Supplemental Figures legends:

Fig. S1. Silencing of the endogenous Cloroplastos alterados gene (*GbCLA1*) in cotton by tobacco rattle virus (TRV)-mediated virus-induced gene silencing (VIGS). (A) The cotyledons of 10-day-old seedlings of *G. barbadense* cv. '7124' were hand-infiltrated with *Agrobacterium* carrying either *TRV:GbCLA1* or VIGS-vector control (*TRV:00*). The photobleaching phenotype was photographed at 20 d post-infiltration. RT-PCR analysis indicated that the transcripts of *GbCLA1* were reduced 12 d after infiltration. (B) Albino phenotypes were firstly observed after 10 d after infiltration and the tender leaves displayed a more obvious photobleaching phenotype.

Fig. S2. The relative percentages of three groups of proteins with different expression patterns and GO functional classification analysis of identified proteins. (A) The relative percentages of three groups of proteins with different regulated patterns (up-regulated, down-regulated and other regulatory patterns). (B) GO functional classification analysis on differentially expressed proteins based on level 2 biological processes. Histograms represent the functional distribution, which is expressed as a percentage of the amount of proteins.

Fig. S3. qPCR analysis of gossypol metabolic-related genes transcripts in control and MeJA treatments. *GbFPS*, *GbCYP706B1*, *GbCAD1* and *WRKY1*, which were involved in gossypol metabolism, were detected at the transcriptional levels by qPCR. Error bars represent the standard deviation for three independent experiments, and three technical replicates were analyzed.

Supplemental Figures:

Fig. S1

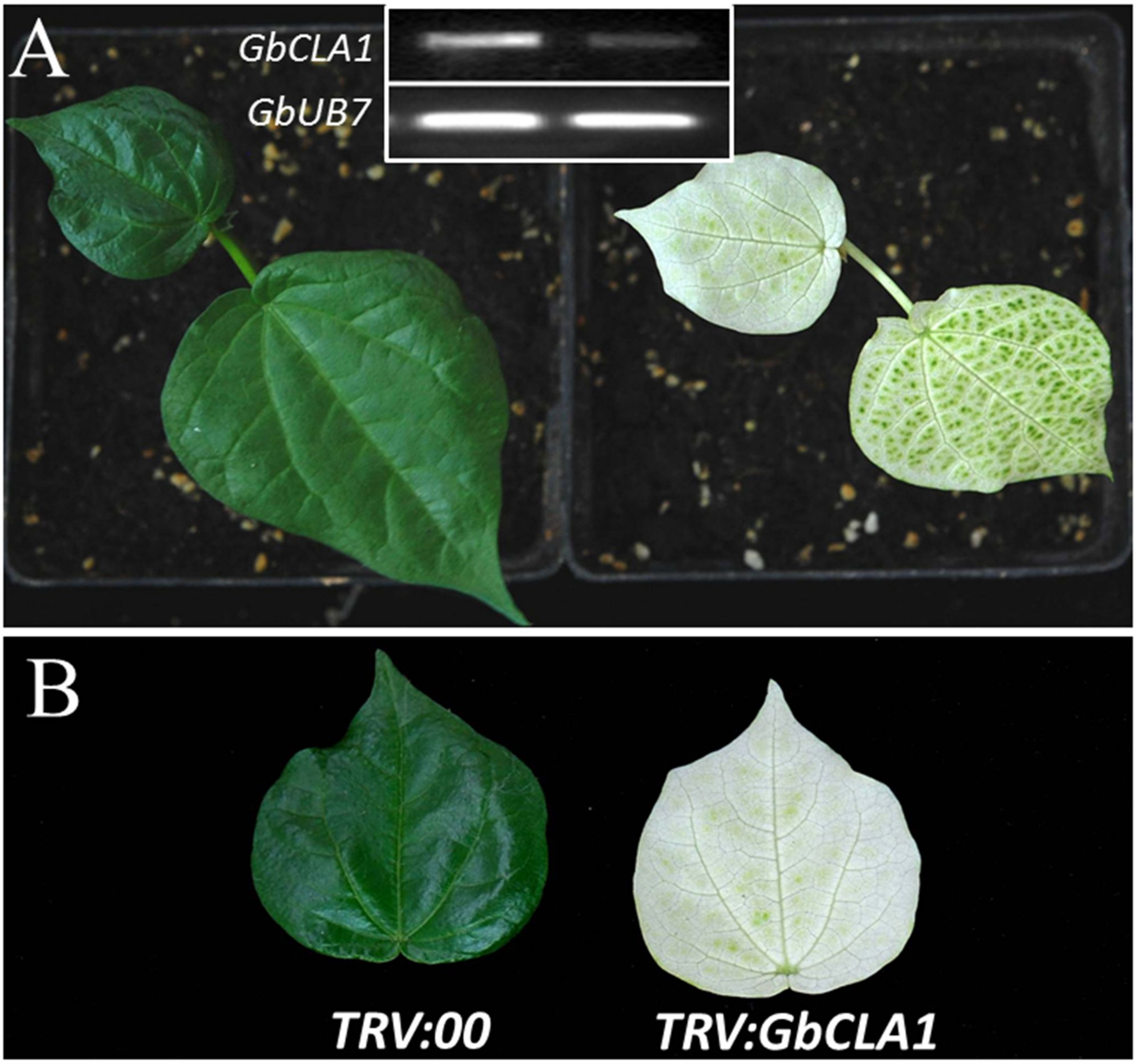


Fig. S2

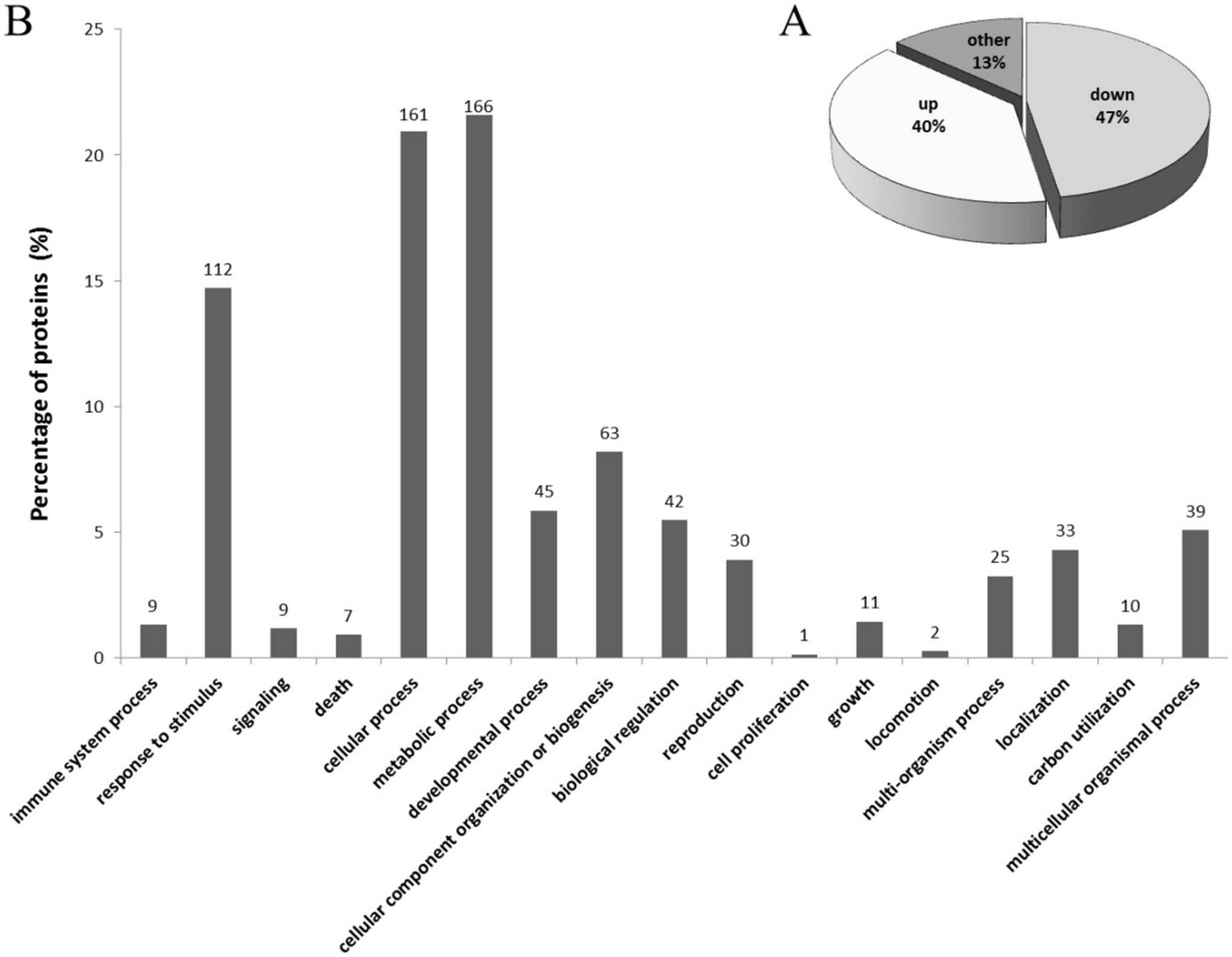
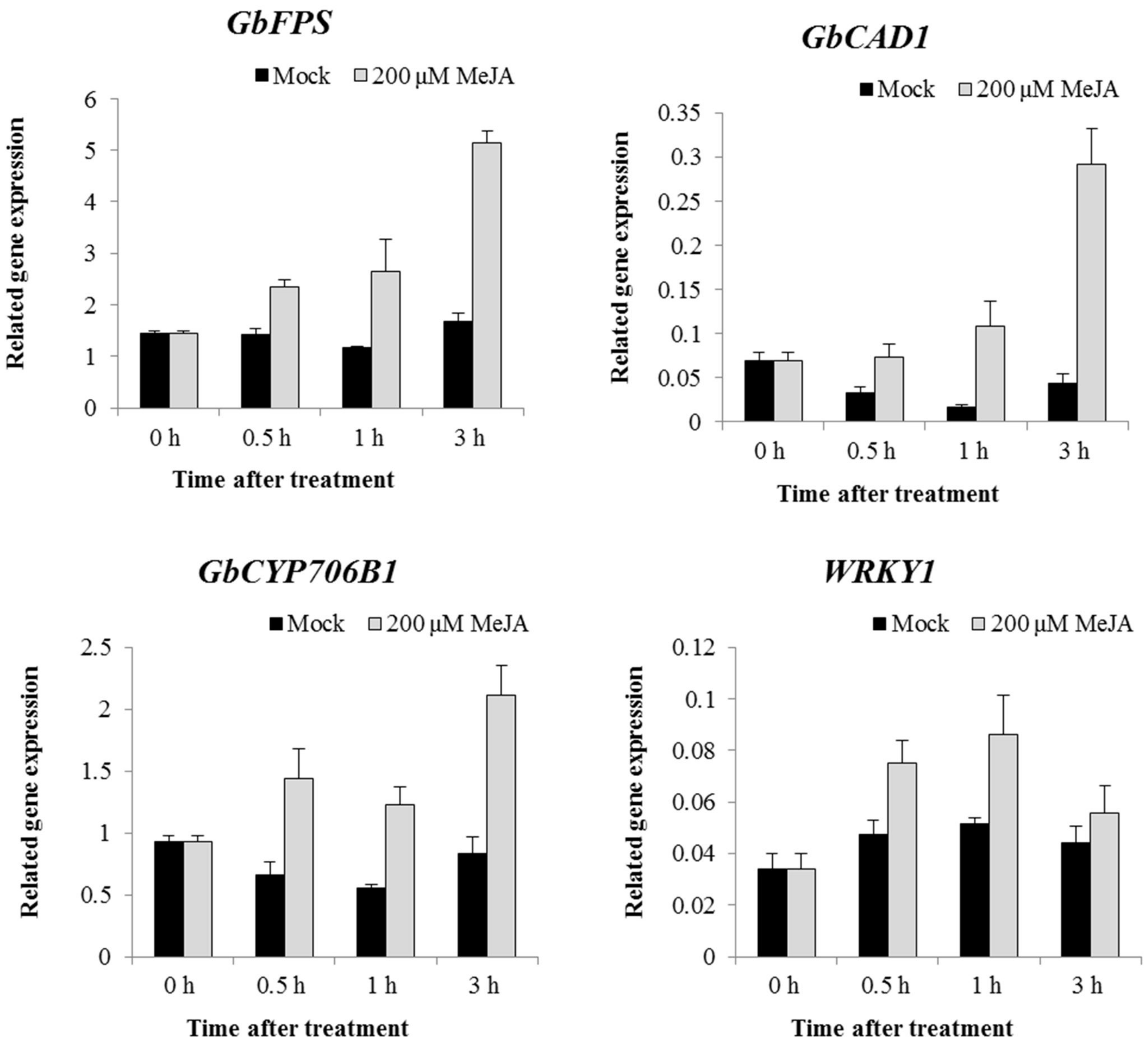

B
Percentage of proteins (%)
25
20
15
10
5
0
9
112
9
7
161
166
45
63
42
30
1
11
2
25
33
10
39
immune system process
response to stimulus
signaling
death
cellular process
metabolic process
developmental process
cellular component organization or biogenesis
biological regulation
reproduction
cell proliferation
growth
locomotion
multi-organism process
localization
carbon utilization
multicellular organismal process
A
other
13%
up
40%
down
47%

Fig. S3


GbFPS
■ Mock □ 200 μM MeJA
Related gene expression
0
1
2
3
4
5
6
0 h
0.5 h
1 h
3 h
Time after treatment
GbCAD1
■ Mock □ 200 μM MeJA
Related gene expression
0
0.05
0.1
0.15
0.2
0.25
0.3
0.35
0 h
0.5 h
1 h
3 h
Time after treatment
GbCYP706B1
■ Mock □ 200 μM MeJA
Related gene expression
0
0.5
1
1.5
2
2.5
0 h
0.5 h
1 h
3 h
Time after treatment
WRKY1
■ Mock □ 200 μM MeJA
Related gene expression
0
0.02
0.04
0.06
0.08
0.1
0.12
0 h
0.5 h
1 h
3 h
Time after treatment

Supplemental tables

Table S1. Primers used for RT

Genes	Sequences	Annealing Temp.(℃)	Length of amplified fragments (bp)
GbCAD1	5'-TACCATAACAACAATGATGCCGAG	58.9	472
	5'-TCCACCACCTACAAATCTCGCTTA		
Gb14-3-3c	5'-ATCGGTGCTCGCCGTGCTTC	59.2	329
	5'-TCGGCGTTGGCAATGTCCTG		
Gb14-3-3d	5'-GCCGTGCTTCCTGGAGGATTG	58.4	279
	5'-GCGTATTCTCAGCAGCGGCTTTC		
GbSSI2	5'-CGCCACGAGACAGCATACACTAA	57.6	382
	5'-CAGAAACCCAACTGAATGGAACAC		
GbLOX1	5'-ACACGATGAACATCAATGCCTT	59.2	361
	5'-TCTCGGAGTTCTTTCCACCAG		
GbJaz1	5'-AAAAGCCTCAAAAAGGAAGACC	59.1	203
	5'-AAGGATAGGATCACCGCAAAA		
GbJar1	5'-TTTGCTGGAACCGCTACGACC	63.2	415
	5'-TGACATTAGGGAAAAGCTCCGG		
GbJaz3	5'-TTCGCTTTGCCTTCGGTTATT	60.7	457
	5'-TGCCTACTCGTTGCCTGTTGT		
GbJaz6	5'-TGGTGGTCAAGTGGCAGTATTT	59.6	391
	5'-ATCGGGTTTAGGTGGCAGAGT		
GbPR4	5'-CAGGAGAAGGAGCGACTGTGA	58.8	284
	5'-TCCCACATCCAAATCTAACCC		
GbBZR1	5'-GGACTGTTGAACCCGATGGCACTA	64.9	285
	5'-CAGGAGCACTGATGGAACCACTATG		
GbBRI1	5'-CACAGCGGAAATGGAAAC	59.6	438
	5'-TAAACATCGCCCTTGGTG		
GbBIN2	5'-TATGGCAGAGCGTGTAGT	58.5	293
	5'-GTGGCATTCTTTGATTAG		
GbUB7	5'-GACTCTACTCAATCCCCACCAGCCT	58.5	321
	5'-CCGCACCTTAGCCGACTACAACATC		
GbCYP706B1	5'-TGACTGATCATGAGAAGCT	59.5	239
	5'-GTGCTGGAGAT TTGATGGT		
GbFPS	5'-GCGGATCTCAGGTCAGCATTT	58.6	334
	5'-TCGGCAATCTAAACCAACAAGG		
GbdHG-6-OMT	5'-AATCCCTTCTGCATAACGCCTA	61.2	255
	5'-GTCCAATCCCTCAAATGCCC		

Table S2. Primers used for qRT

Genes	Sequences	Annealing Temp.(℃)	Length of amplified fragments (bp)
Gb14-3-3c	5'-AGTCTCTGCCTCCGCCGACAACG	66.9	123
	5'-TGCTCAATGGAGGAGATGATGCG		
Gb14-3-3d	5'-ACTTCTTCGTGATAACCTTACTTTGTGGAC	61.8	119
	5'-TCGAAGATTAGGGATTTTACTGTTGTT		
GbLOX1	5'-GCTTATGTTGCTGTAAATGACTCTGG	60.1	111
	5'-CACACTAAGTTGTCGGTTCGTTG		
GbAOS	5'-TGCCACCTGGTCCTTTCATTTC	63.7	193
	5'-GCGTGTTTGGGCTCGGAAGGGTCG		
GbOPR3	5'-AGAGGTCCACTCCTGGCGGCTT	61.3	105
	5'-CCACCTGTTCTTCATTGTAGATTCC		
GbMYC2	5'-GCTCCGCCACTACCGTGCTC	63.9	129
	5'-CTCGAAGCACTTTTTTACGGTGTTC		
GbJaz1	5'-AGCCTCAAAAAGGAAGACCTCAAAC	62.6	109
	5'-TGGCTGCTCAATCACCATAGTAATC		
GbJaz3	5'-TGATTTTGCTCAAGGAGATAACGCT	62.2	138
	5'-TGATTGCCTACTCGTTGCCTGT		
GbJaz6	5'-GGCATCAATATGGCGGTTCAGGAC	66.1	158
	5'-TTCATCGGGTTTAGGTGGCAGAGT		
GbPR4	5'-GAGGGTAAGAAACTCAAGGACTGG	60.8	115
	5'-CTCCATCAGTGTCCAATCGGTT		
GbNPR1	5'-CTAGCTTGCGGAGGGATTGATACC	64.9	128
	5'-GAGATGGCTGACCTGTCAAACTGC		
GbPR1	5'-AAGAATGTGGGTTAGTGAGAGGGT	60.3	90
	5'-ACCACTTGAGTATAATGCCCGC		
GbPR5	5'-AAGGAGTCCACCACAATCACCG	61.2	102
	5'-CTGGCACTGCTATGGCTCGTAT		
GbCAD1	5'-AACCAGAAAAAGGCTGCAACTTCAG	64.4	112
	5'-TCCTTATTGGAAGAAAGAGGGTGATG		
GbFPS	5'-GCTACCGCCTGTTGAAAGATGG	63.2	132
	5'-TCGGCAATCTAAACCAACAAGG		
GbCYP706B1	5'-CAAAGGGCACCAGGGTCTTC	64.0	107
	5'-ACCGAGAGATACTCCGGCACAC		
WRKY1	5'-GCTGAATGTGAGGATTATGGTGCCA	60.9	121
	5'-TCAGAAGGATTTGTGCGGACTTGAACC		
GbUB7	5'-GAAGGCATTCCACCTGACCAAC	58.5	198
	5'-CTTGACCTTCTTCTTCTTGTGCTTG		

Table S3. Primers used for VIGS

Genes	Sequences	Annealing Temp.(℃)	Length of amplified fragments (bp)
GbCAD1	5'-CGACGACAAGACCCTTACCATAACAACAATGATGCCGAG	61.9	472
	5'-GAGGAGAAGAGCCCTTCCACCACCTACAAATCTCGCTTA		
Gb14-3-3c	5'-CGACGACAAGACCCTATCGGTGCTCGCCGTGCTTC	67.2	329
	5'-GAGGAGAAGAGCCCTTCGGCGTTGGCAATGTCCTG		
Gb14-3-3d	5'-CGACGACAAGACCCTGCCGTGCTTCCTGGAGGATTG	66.4	279
	5'-GAGGAGAAGAGCCCTGCGTATTCTCAGCAGCGGCTTTC		
GbSSI2	5'-CGACGACAAGACCCTCGCCACGAGACAGCATACACTAA	62.6	382
	5'-GAGGAGAAGAGCCCTCAGAAACCCAACTGAATGGAACAC		

Table S4. MS/MS identification of differentially expressed protein spots on 2-DE gels from *G. barbadense* cv. '7124' inoculation with *V. dahliae*

ssp no.[a]	Gi no.[b]	protein name	protein score	lon score[c]/sequence[d]	Sequence Coverage	Matched[e]/Searched[f]	Species	Experimental MM[g] (kD)/pI	Theoretical MM[g] (kD)/pI	Fold change[h] (ve/control)
11	gi|48741806	proteasome subunit alpha type 5	334	43/GVNTFSPEGR;73/LFQVEYAIEAIK;43/RITSPLLEPSSVEK;70/ITSPLLEPSSVEK;38/VETQNHR;41/VAPTYHLYTPSEVEAVITR;27/VAPTYHLYTPSEVEAVITRL	20%	7/117	*G. raimondii*	35.39/4.67	34.56/5.36	0.19
12	gi|5049781	14-3-3-like protein (14-3-3a)	115	115/AAQDIALTDLAPTHPIR	8%	1/160	*G. hirsutum*	28.60/4.71	22.87/5.74	0.38
17	gi|13349772	latex-abundant protein	293	118/SAEPGDFLFVHYSGHGTR;71/EQIGDSSKPQDSESESGSGGFR;104SFLHHTVQDAFESR;	23%	3/210	*G. arboreum*	27.41/4.79	25.94/5.18	0.29
24	gi|109862253	elongation factor 1	384	54/ALNDFLSGK;83/AEAADDEDDLDLFGDETEEDKK;46/SSVLMDVKPWDDETDMK;33/KLEEAVR;76/SVEMPGLLWGASK;75/LVAVGYGIK	30%	7/158	*G. hirsutum*	28.83/4.83	27.83/4.89	0.47
25	gi|5050340	chalcone isomerase	465	69/TLFLGGAGER;64/GLEIQGKFIK;104/SAVELTESVEFFR;79/VTMILPLTGQQYSEK;69/VTMILPLTGQQYSEK;43/VSENCVAIWK;34/AIEKFIEVFK;71/LLANSVLES	36%	8/193	*G. hirsutum*	26.80/4.86	24.27/5.77	0.48
40	gi|48748039	cysteine proteinase rd21a	269	39/VVSINDYEDVPVNDEK;78/AVANQPVSVAIEAGGR;70/SFQLYQSGIFDGK;41/GKDYWIVK;41/NSWGSSWGEAGYIR	22%	5/108	*G. raimondii*	26.91/4.51	32.90/4.69	0.05
112	gi|48797299	glycine-rich rna-binding	304	132/LFVGGISYQTDDQGLR;40/YGEVIEAR;19/IIVDRETGR;92/GFGFVTYTSSEDASSALQALDGQTLHGR;21/VNYATER	31%	5/175	*G. raimondii*	32.50/4.49	21.43/5.63	0.24
123	gi|5049148	14-3-3-like protein (14-3-3b)	49	49/EQQVYLAR	4%	1/210	*G. hirsutum*	33.01/4.76	20.49/6.26	0.47
127	gi|5046822	14-3-3 protein (14-3-3c)	148	70/VSASADNEELTVEER;78/SAQDIANAELAPTHPIR	15%	2/126	*G. hirsutum*	34.71/4.78	23.76/5.04	0.35
133	gi|31073060	iron binding protein	162	51/ELNLVPTVPQMSLAR;66/LLNLHNVAER;45/ISEYVAQLR	10%	3/210	*G. hirsutum*	32.40/4.82	37.49/5.76	0.49
150	gi|48742511	thiol protease aleurain-like protein	214	112/YNGGLDTEEAYPYTAK;102/NSWGAQWGDNGYFK	12%	2/158	*G. raimondii*	30.77/4.90	27.09/7.16	0.21
155	gi|48742486	ran binding protein	126	52/LEEVAVSTGEENEDPILDLK;42/FDKEGNQWK;32/FASVENCK	11%	3/147	*G. raimondii*	33.26/4.92	37.28/5.45	2.85
161	gi|13356530	elongation factor 1-beta	181	41/SSVLMDVKPWDDETDMK;46/SVEMPGLLWGASK;65/LVAVGYGIK;29/NEYIQSCDIVAFNK	28%	4/210	*G. arboreum*	29.20/4.60	20.39/4.47	0.33
206	gi|78323677	proliferating cell nuclear antigen	382	52/SEGFEHYR;124/ADDGSDTVTFMFESPTQDK;44/LMDIDSEHLGIPEAEYHAIVR;83/LMDIDSEHLGIPEAEYHAIVR;25/MPSAEFAR;41/MPSAEFAR;57/GDIGTANIVLR;26/IAEMGYIR	24%	8/180	*G. hirsutum*	38.07/4.75	34.11/4.87	0.29
212	gi|78323533	26s proteasome regulatory subunit	370	75/VHPLVIFNICDCYVR;95/VIGTLLGSVLPDGTVDIR;21/EVIVGWYSTGLGVTGGSALIHDFYSR;109/EVSNPIHLTVDTGFR;70/AFVSVNLALGDR	29%	5/210	*G. hirsutum*	35.96/4.92	32.04/5.36	0.36
216	gi|78323733	20s proteasome subunit paf1	498	132/NQYDTDVTTWSPAGR;62/LFQVEYAMEAVK;129/VDDHIGVAIAGLTADGR;121/NECINYSFTYESPLPVGR;55/RFENFTDSSR	25%	5/210	*G. hirsutum*	36.89/4.90	31.55/8.97	0.39

225	gi|5044774	ubiquitin thioesterase otubain-like protein	247	66/VLDQQYAAIR;32/TRGDGNCFFR;40/SFMFSYLEHILESQDR;60/SFMFSYLEHILESQDR;20/SRDQSISDYVVMFFR;27/DQSISDYVVMFFR;42/FVTSGEIR	25%	7/210	*G. hirsutum*	40.27/4.77	26.94/5.82	--
231	gi|109860660	ubiquitin thioesterase otubain-like protein	200	58/VLDQQYAAIR;13/SFMFSYLEHILESQDR;91/EDSISQDELILR;38/FVTSGEIR	16%	4/210	*G. hirsutum*	40.35/4.81	32.79/9.42	0.20
232	gi|78323677	proliferating cell nuclear antigen	312	52/SEGFEHYR;55/ADDGSDTVTFMFESPTQDK;42/MPSAEFAR;87/GDIGTANIVLR;36/QNTTVDKPEEATIIEMNEPVSLTFALR;40/YMNSFTK	26%	6/147	*G. hirsutum*	38.18/4.72	34.11/4.87	0.25
233	gi|5046822	14-3-3 protein	59	59/SAQDIANAELAPTHPIR	8%	1/210	*G. hirsutum*	36.28/4.81	23.76/5.04	0.20
314	gi|84169310	WD-repeat protein	108	37/IWEADIIR;46/TIFSVHWSR;26/EGIIASGAADDAVR	18%	3/202	*G. hirsutum*	45.13/4.76	19.07/5.62	0.24
318	gi|164354844	peroxidase	296	72/FALANVNSAR;18/SAVESSCSGVVSCADILAIAAR;92/DSVVLSGGPTWR;44/CATFDNR;71/GLLGSDQILYSSDLAVSTTK	21%	5/158	*G. hirsutum*	45.01/4.85	36.08/5.63	0.39
322	gi|11207995	40s ribosomal protein sa	137	17/RNDGIYIINLGK;16/FAQYTGCHAIAGR;93/HTPGTFTNQLQTSFSEPR;11/LLILTDPR	29%	4/189	*G. arboreum*	46.11/4.90	19.42/8.74	0.25
328	gi|5048825	spermidine synthase	194	49/VLVLDGVIQLTER;62/VLVIGGGDGGVLR;82/QYFPDVAVGYDDPR	20%	3/210	*G. hirsutum*	44.88/4.88	21.34/4.70	0.31
338	gi|48740287	late embryogenesis abundant protein	405	50/LLSGLIPDAGTIHAHGEETVK;68/STYDDIKPGSIIPYR;72/TGEIPIPYKPDIDMEK;68/FSWEETIAVLHLK;60/DFGSALWDMIR;87/GHINVDTPFGAMK	35%	6/158	*G. raimondii*	42.10/4.63	27.91/4.91	--
405	gi|164261933	ankyrin repeat domain protein	371	38/HILDEIETGGPAAMMK;114/AALASGADKDEEDSEGR;78/TALHFACGYGEVK;83/NTALHYAAGYGR;58/LNNQHEVLK	19%	5/148	*G. hirsutum*	47.93/4.31	38.70/5.10	0.28
407	gi|48748039	cysteine proteinase rd21a	236	25/LPDSVDWR;87/AVANQPVSVAIEAGGR;40/SFQLYQSGIFDGK;84/NSWGSSWGEAGYIR	17%	4/192	*G. raimondii*	49.31/4.40	32.90/4.69	N
411	gi|78330968	uv excision repair protein	135	11/AAYNNPER;48/AVEYLYSGIPEQAEAPPVAR;23/NSPQFQALR;52/LIQEHQGDFLR	16%	4/102	*G. hirsutum*	48.42/4.76	30.05/4.76	0.29
415	gi|78332047	uv excision repair protein	275	43/AAYNNPER;85/AVEYLYSGIPEQAEAPPVAR;52/NSPQFQALR;78/LIQEHQGDFLR;17/LEAMGFDR	18%	5/158	*G. hirsutum*	47.72/4.85	31.43/4.58	0.38
417	gi|164263296	transaldolase	623	70/AISSSNAYNDQFR;71/DIESAYWELVVK;64/LFEPIYDQTDGGDGYVSVEVSPR;76/VTSVASFFVSR;79/AAVAQAALAYR;109/TIDANVSEAEGIYSALEK;84/VGSQLEDEGVESFKK;71/SFDSLLDTLQEK	25%	8/136	*G. hirsutum*	47.94/4.88	50.24/9.66	0.44
418	gi|164263296	transaldolase	628	88/AISSSNAYNDQFR;24/DIESAYWELVVK;128/LFEPIYDQTDGGDGYVSVEVSPR;81/YLHEVVDRPNVYIK;112/YEAVIDAYLDGLEASGLSDLSR;70/VTSVASFFVSR;62/AAVAQAALAYR;63/SFDSLLDTLQEK	26%	8/210	*G. hirsutum*	48.41/4.91	50.24/9.66	0.49
424	gi|48817237	nucleotide exchange factor	53	53/AFYAVSALIR	3%	1/210	*G. raimondii*	51.06/4.86	30.42/5.35	--
502	gi|48878188	target of myb protein 1	297	65/ELFQGPNPADK;25/AFSEVAAER;55/LIDDPQTVVNNR;30/ALMLIEAWGESTSELR;52/ALMLIEAWGESTSELR;99/DNESLAPIFTPPR	24%	6/198	*G. raimondii*	56.15/4.73	28.40/5.11	0.44
506	gi|48747592	phosphoethanolamine methyltransferase	102	49/TYPDNSFDVIYSR;53/DTILHIQDKPALFR	10%	2/154	*G. raimondii*	56.24/4.91	29.66/5.04	3.73
524	gi|45438674	peroxidase	170	170/SDQNLFSTEGADTIEIVNR	17%	1/132	*G. hirsutum*	54.39/4.77	11.71/4.05	N
616	gi|48742071	tubulin beta	416	102/IDVYYNEASGGR;21/SGPIGQIFRPDNFVFGQSGAGNNWAK;152/GHYTEGAELIDAVLDVVR;46/FPGQLNSDLR;58/LAVNLIPFPR37/LHFFMVGFAPLTSR	30%	6/98	*G. raimondii*	58.21/4.87	32.92/5.28	N

706	gi|21091341	protein disulfide isomerase	293	39/GYPTVYFR;112/LAPILEEVAIHYEK;142/LDATANDIVDPNFDVR	17%	3/138	*G. arboreum*	61.74/4.80	24.49/5.53	0.38
707	gi|78324178	rubisco subunit binding protein	405	66/EIAFDQSSR;87/LADAVGLTLGPR;67/NVVLDEFGSPK;80/AIELPNAMENAGAALIR;51/GYISPQFVTNPEK;54/LICEFENAR	23%	6/210	*G. hirsutum*	62.85/4.82	32.30/8.31	0.48
709	gi|5047127	glutamine synthetase	214	7/SMREDGGFEVIK;28/AILNLSLR;82/HKEHISAYGEGNER;97/HETASINTFSWGVANR	26%	4/210	*G. hirsutum*	61.57/4.87	21.09/8.27	0.49
711	gi|32479441	probable nucleoredoxin 1-like	102	55/MPWLAIPFSDSEAR;47/VLTEEGVEIIR	6%	2/158	*G. hirsutum*	66.13/4.89	42.79/4.98	0.29
717	gi|13248313	tetratricopeptide repeat domain-containing protein	68	57/TEFFLNHEALQQVIR;11/LVYTIYAR	12%	2/111	*G. arboreum*	64.53/4.83	20.81/7.89	0.19
719	gi|13350678	protein disulfide isomerase	113	91/VDANEESNKDLANEYEVR;22/SAEDASNFIDEK	13%	2/96	*G. arboreum*	63.35/4.80	25.58/5.30	N
720	gi|13350678	protein disulfide isomerase	156	137/VDANEESNKDLANEYEVR;20/LRSDYEFGHTLDAK	14%	2/210	*G. arboreum*	63.11/4.88	25.58/5.30	N
804	gi|78341095	stromal 70 kda heat shock-related chloroplastic-like	393	114/LSFKDIDEVILVGGSTR;109/DIDEVILVGGSTR;64/IPAVQELVR;105/SEVFSTAADGQTSVEINVLQGER	16%	4/158	*G. hirsutum*	70.45/4.84	32.97/4.64	0.33
1008	gi|193219783	triosephosphate isomerase	716	55/FFVGGNWK;46/IEVSAQNSWIGK;78/GGAFTGEISVEQLK;64/WVILGHSER;68/HVIGEDDQFIGK;79/HVIGEDDQFIGKK;50/TFDVCFQQLK;100/VATPQQAQEVHVAVR;94/EEDIDGFLVGGASLK;83/GPEFATIVNSVT	32%	10/210	*G. hirsutum*	28.81/5.08	37.38/6.36	2.25
1028	gi|84144761	dienelactone hydrolase family	193	70/DHGPDKGYEDAK;61/VPIAILGAEQDHISPPELLK;39/QFDEILK;23/VGHGWSVR	18%	4/144	*G. hirsutum*	27.64/5.04	28.10/5.23	N
1104	gi|11209486	remorin family	62	36/STEVSVDRDAVLAR;26/ISLINAWEESEK	12%	2/210	*G. arboreum*	31.16/5.00	23.13/7.08	0.40
1106	gi|31407188	protein in2-1 homolog b-like protein	414	46/LYLAYPCPYAQR;36/LVPLNLQNRPAWYK;130/DADAAFDHLETALAK;53/FQIYLSEVFNYDLTAGRPK;107/VAAWIEAADKIDAYK	29%	6/158	*G. hirsutum*	30.41/5.03	29.25/6.84	0.42
1114	gi|11209486	remorin family protein	209	44/STEVSVDRDAVLAR;38/RISLINAWEESEK;61/ISLINAWEESEK;42/KLSSIAAWENTK;24/AAIEAELKR	23%	5/201	*G. arboreum*	31.23/5.07	23.13/7.08	0.41
1115	gi|164316384	protein in2-1 homolog b-like protein	421	67/ATETVESLPPTLEANAEQPPLFDGTTR;58/LYTSYPCPFAQR;46/LVPLNLQNRPAWYK;65/KYDDGPFLLGR;69/YDDGPFLLGR;81/DFSLADIAYIPFVER;35/YDTI	28%	7/158	*G. hirsutum*	31.90/5.08	36.29/5.93	8.33
1124	gi|13352433	20s proteasome subunit paf1	95	56/NQYDTDVTTWSPAGR;39/NECINYNFTYESPLPVGR	15%	2/158	*G. arboreum*	34.94/4.97	24.60/9.51	N
1126	gi|5046691	ran binding protein	115	43/FDKEGNQWK;72/FQEVAESQKPK	11%	2/97	*G. hirsutum*	33.92/5.03	20.56/5.49	N
1132	gi|78328997	tubulin folding cofactor b	156	71/LQIEGDASVLLR;72/YSISEDEYNKR;13/EQMASQNPSEFR	11%	3/210	*G. hirsutum*	31.81/5.11	34.70/8.04	0.23
1145	gi|5044913	methylthioadenosine nucleosidase	81	27/FQLIENPHSSFPK;54/IPIPVFDLYGVGLR	12%	2/209	*G. hirsutum*	32.51/4.95	23.14/9.55	0.18
1150	gi|78341942	ribose-5-phosphate isomerase	43	43/LEGLFNELGCEAK	4%	1/194	*G. hirsutum*	29.12/4.96	29.74/7.14	0.11
1207	gi|48808146	glycosyl hydrolase family 38 protein	94	19/TFYTDSNGR;57/EFSVLVDR;17/SLGGSSIVDGQIELMLHR	12%	3/140	*G. raimondii*	35.91/4.99	31.61/4.82	5.43
1217	gi|11209293	20s proteasome subunit paf1	241	70/NQYDTDVTTWSPAGR;120/VDDHIGVAIAGLTADGR;51/NECINYSFTYESPLPVGR	23%	3/133	*G. arboreum*	38.00/5.07	23.90/9.47	2.84

1231	gi|48748981	adenine nucleotide alpha hydrolases-like protein	194	79/FPFSTPIAGSQR;54/IAIAVDLSDESAYAVR;39/LQITPNSTNNR;22/LCLEVER	16%	4/153	*G. raimondii*	37.88/5.03	31.03/5.40	N
1240	gi|54119904	probable carboxylesterase 2-	55	28/GWLYYDK;27/LASFFNQGK	6%	2/95	*G. raimondii*	41.80/5.02	32.40/5.37	2.91
1313	gi|48818461	transducin family protein	185	59/SHILVTAEDESGIHIWDLR;86/EPWIFASLSYDGR;41/VVVESVKPFLSR	19%	3/122	*G. raimondii*	46.18/5.10	26.49/5.57	0.34
1320	gi|345461935	desoxyhemigossypol-6-O-methyltransferase	80	14/ILVHSDFFAR;45/QKLDNDAQEEGYVLTNSSR;21/LFLAAGFSSFK	10%	3/158	*G. barbadense*	43.27/5.02	40.86/5.23	0.34
1335	gi|13350365	transaldolase-like protein	144	46/LAYDTHGIIR;37/LYDEIAVPPER;61/IPSTWQGIEASR	14%	3/210	*G. arboreum*	43.52/4.99	24.86/5.09	N
1406	gi|78324960	3-isopropylmalate dehydrogenase	118	67/LLKPETGLLQLR;51/ELTGGIYFGKPR	8%	2/158	*G. hirsutum*	47.41/5.02	31.78/8.31	2.05
1434	gi|78354144	nucleoporin nup43	105	37/TPGGPVLQFK;68/TSGIVHSIDIHPSR	14%	2/158	*G. hirsutum*	48.85/5.04	18.41/8.48	3.66
1502	gi|5050625	alpha-tubulin	326	71/AVFVDLEPTVIDEVR;65/QLFHPEQLISGK;74/QLFHPEQLISGKEDAANNFAR;67/EIVDLCLDR;48/SLDIERPTYTNLNR	31%	5/158	*G. hirsutum*	55.73/4.99	20.52/6.22	3.62
1507	gi|48752349	alpha-tubulin	549	60/EIVDLCLDR;90/QLFHPEQLISGK;112/LISQIISSLTTSLR;39/SLDIERPTYTNLNR;113/AVFVDLEPTVIDEVR;137/FDGAINVDVTEFQTNLVPYPR	30%	6/146	*G. raimondii*	55.38/5.03	31.65/6.07	N
1513	gi|48814087	aminoacylase-1	155	46/RIEEEWAPASR;46/IGKPEILSGATDAR;64/GINVYESIIEAYTSYIPPGR	17%	3/158	*G. raimondii*	53.31/5.11	29.75/7.24	N
1516	gi|48780251	tubulin alpha-7 chain	437	71/AVFLDLEPTVIDEVR;93/QLFHPEQLISGK;83/LADNCTGLQGFLVFHAVGGGTGSGLGSLLLER;54/LVSQVISSLTASLR;136/FDGALNVDVNEFQTNLVPYPR	34%	5/160	*G. raimondii*	54.83/5.10	30.33/5.43	N
1517	gi|5050625	alpha-tubulin	70	28/AVFVDLEPTVIDEVR;23/EIVDLCLDR;19/SLDIERPTYTNLNR	20%	3/140	*G. hirsutum*	55.60/5.12	20.52/6.22	4.18
1524	gi|315069289	alpha tubulin 1	389	72/AVFVDLEPTVIDEVR;90/QLFHPEQLISGK;34/SLDIERPTYTNLNR;47/LVSQVISSLTASLR;80/FDGALNVDVTEFQTNLVPYPR;67/TIQFVDWCPTGFK	29%	6/151	*G. barbadense*	54.67/5.07	34.24/6.27	N
1526	gi|48748259	alpha-tubulin	402	88/QLFHPEQLISGK;117/LISQIISSLTTSLR;89/AVFVDLEPTVIDEVR;108/FDGAINVDITEFQTNLVPYPR	21%	4/160	*G. raimondii*	55.28/5.14	32.26/5.44	N
1604	gi|48777881	glucose-6-phosphate isomerase	377	120/QGVAITQENSLLDNTAR;28/IEGWVAR;28/FPMFDWVGGR;86/GSTDQHAYIQQLR;115/EGVHNFFVTFI	23%	5/203	*G. raimondii*	59.23/4.97	29.10/4.87	0.40
1615	gi|48777881	glucose-6-phosphate isomerase	86	48/QGVAITQENSLLDNTAR;38/GSTDQHAYIQQLR	11%	2/158	*G. raimondii*	59.41/5.03	29.10/4.87	2.92
1617	gi|13353515	phosphoesterase family protein	179	39/YVDNFHQYDLSFKR;52/LPNYVVIEPR;18/EIYEALR;70/DAWAGSFDIVVNR	19%	4/158	*G. arboreum*	60.73/5.05	26.53/6.15	0.40
1623	gi|48803376	RNA recognition motif-containing	65	43/QVEFYFSDSNIPR;22/TIAASPFEFNVK	9%	2/158	*G. raimondii*	59.13/5.09	28.90/4.85	5.63
1628	gi|54123077	beta-tubulin	167	136/GHYTEGAELVDSVLDVVR;30/IREEYPDR	10%	2/210	*G. hirsutum*	58.19/5.10	27.64/5.85	0.34
1651	gi|21103494	fas-associated factor 2-b-like	57	34/VLEESAPVLVAAR;23/LREEQDAAYR	10%	2/158	*G. arboreum*	60.40/4.97	24.37/7.78	2.23
1652	gi|13354972	vacuolar atpase b subunit	59	46/QIYPPINVLPSLSR;13/NIFQSLDLAWTLLR	10%	2/87	*G. arboreum*	57.95/5.04	28.38/9.91	++
1804	gi|78343945	ubiquitin carboxyl-terminal hydrolase	235	124/KLDVYIDVPDVIDISHIR;111/VDTLISFGFQEEIAR	11%	2/210	*G. hirsutum*	79.24/4.96	31.08/4.98	0.48

2005	gi|13356871	proteasome subunit beta type	634	56/NCFAIASDR;36/NCFAIASDRR;64/RLGVQLQTIATDFQR;126/LGVQLQTIATDFQR;161/LFLGLSGLATDAQTLYQR;79/DFVVAGTASESLYGACESMFK;111/DCLSGWGGHVYVVTPTEVK	31%	7/210	*G. arboreum*	24.60/5.22	29.68/5.36	2.57
2016	gi|84144761	dienelactone hydrolase family	147	58/DHGPDKGYEDAK;28/QFDEILK;32/ASEVDSFVK;28/VGHGWSVR	14%	4/142	*G. hirsutum*	28.09/5.17	28.10/5.23	4.02
2102	gi|164310401	type 2 ribosome-inactivating protein precursor	161	44/DLYNALTER;39/SGDIPILPPR;78/LVYDAQELVLSTLR	11%	3/158	*G. hirsutum*	31.44/5.16	31.48/5.27	3.37
2105	gi|48743646	isopentenyl diphosphate isomerase	608	33/YELLLQQR;99/ESELISENHLGVR;108/KLLDELGIPAEDVPVDQFVPLSR;93/LLDELGIPAEDVPVDQFVPLSR;107/WGEHELDYLLFIVR;106/DVNVHPNPDEVAEAK;36/LSPWFR;26/LVVDNFLFK	34%	8/210	*G. raimondii*	32.58/5.21	30.19/8.50	0.45
2123	gi|48811023	protein phosphatase 2c	177	18/SSMEDFYETR;30/QNLFSNLIR;47/DAGSTASTAILVGDR;40/GGNAFAVSR;41/DHKPDQSDER	21%	5/158	*G. raimondii*	34.06/5.18	27.21/5.75	13.06
2124	gi|48812639	(+)-delta-cadinene synthase (GbCAD1)	310	49/LAFIDSVQR;5/EIEDELENIYHNNNDAENDLYTTSLR;87/GLLELYQASYLR;105/HYLSVYQDIESHNK;39/IDFNMLQFLHR;63/IDFNMLQFLHR	24%	6/210	*G. raimondii*	31.06/5.14	34.02/6.56	3.65
2205	gi|164253821	phenazine biosynthesis	647	98/YYVVDAFTNSAFK;108/GNPAAVCLLEEER;75/GNPAAVCLLEEERDEK;14/ITNSTSPNTR;35/TTTADDIFVVLPSGK;159/GLIVSGAAPSDSEFDFISR;63/LELVAHAASPR;94/GGIVNIHFDEQNQR	30%	8/210	*G. hirsutum*	36.85/5.17	35.14/5.13	2.46
2246	gi|109831589	2-keto-3-deoxy-l-rhamnonate aldolase-like	97	20/AVATTNTPAIIR;33/LPESSAVWAK;26/GYHMVSGAIDVGLFR;18/NAAVEDVRK	17%	4/117	*G. hirsutum*	36.91/5.20	28.92/5.48	10.77
2250	gi|13352653	dna-damage-repair toleration protein	66	66/SLNIEVEDLGITSYYNIGAEVGR	10%	1/158	*G. arboreum*	37.14/5.16	22.53/5.07	0.10
2320	gi|48739156	caffeic acid o-methyltransferase	289	44/ELASQLPTSNPDAPVMLDR;43/LLATYSILTCSLR;63/DAVLEGGIPFNK;42/AYGMTAFEYHGTDPR;30/AYGMTAFEYHGTDPR;96/ILETYDGFEGLK	27%	6/158	*G. raimondii*	45.47/5.26	28.80/5.77	0.48
2415	gi|5046349	s-adenosylmethionine	136	45/TIFHLNPSGR;60/FVIGGPHGDAGLTGR;31/TAAYGHFGR	17%	3/158	*G. hirsutum*	50.34/5.26	21.92/8.81	2.08
2511	gi|82756479	alpha-tubulin	198	86/AIFVDLEPTVIDAVR;28/QLFHPEQLISGK;54/QLFHPEQLISGKEDAANNFAR;31/SLDIERPTYTNLNR	21%	4/210	*G. hirsutum*	54.25/5.24	25.61/5.65	0.05
2518	gi|5049948	tubulin alpha	197	65/AIFVDLEPTVIDEVR;30/QLFHPEQLISGK;30/QLFHPEQLISGKEDAANNFAR;23/EDAANNFAR;16/EIVDLCLDR;34/SLDIERPTYTNLNR	30%	6/158	*G. hirsutum*	54.63/5.16	21.37/5.72	N
2525	gi|78345852	aha1 domain-containing protein	288	94/SLSDLTILDGQGNLR;58/VDGEAYVNIR;81/FGSWPDGIDSTVR;55/LVFNEPEPGVTIIK	16%	4/210	*G. hirsutum*	54.72/5.18	36.24/8.46	--
2611	gi|48801055	n-carbamoyl-l-amino acid	64	64/QIDELSTFSDTPAPSVTR	6%	1/158	*G. raimondii*	59.00/5.25	31.56/5.04	0.49
2633	gi|78328524	chaperonin cpn60-mitochondrial-like isoform 2	67	16/SIEFKDR;52/GYISPYFITNQK	2%	2/210	*G. hirsutum*	60.90/5.17	33.60/9.60	2.43
2733	gi|164281758	pentatricopeptide repeat-containing protein	323	70/LDLYVAAAGINPQR;71/NPLYLGLQQHR;24/AQGRPMIDFPK;158/IVVAGAGSAGIGVVNAAR	13%	4/210	*G. hirsutum*	64.86/5.27	45.55/9.52	2.27

2756	gi|109861556	kh domain-containing protein	47	25/ILDGPPGTQER;22/ALELIASHLR	6%	2/110	*G. hirsutum*	68.79/5.18	36.19/5.98	5.09
2764	gi|48792870	pyruvate kinase	127	20/EWHQMVIER;80/AEDGEIWTFSVR;27/ANLTFWR	9%	3/210	*G. raimondii*	65.01/5.10	30.70/4.84	0.41
3004	gi|31407396	glutathione s-transferase	289	60/VFGYWASPYSYR;100/GVSYEYINEDIFGNK;52/HNPYLPQDPYDK;40/CFPTLWLAAWSAENER;37/VTNEACEYLK	27%	5/158	*G. hirsutum*	26.41/5.33	27.55/7.78	0.29
3105	gi|48797422	aluminum-induced protein	506	104/TANEGIIVIEAYR;39/DRGPYPPDQVVR;45/GPYPPDQVVR;91/ATFIAADADGSVPFFWGTDAEGHLVLADDR;62/GCFFTSSGGLR;89/SYEHPLNELKPVPR	41%	7/104	*G. raimondii*	31.27/5.34	23.99/7.07	5.11
3107	gi|62295807	cysteine-rich repeat secretory protein	234	25/GFGLGSIGQKPNQAYGLALCR;30/TCVVEAGSEIR;42/GAIIWYDNCLFK;79/TKELLSELANQAYSNPK;30/LYGLTQCTR;26/VVGGSCNFR	35%	6/203	*G. hirsutum*	29.89/5.36	25.37/8.24	0.32
3108	gi|48776883	cathepsin b-like cysteine protease	262	42/LPTSFDAR;34/TAWPQCTSIGR;42/HYSVGAYR;112/NGPVEVSFTVYEDFAHYK;32/GWGDDGYFK	19%	5/210	*G. raimondii*	34.42/5.36	31.37/5.98	0.32
3110	gi|84172589	ubiquinone biosynthesis protein	253	107/KNPPAEYQGEQAR;36/NPPAEYQGEQAR;110/EVGISPSIVGSFPR	17%	3/210	*G. hirsutum*	32.08/5.35	16.71/9.77	0.21
3123	gi|11199964	adenine nucleotide alpha hydrolases-like protein	155	116/IGVAVDLSDESAFAVR;39/QIEDEFDAFTASK	15%	2/106	*G. arboreum*	33.77/5.44	20.34/6.86	0.16
3124	gi|73862760	isopentenyl diphosphate isomerase	497	40/YELLLQQR;68/VWTNTCCSHPLYR;87/ESELISENHLGVR;94/WGEHELDYLLFIVR;115/DVNVHPNPDEVAEAK;50/LVVDNFLFK;44/WWDHVEK	31%	7/158	*G. hirsutum*	32.74/5.31	30.03/8.84	4.18
3211	gi|164322600	glutelin type-a	278	69/GFALPHYADCSK;46/FPFLEQVGLNVSR;26/LVLETNATR;56/APWYASDPQVVYVVK;81/GSGEVQIVGL	15%	5/120	*G. hirsutum*	41.56/5.38	45.88/9.32	3.65
3303	gi|78334230	flavanone 3-hydroxylase	794	78/TLQASFVRDEDERPK;77/EFFALPAEEKLR;75/KGGFIVSSHLQGEAVQDWR;116/GGFIVSSHLQGEAVQDWR;78/EIVTYFSYPLR;48/WPDKPEGWVEVTK;51/CPQPDLTLGLKR;187/HTDPGTITLLLQDQVGGLQATR;84/LSIATFQNPAPDATVYPLK	38%	9/210	*G. hirsutum*	45.29/5.30	35.86/5.23	2.06
3326	gi|48741498	flavanone 3-hydroxylase	706	47/TLQASFVR;73/TLQASFVRDEDERPK;100/VAYNQFSNDIPVISLAGIDDVDGKR;42/KGGFIVSSHLQGEAVQDWR;124/GGFIVSSHLQGEAVQDWR;63/EIVTYFSYPLK;82/WPDKPEGWIEVTK;176/HTDPGTITLLLQDQ	38%	8/210	*G. raimondii*	45.18/5.42	30.98/5.45	0.48
3339	gi|164295626	glutamine synthetase	226	11/IIAEYIWIGGSGMDLR;87/HKEHIAAYGEGNER;128/HETADINSFSWGVANR	11%	3/210	*G. hirsutum*	44.90/5.33	46.45/8.54	N
3725	gi|13243658	t-complex protein 1 subunit theta-like	52	52/NPANFDVDNVR	4%	1/158	*G. arboreum*	61.73/5.40	30.22/7.40	0.44
3824	gi|48778421	xaa-pro aminopeptidase	122	57/IGEDPSVDSWISDNLPR;67/NQPPAETNPVIVHPLEFAGR	13%	2/171	*G. raimondii*	72.75/5.42	30.87/5.25	0.48
3827	gi|13244481	xaa-pro aminopeptidase 2	100	74/LTEVTASDKLEGFR;25/GHIALGNAR	8%	2/155	*G. arboreum*	72.01/5.32	28.49/9.25	0.45
4002	gi|48744626	14-3-3 protein (14-3-3d)	266	19/LAEQAER;62/FMETVVSSVVAPDELTVEER;87/FMETVVSSVVAPDELTVEER;98/SAQDIAVSELAPTHPIR;62/DSTLIMQLLR;45/DSTLIMQLLR	18%	6/210	*G. raimondii*	26.51/5.43	32.41/5.01	0.39
4017	gi|109829261	ascorbate peroxidase	624	71/LAWHSAGTFDVK;128/QPAELAHAANNGLDIAVR;81/EDKPHPPPEGR;84/LPNATEGADHLR;45/QVFSNQMGLSDQDIVALSGGHTLGR;71/VLLSDPVFRPLVEK;144/YAADEDAFFADYTEAHLK	42%	7/210	*G. hirsutum*	28.59/5.61	28.61/5.07	0.23

4104	gi|48746857	glutamine synthetase	58	8/IIAEYIWIGGSGMDLR;51/HKEHIAAYGEGNER	9%	2/127	*G. raimondii*	34.41/5.48	34.04/5.81	N
4122	gi|48751326	ascorbate peroxidase	517	71/LAWHSAGTFDVK;153/QPAELAHAANNGLDIAVR;74/EDKPHPPPEGR;83/VLLSDPVFRPLVDK;137/YAADEDAFFADYAEAHLK	25%	5/210	*G. raimondii*	29.34/5.60	31.77/6.82	0.49
4131	gi|48799208	alcohol dehydrogenase-like	241	52/SVASELCQTGVR;26/INCISPAPIPTPMVIR;59/QIAEIYQGIPK;104/YVTGHNLVVDGGFTSFK	22%	4/210	*G. raimondii*	30.98/5.51	27.63/6.42	0.14
4159	gi|48802272	type 2 ribosome-inactivating protein precursor	112	112/YANDYSGLVNVATCDGFVEER	9%	1/175	*G. raimondii*	32.89/5.63	24.25/8.76	0.27
4203	gi|48753495	thiosulfate sulfurtransferase	249	41/VLDASWYMPDEQR;9/VWWMFR;66/VWVLDGGLPR;49/VYQGQTAGPLTFQTK;49/THQHIDAR;36/FDGA	23%	6/210	*G. raimondii*	37.16/5.48	28.95/6.15	2.47
4208	gi|48879364	2-oxoglutarate-dependent	80	18/GVQAEIDFPVIEFR;29/SFAQLMWPDGHPR;33/YMAPPPGEYER	14%	3/158	*G. raimondii*	41.60/5.50	30.85/5.34	2.62
4212	gi|48745618	nad-malate dehydrogenase	354	74/VAILGAAGGIGQPLALLIK;66/GVNVVVIPAGVPR;49/DDLFNINANIVK;79/KLFGVTTLDVVR;60/LFGVTTLDVVR;13/AGAGSATLSMAYAAAR;13/FVESSLR	28%	7/210	*G. raimondii*	39.48/5.55	29.79/5.98	0.27
4252	gi|48797418	phenylcoumaran benzylic ether reductase -like	84	43/FLPSEFGTDPAR;41/TVYIRPPQNILSQR	10%	2/210	*G. raimondii*	39.07/5.62	28.63/5.73	2.83
4333	gi|48813830	stearoyl-acyl-carrier protein desaturase (GbSSI2)	349	19/YLYLCGR;74/ATFISHGNTAR;76/DYADIVEYLVDR;51/LKELIGLSPEGR;67/EAQEFVCGLAPR;62/ESPSVPFSWVSGR	24%	6/155	*G. raimondii*	43.62/5.46	31.86/5.59	2.26
4422	gi|13248670	mitochondrial elongation factor Tu	144	144/ILDQGQAGDNVGLLLR	6%	1/149	*G. arboreum*	48.02/5.59	26.81/9.17	N
4432	gi|164258867	protein disulfide isomerase	483	69/YLKPNLEADHIAPWVK;69/VVVADTFDDMVFK;98/LAPILEEVAVHYENDAK;96/LDATANDIMDPNFDVR;43/GYPTVYFR;108/SADGNISAYEGER	19%	6/210	*G. hirsutum*	48.21/5.55	48.50/9.35	--
4760	gi|164339680	pyruvate decarboxylase	109	26/LKQNNTAYENYHR;22/IFVPEGQPLK;38/VNVLFQHIQK;23/ELLEWGSR	10%	4/210	*G. hirsutum*	63.23/5.50	42.43/8.16	2.80
4803	gi|164313765	xaa-pro aminopeptidase 2	76	76/NQPPAETNPVIVHPLEFAGR	8%	1/210	*G. hirsutum*	72.41/5.44	27.27/4.94	++
5003	gi|315074094	proteasome subunit beta type-6	390	30/TSTGMYVANR;71/ASDKITQLTDNVNVCR;102/SGSAADSQIVSDYVR;56/YFLHQHTIQLGQPATVK;87/TVVINSDGVTR;43/NFYPGDK	28%	6/113	*G. barbadense*	25.25/5.66	29.32/8.46	0.38
5131	gi|48797422	aluminum-induced protein	358	93/TANEGIIVIEAYR;54/DRGPYPPDQVVR;51/GPYPPDQVVR;60/FAFIIYDSSSK;37/GCFFTSSGGLR;63/SYEHPLNELKPVPR	27%	6/158	*G. raimondii*	30.61/5.73	23.99/7.07	0.23
5132	gi|164261388	snf7-like protein	146	14/TRHQIEK;38/SQLQGVSLR;94/VAQAEATGNDDGGIDSDLQAR	16%	3/158	*G. hirsutum*	35.40/5.72	25.60/5.10	N
5141	gi|13349950	phosphomannomutase a1	145	133/KPGLIALFDVDGTLTAPR;12/GTFIEFR	10%	2/210	*G. arboreum*	34.70/5.71	26.04/9.12	0.17
5148	gi|78324615	protein phosphatase	228	70/ANHPMEDYVFAEFK;13/LVIANVGDSR;30/QLSVDHEPASER;72/GGFVSNFPGDVAR;24/VDGQLAVAR	18%	6/210	*G. hirsutum*	31.16/5.69	34.27/6.84	0.43
5159	gi|21090394	soluble inorganic pyrophosphatase	130	64/VLYSSVVYPHNYGFIPR;43/HYTDIKDLPPHR;23/FFEDYKK	16%	3/158	*G. arboreum*	30.56/5.80	25.72/7.10	N
5205	gi|48791016	2-oxoglutarate-dependent	156	47/VREETFGLMK;35/VREETFGLMK;55/ELVEVPVER;54/YMAPPPGEYER	9%	4/158	*G. raimondii*	41.68/5.68	34.53/5.12	2.28
5242	gi|11206427	homoserine kinase	63	63/LGVDQLVLAGLESEAK	6%	1/210	*G. arboreum*	39.33/5.84	26.44/9.30	6.61

5422	gi|48749615	fumarylacetoacetase	274	83/LATAIGDYVVDLSEIAK;40/LLSSTEPTLR;10/NCGTIFR;25/GPQNAIPQNWFHLPIAYHGR;72/ASSIVISGTNINRPR;46/GQGYPTGQSPPYFGPSLK	32%	6/158	*G. raimondii*	47.02/5.77	29.97/6.40	0.46
5721	gi|164262533	acid beta-fructofuranosidase	51	10/TFYDQNK;41/VLVDHSIVESFAQGGR	6%	2/210	*G. hirsutum*	67.91/5.84	39.06/8.94	0.18
6007	gi|78353154	proteasome subunit beta type	229	55/VQFTEYIQK;56/NVALYQFR;48/ETGPSLFYIDYIATLHK;14/GAFGYGSYFSLAMMDR;56/LVVAPPNFVIK	26%	5/210	*G. hirsutum*	24.39/5.87	25.81/7.14	9.52
6009	gi|109891548	gdsl esterase lipase	388	33/GYSGYNTR;80/YAAFQHVPLDEYK;119/TLVLLITPPPIDEDGR;80/HPYVENPSGLPER;28/MQQYTDWR;47/ADLPLIADIDHDDPLK	29%	6/210	*G. hirsutum*	28.06/5.89	28.66/6.38	2.91
6034	gi|109882527	proteasome subunit beta type-1	216	20/TVFASASER;141/DIYTGDKLEIVVINADGIR	11%	3/191	*G. hirsutum*	27.17/6.07	28.46/5.72	N
6105	gi|164296478	gdsl esterase lipase cprd49	341	39/GYFGWNSR;22/RAIQVLDHVFPK;81/LIFLTSPPVNEER;54/YASEHFSHLVR;69/VVNLFTAFQQR;77/TTLNPSEWTFHR	21%	6/210	*G. hirsutum*	29.14/5.86	35.65/6.28	3.58
6109	gi|48747985	6-phosphogluconolactonase	243	64/EKGSFTVVLSGGSLIK;32/GSFTVVLSGGSLIK;62/LAFDGFLSK;60/SNVLSVSTATGFPK;24/DSPKPPPER	18%	5/210	*G. raimondii*	30.41/5.92	28.77/8.61	3.04
6110	gi|78324276	ascorbate peroxidase	59	22/VDKPHPPPEGR;37/LPNATEGADHLR	8%	2/116	*G. hirsutum*	29.20/5.94	30.07/7.62	2.18
6314	gi|5045873	phosphoglycerate kinase	308	146/VDLNVPLDDNFNITDDTR;48/MVAALPDGGVLLLENVR;114/LASLADLYVNDAFGTAHR	26%	3/210	*G. hirsutum*	44.56/5.95	21.82/7.85	2.13
6348	gi|109838718	serine-threonine kinase receptor-associated	369	60/GAVWSVCLDTNALR;91/VWDALTGDVLHSFEHK;45/IYDLNRPDAPPR;32/FWDANHYGLVK;17/FVAGGEDMWVR;124/FSPGGESYASGSEDGTIR	28%	6/210	*G. hirsutum*	40.39/6.02	32.29/8.48	2.37
6422	gi|48743158	gdp-d-mannose 3 -epimerase	186	65/SFTFIDECVEGVLR;59/KLPIHHIPGPEGVR;62/VVGTQAPVQLGSLR	18%	3/210	*G. raimondii*	50.15/6.05	26.21/7.66	4.31
6425	gi|48752415	mitogen-activated protein kinase 4	152	38/YVHSANVLHR;114/LITELIGSPDDASLGFLR	9%	2/210	*G. raimondii*	47.42/6.09	35.57/7.24	2.51
6713	gi|48801140	malate oxidoreductase	254	64/GILYPSIDSIR;62/HITAEVGASVLR;72/AAVAEEVAEGHGDVGPK;56/EETVEYVFR	24%	4/210	*G. raimondii*	61.28/6.01	23.01/5.10	2.14
6832	gi|13350369	transketolase	326	50/NGNTGYDEIR;33/NLGWPYEPFHVPEDVK;72/HVPQGAALEAEWNAK;69/SIITGELPAGWEK;102/ALPTYTPESPADATR	30%	5/158	*G. arboreum*	71.50/6.05	25.21/7.94	0.37
7003	gi|11202870	manganese superoxide dismutase	198	74/HHQTYITNYNK;65/ALEQLHDAIQK;35/NVRPDYLK;24/YASEVYEK	13%	4/210	*G. arboreum*	24.96/6.20	32.17/8.58	8.63
7061	gi|164257288	triosephosphate isomerase	402	45/KFFVGGNWK;50/FFVGGNWK;51/SDFHVAAQNCWVR;58/ALLNESNEFVGDK;51/VIACIGETLEQR;37/VATPAQAQEVHCELRK;110/WLNQNVGADIAASVR	22%	7/158	*G. hirsutum*	28.08/6.32	37.60/9.20	4.02
7204	gi|48750761	catechol o-methyltransferase	86	86/VIVVEAVVPVVPEANAYLR	10%	1/210	*G. raimondii*	41.18/6.17	20.69/6.56	0.46
7205	gi|62295617	alkaloid o-methyltransferase related	135	37/IELDEAMLQGQAEIWR;55/IELDEAMLQGQAEIWR;32/YLYSFADSMALK;48/AHGCEIWDLASR	19%	4/158	*G. hirsutum*	40.62/6.17	23.02/6.49	0.25
7209	gi|48749963	auxin-induced protein pcnt115-like	392	83/FGIDYTDGKR;84/LGVDCIDLYYQHR;119/YIGLSEASASTIR;105/ELGIGIVAYSPLGR	19%	4/210	*G. raimondii*	41.34/6.25	28.52/6.20	N
7212	gi|18099886	auxin-induced protein pcnt115	244	78/YIGISEASPETIR;94/AKEDTSNSSLGVFPR;73/FQGENLEQNR	13%	3/210	*G. arboreum*	40.87/6.29	30.87/6.50	0.33

7318	gi|164257564	beta galactosidase 9	235	26/TDNEPFKR;95/LPHRPVEDLAFAVAR;114/TSGGPFYITSYDYDAPIDEYGLR	10%	3/210	*G. hirsutum*	46.09/6.30	49.18/9.65	3.24
7408	gi|48821513	dihydrolipoyllysine-residue succinyltransferase	112	48/EGETVEPGTR;11/LGFMSGFVK;53/ATVSALQHQPIVNAVIDGDDIIYR	16%	3/206	*G. raimondii*	49.28/6.21	29.16/8.82	3.07
7503	gi|78329865	leucine	124	124/GNTAAAIVSGTVLGLYEDNR	7%	1/210	*G. hirsutum*	55.04/6.12	26.87/8.27	3.27
7511	gi|164358784	succinate-semialdehyde	90	28/IGDALLASTQVR;63/AGLAAYIFTNNVQR	9%	2/210	*G. hirsutum*	55.93/6.20	30.40/8.66	2.85
7518	gi|73864584	6-phosphogluconate dehydrogenase	67	35/GWNLNFGELAR;33/DLFGAHTYER	8%	2/158	*G. hirsutum*	56.12/6.25	27.19/9.37	2.30
7613	gi|48780111	gmp synthase	225	44/LHCVFVDNGLLR;23/LLFKDEVR;44/HPFPGPGLAVR;114/VLGDVTEGNALDIVR	15%	4/210	*G. raimondii*	61.02/6.25	33.45/8.87	2.85
7715	gi|48739022	asparagine synthetase	204	24/ALHLYDCLR;48/ATSAWGLEAR;61/AFDDENHPYLPK;25/EAYYYR;46/FFPQNSAR	17%	5/158	*G. raimondii*	63.21/6.28	29.28/6.48	0.45
7717	gi|48812774	glucose-6-phosphate 1-dehydrogenase	58	58/NVQIIFSEDFGTEGR	5%	1/181	*G. raimondii*	61.25/6.29	33.06/7.94	N
7720	gi|164327830	tcp-1 cpn60 chaperonin family	366	40/HKFDVDTR;68/LVEGLVLDHGSR;107/SEINAGFFYSNAEQR;51/GPNDHTIAQIK;100/NTIEDEAVILGAGAF	21%	5/158	*G. hirsutum*	61.82/6.34	35.31/5.74	0.32
7801	gi|164312069	transketolase	305	47/GLGWHVIWVK;85/NGNTGYDEIR;91/ANSYSVHGSALGAK;83/ALPTYTPESPADATR	11%	4/158	*G. hirsutum*	71.38/6.10	46.70/8.52	0.41
7820	gi|48749600	sucrose synthase	209	72/IQNLNALQHVLR;36/FQEIGLER;37/LLPDAVGTTCGQR;64/VYGTEYSDILR	16%	4/210	*G. raimondii*	76.93/6.33	30.57/6.31	2.01
7822	gi|48743676	long chain acyl-CoA synthetase 4	381	85/DVYISYLPLAHIFDR;88/LLVEDIGELKPSIFCAVPR;135/LILSGAAPLSTHVEEFLR;73/LESVPEMNYDALA	25%	4/210	*G. raimondii*	70.50/6.34	30.84/8.13	0.18
7934	gi|109863329	2-oxoglutarate e1 component	133	133/LTDSFLDGTSSVYLEELQR	7%	1/210	*G. hirsutum*	83.12/6.27	30.29/7.11	3.20
8001	gi|13246902	transmembrane emp24 domain-containing protein	392	83/ADSTWHNSHEGVDLVVK;43/GPTGDQIQDYRDK;64/ISEKFEFVAHQK;48/FEFVAHQK;57/LEEALYNIQFEQHWLEAQTER;96/AFYESAALIGASVLQVYLLR	31%	6/158	*G. arboreum*	28.14/6.37	31.47/7.85	3.65
8003	gi|21094593	cysteine proteinase inhibitor	219	53/FAVDEHNKK;24/ENAMVEFVR;102/EIVHANAEVLEDFAK;40/FKVEVHHK	18%	4/158	*G. arboreum*	28.41/6.42	25.04/6.24	2.44
8118	gi|164249213	short chain alcohol dehydrogenase	242	53/VALITGGASGLGECSAR;69/LDIMFNNAGLIGDGEVR;19/VTDASTDNFKR;30/VFDINVLGGFLGAK;13/ISIGLPHAYK;58/SLAVELGEHGIR	19%	6/177	*G. hirsutum*	33.66/6.46	43.60/9.31	2.13
8129	gi|164321379	caffeoyl-o-methyltransferase	254	45/HQEVGHK;79/SLLQSDALYQYILETSVYPR;16/EPEPMKELR;83/ENYELGLPVIR;30/DFVLELNK	19%	5/210	*G. hirsutum*	35.04/6.58	31.81/5.79	3.88
8213	gi|32479439	aldo keto	156	52/LDVDYIDLYYIIR;34/YIGISEASPETIR;26/DVEEEIIPLCR	10%	4/148	*G. hirsutum*	41.75/6.57	42.01/8.05	2.68
8304	gi|48739277	poly -specific endoribonuclease-b-	154	23/LWQLDLNR;80/QEQAAFIEEISR;52/GGTSGSSSAFEHVFVGEIK	16%	3/210	*G. raimondii*	46.07/6.39	27.77/4.97	2.40
8314	gi|3326420	IAA-conjugate-resistant 4	114	114/FADINNAYEVLSDSEKR	7%	1/210	*G. hirsutum*	45.81/6.47	43.69/7.16	2.64
8434	gi|48745701	hydroxymethylglutaryl- synthase	86	24/LVFNDFVR;62/LAPFSTLTGDESYQSR	8%	2/158	*G. raimondii*	51.72/6.41	30.33/9.53	2.16
8523	gi|5049652	dihydrolipoyl dehydrogenase	278	78/DTLEVDAALIATGR;158/APFTNGLGLENVNVVTQR;42/GFVPVDER	19%	3/210	*G. hirsutum*	55.75/6.51	22.74/6.66	0.20

8607	gi|164270428	adenylyl cyclase associated protein	356	43/RSDFFNHLK;41/SAGDSLSALAWIAYTGK;57/NKDQIHVEWAK;49/ELYLPGLR;72/SHYPLGPVWSASGK;62/KWAVENQIGR;34/WAVENQIGR	16%	7/210	*G. hirsutum*	59.21/6.41	44.82/9.58	2.49
8712	gi|164316346	2-hydroxyacyl- lyase	315	57/KAERPLIVFGK;106/GLVNDDHELAASAAR;104/FILVDVSEEEIKLR;49/DVVPFNFLTPMR	12%	4/158	*G. hirsutum*	61.54/6.48	46.68/10.08	3.24
8801	gi|5049242	transketolase 1	62	62/ALPTYTPESPADATR	7%	1/210	*G. hirsutum*	70.73/6.37	22.75/6.73	2.01
9201	gi|48741079	26s proteasome non-atpase regulatory subunit 14	326	79/AVAVVVDPIQSVK;66/HYYSIAINYR;25/MLLNLHK;49/WTDGLTLR;26/RFDTHSK;81/TNEQTVQEMLNLAIK	21%	6/151	*G. raimondii*	37.11/6.64	30.95/7.31	0.47
9202	gi|48750384	malate dehydrogenase	163	36/ANTFVAEVMGLDPR;58/EIDYLTNR;70/CGVEEIYPLGPLNEYER	14%	3/158	*G. raimondii*	38.13/6.64	29.76/8.74	2.01
9404	gi|48745701	hydroxymethylglutaryl- synthase	176	39/LVFNDFVR;119/LAPFSTLTGDESYQSR;17/SRHEFAPEK	12%	3/210	*G. raimondii*	51.64/6.63	30.33/9.53	2.14
9407	gi|48828974	isocitrate dehydrogenase	335	36/LVPGWTKPICIGR;62/HAFGDQYR;66/SKYEAAGIWYEHR;63/YEAAGIWYEHR;108/GGETSTNSIASIFA	17%	5/210	*G. raimondii*	48.99/6.73	32.47/8.19	0.50
9418	gi|13246368	transcription factor	82	82/SVSINEFLKPAEGER	8%	1/210	*G. arboreum*	51.21/6.68	20.46/8.89	--
9503	gi|48816177	monodehydroascorbate reductase	312	131/EFVIVGGGNAAGYAAR;29/EAYAPYERPALTK;39/LPGFHTCVGSGGER;42/IGGNLPGVHYIR;45/LDTSIIFPENQLLQR;26/LFTPSLAQR	28%	6/210	*G. raimondii*	53.78/6.61	30.16/9.14	2.11
9606	gi|48804741	aldehyde dehydrogenase family 2 member mitochondrial-like	308	96/TLVHESVYDEFVEK;51/DEIFGPVQSISK;74/FKDLEEVVQR;87/ANASSYGLAAGVFTQNIETANTLTR	23%	4/210	*G. raimondii*	57.18/6.66	29.48/6.99	5.27
9615	gi|48810466	methylmalonate-semialdehyde dehydrogenase	228	54/AISFVGSNTAGMHIYGR;16/AISFVGSNTAGMHIYGR;92/DATLNALLAAGFGAAGQR;82/ADSLEDALNIVNR	18%	4/210	*G. raimondii*	56.70/6.85	26.96/9.16	2.19

[a] Sample spot protein number.

[b] NCBI gi number.

[c] Score for matched peptides.

[d] Sequence of matched peptides.

[e] Count of the number of distinct peptide sequences assigned to each protein.

[f] Number of unique peptides identified.

[g] Molecular mass.

[h] Average fold change of $\geqslant 2$ or $\leqslant 0.5$ and $P \leqslant 0.05$, as assessed by a Student *t* -test of three biological replicates. ("$\geqslant 2$" means up-regulated; "$\leqslant 0.5$" means down-regulated; "N" means other regulatory patterns. "++" means no detection in infection samples, while "--" means no detection in Mock sample.)

Information of single-peptide-based protein identifications

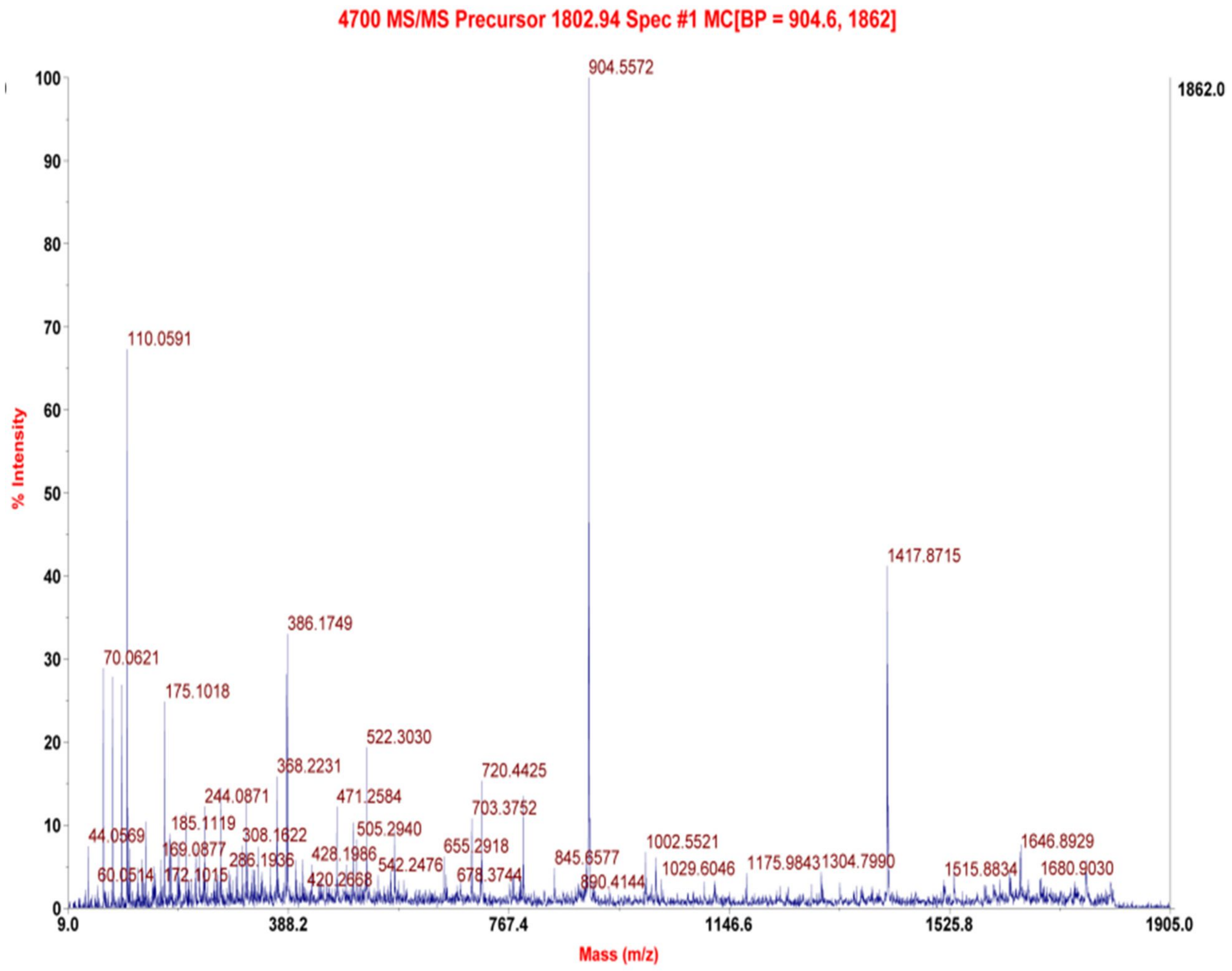
ssp No.: 12

sequence identified： **AAQDIALTDLAPTHPIR**

the precursor m/z and charge observed： **1802.9431**

score/E-value for this peptide： **115/5.1e-009**

Annotated MS/MS spectra:



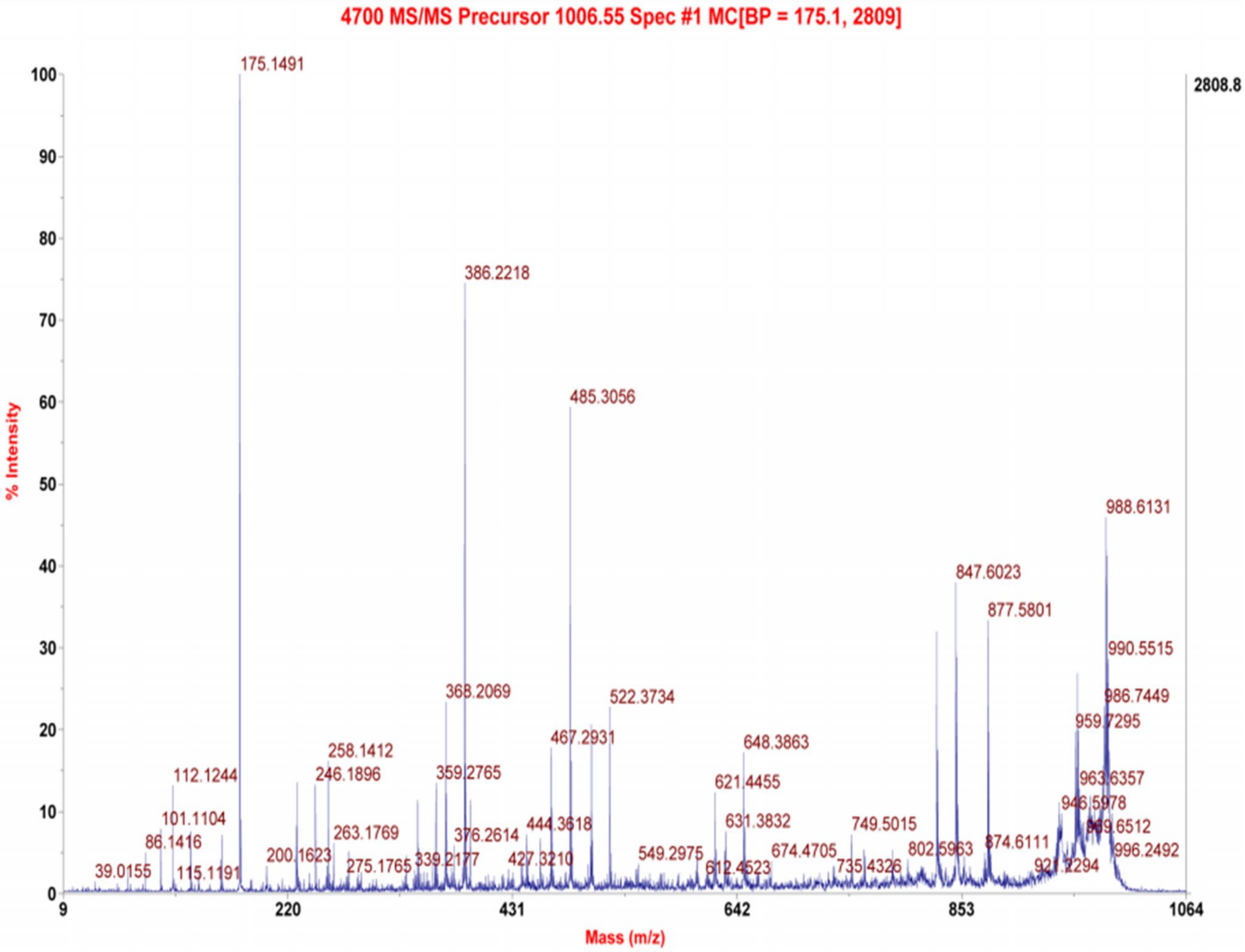
ssp No.: **123**

sequence identified：**EQQVYLAR**

the precursor m/z and charge observed：**1006.5546**

score/E-value for this peptide：**49/0.038**

Annotated MS/MS spectra:



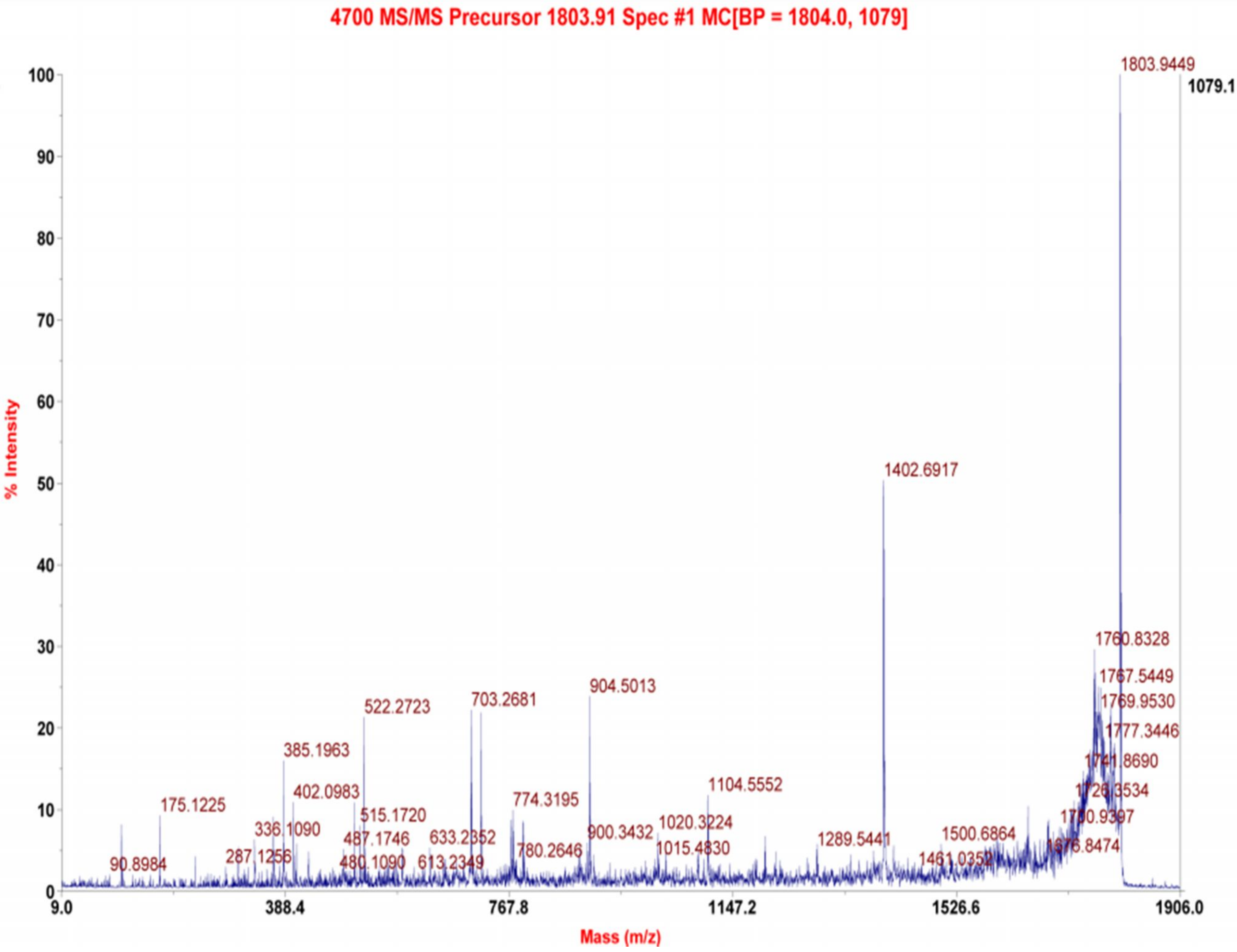
ssp No.: 233

sequence identified： **SAQDIANAELAPTHPIR**

the precursor m/z and charge observed： **1803.9147**

score/E-value for this peptide： **59/0.002**

Annotated MS/MS spectra:



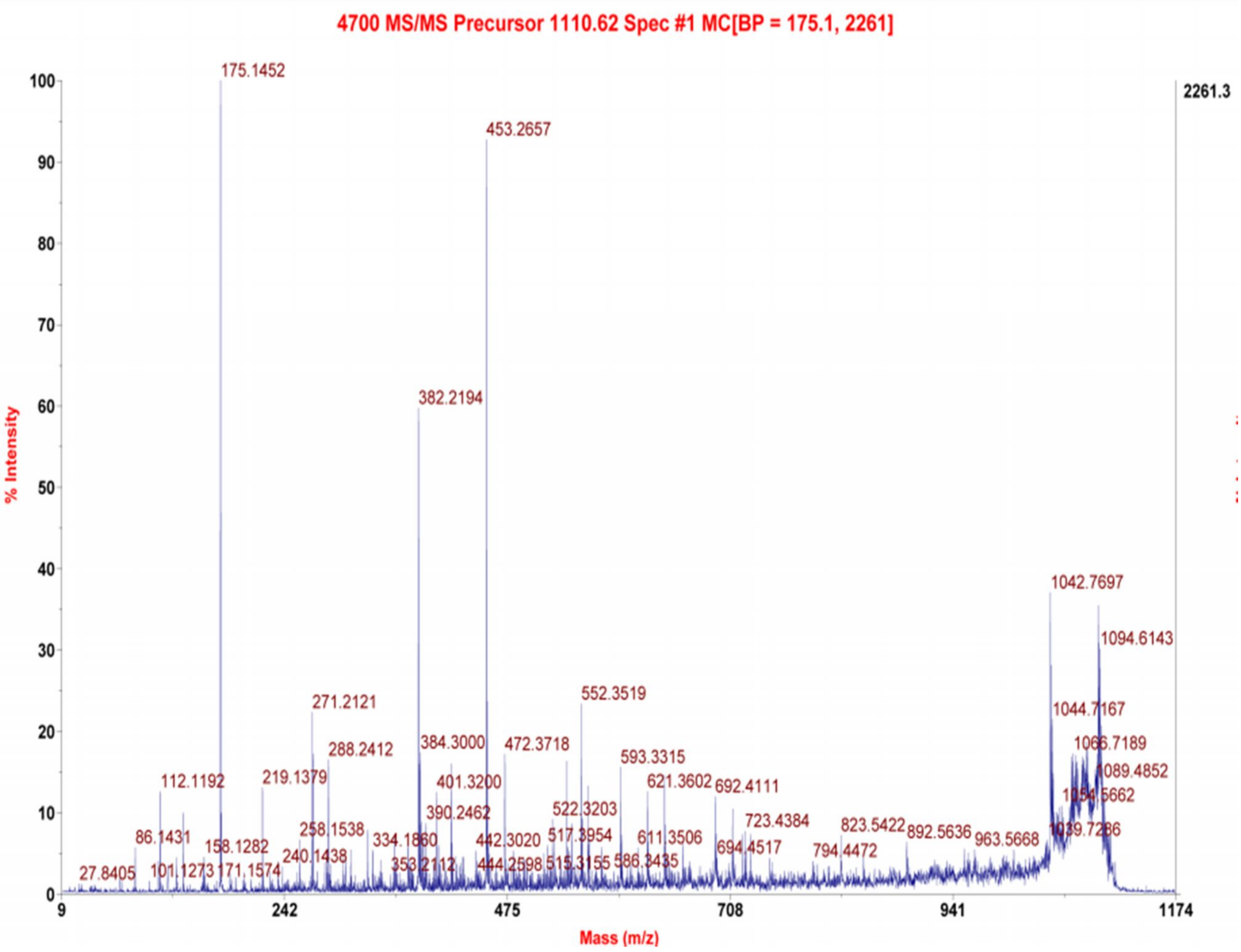
ssp No.: **424**

sequence identified： **AFYAVSALIR**

the precursor m/z and charge observed： **1110.6155**

score/E-value for this peptide： **53/0.013**

Annotated MS/MS spectra:



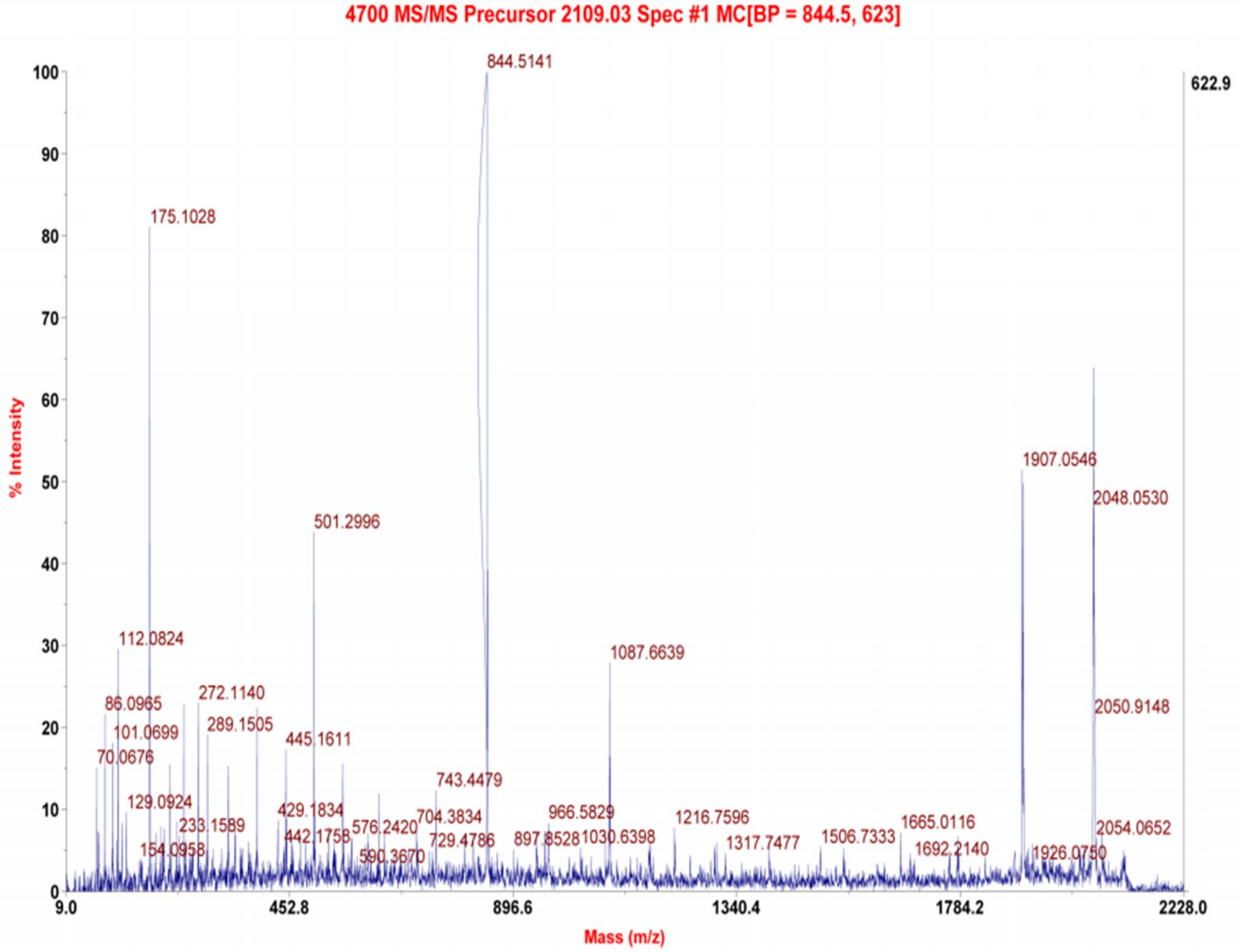
ssp No.: **524**

sequence identified：**SDQNLFSTEGADTIEIVNR**

the precursor m/z and charge observed：**2109.0349**

score/E-value for this peptide：**170/1.1e-014**

Annotated MS/MS spectra:



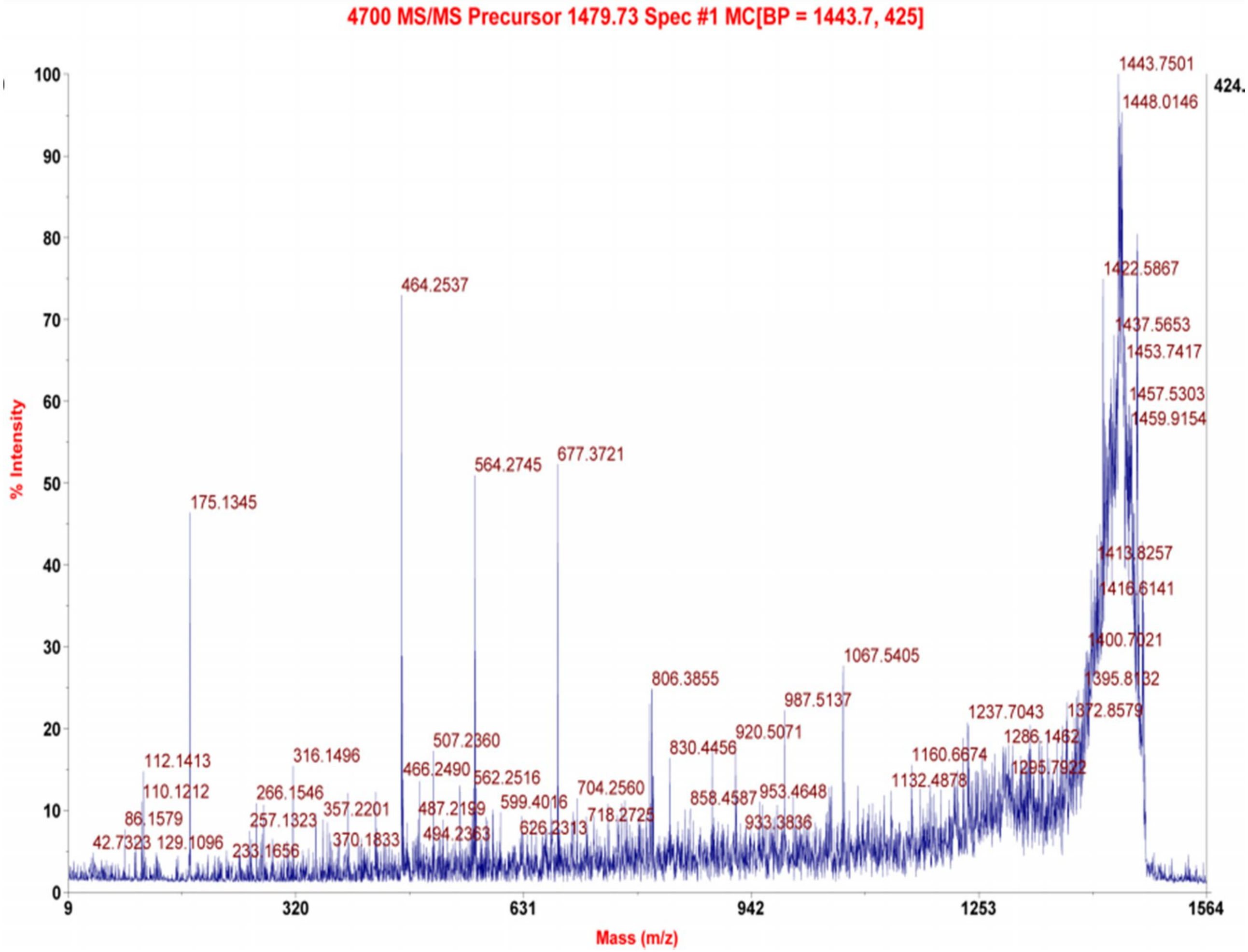
ssp No.: **1150**

sequence identified： **LEGLFNELGCEAK**

the precursor m/z and charge observed： **1479.7294**

score/E-value for this peptide： **43/0.099**

Annotated MS/MS spectra:



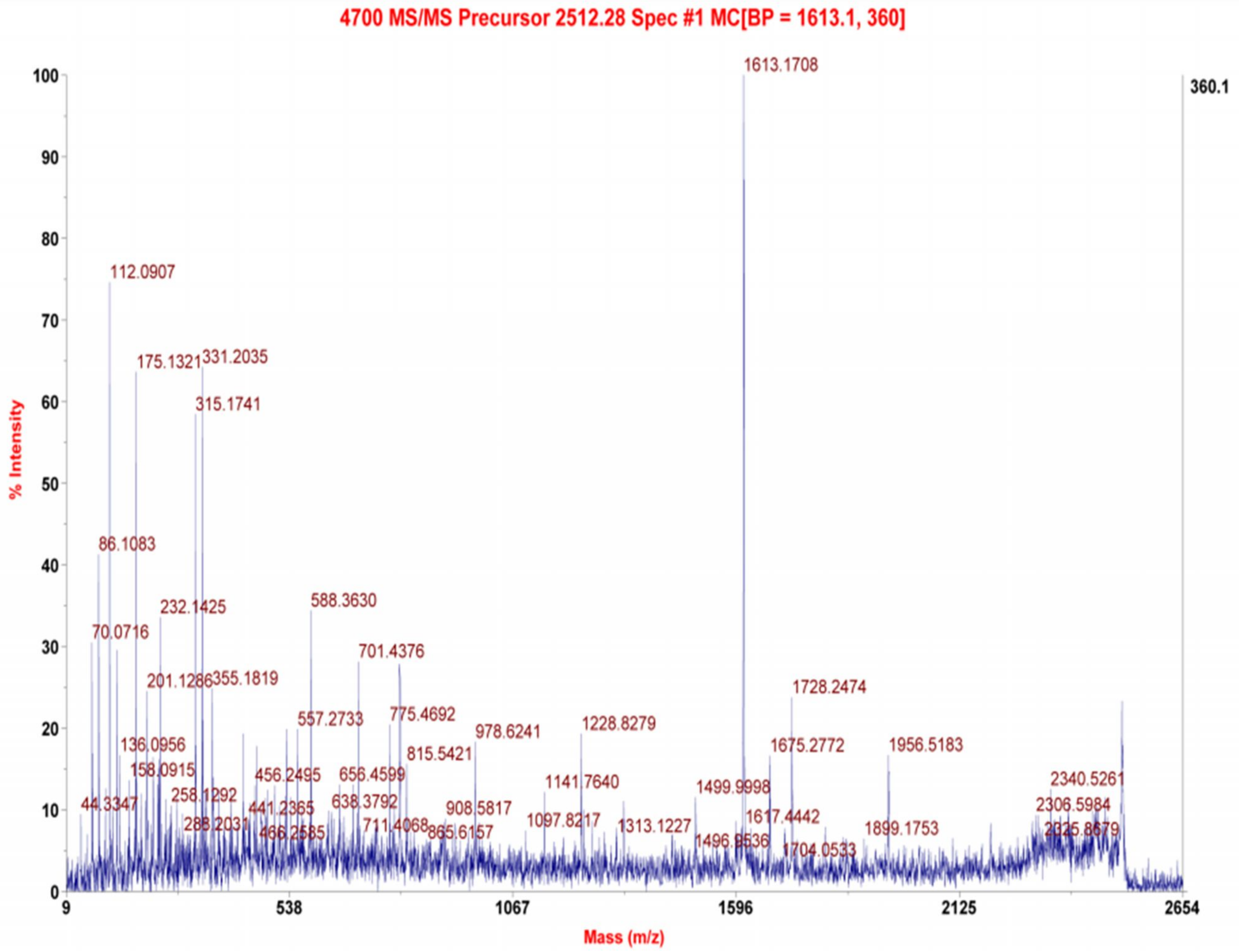
ssp No.: 2250

sequence identified：**SLNIEVEDLGITSYYNIGAEVGR**

the precursor m/z and charge observed：**2512.2803**

score/E-value for this peptide：**66/0.00022**

Annotated MS/MS spectra:



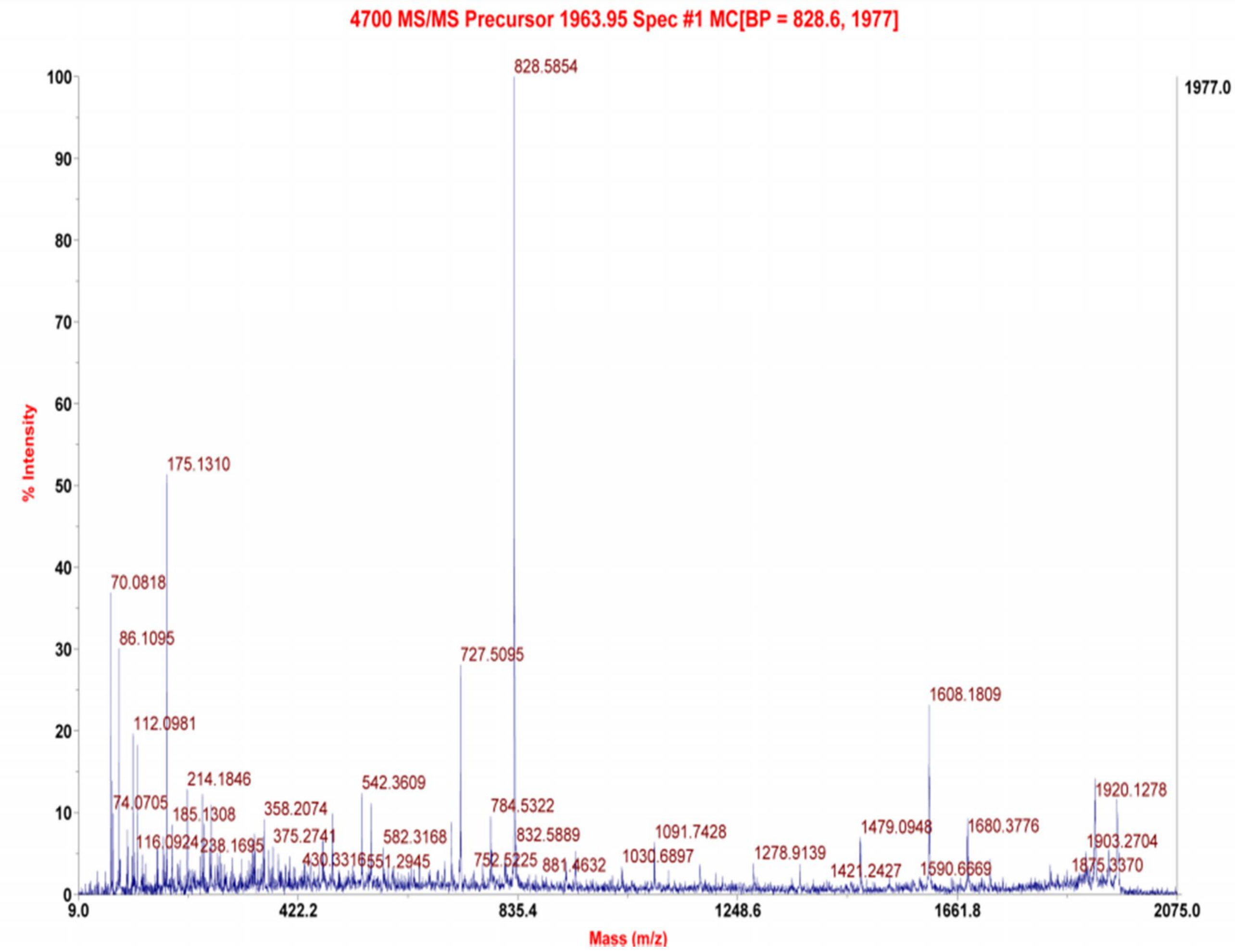
ssp No.: **2611**

sequence identified：**QIDELSTFSDTPAPSVTR**

the precursor m/z and charge observed：**1963.9510**

score/E-value for this peptide：**64/0.00054**

Annotated MS/MS spectra:



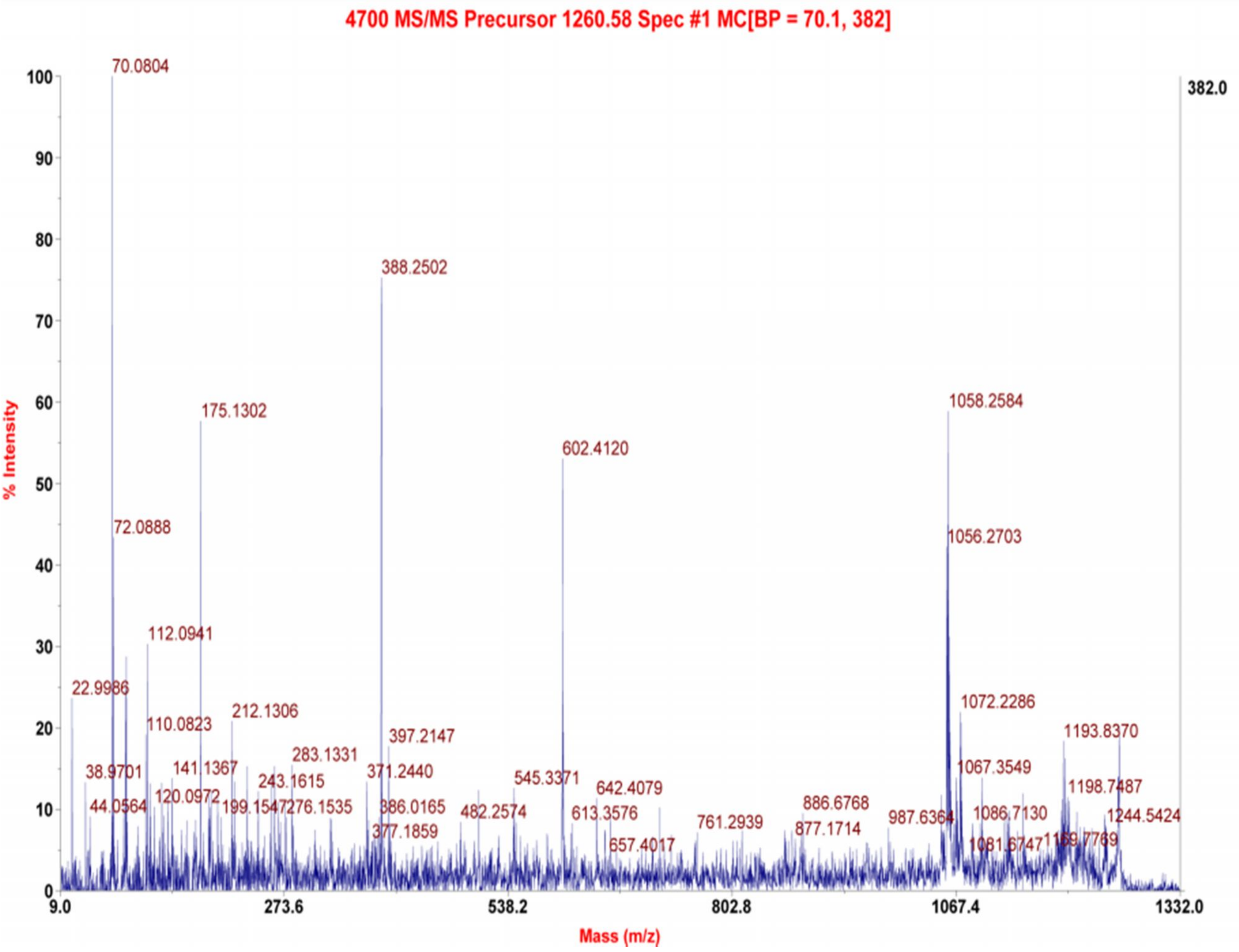
ssp No.: **3725**

sequence identified：**NPANFDVDNVR**

the precursor m/z and charge observed：**1260.5808**

score/E-value for this peptide：**52/0.016**

Annotated MS/MS spectra:



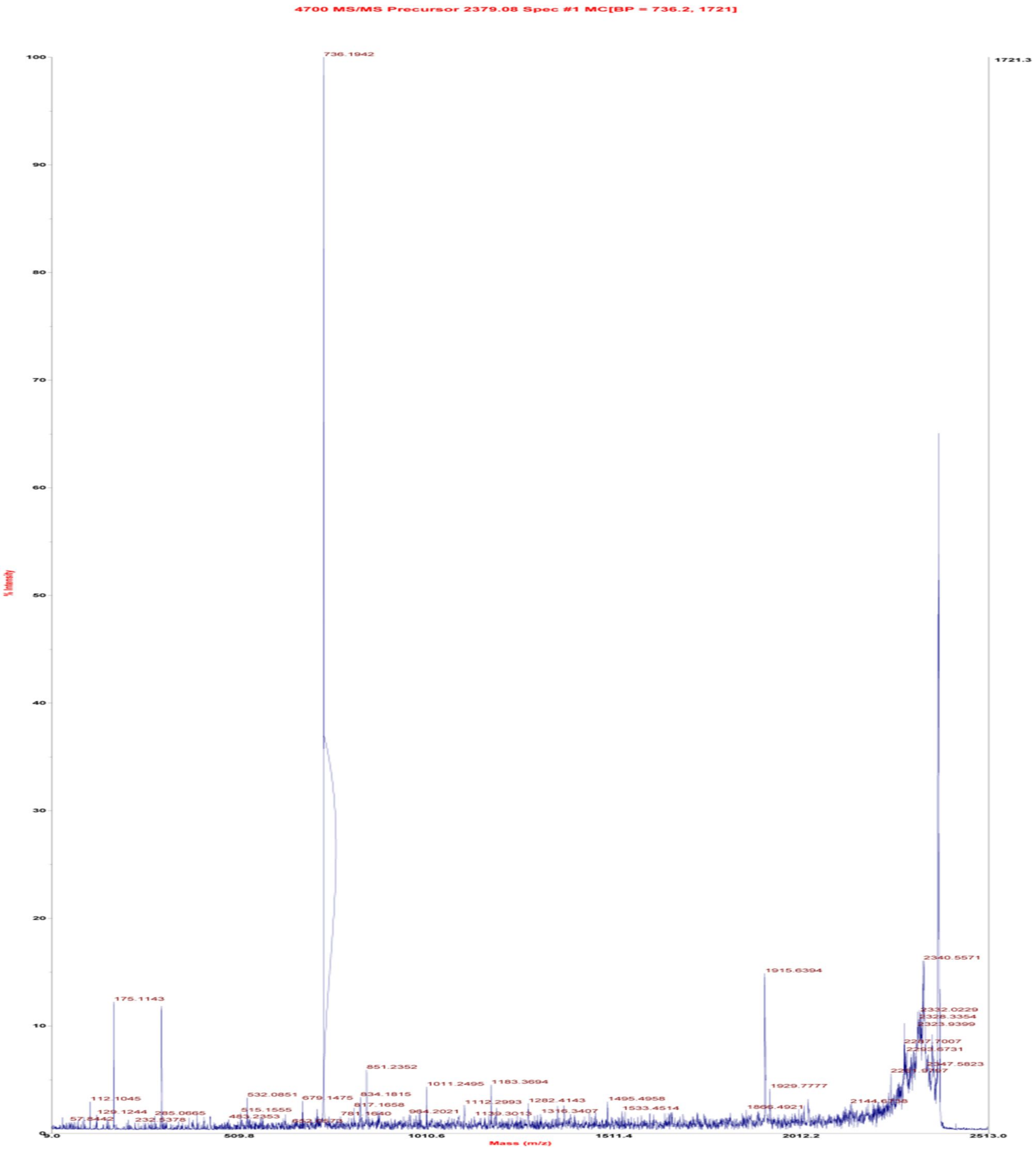
ssp No.: **4159**

sequence identified： **YANDYSGLVNVATCDGFVEER**

the precursor m/z and charge observed： **2379.0769**

score/E-value for this peptide： **112/4.6e-009**

Annotated MS/MS spectra:



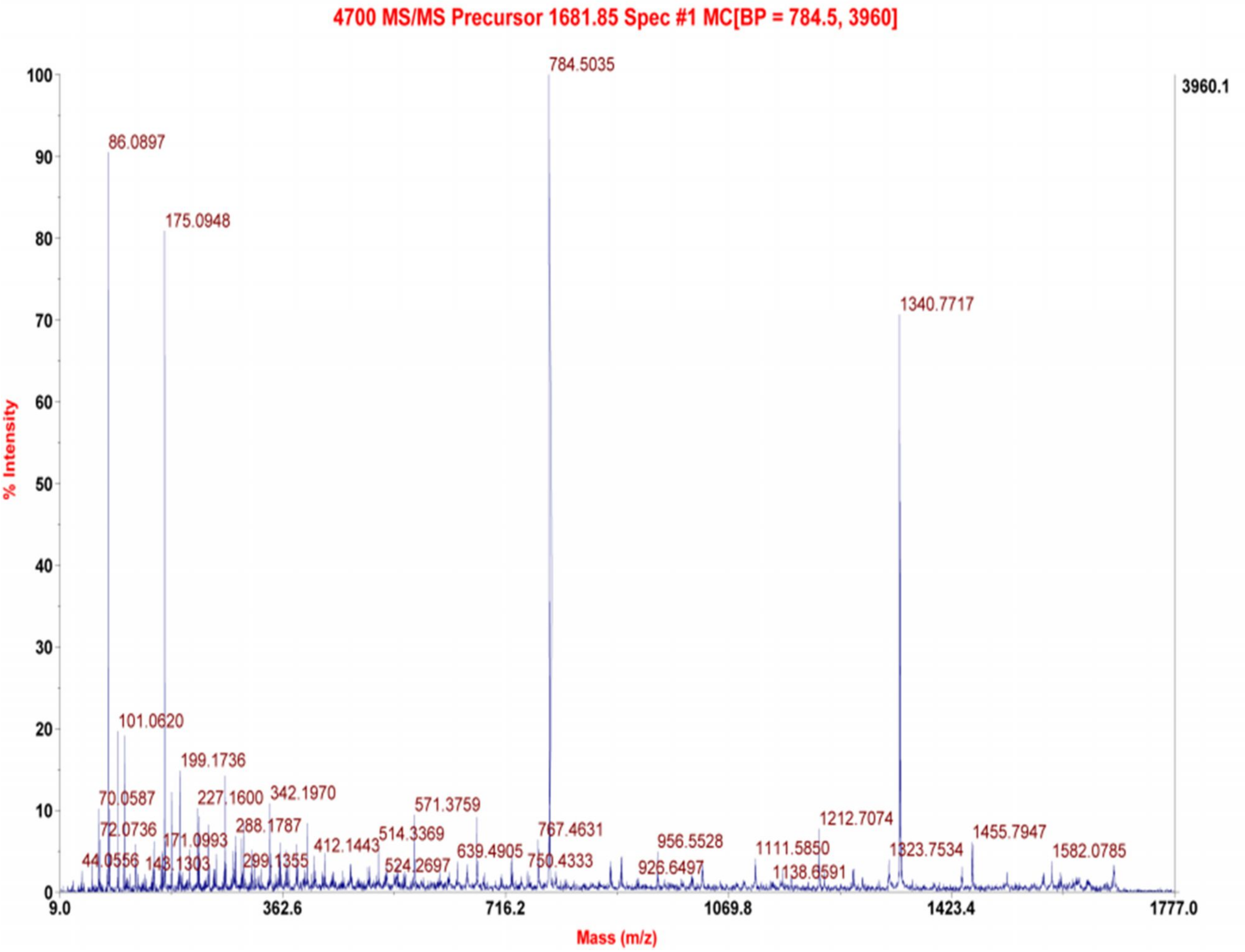
ssp No.: **4422**

sequence identified：**ILDQGQAGDNVGLLLR**

the precursor m/z and charge observed：**1681.8540**

score/E-value for this peptide：**144/7.4e-012**

Annotated MS/MS spectra:



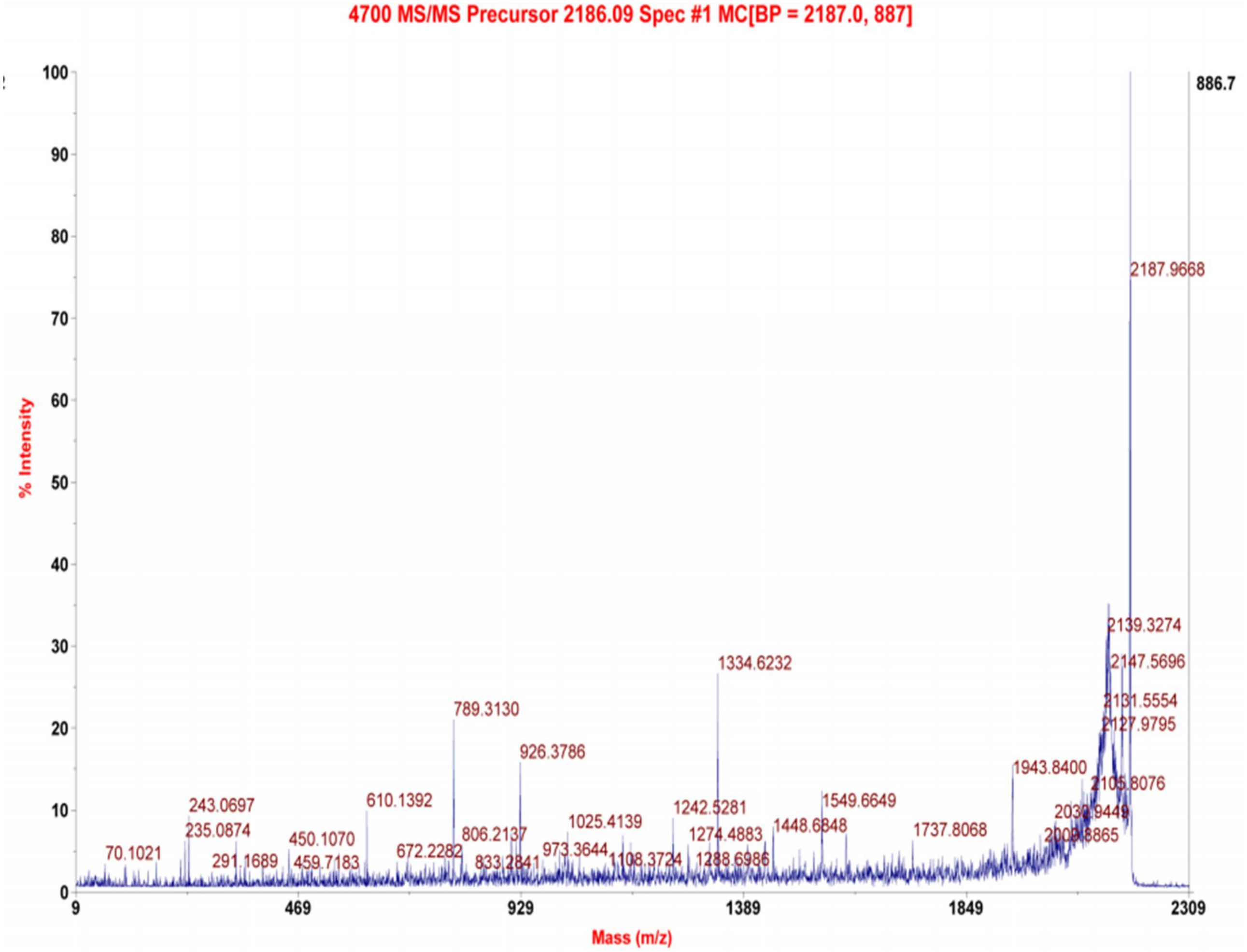
ssp No.: **4803**

sequence identified：**NQPPAETNPVIVHPLEFAGR**

the precursor m/z and charge observed：**2186.0879**

score/E-value for this peptide：**76/3e-005**

Annotated MS/MS spectra:



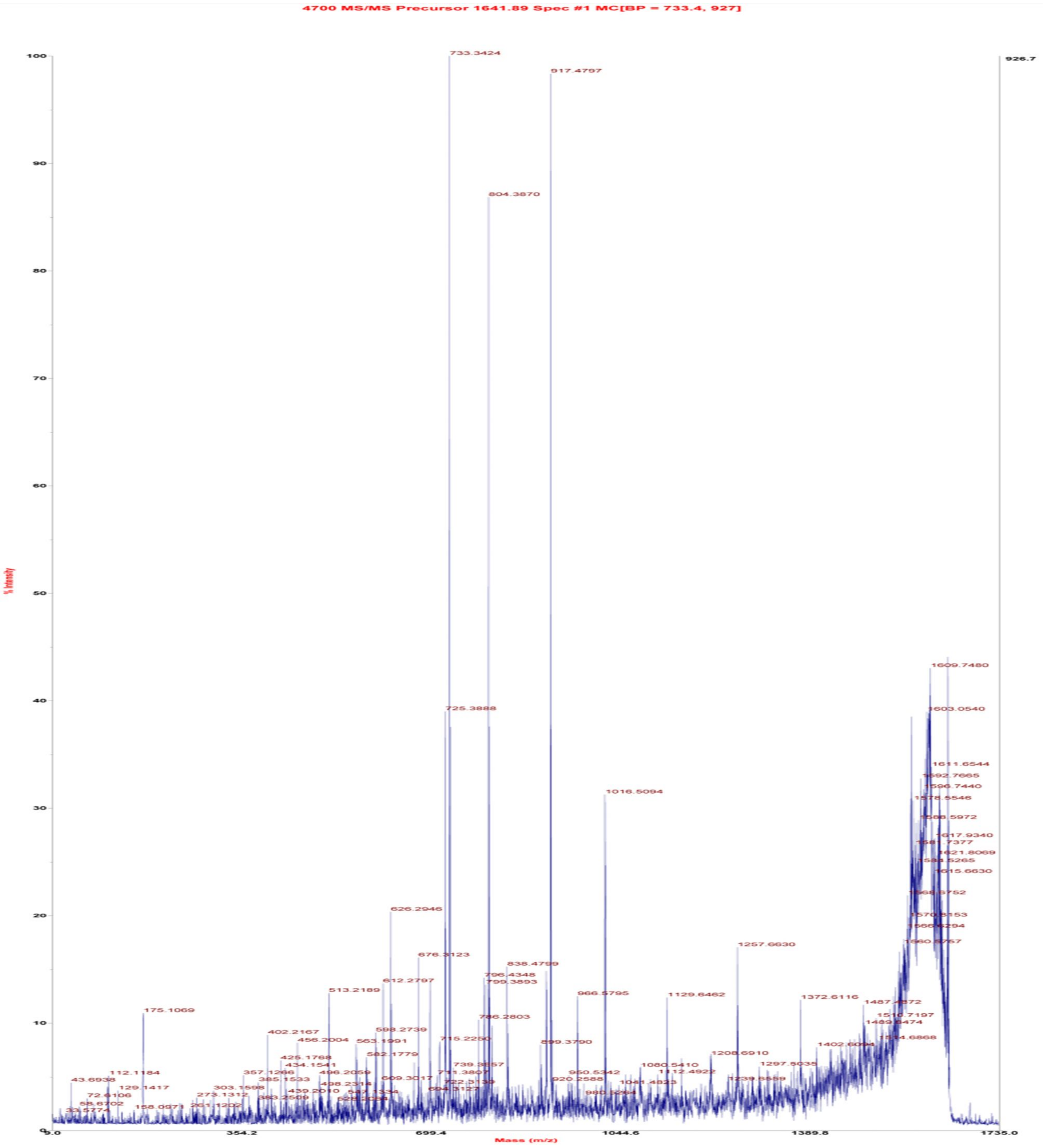
ssp No.: **5242**

sequence identified：**LGVDQLVLAGLESEAK**

the precursor m/z and charge observed：**1641.8945**

score/E-value for this peptide：**63/0.00095**

Annotated MS/MS spectra:



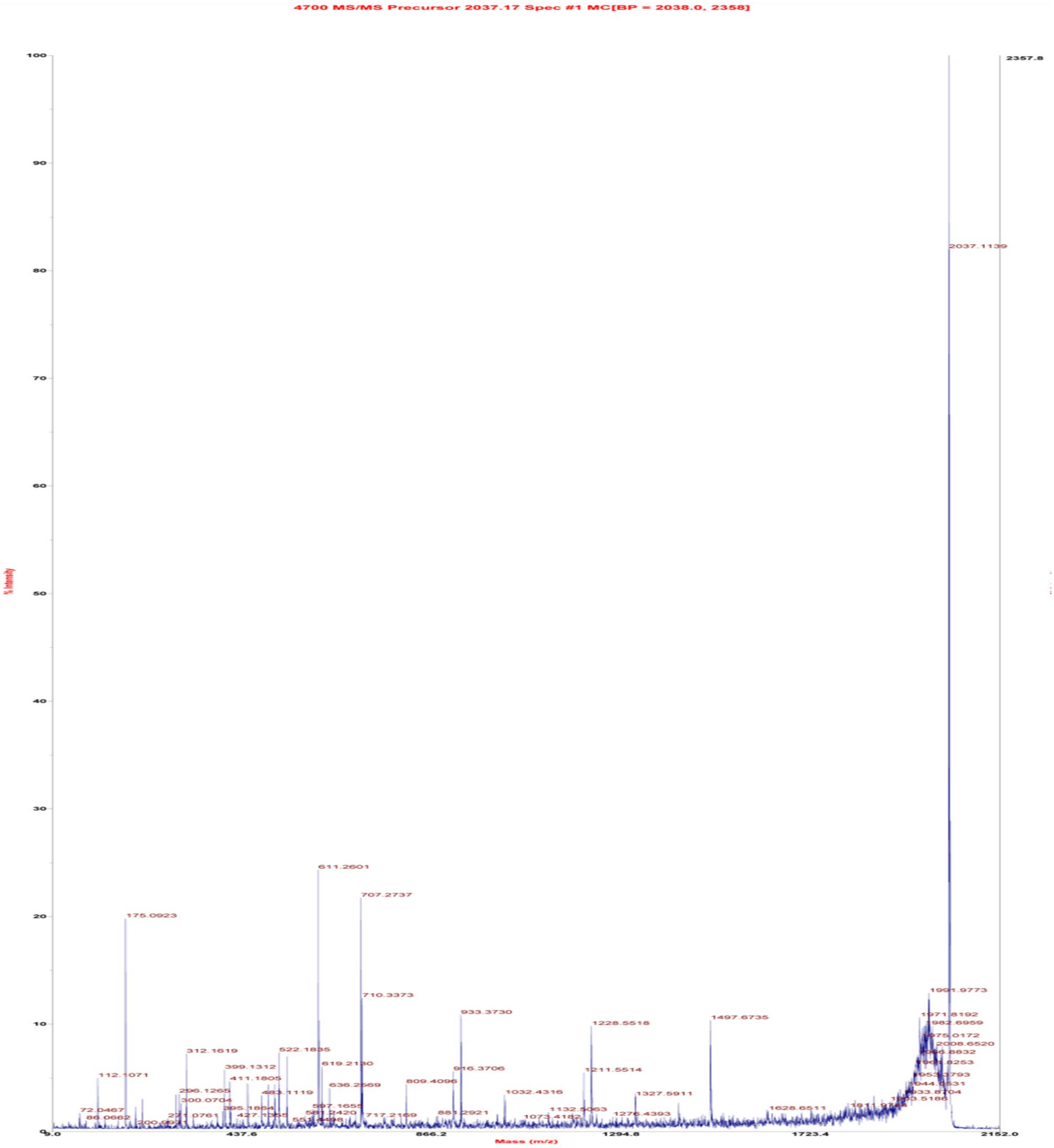
ssp No.: 7204

sequence identified：**VIVVEAVVPVVPEANAYLR**

the precursor m/z and charge observed：**2037.1680**

score/E-value for this peptide：**86/2.2e-006**

Annotated MS/MS spectra:



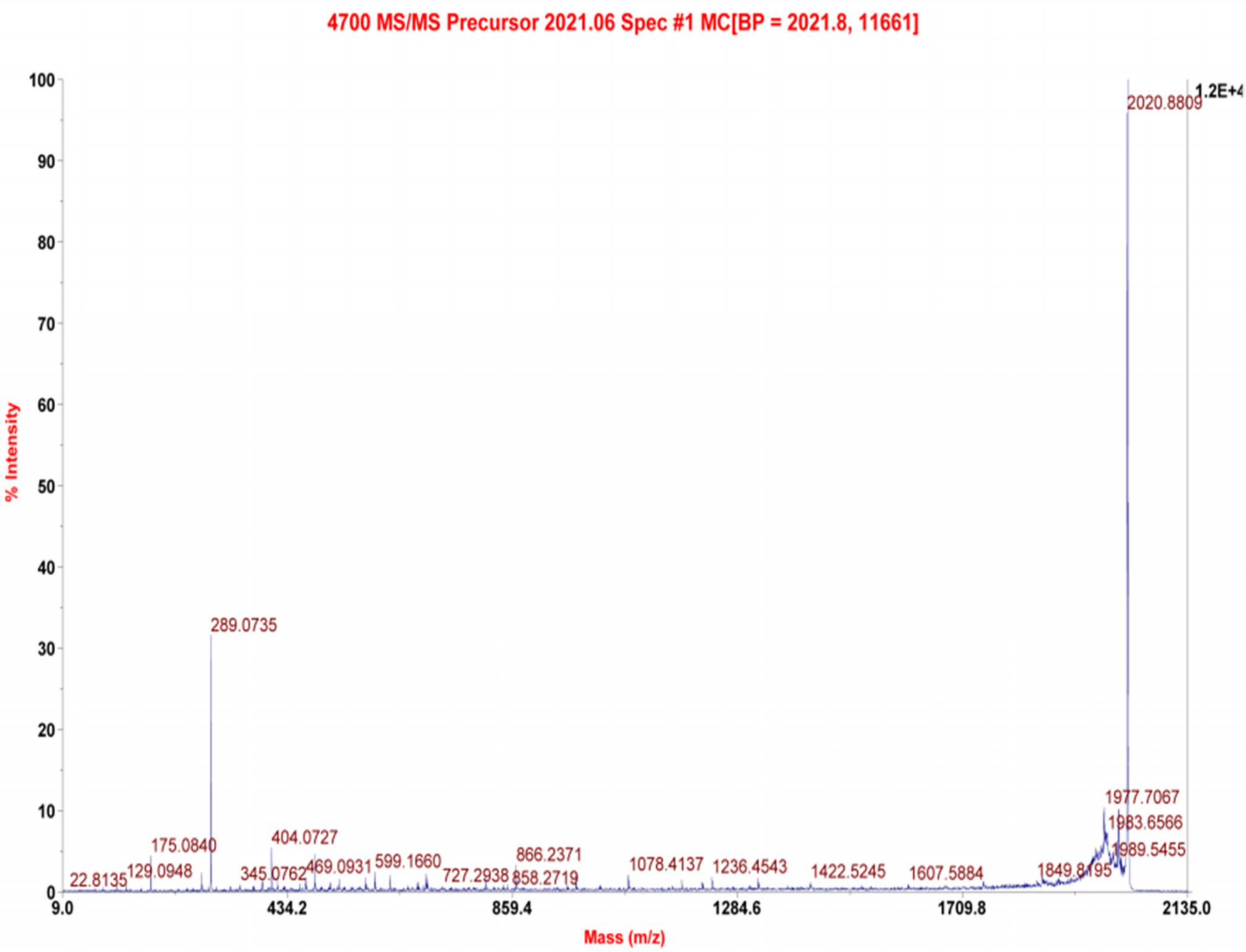
ssp No.: 7503

sequence identified：**GNTAAAIVSGTVLGLYEDNR**

the precursor m/z and charge observed：**2021.0631**

score/E-value for this peptide：**124/5.4e-010**

Annotated MS/MS spectra:



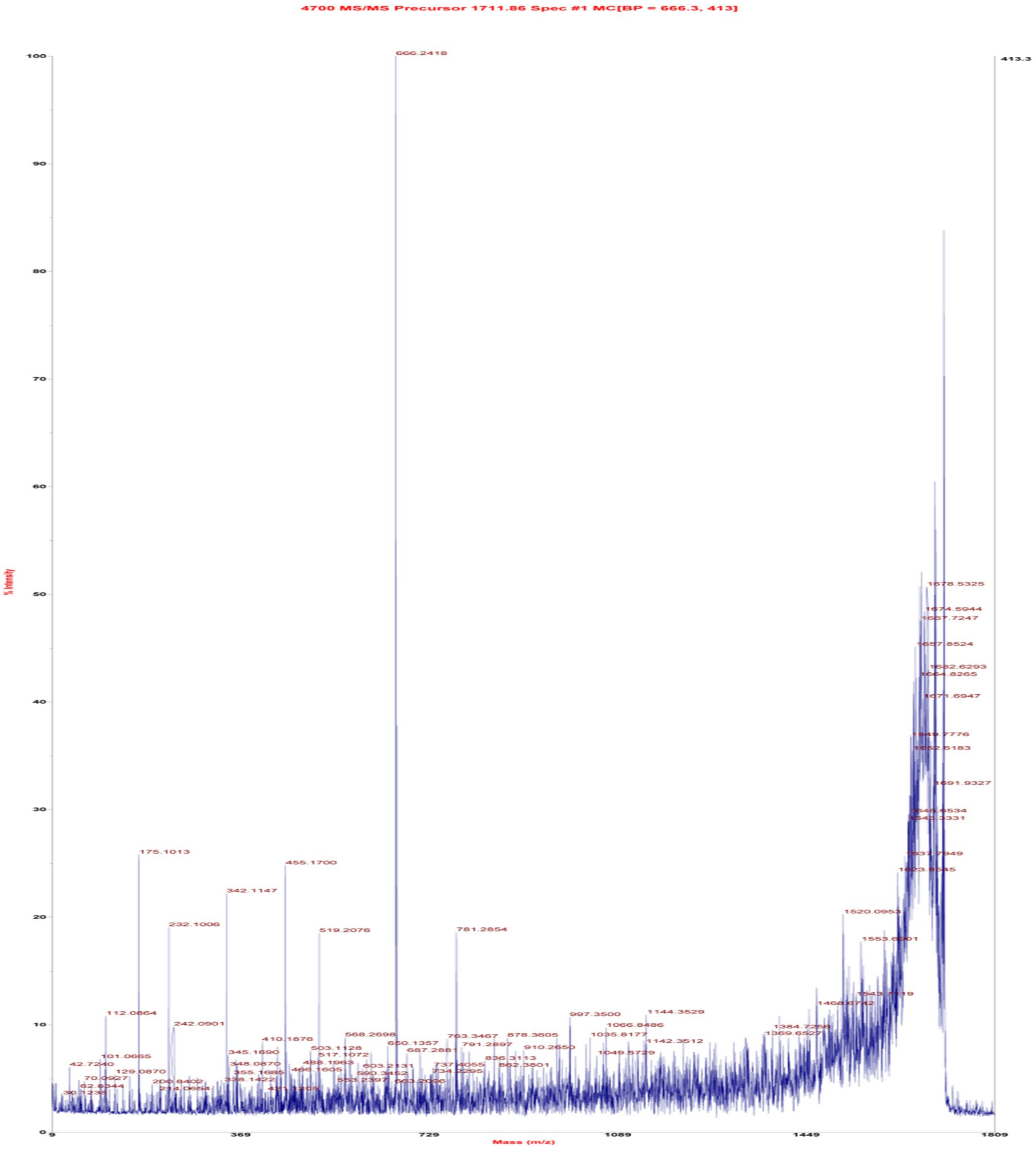
ssp No.: **7717**

sequence identified：**NVQIIFSEDFGTEGR**

the precursor m/z and charge observed：**1711.8552**

score/E-value for this peptide：**58/0.0028**

Annotated MS/MS spectra:



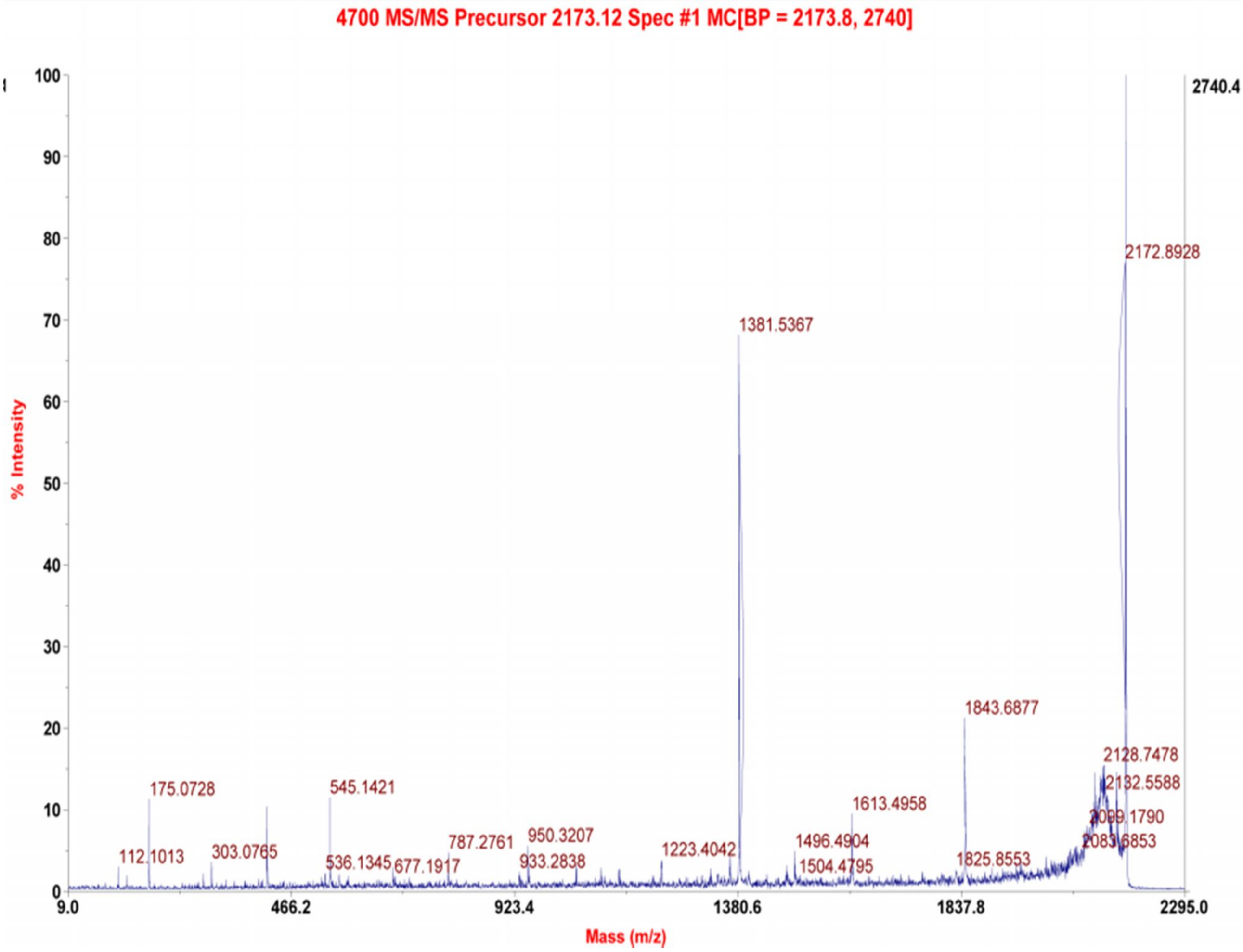
ssp No.: **7934**

sequence identified： **LTDSFLDGTSSVYLEELQR**

the precursor m/z and charge observed： **2173.1211**

score/E-value for this peptide： **133/5.3e-011**

Annotated MS/MS spectra:



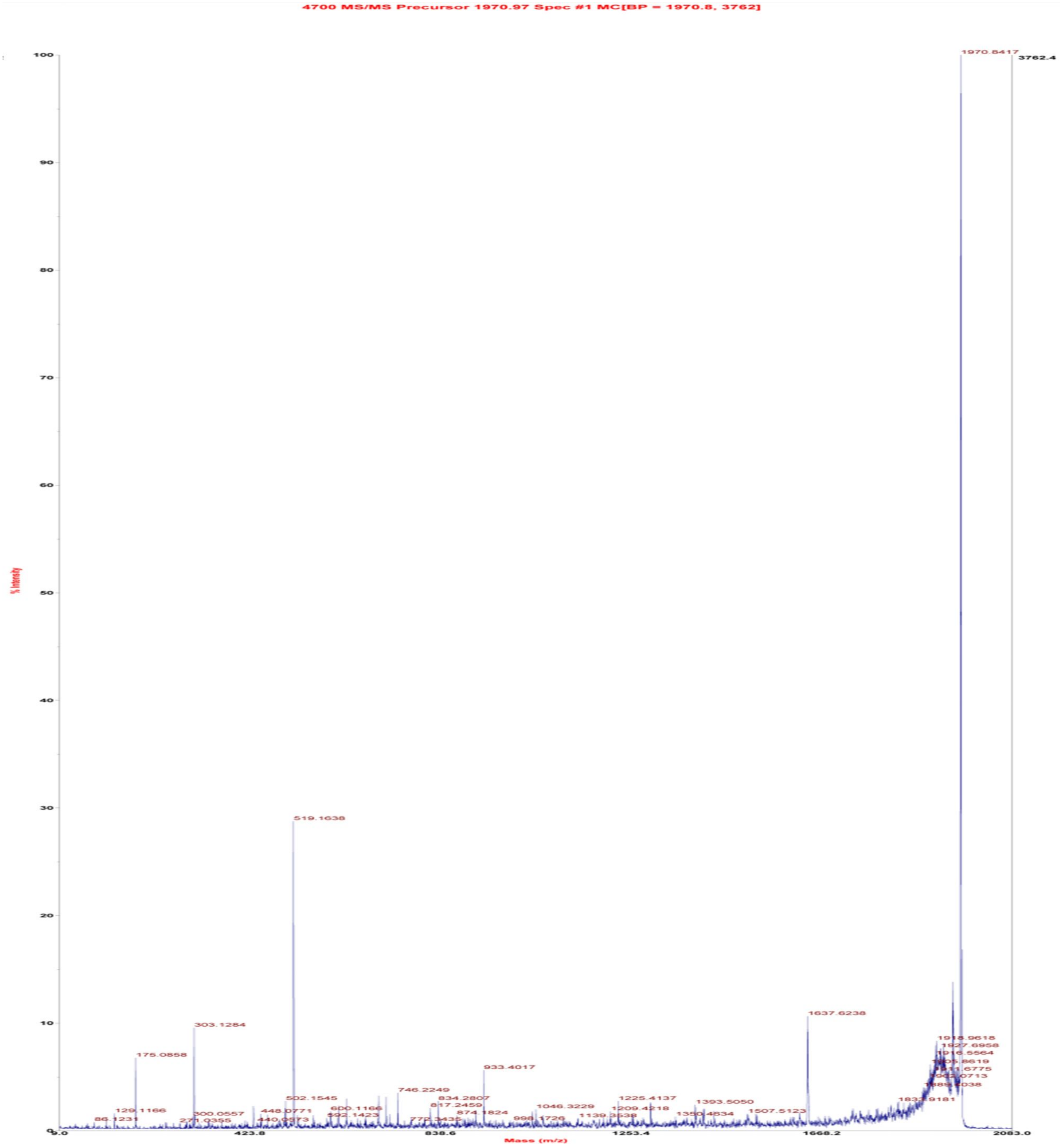
ssp No.: **8314**

sequence identified：**FADINNAYEVLSDSEKR**

the precursor m/z and charge observed：**1970.9670**

score/E-value for this peptide：**114/5.7e-009**

Annotated MS/MS spectra:



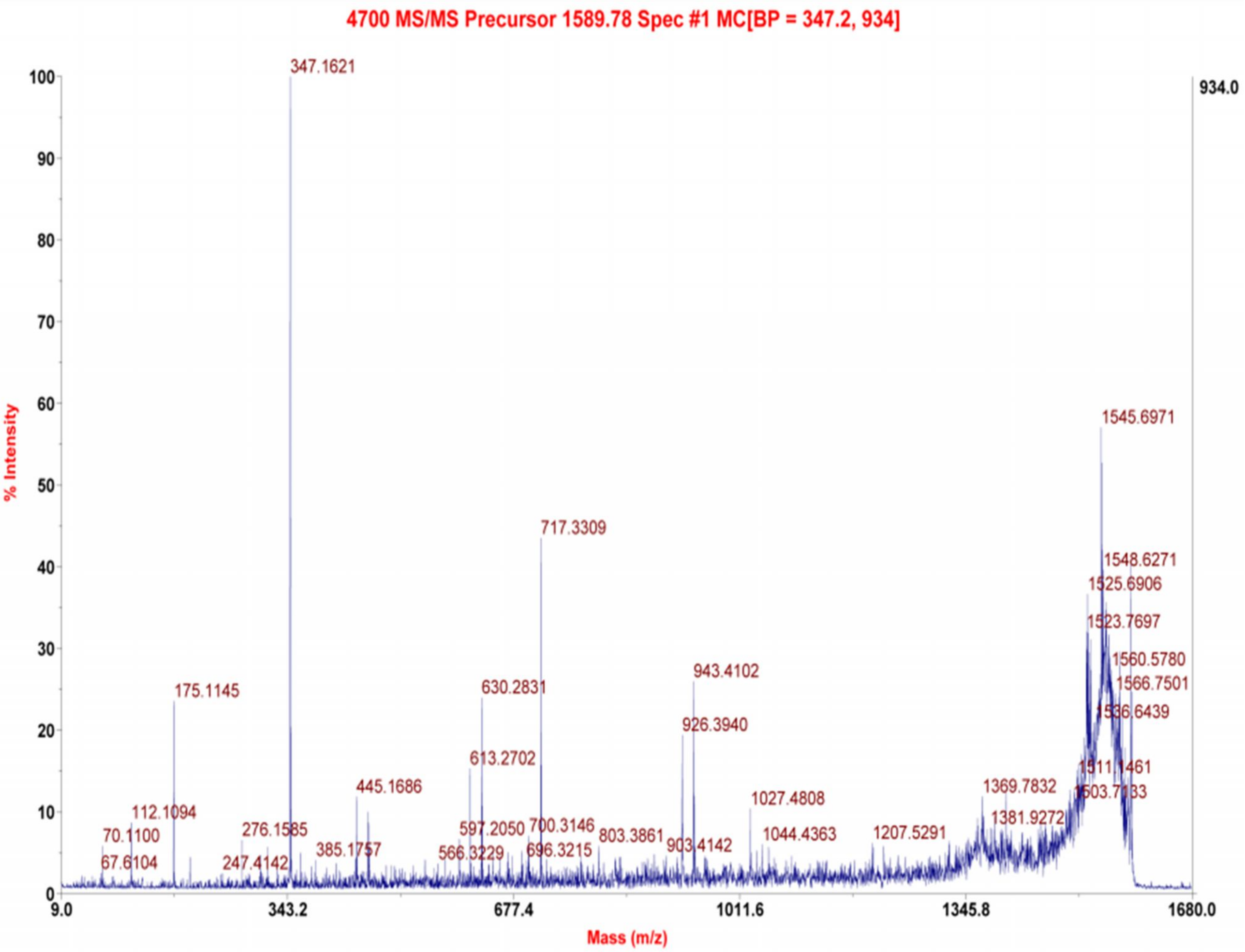
ssp No.: **8801**

sequence identified： **ALPTYTPESPADATR**

the precursor m/z and charge observed： **1589.7849**

score/E-value for this peptide： **62/0.0012**

Annotated MS/MS spectra:



ssp No.: **9418**

sequence identified：**SVSINEFLKPAEGER**

the precursor m/z and charge observed：**1675.9115**

score/E-value for this peptide：**82/1.1e-005**

Annotated MS/MS spectra: