Summary

1. Notes

2. Result Statistics

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

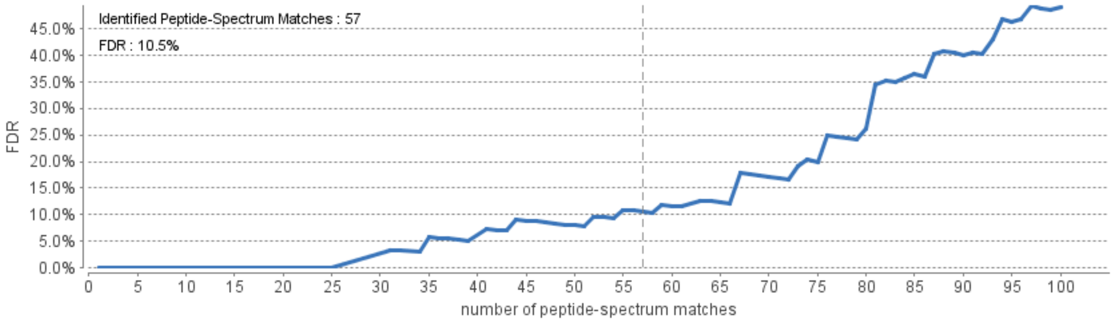
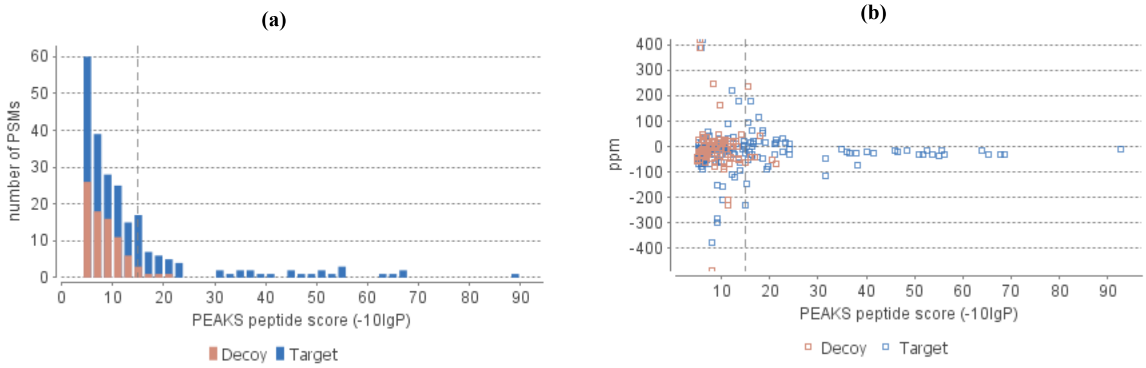
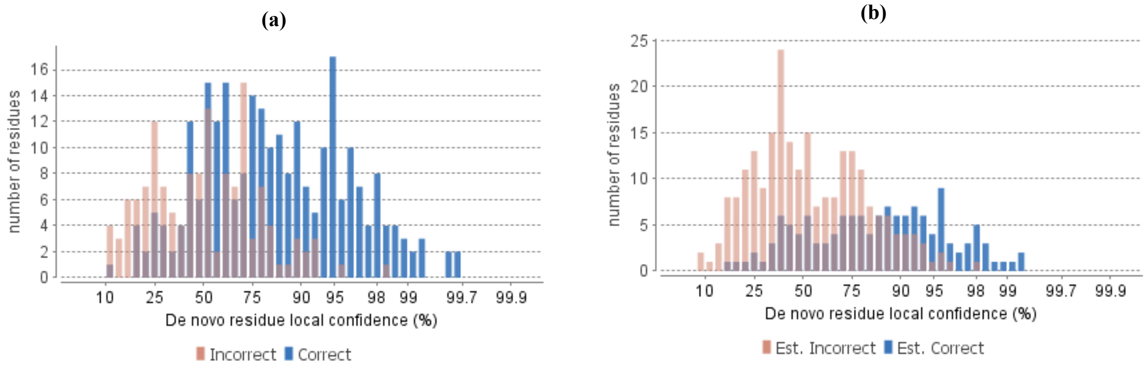


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.


(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1340
# of MS/MS Scans	997

Table 2. Result filtration parameters.

Peptide -10lgP	≥15
Protein -10lgP	≥20
Proteins unique peptides	≥0
De novo ALC Score	≥50%

Table 3. Statistics of filtered result.

Peptide-Spectrum Matches	57
Peptide Sequences	53

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Deamidation	.98	2	Q
Pyro-glu from Q	-17.03	1	N-term

Protein Groups	22
Proteins	124
Proteins (#Unique Peptides)	0 (>2); 1 (=2); 104 (=1);
FDR (Peptide-Spectrum Matches)	10.5%
FDR (Peptide Sequences)	11.3%
FDR (Protein)	3.2%
De Novo Only Spectra	30

3. Experiment Control

Figure 4. Precursor mass error of peptide-spectrum matches (PSM) in filtered result. **(a)** Distribution of precursor mass error in ppm; **(b)** Scatterplot of precursor m/z versus precursor mass error in ppm.

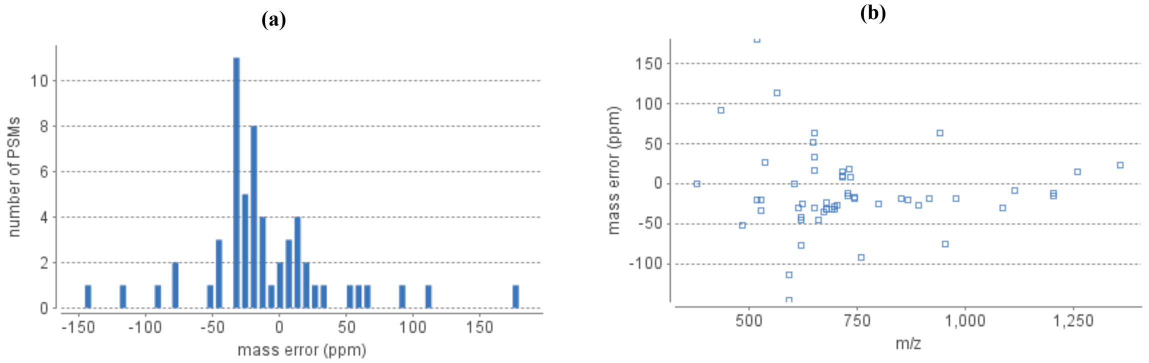


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Q-TOF	0	0	0	0	53

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fragment ion tolerance: 0.1
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 53
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: D_1_180917.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: Quadrupole
MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	4504	tr|A0A023ETG9|A0A023ETG9_AEDAL	128.71	10	4	1	N	49690	Tubulin beta chain OS=Aedes albopictus PE=2 SV=1
1	4494	tr|A0A0P5ZYN7|A0A0P5ZYN7_9CRUS	126.44	20	6	1	Y	50152	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4493	tr|A0A0P6A5L5|A0A0P6A5L5_9CRUS	126.44	20	6	1	Y	48456	Tubulin alpha chain (Fragment) OS=Daphnia magna PE=3 SV=1
4	4505	tr|T1GUQ6|T1GUQ6_MEGSC	123.64	12	4	0	N	42846	Tubulin beta chain OS=Megaselia scalaris PE=3 SV=1
4	4506	tr|R4G588|R4G588_RHOPR	123.64	11	4	0	N	48432	Tubulin beta chain (Fragment) OS=Rhodnius prolixus PE=2 SV=1
4	4509	tr|C7SAG3|C7SAG3_9MUSC	123.64	10	4	0	N	49870	Tubulin beta chain OS=Anastrepha ludens PE=3 SV=1
4	4508	tr|A0A023FK66|A0A023FK66_9ACAR	123.64	10	4	0	N	49838	Tubulin beta chain OS=Amblyomma cajennense PE=2 SV=1
4	4507	tr|C7SAG4|C7SAG4_BACDO	123.64	10	4	0	N	49870	Tubulin beta chain OS=Bactrocera dorsalis GN=TBB2 PE=3 SV=1
4	4513	tr|A0A0P5E5N2|A0A0P5E5N2_9CRUS	123.64	10	4	0	N	50179	Tubulin beta chain OS=Daphnia magna GN=APZ42_016801 PE=3 SV=1
4	4512	tr|A0A069DTP4|A0A069DTP4_9HEMI	123.64	10	4	0	N	50257	Tubulin beta chain OS=Panstrongylus megistus PE=2 SV=1
4	4511	tr|B4QE31|B4QE31_DROSI	123.64	10	4	0	N	50147	Tubulin beta chain OS=Drosophila simulans GN=Dsim\GD25319 PE=3 SV=1
4	4510	tr|V9IK78|V9IK78_APICE	123.64	10	4	0	N	50175	Tubulin beta chain OS=Apis cerana GN=ACCB10461 PE=2 SV=1
4	4516	tr|A0A0J7L622|A0A0J7L622_LASNI	123.64	6	4	0	N	88812	Tubulin beta-1 chain OS=Lasius niger GN=RF55_1586 PE=3 SV=1
7	4525	tr|A0A0P5F7I2|A0A0P5F7I2_9CRUS	123.31	13	3	1	N	51108	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
total 124 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
7	4524	tr|A0A0P5YRH3|A0A0P5YRH3_9CRUS	123.31	14	3	1	N	47483	ATP synthase subunit beta (Fragment) OS=Daphnia magna PE=3 SV=1
7	4523	tr|A0A0P5RWN8|A0A0P5RWN8_9CRUS	123.31	14	3	1	N	45219	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4522	tr|A0A0P6FT42|A0A0P6FT42_9CRUS	123.31	14	3	1	N	44893	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4521	tr|A0A0N8D2L0|A0A0N8D2L0_9CRUS	123.31	16	3	1	N	41594	ATP synthase subunit beta (Fragment) OS=Daphnia magna PE=3 SV=1
7	4520	tr|Q6W4K6|Q6W4K6_DROSI	123.31	16	3	1	N	40608	ATP synthase subunit beta (Fragment) OS=Drosophila simulans GN=ATPsyn-beta PE=4 SV=1
7	4519	tr|D8VIP0|D8VIP0_HELME	123.31	17	3	1	N	37534	ATP synthase subunit beta (Fragment) OS=Heliconius melpomene melpomene PE=4 SV=1
7	4518	tr|G3KAV3|G3KAV3_HELNM	123.31	17	3	1	N	36677	ATP synthase subunit beta (Fragment) OS=Heliconius numata arcuella GN=ATPs PE=4 SV=1
7	4517	tr|G3KAY5|G3KAY5_HELNM	123.31	17	3	1	N	36677	ATP synthase subunit beta (Fragment) OS=Heliconius numata silvana GN=ATPs PE=4 SV=1
7	4540	tr|E0W1G3|E0W1G3_PEDHC	123.31	11	3	1	N	58998	ATP synthase subunit beta OS=Pediculus humanus subsp. corporis GN=8239544 PE=3 SV=1
7	4539	tr|A0A0P5T3L7|A0A0P5T3L7_9CRUS	123.31	11	3	1	N	57546	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4538	tr|A0A0P5BBW0|A0A0P5BBW0_9CRUS	123.31	11	3	1	N	57228	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4537	tr|A0A0P5UBV1|A0A0P5UBV1_9CRUS	123.31	11	3	1	N	57274	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4536	tr|A0A0P5EU29|A0A0P5EU29_9CRUS	123.31	11	3	1	N	57156	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4535	tr|A0A0P5BBX0|A0A0P5BBX0_9CRUS	123.31	11	3	1	N	56983	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4534	tr|A0A0J7KRQ1|A0A0J7KRQ1_LASNI	123.31	12	3	1	N	55523	ATP synthase subunit beta OS=Lasius niger GN=RF55_7041 PE=3 SV=1
7	4533	tr|Q1HPT1|Q1HPT1_BOMMO	123.31	12	3	1	N	54988	ATP synthase subunit beta OS=Bombyx mori GN=Atpsyn-beta PE=2 SV=1
7	4532	tr|I4DIU5|I4DIU5_PAPXU	123.31	12	3	1	N	54872	ATP synthase subunit beta OS=Papilio xuthus GN=RR46_14819 PE=2 SV=1
7	4531	tr|A0A1B0CLT6|A0A1B0CLT6_LUTLO	123.31	12	3	1	N	54969	ATP synthase subunit beta OS=Lutzomyia longipalpis PE=3 SV=1
7	4530	tr|A0A1I8NT76|A0A1I8NT76_STOCA	123.31	12	3	1	N	54485	ATP synthase subunit beta OS=Stomoxys calcitrans GN=106084826 PE=3 SV=1
7	4529	tr|A0A182FTY6|A0A182FTY6_ANOAL	123.31	12	3	1	N	53768	ATP synthase subunit beta OS=Anopheles albimanus PE=3 SV=1
7	4528	tr|E3XEC7|E3XEC7_ANODA	123.31	12	3	1	N	53768	ATP synthase subunit beta OS=Anopheles darlingi GN=AND_006288 PE=3 SV=1
7	4527	tr|A0A0P4WJ96|A0A0P4WJ96_9CRUS	123.31	12	3	1	N	53651	ATP synthase subunit beta OS=Daphnia magna PE=3 SV=1
7	4526	tr|A0A0P5ULZ6|A0A0P5ULZ6_9CRUS	123.31	12	3	1	N	52829	ATP synthase subunit beta (Fragment) OS=Daphnia magna PE=3 SV=1
2	4498	tr|A0A1V9X7H2|A0A1V9X7H2_9ACAR	115.10	16	5	0	Y	50038	Tubulin alpha chain OS=Tropilaelaps mercedesae GN=BIW11_12319 PE=3 SV=1
2	4500	tr|A0A2A3E7F9|A0A2A3E7F9_APICC	112.09	11	4	0	Y	53593	Tubulin alpha-2 chain OS=Apis cerana cerana GN=APICC_04279 PE=4 SV=1
2	4499	tr|A0A088ATP8|A0A088ATP8_APIME	112.09	11	4	0	Y	53663	Tubulin alpha chain OS=Apis mellifera PE=3 SV=1
2	4497	tr|A0A0K2TRK8|A0A0K2TRK8_LEPSM	112.09	12	4	0	Y	50170	Tubulin alpha chain OS=Lepeophtheirus salmonis PE=3 SV=1
2	4496	tr|A0A0L7QLG6|A0A0L7QLG6_9HYME	112.09	12	4	0	Y	49893	Tubulin alpha chain (Fragment) OS=Habropoda laboriosa GN=WH47_10606 PE=3 SV=1
2	4495	tr|A0A154PSW5|A0A154PSW5_9HYME	112.09	12	4	0	Y	49370	Tubulin alpha chain (Fragment) OS=Dufourea novaeangliae GN=WN55_07811 PE=3 SV=1
6	4515	tr|A0A1W4X4A3|A0A1W4X4A3_AGRPL	107.40	10	3	1	N	50100	Tubulin beta chain OS=Agrilus planipennis GN=LOC108738295 PE=3 SV=1
6	4514	tr|A0A0F6PKG8|A0A0F6PKG8_LYGLI	107.40	10	3	1	N	50193	Tubulin beta chain OS=Lygus lineolaris PE=2 SV=1
5	4503	tr|A0A1J1HUL7|A0A1J1HUL7_9DIPT	107.17	6	4	0	Y	132932	CLUMA_CG004748, isoform A OS=Clunio marinus GN=CLUMA_CG004748 PE=3 SV=1
5	4502	tr|A0A1W4XPI9|A0A1W4XPI9_AGRPL	103.40	11	3	0	Y	50922	Tubulin alpha chain OS=Agrilus planipennis GN=LOC108743352 PE=3 SV=1
5	4501	tr|O01943|O01943_GECLA	103.40	11	3	0	Y	49199	Tubulin alpha chain (Fragment) OS=Gecarcinus lateralis PE=2 SV=1
8	4541	tr|A0A023FND3|A0A023FND3_9ACAR	67.98	10	3	1	N	56225	ATP synthase subunit beta (Fragment) OS=Amblyomma cajennense PE=2 SV=1
9	4660	tr|A0A0P6CCE9|A0A0P6CCE9_9CRUS	58.88	11	2	2	N	35810	Glyceraldehyde-3-phosphate dehydrogenase OS=Daphnia magna PE=3 SV=1
11	4715	tr|T1ITF6|T1ITF6_STRMM	51.75	5	1	1	N	42895	Uncharacterized protein OS=Strigamia maritima PE=3 SV=1
11	4714	tr|L7M4J4|L7M4J4_9ACAR	51.75	5	1	1	N	41399	Putative histone macroh2a1.1 strongylocentrotus purpuratus: similar to histone OS=Rhipicephalus pulchellus PE=2 SV=1
11	4713	tr|A0A224YUU6|A0A224YUU6_9ACAR	51.75	5	1	1	N	41492	Core histone macro-H2A.1-like OS=Rhipicephalus zambeziensis PE=3 SV=1
11	4712	tr|A0A293LN19|A0A293LN19_ORNER	51.75	5	1	1	N	39238	Histone H2A (Fragment) OS=Ornithodoros erraticus PE=4 SV=1
11	4711	tr|A0A293LE62|A0A293LE62_ORNER	51.75	5	1	1	N	39238	Histone H2A (Fragment) OS=Ornithodoros erraticus PE=4 SV=1
11	4710	tr|G3MG27|G3MG27_9ACAR	51.75	6	1	1	N	32542	Uncharacterized protein (Fragment) OS=Amblyomma maculatum PE=2 SV=1
11	4709	tr|A0A087U9P4|A0A087U9P4_9ARAC	51.75	12	1	1	N	17993	Histone H2A (Fragment) OS=Stegodyphus mimosarum GN=X975_16210 PE=3 SV=1
11	4708	tr|A0A0A9Z7N0|A0A0A9Z7N0_LYGHE	51.75	14	1	1	N	16371	Histone H2A (Fragment) OS=Lygus hesperus GN=h2afx PE=3 SV=1
11	4707	tr|A0A1B6LDW1|A0A1B6LDW1_9HEMI	51.75	14	1	1	N	15417	Histone H2A OS=Graphocephala atropunctata GN=g.7519 PE=3 SV=1
11	4706	tr|A0A146KQ63|A0A146KQ63_LYGHE	51.75	14	1	1	N	16129	Histone H2A (Fragment) OS=Lygus hesperus GN=h2afx PE=3 SV=1
11	4705	tr|A0A0P6A1I4|A0A0P6A1I4_9CRUS	51.75	14	1	1	N	14860	Histone H2A (Fragment) OS=Daphnia magna PE=3 SV=1
11	4704	tr|A0A1W4WD58|A0A1W4WD58_DROFC	51.75	16	1	1	N	13319	Histone H2A OS=Drosophila ficusphila GN=LOC108102292 PE=3 SV=1
13	4719	tr|A0A1B0GP78|A0A1B0GP78_PHLPP	41.52	2	1	1	N	100688	Histone H4 OS=Phlebotomus papatasi PE=3 SV=1
14	4720	tr|A0A0P6CVG1|A0A0P6CVG1_9CRUS	40.23	6	1	1	N	31798	Malate dehydrogenase OS=Daphnia magna PE=3 SV=1
15	4723	tr|A0A0L7KSH4|A0A0L7KSH4_9NEOP	38.13	3	1	1	N	33687	Glutamate receptor, ionotropic kainate 1 OS=Operophtera brumata GN=OBRU01_21965 PE=4 SV=1
total 124 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
15	4724	tr|A0A075TD97|A0A075TD97_HELAM	38.13	2	1	1	N	62708	Ionotropic glutamate receptor (Fragment) OS=Helicoverpa armigera GN=iGluR3 PE=2 SV=1
15	4725	tr|A0A0L7LL85|A0A0L7LL85_9NEOP	38.13	2	1	1	N	63721	Ionotropic glutamate receptor OS=Operophtera brumata GN=OBRU01_06179 PE=3 SV=1
15	4726	tr|H9JJ96|H9JJ96_BOMMO	38.13	2	1	1	N	67158	Uncharacterized protein OS=Bombyx mori PE=3 SV=1
15	4727	tr|A0A0V0J1A3|A0A0V0J1A3_CYDPO	38.13	1	1	1	N	94424	Putative ionotropic glutamate receptor iGluR5 (Fragment) OS=Cydia pomonella GN=iGluR PE=3 SV=1
15	4728	tr|A0A194Q9S0|A0A194Q9S0_PAPXU	38.13	1	1	1	N	97873	Glutamate receptor, ionotropic kainate 2 OS=Papilio xuthus GN=RR46_08055 PE=3 SV=1
15	4729	tr|A0A2A4JAT1|A0A2A4JAT1_HELVI	38.13	1	1	1	N	97912	Uncharacterized protein (Fragment) OS=Heliothis virescens GN=B5V51_5128 PE=4 SV=1
15	4730	tr|A0A212EM67|A0A212EM67_DANPL	38.13	1	1	1	N	102903	Glutamate receptor ionotropic kainate 2 like protein OS=Danaus plexippus plexippus GN=KGM_215109 PE=3 SV=1
15	4731	tr|A0A0N1IIG3|A0A0N1IIG3_PAPMA	38.13	1	1	1	N	104776	Glutamate receptor, ionotropic kainate 2 OS=Papilio machaon GN=RR48_01726 PE=3 SV=1
16	4750	tr|Q5TWK1|Q5TWK1_ANOGA	31.51	2	1	1	N	61246	AGAP006906-PA OS=Anopheles gambiae GN=3290265 PE=4 SV=3
16	4749	tr|A0A182TCZ3|A0A182TCZ3_9DIPT	31.51	2	1	1	N	61244	Uncharacterized protein OS=Anopheles melas PE=4 SV=1
16	4751	tr|A0A182UV11|A0A182UV11_ANOME	31.51	2	1	1	N	63737	Uncharacterized protein OS=Anopheles merus PE=4 SV=1
16	4752	tr|A0A2C9GS79|A0A2C9GS79_ANOAR	31.51	2	1	1	N	63932	Uncharacterized protein OS=Anopheles arabiensis PE=4 SV=1
16	4753	tr|A0A182L3Q7|A0A182L3Q7_9DIPT	31.51	2	1	1	N	64366	Uncharacterized protein OS=Anopheles coluzzii PE=4 SV=1
16	4754	tr|A0A182WWF7|A0A182WWF7_ANOQN	31.51	1	1	1	N	120340	Uncharacterized protein OS=Anopheles quadriannulatus PE=4 SV=1
17	4755	tr|A0A0K2VDA2|A0A0K2VDA2_LEPSM	31.50	7	1	1	N	8419	Uncharacterized protein (Fragment) OS=Lepeophtheirus salmonis PE=4 SV=1
17	4756	tr|T1GNU9|T1GNU9_MEGSC	31.50	2	1	1	N	28927	Uncharacterized protein OS=Megaselia scalaris PE=4 SV=1
17	4761	tr|A0A067RJ46|A0A067RJ46_ZOONE	31.50	1	1	1	N	45235	von Willebrand factor D and EGF domain-containing protein OS=Zootermopsis nevadensis GN=L798_11028 PE=4 SV=1
17	4822	tr|A0A1J1J4I8|A0A1J1J4I8_9DIPT	31.50	1	1	1	N	63903	CLUMA_CG019121, isoform A OS=Clunio marinus GN=CLUMA_CG019121 PE=4 SV=1
17	4842	tr|E0VC82|E0VC82_PEDHC	31.50	1	1	1	N	77829	Protein pns1, putative OS=Pediculus humanus subsp. corporis GN=8231471 PE=3 SV=1
17	4868	tr|A0A212F9M7|A0A212F9M7_DANPL	31.50	1	1	1	N	97384	Putative NP95 OS=Danaus plexippus plexippus GN=KGM_203968 PE=4 SV=1
17	4880	tr|A0A212FGX5|A0A212FGX5_DANPL	31.50	1	1	1	N	108442	Transient receptor potential cation channel protein painless isoform 1 OS=Danaus plexippus plexippus GN=KGM_211899 PE=3 SV=1
17	4957	tr|A0A0M4F702|A0A0M4F702_DROBS	31.50	0	1	1	N	141392	Metalloendopeptidase OS=Drosophila busckii GN=Dbus_chr3Rg2662 PE=3 SV=1
17	4958	tr|A0A182H9K0|A0A182H9K0_AEDAL	31.50	0	1	1	N	139002	Metalloendopeptidase OS=Aedes albopictus PE=3 SV=1
17	4991	tr|B4LW38|B4LW38_DROVI	31.50	0	1	1	N	161963	Metalloendopeptidase OS=Drosophila virilis GN=Dvir\GJ23651 PE=3 SV=1
17	4996	tr|B4QTR3|B4QTR3_DROSI	31.50	0	1	1	N	164942	Metalloendopeptidase OS=Drosophila simulans GN=tok PE=3 SV=1
17	5000	tr|A0A034VDR1|A0A034VDR1_BACDO	31.50	0	1	1	N	166249	Metalloendopeptidase OS=Bactrocera dorsalis GN=TLD PE=3 SV=1
17	5003	tr|A0A1A9WC30|A0A1A9WC30_9MUSC	31.50	0	1	1	N	174608	Metalloendopeptidase OS=Glossina brevipalpis PE=3 SV=1
17	5018	tr|A0A1A9WXH7|A0A1A9WXH7_9MUSC	31.50	0	1	1	N	177630	Uncharacterized protein OS=Glossina brevipalpis PE=4 SV=1
17	5040	tr|A0A1B6LZH3|A0A1B6LZH3_9HEMI	31.50	0	1	1	N	179787	Uncharacterized protein OS=Graphocephala atropunctata GN=g.24631 PE=4 SV=1
17	5052	tr|A0A1I8PPZ3|A0A1I8PPZ3_STOCA	31.50	0	1	1	N	188941	Metalloendopeptidase OS=Stomoxys calcitrans GN=106084331 PE=3 SV=1
17	5125	tr|A0A088ACM0|A0A088ACM0_APIME	31.50	0	1	1	N	322436	Uncharacterized protein OS=Apis mellifera PE=4 SV=1
17	5121	tr|B4QT41|B4QT41_DROSI	31.50	0	1	1	N	248569	GD21088 OS=Drosophila simulans GN=Dsim\GD21088 PE=4 SV=1
17	5120	tr|A0A224X4P4|A0A224X4P4_9HEMI	31.50	0	1	1	N	249239	Putative nidogen (Fragment) OS=Panstrongylus lignarius PE=4 SV=1
17	5112	tr|A0A232F5I4|A0A232F5I4_9HYME	31.50	0	1	1	N	237992	Uncharacterized protein OS=Trichomalopsis sarcophagae GN=TSAR_012850 PE=4 SV=1
17	5106	tr|A0A1B6LVD0|A0A1B6LVD0_9HEMI	31.50	0	1	1	N	207218	Uncharacterized protein (Fragment) OS=Graphocephala atropunctata GN=g.24646 PE=4 SV=1
32	5135	tr|A0A2A4K6P5|A0A2A4K6P5_HELVI	27.31	0	2	1	N	498248	Uncharacterized protein OS=Heliothis virescens GN=B5V51_1066 PE=4 SV=1
18	1175	tr|E2BYR5|E2BYR5_HARSA	24.05	1	1	1	N	107524	Dynein intermediate chain 2, axonemal OS=Harpegnathos saltator GN=EAI_14044 PE=4 SV=1
19	4758	tr|A0A0K8SP95|A0A0K8SP95_LYGHE	24.00	1	1	1	N	86434	Protein transport protein Sec23A OS=Lygus hesperus GN=SEC23A PE=4 SV=1
10	4759	tr|A0A084VFX3|A0A084VFX3_ANOSI	23.17	2	1	1	N	41010	CYP6M1c OS=Anopheles sinensis GN=ZHAS_00004044 PE=4 SV=1
21	4762	tr|A0A0A9YA46|A0A0A9YA46_LYGHE	22.80	2	1	1	N	44058	Steroid hormone receptor ERR2 OS=Lygus hesperus GN=Esrrb_8 PE=3 SV=1
21	4763	tr|A0A0A9VQS0|A0A0A9VQS0_LYGHE	22.80	2	1	1	N	44457	Steroid hormone receptor ERR2 OS=Lygus hesperus GN=Esrrb_0 PE=3 SV=1
21	4765	tr|A0A0A9Y8J4|A0A0A9Y8J4_LYGHE	22.80	1	1	1	N	48439	Steroid hormone receptor ERR2 OS=Lygus hesperus GN=Esrrb_2 PE=3 SV=1
21	4766	tr|A0A0A9Y9B6|A0A0A9Y9B6_LYGHE	22.80	1	1	1	N	49133	F-box/LRR-repeat protein 12 OS=Lygus hesperus GN=FBXL12 PE=4 SV=1
21	4768	tr|N6U3G5|N6U3G5_DENPD	22.80	1	1	1	N	54464	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_10244 PE=3 SV=1
21	4774	tr|B7QA75|B7QA75_IXOSC	22.80	1	1	1	N	60362	Acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Ixodes scapularis GN=8038202 PE=3 SV=1
21	4777	tr|A0A0A1XHZ0|A0A0A1XHZ0_ZEUCU	22.80	1	1	1	N	65807	Sphingomyelin synthase-related 1 OS=Zeugodacus cucurbitae GN=SMSr_0 PE=4 SV=1
21	4794	tr|A0A0E4GBG0|A0A0E4GBG0_ANOGA	22.80	1	1	1	N	84871	Uncharacterized protein OS=Anopheles gambiae PE=4 SV=1
21	4816	tr|A0A0P6GKE9|A0A0P6GKE9_9CRUS	22.80	1	1	1	N	98080	Eyes shut OS=Daphnia magna PE=4 SV=1
21	4825	tr|A0A0P5YUZ6|A0A0P5YUZ6_9CRUS	22.80	1	1	1	N	122636	Leucine-rich repeat-containing protein OS=Daphnia magna GN=APZ42_023826 PE=4 SV=1
total 124 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
12	4773	tr|A0A087UQW5|A0A087UQW5_9ARAC	21.19	6	1	1	N	10714	Xin actin-binding repeat-containing protein 2 (Fragment) OS=Stegodyphus mimosarum GN=X975_08866 PE=4 SV=1
12	4788	tr|A0A182SD20|A0A182SD20_9DIPT	21.19	4	1	1	N	13061	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
12	4806	tr|A0A0T6BBI1|A0A0T6BBI1_9SCAR	21.19	3	1	1	N	16954	Trypsin (Fragment) OS=Oryctes borbonicus GN=AMK59_1783 PE=3 SV=1
12	4805	tr|A0A182N5F4|A0A182N5F4_9DIPT	21.19	3	1	1	N	16461	Uncharacterized protein OS=Anopheles dirus PE=4 SV=1
12	4859	tr|A0A182SSD0|A0A182SSD0_9DIPT	21.19	1	1	1	N	48967	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
12	4902	tr|A0A1A9XPY1|A0A1A9XPY1_GLOFF	21.19	1	1	1	N	99363	Uncharacterized protein OS=Glossina fuscipes fuscipes PE=4 SV=1
12	4901	tr|A0A1B0BCP2|A0A1B0BCP2_9MUSC	21.19	1	1	1	N	99340	Uncharacterized protein OS=Glossina palpalis gambiensis PE=4 SV=1
12	4912	tr|A0A1B0FND5|A0A1B0FND5_GLOMM	21.19	1	1	1	N	101723	Uncharacterized protein OS=Glossina morsitans morsitans PE=4 SV=1
12	4916	tr|A0A1A9VCZ7|A0A1A9VCZ7_GLOAU	21.19	1	1	1	N	103003	Uncharacterized protein OS=Glossina austeni PE=4 SV=1
22	4815	tr|A0A132AHU8|A0A132AHU8_SARSC	20.93	0	1	1	N	350222	Zinc finger homeobox protein 4-like protein OS=Sarcoptes scabiei GN=QR98_0091340 PE=4 SV=1
total 124 proteins									

tr|A0A023ETG9|A0A023ETG9_AEDAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEVISDEHGI DATGAYCGDS DLQLERINVY YNEATGGKYV PRAVLVDLEP GTMDSVRAGP
81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**ESEGCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP
161 DRIMNTFSVV PSPKVSDTVV EPYNATLSVH QLVENTDESY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMTGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR
321 MSMKEVDEQM LNIQSKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSSTFIGN STAIQEIFKR** IAEQFTAMFR RKAFLHWYTG
401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEEGEFDEEE EGGEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.MSSTFIGNSTAIQEIFKR.I	Y	65.32	2029.0303	-32.6	677.3287	3	26.79	979	1	363	380	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|A0A0P5ZYN7|A0A0P5ZYN7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPR**AVFVDL EPTVIDEVR**T
81 GTYR**QLFHPE QLITGKEDAA NNYARGHYTI GKEIIDLVLD RIR**KLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCLLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGVDSV EGEGEEEGEE Y

d Deam
P Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	244	264	
R.GHYTIGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	106	121	
R.LISQIVSSITASLR.F	Y	52.65	1486.8718	-17.5	744.4302	2	32.35	1168	1	230	243	
R.AVFVDLEPTVIDEVR.T	N	45.87	1700.8984	-18.4	851.4409	2	27.54	1004	1	65	79	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	244	264	Deamidation (NQ)
R.LISQ(+.98)IVSSITASLR.F	Y	22.80	1487.8558	-19.1	744.9210	2	33.11	1189	1	230	243	Deamidation (NQ)
R.GHYTIGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	106	123	
R.Q(-17.03)LFHPEQLITGKEDAANNYAR.G	N	15.06	2397.1711	-25.5	800.0439	3	23.91	883	1	85	105	Pyro-glu from Q
total 8 peptides												

tr|A0A0P6A5L5|A0A0P6A5L5_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deam
P Pyro-

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPR**AVFVDL EPTVIDEVR**T
81 GTYR**QLFHPE QLITGKEDAA NNYARGHYTI GKEIIDLVLD RIR**KLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCLLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	244	264	
R.GHYTIGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	106	121	
R.LISQIVSSITASLR.F	Y	52.65	1486.8718	-17.5	744.4302	2	32.35	1168	1	230	243	
R.AVFVDLEPTVIDEVR.T	N	45.87	1700.8984	-18.4	851.4409	2	27.54	1004	1	65	79	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	244	264	Deamidation (NQ)
R.LISQ(+.98)IVSSITASLR.F	Y	22.80	1487.8558	-19.1	744.9210	2	33.11	1189	1	230	243	Deamidation (NQ)
R.GHYTIGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	106	123	
R.Q(-17.03)LFHPEQLITGKEDAANNYAR.G	N	15.06	2397.1711	-25.5	800.0439	3	23.91	883	1	85	105	Pyro-glu from Q
total 8 peptides												

tr|T1GUQ6|T1GUQ6_MEGSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FWEIISDEHG IDATGAYHGD SDLQLERINV YYNEASGGKY VPRAVLVDLE PGTMDSVRSG PFGQIFRPDN FVFGQSGAGN
81 NWAK**GHYTEG AELVDSVLDV VRK**EAESCDC LQGFQLTHSL GGGTGSGMGT LLISKIREEY PDRIMNTYSV VPSPKVSDTV
161 VEPYNATLSV HQLVENTDET YCIDNEALYD ICFRTLKLTT PTYGDLNHLV SLTMSGVTTC LRFPGQLNAD LRKLAVNMVP
241 FPRLHFFMPG FAPLTSRGSQ QYRALTVPEL TQQMFDAKNM MAACDPRHGR **YLTVAAIFR**G QQLIFVEWIP NNVKTAVCDI
321 PPRGLK**MSAT FIGNSTAIQE LFKR**ISEQFT AMFRRKAFLH WYTGEGMDEM EFTEAESNMN DLVS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	85	103	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	85	102	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	327	344	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	291	299	
total 4 peptides												

tr|R4G588|R4G588_RHOPR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FWEIISDEHG IDPTGAYHGD SDLQLERINV YYNEASGKGG GKYVPRAILV DLEPGTMDSV RSGPFGQIFR PDNFVFGQSG
81 AGNNWAK**GHY TEGAELVDSV LDVVRK**EAES CDCLQGFQLT HSLGGGTGSG MGTLLISKIR EEYPDRIMNT YSVVPSPKVS
161 DTVVEPYNAT LSVHQLVENT DETYCIDNEA LYDICFRTLK LSTPTYGDLN HLVSLTMSGV TTCLRFPGQL NADLRKLAVN
241 MVPFPRLHFF MPGFAPLTSR GSQQYRALTV PELTQQMFDA KNMMAACDPR HGR**YLTVAAI FR**GRMSMKEV DEQMLNIQNK
321 NSSYFVEWIP NNVKTAVCDI PPRGLK**MSAT FIGNSTAIQE LFKR**ISEQFT AMFRRKAFLH WYTGEGMDEM EFTEAESNMN
401 DLVSEYQQYQ EATADEDAEF DEEHEQEVDE N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	88	106	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	88	105	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	347	364	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	294	302	
total 4 peptides												

tr|C7SAG3|C7SAG3_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGGKF WEVISDEHCI DATGTYYGDS DLQLERINVY YNEATGAKYV PRAILVDLEP GTMDSVRSGA
81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**ESEGCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTFSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSF FVEWIPNNCK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** VSEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEEGEFDEDE EGGGDE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.V	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|A0A023FK66|A0A023FK66_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEVISDEHGI DPTGSYHGDS DLQLERINVY YNEASGGKYV PRAILVDLEP GTMDSVRSGP
81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAEGCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTFSVV PSPKVSDTVV EPYNATLSVH QLVENTDETF CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTARGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMREVDEQM LNVQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEEGEFEDEP EADAEA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|C7SAG4|C7SAG4_BACDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGGKF WEVISDEHCI DATGTYYGDS DLQLERINVY YNEATGAKYV PRAILVDLEP GTMDSVRSGA
81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**ESEGCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTFSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSF FVEWIPNNCK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** VSEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEEGEFDEDE EGGGDE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.V	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|A0A0P5E5N2|A0A0P5E5N2_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI QPNGTYHGES ELQLERINVY YNEASGGKYV PRAVLVDLEP GTMDSVRSGP
81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTARGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DDEADFEEDG DHADQDAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|A0A069DTP4|A0A069DTP4_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DPTGAYHGDS DLQLERINVY YNEASGGGKY VPRAILVDLE PGTMDSVRSG
81 PFGQIFRPDN FVFGQSGAGN NWAK**GHYTEG AELVDSVLDV VRK**EAEGCDC LQGFQLTHSL GGGTGSGMGT LLISKIREEY

161 PDRIMNTYSV VPSPKVSDTV VEPYNATLSV HQLVENTDET YCIDNEALYD ICFRTLKLST PTYGDLNHLV SLTMSGVTTC
241 LRFPGQLNAD LRKLAVNMVP FPRLHFFMPG FAPLTSRGSQ QYRALTVPEL TQQMFDAKNM MAACDPRHGR **YLTVAAIFR**G

321 RMSMKEVDEQ MLNIQNKNSS YFVEWIPNNV KTAVCDIPPR GLK**MSATFIG NSTAIQELFK R**ISEQFTAMF RRKAFLHWYT

401 GEGMDEMEFT EAESNMNDLV SEYQQYQEAT ADEDAEFDEE QEQEIDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	105	123	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	105	122	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	364	381	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	311	319	
total 4 peptides												

tr|B4QE31|B4QE31_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DATGAYHGDS DLQLERINVY YNEASGGKYV PRAVLVDLEP GTMDSVRSGP
81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFEEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|V9IK78|V9IK78_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DPTGTYHGDS DLQLERINVY YNEASGGKYV PRAILVDLEP GTMDSVRSGP

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLSTP TYGDLNHLVS LTMSGVTTCL

241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALSVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFDEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	104	122	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	104	121	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 4 peptides												

tr|A0A0J7L622|A0A0J7L622_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQNVNPFSS TQNTPTKAAE EKQSLPKDNH AVSKRLQKEL MVLMMNTEQG VSAFPEGENL FKWIGTITGP RDTVYAGLTY

81 KLTLEFPHSY PYSAPIVRFA TPCFHPNVDT GGNICLDILK DKWSALYDVR TILLSIQSLL SGTIWTDFKP QIENLNTDKL

161 TIVAWDPPGY GKSRPPDRTF PDDFFQRDAA WAHSLMQTLG YSKFSLIGWS NGGITSLLLA STYPESIRRM VVFGANAYIH

241 PDEAKIYENI RDIDKWSERM RTSMIQVYGE DYFRKTWSNW IDAKLRLYEK QNGNVCKEVL SKIKCPTLII HGAKDAIVFP

321 EHPTYLKQNI ANSNLHILEK GAHNLHLRYF EEFNNLFWEI ISDEHGIDPT GTYHGDSDLQ LERINVYYNE ASGGKYVPRA

401 ILVDLEPGTM DSVRSGPFGQ IFRPDNFVFG QSGAGNNWAK **GHYTEGAELV DSVLDVVRK**E AESCDCLQGF QLTHSLGGGT

481 GSGMGTLLIS KIREEYPDRI MNTYSVVPSP KVSDTVVEPY NATLSVHQLV ENTDETYCID NEALYDICFR TLKLSTPTYG

561 DLNHLVSLTM SGVTTCLRFP GQLNADLRKL AVNMVPFPRL HFFMPGFAPL TSRGSQQYRA LSVPELTQQM FDAKNMMAAC

641 DPRHGR**YLTV AAIFR**GRMSM KEVDEQMLNI QNKNSSYFVE WIPNNVKTAV CDIPPRGLK**M SATFIGNSTA IQELFKR**ISE

721 QFTAMFRRKA FLHWYTGEGM DEMEFTEAES NMNDLVSEYQ QYQEATADED AEFDEEQEAE VDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDSVLDVVRK.E	N	68.54	2086.0693	-32.4	696.3412	3	27.51	1003	2	441	459	
K.GHYTEGAELVDSVLDVVR.K	N	55.51	1957.9745	-18.0	979.9769	2	29.62	1074	1	441	458	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	700	717	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	647	655	
total 4 peptides												

tr|A0A0P5F7I2|A0A0P5F7I2_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADEAAIANG KIVAVIGAVV DVQFEDQLPP ILNALEVSNR SPRLILEVAQ HLGENTVRTI AMDGTEGLIR GQPVLDTGSP

81 IKIPVGPETL GRIMNVIGEP IDERGPIVTD KFAAIHAEAP EFVEMNVAQE ILITGIKVVD LLAPYAKGGK IGLFGGAGVG

161 K**TVLIMELIN NVAK**AHGGYS VFAGVGERTR EGNDLYHEMI ESGVISLKDK TSKVALVYGQ MNEPPGARAR **VALTGLTVAE**

241 **YFRDQEGQDV LLFIDNIFR**F TQAGSEVSAL LGRIPSAVGY QPTLATDMGS MQERITTTKK GSITSVQAIY VPADDLTD**PA**

321 **PATTFAHLDA TTVLSR**AIAE LGIYPAVDPL DSTSRMMDPN IIGDVHYNAA RGVQKILQDY KSLQDIIAIL GMDELSEDDK

401 LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPIAETIKGF KMILNGELDH LPEAAFYMVG PIEEVVAKAE KLAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	231	259	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	319	336	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	162	174	
total 3 peptides												

tr|A0A0P5YRH3|A0A0P5YRH3_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADEAAIANG KIVAVIGAVV DVQFEDQLPP ILNALEVSNR SPRLILEVAQ HLGENTVRTI AMDGTEGLIR GQPVLDTGSP
81 IKIPVGPETL GRIMNVIGEP IDERGPIVTD KFAAIHAEAP EFVEMNVAQE ILITGIKVVD LLAPYAKGGK IGLFGGAGVG
161 K**TVLIMELIN NVAK**AHGGYS VFAGVGERTR EGNDLYHEMI ESGVISLKDK TSKVALVYGQ MNEPPGARAR **VALTGLTVAE**
241 **YFRDQEGQDV LLFIDNIFR**F TQAGSEVSAL LGRIPSAVGY QPTLATDMGS MQERITTTKK GSITSVQAIY VPADDLTD**PA**
321 **PATTFAHLDA TTVLSR**AIAE LGIYPAVDPL DSTSRMMDPN IIGDVHYNAA RGVQKILQDY KSLQDIIAIL GMDELSEDDK
401 LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPIAETIKGF KMI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	231	259	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	319	336	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	162	174	
total 3 peptides												

tr|A0A0P5RWN8|A0A0P5RWN8_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSNFQDKPG GLIRGQPVLD TGSPIKIPVG PETLGRIMNV IGEPIDERGP IVTDKFAAIH AEAPEFVEMN VAQEILITGI
81 KVVDLLAPYA KGGKIGLFGG AGVGK**TVLIM ELINNVAK**AH GGYSVFAGVG ERTREGNDLY HEMIESGVIS LKDKTSKVAL
161 VYGQMNEPPG ARAR**VALTGL TVAEYFRDQE GQDVLLFIDN IFR**FTQAGSE VSALLGRIPS AVGYQPTLAT DMGSMQERIT
241 TTKKGSITSV QAIYVPADDL TD**PAPATTFA HLDATTVLSR** AIAELGIYPA VDPLDSTSRM MDPNIIGDVH YNAARGVQKI
321 LQDYKSLQDI IAILGMDELS EDDKLTVARA RKIQRFLSQP FQVAEVFTGH AGKLVPIAET IKGFKMILNG ELDHLPEAAF
401 YMVGPIEEVV AKAEKLAEST A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	175	203	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	263	280	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	106	118	
total 3 peptides												

tr|A0A0P6FT42|A0A0P6FT42_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDGTEGLVRG QRVADTGFPI RIPVGAETLG RIINVIGEPI DERGPIPTDK RAPIHAEAPE FVEMSVQQEI LVTGIKVVDL
81 LAPYAKGGKI GLFGGAGVGK **TVLIMELINN VAK**AHGGYSV FAGVGERTRE GNDLYNEMIE GGVISLKDKT SKVALVYGQM
161 NEPPGARAR**V ALTGLTVAEY FRDQEGQDVL LFIDNIFR**FT QAGSEVSALL GRIPSAVGYQ PTLATDMGSM QERITTTTKG
241 SITSVQAIYV PADDLTD**PAP ATTFAHLDAT TVLSR**AIAEL GIYPAVDPLD STSRIMDPNI IGNEHYNIAR GVQKILQDYK
321 SLQDIIAILG MDELSEEDKL TVARARKIQR FLSQPFQVAE VFTGHAGKLV PLEETIKGFT KILHGELDHL PEVAFYMVGP
401 IEEVVEKAER LAKEAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	170	198	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	258	275	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	101	113	
total 3 peptides												

tr|A0A0N8D2L0|A0A0N8D2L0_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSNFQDKPG GLIRGQPVLD TGSPIKIPVG PETLGRIMNV IGEPIDERGP IVTDKFAAIH AEAPEFVEMN VAQEILITGI
81 KVVDLLAPYA KGGKIGLFGG AGVGK**TVLIM ELINNVAK**AH GGYSVFAGVG ERTREGNDLY HEMIESGVIS LKDKTSKVAL
161 VYGQMNEPPG ARAR**VALTGL TVAEYFRDQE GQDVLLFIDN IFR**FTQAGSE VSALLGRIPS AVGYQPTLAT DMGSMQERIT
241 TTKKGSITSV QAIYVPADDL TD**PAPATTFA HLDATTVLSR** AIAELGIYPA VDPLDSTSRM MDPNIIGDVH YNAARGVQKI
321 LQDYKSLQDI IAILGMDELS EDDKLTVARA RKIQRFLSQP FQVAEVFTGH AGKLVPIAET IKGFKMI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	175	203	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	263	280	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	106	118	
total 3 peptides												

tr|Q6W4K6|Q6W4K6_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EPIDERGPID TDKTAAIHAE APEFVQMSVE QEILVTGIKV VDLLAPYAKG GKIGLFGGAG VGK**TVLIMEL INNVAK**AHGG
81 YSVFAGVGER TREGNDLYNE MIEGGVISLK DKTSKVALVY GQMNEPPGAR AR**VALTGLTV AEYFRDQEGQ DVLLFIDNIF**
161 **R**FTQAGSEVS ALLGRIPSAV GYQPTLATDM GSMQERITTT KKGSITSVQA IYVPADDLTD **PAPATTFAHL DATTVLSR**AI
241 AELGIYPAVD PLDSTSRIMD PNIIGQEHYN VARGVQKILQ DYKSLQDIIA ILGMDELSEE DKLTVARARK IQRFLSQPFQ
321 VAEVFTGHAG KLVPLEQTIK GFSAILAGDY DHLPEVAFYM VGPIEEVVEK ADRLAK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	133	161	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	221	238	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	64	76	
total 3 peptides												

tr|D8VIP0|D8VIP0_HELME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VQFEDSLPPI LNALEVQNRS PRLVLEVAQH LGENTVRTIA MDGTEGLVRG QPVHDCGSPI RIPVGAETLG RIINVIGEPI
81 DERGPIPTDK TAAIHAEAPE FVDMSVQQEI LVTGIKVVDL LAPYAKGGKI GLFGGAGVGK **TVLIMELINN VAK**AHGGYSV
161 FAGVGERTRE GNDLYHEMIE SGVISLKDKT SKVALVYGQM NEPPGARAR**V ALTGLTVAEY FRDQEGQDVL LFIDNIFR**FT
241 QAGSEVSALL GRIPSAVGYQ PTLATDMGTM QERITTTKKG SITSVQAIYV PADDLTD**PAP ATTFAHLDAT TVLSR**AIAEL
321 GIYPAVDPLD STSRIMDPNI IGAEHYNVAR GV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	210	238	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	298	315	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	141	153	
total 3 peptides												

tr|G3KAV3|G3KAV3_HELNM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EDSLPPILNA LEVQNRSPRL VLEVAQHLGE NTVRTIAMDG TEGLVRGQPV HDCGSPIRIP VGAETLGRII NVIGEPIDER
81 GPIPTDKTAA IHAEAPEFVD MSVQQEILVT GIKVVDLLAP YAKGGKIGLF GGAGVGK**TVL IMELINNVAK** AHGGYSVFAG
161 VGERTREGND LYHEMIESGV ISLKDKTSKV ALVYGQMNEP PGARAR**VALT GLTVAEYFRD QEGQDVLLFI DNIFR**FTQAG
241 SEVSALLGRI PSAVGYQPTL ATDMGTMQER ITTTKKGSIT SVQAIYVPAD DLTD**PAPATT FAHLDATTVL SR**AIAELGIY
321 PAVDPLDSTS RIMDPNIIGA EHYN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	207	235	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	295	312	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	138	150	
total 3 peptides												

tr|G3KAY5|G3KAY5_HELNM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EDSLPPILNA LEVQNRSPRL VLEVAQHLGE NTVRTIAMDG TEGLVRGQPV HDCGSPIRIP VGAETLGRII NVIGEPIDER
81 GPIPTDKTAA IHAEAPEFVD MSVQQEILVT GIKVVDLLAP YAKGGKIGLF GGAGVGK**TVL IMELINNVAK** AHGGYSVFAG
161 VGERTREGND LYHEMIESGV ISLKDKTSKV ALVYGQMNEP PGARAR**VALT GLTVAEYFRD QEGQDVLLFI DNIFR**FTQAG
241 SEVSALLGRI PSAVGYQPTL ATDMGTMQER ITTTKKGSIT SVQAIYVPAD DLTD**PAPATT FAHLDATTVL SR**AIAELGIY
321 PAVDPLDSTS RIMDPNIIGA EHYN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	207	235	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	295	312	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	138	150	
total 3 peptides												

tr|E0W1G3|E0W1G3_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSAVSRAAS GVLRAVKTPN IQNEALKVFS AITGTRLLSF DSVFGPTDDD DEKCKEDDKP KSQDKSKSEY ATAPAAKAGK
81 GTSGKIVAVI GAVVDVQFDE NLPAILNALE VSNRSPRLIL EVAQHLGENT VRTIAMDGTE GLVRGQVVTD TGYPIRIPVG
161 AETLGRIMNV IGEPIDERGP IKTDKFAAIH AEAPEFVDMS VEQEILVTGI KVVDLLAPYA KGGKIGLFGG AGVGK**TVLIM**
241 **ELINNVAK**AH GGYSVFAGVG ERTREGNDLY HEMIESGVIS LKDKTSKVAL VYGQMNEPPG ARAR**VALTGL TVAEYFRDQE**
321 **GQDVLLFIDN IFR**FTQAGSE VSALLGRIPS AVGYQPTLAT DMGTMQERIT TTKKGSITSV QAIYVPADDL TD**PAPATTFA**
401 **HLDATTVLSR** AIAELGIYPA VDPLDSTSRI MDPNIIGAEH YNIARGVQKI LQDYKSLQDI IAILGMDELS EDDKLTVARA
481 RKIQRFLSQP FQVAEVFTGH AGKLVPLQET IKGFSQILKG EYDHLPEVAF YMVGPIEEVV AKAETLAKSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	305	333	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	393	410	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	236	248	
total 3 peptides												

tr|A0A0P5T3L7|A0A0P5T3L7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAASSAIAAM LNAVARASSG ILRTVQPTVS HIQNGQSKVL PALLGKRSFY TSQLLSAEAK TAAMADEAAI ANGKIVAVIG
81 AVVDVQFEDQ LPPILNALEV SNRSPRLILE VAQHLGENTV RTIAMDGTEG LIRGQPVLDT GSPIKIPVGP ETLGRIMNVI
161 GEPIDERGPI VTDKFAAIHA EAPEFVEMNV AQEILITGIK VVDLLAPYAK GGKIGLFGGA GVGK**TVLIME LINNVAK**AHG
241 GYSVFAGVGE RTREGNDLYH EMIESGVISL KDKTSKVALV YGQMNEPPGA RAR**VALTGLT VAEYFRDQEG QDVLLFIDNI**
321 **FR**FTQAGSEV SALLGRIPSA VGYQPTLATD MGSMQERITT TKKGSITSVQ AIYVPADDLT D**PAPATTFAH LDATTVLSR**A
401 IAELGIYPAV DPLDSTSRMM DPNIIGDVHY NAARGVQKIL QDYKSLQDII AILGMDELSE DDKLTVARAR KIQRFLSQPF
481 QVAEVFTGHA GKLVPIAETI KGFKMILNGE LDHLPEAAFY MVGPIEEVVA KAEKLAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	294	322	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	382	399	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	225	237	
total 3 peptides												

tr|A0A0P5BBW0|A0A0P5BBW0_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAASSAIAAM LNAVARASSG ILRTVQPTVS HIQNGQSKVL PALLGKRSFY TSQLLSAEAK TAAKAAIANG KIVAVIGAVV
81 DVQFEDQLPP ILNALEVSNR SPRLILEVAQ HLGENTVRTI AMDGTEGLIR GQPVLDTGSP IKIPVGPETL GRIMNVIGEP
161 IDERGPIVTD KFAAIHAEAP EFVEMNVAQE ILITGIKVVD LLAPYAKGGK IGLFGGAGVG K**TVLIMELIN NVAK**AHGGYS
241 VFAGVGERTR EGNDLYHEMI ESGVISLKDK TSKVALVYGQ MNEPPGARAR **VALTGLTVAE YFRDQEGQDV LLFIDNIFR**F
321 TQAGSEVSAL LGRIPSAVGY QPTLATDMGS MQERITTTKK GSITSVQAIY VPADDLTD**PA PATTFAHLDA TTVLSR**AIAE
401 LGIYPAVDPL DSTSRMMDPN IIGDVHYNAA RGVQKILQDY KSLQDIIAIL GMDELSEDDK LTVARARKIQ RFLSQPFQVA
481 EVFTGHAGKL VPIAETIKGF KMILNGELDH LPEAAFYMVG PIEEVVAKAE KLAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	291	319	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	379	396	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	222	234	
total 3 peptides												

tr|A0A0P5UBV1|A0A0P5UBV1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAASSAIAAM LNAVARASSG ILRTVQPTVS HIQNGQSKVL PALLGKRSFY TSQLLSAEAK TAAEAAIANG KIVAVIGAVV
81 DVQFEDQLPP ILNALEVSNR SPRLILEVAQ HLGENTVRTI AMDGTEGLIR GQPVLDTGSP IKIPVGPETL GRIMNVIGEP
161 IDERGPIVTD KFAAIHAEAP EFVEMNVAQE ILITGIKVVD LLAPYAKGGK IGLFGGAGVG K**TVLIMELIN NVAK**AHGGYS
241 VFAGVGERTR EGKDRYHEMI ESGVISLKDK TSKVALVYGQ MNEPPGARAR **VALTGLTVAE YFRDQEGQDV LLFIDNIFR**F
321 TQAGSEVSAL LGRIPSAVGY QPTLATDMGS MQERITTTKK GSITSVQAIY VPADDLTD**PA PATTFAHLDA TTVLSR**AIAE
401 LGIYPAVDPL DSTSRMMDPN IIGDVHYNAA RGVQKTLQDY KSLQDIIAIL GMDELSEDDK LTVARARKIQ RFLSQPFQVA
481 EVFTGHAGKL VPIAETIKGF KMILNGELDH LPEAAFYMVG PIEEVVAKAE KLAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	291	319	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	379	396	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	222	234	
total 3 peptides												

tr|A0A0P5EU29|A0A0P5EU29_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAASSAIAAM LNAVARASSG ILRTVQPTVS HIQNGQSKVL PALLGKRSFY TSQLLSAEAK TAAKAAIANG KIVAVIGAVV
81 DVQFEDQLPP ILNALEVSNR SPRLILEVAQ HLGENTVRTI AMDGTEGLIR GQPVLDTGSP IKIPVGPETL GRIMNVIGEP
161 IDERGPIVTD KFAAIHAEAP EFVEMNVAQE ILITGIKVVD LLAPYAKGGK IGLFGGAGVG K**TVLIMELIN NVAK**AHGGYS
241 VFAGVGERTR GKDRYHEMIE SGVISLKDKT SKVALVYGQM NEPPGARAR**V ALTGLTVAEY FRDQEGQDVL LFIDNIFR**FT
321 QAGSEVSALL GRIPSAVGYQ PTLATDMGSM QERITTTKKG SITSVQAIYV PADDLTD**PAP ATTFAHLDAT TVLSR**AIAEL
401 GIYPAVDPLD STSRMMDPNI IGDVHYNAAR GVQKILQDYK SLQDIIAILG MDELSEDDKL TVARARKIQR FLSQPFQVAE
481 VFTGHAGKLV PIAETIKGFK MILNGELDHL PEAAFYMVGP IEEVVAKAEK LAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	290	318	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	378	395	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	222	234	
total 3 peptides												

tr|A0A0P5BBX0|A0A0P5BBX0_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAIAAMLNA VARASSGILR TVQPTVSHIQ NGQSKVLPAL LGKRSFYTSQ LLSAEAKTAA KAAIANGKIV AVIGAVVDVQ

81 FEDQLPPILN ALEVSNRSPR LILEVAQHLG ENTVRTIAMD GTEGLIRGQP VLDTGSPIKI PVGPETLGRI MNVIGEPIDE

161 RGPIVTDKFA AIHAEAPEFV EMNVAQEILI TGIKVVDLLA PYAKGGKIGL FGGAGVGK**TV LIMELINNVA K**AHGGYSVFA

241 GVGERTREGN DLYHEMIESG VISLKDKTSK VALVYGQMNE PPGARAR**VAL TGLTVAEYFR DQEGQDVLLF IDNIFR**FTQA

321 GSEVSALLGR IPSAVGYQPT LATDMGSMQE RITTTKKGSI TSVQAIYVPA DDLTD**PAPAT TFAHLDATTV LSR**AIAELGI

401 YPAVDPLDST SRMMDPNIIG DVHYNAARGV QKILQDYKSL QDIIAILGMD ELSEDDKLTV ARARKIQRFL SQPFQVAEVF

481 TGHAGKLVPI AETIKGFKMI LNGELDHLPE AAFYMVGPIE EVVAKAEKLA ESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	288	316	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	376	393	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	219	231	
total 3 peptides												

tr|A0A0J7KRQ1|A0A0J7KRQ1_LASNI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMLSAVSKAA AGALRIAKPC LIQNEAAKVS SAFAINKRDY AAKAAAATKT GAQGKVVAVI GAVVDVQFED DLPPILNALE

81 VQNRTPRLVL EVAQHLGEST VRTIAMDGTE GLVRGQNVLD SGYPIRIPVG AETLGRIINV IGEPIDERGP IPTDKLAPIH

161 ADAPEFVEMS VEQEILVTGI KVVDLLAPYA KGGKIGLFGG AGVGK**TVLIM ELINNVAK**AH GGYSVFAGVG ERTREGNDLY

241 HEMIESGVIS LKDKTSKVAL VYGQMNEPPG ARAR**VALTGL TVAEYFRDQE GQDVLLFIDN IFR**FTQAGSE VSALLGRIPS

321 AVGYQPTLAT DMGTMQERIT TTKKGSITSV QAIYVPADDL TD**PAPATTFA HLDATTVLSR** AIAELGIYPA VDPLDSTSRI

401 MDPNIIGAEH YNIARGVQKI LQDYKSLQDI IAILGMDELS EEDKLTVARA RKIQRFLSQP FQVAEVFTGH AGKLVPLQET

481 IKGFQKILAG DYDHLPEVAF YMVGPIEEVV AKAESLAKQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	275	303	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	363	380	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	206	218	
total 3 peptides												

tr|Q1HPT1|Q1HPT1_BOMMO back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLGAISRVGS GILAVKSVAE KSLSECGKIV AVNAVNKRDY AAKSAGKGQG KVVAVIGAVV DVQFEDNLPP ILNALEVQNR

81 SPRLVLEVAQ HLGENTVRTI AMDGTEGLVR GQPVLDSGSP IRIPVGAETL GRIINVIGEP IDERGPIPTD KTAAIHAEAP

161 EFVDMSVQQE ILVTGIKVVD LLAPYAKGGK IGLFGGAGVG K**TVLIMELIN NVAK**AHGGYS VFAGVGERTR EGNDLYHEMI

241 ESGVISLKDK TSKVALVYGQ MNEPPGARAR **VALTGLTVAE YFRDQEGQDV LLFIDNIFR**F TQAGSEVSAL LGRIPSAVGY

321 QPTLATDMGT MQERITTTKK GSITSVQAIY VPADDLTD**PA PATTFAHLDA TTVLSR**AIAE LGIYPAVDPL DSTSRIMDPN

401 IIGAEHYNVA RGVQKILQDY KSLQDIIAIL GMDELSEEDK LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPLEETIKGF

481 SKILAGDYDH LPEVAFYMVG PIEEVVAKAD TLAKNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	271	299	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	359	376	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	202	214	
total 3 peptides												

tr|I4DIU5|I4DIU5_PAPXU back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSTAGRAGL LAARTVVNNS LAEKTPLVAG ALANKRDYAA KAAGKGQGKV VAVIGAVVDV QFEDNLPPIL NALEVQNRSP
81 RLVLEVAQHL GENTVRTIAM DGTEGLVRGQ PVLDSGSPIR IPVGAETLGR IINVIGEPID ERGPIPTDKT AAIHAEAPEF
161 VDMSVEQEIL VTGIKVVDLL APYAKGGKIG LFGGAGVGK**T VLIMELINNV AK**AHGGYSVF AGVGERTREG NDLYHEMIES
241 GVISLKDKTS KVALVYGQMN EPPGARAR**VA LTGLTVAEYF RDQEGQDVLL FIDNIFR**FTQ AGSEVSALLG RIPSAVGYQP
321 TLATDMGTMQ ERITTTKKGS ITSVQAIYVP ADDLTD**PAPA TTFAHLDATT VLSR**AIAELG IYPAVDPLDS TSRIMDPNII
401 GAEHYNVARG VQKILQDYKS LQDIIAILGM DELSEEDKLT VARARKIQRF LSQPFQVAEV FTGHAGKLVP LEETIKGFSK
481 ILQGEYDHLP EVAFYMVGPI EEVVAKAETL AKNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	269	297	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	357	374	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	200	212	
total 3 peptides												

tr|A0A1B0CLT6|A0A1B0CLT6_LUTLO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSAINNAVR VATKRETGKF ISGLVQFNRQ YAAKTAAKAG ASNGRVVAVI GAVVDVQFDE NLPPILNALE VEGRKPRLVL
81 EVAQHLGENT VRTIAMDGTE GLVRGNKVLD TGSPIKIPVG AETLGRIINV IGEPIDERGP IETNKFAAIH AEAPEFVEMS
161 VEQEILVTGI KVVDLLAPYA KGGKIGLFGG AGVGK**TVLIM ELINNVAK**AH GGYSVFAGVG ERTREGNDLY NEMIESGVIS
241 LKDKTSKVAL VYGQMNEPPG ARAR**VALTGL TVAEYFRDQE GQDVLLFIDN IFR**FTQAGSE VSALLGRIPS AVGYQPTLAT
321 DMGSMQERIT TTKKGSITSV QAIYVPADDL TD**PAPATTFA HLDATTVLSR** AIAELGIYPA VDPLDSTSRI MDPNVIGQEH
401 YNVARGVQKI LQDYKSLQDI IAILGMDELS EEDKLTVARA RKIQRFLSQP FQVAEVFTGH AGKLVPLEET IKGFSKILIG
481 EYDHLPEVAF YMVGPIEEVV AKAERLAKEA A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	265	293	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	353	370	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	196	208	
total 3 peptides												

tr|A0A1I8NT76|A0A1I8NT76_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSAARSALS RSDKKVISLL AQSQREYAKA AAKAAAVGNG KIVAVIGAVV DVQFEDQLPP ILNALEVDNR TPRLVLEVAQ
81 HLGENTVRTI AMDGTEGLVR GHKVIDTGFP IRIPVGAETL GRIINVIGEP IDERGPIPTD KTAPIHAEAP EFVDMSVEQE
161 ILVTGIKVVD LLAPYAKGGK IGLFGGAGVG K**TVLIMELIN NVAK**AHGGYS VFAGVGERTR EGNDLYNEMI ESGVISLKDK
241 TSKVALVYGQ MNEPPGARAR **VALTGLTVAE YFRDQEGQDV LLFIDNIFR**F TQAGSEVSAL LGRIPSAVGY QPTLATDMGS
321 MQERITTTKK GSITSVQAIY VPADDLTD**PA PATTFAHLDA TTVLSR**AIAE LGIYPAVDPL DSTSRIMDPN IIGSTHYNVA
401 RGVQKILQDY KSLQDIIAIL GMDELSEEDK LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPLEETIKGF TQILAGEYDH
481 LPEVAFYMVG PIEEVVEKAE RLAKEAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	261	289	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	349	366	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	192	204	
total 3 peptides												

tr|A0A182FTY6|A0A182FTY6_ANOAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSSMKTLVS AAVRADQVLA RTYAAKAAAA AAGAQGKVVA VIGAVVDVQF DDNLPPILNA LEVQGRTARL VLEVAQHLGE
81 NTVRTIAMDG TEGLVRGQRV LDTGSPIRIP VGAETLGRII NVIGEPIDER GPIETNLSAP IHAEAPEFIE MSVEQEILVT
161 GIKVVDLLAP YAKGGKIGLF GGAGVGK**TVL IMELINNVAK** AHGGYSVFAG VGERTREGND LYNEMIEGGV ISLKDKSSKV
241 ALVYGQMNEP PGARAR**VALT GLTVAEYFRD QEGQDVLLFI DNIFR**FTQAG SEVSALLGRI PSAVGYQPTL ATDMGSMQER
321 ITTTKKGSIT SVQAIYVPAD DLTD**PAPATT FAHLDATTVL SR**AIAELGIY PAVDPLDSTS RIMDPNIIGA EHYNIARGVQ
401 KILQDYKSLQ DIIAILGMDE LSEEDKLTVA RARKIQRFLS QPFQVAEVFT GHAGKLVPLE ETIKGFTKIL NGELDHLPEV
481 AFYMVGPIEE VVEKAERLAK EAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	257	285	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	345	362	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	188	200	
total 3 peptides												

tr|E3XEC7|E3XEC7_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSSMKTLVS AAVRADQVLA RTYAAKAAAA AAGAQGKVVA VIGAVVDVQF DDNLPPILNA LEVQGRTARL VLEVAQHLGE
81 NTVRTIAMDG TEGLVRGQRV LDTGSPIRIP VGAETLGRII NVIGEPIDER GPIETNLSAP IHAEAPEFIE MSVEQEILVT
161 GIKVVDLLAP YAKGGKIGLF GGAGVGK**TVL IMELINNVAK** AHGGYSVFAG VGERTREGND LYNEMIEGGV ISLKDKSSKV
241 ALVYGQMNEP PGARAR**VALT GLTVAEYFRD QEGQDVLLFI DNIFR**FTQAG SEVSALLGRI PSAVGYQPTL ATDMGSMQER
321 ITTTKKGSIT SVQAIYVPAD DLTD**PAPATT FAHLDATTVL SR**AIAELGIY PAVDPLDSTS RIMDPNIIGA EHYNIARGVQ
401 KILQDYKSLQ DIIAILGMDE LSEEDKLTVA RARKIQRFLS QPFQVAEVFT GHAGKLVPLE ETIKGFTKIL NGELDHLPEV
481 AFYMVGPIEE VVEKAERLAK EAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	257	285	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	345	362	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	188	200	
total 3 peptides												

tr|A0A0P4WJ96|A0A0P4WJ96_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKLERRRSTL LRWLTKTETA AMADEAAIAN GKIVAVIGAV VDVQFEDQLP PILNALEVSN RSPRLILEVA QHLGENTVRT
81 IAMDGTEGLI RGQPVLDTGS PIKIPVGPET LGRIMNVIGE PIDERGPIVT DKFAAIHAEA PEFVEMNVAQ EILITGIKVV
161 DLLAPYAKGG KIGLFGGAGV GK**TVLIMELI NNVAK**AHGGY SVFAGVGERT REGNDLYHEM IESGVISLKD KTSKVALVYG
241 QMNEPPGARA R**VALTGLTVA EYFRDQEGQD VLLFIDNIFR** FTQAGSEVSA LLGRIPSAVG YQPTLATDMG SMQERITTTK
321 KGSITSVQAI YVPADDLTD**P APATTFAHLD ATTVLSR**AIA ELGIYPAVDP LDSTSRMMDP NIIGDVHYNA ARGVQKILQD
401 YKSLQDIIAI LGMDELSEDD KLTVARARKI QRFLSQPFQV AEVFTGHAGK LVPIAETIKG FKMILNGELD HLPEAAFYMV
481 GPIEEVVAKA EKLAESTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	252	280	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	340	357	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	183	195	
total 3 peptides												

tr|A0A0P5ULZ6|A0A0P5ULZ6_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLNAVARASS GILRTVQPTV SHIQNGQSKV LPALLGKRSF YTSQLLSAEA KTAAKAAIAN GKIVAVIGAV VDVQFEDQLP

81 PILNALEVSN RSPRLILEVA QHLGENTVRT IAMDGTEGLI RGQPVLDTGS PIKIPVGPET LGRIMNVIGE PIDERGPIVT

161 DKFAAIHAEA PEFVEMNVAQ EILITGIKVV DLLAPYAKGG KIGLFGGAGV GK**TVLIMELI NNVAK**AHGGY SVFAGVGERT

241 REGNDLYHEM IESGVISLKD KTSKVALVYG QMNEPPGARA R**VALTGLTVA EYFRDQEGQD VLLFIDNIFR** FTQAGSEVSA

321 LLGRIPSAVG YQPTLATDMG SMQERITTTK KGSITSVQAI YVPADDLTD**P APATTFAHLD ATTVLSR**AIA ELGIYPAVDP

401 LDSTSRMMDP NIIGDVHYNA ARGVQKILQD YKSLQDIIAI LGMDELSEDD KLTVARARKI QRFLSQPFQV AEVFTGHAGK

481 LVPIAETIKG FKMI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	92.63	3341.7295	-8.2	1114.9080	3	43.95	1576	1	282	310	
D.PAPATTFAHLDATTVLSR.A	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	370	387	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	213	225	
total 3 peptides												

tr|A0A1V9X7H2|A0A1V9X7H2_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETGAGK HVPRAVYVDL EPTVVDEVRT

d Deam

P Pyro-

81 GTYR**QLFHPE QLITGKEDAA NNYARGHYTI GKELIDLVLD RIR**KLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

161 YGKKSKLEFA VYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQHTVAE ITNACFEPAN QMVKCDPRHG KYMACCLLYR

321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDTAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGIDSN EGGAEDDGGD EF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	244	264	
R.GHYTIGKELIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	106	121	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	230	243	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	244	264	Deamidation (NQ)
R.GHYTIGKELIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	106	123	
R.Q(-17.03)LFHPEQLITGKEDAANNYAR.G	N	15.06	2397.1711	-25.5	800.0439	3	23.91	883	1	85	105	Pyro-glu from Q
total 6 peptides												

tr|A0A2A3E7F9|A0A2A3E7F9_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MYIENAFCSR TIDCREAWTS PEGSFVHLGG RIEKREVLSV HIGQGGVQMG NACWELYCLE HGIQPDGMLP PTSCSSDEGF

d Deam

81 QTFFSETGGG KYVPRAVFLD LEPTVIDEVR TGTYHQLFHP EQLISGKEDA ANNYAR**GHYT LGKEIIDLVL DRIR**KIADMC

161 TGLQGFLIFH AFGGGTGSGF TSLLMERLSM DYGKKAKLEF AIYPSPQIST AVVEPYNAIL TTHTTLEHSD CAFLVDNEAI

241 YDICRRNLDI ERPTYTNLNR **LIGQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL ATYAPIVSIE KAYHEQLTVM

321 ELTSSCFEPA MQMVKCNPQR GKYMACCLLY RGDVVPKDVN ASIATIKTKR AIQFVDWCPT GFKVGINYQP PTVVPGGDLA

401 KVQRAMAMLA NTTAIAEAWT RLNRKFDLMF GKRAFVHWYV AESMDESEFN EAREDLAALE KDYEEVGMDS TDAGEGEDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	275	295	
R.GHYTLGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	137	152	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	261	274	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	275	295	Deamidation (NQ)
R.GHYTLGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	137	154	
total 5 peptides												

tr|A0A088ATP8|A0A088ATP8_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MCMKNAFCPR TIDLQLSRRD FTLRMFCSFS GIGKREVLSV HIGQGGVQMG NACWELYCLE HGIQPDGMLP PTSCSSDEGF d Deam
81 QTFFSETGGG KYVPRAVFLD LEPTVIDEVR TGTYHQLFHP EQLISGKEDA ANNYAR**GHYT LGKEIIDLVL DRIR**KIADMC
161 TGLQGFLIFH AFGGGTGSGF TSLLMERLSM DYGKKAKLEF AIYPSPQIST AVVEPYNAIL TTHTTLEHSD CAFLVDNEAI
241 YDICRRNLDI ERPTYTNLNR **LIGQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL ATYAPIVSIE KAYHEQLTVM
321 ELTSSCFEPA MQMVKCNPQR GKYMACCLLY RGDVVPKDVN ASIATIKTKR AIQFVDWCPT GFKVGINYQP PTVVPGGDLA
401 KVQRAMAMLA NTTAIAEAWT RLNRKFDLMF GKRAFVHWYV AESMDESEFN EAREDLAALE KDYEEVGMDS TDAGEGEDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	275	295	
R.GHYTLGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	137	152	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	261	274	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	275	295	Deamidation (NQ)
R.GHYTLGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	137	154	
total 5 peptides												

tr|A0A0K2TRK8|A0A0K2TRK8_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGSQMGNAC WELYCLEHGI QPDGHMPSDK TVGSADDSFN TFFSETGAGK HVPRAVFVDL EPTVIDEIRT d Deam
81 GTYRQLFHPE QLVTGKEDAA NNYAR**GHYTI GKEILDLVLD RIR**KLSDNCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVATA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVSE VTNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSL DPEDEEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	244	264	
R.GHYTIGKEILDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	106	121	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	230	243	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	244	264	Deamidation (NQ)
R.GHYTIGKEILDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	106	123	
total 5 peptides												

tr|A0A0L7QLG6|A0A0L7QLG6_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QREVLSVHIG QGGVQMGNAC WELYCLEHGI QPDGMLPPQS CSSDEGFQTF FSETGGGKYV PRAVFLDLEP TVIDEVRTGT d Deam
81 YHQLFHPEQL ISGKEDAANN YAR**GHYTLGK EIIDLVLDRI R**KTADMCSGL QGFLIFHAFG GGTGSGFTSL LMERLSMDYG
161 KKAKLEFAIY PSPQISTAVV EPYNAILTTH TTLEHSDCAF LVDNEAIYDI CRRNLDIERP TYTNLNR**LIG QIVSSITASL**
241 **RFDGALNVDL TEFQTNLVPY PR**IHFPLATY APIVSIEKAY HEQLTVMELT SSCFEPAMQM VKCNPQRGKY MACCLLYRGD
321 VVPKDVNASI ATIKTKRAIQ FVDWCPTGFK VGINYQPPTV VPGGDLAKVQ RAMAMLANTT AIAEAWTRLN RKFDLMFGKR
401 AFVHWYVQES MDESEFNEAR EDLAALEKDY EEVGMDSTDA GEGEDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	242	262	
R.GHYTLGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	104	119	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	228	241	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	242	262	Deamidation (NQ)
R.GHYTLGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	104	121	
total 5 peptides												

tr|A0A154PSW5|A0A154PSW5_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deam

1 REVLSVHIGQ GGVQMGNACW ELYCLEHGIQ PDGMLPPQSC SSDEGFQTFF SETGGGKYVP RAVFLDLEPT VIDEVRTGTY
81 HQLFHPEQLI SGKEDAANNY AR**GHYTLGKE IIDLVLDRIR** KIADMCSGLQ GFLIFHAFGG GTGSGFTSLL MERLSMDYGK

161 KAKLEFAIYP SPQISTAVVE PYNAILTTHT TLEHSDCAFL VDNEAIYDIC RRNLDIERPT YTNLNR**LIGQ IVSSITASLR**

241 **FDGALNVDLT EFQTNLVPYP R**IHFPLATYA PIVSIEKAYH EQLTVMELTS SCFEPAMQMV KCNPHRGKYM ACCLLYRGDV

d

321 VPKDVNASIA TIKTKRAIQF VDWCPTGFKV GINYQPPTVV PGGDLAKVQR AMAMLANTTA IAEAWTRLNR KFDLMFGKRA
401 FVHWYVAESM DESEFNEARE DLAALEKDYE EVGMDSTDAG EGE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	241	261	
R.GHYTLGKEIIDLVLDR.I	N	53.63	1841.0046	-30.0	614.6571	3	28.97	1053	1	103	118	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	227	240	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	241	261	Deamidation (NQ)
R.GHYTLGKEIIDLVLDRIR.K	N	20.91	2110.1897	-34.4	528.5366	4	31.29	1130	1	103	120	
total 5 peptides												

tr|A0A1W4X4A3|A0A1W4X4A3_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DPTGAYHGDS DLQLERINVY YNEASGGKYV PRAILVDLEP GTMDSVRSGP
81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDAVLDVV RK**EAESCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFDEEA EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDAVLDVVRK.E	Y	67.89	2070.0745	-32.3	691.0098	3	29.83	1081	1	104	122	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 3 peptides												

tr|A0A0F6PKG8|A0A0F6PKG8_LYGLI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DPTGSYHGDS DLQLERINVY YNEASGGKYV PRAILVDLEP GTMDSVRSGP
81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDAVLDVV RK**EAEGCDCL QGFQLTHSLG GGTGSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLSTP TYGDLNHLVS LTMSGVTTCF
241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTSRGSQQ YRALSVPELT AQMFDSKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFKR** ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFDEEQ EQEIEEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GHYTEGAELVDAVLDVVRK.E	Y	67.89	2070.0745	-32.3	691.0098	3	29.83	1081	1	104	122	
K.MSATFIGNSTAIQELFKR.I	N	55.02	2013.0353	-35.1	671.9955	3	27.94	1017	1	363	380	
R.YLTVAAIFR.G	N	36.00	1052.6018	-21.0	527.2971	2	26.15	958	1	310	318	
total 3 peptides												

tr|A0A1J1HUL7|A0A1J1HUL7_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deam
P Pyro-

1 MTKMRECISI HVGQAGVQIG NACWELYCLE HGIQPDGQMP SDKTIGGGDD SFNTFFSETG AGKHVPRAVF VDLEPTVVDE
81 VRTGTYR**QLF HPEQLITGKE DAANNYAR**GH YTIGKEIVDV VLDRIRKLAD QCTGLQGFLI FHSFGGGTGS GFTSLLMERL
161 SVDYGKKSKL EFAIYPAPHI STARECISIH VGQAGVQIGN ACWELYCLEH GIQPDGQMPS DKTMGGGDDS FTTFFSETGG
241 GHYVPR**AVFV DLEPTVIDEV R**TGTYRQLFH PEQLITGKED AANNYARGHY TIGKEIVDVV LDRIRKLADQ CTGLQGFLIF
321 HSFGGGTGSG FTSLLMERLS IDYGKKSKLE FAIYPAPHIS TAVVEPYNSI LTTHTTLEHS DCAFMVDNEA IFDICRRNLD
401 IERPTYTNLN R**LIGQIVSSI TASLRFDGAL NVDLTEFQTN LVPYPR**IHFP LVTYAPVISA EKAYHEQLSV AEITNACFEP
481 ANQMVKCDPR HGKYMACCML YRGDVVPKDV NAAIATIKTK RTIQFVDWCP TGFKVGINYQ PPTVVPGGDL GKVQRAVCML
561 SNTTAIAEAW ARLDHKFDLM YAKRAFVHWY VGEGMEEGEF SEAREDLAAL EKDYEEVGMD SGDPEDEGGR EKLNFITDRN
641 LFSHSSFDRH IVQTFPKLSL YFPIIPENLI KIIQNVHVGQ AGVQIGNACW ELYCLEHGIQ PDGQMPSDKT IGGGDDSFNT
721 FFSETGAGKH VPRAVFVDLE PTVVDEVRTG TYRQLFHPEQ LITGKEDAAN NYARGHYTIG KEIVDLVLDR IRKLADQCTG
801 LQGFLIFHSF GGGTGSGFTS LLMERLSVDY GKKSKLEFAI YPAPQVSTAV VEPYNSILTT HTTLEHSDCA FMVDNEAIYD
881 ICRRNLDIER PTYTNLNRLI GQIVSSITAS LRFDGALNVD LTEFQTNLVP YPRIHFPLVT YAPVISAEKA YHEQNSVAEI
961 TNACFEPANQ MVKCDPRHGK YMACCMLYRG DVVPKDVNAA IATIKTKRTI QFVDWCPTGF KVGINYQPPT VVPGGDLAKV
1041 QRAVCMLSNT TAIAEAWARL DHKFDLMYAK RAFVHWYVGE GMEEGEFSEA REDLAALEKD YEEVGMDSGD AEEESVNDDI
1121 MNRECISIHV GQAGVQIGNA CWELYCLEHG IQPDGQMPSD KTIGGGDDSF TTFFSETGAG KHVPRAVXIF KGPTRSMKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	426	446	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	412	425	
R.AVFVDLEPTVIDEVR.T	N	45.87	1700.8984	-18.4	851.4409	2	27.54	1004	1	247	261	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	426	446	Deamidation (NQ)
R.Q(-17.03)LFHPEQLITGKEDAANNYAR.G	N	15.06	2397.1711	-25.5	800.0439	3	23.91	883	1	88	108	Pyro-glu from Q
total 5 peptides												

tr|A0A1W4XPI9|A0A1W4XPI9_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deam

1 MKSHYHHFQR ECISVHCGQA GIQIGNACWE LYCLEHGIQP DGHMPSDKCG GDDSFNTFFC ETGAGKHVPR **AVFVDLEPTV**
81 **IDEVR**TGTYR QLFHPEQLIS GKEDAANNYA RGHYSVGKEM IDLVLDRIRK LSDQCTGLQG FLIFHSFGGG TGSGFTSLLM
161 EKLSIDFGKK SKLEFAIYPA PQIATAVVEP YNSILTTHTT LEHSDAAFMV DNEAIYDICR RNLDIDRPTY TNLNR**LIGQI**
241 **VSSITASLRF DGALNVDLTE FQTNLVPYPR** IHFPLVTYAP VISSEKAFHE QLSVNDITTA CFEPANQMVK CDPRHGKYMA
321 CCMLYRGDVV PKDVNAAIGI IKTKRTIQFV DWCPTGFKVG INYQPPTVVP GGDLAKVQRA VCMLSNTTAI AEAWARLDHK
401 FDLMYAKRAF VHWYVGEGME EGEFSEARED TAALERDYEE VGMDSNDGEA ECAEEF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	250	270	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	236	249	
R.AVFVDLEPTVIDEVR.T	N	45.87	1700.8984	-18.4	851.4409	2	27.54	1004	1	71	85	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	250	270	Deamidation (NQ)
total 4 peptides												

tr|O01943|O01943_GECLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

d Deam

1 HVGQAGVQIG NACWELYCLE HGIQPDGSMP SDKLAGQHDG SFSTFFSESG AGNHVPR**AVF VDLEPTVIDE VR**TGTYRKLF
81 HPEQLLTGKE DAANNYARGH YTIGKELIDL TMERVRKLAD QCSGLQGFLI FHSFGGGTGS GFTSLMMERL SLDYGKKSKL
161 EFAIYPAPQV ATAVVEPYNS ILTTHTTLEH SDCAFMVDNE AIYDICRRNL DIERPTYTNL NR**LIGQIVSS ITASLRFDGA**
241 **LNVDLTEFQT NLVPYPR**IHF PLVTYAPVVS SAKANHEQLS VAEITSACFE PANQMVKCDP RHGKYMACCL LYRGDVVPKD
321 VNCLIATIKT KRSIQFVDWC PTGFKVGINY QAPTVVPGGD LAKVNRAVCM LSNTTAIGEA WARLDHKFDL MYAKRAFVHW
401 YVGEVMEEGE FSEAREDLAA LEKDYEEVGL DSTDEAEEEP EEF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FDGALNVDLTEFQTNLVPYPR.I	N	63.91	2408.2012	-15.4	1205.0894	2	31.68	1145	1	237	257	
R.LIGQIVSSITASLR.F	N	48.39	1456.8613	-14.8	729.4272	2	31.20	1127	1	223	236	
total 4 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AVFVDLEPTVIDEVR.T	N	45.87	1700.8984	-18.4	851.4409	2	27.54	1004	1	58	72	
R.FDGALNVDLTEFQ(+.98)TNLVPYPR.I	N	24.08	2409.1851	-12.7	1205.5845	2	33.59	1205	2	237	257	Deamidation (NQ)
total 4 peptides												

tr|A0A023FND3|A0A023FND3_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TMLSVVGRAC SSVLKAAKPA ASLVKVNGAN SKLLPALCAT HPSSRRHAAA QAGAKAGNGH IVAVIGAVVD VQFDDNLPPI
81 LNALEVEGRK PRLVLEVAQH LGENTVRTIA MDGTEGLVRG QKVKDTQSPI KIPVGPETLG RIMNVIGEPI DERGPIPSDK
161 FLAIHQEAPE FVEMSVEQEI LVTGIKVVDL LAPYSKGGKI GLFGGAGVGK **TVLIMELINN VAK**AHGGYSV FAGVGERTRE
241 GNDLYHEMIE GGVISLKDKS SKVSLVYGQM NEPPGARARV ALTGLSVAEY FRDQEGQDVL LFIDNIFRFT QAGSEVSALL
321 GRIPSAVGYQ PTLATDMGTM QERITTTKKG SITSVQAIYV PADDLTD**PAP ATTFAHLDAT TVLSR**GIAEL GIYPAVDPLD
401 STSRIMDPNV VGQEHYDIAR GVQKILQDYK **SLQDIIAILG MDELSEEDKL TVSR**ARKIQR FLSQPFQVAE VFTGQAGKFV
481 PIADTISGFK SILNGEMDHL PEVAFYMVGP IEEVREKAEK LAAEAT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.PAPATTFAHLDATTVLSR.G	N	38.04	1867.9791	-25.0	623.6514	3	22.48	836	1	368	385	
K.SLQDIIAILGMDELSEEDKLTVSR.A	Y	36.57	2674.3735	-27.9	892.4402	3	36.44	1300	1	431	454	
K.TVLIMELINNVAK.A	N	34.97	1456.8323	-12.1	729.4146	2	33.90	1215	1	211	223	
total 3 peptides												

tr|A0A0P6CCE9|A0A0P6CCE9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVKVGVNGFG RIGRLVTRAA ICSGKVEIVA INDPFIDLNY MVYMFQYDST HGKFNGTVKA ENGKLVINGK PITIFQERDP
81 TNIKWGEAGA EYVVESTGVF TTMEKAGAHL KGGAKRVIIS APSADAPMFV MGVNHEKYDN SLKIVSNASC TTNCLAPLAK
161 **VIHDNFGIVE GLMTTVHAIT ATQK**TVDGPS GKLWRDGRGA AQNIIPASTG AAKAVGKVIP ELNGKLTGMA FRVPTPNVSV
241 VDLTCRLEKP AKYDDIKKVV KQASEGPLKG ILGYTEDQVV SCDFNSNSHS STFDAGAGIA LNDNFVKLIS WYDNEYGYSN
321 R**VVDLMAYMA SKE**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VIHDNFGIVEGLMTTVHAITATQK.T	Y	50.94	2594.3525	-31.0	649.5753	4	33.69	1208	2	161	184	
R.VVDLMAYMASKE	Y	15.88	1355.6465	-23.3	678.8147	2	25.38	932	1	322	333	
total 2 peptides												

tr|T1ITF6|T1ITF6_STRMM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGGKKRN KSTTRSAKAG VLFPVGRLHR YLRKGTHHQR IGAGAPVYL**A AVIEYLTAEI LELAGNAAR**D NKKGRVTPRH
81 ILLAVANDEE LHQLLKGVTI ASGGVLPKIH PELLAKKKGG KFVFVNNPVS MAPVSPPYKK PKLSPAKSPK KSPVVNKTVK
161 GKPKGKGAKD NTTNSASGGT GITILSEKKL FLGQKLTVIQ GDIVNVTADA IINPTNASFY MGGEIGQTLE KVGGKEFQQE
241 IKDLISSNGQ LDSADAAICP GHNFPAKYVI HCNAPTFGSN NSNDLLEKTV KNCLTLADEK NIKSLAVPPF GTGNVTDAEA
321 LLGKTVKNCL VLADSKNLKS LALPSVGSGR AGFPKQQAAQ IILKAISNYF VNVMSSSLKQ IYFVLYDMES IGIYTSELAK
401 LDS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|L7M4J4|L7M4J4_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSARGGKKRC KAVSKSTKAG VLFPVGRIGR YLRKSTHHFR IAAGAPVYM**A AVIEYLTAEI LELAGNAAR**D NKKNRVTPRH
81 ILLAIANDDE LHQLLRGVTI ASGGVLPRIQ PELLARKKGN KFVMPSPKHQ PSALPVRVDN TPSKSHQAAV AAAAAAKPSS
161 APPPPKKVAA TAASKKQLPP TPATPTKEKS KGKGKESTGA ESSHATVTVL SEKKLFLGQK LTVIQGDMAS VTVDAAVHPT
241 NANFSLAGEV GQVLEKAGGK EFQQEVKELL GSHGPLESAG VAICPGHHFP AKHVIHCHVP TGANAVEHLE KCVRNCLELA
321 DDKNIRVLAI PPLITHNTSP SQKQLAAQAV LRAISSYFVN VMGSSLKQVL FVLSDMESIG IYASELAKLD S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|A0A224YUU6|A0A224YUU6_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSARGGKKRC KAVSKSTKAG VLFPVGRIGR YLRKSTHHFR IAAGAPVYM**A AVIEYLTAEI LELAGNAAR**D NKKNRVTPRH
81 ILLAIANDDE LHQLLRGVTI ASGGVLPRIQ PELLARKKGN KFVMPSPKHQ PSALPMRINN TPSKPHQAAV TAAAAAKPTS
161 APPPPKKVAA TAASKKQLPP TPAAPAKEKS KGKGKESTGA EPSHTTVTVL SEKKLFLGQK LTVIQGDMAS VTVDAAVHPT
241 NANFSLAGEV GQVLEKAGGK EFQQEVKELL ASHGPLESAG VAICPGHHFP AKHVIHCHVP TGANAVEHLE KCVRNCLELA
321 DDKNIRVLAI PPLITHNTSP SQKQLAAQAV LRAISSYFVN VMGSSLKQVL FVLSDMESIG IYASELAKLD S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|A0A293LN19|A0A293LN19_ORNER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSARGGKKRS KSVSKSTKAG VLFPVGRMRR YLRKGTHHFR IGAGAPVYM**A AVIEYLTAEI LELAGNAAR**D NKKGRVTPRH
81 ILLAIANDDE LHQLLKGVTI ASGGVLPRLL PELLARKKGG KFIMPSPKHQ PSSTTTYTPP KSPPKKNPPK KLTQAVLAAK
161 EKGKGAKGKD VQSSGSEQTH ASVTVLSEKK LFLGQKLTVI QGDIVNVTAD ALIHPTNMTL SLSGEVGQAL EKSGGKEFVQ
241 EVKDLLASNG PLESAGAAIC SGHNFPAKFV VHCNLPANSV ANGSELLEKC VRNCLSLADE KNIRALAVPA LGTHSAGFTK
321 QQAAQVILKA ISNYFVNIMS SSLKQIYFVL SDMESIGIYT SELAKLDS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|A0A293LE62|A0A293LE62_ORNER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSARGGKKRS KSVSKSTKAG VLFPVGRMRR YLRKGTHHFR IGAGAPVYM**A AVIEYLTAEI LELAGNAAR**D NKKGRVTPRH
81 ILLAIANDDE LHQLLKGVTI ASGGVLPRLL PELLARKKGG KFIMPSPKHQ PSSTTTYTPP KSPPKKNPPK KLTQAVLAAK
161 EKGKGAKGKD VQSSGSEQTH ASVTVLSEKK LFLGQKLTVI QGDIVNVTAD ALIHPTNMTL SLSGEVGQAL EKSGGKEFVQ
241 EVKDLLASNG PLESAGAAIC SGHNFPAKFV VHCNIPANSV ANGSELLEKC VRNCLSLADE KNIRALAVPA LGTHSAGFTK
321 QQAAQVILKA ISNYFVNIMS SSLKQIYFVL SDMESIGIYT SELAKLDS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|G3MG27|G3MG27_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSARGGKKRC KAVSKSAKAG VLFPVGRIGR YLRKSTHHFR IGAGAPVYM**A AVIEYLTAEI LELAGNAAR**D TKKGRVTPRH
81 ILLAIANDDE LHQLLRGVTI ASGGVLPRIL PELLARKKGN KFIMPSPKHQ SPTVNVIIPP PKAKPVNKPV PPPPPKKAVT
161 AASKKQTAPL LPSAPTPLKD KGRSAKGKDA AGGELSHSSV TVLSEKKLFL GQKLTVIQGD VASVTADAAI HPTNANFSLS
241 GEVGQVLDKV GGKEFQQEVK ELLASHGPLE SSGVAICPGH HFPAKHVLHC HVPPASGANA AELLEKCVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	50	69	
total 1 peptides												

tr|A0A087U9P4|A0A087U9P4_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 M**AAVIEYLTA EILELAGNAA R**DNKKGRVTP RHILLAVAND EELHLLLKNV TIASGGVLPR IEPELLAKKK GRFVTMPSPR

81 SGPSSPAPAS STKKAKPVYT SPKKMPRKAS ASIKGKGKGK GKASKDLPNS LSNQAGAVTM LSEKKLFLGQ KLIVIQGDII

161 NVTSDAVLHP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVIEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	2	21	
total 1 peptides												

tr|A0A0A9Z7N0|A0A0A9Z7N0_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IEKIMAKGKG GLANVDRTKP RKPRKTRSQK AGLQFPVLQI HRALKKGRFA KKIFGGAPVY L**AAVLEYLTA ELLELAGNAA**

81 **R**DNKKSRVIP RHLQLAVRND EELNKLLAGV TISEGGVLPF IHNVLLQKKT REYEKKDGQK NMSQEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AAVLEYLTAELLELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	62	81	
total 1 peptides												

tr|A0A1B6LDW1|A0A1B6LDW1_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAPVPASGSG RGKKDATKRV SKATKAGLTF PPSRFIRMLK KGKYSSKIGV GAGVYL**AAVL EYLTAEILEL AGNAAR**DNKK

81 SRVIPRHIQL AIRNDEELSK LLGSVVLPAG GVLPHIQAVL LPKKGKESQV GPAKGGKTSN TLSQEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AAVLEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	57	76	
total 1 peptides												

tr|A0A146KQ63|A0A146KQ63_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KIMAKGKGGL ANVDRTKPRK PRKTRSQKAG LQFPVLQIHR ALKKGRFAKK IFGGAPVYL**A AVLEYLTAEL LELAGNAAR**D

81 NKKSRVIPRH LQLAVRNDEE LNKLLAGVTI SEGGVLPFIH NVLLQKKTRE YEKKDGQKNM SQEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AAVLEYLTAELLELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	60	79	
total 1 peptides												

tr|A0A0P6A1I4|A0A0P6A1I4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGKARAKAKS GRGKQGGKAR AKAKSRSSRA GLQFPVGRVH RLLRKGNYAE RVGAGAPVYM **AAVLEYLTAE ILELAGNAAR**

81 DNKKTRIIPR HLQLAIRNDE ELNKLLGRVT IAQGGVLPNI QAVLLPKKTE SHHKAKGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVLEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	61	80	
total 1 peptides												

tr|A0A1W4WD58|A0A1W4WD58_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKSGKA RTKAKTRSSR AGLQFPVGRV HRFLRKGSYA QRVGAGAPVY M**AAVLEYLTA EILELAGNAA R**DNKKSRIIP

81 RHLQLAVRND EELNKLLGGV TIAQGGVLPN IQAVLLPKKT AKSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.AAVLEYLTAEILELAGNAAR.D	Y	51.75	2087.1262	-29.3	696.6956	3	45.15	1623	1	52	71	
total 1 peptides												

tr|A0A1B0GP78|A0A1B0GP78_PHLPP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDLLSVPLK KPAEVDVVKP LKNLILSSYG SSDKIANYTE AVNEFSKLRN SAIWKFFEKF ESSLDIVYNY YDQLCGLETK

81 IPVQELQIPF KWKDAFSKGS IFGGRASLTL SSLGYEKVCV LFNIAALQSA VAGAQSLDSD EGLRLATKLY QQSAGIFTHL

161 KAAVPAAIPQ EPTPDLYQEV LTVLTNLMVA QAQEIFVVKA IRDKMKEQVI AKLCCQCEEF YAESLRGLQK ESVRNLWEKE

241 WITTVAGKQA GFHAMTQLYT SLACRANKKV GEEIARLQHA VELFKAAQSR SGKSSMFQEY AERAQRNLVE SKKDNDFIYN

321 EIIPDVKTLD GPGKAQLAKA ITLSSPLGSN YKDLFGDLVP VALHQALSAC EARKTEMVNV EIQKLREATQ MLNSVLASLN

401 LPAAIESTAG GSGLPPSLQD KAKGVRDNGG VSQITRMFKE LPEALTRNKE ILDECDRMLN DERDSDNALK NQFKERWTRT

481 PSEKLTEVFR SNIAKYRDII NKAVQADAIV RGKFESHMNG IEILSKSPDE LERSVPNTGS AGVSNSPSVM KLRSLMESVE

561 TIKAERDAIE AELKSATINM KEQFLSALAK DGAINEPALS VAEIGKTLAP LQAQVQESIK RQEGILSEVQ SAHTTFTNES

641 GGASNTRDAL LIQLAAAYDT FMELQGNLKE GTKFYNELTE LLVTFQNKIS DFCFARKTEK DELMKDLTQQ TSRAVAPTPQ

721 LPAHHATTPA VPTSTVDGSV PYPASGMANM PMPYGASPAA PYPTYVAPPM PQGFNPYAPL PYPQTPYYQG FPQGPPPSHY

801 ATYPGSLAHQ QQQQQPGQPG YPRGAKRHRK VLRDNIQGIT KPAIRRLARR GGVKRISGLI YEETRGVLK**V FLENVIRDAV**

881 **TYTEHAK**RKT VTAMDVVYAL KRQGRTLYGF GG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VFLENVIRDAVTYTEHAK.R	Y	41.52	2104.0952	-27.2	702.3533	3	29.94	1086	1	870	887	
total 1 peptides												

tr|A0A0P6CVG1|A0A0P6CVG1_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMGVLDGVLM ELQDCALPLL QDVIATDKEE IAFKDLDVAV LVGSMPRREG MERKDLLKAN VKIFKSQGTA LEKYAKKSVK

81 VIVVGNPANT NCLTASKSAP SIPKENFSCL TRLDHNRAKS QIALKLGVTA DDVKNVIIWG NHSSTQYPDV NHAKVKLQGK

161 EVGVYEALKD DSWLKGEFIT TVQQRGAAVI KARKLSSAMS AAKAIADHIR DIWFGTPEGE FVSMGVISDG NSYGVPDDLL

241 YSFPVVIKNK TWKFVEGLPI NDFSREKMDL TAK**ELTEEKE TAFEFLSSA**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.ELTEEKETAFEFLSSA	Y	40.23	1829.8571	-19.0	915.9185	2	26.83	980	1	274	289	
total 1 peptides												

tr|A0A0L7KSH4|A0A0L7KSH4_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQLIDEECRT LKYDREVSDL LQSSSTGLPI LCQQFWVEVG KISNSDGMLK YKNITSFSAV FTEEARGGSS ELAFKYAVYR

81 INKEKSLLPN STLVYDIQYT PERDSFKTYK KACAQIKSGA VALFSGEGVT LGATLGALCR SLRAPHMLAA PAPAALHSTN

161 STFTVNLYPP RELMVKAFSD LIGYLNWTRM GVIYEDYGYG ELNMLDLGDG RDMYAVRVSD AEEYRRALAL IKAQRIGNII

241 VDTDPTKMRQ LGRALQLMRL SGGEGGGTVL AGHWTPGEGL AITDPAAYKR **DPPPNVTLT**V VTVEVSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	291	299	
total 1 peptides												

tr|A0A075TD97|A0A075TD97_HELAM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IHPGNVSCDK DTPSLHGKAI YDNINTIQAH GLTGPLEFKQ GIRKNFHLQL MRLTGGEKGG MVVSGTWSPA EGLAITDPAA

81 YTR**DPPPNVT LT**VVTVEEKP YVMVKEGWNL QGNARFEGFC IDLLARVAAR AGFHYRLRLV PDNMYGARDP DTGHWNGIVR

161 ELMDRKADIA VASMTINYAR EAVIDFTKPF MNLGIGILFK VPTSQPTRLF SFLNPLAIEI WLYVLAAYIL VSFTLFVMAR

241 FSPYEWSTST HVCGHETKLL TNQFSVCNSF WFITGTFLRQ GSGLNPKATS TRIVGGIWWF FTLIILSSYT ANLAAFLTVE

321 RTVLPIQSAA DLAAQHHIHY GTLNGGSTMS FFRDSNIDIY QKMWEHMSSA SPPALVSSYE EGVRRVLAGN YAFLMESTML

401 DHRVQRDCNL TQIGGLLDSK GYGIATWKGS PWRDKISLAI LELQEKGVIQ ILYDKWWKNT GDVCNRDGKD SKANPLGVQN

481 IGGVFVTLLC GLALAIVVAI LEFCWNTKKN ASQGRQSLCS EMGQELRTAM RGGSSSRTVL RPGCSRCSPA THVPPATSRY

561 QHSRSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	84	92	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
total 1 peptides												

tr|A0A0L7LL85|A0A0L7LL85_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGWRLVDRS ADRVQEALKA IGATEGLQAD EVSCEKDAPW ALGRTLLDNI NTLQLMRLSG GEGGGTVLAG HWTPGEGLAI

81 TDPAAYKR**DP PPNVTLT**VVT VEEKPYVMVK EGWNLQGNAR FEGFCIDLLA KVAARAGFHY RLRLVPDNMY GARDPNTGHW

161 NGIVRELVDR VSAAGSAFLN PLAIEIWLYV LAAYILVSFT LFVMARFSPY ECVCNSFWFI TGTFLRQGSG LNPKVMPSDF

241 HPYSRRHMVV FHADHPLVVH REPGCLPDSG THSVAHTERG RPRGAEQYTD SNIDIYQKMW LHMSTTSPPA LVPSYEEGVR

321 RVLSGNYAFL MESTMLDHRV QRDCNLTQIG GLLDSKRDCN LTQIGGLLDS KRDCNLTQIG GLLDSKRDCN LTQIGGLLNS

401 KVSLLNSEER GVIQILYDKW WKNTGDVCNR DGKDSKANPL GVQNIGGVFV TLLCGLALAI VVAILEFCWN TRKNATQGRQ

481 SLCRLRQVLP GHTRAARTLQ IRGNVHTQTT TPVARCRNSV DGGRHQTLEK FNGHSQKDHV VRVERAQRKE TCSNRSLELL

561 ITYKFYEYFT Y

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	89	97	
total 1 peptides												

tr|H9JJ96|H9JJ96_BOMMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRPEWRWIVV VLNVVGALSP VIKIGALFTE DERGGSEELA FKYSVYRINK ERSVLANSTL VYDIQYAPAK DTFKTYKRAC

81 SQVKSGAVAL FSSGGDLLGS TLDAICRSLH APHMLVAPQT RPTLNNESFT INLYPPRGLL NEAFGDLIGY LNWTRMGVLY

161 EDFGYGDLSI LDIAKDGRDM YAVRCVDPKD YRKSLIQLKA QRIKNVIVDT DPARFRQLAR ADMELFDLED FYYNRVNMSG

241 WRLVDRDSDK VKDALQVMEK FHPIGASILS GGHIRTAPAL LYDAVQVLAL AMSSTELVQT KNVSCDKDSP WPHGRALLEN

321 INTVQAHGLT GPIQLKDGIR TNFSLQLMRL SGGETGGTVL AGEWRPGEGL VITDPAAYRR **DPPPNVTLT**V VTVEEKPYVM

401 VKEGWNLQGN ARFEGFCIDL LARVAARAGF HYRLRLVPDN MYGARDPETG QWNGIVRELM DRKADIAVAS MTINYAREAV

481 IDFTKPFMNL GIGILFKVPT SQPTRLFSFL NPLAIEIWLY VLAAYVLVSF TLFVMARFSP YEWSTTTHVC GHETKLLTNQ

561 FSVCNSFWFI TGTFLRQGSG LNPKVTVRLI GDSLAVEFDL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	381	389	
total 1 peptides												

tr|A0A0V0J1A3|A0A0V0J1A3_CYDPO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWAWCGWLVA VHAVAAVSPV IKIGAILTDE ARGGSTELAF KYAVYRINKE RSVLPDSTLV YAIQYIPAGD SFRSYKKACH

81 EIKSGAVALF SSGGPTLSRS LNALCRSLNI IHLSSSADTA SQEDNDPDSF TVNLYPARQV MDRAFADLTA YLNWTRMGVI

161 YEDYGYGELN IANIAKDGRD MYCVRASHEY RRALTLLKAQ GVTHIIVDTD PKKLRQLARA ILQLQMNNEN YHYIFTSFDM

241 ELFDLEDFYY NRVNMSGWRL VDRDSDKVKD TLLVMEKFHP IGASILTGGH IKTEPALLYD AIQVLAMALA ASKEVGPTNA

321 SCDDETIWSN GKDIMENINK IHAHGLTGPI QFQNGVRTNF SLQLMRLVGG EKGGTVVSGH WNPGDGLTIT DPAAYKR**DPP**

401 **PNVTLT**IVTV EEKPYVMVKE GWNLQGNARF EGFCIDLLAR VAAQAGFAYR LRLVPDNMYG ARDPDTGQWN GIVRELVDRK

481 ADIAVASMTI NYAREAVIDF TKPFMNLGIG ILFKVPTSQP TRLFSFLNPL AIEIWLYVLA AYILVSFTLF VMARFSPYEW

561 SSSTHVCGHE TKLLTNQFSV CNSLWFITGT FLRQGSGLNP KATSTRIVGG IWWFFTLIIL SSYTANLAAF LTVERTVLPI

641 QSAADLAAQN SVQYGTLNGG STMTFFRDSN IDIYQKMWQH MSTTSPPALV SSYEEGVRRV LQGNYAFLME STMLDHRVQR

721 DCNLTQIGGL LDSKGYGIAT WKGSPWRDRI SLAILELQEK GVIQILYDKW WKNTGDVCNR DGKDSKANPL GVQNIGGVFV

801 TLLCGLALAI VVAILEFCWH TKKNASHGRQ SLCSEMGQEL RTAMRGGSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.I	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	398	406	
total 1 peptides												

tr|A0A194Q9S0|A0A194Q9S0_PAPXU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWREWRWLLV LLNAVAALSP VIKIGAIFTE EARGGSAELA FKYAVYRINK ERNLLPGSTL VYDIQYTTSR DTFRTYKKAC
81 TQIRAGAVAL LNSAGPLLGA TLGAMCRTLH APHLTVAHNM PESVNTSDFF TINLYPSRDL MDKAFAELTA YLNWTRMGII
161 YEDYGYGEIN ILNMASDGRD MYTVRCADSK DYRRGLQQLK AQRISHIIVD TDPKHLRQFS RAILQLQMNN ENYHYIFTSF
241 DMELFDLEDF YYNRVNMSGW RLVDRDSDKV KEALQIMQKF HPISANILTG GHIKTEPALL YDAVQILALG LASTKEVHTA
321 NMSCESGMSW IHGKTLRDNI NKIQAHGLTG PIEFSNGVRT KFKLQLMRLA GGEAGGPVLA GSWDPDQGLQ LSDPAAYRR**D**
401 **PPPNVTLT**VV TVEEKPYVMV KEGWNLQGNA RFEGFCIDLL ARVAARAGFH YTLRLVPDNM YGAWDPDTGQ WNGIVRELMD
481 RKADIAVASM TINYAREAVI DFTKPFMNLG IGILFKVPTS QPTRLFSFLN PLAIEIWLYV LAAYILVSFT LFVMARFSPY
561 EWSSSTHVCG HETKLLTNQF SVCNSFWFIT GTFLRQGSGL NPMATSTRIV GGIWWFFTLI ILSSYTANLA AFLTVERTVL
641 PIQSAADLAA QNHVQYGTLN GGSTMTFFRD SNIDIYQKMW QHMSTASPPS LVSSYEEGVR RVLAGNYAFL MESTMLDHRV
721 QRDCNLTQIG GLLDSKGYGI ATWKGSPWRD RISLAILDLQ EKGVIQILYD KWWKNTGDVC NRDGMAPLKL LRGVFVTLLC
801 GLALAIVVAI LEFCWNTKKN ASHGRQSLCS EMGQELRTAM RGGSSRTVLR PGCSRCSPAT HVPPAPSRYE VC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	400	408	
total 1 peptides												

tr|A0A2A4JAT1|A0A2A4JAT1_HELVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWPGWRWVVL MVNAVAALSP VVKIGAIFTE DARGGSTELA FKYAVYRINK ERILLPNSTL VYDIQYTPSR DTFKTYKKAC
81 AQIQSGAVAL FSSVGPLLGN TLDHMSTSLH SPHLTIGPFA PENLNHTFTI NLYPPKDLLT KAFAEFLSYL NWTRMGVIYE
161 DYGYGEPNIL DIAKDGRDMY AVRCRDAKEY RRGLALLKAQ QIEHIVVDTD PKRVRQLARA ILQLQMNNED YHYVFTSFDF
241 ELFDMEDFYY NRVNMSGWRL VDRHSDKVKE SLQVMEKFHP IGASIISGGH IKTEPALLYD AVQILCQALA LTEDIHPGNV
321 SCDKDTPSLH GKAIYDNINT IQAHGLTGPL EFKQGVRKNF HLQLMRLTGG EKGGMVVSGT WSPAEGLAIT DPAAYTR**DPP**
401 **PNVTLT**VVTV EEKPYVMVKE GWNLQGNARF EGFCIDLLAR VAARAGFHYR LRLVPDNMYG ARDPDTGHWN GIVRELMDRK
481 ADIAVASMTI NYAREAVIDF TKPFMNLGIG ILFKVPTSQP TRLFSFLNPL AIEIWLYVLA AYILVSFTLF VMARFSPYEW
561 STSTHVCGHE TKLLTNQFSV CNSFWFITGT FLRQGSGLNP KATSTRIVGG IWWFFTLIIL SSYTANLAAF LTVERTVLPI
641 QSAADLAAQH HIHYGTLNGG STMSFFRDSN IDIYQKMWEH MSSASPPALV SSYEEGVRRV LAGNYAFLME STMLDHRVQR
721 DCNLTQIGGL LDSKGYGIAT WKGSPWRDKI SLAILELQEK GVIQILYDKW WKNTGDVCNR DGKDSKANPL GVQNIGGVFV
801 TLLCGLALAI VVAILEFCWN TKKNASQGRQ SLCSEMGQEL RTAMRGGSSS RTVLRAGCSR CSPATHVPPA TSRYQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	398	406	
total 1 peptides												

tr|A0A212EM67|A0A212EM67_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWKEWRWLVL ILNAVAALSP VIKIGAIFTE EARGGSAELA FKYAVYRINK ERNLLPESTL VYDIQYTTTR DSFRTYKKAC
81 TQIKSGAIAI FSSAGPLLGS TLSAMCRTLH APHLTVAPHV VESPGLCCDY TINLYPSRDL LDTAFVDLTA FLNWTRMGII
161 YEDYGNGELN IVRLARDGRD MYAVRCESRD YRRALAQLKA QDIKHIIVDT DPKHLRLLSR AILQLQMNNE NYHYIFTTFD
241 MELFDLEDFL YNRVNMSGWR LVDRDSDKVK DVLTVMEKFH PIGASILSGG HIKTEPALIY DAVQVLALAL ASTRDVSATN
321 ASCDTETTVA YGSVLLENIN KVQAHGLTGP IAFTNGNRKT FNLQLMRLSA ERRAAVLAGH WTKDGGLEVT DPAAYRR**DPP**
401 **PNVTLT**VVTV EEKPYVMVKE GWNLQGNARF EGFCIDLLAR VAARAGFSYR LRLVPGNVYG ARDPATGQWN GIVRELVDRK
481 ADIAVASMTI NYAREAVIDF TKPFMNLGIG ILFKVPSSQP TRLFSFLNPL AVEIWLYVLA AYILVSFTLF VMARFSPYEW
561 SSSTHICGHE TKLLTNQFSV CNSFWFITGT FLRQGSGLNP KATSTRIVGG IWWFFTLIIL SSYTANLAAF LTVERTVLPI
641 QSAADLAAQN SVQYGTLSGG STMTFFRDSN IDIYQRMWDH MSRASPPALV ASYEEGVRRV LAGNYAFLME STMLDHRVQR
721 DCNLTQVGGL LDSKGYGIAT WKGSPWRDKI SLAILELQEK GVIQILYDKW WKNTGDVCNR DGKDSKANPL GVQNIGGVFV
801 TLLCGLVLAI VVAILEFCWN TKKNASQGRQ SLCSEMGQEL SAALRGGKSR AAPRPCCTRC DRGTHVPTGD VCEYGGVEGA
881 EMVIALSAAR RLRPRFPCAR VRSPSSSSTG CGFKFGSCRE FFINE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	398	406	
total 1 peptides												

tr|A0A0N1IIG3|A0A0N1IIG3_PAPMA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWREWRWLLV LLNAVAALSP VIKIGAIFTE EARGGSAELA FKYAVYRINK ERNLLPGSTL VYDIQYTTTR DTFRTYKKAC

81 TQIRAGAVAL LNSAGPLLGA TLGAMCRSLH APHLTVAHNM PESVNRSDFF TINLYPSRDL MDKAFAELTA YLNWTRMGII

161 YEDYGYGEIN ILNMARDGRD MYTVRCADSK DYRRGLQQLK AQRISHIIVD TDPKHLRQFS RAILQLQMNN ENYHYIFTSF

241 DMELFDLEDF YYNRVNMSGW RLVDRDSDKV KEALQVMQKF HPIGANILTG GHIKTEPALL YDAVQILALG LASTKEVHTA

321 NMSCESGMAW IHGKTLRDNI NKIQAHGLTG PIEFSHGIRT KFKLQLMRLE GGEGGGAVLA GSWDPDEGLQ LSDPAAYRR**D**

401 **PPPNVTLT**VV TVEEKPYVMV KEGWNLQGNA RFEGFCIDLL ARVAARAGFH YTVRLVPDNM YGAWDPDTGQ WNGIVRELMD

481 RKADIAVASM TINYAREAVI DFTKPFMNLG IGILFKVPTS QPTRLFSFLN PLAIEIWLYV LAAYILVSFT LFVMARFSPY

561 EWSSSTHVCG HETKLLTNQF SVCNSFWFIT GTFLRQGSGL NPMATSTRIV GGIWWFFTLI ILSSYTANLA AFLTVERTVL

641 PIQSAADLAA QNHVQYGTLN GGSTMTFFRD SNIDIYQKMW QHMSTASPPS LVSSYEEGVR RVLAGNYAFL MESTMLDHRV

721 QRDCNLTQIG GLLDSKGYGI ATWKGSPWRD RISLAILDLQ EKGVIQILYD KWWKNTGDVC NRDGKDSKAN PLGVQNIGGV

801 FVTLLCGLAL AIVVAILEFC WNTKKNASHG RQSLCSEMGQ ELRTAMRGGS SRTVLRPGCS RCSPATHVPP APSRYEYCRT

881 QGAAVVVARG ARARIRARIA RAPRPPAPRT RPTRPTRPAH PTHPTHPAPA TLQALQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DPPPNVTLT.V	Y	38.13	952.4866	-75.6	953.4218	1	12.91	568	1	400	408	
total 1 peptides												

tr|Q5TWK1|Q5TWK1_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSALLLLCCW LALLPSPEAH TIIERPSRPS PEDYRYQRAL LASEESALAF GADIPLAGNE ILVNNHLMDL KRDELEKGYT

81 NPFNFSPARH FFEVLDQINA SPLFRFVREL PKGAVLHAHD TALASTEVIV KATYQPHLWQ RGCFEHGRQP EFLFSRTKPT

161 APQRGNKHND GDDDDDWELV QTVRERMGPA RYDEHVRQLF SLYTLDPQTA YRSINDVWDR FSQIFLAFNP IVTYRPVWEF

241 YFREALREFH EDNV**LYLEFR GLLPT**LYDLD GKTYGPEEVV QIYRTITEEF KATHPRFAGT KFIYAPLRLV DNQTMDQYLS

321 LAERLHRLHG DYVVAFDLVG QEDLGRQLLD FVPQLLQLPA SINFVFHAGE TNWNGMPSDG NLFDAIMLGT KRIGHGYSLL

401 KHPLLLEKVR QRNICVEINP VSNQVLRLVA DHRNHPASVL FASDFPLVVS SDDPSFWRAA PLSHDFYMAF LGMTRVGQDL

481 RVFKKLALNS IRYSLMSDRE KEVALGKFEL AWDGFIDRKA EQLRASSRNE V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	255	265	
total 1 peptides												

tr|A0A182TCZ3|A0A182TCZ3_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LLLLCCGLAL LPSPEAHTII ERPSRPSPED YRYQRALLAS EEAALAFGAD ITLDGNEILV NNHLMDLKRE ELEKGYTNPF

81 NFSPARHFFE VLDQINASPL FRFVRELPKG AVLHAHDTAL ASTEVIVKAT YQPHLWQRGR FEHGRQPEFI FSRTKPTAPQ

161 RGNKHNDDDD DDDDDDWELV QTVRERMGPA RYDEHVRQLF SLYTPDPQTA YRSINDVWDR FSQIFLAFNP IVTYRPVWEF

241 YFREALREFH EDNV**LYLEFR GLLPT**LYDLD GKTYGPEEVV QIYRTITEDF KATHPRFAGT KFIYAPLRLV DNQTMDQYLS

321 LAERLHRLHG DYVVAFDLVG QEDLGRQLLD FVPQLLELPA SINFVFHAGE TNWNGMPSDG NLFDAIMLGT KRIGHGYSLL

401 KHPLLLEKVR QRNICVEINP VSNQVLRLVA DHRNHPASVL FASDFPLVVS SDDPSFWRAA PLSHDFYMAF LGMTTVGQDL

481 RVFKKLALNS IRYSLMSDRE KEVALGKFQL AWDGFIDRKA EQLRASSRNE V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	255	265	
total 1 peptides												

tr|A0A182UV11|A0A182UV11_ANOME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARLAKQPSA FRCRTIVFQP KLTCSSSLLL LCCWLALLPS PEAHTIIERP SRPSPEDYRY QRALLASEEA DLAFGADITL

81 DGNEVLVNNH LMDLKREELE KGYTNPFNFS PARHFFEVLD QINASPLFRF VRELPKGAVL HAHDTALAST EVIVKATYQP

161 HLWQRGRFEH GRQPEFLFSR TKPTAPQRGN NHDDDDDWEL VQTVRERMGP ARYDEHVRQL FSLYTPDPQT AYRSINDVWD

241 RFSQIFLAFN PIVTYRPVWE FYFREALREF HEDNV**LYLEF RGLLPT**LYDL DGKTYGPEEV IQIYRTITEE FKATHPRFAG

321 TKFIYAPLRL VDNQTMDQYL SLAERLHRLH GDYVVAFDLV GQEDLGRQLL DFVPQLLELP ASINFVFHAG ETNWNGMPSD

401 GNLFDAIMLG TKRIGHGYSL LKHPLLLEKV RQRNICVEIN PVSNQVLRLV ADHRNHPASA LFASDFPLVV SSDDPSFWRA

481 APLSHDFYMA FLGMTKVGQD LRVFKKLALN SIRYSLMSDR EKEVALGKFQ LAWDGFIDRK AEQLRASSRN EV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	276	286	
total 1 peptides												

tr|A0A2C9GS79|A0A2C9GS79_ANOAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARLAKQPTA FRCRTIVFQP KLTCSSSLLL LCCWLALLPS PEAHTIIERP SRPSPEDYRY QRALLASEEA DLAFGADIPL

81 AGNEILVNNH LMDLKRQELE KGYTNPFNFS PARHFFEVLD QINASPLFRF VRELPKGAVL HAHDTALAST EVIVKATYQP

161 HLWQRGCFEH GRQPEFLFSR TKPTAPQRGN KHNDDDDDDW ELVQTVRERM GPARYDEHVR QLFSLYTPDP QTAYHSINDV

241 WDRFSQIFLA FNPIVTYRPV WEFYFREALR EFHEDNV**LYL EFRGLLPT**LY DLDGKTYGPE EVVQIYRTIT EEFKATHPRF

321 AGTKFIYAPL RLVDNQTMDQ YLSLAERLHR LHDDYVVAFD LVGQEDLGRQ LLDFVPQLLE LPASINFVFH AGETNWNGMP

401 SDGNLFDAIM LGTKRIGHGY SLLKHPLLLE KVRQRNICVE INPVSNQVLR LVADHRNHPA SVLFASDFPL VVSSDDPSFW

481 RAAPLSHDFY MAFLGMTTVG QDLRVFKKLA LNSIRYSLMS DREKEVALGK FQLAWDGFID RKAEQLRASS RNEV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	278	288	
total 1 peptides												

tr|A0A182L3Q7|A0A182L3Q7_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LTTTMARLAK QPSAFRCRTI VFQPKLTCSS SLLLLCCWLA LLPSPEAHTI IERTSRPSPE DYRYQRALLA SEEADLAFGA

81 DIPLAGNEIL VNNHLMDLKR QELEKGYTNP FNFSPARHFF EVLDQINASP LFRFVRELPK GAVLHAHDTA LASTEVIVKA

161 TYQPHLWQRG RFEHGRQPEF LFSRTKPTAP QRGNKHNDDD DDDWELVQAV RERMGPARYD EHVRQLFSLY TPDPQTAYRS

241 INDVWDRFSQ IFLAFNPIVT YRPVWEFYFR EALREFHEDN V**LYLEFRGLL PT**LYDLDGKT YGPEEVVQIY RTITEEFKAT

321 HPRFAGTKFI YAPLRLVDNQ TMDQYLSLAE RLHRLHGDYV VAFDLVGQED LGRQLLDFVP QLLELPASIN FVFHAGETNW

401 NGMPSDGNLF DAIMLGTKRI GHGYSLLKHP LLLEKVRQRN ICVEINPVSN QVLRLVADHR NHPASVLFAS DFPLVVSSDD

481 PSFWRAAPLS HDFYMAFLGM TTVGQDLRVF KKLALNSIRY SLMSDREKEV ALGKFQLAWD GFIDRKAEQL RASTWNEV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	282	292	
total 1 peptides												

tr|A0A182WWF7|A0A182WWF7_ANOQN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MARLAKQPSA FRCRTIVFQP KLTCSSSLLL LCCWLALLPS PEAHTIIERP SRPSPEDYRY QRALLASEEA DLAFGADMTL
  81  DGNEILVNNH LMDLKREELE KGYTNPFSFS PARHFFEVLD QINASPLFRF VRELPKGAVL HAHDTALAST EVIVKATYQP
 161  HLWQRGCFEH GRQPEFLFSR TKPTAPQRGN KHDDDDDWEL VQTVRERMGP ARYDEHVRQL FSLFTPDPQT AYRSINDVWD
 241  RFSQIFLAFN PIVTYRPVWE FYFREALREF HEDNVLYLEF RGLLPTLYDL DGKTYGPEEV VQIYRTITEE FKATHPRFAG

 321  TKFIYAPLRL VDNQTMDQYL SLAERLHRLH GDYVVAFDLV GQEDLGRQLL DFVPQLLELP ASINFVFHAG ETNWNGMPSD
 401  GNLFDAIMLG TKRIGHGYSL LKHPLLLEKV RQRNICVEIN PVSNQVLRLV ADHRNHPASV LFASDFPLVV SSDDPSFWRA
 481  APLSHDFYMA FLGMTTVGQD LRVFKKLALN SIRYSLMSDR EKEVALGKFQ LAWDDFIDRK AEQLRASSRN ERMARPAYDE
 561  FCRQREEFFA REQGRGLGAN LVLSPAEQRL NQYVMHLKQL ELAKGVENPY ELVSARHFFE MLDRINESPL FRLIQKMPKG
 641  GVLHAHDTAI GSTELIVRAT RHAHLWQSGS IPQAAADPMP VYTFSRNKPA AEGEWRLVAD IRSTMGDAAY EAAIRKMFTL
 721  YTTDPLNEHR DINDVWRKFM ALFICFEPMV TYRPVWEEYY YGCLEELLAD NVTYLEFRGL LPPVYDLDDR KYTPEEIVQM
 801  YVDQSEKFLR ANPKFAGVKF IYAPLKFCDD STFDGYLTLV QTLKARFPTF IAGFDLVGQE DLGRPHTDFN ERLLRLPAGI
 881  NFFFHAGETN WTGRRDENLI DAILLGTMRI GHGFAAIKHP VVLEEIKKRN ICIELNPISN QVLKLVQDFR NHPGGFYFSD
 961  NYPVVVSSDD PSFWCASPLS HDFFVAFMGL ASARADLRLL KQLALNSIEY SSMEGEEKTI ATQKWTAAWN EYVEEMLKTI
1041  PAEF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LYLEFRGLLPT.L	Y	31.51	1320.7441	-46.1	661.3489	2	21.40	802	1	276	286	
total 1 peptides												

tr|A0A0K2VDA2|A0A0K2VDA2_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  NSNAIPWDVY SQSKQIIVPF TVFNGKVDLW HRQYWQMLSG SFIQWCHNGY KEEEKGGVGP YPTYGPSLIL PTL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.CHNGY.K	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	46	50	
total 1 peptides												

tr|T1GNU9|T1GNU9_MEGSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MKSLVLVICS LWILQGCVEC HNGYFYPKPK YVVTIEPSIE VFSKTIQYEE TPVTQGYSQK HYKGHSYAQG HTTTPTKKYD

  81  TGHYQGHTAQ NIPKSSHVYS SGHYNSSPAH VTSSVHKYRP VQVASSGQKS GHYGSQKSTS GILIHKSVPI YSTGHKSSYN
 161  SGHYSPVQSS HNQIATNEKK GYGTYTKNTG HYTPLVQLPS IESTAKTPTT YNMYAPMSIH ARQLIMDMGD IKISVPLSSD
 241  GITADGEYLL KIPIYNKVTK K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.CHNGY.F	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	20	24	
total 1 peptides												

tr|A0A067RJ46|A0A067RJ46_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MRSLGILASI LALAVGFGGA KVVESEHALR SGRDAEQRGM PSNCPTGSAV LQVQSQSDIF LGNSSMGGFE LLRYVCGWTK
  81  APVEAPSGWV MGNGPNGQRV NVTIYKNEYR TFPVCCPGYV RNEEDICVPK CKGECVNGLC TSPGKCQCFD GFTLNDLGNC
 161  VVTCPCGCPY GECSGNRCTC NPGYALDSSG KVCNPVCEKA CERGDCVSPN NCSCYHGYKK HPQRSHVCVP HCDDPCENGT
 241  CTAPDICSCD SGYYKSQFKC LPYCTSCQNG RCVKPYTCVC HNGYGAEQGK CEPVCDSLCV NAKCTAPNTC TCHRGYVHST

 321  AHMCVPRCFP SCINAECVTP NVCQCNPGYI KKKPHKCVFD VIGGNLGRYA NEFNWHSDRA VQGLWRNKTS PTKFISMEKY
 401  PKFSYFDKKD HKKASG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.CHNGY.G	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	280	284	
total 1 peptides												

tr|A0A1J1J4I8|A0A1J1J4I8_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMRSWTRLSS EAMLKIFLAI FLLNILNCDH KVESAFEDLS STCKNQFIFF NDALLARRDW ALKMFDTWGK FQHSVLDGNV
81 NNFGDYDLCR SFVHESPVTS IGTVNGEYCL VSYIGAEEDI EPFDINFDWK ELGSLARSQN LYLTTGICLP KSCTKKDVDE
161 IANIVFSNAN LNVTSVSCES KPYLRFSNRL LAVFIFIGLL ITVIASTVYE LFMIHRDSEG KFNLIKIYLH RFLRYTPVLL
241 FLVLFFMSFM QLLGSGPIFE RTLEDWLPNC YNYWWSTLLH IATYTNIDNL CLNWTWYLSA DFQLFLVSPI LIYPAWRWKW
321 KIFAVAFPIA MLSFLIYIFV VSITYEFLVF VGPLQSQGQF DYDRLLYYPT HARAGPWIIG MALGFIMYQL KGIKPHINKY
401 LATFLWVASF SLLTVVVLGY FPFQQADEYF TINKIVNASY NAFYRSGWAL SLAWIIFA**CH NGY**GGIINWF LSLPQFQPLA

481 RMSLSVYLSH RIFQIISVAT IRQPIYLSPF NLLHVYFGDV IMSLIVGIAV YLCIEAPFAV LEARLSGDDT KKN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.CHNGY.G	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	459	463	
total 1 peptides												

tr|E0VC82|E0VC82_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKGSKYHNYP EKRLFRRRSC TDILCLALFI GCLAGWVCLG YFAVRTTPPN ELFAPTDYRN RRCGYDDGVK DRPYVLYFDL
81 LECVPPKASI FQCHTTRVCV SECPKENFYL KQHLNNFYDA RSLRNKLICK DDFDKSKIRD KESAMKAIES KECAEWYLES
161 KPVYRRCLYD CIELYKPDFI VTYLNEKPEN VTQLTNTHLH FDTVYYHVLN SITDKDTIFR LAINKESDEF RSKIEKWEKS
241 EISGAVGRQF FDASKFVAEF GHAIFQDLTI IWPWILIHVC GAAIISFFYI IIMRWISGIL VWLSVFSSIG LLSYSKHRIH
321 LAIELIKEGS KAVMCSWSAV VFPLFLWLLQ LIFIAYAILL FAYLINSGIP VKRVKGLIES SECI**CHNGY**V ENSSCDEKTF

401 DKYCHRINSN DIPCSTAKCV FSNEETKKQS IYFHLYNLFM IFWCLFFVSG FGQMVLASTF STYYWTFNKD NLPVFMVGGS
481 VWKVIRYHLG TVSLGSLLLA LCNWIRVIIE YIYYYINKYD NCLIKFIKCC CSCFFWLLNA FLKFLNKNAY VMCAIHGKNF
561 CTSAKIAFEL LSRNILRVII LDRVTNFLFF LGKVTVTTCV GIIAFYFFTN PVPSIEDILN QEKRYKVDYY FVPMIIICAA
641 GYFISSLFFK VYSMAVDTLF LCARKYI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.CHNGY.V	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	385	389	
total 1 peptides												

tr|A0A212F9M7|A0A212F9M7_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MHVRVRMFGK PDTIVVVESK LTKLQQFRRI IKEKFDVEPK LQRLFYGGKL LEDGYTFHDY NIKLNDVIQL IAVPQTVESE
81 DEKKSLDNQE QVKESDFEEK TIVYTDVTST VYAVGDLVDV KDREQGAWLE GKIVRIVLDP KVNYENEQNK EDLNSSLDNK
161 NDLENKPPSN ISEQSNTQKI GIAKYFTKQT NGKRLSKDFK VKTVKVTAEN VLYKVQLDDD EEDSELFCKL KEIRPRARHE
241 IDVKDLMPGQ KVMINHNTDE PLEKGYWYDF KVDEIKKLRT SYEIVGTLYL GPDSVPQNDT KVKIHDKIFT IEEPVPLEKR
321 TEDYLKSIQE TPAARSKPLN CLKCRDNEEE PCKECGCYLC AQKNDPDKII LCDE**CHNGY**H MVCLKPPLTV LPDDDWYCPS

401 CKRDPNDVIA PGASKQAKKS NTSKTNRDWG RGMACVGKTK TCPMPLNHFG PIPGIEVGMC WRFRIQLSES GVHRPPVSGI
481 HGRDIEGAYS IVLSGGYEDD VDNGYEFTYT GSGGRNLSGN KRTAEQSCDQ TLTRENKALA RNCAVDKVSE DGGDAGDDWR
561 RGKPVRVVRS CKMMKHFPKY APQEGIRYDG IYKVVKYYPE RGLSGYIVWK YLLRRDDPSP APWETGAKKY NIVYPDGYLE
641 AEAEKKALKE KATNSKKSSK RVKRNESSSS ETDSSPVVKK RKVQKTPQNG KVRKKQSLSD SSESSSEIEK STSKDTNPKK
721 ENRKSVIPSI FTKSPKNKKV KAEEPLSGEE KESVMADTLN SKLWGDCLDV CEKQGKKEFI EHVTQVFLCI ICQDVAVNPV
801 TTPCSHNFCI GCLKLAFKSS DSQGCPCCRQ SLAKMEVQVN EQLKKALQTI LKGYDAGKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.CHNGY.H	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	375	379	
total 1 peptides												

tr|A0A212FGX5|A0A212FGX5_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTKDSYEMNN RLSRGGSLFG GDPQVQLRTA LRSNDYGTFK KLVSYGAVDL EHVYPYPDYK TCLEIAVSEP NKIEFIKLLL
81 QHEVQVNKIN ETHGGAPIHF AVENGNAEAL EVLLEDDRID LDTRWKGNTA LLMAIKQIQD LDEDREHDLD IYEDMVEKLL
161 KAGCNANSPD LRGITPVYSA AKQGLERVVT LILDYSKDPI DLDTYKDIKG KTARYYLKEA FPHLLPKFDS AVENIEPSID
241 KDLLFSYLLR HEEDNFIRDF TKLSRKNEHR AMLAADNGMN TMLQLAVDKG LEKVVQTLLS AGADVNATCS GNNRRPIAIA
321 **CHNGY**HKILK MFIDSDSSLF DPVNSESLVQ ITVKGMRKAV ESPKINYKAC LNLLLKHPKV NVDINHQDMK DNTALHYAAR

401 SGDSETVLDL LRNGACVGLN NAFDEPPLAD INAKTLETYL DECITTNSER PSDENYEIHM KYSFLVYPNN SLENELCQVP
481 LMEKSNNNND SIRKCDAILA PETEALLYMT RNEELRPLLK HPVITSFLYL KWQRISCLFY ANITFYSLLW LCLILYIILG
561 YGVEGRKNKS VEALNVLTHV GAVIGLILLI MRELFQLLVS PTRYLQSIEN WMEIALIFVT AWILGYDAAE ESTKQQLSAV
641 AILLSSAELV LLIGQFPTLS TNIVMLRTVS WNFFKFLLWY CILIIAFALS FYTLFRKVIS EGDQKAPNLN EQASEDEDED
721 FFEDPGSSLF KTIVMLTGEF DAGSIKFSTF PVTSHLIFTV FVFMVPIVLF NLLNGLAVSD TQEIRADAEL VGHISRVKLI
801 SYFESVLIGK AYTKPRRCWS WLPAYLQNVH FIKPQMLCIK PFAKRICLFP HFLPRFRIIV MPNQNNRIEI PRPEPLMKAG
881 DDYEDIEGGK CCFEGCQSLR LERRIVKNAK FIISRRTQVS EFDEIKSRLS AYENKISGLE VALKKILTRM DIP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.CHNGY.H	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	321	325	
total 1 peptides												

tr|A0A0M4F702|A0A0M4F702_DROBS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGDIVLTARD KIPDPKHSIV KNERMLSNQP SAVDASSVKH SSSFHLYIEN FKHVYNEGLQ VEEEGLTDVI RKKTKMSNFN
81 NIWLNSEGRS AVKHYVHIPL DISQQNADLW LPKRNLRLAN KLHATPEFLK HSKTRFLRRK VDVRKIQSNN KDIEDDSGKH
161 FITEQRHYIV PTPFPTLRST IPNVYSNAGG NGMLLNNKDV DFIHSHGMTR KEDRRIHKTR NHHRYNCNKK KSHFRGDLNQ
241 TIDQKAQNYL NSGRQHSKWL QGKNNQIVWQ SFNTSKSVQP SQVFENKLNI IHQQQIASHN RVSRAVTAKK ERIWDYGVIP
321 YEIDGNFSGL HKALFKQAMR HWENSTCIKF VERDAEIHPN YIVFTIRNCG CCSFVGKRGN GPQAISIGRN CDKFGIVVHE
401 LGHVVGFWHE HTRPDREKHV VIEHNNIMKG QDYNFNMLSM DEVNSLGMAY DYDSIMHYAR NTFSKGTYLD TILPIEVKGR
481 KRPEIGQRLR LSQGDIAQAN LLYKCPKCGR TFQESTGIFS SPVYYTAGAL SNETEHCEWR ITATHGERVV LRLENMNIFK
561 SNNCETDYLE IRDGYYIKSP LIGRYCGKVA KEVITTLSSR MLLTYINKHR EDGYRGFKAE FDVVCGGNLS VDDSEGRLES
641 PNYPLDYLPN KECLWKISVP KGFQVALKFQ SFEVENHDSC VYDYVEVRDG DAQDAPLIGV FCGYKPPPNL KSSGNLMYVK
721 FVSDTSVQKA GFSAVFMKEV DECETQNHGC EHECINTLGG YECSCHIGYE LHSDKKHCED ACGGLIEYPN GTITSPSFPE
801 MYPILKECIW EIIAPPKHKI SLNFTHFDLE GTEHQQSDCG YDSVTIYSKL TENRLKRMGT YCGTSIPPTI TSDSNALRVE
881 FHSDKSIQRS GFAAVFFTDI DECAVNNGGC QHECRNTIGS YLCF**CHNGY**S LHENGHDCKE GECKYEISSS FGSIYSPSYP

961 DNYPPNADCV WHFSTTPGHR IKLIFNEFNV ESHQECAYDN VAIYDGESEL SSLLGRFCGD KIPYPISSTS NQLYMALKTD
1041 KNKQMNGFTA LHSTSCGGYL RASSNVQQFY SHARFSNLDY DDNMDCEWTI QAPPNSNVQL LFLTFDIESS ENCTYDYVQV
1121 FSGMEDISGP MYGQYCGNLL PQDIISLTDS LLVRFKTDSS VHMKGFSVSY VAVDPFENSE EDVESLYSSE MATPFPGSLK
1201 SIFKEETEES DDYSDFSGNQ LAKGNFRGRF SYPISYSTWT N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	925	929	
total 1 peptides												

tr|A0A182H9K0|A0A182H9K0_AEDAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MGDIALPNVD YETEWQKQRL NKTFQQELEK LKQEVYHEGL QVEEEGLTDI IRKKTKQLSP DLNQPSKSLN EATVYISGSQ
  81 AVDHKSLNQI SHNDRDNAII DSYSNGESQI KATIIDNNDN IILRNTSGTD IHQVGPQEGN SASTSNGSDS STIIKKKKNT
 161 KAADVRNIDH NRIQSDTKDI VIDDASDNII SNNHASRKTM ASRTLLTPPP TPTPKPARTT QANRFSNSGG NGRTLEDVQV
 241 LNGDGTITAH KRHHRRRRQG NGRKNNGTNP DETTVQIDGK QKKKTLDANS DTYKARLERL KTDLGNPTLS VNDLNLKRSK
 321 SKPKPFAGGK KAPKDKQPAG NKNKESRALP SKVKQIGGKP PGNGGAQRHT PSSSTRILDD IIIEEKVQGA AATVGTGDDL
 401 IRDRKGNVVK SSFLEAHLAT EQRQLPVDGA RSSRAATASH HRATRAATAK KERIWDFGVI PYEIDGNFSG LHKALFKQAM
 481 RHWENYTCIK FVERNPIDHP NYIVFTERQC GCCSFVGKRG NGPQAISIGK NCDKFGIVVH ELGHVVGFWH EHTRPDRENH
 561 VVIEKNNIMV GQEYNFNKLT EDEVNSLGLP YDYDSIMHYA RNTFSKGTYL DTIFPIEIPS RKRPEIGQRL RLSEGDIAQA
 641 NLLYKCAKCG RTFQENSASF TSPSYYSLVP PSEPERCEWR ITATHGERIV LNITDLDIFK SNNCRSDYLE IRDGYWHKSP
 721 ILGKFCGSGK VNDLIKSTGS RMLLTYTTTF RQINMRGFAA SYEAVCGGSV NLESGGRLES PNYPMDYLPN KECIWKITVP
 801 KDYQVALKFQ SFEVENHDNC VYDYVEVRDG ESADSRIIGV FCGYKIPPDM RSSTNKMFVK FVSDGSVQKA GFSATFMKEV
 881 DECERMDHGC EHECINTLGG YECACYIGYE LHSDKKSCEN ACGGTLKQTN GSILSPSFPN EYPILKECVW EIIAPPQHKI
 961 TLNFTHFELE GNTFYQASEC EYDSVAVYSK VNEDSLKRHG VYCGNKIPPT ITSEGNTLRV EFKSDKTIQK SGFAAIYSTD
1041 VDECAVNNGG CQHECKNTLG SYVCSCHNGY TLQDNGHDCK EGGCKYEVSS PNGQIFSPNY PDYYPPKKDC VWHFTTTPGH

1121 RIRLVFNVFD IEPHQNPPEI ISMNQALLVR FRSDDTVGFK GFSASYVAIN PFGKGHSEDD ELVDSAEITP FPGSLKNTVI
1201 KADEDVDEDE DEDYEIIVHH RHLNPKVRYA VRNEIRSSQA ID
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.CHNGY.T	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1066	1070	
total 1 peptides												

tr|B4LW38|B4LW38_DROVI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MALQSRLGAG RGGRVMSYTN YALLVATALL VLISAHVKSA KLHGDPLVAP TSMDNVAIVE KHERDNNKYV KEYVKESAAT
  81 HPYHQHGHGQ HKSHLHHLHH LPLQNNLRAY HSKYSIEQLL HMQVAPKVSN DIDMDPCKAG GFMGDIALPD GDEGPVVAHT
 161 PIDDEEPEEE KLTPKTATNH MLADAPEPAK YNATFQLDLE KLKQEVYNEG LQVEEEGLTD IIRKKTKLPS VGIVSHTTGQ
 241 PLTKASGISN NDASLSANEP LKPSAQTLSD IANPPSYKNE VLTPPESQAI QRRRTASNAR MSVAPALLQL NKTQTLHRNV
 321 DMRKIQSNNK DIEDDSGNNF VAERRQHIVP TSLPTQRSTM PNVYSNAGGN GMHLDDDVDF LHAHGIVRRR HRRGPKHRNS
 401 HWTDYVSKVQ RLREELDRPH GQSPHLSQRQ HPHSHKKQKH GQHRRRGRGR STPSPLNVFS TQAQIDEQQR TDNMNSLQIP
 481 KADTRVPDTD SPRQHHRVAR AVTAKKERIW DYGVIPYEID GNFSGLHKAL FKQAMRHWEN STCIKFVERD AEIHPNYIVF
 561 TIRNCGCCSF VGKRGNGPQA ISIGRNCDKF GIVVHELGHV VGFWHEHTRP DREKHVVIEH NNIMKGQDYN FNMLSVDEVN
 641 SLGMAYDYDS IMHYARNTFS KGTYLDTILP IEVKGRKRPE IGQRLRLSQG DIAQANLLYK CPKCGRTFQE STGIFSSPIY
 721 YTAGAVSNET EHCEWRITAT HGERVVLRLE DMNIFKSNNC ETDYLEVRDG YYFKSPLIGR FCGKVANDVI TTQSSRMLLT
 801 YVNTHRGDGY RGFKAEFDVV CGGDLSVDDS EGRLESPNYP LDYLPNKECV WKITVPKSFQ VALKFQSFEV ENHDSCVYDY
 881 VEVRDGPAQD APLIGVFCGY KPPPNMKSSG NSMYVKFVSD TSVQKAGFSA VFMKEVDECE TQNHGCEHEC INTLGGYECS
 961 CHIGYELHSD KKHCEDACGG VIEYPNGTIT SPSYPEFYPV LKECIWEIVA PPKHKISLNF THFDLEGTAH QQSDCGYDSV
1041 TIYSKLSENR LKRIGTFCGS AIPPTATSDS NALRVEFHSD KSIQRTGFAA VFFTDIDECA VNNGGCQHEC RNTIGSYMCF
1121 CHNGYSLHEN GHDCKEGECK NEISAPFGTI YSPNYPDNYP PNADCVWHFS TTPGHRIKLI FNEFNVESHQ ECAYDNVAIY

1201 DGESELSSLL GRFCGEKIPY PISSTTNQLY MVLKTDKNKQ MNGFTAMHST SCGGYLRATN HVQQFYSHSR FSNQDYDDNA
1281 DCEWTIQAPP NSNVQLLFLT FDIESSENCT YDYVQVFSGM EDTSGPMYGQ YCGNVLPQDI ISMTDSLLVR FKTDSSVPMK
1361 GFSASYVAVD PFENSDEDVE NSYSSEMVTP FPGSLKSIYK EDTEETDDYS DFSENQLVNA QYRRRHTFPI SYSSWTN
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1121	1125	
total 1 peptides												

tr|B4QTR3|B4QTR3_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MRRRRGTPLG VSWTNCVLLL ATGLLVVLIS VHAKNPRPHR GLPAPAPAPV PASVDQVATE NDHRREPTVD GSVLQRLSGS
  81 DRAVDADEDV DEDGDEGLKH QHLEHRQQFD AYLGTIRRLR RPYRSKYTIE QLMRLHVTPK VSEDIDMDPC KAGGFMGDIA
 161 LPEGDSGPVV AHTPIDDEEQ ERQEVEQLLA DSPSPVHDPA SVSGAANSGP TKFNATFQLD LEKLKQEVYH EGLQVEEEGL
 241 TDIIRKKTKL PSSGPVNLKA GQSQSQSQSA NEPVKPGSES PSDYAQASSY KNEVLPPSEQ RIHADKPARL TLAEIGPKSS
 321 NKTQSLHRNV DTRKIQSDNK DIEDDSGNNF VAERRPSQIV PTSLPEQRST PAHVYSNAGG NGMQLDDEVD FLHSRGVVRR
 401 RHRRGPKQRR SNQHLEHEAK LQRLKEELSR PVIEGHHRQS HHQKQAQHRQ HHQSHHRKKH RRQQQHHRRR GQSTTQYVNH
 481 SPPGFNQSQQ AQQQSVPEMD LLKAEAPKDE EPLRHRVARA VTAKKERIWD YGVIPYEIDG NFSGIHKALF KLAMRHWENS
 561 TCIKFVERDP EIHPNYIVFT VRSCGCCSFV GKRGNGPQAI SIGRNCDKFG IVVHELGHVV GFWHEHTRPD REKHVVIEHN
 641 NIMKGQDYNF NMLSPDEVDS LGMAYDYDSI MHYARNTFSK GTYLDTILPI EMKGRKRPEI GQRLRLSQGD IAQANLLYKC
 721 PKCGRTFQES SGIFASPSHY TAGALSNETE HCEWRITATY GERVELKLED MNIFKSNNCE TDYLEIRDGY FEKSPLIGRF
 801 CGKVDKEVIR TESSRMLLTY VNTHRIEGFR GFKAEFDVVC GGELSVDDAV GRLESPNYPL DYLPNKECVW KITVPDSYQV
 881 ALKFQSFEVE NHDSCVYDYV EVRDGPGQDA PLIGVFCGYK PPPNMKSSGN SMYVKFVSDT SVQKAGFSAV FMKEVDECET
 961 QNHGCEHECI NTLGGYECSC RIGFELHSDK KHCEDACGGV IEYPNGTITS PSFPETYPLL KECIWEIVAP PKHRISLNFT
1041 HFDLEGTAHQ QSDCGYDSVT VYSKLGENRL KRIGTFCGSS IPPTATSESN ALRLEFHSDK SIQRSGFAAV FFTDIDECAV
1121 NNGGCQHECR NTIGSYICMC HNGYSMHENG HDCKEGECKY EISAPFGSIF SPNYPDSYPP NADCVWHFIT TPGHRIKLIF

1201 NEFDVESHQE CTYDNVAVYD GESESSSVLG RFCGDKIPFP ISSTSNQMYM VLKTDKNKQK NGFTASHSTA CGGYLRATSQ
1281 VQQFYSHARF GNQDYDDGMD CEWTIAAPDN SYVQLIFLTF DIESSENCTF DYVQVFSDID DVYGQYGPMY GQYCGNVLPQ
1361 DINSMTHSLL VRFKTDSSVP MKGFSASYVA VPNSGEYDHS DEDVENSYSS EMVTPFPGSL KSIYIEDTQE ETDEYSDFSG
1441 NQLVLNGQYR GRYSLPNRYY SGKA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1140	1144	
total 1 peptides												

tr|A0A034VDR1|A0A034VDR1_BACDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MLNNHHYQSK YTIEELMNMK IQNRLSDDID MDPCKAGGFM GDIALPDINY DGDPIVAHTF VIPLKKRLDN GGGNESSAKQ
  81 DKYEDDDADA GQWQSDSATN KPITPIKFNA SFQQELEILK QEVYHEGLQV EEEGLTHIIR KKTKLPSTRF DFKDSKNELS
 161 SNDPALSANE PVKPRSFSSN TNYLMKNLKN EVITNSKDNS NGNGNHYKHN PAYQPVDGSV FNEKPGSSDK STDTDTNKTH
 241 PLSVSQQQKL RQRALSSGNG GTGGLYTQPG KATTFDANGK VESIALHRSG EYFGPSVSNE RSIDAEKLRK SLFGISNRNV
 321 DQRKIQSNTK DIDVDAGNNF VAERRMVILP TSLPTQRSTL PNVYSNAGGN GMKLDDVDFL HPEGPVRRRH RRGRKHRRSS
 401 DFRHTDFNIK LQRLKEELNR PVHTAHEYQT QVHREMHSIT KLHTQNNKKV AKIKAENTDD ANARLLELEY ERHNQQLMTE
 481 WQQQHNQTKN FNYSSHQGDG RGGMARSVVE VNANTAGKSD NKVKASLEME LQNAENSRLS RSRNRMVRAV TAKKERIWDY
 561 GVIPYEIDGN FSGLHKALFK QAMRHWENST CIKFIERDPE IHPNYIVFTV RSCGCCSFVG KRGNGAQAIS IGRNCDKFGI
 641 VVHELGHVVG FWHEHTRPDR EKHVVIEHNN IMKGQDYNFN KLTPEEVDSL GLPYDYDSIM HYARNTFSKG TYLDTILPIE
 721 VKGKKRPEIG QRLRLSAGDI AQANLLYKCP KCGRTFQENT GIFASPSYYT AGALTNETEI CEWRITATHG ERVVLKLENM
 801 NIFKSNNCQT DYLEVRDGYY IKSPLIKRFC GKVNGEILKT ESSRMLLTYV NTHRMEGYRG FKAEFDVICG GEMSVDDSEG
 881 RLESPNYPLD YLPSKECVWK ITVPRGYQVA LKFQSFEVEN HDSCVYDYVE VRDGATEDSQ LIGVFCGYKP PPNMKSSGNA
 961 MYVKFLSDSS VQKAGFSAIF MKEVDECETQ NHGCEHDCIN TLGGYECSCH IGYELHSDKK HCEDACGGVI EYPNGTISSP
1041 SFPDTYPVLK ECIWEIIAPP KHKISLNFTH FDLEGNTQQQ TDCGYDSVTV YSKLSENRLK RIGTYCGTAI PPTATSEGNA
1121 LRIEFHSDKT IQGTGFAAVF FTDIDECSTN NGGCQHECRN TIGSYMCFCH NGYSLHENGH DCKEGECKHE ISAPFGTIYS

1201 PNFPDLYPPN ADCVWHFSTT PGHRIKLIFN EFNVESHQEC AYDNVAVYDG ESESSSLLGH FCGDKIPYPI SSTTNQLYMV
1281 FKTDKNKQMA GFTAIHSTSC GGYLRATNQI QQFYSHALFG NRNYNENMDC EWTIQAPASS NVQLLFLTFD IEASENCTYD
1361 YVQVYSGMED TSGPMYGQYC GNTLPQDIIS LTDSLLVRFK TDDTVTMKGF SASYVAVDPF ENSEEDFNSY SAERATPFPG
1441 SLKSIYEDSD EYGDFSENQL IARPRGRYYN NF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1169	1173	
total 1 peptides												

tr|A0A1A9WC30|A0A1A9WC30_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQTHIRGRN RRYVAIANYA TFTLTAIFVL ISACARSAQV NFNTFSSLPS PYESSLNIKV QSTRPQASPD ETFASSLDVP

81 ENALSIHADD KNVSPSKEHI ALESSRTQIV QEPEQFRPDI KSYHHSHHSY HSHHQNEPYH GHGVNRTGQQ RRQHRRKNLG

161 SDLWLHHRYY QPQHQHQHHH RNHYRDHNMI PQSQHIIRID PVQQLIVPAQ VPKHKYRSKY TIEELLNTKF ERKISDDIDM

241 DPCKAGGFMG DIALPETTYD DYPIVAHTTI GKVLETSPSR EAIIKFNDTF QKEMEILKQE VYHEGLQVEE EGLTDIIRRK

321 TKLPSIKPEL NTDFLSNANE LVKPFHYHQS RESYNYMDKN HKNDVISSEG FLNQIKRNPS AGREEHTTVN AKEDDEETDK

401 EDFKKIYHHT PGKKFSFPTE KTYIYSPPEK VNKPPVGLSN RNVDQRKIQS NTKDIELDAN NNFVSERKFV ILPTASPTQR

481 TTLPNVYSNA GGNGMKMDDI QEFKGSSTIV RRKHRRRRKN ELNPPVQKHP TIDHHHHHQQ LMAKENNHQI VDIQSNEVFV

561 KHLLHVDNHS EPLAVFPSRD NDDEFSLISE RRRSIRAVTA KKERIWDYGV IPYEIDGNFS GLHKALFKQA MRHWENFTCI

641 KFVERDTELH PNYIVFTIRG CGCCSFVGKR GNGPQAISIG RNCDKFGIVV HELGHVVGFW HEHTRPDREK HVIIDHINIM

721 KGQDYNFNKL TPDEVDSLGM AYDYDSIMHY ARNTFSKGTY LDTILPIEIK GKKRPEIGQR LRLSSGDIAQ ANLLYKCPKC

801 GRTFQENTGL FASPSYYTGG ALTNETEHCE WRITATHGER VILRIENLNI FKSEHCQSDY LEIRDGYYHK SPLIARFCGK

881 VSNEALKTET SRMLLTYVNA HRTNGFRGFK AEFEVICGGE ITIDENEGRL ESPNYPLDYL PNKECVWKIT APKGYQVALK

961 FQSFEVENHD SCVYDFVEVR DGPTQDSPLI GVFCGYKPPP NMKSSGDVMY MKFVSDTSVQ KPGFSATFMK EVDECETKNH

1041 GCEHECINTL GGYECNCRIG YELHSDKKHC EDACGGVIEY PNGTITSPSF PDNYPILKDC IWEIIAPPKH KISLNFTHFD

1121 LEGAAHHQSE CGYDKVTIYS KLSENRLKRI GTFCGSSMPP AATSEGNALR IEFHSDKSIQ STGFAAVFFT DVDECSVNNG

1201 GCQHECRNTI GSYICS**CHNG** **Y**SLHENGHDC KEGECKHEIS APFGTIYSPN YPDSYPPNAD CVWHFLTTPG HRIKLIFNEF

1281 KLESHQECAY DNVAIYDGDS ESSSILGRFC GDKIPYPISS STNQLYMVLK TDKNKQHNGF TAVHSTSCGG YLRATNQIQQ

1361 FYSHARYGNQ PYDANMDCEW LIQAPPSSNV QLIFLTFDLE TSENCTYDYV QVFSGMEDTS GPMYGQYCTN TLPQDIISIT

1441 DSLLVRFKTD GSITMKGFSA SYVAVDPFEN SEEDPTSYSS EMVTPFPGSL KSIYKEDGSH ETDDYNDFNE NQLIVNNPYL

1521 KRYRREN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1217	1221	
total 1 peptides												

tr|A0A1A9WXH7|A0A1A9WXH7_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKRYLLQFLF VAIVCSRVLS SPLAQTEIPQ DDDDDDWDDE DESSEADDDG RIYKNPRNSP STECPRDEEQ ATLLGQKCLR

81 KCSSDEDCKS KKKKCLCDGV CEFLLNSGLV QQDRECPELA QPTLGQVTVA GRHFGARASY SCPHGYHVVG LQSRLCQADG

161 NWAGAEPACK QNIYCLKPPQ IEHARNSALP EQETFDLDST VQYH**CHNGY**V TNGFPRAKCL AIDGQASWYG PDIQCEPRSC

241 GQPPDPANGW HSGECYTYGC KITYNCGNSY ELVGKHERTC QSDGSWTPKE LPTCVLVTSV ICPTPENPKN GKATYTTLAY

321 NSVVSYECRY GYTLVGESSS RSSIIFRCQP EMLMQGHASS VCQIDGRWRN PLPECLAPCV VPTISQGFVV PIEIITDENG

401 TIIITPTTTQ SPVISPSGYV DKVKHGTSLD VKCDENYEFP VSLLSPPTCH NGTWSIIPRC VPARCKNMPK PPKHGMVLAP

481 KTEHGMKARF KCKDGFKLVS PEGKDVTDFN AYILTCSFGN WTGETPHCQE VFCSFPGYIP NGKVLLVGNM GLYDYRPYVK

561 KIVNNKQIMY DCDKGYVLDV GPPGATCVGG KWRPLELPQC LLGQHPRLRW NRRRRSIEMR YIGSTYRMRE TRDLEKKLRY

641 EIYQHFPQWK NVANEIGHKL RKRNKRTPTE LEEAYSKYYQ RIRQKYQNYV KHLLGYNRMQ NPLEFLNTNK KIQLQDGRWY

721 SFYDSPDHLT RFKANQKSRT LANDFNLYDY EDFDGAHRTV GKIPMPNIYQ NSRYSSNRRQ NEPLLDGNNS FHYIMEASKK

801 LQKPSNETDF IQQLKAQIIR KRRKRSSSYL QSGEPDATGH LENKEGRKRL RGPCEDLDWD SFANITTVRQ GKAPGRNSVG

881 IILYLECNPG FKLNIKDENV TVRCIRGIWK PETPKCISAP CLVPLVENGK YYKVEPHTKQ LSDKPSLTPL STYEEIQSNE

961 FITLECEDGY KIQGSAQLRC AHGSWSVNAF SECVSILCTL PNITGLTYEG GYRAGLTIGH MSTVSVRCNY STNTLPIEMN

1041 CNKGILSPQN IHCESGMRKS REEILQDNEE ETNARSNSVS ISHSLDSSDM EESSNSTDDT TEEAKMCGPP SITDGALVYK

1121 NGDLEIEGGY ESGTEIFFNC IPSASGERNT WKIICENGHW IGRSYNCANG TCMFKNNEPN VVSFYNDLEI REDIVEFPPG

1201 AAIISRCTDI GKFELVGSIE RTCIHSEWTG TKPACYGLNQ ENDYAMEKAP TILFRHQNGP IAQSNDGKLI VYPGTTLHME

1281 CLWMRRFGNP KWSVSHSFRN YSEGWVTDEG RDATLEYRLT ISNAQSEDSG IFSCQTPARH EHSVEVVVKS INCPEIPIRR

1361 GLIVSTNGTK LSTRVLLSCS NGNSLIGSSE LFCLPSGNWS APLPVCESVE CGDIPLPNNV SSPRVSVLSR EVGGRAAFSC

1441 ASGYGLRGPS EAICLPTGEW AVPFPTCIEV QCDNPGAPQN GYAQGSAPYR AGDVVQFNCN PEYMMQGQPI IACQDNGRWS

1521 GVLPKCVQAC SYPGTAISGH MSSVQFYYAI GESVTFTCDA GLELRGPKMV KCLKNGKWSG AIPQCVATD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.CHNGY.V	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	205	209	
total 1 peptides												

tr|A0A1B6LZH3|A0A1B6LZH3_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MDECKDNPRI CSGGRCSNTV GSFSCACTDG LLPGPGGSSC LDVNECESGR DVCGNGECDN TIGSFICRCE DGYSVKPGRG
  81 PQCTDDDECV LETHQCDINA HCINNPGSFS CKCPDGFTGN GISCRDINEC LTNNGGCDQN AQCINTDGSF KCVCDSGFRG
 161 DGYSCQDVDE CTESPTLCEN GHCLNYPGSF RCECEMGFMH PDDKSETACI DINECMMFNN LCVYGRCENI FGMFRCECNE
 241 GYQLDNSGGN CTDVNECDSP QACLYGTCMN TQGSFICQCP PNYQLVPAGN ACVDKRESRC YLEVEEWRGR QRCSQEMGSP
 321 VTKATCCCSV GKAWGPQCEL CPKINSDEYK ALCPGGIGYR PNTLTVVLED INECEEHEGI CKNGHCTNTF GSFMCSCHTG
 401 FRLDETQVNC VDINECQERP NICGVGYCVN DDGSYHCVCP EGYMLLPNGK ECVDMRKELC YLSYAEGQCT QPMTNEQTRM
 481 LCCCSMGQAW GHPCQPCPTD KTEEYLLLCG NQPGQIMDPM TNASVEIDEC TLMPTMCNHG SCLNTPGSFE CDCNRGFVYD
 561 IESHQCIDDN ECLRIPSPCR GNAQCVNSPG SFECQCPEGY KLGMSMRDCV DIDECLERPG ICENGDCNNF QGSFQCVCHN

 641 GYQLTVSRET CTDTDECTRH PNICNNGTCI NAVGSFKCHC FPGFKLSHNN DCIDVDECYI MPYLCRNGRC RNMIGSFRCE

 721 CADGYSLSAD NQHCQDVDEC QETGGMCGPA GRCQNLMGSF QCSCPSGYRL NPDKTKCVDV NECQDSAGIC EGGACINTDG
 801 GFICECPDGY VLSQNGMKCI DVRKDMCFDV LHMDRCSMAR REPMTVKECC CSMGAAWGRY CEQCPKDGTE EFWKLCPQGP
 881 GRMDTGEDLN ECDFMPHACD GGDCINTDGS FRCECPAGYI LDGTGKRCID DNECMSGAGI CGNGTCSNLI GGFECSCTEG
 961 FAPGPMQACE DINECLELNN QCAFRCHNVP GSYRCICPYG YALAPDGRHC VDVDECVTPA NNCKYNCKNL IGSFMCNCPE
1041 GYSQMGMSDD CRDVNECLTQ PNVCVNGRCV NLQGSFRCDC FEGFKSSYDF KQCIDERQGY CFRKLMNGRC SSHSDGLMAV
1121 TKADCCCTMG AAWGPYCELC PSPGSDDYQQ LCLDTGYSID GSDIDECHTI PDLCRNGKCI NTLGSYRCLC NKGFKPDHSG
1201 KHCKDVNECE QKPAPCQFAC QNTEGSFICS CGAGYVLHSD GTSCADLDEC ATGQHLCQHQ CVNTQGSYSC SCPDGYSQAG
1281 DHCLDVDECE SGHLCPGPGR CINTLGSFRC LCPRGYKLDK TGSYCSDSDE CTDDSKCEHG CQNFMGTYRC GCPDGFLQHV
1361 YYNQCVDDNE CSENPCGDQK CFNTMGSYRC GCPDGFQFDQ ALVVCVQVAS SCVGSPCAFG CSPSAGGAGF QCGCPSGYER
1441 IGQGHCLSTI NPAGLGYGGA PNLGSNIPTY PIDQDPYAVP HDRLISTEGC FSCKVNGRHR RMIAESKFFN SRDTLYDAKK
1521 LRELWRSRMS RHRRHHHGDK ARVQQPHRVL KVSLAQTKHR TRILKLQPAI KNDFEYSITK GNENGHFEMV RKHGVWALHF
1601 RRRLKHAGTF PLEITGSRVM PAASNDIWEA PLALHVTIVA SS
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.CHNGY.Q	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	638	642	
total 1 peptides												

tr|A0A1I8PPZ3|A0A1I8PPZ3_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MEKLKVHRGK WRQHCRYGNL KNYAAFIIAT IFVVIMACAK SAHLNVNTLS LAAVTGSSPL RATAKPVQQN SSSASSLSLS
  81 KLEQIPLTVL ELQETPRPQS PQHMPLAAPA TATRNALNTA AAIDNEEEEG ENEANSLLPP ITASAMQQQD ELLERQGQLA
 161 EFYSLQNIQQ QNHPHSGHQY HQHQHQHHHH HHYSQQQETN LQPDDNESQE HKHNPQSSNH HNHQHEHHRH SHHSHHNHRH
 241 LQLEPNQIEE EGVGGDNHQR MVEDKISLIT EHHEEPQQPH HRNYANEGKN SNQASLNGHS HRSRYSIEDL LHNKFEKKVS
 321 NDIYMDPCKA GGFMGDIALP DVQYDDDYPL VAYTQMWEEL PQSDAPLNDA PMKFNDTFQK EMEILKQEVY NEGLQVEEEG
 401 LTDIIRRKTK LPSSKSDFNM DPLQSANELI KPKNNLNYDP INYKNDVISS EDHEARKYSM SLPTKANGMP TEDLYLSKGS
 481 VDKGFNMTKD KFDTSLAHNE KSLTEAEKYN KTTPGMLNRN VDQRKIQSNT KDIELDTGNN FVSERKIVIL PTALPAQRST
 561 LPNVYSNAGG NGMKLDDIQE LKGSSTIIKR RNRRGRKNRR SFNQHSRLDY NLRMQKLKEE LMRPVGEGKK QHHHHHHQHY
 641 QHQEKPHHQD QQEPNKKFTE KISNNVTDNE TMNDDMRYSK FGDMFSDIET EDEVRHGADI VPAYEAEEND EFSFVREHRR
 721 LPRAVTAKKE RVWDYGVIPY EIDGNFSGLH KALFKQAMRH WENSTCIKFV EREPEHHSNY IVFTIRGCGC CSFVGKRGNG
 801 PQAISIGRNC DKFGIVVHEL GHVVGFWHEH TRPDREKHVI IEHNNIMKGQ DYNFNKLTPD EVDSLGMAYD YDSIMHYARN
 881 TFSKGTYLDT ILPIEVKGRK RPEIGQRLRL SAGDIAQANL LYKCPKCGRT FQENTGIFAS PSYYTAGALS NETEHCEWRI
 961 TATHGERVVL KLENLNIFKS ENCQSDYLEI RDGYWHQSPL IARFCGKVNS ETLTTVSSRM LLTYVNTHRT EGYRGFKAEF
1041 DVICGGELNI DDTEGRLESP NYPLEYLPNK ECIWKITVPK GYQVALKFQS FEVENHDSCV YDYVEIRDGP TQDSPLIGVF
1121 CGYKPPPNMK SIGDSMFVKF VSDTSVQKPG FSATFMKEVD ECETQNHGCE HECINTLGGY ECSCHIGYEL HSDKKHCEDA
1201 CGGVIEYPNG TITSPSFPDT YPFLKDCIWE IIAPPKHKIS LNFTHFDLEG ATHHQSECGY DKVTIYSKLG DDRLKKIGSF
1281 CGSSIPPTAT SEENALRVEF HSDKSIQKSG FAAVFFTDID ECSINNGGCQ HECRNTIGSY MCSCHNGYSL HENGHDCKEG

1361 ECKHEISAPF GTIYSPNYPD LYPPNADCVW HFSTTPGHRI KLIFNEFKVE SHQECAYDNV AIYDGDSESS SLLGRFCGEK
1441 IPYPISSSTN QLYMVLKTDK NKQHSGFTAV HSTSCGGYLR ATNQVQQFYS HSRFGNLNYD INMDCEWTIQ ASPNSYVQLI
1521 FLTFDLESSE NCTYDYVQVF SGMEENSGPM YGQYCGNTIP QDIISLTDSL LVRFKTDSSV ILKGFSASYV AVNPFDNSDE
1601 DANSYSSELA TPFPGSLKSI YKEEDSQETD DYNDFNDNQL NVNSPYYNRN RYQNRF
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1344	1348	
total 1 peptides												

tr|A0A088ACM0|A0A088ACM0_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MGWVLSTIIW ITIWSCLLRG FELAPQISPK QIPCDKTRKV FTDSWGIISD GPLGSNYTQD SHCEWLIKAN NSRQFITLSF
  81 RTMGTECSYD YVFVYDGDSF RSPLLGSFSG KTEPQQVTSS SGYMLILLYS DTNYVLDGFH AEFSVTNCSN NCTNHGKCID
 161 NTCFCEDDWG GRDCSRALCP NNCSYSGKCD LKRCHCHNGY SGQSCSLHKM HPESNKWHWL SHSEGGLRPR AAHTAVYIKE

 241 TDSLYVFGGY DLNYILDNLE VYRFNISQWE DEYGNELEGI SSAEHLDPIL LALELKGTNA DEKELYGLRT SSFIWKLLSG
 321 IKDNNNTFNS RNLANVEKRY GWSEFRIGDR EKKIHETKDN ETSRSTVRIE RNDDLKRKHS RHPRPRYAQT ARHRRNLENL
 401 DFYKKFHTSN IKSDILNWEE EIAEDSIGDN IYVQEPKIRD ELFKDESIKS SIDKLPKPSP RYGHAACRYD GGFVIYGGKV
 481 QDGSLSNELW YYNVNTRSWT LRAKNSPFYP PQLTRHTLTL ANNYIYLFGG STVDGEFSSN LYKIKLNLSD PTATTEKWKE
 561 VHPRGGKELD VRVVAHSTVY HQATNSLLIY GGVVASVARF SKLSDRMFVF QLDKKVWSEI HYPRAHLRDT YVPRERAFHT
 641 CNIIGNYLVV FGGYSHRHNK EEICYDNQMY LYHLGCHAWV SHDVLGLNDK DSRYPKQQGV FAHAADVRNG NTLLLVGGYH
 721 GNVNADLLAY TLPPMLAPGD EDNIEPEQIC SRHKSLMECT ANPECGWCSA DEICYGRTIG SNCTTNLQTT RCLGVCPALG
 801 DCHSCLIHGQ PGGGWGTTAR GKKSVSNKLN RGTCTWCVQN ARCHHKDDNY GVCGLRDDTL SQIPGWWGSK GTEIIKVEEC
 881 REMDKRPGLT FLKYKPPVNF TQPDSVTIVN ATTVDFSVPS MQGAKTESAL GGEMIARLIG FLRPPQDFWD STLEHLKICV
 961 SYNSATLHVS RSDDPQELEL VANLTADTSQ CIPTKWPDGY QMMLLPGRYL LDFESKRMVT ASYAYASKME IIHNKKTENP
1041 KVFTFEYLEP FQNGSCQQYK NCLHCLTDSS CGWCDIINKC LSRSINETES CIADVEWDED GNPIREWHYL TITPSACANC
1121 SNYISCESCV NSNLCEWWTE EARCARIGRL PNAVVSFDQC PIPCRQRSNC TQCLDERGRC VWCEATQECF SFSVYTSEYQ
1201 FGLCREWMDQ AGLMGVTSRS GSSLTGNDQC KSCTRHTNCS SCLHSLSCGW CYSLENPIIG ACVQGDFNQP HVNCSLIINE
1281 YQNTTLEIDE SGWAYAQCPD VDECDLGLHD CHLNAVCTNT HGSFSCQCKR GFNGDGKENC TKTCYEKCVN GYCSEAPDYK
1361 CECNLGWTGP DCRTNCGCYN HSTCIQGPGI CDKCQDWTTG TYCEECKAGS YGNATTPLGC KKCNCNEHGD KDLGICDRQT
1441 GYYGDPRDGG MCYYSCMSRG MLGGEGNGKQ GLGSRHSQLS LWESHFGDSP TRECLWIVSP KTDLSSDNML SGIQNVIQFT
1521 IHDDINVSCQ ENSVYVYDGL PEFVSSVTSH QSQLLGVYCT ESTDYPVTVE AKSGFLTVHY KQLDEVEGFN ASYLIMTCNN
1601 CPGNRECRNG NCLCKAGFVG INCDIEICPN NCTSTKKQGI CDKGYGRCVC IPGYGGRDCS IKIKEHQLIF TELFNSEYLA
1681 DHLDHLRKTL PRFGHTLVAD RRGSLWMFGG YSLSHGPLND IRLFDTKNNT WMPITVESTS KASMPQGRYF HALKYLQNQR
1761 WMQIIQDKFK KEPPSLAGHT LTLRRNGESE SLILIGGFSP KYGYLDTVWE FNLETEAWDT INTIGNGPLG VYGHSTVYHS
1841 KSDSFYIFGG YTYAINRTFI SNKLYALNYK TRMWSVLPPF DDDLTDGSSL PQARFLHSAV TTDEYMVIFG GRQNPHNTSD
1921 SLIAYKYSCN LWIRLITKDM EVIGYPPPPA YAHAMTHADP ESNAVYVVGG FDGGIKSHVT LISIPEDLCN LWTDKITCRK
2001 YFGCSFCSVI TISGNNASFC FSNEISINKD DRCDINVTQA QRSNGIFCNL EWMMSRKCQN FKTCTECLAE WPYYKSEEPV
2081 CKWCTNCSNG KCIPSEKDCD ELNKCSVRQK SVTDVNQCGE RQCPASDCEK CNNLEGCVWT RQVLKTYSAN ITGQGICTEG
2161 SLEAPADHPA GGTCEMLYYQ QLPTVELLKF LEISDNVTML IPNVMSKPIF SWHYVRCPPE NECMNGHHTC STKSEKCFDL
2241 EEGFECMCGD GYKTETPSSF NEFGRKICVP MCTQGCVRGT CIEPNICRCD FGYVGANCSI QCQCNGHSNC AGPDKLDVCL
2321 ECHNNTMGPQ CDKCRPLFVG NPADNGQCVP CLEYCNGHTR ICINESMTVP DPNSIEKMSI ELLEKQLVEG PVAKAKCVNC
2401 GNNTRGDKCG ECMIGYFRGT EDLRDICRSC QCHGHGFTCD PVTGEKCNCG NNTESDPTCT SGPMKSTNTG SSPCWMVQCS
2481 KCKENYAGTP TMGHQCYKTV TVDNKMCFDS KLIGGSYDEC KMKPKPLNPG QTVFYMVQPR FMNVDIRVMV DVTQGALDLF
2561 LSPRDDSFVV TLNSTTGYQD VELDSRFMWR KNSHNMWLDE QTRSQMRLVE FQPHNTFSFA LNGTTTEPTW NTGPQYIVME
2641 RYAEGLATFL TIENRNTFLV VRNLTNRLVL TLPQDKHELH ETKFHIALRA IDPVHPEISG RAAYGMIFFR QDQLHIDLFV
2721 FFSVFFSCFF LFLAGCVVAW KTKQAADVRR ARRRHVVEML HMAKRPFASA TIIYDRDGND CNPSSPQRKS RRNKLVSFHS
2801 DVRPVAVEPT DDGVAAVATV FIRLPGGRQA PVKLALGSSL ILLTRVYPVN SRVFLRRRNS HALN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.CHNGY.S	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	196	200	
total 1 peptides												

tr|B4QT41|B4QT41_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MAKIANASLS QQQKQRQAAT ATTTTTTVAA SVETATTTAR SRDRTKSAAQ ITSHLLKRAI SVYSSPQWIP LFILIYLATD
  81 VASVAVPTKE AYFNGSTYLR LTTPMPIWDH SAISFRSCRG GEILAQQYNK NSIVISVLND FLQISLAGPA VHGPNNRLDV
 161 KLPYQLLDNR WHTLQFKYEY GNLYLHVDRA ASIFANSTYN SQFLTNQDIG YKDAILILGN SFSGCLLDGP GLQFVNNSTV
 241 QNVVFGHCPL TPGPCSDHDL FTRLPDNFCL NDPCMGHGTC SSSPEGYECR CTARYSGKNC QKDNGSPCAK NPCENGGSCL
 321 ENSRGDYQCF CDPNHSGQHC ETEVNIHPLC QTNPCLNNGA CVVIGGSGAL TCECPKGYAG ARCEVDTDEC ASQPCQNNGS
 401 CIDRINGFSC DCSGTGYTGA FCQTNVDECD KNPCLNGGRC FDTYGWYTCQ CLDGWGGEIC DRPMTCQTQQ CLNGGTCLDK
 481 PIGFQCLCPP EYTGELCQIA PSCAQQCPID SECVGGKCVC KPGSSASDLE PLTPLELDIL DATLCPSEKK KRYISPEWLK
 561 RKRCELKLRP IGHCLPTTTT PTPEQEPTTT PRTTANPNPA IPNTLTTTTK IPPITTSRTP VGTTTGSRKP PQQPLQSPTQ
 641 RSASLNACPQ ENCLNGGTCL GYSGNYSCIC ASGYTGYNCQ TSTGGGASAL ALTPINCNAT NGKCLNGGTC SMNGTHCYCA
 721 VGYSGDRCEK AENCSPLNCQ EPMVCVQNQC LCPENKVCNQ CATQPCQNGG ECVDLPNGDY ECKCTRGWTG RTCGNDVDEC
 801 TLHPKICGNG ICKNEKGSYK CYCTPGFTGV HCDSDVDECL SFPCLNGATC HNKVGYEGEN CEVDIDECGS NPCSNGSTCI
 881 DRINNFTCNC IPGMTGRICD IDIDDCVGDP CLNGGQCIDQ LGGFRCDCSG TGYEGENCEL NIDECLSNPC TNGAKCLDRV
 961 KDYFCDCHNG YKGKNCEQDI NECESNPCQY NGNCLERSNM TLYQMSRITD LPKVFSQPFS FENASGYECV CVPGIIGKNC

1041 EININECDSN PCSKHGNCND GIGTYTCECE PGFEGTHCEI NIDECDRYNP CQRGTCYDQI DDYDCDCDAN YGGKNCSVLL
1121 KGCDQNPCLN GGACLPYLIN EVTHLYNCTC ENGFQGDKCE KTTTLSMVAT SLISVTTERE EGYDINLQFR TTLPNGVLAF
1201 GTTGEKNEPV SYILELINGR LNLHSSLLNK WEGVFIGSKL NDSNWHKVFV AINTSHLVLS ANDEQAIFPV GSYETANNSQ
1281 PSFPRTYLGG TIPNLKSYLR HLTHQPSAFV GCMQDIMVNG KWIFPEEQDA NVSYTKLENV QSGCPRTEQC KPNPCHSNGE
1361 CTDLWHTFAC HCPRPFFGHT CQHNMTAATF GHENTTHSAV IVETTDVARR AIRSILDISM FIRTREPTGQ VFYLGTDPRK
1441 APTKNIGDSY VAAKLHGGEL LVKMQFSGTP EAYTVGGQKL DNGYNHLIEV VRNQTLVQVK LNGTEYFRKT LSTTGLLDAQ
1521 VLYLGGPAPT RESLLGATTE PGIIPVPGAG VPIEDTTVPK EADDSRDYFK GIIQDVKVSN GSLNLIVEMY SLNVTDVQVN
1601 AKPLGAVTID RASVLPGEVS DDLCRKNPCL HNAECRNTWN DYTCKCPNGY KGKNCQEIEF CQHVTCPGQS LCQNLDDGYE
1681 CVTNTTFTGQ ERSPLAFFYF QEPQSDDIVS ETAPKQTFKP VIDIAFRTRA GGTLLYIDNV DGFFEIGVNG GRVTITWKLS
1761 ALHFGESARF EKENTDGEWS RIYLRAHNSK LEGGWKGWES MVDPTPAFST DIDQAAFQSL IATSTQVYLG GMPESRQARG
1841 STLSAQQGSQ FKGCVGEARV GDLLLPYFSM AELYSRTNVS VQQKAQFRLN ATRPEEGCIL CFQSDCKNDG FCQSPSDEYA
1921 CTCQPGFEGD DCGTDIDECL NTECLNNGTC INQVAAFFCQ CQPGFEGQHC EQNIDECADQ PCHNGGNCTD LIASYVCDCP
2001 EDYMGPQCDV LKQMTCENEP CRNGSTCQNG FNASTGNNFT CTCVPGFEGP LCDIPFCEIT PCDNGGLCLT TGAVPMCKCS
2081 LGYTGRLCEQ DINECESNPC QNGGQCKDLV GRYECDCQGT GFEGIRCEND IDECNVEGDY CGGLGRCFNK PGSFQCICQK
2161 PYCGAYCNFT DPCNATDLCS NGGRCVESCG AKPDYYCECP EGFAGKNCTA PITAKEDGPS TTDIAIIVIP VVVVLLLIAG
2241 ALLGTFLVMA RNKRATRGTY SPSAQEYCNP LLEMDNVLKP PPEERLI
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.CHNGY.K	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	967	971	
total 1 peptides												

tr|A0A224X4P4|A0A224X4P4_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 DNDECLGQNP PCQNGRCINT IGSFKCECHI GFNLGPDGRS CVDTQRDLCY SSYQNGVCSK PSLMAVTKSS CCCCASFIDH
  81 HLAWGTPCEL CPLPGSEEFH RLCPHGVGMT SGGKDINECA QDPYLCVNGA CENIMGSYRC VCNPGFEEDL MRKTCVDIDE
 161 CKLYDNICSG GQCRNTPGSF QCTCPAGTQL NVVMHVCEDI NECEELGGEP CLNGDCINTM GSYICECPPG SIIDHTGRVC
 241 IDNRKGTCWT QVRDRCENSL PQLTSKSECC CSLGSAWGSP CEPCHHVCDC AKGYAKIDGK VCKDINECEL NSGVCRGGGT
 321 CVNTEGSFTC VCLSGLSLDS TGTVCIDVRQ ESCFTEYKHG QGSGVIEGLY PRTICCCSGV GKAWGGPAGG SRCEVCPKQG
 401 TPGFNDLCPK GYGFVDRKDI NECIEFPGMC SNGRCKNTMG GFNCRCNQGY ALDENGIKCV DIDECNIMHG VCGNGTCQNI
 481 AGSFKCDCKE GYESTMMMQV CMDINECDRT PGLCRGGQCV NTPGSFKCNC PPGHELSPDK RSCKDIDECS RTSGICSNGV
 561 CENMMGTYQC VCDDGYQHAG ITSHCEDIDE CASNNGGCTS ICVNTPGSFY CDCHSGFVMR LDGRSCIDVD ECKENPRICN
 641 GGKCTNTVGS FTCQCTKGLL PGPDGSSCVD INECDGDSNV CGNGDCDNTI GSFICHCEIG YSAKPRGGPY CTDEDECQLM
 721 IHNCDYNADC INNPGSFSCR CKDGFNGDGI TCRDINECLT NNGGCNQNAQ CINIEGSFKC VCDSGFRGDG YTCTDIDECI
 801 ENPMLCENGN CLNYPGSFRC ECEMGFMHPN DNSETACVDI NECNAFDNIC VHGQCSNLIG TFKCICGEGF QLDDSRGNCT
 881 DVNECDSPKA CMYGKCINTI GSYLCQCPPN YQLVPAGNAC VDKRESRCYQ QVDDSYGRPS CTKEMGSAVT KATCCCSLGR
 961 GWGIMCELCP RPGTREYNDL CPGGTGLRPN KTTVRLEDIN ECEDHENICK NGHCTNTFGS FMCSCNDGYR LNPQLATCVD
1041 IDECFERPKV CGVGICVNLD GSYHCICPSG YMLLPNGKEC VDMRKEKCYM EYVDGTCAHP MSNHQTKMVC CCSMGEAWGS
1121 PCEPCPRPRS KDYLDLCGTQ PGQILNPMTN QSEEIDECTL MPTMCNHGSC MNTPGSFECH CNRGFSYDAD SHQCIDEDEC
1201 LRSPSPCRGN AHCVNSPGSF ECQCPPGYKL SMSQRDCIDI DECERPGVCA HGSCNNFQGS FQCICHNGYK LHHGTCVDID

1281 ECHRHPNICN NGTCSNTEGS FTCRCHTGFK LSHNNDCIDV DECRTKSYLC RNGRCRNVIG SYKCECPEGY ILSQDLLHCR
1361 DLNECVERTG ICPPPGTCQN TMGSFICSCP AGYHLSSDKK TCIDIDECVE RRGICEGGKC TNTEGGVLCE CPEGFILSDT
1441 KIKCIDVRQD MCYDSYERGY CKEPKMKPIT MKECCCSMGK AWGRHCELCP EQGSEEFLKL CPQGTGRSEN GADLNECQFM
1521 PNICTGGDCI NTDGSFRCEC PTGYVLDPSG KNCIDYNECK TSNICGNGTC VNIEGSFECT CNAGFASGPM QTCEDINECI
1601 EMGKQCAFRC HNVPGSFRCI CPYGYTLAPD GRHCQDVDEC TTPANNCKFQ CKNLIGSFMC ICPEGYTQVG MSDDCRDINE
1681 CKLSSEICEN GYCINLEGSY RCDCFPGFKP NYDRKKCIDE RKGYCFPYLS NGRCVMMPGD VRKGVTKADC CCTMGAAWGP
1761 LCEPCPQPGT ARYTNLCLES GININGQDIN ECQTLPDLCK HGTCINTLGS YRCLCNKGFK ADYVGTHCRD INECAQSPPP
1841 CKYSCQNTEG SFICSCPKGF ELSPDGVSCL DIDECETRQH ICQQNCVNTQ GGYQCSCEKG YRQDGDQCID IDECDASEGY
1921 CPPPGNCINT LGSFRCLCPR GFKLDASGEF CRDKDECTDD TKCEHGCQNI RGSYRCSCPE GFVKHVYYNH CVDDDECSRS
2001 PCGDSKCVNT IGSYRCGCAD GFQFDQTLSA CVQISPACIG SLCSFGCLPS NHGGYTCGCP SGYQKIGQGH CLSTINPMGY
2081 DSMETTIFRH FQAAETYRIP NGKIISTEGC FSCKTNGRHR RMTNGTFRAS RKKYDTEPSI RQRHYWKYKN IARHKRHHIN
2161 SLVTTDKIIA DHIKPKWIHE SKVLKITLLQ TKHRMRIIKI MSAIKNGYEY IITRGNENGH FEMVQRHGVW ALHFKRRLKV
2241 PGVFILEITG KPFNMTLLKS LAEQPLVLHI KLLVV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.CHNGY.K	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1265	1269	
total 1 peptides												

tr|A0A232F5I4|A0A232F5I4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MERGKSGTGR GSKNKIAPHP SDFIALGSKS TSRSDAPDTK RPGVGLTKPG LSSSTSTSND RKKEGSSLQS LIPPKKPKLA
  81 GHPVAPSTRP SVSHTETWEV ITIECDPADL VPLVLEANDA DDGEKLIGLV CGGIKILKNL RWKPDPVVCM GLLYLVKIRP
 161 SIFTNHCILH ALASLLKRDQ SHAFKNKGNP MVSVLAANLL MRGFHDKKEW PEVFIKVYIE DALGDRVWVD NEECKGFVDN
 241 ILTGFNTRIP PKSVLQPELS VMTPRSDCNS PSTLLDDELS GTSAIQIIGD KDKVDLPVCP RYAHCVEVVE NIILEVIKEQ
 321 LNRRQPETIT RNFLKLLSTA CGFVEIRNIA AQKLEMWLHN PKLMRPAQEL LSFICYNCTS HTQRDVEVIS QLVKMRLKTK
 401 AVINLYLNGV KELIGLHPEN LSTILKHTIY NELSNARNPN NMPMLAVMFQ TSPEASAKLL AEIFQELLLN RDDYLRPIRA
 481 LLREIVRVCR HDINLTILAR ALMATRVEVA QQIASFEFKD RMFIAIIDLI SLCMFLAISP QVKDVAIQCQ RGDKKDINVL
 561 YQFQNLVTSI QYETVFWLQS TANQIYGIMY KEPFLHALHK VMMLESPEHY YKPDNFPPET DRALYMRLVS EVPLLESTFK
 641 LFALAFIGKL SFINPKDQLP TCSINNSEMI ELTDHLVRRA AMTSSETFPL LHIKNTEIFE LVFHMCTYQP PAAASINIPS
 721 DYIPPTLAVS NLYWKGWIML LMIAAHNPST IGELGWQQYP ILRILMEMCI TNHFSYPPPT MALPEIVEEN RAKELRLETL
 801 ERQQILHYET YLAKASNPER QICEQTSLLL SQTITMDPTG IPRTPPQHVL DLIQSLNTTH RLGHLLCRSR KPDFLLDIIQ
 881 RQQSTSSQSM PWLAGLVQNS EGSLNQLPVQ CLCEFLLSST IGQADKQSRQ EQLLAHLQLL LTDPLQDSQH AYEVLEYFLR
 961 RLSSQSSASR LQAITGLKLV LNSIPTEDEP MEIDGENEQH NLSASSETWL LKKLPSIPHF HAVRSLVAKA LRSACQVENN
1041 PDLVQAYIAY LATHTPEDDL PDLINLVNEI SQLVVERNTI VAAILPQPDI DSLQAKQTLY AFLSIYCNYL NKARAPRLDG
1121 SRFTWSESQD LILVEWATGE ECTMHILVVH AMIILLTYDQ VDNDELFNQL LETWFPEETE PPKAFLLDTS EEALLIPDWL
1201 KLRIIRSNIP RLVDAALRDL DPYQLVLFIQ SFGVPVNAMT KLLHLLDAAV QIEPMSVTNH VLDKTYMAQL VKILHNRGAS
1281 GGLVFLQHVQ LQAQQLPDES LPPISTRLEN LPSSTNLPKH TIVQLSTAKT DVPNLINQLF IEKIPINQKT DAYRKLHKIL
1361 TKDLHKSGAD GDRGTVVLAV KHILSVLSSI QVKEFLASLV HMSQYSCTLM RVILLPLKRP RTCPQTLELA HSMCCNLIQL
1441 IGDVNAPILA ILRDFTNLHV SRAPRHKELA ALTQTQDPGS ILENTDPLDL ENVGRRLLDI CMNQQRNDVL VESMARLLVA
1521 DSEQGSIKPR TGLLIDWLAS VEPELIDTCP NLQIRLLFGK TNVYVRIDES VVSSHSCRPY LLTLLTHGAS WATLYKCVGH
1601 LLNQCHNGYD PTAVLDFLWA LTCNPKLWQG REKYSTKNDI PENILMLTNE QLLVLVMYLI EEAVILCERQ NRKTAITQME

1681 TRLDLLLCCC SAEDELTMGV VKYLADQMTN SNGVHADMFH QFLLHLYMKV PKIICYLNTF QAKKMVNNAN ISDWTGSILD
1761 CMSHTLLTAL ASQRQKSSKS RELELCARKM AAVHPILVLR QLPLLASSLM GWCDLEYSQF RSGHHLNLFT QVMGLLELLQ
1841 PHLFNEEHRK GLENTLENYF YCFQNYCNKD SSFQNYSNKD DLIPLLNRFS LLLQAYVVHD EQHALKYIQQ HAYILHDLQA
1921 HYLSLESLRS LVSGIPIPRE GENGETVLIT STFRRNAPTP PSAHWAGWVA SLTKMQGDEV HSALHEIDTL SSRKPSVLEP
2001 IIDNIADLLV SPQGNIRNLA HVLIARALKH RPYPNLGVLS AFQRCLDSSR ADILMSALDR LPDYVLCMQE YALPLMQKVF
2081 ELGVNSNVNT IPYINKSITL LNTQKGC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.CHNGY.D	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	1605	1609	
total 1 peptides												

tr|A0A1B6LVD0|A0A1B6LVD0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 SLCCCSTVGK AWGGPSDGTR CEQCPRQGTD THHELCPKGY GFIDRKDINE CTEFPGMCTN GRCKNTIGGF NCRCNQGYAL
  81 DENGIKCIDI DECSIMHGVC GDGICRNTPG NFECDCKEGY ESSSMMQICV DINECDRTPG LCRGGVCHNM PGSYRCNCPA
 161 GHELAPDKQS CKDIDECSRT SGICSNGVCE NMMGTYQCVC DDGYQQTDMK SHCEDIDECS NSNGGCQGVC VNTAGSFSCA
 241 CSAGYRLVSD GRGCVDMDEC KDNPRICSGG RCSNTVGSFS CACTDGLLPG PGGSSCLDVN ECESGRDVCG NGECDNTIGS
 321 FICRCEDGYS VKPGRGPQCT DDDECVLETH QCDINAHCIN NPGSFSCKCP DGFTGNGISC RDINECLTNN GGCDQNAQCI
 401 NTDGSFKCVC DSGFRGDGYS CQDVDECTES PTLCENGHCL NYPGSFRCEC EMGFMHPDDK SETACIDINE CMMFNNLCVY
 481 GRCENIFGMF RCECNEGYQL DNSGGNCTDV NECDSPQACL YGTCMNTQGS FICQCPPNYQ LVPAGNACVD KRESRCYLEV
 561 EEWRGRQRCS QEMGSPVTKA TCCCSVGKAW GPQCELCPKI NSDEYKALCP GGIGYRPNTL TVVLEDINEC EEHEGICKNG
 641 HCTNTFGSFM CSCHTGFRLD ETQVNCVDIN ECQERPNICG VGYCVNDDGS YHCVCPEGYM LLPNGKECVD MRKELCYLSY
 721 AEGQCTQPMT NEQTRMLCCC SMGQAWGHPC QPCPTDKTEE YLLLCGNQPG QIMDPMTNAS VEIDECTLMP TMCNHGSCLN
 801 TPGSFECDCN RGFVYDIESH QCIDDNECLR IPSPCRGNAQ CVNSPGSFEC QCPEGYKLGM SMRDCVDIDE CLERPGICEN
 881 GDCNNFQGSF QCVCHNGYQL TVSRETCTDT DECTRHPNIC NNGTCINAVG SFKCHCFPGF KLSHNNDCID VDECYIMPYL

 961 CRNGRCRNMI GSFRCECADG YSLSADNQHC QDVDECQETG GMCGPAGRCQ NLMGSFQCSC PSGYRLNPDK TKCVDVNECQ
1041 DSAGICEGGA CINTDGGFIC ECPDGYVLSQ NGMKCIDVRK DMCFDVLHMD RCSMARREPM TVKECCCSMG AAWGRYCEQC
1121 PKDGTEEFWK LCPQGPGRMD TGEDLNECDF MPHACDGGDC INTDGSFRCE CPAGYILDGT GKRCIDDNEC MSGAGICGNG
1201 TCSNLIGGFE CSCTEGFAPG PMQACEDINE CLELNNQCAF RCHNVPGSYR CICPYGYALA PDGRHCVDVD ECVTPANNCK
1281 YNCKNLIGSF MCNCPEGYSQ MGMSDDCRDV NECLTQPNVC VNGRCVNLQG SFRCDCFEGF KSSYDFKQCI DERQGYCFRK
1361 LMNGRCSSHS DGLMAVTKAD CCCTMGAAWG PYCELCPSPG SDDYQQLCLD TGYSIDGSDI DECHTIPDLC RNGKCINTLG
1441 SYRCLCNKGF KPDHSGKHCK DVNECEQKPA PCQFACQNTE GSFICSCGAG YVLHSDGTSC ADLDECATGQ HLCQHQCVNT
1521 QGSYSCSCPD GYSQAGDHCL DVDECESGHL CPGPGRCINT LGSFRCLCPR GYKLDKTGSY CSDSDECTDD SKCEHGCQNF
1601 MGTYRCGCPD GFLQHVYYNQ CVDDNECSEN PCGDQKCFNT MGSYRCGCPD GFQFDQALVV CVQVASSCVG SPCAFGCSPS
1681 AGGAGFQCGC PSGYERIGQG HCLSTINPAG LGYGGAPNLG SNIPTYPIDQ DPYAVPHDRL ISTEGCFSCK VNGRHRRMIA
1761 ESKFFNSRDT LYDAKKLREL WRSRMSRHRR HHHGDKARVQ QPHRVLKVSL AQTKHRTRIL KLQPAIKNDF EYSITKGNEN
1841 GHFEMVRKHG VWALHFRRRL KHAGTFPLEI TGSRVMPAAS NDIWEAPLAL HVTIVASS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.CHNGY.Q	Y	31.50	592.2064	-114.6	593.1458	1	4.61	218	1	894	898	
total 1 peptides												

tr|A0A2A4K6P5|A0A2A4K6P5_HELVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MYLEKTAIHV LRYNMYINGY PCLINLNANY LCVFLAINID ASCSEEVPVP KRNLDQRLAR SAWNHFQQDC TRTLCRCEIM
  81 QEKKPLKKLR KKQNLILTTL QLMSRKEISK ILRAKVNALC VIEIHSRDTV DRMYKMEPIF QNPMGLPVAK AMSSEDGECV
 161 EWKYNLVLDG PAEVWLSGLE HTMRVVLRDQ LILTRAALRK CRYQRETWIN DWPDCTRTLC RCEIMQEKKP LKKLRKKQNL
 241 ILTTLQLMSR KEISKILRAK VNALCVIEIH SRDTVDRMYK MGCMNVTAFE WFSQLKFYWD REREDCYIKQ TNTNSIYTYE
 321 YIGNSGRLVI TPLTDRCYIT LTTALHLFRG GSPQGPAGTG KTETTKDLGR ALARWVVVTN CSDGLDYKSM AKCFSGIAQS
 401 GCWGCFDEFN RINIEVLSVV AQQILAVLLA LSLFQKRFIF EGADIKLDPN CGIFITMNPG YAGRTELPDN LKSMFRPIAM
 481 CVPDSLIIAE NTLFSDGFTA YKVNAKKVFT LYQLAMQQLS KQEHYDFGLR SMVALLRYAG IKRRAYPHLP EQEMVILAMR
 561 DMNVARLTAK DVPLFDGIMQ DIFPDVEIPT LDYELLETAI TAEMRLAGLQ PVKAALHKVI QTYETKNSRH SSILLGDTNT
 641 AKSVSWRMLA LTTTRLHNEK QPGFEIVHTF PMNPKALTLG ELYGEYNLAT GEWKDGVLSS IMRTTCQGRT ELPDNLKSMF
 721 RPIAMCVPDS LIIAENTLFS DGFTAYKVNA KKVFTLYQLA MQQLSKQEHY DFGLRSMVAL LRYAGIKRRA YPHLPEQEMV
 801 ILAMRDMNVA RLTAKDVPLF DGIMQDIFPD VEIPTLDYEL LETAITAEMR LAGLQPVKAA LHKVIQTYET KNSRHSSILL
 881 GDTNTAKSVS WRMLALTTTR LHNEKQPGFE IVHTFPMNPK ALTLGELYGE YNLATGEWKD GVLSSIMRTT CQGGVGSKWG
 961 EGGAVTGGVV VRGRAAVTGE VAVRGDVAVR GEVAVSREMA VTGGVAVSRE MAVTGGVAVT GGVAVRGGVA ARGAVAVRRG
1041 VAVRGGVAVK VKVAVRRAVE VKCGEGSSKG CYVLIYLLQD FKIKVTLTRI YHTDESPDNK WIIFDGPVDA IWIENLNSVM
1121 DDNKLLTLVN SERISMPSQV TLLIETLDLA VASPATVSRN GMVYNDYKDW GWWPFVNSWL ETIDYPEYRE MLRRFFLSIL
1201 TPVLELKRLY LREGESVRGQ ELTGVRCLCR LLGLLPEPAP ALPDEQTDIE GLAKMRFLFA MIWSVCATLE EDPRRRLDNW
1281 IREHEGIFPL KDTVYDYFVD ERLQQFKPWE EKLPDNWRFN PVAGFHTILV PTMEFIRVQV IALDMLKAGY GVLVGGPTGT
1361 GKTFLIQGTL NMLDPSKYSM QVINMSAQTT AANVQDIIES RLEKRTKGNY VPAGGKKMIA FMDDINMPVR DYYGSQPPLE
1441 LVRLWHDYGY WFDRAKQWRK NVKNMVLCGA AGPPGGARSP LPARLLSCFH AFYLPSPTQQ QLVKIFGTML GQHLQEFDEE
1521 TKSVGKTVLV ATIDMFNNIV AKLLPTPSKM HYLFNLRDIS KIFQGLLRSN KDYTNTKARF LRLWIHECFR VFCDRLTEEK
1601 DRDWFMNHIG DMLGKHFELT FHALCPTKSP PLFGHFLNPY EVYDDMNDPD ALRKYITAQM EEYNSCPGVV KMDLVLFKDA
1681 IEHVCRIVRV ISQPRGNLLC VGIGGSGRTC LTRLATYICE YHSFTVVVTK TYGLKDFRED LKVHLLRMHQ LFLLKSSHFL
1761 NIRCDKVGRT SYHDEFLRVS EGTINRIQSD PRHDNELVPG VAARGAAGGG VPLPARRRAA RLHHWTQGED TAGSSLIHAT
1841 TTNWFLEWPR EALLEVAYRF LHGVELLASI TGPRGEDTAG SSLIHATTTN WFLEWPREAL LEVAYRFLHG VELLASITGP
1921 RGEDTAGSSL IHATTTNWFL EWPREALLEV AYRFLHGVEL LASITGPRGE DTAGSSLIHA TTTNWFLEWP REALLEVAYR
2001 FLHGVELLAS ITGPRGEDTA GSSLIHATTT NWFLEWPREA LLEVAYRFLH GVELLASITG PRGEDTAGSS LIHATTTNWF
2081 LEWPREALLE VAYRFLHGVE LLASITGPRG EDTAGSSLIH ATTTNWFLEW PREALLEVAY RFLHGVELLA SITGPRGEDT
2161 AGSSLIHATT TNWFLEWPRE ALLEVAYRFL HGVELLASIT GPRGEDTAGS SLIHATTTNW FLEWPREALL EVAYRFLHGV
2241 ELLASITGPR GEDTAGSSLI HATTTNWFLE WPREALLEVA YRFLHGVELL ASITGPRGED TAGSSLIHAT TTNWFLEWPR
2321 EALLEVAYRF LHGVELLASI TGPRGEDTAG SSLIHATTTN WFLEWPREAL LEVAYRFLHG VELLASITGP RGEDTAGSSL
2401 IHATTTNWFL EWPREALLEV AYRFLHGVEL LASITGPRGE DTAGSSLIHA TTTNWFLEWP REALLEVAYR FLHGVELLAS
2481 ITGPRGEDTA GSSLIHATTT NWFLEWPREA LLEVAYRFLH GVELLASITG PRGEDTAGSS LIHATTTNWF LEWPREALLE
2561 VAYRFLHGVE LLASITGPRG EDTAGSSLIH ATTTNWFLEW PREALLEVAY RFLHGVELLA SITGPRGEDT AGSSLIHATT
2641 TNWFLEWPRE ALLEVAYRFL HGVELLASIT GPRGEDTAGS SLIHATTTNW FLEWPREALL EVAYRFLHGV ELLASITGPR
2721 GEDTAGSSLI HATTTNWFLE WPREALLEVA YRFLHGVELL ASITGPRGED TAGSSLIHAT TTNWFLEWPR EALLEVAYRF
2801 LHGVELLASI TGPRGEDTAG SSLIHATTTN WFLEWPREAL LEVAYRFLHG VELLASITGP RVRRMESLIE SREDVLRASV
2881 ASIMSLIHSS VGRYSLRMWQ EMRRTNYVTP TNYLELVAGY KEMLSAKRNE IALQANKLRN GLGKVEETTK LVGQMSEELA
2961 EAQVQVGLYT EQCIEYMGVI NVQQRNADEQ QRSVAARSKK TMEEEVQCKK LADAAMRDLA SAMPALEEAI KALDALNKKD
3041 ITEVKSYAKP PQKVEMVLEA VLILLQKEPT WAEAKRQLGD QYFLDRLRDF DKDNISDKTL KKIGTYTVKP DFDPEIVGTV
3121 SSAAKSLCLW VRAIEKYGKI FKIVKPKKER LEEALESLRM KQQILAEARA KLRELSEMIA RLQREYDEKV AQKEELERRS
3201 RMLQLKLERA EALITGLSGE KERWEMTVER LDKEFDNLPG DCLIATGFVA YLGPFVSEYR ESLMEDWFLE VCNESLPVTM
3281 DLSMKKFLLD DATLRDWNYM GLPDDNFSAE NGIIVVRATR WPLAVDPQGQ ALIWISRLEE KNGIQNVGEV LDPSIAPILE
3361 KAVVTIGSSK VIKFNDKMVS YHPDFHLYLT TKLGNPVYTP ETLTKTTMVN FAVKEQGLTA QLLGIVVRKE RPQLEQMKDT
3441 LVLSIAHNKK VLVDLENDLL RIMYESQVPL LENEELFITL QTSQRTSLDV KEALITSQVT EKEIDSARAG YVPVAVRASV
3521 LFFALNDLSR IDPMYQFSLD AYIDLFTYSI DRSPKAGELE DRINNLNEFH TYAVYKNTCR ALFERHKLLL SFHIVSRILF
3601 QMGKMSRNEY MFLLKGGVVL DRSEQPDNPT NWMPDDCWDN ITEMDKLPGF HGIVDVFESL SKEWKEWYLH PEPESQPLIG
3681 DWNDICSDFQ KILFVRSLRV DRVSACITTF IINVLGPRYV EPPVLDIRAA WEESSWKTSL LFVLSPGVDP TAALIQLAQD
3761 VKMFDRFASL SLGQGQAPTA TRMLSHGMKE GGWVFLANCH LACEWLGSLR GLDNPKIHPR FRLWLSSMPD DKFPLHMLQR
3841 SIKMTTEPPQ GLKGNLVRLF ANINEDKFDE ATPKYRRLLF CVSFFHCTLI ARKRFRQLGY NAVYSFNDAD FDVSDNLLAN
3921 YLEEYEEVPW DALRYLFAII NYGGHITDDW DKRVLIAYIN QFFNEDALET PFYRLSSIPA YHIPRDGSLE SYRDFLDLLP
4001 AYERAESLGQ HASADVATLA QDALIMCSTL FALASTGGGG AGGGEDQKVD ELAQEMLVKL PARIDMETTE RMMGPEIVMP
4081 MCVSLLQEIG YYNVLINMIT MGLKELRRAI EGLVVMSEML ETMYLCIFEG RTPSFWLRGR PSMKPLGAWC RELFLRGAHL
4161 QGWANAPRSP PTLCWLPAFV APTGFLTAVM QELRRAIEGL VVMSEMLETM YLCIFEGRTP SFWLRGRPSM KPLGAWCREL
4241 FLRGAHLQGW ANAPRSPPTL CWLPAFVAPT GFLTAVMQTT ARGESWPIDT LCWEFTVMPL EEAGFVRPPR DGGVYIRGQY
4321 LEGASWFRKE GHLQEPLPMQ LVFPMSPIHF KPVRITGKRL RNRYVCPCYY YPLRMGAFVV AVDLPAGKES SDFWVKRGTA
4401 MLCTLAT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.FITLQ.T	Y	19.63	620.3533	-78.0	621.3122	1	25.56	938	1	3477	3481	
I.GGSGR.T	N	15.37	432.2081	91.7	433.2550	1	9.65	438	1	1704	1708	
total 2 peptides												

tr|E2BYR5|E2BYR5_HARSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEIKQVFLKT RAEFGKQCIF DTWGPHMDEE IRPNPAAMAD YIMRTHCNVG VLHTKQFALH EAQTASGQTK SSGMFHFEGG

81 WPREINPKDE ETTMRFRRRI EKDEEWAPKL RNLFQQMEHN VLQNGALNIY EQYFDDMVPT ELMKIRDLRT LNVYENPRAL

161 VRSVNDISWS PDSGSKMVVS YYSEFGVQPE DNIAHIWQID NPNEPWVTLK ATSAPLVSEF NPRDPSVLAS GLMSGQVCSW

241 DIRTGSTPTQ TSHCRFSHRD AVTTVKWITS KSNTEFFSGS VNGRAMWWDT RKLREPVEIL TFDLQTPNEP QMDRAIGVSS

321 ANFEASLSAK FMFGLDNGLV ISGSRKAHTP AEKLAWSFDA HYGPVFSVDR NGSNPKIFLT VGDCIARVWA EDTRDGNLVS

401 TRFIREEPVR GCWNKARHSI FYVTTRSGVL TVWDLLVGLG NPILSVQICE EKLSAIAAHE RGDLLAIGNS AGNVYLVELT

481 EALYSFDKNE KNNFSSYLEC CSRFAKAIDT RLKEIKLTRT YATEDESRST LEVTRGKRKD KTLPKILGRK GQKMQESQDK

561 LKNYRKRERS TKKNKRRLKD EFDDFRIVEE KFFEVVEKEK LKYEGDERVL TPSKISVTKV ASRKIDKNFV TTADEAKDDT

641 AKMPAKKIAV PKKTKIAIPT AEAEKSVEQE KPEE**TLPASA EAIAESPT**EE ISKRSKRKRR KRLMPVAFSL PRPCKVGICK

721 PDICCRGKLS TRAVVRFADR AKWIRGEVRD GEERSKGDVA ARTAVEARRK KRDSWTKLMR AYERKASSKE TIASLWEMTE

801 LPEELREAVR EAKREIRQAE RSGKTRTRAE KLAKRAPTRS VTAAEKSREA PRSSQEDEEG DPAKEVTARS TMARILAARK

881 GKRAVMMDPC TPWKPPSLLK DLQSLLGGPL PESIEEKTNL GMARIKELEA ARGGVYPRIS DFHSID

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TLPASAEAIAESPT.E	Y	24.05	1356.6772	-32.4	679.3239	2	18.91	723	1	675	688	
total 1 peptides												

tr|A0A0K8SP95|A0A0K8SP95_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTTYEEFIQQ SEERDGIRFT WNVWPSSRIE ATRLVVPVGC LYQPLKERTD LPAIQYDPVL CTRNTCRAIL NPMCQVDYRA

81 KLWVCNFCFQ RNPFPPQYAA ISEQHQPAEL IPSFSTIEYT ISRAQFLPPI FLLVVDTCLD DDELGALKDS LQTSLSLLPT

161 NSLVGLITFG KMVQVHELGC EGCSRSYVFR GTKDLTSKQV QDMLGIGKVS ASPQQQQRA MGGQQPFPTN RFIQPIQSCD

241 MSLTDLLGEM QRDPWPVGQG KRPLRSTGAA LAIAIGLLEC SYPNTGAKVM LFLGGPCSQG PGQVVNDDLR EPIRSHHDIQ

321 KDNARYMKKA IKHYDSLALR AATNGHSVDI YSCALDQTGL AEMKQCCNST GGHMVMGDTF NSTLFKQTFQ RVLSRDQKGE

401 FKMAFNGVVE VKTSRELKVM GAIGPCVSLN TKGPCVSE**TD IGLGGT**CQWK FCTFNQNTTA AMFFEVVNQH AAPIPQGGRG

481 CIQFITQYQH ASGQRRIRVT TVARNWADAT TNMHHVSAGF DQEAGAVLMA RMVVHRAETD DGPDVMRWAD RMLIRLCQKF

561 GEYNKDDPNS FRLPENFSLY PQFMYHLRRS QFLQVFNNSP DETSYYRHIL MREDLSQSLI MIQPILYSYS FNGPEPVLLD

641 TSSIQPDRIL LMDTFFQILI FHGETIAQWR AQRYQDLPEY ENFKQLLQAP VDDAKEILHT RFPMPRYIDT EQGGSQARFL

721 LSKVNPSQTH NNMYGYGGES GAPVLTDDVS LQVFMEHLKK LAVSSTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDIGLGGT.C	Y	24.00	732.3654	8.5	733.3788	1	19.35	741	1	439	446	
total 1 peptides												

tr|A0A084VFX3|A0A084VFX3_ANOSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSPIEVLIA VLAVLGALVY CVVRKHSYWK DHGVPHPKPV FPIGSFKDVG SKVHFVGALE RYYREYKGKH PFVGVYMLL**T**

81 **PVAMPT**DLEL VKAMLVRDFQ HFHDRGVYCN EKDDPLSGHL FNLEGQRWRH LRNRITPTFT SGKMRTMFPT IVAAGRQLAD

161 YMDETVRERD ELELKDVVSR FTTDVIGTCA FGIECNSMRD PDAKFRAMGR RIIEKQPPQW VNLMVQFSPR LCXXXXXXXS

241 FFMQVVRDTV DYRMANGVQR NDFMDLMIRM LQNEENPDES LTFNEVAAQA FVFFFAGFET SSTLLTWTLY ELALNQDIQE

321 KGRQSVNEIL DQHGGELTYD AVSEMKYLDQ ILKGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPVAMPT.D	Y	23.17	715.3575	15.2	716.3756	1	20.01	755	2	80	86	
total 1 peptides												

tr|A0A0A9YA46|A0A0A9YA46_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARPVKTPRM SDGSGNIIMV GVIKKEEELS PFGPPPSPNS AMYSPPATLL SNEEDLKDDE SPRRLCLVCG DVASGFHYGV
81 ASCEACKAFF KRTIQGNIEY NCPAANDCEI NKRRRKACQA CRFQKCLEKG MLKEGVRLDR VRGGRQKYRR NNEVPYIVSV
161 TSQNKPSLED NKLLEILLGC EPEILSIVPE RDGRPVLSPL NILSELYDKE LVNVIGWAKQ IPGF**TDLSLT** NQMRLLQSTW
241 TEILTLSLAF RSLPPSGKLN FAVDFIIDEM LAQECGAMDL YQLCLVITDR LQNCSICKEE YILLKALVLA NSDVRLDEAL
321 ALKQFRESIV SALMDCVGIM RGNSAEMANI LLCLPVLRQA DHTLRSFWTN VHRRGAVVMN KLFIEMLDPP LRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSLT.N	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	225	230	
total 1 peptides												

tr|A0A0A9VQS0|A0A0A9VQS0_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARPVKTPRM SDGSGNIIMV GVIKKEEELS PFGPPPSPNS AMYSPPATLL SNEEDLKDDE SPRRLCLVCG DVASGFHYGV
81 ASCEACKAFF KRTIQGNIEY NCPAANDCEI NKRRRKACQA CRFQKCLEKG MLKEGVRLDR VRGGRQKYRR NNEVPYIVSV
161 TSQNKPSLEV IVSDNKLLEI LLGCEPEILS IVPERDGRPV LSPLNILSEL YDKELVNVIG WAKQIPGF**TD LSLT**NQMRLL
241 QSTWTEILTL SLAFRSLPPS GKLNFAVDFI IDEMLAQECG AMDLYQLCLV ITDRLQNCSI CKEEYILLKA LVLANSDVRL
321 DEALALKQFR ESIVSALMDC VGIMRGNSAE MANILLCLPV LRQADHTLRS FWTNVHRRGA VVMNKLFIEM LDPPLRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSLT.N	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	229	234	
total 1 peptides												

tr|A0A0A9Y8J4|A0A0A9Y8J4_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARPVKTPRM SDGSGNIIMV GVIKKEEELS PFGPPPSPNS AMYSPPATLL SNEVSFCDGV IGEIPQCSPE SPDQHFCTST
81 TTALADANTS IGEDLKDDES PRRLCLVCGD VASGFHYGVA SCEACKAFFK RTIQGNIEYN CPAANDCEIN KRRRKACQAC
161 RFQKCLEKGM LKEGVRLDRV RGGRQKYRRN NEVPYIVSVT SQNKPSLEVI VSDNKLLEIL LGCEPEILSI VPERDGRPVL
241 SPLNILSELY DKELVNVIGW AKQIPGF**TDL SLT**NQMRLLQ STWTEILTLS LAFRSLPPSG KLNFAVDFII DEMLAQECGA
321 MDLYQLCLVI TDRLQNCSIC KEEYILLKAL VLANSDVRLD EALALKQFRE SIVSALMDCV GIMRGNSAEM ANILLCLPVL
401 RQADHTLRSF WTNVHRRGAV VMNKLFIEML DPPLRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSLT.N	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	268	273	
total 1 peptides												

tr|A0A0A9Y9B6|A0A0A9Y9B6_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRGVKNKSDS DCSELEPEAK KCKTEESPPE AKTILTEELE SDEKSTTTAT PDSSFNLPTP QPSEQAPRFV KPPRSPSPEP
81 SYPSLLNLSD DVLLHILSFI GPSDLVSLAH CSERLNNIAR DKSLWRVCDL RPRILSLNRL HNVLHWLQPV TLSFASCGPL
161 EIMPPLKEGE TIEPTWLLSF MILLSKYAPN LKTLVLENHI IDCNKILIED FPPSVENLSL KSCIFKNVPK QSSYFLGIHS
241 SMSRLRALDL TDSSWFVPHS LLALSKCAVL EELVLDGCDV SECMPYASLA ANYGFCNLRL LDLRNTAVSD VEVSCFNKMK
321 TLRHLYISAS EEVQPLRLPY SFSYV**TDLSI T**AFGESPAVH RQVLGRQVQV VGRPPCLIET LLLNNYPGIT DLTLRHVVVA
401 MPHLKLLDLT NTGVTSEGLA KFKTDRPSVT LVVSPNMIPS EA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.TDLSIT.A	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	346	351	
total 1 peptides												

tr|N6U3G5|N6U3G5_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSVGSEFIT NIWVPDTFFV NEKTSSFHKA TTSNEFIRIH HSGSITRSIR LTITASCPMN LQYFPMDRQL CHIEIESFGY
81 TMKDITYKWQ TGPTSVGISN EVQLPQFRVL GHRQKT**TDIS LT**TGNVQCSL QRTDFLIETC SKKLPKGFLP LVARVRVKRA

161 IQSVTPCETS GISGTKVPTR SAYRTRSRCP NSRFSDIGKE PWRSPSPQVH PLCPIWGLVT LALPQSGLFA GFGTSYIVVP
241 TGNYSRLACE IQFVRSMGYY LIQIYIPSGL IVIISWVSFW LNRNATPARV ALGVTTVLTM TTLMSSTNAA LPKISYVKSI
321 DVYLGTCFVM VFASLLEYAT VGYMAKRIQM RKNRFLAIQK IAEQKKLNVD GGPDDHLPKQ TEAVRFKVHD PKAHSKGGTL
401 ESTVNGGRGG REGGADDEVA GGPPIPQHIM HPNKDINKLY GITPSDIDKY SRIVFPVCFV CFNLMYWIIY LHISDVVADD
481 LVLLEVDK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TDISLT.T	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	117	122	
total 1 peptides												

tr|B7QA75|B7QA75_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NSPGLPNYRK VLLPALSPTM ETGTVISWEK KEGDKLNKGD LLCEIETDKS VMSFESPEEG YLAKIIVPAG TKDIHLGRVL
81 CILVYSEADI AAFGDFESDR TTVPAGQPKA AASAPASAPA STQMNYIDIP RTSMRQVMLV LLPALSPTME MGTIISWEKK
161 EGDKLNEGDL LCEIETDKAT MGFETPEEGY LAKIIIPAGT KDVPLGKLLC ILVYDEADVA AFKDFVDDGT AAPTAQPKAA
241 AAPAAPAPAP APTAAPAPAP ALTPTTPTPS MAGAPAAGVG GRLFASPLAK RLAAEQGLNL AQIPVGSGPG GRIVAQDLAS
321 AVPMAAAAAP VAAGTKY**TDI SLT**SMRQTIA KRLLQSKQTI PHYYLSVDIN MDAVMKLREE FNKAMEKENI KLSVNDFVIK

401 ATALACKKVP QANSSWQETF IREYKSVDVN MAVSTPEGLI TPIVFGAEKK ARMLLISEET KSLASKARDK KLQPHEFQGG
481 TITVSNLGMF GVKNFSAIIN PPQACILAVG CTEDVLVPDE NSNTGYRAVK MMSVTLSCDH RVVDGAVGAQ WLQHFKRLLE
561 RPDLMLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.TDISLT.S	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	338	343	
total 1 peptides												

tr|A0A0A1XHZ0|A0A0A1XHZ0_ZEUCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MANVNVNHGH NSNDIKVTNS AHDIIKPIAE RTSREWQGED VVKWAENQGL DCNVITCLAA EHIDGSDLLE LTENDIRDFR
81 YHLQYNLTMS DMKKLWVAVR KLQNTNSSAS HNFLQRNTLG SSDCSQFNRH CIHQSCGSPS CCNLNVCNCH IERNGVGYYS
161 DVCSPPNPPT LNGSVEDDNM SPPMSVDGRA TNIPPELFKT AISLGYSFLV TWITSFVMVI VHERVPDMKR YPPLPDIFLD
241 NVPHIPWAFH MCEITGTLLF IIWCCVCIFH KYRLVLLRRF FALAGTVFLL RCVTMLITSL SVPGTHLQCN QNDYAVDD**TD**

321 **LSIT**EALQLR ISRAYTIWSG LGMSIQGVRT CGDYMFSGHT VALTLLNFFI TEYTPRNLYF LHTMTWLLNM FGIFFILAAH

401 EHYSIDVFVA FYITSRLFLY YHTLANNQAL MSHDSTRTRI WFPMFSYFEN SIDGIVPNEF DSIGDLLDCL CQLVLSFKDT
481 CMLTARRIWI EVPPISSSEN LPSLSNAPDS LKLLNKPSQT RDGFGTTISA NVSNTLTPSQ PIFDVSKKMT HGIFKSFEPT
561 SDTPITKLSA SSNNIQGDKK HQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.TDLSIT.E	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	319	324	
total 1 peptides												

tr|A0A0E4GBG0|A0A0E4GBG0_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALREGLGSR STSSSLRLEE GSAGRRTNFS SFSSSFDEFG PPYADLPMEI LVKIFTYLTP SDRREASQTC RRWCEASHHT
81 AFLENFWLVL HRQPFDANGP PVRDLLQSFR HFPNVHLSEV DFERIGNFFT HFGPHIRRIV LRACEIQERD LTAILRRLPA
161 LRALTIESCR DLFMCVRLFE DAAEREELRQ TLSNV**TDLSL T**HNQYLSDAI LHRMVEIMPS LRALALAGCH ISFHKGLYRK

241 FYPGDGKQPS ESVLTFHYVS QLIEQRKGSL RALDFGETLV DDNALEVLAG MSPALCLERL ELNRCEQLSS RGLGTLITAQ
321 AAHLQHLNLS KTFRLTDSCL LQICRELRGL RVLKMRECRA LSNQGVRELV QLPALEVLDI SYCEDVNGAG LLEGIASRPN
401 ETLRELRVRA LNLCERSIIA ISEQLSALRI LDLGYCFHAV SDLCVQFIFR NLVRLTELDL ESCRKLSDEG LTGLGMLPII
481 QRHEQQQQPT AQPGASLGNG SVEGNAAPAD DQARPATPEP EPALQAATAH MRISLRSRAE REIVEDAERK KQLLEAMQRK
561 DNLQSARDDG TTFSGYSIGR LQQLRVLNLT GCNRLTDVTL LCNFKLLELR DLYLAQCQQI SVDGIRALVR GCPAVERLDL
641 SECHSINDRA VEQIAFHLHR LRTLSLRRCY QLTDFSLDYI ACHARRLREL DVRGCKHMCA DPAMRLVNLP LLATILPGKQ
721 DENGANGVFG AGSSASSPSL PPAPPPPAAP SRASMRI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.TDLSLT.H	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	196	201	
total 1 peptides												

tr|A0A0P6GKE9|A0A0P6GKE9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSTVSTMTSI TVVTPQRSTV TAMTPLQDPI TTLPSLLSTL ELESDPTTPE WTTWISTITT NLSRDIENTI WTTMGVSEET
81 TTMSINGSMV QDLPTTISDE TSTITSTDAL DTTTAVADTM TPMTHQTATQ FKTTVQSSIG TTFVPFLPES TIKPETSEGE
161 RESKSSTTVT RPMSSSSTAS TTVISHSTRL GHGISSTATT IAANTLFTLR NDRHTEDVTA GGTTTIHLPT NGRPPEADHV
241 PAATEHETDM TTNGHFELDN RPLLHPDDNT TESSLP**TDLS LT**LTTVSREL VDVSNQTTTT TTTTTMVKVL AVEPPLMDPS

321 LLPGEIPANS CDSNTCMNGG TCVMTAEGWQ CRCSWRNEGR RCETDRKLKV PQFHGNSYLS YAVADRTQAD DQNQQQVLEA
401 RLEFSTMAPL GLIAYIHSID AHVYLAVYVE RGALKFRLSC GRQQMTLVET KYNVSDGDIH AIFMRFLKVE DRNSSSSFCM
481 GSVKLNNSYS MNGEQRLADD EHFTWPGRLH IGGRPYGVPT PAELVFLPGI VGCAYNLEID GQRLDMIADA VQGKALDECP
561 DRRANCGGLR CLNGGICRAN FDSNAQQNGD QQFDERGGGC ICPMGWVGDQ CEIRQCPCNP CQVNSTCLMS SNDQMICVCS
641 YGRIGSLCEI AVNVTRPQFD GTFMGHSSYL SLTPPPFIRE HFEMKFSFVT DDARQVALLL FIGQPINADQ VTLAGIEEKK
721 DFLAVSFIRG HVALTWDLGS GARRIFTARP VSVSTMGGHS VHVGMRGRVA WLQVNNQPTV TGRSPGLMSV LNAHPSLFLG
801 GHSSFNHSRL PSDLPLHSGF RGCIYDLVFR SREFADRDQE FDHHNTINHW LPVVQSGRGV RQCSIPSCRL RMSKNSGENM
881 TSLGSNDVEE PFEDVC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDLSLT.L	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	277	282	
total 1 peptides												

tr|A0A0P5YUZ6|A0A0P5YUZ6_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDTNDDRGAG EAMLKGSGAR RMATSSGWRK MLMCCLKPEE DDVQVLDYEH SSLSDVPAEV FNHERTLEIL RLDCNQIADL
81 PRPLFHCHGL KELWLSDNDI SVLPPALASL IHLQVLDISK NSLTEVPDAI SGLKALITLD LSVNPLGKLP EGATKLLSLE
161 SLNLSDTFLE FLPANFGRLT KLRLLELREN QLASLPKSMA RLTALKRLDM GQNDLCDLPE VVGSIPSLTE LWVDGNKLDV
241 LPEFLGHLQN LVHLDASRNC LHGIAPTIGL CKSL**TDLSLT** SNNLANLPEE VGDLTLLTVL RVDDNRLTCL PDSLGRLSHL

321 EELQAGQNRL SKLPTSIGLL RKLETLMLNE NLLDELPVEL GSCQRLTVLS LRKNRLDHLP PEMGHLSRLR VVNLSCNRLL
401 HLPVSFLKLP SLSALWLSEA QTKPVVPLQT DIDSSTGHKV LTCFLLPQSA DPEAEEQTPA DKGSPNVVTA RSPTHIKFAF
481 DGEADPKAGK LMRNPTPYPK ELKALAKHAQ HIQQHHPVSP TSRNSVELPT TGTTSSSSSE SNAKLKKQPE PLPVAVVPPQ
561 PAAPSTTITV HVDPSVTIVS KSSDEPRPVQ SEPSNAPVRP KPEIVLESPQ PLAAPSNESQ PEVPPLLPLV HTASPLQSKR
641 NVSVENLADP EVDPPKPNGI PAAAEHSPRS AEIEIKEARV LRPLMSAADG LDKVKNPTDV VDRSSQPDLT AEIKQQQQPP
721 PYHVAAVYSK RAAEFNHATS LPRTQSTDSG FTVEGTSGER RDSSPSRDSG RGPSIEPLED NAQPSGSPGP VQSVVAAKRP
801 VDLPLNGSLA DREKMTPLAL KRATYIIDNS LSPNDGSEAV EETGDLQSVA ALRQAAREVF LSASPKESPL PGHKQTSWDV
881 PISVHTTNGS SNTLSAANVV GLPPAGNSSE NGGQQPPAKI QGRLPPPKYH VTSNGFRDTS AELKSPPPAN ASSRIPLASH
961 NRLPSGLPRQ LSNLSNSSLL DGPIVNKSAP LLPPKKRDSP PPPTLQPKLS TSRIPPPQVH TPVLASPLTP LSLKTNFSPL
1041 PVHNARMVTP TTTPITPTTN NNDFEANQTN KITPSQPLNT RIPLPKYSAS DISKTGVSPG SRIPTRLPTP TTSIPSISKS
1121 KLSADLTGSP SLAAYTSRIQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TDLSLT.S	Y	22.80	648.3330	33.5	649.3620	1	9.87	453	1	275	280	
total 1 peptides												

tr|A0A087UQW5|A0A087UQW5_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDLCSICGKK VYPMEKMETS GMRLHKNCFR C**AHCCC**MLRL ENYTKSGRRL YCTPHFKQLF ISRGNYDEGF GREQHKEKWN

81 RSCNNTPIPR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.AHCCC.M	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	32	36	
total 1 peptides												

tr|A0A182SD20|A0A182SD20_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEWIAIQKK KKRRSSSRKR ALWAGHDRSE KDRNEANTMI VTRNLGHIFE ISSIQVGYSV TNTKYTKAPF LC**AHCCC**CII

81 QFIRAGLVVI VLPKKDTVSR NNSTGRIIHF AQTNG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.AHCCC.C	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	73	77	
total 1 peptides												

tr|A0A0T6BBI1|A0A0T6BBI1_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASLFLIVLI LSTVSALPSH DRVKRVVKGT PTPIEKIPYQ VALVVDNFPI CGGSIIREDI ILTA**AHCCC**S YLPNDTLIYA

81 GMYNKEDMPN LKGIRVKDVK IHELYNYTGE STPDDIALIV LEENLSFNRT INKIDLVEED YEIPVNATVS GW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AHCCC.S	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	65	69	
total 1 peptides												

tr|A0A182N5F4|A0A182N5F4_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALAVLPTPG LERNGRSRTL RTTHVNKQDE RKQPLSSFHP MRNARNTS**AH CCC**TLDTTLS VVLMVVVVMV VVVAEMMVVM

81 STLVAATSRT AVAIDVGNGS GGSTRGTKSI QILTAGGPWL SIGEVTWPQL ELISLRFAHG RTDHYDQHDE HG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.AHCCC.T	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	49	53	
total 1 peptides												

tr|A0A182SSD0|A0A182SSD0_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRSFFDRKTI PLLVIIVGLS AALIAVCIDA YAGDSDDEVD RPKQPDGEAP LECERPSVTT ASGALVKRSA FCSGDLIFED
81 NFDRLDLATW EHEHTLAGGG NWEFQYYLNN RRNSYVKDGI FFIRPTLLAD DAGEEFLSSG FLSIHGGTPC TNPTNYGCER
161 QGTPTNYLNP IKSARVRTIH SFNFKYGKVE IRAKLPTGEW LWPALWLMPK MNQYGTWPAS GEIDLMESRG NQDYSVDGNQ
241 LGVEHIGTTL HFGPYPGLNG YEMATSAKYS PAGQGFNKGF HRYQLEWTPE FMRFSVDDEQ VMQVDGNFWQ LGGFDQRAPN
321 TPNPWVTGGK MAPFDEEFYI IMNLAVGGTN GFFPDTPPAT NANGNKPWSN QSPTAFRDFW QGRSDWLPTW KLQENESVEA
401 SLQVDYPL**AH CCC**KYHSETL ARLVQARKGY VFVPSE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AHCCC.K	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	409	413	
total 1 peptides												

tr|A0A1A9XPY1|A0A1A9XPY1_GLOFF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSLDLLLLN VDTLFEQHSV TEIEMVHKRI EEVIENKKEE LRTMVGERYR DLLKAADTIT AMKESTKELI TQVESISGYC
81 KNLNDQQLVG FKTETDKSIN LNKRIVKLQD NYFSTMVQIN LLTCLPEIIW SHLDQEQYYA ATELFIFSRH ISTGLQLDSN
161 DLMRKLPIAK KQWEILKPFQ KTIKQQVLFA LERETLTIDV LVDCLIALLL LDHTTLENAF KCFLKLRTST VLHCLSNDNN
241 GRAKDRILTT LKVLNDSLEL IHQCFFENGA IFVKLNEYTN VNALPTINRV NCLDVHFDNA LPDIILNFKG KFDTTTLSKD
321 SINLALEKWL KDIQDLVENQ LKQLFDLIAN MQIIQEIKTD ANNIRKPGIL RSFSNQFNHL EALDFYELHY VPLINQRIRN
401 IINDNLSSAI NEMQAFIKNL LEIEEEEELN SNKKQKEYIW QENATDLPNS LAQVLNGDLK TNNLLMKSKG YDTRIINVCH
481 ELDEKLAGII NEMNILLKES STKVEDKILL VDFLSATAQE HLNHFINQLG NLQRSLKGRS ALLFL**AHCCC** ALLELCPHLK

561 ICLCQKSSWR QLLRASTSSV VTERWRQICS ALEEQIYHIW LRIIEDVLEE FDCKRLMPQT ITNDVILKDF TPSLCLQTYF
641 YTFILKITEV IPQTLPSKVL QILNEKLLQQ LIDYYHSLLN DQLTQKVAQQ IYFDLKFLQH SFELSNEQKE QFEVLQNSCK
721 KLIDPFDFEL LFTHNLNNVK KAVNRFSCLL GVLTSLNVQS VHVDATHATN MTQDKDPNIL NLCSSSSTML WFPLLPIVTN
801 SNANNNNTNI AAPVQEHKKT SYDTDKSVTP THKSNTAARK NDSKSKSGAV SFFGAMSQDW FR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AHCCC.A	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	546	550	
total 1 peptides												

tr|A0A1B0BCP2|A0A1B0BCP2_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSLDLLLLN VDTLFEQHSV TEIEMVHKRI EEVIENKKEE LRTMVGERYR DLLKAADTIT AMKESTKELI TQVESISGYC

81 KNLNDQQLVG FKTETDKSIN LNKRIVKLQD NYFSTMVQIN LLTCLPEIIW SHLDQGQYYA ATELFLFSRH ISTGLQLDSN

161 DLMRKLPIAK KQWEILKPFQ KTIKQQVLFA LERENLTIDV LVDCLIALLL LDHTTLENAF KCFLKLRTST VLHCLSNDNN

241 GRAKDRILTT LKVLNDSLEL IHQCFFENGA IFVKLNEYTN VKALPTITRV NCLDVHFDNA LPDIILNFKG KFDTTTLSKD

321 SINLALEKWL KDIQDLVENQ LKQLFNLIAN MQIIQEIKTD ANNIRKPGIL RSFSNQFNHL EALDFYELHY VPLINQRIRN

401 IINDNLSNAI NEMQAFTKNL LEIEEEEELN SNKKQKEYIW QENATDLPNS LAQVLNGDLK TNNLLMKSKG YDTRIINVCH

481 ELDEKLAGII NEMNILLKES STKVEDKILL VDFLSATAQE HLNHFINQLG NLQRSLKGRS ALLFL**AHCCC** ALLELCPHLK

561 ICLCQKSSWR QLLRASTSSV VTERWRQICN ALEEQIFHIW LRIIEDVLEE FDCKRLMPQT ITNDVILKDF TPSLCLQTYF

641 YTFILKITEV VPQTLPSKVL QILNEKLLQQ LIDYYHSLLN DQLTQKVAQQ IYFDLKFLQH SFELSNEQKE QFEVLQNSCK

721 KLIDPFDFEL LFTHNLNNVK KAVNRFSCLL GVLTSLNVQS VHVDATHATN MTQDRDPNIL NLCSSSSTML WFPLLPIVTN

801 SNANNNNTNI AAPVQEHKKT SYDPDKSVTP THKSNTAARK NDSKSKSGAV SFFGAMSQDW FR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AHCCC.A	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	546	550	
total 1 peptides												

tr|A0A1B0FND5|A0A1B0FND5_GLOMM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSLDLLLLN VDTLFEQHSV AEVEMVHKRI EEVIENKKEE LRTMVGERYR DLLKAADTIT AMKESTKELI TQVESISGYC

81 KNLNDQQLVG FKTETDKSIN LNKRIVKLQD NYFSTMVQIN LLTCLPEIIW SHLDQEQYYA ATELFIFSRH ISTGLQLDSN

161 DLMRKLPIAK KQWEILKPFQ KTIKQQVLFA LERENLTIDV LVDCLIALLL LDRTTLENAF KCFLKLRTST VLHCLSNDNN

241 GRAKDRILIS LKVLNDSLEL IQQCFFENGA VFVKLNEYTN LNAPPTIARI NCPDVHFDNA LPDIILNFKG KFDTTTLSKD

321 SINLALEKWL KDIQDLVENQ LKQLFDLIVN MQIIQEIKTD ANNIRKPGIL RSFSNQLNHL ESLDFYELHY VPLINQRIRN

401 IINDNLSNAI NEMHAFIKNL LEIEEAGKEE ELNINEQQKE CIWQENATDL PNSLAQVLND DLKTNNLLMK SKGYDTRIIN

481 VCHELDEKLA GIIDEMNILL EESSTKVEDK ILLVDFLSET AQEHLNHFIN QLWNLQRSLK GRSTLLFL**AH CCC**ALLELCP

561 HLKICLCQKS SWRQLLGAST SSVVTERWRQ ICNAMEEQIY HIWLRIIEDI LEEFDCKRLM PQTITNDVIL KDFTPSLCLQ

641 TYFYMLISKI TEVVPQTLPS KVLKILNEKL LQQLIDYYHS LLNDQLTQKV ALQIYFDLKF LQHSFEFVKE QKEQFEALQN

721 SCKKLIDPFD FELLFTHNLN NVKKAVNRFS CLLGVLTSLN VQSVHVDATN TTNVIQDKDP NILNLCSSSS TMLWFPLLPI

801 VTNSNANNNN INIAGSVQEH KKTSYDTDKP VTPTRKTNIA APPAGAALFL PPLLSTAVAT AAPPPAFFCK DCKIFSYLFR

881 LQYR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AHCCC.A	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	549	553	
total 1 peptides												

tr|A0A1A9VCZ7|A0A1A9VCZ7_GLOAU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSLDLLLLN VDTLFEQHSV TEVEMVHKRI EKVIENKKEE LRTMVGERYR DLLKAADTIT AMKESTKELI TQVERISGYC

81 KNLNDQQLVG FKTETDKSIN LNKRIVKLQD NYFSTMVQIN LLTCLPEIIW SHLDEEQYYA ATELFIFSRH ISTGLQLDSN

161 DLMRKLPIAK KQWEILKPFQ KTIKQQVLFA LERENLTIDV LVDCLIALLL LDRTTLENAF KCFLKLRTST VLHCLSNDNN

241 GRAKDRILTS LKVLNDSLEL IQQCFFENGA IFVRLDEYTN FNAPPTITRI NCPDVHFDNA LPDIILNFKG KFDTTTLSKD

321 SINLALEKWL KDIQDLVENQ LKQLFDLIVN MQIIQEIKTD ANNIRKPGIL RSFSNQVNHL ESLDFYELHY VPLINQRIRN

401 IINDNLSNAL NEMQAFIKNL LEIEEAGEEE ELNINEQQQK ECIWQENATD LPNSLAQVLN ADLKTNNLLM KSKGYDTRII

481 NVCHELDEKL GGIINEMNIL LEESSTKVED KILLVDFLSE TAQEHLNHFI NQLCNLQRSL KGRSALFFL**A HCCC**ALLELC

561 PHLKICLCQK SSWRQLLGAS TSSVVTERWR QICNALEEQI YQIWLRIIED ILEEFDCKRL MPQTITNDVI LKDFTHWESI

641 TLEQGDYHPD QLPQTSVPVP VQPSLCLQTY FYMLILKITE VVPQTLPSKV LKILNEKLLQ QLIDYYHSLL NDQLTQKVAL

721 QIYFDLKFLQ HSFELLKEQK EQFEALQNSC KKLIDPFDFE LLFTHNLNNV KRAVNRFSCL LGVLTSLNVQ SVHVDATNAT

801 NVTQDKDPNI LNLCSSSSTM LWFPLLPIVT NSNPDNNNTN IAESVQEHKK SSYDTDKPVT PTRKSNIAAR KSDSKSKSGA

881 ASFFGAMSQD WFR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AHCCC.A	Y	21.19	535.1342	26.1	536.1554	1	6.22	295	2	550	554	
total 1 peptides												

tr|A0A132AHU8|A0A132AHU8_SARSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MSSSPPAATT AVSPLSNDSH LLSTKNSSIL LDDQQAMITS SASLHQDITN DIEDDDGDGT ESLTSSLSDV ETFNGKIVYN
  81 PDGSAYIIEG PDSDGSEVEA EISQEGSIID ARGQSPNYGS ISFPQIVSAF HISRSYSNEI YPSPFLESPK QTSTISTESK
 161 ISDLPVMHSY RVFSLRNKKC SSSKYKSSSS QIDENDEIID ENIDKCNKEN FTFDDDDDTI EQESRLQALN NCSTVPVKPI
 241 LMCFICKLSF GYTKSFVAHS IGEHHLSLND EERKVLQSKN TSAIIQGVGK EKEPLLSFLR PKSSTPAPFR SLISHHPTQS
 321 QQLQPQQKPQ QQSLDAQQLL AVQMAAVASA LRSSSDSLPV LNSKNTNECS SSSSINELAN NSAFSSPTNS PDRSSMTNNA
 401 EDGEIVGDCV DEKKVEKLSI SQTTNNLDED EEMMMANKTN PSEDGDDDED ENDDDGTVDN KINRFDERSS NSVGDCDVAS
 481 AVASQFASEL ADLANLEKFA QAAAVAAAAQ QQQMDLHSIA AVMAAAVAAS ANKSSHLNQI SSPATKVSPT SSSSSSSSSV
 561 SSSSSKANQS TNFNNNGLLV CPDSKNISLL FNHHSNSPST DSDASNLLAS VGNHSTTARQ TSTNSNHPPL LIQHSRNSCK
 641 TLKCPKCNWH YKYQETLEIH MKEKHPENEM NCIYCLTNQP HPRLARGETY TCGYKPYRCD VCNYSTTTKG NLSIHMQSDK
 721 HINNVQELQN GNIPSTAEHL LQSQALTAAV AQAANGNNTS PITNNNSSAL TTNSSATGSG SPVPTSSAAN LAKIVAQQQQ
 801 ESQKNSSKIS SNHHFHSNSS LTPPTTPNSN ANSSNSINSS SSKQKATWRC DVCNYETNVA RNLRIHMTSE KHTHNIMILK
 881 QNVSQMQQLN ALQQGILNPE QLLQLNPGLF AAAAAAAAAG MTNNAAGSNG TNPIIGALGS VNGPNADGNG MQPEVALADM
 961 AYNHALLMMA SQQQQRNMVA LMQQQQQPNT DSKLSSPSSS SSTSSTIPTT LSNASVNDSQ ATFDMEHPDS SISVIANSIP
1041 LNDPNQLFDC CVCGSFSTDS IETLNHHLQL NRTGIREDEV LLTIDDEMNK IAPALLNQFG LNSTDSLLLK NALIEQQAKL
1121 NQFQNLENDQ SQQSQQSESI STTNTINCPF CSYQNDSEIR IQMHILVSHP HQHQQSAIKS LSALADDSSA NQSKLTPPPS
1201 LIPSILCPLC QEPFHERNNL ENHLVEIHSV TKEGVQRLML LVDTTELDKF HSSSSPAIQN NQNKMSTNEK KKLRKNSNDR
1281 SDTAEDDQDE RKSNDDEETS PCADSTSKQI DDEPMMIDTN NLNEFGNLPA AVLDLLHCPG CQRMFLNLEE LFAHMIIEMH
1361 LKPTAQGQFQ CWRNDCQQQF SSLQSVQIHF RDQHFLKCAK LLNTVGANFG NNILNTNPPN AAVSDRHVYK YRCSQCSLAF
1441 KTIEKLQIHS QYHLIRAATQ CVVCSRSFRS IESLQKHMES SHSNLNDEEL EQYRNNLLQN HLLLTLGRNG GVLDPSTTEL
1521 LKKESLRSDD IDDQSMDLDN GGGALDLASY QSKQEQDDHH FVNHAQLAID NNNLGANSNT ALLNGNTEQS SANSLEDYLN
1601 SQQIAEESYN DPSRKYKCHR CKMAFTKQSY LTAHNKILLH RKGEKMNYPL EKYLDPNRPF KCEICKESFT QKNILLVHYN
1681 SVSHLHRLKQ SMKESSAAVA ASVAASQSSI SPNSSMTNHD DENNDTNNEN KLFKCNLCKV SYSMPSSLHN HLRSTLHQTR
1761 TSKLHELAQS GQLDLSLPLI EPLNYFNSTT NNNNNNGSIN NLKNSNLNTN QSTASAVKFA EIFGNDPQQQ QALSLQQAAL
1841 NLAISNGTNQ SAQFMPINGQ SSTSSPFTCS KCQAAFISKE AQLQHQHLCG LFGNLTNVNN NNNNYDQTTA ALASNNINHQ
1921 SNLTTQANKQ LSKLSSLSGS LYKNKPQLYK HLLETWGFEI VMQFNESNQK ILSAKDSTDP ESQSSNQRPI ENGDLSEQTS
2001 SSQPIADSNN ETDGNISEEK NVQNSTDDVN EDDGVVDRKD AVKDDQEEKD DDDDDVTRPK SNTKENVENS EGLNKDGLDK
2081 RVNQGIENES TSKQEENSIT PPELNKCQCD ICFQEFSSIW VLKAHREEIH KDLVPLTVVE SFADEFRNEY DRKFSSTSSN
2161 ETDGNESTVM VNKNNEPSSL ENQSINSSNL NFDANSNGHT AVNLSESNLH SITSVANNNH SSPCSSPNLT PNDALNLTGT
2241 GHLTDPISAL NPLTDQQANG LAQLLPNLGA NATPAEIAAA NQMAAQIQFS QLLMSMGLAG MAAGMPMSGG MPFAAAAAMG
2321 IPPQLLPMMM ADPMMAAAAA FNNPALAAAA AAQLNQAQAA VAAQQQQQQS TISQSNPRVA SPTPVSNPTA ILPVVNQSNL

2401 TTNPSSNAVA VAAASAAAAQ QQKRARTRIS DEQLKVLRQY FDINNSPTEE QLIEMSQKSG LPMKVIKHWF RNTLFKERQR
2481 NKDSPYNFNN PPSTYLNLDE YEKTGEAKVF TLDDLKKCDQ NQHSLNSGNN LMMVNNSQEN LASKENKSST KEKPNDSESE
2561 YEAKISNDLK SSSSNKDTDY ATSDDEEIKR SSQPKDFLHN SDIVDSNQRL SKHQSCLPLS VTPVQDFDQL SKSMSFNMGS
2641 PQPSESSMSS SAFESTNNGS ANTSSLFAGL ANFSPGSLSS SQNMASSLQM ALDAQRSQLA AAAVAANSSK MLSSASVANV
2721 SSHSSSGKRA NRTRFTDYQI KVLQEFFESN AYPKDDDLEY LSKLLNLSPR VIVVWFQNAR QKARKVYENQ PPSTPVGEDD
2801 GSGRFQRTPG LNYQCKKCLQ VFQRYYELIK HQKNSCFKDE NPLASQIRLA AEARAQASSP TMSRDSSTPI DCTRSATTTP
2881 EKLSMNLLAS PNSAASPLNN GQNGPKSSPN STNTSIGSSA TTTPTNQNET SQTFRCDKCP MVFNRIDLWR DHQIVHLVNS
2961 NLFNAAAANP FGLMQLEAAQ QQQSQLLNIS PQPSPTAMIG HGSKRKILHD DDNDEDESCD FDSMSGNGNS NSSDQTPRDK
3041 RLRTTILPEQ LDYLYQKYQI DSNPSRKMLE SIAKEVGLKK RVVQVWFQNT RARERKGQFR AHQQVIHKRC PFCRALFKAR
3121 SALESHLATR HADQYTKGDI NIDNLPDGDP SEDGELAINE TSNVDSSQMA DVMKRYEDSF KKYLDELNIQ GECL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TPVSNPT.A	Y	20.93	714.3548	7.7	715.3676	1	20.11	766	1	2383	2389	
total 1 peptides												