

Table 1 supplementary data: Mascot Search Results using the *Helianthus* EST database

Search Parameters

Type of search	: MS/MS Ion Search	Peptide Mass Tolerance	: ± 0.5 Da
Enzyme	: Trypsin	Fragment Mass Tolerance	: ± 0.4 Da
Variable modifications	: Deamidation (NQ), Oxidation (M)	Max Missed Cleavages	: 2
Mass values	: Monoisotopic	Instrument type	: ESI-TRAP
Protein Mass	: Unrestricted	Number of queries	: 72

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 48 indicate identity or extensive homology (p<0.05).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

1	gij33135602 gb CF096535.1 CF096535	Mass: 18282	Score: 94	Queries matched: 2	Frame: 4				
	QHN23104.yg.ab1 QH_N sunflower <i>H. argophyllus</i> (drought stress) <i>Helianthus argophyllus</i> cDNA clone QHN								
	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	537.38	1072.74	1072.50	0.24	0	34	1.7	1	R.YYVDLMNR.Q
	795.60	1589.19	1588.82	0.37	0	60	0.0045	1	K.MGQLSVLTGTQGEIR.S
2	gij33122964 gb CF083921.1 CF083921	Mass: 20118	Score: 85	Queries matched: 2	Frame: 6				
	QHL21A22.yg.ab1 QH_L sunflower <i>H. paradoxus</i> (salt stress) <i>Helianthus paradoxus</i> cDNA clone QHL21A22								
	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	537.38	1072.74	1072.50	0.24	0	34	1.7	1	R.YYVDLMNR.Q
	637.48	1272.94	1272.72	0.22	0	51	0.036	1	R.AQAFVIENLR.R

Proteins matching the same set of peptides:

gij90456162 gb DY918041.1 DY918041	Mass: 31687	Score: 85	Queries matched: 2	Frame: 1
CHAY13806.b1_L20.ab1 CHA(XYZ) common wild sunflower <i>Helianthus annuus</i> cDNA clone CHAY13806, mRNA sequence				
gij90463868 gb DY925747.1 DY925747	Mass: 30551	Score: 85	Queries matched: 2	
CHAY9260.b1_G11.ab1 CHA(XYZ) common wild sunflower <i>Helianthus annuus</i> cDNA clone CHAY9260, mRNA sequence				
gij90464214 gb DY926093.1 DY926093	Mass: 30167	Score: 85	Queries matched: 2	Frame: 3
CHAY9615.b1_M03.ab1 CHA(XYZ) common wild sunflower <i>Helianthus annuus</i> cDNA clone CHAY9615, mRNA sequence				
gij90464312 gb DY926191.1 DY926191	Mass: 34788	Score: 85	Queries matched: 2	Frame: 3
CHAY9714.b1_D05.ab1 CHA(XYZ) common wild sunflower <i>Helianthus annuus</i> cDNA clone CHAY9714, mRNA sequence				
gij90471082 gb DY932940.1 DY932940	Mass: 29935	Score: 85	Queries matched: 2	
CHPX11210.b1_C19.ab1 CHP(XYZ) plains sunflower <i>Helianthus petiolaris</i> cDNA clone CHPX11210, mRNA sequence				
gij90471088 gb DY932946.1 DY932946	Mass: 32855	Score: 85	Queries matched: 2	Frame: 2
CHPX11216.b1_O19.ab1 CHP(XYZ) plains sunflower <i>Helianthus petiolaris</i> cDNA clone CHPX11216, mRNA sequence				
gij90485841 gb DY947699.1 DY947699	Mass: 32705	Score: 85	Queries matched: 2	Frame: 3
CHPY3056.b1_P20.ab1 CHP(XYZ) plains sunflower <i>Helianthus petiolaris</i> cDNA clone CHPY3056, mRNA sequence				
gij90490829 gb DY952687.1 DY952687	Mass: 31326	Score: 85	Queries matched: 2	Frame: 3
CHPY8984.b1_P13.ab1 CHP(XYZ) plains sunflower <i>Helianthus petiolaris</i> cDNA clone CHPY8984, mRNA sequence				
gij125422554 gb EL434526.1 EL434526	Mass: 34357	Score: 85	Queries matched: 2	Frame: 3
CHTL2351.b2_M11.ab1 CHT(LMS) Jerusalem artichoke <i>Helianthus tuberosus</i> cDNA clone CHTL2351, mRNA sequence				
gij125422747 gb EL434719.1 EL434719	Mass: 33660	Score: 85	Queries matched: 2	Frame: 3
CHTL2565.b2_L18.ab1 CHT(LMS) Jerusalem artichoke <i>Helianthus tuberosus</i> cDNA clone CHTL2565, mRNA sequence				
gij125439584 gb EL451281.1 EL451281	Mass: 33343	Score: 85	Queries matched: 2	Frame: 1
CHTM4174.b2_L12.ab1 CHT(LMS) Jerusalem artichoke <i>Helianthus tuberosus</i> cDNA clone CHTM4174, mRNA sequence				
gij125448072 gb EL459768.1 EL459768	Mass: 34644	Score: 85	Queries matched: 2	Frame: 3
CHTS1347.b2_E02.ab1 CHT(LMS) Jerusalem artichoke <i>Helianthus tuberosus</i> cDNA clone CHTS1347, mRNA sequence				

Peptide matches not assigned to protein hits: (no details means no match)

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
457.90	913.80	913.53	0.26	1	45	0.14	1	ARVTILGQG
637.56	1909.64	1910.07	-0.43	0	35	1.1	1	ILIEDGISAHITSLTSLK
737.86	2210.55	2210.98	-0.43	2	35	1.1	1	QLCWMKSLTMYNRYNDK + 2 Deamidation (NQ); Oxidation (M)
530.90	1059.79	1059.56	0.24	1	34	2	1	VNNIINKSR + 3 Deamidation (NQ)
595.95	1189.89	1189.65	0.25	1	31	3.5	1	ARLNLGLGFVNK + 2 Deamidation (NQ)
637.55	1909.62	1910.07	-0.46	0	30	3.4	1	ILIEDGISAHITSLTSLK
637.54	1909.60	1910.07	-0.47	0	30	3.4	1	ILIEDGISAHITSLTSLK
449.31	896.61	896.41	0.21	0	29	4.8	1	TMLNNFR + 2 Deamidation (NQ)
637.63	1909.86	1910.01	-0.15	2	28	6.2	1	TVDERFLIGIMCKTLR + Oxidation (M)
516.41	1030.80	1030.58	0.22	1	26	11	1	VLDNRVSTK
506.32	1010.63	1010.41	0.23	0	25	13	1	HYHLDPDN + Deamidation (NQ)
637.63	3183.10	3183.60	-0.49	1	23	9.7	1	CQLQFNQGGKIYVWWWVEVGGQLMMVK + 2 Deamidation (NQ)
637.54	1909.59	1910.07	-0.48	0	22	20	1	ILIEDGISAHITSLTSLK
637.57	1909.70	1910.07	-0.38	0	22	21	1	ILIEDGISAHITSLTSLK
637.63	1273.24	1273.57	-0.33	0	22	29	1	LXSNNFQVAR + Deamidation (NQ)
637.56	2546.19	2546.37	-0.17	2	22	17	1	QSLSPKIQGKLTCLHVPFVSNHL + Deamidation (NQ)
637.56	1273.10	1273.54	-0.44	0	22	32	1	IYENLMTGCMV + Deamidation (NQ)
637.49	1272.96	1272.67	0.30	1	20	47	1	SLGSITIRTNPN + Deamidation (NQ)
426.37	1701.45	1701.79	-0.34	0	19	46	1	FDFSLSGTSLDMAAPK + Oxidation (M)
637.57	1273.13	1273.59	-0.46	0	19	58	1	LXSGNAITQMV + Deamidation (NQ); Oxidation (M)
637.54	1273.07	1273.54	-0.47	0	19	62	1	IYENLMTGCMV + Deamidation (NQ)
637.54	3182.66	3182.46	0.19	2	19	26	1	DIKEVISEVSDSDHDGRINYDEFVAMMR
637.63	2546.48	2546.06	0.42	0	19	38	1	SNCXHSNMYLHFPWHVLMYGV + Deamidation (NQ)
637.55	1273.08	1273.54	-0.46	0	18	63	1	IYENLMTGCMV + Deamidation (NQ)
637.54	2546.12	2546.16	-0.04	1	18	39	1	AFLIYDNVHSLFGCGFNSNNRR + 3 Deamidation (NQ)
637.57	3182.83	3182.46	0.36	2	18	27	1	DIKEVISEVSDSDHDGRINYDEFVAMMR
430.31	1717.23	1716.81	0.42	0	18	60	1	EHQQPQFMTSLNIK + Deamidation (NQ); Oxidation (M)
637.57	2546.26	2546.06	0.20	0	18	42	1	SNCXHSNMYLHFPWHVLMYGV + Deamidation (NQ)
637.55	2546.16	2546.37	-0.21	2	18	43	1	QSLSPKIQGKLTCLHVPFVSNHL + Deamidation (NQ)
637.54	2546.14	2546.37	-0.23	2	18	43	1	QSLSPKIQGKLTCLHVPFVSNHL + Deamidation (NQ)
676.49	1350.97	1350.65	0.32	0	17	81	1	QNVLAPSGPGPLCP + 2 Deamidation (NQ)
434.91	867.80	867.45	0.36	0	17	84	1	ISPVSQTH
602.46	1202.90	1202.67	0.23	1	17	1e+002	1	ASIEQILAKCK
563.63	1687.87	1687.98	-0.10	2	17	88	1	RIFLSVQFPLPSKR + Deamidation (NQ)
430.31	1287.92	1287.57	0.35	1	16	1.1e+002	1	HQKLXFGCTSR + Deamidation (NQ)
692.50	1382.99	1382.75	0.24	2	16	1.1e+002	1	NGSKTKIPQNAPK + Deamidation (NQ)
637.54	1273.06	1273.56	-0.50	0	16	1.1e+002	1	FNGVTSSSENYR + Deamidation (NQ)
563.63	1125.25	1125.41	-0.16	1	16	1.2e+002	1	QMMRFMFC + Deamidation (NQ); 2 Oxidation (M)
524.39	1046.76	1046.41	0.35	0	16	1.3e+002	1	AYGDCNTR + Deamidation (NQ)
434.90	1301.68	1301.63	0.04	0	16	1.2e+002	1	TGISNQiANDNR
457.43	1825.69	1825.91	-0.22	2	16	1e+002	1	NTGALNDFRVHRAQPK + 3 Deamidation (NQ)
742.55	2224.63	2224.14	0.49	0	15	96	1	YGSTGSLLVIQGNTMDLTINK
637.56	3182.74	3182.48	0.26	2	15	59	1	GMDVCITTAQTDKEAYKLLALMGMPFR + Deamidation (NQ); 3 Oxidation (M)
426.37	1276.09	1275.61	0.47	2	14	1.9e+002	1	TYSGCHLRRSP
426.37	850.72	850.45	0.27	1	14	2.1e+002	1	YTLIRDA
637.55	3182.70	3182.63	0.07	1	13	84	1	QRLPNICLLPMVSLQVSAIQQWTCPS + Deamidation (NQ); Oxidation (M)
453.76	905.51	905.48	0.03	0	13	2.5e+002	1	GGVGHAGPVR
637.54	3182.67	3182.54	0.13	2	13	91	1	PNLMNQNHPILMPCNHHTLIPNNRQVR + 5 Deamidation (NQ)
481.34	960.67	960.44	0.23	1	13	2.7e+002	1	RGGGGTDEGR
457.43	912.84	912.43	0.41	1	13	2.2e+002	1	SGKGQPPGDA
430.31	2146.54	2146.99	-0.45	2	12	1.9e+002	1	TRASVTYLLYRXDSNYVD + Deamidation (NQ)
457.43	1369.26	1369.64	-0.38	0	12	2.6e+002	1	ASNLASFTNSLFP + 2 Deamidation (NQ)
483.20	1446.58	1446.88	-0.30	2	12	2.7e+002	1	LHRPTNKIIAKR + Deamidation (NQ)
523.36	1044.70	1044.51	0.19	0	11	3.5e+002	1	PQNGTSLNIT + Deamidation (NQ)
430.31	858.62	858.36	0.26	0	11	4e+002	1	HCSHGYSR

457.43	2282.11	2282.27	-0.16	1	11	2.3e+002	1	ANLISYLAEMILFCIIKVV + Deamidation (NQ); Oxidation (M)
505.18	1008.34	1008.40	-0.06	0	11	3.7e+002	1	PDYGCSDPR
426.37	2126.81	2127.17	-0.36	1	11	2.8e+002	1	TLQAITILRFLPNNIQNR + 3 Deamidation (NQ)
415.29	828.56	828.38	0.18	2	9	5.7e+002	1	CRRSHGN
483.20	964.39	964.50	-0.12	0	9	5.6e+002	1	SYHFTLVV
459.35	916.68	916.46	0.22	1	9	6.6e+002	1	AIADNREK + Deamidation (NQ)
483.19	1446.53	1446.75	-0.22	2	9	5.6e+002	1	HLFHTGHRRR
563.63	2813.12	2813.37	-0.24	2	9	3.2e+002	1	SSMIEDVAAVAGNGDDGLRIRYFVK + Oxidation (M)
483.19	964.36	964.51	-0.15	1	9	6.7e+002	1	LGPATNHRV + Deamidation (NQ)
483.19	1928.71	1929.00	-0.29	1	8	5.4e+002	1	APPSKSDVPNSFPALVFR + Deamidation (NQ)
483.20	2410.97	2411.31	-0.34	2	7	6.1e+002	1	TTSLEIQPRKSPHICPQITSS
483.20	1928.77	1928.82	-0.05	1	6	8.8e+002	1	SFDGAGAADGGAYGGEQSRR + Deamidation (NQ)
483.19	2410.89	2411.20	-0.31	1	6	7.5e+002	1	IVVVHQFHNPLFCWRSQVWS + Deamidation (NQ)
563.63	2250.50	2250.23	0.27	1	5	9.2e+002	1	LLSNTSMSELLPVSQTRVFLK + Deamidation (NQ); Oxidation (M)

Table 2 supplementary data: Mascot Search Results using the *Viridiplantae* database

Search Parameters

Type of search	: MS/MS Ion Search	Peptide Mass Tolerance	: ± 0.5 Da
Enzyme	: Trypsin	Fragment Mass Tolerance	: ± 0.4 Da
Variable modifications	: Deamidation (NQ), Oxidation (M)	Max Missed Cleavages	: 2
Mass values	: Monoisotopic	Instrument type	: ESI-TRAP
Protein Mass	: Unrestricted	Number of queries	: 72

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 43 indicate identity or extensive homology ($p < 0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

1 Q401B7_PANGI **Mass: 38792** **Score: 60** **Queries matched: 1**
 Peroxidase.- *Panax ginseng* (Korean ginseng).

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
795.60	1589.19	1588.82	0.37	0	60	0.0012	1	K.MGQLSVLTGTQGEIR.G

2 Q8SA59_HELAN **Mass: 60932** **Score: 54** **Queries matched: 2**
 Carbohydrate oxidase.- *Helianthus annuus* (Common sunflower).

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
457.90	913.80	913.56	0.24	0	45	0.039	1	R.NLVTLLNK.D
676.49	1350.97	1350.73	0.24	0	9	1.2e+002	3	R.AIFPTLYLGNSR.N

Proteins matching the same set of peptides:

CAC07597 **Mass: 60913** **Score: 54** **Queries matched: 2**

Sequence 15 from Patent WO9950428.- *Helianthus annuus* (Common sunflower).

CAB42582 **Mass: 59948** **Score: 54** **Queries matched: 2**

SEQUENCE 15 FROM PATENT WO9813478.- *Helianthus annuus* (Common sunflower).

CAB42584 **Mass: 59967** **Score: 54** **Queries matched: 2**

SEQUENCE 19 FROM PATENT WO9813478.- *Helianthus annuus* (Common sunflower).

3 Q5QQS6_ZINEL **Mass: 14015** **Score: 51** **Queries matched: 1**
 Putative peroxidase (EC 1.11.1.7) (Fragment).- *Zinnia elegans* (Zinnia).

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
637.48	1272.94	1272.72	0.22	0	51	0.008	1	R.AQAFVIENLR.R

Peptide matches not assigned to protein hits: (no details means no match)

Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
537.38	1072.74	1072.50	0.24	0	34	0.35	1	YYVDLMNR
530.90	1059.79	1059.47	0.32	1	34	0.6	1	DPDNINNKK + 3 Deamidation (NQ)
595.95	1189.89	1189.60	0.29	0	32	0.69	1	QVLQTLCEQK + Deamidation (NQ)
449.31	896.61	896.37	0.24	0	29	0.78	1	MTVQNMR + 2 Deamidation (NQ); Oxidation (M)
516.41	1030.80	1030.57	0.23	1	26	2.2	1	VINASSPSKK + Deamidation (NQ)
692.50	1382.99	1382.68	0.32	1	25	2.7	1	EVEAKFMVSSEK
637.63	2546.48	2546.16	0.32	0	24	4.7	1	TEYTAYVSEGLGNIQNWNEVMK + Deamidation (NQ)
742.55	2224.63	2225.09	-0.45	2	23	5	1	CGPMHGVPVLLKDNMATRDR + Oxidation (M)
637.56	3182.74	3182.58	0.16	2	22	5.2	1	NRYREFIAEVLMMNPGLLILDEGHNPR + 3 Deamidation (NQ)
637.49	1272.96	1272.67	0.30	0	19	12	1	NGDSLAITVINR + Deamidation (NQ)
637.57	2546.26	2546.21	0.06	0	19	15	1	IHINQLCNHSFYFLGYFSSVR + 2 Deamidation (NQ)
637.63	3183.10	3183.42	-0.32	2	19	13	1	AEAIRMEEDEGEEKGNFSLGWQGHGIF + Deamidation (NQ)
637.54	2546.12	2546.21	-0.08	0	18	16	1	IHINQLCNHSFYFLGYFSSVR + 2 Deamidation (NQ)
637.56	2546.19	2546.43	-0.24	0	18	19	1	QGLDLLLAILVEDKPISLAPNSAR + Deamidation (NQ)
434.91	867.80	867.52	0.29	0	17	12	1	LSPVSPLR
637.57	1909.70	1910.06	-0.36	1	17	29	1	NLIPGPRGFPLVGSMSLR
637.54	1909.60	1909.96	-0.35	1	16	31	1	DLPELEGFFLGKNEFR
637.55	1909.62	1909.96	-0.34	1	16	34	1	DLPELEGFFLGKNEFR
637.63	1909.86	1909.89	-0.03	1	16	34	1	NPPRDRPQSLTNNGGQR + 4 Deamidation (NQ)
637.56	1909.64	1910.02	-0.38	2	16	36	1	FFKDP LIHYVRYQ GK
637.54	2546.14	2546.29	-0.15	1	16	29	1	LNPSMVRSQMLENAFIIDNPIK + Deamidation (NQ); Oxidation (M)
457.43	1825.69	1825.76	-0.07	0	16	29	1	DTGSPFMMDAIYTAMK + 3 Oxidation (M)
637.55	2546.16	2546.29	-0.13	1	16	30	1	LNPSMVRSQMLENAFIIDNPIK + Deamidation (NQ); Oxidation (M)
637.57	3182.83	3182.58	0.24	2	15	26	1	NRYREFIAEVLMMNPGLLILDEGHNPR + 3 Deamidation (NQ)
506.32	1010.63	1010.47	0.16	0	15	29	1	CQINSFIGK + 2 Deamidation (NQ)
637.54	1909.59	1909.90	-0.31	0	14	49	1	TNVAMLTILQLEMNR + 4 Deamidation (NQ); 2 Oxidation (M)
737.86	2210.55	2210.84	-0.29	0	14	40	1	YMTMDSMTNDELSSNPK + 2 Deamidation (NQ)
637.55	3182.70	3182.66	0.04	2	13	41	1	ENQRLFLFLVNSHVYECESVLVFLRK + Deamidation (NQ)
637.54	3182.67	3182.66	0.01	2	13	42	1	ENQRLFLFLVNSHVYECESVLVFLRK + Deamidation (NQ)
637.57	1273.13	1273.59	-0.46	0	13	48	1	IVGCGGFGMVYR + Oxidation (M)
457.43	912.84	912.49	0.35	0	13	35	1	ADSSPPLVK
426.37	850.72	850.38	0.34	0	13	39	1	YIQQDNA
637.54	1273.06	1272.64	0.42	1	13	54	1	LDGRHNLFAK
637.63	1273.24	1273.72	-0.48	0	13	57	1	IIFMLQLPGAR + Oxidation (M)
637.54	3182.66	3182.58	0.07	2	12	51	1	NRYREFIAEVLMMNPGLLILDEGHNPR + 3 Deamidation (NQ)
426.37	1276.09	1275.63	0.46	1	12	62	1	HQGGLQPEPRR + 2 Deamidation (NQ)
457.43	1369.26	1369.67	-0.40	1	12	62	1	GSKALISEYGCSR
434.90	1301.68	1301.72	-0.04	1	12	60	1	TLGLSVEADKAAK
453.76	905.51	905.42	0.09	0	12	64	1	NPNVASFR + 2 Deamidation (NQ)
481.34	960.67	960.52	0.15	1	12	67	1	ERVSLVR
676.49	1350.97	1350.75	0.22	2	12	67	1	RHGMHFRVLAK
457.43	2282.11	2282.04	0.07	2	12	76	1	ANSMASAKVWENNQGAESKIK + 4 Deamidation (NQ); Oxidation (M)

426.37	1701.45	1701.89	-0.44	1	11	72	1	ISNKIGQLSNSNGQIK + 2 Deamidation (NQ)
426.37	2126.81	2127.13	-0.32	2	11	83	1	LTKREINAVQPDPDTPQFLR + 2 Deamidation (NQ)
602.46	1202.90	1202.59	0.31	0	11	80	1	EAIHQIANDSR
505.18	1008.34	1008.52	-0.18	0	11	63	1	LVGYISSDR
523.36	1044.70	1044.39	0.31	0	11	94	1	QCEEGFGMK + Deamidation (NQ); Oxidation (M)
430.31	1287.92	1287.61	0.31	0	11	89	1	YLEVNFQFNGK + Deamidation (NQ)
459.35	916.68	916.48	0.20	0	11	89	1	LAANMLQR + Deamidation (NQ)
524.39	1046.76	1046.44	0.33	0	10	1e+002	1	QYDAMEFK + Oxidation (M)
563.63	2813.12	2813.47	-0.35	1	9	1.2e+002	1	LGVPPVDLVLSSPWLPLDHRCLCQR + Deamidation (NQ)
430.31	1717.23	1716.89	0.34	0	9	1.6e+002	1	NVVVYGPALWATGTNR
483.20	1446.58	1446.70	-0.12	0	8	1.6e+002	1	HIGVQSACVFSSGR
430.31	858.62	858.43	0.18	0	8	1.6e+002	1	AHTDFIR
563.63	1125.25	1125.67	-0.42	1	8	1.2e+002	1	RLPVPAFQAK
637.56	1273.10	1272.60	0.50	2	8	1.6e+002	1	XLARXPXQTVR
415.29	828.56	828.49	0.07	1	8	1.6e+002	1	IGRSIQR
563.63	1687.87	1687.93	-0.05	2	7	1.8e+002	1	EIQEVKERLAAGFAK
483.19	1446.53	1446.86	-0.33	2	7	2.4e+002	1	KNFPLVTLLKMK + Oxidation (M)
637.54	1273.07	1272.60	0.47	2	7	2.1e+002	1	XLARXPXQTVR
637.55	1273.08	1272.60	0.48	2	7	2.1e+002	1	XLARXPXQTVR
430.31	2146.54	2146.14	0.40	2	6	2.3e+002	1	HLIMRFNSLTLKGSHTK + Deamidation (NQ); Oxidation (M)
483.20	2410.97	2411.13	-0.17	1	5	3e+002	1	LHTSDGLEFAFLGESNGTKEMK + Deamidation (NQ)
483.19	964.36	964.57	-0.21	2	5	2.8e+002	1	IHREVR
483.20	964.39	964.58	-0.20	1	5	2.8e+002	1	LLEAKVHR
563.63	2250.50	2250.03	0.47	2	5	3.8e+002	1	ILKSSRMEEPDCPEGSVSDR + Oxidation (M)
483.20	1928.77	1928.95	-0.18	1	4	4.1e+002	1	HRLQSGNGLLCGGNFLNK + 2 Deamidation (NQ)
483.19	2410.89	2411.09	-0.19	2	4	3.6e+002	1	FCNGEMMGRKIELHAATNGCTK + Deamidation (NQ)
483.19	1928.71	1928.95	-0.24	1	2	7.2e+002	1	HRLQSGNGLLCGGNFLNK + 2 Deamidation (NQ)