	873.4	872.4	7
8	805.5	403.3		787.5	I	761.4	381.2	744.4	743.4	6
9	934.5	467.8		916.5	E	648.3		631.3	630.3	5
10	1048.6	524.8	1031.5	1030.6	N	519.3		502.2	501.2	4
11	1149.6	575.3	1132.6	1131.6	T	405.2		388.2	387.2	3
12	1278.7	639.8	1261.6	1260.7	E	304.2		287.1	286.2	2
13	1452.8	726.9	1435.7	1434.8	R	175.1		158.1		1

Peptide sequence: FFVVYTDGSGVELLR

Exclusive (unique to this protein): FALSE

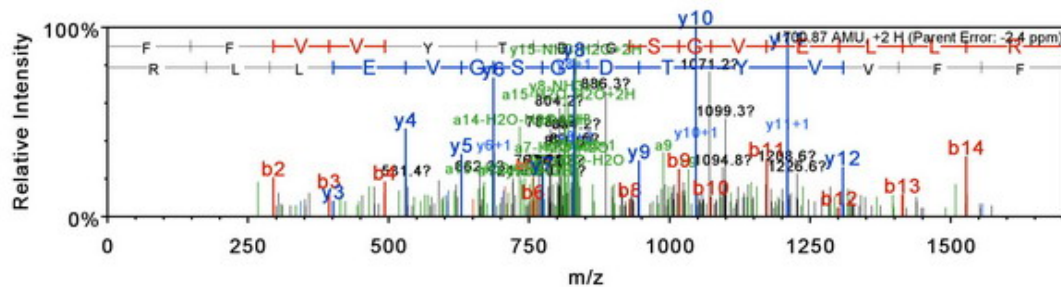
SEQUEST XCorr score: 4.22 SEQUEST DCn score: 0.546

Fix modifications: None

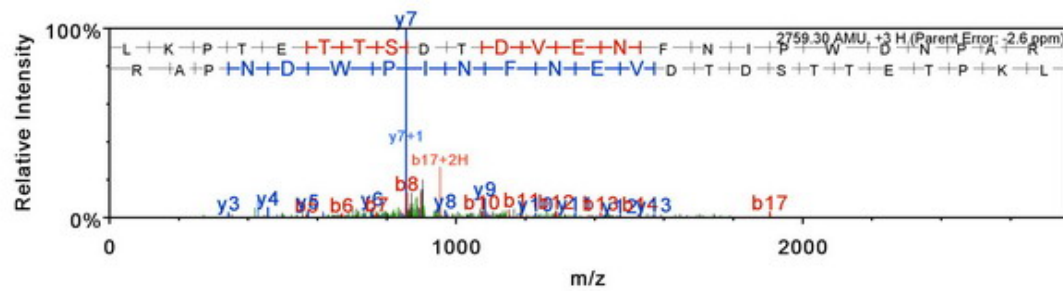
Variable modifications: None

Charge: 2 Observed m/z: 851.4445

Actual minus calculated peptide mass (AMU): -0.0040256



Charge: 3 Observed m/z: 920.7734
Actual minus calculated peptide mass (AMU): -0.0070758



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	2760.3	1380.7	2743.3	2742.3	24
2	242.2	121.6	225.2		K	2647.2	1324.1	2630.2	2629.2	23
3	339.2	170.1	322.2		P	2519.1	1260.1	2502.1	2501.1	22
4	440.3	220.7	423.3	422.3	T	2422.1	1211.5	2405.1	2404.1	21
5	569.3	285.2	552.3	551.3	E	2321.0	1161.0	2304.0	2303.0	20
6	670.4	335.7	653.4	652.4	T	2192.0	1096.5	2175.0	2174.0	19
7	771.4	386.2	754.4	753.4	T	2090.9	1046.0	2073.9	2072.9	18
8	858.5	429.7	841.4	840.5	S	1989.9	995.5	1972.9	1971.9	17
9	973.5	487.3	956.5	955.5	D	1902.9	951.9	1885.8	1884.9	16
10	1074.5	537.8	1057.5	1056.5	T	1787.8	894.4	1770.8	1769.8	15
11	1189.6	595.3	1172.5	1171.5	D	1686.8	843.9	1669.8	1668.8	14
12	1288.6	644.8	1271.6	1270.6	V	1571.8	786.4	1554.7	1553.8	13
13	1417.7	709.3	1400.6	1399.7	E	1472.7	736.9	1455.7	1454.7	12
14	1531.7	766.4	1514.7	1513.7	N	1343.7	672.3	1326.6	1325.6	11
15	1678.8	839.9	1661.8	1660.8	F	1229.6	615.3	1212.6	1211.6	10
16	1792.8	896.9	1775.8	1774.8	N	1082.5	541.8	1065.5	1064.5	9
17	1905.9	953.5	1888.9	1887.9	I	968.5	484.8	951.5	950.5	8
18	2003.0	1002.0	1985.9	1985.0	P	855.4	428.2	838.4	837.4	7
19	2189.0	1095.0	2172.0	2171.0	W	758.4	379.7	741.3	740.4	6
20	2304.1	1152.5	2287.0	2286.1	D	572.3		555.3	554.3	5
21	2418.1	1209.6	2401.1	2400.1	N	457.3		440.2		4
22	2515.2	1258.1	2498.1	2497.2	P	343.2		326.2		3
23	2586.2	1293.6	2569.2	2568.2	A	246.2		229.1		2
24	2760.3	1380.7	2743.3	2742.3	R	175.1		158.1		1

Peptide sequence: TLEVIETAPLPVPEVVYPFR

Exclusive (unique to this protein): TRUE

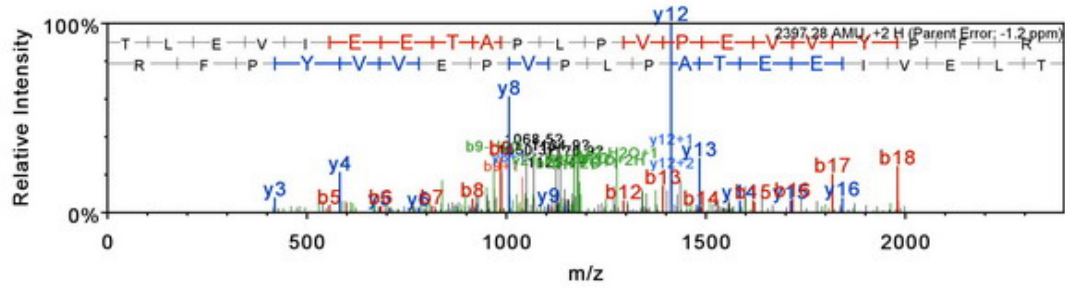
SEQUEST XCorr score: 3.63 SEQUEST DCn score: 0.634

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 1199.6479

Actual minus calculated peptide mass (AMU): -0.00293



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	2398.3	1199.7	2381.3	2380.3	21
2	215.1			197.1	L	2297.2	1149.1	2280.2	2279.2	20
3	344.2			326.2	E	2184.2	1092.6	2167.1	2166.2	19
4	443.3			425.2	V	2055.1	1028.1	2038.1	2037.1	18
5	556.3			538.3	I	1956.1	978.5	1939.0	1938.0	17
6	685.4	343.2		667.4	E	1843.0	922.0	1825.9	1825.0	16
7	814.4	407.7		796.4	E	1713.9	857.5	1696.9	1695.9	15
8	915.5	458.2		897.5	T	1584.9	792.9	1567.9	1566.9	14
9	986.5	493.8		968.5	A	1483.8	742.4	1466.8	1465.8	13
10	1083.6	542.3		1065.5	P	1412.8	706.9	1395.8	1394.8	12
11	1196.6	598.8		1178.6	L	1315.7	658.4	1298.7	1297.7	11
12	1293.7	647.4		1275.7	P	1202.7	601.8	1185.6	1184.7	10
13	1392.8	696.9		1374.8	V	1105.6	553.3	1088.6	1087.6	9
14	1489.8	745.4		1471.8	P	1006.5	503.8	989.5	988.5	8
15	1618.9	809.9		1600.9	E	909.5	455.3	892.5	891.5	7
16	1717.9	859.5		1699.9	V	780.4	390.7	763.4		6
17	1817.0	909.0		1799.0	V	681.4		664.4		5
18	1980.1	990.5		1962.1	Y	582.3		565.3		4
19	2077.1	1039.1		2059.1	P	419.2		402.2		3
20	2224.2	1112.6		2206.2	F	322.2		305.2		2
21	2398.3	1199.7	2381.3	2380.3	R	175.1		158.1		1

Peptide sequence: VLLQVLQEAHQYR

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 3.52 SEQUEST DCn score: 0.603

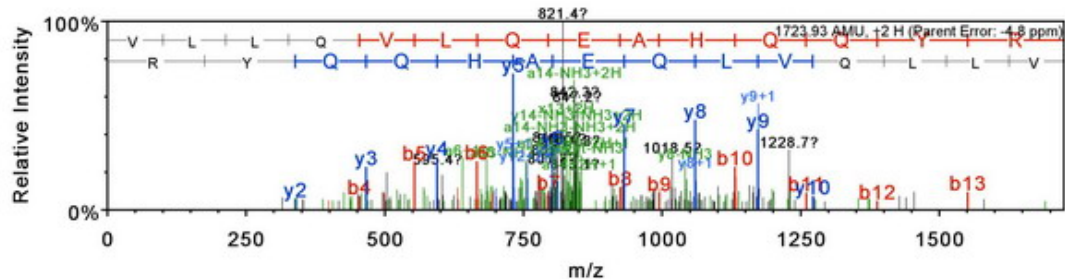
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 862.9722

Actual minus calculated peptide mass (AMU): -0.008301



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1724.9	863.0	1707.9	1706.9	14
2	213.2				L	1625.9	813.4	1608.9	1607.9	13
3	326.2				L	1512.8	756.9	1495.8	1494.8	12
4	454.3		437.3		Q	1399.7	700.4	1382.7	1381.7	11
5	553.4		536.3		V	1271.7	636.3	1254.6	1253.6	10
6	666.5	333.7	649.4		L	1172.6	586.8	1155.5	1154.6	9
7	794.5	397.8	777.5		Q	1059.5	530.3	1042.5	1041.5	8
8	923.6	462.3	906.5	905.6	E	931.4	466.2	914.4	913.4	7
9	994.6	497.8	977.6	976.6	A	802.4	401.7	785.4		6
10	1131.7	566.3	1114.6	1113.6	H	731.4	366.2	714.3		5
11	1259.7	630.4	1242.7	1241.7	Q	594.3		577.3		4
12	1387.8	694.4	1370.7	1369.8	Q	466.2		449.2		3
13	1550.8	775.9	1533.8	1532.8	Y	338.2		321.2		2
14	1724.9	863.0	1707.9	1706.9	R	175.1		158.1		1

Gene symbol: LOC621832;Nutf2;LOC100043462;LOC100044514

Protein name: Nuclear transport factor 2

Protein accession numbers: IPI00124149

Peptide sequence: NINDAWVCTNDMFR

Exclusive (unique to this protein): TRUE

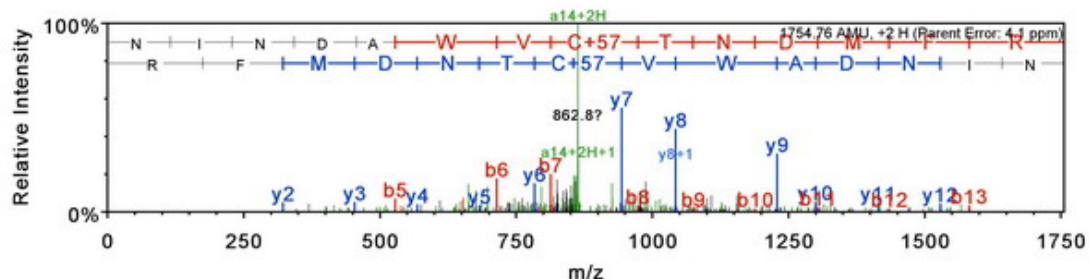
SEQUEST XCorr score: 3.23 SEQUEST DCn score: 0.72

Fix modifications: C8: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2 Observed m/z: 878.3867

Actual minus calculated peptide mass (AMU): 0.007202



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1755.8	878.4	1738.7	1737.8	14
2	228.1		211.1		I	1641.7	821.4	1624.7	1623.7	13
3	342.2		325.2		N	1528.6	764.8	1511.6	1510.6	12
4	457.2		440.2	439.2	D	1414.6	707.8	1397.6	1396.6	11
5	528.2		511.2	510.2	A	1299.6	650.3	1282.5	1281.5	10
6	714.3	357.7	697.3	696.3	W	1228.5	614.8	1211.5	1210.5	9
7	813.4	407.2	796.4	795.4	V	1042.5	521.7	1025.4	1024.4	8
8	973.4	487.2	956.4	955.4	C+57	943.4	472.2	926.4	925.4	7
9	1074.5	537.7	1057.4	1056.5	T	783.4	392.2	766.3	765.3	6
10	1188.5	594.8	1171.5	1170.5	N	682.3		665.3	664.3	5
11	1303.5	652.3	1286.5	1285.5	D	568.3		551.2	550.2	4
12	1434.6	717.8	1417.5	1416.6	M	453.2		436.2		3
13	1581.7	791.3	1564.6	1563.6	F	322.2		305.2		2
14	1755.8	878.4	1738.7	1737.8	R	175.1		158.1		1

Gene symbol: LOC638385

Protein name: similar to High mobility group protein 1

Protein accession numbers: IPI00661255

Peptide sequence: MSSYAFFVQTCR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.68 SEQUEST DCn score: 0.174

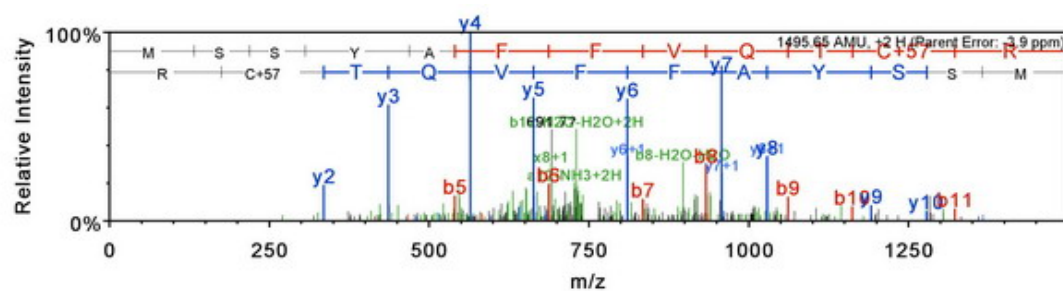
Fix modifications: C11: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2

Observed m/z: 748.8343

Actual minus calculated peptide mass (AMU): -0.005859



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.1				M	1496.7	748.8	1479.6	1478.7	12
2	219.1			201.1	S	1365.6	683.3	1348.6	1347.6	11
3	306.1			288.1	S	1278.6	639.8	1261.6	1260.6	10
4	469.2			451.2	Y	1191.6	596.3	1174.5	1173.5	9
5	540.2			522.2	A	1028.5	514.8	1011.5	1010.5	8
6	687.3	344.1		669.3	F	957.5	479.2	940.4	939.5	7
7	834.4	417.7		816.3	F	810.4	405.7	793.4	792.4	6
8	933.4	467.2		915.4	V	663.3		646.3	645.3	5
9	1061.5	531.2	1044.5	1043.5	Q	564.3		547.2	546.3	4
10	1162.5	581.8	1145.5	1144.5	T	436.2		419.2	418.2	3
11	1322.5	661.8	1305.5	1304.5	C+57	335.2		318.1		2
12	1496.7	748.8	1479.6	1478.7	R	175.1		158.1		1

Gene symbol: LOC667026

Protein name: similar to MTH2 protein

Protein accession numbers: IPI00462401

Peptide sequence: FASVVNSFVEK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.58 SEQUEST DCn score: 0.513

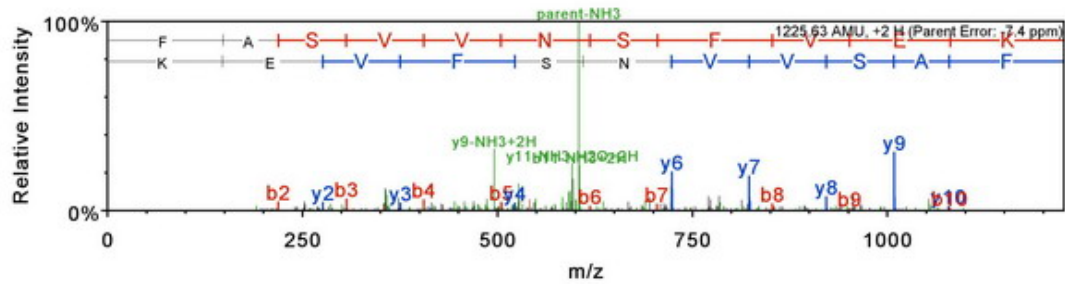
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 613.8204

Actual minus calculated peptide mass (AMU): -0.009033



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1226.6	613.8	1209.6	1208.6	11
2	219.1				A	1079.6	540.3	1062.5	1061.6	10
3	306.2			288.1	S	1008.5	504.8	991.5	990.5	9
4	405.2			387.2	V	921.5	461.3	904.5	903.5	8
5	504.3			486.3	V	822.4	411.7	805.4	804.4	7
6	618.3	309.7	601.3	600.3	N	723.4	362.2	706.3	705.4	6
7	705.4	353.2	688.3	687.4	S	609.3		592.3	591.3	5
8	852.4	426.7	835.4	834.4	F	522.3		505.3	504.3	4
9	951.5	476.3	934.5	933.5	V	375.2		358.2	357.2	3
10	1080.5	540.8	1063.5	1062.5	E	276.2		259.1	258.1	2
11	1226.6	613.8	1209.6	1208.6	K	147.1		130.1		1

Gene symbol: LOC668706

Protein name: similar to 60S ribosomal protein L12

Protein accession numbers: IPI00338838,IPI00754405,IPI00849793

Peptide sequence: HSGNITFDEIVNIAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.73 SEQUEST DCn score: 0.514

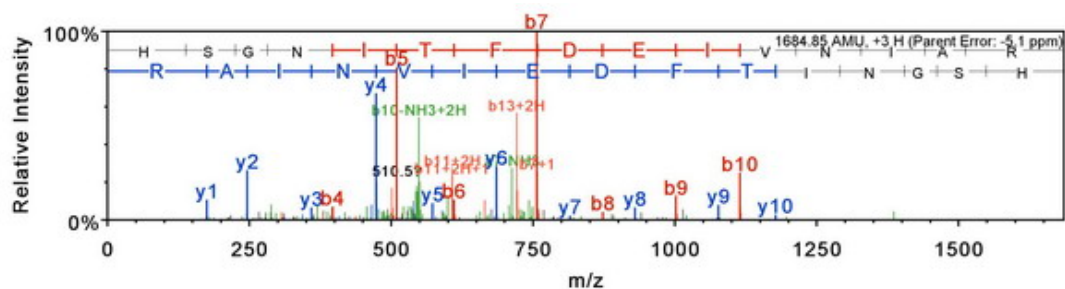
Fix modifications: None

Variable modifications: None

Charge: 3

Observed m/z: 562.6227

Actual minus calculated peptide mass (AMU): -0.0085453



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	138.1	69.5			H	1685.9	843.4	1668.8	1667.9	15
2	225.1	113.1		207.1	S	1548.8	774.9	1531.8	1530.8	14
3	282.1	141.6		264.1	G	1461.8	731.4	1444.7	1443.8	13
4	396.2	198.6	379.1	378.2	N	1404.8	702.9	1387.7	1386.7	12
5	509.3	255.1	492.2	491.2	I	1290.7	645.9	1273.7	1272.7	11
6	610.3	305.7	593.3	592.3	T	1177.6	589.3	1160.6	1159.6	10
7	757.4	379.2	740.3	739.4	F	1076.6	538.8	1059.5	1058.6	9
8	872.4	436.7	855.4	854.4	D	929.5	465.3	912.5	911.5	8
9	1001.4	501.2	984.4	983.4	E	814.5	407.7	797.5	796.5	7
10	1114.5	557.8	1097.5	1096.5	I	685.4	343.2	668.4		6
11	1213.6	607.3	1196.6	1195.6	V	572.4		555.3		5
12	1327.6	664.3	1310.6	1309.6	N	473.3		456.3		4
13	1440.7	720.9	1423.7	1422.7	I	359.2		342.2		3
14	1511.8	756.4	1494.7	1493.7	A	246.2		229.1		2
15	1685.9	843.4	1668.8	1667.9	R	175.1		158.1		1

Peptide sequence: QAQIEVVPSASALIHK

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 3.42 SEQUEST DCn score: 0.644

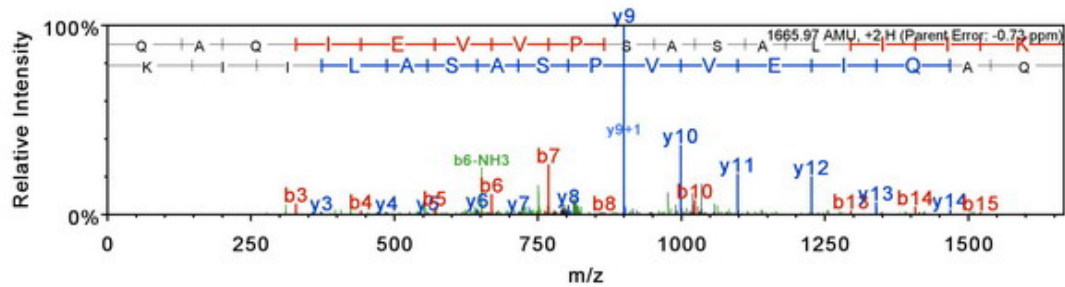
Fix modifications: None

Variable modifications: None

Charge: 2

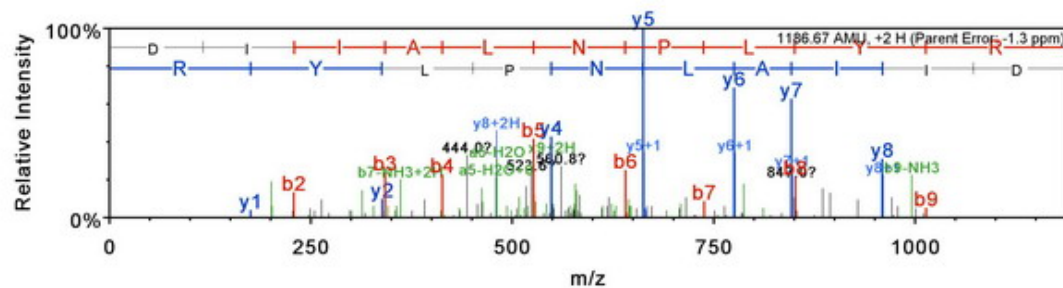
Observed m/z: 833.9906

Actual minus calculated peptide mass (AMU): -0.0012249



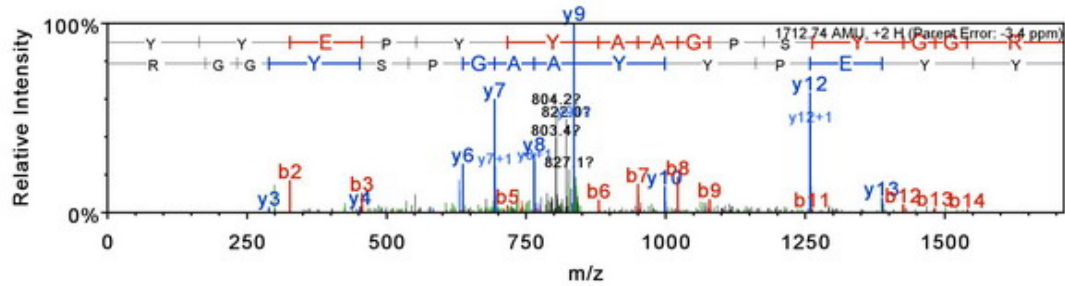
B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	1667.0	834.0	1650.0	1649.0	16
2	200.1		183.1		A	1538.9	770.0	1521.9	1520.9	15
3	328.2		311.1		Q	1467.9	734.4	1450.9	1449.9	14
4	441.3		424.2		I	1339.8	670.4	1322.8	1321.8	13
5	570.3		553.3	552.3	E	1226.7	613.9	1209.7	1208.7	12
6	669.4	335.2	652.3	651.4	V	1097.7	549.4	1080.7	1079.7	11
7	768.4	384.7	751.4	750.4	V	998.6	499.8	981.6	980.6	10
8	865.5	433.2	848.5	847.5	P	899.6	450.3	882.5	881.6	9
9	952.5	476.8	935.5	934.5	S	802.5	401.8	785.5	784.5	8
10	1023.6	512.3	1006.5	1005.5	A	715.5	358.2	698.5	697.5	7
11	1110.6	555.8	1093.5	1092.6	S	644.4	322.7	627.4	626.4	6
12	1181.6	591.3	1164.6	1163.6	A	557.4		540.4		5
13	1294.7	647.9	1277.7	1276.7	L	486.4		469.3		4
14	1407.8	704.4	1390.8	1389.8	I	373.3		356.3		3
15	1520.9	760.9	1503.8	1502.9	I	260.2		243.2		2
16	1667.0	834.0	1650.0	1649.0	K	147.1		130.1		1

Gene symbol: Lonp1
Protein name: Lon protease homolog
Protein accession numbers: IPI00319518,IPI00761408
Peptide sequence: DIIALNPLYR
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 2.98 SEQUEST DCn score: 0.563
Fix modifications: None
Variable modifications: None
Charge: 2 Observed m/z: 594.3426
Actual minus calculated peptide mass (AMU): -0.0015855



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	116.0			98.0	D	1187.7	594.3	1170.7	1169.7	10
2	229.1			211.1	I	1072.7	536.8	1055.6		9
3	342.2			324.2	I	959.6	480.3	942.5		8
4	413.2			395.2	A	846.5	423.8	829.5		7
5	526.3			508.3	L	775.5	388.2	758.4		6
6	640.4	320.7	623.3	622.4	N	662.4		645.3		5
7	737.4	369.2	720.4	719.4	P	548.3		531.3		4
8	850.5	425.8	833.5	832.5	L	451.3		434.2		3
9	1013.6	507.3	996.5	995.6	Y	338.2		321.2		2
10	1187.7	594.3	1170.7	1169.7	R	175.1		158.1		1

Gene symbol: Lpp
Protein name: Isoform 1 of Lipoma-preferred partner homolog
Protein accession numbers: IPI00221494,IPI00656290
Peptide sequence: YYEPYAAAGPSYGGR
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 3.59 SEQUEST DCn score: 0.757
Fix modifications: None
Variable modifications: None
Charge: 2 Observed m/z: 857.3785
Actual minus calculated peptide mass (AMU): -0.005737



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1713.8	857.4	1696.7	1695.7	15
2	327.1				Y	1550.7	775.9	1533.7	1532.7	14
3	456.2			438.2	E	1387.6	694.3	1370.6	1369.6	13
4	553.2			535.2	P	1258.6	629.8	1241.6	1240.6	12
5	716.3			698.3	Y	1161.5	581.3	1144.5	1143.5	11
6	879.4	440.2		861.4	Y	998.5	499.7	981.4	980.5	10
7	950.4	475.7		932.4	A	835.4	418.2	818.4	817.4	9
8	1021.4	511.2		1003.4	A	764.4	382.7	747.3	746.4	8
9	1078.5	539.7		1060.4	G	693.3	347.2	676.3	675.3	7
10	1175.5	588.3		1157.5	P	636.3	318.7	619.3	618.3	6
11	1262.5	631.8		1244.5	S	539.3		522.2	521.3	5
12	1425.6	713.3		1407.6	Y	452.2		435.2		4
13	1482.6	741.8		1464.6	G	289.2		272.1		3
14	1539.6	770.3		1521.6	G	232.1		215.1		2
15	1713.8	857.4	1696.7	1695.7	R	175.1		158.1		1

Gene symbol: Lrch4

Protein name: Leucine-rich repeat and calponin homology domain-containing protein 4

Protein accession numbers: IPI00121785

Peptide sequence: NQLSTLPDELGDLPLVR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.34 SEQUEST DCn score: 0.594

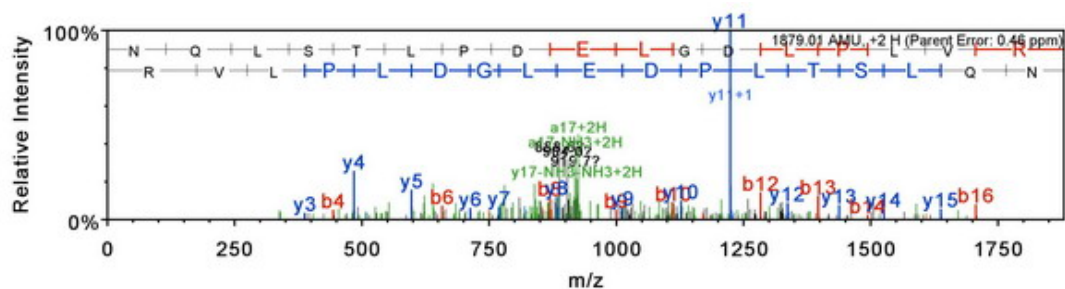
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 940.5109

Actual minus calculated peptide mass (AMU): 0.0008545



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1880.0	940.5	1863.0	1862.0	17
2	243.1		226.1		Q	1766.0	883.5	1748.9	1748.0	16
3	356.2		339.2		L	1637.9	819.5	1620.9	1619.9	15
4	443.2		426.2	425.2	S	1524.8	762.9	1507.8	1506.8	14
5	544.3		527.3	526.3	T	1437.8	719.4	1420.8	1419.8	13
6	657.4	329.2	640.3	639.4	L	1336.8	668.9	1319.7	1318.7	12
7	754.4	377.7	737.4	736.4	P	1223.7	612.3	1206.6	1205.7	11
8	869.4	435.2	852.4	851.4	D	1126.6	563.8	1109.6	1108.6	10
9	998.5	499.7	981.5	980.5	E	1011.6	506.3	994.6	993.6	9
10	1111.6	556.3	1094.5	1093.5	L	882.5	441.8	865.5	864.5	8
11	1168.6	584.8	1151.6	1150.6	G	769.5	385.2	752.4	751.5	7
12	1283.6	642.3	1266.6	1265.6	D	712.4	356.7	695.4	694.4	6
13	1396.7	698.9	1379.7	1378.7	L	597.4		580.4		5
14	1493.8	747.4	1476.7	1475.7	P	484.3		467.3		4
15	1606.8	803.9	1589.8	1588.8	L	387.3		370.3		3
16	1705.9	853.5	1688.9	1687.9	V	274.2		257.2		2
17	1880.0	940.5	1863.0	1862.0	R	175.1		158.1		1

Gene symbol: Lrpap1

Protein name: Alpha-2-macroglobulin receptor-associated protein precursor

Protein accession numbers: IPI00469307

Peptide sequence: IQEYNVLLDTLSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.18 SEQUEST DCn score: 0.383

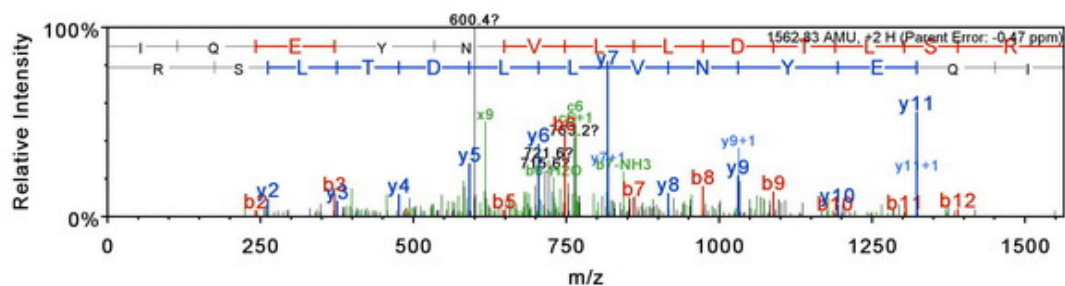
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 782.4228

Actual minus calculated peptide mass (AMU): -0.0007324



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1563.8	782.4	1546.8	1545.8	13
2	242.2		225.1		Q	1450.8	725.9	1433.7	1432.7	12
3	371.2		354.2	353.2	E	1322.7	661.9	1305.7	1304.7	11
4	534.3		517.2	516.3	Y	1193.7	597.3	1176.6	1175.6	10
5	648.3		631.3	630.3	N	1030.6	515.8	1013.6	1012.6	9
6	747.4	374.2	730.3	729.4	V	916.6	458.8	899.5	898.5	8
7	860.5	430.7	843.4	842.4	L	817.5	409.2	800.5	799.5	7
8	973.5	487.3	956.5	955.5	L	704.4	352.7	687.4	686.4	6
9	1088.6	544.8	1071.5	1070.5	D	591.3		574.3	573.3	5
10	1189.6	595.3	1172.6	1171.6	T	476.3		459.3	458.3	4
11	1302.7	651.9	1285.7	1284.7	L	375.2		358.2	357.2	3
12	1389.7	695.4	1372.7	1371.7	S	262.1		245.1	244.1	2
13	1563.8	782.4	1546.8	1545.8	R	175.1		158.1		1

Gene symbol: Lrrc57

Protein name: 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810002D13 product:hypothetical Leucine-rich repeat, typical subtype containing protein, full insert sequence

Protein accession numbers: IPI00323479,IPI00473453,IPI00623216

Peptide sequence: ELPSTFGQLSALK

Exclusive (unique to this protein): TRUE

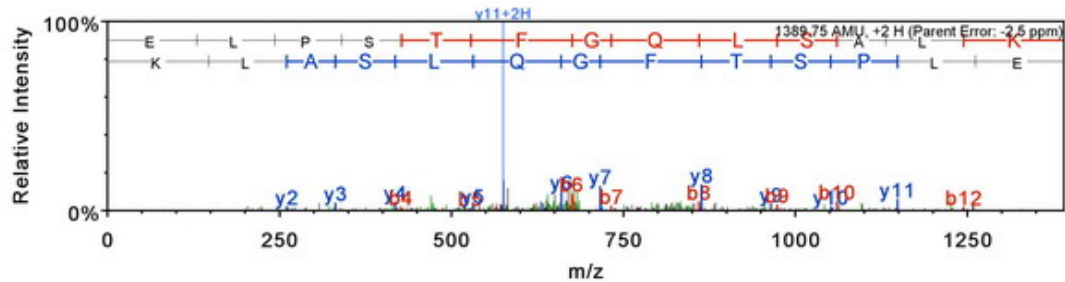
SEQUEST XCorr score: 3.1 SEQUEST DCn score: 0.56

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 695.8814

Actual minus calculated peptide mass (AMU): -0.003418



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1390.8	695.9	1373.7	1372.8	13
2	243.1			225.1	L	1261.7	631.4	1244.7	1243.7	12
3	340.2			322.2	P	1148.6	574.8	1131.6	1130.6	11
4	427.2			409.2	S	1051.6	526.3	1034.5	1033.6	10
5	528.3			510.3	T	964.6	482.8	947.5	946.5	9
6	675.3	338.2		657.3	F	863.5	432.3	846.5	845.5	8
7	732.4	366.7		714.4	G	716.4	358.7	699.4	698.4	7
8	860.4	430.7	843.4	842.4	Q	659.4	330.2	642.4	641.4	6
9	973.5	487.3	956.5	955.5	L	531.4		514.3	513.3	5
10	1060.5	530.8	1043.5	1042.5	S	418.3		401.2	400.3	4
11	1131.6	566.3	1114.5	1113.6	A	331.2		314.2		3
12	1244.7	622.8	1227.6	1226.6	L	260.2		243.2		2
13	1390.8	695.9	1373.7	1372.8	K	147.1		130.1		1

Gene symbol: Lypd4

Protein name: Ly6/PLAUR domain-containing protein 4 precursor

Protein accession numbers: IPI00225951

Peptide sequence: VTEVINVLDK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.79 SEQUEST DCn score: 0.548

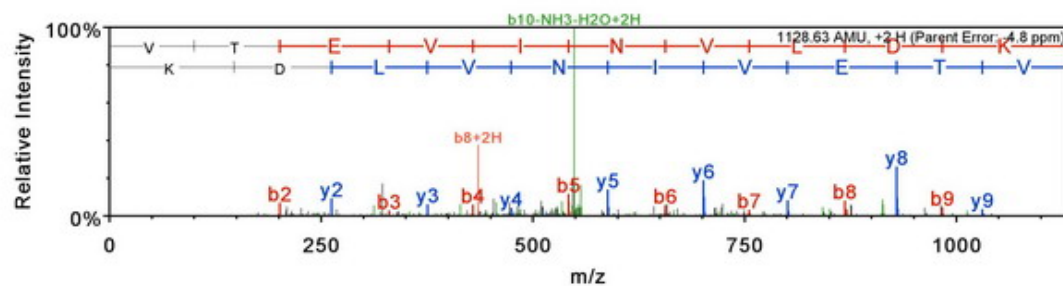
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 565.3247

Actual minus calculated peptide mass (AMU): -0.005371



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1129.7	565.3	1112.6	1111.6	10
2	201.1			183.1	T	1030.6	515.8	1013.6	1012.6	9
3	330.2			312.2	E	929.5	465.3	912.5	911.5	8
4	429.2			411.2	V	800.5	400.8	783.5	782.5	7
5	542.3			524.3	I	701.4	351.2	684.4	683.4	6
6	656.4	328.7	639.3	638.4	N	588.3		571.3	570.3	5
7	755.4	378.2	738.4	737.4	V	474.3		457.3	456.3	4
8	868.5	434.8	851.5	850.5	L	375.2		358.2	357.2	3
9	983.5	492.3	966.5	965.5	D	262.1		245.1	244.1	2
10	1129.7	565.3	1112.6	1111.6	K	147.1		130.1		1

Gene symbol: Lyz

Protein name: Lysozyme C type P precursor

Protein accession numbers: IPI00113427

Peptide sequence: STDYGIFQINSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.38 SEQUEST DCn score: 0.653

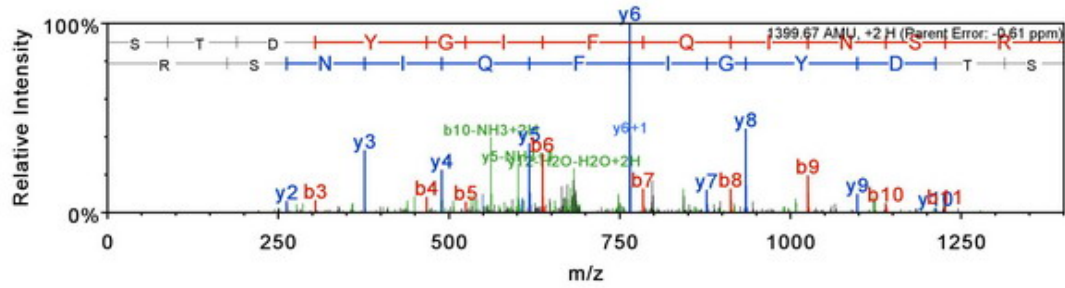
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 700.844

Actual minus calculated peptide mass (AMU): -0.0008545



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1400.7	700.8	1383.7	1382.7	12
2	189.1			171.1	T	1313.7	657.3	1296.6	1295.6	11
3	304.1			286.1	D	1212.6	606.8	1195.6	1194.6	10
4	467.2			449.2	Y	1097.6	549.3	1080.5	1079.6	9
5	524.2			506.2	G	934.5	467.8	917.5	916.5	8
6	637.3	319.2		619.3	I	877.5	439.3	860.5	859.5	7
7	784.4	392.7		766.3	F	764.4	382.7	747.4	746.4	6
8	912.4	456.7	895.4	894.4	Q	617.3		600.3	599.3	5
9	1025.5	513.3	1008.5	1007.5	I	489.3		472.3	471.3	4
10	1139.5	570.3	1122.5	1121.5	N	376.2		359.2	358.2	3
11	1226.6	613.8	1209.5	1208.6	S	262.1		245.1	244.1	2
12	1400.7	700.8	1383.7	1382.7	R	175.1		158.1		1

Gene symbol: Maea

Protein name: Isoform 1 of Macrophage erythroblast attacher

Protein accession numbers: IPI00122269,IPI00845788

Peptide sequence: IQEFIELVR

Exclusive (unique to this protein): TRUE

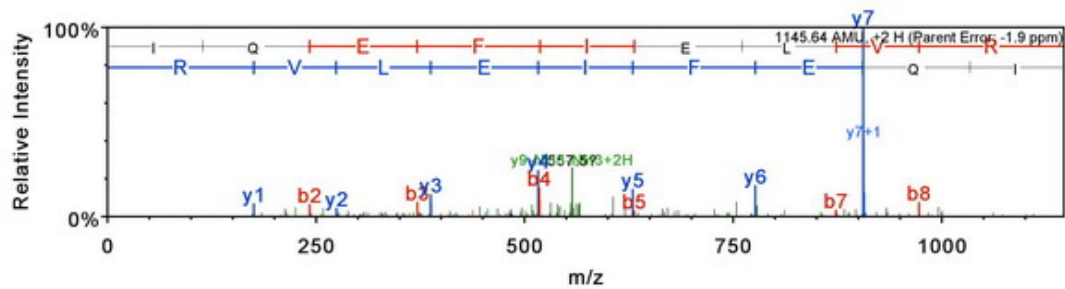
SEQUEST XCorr score: 2.8 SEQUEST DCn score: 0.467

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 573.829

Actual minus calculated peptide mass (AMU): -0.0021955



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1146.7	573.8	1129.6	1128.6	9
2	242.2		225.1		Q	1033.6	517.3	1016.5	1015.6	8
3	371.2		354.2	353.2	E	905.5	453.3	888.5	887.5	7
4	518.3		501.2	500.3	F	776.5	388.7	759.4	758.5	6
5	631.4		614.3	613.3	I	629.4		612.4	611.4	5
6	760.4	380.7	743.4	742.4	E	516.3		499.3	498.3	4
7	873.5	437.2	856.5	855.5	L	387.3		370.3		3
8	972.5	486.8	955.5	954.5	V	274.2		257.2		2
9	1146.7	573.8	1129.6	1128.6	R	175.1		158.1		1

Gene symbol: Mbd3

Protein name: Isoform 1 of Methyl-CpG-binding domain protein 3

Protein accession numbers: IPI00131067,IPI00466458,IPI00830772,IPI00830957

Peptide sequence: LSGLSAFDIAEELVR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.03 SEQUEST DCn score: 0.567

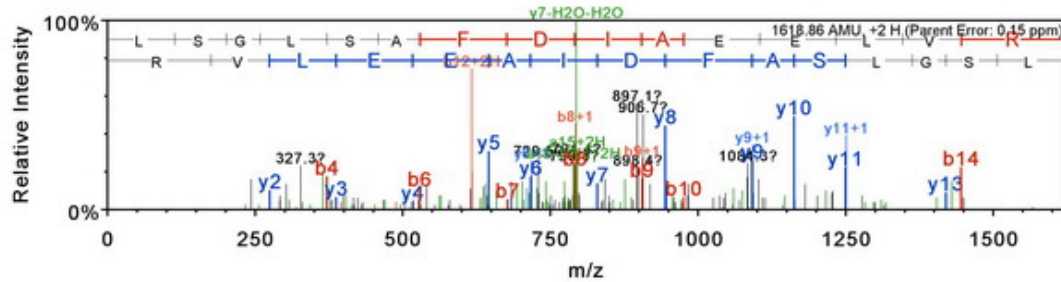
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 810.4363

Actual minus calculated peptide mass (AMU): 0.0002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1619.9	810.4	1602.8	1601.9	15
2	201.1			183.1	S	1506.8	753.9	1489.8	1488.8	14
3	258.1			240.1	G	1419.8	710.4	1402.7	1401.7	13
4	371.2			353.2	L	1362.7	681.9	1345.7	1344.7	12
5	458.3			440.3	S	1249.6	625.3	1232.6	1231.6	11
6	529.3	265.1		511.3	A	1162.6	581.8	1145.6	1144.6	10
7	676.4	338.7		658.4	F	1091.6	546.3	1074.5	1073.6	9
8	791.4	396.2		773.4	D	944.5	472.8	927.5	926.5	8
9	904.5	452.7		886.5	I	829.5	415.2	812.5	811.5	7
10	975.5	488.3		957.5	A	716.4	358.7	699.4	698.4	6
11	1104.6	552.8		1086.5	E	645.4		628.3	627.4	5
12	1233.6	617.3		1215.6	E	516.3		499.3	498.3	4
13	1346.7	673.9		1328.7	L	387.3		370.3		3
14	1445.8	723.4		1427.7	V	274.2		257.2		2
15	1619.9	810.4	1602.8	1601.9	R	175.1		158.1		1

Gene symbol: Mcm2

Protein name: CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730064M13 product:minichromosome maintenance deficient 2 mitotin (*S. cerevisiae*), full insert sequence

Protein accession numbers: IPI00323820

Peptide sequence: ESLVVNYEDLAAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.12 SEQUEST DCn score: 0.511

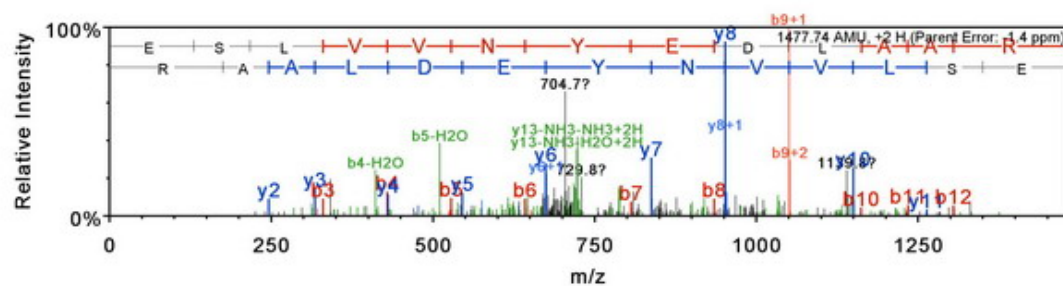
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 739.8774

Actual minus calculated peptide mass (AMU): -0.002075



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1478.8	739.9	1461.7	1460.7	13
2	217.1			199.1	S	1349.7	675.4	1332.7	1331.7	12
3	330.2			312.2	L	1262.7	631.8	1245.7	1244.7	11
4	429.2			411.2	V	1149.6	575.3	1132.6	1131.6	10
5	528.3			510.3	V	1050.5	525.8	1033.5	1032.5	9
6	642.4	321.7	625.3	624.3	N	951.5	476.2	934.4	933.4	8
7	805.4	403.2	788.4	787.4	Y	837.4	419.2	820.4	819.4	7
8	934.5	467.7	917.4	916.4	E	674.4	337.7	657.3	656.3	6
9	1049.5	525.2	1032.5	1031.5	D	545.3		528.3	527.3	5
10	1162.6	581.8	1145.5	1144.5	L	430.3		413.3		4
11	1233.6	617.3	1216.6	1215.6	A	317.2		300.2		3
12	1304.6	652.8	1287.6	1286.6	A	246.2		229.1		2
13	1478.8	739.9	1461.7	1460.7	R	175.1		158.1		1

Gene symbol: Mcm3

Protein name: DNA replication licensing factor MCM3

Protein accession numbers: IPI00108338

Peptide sequence: LLNNAFEELVAFQR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.82 SEQUEST DCn score: 0.607

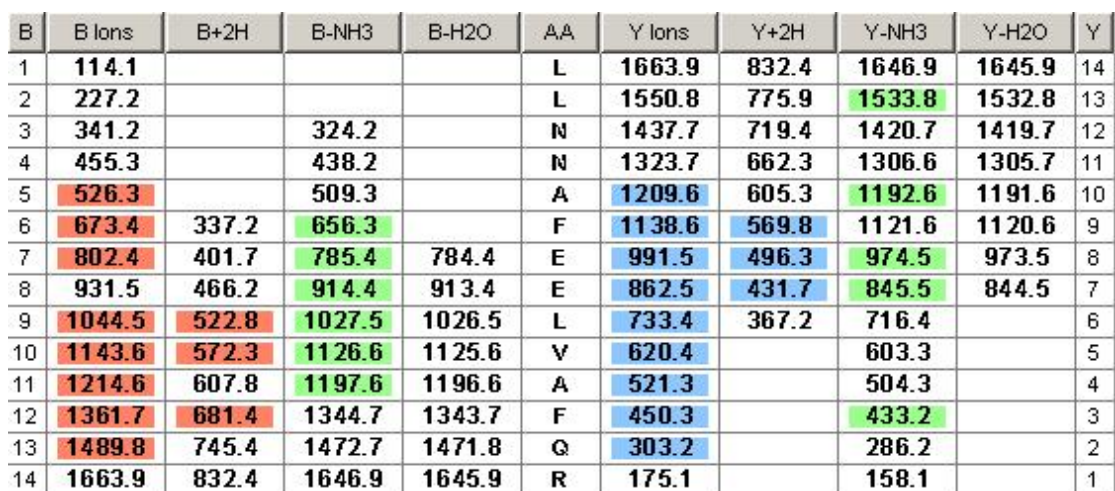
Fix modifications: None

Variable modifications: None

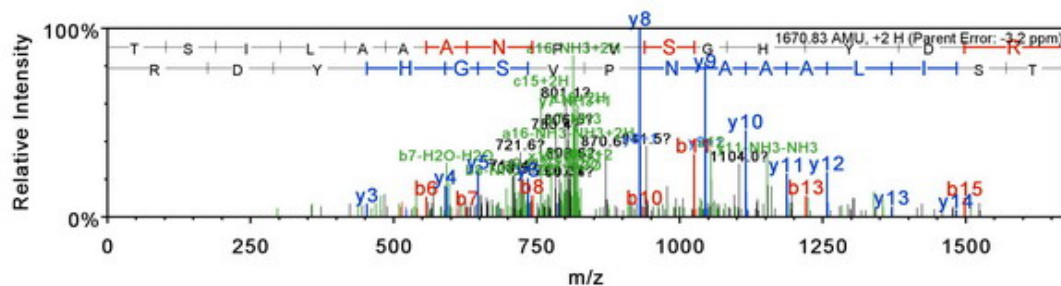
Charge: 2

Observed m/z: 832.4463

Actual minus calculated peptide mass (AMU): 0.00415



Actual minus calculated peptide mass (AMU): -0.005371



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1671.9	836.4	1654.8	1653.8	16
2	189.1			171.1	S	1570.8	785.9	1553.8	1552.8	15
3	302.2			284.2	I	1483.8	742.4	1466.7	1465.8	14
4	415.3			397.3	L	1370.7	685.8	1353.7	1352.7	13
5	486.3			468.3	A	1257.6	629.3	1240.6	1239.6	12
6	557.3	279.2		539.3	A	1186.6	593.8	1169.5	1168.5	11
7	628.4	314.7		610.4	A	1115.5	558.3	1098.5	1097.5	10
8	742.4	371.7	725.4	724.4	N	1044.5	522.8	1027.5	1026.5	9
9	839.5	420.2	822.4	821.5	P	930.4	465.7	913.4	912.4	8
10	938.5	469.8	921.5	920.5	V	833.4	417.2	816.4	815.4	7
11	1025.6	513.3	1008.5	1007.6	S	734.3	367.7	717.3	716.3	6
12	1082.6	541.8	1065.6	1064.6	G	647.3	324.2	630.3	629.3	5
13	1219.6	610.3	1202.6	1201.6	H	590.3	295.6	573.2	572.3	4
14	1382.7	691.9	1365.7	1364.7	Y	453.2		436.2	435.2	3
15	1497.7	749.4	1480.7	1479.7	D	290.2		273.1	272.1	2
16	1671.9	836.4	1654.8	1653.8	R	175.1		158.1		1

Gene symbol: Mcts2

Protein name: ES cells cDNA, RIKEN full-length enriched library, clone:2400002F11
product: MULTIPLE COPIES IN A T-CELL MALIGNANCIES

Protein accession numbers: IPI00131888

Peptide sequence: FVLSGANIMCPGLTSPGAK

Exclusive (unique to this protein): TRUE

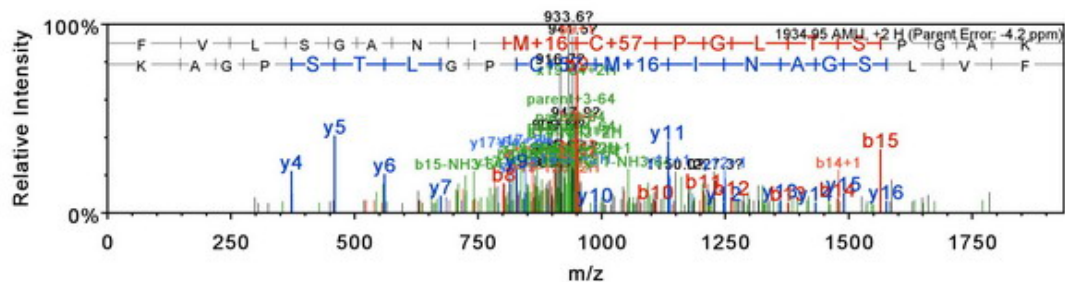
SEQUEST XCorr score: 3.15 SEQUEST DCn score: 0.495

Fix modifications: C10: Carbamidomethyl (+57.02)

Variable modifications: M9: Oxidation (+16.00)

Charge: 2 Observed m/z: 968.4836

Actual minus calculated peptide mass (AMU): -0.008057



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1936.0	968.5	1918.9	1918.0	19
2	247.1				V	1788.9	895.0	1771.9	1770.9	18
3	360.2				L	1689.8	845.4	1672.8	1671.8	17
4	447.3			429.3	S	1576.8	788.9	1559.7	1558.7	16
5	504.3			486.3	G	1489.7	745.4	1472.7	1471.7	15
6	575.3	288.2		557.3	A	1432.7	716.9	1415.7	1414.7	14
7	689.4	345.2	672.3	671.4	N	1361.7	681.3	1344.6	1343.7	13
8	802.5	401.7	785.4	784.4	I	1247.6	624.3	1230.6	1229.6	12
9	949.5	475.2	932.5	931.5	M+16	1134.5	567.8	1117.5	1116.5	11
10	1109.5	555.3	1092.5	1091.5	C+57	987.5	494.3	970.5	969.5	10
11	1206.6	603.8	1189.5	1188.5	P	827.5	414.2	810.4	809.5	9
12	1263.6	632.3	1246.6	1245.6	G	730.4	365.7	713.4	712.4	8
13	1376.7	688.8	1359.6	1358.7	L	673.4	337.2	656.4	655.4	7
14	1477.7	739.4	1460.7	1459.7	T	560.3	280.7	543.3	542.3	6
15	1564.8	782.9	1547.7	1546.7	S	459.3		442.2	441.3	5
16	1661.8	831.4	1644.8	1643.8	P	372.2		355.2		4
17	1718.8	859.9	1701.8	1700.8	G	275.2		258.1		3
18	1789.9	895.4	1772.8	1771.9	A	218.2		201.1		2
19	1936.0	968.5	1918.9	1918.0	K	147.1		130.1		1

Gene symbol: Mgea6

Protein name: Cutaneous T-cell lymphoma-associated antigen 5 homolog

Protein accession numbers: IPI00153633,IPI00654285

Peptide sequence: GPENLLDHQMNTER

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.69 SEQUEST DCn score: 0.475

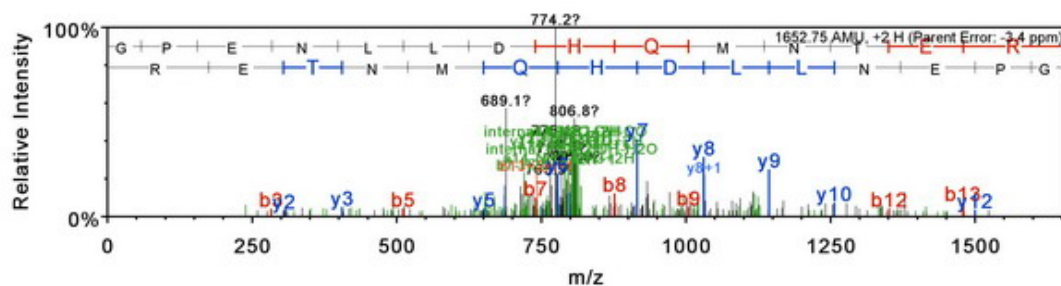
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 827.3839

Actual minus calculated peptide mass (AMU): -0.0056153



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1653.8	827.4	1636.7	1635.8	14
2	155.1				P	1596.7	798.9	1579.7	1578.7	13
3	284.1			266.1	E	1499.7	750.4	1482.7	1481.7	12
4	398.2		381.1	380.2	N	1370.7	685.8	1353.6	1352.6	11
5	511.3		494.2	493.2	L	1256.6	628.8	1239.6	1238.6	10
6	624.3	312.7	607.3	606.3	L	1143.5	572.3	1126.5	1125.5	9
7	739.4	370.2	722.3	721.4	D	1030.4	515.7	1013.4	1012.4	8
8	876.4	438.7	859.4	858.4	H	915.4	458.2	898.4	897.4	7
9	1004.5	502.7	987.5	986.5	Q	778.4	389.7	761.3	760.3	6
10	1135.5	568.3	1118.5	1117.5	M	650.3		633.3	632.3	5
11	1249.6	625.3	1232.5	1231.5	N	519.3		502.2	501.2	4
12	1350.6	675.8	1333.6	1332.6	T	405.2		388.2	387.2	3
13	1479.7	740.3	1462.6	1461.6	E	304.2		287.1	286.2	2
14	1653.8	827.4	1636.7	1635.8	R	175.1		158.1		1

Gene symbol: Mipep

Protein name: CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730088G21 product:mitochondrial intermediate peptidase, full insert sequence

Protein accession numbers: IPI00222838,IPI00753039,IPI00757068

Peptide sequence: ALQGTIAQTPETVMQFLEK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.96 SEQUEST DCn score: 0.481

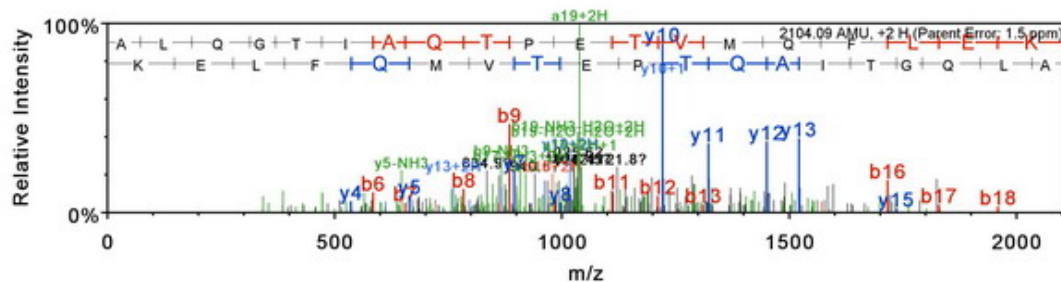
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1053.0532

Actual minus calculated peptide mass (AMU): 0.0031752



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2105.1	1053.0	2088.1	2087.1	19
2	185.1				L	2034.1	1017.5	2017.0	2016.1	18
3	313.2		296.2		Q	1921.0	961.0	1904.0	1903.0	17
4	370.2		353.2		G	1792.9	897.0	1775.9	1774.9	16
5	471.3		454.2	453.3	T	1735.9	868.5	1718.9	1717.9	15
6	584.3	292.7	567.3	566.3	I	1634.9	817.9	1617.8	1616.8	14
7	655.4	328.2	638.4	637.4	A	1521.8	761.4	1504.7	1503.8	13
8	783.4	392.2	766.4	765.4	Q	1450.7	725.9	1433.7	1432.7	12
9	884.5	442.8	867.5	866.5	T	1322.7	661.8	1305.6	1304.7	11
10	981.5	491.3	964.5	963.5	P	1221.6	611.3	1204.6	1203.6	10
11	1110.6	555.8	1093.5	1092.6	E	1124.6	562.8	1107.5	1106.6	9
12	1211.6	606.3	1194.6	1193.6	T	995.5	498.3	978.5	977.5	8
13	1310.7	655.9	1293.7	1292.7	V	894.5	447.7	877.5	876.5	7
14	1441.7	721.4	1424.7	1423.7	M	795.4	398.2	778.4	777.4	6
15	1569.8	785.4	1552.8	1551.8	Q	664.4		647.3	646.4	5
16	1716.9	858.9	1699.8	1698.9	F	536.3		519.3	518.3	4
17	1830.0	915.5	1812.9	1811.9	L	389.2		372.2	371.2	3
18	1959.0	980.0	1942.0	1941.0	E	276.2		259.1	258.1	2
19	2105.1	1053.0	2088.1	2087.1	K	147.1		130.1		1

Gene symbol: Morc3

Protein name: Microrchidia 3

Protein accession numbers: IPI00755119

Peptide sequence: SDPGITVSTQTDAPGLTVK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.65 SEQUEST DCn score: 0.596

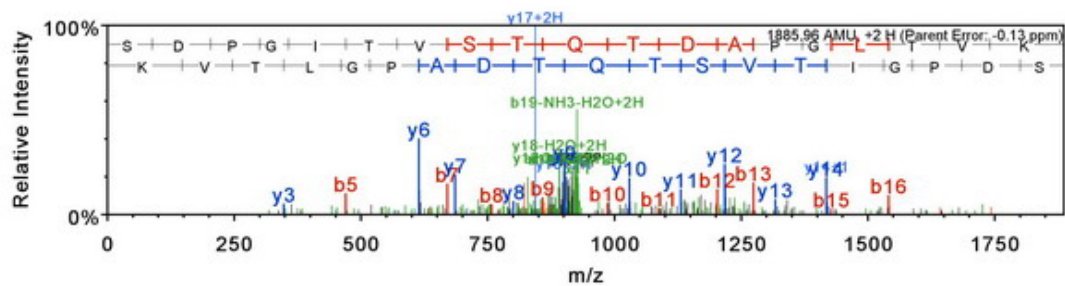
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 943.9896

Actual minus calculated peptide mass (AMU): -0.0002441



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1887.0	944.0	1869.9	1869.0	19
2	203.1			185.1	D	1799.9	900.5	1782.9	1781.9	18
3	300.1			282.1	P	1684.9	843.0	1667.9	1666.9	17
4	357.1			339.1	G	1587.9	794.4	1570.8	1569.9	16
5	470.2			452.2	I	1530.8	765.9	1513.8	1512.8	15
6	571.3	286.1		553.3	T	1417.8	709.4	1400.7	1399.7	14
7	670.3	335.7		652.3	V	1316.7	658.9	1299.7	1298.7	13
8	757.4	379.2		739.4	S	1217.6	609.3	1200.6	1199.6	12
9	858.4	429.7		840.4	T	1130.6	565.8	1113.6	1112.6	11
10	986.5	493.7	969.5	968.5	Q	1029.6	515.3	1012.5	1011.6	10
11	1087.5	544.3	1070.5	1069.5	T	901.5	451.3	884.5	883.5	9
12	1202.5	601.8	1185.5	1184.5	D	800.5	400.7	783.4	782.4	8
13	1273.6	637.3	1256.6	1255.6	A	685.4	343.2	668.4	667.4	7
14	1370.6	685.8	1353.6	1352.6	P	614.4	307.7	597.4	596.4	6
15	1427.7	714.3	1410.6	1409.7	G	517.3		500.3	499.3	5
16	1540.8	770.9	1523.7	1522.7	L	460.3		443.3	442.3	4
17	1641.8	821.4	1624.8	1623.8	T	347.2		330.2	329.2	3
18	1740.9	870.9	1723.8	1722.9	V	246.2		229.2		2
19	1887.0	944.0	1870.0	1869.0	K	147.1		130.1		1

Gene symbol: Mrpl19

Protein name: Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630024D24 product:mitochondrial ribosomal protein L19, full insert sequence

Protein accession numbers: IPI00135311

Peptide sequence: FLSPEFIPPR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.63 SEQUEST DCn score: 0.499

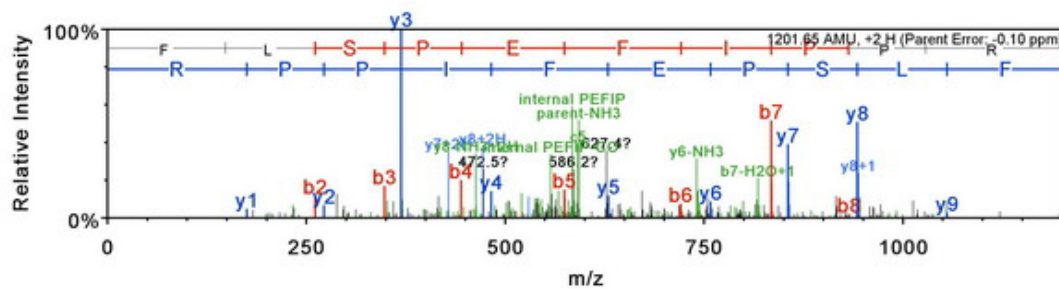
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 601.8326

Actual minus calculated peptide mass (AMU): -0.0001221



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1202.7	601.8	1185.6	1184.7	10
2	261.2				L	1055.6	528.3	1038.6	1037.6	9
3	348.2			330.2	S	942.5	471.8	925.5	924.5	8
4	445.3			427.2	P	855.5	428.2	838.5	837.5	7
5	574.3			556.3	E	758.4	379.7	741.4	740.4	6
6	721.4	361.2		703.4	F	629.4		612.4		5
7	834.4	417.7		816.4	I	482.3		465.3		4
8	931.5	466.3		913.5	P	369.2		352.2		3
9	1028.5	514.8		1010.5	P	272.2		255.2		2
10	1202.7	601.8	1185.6	1184.7	R	175.1		158.1		1

Gene symbol: Mrpl21

Protein name: Isoform 1 of 39S ribosomal protein L21, mitochondrial precursor

Protein accession numbers: IPI00133965

Peptide sequence: VNELIATGQYGR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.48 SEQUEST DCn score: 0.577

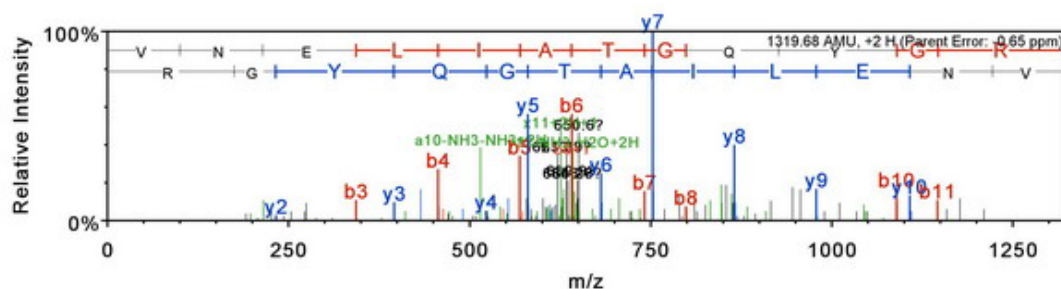
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 660.8491

Actual minus calculated peptide mass (AMU): -0.0008545



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1320.7	660.9	1303.7	1302.7	12
2	214.1		197.1		N	1221.6	611.3	1204.6	1203.6	11
3	343.2		326.1	325.2	E	1107.6	554.3	1090.5	1089.6	10
4	456.3		439.2	438.2	L	978.5	489.8	961.5	960.5	9
5	569.3		552.3	551.3	I	865.5	433.2	848.4	847.4	8
6	640.4	320.7	623.3	622.4	A	752.4	376.7	735.3	734.4	7
7	741.4	371.2	724.4	723.4	T	681.3	341.2	664.3	663.3	6
8	798.4	399.7	781.4	780.4	G	580.3		563.3		5
9	926.5	463.8	909.5	908.5	Q	523.3		506.2		4
10	1089.6	545.3	1072.5	1071.5	Y	395.2		378.2		3
11	1146.6	573.8	1129.5	1128.6	G	232.1		215.1		2
12	1320.7	660.9	1303.7	1302.7	R	175.1		158.1		1

Gene symbol: Mrpl24

Protein name: 39S ribosomal protein L24, mitochondrial precursor

Protein accession numbers: IPI00162769

Peptide sequence: NWVVLEGLNTHYR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.49 SEQUEST DCn score: 0.501

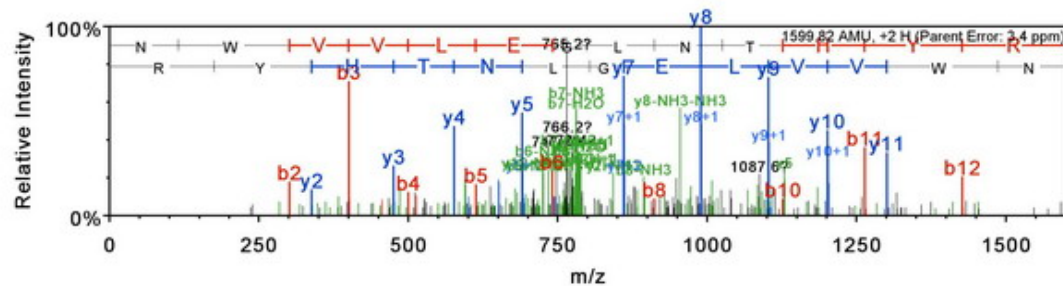
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 800.9184

Actual minus calculated peptide mass (AMU): 0.005371



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1600.8	800.9	1583.8	1582.8	13
2	301.1		284.1		W	1486.8	743.9	1469.8	1468.8	12
3	400.2		383.2		V	1300.7	650.9	1283.7	1282.7	11
4	499.3		482.2		V	1201.6	601.3	1184.6	1183.6	10
5	612.4		595.3		L	1102.6	551.8	1085.5	1084.5	9
6	741.4	371.2	724.4	723.4	E	989.5	495.2	972.5	971.5	8
7	798.4	399.7	781.4	780.4	G	860.4	430.7	843.4	842.4	7
8	911.5	456.3	894.5	893.5	L	803.4	402.2	786.4	785.4	6
9	1025.5	513.3	1008.5	1007.5	N	690.3	345.7	673.3	672.3	5
10	1126.6	563.8	1109.6	1108.6	T	576.3	288.7	559.3	558.3	4
11	1263.7	632.3	1246.6	1245.6	H	475.2	238.1	458.2		3
12	1426.7	713.9	1409.7	1408.7	Y	338.2		321.2		2
13	1600.8	800.9	1583.8	1582.8	R	175.1		158.1		1

Gene symbol: Mrpl47

Protein name: 39S ribosomal protein L47, mitochondrial precursor

Protein accession numbers: IPI00322422

Peptide sequence: NMLLTLEQEAQ

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.01 SEQUEST DCn score: 0.515

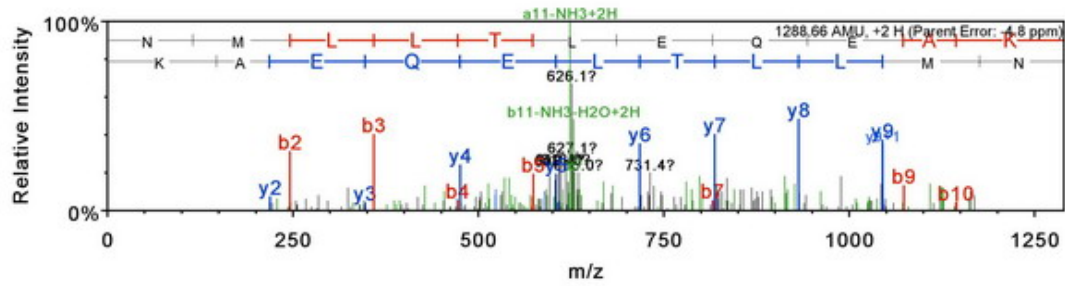
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 645.3397

Actual minus calculated peptide mass (AMU): -0.006226



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1289.7	645.3	1272.7	1271.7	11
2	246.1		229.1		M	1175.6	588.3	1158.6	1157.6	10
3	359.2		342.2		L	1044.6	522.8	1027.6	1026.6	9
4	472.3		455.2		L	931.5	466.3	914.5	913.5	8
5	573.3		556.3	555.3	T	818.4	409.7	801.4	800.4	7
6	686.4	343.7	669.4	668.4	L	717.4	359.2	700.4	699.4	6
7	815.4	408.2	798.4	797.4	E	604.3		587.3	586.3	5
8	943.5	472.3	926.5	925.5	Q	475.3		458.2	457.2	4
9	1072.5	536.8	1055.5	1054.5	E	347.2		330.2	329.2	3
10	1143.6	572.3	1126.5	1125.6	A	218.2		201.1		2
11	1289.7	645.3	1272.7	1271.7	K	147.1		130.1		1

Gene symbol: Mrpl49

Protein name: Mitochondrial 39S ribosomal protein L49

Protein accession numbers: IPI00131988

Peptide sequence: TPITQVNEVTGTLR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.59 SEQUEST DCn score: 0.526

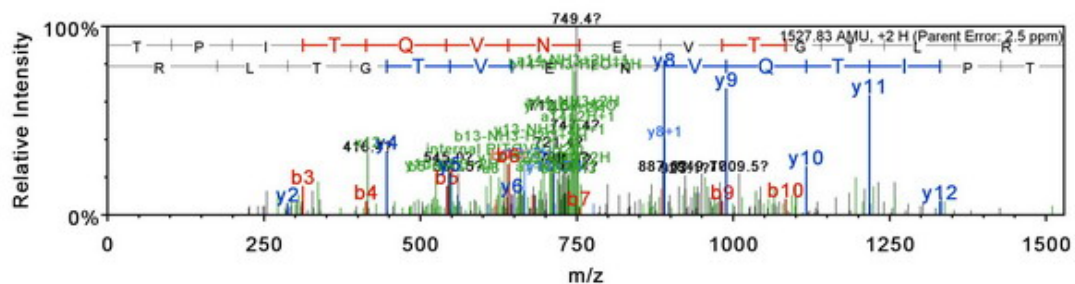
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 764.9227

Actual minus calculated peptide mass (AMU): 0.003784



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1528.8	764.9	1511.8	1510.8	14
2	199.1			181.1	P	1427.8	714.4	1410.8	1409.8	13
3	312.2			294.2	I	1330.7	665.9	1313.7	1312.7	12
4	413.2			395.2	T	1217.7	609.3	1200.6	1199.6	11
5	541.3		524.3	523.3	Q	1116.6	558.8	1099.6	1098.6	10
6	640.4	320.7	623.3	622.4	V	988.5	494.8	971.5	970.5	9
7	754.4	377.7	737.4	736.4	N	889.5	445.2	872.5	871.5	8
8	883.5	442.2	866.4	865.4	E	775.4	388.2	758.4	757.4	7
9	982.5	491.8	965.5	964.5	V	646.4	323.7	629.4	628.4	6
10	1083.6	542.3	1066.5	1065.6	T	547.3		530.3	529.3	5
11	1140.6	570.8	1123.6	1122.6	G	446.3		429.3	428.3	4
12	1241.6	621.3	1224.6	1223.6	T	389.3		372.2	371.2	3
13	1354.7	677.9	1337.7	1336.7	L	288.2		271.2		2
14	1528.8	764.9	1511.8	1510.8	R	175.1		158.1		1

Gene symbol: Mrps25

Protein name: Mitochondrial 28S ribosomal protein S25

Protein accession numbers: IPI00315671

Peptide sequence: IMTVNYNTYGE LGE GAR

Exclusive (unique to this protein): TRUE

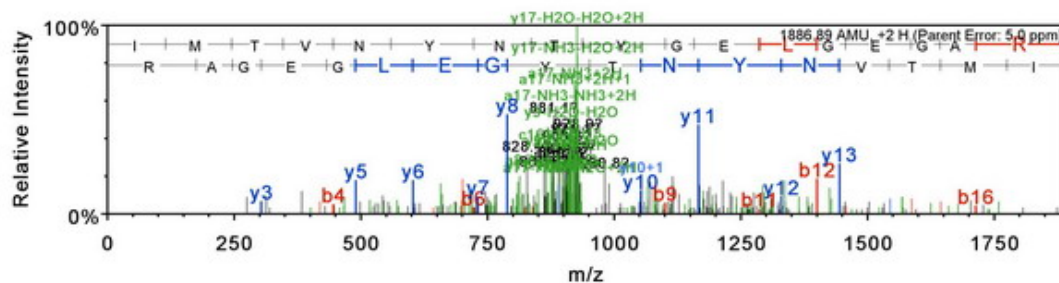
SEQUEST XCorr score: 2.72 SEQUEST DCn score: 0.478

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 944.4542

Actual minus calculated peptide mass (AMU): 0.009399



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1887.9	944.5	1870.9	1869.9	17
2	245.1				M	1774.8	887.9	1757.8	1756.8	16
3	346.2			328.2	T	1643.8	822.4	1626.7	1625.8	15
4	445.3			427.2	V	1542.7	771.9	1525.7	1524.7	14
5	559.3		542.3	541.3	N	1443.7	722.3	1426.6	1425.6	13
6	722.4	361.7	705.3	704.3	Y	1329.6	665.3	1312.6	1311.6	12
7	836.4	418.7	819.4	818.4	N	1166.5	583.8	1149.5	1148.5	11
8	937.5	469.2	920.4	919.4	T	1052.5	526.8	1035.5	1034.5	10
9	1100.5	550.8	1083.5	1082.5	Y	951.5	476.2	934.4	933.4	9
10	1157.5	579.3	1140.5	1139.5	G	788.4	394.7	771.4	770.4	8
11	1286.6	643.8	1269.5	1268.6	E	731.4	366.2	714.3	713.4	7
12	1399.7	700.3	1382.6	1381.7	L	602.3	301.7	585.3	584.3	6
13	1456.7	728.8	1439.7	1438.7	G	489.2		472.2	471.2	5
14	1585.7	793.4	1568.7	1567.7	E	432.2		415.2	414.2	4
15	1642.7	821.9	1625.7	1624.7	G	303.2		286.2		3
16	1713.8	857.4	1696.8	1695.8	A	246.2		229.1		2
17	1887.9	944.5	1870.9	1869.9	R	175.1		158.1		1

Gene symbol: Mrps9

Protein name: Mrps9 protein (Fragment)

Protein accession numbers: IPI00480261

Peptide sequence: LSDEDYAQFIR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.29 SEQUEST DCn score: 0.479

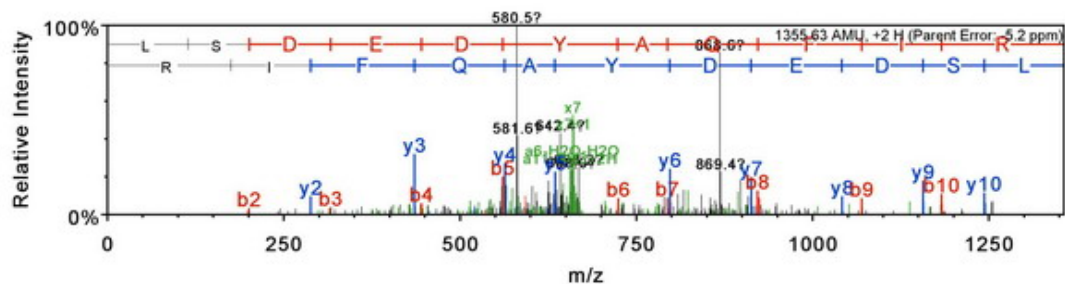
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 678.8222

Actual minus calculated peptide mass (AMU): -0.0070758



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1356.6	678.8	1339.6	1338.6	11
2	201.1			183.1	S	1243.6	622.3	1226.5	1225.5	10
3	316.2			298.1	D	1156.5	578.8	1139.5	1138.5	9
4	445.2			427.2	E	1041.5	521.3	1024.5	1023.5	8
5	560.2			542.2	D	912.5	456.7	895.4	894.5	7
6	723.3	362.2		705.3	Y	797.4	399.2	780.4		6
7	794.3	397.7		776.3	A	634.4		617.3		5
8	922.4	461.7	905.4	904.4	Q	563.3		546.3		4
9	1069.5	535.2	1052.4	1051.4	F	435.3		418.3		3
10	1182.5	591.8	1165.5	1164.5	I	288.2		271.2		2
11	1356.6	678.8	1339.6	1338.6	R	175.1		158.1		1

Gene symbol: Mta1

Protein name: Mta1 protein

Protein accession numbers: IPI00624969,IPI00776055,IPI00853911

Peptide sequence: VGDYVYFENSSSNPYLIR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.73 SEQUEST DCn score: 0.627

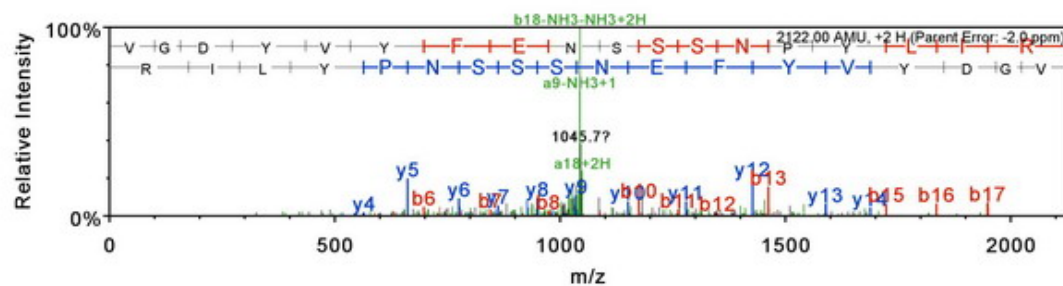
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1062.006

Actual minus calculated peptide mass (AMU): -0.00415



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	2123.0	1062.0	2106.0	2105.0	18
2	157.1				G	2023.9	1012.5	2006.9	2005.9	17
3	272.1			254.1	D	1966.9	984.0	1949.9	1948.9	16
4	435.2			417.2	Y	1851.9	926.5	1834.9	1833.9	15
5	534.3			516.3	V	1688.8	844.9	1671.8	1670.8	14
6	697.3	349.2		679.3	Y	1589.8	795.4	1572.7	1571.8	13
7	844.4	422.7		826.4	F	1426.7	713.9	1409.7	1408.7	12
8	973.4	487.2		955.4	E	1279.6	640.3	1262.6	1261.6	11
9	1087.5	544.2	1070.5	1069.5	N	1150.6	575.8	1133.6	1132.6	10
10	1174.5	587.8	1157.5	1156.5	S	1036.5	518.8	1019.5	1018.5	9
11	1261.5	631.3	1244.5	1243.5	S	949.5	475.3	932.5	931.5	8
12	1348.6	674.8	1331.5	1330.6	S	862.5	431.7	845.5	844.5	7
13	1462.6	731.8	1445.6	1444.6	N	775.5	388.2	758.4		6
14	1559.7	780.3	1542.6	1541.7	P	661.4		644.4		5
15	1722.7	861.9	1705.7	1704.7	Y	564.4		547.3		4
16	1835.8	918.4	1818.8	1817.8	L	401.3		384.3		3
17	1948.9	975.0	1931.9	1930.9	I	288.2		271.2		2
18	2123.0	1062.0	2106.0	2105.0	R	175.1		158.1		1

Gene symbol: Mtap7

Protein name: Isoform 2 of Ensconsin

Protein accession numbers: IPI00380510

Peptide sequence: LSSSATLLNSPDR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.96 SEQUEST DCn score: 0.605

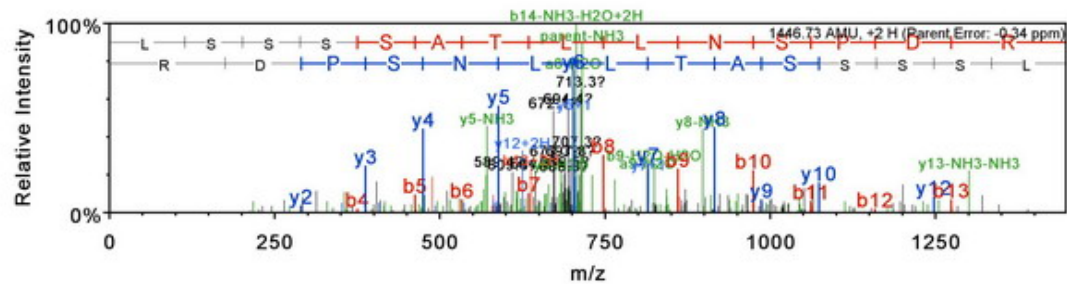
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 724.3733

Actual minus calculated peptide mass (AMU): -0.0004883



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1447.7	724.4	1430.7	1429.7	14
2	201.1			183.1	S	1334.7	667.8	1317.6	1316.6	13
3	288.2			270.1	S	1247.6	624.3	1230.6	1229.6	12
4	375.2			357.2	S	1160.6	580.8	1143.6	1142.6	11
5	462.2			444.2	S	1073.6	537.3	1056.5	1055.5	10
6	533.3	267.1		515.3	A	986.5	493.8	969.5	968.5	9
7	634.3	317.7		616.3	T	915.5	458.3	898.5	897.5	8
8	747.4	374.2		729.4	L	814.4	407.7	797.4	796.4	7
9	860.5	430.7		842.5	L	701.4	351.2	684.3	683.4	6
10	974.5	487.8	957.5	956.5	N	588.3		571.3	570.3	5
11	1061.5	531.3	1044.5	1043.5	S	474.2		457.2	456.2	4
12	1158.6	579.8	1141.6	1140.6	P	387.2		370.2	369.2	3
13	1273.6	637.3	1256.6	1255.6	D	290.2		273.1	272.1	2
14	1447.7	724.4	1430.7	1429.7	R	175.1		158.1		1

Gene symbol: mt-Atp8

Protein name: ATP synthase protein 8

Protein accession numbers: IPI00116896

Peptide sequence: IYLPHSLPQQ

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.58 SEQUEST DCn score: 0.469

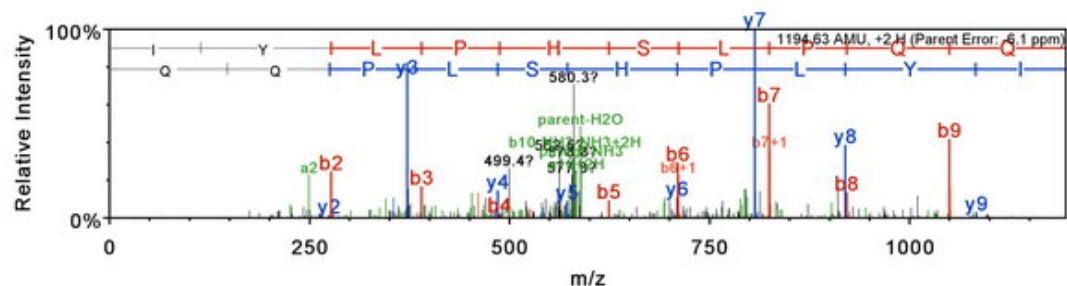
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 598.3241

Actual minus calculated peptide mass (AMU): -0.007324



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1195.7	598.3	1178.6	1177.6	10
2	277.2				Y	1082.6	541.8	1065.5	1064.5	9
3	390.2				L	919.5	460.3	902.5	901.5	8
4	487.3				P	806.4	403.7	789.4	788.4	7
5	624.4	312.7			H	709.4	355.2	692.3	691.4	6
6	711.4	356.2		693.4	S	572.3		555.3	554.3	5
7	824.5	412.7		806.5	L	485.3		468.3		4
8	921.5	461.3		903.5	P	372.2		355.2		3
9	1049.6	525.3	1032.5	1031.6	Q	275.1		258.1		2
10	1195.7	598.3	1178.6	1177.6	Q	147.1		130.1		1

Gene symbol: Mtx1

Protein name: Metaxin-1

Protein accession numbers: IPI00112327

Peptide sequence: QGADTLAFMSLLEEK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.5 SEQUEST DCn score: 0.574

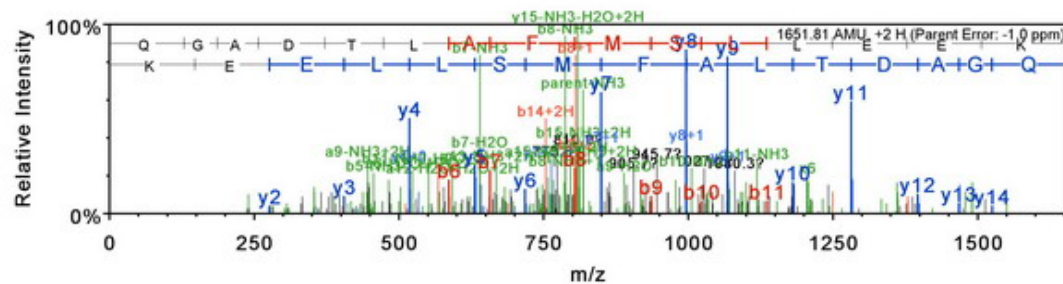
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 826.9134

Actual minus calculated peptide mass (AMU): -0.001709



Gene symbol: Myh7b

Protein name: Novel protein

Protein accession numbers: IPI00755200

Peptide sequence: HSHEEALEALET LKR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.52 SEQUEST DCn score: 0.473

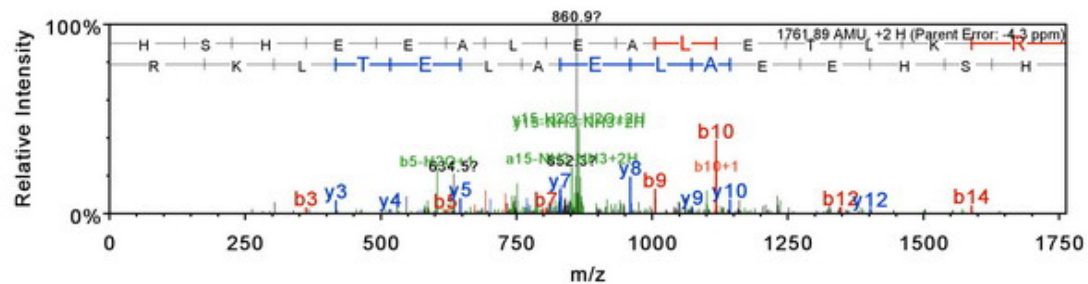
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 881.9546

Actual minus calculated peptide mass (AMU): -0.007568



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	138.1	69.5			H	1762.9	882.0	1745.9	1744.9	15
2	225.1	113.1		207.1	S	1625.9	813.4	1608.8	1607.8	14
3	362.2	181.6		344.2	H	1538.8	769.9	1521.8	1520.8	13
4	491.2	246.1		473.2	E	1401.8	701.4	1384.7	1383.8	12
5	620.2	310.6		602.2	E	1272.7	636.9	1255.7	1254.7	11
6	691.3	346.1		673.3	A	1143.7	572.3	1126.7	1125.7	10
7	804.4	402.7		786.4	L	1072.6	536.8	1055.6	1054.6	9
8	933.4	467.2		915.4	E	959.6	480.3	942.5	941.5	8
9	1004.4	502.7		986.4	A	830.5	415.8	813.5	812.5	7
10	1117.5	559.3		1099.5	L	759.5	380.2	742.5	741.5	6
11	1246.6	623.8		1228.6	E	646.4	323.7	629.4	628.4	5
12	1347.6	674.3		1329.6	T	517.4	259.2	500.3	499.3	4
13	1460.7	730.9		1442.7	L	416.3	208.7	399.3		3
14	1588.8	794.9	1571.8	1570.8	K	303.2	152.1	286.2		2
15	1762.9	882.0	1745.9	1744.9	R	175.1		158.1		1

Gene symbol: Myh9

Protein name: Myosin-9

Protein accession numbers: IPI00123181,IPI00788324

Peptide sequence: AGVLAHLEEER

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 3 SEQUEST DCn score: 0.515

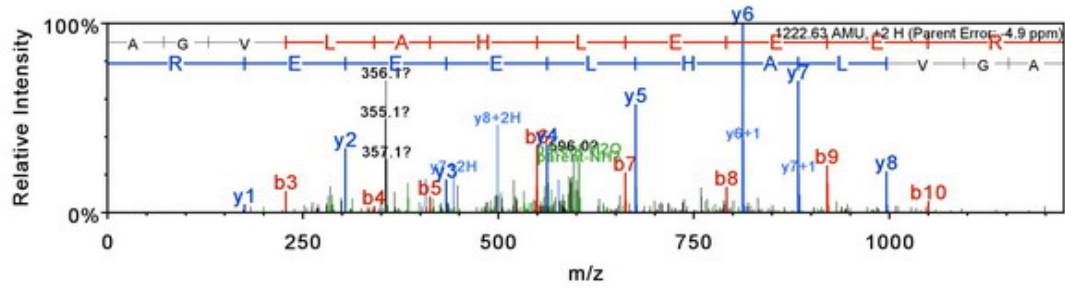
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 612.3202

Actual minus calculated peptide mass (AMU): -0.005949



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1223.6	612.3	1206.6	1205.6	11
2	129.1				G	1152.6	576.8	1135.6	1134.6	10
3	228.1				V	1095.6	548.3	1078.5	1077.6	9
4	341.2				L	996.5	498.8	979.5	978.5	8
5	412.3				A	883.4	442.2	866.4	865.4	7
6	549.3	275.2			H	812.4	406.7	795.4	794.4	6
7	662.4	331.7			L	675.3		658.3	657.3	5
8	791.4	396.2		773.4	E	562.3		545.2	544.2	4
9	920.5	460.8		902.5	E	433.2		416.2	415.2	3
10	1049.5	525.3		1031.5	E	304.2		287.1	286.2	2
11	1223.6	612.3	1206.6	1205.6	R	175.1		158.1		1

Peptide sequence: RHEMPPHIYAITDTAYR

Exclusive (unique to this protein): TRUE

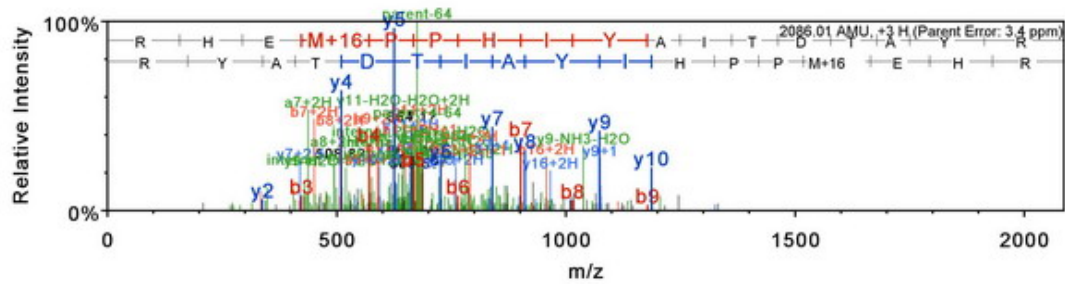
SEQUEST XCorr score: 3.55 SEQUEST DCn score: 0.428

Fix modifications: None

Variable modifications: M4: Oxidation (+16.00)

Charge: 3 Observed m/z: 696.3453

Actual minus calculated peptide mass (AMU): 0.0070758



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	157.1	79.1	140.1		R	2087.0	1044.0	2070.0	2069.0	17
2	294.2	147.6	277.1		H	1930.9	966.0	1913.9	1912.9	16
3	423.2	212.1	406.2	405.2	E	1793.9	897.4	1776.8	1775.8	15
4	570.3	285.6	553.2	552.2	M+16	1664.8	832.9	1647.8	1646.8	14
5	667.3	334.2	650.3	649.3	P	1517.8	759.4	1500.8	1499.8	13
6	764.4	382.7	747.3	746.3	P	1420.7	710.9	1403.7	1402.7	12
7	901.4	451.2	884.4	883.4	H	1323.7	662.3	1306.6	1305.7	11
8	1014.5	507.8	997.5	996.5	I	1186.6	593.8	1169.6	1168.6	10
9	1177.6	589.3	1160.5	1159.5	Y	1073.5	537.3	1056.5	1055.5	9
10	1248.6	624.8	1231.6	1230.6	A	910.5	455.7	893.4	892.5	8
11	1361.7	681.3	1344.7	1343.7	I	839.4	420.2	822.4	821.4	7
12	1462.7	731.9	1445.7	1444.7	T	726.3	363.7	709.3	708.3	6
13	1577.8	789.4	1560.7	1559.7	D	625.3		608.3	607.3	5
14	1678.8	839.9	1661.8	1660.8	T	510.3		493.2	492.3	4
15	1749.8	875.4	1732.8	1731.8	A	409.2		392.2		3
16	1912.9	957.0	1895.9	1894.9	Y	338.2		321.2		2
17	2087.0	1044.0	2070.0	2069.0	R	175.1		158.1		1

Peptide sequence: TQLEELEDELQATEDAK

Exclusive (unique to this protein): FALSE

SEQUEST XCorr score: 6.55 SEQUEST DCn score: 0.66

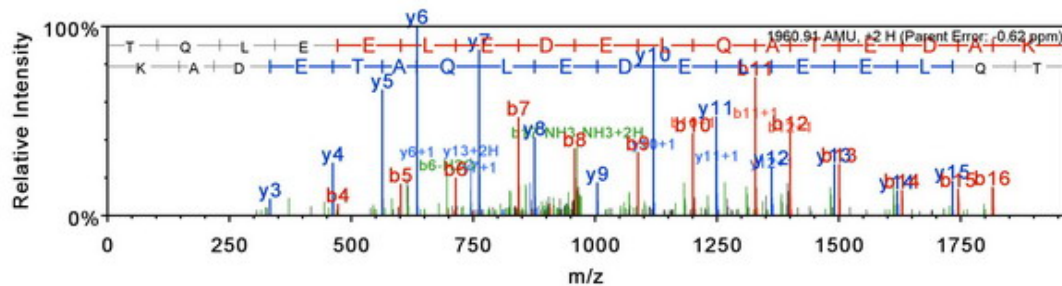
Fix modifications: None

Variable modifications: None

Charge: 2

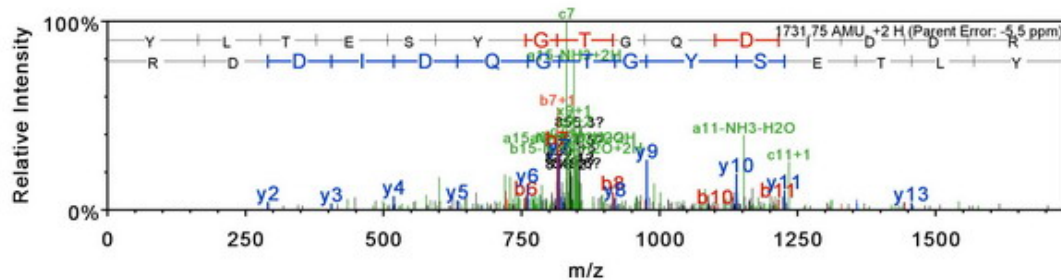
Observed m/z: 981.4631

Actual minus calculated peptide mass (AMU): -0.0012249



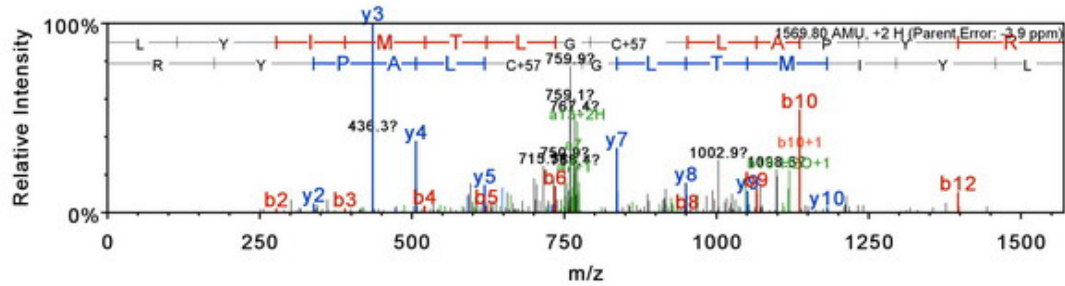
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	1961.9	981.5	1944.9	1943.9	17
2	230.1		213.1	212.1	Q	1860.9	930.9	1843.9	1842.9	16
3	343.2		326.2	325.2	L	1732.8	866.9	1715.8	1714.8	15
4	472.2		455.2	454.2	E	1619.7	810.4	1602.7	1601.7	14
5	601.3		584.3	583.3	E	1490.7	745.9	1473.7	1472.7	13
6	714.4	357.7	697.3	696.4	L	1361.6	681.3	1344.6	1343.6	12
7	843.4	422.2	826.4	825.4	E	1248.6	624.8	1231.5	1230.5	11
8	958.4	479.7	941.4	940.4	D	1119.5	560.3	1102.5	1101.5	10
9	1087.5	544.2	1070.5	1069.5	E	1004.5	502.8	987.5	986.5	9
10	1200.6	600.8	1183.5	1182.5	L	875.5	438.2	858.4	857.4	8
11	1328.6	664.8	1311.6	1310.6	Q	762.4	381.7	745.3	744.4	7
12	1399.7	700.3	1382.6	1381.7	A	634.3	317.7	617.3	616.3	6
13	1500.7	750.9	1483.7	1482.7	T	563.3		546.2	545.3	5
14	1629.8	815.4	1612.7	1611.7	E	462.2		445.2	444.2	4
15	1744.8	872.9	1727.8	1726.8	D	333.2		316.2	315.2	3
16	1815.8	908.4	1798.8	1797.8	A	218.2		201.1		2
17	1961.9	981.5	1944.9	1943.9	K	147.1		130.1		1

Gene symbol: Myo6
Protein name: MKIAA0389 protein
Protein accession numbers: IPI00462752,IPI00776145
Peptide sequence: YLTESYGTGQDIDDR
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 2.85 SEQUEST DCn score: 0.601
Fix modifications: None
Variable modifications: None
Charge: 2 Observed m/z: 866.8826
Actual minus calculated peptide mass (AMU): -0.009522



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	164.1				Y	1732.8	866.9	1715.7	1714.8	15
2	277.2				L	1569.7	785.4	1552.7	1551.7	14
3	378.2			360.2	T	1456.6	728.8	1439.6	1438.6	13
4	507.3			489.2	E	1355.6	678.3	1338.5	1337.6	12
5	594.3			576.3	S	1226.5	613.8	1209.5	1208.5	11
6	757.3	379.2		739.3	Y	1139.5	570.3	1122.5	1121.5	10
7	814.4	407.7		796.4	G	976.4	488.7	959.4	958.4	9
8	915.4	458.2		897.4	T	919.4	460.2	902.4	901.4	8
9	972.4	486.7		954.4	G	818.4	409.7	801.3	800.4	7
10	1100.5	550.8	1083.5	1082.5	Q	761.3	381.2	744.3	743.3	6
11	1215.5	608.3	1198.5	1197.5	D	633.3		616.3	615.3	5
12	1328.6	664.8	1311.6	1310.6	I	518.3		501.2	500.3	4
13	1443.6	722.3	1426.6	1425.6	D	405.2		388.2	387.2	3
14	1558.7	779.8	1541.6	1540.6	D	290.2		273.1	272.1	2
15	1732.8	866.9	1715.7	1714.8	R	175.1		158.1		1

Gene symbol: Nat13
Protein name: Isoform 5 of N-acetyltransferase NAT13
Protein accession numbers: IPI00845580
Peptide sequence: LYIMTLGCLAPYR
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 2.67 SEQUEST DCn score: 0.545
Fix modifications: C8: Carbamidomethyl (+57.02)
Variable modifications: None
Charge: 2 Observed m/z: 785.9073
Actual minus calculated peptide mass (AMU): -0.006104



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1570.8	785.9	1553.8	1552.8	13
2	277.2				Y	1457.7	729.4	1440.7	1439.7	12
3	390.2				I	1294.7	647.8	1277.6	1276.7	11
4	521.3				M	1181.6	591.3	1164.5	1163.6	10
5	622.3			604.3	T	1050.5	525.8	1033.5	1032.5	9
6	735.4	368.2		717.4	L	949.5	475.3	932.5		8
7	792.4	396.7		774.4	G	836.4	418.7	819.4		7
8	952.5	476.7		934.5	C+57	779.4	390.2	762.4		6
9	1065.5	533.3		1047.5	L	619.4		602.3		5
10	1136.6	568.8		1118.6	A	506.3		489.3		4
11	1233.6	617.3		1215.6	P	435.2		418.2		3
12	1396.7	698.9		1378.7	Y	338.2		321.2		2
13	1570.8	785.9	1553.8	1552.8	R	175.1		158.1		1

Gene symbol: Nbr1

Protein name: Neighbor of Brca1 gene 1

Protein accession numbers: IPI00648777

Peptide sequence: GAEGEPGIESGLEPTEAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.99 SEQUEST DCn score: 0.493

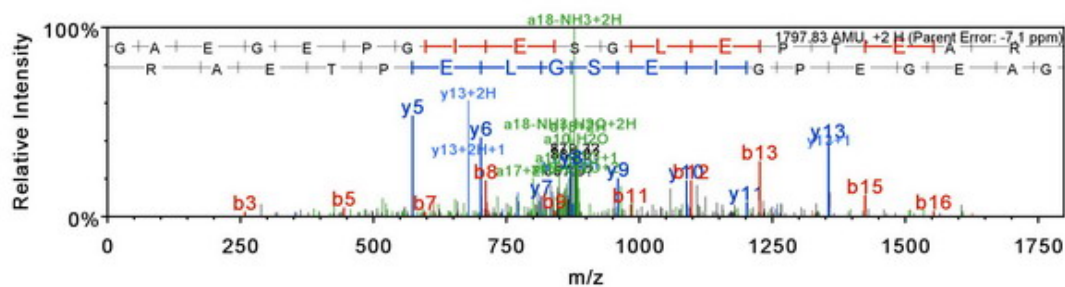
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 899.9206

Actual minus calculated peptide mass (AMU): -0.0127



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1798.9	899.9	1781.8	1780.8	18
2	129.1				A	1741.8	871.4	1724.8	1723.8	17
3	258.1			240.1	E	1670.8	835.9	1653.8	1652.8	16
4	315.1			297.1	G	1541.7	771.4	1524.7	1523.7	15
5	444.2			426.2	E	1484.7	742.9	1467.7	1466.7	14
6	541.2	271.1		523.2	P	1355.7	678.3	1338.7	1337.7	13
7	598.3	299.6		580.2	G	1258.6	629.8	1241.6	1240.6	12
8	711.3	356.2		693.3	I	1201.6	601.3	1184.6	1183.6	11
9	840.4	420.7		822.4	E	1088.5	544.8	1071.5	1070.5	10
10	927.4	464.2		909.4	S	959.5	480.2	942.5	941.5	9
11	984.4	492.7		966.4	G	872.5	436.7	855.4	854.4	8
12	1097.5	549.3		1079.5	L	815.4	408.2	798.4	797.4	7
13	1226.5	613.8		1208.5	E	702.3	351.7	685.3	684.3	6
14	1323.6	662.3		1305.6	P	573.3		556.3	555.3	5
15	1424.7	712.8		1406.6	T	476.3		459.2	458.2	4
16	1553.7	777.4		1535.7	E	375.2		358.2	357.2	3
17	1624.7	812.9		1606.7	A	246.2		229.1		2
18	1798.9	899.9	1781.8	1780.8	R	175.1		158.1		1

Gene symbol: Ndufa12

Protein name: NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 12

Protein accession numbers: IPI00344004

Peptide sequence: FNVSATPEQYVPYSTTR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.88 SEQUEST DCn score: 0.649

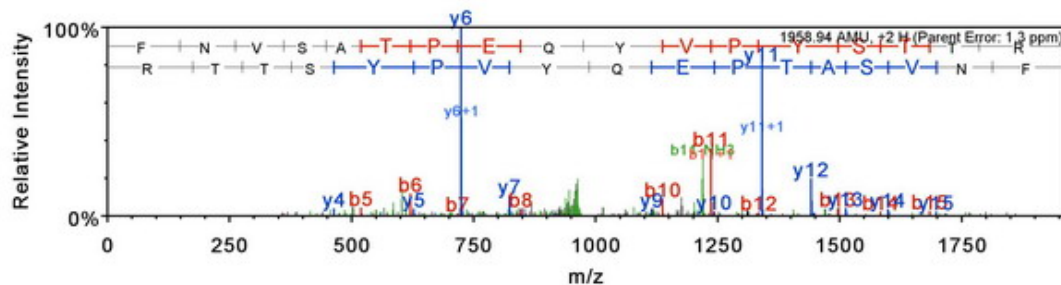
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 980.4777

Actual minus calculated peptide mass (AMU): 0.002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1960.0	980.5	1942.9	1941.9	17
2	262.1		245.1		N	1812.9	906.9	1795.9	1794.9	16
3	361.2		344.2		V	1698.8	849.9	1681.8	1680.8	15
4	448.2		431.2	430.2	S	1599.8	800.4	1582.7	1581.8	14
5	519.3		502.2	501.3	A	1512.7	756.9	1495.7	1494.7	13
6	620.3	310.7	603.3	602.3	T	1441.7	721.4	1424.7	1423.7	12
7	717.4	359.2	700.3	699.4	P	1340.7	670.8	1323.6	1322.6	11
8	846.4	423.7	829.4	828.4	E	1243.6	622.3	1226.6	1225.6	10
9	974.5	487.7	957.4	956.5	Q	1114.5	557.8	1097.5	1096.5	9
10	1137.5	569.3	1120.5	1119.5	Y	986.5	493.8	969.5	968.5	8
11	1236.6	618.8	1219.6	1218.6	V	823.4	412.2	806.4	805.4	7
12	1333.6	667.3	1316.6	1315.6	P	724.4	362.7	707.3	706.4	6
13	1496.7	748.9	1479.7	1478.7	Y	627.3		610.3	609.3	5
14	1583.7	792.4	1566.7	1565.7	S	464.3		447.2	446.2	4
15	1684.8	842.9	1667.8	1666.8	T	377.2		360.2	359.2	3
16	1785.8	893.4	1768.8	1767.8	T	276.2		259.1	258.2	2
17	1960.0	980.5	1942.9	1941.9	R	175.1		158.1		1

Gene symbol: Ndufa12l

Protein name: Mimitin, mitochondrial precursor

Protein accession numbers: IPI00330551

Peptide sequence: EVDYEAGDIPTWEAWIR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 5.12 SEQUEST DCn score: 0.71

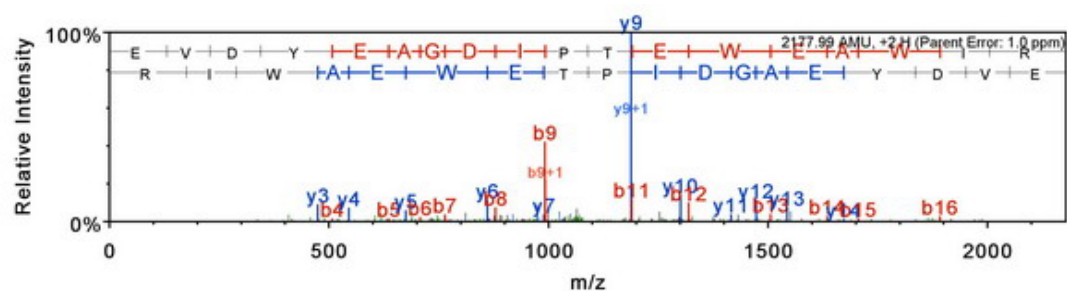
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 1090.0044

Actual minus calculated peptide mass (AMU): 0.0021955



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	2179.0	1090.0	2162.0	2161.0	18
2	229.1			211.1	V	2050.0	1025.5	2032.9	2032.0	17
3	344.2			326.1	D	1950.9	976.0	1933.9	1932.9	16
4	507.2			489.2	Y	1835.9	918.4	1818.8	1817.9	15
5	636.3			618.2	E	1672.8	836.9	1655.8	1654.8	14
6	707.3	354.2		689.3	A	1543.8	772.4	1526.7	1525.7	13
7	764.3	382.7		746.3	G	1472.7	736.9	1455.7	1454.7	12
8	879.3	440.2		861.3	D	1415.7	708.4	1398.7	1397.7	11
9	992.4	496.7		974.4	I	1300.7	650.8	1283.6	1282.7	10
10	1089.5	545.2		1071.5	P	1187.6	594.3	1170.6	1169.6	9
11	1190.5	595.8		1172.5	T	1090.5	545.8	1073.5	1072.5	8
12	1319.6	660.3		1301.5	E	989.5	495.3	972.5	971.5	7
13	1505.6	753.3		1487.6	W	860.4	430.7	843.4	842.4	6
14	1634.7	817.9		1616.7	E	674.4		657.3	656.4	5
15	1705.7	853.4		1687.7	A	545.3		528.3		4
16	1891.8	946.4		1873.8	W	474.3		457.3		3
17	2004.9	1003.0		1986.9	I	288.2		271.2		2
18	2179.0	1090.0	2162.0	2161.0	R	175.1		158.1		1

Gene symbol: Ndufa13

Protein name: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Protein accession numbers: IPI00230715

Peptide sequence: LLIEDLEAR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.68 SEQUEST DCn score: 0.318

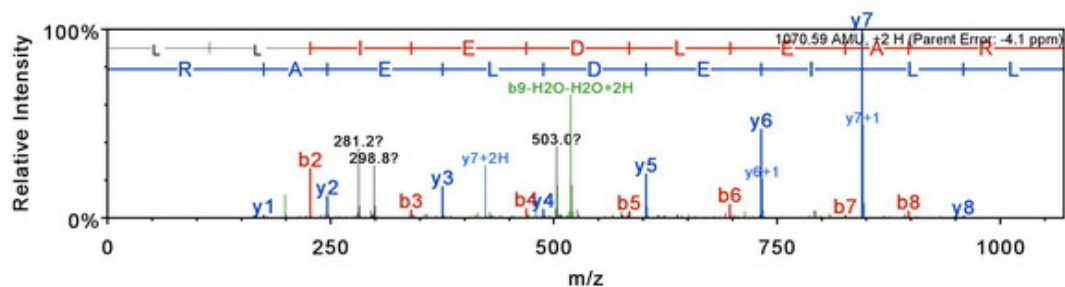
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 536.3043

Actual minus calculated peptide mass (AMU): -0.004395



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1071.6	536.3	1054.6	1053.6	9
2	227.2				L	958.5	479.8	941.5	940.5	8
3	340.3				I	845.4	423.2	828.4	827.4	7
4	469.3			451.3	E	732.4	366.7	715.3	714.3	6
5	584.3			566.3	D	603.3		586.3	585.3	5
6	697.4	349.2		679.4	L	488.3		471.3	470.3	4
7	826.5	413.7		808.5	E	375.2		358.2	357.2	3
8	897.5	449.3		879.5	A	246.2		229.1		2
9	1071.6	536.3	1054.6	1053.6	R	175.1		158.1		1

Gene symbol: Neb

Protein name: similar to Nebulin

Protein accession numbers: IPI00755239

Peptide sequence: VSKTILNWFITXMWPR

Exclusive (unique to this protein): TRUE

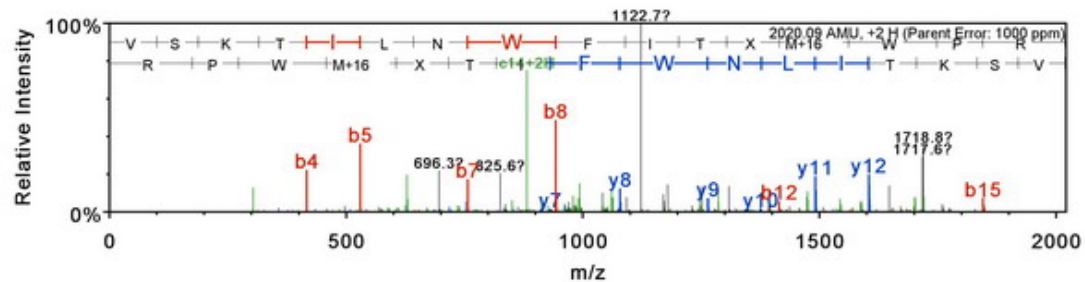
SEQUEST XCorr score: 2.66 SEQUEST DCn score: 0.289

Fix modifications: None

Variable modifications: M13: Oxidation (+16.00)

Charge: 2 Observed m/z: 1011.0513

Actual minus calculated peptide mass (AMU): 2.074



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	2019.0	1010.0	2002.0	2001.0	16
2	187.1			169.1	S	1920.0	960.5	1902.9	1901.9	15
3	315.2	158.1	298.2	297.2	K	1832.9	917.0	1815.9	1814.9	14
4	416.3	208.6	399.2	398.2	T	1704.8	852.9	1687.8	1686.8	13
5	529.3	265.2	512.3	511.3	I	1603.8	802.4	1586.8	1585.8	12
6	642.4	321.7	625.4	624.4	L	1490.7	745.9	1473.7	1472.7	11
7	756.5	378.7	739.4	738.5	N	1377.6	689.3	1360.6	1359.6	10
8	942.5	471.8	925.5	924.5	W	1263.6	632.3	1246.5	1245.6	9
9	1089.6	545.3	1072.6	1071.6	F	1077.5	539.3	1060.5	1059.5	8
10	1202.7	601.9	1185.7	1184.7	I	930.4	465.7	913.4	912.4	7
11	1303.7	652.4	1286.7	1285.7	T	817.3	409.2	800.3	799.3	6
12	1414.7	707.9	1397.7	1396.7	X	716.3		699.3		5
13	1561.8	781.4	1544.8	1543.8	M+16	605.3		588.3		4
14	1747.9	874.4	1730.8	1729.9	W	458.3		441.2		3
15	1844.9	923.0	1827.9	1826.9	P	272.2		255.2		2
16	2019.0	1010.0	2002.0	2001.0	R	175.1		158.1		1

Gene symbol: Nedd1

Protein name: Isoform 1 of Protein NEDD1

Protein accession numbers: IPI00110438

Peptide sequence: FIQNMIQETLDDFR

Exclusive (unique to this protein): TRUE

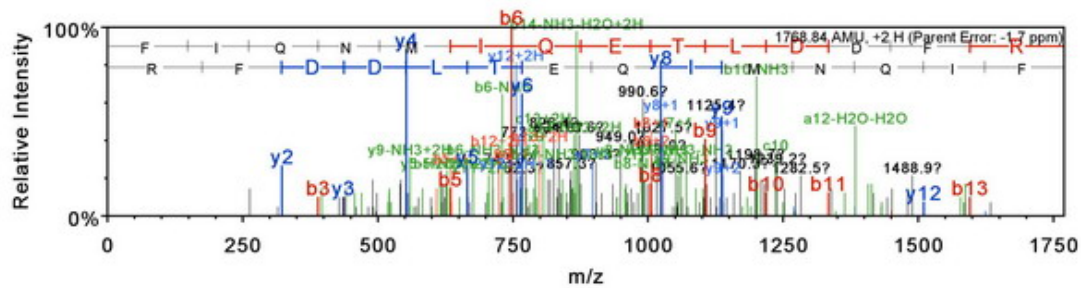
SEQUEST XCorr score: 3.22 SEQUEST DCn score: 0.54

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 885.4291

Actual minus calculated peptide mass (AMU): -0.00293



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1769.9	885.4	1752.8	1751.8	14
2	261.2				I	1622.8	811.9	1605.8	1604.8	13
3	389.2		372.2		Q	1509.7	755.4	1492.7	1491.7	12
4	503.3		486.2		N	1381.6	691.3	1364.6	1363.6	11
5	634.3		617.3		M	1267.6	634.3	1250.6	1249.6	10
6	747.4	374.2	730.4		I	1136.6	568.8	1119.5	1118.5	9
7	875.5	438.2	858.4		Q	1023.5	512.2	1006.5	1005.5	8
8	1004.5	502.8	987.5	986.5	E	895.4	448.2	878.4	877.4	7
9	1105.5	553.3	1088.5	1087.5	T	766.4	383.7	749.4	748.4	6
10	1218.6	609.8	1201.6	1200.6	L	665.3		648.3	647.3	5
11	1333.7	667.3	1316.6	1315.6	D	552.2		535.2	534.2	4
12	1448.7	724.8	1431.7	1430.7	D	437.2		420.2	419.2	3
13	1595.7	798.4	1578.7	1577.7	F	322.2		305.2		2
14	1769.9	885.4	1752.8	1751.8	R	175.1		158.1		1

Gene symbol: Nif3l1

Protein name: Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500035A02 product:Ngg1 interacting factor 3-like 1 (S. pombe), full insert sequence

Protein accession numbers: IPI00230615

Peptide sequence: GVGGVSVTSFPA

Exclusive (unique to this protein): TRUE

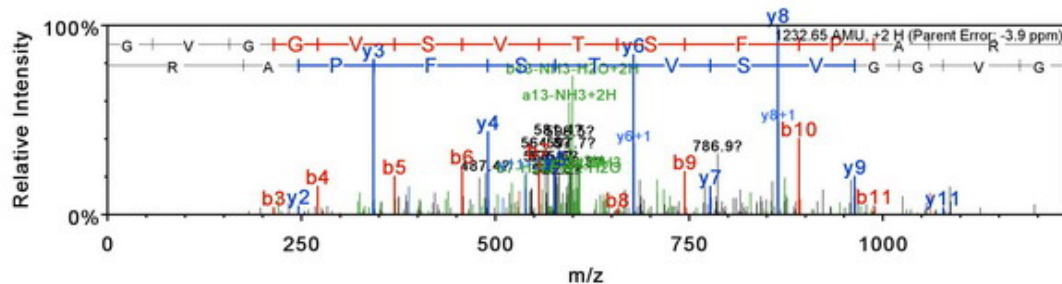
SEQUEST XCorr score: 3.09 SEQUEST DCn score: 0.582

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 617.3311

Actual minus calculated peptide mass (AMU): -0.004761



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1233.7	617.3	1216.6	1215.7	13
2	157.1				V	1176.6	588.8	1159.6	1158.6	12
3	214.1				G	1077.6	539.3	1060.5	1059.6	11
4	271.1				G	1020.6	510.8	1003.5	1002.5	10
5	370.2				V	963.5	482.3	946.5	945.5	9
6	457.2	229.1		439.2	S	864.5	432.7	847.4	846.5	8
7	556.3	278.7		538.3	V	777.4	389.2	760.4	759.4	7
8	657.4	329.2		639.4	T	678.4	339.7	661.3	660.4	6
9	744.4	372.7		726.4	S	577.3		560.3	559.3	5
10	891.5	446.2		873.5	F	490.3		473.3		4
11	988.5	494.8		970.5	P	343.2		326.2		3
12	1059.5	530.3		1041.5	A	246.2		229.1		2
13	1233.7	617.3	1216.6	1215.7	R	175.1		158.1		1

Gene symbol: Nipsnap3a

Protein name: Protein NipSnap3A

Protein accession numbers: IPI00132444

Peptide sequence: VHVLWWNESADSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.92 SEQUEST DCn score: 0.675

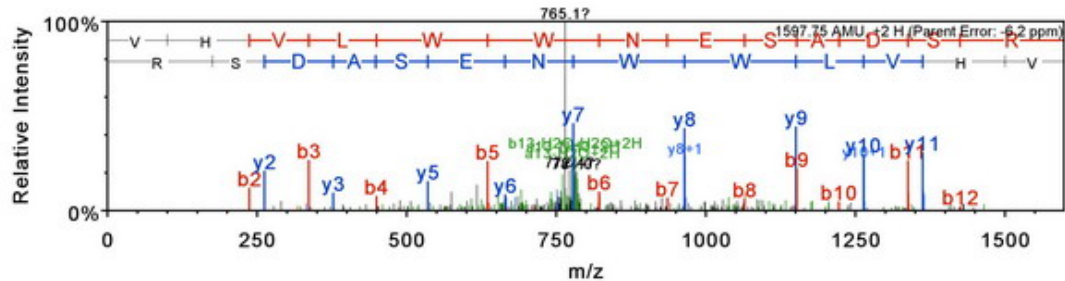
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 799.8847

Actual minus calculated peptide mass (AMU): -0.009888



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1598.8	799.9	1581.7	1580.8	13
2	237.1	119.1			H	1499.7	750.4	1482.7	1481.7	12
3	336.2	168.6			V	1362.6	681.8	1345.6	1344.6	11
4	449.3	225.2			L	1263.6	632.3	1246.5	1245.6	10
5	635.4	318.2			W	1150.5	575.8	1133.5	1132.5	9
6	821.5	411.2			W	964.4	482.7	947.4	946.4	8
7	935.5	468.3	918.5		N	778.3	389.7	761.3	760.3	7
8	1064.5	532.8	1047.5	1046.5	E	664.3	332.7	647.3	646.3	6
9	1151.6	576.3	1134.5	1133.5	S	535.3		518.2	517.2	5
10	1222.6	611.8	1205.6	1204.6	A	448.2		431.2	430.2	4
11	1337.6	669.3	1320.6	1319.6	D	377.2		360.2	359.2	3
12	1424.7	712.8	1407.6	1406.7	S	262.1		245.1	244.1	2
13	1598.8	799.9	1581.7	1580.8	R	175.1		158.1		1

Gene symbol: Nit2

Protein name: Nit protein 2

Protein accession numbers: IPI00119945

Peptide sequence: GCQLLVYPGAFNLTTGPAHWELLQR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.05 SEQUEST DCn score: 0.556

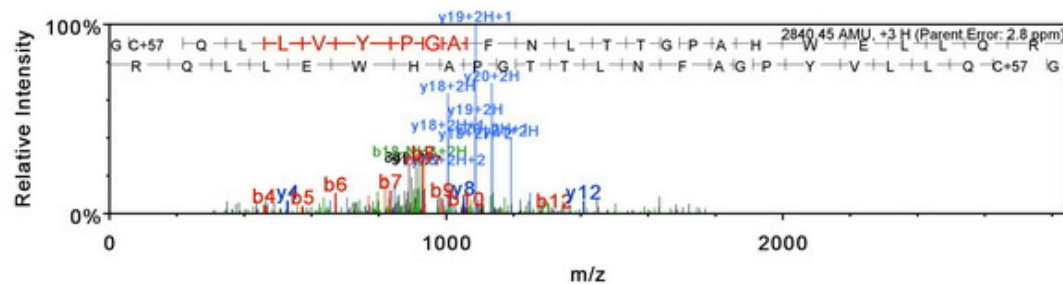
Fix modifications: C2: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 3

Observed m/z: 947.8248

Actual minus calculated peptide mass (AMU): 0.007813



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	2841.5	1421.2	2824.4	2823.4	25
2	218.1				C+57	2784.4	1392.7	2767.4	2766.4	24
3	346.1		329.1		Q	2624.4	1312.7	2607.4	2606.4	23
4	459.2		442.2		L	2496.3	1248.7	2479.3	2478.3	22
5	572.3		555.3		L	2383.3	1192.1	2366.2	2365.3	21
6	671.4	336.2	654.3		V	2270.2	1135.6	2253.2	2252.2	20
7	834.4	417.7	817.4		Y	2171.1	1086.1	2154.1	2153.1	19
8	931.5	466.2	914.4		P	2008.0	1004.5	1991.0	1990.0	18
9	988.5	494.8	971.5		G	1911.0	956.0	1894.0	1893.0	17
10	1059.5	530.3	1042.5		A	1854.0	927.5	1836.9	1836.0	16
11	1206.6	603.8	1189.6		F	1782.9	892.0	1765.9	1764.9	15
12	1320.6	660.8	1303.6		N	1635.9	818.4	1618.8	1617.9	14
13	1433.7	717.4	1416.7		L	1521.8	761.4	1504.8	1503.8	13
14	1534.8	767.9	1517.8	1516.8	T	1408.7	704.9	1391.7	1390.7	12
15	1635.8	818.4	1618.8	1617.8	T	1307.7	654.4	1290.7	1289.7	11
16	1692.8	846.9	1675.8	1674.8	G	1206.6	603.8	1189.6	1188.6	10
17	1789.9	895.5	1772.9	1771.9	P	1149.6	575.3	1132.6	1131.6	9
18	1860.9	931.0	1843.9	1842.9	A	1052.6	526.8	1035.5	1034.5	8
19	1998.0	999.5	1981.0	1980.0	H	981.5	491.3	964.5	963.5	7
20	2184.1	1092.5	2167.0	2166.1	WV	844.5	422.7	827.4	826.5	6
21	2313.1	1157.1	2296.1	2295.1	E	658.4		641.4	640.4	5
22	2426.2	1213.6	2409.2	2408.2	L	529.4		512.3		4
23	2539.3	1270.1	2522.3	2521.3	L	416.3		399.2		3
24	2667.3	1334.2	2650.3	2649.3	Q	303.2		286.2		2
25	2841.5	1421.2	2824.4	2823.4	R	175.1		158.1		1

Gene symbol: Nme5

Protein name: Isoform 1 of Nucleoside diphosphate kinase homolog 5

Protein accession numbers: IPI00336782

Peptide sequence: FMFPAVIEPIPIGQAAK

Exclusive (unique to this protein): TRUE

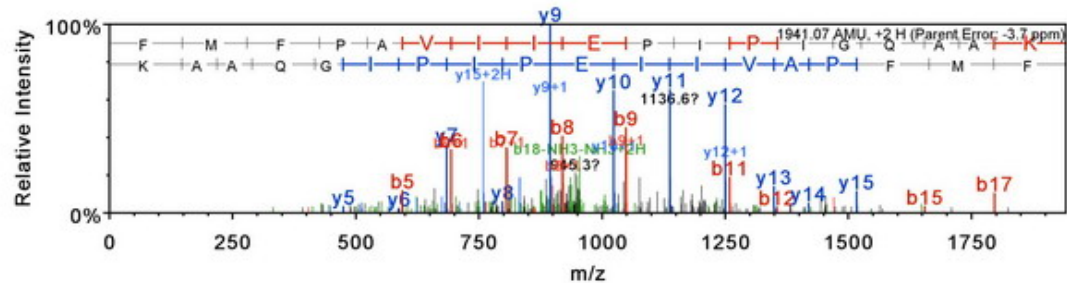
SEQUEST XCorr score: 3.84 SEQUEST DCn score: 0.631

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 971.5443

Actual minus calculated peptide mass (AMU): -0.007202



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.1				F	1942.1	971.6	1925.1	1924.1	18
2	279.1				M	1795.0	898.0	1778.0	1777.0	17
3	426.2				F	1664.0	832.5	1647.0	1646.0	16
4	523.2				P	1516.9	759.0	1499.9	1498.9	15
5	594.3				A	1419.9	710.4	1402.8	1401.9	14
6	693.3	347.2			V	1348.8	674.9	1331.8	1330.8	13
7	806.4	403.7			I	1249.8	625.4	1232.7	1231.7	12
8	919.5	460.3			I	1136.7	568.8	1119.6	1118.7	11
9	1048.5	524.8		1030.5	E	1023.6	512.3	1006.6	1005.6	10
10	1145.6	573.3		1127.6	P	894.5	447.8	877.5		9
11	1258.7	629.9		1240.7	I	797.5	399.3	780.5		8
12	1355.7	678.4		1337.7	P	684.4	342.7	667.4		7
13	1468.8	734.9		1450.8	I	587.4	294.2	570.3		6
14	1525.9	763.4		1507.8	G	474.3		457.2		5
15	1653.9	827.5	1636.9	1635.9	Q	417.3		400.2		4
16	1725.0	863.0	1707.9	1706.9	A	289.2		272.2		3
17	1796.0	898.5	1779.0	1778.0	A	218.2		201.1		2
18	1942.1	971.6	1925.1	1924.1	K	147.1		130.1		1

Gene symbol: Nphp1

Protein name: Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420025P16
product:nephronophthisis 1

Protein accession numbers: IPI00753158

Peptide sequence: ASYFLQPELTTSQLAFR

Exclusive (unique to this protein): TRUE

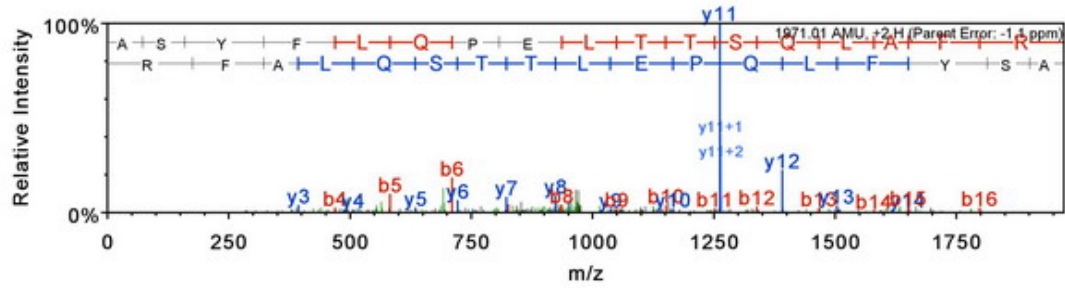
SEQUEST XCorr score: 4.13 SEQUEST DCn score: 0.645

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 986.5118

Actual minus calculated peptide mass (AMU): -0.0021955



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1972.0	986.5	1955.0	1954.0	17
2	159.1			141.1	S	1901.0	951.0	1884.0	1883.0	16
3	322.1			304.1	Y	1814.0	907.5	1796.9	1795.9	15
4	469.2			451.2	F	1650.9	826.0	1633.9	1632.9	14
5	582.3			564.3	L	1503.8	752.4	1486.8	1485.8	13
6	710.4	355.7	693.3	692.3	Q	1390.7	695.9	1373.7	1372.7	12
7	807.4	404.2	790.4	789.4	P	1262.7	631.8	1245.7	1244.7	11
8	936.5	468.7	919.4	918.4	E	1165.6	583.3	1148.6	1147.6	10
9	1049.5	525.3	1032.5	1031.5	L	1036.6	518.8	1019.6	1018.6	9
10	1150.6	575.8	1133.5	1132.6	T	923.5	462.3	906.5	905.5	8
11	1251.6	626.3	1234.6	1233.6	T	822.5	411.7	805.4	804.4	7
12	1338.7	669.8	1321.6	1320.7	S	721.4	361.2	704.4	703.4	6
13	1466.7	733.9	1449.7	1448.7	Q	634.4		617.3		5
14	1579.8	790.4	1562.8	1561.8	L	506.3		489.3		4
15	1650.8	825.9	1633.8	1632.8	A	393.2		376.2		3
16	1797.9	899.5	1780.9	1779.9	F	322.2		305.2		2
17	1972.0	986.5	1955.0	1954.0	R	175.1		158.1		1

Gene symbol: Nqo2

Protein name: Ribosyldihydronicotinamide dehydrogenase

Protein accession numbers: IPI00266614,IPI00268553

Peptide sequence: GFAFDIPGFYDSGFLK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.67 SEQUEST DCn score: 0.377

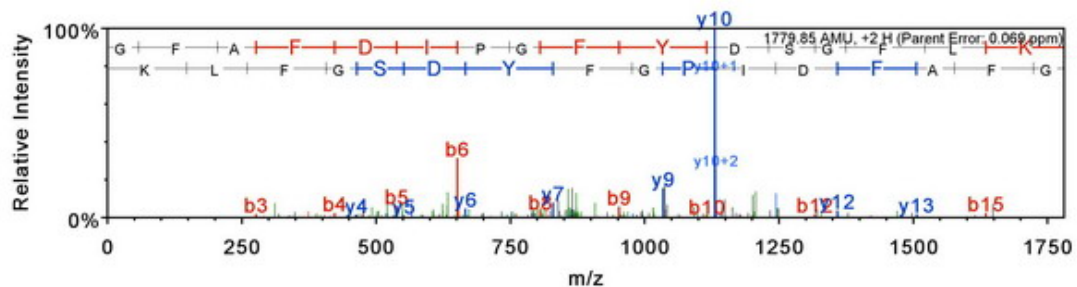
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 890.9333

Actual minus calculated peptide mass (AMU): 0.0001221



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	58.0				G	1780.9	890.9	1763.8	1762.9	16
2	205.1				F	1723.8	862.4	1706.8	1705.8	15
3	276.1				A	1576.8	788.9	1559.7	1558.8	14
4	423.2				F	1505.7	753.4	1488.7	1487.7	13
5	538.2			520.2	D	1358.7	679.8	1341.6	1340.7	12
6	651.3	326.2		633.3	I	1243.6	622.3	1226.6	1225.6	11
7	748.4	374.7		730.4	P	1130.5	565.8	1113.5	1112.5	10
8	805.4	403.2		787.4	G	1033.5	517.3	1016.5	1015.5	9
9	952.5	476.7		934.5	F	976.5	488.7	959.5	958.5	8
10	1115.5	558.3		1097.5	Y	829.4	415.2	812.4	811.4	7
11	1230.5	615.8		1212.5	D	666.4	333.7	649.3	648.3	6
12	1317.6	659.3		1299.6	S	551.3		534.3	533.3	5
13	1374.6	687.8		1356.6	G	464.3		447.3		4
14	1521.7	761.3		1503.7	F	407.3		390.2		3
15	1634.8	817.9		1616.7	L	260.2		243.2		2
16	1780.9	890.9	1763.8	1762.9	K	147.1		130.1		1

Gene symbol: Nt5c

Protein name: 5'(3')-deoxyribonucleotidase, cytosolic type

Protein accession numbers: IPI00124639,IPI00648626

Peptide sequence: WVEQNLGPEFVER

Exclusive (unique to this protein): TRUE

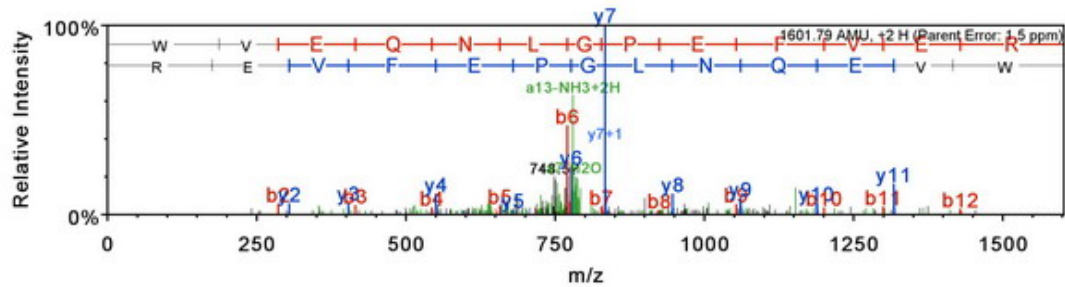
SEQUEST XCorr score: 3.41 SEQUEST DCn score: 0.488

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 801.9009

Actual minus calculated peptide mass (AMU): 0.002441



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	187.1				W	1602.8	801.9	1585.8	1584.8	13
2	286.2				V	1416.7	708.9	1399.7	1398.7	12
3	415.2			397.2	E	1317.6	659.3	1300.6	1299.6	11
4	543.3		526.2	525.3	Q	1188.6	594.8	1171.6	1170.6	10
5	657.3		640.3	639.3	N	1060.5	530.8	1043.5	1042.5	9
6	770.4	385.7	753.4	752.4	L	946.5	473.8	929.5	928.5	8
7	827.4	414.2	810.4	809.4	G	833.4	417.2	816.4	815.4	7
8	924.5	462.7	907.4	906.5	P	776.4	388.7	759.4	758.4	6
9	1053.5	527.3	1036.5	1035.5	E	679.3		662.3	661.3	5
10	1200.6	600.8	1183.5	1182.6	F	550.3		533.3	532.3	4
11	1299.6	650.3	1282.6	1281.6	V	403.2		386.2	385.2	3
12	1428.7	714.8	1411.7	1410.7	E	304.2		287.1	286.2	2
13	1602.8	801.9	1585.8	1584.8	R	175.1		158.1		1

Gene symbol: Nudcd3

Protein name: Isoform 1 of NudC domain-containing protein 3

Protein accession numbers: IPI00268927

Peptide sequence: SMATVDEEEQAVLDR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.96 SEQUEST DCn score: 0.495

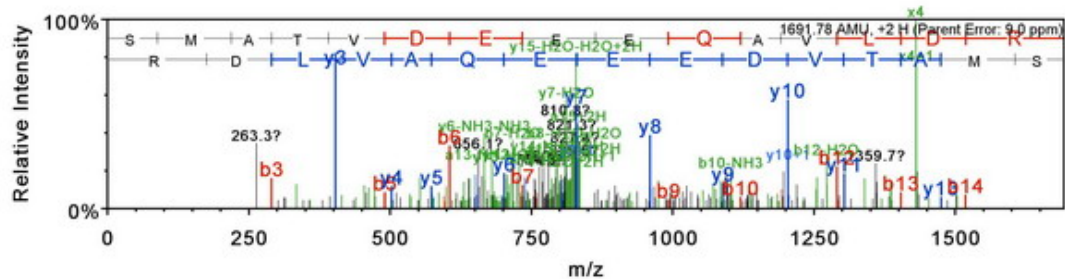
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 846.8991

Actual minus calculated peptide mass (AMU): 0.01526



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1692.8	846.9	1675.8	1674.8	15
2	219.1			201.1	M	1605.7	803.4	1588.7	1587.7	14
3	290.1			272.1	A	1474.7	737.9	1457.7	1456.7	13
4	391.2			373.2	T	1403.7	702.3	1386.6	1385.7	12
5	490.2			472.2	V	1302.6	651.8	1285.6	1284.6	11
6	605.3	303.1		587.3	D	1203.5	602.3	1186.5	1185.5	10
7	734.3	367.7		716.3	E	1088.5	544.8	1071.5	1070.5	9
8	863.4	432.2		845.3	E	959.5	480.2	942.5	941.5	8
9	992.4	496.7		974.4	E	830.4	415.7	813.4	812.4	7
10	1120.5	560.7	1103.4	1102.4	Q	701.4	351.2	684.4	683.4	6
11	1191.5	596.3	1174.5	1173.5	A	573.3		556.3	555.3	5
12	1290.5	645.8	1273.5	1272.5	V	502.3		485.3	484.3	4
13	1403.6	702.3	1386.6	1385.6	L	403.2		386.2	385.2	3
14	1518.7	759.8	1501.6	1500.7	D	290.2		273.1	272.1	2
15	1692.8	846.9	1675.8	1674.8	R	175.1		158.1		1

Gene symbol: Nup107

Protein name: Nuclear pore complex protein Nup107

Protein accession numbers: IPI00221767

Peptide sequence: VLIQANQEDNFGTATPR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.38 SEQUEST DCn score: 0.545

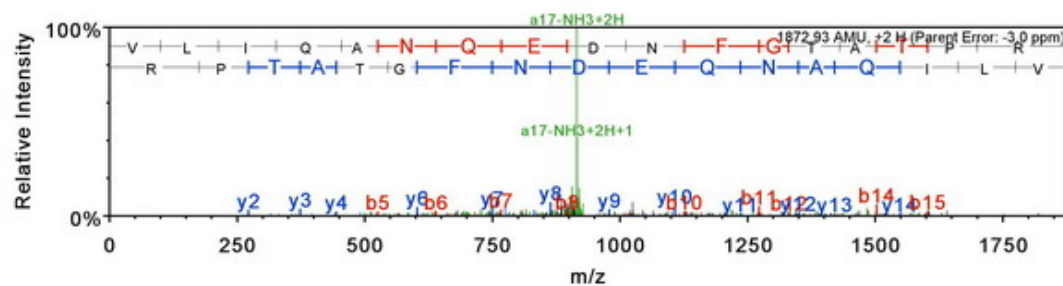
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 937.4716

Actual minus calculated peptide mass (AMU): -0.0056153



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1873.9	937.5	1856.9	1855.9	17
2	213.2				L	1774.9	887.9	1757.9	1756.9	16
3	326.2				I	1661.8	831.4	1644.8	1643.8	15
4	454.3		437.3		Q	1548.7	774.9	1531.7	1530.7	14
5	525.3		508.3		A	1420.7	710.8	1403.6	1402.6	13
6	639.4	320.2	622.4		N	1349.6	675.3	1332.6	1331.6	12
7	767.4	384.2	750.4		Q	1235.6	618.3	1218.5	1217.6	11
8	896.5	448.8	879.5	878.5	E	1107.5	554.3	1090.5	1089.5	10
9	1011.5	506.3	994.5	993.5	D	978.5	489.7	961.4	960.5	9
10	1125.5	563.3	1108.5	1107.5	N	863.4	432.2	846.4	845.4	8
11	1272.6	636.8	1255.6	1254.6	F	749.4	375.2	732.4	731.4	7
12	1329.6	665.3	1312.6	1311.6	G	602.3	301.7	585.3	584.3	6
13	1430.7	715.9	1413.7	1412.7	T	545.3		528.3	527.3	5
14	1501.7	751.4	1484.7	1483.7	A	444.3		427.2	426.3	4
15	1602.8	801.9	1585.8	1584.8	T	373.2		356.2	355.2	3
16	1699.8	850.4	1682.8	1681.8	P	272.2		255.2		2
17	1873.9	937.5	1856.9	1855.9	R	175.1		158.1		1

Gene symbol: Nup133

Protein name: Nuclear pore complex protein Nup133

Protein accession numbers: IPI00320303

Peptide sequence: ENVSLLAEDLEESLTSSVGGR

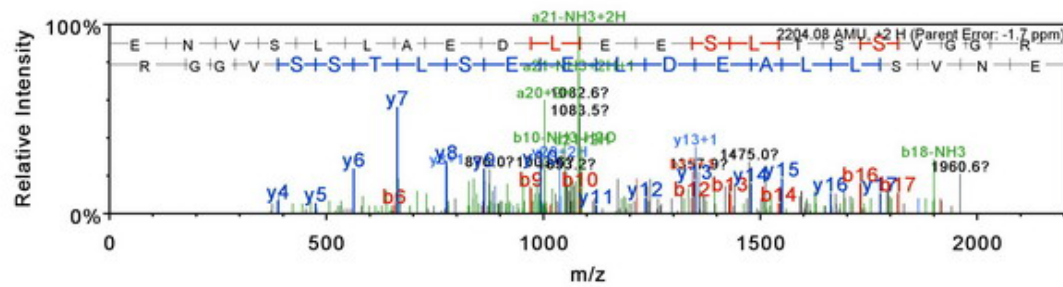
Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.11 SEQUEST DCn score: 0.576

Fix modifications: None

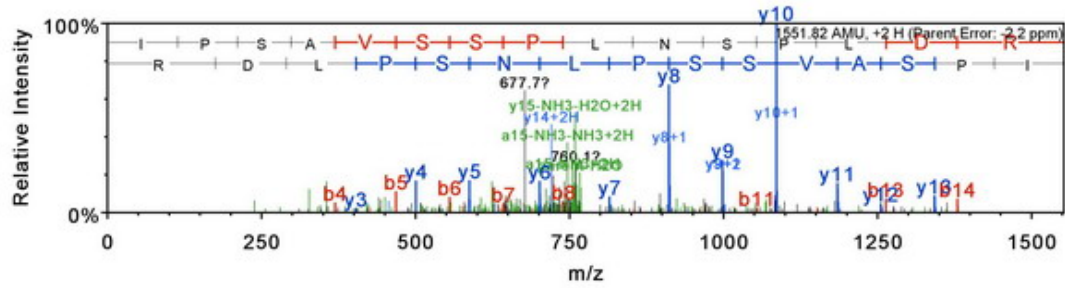
Variable modifications: None

Charge: 2 Observed m/z: 1103.0464
Actual minus calculated peptide mass (AMU): -0.003662



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	2205.1	1103.0	2188.1	2187.1	21
2	244.1		227.1	226.1	N	2076.1	1038.5	2059.0	2058.0	20
3	343.2		326.1	325.2	V	1962.0	981.5	1945.0	1944.0	19
4	430.2		413.2	412.2	S	1862.9	932.0	1845.9	1844.9	18
5	543.3		526.3	525.3	L	1775.9	888.5	1758.9	1757.9	17
6	656.4	328.7	639.3	638.4	L	1662.8	831.9	1645.8	1644.8	16
7	727.4	364.2	710.4	709.4	A	1549.7	775.4	1532.7	1531.7	15
8	856.4	428.7	839.4	838.4	E	1478.7	739.9	1461.7	1460.7	14
9	971.5	486.2	954.4	953.5	D	1349.7	675.3	1332.6	1331.6	13
10	1084.5	542.8	1067.5	1066.5	L	1234.6	617.8	1217.6	1216.6	12
11	1213.6	607.3	1196.6	1195.6	E	1121.5	561.3	1104.5	1103.5	11
12	1342.6	671.8	1325.6	1324.6	E	992.5	496.8	975.5	974.5	10
13	1429.7	715.3	1412.6	1411.7	S	863.5	432.2	846.4	845.5	9
14	1542.8	771.9	1525.7	1524.7	L	776.4	388.7	759.4	758.4	8
15	1643.8	822.4	1626.8	1625.8	T	663.3	332.2	646.3	645.3	7
16	1730.8	865.9	1713.8	1712.8	S	562.3	281.7	545.3	544.3	6
17	1817.9	909.4	1800.8	1799.9	S	475.3		458.2	457.3	5
18	1916.9	959.0	1899.9	1898.9	V	388.2		371.2		4
19	1974.0	987.5	1956.9	1955.9	G	289.2		272.1		3
20	2031.0	1016.0	2014.0	2013.0	G	232.1		215.1		2
21	2205.1	1103.0	2188.1	2187.1	R	175.1		158.1		1

Gene symbol: Nup153
Protein name: Nucleoporin 153
Protein accession numbers: IPI00330624
Peptide sequence: IPSAVSSPLNSPLDR
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 3.1 SEQUEST DCn score: 0.695
Fix modifications: None
Variable modifications: None
Charge: 2 Observed m/z: 776.919
Actual minus calculated peptide mass (AMU): -0.003418



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1552.8	776.9	1535.8	1534.8	15
2	211.1				P	1439.8	720.4	1422.7	1421.7	14
3	298.2			280.2	S	1342.7	671.9	1325.7	1324.7	13
4	369.2			351.2	A	1255.7	628.3	1238.6	1237.7	12
5	468.3			450.3	V	1184.6	592.8	1167.6	1166.6	11
6	555.3	278.2		537.3	S	1085.6	543.3	1068.5	1067.5	10
7	642.4	321.7		624.3	S	998.5	499.8	981.5	980.5	9
8	739.4	370.2		721.4	P	911.5	456.3	894.5	893.5	8
9	852.5	426.8		834.5	L	814.4	407.7	797.4	796.4	7
10	966.5	483.8	949.5	948.5	N	701.4	351.2	684.3	683.4	6
11	1053.6	527.3	1036.5	1035.5	S	587.3		570.3	569.3	5
12	1150.6	575.8	1133.6	1132.6	P	500.3		483.3	482.3	4
13	1263.7	632.4	1246.7	1245.7	L	403.2		386.2	385.2	3
14	1378.7	689.9	1361.7	1360.7	D	290.2		273.1	272.1	2
15	1552.8	776.9	1535.8	1534.8	R	175.1		158.1		1

Gene symbol: Nup188

Protein name: Nucleoporin 188

Protein accession numbers: IPI00420602

Peptide sequence: IPQGTVGQVMLDDR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.62 SEQUEST DCn score: 0.468

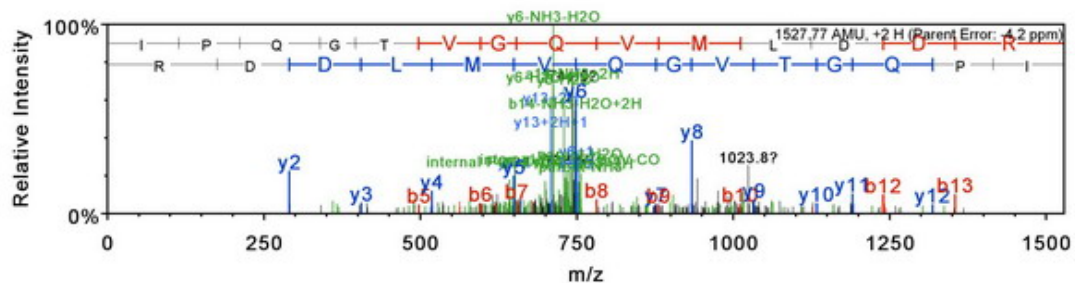
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 764.8905

Actual minus calculated peptide mass (AMU): -0.00647



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1528.8	764.9	1511.8	1510.8	14
2	211.1				P	1415.7	708.4	1398.7	1397.7	13
3	339.2		322.2		Q	1318.6	659.8	1301.6	1300.6	12
4	396.2		379.2		G	1190.6	595.8	1173.6	1172.6	11
5	497.3		480.3	479.3	T	1133.6	567.3	1116.5	1115.5	10
6	596.3	298.7	579.3	578.3	V	1032.5	516.8	1015.5	1014.5	9
7	653.4	327.2	636.3	635.4	G	933.5	467.2	916.4	915.4	8
8	781.4	391.2	764.4	763.4	Q	876.4	438.7	859.4	858.4	7
9	880.5	440.8	863.5	862.5	V	748.4	374.7	731.3	730.4	6
10	1011.5	506.3	994.5	993.5	M	649.3		632.3	631.3	5
11	1124.6	562.8	1107.6	1106.6	L	518.3		501.2	500.3	4
12	1239.6	620.3	1222.6	1221.6	D	405.2		388.2	387.2	3
13	1354.7	677.8	1337.6	1336.7	D	290.2		273.1	272.1	2
14	1528.8	764.9	1511.8	1510.8	R	175.1		158.1		1

Gene symbol: Nup214

Protein name: nucleoporin 214

Protein accession numbers: IPI00229722

Peptide sequence: LNQLVDSLQQLR

Exclusive (unique to this protein): TRUE

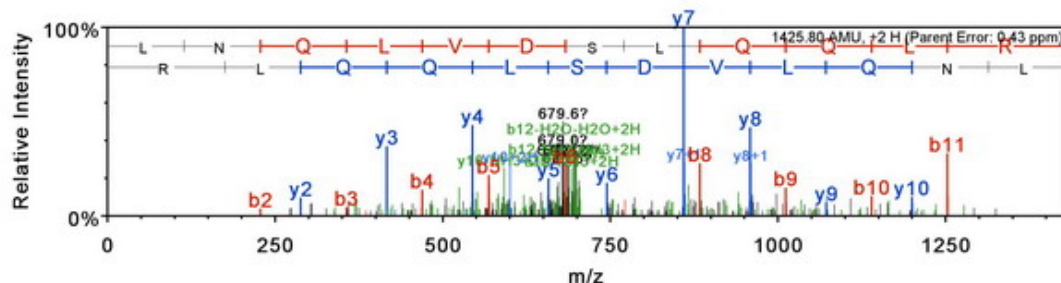
SEQUEST XCorr score: 3.43 SEQUEST DCn score: 0.487

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 713.9052

Actual minus calculated peptide mass (AMU): 0.0006104



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1426.8	713.9	1409.8	1408.8	12
2	228.1		211.1		N	1313.7	657.4	1296.7	1295.7	11
3	356.2		339.2		Q	1199.7	600.3	1182.7	1181.7	10
4	469.3		452.3		L	1071.6	536.3	1054.6	1053.6	9
5	568.4		551.3		V	958.5	479.8	941.5	940.5	8
6	683.4	342.2	666.4	665.4	D	859.5	430.2	842.4	841.5	7
7	770.4	385.7	753.4	752.4	S	744.4	372.7	727.4	726.4	6
8	883.5	442.3	866.5	865.5	L	657.4		640.4		5
9	1011.6	506.3	994.5	993.5	Q	544.3		527.3		4
10	1139.6	570.3	1122.6	1121.6	Q	416.3		399.2		3
11	1252.7	626.9	1235.7	1234.7	L	288.2		271.2		2
12	1426.8	713.9	1409.8	1408.8	R	175.1		158.1		1

Gene symbol: Nup35

Protein name: Nucleoporin NUP53

Protein accession numbers: IPI00469331

Peptide sequence: SIYDDISSPGLGSTPLTSR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 4.11 SEQUEST DCn score: 0.627

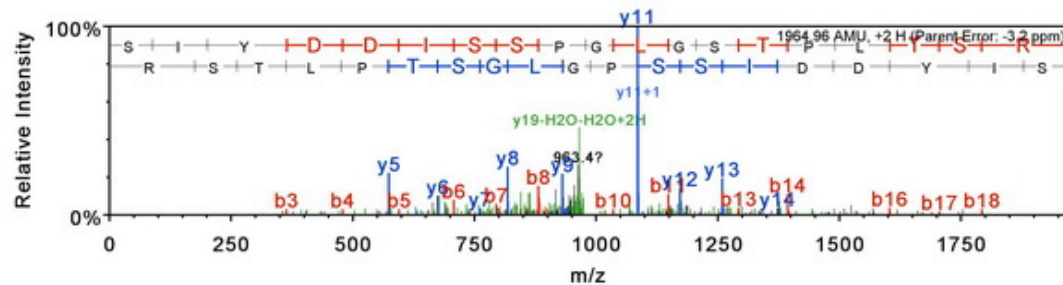
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 983.4894

Actual minus calculated peptide mass (AMU): -0.006226



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1966.0	983.5	1949.0	1948.0	19
2	201.1			183.1	I	1879.0	940.0	1861.9	1860.9	18
3	364.2			346.2	Y	1765.9	883.4	1748.8	1747.9	17
4	479.2			461.2	D	1602.8	801.9	1585.8	1584.8	16
5	594.2			576.2	D	1487.8	744.4	1470.7	1469.8	15
6	707.3	354.2		689.3	I	1372.7	686.9	1355.7	1354.7	14
7	794.4	397.7		776.4	S	1259.7	630.3	1242.6	1241.7	13
8	881.4	441.2		863.4	S	1172.6	586.8	1155.6	1154.6	12
9	978.4	489.7		960.4	P	1085.6	543.3	1068.6	1067.6	11
10	1035.5	518.2		1017.5	G	988.5	494.8	971.5	970.5	10
11	1148.5	574.8		1130.5	L	931.5	466.3	914.5	913.5	9
12	1205.6	603.3		1187.6	G	818.4	409.7	801.4	800.4	8
13	1292.6	646.8		1274.6	S	761.4	381.2	744.4	743.4	7
14	1393.7	697.3		1375.6	T	674.4	337.7	657.4	656.4	6
15	1490.7	745.9		1472.7	P	573.3		556.3	555.3	5
16	1603.8	802.4		1585.8	L	476.3		459.3	458.3	4
17	1704.8	852.9		1686.8	T	363.2		346.2	345.2	3
18	1791.9	896.4		1773.9	S	262.1		245.1	244.1	2
19	1966.0	983.5	1949.0	1948.0	R	175.1		158.1		1

Gene symbol: Nup98

Protein name: Nup98 protein (Fragment)

Protein accession numbers: IPI00474558

Peptide sequence: LMPEDYALEELR

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 2.8 SEQUEST DCn score: 0.585

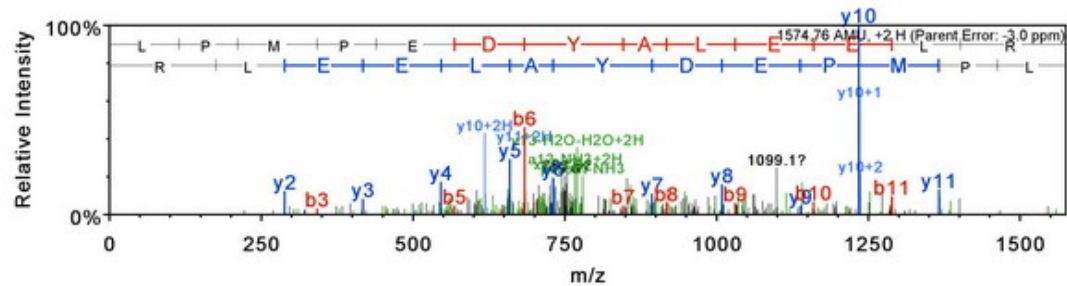
Fix modifications: None

Variable modifications: None

Charge: 2

Observed m/z: 788.3881

Actual minus calculated peptide mass (AMU): -0.004761



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1575.8	788.4	1558.8	1557.8	13
2	211.1				P	1462.7	731.9	1445.7	1444.7	12
3	342.2				M	1365.6	683.3	1348.6	1347.6	11
4	439.2				P	1234.6	617.8	1217.6	1216.6	10
5	568.3			550.3	E	1137.5	569.3	1120.5	1119.5	9
6	683.3	342.2		665.3	D	1008.5	504.8	991.5	990.5	8
7	846.4	423.7		828.4	Y	893.5	447.2	876.5	875.5	7
8	917.4	459.2		899.4	A	730.4	365.7	713.4	712.4	6
9	1030.5	515.8		1012.5	L	659.4		642.4	641.4	5
10	1159.5	580.3		1141.5	E	546.3		529.3	528.3	4
11	1288.6	644.8		1270.6	E	417.3		400.2	399.2	3
12	1401.7	701.3		1383.7	L	288.2		271.2		2
13	1575.8	788.4	1558.8	1557.8	R	175.1		158.1		1

Gene symbol: Odf1

Protein name: Outer dense fiber protein

Protein accession numbers: IPI00230559

Peptide sequence: SCGLCDLYPPCCLCDYK

Exclusive (unique to this protein): TRUE

SEQUEST XCorr score: 3.43 SEQUEST DCn score: 0.832

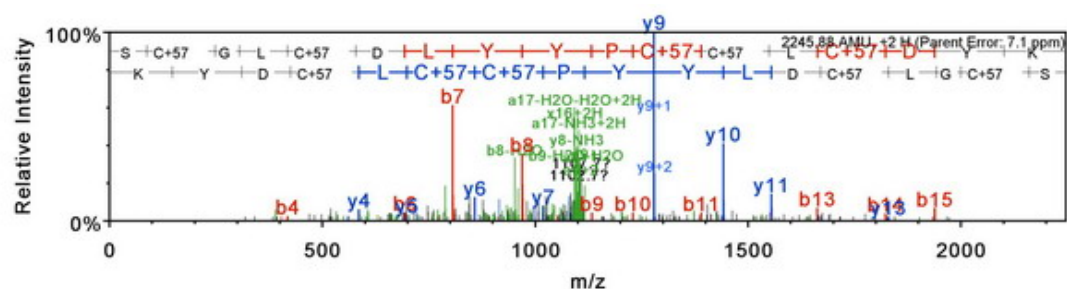
Fix modifications: C2: Carbamidomethyl (+57.02), C5: Carbamidomethyl (+57.02), C11: Carbamidomethyl (+57.02), C12: Carbamidomethyl (+57.02), C14: Carbamidomethyl (+57.02)

Variable modifications: None

Charge: 2

Observed m/z: 1123.9464

Actual minus calculated peptide mass (AMU): 0.01587



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	2246.9	1123.9	2229.8	2228.9	17
2	248.1			230.1	C+57	2159.8	1080.4	2142.8	2141.8	16
3	305.1			287.1	G	1999.8	1000.4	1982.8	1981.8	15
4	418.2			400.2	L	1942.8	971.9	1925.8	1924.8	14
5	578.2			560.2	C+57	1829.7	915.4	1812.7	1811.7	13
6	693.2	347.1		675.2	D	1669.7	835.3	1652.6	1651.7	12
7	806.3	403.7		788.3	L	1554.6	777.8	1537.6	1536.6	11
8	969.4	485.2		951.4	Y	1441.6	721.3	1424.5	1423.5	10
9	1132.4	566.7		1114.4	Y	1278.5	639.8	1261.5	1260.5	9
10	1229.5	615.3		1211.5	P	1115.4	558.2	1098.4	1097.4	8
11	1389.5	695.3		1371.5	C+57	1018.4	509.7	1001.4	1000.4	7
12	1549.6	775.3		1531.5	C+57	858.4	429.7	841.3	840.3	6
13	1662.6	831.8		1644.6	L	698.3		681.3	680.3	5
14	1822.7	911.8		1804.7	C+57	585.2		568.2	567.2	4
15	1937.7	969.4		1919.7	D	425.2		408.2	407.2	3
16	2100.8	1050.9		2082.8	Y	310.2		293.2		2
17	2246.9	1123.9	2229.8	2228.9	K	147.1		130.1		1

Gene symbol: Oplah

Protein name: 5-oxoprolinase

Protein accession numbers: IPI00169473

Peptide sequence: SQISTESFLHLR

Exclusive (unique to this protein): TRUE

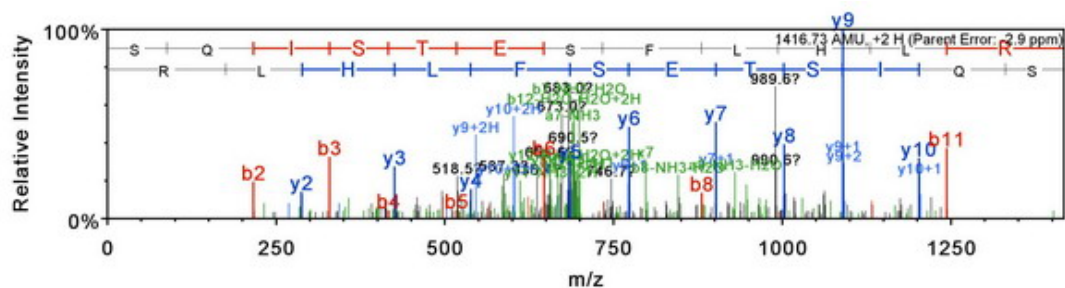
SEQUEST XCorr score: 3.04 SEQUEST DCn score: 0.46

Fix modifications: None

Variable modifications: None

Charge: 2 Observed m/z: 709.3738

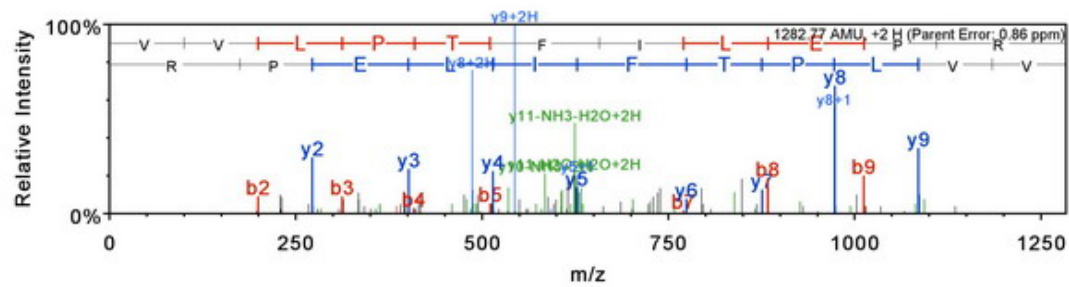
Actual minus calculated peptide mass (AMU): -0.00415



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1417.7	709.4	1400.7	1399.7	12
2	216.1		199.1	198.1	Q	1330.7	665.9	1313.7	1312.7	11
3	329.2		312.2	311.2	I	1202.7	601.8	1185.6	1184.6	10
4	416.2		399.2	398.2	S	1089.6	545.3	1072.5	1071.6	9
5	517.3		500.2	499.3	T	1002.5	501.8	985.5	984.5	8
6	646.3	323.7	629.3	628.3	E	901.5	451.3	884.5	883.5	7
7	733.3	367.2	716.3	715.3	S	772.5	386.7	755.4	754.4	6
8	880.4	440.7	863.4	862.4	F	685.4	343.2	668.4		5
9	993.5	497.3	976.5	975.5	L	538.4	269.7	521.3		4
10	1130.5	565.8	1113.5	1112.5	H	425.3	213.1	408.2		3
11	1243.6	622.3	1226.6	1225.6	L	288.2		271.2		2
12	1417.7	709.4	1400.7	1399.7	R	175.1		158.1		1

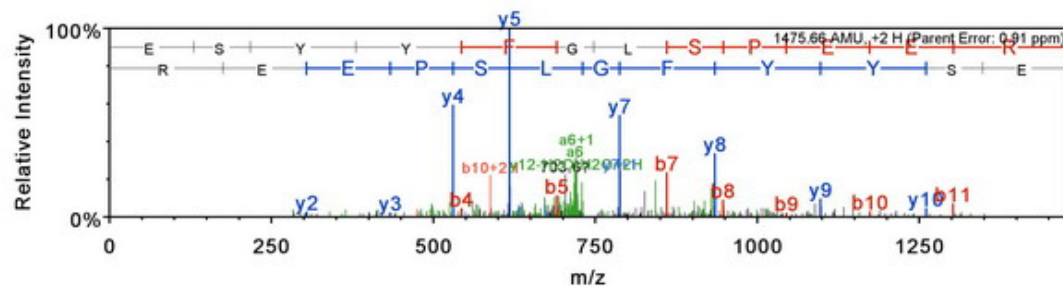
Variable modifications: None

Charge: 2 Observed m/z: 642.3909
Actual minus calculated peptide mass (AMU): 0.001099



B	B ions	B+2H	B-NH3	B-H2O	AA	Y ions	Y+2H	Y-NH3	Y-H2O	Y
1	100.1				V	1283.8	642.4	1266.8	1265.8	11
2	199.1				V	1184.7	592.9	1167.7	1166.7	10
3	312.2				L	1085.6	543.3	1068.6	1067.6	9
4	409.3				P	972.6	486.8	955.5	954.5	8
5	510.3			492.3	T	875.5	438.3	858.5	857.5	7
6	657.4	329.2		639.4	F	774.5	387.7	757.4	756.4	6
7	770.5	385.7		752.5	I	627.4		610.4	609.4	5
8	883.6	442.3		865.6	L	514.3		497.3	496.3	4
9	1012.6	506.8		994.6	E	401.2		384.2	383.2	3
10	1109.7	555.3		1091.7	P	272.2		255.2		2
11	1283.8	642.4	1266.8	1265.8	R	175.1		158.1		1

Gene symbol: Otud4
Protein name: HIV-1 induced protein HIN-1
Protein accession numbers: IPI00137459
Peptide sequence: ESYYFGLSPEER
Exclusive (unique to this protein): TRUE
SEQUEST XCorr score: 2.93 SEQUEST DCn score: 0.373
Fix modifications: None
Variable modifications: None
Charge: 2 Observed m/z: 738.8369
Actual minus calculated peptide mass (AMU): 0.001343



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.1			112.0	E	1476.7	738.8	1459.6	1458.7	12
2	217.1			199.1	S	1347.6	674.3	1330.6	1329.6	11
3	380.2			362.1	Y	1260.6	630.8	1243.6	1242.6	10
4	543.2			525.2	Y	1097.5	549.3	1080.5	1079.5	9
5	690.3			672.3	F	934.5	467.7	917.4	916.5	8
6	747.3	374.2		729.3	G	787.4	394.2	770.4	769.4	7
7	860.4	430.7		842.4	L	730.4	365.7	713.4	712.4	6
8	947.4	474.2		929.4	S	617.3		600.3	599.3	5
9	1044.5	522.7		1026.5	P	530.3		513.2	512.3	4
10	1173.5	587.3		1155.5	E	433.2		416.2	415.2	3
11	1302.5	651.8		1284.5	E	304.2		287.1	286.2	2
12	1476.7	738.8	1459.6	1458.7	R	175.1		158.1		1