

**Table 1. Intracellular peptides identified on inguinal adipose tissue of WT or THOP1<sup>-/-</sup>**

Precursor Protein name	Peptide sequence	RT	L1_m/z	L2_m/z	I_m/z	H_m/z	z	T	Avg. mass	SD	Obs. mass	Theor. mass	ppm
Macrophage migration inhib. factor	LSELTQQLAQATGKPAQ	64,7	920,5638	922,558	924,5377	928,5586	2	2	1783,0083	0,045	1783,008	1782,9549	29,9
Histone H2A type 1-B	AQGGVLPNIQAVLLPK	96,9	837,5191	839,5303	841,5442	845,5635	2	2	1616,9778	0,024	1616,978	1616,9687	5,6
Histone H2B type 2-B	KQVHPDTGISSKAMGImNS	37,6	701,0305	703,054	705,0552	709,0762	3	3	2016,0107	0,041	2016,011	2015,9792	15,6
Elongation factor 2	ASVLTAQPRIMEPI	80,1	777,4376	778,4376	779,4517	781,4618	2	1	1524,836	0,014	1524,836	1524,8407	-3,12
Creatine kinase M-type	DISNADRLGSSEVEQ	49,1	824,4038	825,4003	826,4043	828,4151	2	1	1618,7534	0,011	1618,753	1618,66	57,7
Creatine kinase M-type	DISNADRLGSSEVEQV	59,5	873,929	874,9346	875,9405	877,9507	2	1	1717,819	0,011	1717,819	1717,8191	-0,06
Creatine kinase M-type	IDDHFLFDKPVSPLL	99,3	906,5032	908,5107	910,5258	914,5468	2	2	1754,9425	0,022	1754,942	1754,9316	6,18
Apolipoprotein A-I	LETlKTQVQSVIDKA	73,2	586,3524	588,364	590,3767	594,3958	3	3	1671,9655	0,036	1671,965	1671,948	10,5
Apolipoprotein A-II	FSSLMNLEEKPAAPAA	71,5	830,9321	832,9461	834,9584	838,9783	2	2	1603,8067	0,024	1603,807	1603,7989	4,83
Apolipoprotein A-II	HEQLTPLVRSAGTSLVN	60	925,5099	926,5137	927,5212	929,5321	2	1	1820,9801	0,011	1820,98	1820,9817	-0,91
Serum albumin	SQTFPNADFAEITKL	93,2	869,46	871,4683	873,4811	877,4998	2	2	1680,8538	0,023	1680,854	1680,8432	6,31
Non-specific lipid-transfer protein	ADSDLLALMTGKMNPQSA	99	959,9837	961,9929	964,0899	968,0289	2	2	1861,9469	0,103	1861,947	1861,8987	25,9
Hemoglobin subunit alpha	GAEALERMFASFPTTK	87,8	906,5109	908,4832	910,4923	914,5168	2	2	1754,9008	0,033	1754,901	1754,834	38,1
Hemoglobin subunit alpha	FDVSHGSAQVK	24,6	615,8264	617,8394	619,8522	623,8708	2	2	1173,5936	0,025	1173,594	1173,5851	7,24
Hemoglobin subunit alpha	IGGHGAEYGAEALER	39,5	779,3855	780,3916	781,3956	783,4088	2	1	1528,7324	0,009	1528,732	1528,7343	-1,28
Hemoglobin subunit alpha	SVSTVLTSK	35,3	489,298	491,3106	493,3228	497,342	2	2	920,5359	0,024	920,5359	920,5251	11,7
Acyl-CoA-binding protein	QATVGDVNTDRPGLDLKKGK	58,5	727,7425	729,7576	731,7711	735,7884	3	3	2096,1435	0,040	2096,144	2096,1299	6,49

RT= retention time; m= methionine oxidized; L1 or L2 =Light; I=Intermediary; H=Heavy; z=charge; T= number of tags; SD= standard deviation; Avg=Average mass; Obs=Observed; theor.=theoric

# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **LSELTQQLAQATGKPAQ**

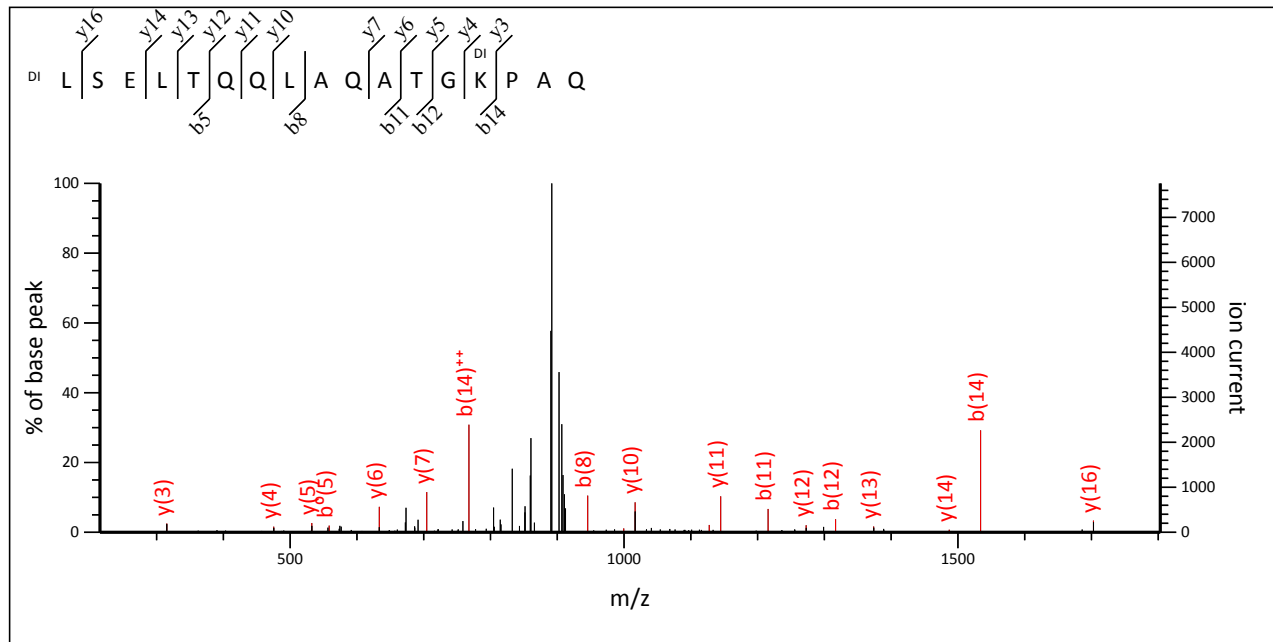
Found in **MIF\_MOUSE** in **SwissProt**, Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2

Match to Query 14599: 1847.062548 from(924.538550,2+) intensity(2914775.6000) scans(14738-14751) rawscans(sn14738:sn14751)  
rtinseconds(3887.7387-3890.5887) index(9352)

Title: 9353: Sum of 2 scans in range 14738 (rt=3887.74) to 14751 (rt=3890.59) [D:\Users\Mayara - HMS Fusion

data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



215.18 to 1803.06



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1847.0604

Variable modifications:

N-term : Dimethyl:2H(4) (N-term)

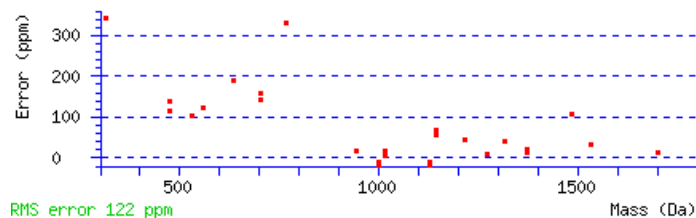
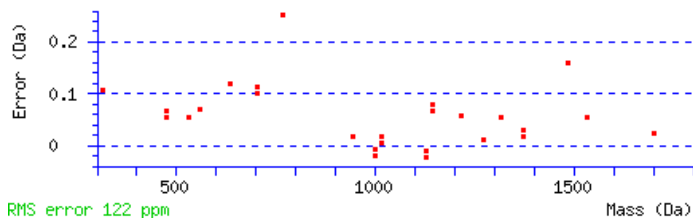
K14 : Dimethyl:2H(4) (K)

Ions Score: 103 Expect: 1.3e-008

Matches : 26/170 fragment ions using 26 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	146.1477	73.5775					L							17
2	233.1798	117.0935			215.1692	108.0882	S	1702.9272	851.9672	1685.9007	843.4540	1684.9166	842.9620	16
3	362.2224	181.6148			344.2118	172.6095	E	1615.8952	808.4512	1598.8686	799.9379	1597.8846	799.4459	15
4	475.3064	238.1569			457.2959	229.1516	L	1486.8526	743.9299	1469.8260	735.4167	1468.8420	734.9246	14
5	576.3541	288.6807			558.3435	279.6754	T	1373.7685	687.3879	1356.7420	678.8746	1355.7579	678.3826	13
6	704.4127	352.7100	687.3861	344.1967	686.4021	343.7047	Q	1272.7208	636.8641	1255.6943	628.3508	1254.7103	627.8588	12
7	832.4713	416.7393	815.4447	408.2260	814.4607	407.7340	Q	1144.6623	572.8348	1127.6357	564.3215	1126.6517	563.8295	11
8	945.5553	473.2813	928.5288	464.7680	927.5448	464.2760	L	1016.6037	508.8055	999.5771	500.2922	998.5931	499.8002	10
9	1016.5924	508.7999	999.5659	500.2866	998.5819	499.7946	A	903.5196	452.2634	886.4931	443.7502	885.5091	443.2582	9
10	1144.6510	572.8291	1127.6245	564.3159	1126.6405	563.8239	Q	832.4825	416.7449	815.4560	408.2316	814.4719	407.7396	8
11	1215.6881	608.3477	1198.6616	599.8344	1197.6776	599.3424	A	704.4239	352.7156	687.3974	344.2023	686.4134	343.7103	7
12	1316.7358	658.8715	1299.7093	650.3583	1298.7253	649.8663	T	633.3868	317.1970	616.3603	308.6838	615.3762	308.1918	6
13	1373.7573	687.3823	1356.7307	678.8690	1355.7467	678.3770	G	532.3391	266.6732	515.3126	258.1599			5

14	1533.9087	767.4580	1516.8821	758.9447	1515.8981	758.4527	K	475.3177	238.1625	458.2911	229.6492			4
15	1630.9614	815.9843	1613.9349	807.4711	1612.9508	806.9791	P	315.1663	158.0868	298.1397	149.5735			3
16	1701.9985	851.5029	1684.9720	842.9896	1683.9880	842.4976	A	218.1135	109.5604	201.0870	101.0471			2
17							Q	147.0764	74.0418	130.0499	65.5286			1



NCBI BLAST search of [LSELTQQLAQATGKPAQ](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

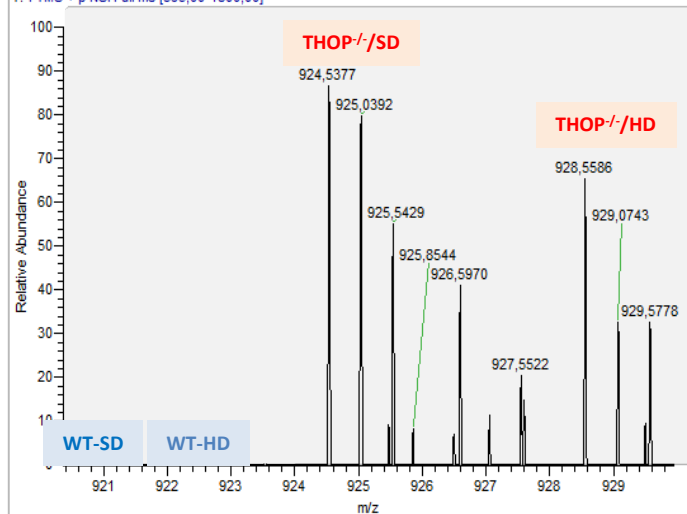
#### All matches to this query

Score	Mr(calc)	Delta	Sequence
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18.4	1846.9858	0.0768	<a href="#">SSSFSEIEIQAVVPYR</a>
15.2	1846.9497	0.1128	<a href="#">DSAVSVPTTQANATRRGS</a>
14.9	1846.9930	0.0696	<a href="#">GVGAVPAAAAGSAGAAASLGNAT</a>
14.0	1846.9975	0.0650	<a href="#">VFSLTQQPVRMEAAKA</a>
13.8	1846.8692	0.1933	<a href="#">EDLEMRPGDMITLLE</a>
13.3	1846.9887	0.0738	<a href="#">DSSITGELEKQLLQAN</a>
13.1	1847.0780	-0.0154	<a href="#">ALCLQTQLLPYLALLT</a>
12.6	1846.9207	0.1419	<a href="#">ELLRMGEVQTAQDNR</a>
12.3	1847.0040	0.0585	<a href="#">LEWAASSVEVTAVAAKN</a>

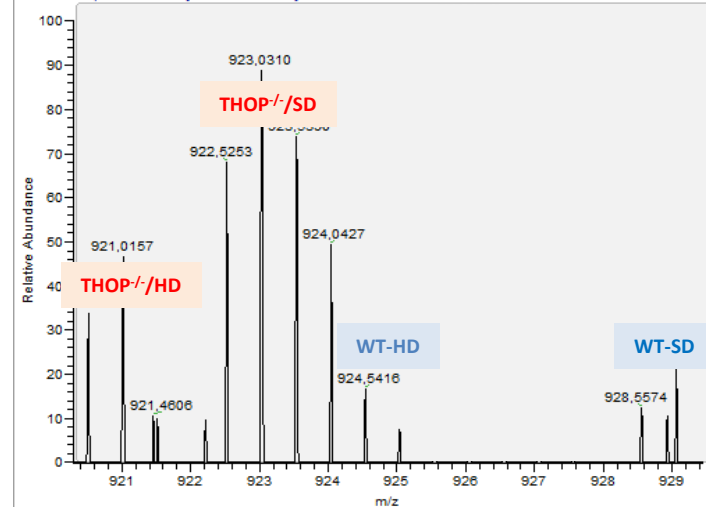
Mascot: <http://www.matrixscience.com/>

# LSELTQQQLAQATGKPAQ

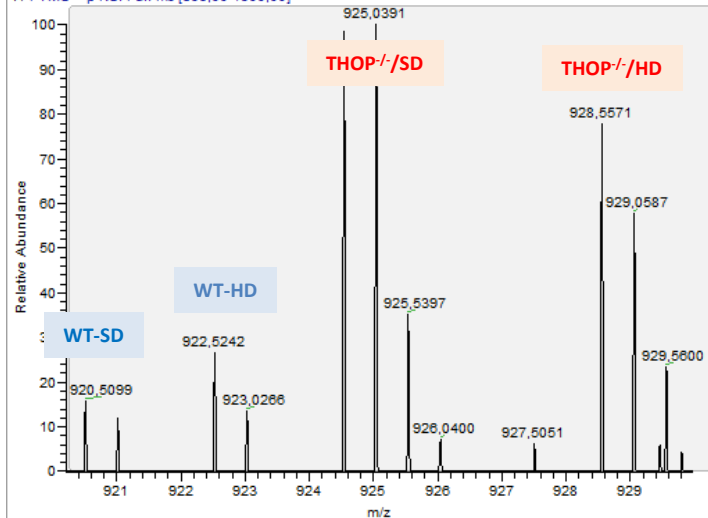
170711PESSAM02977\_May1 #14602-14797 RT: 64.34-64.91 AV: 10 NL: 3,18E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



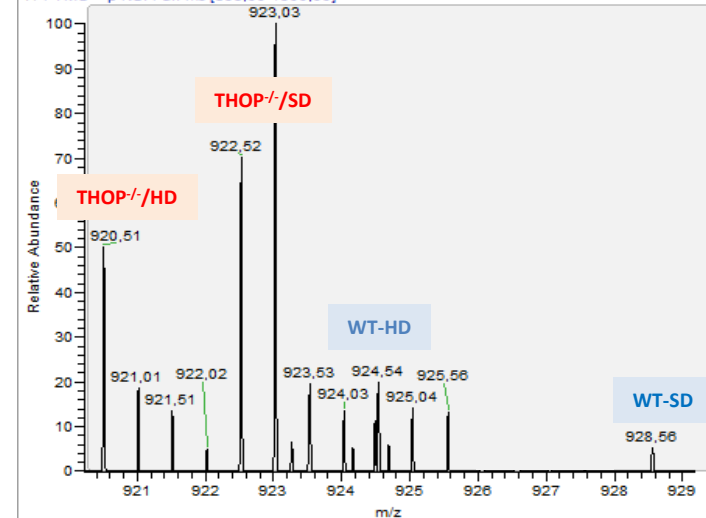
170711PESSAM02978\_May2 #14113-14267 RT: 63.68-64.19 AV: 8 NL: 3,67E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



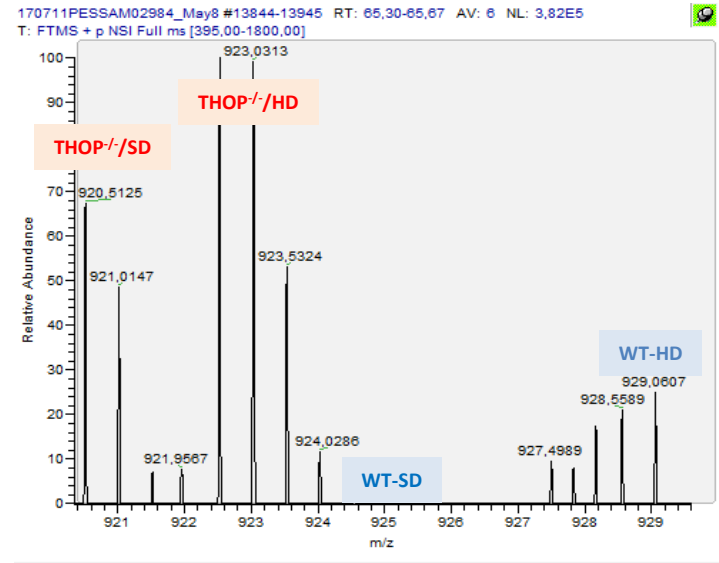
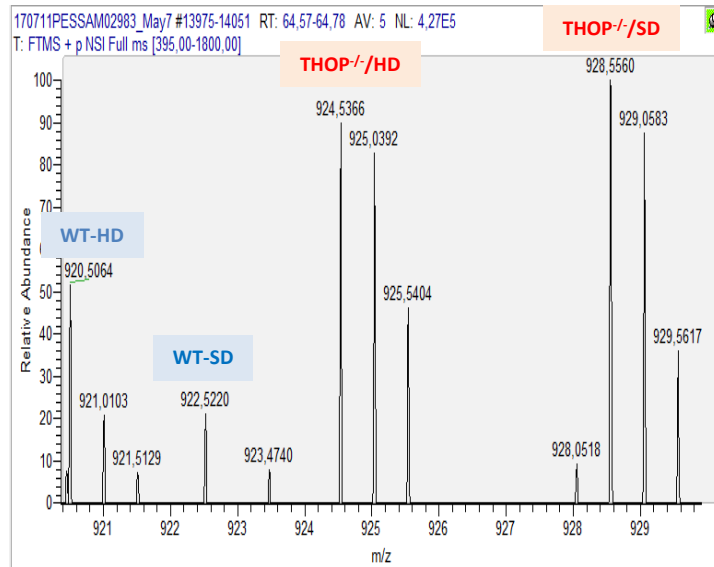
170711PESSAM02981\_May5 #13459-13596 RT: 59.97-60.38 AV: 8 NL: 7,08E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



170711PESSAM02982\_May6 #13598-13790 RT: 64.37-64.99 AV: 10 NL: 3,63E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



# LSELTQQLAQTGKPAQ



# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **AQGGVLPNIQAVLLPK**

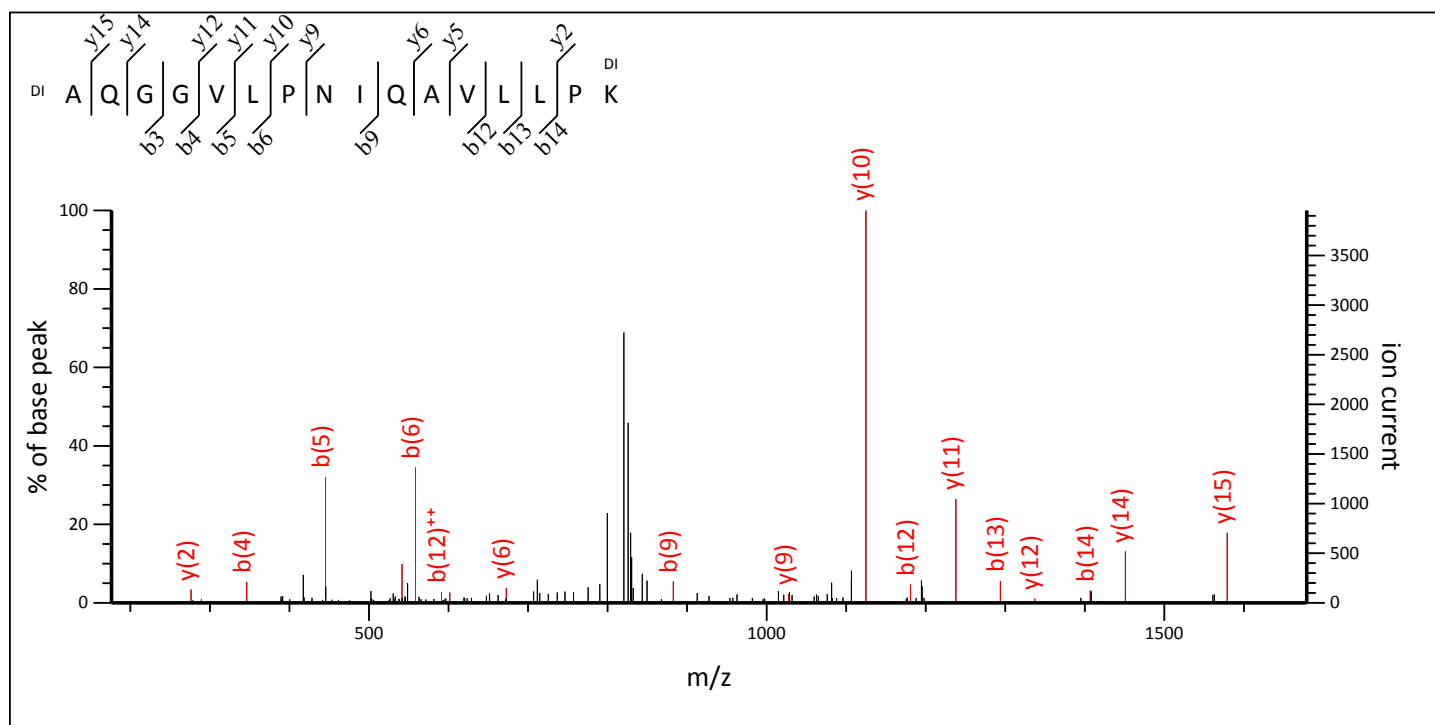
Found in **H2A2B\_MOUSE** in **SwissProt**, Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3

Match to Query 12540: 1681.073268 from(841.543910,2+) intensity(2031343.0000) scans(22590-22787)

rawscans(sn22590:sn22787) rtinseconds(5814.52-5872.8208) index(14871)

Title: 14872: Sum of 2 scans in range 22590 (rt=5814.52) to 22787 (rt=5872.82) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



176.3

to 1679.05



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1681.0742

Variable modifications:

N-term : Dimethyl:2H(4) (N-term)

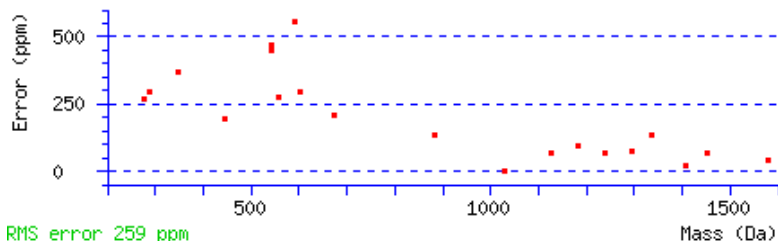
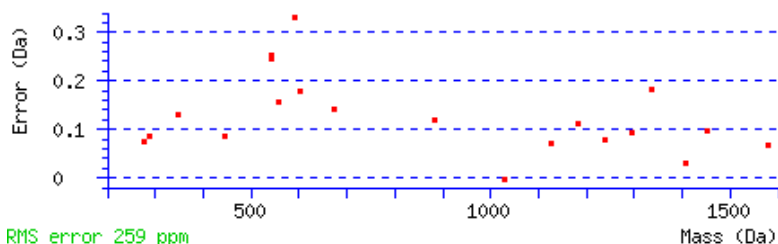
K16 : Dimethyl:2H(4) (K)

Ions Score: 66 Expect: 5.2e-005

Matches : 20/118 fragment ions using 38 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	104.1008	52.5540			A					16
2	232.1594	116.5833	215.1328	108.0701	Q	1578.9879	789.9976	1561.9614	781.4843	15
3	289.1808	145.0941	272.1543	136.5808	G	1450.9294	725.9683	1433.9028	717.4550	14
4	346.2023	173.6048	329.1758	165.0915	G	1393.9079	697.4576	1376.8814	688.9443	13
5	445.2707	223.1390	428.2442	214.6257	V	1336.8864	668.9469	1319.8599	660.4336	12
6	558.3548	279.6810	541.3282	271.1678	L	1237.8180	619.4127	1220.7915	610.8994	11
7	655.4075	328.2074	638.3810	319.6941	P	1124.7340	562.8706	1107.7074	554.3573	10

8	769.4505	385.2289	752.4239	376.7156	N	<b>1027.6812</b>	514.3442	1010.6547	505.8310	9
9	<b>882.5345</b>	441.7709	865.5080	433.2576	I	913.6383	457.3228	896.6117	448.8095	8
10	1010.5931	505.8002	993.5666	497.2869	Q	800.5542	400.7807	783.5277	392.2675	7
11	1081.6302	<b>541.3188</b>	1064.6037	532.8055	A	<b>672.4956</b>	336.7515	655.4691	328.2382	6
12	<b>1180.6986</b>	<b>590.8530</b>	1163.6721	582.3397	V	<b>601.4585</b>	301.2329	584.4320	292.7196	5
13	<b>1293.7827</b>	647.3950	1276.7562	638.8817	L	502.3901	251.6987	485.3636	243.1854	4
14	<b>1406.8668</b>	703.9370	1389.8402	695.4237	L	389.3060	195.1567	372.2795	186.6434	3
15	1503.9195	752.4634	1486.8930	743.9501	P	<b>276.2220</b>	138.6146	259.1954	130.1014	2
16					K	179.1692	90.0882	162.1427	81.5750	1



NCBI **BLAST** search of [AQGGVLPNIQAVLLPK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

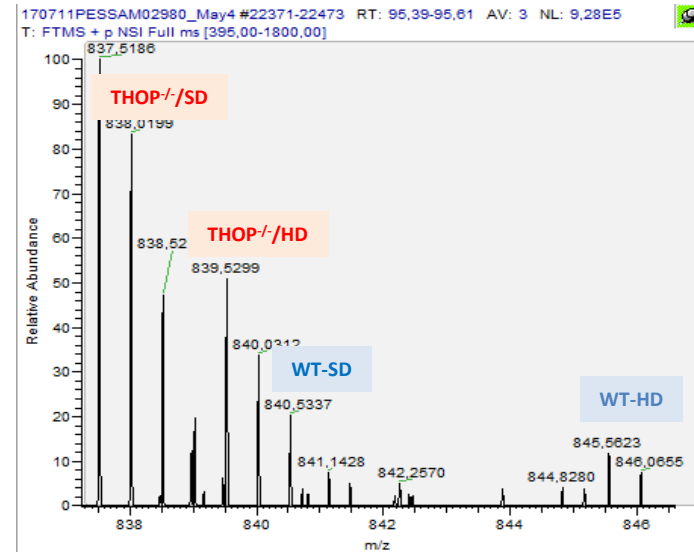
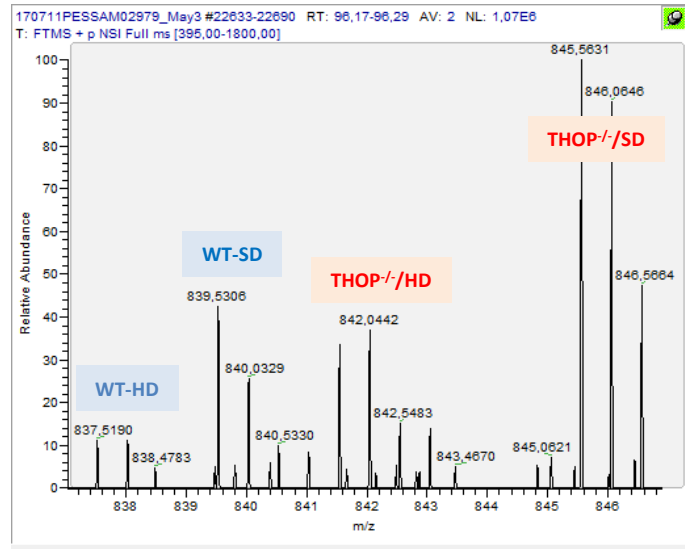
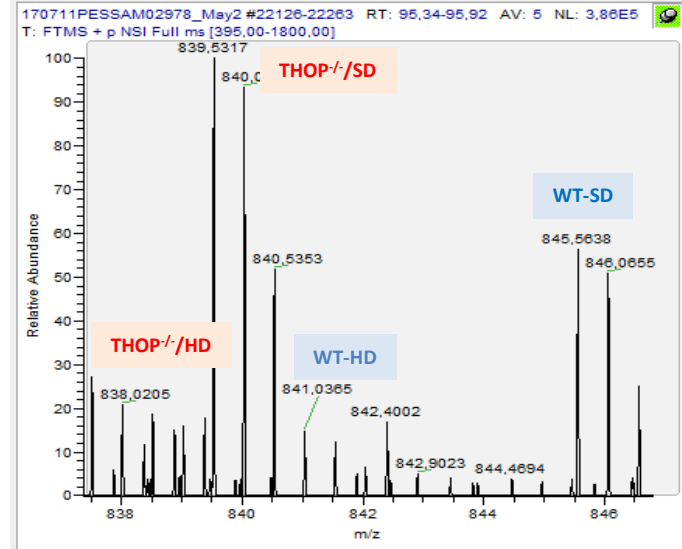
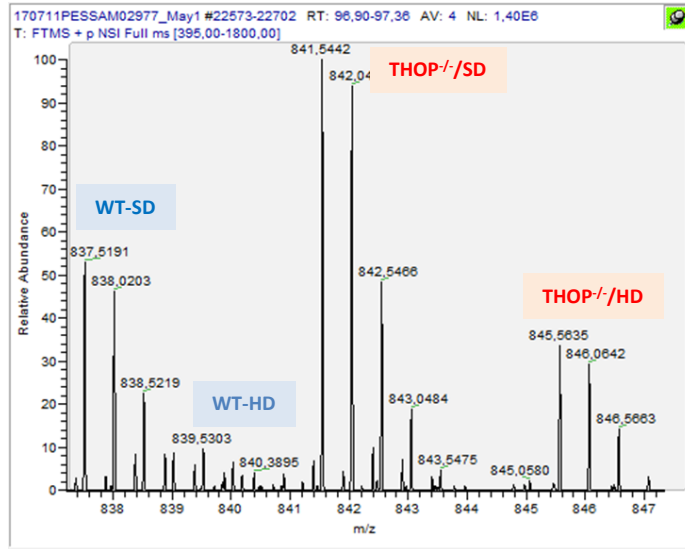
Other BLAST [web gateways](#)

#### All matches to this query

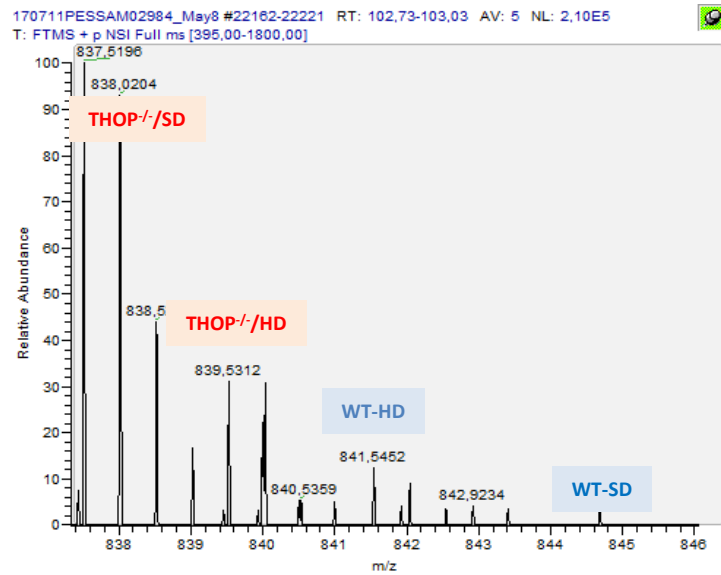
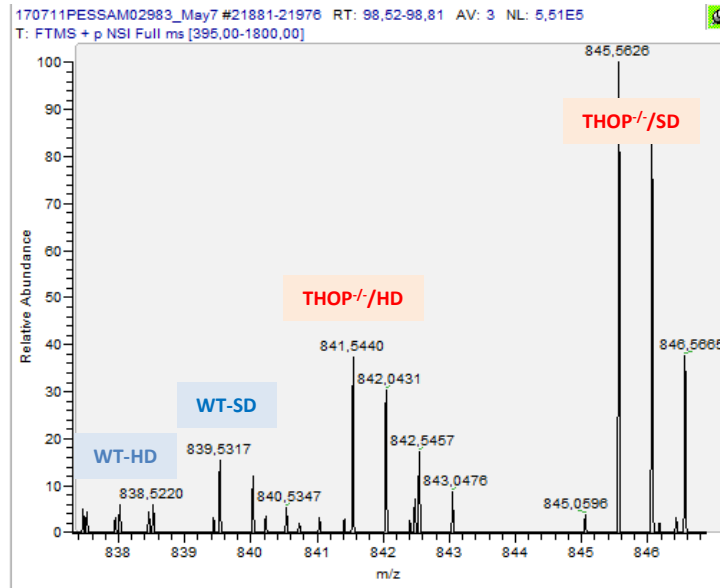
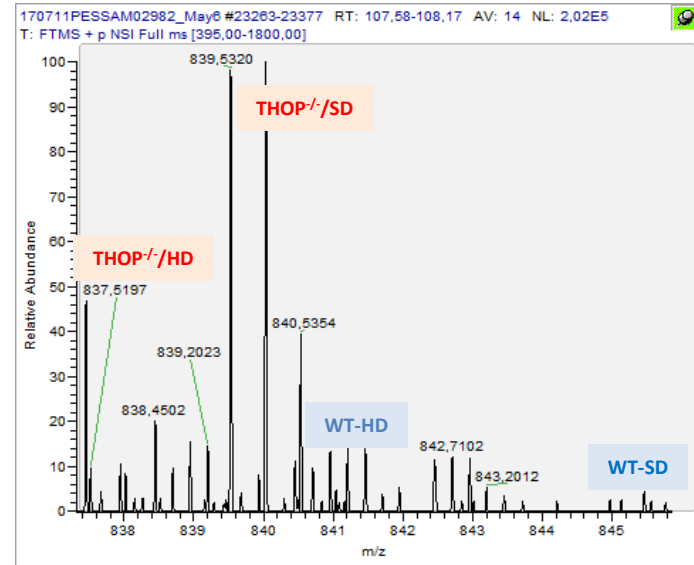
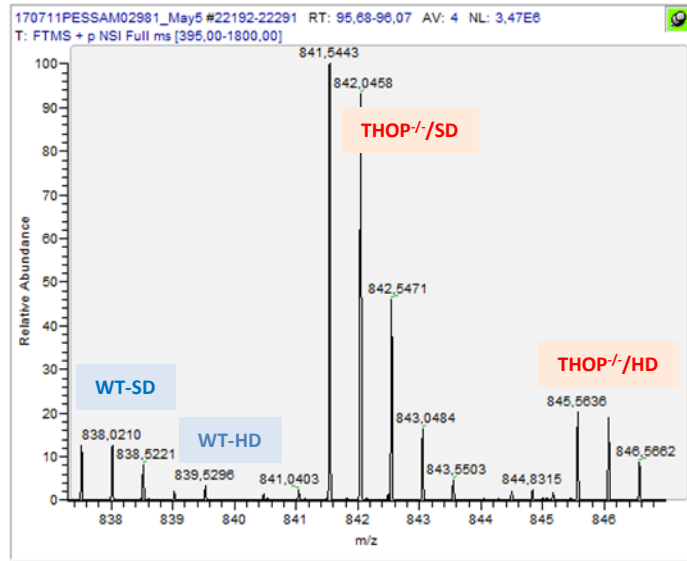
Score	Mr(calc)	Delta	Sequence
65.7	1681.0742	-0.0009	<a href="#">AQGGVLPNIQAVLLPK</a>
19.6	1680.8467	0.2266	<a href="#">MDAVLLVIAQTFMDA</a>
19.4	1680.9826	0.0906	<a href="#">AWAAMALTFLLVLLT</a>
19.4	1680.8215	0.2518	<a href="#">MVMPNLYGNIVNNV</a>
18.5	1680.8458	0.2275	<a href="#">TDTGSAEQFDLVILT</a>
18.1	1680.8252	0.2481	<a href="#">AGLEIMEQMALLQE</a>
18.0	1680.7885	0.2848	<a href="#">DSAVPCAMMLELARA</a>
17.8	1680.9484	0.1248	<a href="#">GDDSLKMHVVKILT</a>
17.5	1681.0906	-0.0173	<a href="#">IEKLELPLKQKGVG</a>
17.4	1681.0207	0.0526	<a href="#">LRPLELPVTPVIEQ</a>

Mascot: <http://www.matrixscience.com/>

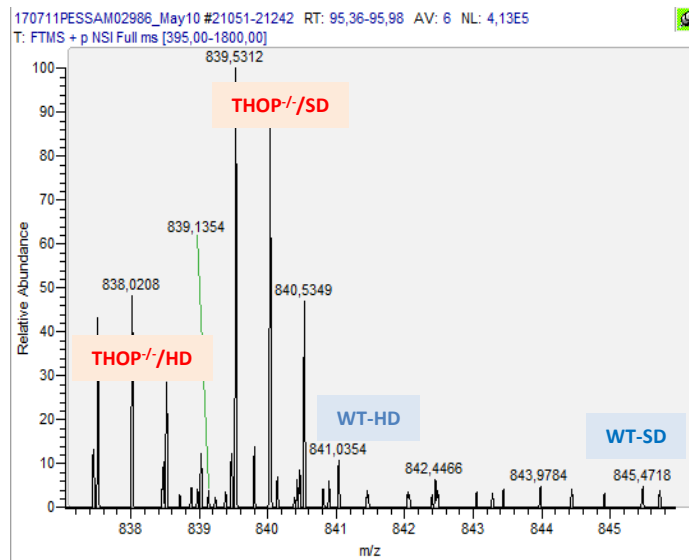
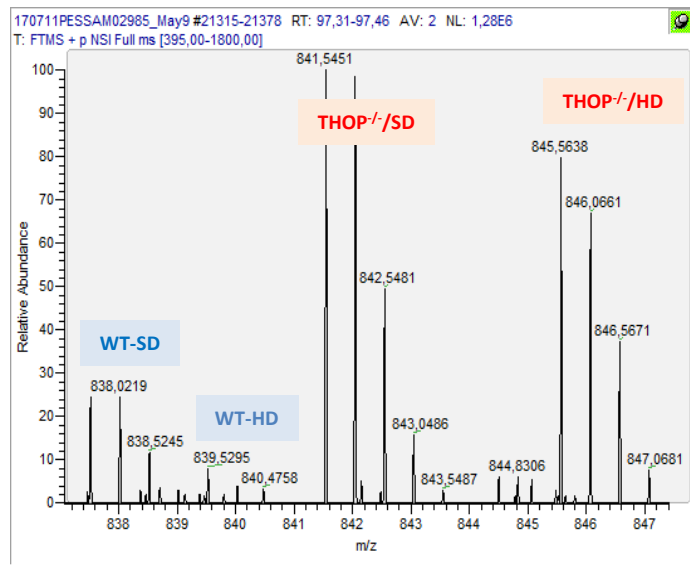
# AQGGVLPNIQAVLLPK



# AQGGVLPNIQAVLLPK

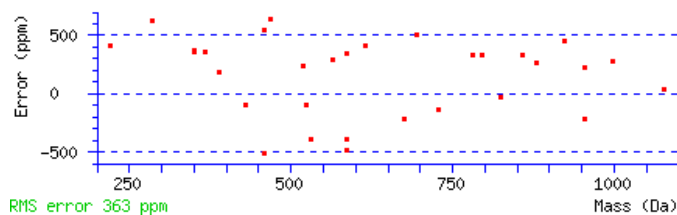
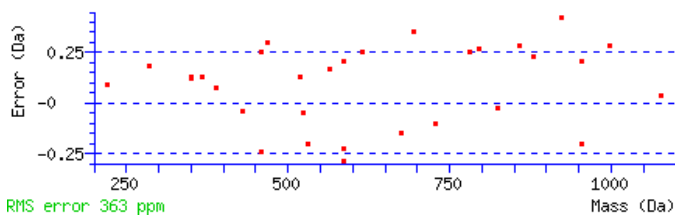


# AQGGVLPNIQAVLLPK





15	1646.0061	823.5067	1628.9796	814.9934	1627.9956	814.5014	G	537.2337	269.1205	520.2072	260.6072	519.2232	260.1152	5
16	1759.0902	880.0487	1742.0637	871.5355	1741.0796	871.0435	I	480.2123	240.6098	463.1857	232.0965	462.2017	231.6045	4
17	1906.1256	953.5664	1889.0991	945.0532	1888.1150	944.5612	M	367.1282	184.0677	350.1016	175.5545	349.1176	175.0625	3
18	2020.1685	1010.5879	2003.1420	1002.0746	2002.1580	1001.5826	N	220.0928	110.5500	203.0662	102.0368	202.0822	101.5448	2
19							S	106.0499	53.5286			88.0393	44.5233	1



NCBI BLAST search of [KQVHPDTGISSKAMGIMNS](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

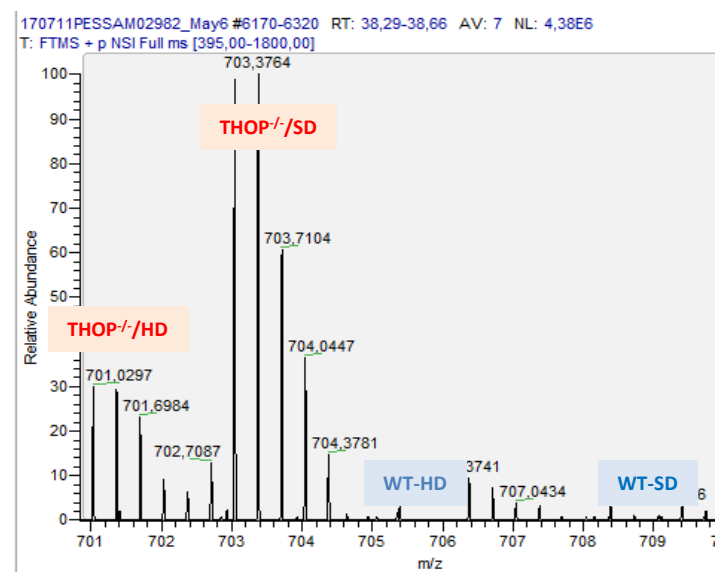
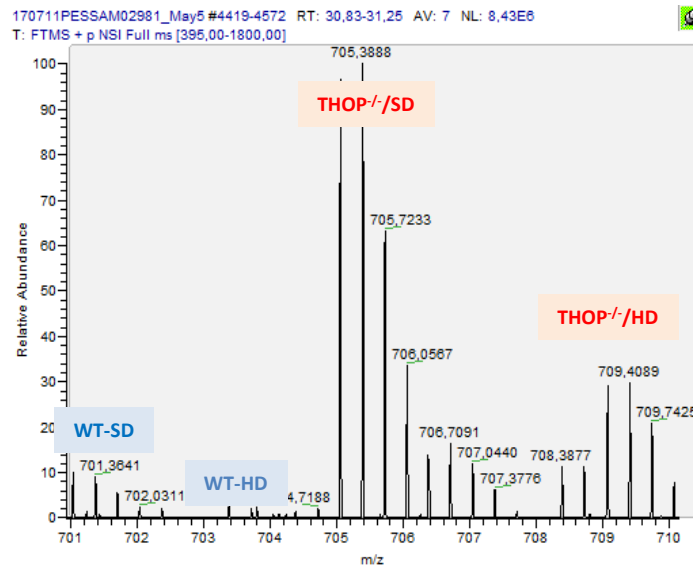
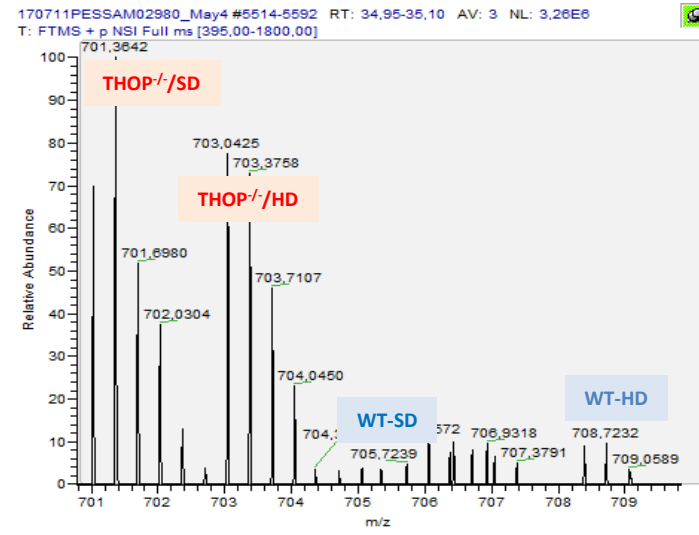
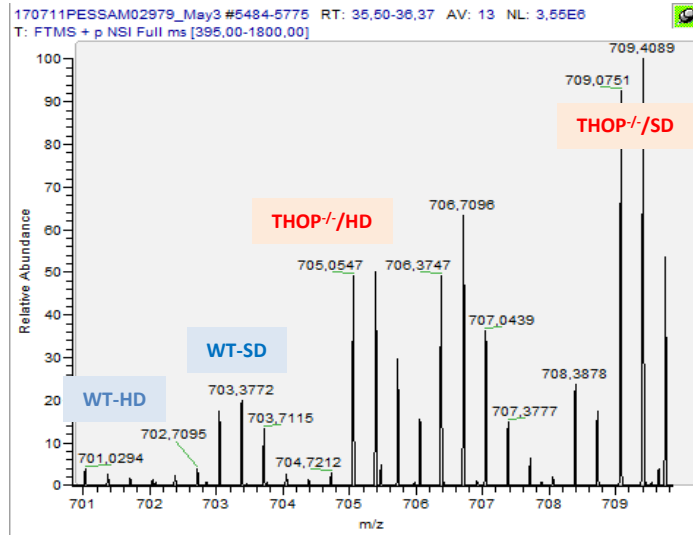
Other BLAST [web gateways](#)

#### All matches to this query

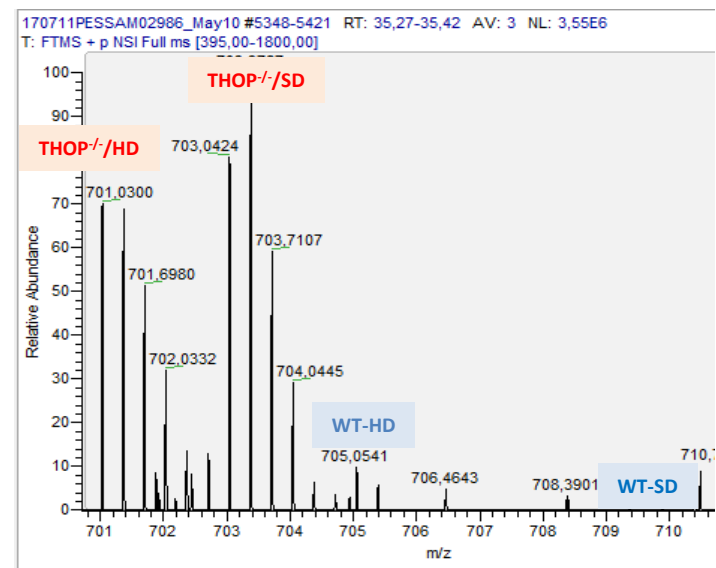
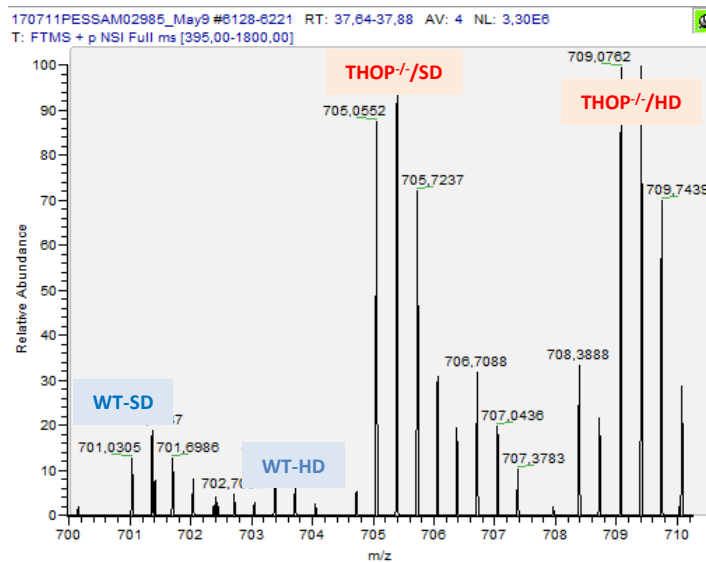
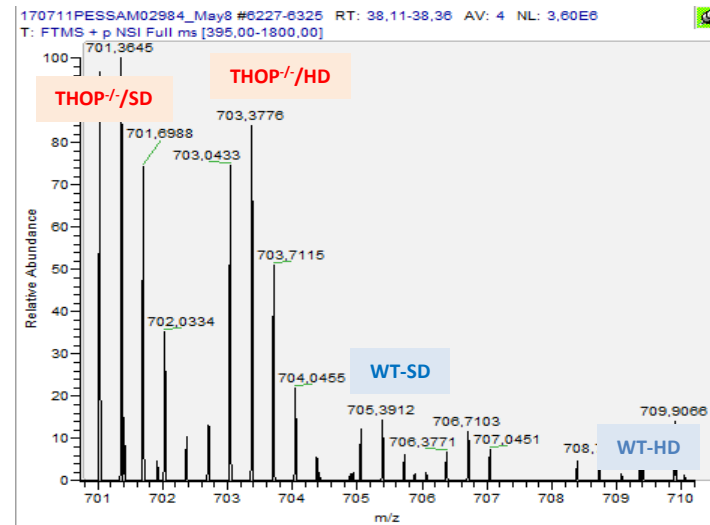
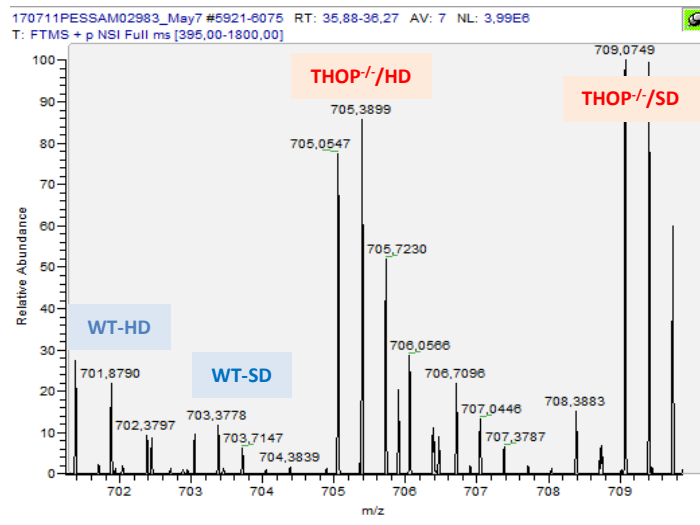
Score	Mr(calc)	Delta	Sequence
33.4	2124.2039	0.0013	<a href="#">KQVHPDTGISSKAMGIMNS</a>
23.1	2123.9537	0.2514	<a href="#">TGLETIGRDTCPGEMGAEMI</a>
22.1	2124.0193	0.1858	<a href="#">TLTDEDESPEGSRGGLEFSN</a>
21.4	2123.9948	0.2103	<a href="#">FMLGTIPFPEGMGGSVYFS</a>
21.0	2124.1352	0.0700	<a href="#">APVVNESGAILGMVTLGNMLS</a>
20.8	2124.0752	0.1299	<a href="#">YFHRDRLNTGSKDLFAE</a>
20.7	2124.0751	0.1300	<a href="#">YNIVLFLTTFQESLGMSN</a>
20.6	2124.1430	0.0621	<a href="#">LSSLGQIDGWSSMQLRAVV</a>
19.8	2124.0918	0.1133	<a href="#">RERMDDSSYTSKLLSCK</a>
19.4	2123.9892	0.2159	<a href="#">SVSLLSALATSDPGQMDSSQS</a>

Mascot: <http://www.matrixscience.com/>

# KQVHPDTGISSKAMGI<sub>m</sub>NS



# KQVHPDTGISSKAMGImNS



# Mascot Search Results

## Peptide View

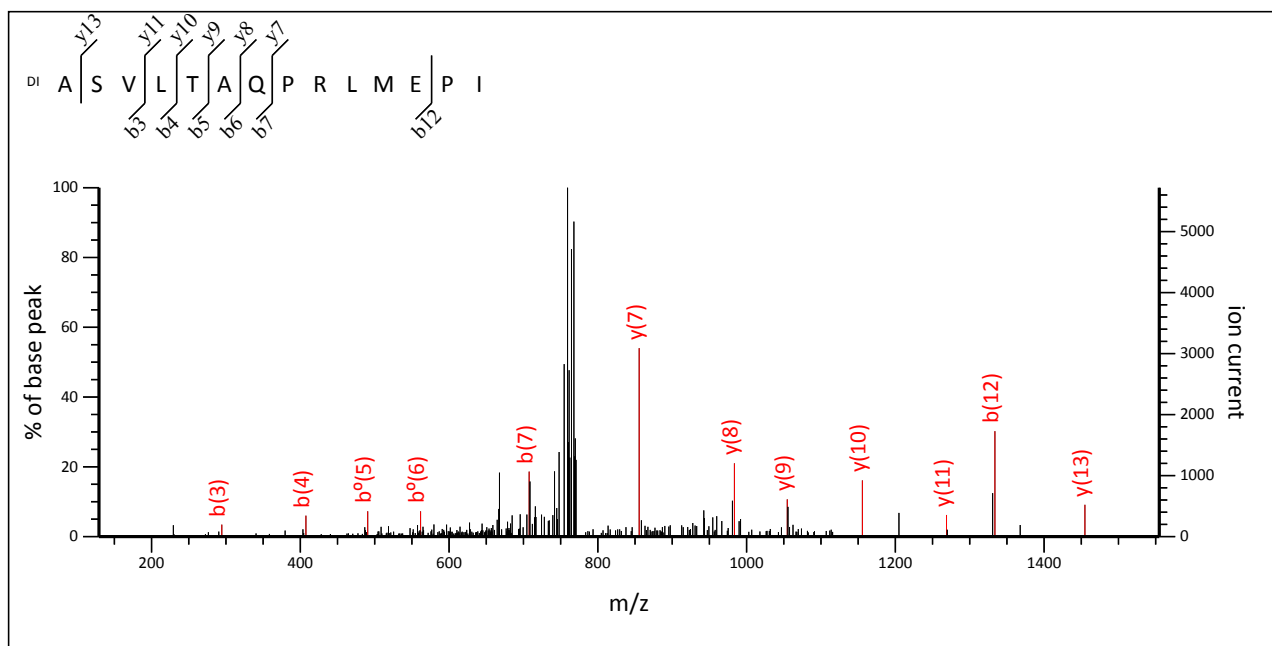
MS/MS Fragmentation of **ASVLTAQPR**LMPEI

Found in **EF2\_MOUSE** in **SwissProt**, Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2

Match to Query 10834: 1560.910508 from(781.462530,2+) intensity(2986679.8000) scans(18798) rawscans(sn18798)  
rtinseconds(4807.0934) index(12263)

Title: 12264: Scan 18798 (rt=4807.09) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



129.28

to

1554.87



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1560.9090

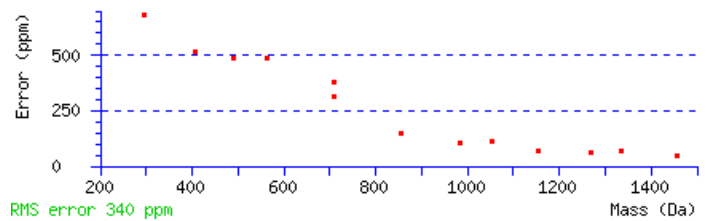
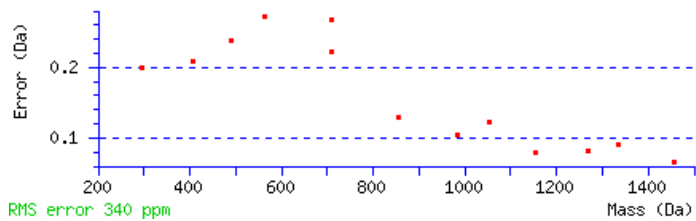
Variable modifications:

N-term : Dimethyl:2H(6)13C(2) (N-term)

Ions Score: 48 Expect: 0.022

Matches : 13/128 fragment ions using 13 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	108.1201	54.5637					A							14
2	195.1521	98.0797			177.1415	89.0744	S	1454.8036	727.9054	1437.7770	719.3921	1436.7930	718.9001	13
3	294.2205	147.6139			276.2099	138.6086	V	1367.7715	684.3894	1350.7450	675.8761	1349.7610	675.3841	12
4	407.3046	204.1559			389.2940	195.1506	L	1268.7031	634.8552	1251.6766	626.3419	1250.6926	625.8499	11
5	508.3522	254.6798			490.3417	245.6745	T	1155.6191	578.3132	1138.5925	569.7999	1137.6085	569.3079	10
6	579.3894	290.1983			561.3788	281.1930	A	1054.5714	527.7893	1037.5448	519.2761	1036.5608	518.7840	9
7	707.4479	354.2276	690.4214	345.7143	689.4374	345.2223	Q	983.5343	492.2708	966.5077	483.7575	965.5237	483.2655	8
8	804.5007	402.7540	787.4742	394.2407	786.4901	393.7487	P	855.4757	428.2415	838.4491	419.7282	837.4651	419.2362	7
9	960.6018	480.8045	943.5753	472.2913	942.5912	471.7993	R	758.4229	379.7151	741.3964	371.2018	740.4124	370.7098	6
10	1073.6859	537.3466	1056.6593	528.8333	1055.6753	528.3413	L	602.3218	301.6645			584.3112	292.6593	5
11	1204.7264	602.8668	1187.6998	594.3535	1186.7158	593.8615	M	489.2377	245.1225			471.2272	236.1172	4
12	1333.7690	667.3881	1316.7424	658.8748	1315.7584	658.3828	E	358.1973	179.6023			340.1867	170.5970	3
13	1430.8217	715.9145	1413.7952	707.4012	1412.8112	706.9092	P	229.1547	115.0810					2
14							I	132.1019	66.5546					1



NCBI **BLAST** search of [ASVLTAQPRLMEPI](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

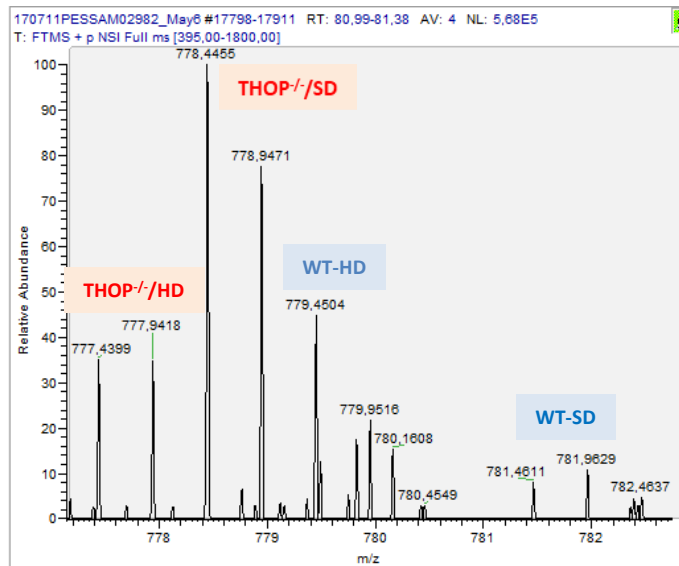
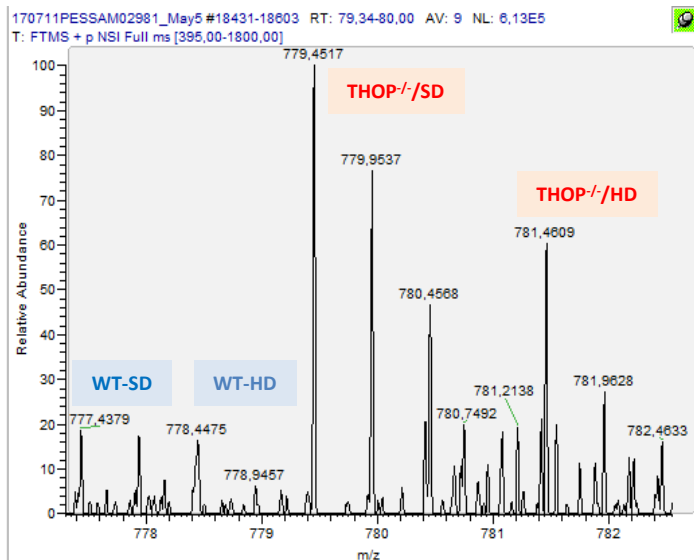
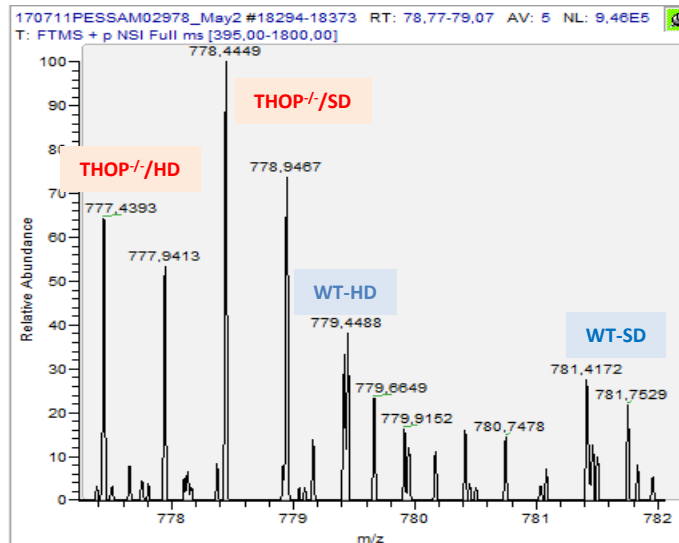
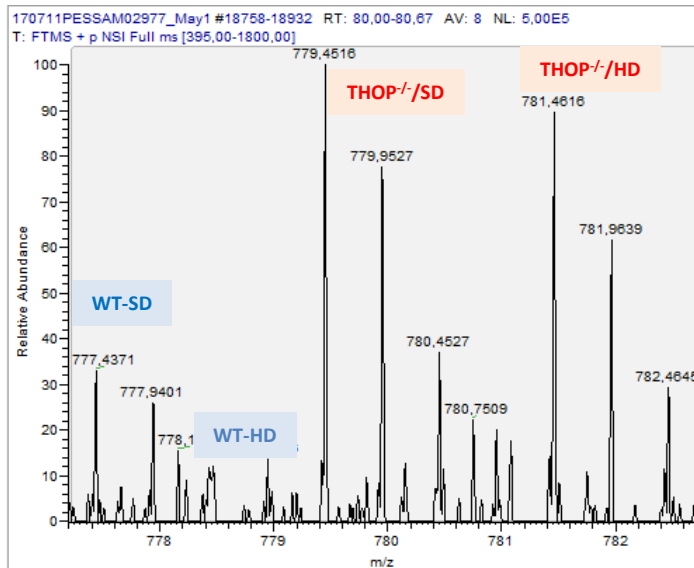
Other BLAST [web gateways](#)

#### All matches to this query

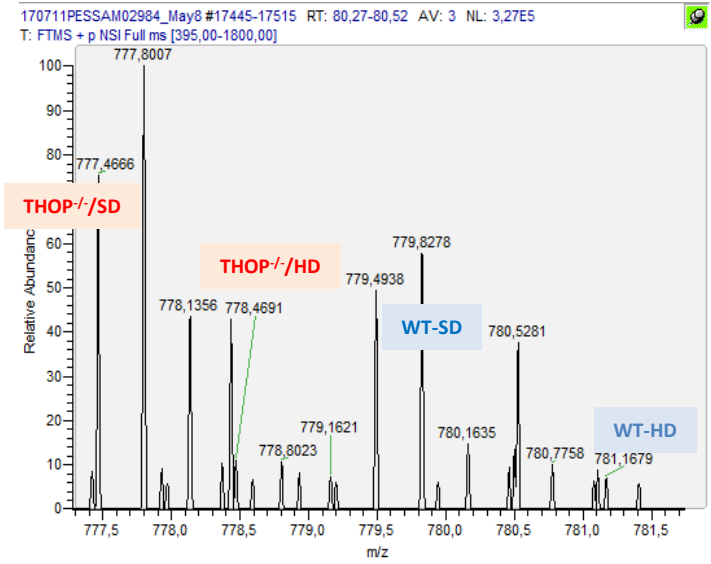
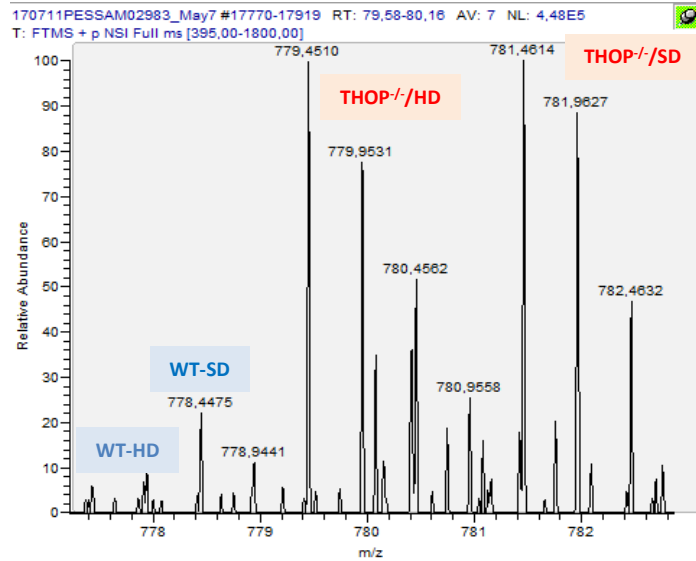
Score	Mr(calc)	Delta	Sequence
48.5	1560.9090	0.0015	<a href="#">ASVLTAQPRLMEPI</a>
29.5	1560.8850	0.0255	<a href="#">FLRFCKQATLQE</a>
28.0	1560.9007	0.0098	<a href="#">AEGLTCLIKVGAEAD</a>
26.9	1560.7915	0.1190	<a href="#">GEALTAEKEHMEE</a>
22.4	1560.9279	-0.0174	<a href="#">KLPIYALAQTLGAF</a>
20.6	1560.8868	0.0237	<a href="#">QELTSKQGGRCSVP</a>
19.3	1560.8624	0.0482	<a href="#">RLRLNEEATLQE</a>
18.9	1560.7781	0.1324	<a href="#">QELTAMRMSRDTA</a>
18.9	1560.7781	0.1324	<a href="#">QELTAMRMSRDTA</a>
17.6	1560.8483	0.0622	<a href="#">DRDALVGLAVLLGCD</a>

Mascot: <http://www.matrixscience.com/>

# ASVLTAQPRLMEPI



# ASVLTAQPRLMEPI



# Mascot Search Results

## Peptide View

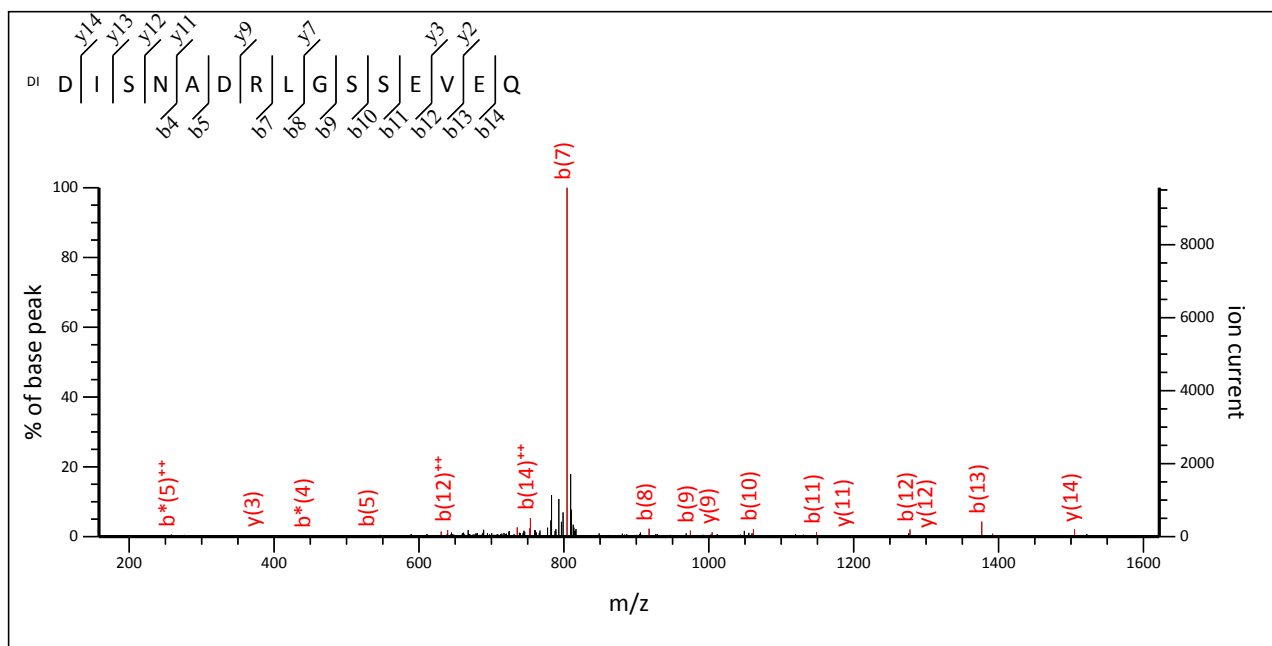
MS/MS Fragmentation of **DISNADRLGSVEEQ**

Found in **KCRM\_MOUSE** in **SwissProt**, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 12401: 1650.795028 from(826.404790,2+) intensity(1203988.6000) scans(9733) rawscans(sn9733) rtinseconds(2944.0576) index(6186)

Title: 6187: Scan 9733 (rt=2944.06) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02979\_May3.raw]

Data file 170711PESSAM02979\_May3.temp.mgf



158.26

to

1621.86



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1650.7999

Variable modifications:

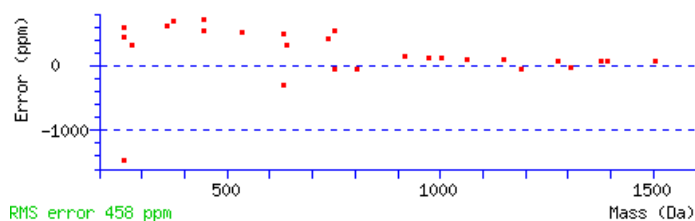
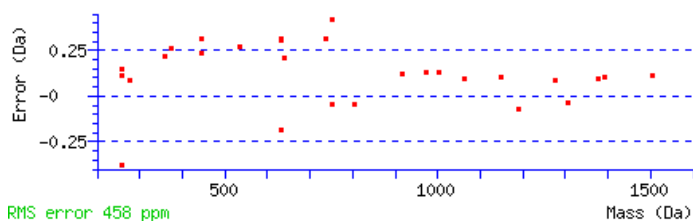
N-term : Dimethyl:2H(4) (N-term)

Ions Score: 75 Expect: 8.1e-005

Matches : 28/160 fragment ions using 37 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	148.0906	74.5490			130.0801	65.5437	D							15
2	261.1747	131.0910			243.1641	122.0857	I	1504.7238	752.8655	1487.6972	744.3523	1486.7132	743.8603	14
3	348.2067	174.6070			330.1962	165.6017	S	1391.6397	696.3235	1374.6132	687.8102	1373.6292	687.3182	13
4	462.2496	231.6285	445.2231	223.1152	444.2391	222.6232	N	1304.6077	652.8075	1287.5811	644.2942	1286.5971	643.8022	12
5	533.2868	267.1470	516.2602	258.6337	515.2762	258.1417	A	1190.5648	595.7860	1173.5382	587.2727	1172.5542	586.7807	11
6	648.3137	324.6605	631.2872	316.1472	630.3031	315.6552	D	1119.5277	560.2675	1102.5011	551.7542	1101.5171	551.2622	10
7	804.4148	402.7110	787.3883	394.1978	786.4042	393.7058	R	1004.5007	502.7540	987.4742	494.2407	986.4901	493.7487	9
8	917.4989	459.2531	900.4723	450.7398	899.4883	450.2478	L	848.3996	424.7034	831.3731	416.1902	830.3890	415.6982	8
9	974.5203	487.7638	957.4938	479.2505	956.5098	478.7585	G	735.3155	368.1614	718.2890	359.6481	717.3050	359.1561	7
10	1061.5524	531.2798	1044.5258	522.7665	1043.5418	522.2745	S	678.2941	339.6507	661.2675	331.1374	660.2835	330.6454	6
11	1148.5844	574.7958	1131.5578	566.2826	1130.5738	565.7906	S	591.2620	296.1347	574.2355	287.6214	573.2515	287.1294	5
12	1277.6270	639.3171	1260.6004	630.8039	1259.6164	630.3119	E	504.2300	252.6186	487.2035	244.1054	486.2195	243.6134	4
13	1376.6954	688.8513	1359.6689	680.3381	1358.6848	679.8461	V	375.1874	188.0974	358.1609	179.5841	357.1769	179.0921	3
14	1505.7380	753.3726	1488.7114	744.8594	1487.7274	744.3674	E	276.1190	138.5631	259.0925	130.0499	258.1084	129.5579	2

15						Q	147.0764	74.0418	130.0499	65.5286			1
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NCBI **BLAST** search of [DISNADRLGSSEVEQ](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

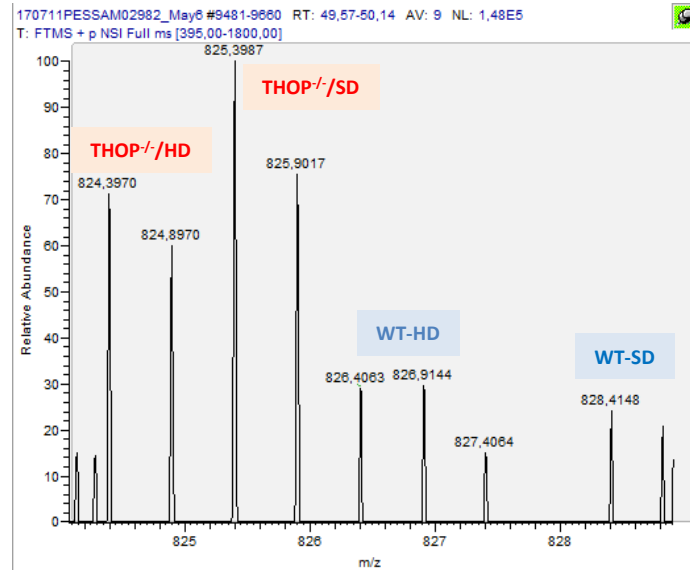
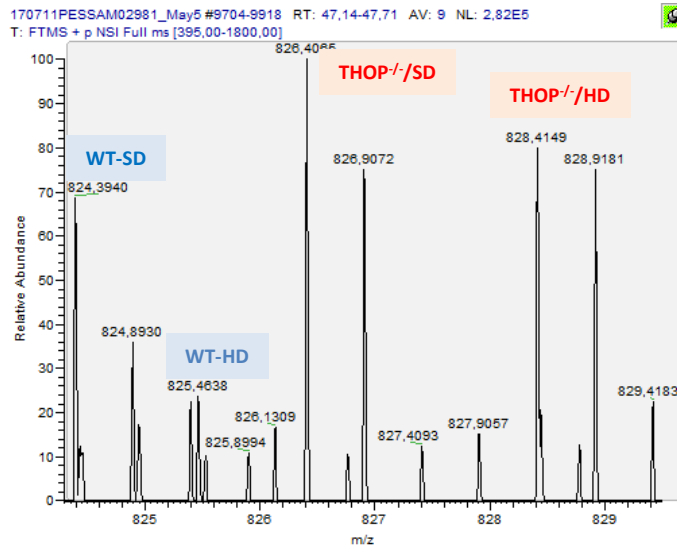
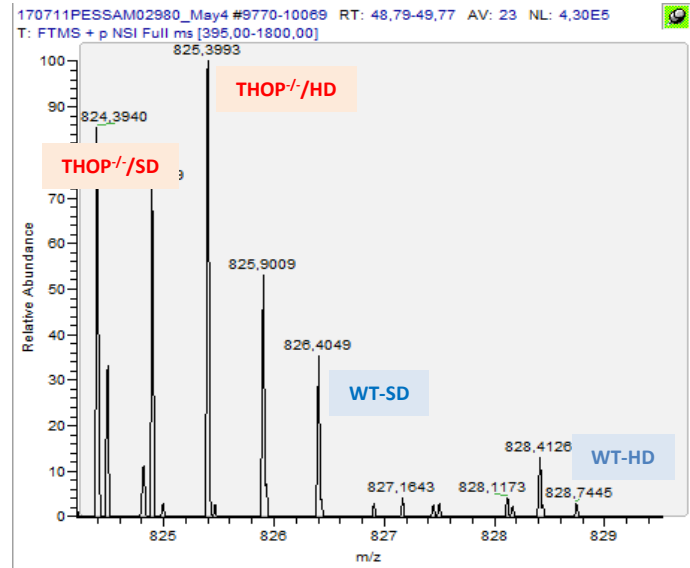
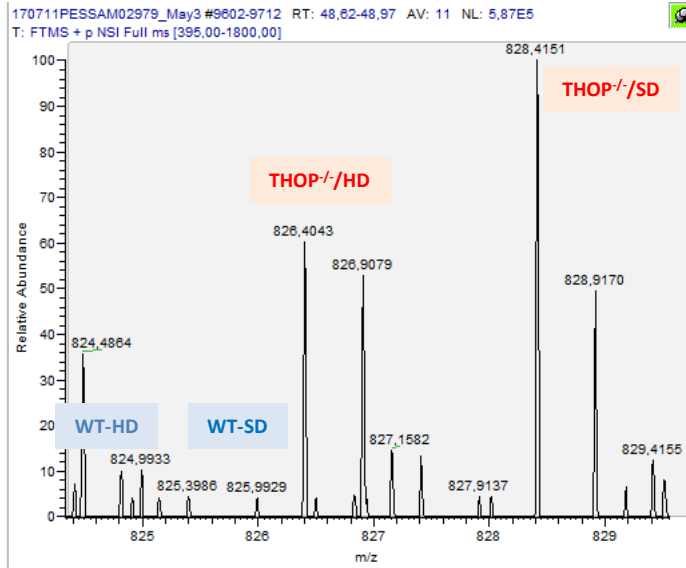
Other BLAST [web gateways](#)

#### All matches to this query

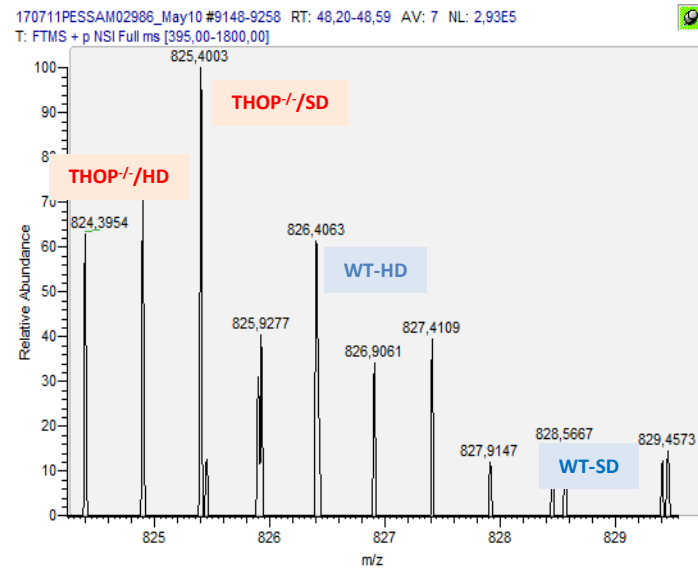
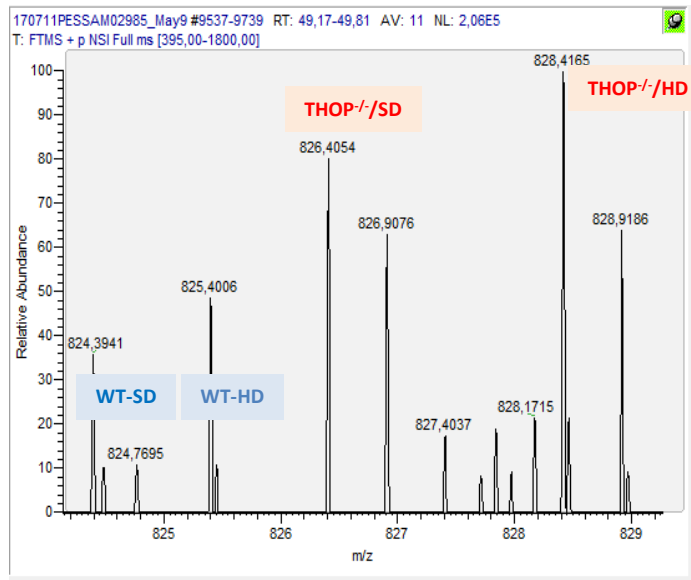
Score	Mr(calc)	Delta	Sequence
75.0	1650.7999	-0.0048	<a href="#">DISNADRLGSSEVEQ</a>
30.3	1650.9810	-0.1860	<a href="#">RLSNVSLTGLGTVRT</a>
25.1	1650.7634	0.0316	<a href="#">RSVEEAVNGSEEEENA</a>
24.1	1651.0120	-0.2170	<a href="#">VSGTTLRGLIKLNDT</a>
23.7	1650.8875	-0.0925	<a href="#">ARVTWCAVGSEEKR</a>
22.9	1650.7828	0.0123	<a href="#">DQVSAYGFITNNYQ</a>
22.4	1650.7407	0.0544	<a href="#">SEQEVNELCQSVQE</a>
21.9	1650.9506	-0.1556	<a href="#">EVLCSVSLKLWQE</a>
21.8	1650.7948	0.0002	<a href="#">TSSASSVTGVVNGESLE</a>
21.6	1650.8626	-0.0676	<a href="#">DQVSEDTVEMPLPK</a>

Mascot: <http://www.matrixscience.com/>

# DISNADRLGSSEVEQ



# DISNADRLGSSEVEQ



# Mascot Search Results

## Peptide View

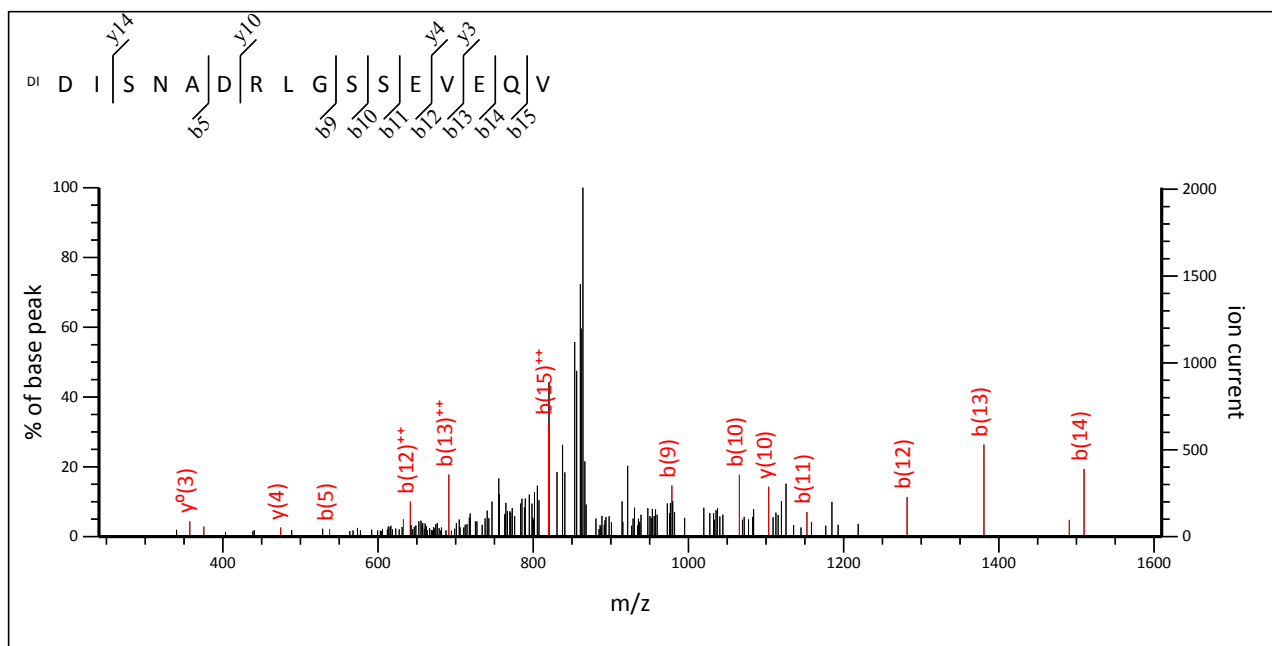
MS/MS Fragmentation of **DISNADRLGSSEVEQV**

Found in **KCRM\_MOUSE** in **SwissProt**, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 13809: 1753.890468 from(877.952510,2+) intensity(1823285.3000) scans(13413) rawscans(sn13413)  
rtinseconds(3585.2932) index(8910)

Title: 8911: Scan 13413 (rt=3585.29) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02981\_May5.raw]

Data file 170711PESSAM02981\_May5.temp.mgf



240.37

to

1609.83



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1753.8875

Variable modifications:

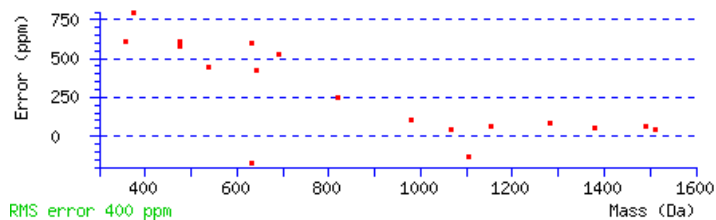
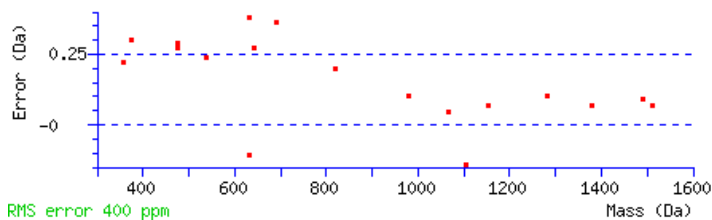
N-term : Dimethyl:2H(6)13C(2) (N-term)

Ions Score: 34 Expect: 0.46

Matches : 18/168 fragment ions using 31 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	152.1099	76.5586			134.0993	67.5533	D							16
2	265.1940	133.1006			247.1834	124.0953	I	1603.7922	802.3997	1586.7657	793.8865	1585.7816	793.3945	15
3	352.2260	176.6166			334.2154	167.6113	S	1490.7081	745.8577	1473.6816	737.3444	1472.6976	736.8524	14
4	466.2689	233.6381	449.2424	225.1248	448.2583	224.6328	N	1403.6761	702.3417	1386.6496	693.8284	1385.6655	693.3364	13
5	537.3060	269.1566	520.2795	260.6434	519.2955	260.1514	A	1289.6332	645.3202	1272.6066	636.8070	1271.6226	636.3149	12
6	652.3330	326.6701	635.3064	318.1568	634.3224	317.6648	D	1218.5961	609.8017	1201.5695	601.2884	1200.5855	600.7964	11
7	808.4341	404.7207	791.4075	396.2074	790.4235	395.7154	R	1103.5691	552.2882	1086.5426	543.7749	1085.5586	543.2829	10
8	921.5181	461.2627	904.4916	452.7494	903.5076	452.2574	L	947.4680	474.2376	930.4415	465.7244	929.4575	465.2324	9
9	978.5396	489.7734	961.5131	481.2602	960.5290	480.7682	G	834.3840	417.6956	817.3574	409.1823	816.3734	408.6903	8
10	1065.5716	533.2895	1048.5451	524.7762	1047.5611	524.2842	S	777.3625	389.1849	760.3359	380.6716	759.3519	380.1796	7
11	1152.6037	576.8055	1135.5771	568.2922	1134.5931	567.8002	S	690.3305	345.6689	673.3039	337.1556	672.3199	336.6636	6
12	1281.6463	641.3268	1264.6197	632.8135	1263.6357	632.3215	E	603.2984	302.1529	586.2719	293.6396	585.2879	293.1476	5
13	1380.7147	690.8610	1363.6881	682.3477	1362.7041	681.8557	V	474.2558	237.6316	457.2293	229.1183	456.2453	228.6263	4
14	1509.7573	755.3823	1492.7307	746.8690	1491.7467	746.3770	E	375.1874	188.0974	358.1609	179.5841	357.1769	179.0921	3

15	1637.8158	819.4116	1620.7893	810.8983	1619.8053	810.4063	Q	246.1448	123.5761	229.1183	115.0628			2
16							V	118.0863	59.5468					1



NCBI **BLAST** search of [DISNADRLGSSEVEQV](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

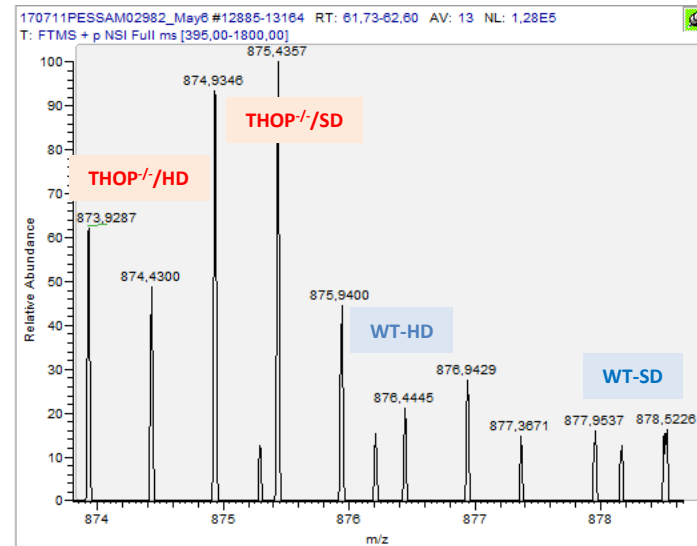
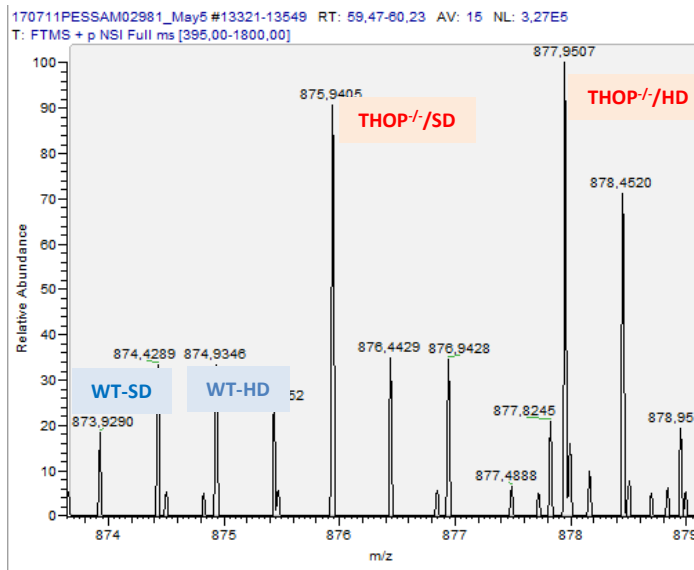
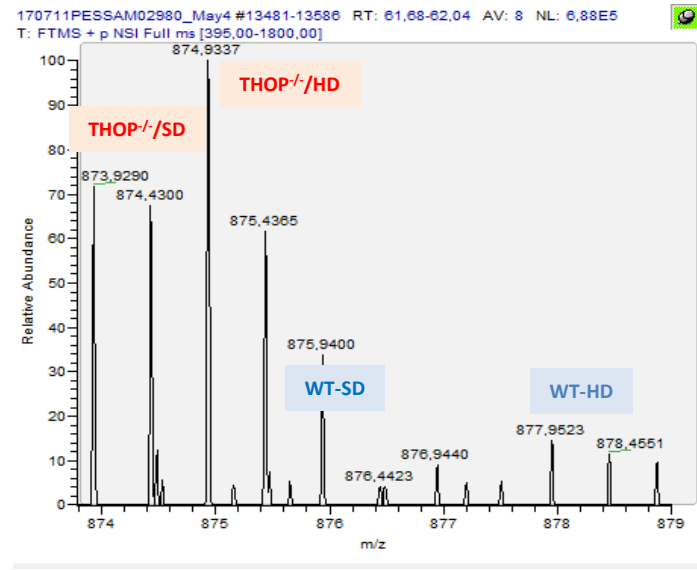
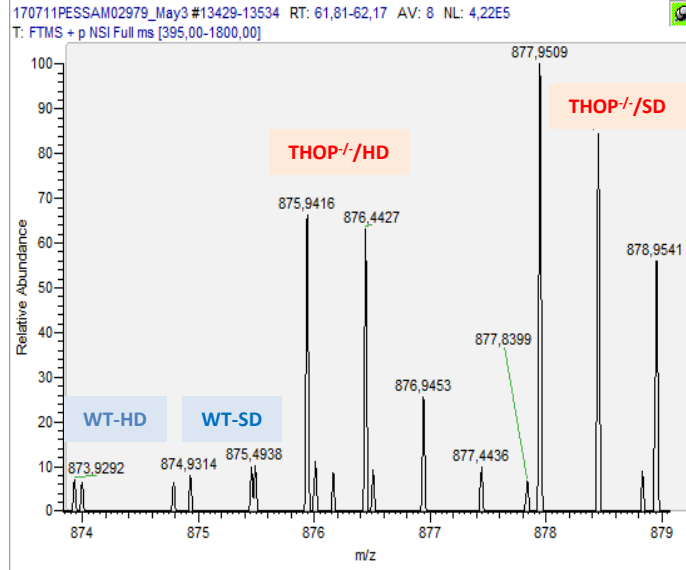
Other BLAST [web gateways](#)

#### All matches to this query

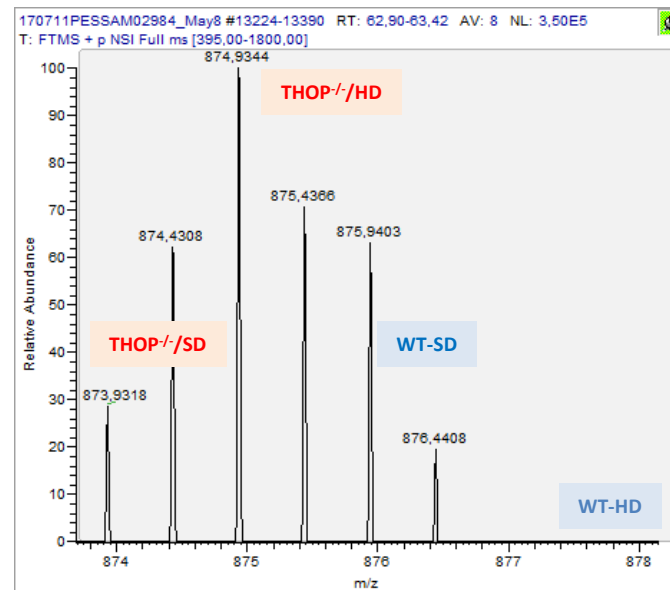
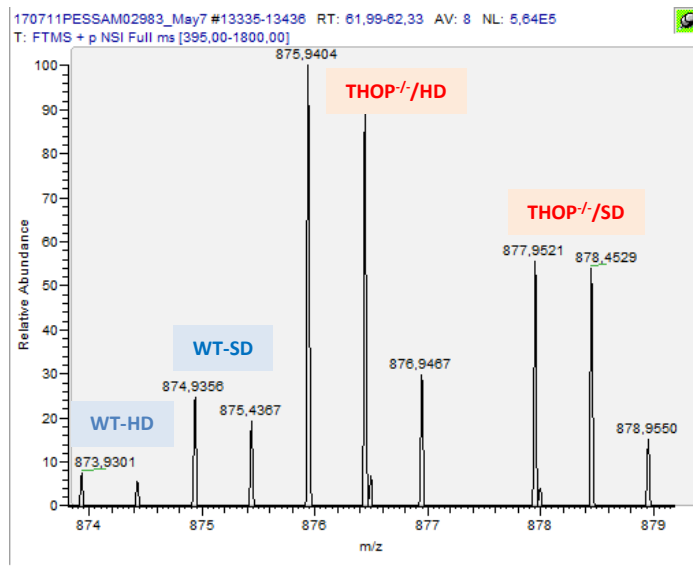
Score	Mr(calc)	Delta	Sequence
33.7	1753.8875	0.0029	<a href="#">DISNADRLGSSEVEQV</a>
28.9	1753.8808	0.0097	<a href="#">EDTFKKCSSEVEAK</a>
22.5	1754.0066	-0.1161	<a href="#">ILTEGQVKNSEVEQV</a>
21.3	1753.9308	-0.0404	<a href="#">KGGPGA AVEPSEGEEVQ</a>
20.4	1753.9284	-0.0379	<a href="#">FRDEELKCTVVELN</a>
19.9	1754.0025	-0.1121	<a href="#">NVTAEKEVSTGTVLRS</a>
19.9	1753.7428	0.1477	<a href="#">ENGSDISSAENEQTEA</a>
19.8	1753.9873	-0.0968	<a href="#">GPPGHKGEGKDMVISR</a>
19.5	1753.9826	-0.0921	<a href="#">GLLTTT VTLQQPVELN</a>
19.1	1753.9195	-0.0291	<a href="#">GNEVDGMSRPLRPRP</a>

Mascot: <http://www.matrixscience.com/>

# DISNADRLGSSEVEQV



# DISNADRLGSSEVEQV



# Mascot Search Results

## Peptide View

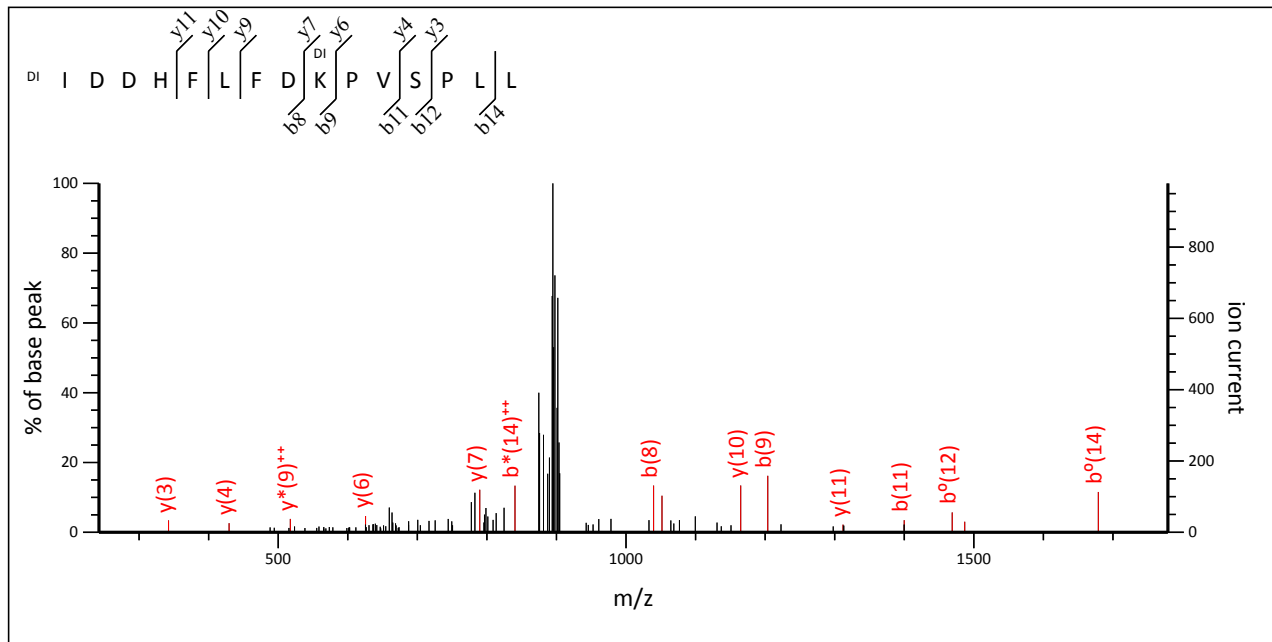
MS/MS Fragmentation of **IDDHFLFDKPVSP**LL

Found in **KCRM\_MOUSE** in **SwissProt**, Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1

Match to Query 14384: 1827.078528 from(914.546540,2+) intensity(746218.2800) scans(23165-23196) rawscans(sn23165:sn23196) rtinseconds(5986.6983-5996.3487) index(15276)

Title: 15277: Sum of 2 scans in range 23165 (rt=5986.7) to 23196 (rt=5996.35) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



242.33

to 1779



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1827.0757

Variable modifications:

N-term : Dimethyl:2H(6)13C(2) (N-term)

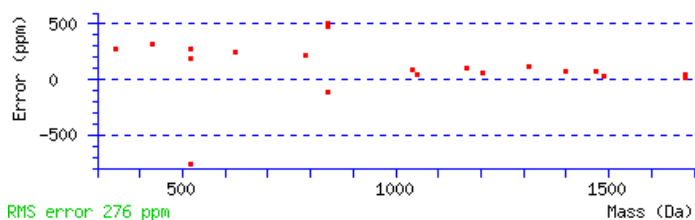
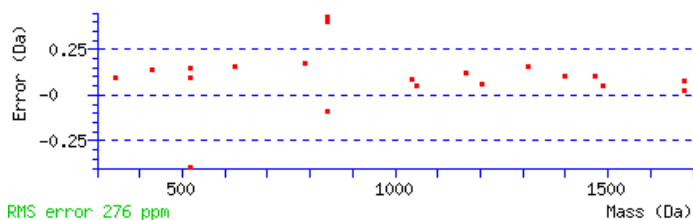
K9 : Dimethyl:2H(6)13C(2) (K)

Ions Score: 46 Expect: 0.0018

Matches : 20/132 fragment ions using 25 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	150.1670	75.5871					I							15
2	265.1940	133.1006			247.1834	124.0953	D	1678.9232	839.9652	1661.8967	831.4520	1660.9126	830.9600	14
3	380.2209	190.6141			362.2103	181.6088	D	1563.8963	782.4518	1546.8697	773.9385	1545.8857	773.4465	13
4	517.2798	259.1435			499.2692	250.1383	H	1448.8693	724.9383	1431.8428	716.4250	1430.8588	715.9330	12
5	664.3482	332.6777			646.3377	323.6725	F	1311.8104	656.4088	1294.7839	647.8956	1293.7998	647.4036	11
6	777.4323	389.2198			759.4217	380.2145	L	1164.7420	582.8746	1147.7154	574.3614	1146.7314	573.8694	10
7	924.5007	462.7540			906.4901	453.7487	F	1051.6579	526.3326	1034.6314	517.8193	1033.6474	517.3273	9
8	1039.5276	520.2675			1021.5171	511.2622	D	904.5895	452.7984	887.5630	444.2851	886.5789	443.7931	8
9	1203.6983	602.3528	1186.6717	593.8395	1185.6877	593.3475	K	789.5626	395.2849	772.5360	386.7716	771.5520	386.2796	7
10	1300.7510	650.8792	1283.7245	642.3659	1282.7405	641.8739	P	625.3919	313.1996			607.3814	304.1943	6
11	1399.8195	700.4134	1382.7929	691.9001	1381.8089	691.4081	V	528.3392	264.6732			510.3286	255.6679	5
12	1486.8515	743.9294	1469.8249	735.4161	1468.8409	734.9241	S	429.2708	215.1390			411.2602	206.1337	4
13	1583.9042	792.4558	1566.8777	783.9425	1565.8937	783.4505	P	342.2387	171.6230					3

14	1696.9883	848.9978	1679.9618	840.4845	1678.9777	839.9925	L	245.1860	123.0966					2
15							L	132.1019	66.5546					1



NCBI **BLAST** search of [IDDHFLFDKPVSPLL](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

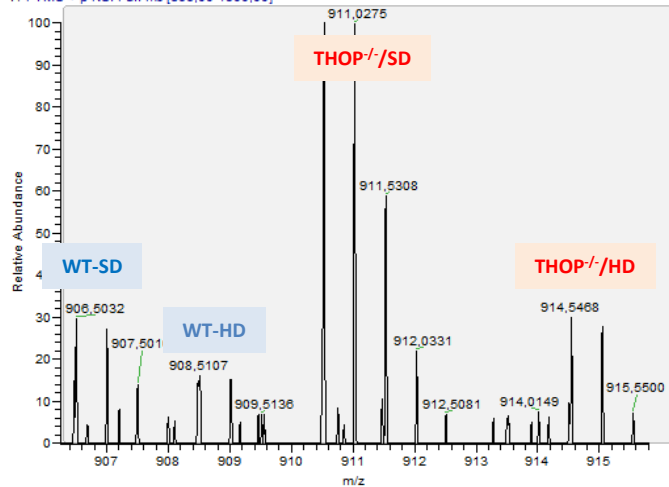
#### All matches to this query

Score	Mr(calc)	Delta	Sequence
46.4	1827.0757	0.0028	<a href="#">IDDHFLFDKPVSPLL</a>
16.2	1827.1069	-0.0284	<a href="#">QLLSKTPGSRSQPLPL</a>
15.8	1827.0717	0.0068	<a href="#">PVDAKVGLGISQSSSLP</a>
15.1	1826.9560	0.1225	<a href="#">LCPSVPSNSVSQLOKAN</a>
12.6	1826.8972	0.1813	<a href="#">PASSASEVASTESMPVTL</a>
11.2	1827.0618	0.0167	<a href="#">VTASPVIAVTNFRQV</a>
11.1	1826.9384	0.1401	<a href="#">IMSIFWGMDMVILAI</a>
11.0	1826.8886	0.1899	<a href="#">MARSRGHLWAYSPEP</a>
10.9	1827.0135	0.0651	<a href="#">ASMPDNTAAQKVSHLLG</a>
10.9	1826.9978	0.0807	<a href="#">LITEAQTQASGAGNKFQ</a>

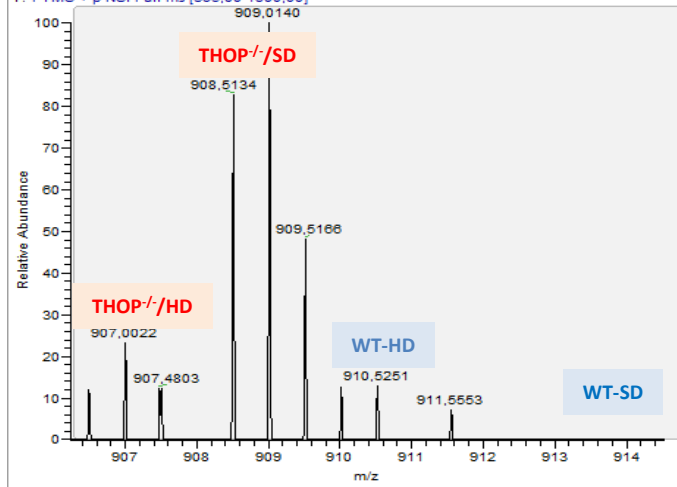
Mascot: <http://www.matrixscience.com/>

# IDDHFLFDKPVSPLL

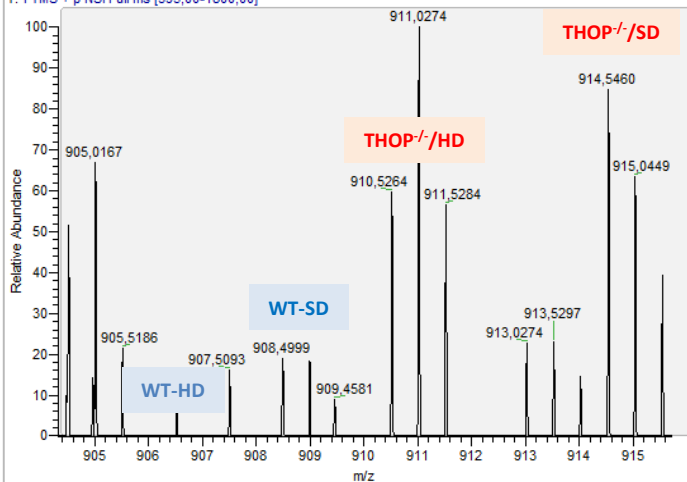
170711PESSAM02977\_May1 #23049-23446 RT: 99.33-101.22 AV: 14 NL: 5,82E4  
T: FTMS + p NSI Full ms [395,00-1800,00]



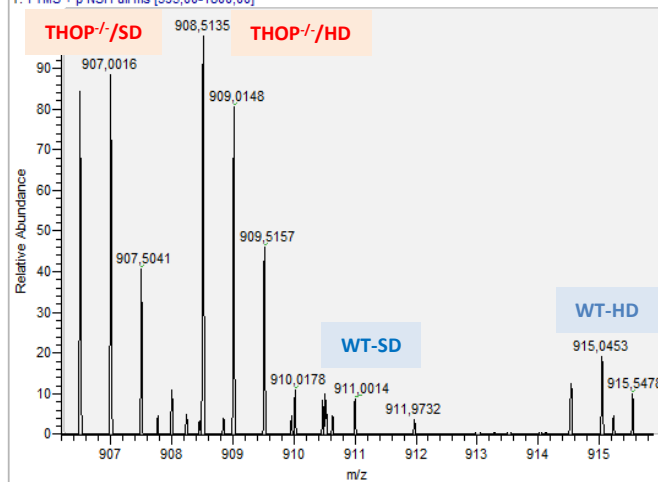
170711PESSAM02978\_May2 #22636-22732 RT: 97.90-98.20 AV: 3 NL: 2,95E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



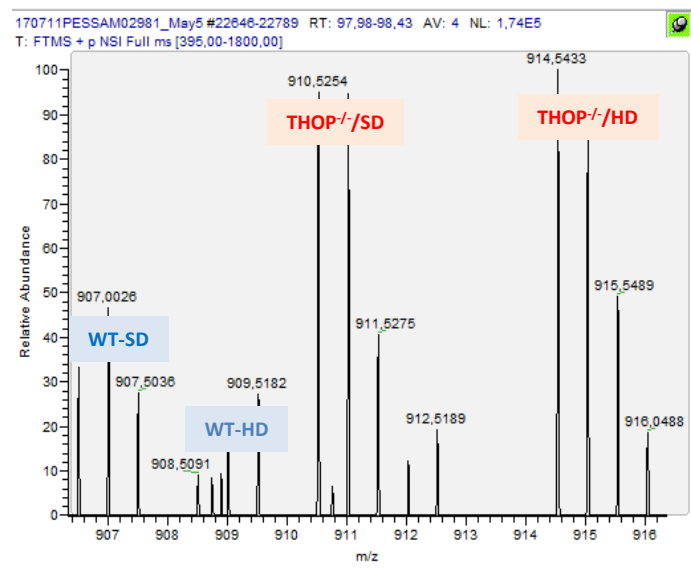
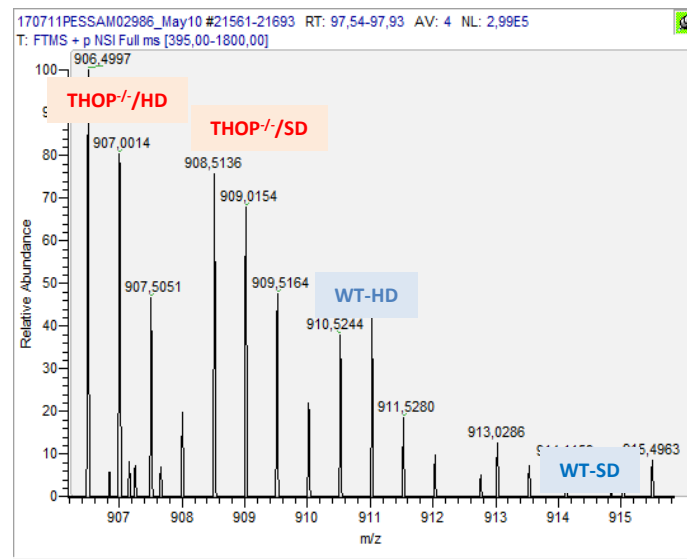
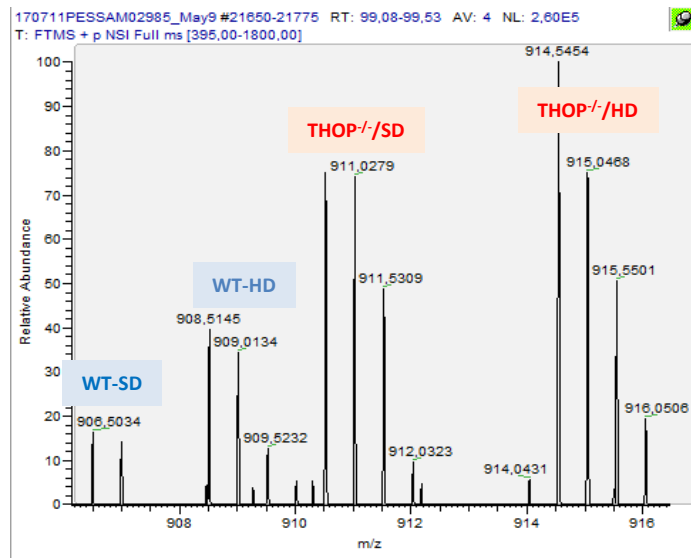
170711PESSAM02979\_May3 #23088-23167 RT: 98.01-98.13 AV: 2 NL: 3,83E5  
T: FTMS + p NSI Full ms [395,00-1800,00]



170711PESSAM02980\_May4 #22829-23268 RT: 97.26-98.84 AV: 14 NL: 1,56E5  
T: FTMS + p NSI Full ms [395,00-1800,00]

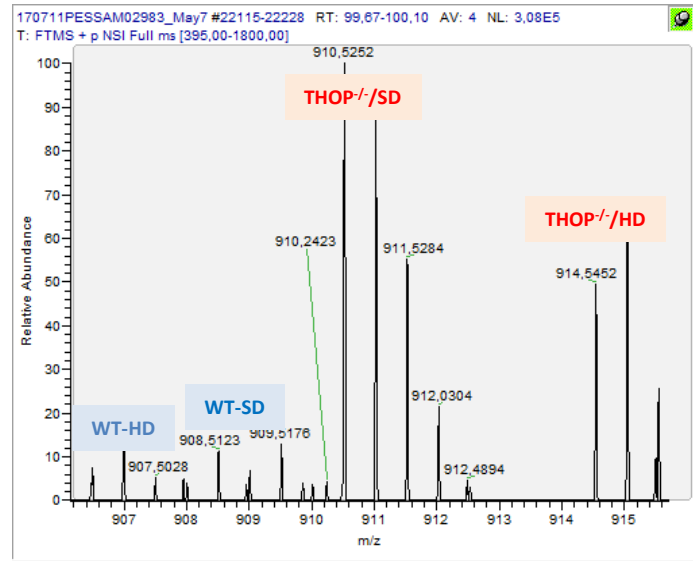


# IDDHFLFDKPVSPLL



May6 –not found

# IDDHFLFDKPVSPLL



May8 –not found

# Mascot Search Results

## Peptide View

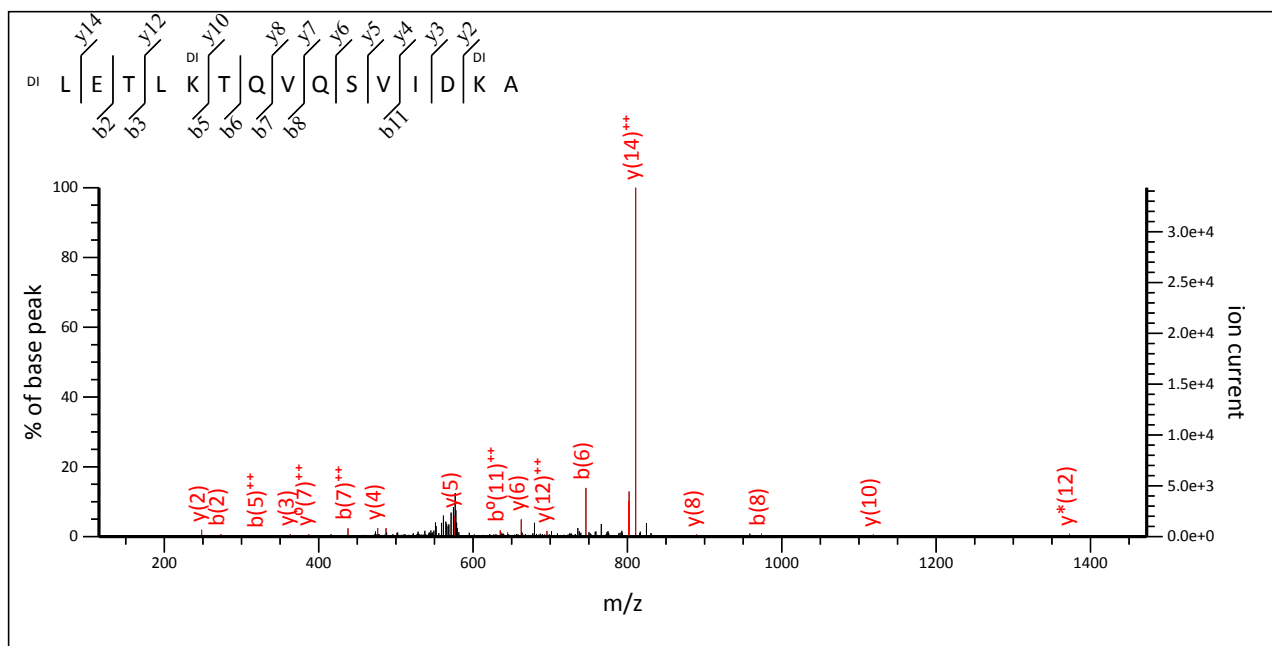
MS/MS Fragmentation of **LETTLKTQVQSVIDKA**

Found in **APOA1\_MOUSE** in **SwissProt**, Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=2

Match to Query 13752: 1762.070802 from(588.364210,3+) intensity(4227358.0000) scans(16013) rawscans(sn16013) rtinseconds(4398.351) index(10848)

Title: 10849: Scan 16013 (rt=4398.35) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02985\_May9.raw]

Data file 170711PESSAM02985\_May9.temp.mgf



115.3

to

1472.81



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1762.0815

Variable modifications:

N-term : Dimethyl:2H(2) (N-term)

K5 : Dimethyl:2H(2) (K)

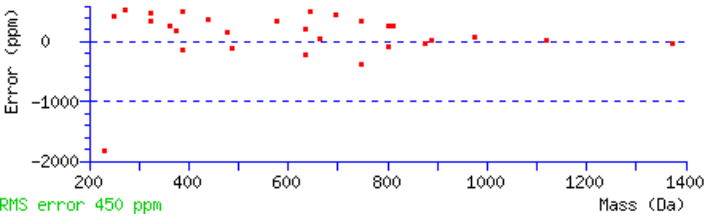
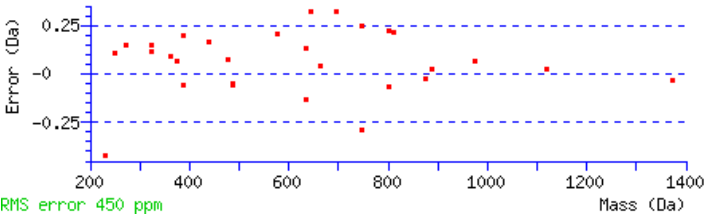
K14 : Dimethyl:2H(2) (K)

Ions Score: 38 Expect: 0.015

Matches : 30/152 fragment ions using 56 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	144.1383	72.5728					L							15
2	273.1809	137.0941			255.1703	128.0888	E	1619.9578	810.4825	1602.9313	801.9693	1601.9473	801.4773	14
3	374.2286	187.6179			356.2180	178.6126	T	1490.9152	745.9612	1473.8887	737.4480	1472.9047	736.9560	13
4	487.3126	244.1600			469.3021	235.1547	L	1389.8675	695.4374	1372.8410	686.9241	1371.8570	686.4321	12
5	645.4545	323.2309	628.4280	314.7176	627.4440	314.2256	K	1276.7835	638.8954	1259.7569	630.3821	1258.7729	629.8901	11
6	746.5022	373.7547	729.4757	365.2415	728.4917	364.7495	T	1118.6416	559.8244	1101.6150	551.3111	1100.6310	550.8191	10
7	874.5608	437.7840	857.5342	429.2708	856.5502	428.7788	Q	1017.5939	509.3006	1000.5673	500.7873	999.5833	500.2953	9
8	973.6292	487.3182	956.6027	478.8050	955.6186	478.3130	V	889.5353	445.2713	872.5088	436.7580	871.5247	436.2660	8
9	1101.6878	551.3475	1084.6612	542.8343	1083.6772	542.3422	Q	790.4669	395.7371	773.4403	387.2238	772.4563	386.7318	7
10	1188.7198	594.8635	1171.6933	586.3503	1170.7093	585.8583	S	662.4083	331.7078	645.3818	323.1945	644.3978	322.7025	6
11	1287.7882	644.3978	1270.7617	635.8845	1269.7777	635.3925	V	575.3763	288.1918	558.3497	279.6785	557.3657	279.1865	5
12	1400.8723	700.9398	1383.8457	692.4265	1382.8617	691.9345	I	476.3079	238.6576	459.2813	230.1443	458.2973	229.6523	4
13	1515.8992	758.4533	1498.8727	749.9400	1497.8887	749.4480	D	363.2238	182.1155	346.1973	173.6023	345.2132	173.1103	3

14	1674.0412	837.5242	1657.0146	829.0109	1656.0306	828.5189	K	248.1969	124.6021	231.1703	116.0888			2
15							A	90.0550	45.5311					1



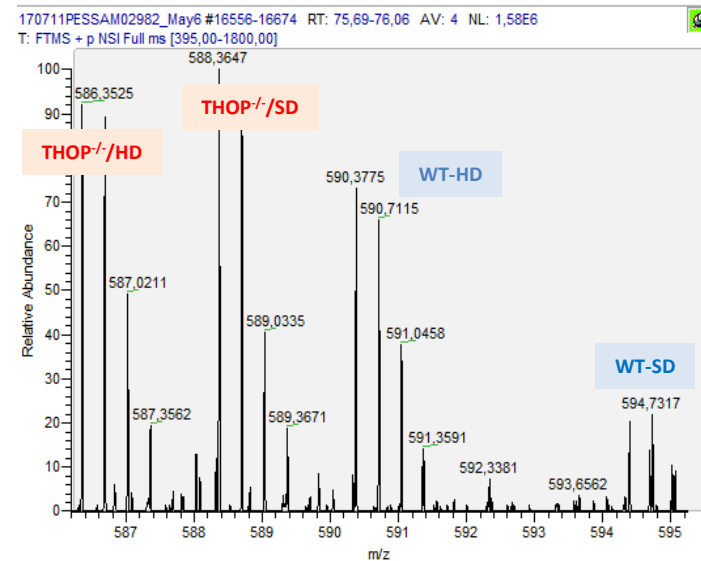
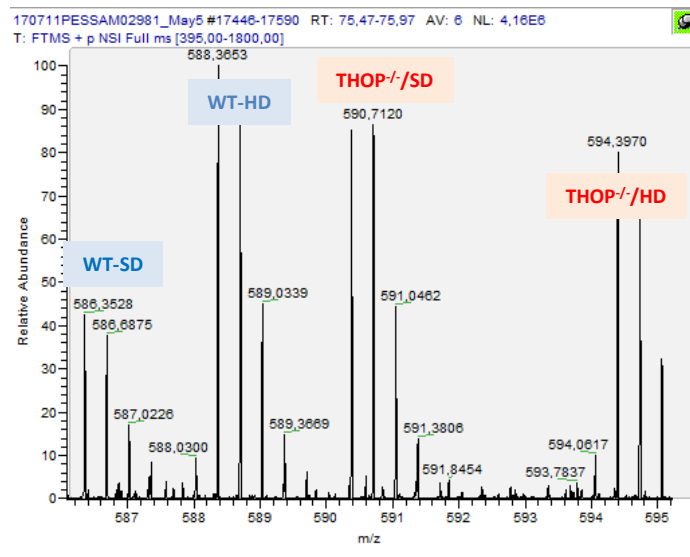
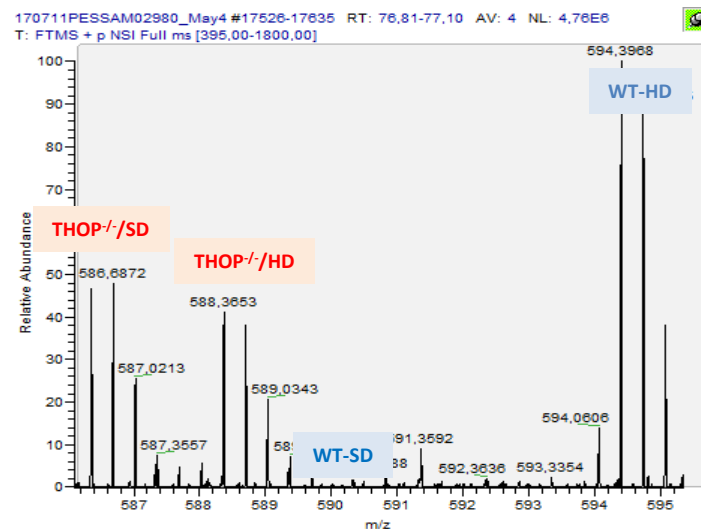
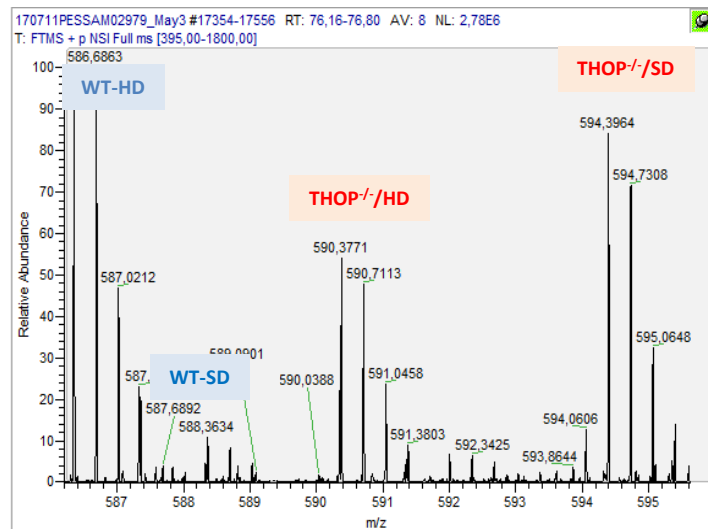
NCBI BLAST search of [LETLKTQVQSVIDKA](#)  
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)  
Other BLAST [web gateways](#)

All matches to this query

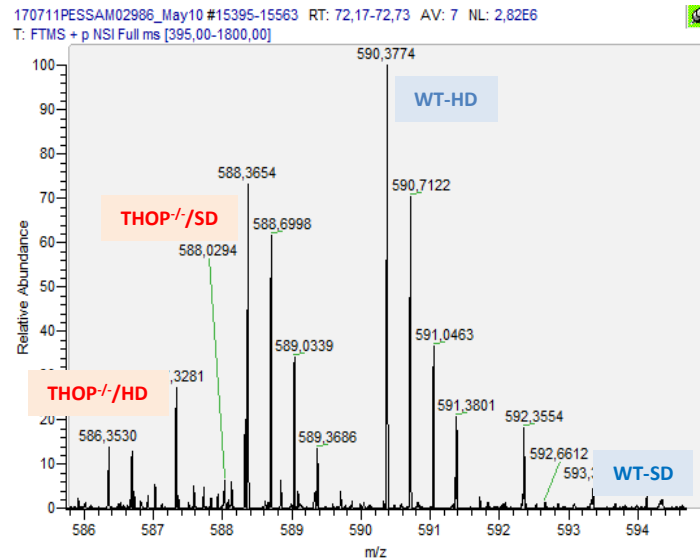
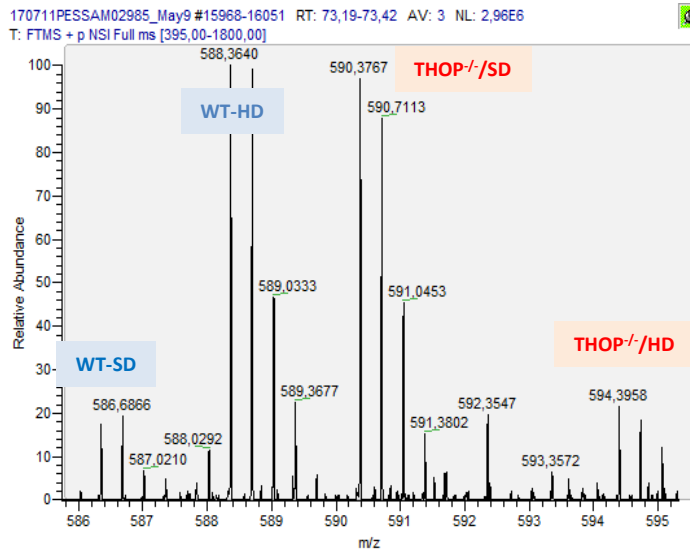
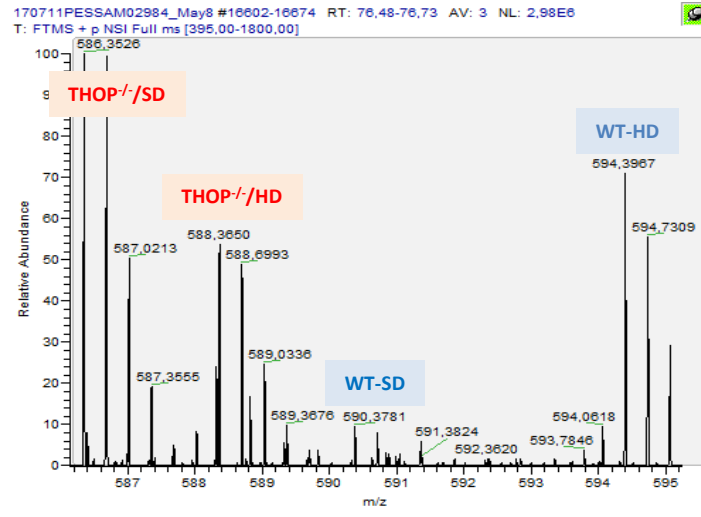
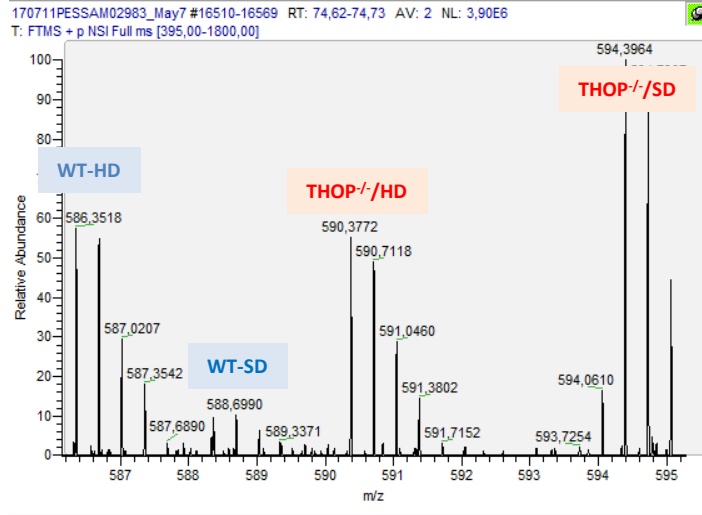
Score	Mr(calc)	Delta	Sequence
38.2	1762.0815	-0.0107	<a href="#">LETLKTQVQSVIDKA</a>
18.3	1761.9625	0.1083	<a href="#">LEITQDSHKGVPLEH</a>
17.4	1762.1008	-0.0300	<a href="#">LAGLGLGLSLIFIAVYL</a>
16.6	1762.0829	-0.0121	<a href="#">NNLQLLSQVLPRLKA</a>
16.5	1762.0136	0.0572	<a href="#">LAIVALISIIYMLH</a>
16.3	1762.0829	-0.0121	<a href="#">IHKAASVGDVAKVQHI</a>
16.2	1761.9036	0.1672	<a href="#">ASGLPLVTEETPPPPGE</a>
16.2	1761.9108	0.1600	<a href="#">AEPAGLSLRADSDSGSK</a>
16.1	1761.8818	0.1890	<a href="#">GGSMPSAAISQLSSELL</a>
16.0	1762.0262	0.0446	<a href="#">SAGAVTVLKAPNRELM</a>

Mascot: <http://www.matrixscience.com/>

# LETLKTQVQSVIDKA



# LETLKTQVQSVIDKA



# Mascot Search Results

## Peptide View

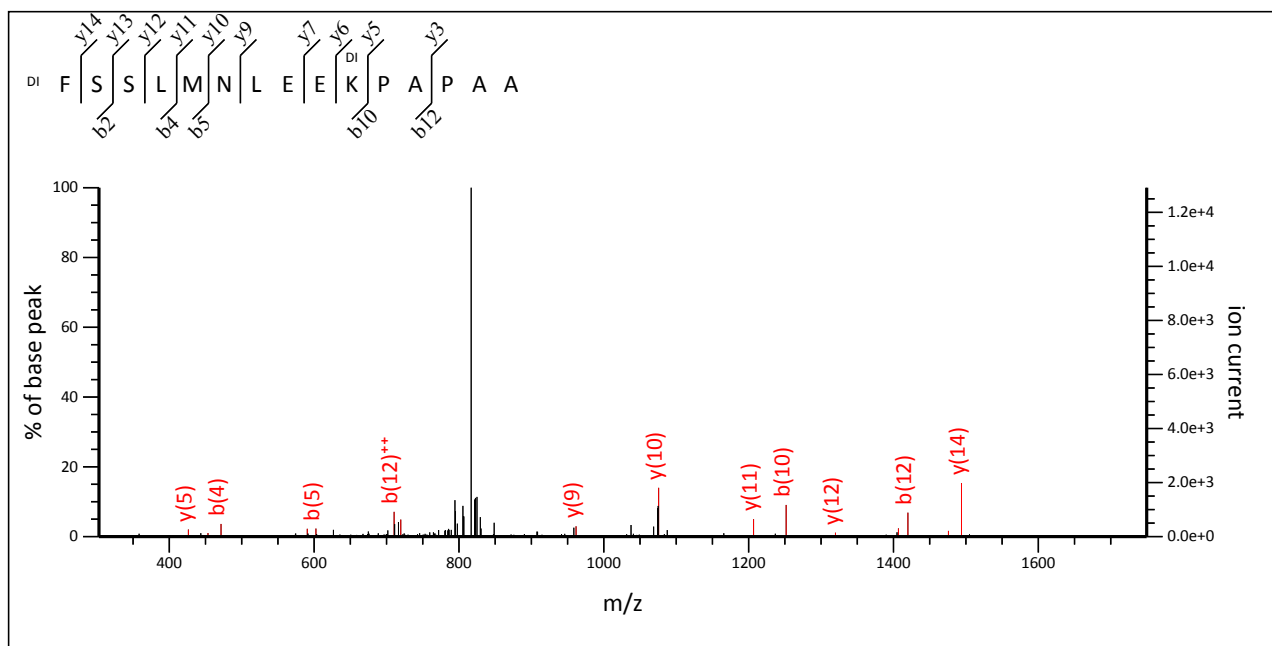
MS/MS Fragmentation of **FSSLMNLEEK**PAPAA

Found in **APOA2\_MOUSE** in **SwissProt**, Apolipoprotein A-II OS=Mus musculus GN=Apoa2 PE=1 SV=2

Match to Query 12466: 1675.941268 from(838.977910,2+) intensity(1987756.5000) scans(16579) rawscans(sn16579)  
rtinseconds(4288.0265) index(10657)

Title: 10658: Scan 16579 (rt=4288.03) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.tmp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1675.9429

Variable modifications:

N-term : Dimethyl:2H(6)13C(2) (N-term)

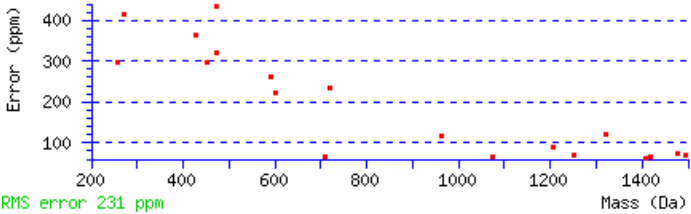
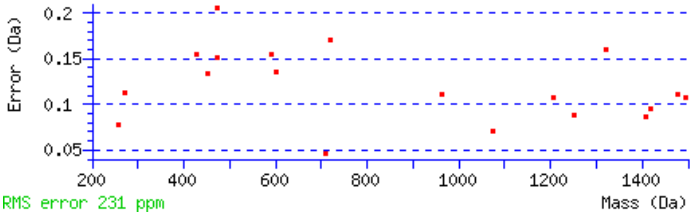
K10 : Dimethyl:2H(6)13C(2) (K)

Ions Score: 74 Expect: 6.1e-006

Matches : 19/134 fragment ions using 25 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	184.1514	92.5793					F							15
2	271.1834	136.0953			253.1728	127.0900	S	1493.8061	747.4067	1476.7796	738.8934	1475.7956	738.4014	14
3	358.2154	179.6113			340.2049	170.6061	S	1406.7741	703.8907	1389.7475	695.3774	1388.7635	694.8854	13
4	471.2995	236.1534			453.2889	227.1481	L	1319.7421	660.3747	1302.7155	651.8614	1301.7315	651.3694	12
5	602.3400	301.6736			584.3294	292.6683	M	1206.6580	603.8326	1189.6315	595.3194	1188.6474	594.8274	11
6	716.3829	358.6951	699.3563	350.1818	698.3723	349.6898	N	1075.6175	538.3124	1058.5910	529.7991	1057.6070	529.3071	10
7	829.4670	415.2371	812.4404	406.7238	811.4564	406.2318	L	961.5746	481.2909	944.5480	472.7777	943.5640	472.2857	9
8	958.5095	479.7584	941.4830	471.2451	940.4990	470.7531	E	848.4905	424.7489	831.4640	416.2356	830.4800	415.7436	8
9	1087.5521	544.2797	1070.5256	535.7664	1069.5416	535.2744	E	719.4479	360.2276	702.4214	351.7143	701.4374	351.2223	7
10	1251.7228	626.3650	1234.6962	617.8518	1233.7122	617.3597	K	590.4053	295.7063	573.3788	287.1930			6
11	1348.7755	674.8914	1331.7490	666.3781	1330.7650	665.8861	P	426.2347	213.6210					5
12	1419.8127	710.4100	1402.7861	701.8967	1401.8021	701.4047	A	329.1819	165.0946					4
13	1516.8654	758.9363	1499.8389	750.4231	1498.8549	749.9311	P	258.1448	129.5761					3

15/07/2019	Mascot Search Results: Peptide View													
14	1587.9025	794.4549	1570.8760	785.9416	1569.8920	785.4496	A	161.0921	81.0497					2
15							A	90.0550	45.5311					1



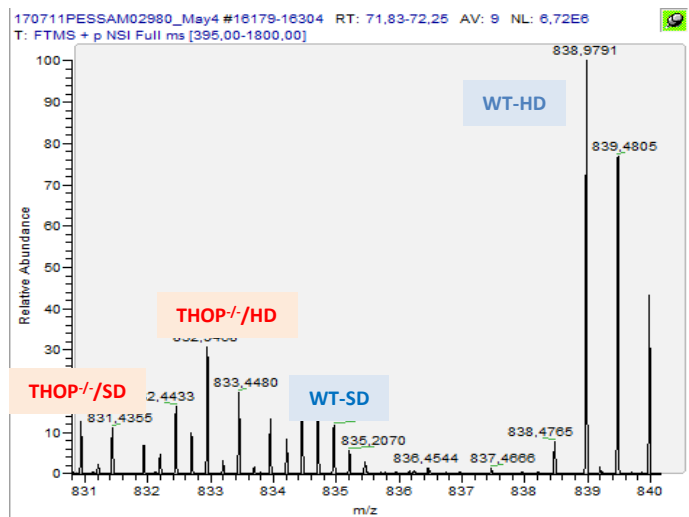
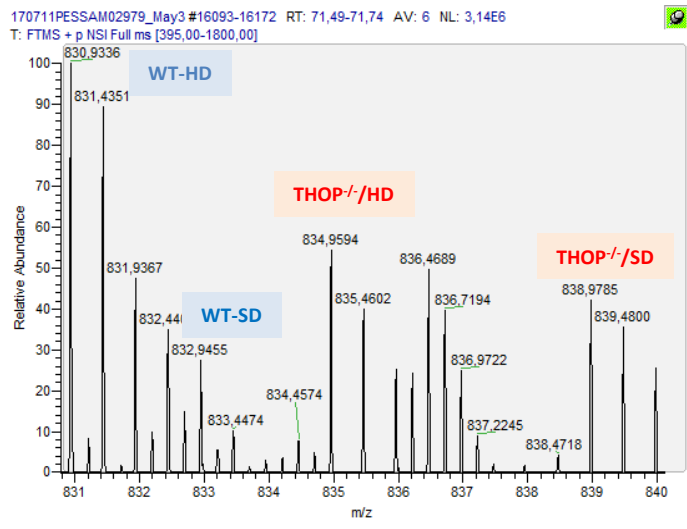
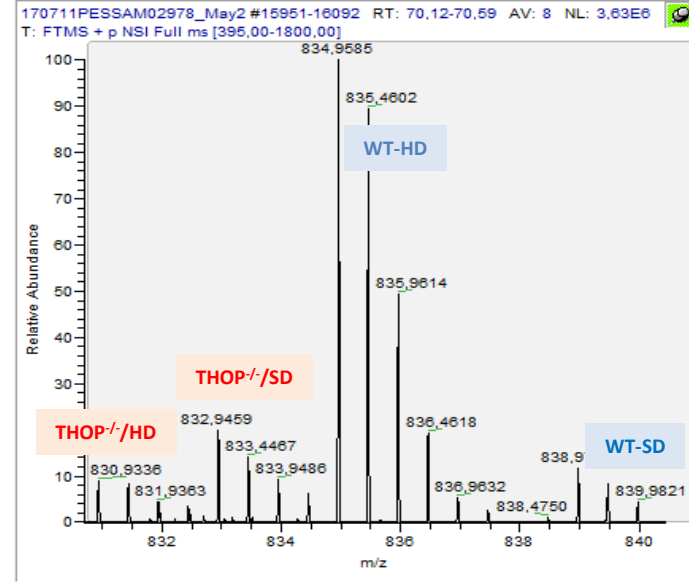
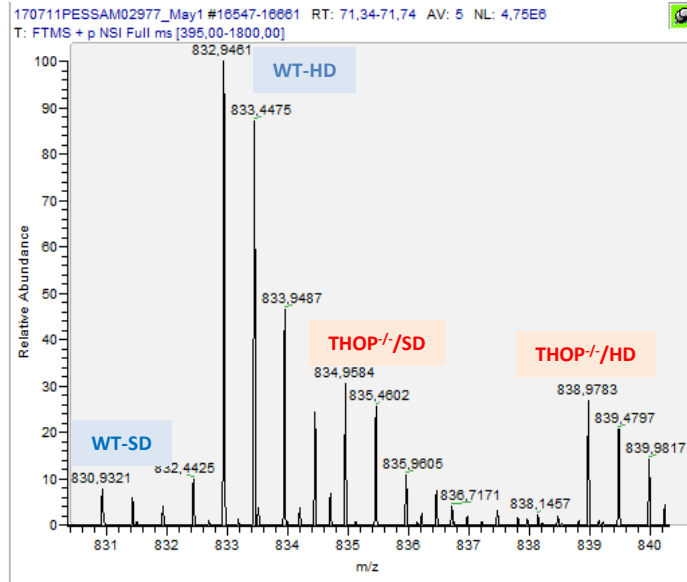
NCBI **BLAST** search of [FSSLMNLEEKAPAA](#)  
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)  
 Other BLAST [web gateways](#)

All matches to this query

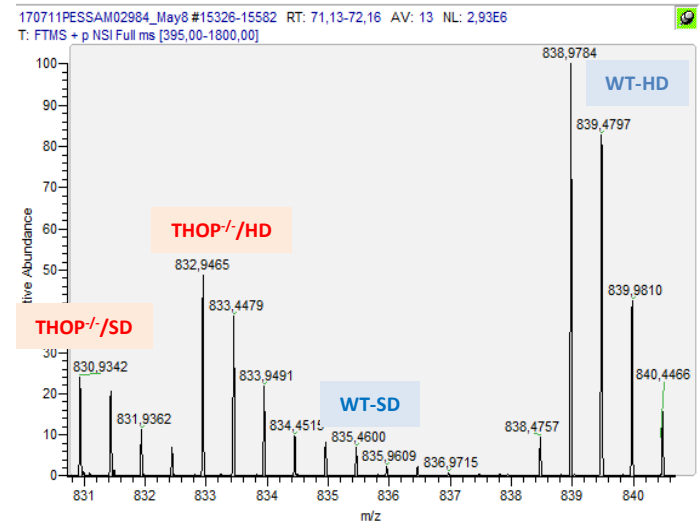
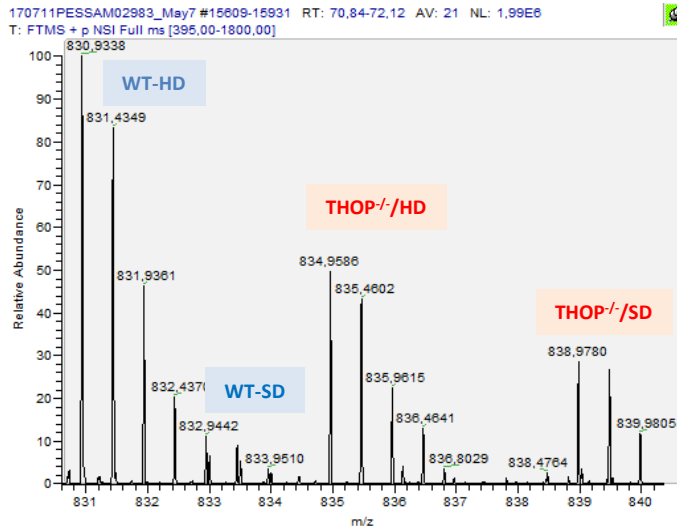
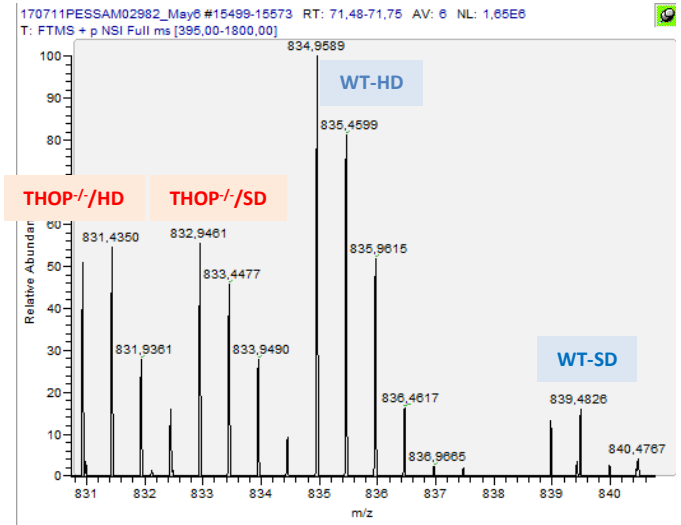
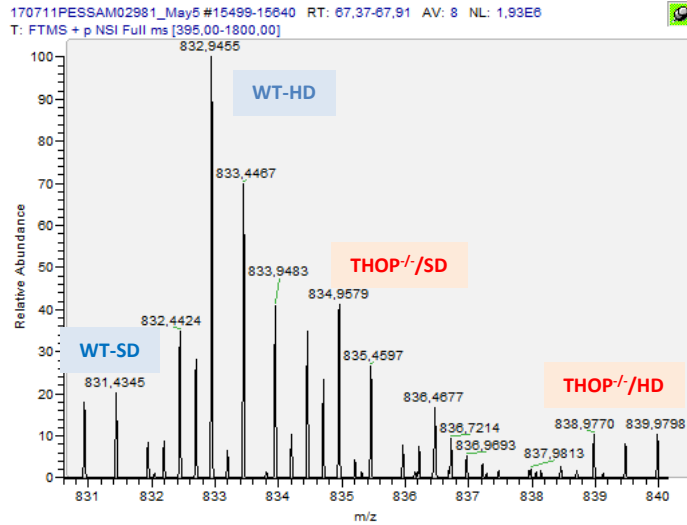
Score	Mr(calc)	Delta	Sequence
74.2	1675.9429	-0.0016	<a href="#">FSSLMNLEEKAPAA</a>
18.0	1675.6775	0.2638	<a href="#">FSSMIADDMSNYDE</a>
15.8	1675.8095	0.1317	<a href="#">ELSLCHITGMREML</a>
15.3	1675.7402	0.2011	<a href="#">HGGGTGGGGGAGGQAMDPAA</a>
15.3	1675.8516	0.0897	<a href="#">EISLPTTSTIIDGSQS</a>
14.4	1675.9007	0.0405	<a href="#">ILCLIYTLNFAIDH</a>
14.4	1675.9912	-0.0500	<a href="#">LKHLIENFIPL</a>
14.1	1675.9468	-0.0056	<a href="#">ASASLSGTSALTGLTKR</a>
13.9	1675.8095	0.1317	<a href="#">ELSLCHITGMREML</a>
13.2	1675.8473	0.0940	<a href="#">RKNMPCICIHA</a>

Mascot: <http://www.matrixscience.com/>

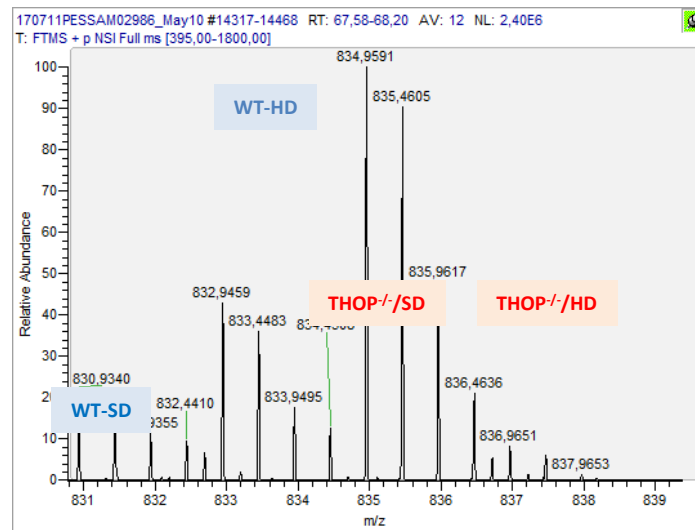
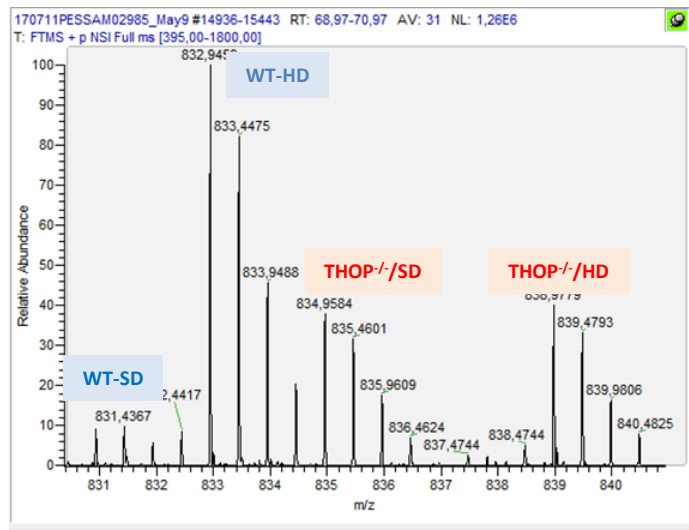
# FSSLMNLEEKPAAPAA



# FSSLMNLEEKPAAPAA



# FSSLMNLEEKPAAPAA



# Mascot Search Results

## Peptide View

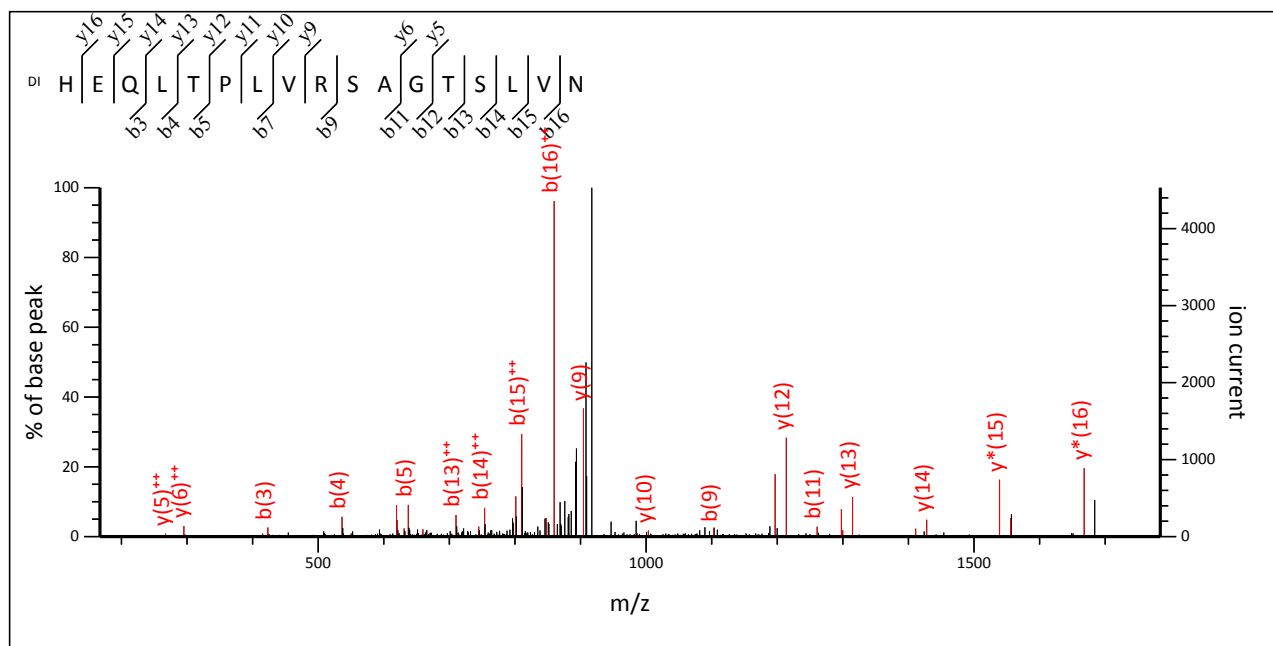
MS/MS Fragmentation of **HEQLTPLVRSAGTSLVN**

Found in **APOA2\_MOUSE** in **SwissProt**, Apolipoprotein A-II OS=Mus musculus GN=Apoa2 PE=1 SV=2

Match to Query 14687: 1849.006168 from(925.510360,2+) intensity(1484091.9000) scans(12825) rawscans(sn12825) rtinseconds(3595.332) index(8313)

Title: 8314: Scan 12825 (rt=3595.33) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02983\_May7.raw]

Data file 170711PESSAM02983\_May7.temp.mgf



167.25 to 1784.03



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1849.0058

Variable modifications:

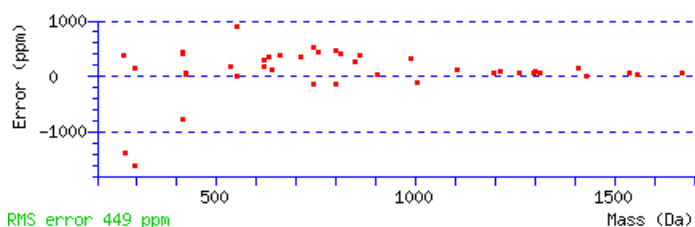
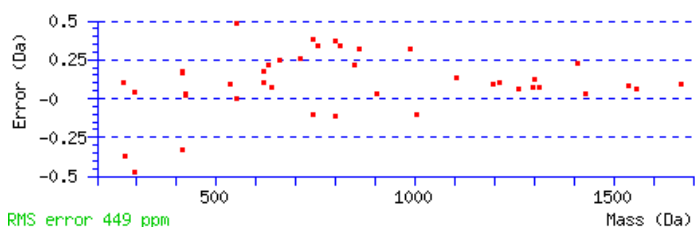
N-term : Dimethyl (N-term)

Ions Score: 39 Expect: 0.0088

Matches : 41/180 fragment ions using 77 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	166.0975	83.5524					H							17
2	<b>295.1401</b>	148.0737			277.1295	139.0684	E	1684.9228	842.9651	<b>1667.8963</b>	834.4518	1666.9123	833.9598	16
3	<b>423.1987</b>	212.1030	406.1721	203.5897	405.1881	203.0977	Q	<b>1555.8802</b>	778.4438	<b>1538.8537</b>	769.9305	1537.8697	769.4385	15
4	<b>536.2827</b>	<b>268.6450</b>	519.2562	260.1317	518.2722	259.6397	L	<b>1427.8217</b>	714.4145	<b>1410.7951</b>	705.9012	1409.8111	705.4092	14
5	<b>637.3304</b>	319.1688	<b>620.3039</b>	310.6556	<b>619.3198</b>	310.1636	T	<b>1314.7376</b>	657.8724	<b>1297.7110</b>	649.3592	1296.7270	648.8672	13
6	734.3832	367.6952	717.3566	359.1819	716.3726	358.6899	P	<b>1213.6899</b>	607.3486	<b>1196.6634</b>	598.8353	1195.6793	598.3433	12
7	<b>847.4672</b>	<b>424.2373</b>	830.4407	<b>415.7240</b>	829.4567	<b>415.2320</b>	L	1116.6371	558.8222	1099.6106	<b>550.3089</b>	1098.6266	<b>549.8169</b>	11
8	946.5356	473.7715	929.5091	465.2582	928.5251	464.7662	V	<b>1003.5531</b>	502.2802	<b>986.5265</b>	493.7669	985.5425	493.2749	10
9	<b>1102.6368</b>	551.8220	1085.6102	543.3087	1084.6262	542.8167	R	<b>904.4847</b>	452.7460	887.4581	444.2327	886.4741	443.7407	9
10	1189.6688	595.3380	1172.6422	586.8248	1171.6582	586.3327	S	748.3836	374.6954	731.3570	366.1821	730.3730	365.6901	8
11	<b>1260.7059</b>	<b>630.8566</b>	1243.6793	622.3433	1242.6953	621.8513	A	661.3515	331.1794	644.3250	322.6661	643.3410	322.1741	7
12	1317.7274	<b>659.3673</b>	1300.7008	650.8540	<b>1299.7168</b>	650.3620	G	590.3144	<b>295.6608</b>	573.2879	287.1476	572.3039	286.6556	6
13	1418.7750	<b>709.8912</b>	1401.7485	701.3779	1400.7645	700.8859	T	533.2930	<b>267.1501</b>	516.2664	258.6368	515.2824	258.1448	5
14	1505.8071	<b>753.4072</b>	1488.7805	<b>744.8939</b>	1487.7965	<b>744.4019</b>	S	432.2453	216.6263	<b>415.2187</b>	208.1130	414.2347	207.6210	4

15	1618.8911	809.9492	1601.8646	801.4359	1600.8806	800.9439	L	345.2132	173.1103	328.1867	164.5970			3
16	1717.9595	859.4834	1700.9330	850.9701	1699.9490	850.4781	V	232.1292	116.5682	215.1026	108.0550			2
17							N	133.0608	67.0340	116.0342	58.5207			1



NCBI BLAST search of [HEQLTPLVRSAGTSLVN](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

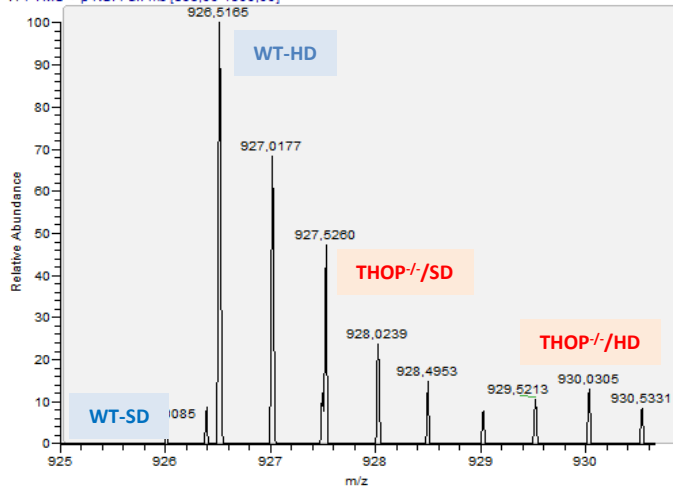
#### All matches to this query

Score	Mr(calc)	Delta	Sequence
39.2	1849.0058	0.0004	<a href="#">HEQLTPLVRSAGTSLVN</a>
16.9	1848.9159	0.0903	<a href="#">EGFEQAARDYTLRTE</a>
16.5	1848.9059	0.1002	<a href="#">AISDIMSSDQETYSCK</a>
16.3	1849.0713	-0.0651	<a href="#">PALLLTALEQHVLYLQ</a>
15.4	1848.9846	0.0216	<a href="#">IQQALHRPPSSAAQYL</a>
15.2	1849.0273	-0.0211	<a href="#">EEQLTLVRLSRPCAQA</a>
14.6	1849.0098	-0.0036	<a href="#">VTPATEPRNAQTQLQLY</a>
14.5	1849.0814	-0.0752	<a href="#">RDKEFQSHLTSHEK</a>
14.5	1848.8418	0.1644	<a href="#">FSPEDYQSTAGTLEFQ</a>
14.4	1849.1164	-0.1102	<a href="#">LAQALNEALKPTLQYL</a>

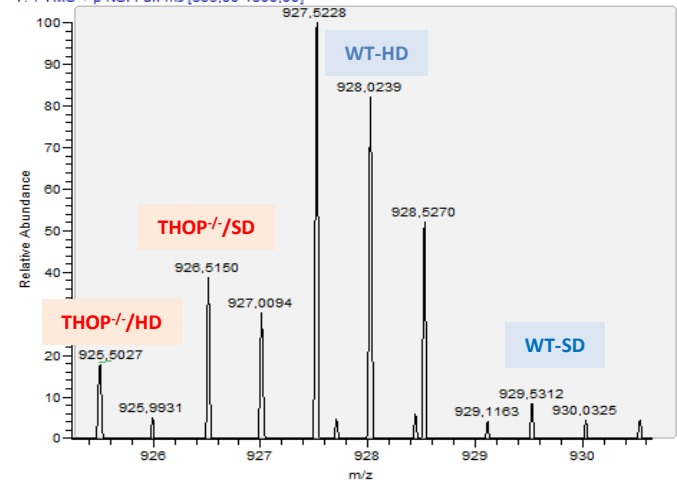
Mascot: <http://www.matrixscience.com/>

# HEQLTPLVRSAGTSLVN

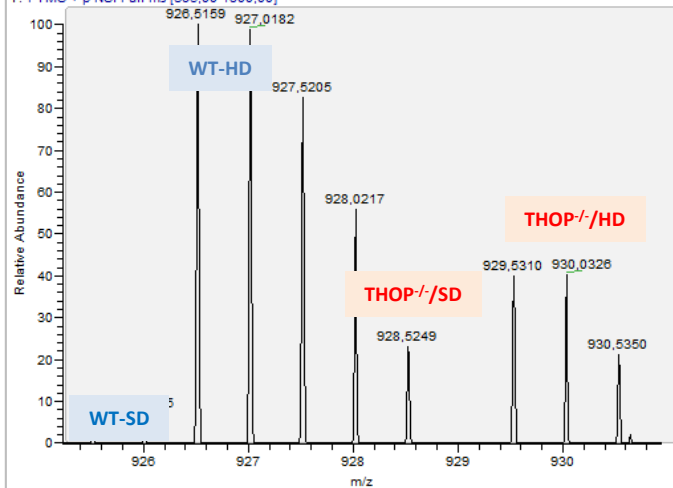
170711PESSAM02977\_May1 #13830-13956 RT: 61.52-61.89 AV: 7 NL: 8.11E5  
T: FTMS + p NSI Full ms [395.00-1800.00]



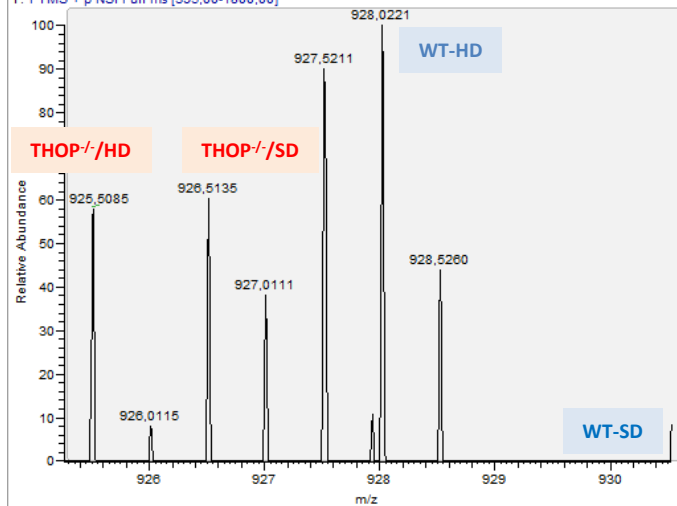
170711PESSAM02978\_May2 #13265-13557 RT: 60.69-61.63 AV: 19 NL: 3.00E5  
T: FTMS + p NSI Full ms [395.00-1800.00]



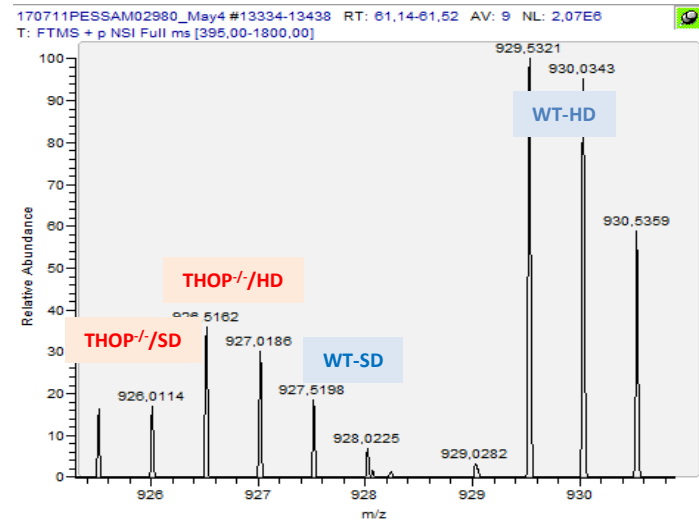
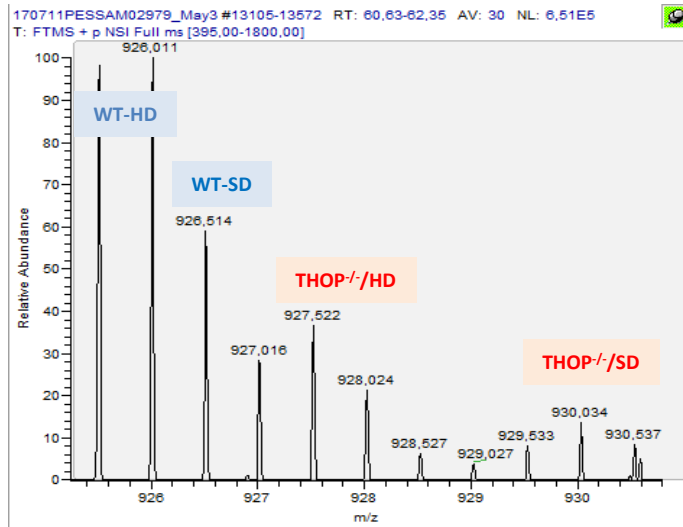
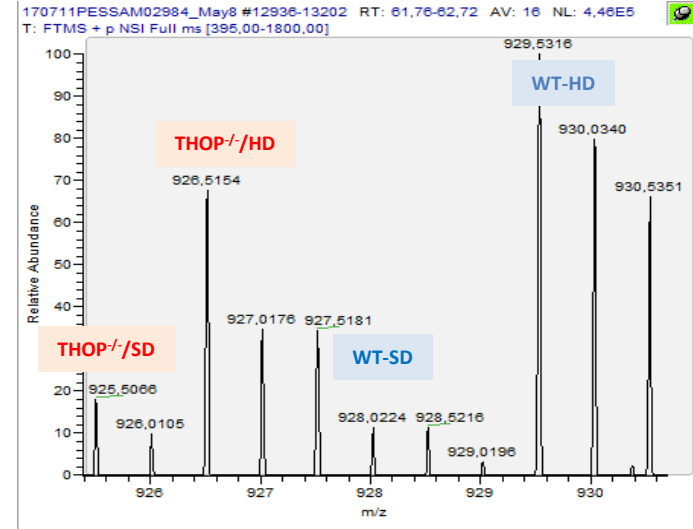
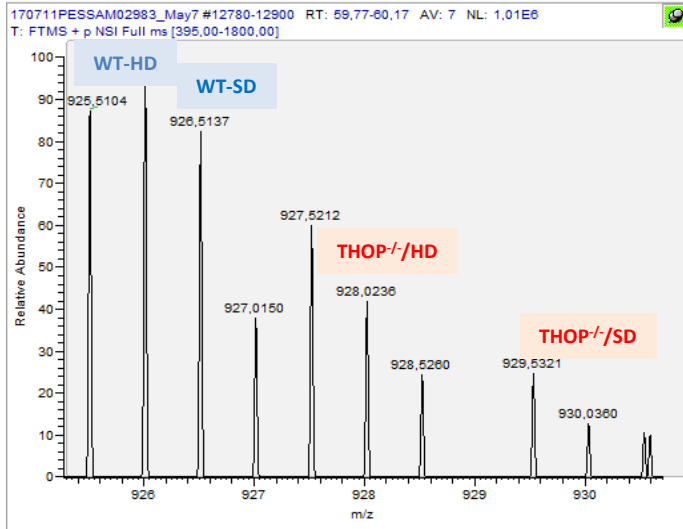
170711PESSAM02981\_May5 #12069-12203 RT: 54.87-55.30 AV: 11 NL: 1.65E6  
T: FTMS + p NSI Full ms [395.00-1800.00]



170711PESSAM02982\_May6 #12646-12803 RT: 60.71-61.29 AV: 12 NL: 2.09E5  
T: FTMS + p NSI Full ms [395.00-1800.00]



# HEQLTPLVRSAGTSLVN



# Mascot Search Results

## Peptide View

MS/MS Fragmentation of **SQTFPNADFAEITKL**

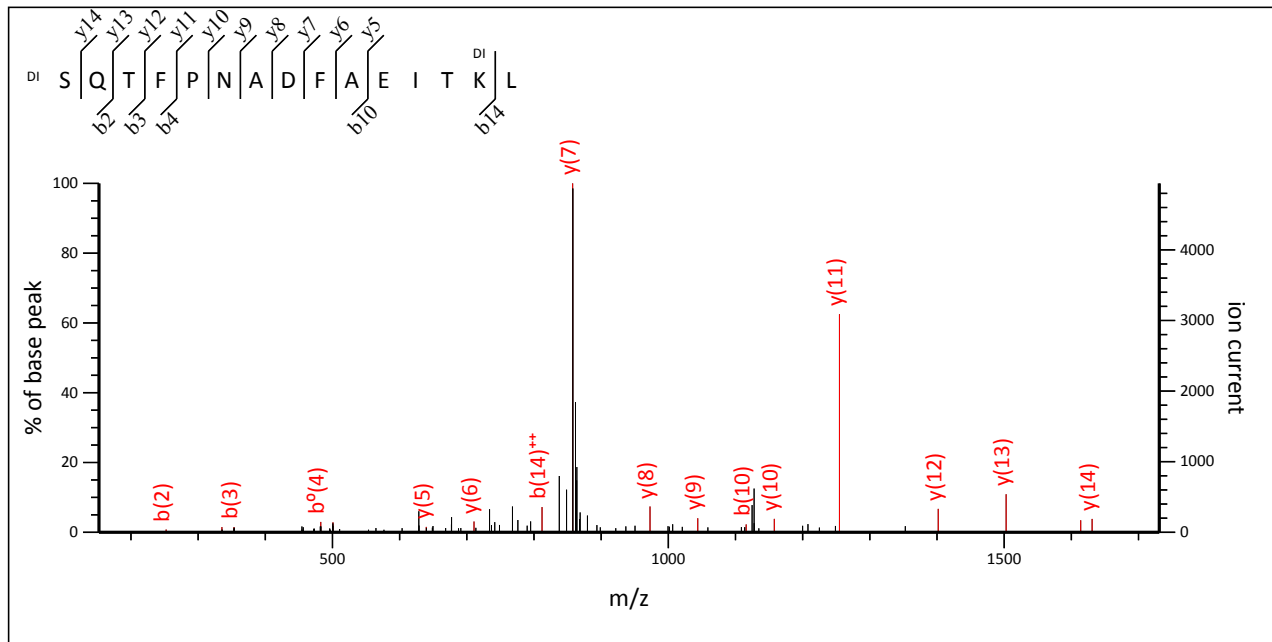
Found in **ALBU\_MOUSE** in **SwissProt**, Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3

Match to Query 13506: 1752.982588 from(877.498570,2+) intensity(2773684.7000) scans(21840-21901) rawscans(sn21840:sn21901)  
rtinseconds(5595.796-5612.719) index(14323)

Title: 14324: Sum of 3 scans in range 21840 (rt=5595.8) to 21901 (rt=5612.72) [D:\Users\Mayara - HMS Fusion

data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



152.37

to

1730.94



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1752.9872

Variable modifications:

N-term : Dimethyl:2H(6)13C(2) (N-term)

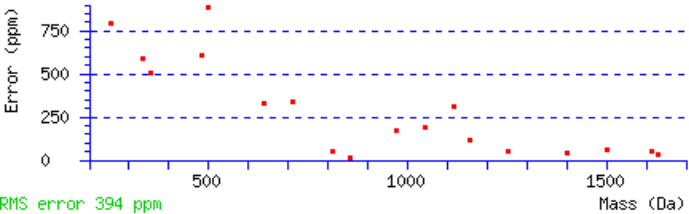
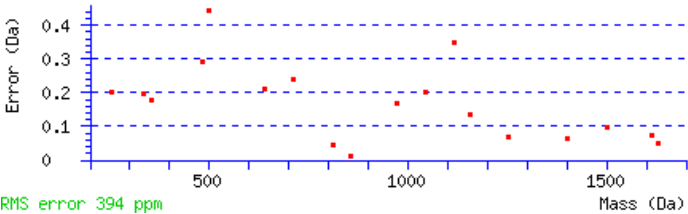
K14 : Dimethyl:2H(6)13C(2) (K)

Ions Score: 59 Expect: 9.9e-005

Matches : 18/160 fragment ions using 44 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>*++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	124.1150	62.5611			106.1044	53.5558	S							15
2	252.1736	126.5904	235.1470	118.0771	234.1630	117.5851	Q	1630.8868	815.9470	1613.8603	807.4338	1612.8763	806.9418	14
3	353.2212	177.1143	336.1947	168.6010	335.2107	168.1090	T	1502.8282	751.9178	1485.8017	743.4045	1484.8177	742.9125	13
4	500.2896	250.6485	483.2631	242.1352	482.2791	241.6432	F	1401.7806	701.3939	1384.7540	692.8806	1383.7700	692.3886	12
5	597.3424	299.1748	580.3159	290.6616	579.3318	290.1696	P	1254.7122	627.8597	1237.6856	619.3464	1236.7016	618.8544	11
6	711.3853	356.1963	694.3588	347.6830	693.3748	347.1910	N	1157.6594	579.3333	1140.6328	570.8201	1139.6488	570.3280	10
7	782.4224	391.7149	765.3959	383.2016	764.4119	382.7096	A	1043.6165	522.3119	1026.5899	513.7986	1025.6059	513.3066	9
8	897.4494	449.2283	880.4228	440.7151	879.4388	440.2231	D	972.5793	486.7933	955.5528	478.2800	954.5688	477.7880	8
9	1044.5178	522.7625	1027.4913	514.2493	1026.5072	513.7573	F	857.5524	429.2798	840.5259	420.7666	839.5418	420.2746	7
10	1115.5549	558.2811	1098.5284	549.7678	1097.5444	549.2758	A	710.4840	355.7456	693.4574	347.2324	692.4734	346.7403	6
11	1244.5975	622.8024	1227.5710	614.2891	1226.5869	613.7971	E	639.4469	320.2271	622.4203	311.7138	621.4363	311.2218	5
12	1357.6816	679.3444	1340.6550	670.8312	1339.6710	670.3391	I	510.4043	255.7058	493.3777	247.1925	492.3937	246.7005	4
13	1458.7293	729.8683	1441.7027	721.3550	1440.7187	720.8630	T	397.3202	199.1637	380.2937	190.6505	379.3097	190.1585	3

14	1622.8999	811.9536	1605.8733	803.4403	1604.8893	802.9483	K	296.2725	148.6399	279.2460	140.1266			2
15							L	132.1019	66.5546					1



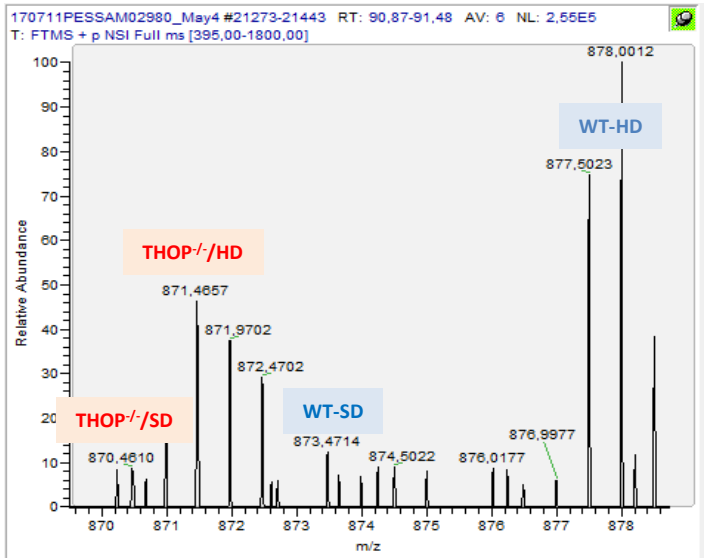
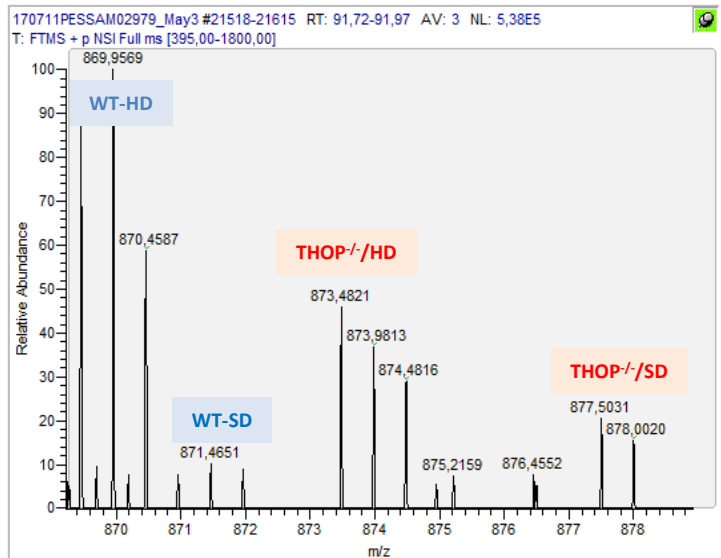
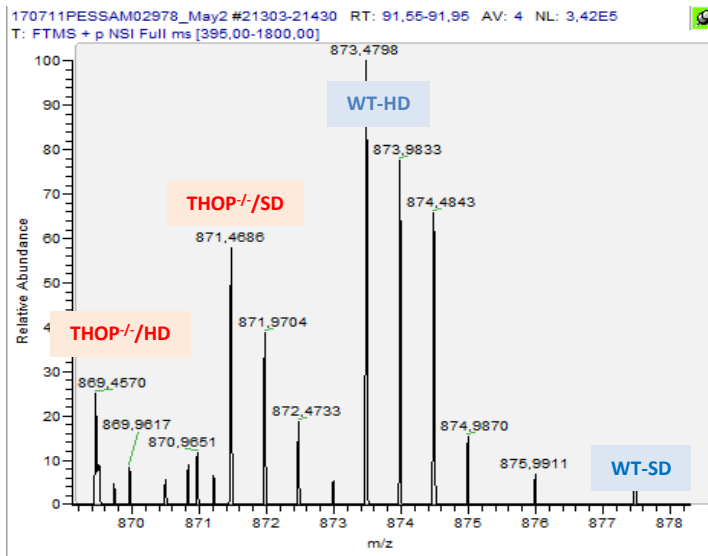
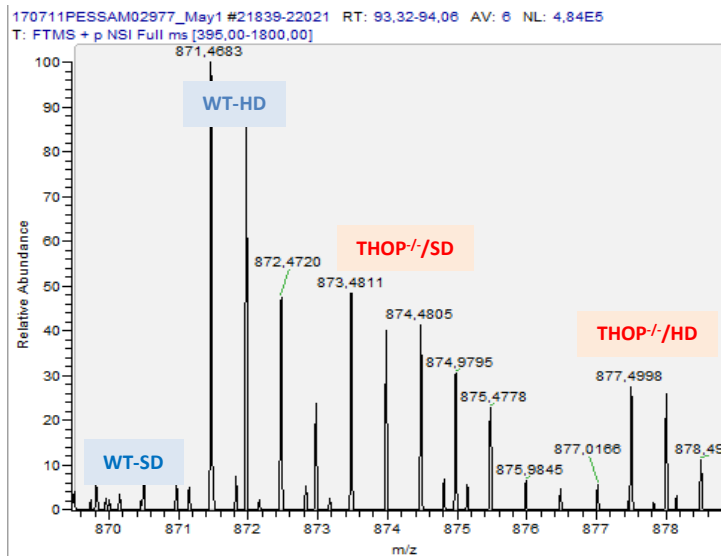
NCBI BLAST search of [SQTFPNADFAEITKL](#)  
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)  
Other BLAST [web gateways](#)

All matches to this query

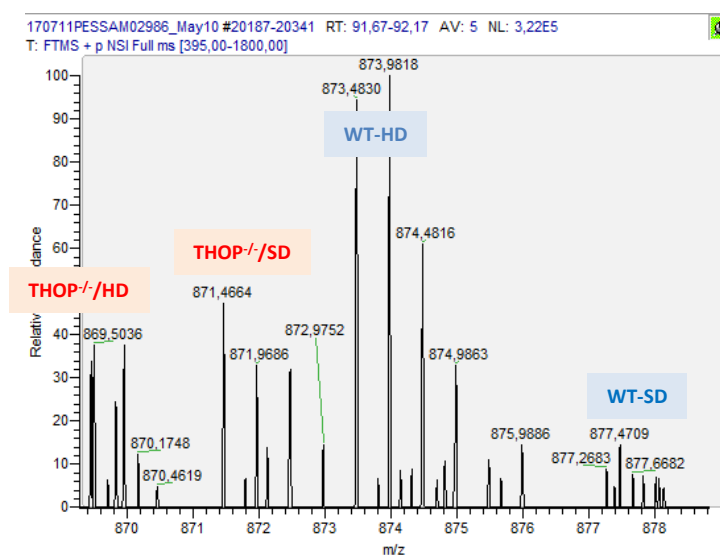
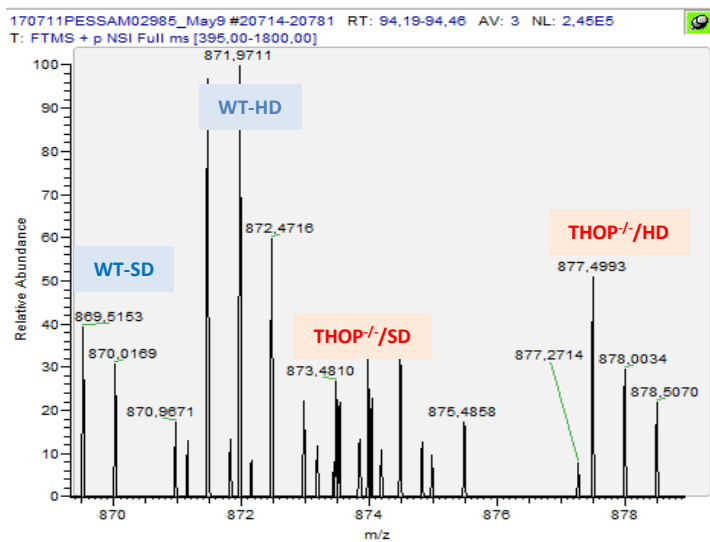
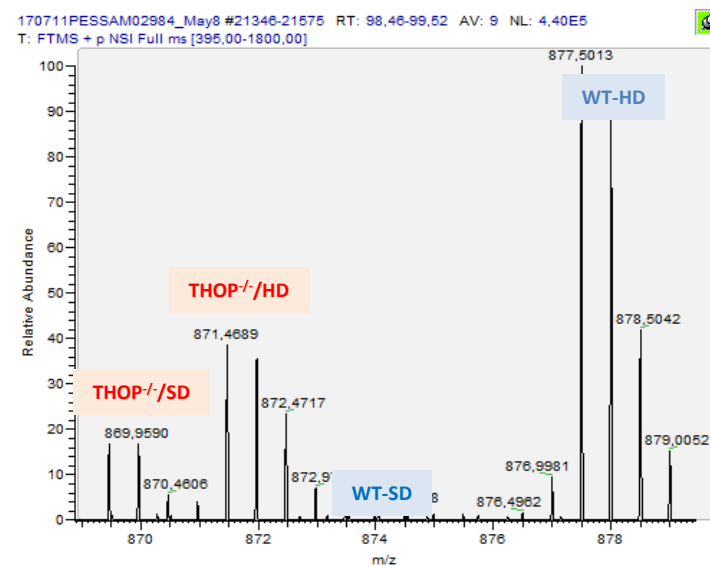
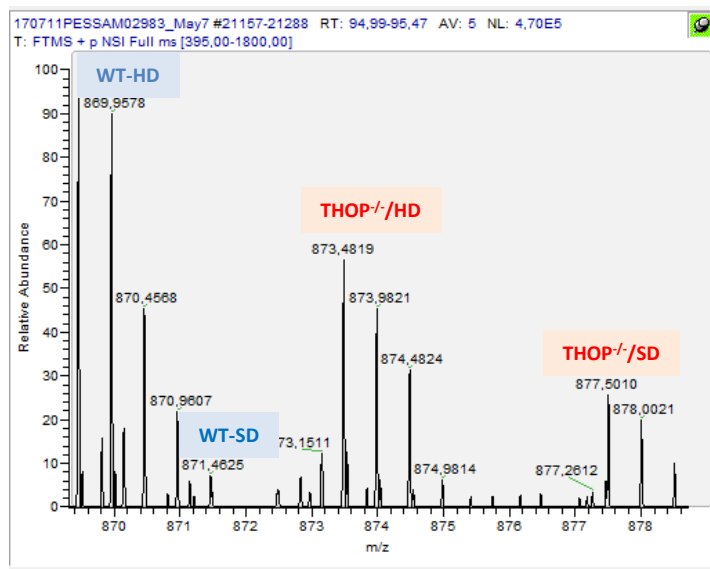
Score	Mr(calc)	Delta	Sequence
59.0	1752.9872	-0.0047	<a href="#">SQTFPNADFAEITKL</a>
15.6	1752.9895	-0.0070	<a href="#">GILSPGVALGTAGGAMSSK</a>
12.3	1753.0552	-0.0726	<a href="#">HLPPTLAAPGQPLRVL</a>
10.9	1752.9762	0.0063	<a href="#">SQTMAPLKTVGTLGMM</a>
10.8	1752.9633	0.0192	<a href="#">LFTPGSRIESILMSL</a>
10.5	1752.9183	0.0643	<a href="#">SIMQSQSVMLPLVPGD</a>
10.1	1752.9035	0.0790	<a href="#">TNTNGTNGNLVPVTN</a>
10.1	1752.9048	0.0777	<a href="#">GSAPRHGSARSGPAPEPS</a>
9.9	1753.0387	-0.0561	<a href="#">KKEDIFASSPMSGTK</a>
9.9	1752.7168	0.2658	<a href="#">NCCEDTQASMQQVHQ</a>

Mascot: <http://www.matrixscience.com/>

# SQTFPNADFAEITKL



# SQTFPNADFAEITKL



# Mascot Search Results

## Peptide View

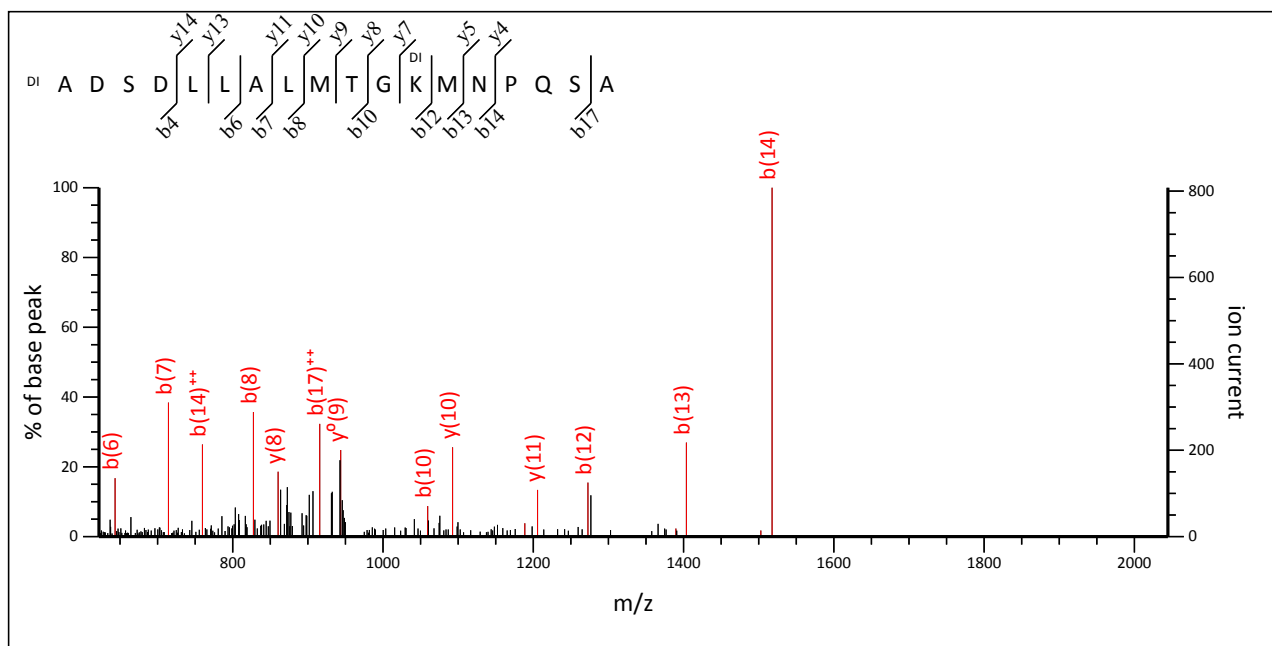
MS/MS Fragmentation of **ADSDLLALMTGKMNPQSA**

Found in **NLTP\_MOUSE** in **SwissProt**, Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3

Match to Query 15454: 1917.951368 from(959.982960,2+) intensity(389329.7200) scans(21991) rawscans(sn21991) rtinseconds(5940.3122) index(14787)

Title: 14788: Scan 21991 (rt=5940.31) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02983\_May7.raw]

Data file 170711PESSAM02983\_May7.temp.mgf



621.98

to

2044.58



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1917.9540

Variable modifications:

N-term : Dimethyl (N-term)

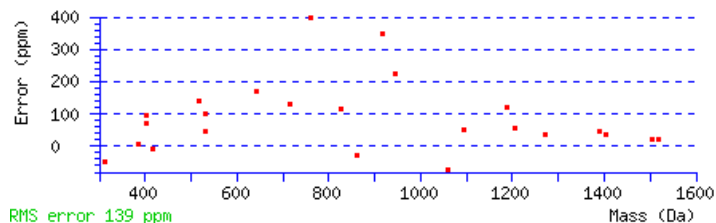
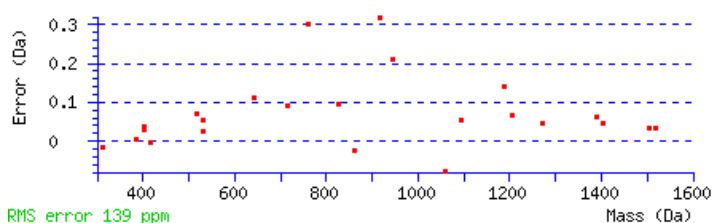
K12 : Dimethyl (K)

Ions Score: 78 Expect: 1.5e-005

Matches : 24/174 fragment ions using 25 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	100.0757	50.5415					A							18
2	215.1026	108.0550			197.0921	99.0497	D	1819.8928	910.4501	1802.8663	901.9368	1801.8823	901.4448	17
3	302.1347	151.5710			284.1241	142.5657	S	1704.8659	852.9366	1687.8394	844.4233	1686.8553	843.9313	16
4	417.1616	209.0844			399.1510	200.0792	D	1617.8339	809.4206	1600.8073	800.9073	1599.8233	800.4153	15
5	530.2457	265.6265			512.2351	256.6212	L	1502.8069	751.9071	1485.7804	743.3938	1484.7964	742.9018	14
6	643.3297	322.1685			625.3192	313.1632	L	1389.7229	695.3651	1372.6963	686.8518	1371.7123	686.3598	13
7	714.3668	357.6871			696.3563	348.6818	A	1276.6388	638.8230	1259.6123	630.3098	1258.6282	629.8178	12
8	827.4509	414.2291			809.4403	405.2238	L	1205.6017	603.3045	1188.5751	594.7912	1187.5911	594.2992	11
9	958.4914	479.7493			940.4808	470.7441	M	1092.5176	546.7625	1075.4911	538.2492	1074.5071	537.7572	10
10	1059.5391	530.2732			1041.5285	521.2679	T	961.4771	481.2422	944.4506	472.7289	943.4666	472.2369	9
11	1116.5605	558.7839			1098.5500	549.7786	G	860.4295	430.7184	843.4029	422.2051	842.4189	421.7131	8
12	1272.6868	636.8470	1255.6603	628.3338	1254.6762	627.8418	K	803.4080	402.2076	786.3815	393.6944	785.3974	393.2024	7
13	1403.7273	702.3673	1386.7007	693.8540	1385.7167	693.3620	M	647.2817	324.1445	630.2552	315.6312	629.2712	315.1392	6

14	1517.7702	759.3887	1500.7437	750.8755	1499.7596	750.3835	N	516.2413	258.6243	499.2147	250.1110	498.2307	249.6190	5
15	1614.8230	807.9151	1597.7964	799.4019	1596.8124	798.9098	P	402.1983	201.6028	385.1718	193.0895	384.1878	192.5975	4
16	1742.8816	871.9444	1725.8550	863.4311	1724.8710	862.9391	Q	305.1456	153.0764	288.1190	144.5631	287.1350	144.0711	3
17	1829.9136	915.4604	1812.8870	906.9472	1811.9030	906.4551	S	177.0870	89.0471			159.0764	80.0418	2
18							A	90.0550	45.5311					1



NCBI **BLAST** search of [ADSDLLALMTGKMNPQSA](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

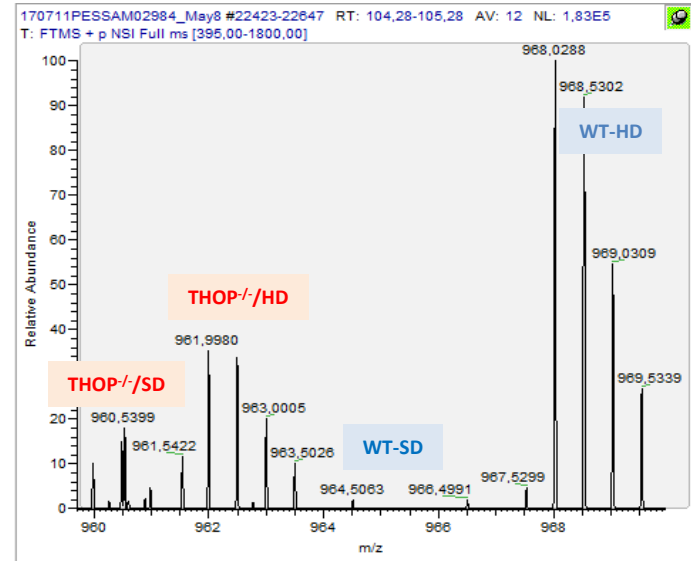
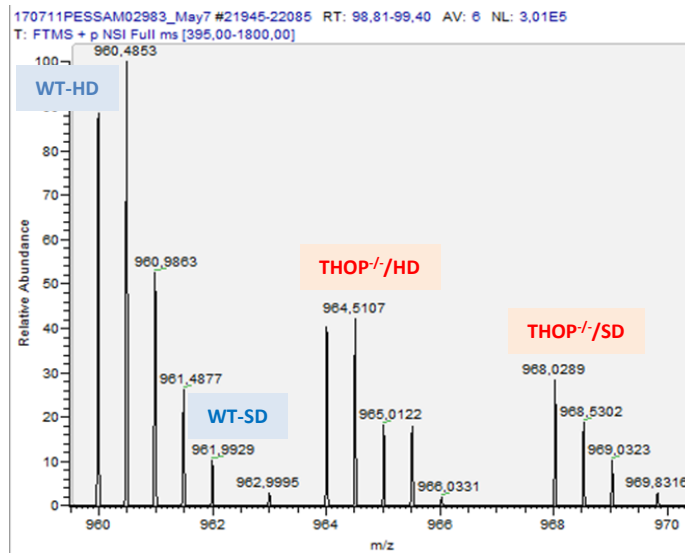
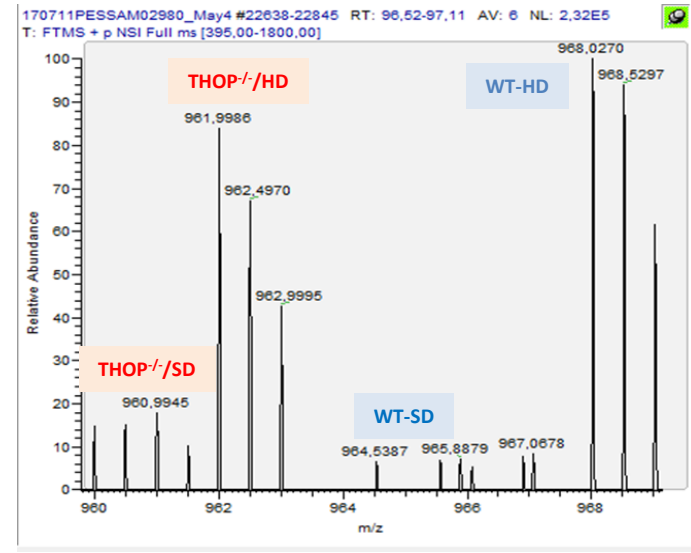
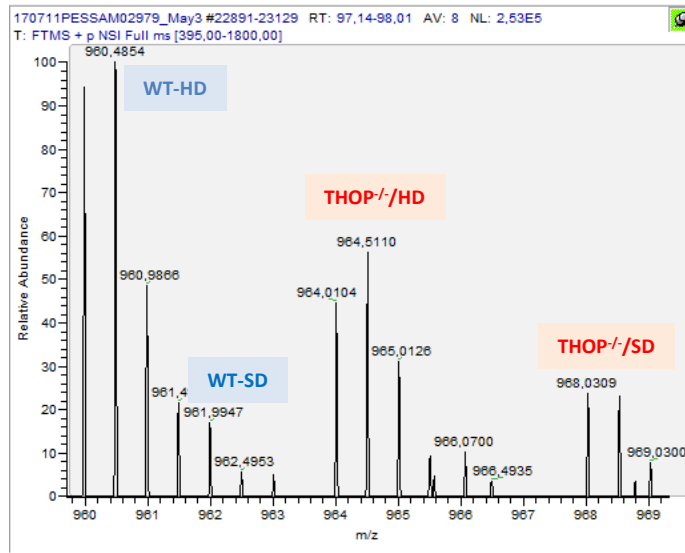
Other BLAST [web gateways](#)

#### All matches to this query

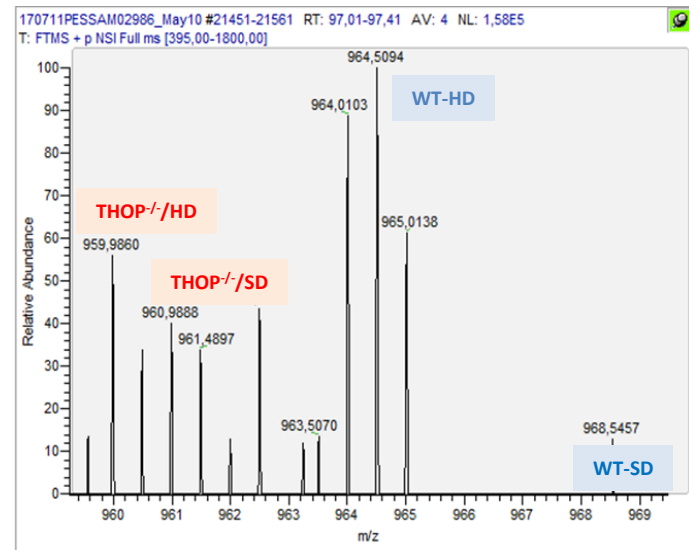
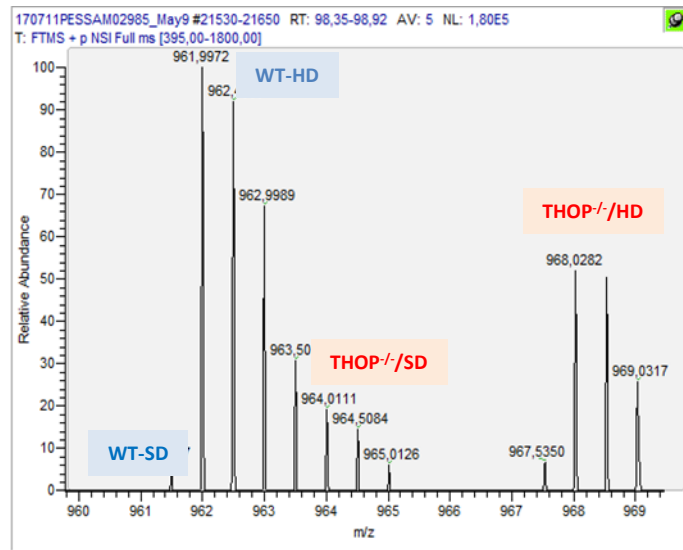
Score	Mr(calc)	Delta	Sequence
77.8	1917.9540	-0.0026	<a href="#">ADSDLLALMTGKMNPQSA</a>
25.6	1918.0485	-0.0971	<a href="#">MQLSIALDINFESIIDK</a>
23.2	1918.0303	-0.0789	<a href="#">PYSYISLITMAIQQAPS</a>
22.2	1918.0138	-0.0624	<a href="#">AGGAAAGLSPPAPAPFPLEPG</a>
21.6	1917.9694	-0.0180	<a href="#">PAGGSGGGLSDSGRNSLTSLP</a>
21.6	1918.1900	-0.2386	<a href="#">KDLLLLAAELGKMLLER</a>
20.0	1917.9578	-0.0064	<a href="#">MEAQLASQSTQRTGKGQ</a>
19.9	1918.0921	-0.1407	<a href="#">EAENEKMKAI GARNLL</a>
19.5	1918.1342	-0.1828	<a href="#">WRIYRPTTGALLLLTA</a>
19.3	1918.1007	-0.1494	<a href="#">VPLVIGCAVSCMALLTLA</a>

Mascot: <http://www.matrixscience.com/>

# ADSDLLALMTGKMNPQSA

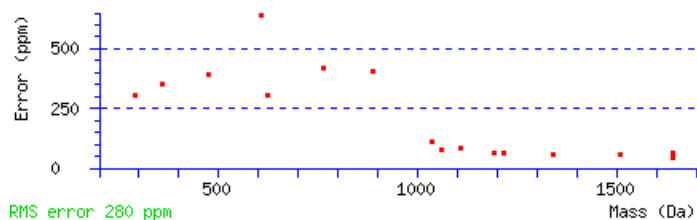
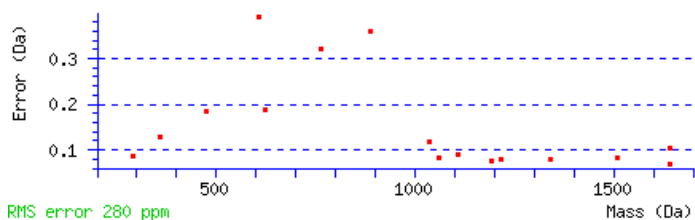


# ADSDLLALMTGKMNPQSA





14	1538.7672	769.8872	1521.7406	761.3740	1520.7566	760.8819	T	379.2551	190.1312	362.2286	181.6179	361.2445	181.1259	3
15	1639.8149	820.4111	1622.7883	811.8978	1621.8043	811.4058	T	278.2074	139.6074	261.1809	131.0941	260.1969	130.6021	2
16							K	177.1598	89.0835	160.1332	80.5702			1



NCBI BLAST search of [GAEALERMFASFPTTK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

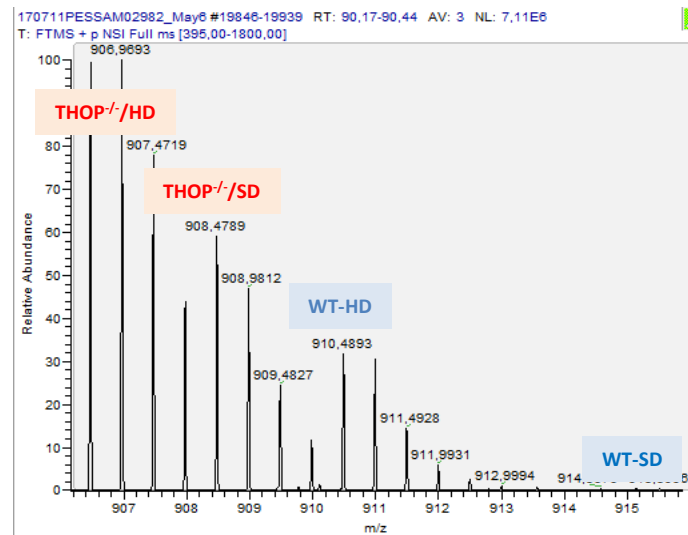
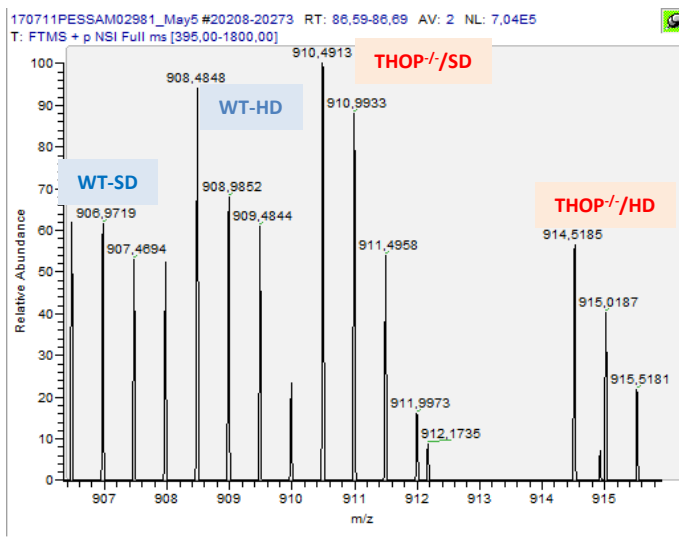
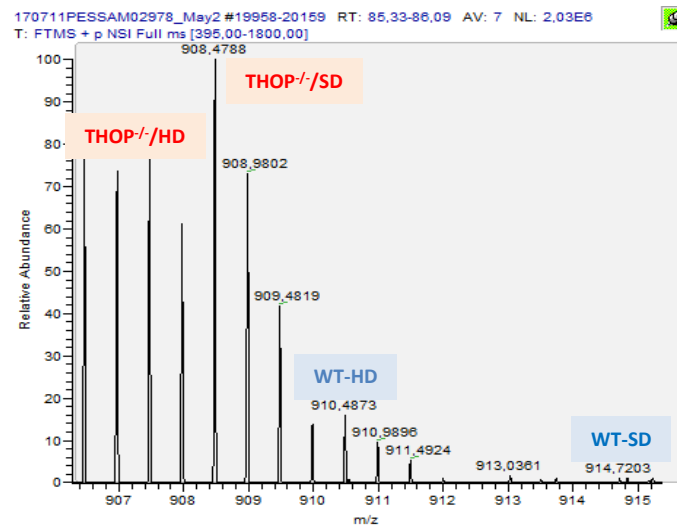
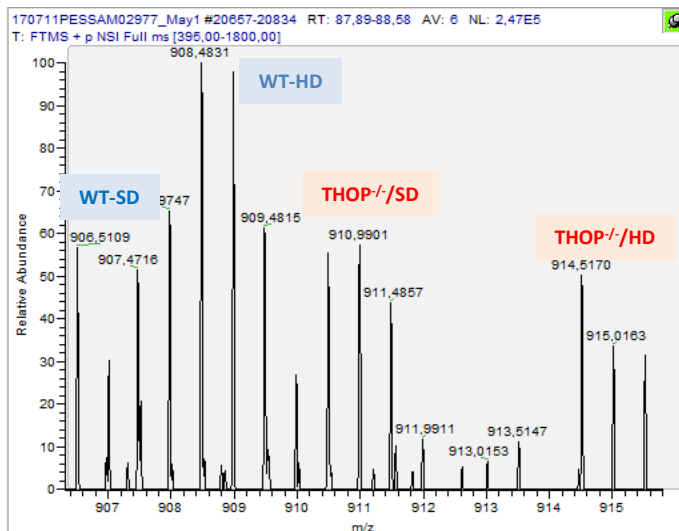
Other BLAST [web gateways](#)

#### All matches to this query

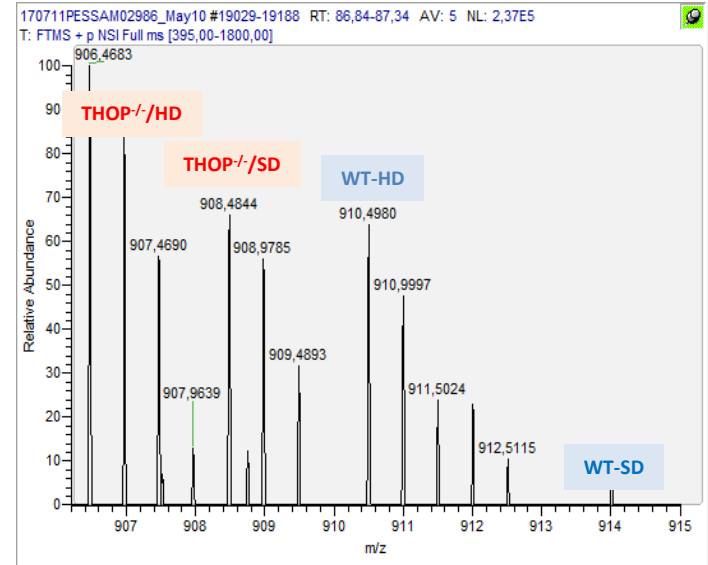
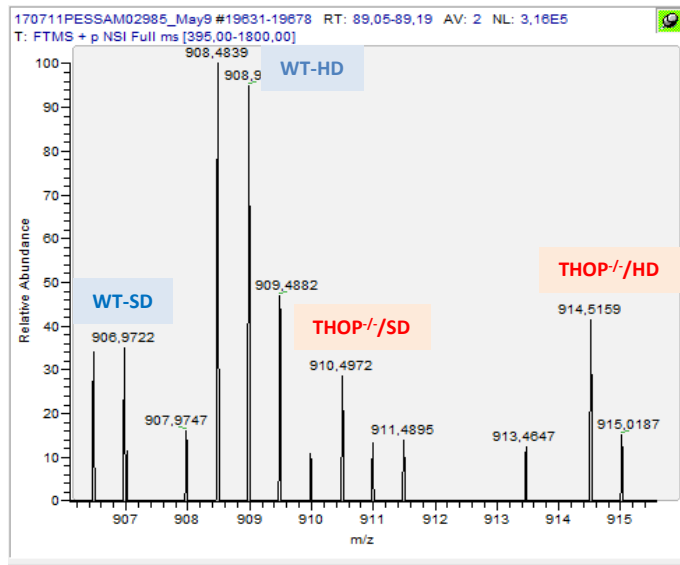
Score	Mr(calc)	Delta	Sequence
52.5	1814.9600	-0.0089	<a href="#">GAEALERMFASFPTTK</a>
18.8	1814.9854	-0.0343	<a href="#">SVPRFSAAAACSNITRL</a>
17.2	1815.1671	-0.2160	<a href="#">VKASTCKPFLFLLTK</a>
14.0	1814.8331	0.1180	<a href="#">GMSLGMSATTHYHTYL</a>
13.1	1814.7787	0.1724	<a href="#">NNSAGMAASPEMMGLGDV</a>
13.1	1815.0001	-0.0490	<a href="#">LIGIYATALSASMSSLIG</a>
12.7	1814.8506	0.1005	<a href="#">NVATSESDLSMRTL</a>
12.4	1815.0029	-0.0518	<a href="#">KSADFFPGLSAFLSQE</a>
12.0	1815.0103	-0.0592	<a href="#">EEFMLPLKQVLEL</a>
11.4	1814.7822	0.1690	<a href="#">AVGYSWPGAFSMADSSP</a>

Mascot: <http://www.matrixscience.com/>

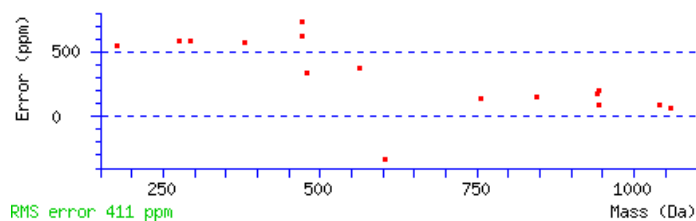
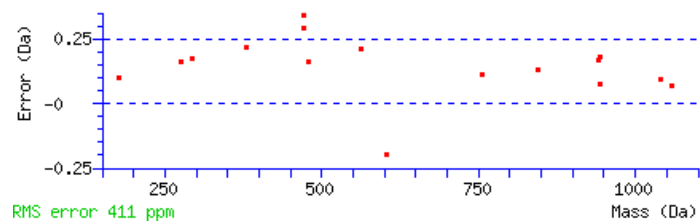
# GAEALERMFASFPPTTK



# GAEALERMFASFPTTK







NCBI **BLAST** search of [FDVSHGSAQVK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

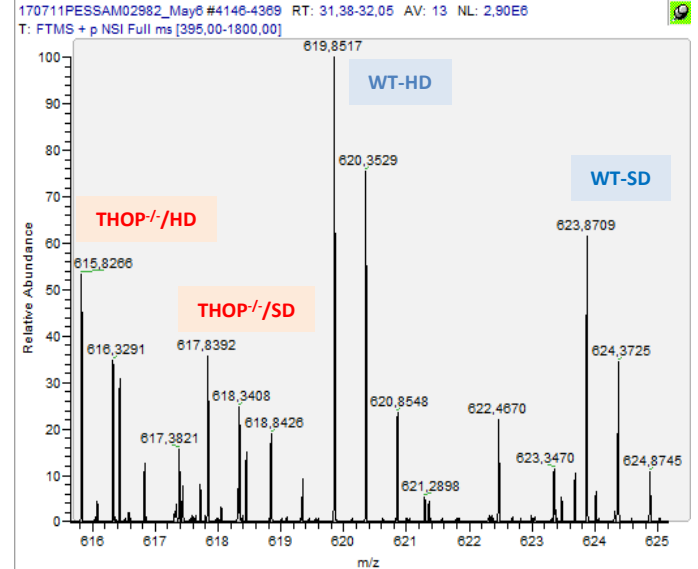
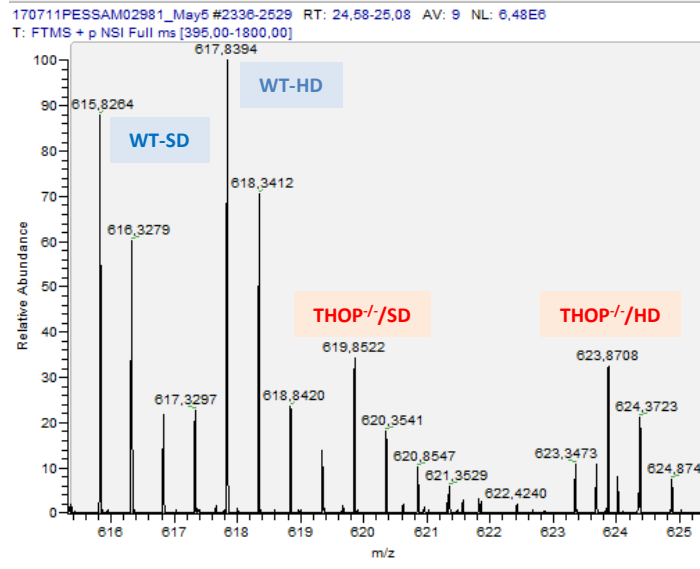
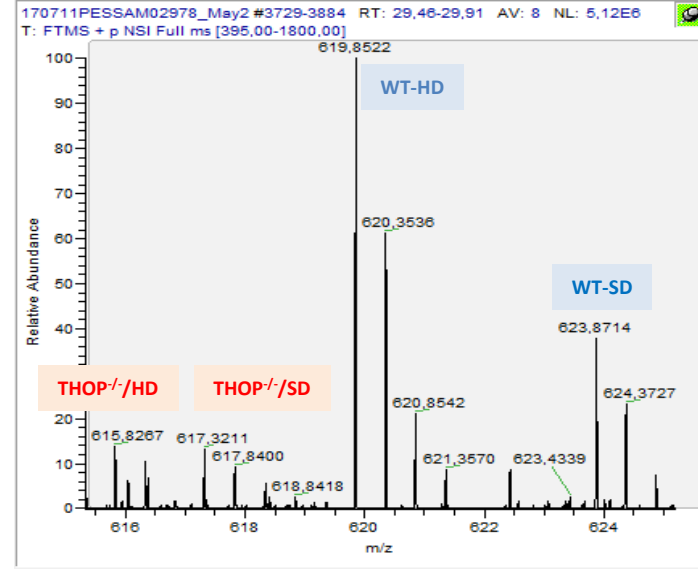
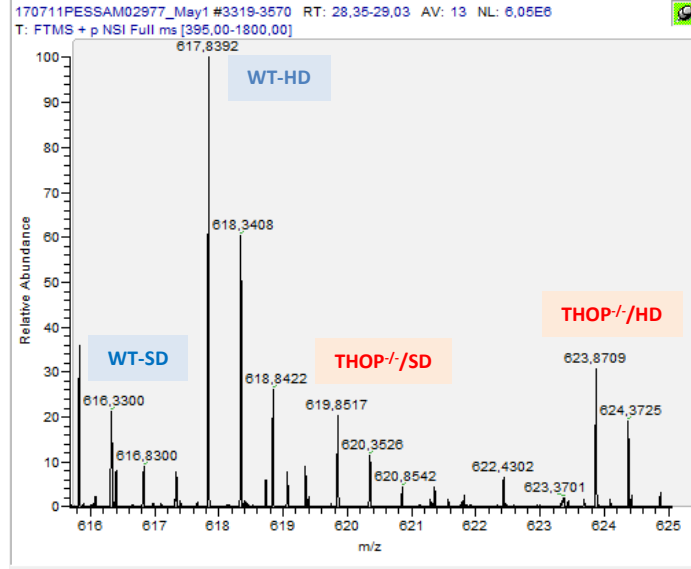
Other BLAST [web gateways](#)

#### All matches to this query

Score	Mr(calc)	Delta	Sequence
50.8	1233.6718	-0.0071	<a href="#">FDVSHGSAQVK</a>
28.7	1233.6176	0.0471	<a href="#">MDVSEHLPSR</a>
20.9	1233.6241	0.0405	<a href="#">FDVSAPGSGGLTP</a>
17.2	1233.6639	0.0008	<a href="#">TPVKMPPSNTS</a>
16.7	1233.7043	-0.0396	<a href="#">IGVIFMASPVL</a>
16.6	1233.6791	-0.0145	<a href="#">MITSHEPPKT</a>
16.6	1233.5105	0.1542	<a href="#">MTLSTEMSDAS</a>
15.5	1233.6577	0.0070	<a href="#">IMVSAIGNDGPL</a>
14.7	1233.5980	0.0667	<a href="#">VDVSTEAMYAA</a>
14.4	1233.7243	-0.0596	<a href="#">CDVSKTLLHL</a>

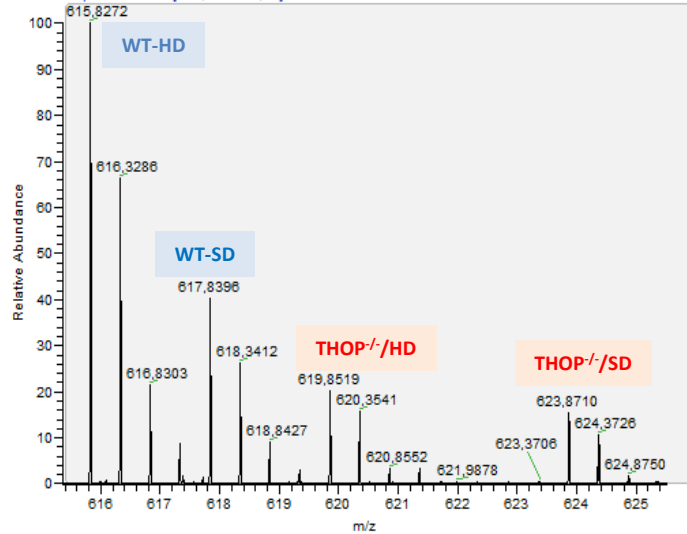
Mascot: <http://www.matrixscience.com/>

# FDVSHGSAQVK

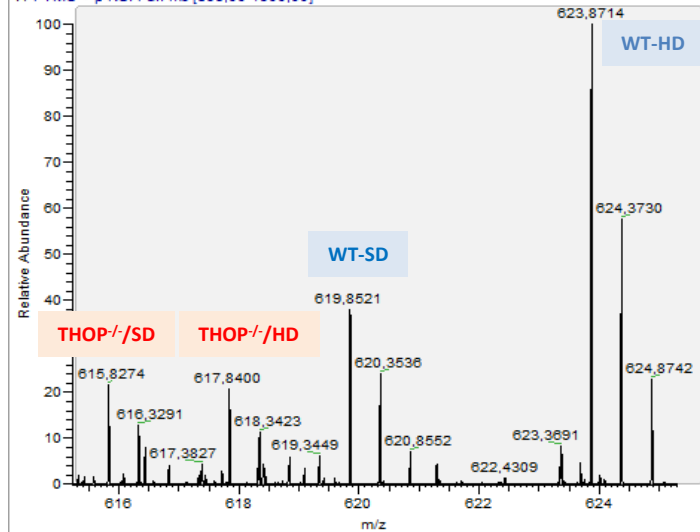


# FDVSHGSAQVK

170711PESSAM02983\_May7 #4188-4288 RT: 30,27-30,53 AV: 7 NL: 8,74E6  
T: FTMS + p NSI Full ms [395,00-1800,00]

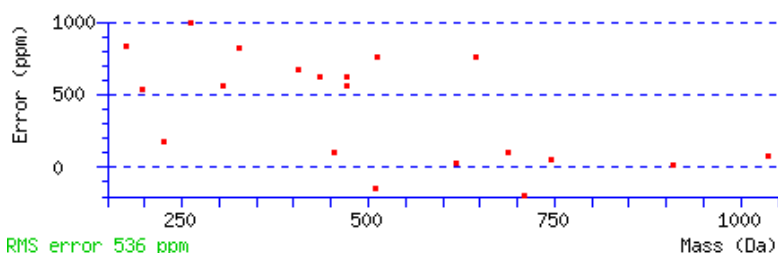
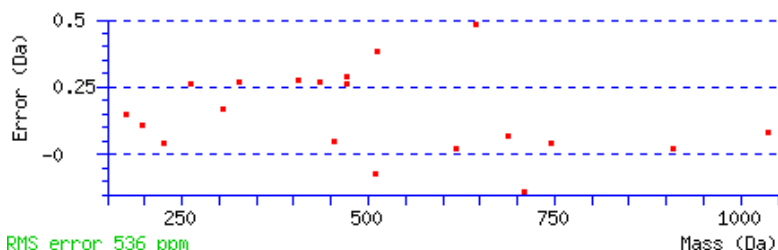


170711PESSAM02984\_May8 #4209-4398 RT: 31,29-31,89 AV: 14 NL: 5,66E6  
T: FTMS + p NSI Full ms [395,00-1800,00]





9	870.4104	435.7089	852.3999	426.7036	G	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	7
10	941.4476	471.2274	923.4370	462.2221	A	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
11	1070.4902	535.7487	1052.4796	526.7434	E	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	5
12	1141.5273	571.2673	1123.5167	562.2620	A	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
13	1254.6113	627.8093	1236.6008	618.8040	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
14	1383.6539	692.3306	1365.6434	683.3253	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15					R	175.1190	88.0631	158.0924	79.5498			1



NCBI BLAST search of [IGGHGAEYGAELER](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

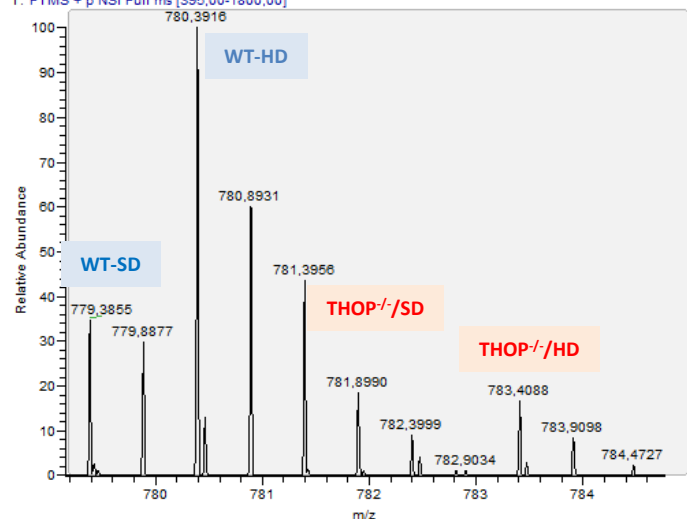
#### All matches to this query

Score	Mr(calc)	Delta	Sequence
44.5	1556.7583	0.0010	<a href="#">IGGHGAEYGAELER</a>
20.4	1556.8708	-0.1115	<a href="#">AYIHEKGMHRD</a>
18.9	1556.8218	-0.0625	<a href="#">ELEAEKAGTVSMY</a>
17.4	1556.7028	0.0565	<a href="#">EMGDEYVERAVT</a>
17.4	1556.8546	-0.0953	<a href="#">LPMMEYIPEKRA</a>
17.4	1556.8546	-0.0953	<a href="#">LPMMEYIPEKRA</a>
16.8	1556.9713	-0.2120	<a href="#">SAKGAERVITLKM</a>
16.6	1556.9054	-0.1461	<a href="#">DLPYEYLKPSRI</a>
15.3	1556.8675	-0.1082	<a href="#">KGNGGEHGPPGPPGP</a>
14.6	1556.8596	-0.1003	<a href="#">IAGLNMLSAISIER</a>

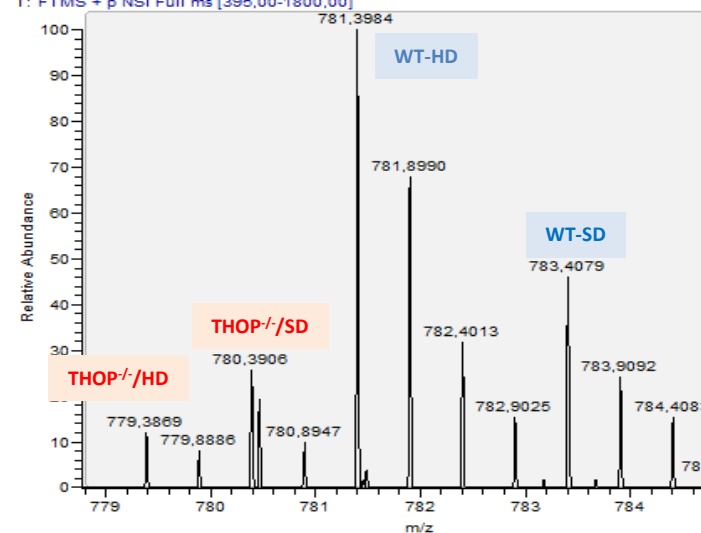
Mascot: <http://www.matrixscience.com/>

# IGGHGAEYGAELER

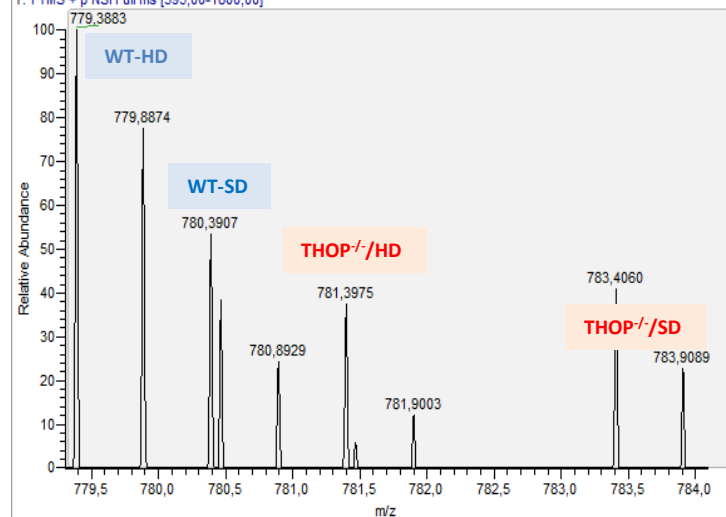
170711PESSAM02977\_May1 #6988-7471 RT: 39,51-41,00 AV: 28 NL: 1,18E6  
T: FTMS + p NSI Full ms [395,00-1800,00]



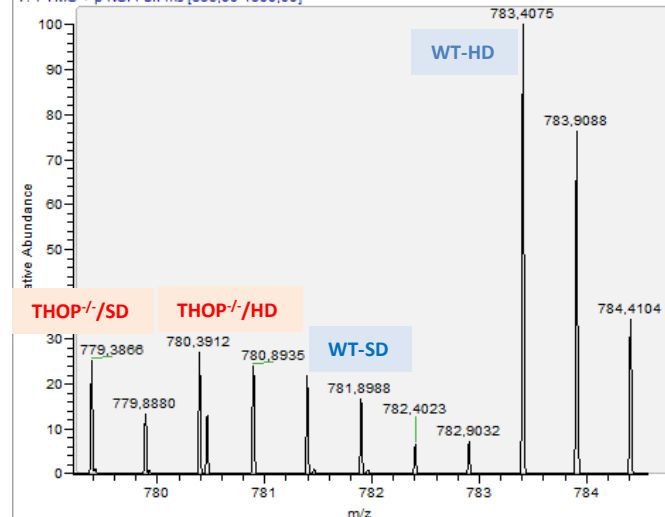
170711PESSAM02978\_May2 #6980-7148 RT: 40,01-40,52 AV: 9 NL: 1,53E6  
T: FTMS + p NSI Full ms [395,00-1800,00]



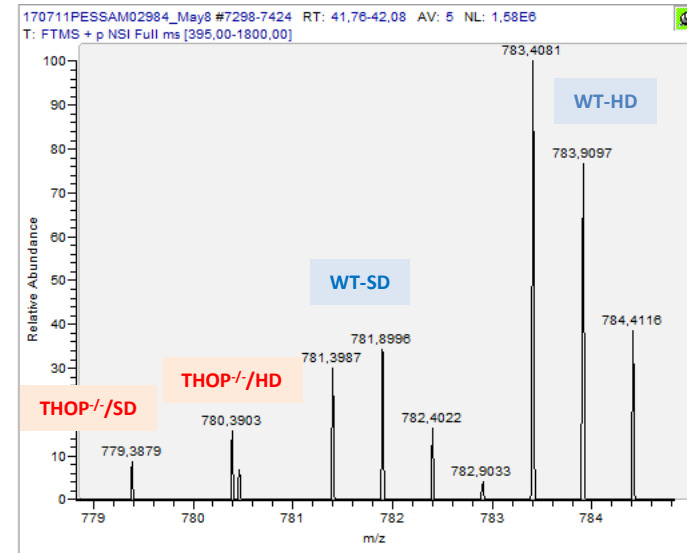
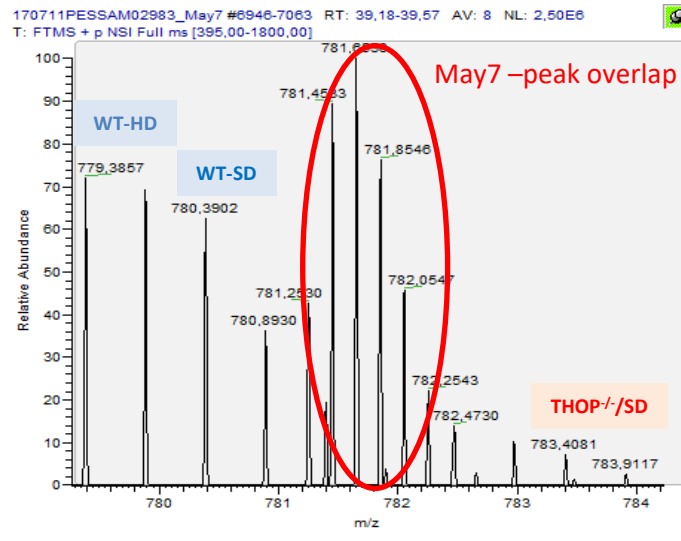
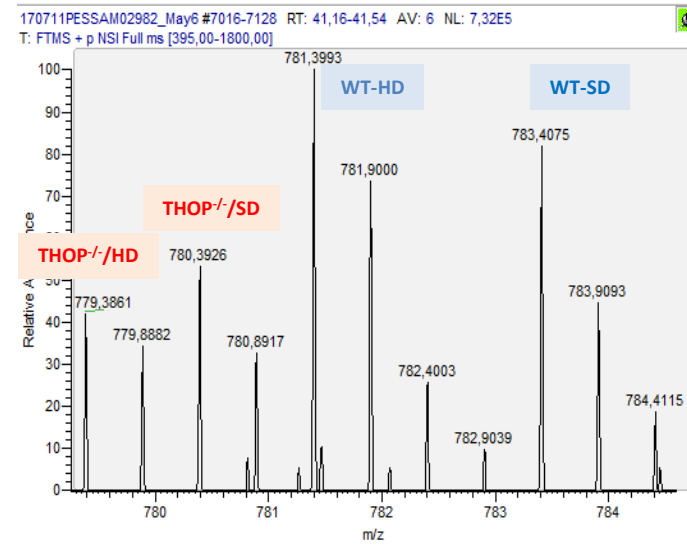
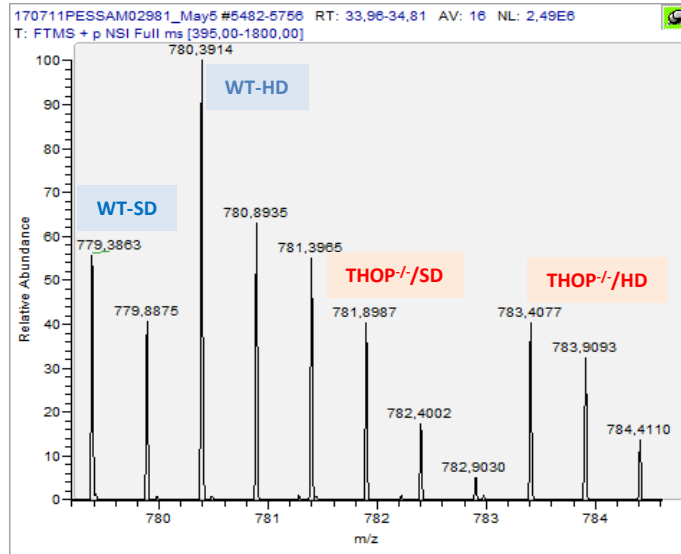
170711PESSAM02979\_May3 #6434-6533 RT: 38,60-38,80 AV: 4 NL: 1,17E6  
T: FTMS + p NSI Full ms [395,00-1800,00]



170711PESSAM02980\_May4 #6592-6767 RT: 38,42-38,92 AV: 10 NL: 3,08E6  
T: FTMS + p NSI Full ms [395,00-1800,00]



# IGGHGAEYGAELER



# Mascot Search Results

## Peptide View

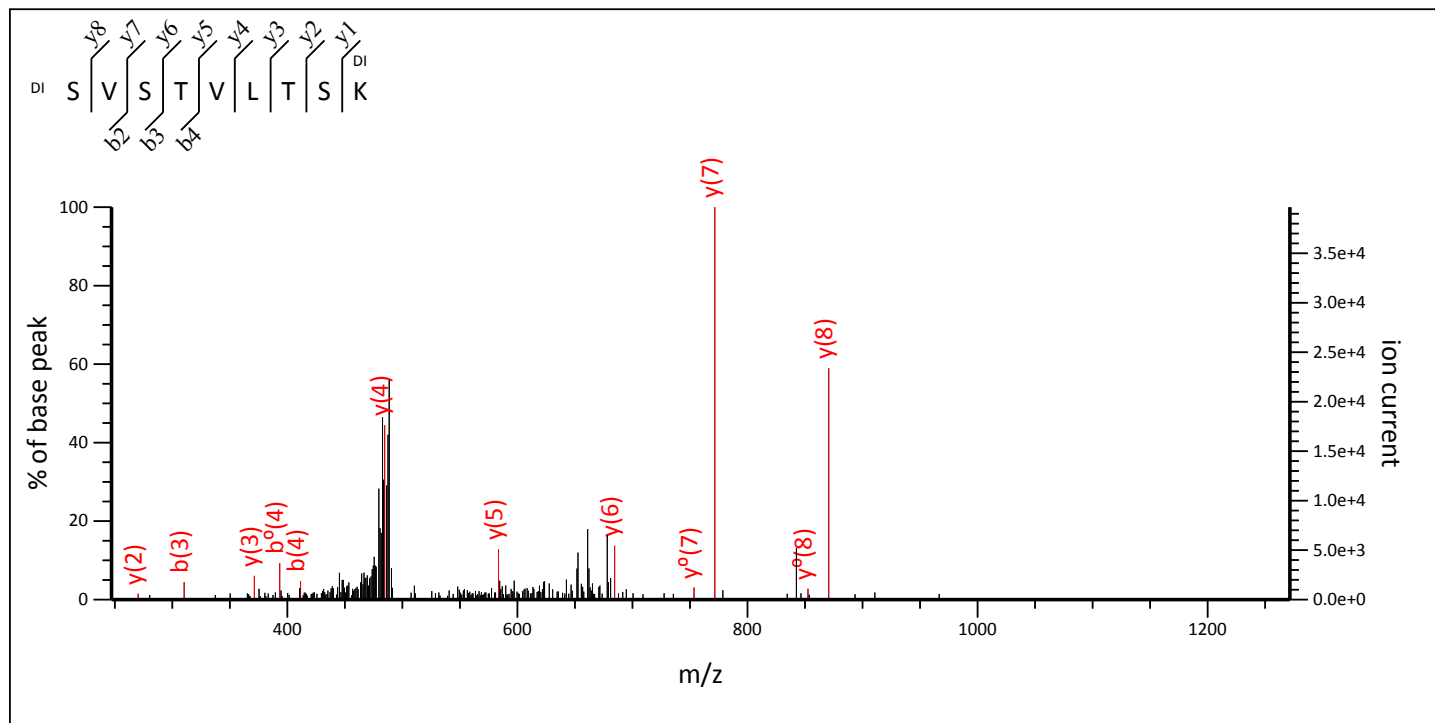
MS/MS Fragmentation of **SVSTVLTSK**

Found in **HBA\_MOUSE** in **SwissProt**, Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2

Match to Query 2839: 992.668188 from(497.341370,2+) intensity(14296911.0000) scans(5675) rawscans(sn5675)  
rtinseconds(2123.5117) index(3301)

Title: 3302: Scan 5675 (rt=2123.51) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



247.13

to 1271.51



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 992.6692

Variable modifications:

N-term : Dimethyl:2H(6)13C(2) (N-term)

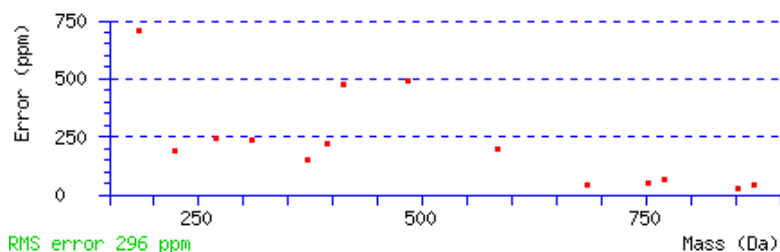
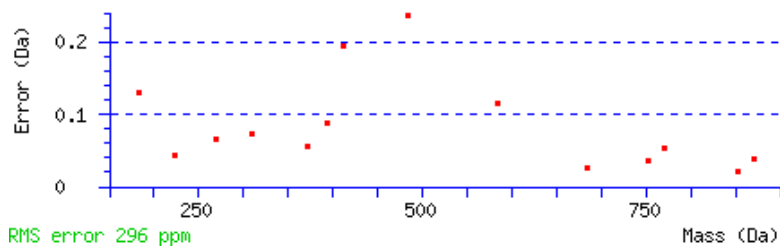
K9 : Dimethyl:2H(6)13C(2) (K)

Ions Score: 62 Expect: 0.023

Matches : 14/78 fragment ions using 25 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y*	y <sup>*++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	124.1150	62.5611	106.1044	53.5558	S							9
2	223.1834	112.0953	205.1728	103.0900	V	870.5688	435.7880	853.5422	427.2748	852.5582	426.7827	8
3	310.2154	155.6113	292.2049	146.6061	S	771.5004	386.2538	754.4738	377.7405	753.4898	377.2485	7
4	411.2631	206.1352	393.2525	197.1299	T	684.4683	342.7378	667.4418	334.2245	666.4578	333.7325	6
5	510.3315	255.6694	492.3209	246.6641	V	583.4207	292.2140	566.3941	283.7007	565.4101	283.2087	5
6	623.4156	312.2114	605.4050	303.2061	L	484.3522	242.6798	467.3257	234.1665	466.3417	233.6745	4
7	724.4633	362.7353	706.4527	353.7300	T	371.2682	186.1377	354.2416	177.6245	353.2576	177.1324	3
8	811.4953	406.2513	793.4847	397.2460	S	270.2205	135.6139	253.1940	127.1006	252.2099	126.6086	2

9					K	183.1885	92.0979	166.1619	83.5846			1
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NCBI **BLAST** search of [SVSTVLTSK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

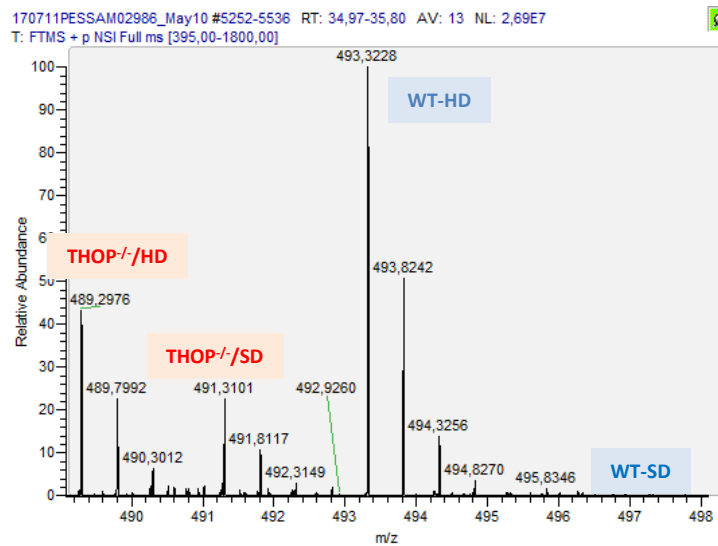
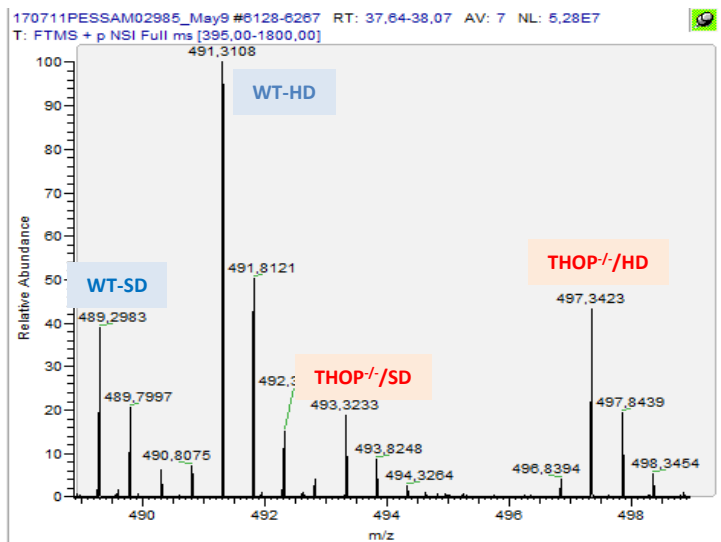
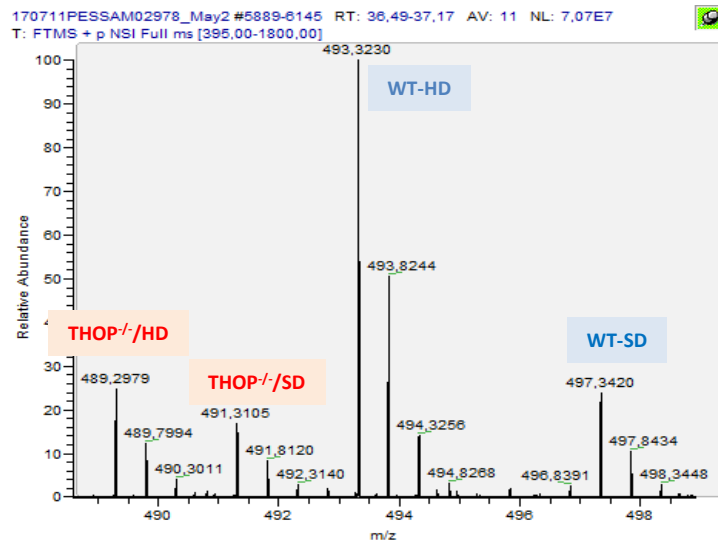
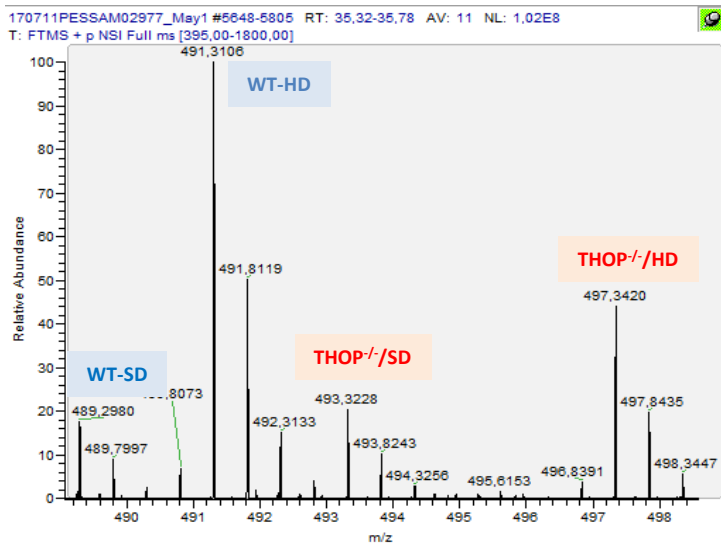
Other BLAST [web gateways](#)

#### All matches to this query

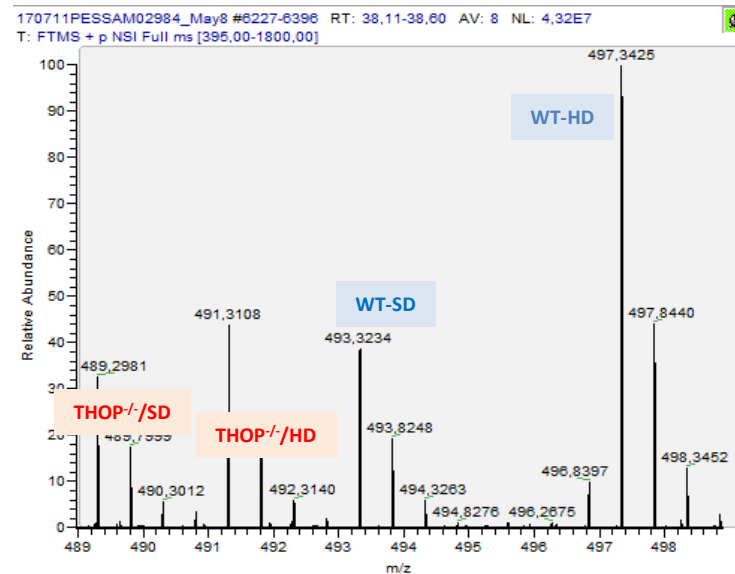
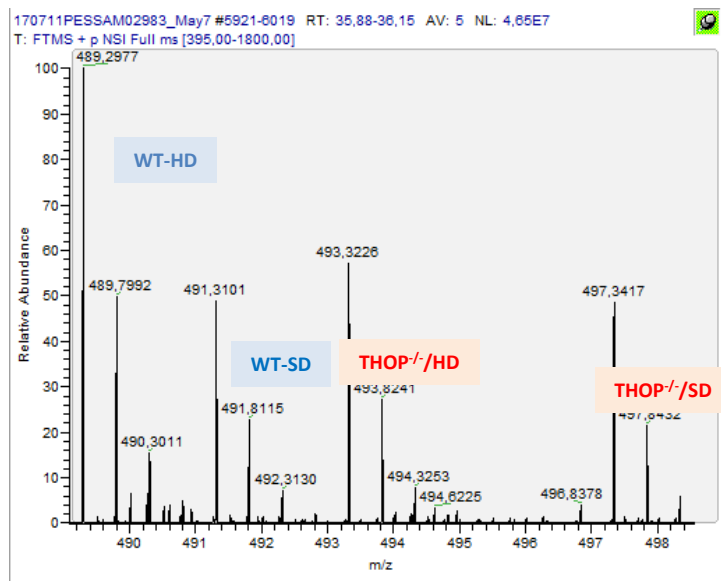
Score	Mr(calc)	Delta	Sequence
62.2	992.6692	-0.0010	<a href="#">SVSTVLTSK</a>
44.8	992.6328	0.0354	<a href="#">GSSTVITSK</a>
26.9	992.5030	0.1652	<a href="#">SVSSFAVGGM</a>
26.2	992.5179	0.1503	<a href="#">INDLLSFG</a>
25.4	992.5787	0.0895	<a href="#">SVSSPMADK</a>
24.6	992.5360	0.1321	<a href="#">SVVAGFSSGF</a>
23.6	992.4485	0.2197	<a href="#">PGDLSVSSTC</a>
23.2	992.4848	0.1833	<a href="#">DNLLVTSMG</a>
22.8	992.5212	0.1469	<a href="#">VAKSVTSGM</a>
21.7	992.5787	0.0895	<a href="#">SVGMGDVEK</a>

Mascot: <http://www.matrixscience.com/>

# SVSTVLTSK



# SVSTVLTSK



# Mascot Search Results

## Peptide View

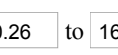
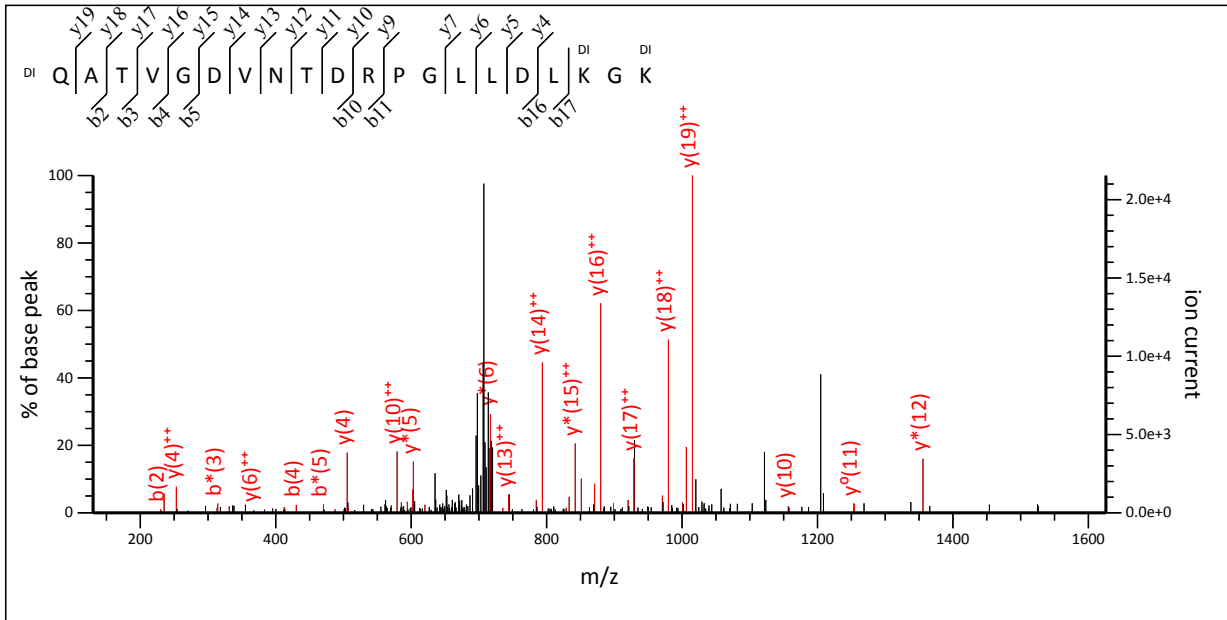
MS/MS Fragmentation of **QATVGDVNTDRPGLLDLKGK**

Found in **ACBP\_MOUSE** in **SwissProt**, Acyl-CoA-binding protein OS=Mus musculus GN=Dbi PE=1 SV=2

Match to Query 17147: 2186.250912 from(729.757580,3+) intensity(10054624.0000) scans(12874) rawscans(sn12874) rtinseconds(3491.9313) index(8013)

Title: 8014: Scan 12874 (rt=3491.93) [D:\Users\Mayara - HMS Fusion data\170711PESSAM02977\_May1.raw]

Data file 170711PESSAM02977\_May1.temp.mgf



Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 2186.2634

Variable modifications:

N-term : Dimethyl:2H(2) (N-term)

K18 : Dimethyl:2H(2) (K)

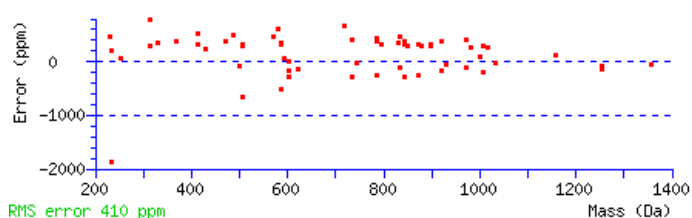
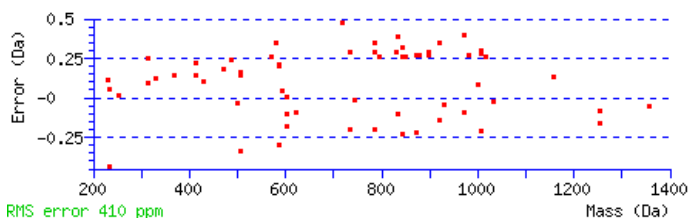
K20 : Dimethyl:2H(2) (K)

Ions Score: 41 Expect: 0.0066

Matches : 63/216 fragment ions using 104 most intense peaks ([help](#))

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	159.1128	80.0600	142.0863	71.5468			Q							20
2	230.1499	115.5786	213.1234	107.0653			A	2029.1652	1015.0862	2012.1386	1006.5730	2011.1546	1006.0809	19
3	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	T	1958.1281	979.5677	1941.1015	971.0544	1940.1175	970.5624	18
4	430.2660	215.6366	413.2395	207.1234	412.2554	206.6314	V	1857.0804	929.0438	1840.0538	920.5306	1839.0698	920.0385	17
5	487.2875	244.1474	470.2609	235.6341	469.2769	235.1421	G	1758.0120	879.5096	1740.9854	870.9964	1740.0014	870.5043	16
6	602.3144	301.6608	585.2879	293.1476	584.3039	292.6556	D	1700.9905	850.9989	1683.9640	842.4856	1682.9799	841.9936	15
7	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	V	1585.9636	793.4854	1568.9370	784.9721	1567.9530	784.4801	14
8	815.4258	408.2165	798.3992	399.7032	797.4152	399.2112	N	1486.8952	743.9512	1469.8686	735.4379	1468.8846	734.9459	13
9	916.4734	458.7404	899.4469	450.2271	898.4629	449.7351	T	1372.8522	686.9298	1355.8257	678.4165	1354.8417	677.9245	12
10	1031.5004	516.2538	1014.4738	507.7406	1013.4898	507.2485	D	1271.8045	636.4059	1254.7780	627.8926	1253.7940	627.4006	11
11	1187.6015	594.3044	1170.5749	585.7911	1169.5909	585.2991	R	1156.7776	578.8924	1139.7511	570.3792	1138.7670	569.8872	10
12	1284.6543	642.8308	1267.6277	634.3175	1266.6437	633.8255	P	1000.6765	500.8419	983.6499	492.3286	982.6659	491.8366	9
13	1341.6757	671.3415	1324.6492	662.8282	1323.6652	662.3362	G	903.6237	452.3155	886.5972	443.8022	885.6132	443.3102	8
14	1454.7598	727.8835	1437.7332	719.3703	1436.7492	718.8782	L	846.6023	423.8048	829.5757	415.2915	828.5917	414.7995	7
15	1567.8438	784.4256	1550.8173	775.9123	1549.8333	775.4203	L	733.5182	367.2627	716.4917	358.7495	715.5076	358.2575	6

16	1682.8708	841.9390	1665.8442	833.4258	1664.8602	832.9338	D	620.4341	310.7207	603.4076	302.2074	602.4236	301.7154	5
17	1795.9549	898.4811	1778.9283	889.9678	1777.9443	889.4758	L	505.4072	253.2072	488.3806	244.6940			4
18	1954.0968	977.5520	1937.0702	969.0387	1936.0862	968.5467	K	392.3231	196.6652	375.2966	188.1519			3
19	2011.1182	1006.0628	1994.0917	997.5495	1993.1077	997.0575	G	234.1812	117.5942	217.1547	109.0810			2
20							K	177.1598	89.0835	160.1332	80.5702			1



NCBI BLAST search of [QATVGDVNTDRPGLLDLKGK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

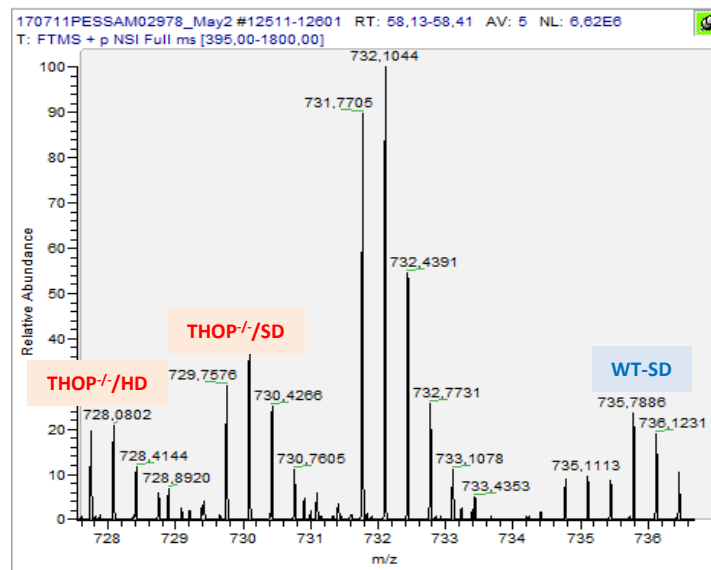
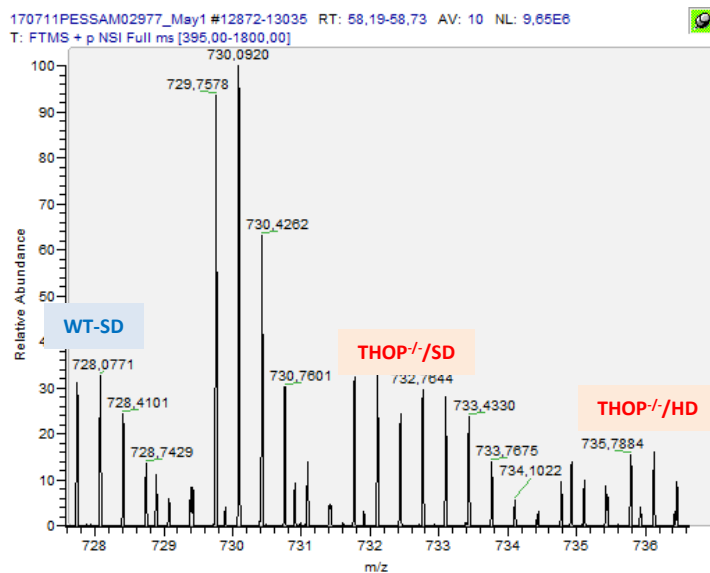
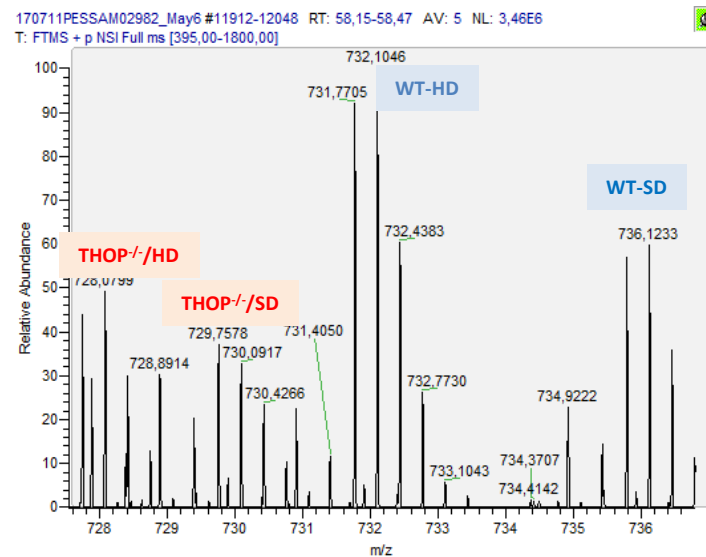
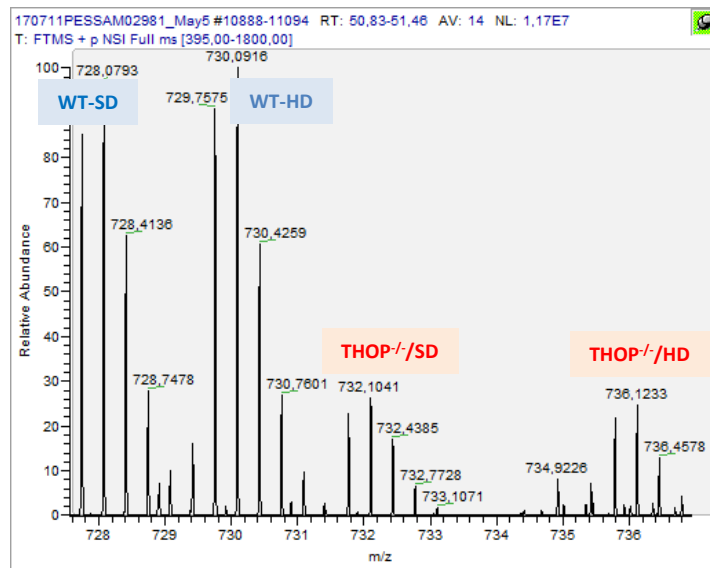
Other BLAST [web gateways](#)

#### All matches to this query

Score	Mr(calc)	Delta	Sequence
41.4	2186.2634	-0.0125	<a href="#">QATVGDVNTDRPGLLDLKGK</a>
17.4	2186.1636	0.0873	<a href="#">APRKPPSSELLESRDHYA</a>
15.9	2186.0460	0.2049	<a href="#">ANDVGMIQTAHVGVGISGNEGM</a>
15.7	2186.1623	0.0886	<a href="#">SATDRKIIIFQVIDYVSAY</a>
14.2	2186.0416	0.2093	<a href="#">YSTPSPATIETQSSSSEEIV</a>
13.0	2186.0678	0.1831	<a href="#">QATVGNYSYKCNTEEHIEVS</a>
12.9	2186.1486	0.1023	<a href="#">YVVFLKLFLETAEQHEM</a>
12.5	2186.1261	0.1248	<a href="#">PPAGDDGSGSRPQRLLWQTA</a>
11.7	2186.0060	0.2449	<a href="#">SNGNRRHSEDESLGSSGRV</a>
11.3	2186.1253	0.1256	<a href="#">VTPVPGQTLVTMATATVTANNG</a>

Mascot: <http://www.matrixscience.com/>

# QATVGDVNTDRPGLLDLKGG



QATVGDVNTDRPGLLDLKGG

May7 –not found

