



Mass Spectrometry Report

Jan 20, 2006

Hanson Institute
Protein Core Facility

Sample: C:\MS Files\20-1-06\06-006-1.raw

Samples for identification by mass spectrometry were digested with trypsin under standardised conditions. The resulting peptides were reduced with TCEP and desalted through a C18 reverse phase silica column into the Q-Tof2 Mass Spectrometer, via a NanoSource.

The spectrometer was calibrated against the fragmentation pattern of [Glu]-Fibrino peptide B and found to be accurate to within 30 ppm.

Data was collected as intensity versus mass over charge (Th, Thompsons) and multiply charged ions (+2, +3, +4) were automatically detected and subjected to fragmentation.

The collected fragmentation data was the analysed using ProteinLynx software and searched against a FASTA protein database.

Protein identification matches were assigned if 2 or more sequenced peptides were identified from a protein in the database.

Regards,

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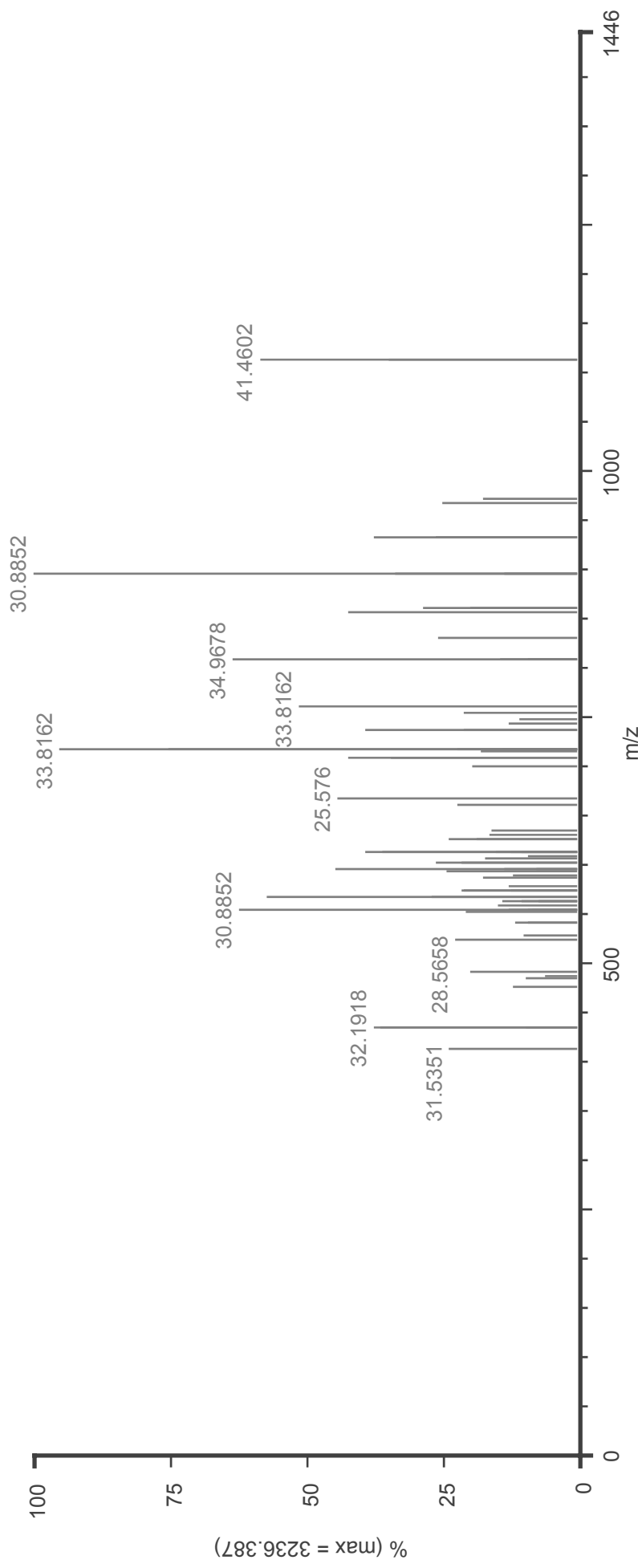
Workflow Template: Medium NCBI Search

Property	Value
Query Type	Databank Search
Search Type	PLGS
Databank	NCBI0505-1.0
Fragment Tolerance	0.1 Da
High MW Filter	200000
Low MW Filter	0
High Pi Filter	14.0
Low Pi Filter	0.0
Mass Tolerance	100.0Da
Min Peptides	2
Min Std. Deviation	0.0050
Digestor 1	Trypsin
Query Type	Automod Search
Consider Mods	true
Consider Subs.	true
Max. Mods & Subs	1
Fragment Tolerance	0.1
Mass Tolerance	50.0 Da
Min. Mass Std. Deviation	0.0050
Digestor 1	Trypsin

Sample: C:\MS Files\20-1-06\06-006-1.raw

Acc #	Protein Description	Peptides	Coverage	Score
37999050	essential protein for meiotic synapsis Oryza sativa japonica cultivar ...	5	7.377	14.7098





Protein Match Details

Sample: C:\MS Files\20-1-06\06-006-1.raw
Accession: 37999050
Name: 37999050
Description: essential protein for meiotic synapsis Oryza sativa japonica cultiv
Confidence: 100.0
Coverage: 7.377
Matches: 5
Score: 14.7098

37999050 Coverage Map					
1	MVMAQKTEA	EITEQDSLLL	TRNLLFAIY	NISYIRGLFP	EKYFNDKSVP
51	ALEMKIKKLM	PMDTESRRLI	DWMEKGVYDA	LQKKYIKTLL	FCICEKEEGP
101	MIEEYAFSFS	YPNTSGDEVA	MNLSRTGSKK	NSATFISNAA	EVTDDQMR S
151	ACKMIRTLVS	LMETLDDQME	ERTILMKLLY	YDDVTPEDEY	PPFFKCCADN
201	EAINIWNKNP	LKMEVGNVNS	KHLVLALKVK	SVLDPCDDNN	VNSEDDNMSL
251	DNESDQDNDF	SDTEVRPSEA	ERYIVAPNDG	TCKGQGTIS	EDDTQDPVHE
301	EELTAQVREW	ICSRDTESE	VSDVLVNFPP	ISMEMVEDIM	ERLLKDGLLS
351	RAKKDSYSVN	KIADPTTPhi	KKEVIMQNVS	PTEGTKNSNG	DLMYMKALYH
401	ALPMDYVSVG	KLHGKLDGEA	SQNMVRKLI	KMVQDGYVKN	SANRRLGKAV
451	IHSEVTNRKL	LETKKILEVD	IAEQMAIDTN	AEPGEPEKRD	HLSGHEMRDG
501	STMGCLQSVG	SDLTRTRREL	EPQQNVSMQS	GGEASTVDKD	PSRTPTSVRE
551	QASVCSLESG	VLGQKVRKSL	AGAGGTQCSC	DKRFRKASTV	KEPILQYVKR
601	QKSQVQVQVQ				



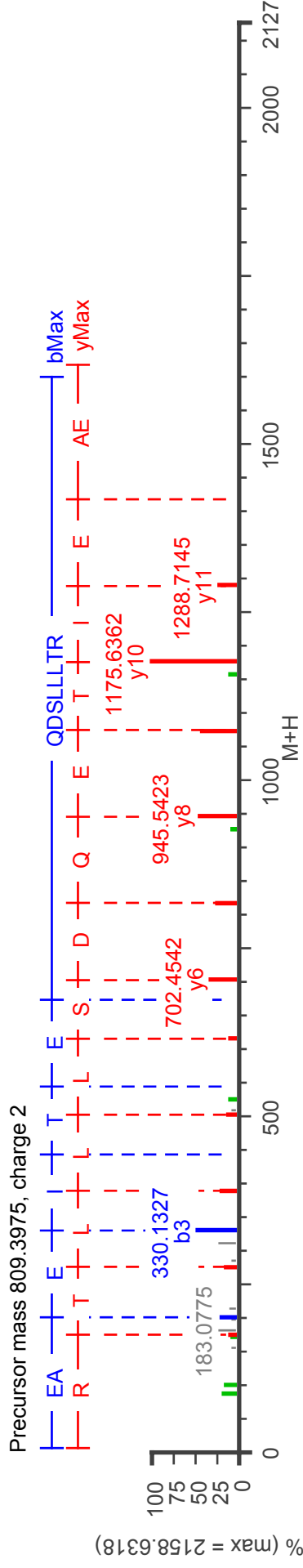
Peptide Match # 1

Sequence: *EAEITEQDSLLLTR*

Score: 220.5093

Mass: 1616.8258

Modifications: None



	E	A	E	E	I	T	E	Q	D	S	L	L	L	T	R
a	102.055 (0.001)	173.093 (0.002)	302.135 (-0.003)	415.219 (0.001)	516.267 (0.001)	645.31	773.368	888.395	975.427	1088.511	1201.595	1314.679	1415.727	--	
b	130.05	201.088 (0)	330.13 (-0.003)	443.214 (0.004)	544.262 (-0.004)	673.304 (0.017)	801.363	916.39	1003.422	1116.506	1229.59	1342.674	1443.722	--	
v''	--	1488.791	1417.754 (0.01)	1288.711 (-0.003)	1175.627 (-0.009)	1074.58 (-0.011)	945.537 (-0.005)	817.478 (0.002)	702.451 (-0.003)	615.419 (0.024)	502.335 (-0.004)	389.251 (-0.005)	276.167 (-0.002)	175.119 (0.001)	
z	--	1471.765	1400.727	1271.685 (-0.001)	1158.601 (-0.004)	1057.553 (0.004)	928.51 (-0.015)	800.452 (0.013)	685.425 (0.083)	598.393 (0.027)	485.309 (0.025)	372.225 (-0.01)	259.141 (0.016)	158.093	

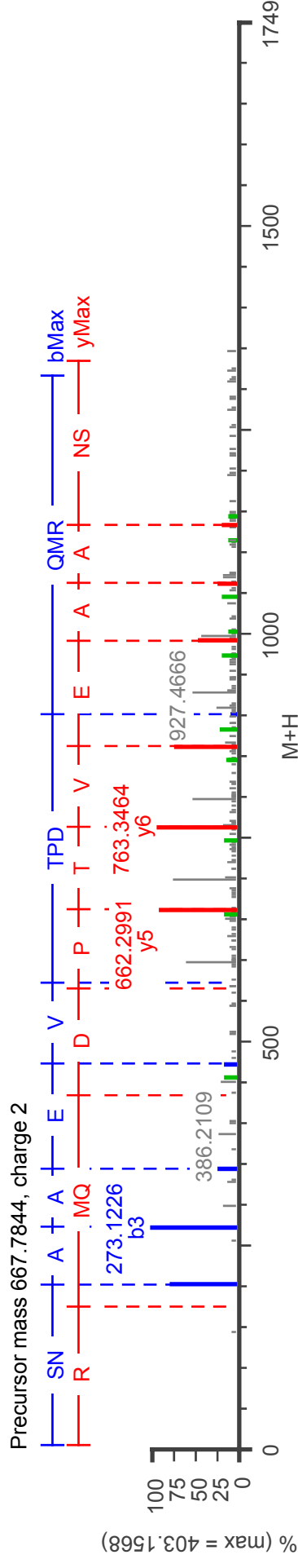
Peptide Match # 2

Sequence: SNAAEVTPDQMR

Score: 106.0126

Mass: 1333.5931

Modifications: Hydroxyl DKNP (9)



	S	N	A	A	E	V	T	P	D	Q	M	R	
a	60.045 (0.001)	174.088	245.125	316.162 (-0.003)	445.205 (-0.002)	544.273 (0.004)	645.321 (0.044)	742.373	873.395	1001.454 (0.024)	1132.495	--	
b	88.04	202.083 (0.001)	273.12 (-0.003)	344.157 (-0.005)	473.2 (-0.006)	572.268 (-0.002)	673.316	770.368	901.39 (-0.049)	1029.449	1160.489	--	
y"	--	1247.569	1133.526 (-0.024)	1062.489 (-0.005)	991.452 (-0.006)	862.409 (-0.003)	763.341 (-0.006)	662.293 (-0.006)	565.24 (0.011)	434.219 (0.008)	306.16	175.119 (0.002)	
z	--	1230.542	1116.5	1045.462 (-0.071)	974.425 (-0.004)	845.383 (0.023)	746.314 (0.019)	645.267 (-0.011)	548.214	417.192	289.133	158.093	

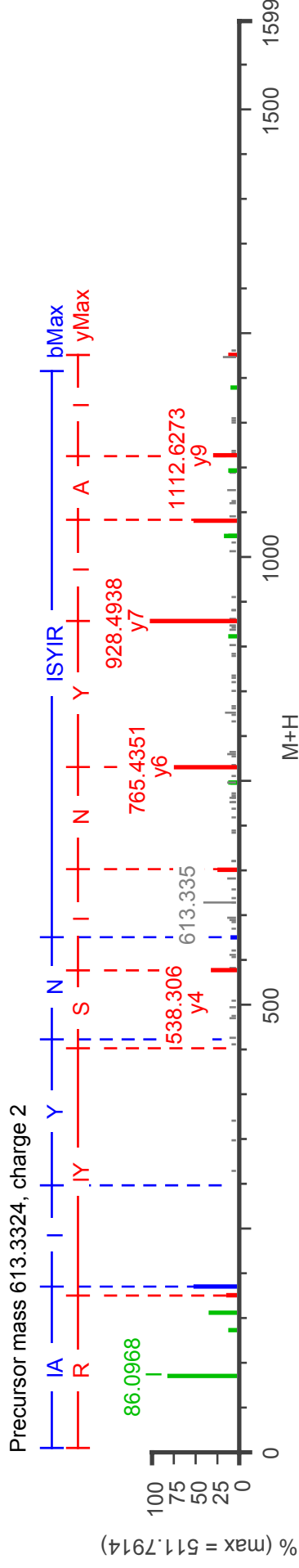
Peptide Match # 3

Sequence: *I A I Y N I S Y I R*

Score: 86.9647

Mass: 1224.6866

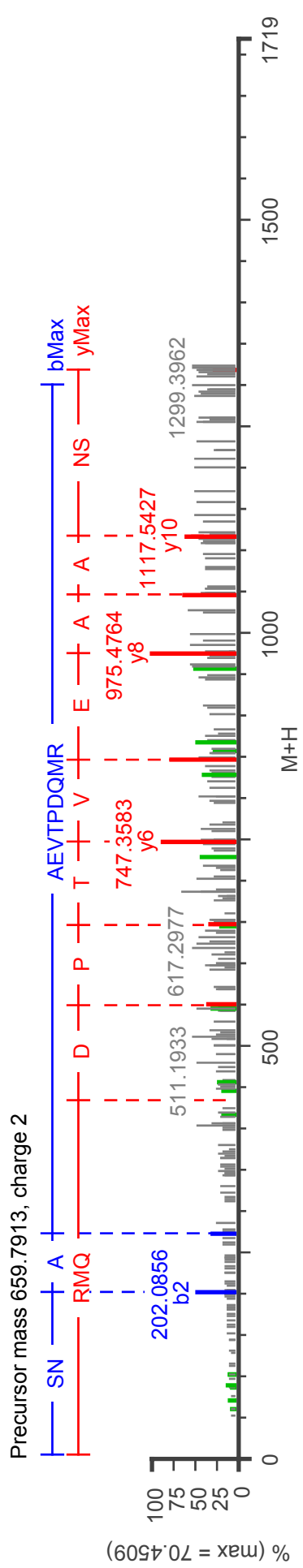
Modifications: None



a	86.097 <i>(0)</i>	157.134 <i>(0.002)</i>	270.218	433.281 <i>(0.095)</i>	547.324	660.408	747.44 <i>(0.029)</i>	910.504 <i>(0.051)</i>	1023.588 <i>(0.078)</i>	--
b	114.092	185.129 <i>(-0.002)</i>	298.213 <i>(0.007)</i>	461.276 <i>(0.022)</i>	575.319 <i>(-0.062)</i>	688.403	775.435	938.499	1051.583	--
v''	--	1112.61 <i>(-0.017)</i>	1041.573 <i>(-0.01)</i>	928.489 <i>(-0.005)</i>	765.426 <i>(-0.009)</i>	651.383 <i>(-0.015)</i>	538.299 <i>(-0.007)</i>	451.267 <i>(-0.004)</i>	288.204	175.119 <i>(-0.007)</i>
z	--	1095.584 <i>(0.012)</i>	1024.547 <i>(0.008)</i>	911.463 <i>(-0.009)</i>	748.399 <i>(-0.011)</i>	634.356 <i>(0.076)</i>	521.272 <i>(0.099)</i>	434.24	271.177 <i>(0.03)</i>	158.093 <i>(0)</i>

Peptide Match # 4

Sequence: SNAAEVTPDQMR
Score: 26.6958
Mass: 1317.5984
Modifications: None

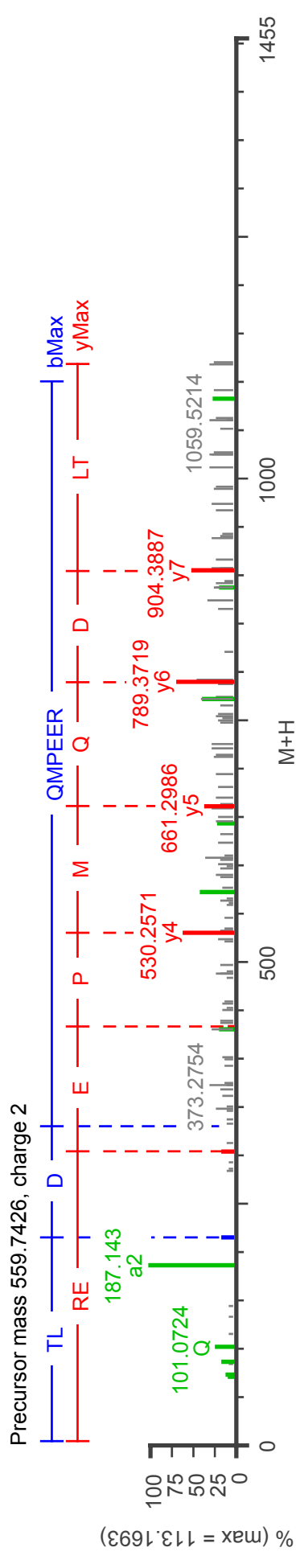


a	60.045 (0.008)	174.088	245.125	316.162	445.205 (0.074)	544.273 (0.003)	645.321 (-0.006)	742.373	857.4 (0.059)	985.459	1116.5	--
b	88.04	202.083 (-0.003)	273.12 (-0.001)	344.157	473.2	572.268	673.316	770.368	885.395	1013.454	1144.494	--
y"	--	1231.574	1117.531 (-0.011)	1046.494 (-0.016)	975.457 (-0.019)	846.414 (0.002)	747.346 (-0.012)	646.298 (-0.016)	549.246 (0.025)	434.219 (0)	306.16	175.12
z	--	1214.548	1100.505	1029.468	958.43	829.388	730.319	629.272	532.219	417.192 (0.021)	289.134	158.093



Peptide Match # 5

Sequence: TLDQMPEER
Score: 25.8123
Mass: 1117.5074
Modifications: None



a	74.061 (-0)	187.145 (0.002)	302.172	430.23 (-0.028)	561.271	658.323	787.366	916.409	--
b	102.056	215.14 (-0.001)	330.167 (-0.004)	458.225	589.266	686.318	815.361	944.404	--
v''	--	1017.468	904.383 (-0.005)	789.357 (-0.015)	661.298 (-0.001)	530.257 (0)	433.205 (-0.085)	304.162 (-0.005)	175.12
z	--	1000.441	887.357 (-0.004)	772.33 (-0.034)	644.271 (-0.062)	513.231	416.178	287.136	158.093

