

MASCOT Search Results

Protein View: 349

Prot-1 [agafab 20160316]

Database: small-www
Score: 9207
Nominal mass (M_r): 39892
Calculated pI: 7.90

Sequence similarity is available as [an NCBI BLAST search of 349 against nr](#).

Search parameters

MS data file: \\212.87.29.88\orbital\FA\03-marzec2016\60324460bro_Prot-1.raw
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: [Methylthio \(C\)](#)
Variable modifications: [Oxidation \(M\)](#)

Protein sequence coverage: 35%

Matched peptides shown in ***bold red***.

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1 RAFFHNKGGN DIIPNSYIVV MKDGISTQEF ESHISSVSAT HAKRSTELVG
51 HKDSFNINGW RAYNGHFDAA TLESILNDDN VKYVEHDRVV KISALTTQPN
101 APSWGLGRIS HRSPGNKDFV YDDTAGQGIT IYGVDTGIDI NHPDFGGRAR
151 WGTNTVDNAN NDGHGHGTHT AGTFAGNAYG IAKKASVVAV KVLSASGSGS
201 NAGVIKGIDW CVTDARSKGA LGKAALNLSL GGGFNQATND AVTRAQTAGI
251 FVAVAAGNDN KDARNYSPAS APAVCTVASS TIDDQKSSFS NWGSIVDIYA
301 PGSNIISDAP GGGVRTMSGT SMASPHVCGA GAAMLAQGVP VGQVCDRLKQ
351 IGNAVVRNPG TSTTNRLLYN GSGQGSHHHH HH

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Unformatted sequence string: [382 residues](#) (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Query	Star	En	Observe	Mr (expt)	Mr (calc)	ppm	M _e ^{Score}	Expect	Rank	U	Peptide
4310	109	-11 7	498.272 6	994.530 6	994.530 8	-0.16	177	2.1e-08	1Score > 13	indicat es	UR.ISHRSPGNK.D
4311	109	-11 7	332.517 5	994.530 7	994.530 8	-0.14	137	0.00021	1Score > 13	indicat es	UR.ISHRSPGNK.D

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Score} e	Expect	Rank	U	Peptide
2487 <u>0</u>	151	-18 3	832.380 0	3325.49 09	3325.48 86	0.72	047	2.1e- 05	indicat es	U	R.WGTNTVDNANNDGHHGHGHTHTAGTFAGNAYG IAK.K
1Score > 13 identit y											
2487 <u>1</u>	151	-18 3	832.380 1	3325.49 15	3325.48 86	0.88	045	2.9e- 05	indicat es	U	R.WGTNTVDNANNDGHHGHGHTHTAGTFAGNAYG IAK.K
1Score > 13 identit y											
2487 <u>3</u>	151	-18 3	832.380 3	3325.49 23	3325.48 86	1.11	044	4.4e- 05	indicat es	U	R.WGTNTVDNANNDGHHGHGHTHTAGTFAGNAYG IAK.K
1Score > 13 identit y											
2487 <u>4</u>	151	-18 3	832.380 9	3325.49 47	3325.48 86	1.83	056	2.8e- 06	indicat es	U	R.WGTNTVDNANNDGHHGHGHTHTAGTFAGNAYG IAK.K
1Score > 13 identit y											
2487 <u>5</u>	151	-18 3	832.381 1	3325.49 52	3325.48 86	1.99	042	7.1e- 05	indicat es	U	R.WGTNTVDNANNDGHHGHGHTHTAGTFAGNAYG IAK.K
1Score > 13 identit y											

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1519	184	-19 1	401.263 6	800.512 7	800.512 0	0.86	186	2.6e- 09	1Score > 13 indicat es identit y		UK.KASVVAVK.V
9860	192	-20 6	673.868 3	1345.72 20	1345.72 01	1.37	0148	1.5e- 15	1Score > 13 indicat es identit y		UK.VLSASGSGSNAGVIK.G
9861	192	-20 6	673.868 5	1345.72 24	1345.72 01	1.69	0126	2.3e- 13	1Score > 13 indicat es identit y		UK.VLSASGSGSNAGVIK.G
1903 9	224	-24 4	697.357 3	2089.05 00	2089.05 52	-2.49	042	6.8e- 05	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1904 0	224	-24 4	697.357 6	2089.05 09	2089.05 52	-2.09	038	0.0001 6	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M _e Score	Expect	Rank	U	Peptide
1904 <u>2</u>	224	-24 4	1045.53 30	2089.05 14	2089.05 52	-1.81	0117	2.1e- 12	13	indicates identity	UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>3</u>	224	-24 4	1045.53 34	2089.05 22	2089.05 52	-1.42	0112	6.1e- 12	13	indicates identity	UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>4</u>	224	-24 4	697.358 5	2089.05 37	2089.05 52	-0.71	032	0.0006 3	13	indicates identity	UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>5</u>	224	-24 4	697.358 9	2089.05 49	2089.05 52	-0.14	0112	7e-12	13	indicates identity	UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>6</u>	224	-24 4	1045.53 48	2089.05 50	2089.05 52	-0.083	0107	2.1e- 11	13	indicates identity	UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Score} e	Expect	Rank	U	Peptide
1904 <u>7</u>	224	-24 4	697.359 1	2089.05 56	2089.05 52	0.16	0122	6.2e- 13	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>8</u>	224	-24 4	1045.53 51	2089.05 56	2089.05 52	0.20	0180	1e-18	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1904 <u>9</u>	224	-24 4	697.359 2	2089.05 59	2089.05 52	0.31	0117	1.8e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>0</u>	224	-24 4	697.359 3	2089.05 62	2089.05 52	0.46	082	6.1e- 09	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>1</u>	224	-24 4	1045.53 54	2089.05 62	2089.05 52	0.49	0110	1.1e- 11	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1905 <u>2</u>	224	-24 4	697.359 5	2089.05 65	2089.05 52	0.62	0109	1.4e- 11	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>3</u>	224	-24 4	1045.53 56	2089.05 66	2089.05 52	0.68	0180	9.5e- 19	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>4</u>	224	-24 4	697.359 5	2089.05 67	2089.05 52	0.69	056	2.6e- 06	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>5</u>	224	-24 4	1045.53 58	2089.05 70	2089.05 52	0.87	0180	1e-18	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1905 <u>6</u>	224	-24 4	697.359 9	2089.05 77	2089.05 52	1.20	0108	1.7e- 11	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	MScore	Expect	Rank	U	Peptide
19057	224	249	697.359	2089.0578	2089.0552	1.21	0119	1.1e-12	13		UK.AALNLSLGGGFNQATNDAVTR.A
											1Score > 13 indicates identity
19058	224	249	697.359	2089.0578	2089.0552	1.25	0107	2.2e-11	13		UK.AALNLSLGGGFNQATNDAVTR.A
											1Score > 13 indicates identity
19059	224	2462	1045.53	2089.0578	2089.0552	1.26	0176	2.6e-18	13		UK.AALNLSLGGGFNQATNDAVTR.A
											1Score > 13 indicates identity
19060	224	249	697.359	2089.0580	2089.0552	1.33	0121	7.5e-13	13		UK.AALNLSLGGGFNQATNDAVTR.A
											1Score > 13 indicates identity
19061	224	2463	1045.53	2089.0580	2089.0552	1.35	089	1.2e-09	13		UK.AALNLSLGGGFNQATNDAVTR.A
											1Score > 13 indicates identity

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1906 <u>2</u>	224	-24 4	1045.53 63	2089.05 80	2089.05 52	1.35	0160	9.7e- 17	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>3</u>	224	-24 4	1045.53 64	2089.05 82	2089.05 52	1.45	0111	8.6e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>4</u>	224	-24 4	697.360 1	2089.05 83	2089.05 52	1.48	0114	3.7e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>5</u>	224	-24 4	697.360 1	2089.05 85	2089.05 52	1.56	0116	2.4e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>6</u>	224	-24 4	697.360 2	2089.05 88	2089.05 52	1.71	0116	2.3e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1906 <u>7</u>	224	-24 4	697.360 2	2089.05 89	2089.05 52	1.77	0111	7.4e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>8</u>	224	-24 4	1045.53 68	2089.05 90	2089.05 52	1.83	052	6.7e- 06	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1906 <u>9</u>	224	-24 4	1045.53 68	2089.05 90	2089.05 52	1.83	0180	1e-18	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>1</u>	224	-24 4	697.360 5	2089.05 96	2089.05 52	2.07	040	9.3e- 05	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>2</u>	224	-24 4	1045.53 71	2089.05 96	2089.05 52	2.12	0161	8.7e- 17	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1907 <u>3</u>	224	-24 4	1045.53 75	2089.06 04	2089.05 52	2.50	0170	1.1e- 17	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>4</u>	224	-24 4	1045.53 75	2089.06 04	2089.05 52	2.50	0176	2.6e- 18	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>5</u>	224	-24 4	1045.53 75	2089.06 04	2089.05 52	2.50	0164	4.4e- 17	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>6</u>	224	-24 4	697.360 8	2089.06 05	2089.05 52	2.55	0102	6.4e- 11	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>7</u>	224	-24 4	697.360 8	2089.06 05	2089.05 52	2.55	095	3.4e- 10	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	MScore	Expect	Rank	U	Peptide
1907 <u>8</u>	224	-24 4	1045.53 76	2089.06 06	2089.05 52	2.60	0104	3.7e- 11	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1907 <u>9</u>	224	-24 4	1045.53 78	2089.06 10	2089.05 52	2.79	0173	4.9e- 18	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>0</u>	224	-24 4	697.361 0	2089.06 12	2089.05 52	2.86	072	6.5e- 08	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>1</u>	224	-24 4	697.361 0	2089.06 13	2089.05 52	2.89	0109	1.2e- 11	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>2</u>	224	-24 4	697.361 1	2089.06 14	2089.05 52	2.95	098	1.4e- 10	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1908 <u>3</u>	224	-24 4	1045.53 81	2089.06 16	2089.05 52	3.08	0168	1.4e- 17	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>4</u>	224	-24 4	1045.53 85	2089.06 24	2089.05 52	3.46	085	3.5e- 09	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>5</u>	224	-24 4	1045.53 85	2089.06 24	2089.05 52	3.46	0114	4.4e- 12	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>6</u>	224	-24 4	697.361 5	2089.06 26	2089.05 52	3.52	0127	1.9e- 13	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1908 <u>7</u>	224	-24 4	1045.53 86	2089.06 26	2089.05 52	3.55	0159	1.2e- 16	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	MScore	Expect	Rank	U	Peptide
1908	224	-24 4	697.361 7	2089.06 32	2089.05 52	3.80	095	3.4e- 10	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1908	224	-24 4	1045.53 89	2089.06 32	2089.05 52	3.84	0161	8.5e- 17	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1909	224	-24 4	697.361 8	2089.06 35	2089.05 52	3.95	0105	3.4e- 11	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1909	224	-24 4	697.361 9	2089.06 38	2089.05 52	4.10	090	9.3e- 10	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A
1909	224	-24 4	1045.53 97	2089.06 48	2089.05 52	4.61	0152	6.3e- 16	1Score > 13 indicates identity		UK.AALNLSLGGGFNQATNDAVTR.A

Quer y	Star t	En d	Observe d	Mr(expt)	Mr(calc)	ppm	M ^{Scor} e	Expect	Rank	U	Peptide
1909 <u>3</u>	224	-24 4	1045.54 04	2089.06 62	2089.05 52	5.28	0170	9.3e- 18	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1909 <u>4</u>	224	-24 4	697.363 2	2089.06 76	2089.05 52	5.94	082	6.3e- 09	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1909 <u>5</u>	224	-24 4	1045.54 31	2089.07 16	2089.05 52	7.86	0142	6.6e- 15	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
1909 <u>6</u>	224	-24 4	1045.54 49	2089.07 52	2089.05 52	9.59	0135	3.3e- 14	1Score > 13 indicat es identit y		UK.AALNLSLGGGFNQATNDAVTR.A
2371 <u>1</u>	287	-31 5	1462.21 28	2922.41 10	2922.41 48	-1.29	0148	1.7e- 15	1Score > 13 indicat es identit y	U T	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.

Query	Star	En	Observe	Mr(expt)	Mr(calc)	ppm	M ^{Score}	Expect	Rank	U	Peptide
2371 <u>2</u>	287	-31 5	1462.21 34	2922.41 22	2922.41 48	-0.88	0137	2.2e- 14	indicat es	U _T	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.
									1Score > 13 identit y		
2371 <u>3</u>	287	-31 5	1462.21 51	2922.41 56	2922.41 48	0.29	0127	1.9e- 13	indicat es	U _T	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.
									1Score > 13 identit y		
2371 <u>4</u>	287	-31 5	975.146 8	2922.41 87	2922.41 48	1.33	0128	1.6e- 13	indicat es	U _T	K.SSFSNWGSIVDIYAPGSNIISDAPGGGVR.
									1Score > 13 identit y		
6304	348	-35 7	549.342 6	1096.67 07	1096.67 17	-0.85	177	2.2e- 08	indicat es		UR.LKQIGNAVVR.N
									1Score > 13 identit y		
6305	348	-35 7	366.564 2	1096.67 07	1096.67 17	-0.84	194	4e-10	indicat es		UR.LKQIGNAVVR.N
									1Score > 13 identit y		

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M _e Score	Expect	Rank	U	Peptide
6306	348	-35 7 7	549.342	1096.67 07	1096.67 17	-0.83	174	3.9e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6307	348	-35 7 2	366.564	1096.67 09	1096.67 17	-0.73	194	4e-10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6308	348	-35 7 7	549.342	1096.67 09	1096.67 17	-0.67	177	2.2e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6309	348	-35 7 3	366.564	1096.67 12	1096.67 17	-0.46	194	3.9e- 10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6310	348	-35 7 3	366.564	1096.67 12	1096.67 17	-0.43	194	3.9e- 10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N

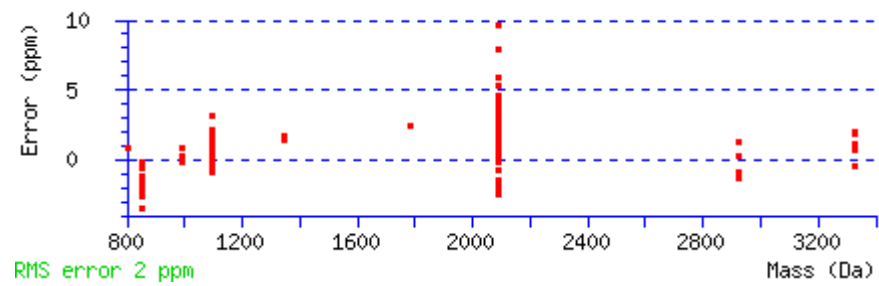
Query	Start	End	Observed	Mr(expt)	Mr(calc)	ppm	M _e Score	Expect	Rank	U	Peptide
6311	348	-35 7 4	366.564	1096.67 13	1096.67 17	-0.37	194	3.9e- 10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6312	348	-35 7 0	549.343	1096.67 15	1096.67 17	-0.12	174	3.8e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6313	348	-35 7 1	549.343	1096.67 17	1096.67 17	0.006	176	2.3e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6314	348	-35 7 1	549.343	1096.67 17	1096.67 17	0.061	177	2.2e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6315	348	-35 7 6	366.564	1096.67 21	1096.67 17	0.37	194	3.9e- 10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M _e Score	Expect	Rank	U	Peptide
6316	348	-35 7 3	549.343	1096.67 21	1096.67 17	0.44	175	2.8e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6317	348	-35 7 7	366.564	1096.67 23	1096.67 17	0.61	194	4e-10	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6318	348	-35 7 6	549.343	1096.67 25	1096.67 17	0.81	174	3.8e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6319	348	-35 7 7	549.343	1096.67 29	1096.67 17	1.12	174	4.2e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6320	348	-35 7 9	549.343	1096.67 33	1096.67 17	1.47	166	2.8e- 07	1Score > 13 indicates identity		UR.LKQIGNAVVR.N

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M _e Score	Expect	Rank	U	Peptide
6322	348	-35 7 9	549.343	1096.67 33	1096.67 17	1.54	174	4.3e- 08	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6323	348	-35 7 0	549.344	1096.67 35	1096.67 17	1.65	168	1.5e- 07	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6324	348	-35 7 3	549.344	1096.67 41	1096.67 17	2.19	155	3.4e- 06	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
6325	348	-35 7 8	549.344	1096.67 50	1096.67 17	3.09	149	1.1e- 05	1Score > 13 indicates identity		UR.LKQIGNAVVR.N
2210	350	-35 7 1	428.752	855.489 7	855.492 6	-3.46	056	2.5e- 06	1Score > 13 indicates identity		UK.QIGNAVVR.N

Query	Start	End	Observed	Mr(expt)	Mr(calc)	ppm	M _e Score	Expect	Rank	U	Peptide
2213	350	-35 7 5	428.752	855.490 4	855.492 6	-2.66	056	2.5e- 06	1Score > 13 indicates identity	UK.QIGNAVVR.N	
2214	350	-35 7 5	428.752	855.490 4	855.492 6	-2.59	056	2.5e- 06	1Score > 13 indicates identity	UK.QIGNAVVR.N	
2215	350	-35 7 5	428.752	855.490 5	855.492 6	-2.45	056	2.5e- 06	1Score > 13 indicates identity	UK.QIGNAVVR.N	
2217	350	-35 7 7	428.752	855.490 8	855.492 6	-2.10	051	8.6e- 06	1Score > 13 indicates identity	UK.QIGNAVVR.N	
2218	350	-35 7 9	428.752	855.491 1	855.492 6	-1.75	056	2.6e- 06	1Score > 13 indicates identity	UK.QIGNAVVR.N	

Query	Start	End	Observed	Mr (expt)	Mr (calc)	ppm	M _e Score	Expect	Rank	U	Peptide
2226	350	-35 7 4	428.753	855.492 1	855.492 6	-0.58	058	1.7e- 06	indicat es identit y	UK.QIGNAVVR.N	1Score > 13
2227	350	-35 7 4	428.753	855.492 3	855.492 6	-0.37	053	4.9e- 06	indicat es identit y	UK.QIGNAVVR.N	1Score > 13
2228	350	-35 7 5	428.753	855.492 4	855.492 6	-0.23	058	1.5e- 06	indicat es identit y	UK.QIGNAVVR.N	1Score > 13
16290	350	-36 6 7	595.651	1783.93 32	1783.92 89	2.41	165	3.2e- 07	indicat es identit y	UK.QIGNAVVRNPGTSTTNR.L	1Score > 13



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