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.

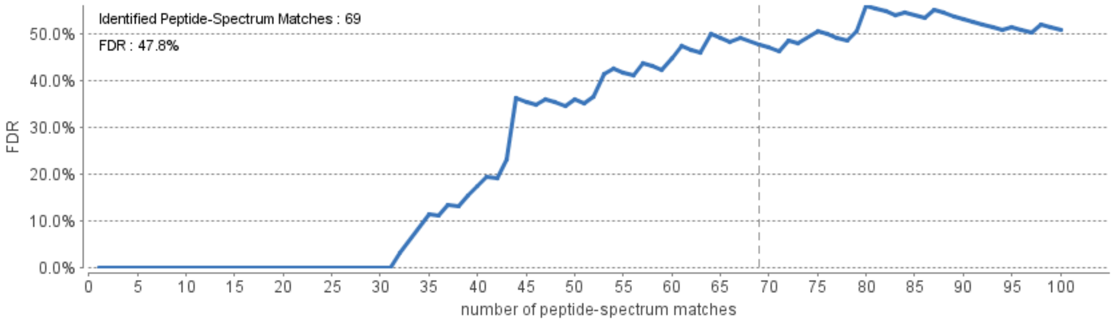

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

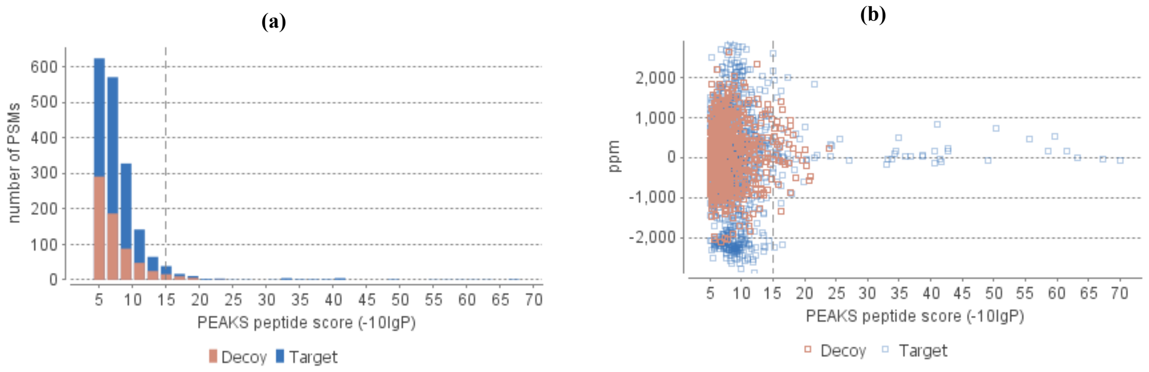

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

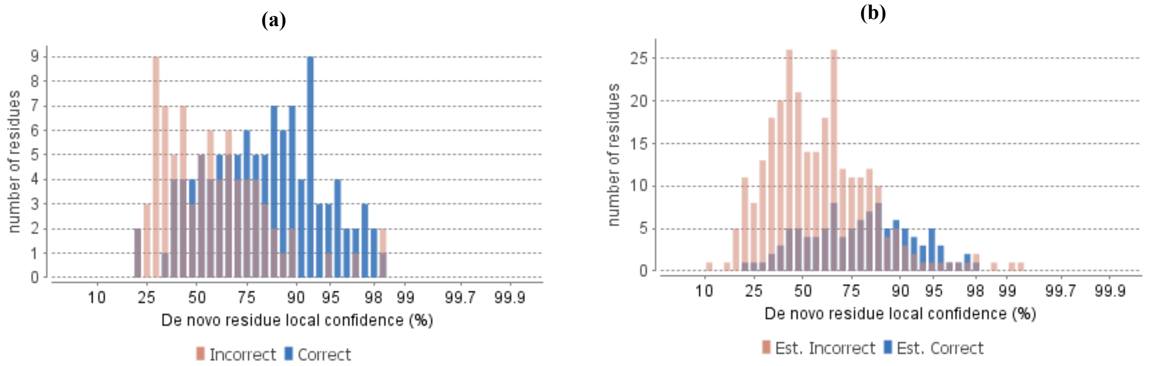

Table 1. Statistics of data.

# of MS Scans	1541
# of MS/MS Scans	4028

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	69
Peptide Sequences	69

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	8	C
Pyro-glu from Q	-17.03	3	N-term
Oxidation	15.99	3	M
Acetylation	42.01	1	Protein N-term
Deamidation	.98	1	Q

Protein Groups	20
Proteins	97
Proteins (#Unique Peptides)	10 (>2); 6 (=2); 81 (=1);
FDR (Peptide-Spectrum Matches)	47.8%
FDR (Peptide Sequences)	47.8%
FDR (Protein)	14.4%
De Novo Only Spectra	43

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.

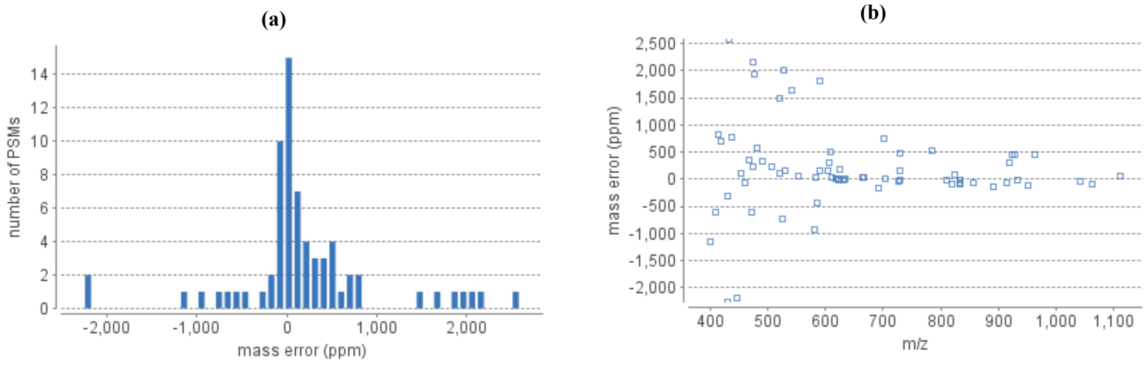

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
LTQ	57	10	2	0	0

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Oxidation (M): 15.99
Fragment ion tolerance: 0.5
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: 92
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: IT_douglas_3_20170921_03.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: Linear Ion Trap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
4	78957	tr|E2DV16|E2DV16_9HYME	117.80	16	5	3	Y	53582	Sodium/potassium-transporting ATPase subunit alpha (Fragment) OS=Townsendiella sp. JS-2010 PE=3 SV=1
3	4599	tr|A0A182J1K8|A0A182J1K8_9DIPT	113.14	14	4	4	Y	49908	Tubulin alpha chain OS=Anopheles atroparvus PE=3 SV=1
3	4601	tr|Q7PUE2|Q7PUE2_ANOGA	113.14	14	4	4	Y	49908	Tubulin alpha chain OS=Anopheles gambiae GN=1281950 PE=3 SV=5
3	4595	tr|A7UIK9|A7UIK9_MONAT	113.14	14	4	4	Y	49908	Tubulin alpha chain OS=Monochamus alternatus PE=2 SV=1
5	36913	tr|A0A0R1E113|A0A0R1E113_DROYA	101.27	5	3	1	Y	111160	Sodium/potassium-transporting ATPase subunit alpha OS=Drosophila yakuba GN=Dyak\GE25699 PE=3 SV=1
2	11772	tr|A0A0P6CE35|A0A0P6CE35_9CRUS	77.77	15	5	5	Y	32931	ADP/ATP translocase OS=Daphnia magna PE=3 SV=1
1	36579	tr|A0A1W4W573|A0A1W4W573_AGRPL	74.53	13	4	4	Y	32970	prohibitin-2 isoform X2 OS=Agrilus planipennis GN=LOC108732799 PE=4 SV=1
1	36584	tr|A0A1Y1M0C5|A0A1Y1M0C5_PHOPY	74.53	13	4	4	Y	33089	Uncharacterized protein OS=Photinus pyralis PE=4 SV=1
1	36587	tr|A0A151X2A0|A0A151X2A0_9HYME	74.53	13	4	4	Y	33532	Prohibitin-2 OS=Trachymyrmex zeteki GN=ALC60_06697 PE=4 SV=1
1	36588	tr|A0A1W4W553|A0A1W4W553_AGRPL	74.53	13	4	4	Y	33255	prohibitin-2 isoform X1 OS=Agrilus planipennis GN=LOC108732799 PE=4 SV=1
1	36591	tr|A0A067QGU8|A0A067QGU8_ZOONE	74.53	12	4	4	Y	35988	Prohibitin-2 OS=Zootermopsis nevadensis GN=L798_03226 PE=4 SV=1
total 97 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
18	36538	tr|V9IID0|V9IID0_APICE	70.05	4	1	1	Y	53350	Mitochondrial-processing peptidase subunit beta OS=Apis cerana GN=ACCB10194 PE=2 SV=1
18	78964	tr|A0A088A820|A0A088A820_APIME	70.05	4	1	1	Y	53349	Uncharacterized protein OS=Apis mellifera GN=LOC410022 PE=3 SV=1
18	36537	tr|A0A0L7RBG9|A0A0L7RBG9_9HYME	70.05	4	1	1	Y	48763	Mitochondrial-processing peptidase subunit beta OS=Habropoda laboriosa GN=WH47_03430 PE=3 SV=1
12	22030	tr|A0A151J3L9|A0A151J3L9_9HYME	67.30	3	1	1	N	59328	ATP synthase subunit alpha OS=Trachymyrmex cornetzi GN=ALC57_10733 PE=3 SV=1
12	22029	tr|A0A1B0C955|A0A1B0C955_LUTLO	67.30	3	1	1	N	58520	ATP synthase subunit alpha OS=Lutzomyia longipalpis PE=3 SV=1
12	22035	tr|A0A1L8E154|A0A1L8E154_9DIPT	67.30	3	1	1	N	59331	ATP synthase subunit alpha OS=Nyssomyia neivai PE=3 SV=1
12	22036	tr|A0A182XJA6|A0A182XJA6_ANOQN	67.30	3	1	1	N	59401	ATP synthase subunit alpha OS=Anopheles quadriannulatus PE=3 SV=1
12	22039	tr|A0A1J1J483|A0A1J1J483_9DIPT	67.30	3	1	1	N	59428	ATP synthase subunit alpha OS=Clunio marinus GN=CLUMA_CG020197 PE=3 SV=1
12	22040	tr|A0A182N7Z7|A0A182N7Z7_9DIPT	67.30	3	1	1	N	59387	ATP synthase subunit alpha OS=Anopheles dirus PE=3 SV=1
12	22041	tr|Q7PHI8|Q7PHI8_ANOGA	67.30	3	1	1	N	59452	ATP synthase subunit alpha OS=Anopheles gambiae GN=1274812 PE=3 SV=2
12	22044	tr|S4VDE6|S4VDE6_LOCMI	67.30	3	1	1	N	59564	ATP synthase subunit alpha OS=Locusta migratoria manilensis GN=atp5a1 PE=2 SV=1
12	22050	tr|A0A1B6KWM9|A0A1B6KWM9_9HEMI	67.30	3	1	1	N	61429	ATP synthase subunit alpha (Fragment) OS=Graphocephala atropunctata GN=g.30172 PE=3 SV=1
12	22062	tr|A0A1B0D1L3|A0A1B0D1L3_PHLPP	67.30	5	1	1	N	34054	Uncharacterized protein OS=Phlebotomus papatasi PE=4 SV=1
12	22043	tr|A0A067QI29|A0A067QI29_ZOONE	67.30	3	1	1	N	59515	ATP synthase subunit alpha OS=Zootermopsis nevadensis GN=L798_03658 PE=3 SV=1
12	22026	tr|B4QHN0|B4QHN0_DROSI	67.30	3	1	1	N	51137	GD11704 OS=Drosophila simulans GN=Dsim\GD11704 PE=3 SV=1
12	22027	tr|A0A182TC06|A0A182TC06_9DIPT	67.30	3	1	1	N	53866	Uncharacterized protein OS=Anopheles maculatus PE=3 SV=1
12	22028	tr|A0A182YNR5|A0A182YNR5_ANOST	67.30	3	1	1	N	57574	ATP synthase subunit alpha OS=Anopheles stephensi PE=3 SV=1
12	22033	tr|B4LIV0|B4LIV0_DROVI	67.30	3	1	1	N	59176	ATP synthase subunit alpha OS=Drosophila virilis GN=Dvir\GJ22050 PE=3 SV=1
12	22034	tr|A0A0M4EW76|A0A0M4EW76_DROBS	67.30	3	1	1	N	59338	ATP synthase subunit alpha OS=Drosophila busckii GN=Dbus_chr2Rg1866 PE=3 SV=1
12	22031	tr|A0A151XGV4|A0A151XGV4_9HYME	67.30	3	1	1	N	59635	ATP synthase subunit alpha OS=Trachymyrmex zeteki GN=ALC60_01388 PE=3 SV=1
12	22032	tr|A0A195CV10|A0A195CV10_9HYME	67.30	3	1	1	N	59555	ATP synthase subunit alpha OS=Cyphomyrmex costatus GN=ALC62_04768 PE=3 SV=1
12	21998	tr|A0A087ZQI5|A0A087ZQI5_APIME	67.30	3	1	1	N	59512	ATP synthase subunit alpha OS=Apis mellifera GN=Atp5a1 PE=3 SV=1
12	21999	tr|A0A0N0BIY2|A0A0N0BIY2_9HYME	67.30	3	1	1	N	59519	ATP synthase subunit alpha OS=Melipona quadrifasciata GN=WN51_07748 PE=3 SV=1
12	22000	tr|V9IFD6|V9IFD6_APICE	67.30	3	1	1	N	59526	ATP synthase subunit alpha OS=Apis cerana GN=ACCB04724 PE=2 SV=1
12	22048	tr|A0A0J9RIM8|A0A0J9RIM8_DROSI	67.30	3	1	1	N	59438	ATP synthase subunit alpha OS=Drosophila simulans GN=Dsim\GD11704 PE=3 SV=1
12	22049	tr|A0A1A9WYG7|A0A1A9WYG7_9MUSC	67.30	3	1	1	N	59478	ATP synthase subunit alpha OS=Glossina brevipalpis PE=3 SV=1
12	78965	tr|A0A1B0BN74|A0A1B0BN74_9MUSC	67.30	3	1	1	N	59476	ATP synthase subunit alpha OS=Glossina palpalis gambiensis PE=3 SV=1
12	22037	tr|A0A182FH95|A0A182FH95_ANOAL	67.30	3	1	1	N	59383	ATP synthase subunit alpha OS=Anopheles albimanus PE=3 SV=1
12	22038	tr|W5J4R5|W5J4R5_ANODA	67.30	3	1	1	N	59383	ATP synthase subunit alpha OS=Anopheles darlingi GN=AND_008921 PE=3 SV=1
12	22042	tr|A0A069DZ92|A0A069DZ92_9HEMI	67.30	3	1	1	N	59539	ATP synthase subunit alpha OS=Panstrongylus megistus PE=2 SV=1
12	22046	tr|A0A182MRL5|A0A182MRL5_9DIPT	67.30	3	1	1	N	59343	ATP synthase subunit alpha OS=Anopheles culicifacies PE=3 SV=1
12	22047	tr|A0A1A9TPM8|A0A1A9TPM8_ANOST	67.30	3	1	1	N	59357	ATP synthase subunit alpha OS=Anopheles stephensi PE=3 SV=1
12	22051	tr|A0A232FBT4|A0A232FBT4_9HYME	67.30	3	1	1	N	61799	ATP synthase subunit alpha OS=Trichomalopsis sarcophagae GN=TSAR_007587 PE=3 SV=1
12	22045	tr|A0A0J7N062|A0A0J7N062_LASNI	67.30	3	1	1	N	59948	ATP synthase subunit alpha OS=Lasius niger GN=RF55_15079 PE=3 SV=1
6	36527	tr|A0A0M4EGW1|A0A0M4EGW1_DROBS	66.29	7	2	2	N	30414	L-2-37Cc OS=Drosophila busckii GN=Dbus_chr3Lg30 PE=4 SV=1
6	36528	tr|B4M935|B4M935_DROVI	66.29	7	2	2	N	30412	Uncharacterized protein, isoform A OS=Drosophila virilis GN=Dvir\GJ17994 PE=4 SV=1
6	36529	tr|B4Q9G9|B4Q9G9_DROSI	66.29	7	2	2	N	30384	GD21777 OS=Drosophila simulans GN=Dsim\GD21777 PE=4 SV=1
6	36530	tr|D0QWC7|D0QWC7_DROMI	66.29	7	2	2	N	30392	GA10498 OS=Drosophila miranda GN=GA10498 PE=4 SV=1
6	36531	tr|W8BWG2|W8BWG2_CERCA	66.29	7	2	2	N	30323	Protein l(2)37Cc OS=Ceratitis capitata GN=L2CC PE=2 SV=1
11	36524	tr|A0A289ZEQ2|A0A289ZEQ2_EULVE	61.65	4	1	1	Y	35925	Mitochondrial lactate dehydrogenase A chain OS=Eulimnogammarus verrucosus PE=2 SV=1
11	36539	tr|A0A1Y1K9I6|A0A1Y1K9I6_PHOPY	61.65	5	1	1	Y	25783	L-lactate dehydrogenase (Fragment) OS=Photinus pyralis PE=3 SV=1
11	36525	tr|A0A0L7LHX0|A0A0L7LHX0_9NEOP	61.65	5	1	1	Y	26220	L-lactate dehydrogenase OS=Operophtera brumata GN=OBRU01_08219 PE=3 SV=1
11	36540	tr|A0A0P6CBY2|A0A0P6CBY2_9CRUS	61.65	4	1	1	Y	30079	L-lactate dehydrogenase (Fragment) OS=Daphnia magna PE=3 SV=1
7	36606	tr|A0A0K8RPB2|A0A0K8RPB2_IXORI	57.21	14	2	2	N	19878	Putative heteroproteinous nuclear ribonucleoprotein k (Fragment) OS=Ixodes ricinus PE=2 SV=1
19	36929	tr|H8WUA0|H8WUA0_9ARAC	42.76	19	1	1	N	6001	Histone H4 (Fragment) OS=Zalmoxis pygmaeus GN=H4 PE=3 SV=1
20	78968	tr|A0A1B0CQK0|A0A1B0CQK0_LUTLO	41.03	12	1	1	N	7440	Histone H2B OS=Lutzomyia longipalpis PE=3 SV=1
total 97 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
21	36535	tr|A0A0A9YXM3|A0A0A9YXM3_LYGHE	38.71	3	1	1	Y	41634	Triosephosphate isomerase OS=Lygus hesperus GN=Tpi PE=3 SV=1
14	36849	tr|A0A034WXL0|A0A034WXL0_RHIMP	36.78	2	1	1	N	55598	Heat shock protein 90 1 (Fragment) OS=Rhipicephalus microplus PE=4 SV=1
14	36666	tr|A0A023FKD7|A0A023FKD7_9ACAR	36.78	1	1	1	N	85386	Putative heat shock protein hsp 90-alpha isoform 1 (Fragment) OS=Amblyomma cajennense PE=2 SV=1
14	36855	tr|B5TGR4|B5TGR4_TRIVP	36.78	2	1	1	N	83013	90 kDa heat shock protein OS=Trialeurodes vaporariorum GN=hsp90 PE=2 SV=1
14	36846	tr|A0A0P6CIM3|A0A0P6CIM3_9CRUS	36.78	9	1	1	N	14090	Heat shock HSP 90-alpha-like protein (Fragment) OS=Daphnia magna PE=4 SV=1
14	36847	tr|A0A1P8LG21|A0A1P8LG21_9CUCU	36.78	5	1	1	N	23631	Heat shock protein (Fragment) OS=Dendroctonus armandi GN=Hsp90-2 PE=2 SV=1
14	36848	tr|E2ILN7|E2ILN7_9CUCU	36.78	4	1	1	N	34142	Heat shock protein 90 (Fragment) OS=Cryptolaemus montrouzieri PE=2 SV=1
14	36850	tr|A0A087UN67|A0A087UN67_9ARAC	36.78	2	1	1	N	80063	Heat shock protein 83 (Fragment) OS=Stegodyphus mimosarum GN=X975_24927 PE=3 SV=1
14	36851	tr|A0A0B4L0J0|A0A0B4L0J0_9CUCU	36.78	2	1	1	N	82121	Heat shock protein 90 OS=Lissorhoptrus oryzophilus GN=HSP90b PE=2 SV=1
14	36852	tr|A0A1W4X044|A0A1W4X044_AGRPL	36.78	2	1	1	N	82659	heat shock protein 83-like OS=Agrilus planipennis GN=LOC108737432 PE=3 SV=1
14	36853	tr|A0A1Z2RU91|A0A1Z2RU91_HERIL	36.78	2	1	1	N	82636	Heat shock protein 90 OS=Hermetia illucens PE=2 SV=1
14	36854	tr|H9B0B8|H9B0B8_9HYME	36.78	2	1	1	N	83332	Heat shock protein 90 OS=Quadrastichus erythrinae PE=2 SV=1
14	36856	tr|A0A131Z059|A0A131Z059_RHIAP	36.78	2	1	1	N	83992	Molecular chaperone HtpG OS=Rhipicephalus appendiculatus PE=3 SV=1
14	36857	tr|A0A224YTX2|A0A224YTX2_9ACAR	36.78	2	1	1	N	83964	Molecular chaperone HtpG OS=Rhipicephalus zambeziensis PE=3 SV=1
14	36858	tr|A0A0K8R8N9|A0A0K8R8N9_IXORI	36.78	2	1	1	N	84236	Putative heat shock protein hsp 90-alpha isoform 1 OS=Ixodes ricinus PE=2 SV=1
14	36859	tr|B7QI01|B7QI01_IXOSC	36.78	2	1	1	N	84279	Hsp90 protein, putative OS=Ixodes scapularis GN=8041558 PE=3 SV=1
14	36669	tr|L7MEG0|L7MEG0_9ACAR	36.78	1	1	1	N	87541	Putative heat shock protein (Fragment) OS=Rhipicephalus pulchellus PE=2 SV=1
22	78998	tr|A0A2A3EHN0|A0A2A3EHN0_APICC	34.98	3	1	1	N	64484	Delta-1-pyrroline-5-carboxylate dehydrogenase OS=Apis cerana cerana GN=APICC_06300 PE=4 SV=1
22	78996	tr|V9IL90|V9IL90_APICE	34.98	4	1	1	N	63561	Delta-1-pyrroline-5-carboxylate dehydrogenase OS=Apis cerana GN=ACCB12403 PE=2 SV=1
22	78997	tr|A0A088A1I8|A0A088A1I8_APIME	34.98	4	1	1	N	63522	Uncharacterized protein OS=Apis mellifera GN=LOC551113 PE=4 SV=1
8	40434	tr|A0A0Q9XTW1|A0A0Q9XTW1_DROMO	24.15	0	1	1	N	197142	Uncharacterized protein, isoform M OS=Drosophila mojavensis GN=Dmoj\GI14008 PE=4 SV=1
8	39750	tr|A0A0P5C1N7|A0A0P5C1N7_9CRUS	24.15	0	1	1	N	635902	Putative Microtubule-actin cross-linking factor OS=Daphnia magna PE=4 SV=1
8	80084	tr|A0A1B6LCG7|A0A1B6LCG7_9HEMI	24.15	2	1	1	N	34702	Uncharacterized protein (Fragment) OS=Graphocephala atropunctata GN=g.24431 PE=4 SV=1
8	82673	tr|A0A0Q5VMA2|A0A0Q5VMA2_DROER	24.15	0	1	1	N	618126	Uncharacterized protein, isoform G OS=Drosophila erecta GN=Dere\GG22462 PE=4 SV=1
8	36559	tr|A0A1I8PMC0|A0A1I8PMC0_STOCA	24.15	0	1	1	N	994180	Uncharacterized protein OS=Stomoxys calcitrans GN=106087979 PE=4 SV=1
8	36533	tr|A0A0P9C0Q5|A0A0P9C0Q5_DROAN	24.15	0	1	1	N	988224	Uncharacterized protein, isoform W OS=Drosophila ananassae GN=Dana\GF11157 PE=4 SV=1
8	37166	tr|A0A0Q9WS80|A0A0Q9WS80_DROWI	24.15	0	1	1	N	984479	Uncharacterized protein, isoform G OS=Drosophila willistoni GN=Dwil\GK17953 PE=4 SV=1
8	37169	tr|A0A0R1DVJ7|A0A0R1DVJ7_DROYA	24.15	0	1	1	N	1002729	Uncharacterized protein, isoform V OS=Drosophila yakuba GN=Dyak\GE13333 PE=4 SV=1
8	37167	tr|A0A1I8MXA4|A0A1I8MXA4_MUSDO	24.15	0	1	1	N	994016	Uncharacterized protein OS=Musca domestica GN=101893893 PE=4 SV=1
8	82516	tr|A0A0J9U1A2|A0A0J9U1A2_DROSI	24.15	0	1	1	N	982574	Uncharacterized protein, isoform G OS=Drosophila simulans GN=Dsim\GD25734 PE=4 SV=1
8	36617	tr|A0A1W4VPU6|A0A1W4VPU6_DROFC	24.15	0	1	1	N	1003103	microtubule-actin cross-linking factor 1 isoform X7 OS=Drosophila ficusphila GN=LOC108096522 PE=4 SV=1
8	36616	tr|A0A1W4VBG9|A0A1W4VBG9_DROFC	24.15	0	1	1	N	1003526	microtubule-actin cross-linking factor 1 isoform X8 OS=Drosophila ficusphila GN=LOC108096522 PE=4 SV=1
36	39097	tr|B4LHD0|B4LHD0_DROVI	22.67	0	2	1	N	369336	Uncharacterized protein OS=Drosophila virilis GN=Dvir\GJ12692 PE=4 SV=2
15	36906	tr|A0A293N017|A0A293N017_ORNER	22.09	4	1	1	N	24546	Caspase-3-like protein 2 (Uncharacterized protein) (Fragment) OS=Ornithodoros erraticus PE=4 SV=1
15	36907	tr|A0A293N044|A0A293N044_ORNER	22.09	4	1	1	N	28676	Caspase-3-like protein 2 (Uncharacterized protein) (Fragment) OS=Ornithodoros erraticus PE=4 SV=1
10	36875	tr|A0A0L0C4S2|A0A0L0C4S2_LUCCU	21.66	0	1	1	N	297672	Cadherin-related tumor suppressor OS=Lucilia cuprina GN=FF38_09502 PE=4 SV=1
10	36876	tr|A0A1A9W0E4|A0A1A9W0E4_9MUSC	21.66	0	1	1	N	300161	Uncharacterized protein OS=Glossina brevipalpis PE=4 SV=1
10	36877	tr|A0A1I8MA30|A0A1I8MA30_MUSDO	21.66	0	1	1	N	378500	Uncharacterized protein OS=Musca domestica PE=4 SV=1
9	39345	tr|B4N084|B4N084_DROWI	21.61	0	1	1	N	113507	Alpha-mannosidase OS=Drosophila willistoni GN=Dwil\GK24528 PE=3 SV=1
9	41033	tr|A0A1I8NPG9|A0A1I8NPG9_STOCA	21.61	0	1	1	N	569745	Uncharacterized protein OS=Stomoxys calcitrans GN=106082007 PE=4 SV=1
total 97 proteins									

tr|E2DV16|E2DV16_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AVLCFIAYSI QASTSEDPND DNLYLGIVLA AVVIVTGIFS YYQESKSSKI MESFKNMVPQ FATVIREGEK **LMLRAEELVL**

81 **GDVVEVK**FGD RIPADIRIIE SRGFKVDNSS LTGESEPQSR SPEFTHENPL ETK**NLAFFST NAVEGTAK**GV VICCGDQTVM

161 GRIAGLASGL DTGETPIAKE IHHFIHLITG VAVFLGVTFF IIAFILGYHW LDAVIFLIGI IVANVPEGLL ATVTVCLTLT

241 AKRMASKNCL VK**NLEAVETL GSTSTICSDK** TGTLTQNR**MT VAHMWFDNQI IEADTTEDQS GLQYDR**TSPG FKALAKIATL

321 CNRAEFKAGQ ENQPILKREV NGDASEAALL KCMELALGDV MGIRKRNKKV CEIPFNSTNK YQVSIHESDN PDDPRHLLVM

401 KGAPERILDR CSTIFIGGKE KVLDEEMKEA FNNAYLELGG LGERVLGFCD YTLPSDKFPI GFKFNCDDPN FPVDGLRFVG

481 LMSMIDPP

C Carba
O Oxida
☒ Mutat

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLAFFSTNAVEGTAK.G	N	59.61	1568.7834	523.3	785.8094	2	35.82	3064	1	134	148	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	N	55.70	1923.9095	455.0	963.3998	2	33.46	2800	1	253	270	Carbamidomethylation
R.AEELVLGDVVEVK.F	Y	50.45	1398.7605	742.1	700.9066	2	36.12	3098	1	75	87	
R.M(+15.99)TVAHMWFDNQIIEADTTEDQSGLQYDR.T	Y	38.71	3329.4604	68.6	1110.9036	3	37.27	3228	1	279	306	Oxidation (M)
K.LMLRAA(sub E)ELVLGDVVEVK.F	Y	19.21	1854.0648	465.5	928.4712	2	37.91	3300	1	71	87	Mutation
total 5 peptides												

tr|A0A182J1K8|A0A182J1K8_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDVVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLR**FDGALNV DLTEFQTNLV PYPRIHFPLV TYAPVISAEK **AYHEQLSVAE ITNACFEPAN QMVK**CDPRHG KYMACCMLYR

321 GDVVPK**DVNA AIATIK**TKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQR**AVCMLSN TTAIAEAWAR** LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSG EGEGEGAEEY

C Carba
O Oxida

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AVC(+57.02)MLSNTTAIAEAWAR.L	Y	63.18	1863.8971	-21.0	932.9363	2	38.35	3349	1	374	390	Carbamidomethylation
R.LIGQIVSSITASLR.F	Y	58.69	1456.8613	166.1	729.5589	2	41.05	3654	1	230	243	
K.DVNAAIATIK.T	Y	42.67	1014.5709	235.1	508.4120	2	31.46	2576	1	327	336	
K.AYHEQLSVAEITNAC(+57.02)FEPANQM(+15.99)VK.C	Y	25.52	2765.2788	448.0	923.1798	3	35.01	2973	1	281	304	Carbamidomethylation; Oxidation (M)
K.AYHEQLSVAEITNAC(+57.02)FEPANQMVK.C	Y	24.31	2749.2839	308.5	917.7180	3	36.13	3099	1	281	304	Carbamidomethylation
total 5 peptides												

tr|Q7PUE2|Q7PUE2_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDVVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLR**FDGALNV DLTEFQTNLV PYPRIHFPLV TYAPVISAEK **AYHEQLSVAE ITNACFEPAN QMVK**CDPRHG KYMACCMLYR

321 GDVVPK**DVNA AIATIK**TKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQR**AVCMLSN TTAIAEAWAR** LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSG EGEGEGAEEY

C Carba
O Oxida

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AVC(+57.02)MLSNTTAIAEAWAR.L	Y	63.18	1863.8971	-21.0	932.9363	2	38.35	3349	1	374	390	Carbamidomethylation
R.LIGQIVSSITASLR.F	Y	58.69	1456.8613	166.1	729.5589	2	41.05	3654	1	230	243	
K.DVNAAIATIK.T	Y	42.67	1014.5709	235.1	508.4120	2	31.46	2576	1	327	336	
K.AYHEQLSVAEITNAC(+57.02)FEPANQM(+15.99)VK.C	Y	25.52	2765.2788	448.0	923.1798	3	35.01	2973	1	281	304	Carbamidomethylation; Oxidation (M)
K.AYHEQLSVAEITNAC(+57.02)FEPANQMVK.C	Y	24.31	2749.2839	308.5	917.7180	3	36.13	3099	1	281	304	Carbamidomethylation
total 5 peptides												

tr|A7UIK9|A7UIK9_MONAT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

C Carba
O Oxida

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

295

241 **SLR**FDGALNV DLTEFQTNLV PYPRIHFPLV TYAPVISAEK **AYHEQLSVAE ITNACFEPAN QMVK**CDPRHG KYMACCMLYR

321 GDVVPK**DVNA AIATIK**TKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQR**AVCMLSN TTAIAEAWAR** LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSG EGEGEGAEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AVC(+57.02)MLSNTTAIAEAWAR.L	Y	63.18	1863.8971	-21.0	932.9363	2	38.35	3349	1	374	390	Carbamidomethylation
R.LIGQIVSSITASLR.F	Y	58.69	1456.8613	166.1	729.5589	2	41.05	3654	1	230	243	
K.DVNAAIATIK.T	Y	42.67	1014.5709	235.1	508.4120	2	31.46	2576	1	327	336	
K.AYHEQLSVAEITNAC(+57.02)FEPANQM(+15.99)VK.C	Y	25.52	2765.2788	448.0	923.1798	3	35.01	2973	1	281	304	Carbamidomethylation; Oxidation (M)
K.AYHEQLSVAEITNAC(+57.02)FEPANQMVK.C	Y	24.31	2749.2839	308.5	917.7180	3	36.13	3099	1	281	304	Carbamidomethylation
total 5 peptides												

tr|A0A0R1E113|A0A0R1E113_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPAKVNKKEN LDDLKQELDI DFHKISPEEL YQRFQTHPEN GLSHAKAKEN LERDGPNALT PPKQTPEWVK FCKNLFGGFA

C Carba

81 MLLWIGAILC FVAYSIQAST SEEPADDNLY LGIVLSAVVI VTGIFSYYQE SKSSKIMESF KNMVPQFATV IREGEKLTLR

161 AEDLVLGDVV EVKFGDRIPA DIRIIEARNF KVDNSSLTGE SEPQSRGAEF THENPLETK**N LAFFSTNAVE GTAK**GVVISC

241 GDHTVMGRIA GLASGLDTGE TPIAKEIHHF IHLITGVAVF LGVTFFVIAF ILGYHWLDAV IFLIGIIVAN VPEGLLATVT

353

321 VCLTLTAKRM ASKNCLVK**NL EAVETLGSTS TICSDK**TGTL TQNRMTVAHM WFDNQIIEAD TTEDQSGVQY DRTSPGFKAL

401 SRIATLCNRA EFKGGQDGVP ILKKEVSGDA SEAALLKCME LALGDVMNIR KRNKKIAEVP FNSTNKYQVS IHETEDSNDP

481 RYLLVMKGAP ERILERCSTI FINGKEKVLD EEMKEAFNNA YMELGGLGER VLGFCDFMLP SDKYPNGFKF NTDDINFPID

561 NLRFVGLMSM IDPPRAAVPD AVAKCRSAGI KVIMVTGDHP ITAKAIAKSV GIISEGNETV EDIAQRLNIP ISEVNPREAK

641 AAVVHGAELR DVSSDQLDEI LRYHTEIVFA RTSPQQKLII VEGCQRMGAI VAVTGDGVND SPALK**KADIG VAMGIAGSDV**

721 **SK**QAADMILL DDNFASIVTG VEEGRLIFDN LKKSIAYTLT SNIPEISPFL AFILCDIPLP LGTVTILCID LGTDMIPAIS

801 LAYEGPEADI MKRRPRNPEI DNLVNERLIS MAYGQIGMIQ AAAGFFVYFV IMAENGFLPK KLFGIRKMWD SKAVNDLTDS

881 YGQEWTYRDR KTLEYTCHTA FFISIVVVQW ADLIICKTRR NSIFQQGMRN WALNFGLVFE TVLAAFLSYC PGMEKGLRMY

961 PLKLVWWFPA IPFALAIFIY DETRRFYLRR NPGGWLEQET YY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLAFFSTNAVEGTAK.G	N	59.61	1568.7834	523.3	785.8094	2	35.82	3064	1	220	234	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	N	55.70	1923.9095	455.0	963.3998	2	33.46	2800	1	339	356	Carbamidomethylation
K.KADIGVAMGIAGSDVSK.Q	Y	41.41	1617.8396	-24.2	809.9075	2	31.86	2620	1	706	722	
total 3 peptides												

tr|A0A0P6CE35|A0A0P6CE35_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

2

1 M**TDAAVSFAK** DFLAGGVAAA ISK**TAVAPIE R**VKLLLQVQH ASKQITADKQ YKGIIDCVVR IPKEQGVLSF WRGNLANVIR

A Acety
O Oxida

81 YFPTQALNFA FKDKYKQIFL GGVDKRTQFW RYFAGNLASG GAAGATSLCF VYPLDFARTR LAADVGKAGA EREFKGLGDC

23940

161 LVK**IYKSDGI K**GLYQG**FNVS VQGIIIYR**AA YFGIYDTAKG MLPDPKNTHI FISWMIAQSV TAVAGLTSYP FDTVRRR**MMM**

241 **QSGR**KGTDIM YTGTLDCWRK IARDEGSKAF FKGAWSNVLR GMGGAFVLVL YDEIKKYT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.T(+42.01)DAAVSFAK.D	Y	41.70	950.4709	-120.0	951.3641	1	31.91	2627	1	2	10	Acetylation (Protein N-term)
G.FNVSVQGIIIYR.A	Y	35.92	1407.7874	17.5	704.9133	2	37.95	3304	1	177	188	
K.IYKSDGIK.G	Y	27.01	922.5123	-58.0	462.2367	2	24.26	1777	1	164	171	
K.TAVAPIER.V	Y	20.32	855.4814	-65.7	856.4325	1	26.64	2037	1	24	31	
total 5 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MM(+15.99)M(+15.99)QSGR.K	Y	20.09	871.3351	776.6	437.0132	2	22.28	1578	1	238	244	Oxidation (M)
total 5 peptides												

tr|A0A1W4W573|A0A1W4W573_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQSKLNDLA GKFGKGGPPG LGIGLKLLGV GAVAAYGVSQ SLYTVEGGHR AIVFNRIGGI QNDIFTEGLH FRIPWFQYPI
81 IYDIRSRPRK ISSPTGSKDL QMVNISLRVL SRPDASQLPT MYRNLGLDYD EKVLPSICNE VLKSVVAKFN AAQLITQRSQ
161 VSLLVRRELV ERAKDFNIIL DDVSITELSF GK**EYTAAVEA KQVAQQEAQR** AAFFVERAKQ EKQ**QKIVQAE GEAEAAK**MLG
241 EAMSR**NPGYL K**LRKIRAAQN IARTIANSQN KVYLSGNGLM LNISDPEFDE QSNKLIKL

d Deam
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QVAQQEAQR.A	Y	40.62	1056.5312	153.3	529.3539	2	22.95	1645	1	202	210	
K.Q(-17.03)VAQQEAQ(+.98)R.A	Y	34.21	1040.4886	104.9	521.3062	2	25.80	1943	1	202	210	Pyro-glu from Q; Deamidation (NQ)
Q.Q(-17.03)KIVQAEGEAEAAK.M	Y	33.78	1453.7412	-46.6	727.8440	2	28.51	2245	1	224	237	Pyro-glu from Q
R.NPGYLK.L	Y	32.94	690.3701	-166.1	691.2626	1	25.29	1890	1	246	251	
K.EYTAAVEAK.Q	Y	24.15	980.4814	323.4	491.4066	2	26.13	1981	1	193	201	
K.Q(-17.03)VAQQEAQR.A	Y	20.21	1039.5046	-46.3	1040.4637	1	25.23	1883	1	202	210	Pyro-glu from Q
total 6 peptides												

tr|A0A1Y1M0C5|A0A1Y1M0C5_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQSKLNDLA SKFGKGGPPG LGLGLKLLGV GAAAAYGVAQ SMYTVEGGHR AIIFSRIGGV QKEIYAEGLH FRIPWFQYPI
81 IYDIRSRPRK ISSPTGSKDL QMVNISLRVL SRPEASAIPV MYRQLGLDYD EKVLPSICNE VLKSVVAKFN AAQLITQRQQ
161 VSLLVRRELV ERAKDFNIIL DDVSITELSF GK**EYTAAVEA KQVAQQEAQR** AAFVVERAKQ ERQ**QKIVQAE GEAEAAK**MLG
241 EAIGL**NPGYL K**LRKIRAAQN IARTIANSQN RVYLNGNSLM LNIQDPEFDD QSNKLKSKK

d Deam
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QVAQQEAQR.A	Y	40.62	1056.5312	153.3	529.3539	2	22.95	1645	1	202	210	
K.Q(-17.03)VAQQEAQ(+.98)R.A	Y	34.21	1040.4886	104.9	521.3062	2	25.80	1943	1	202	210	Pyro-glu from Q; Deamidation (NQ)
Q.Q(-17.03)KIVQAEGEAEAAK.M	Y	33.78	1453.7412	-46.6	727.8440	2	28.51	2245	1	224	237	Pyro-glu from Q
L.NPGYLK.L	Y	32.94	690.3701	-166.1	691.2626	1	25.29	1890	1	246	251	
K.EYTAAVEAK.Q	Y	24.15	980.4814	323.4	491.4066	2	26.13	1981	1	193	201	
K.Q(-17.03)VAQQEAQR.A	Y	20.21	1039.5046	-46.3	1040.4637	1	25.23	1883	1	202	210	Pyro-glu from Q
total 6 peptides												

tr|A0A151X2A0|A0A151X2A0_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQNKFSEMA SRFTKGTNGV PMSLKFLAAA GVAAYSVSKA MYTVEAGHRA IIFSRLGGIQ KDILTEGLHF RVPWFQYPII
81 YDIRSRPRKL SSPTGSKDLQ MVNISLRVLS RPDASTLPSM YRQLGLDYDE KVLPSICNEV LKSVVAKFNA SQLITQRQQV
161 SIMVRKELTE RARDFNIVLD DVSITELSFG K**EYTAAVEAK QVAQQEAQR**A AFVVERAKQE RQ**QKIVQAEG EAEAAK**MMYL
241 GLAVGQ**NPGY LK**LRKIRAAQ NISRTIANSQ NRIFLSGNSL MLNIQDPTFD EGSDKLKSKK

d Deam
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QVAQQEAQR.A	Y	40.62	1056.5312	153.3	529.3539	2	22.95	1645	1	201	209	
K.Q(-17.03)VAQQEAQ(+.98)R.A	Y	34.21	1040.4886	104.9	521.3062	2	25.80	1943	1	201	209	Pyro-glu from Q; Deamidation (NQ)
Q.Q(-17.03)KIVQAEGEAEAAK.M	Y	33.78	1453.7412	-46.6	727.8440	2	28.51	2245	1	223	236	Pyro-glu from Q
Q.NPGYLK.L	Y	32.94	690.3701	-166.1	691.2626	1	25.29	1890	1	247	252	
K.EYTAAVEAK.Q	Y	24.15	980.4814	323.4	491.4066	2	26.13	1981	1	192	200	
K.Q(-17.03)VAQQEAQR.A	Y	20.21	1039.5046	-46.3	1040.4637	1	25.23	1883	1	201	209	Pyro-glu from Q
total 6 peptides												

tr|A0A1W4W553|A0A1W4W553_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQSKLNDLA GKFGKGGPPG LGIGLKLLGV GAVAAYGVSQ SLYTVEGGHR AIVFNRIGGI QNDIFTEGLH FRIPWFQYPI
81 IYDIRSRPRK ISSPTGSKDL QMVNISLRVL SRPDASQLPT MYRNLGLDYD EKVLPSICNE VLKSVVAKFN AAQLITQRSQ
161 VSLLVRRELV ERAKDFNIIL DDVSITELSF GK**EYTAAVEA KQVAQQEAQR** AAFFVERAKQ EKQ**QKIVQAE GEAEAAK**MLG
241 EAMSR**NPGYL K**LRKIRAAQN IARTIANSQN KVYLSGNGLM LNISDPEFDE QSNKLIKRKN

d Deam
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QVAQQEAQR.A	Y	40.62	1056.5312	153.3	529.3539	2	22.95	1645	1	202	210	
K.Q(-17.03)VAQQEAQ(+.98)R.A	Y	34.21	1040.4886	104.9	521.3062	2	25.80	1943	1	202	210	Pyro-glu from Q; Deamidation (NQ)
Q.Q(-17.03)KIVQAEGEAEAAK.M	Y	33.78	1453.7412	-46.6	727.8440	2	28.51	2245	1	224	237	Pyro-glu from Q
R.NPGYLK.L	Y	32.94	690.3701	-166.1	691.2626	1	25.29	1890	1	246	251	
K.EYTAAVEAK.Q	Y	24.15	980.4814	323.4	491.4066	2	26.13	1981	1	193	201	
K.Q(-17.03)VAQQEAQR.A	Y	20.21	1039.5046	-46.3	1040.4637	1	25.23	1883	1	202	210	Pyro-glu from Q
total 6 peptides												

tr|A0A067QGU8|A0A067QGU8_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQSKLNDLA GRFGKGPKGV GTGLKILAVA GAALYGASQS MYTVEGGHRA IIFSRIGGVQ QEVFPEGLHF RIPWFQYPII
81 YDIRSRPRKI SSPTGSKDLQ MVNISLRVLS RPDAISLPIM YRQLGLDYDE KVLPSICNEV LKSVVAKFNA SQLITQRQQV
161 SLLVRRELTE RARDFNIILD DVSITELSFG K**EYTAAVEAK QVAQQEAQR**A AFVVERAKQE RQ**QKIVQAEG EAEAAK**MLGE
241 AVSQ**NPGYLK** LRKIRAAQSI SRTIANSQNR VFLSGSSLML NISEPTFDDL SEKLKSEDSV SHTGGDGSRS LVFDSAVRSA
321 TLLFRH

d Deam
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QVAQQEAQR.A	Y	40.62	1056.5312	153.3	529.3539	2	22.95	1645	1	201	209	
K.Q(-17.03)VAQQEAQ(+.98)R.A	Y	34.21	1040.4886	104.9	521.3062	2	25.80	1943	1	201	209	Pyro-glu from Q; Deamidation (NQ)
Q.Q(-17.03)KIVQAEGEAEAAK.M	Y	33.78	1453.7412	-46.6	727.8440	2	28.51	2245	1	223	236	Pyro-glu from Q
Q.NPGYLK.L	Y	32.94	690.3701	-166.1	691.2626	1	25.29	1890	1	245	250	
K.EYTAAVEAK.Q	Y	24.15	980.4814	323.4	491.4066	2	26.13	1981	1	192	200	
K.Q(-17.03)VAQQEAQR.A	Y	20.21	1039.5046	-46.3	1040.4637	1	25.23	1883	1	201	209	Pyro-glu from Q
total 6 peptides												

tr|V9IID0|V9IID0_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MATCLLKVSS ALRAYSNKSS LVKIQKQWRS TSASLKEILM NQPPTQVTTL DCGMRIATED SGAPTATVGL WIDAGSRFET
81 DENNGVAHFM EHMAFKGTTK RSQTDLELEI ENMGAHLNAY TSREQTVFYA KCLAEDVPKA VEILSDIIQN SKLGENEIER
161 ERGVILREMQ EVETNLQEVV FDHLHASAYQ GTPLGRTILG PTKNIKSITR NDLLNYVRSY YGPPRFILAG AGGVNHNALV
241 ELAQKHFGQM KGPFYDEIPS ILEPCRYTGS EIRVRDDTIP LAHVAIAVEG AGWTDPDNIP LMVANTLMGA WDRSQGGGVN
321 NISYLAEASA TDGLCHSYQS FNTCYQDTGL WGIYFVCDPM EIQDFVFNVQ REWMRLCTTV TEKEVDRAKN ILK**TNMLLQL**
407
401 **DGTTAICEDI GR**QMLCYNRR IPLHELEARI DSVNASNIHD IGMKYIYDQC PVIAAVGPIE NLLDYNLIRA GMYRLRV

c Carba

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TNMLLQLDGTTAIC(+57.02)EDIGR.Q	Y	70.05	2120.0242	-78.4	1060.9363	2	38.04	3314	1	394	412	Carbamidomethylation
total 1 peptides												

tr|A0A088A820|A0A088A820_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MATCLLKVSS ALRAYSNKNS LVKIQKQWRS TSASLKEILM NQPPTQVTTL DCGMRIATED SGAPTATVGL WIDAGSRFET
81 DENNGVAHFM EHMAFKGTTK RSQTDLELEI ENMGAHLNAY TSREQTVFYA KCLAEDVPKA VEILSDIIQN SKLGENEIER
161 ERGVILREMQ EVETNLQEVV FDHLHASAYQ GTPLGRTILG PTKNIKSITR NDLLNYVKSY YGPPRFILAG AGGVNHNALV
241 ELAQKHFGQM KGPFYDEIPS ILEPCRYTGS EIRVRDDTIP LAHVAIAVEG AGWTDPDNIP LMVANTLMGA WDRSQGGGVN
321 NISYLAEASA TDGLCHSYQS FNTCYQDTGL WGIYFVCDPM EIQDFVFNVQ REWMRLCTTV TEKEVDRAKN ILK**TNMLLQL**
407
401 **DGTTAICEDI GR**QMLCYNRR IPLHELEARI DSVNASNIHD IGMKYIYDQC PVIAAVGPIE NLLDYNLIRA GMYRLRV

c Carba

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TNMLLQLDGTTAIC(+57.02)EDIGR.Q	Y	70.05	2120.0242	-78.4	1060.9363	2	38.04	3314	1	394	412	Carbamidomethylation
total 1 peptides												

tr|A0A0L7RBG9|A0A0L7RBG9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPATEVTTLD CGMRVATEDS GAPTATVGLW IDAGSRFETD ENNGVAHFME HMAFKGTTKR SQTDLELEIE NMGAHLNAYT C Carba
81 SREQTVFYAK CLSEDVPKAV EILSDIIQNS KLGESEIERE RCVILREMQE IETNLQEVVF DHLHASAYQG TPLGRTILGP
161 TQNIKSITRN DLVDYVKKHY GPPRFILAGA GGVNHNALVD LAQKHFGQMK GPFYDEIPPL LEPCRYTGCE IRVRDDNIPL
241 AHIAIAVEGA GWADADNIPL MVANTLMGAW DRSQGGGVNN ICFLAEAAAT DGLCHSYQSF NTCYQDTGLW GIYFVSDPMM
366
C
321 LEHFVYNIQR EWMRLCTTVT EREVERAKTA LK**TNMLLQLD GTTAICEDIG R**QMLCYNRRI PLHELETRIN SVTASNIHDV
C
401 AMKYIYDQCP VVAAVGPIEN LPDYNLIRSG MYRLRV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TNMLLQLDGTTAIC(+57.02)EDIGR.Q	Y	70.05	2120.0242	-78.4	1060.9363	2	38.04	3314	1	353	371	Carbamidomethylation
total 1 peptides												

tr|A0A151J3L9|A0A151J3L9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGLLSLRLAS ALIRHLPNAT QINWPATAIA SHKYHVSCSR RSAEISAILE ERILGSAPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEQL LGRVVDALGN PIDGKGPLNS
161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDGG EEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAINYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ENLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR LTELLKQGQY VPMAIEEQVA
481 VIYCGVRGYL DKMDPTKITG FEKEFLAHIR STQQDLLATI AKENVISEAS DAKLKKVVTD FLSSFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	83	97	
total 1 peptides												

tr|A0A1B0C955|A0A1B0C955_LUTLO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSLLSARLAA SVARNLPRTS SQVAKILYPA TSLAARKFHV SSQRNAEISA ILEERILGAA PKADLDETGR VLSIGDGIAR
81 VYGLK**NIQAD EMVEFSSGLK** GMALNLEPDN VGVVVFGNDK LIKEGDIVKR TGAIVDVPVG EELLGRVVDA LGNPIDGKGA
161 ITSKTRFRVG IKAPGIIPRI SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTSLAI DTIINQKRFN DGQDETKKLY
241 CIYVAIGQKR STVAQIVKRL TDTGAMNYSI IVSATASDAA PLQYLAPYSG CAMGEFFRDN GKHALIIYDD LSKQAVAYRQ
321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVRLTELLKQ GQLLSSIAVV
481 RGHLDKMDPQ KITKFEKEFT EHVKSNEKAL LQQIATDGKI TEQTDAKLKE IVTKFLATFT G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	86	100	
total 1 peptides												

tr|A0A1L8E154|A0A1L8E154_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSLLSARLAA SVARNLPRTS SQVAKIIYPA TSLAARKFHL SSQRNAEISA ILEERILGAA PKADLDETGR VLSIGDGIAR
 81  VYGLKNIQAD EMVEFSSGLK GMALNLEPDN VGVVVFGNDK LIKEGDIVKR TGAIVDVPVG EELLGRVVDA LGNPIDGKGA
161  ITSKTRFRVG IKAPGIIPRI SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTSLAI DTIINQKRFN DGQDESKKLY
241  CIYVAIGQKR STVAQIVKRL TDSGAMGYSV IVSATASDAA PLQYLAPYSG CAMGEFFRDN GKHALIIYDD LSKQAVAYRQ
321  MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401  IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVRLTELLKQ GQYVPMAIEE
481  QVAVIYCGVR GHLDKMDPQK ITKFEKEFTE HVKSSEKALL SQIAADGQIT EQTDAKLKDV VAKFLATFAG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	86	100	
total 1 peptides												

tr|A0A182XJA6|A0A182XJA6_ANOQN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGA APKADLEETG RVLSIGDGIA
 81  RVYGLKNIQA DEMVEFSSGL KGMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG
161  EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241  YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321  QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401  GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481  EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A1J1J483|A0A1J1J483_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMLSARLAA SVARNLPRSA QQVARAVIPA SQIVARKIHL STPAKGAEIS TILEERILGA APKADLEETG RVLSIGDGIA
 81  RVYGLKNIQA DEMVEFSSGL KGMALNLEPD NVGVVVFGND RLIREGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGRG
161  EIKTGQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241  YCIYVAIGQK RSTVAQIVKR LTDAGAMDYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321  QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401  GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481  EQVAVIYCGV RGHLDKMDPA KITSFEKEFL AHITTNEQGL LKQIATEGKI SDEVDAKLKS IVTNFLSTFT G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A182N7Z7|A0A182N7Z7_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMISARLAA SVARSLPRTA SQVAKIAVPA VSVAARNFHV STANRGAEIS SILEERILGA APKADLEETG RVLSIGDGIA
 81  RVYGLKNIQA DEMVEFSSGL KGMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG
161  EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241  YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321  QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401  GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481  EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|Q7PHI8|Q7PHI8_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISVRLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STAHRGAEIS AILEERILGA APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG
161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|S4VDE6|S4VDE6_LOCMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSFRLAS AVAKHLPAAT PQISGLTWPA AQITNRNIHV SCSQRAAEIS SILEERILGA APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND RLIKEGDIVK RTGAIVDVPV GEELLGRVVD ALGNPIDGKG
161 PLKASKRFRV GIKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGEDEKKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAIGYS IIVSATASDA APLQYLAPYS GCAMGEFFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNDAHGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TRAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGHLDKLDPS KITAFEKEFL QHIKTSEAAL LANIAKEGKI TDEIDVKLKK IVTDFVANFQ G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A1B6KWM9|A0A1B6KWM9_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PIRRLFSCSP SSSRFRAGGK MAQLSVRLAS ALAKQLSVAV PQVVWPTAQV ASRKLHVSCS QRAAEISSIL EDRILGNAPK
81 ADLEETGRVL SIGDGIARVY GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDKLI KEGDIVKRTG AIVDVPVGED
161 LLGRVVDALG NTIDGKGPLK NVTRARVGVK APGIIPRISV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT
241 IINQQRFNNA EDEKKKLYCI YVAIGQKRST VAQIVKRLTD SGSMKYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK
321 HALIIYDDLS KQAVAYRQMS LLLRRPPGRE AYPGDVFYLH SRLLERAAKM SEANGGGSLT ALPVIETQAG DVSAYIPTNV
401 ISITDGQIFL ETELFYKGIR PAINVGLSVS RVGSAAQTRA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV
481 RLTELLKQGQ YVPMAIEEQV AVIYCGVRGH LDKLDPAKIT AFEKEFLAHV KASHKDVLAS IAKEGKINEE TDAKMKGIVQ
561 SFLSSFTAS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	104	118	
total 1 peptides												

tr|A0A1B0D1L3|A0A1B0D1L3_PHLPP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAHLARVAAS VARSLPKTSS QVTRILYPAT SLAARKFHVS SQKNAEISAI LEERILGAAP KADLDETGRV LSIGDGIARV
81 YGLK**NIQADE MVEFSSGLK**G MALNLEPDNV GVVVFGNDKL IKEGDIVKRT GAIVDVPVGE ELLGRVVDAL GNPIDGKGAI
161 TSKTRFRVGL KAPGIIPRIS VREPMQTGIK AVDSLVPIGR GQRELIIGDR QTGKTALAID TIINQKRFND GQDESKKLYC
241 IYVAIGQKRS TVAQIVKRLT DTGAMNYSII VSATASDAAP LQYLAPYSGC AMGEYHSHLN TFFPFSYLPI SDSLQFV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	85	99	
total 1 peptides												

tr|A0A067QI29|A0A067QI29_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAT SVARHFPSAA PQVANLTWPA AQVASRKLHV SCSQRAAEIS SILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEAD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GADLLGRVVD ALGNPIDGKG

161 PFKSVTRARV GVKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NEGDDEKKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAIGYT IIVSATASDA APLQYLAPYS GCAMGEFFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNETNGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TRAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGHLDKLDPA KITAFEKEFL QHIKTSHKDL LAIIAKEGKI NEDADAKLKK IVSEFLISFT S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|B4QHN0|B4QHN0_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIFSARLAS SVARNLPKAA NQVACKAAYP AASLAARKLH VASTQRSAEI SNILEERILG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGDELLGRVV DALGNAIDGK

161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNEAQDESKK
241 LYCIYVAIGQ KRSTVAQIVK RLTDSGAMGY SVIVSATASD MSPAMGGGSL TALPVIETQA GDVSAYIPTN VISITDGQIF
321 LETELFYKGI RPAINVGLSV SRVGSAAQTK AMKQVAGSMK LELAQYREVA AFAQFGSDLD AATQQLLNRG VRLTELLKQG
401 QYVPMAIEDQ VAVIYCGVRG HLDKMDPAKI TKFEKEFLQH IKTSEQALLD TIAKDGAISE SSDAKLKDIV AKFMSTFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	88	102	
total 1 peptides												

tr|A0A182TC06|A0A182TC06_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VAKIAVPAVS VAARNFHVST ANRGAEISAI LEERILGSAP KADLEETGRV LSIGDGIARV YGLK**NIQADE MVEFSSGLK**G

81 MALNLEPDNV GVVVFGNDKL IKEGDIVKRT GAIVDVPVGD EILGRVVDAL GNAIDGKGEI KTKQRFRVGI KAPGIIPRVS
161 VREPMQTGIK AVDSLVPIGR GQRELIIGDR QTGKTALAID TIINQKRFND GQDESKKLYC IYVAIGQKRS TYLAPYSGCA
241 MGEYFRDNGK HALIIYDDLS KQAVAYRQMS LLLRRPPGRE AYPGDVFYLH SRLLERAAKM SPTLGGGSLT ALPVIETQAG
321 DVSAYIPTNV ISITDGQIFL ETELFYKGIR PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA
401 ATQQLLNRGV RLTELLKQGQ YVPMAIEEQV AVIYCGVRGY LDKMDPGKIT KFEKEFLAHV KTNEKALLQQ IASEGKISDE
481 ADAKLKSVVT SFLSTFSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	65	79	
total 1 peptides												

tr|A0A182YNR5|A0A182YNR5_ANOST

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNWTVAKIAV PAVSVAARNF HVSTANRGAE ISAILEERIL GSAPKADLEE TGRVLSIGDG IARVYGLK**NI QADEMVEFSS**

81 **GLK**GMALNLE PDNVGVVVFG NDKLIKEGDI VKRTGAIVDV PVGDEILGRV VDALGNAIDG KGEIKTKQRF RVGIKAPGII

161 PRVSVREPMQ TGIKAVDSLV PIGRGQRELI IGDRQTGKTA LAIDTIINQK RFNDGQDESK KLYCIYVAIG QKRSTVAQIV
241 KRLTDAGAMN YTIIVSATAS DAAPLQYLAP YSGCAMGEYF RDNGKHALII YDDLSKQAVA YRQMSLLLRR PPGREAYPGD
321 VFYLHSRLLE RAAKMSPTLG GGSLTALPVI ETQAGDVSAY IPTNVISITD GQIFLETELF YKGIRPAINV GLSVSRVGSA
401 AQTKAMKQVA GSMKLELAQY REVAAFAQFG SDLDAATQQL LNRGVRLTEL LKQGQYVPMA IEEQVAVIYC GVRGYLDKMD
481 PGKITKFEKE FLAHVKTNEK ALLQQIASEG KISDDADAKL KSVVTSFMST FSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	69	83	
total 1 peptides												

tr|B4LIV0|B4LIV0_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MISARLASSV ARNLPKAAAQ VACKAAYPAT SLAARKLHVA STQRSAEISS VLEERILGVA PKADLEETGR VLSIGDGIAR

81 VYGLN**NIQAD EMVEFSSGLK** GMALNLEADN VGVVVFGNDK LIKQGDIVKR TGAIVDVPVG NELLGRVVDA LGNAIDGKGA

161 INTKDRFRVG IKAPGIIPRV SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTALAI DTIINQKRFN DGQDESKKLY

241 CIYVAIGQKR STVAQILKRL TDSGAMGYTI IVSATASDAA PLQYLAPYSG CAMGEFFRDK GKHALIIYDD LSKQAVAYRQ

321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG

401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DASTQQLLNR GVRLTELLKQ GQYVPMAIED

481 QVAVIYCGVR GHLDKMDPSK ITKFEKEFLQ HIKTSEQGLL DGIAKDGQIS EAADAKLKDI VQKFMSTFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	86	100	
total 1 peptides												

tr|A0A0M4EW76|A0A0M4EW76_DROBS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MISARLASSV ARNLPKAASQ VACKAAYPAA TLAARKFHVA STQRSAEISN ILEERILGVA PKADLEETGR VLSIGDGIAR

81 VYGLN**NIQAD EMVEFSSGLK** GMALNLEPDN VGVVVFGNDK LIKQGDIVKR TGAIVDVPVG DELLGRVVDA LGNAIDGRGA

161 INTKDRFRVG IKAPGIIPRV SVRDPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTALAI DTIINQKRFN DGQDDTKKLY

241 CIYVAIGQKR STVAQIVKRL TDSGAMDYSV IVSATASDAA PLQYLAPYSG CAMGEYFRDK GKHALIIYDD LSKQAVAYRQ

321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG

401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVRLTELLKQ GQYVPMSIED

481 QVAVIYCGVR GHLDKMDPAK ITKFEKEFLQ HIKTTEQGLL DTIAKEGQIS QASDAKLKDV VTKFMATFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	86	100	
total 1 peptides												

tr|A0A151XGV4|A0A151XGV4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS FLTRHLPNTT AQINWPVTAI ASRKYHVSCS RHSAEISAIL EERILGSAPK ANLEETGRVL SIGDGIARVY

81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEQ LLGRVVDALG NPIDGKGPLN

161 NKLRFRIGTK APGIIPRVSV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDG GEEKKKLYCI

241 YVAIGQKRST VAQIVKRLTD SSAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK HALIIYDDLS KQAVAYRQMS

321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NENLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR

401 PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV RLTELLKQGQ YVPMAIEEQV

481 AVIYCGVRGY LDKMDPTKIT GFEKEFLAHI RSTQQDLLAT IAKENVISEA SDTKLKKVVI DFLSSFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	84	98	
total 1 peptides												

tr|A0A195CV10|A0A195CV10_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SLARHLPNTT GQINWSVTTI ASRKYHVSCN RRSAEISAIL EERILGSAPK ANLEETGRVL SIGDGIARVY

81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEQ LLGRVVDALG NPIDGKGPLN

161 NKLRFRIGTK APGIIPRVSV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDG GEEKKKLYCI

241 YVAIGQKRST VAQIVKRLTD SGAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK HALIIYDDLS KQAVAYRQMS

321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NENLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR

401 PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV RLTELLKQGQ YVPMAIEEQV

481 AVIYCGVRGY LDKMDPSKIT SFEKEFLAHI RATQQDLLAT IAKENVISEA SDAKLKKVVT DFLSSFSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	84	98	
total 1 peptides												

tr|A0A087ZQI5|A0A087ZQI5_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLVS SIARQLPNTT IQVKWPLSIS SCKYHVSCSR RSAEISSILE ERILGASPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS
161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG EEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAMDYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR LTELLKQGQY VPMAIEEQVA
481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TSQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	83	97	
total 1 peptides												

tr|A0A0N0BIY2|A0A0N0BIY2_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SIARQLPNNS IQIKWPLCIA SCKYHVSCSR RSAEISSILE ERILGSAPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIR EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS
161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG DEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAINYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR LTELLKQGQY VPMAIEEQVA
481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TNQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	83	97	
total 1 peptides												

tr|V9IFD6|V9IFD6_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLVS SIARQLPNTT IQVKWPLSIS SCKYHVSCSR RSAEISSILE ERILGATPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS
161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG EEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAMDYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR LTELLKQGQY VPMAIEEQVA
481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TSQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	83	97	
total 1 peptides												

tr|A0A0J9RIM8|A0A0J9RIM8_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIFSARLAS SVARNLPKAA NQVACKAAYP AASLAARKLH VASTQRSAEI SNILEERILG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGDELLGRVV DALGNAIDGK
161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNEAQDESKK
241 LYCIYVAIGQ KRSTVAQIVK RLTDSGAMGY SVIVSATASD AAPLQYLAPY SGCAMGEYFR DKGKHALIIY DDLSKQAVAY
321 RQMSLLLRRP PGREAYPGDV FYLHSRLLER AAKMSPAMGG GSLTALPVIE TQAGDVSAYI PTNVISITDG QIFLETELFY
401 KGIRPAINVG LSVSRVGSAA QTKAMKQVAG SMKLELAQYR EVAAFAQFGS DLDAATQQLL NRGVRLTELL KQGQYVPMAI
481 EDQVAVIYCG VRGHLDKMDP AKITKFEKEF LQHIKTSEQA LLDTIAKDGA ISESSDAKLK DIVAKFMSTF QG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	88	102	
total 1 peptides												

tr|A0A1A9WYG7|A0A1A9WYG7_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAT SVARSLPKAA QQVAAKAAYP VATLAARKLH VSSSQRGAEI SSILEERIMG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGSEILGRVV DALGNAIDGK

161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNDGQDETKK
241 LYCIYVAIGQ KRSTVAQIVK RLSDAGAMDY TIIVSATASD AAPLQYLAPY SGCAMGEYFR DKGKHALIIY DDLSKQAVAY
321 RQMSLLLRRP PGREAYPGDV FYLHSRLLER AAKMSPAMGG GSLTALPVIE TQAGDVSAYI PTNVISITDG QIFLETELFY
401 KGIRPAINVG LSVSRVGSAA QTKAMKQVAG SMKLELAQYR EVAAFAQFGS DLDAATQQLL NRGVRLTELL KQGQYVPMSI
481 EDQVAVIYCG VRGHLDKMDP AKITKFEKEF LQHIKTSEQS LLSQIAQEGK ISEGADAKLK EVVTKFLSTF QG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	88	102	
total 1 peptides												

tr|A0A1B0BN74|A0A1B0BN74_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAT SVARSLPKAA QQIGVKAAYP VATLAARKLH VSSAQRGAEI SSILEERIMG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGSEILGRVV DALGNAIDGK

161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNDGQDESKK
241 LYCIYVAIGQ KRSTVAQIVK RLSDAGAMDY TIIVSATASD AAPLQYLAPY SGCAMGEYFR DKGKHALIIY DDLSKQAVAY
321 RQMSLLLRRP PGREAYPGDV FYLHSRLLER AAKMSPAMGG GSLTALPVIE TQAGDVSAYI PTNVISITDG QIFLETELFY
401 KGIRPAINVG LSVSRVGSAA QTKAMKQVAG SMKLELAQYR EVAAFAQFGS DLDAATQQLL NRGVRLTELL KQGQYVPMSI
481 EDQVAVIYCG VRGHLDKMDP AKITKFEKEF LQHIKTSEQS LLSQIAQEGK ISEGADAKLK EVVTKFLSTF QG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	88	102	
total 1 peptides												

tr|A0A182FH95|A0A182FH95_ANOAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA GQVAKIAVPA VSVAARNFHV ATPNRGAEIS SILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGAG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|W5J4R5|W5J4R5_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA GQVAKIAVPA VSVAARNFHV ATPNRGAEIS SILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGAG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A069DZ92|A0A069DZ92_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALISARVLS SVARQFTSSV PQVGNLSWAG SQNTFRALHV SCSHRAAEIS SILEERILGS APKTDLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLISEGDIVK RTGAIVDVPV GEDLLGRVVD ALGNPIDGKG
161 PLATKNRMRV GIKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NEGDEEKKKL
241 YCIYVAIGQK RSTVAQIVKR LTDTGSMQYT IIVSATASDA APLQYLAPYS GCAMGEHFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNDANGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLA RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGHLDKLDPS KITAFEKEFL QHIKSSHRDL LASIAKEGKI TDDVDGKLKE IVTSFIAGFQ G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A182MRL5|A0A182MRL5_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG
161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPG KITKFEKEFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A1A9TPM8|A0A1A9TPM8_ANOST

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG
161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPG KITKFEKEFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	87	101	
total 1 peptides												

tr|A0A232FBT4|A0A232FBT4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLTVRLAA SVARQLPSTQ VSWPAAVVAS RKYHVSCSRR SAEISSILEE RILGASSKTN LEETGRVLSI GDGIARVYGL
81 K**NIQADEMVE FSSGLK**GMAL NLEPDNVGIV VFGNDRHIKE GDIVKRTGAI VDVPVGNELL GRVVDALGNP IDGKGPLNNK
161 LRFRIGTKAP GIIPRESVRE PMQTGIKAVD SLVPIGRGQR ELIIGDRQTG KTALAIDTII NQKRFNEAGD ENKKLYCIYV
241 AVGQKRSTVA QIVKRLTDAG AINYSIIVSA TASDAAPLQY LAPYSGCAMG EFFRYDIAEF NDLKSIVDNG KHALIIYDDL
321 SKQAVAYRQM SLLLRRPPGR EAYPGDVFYL HSRLLERAAK MNKSLGGGSL TALPVIETQA GDVSAYIPTN VISITDGQIF
401 LETELFYKGI RPAINVGLSV SRVGSAAQTK AMKQVAGSMK LELAQYREVA AFAQFGSDLD AATQQLLNRG VRLTELLKQG
481 QYERSISNGF VLSVPMAIEE QVAVIYCGVR GYLDKMDPAK ITAFEKEFLA HIKATQQDLL ATIAKENIIS EASDAKLKKV
561 VTDFLSSFGA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	82	96	
total 1 peptides												

tr|A0A0J7N062|A0A0J7N062_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SLVRHLPNAT AQITWPATAV ASCKYHVSCS RRSVEISSIL EERILGSAPQ TNLEETGRVI SIGDGIARVY
81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEE LLGRVVDALG NPIDGKGPLN
161 NKLRFRIGTK APGIIPRESV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDA GEEKKKLYCI
241 YVAIGQKRST VAQIVKRLTD SGAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGR HALIIYDDLS KQAVAYRQMS
321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NETLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR
401 PAINVGLSVS RVGSAAQTKA MKQVSYVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVRLTELLK QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPT KITAFEKEFL AHIRSTQQDL LATIAKENII NEASDAKLKK IVTDFLSSFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	67.30	1666.7872	-24.7	834.3803	2	35.91	3074	1	84	98	
total 1 peptides												

tr|A0A0M4EGW1|A0A0M4EGW1_DROBS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAQFFNRIG QMGLGVALLG GVVNSALYNV EGGHRAVIFD RFTGIKENVV GEGTHFFIPW VQRPIIFDIR SQPR**NVPVIT**
81 **GSK**DLQNVNI TLRILYRPIP DELPKIYTIL GQDYDERVLP SIAPEVLKAV VAQFDAGELI TQREMVSQRV SQELTVRAKQ
161 FGFILDDISL THLTFGREFT QAVEMKQVAQ QEAEKAR**FVV EKAEQQK**LAS IISAEGDAAA ADLLAKSFGE AGDGLVELRR
241 IEAAEDIAYQ LSRSRGVAYL PSGQSTLLNL PSTIAQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NVPVITGSK.D	Y	49.00	913.5233	-60.4	914.4753	1	27.90	2178	1	75	83	
R.FVVEKAEQQK.L	Y	34.57	1204.6451	148.3	603.4192	2	25.62	1924	1	198	207	
total 2 peptides												

tr|B4M935|B4M935_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAQFFNRIG QMGLGVALLG GVVNSALYNV EGGHRAVIFD RFTGIKEHVV GEGTHFFIPW VQRPIIFDIR SQPR**NVPVIT**
81 **GSK**DLQNVNI TLRILYRPIP DELPKIYTIL GQDYDERVLP SIAPEVLKAV VAQFDAGELI TQREMVSQRV SQELTVRAKQ
161 FGFILDDISL THLTFGREFT LAVEMKQVAQ QEAEKAR**FVV EKAEQQK**LAS IISAEGDAEA AGLLAKSFGE AGDGLVELRR
241 IEAAEDIAYQ LSRSRGVAYL PSGQSTLLSL PSNMGQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NVPVITGSK.D	Y	49.00	913.5233	-60.4	914.4753	1	27.90	2178	1	75	83	
R.FVVEKAEQQK.L	Y	34.57	1204.6451	148.3	603.4192	2	25.62	1924	1	198	207	
total 2 peptides												

tr|B4Q9G9|B4Q9G9_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAQFFNRIG QMGLGVAVLG GVVNSALYNV EGGHRAVIFD RFTGIKENVV GEGTHFFIPW VQRPIIFDIR SQPR**NVPVIT**

81 **GSK**DLQNVNI TLRILYRPIP DQLPKIYTIL GQDYDERVLP SIAPEVLKAV VAQFDAGELI TQREMVSQRV SQELTVRAKQ

161 FGFILDDISL THLTFGREFT LAVEMKQVAQ QEAEKAR**FVV EKAEQQK**LAS IISAEGDAEA AGLLAKSFGE AGDGLVELRR

241 IEAAEDIAYQ LSRSRGVAYL PSGQSTLLNL PSTIAQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NVPVITGSK.D	Y	49.00	913.5233	-60.4	914.4753	1	27.90	2178	1	75	83	
R.FVVEKAEQQK.L	Y	34.57	1204.6451	148.3	603.4192	2	25.62	1924	1	198	207	
total 2 peptides												

tr|D0QWC7|D0QWC7_DROMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASQFFNRIG QMGLGVAVLG GVVNSALYNV EGGHRAVIFD RFTGIKEHVV GEGTHFFIPW VQRPIIFDIR SQPR**NVPVIT**

81 **GSK**DLQNVNI TLRILYRPIP DQLPKIYTIL GQDYDERVLP SIAPEVLKAV VAQFDAGELI TQREMVSQRV SQELTLRANQ

161 FGFILDDISL THLTFGREFT LAVEMKQVAQ QEAEKAR**FVV EKAEQQK**LAS IISAEGDAAA AGLLAKSFGE AGDGLVELRR

241 IEAAEDIAYQ LSRSRGVAYL PSGQNTLLNL PSTIAQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NVPVITGSK.D	Y	49.00	913.5233	-60.4	914.4753	1	27.90	2178	1	75	83	
R.FVVEKAEQQK.L	Y	34.57	1204.6451	148.3	603.4192	2	25.62	1924	1	198	207	
total 2 peptides												

tr|W8BWG2|W8BWG2_CERCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAQFFNRIG QLGLGVAVLG GVVNSALYNV DGGHRAVIFD RFTGVQQEVV GEGTHFFIPW VQRPIIYDIR SQPR**NVPVIT**

81 **GSK**DLQNVNI TLRILYRPIP DQLPKIYTIL GQDYDERVLP SIAPEVLKAV VAQFDAGELI TQREMVSQRV SEELTERAKQ

161 FGFILDDISL THLTFGREFT QAVEMKQVAQ QEAEKAR**FVV EKAEQQK**LAS IISAEGDASA AGLLAKAFGE AGDGLVELRR

241 IEAAEDIAYQ LSRSRGVAYL PGGQNTLLNL PASLAQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NVPVITGSK.D	Y	49.00	913.5233	-60.4	914.4753	1	27.90	2178	1	75	83	
R.FVVEKAEQQK.L	Y	34.57	1204.6451	148.3	603.4192	2	25.62	1924	1	198	207	
total 2 peptides												

tr|A0A289ZEQ2|A0A289ZEQ2_EULVE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADSIAAQLM EEIVPALDKS GGKVTVVGVG QVGMACAFSL LTQSICSELA LVDVDANKLR GEMLDLQHGL TFLRNIKIDA

C Carba

81 SPDFAVTAGS RVCIVTAGAR QKEGESRLSL VQRNTDIFKG IIPKLVEYSP DTILLIVSNP VDILTYVAQK LSGLPKNR**VI**

164
C

161 **GSGCNLDSAR** FRFHLSQRLN VAPNSAHGWI VGEHGDSSVP VWSGVNVAGV RLRDLNPDIG TPSDPDKYNE LHKEVVNSAY

C

241 EIIKLKGYTS WAIGLSVASL VSSIMKNQRR CYAISVNVQG HHGIEEDVFL SLPSVLGENG VTHVIKQTLT AEEVAQLQKS

321 AKTLWDVQAG LKF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIGSGC(+57.02)NLDSAR.F	Y	61.65	1247.5928	173.8	624.9121	2	27.64	2149	1	159	170	Carbamidomethylation
total 1 peptides												

tr|A0A1Y1K9I6|A0A1Y1K9I6_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

67
C

1 GVRPRKGVTR IDIASDNVKL LRSIIPNVVR HSPNSIILII SNPVDVLTWA TAQLTGLPKH Q**VIGSGCNLD SAR**LRYLMSE C Carba

C

81 IYGVACSSCQ GWILGEHGNS SAPMYSTWTV GGAYVSDLNT SMGSANDVDN WQGIYERMRE GGATVNSFKG YTNWAVALSA

161 TDIINTIIHD TRKVHAVTVC ANGYYGLKTD VYLSLPSVLC KNGILDIVQM DVPQSEWEKL NASAEYLYSI QKKISL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.VIGSGC(+57.02)NLDSAR.L	Y	61.65	1247.5928	173.8	624.9121	2	27.64	2149	1	62	73	Carbamidomethylation
total 1 peptides												

tr|A0A0L7LHX0|A0A0L7LHX0_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADKLKGELM DLQHGSAFLR HAKITASSDY SVSAGSAICV VTAGVRQKEG DPDTILLIAS NPVDILTYVA WKISGLPKHR C Carba

86
C

81 **VIGSGCNLDS AR**FRYLLSEK LGIATTSVHG YIIGEHGDTS VRLADLNPKM GADNDPENWK ETHVQVVQSA YQVIKMKGYT

C

161 SWAIGLSIAE LCGAILSNAN SVHPVSTFLK GEHGIAEEVF LSLPCVLGRC GVTDVIRQPL TDSELAQLSK SAELMAKVQK

241 GIKF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIGSGC(+57.02)NLDSAR.F	Y	61.65	1247.5928	173.8	624.9121	2	27.64	2149	1	81	92	Carbamidomethylation
total 1 peptides												

tr|A0A0P6CBY2|A0A0P6CBY2_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MATLKDQLIV NLLKEEQAPQ NKITVVGVGA VGMACAISIL MKDLADELAL VDVMEDKLKG EMMDLQHGSL FLKTPKIVSS C Carba

81 KDYCVTANSK LVIITAGARQ QEGESRLNLV QRNVNIFKFI IPNIVKYSPH CKLLIVSNPV DILTYVAWKI SGFPKNR**VIG**

163
C

161 **SGCNLDSAR**F RYLMGERLGV HALSCHGWVL GEHGDSSVPV WSGVNVAGVS LKSLNPELGT DADKEQWKEV HKQVVDSAYE

C

241 VIKLKGYTSW AIGLSVADLA ESIMKNLRRV HPIS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VIGSGC(+57.02)NLDSAR.F	Y	61.65	1247.5928	173.8	624.9121	2	27.64	2149	1	158	169	Carbamidomethylation
total 1 peptides												

tr|A0A0K8RPB2|A0A0K8RPB2_IXORI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QWYHARALRS VLRGVLGSLK CCGTPLSSVS SAAPTSTSCL RSVSLTDLLV FPYKSKKMET EQPEETSPTL KPNGEFGKRP

81 AEDMEEEQAF KRSRNTDEMV ELRILLQSK**N AGAVIGK**GGK NIKALR**TDYN ASVSVPDSSG PER**ILSISAD IETIGEILKK

161 IIPTLGRGPA VAITHCNQPA PARI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TDYNASVSVPDSSGPER.I	Y	40.60	1779.7911	-141.7	890.7767	2	29.41	2346	1	127	143	
K.NAGAVIGK.G	Y	33.20	728.4181	-24.1	729.4078	1	24.61	1815	1	110	117	
total 2 peptides												

tr|H8WUA0|H8WUA0_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KPAIRRLARR GGVKR**ISGLI YEETR**GVLKV FLENVIRDAV TYTEHAKXKT VTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.ISGLIYEETR.G	Y	42.76	1179.6135	160.1	590.9084	2	32.09	2647	1	16	25	
total 1 peptides												

tr|A0A1B0CQK0|A0A1B0CQK0_LUTLO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIMNSFVND IFERIAAEAS RLAHYNKRST ITSREIQTAV RLLLPGELAK HAVSEGTKAV TKYTSSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HAVSEGTK.A	Y	41.03	827.4137	818.6	415.0528	2	2.23	160	1	51	58	
total 1 peptides												

tr|A0A0A9YXM3|A0A0A9YXM3_LYGHE

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 MNTAYYSIGI GVKRVLERGA WRGEPRVVRM LSYSYRCKKL RPWTMMGFGI PFLGGLGGGG DAHGKFKALD VQMLATDGAD C Carba
81 KSKSGVGNLE TPTMGTEPIE KDRKFVTGGN FKMNGSKKEL ETIIGHLSKA KLDPNVEVFV SPPAVYMEHT KKLLPKNIAL
161 AAQNCYMKEK GPFTGEISPG MIKDVGGTWV ILGHSERRVL FGESDNLIGE KICRALHDGL KVVACIGESL KERESGQAEE
241 VILDQLDTIA SSCCGSWANI VIAYEPVWAI GTGKVATPEQ AQEMHCVIRS WIKDNLSECA SDVVRIIYGG SVTKDNCREL
C
321 AKMPDIDGFL VGGASIKEEF VDIINVLKDY NDQVKSKESA AAKAAKKDDK KPKKEDKKAK K

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTKDNC(+57.02).R	Y	38.71	1325.6285	42.5	663.8497	2	29.18	2321	1	306	317	Carbamidomethylation
total 1 peptides												

tr|A0A034WXL0|A0A034WXL0_RHIMP

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 KIEDVEDDDE SADKDKKKKK KIKEKYSEDE ELNKTKPIWM RNPDDISQEE YGEFYKSLTN DWEDHLAVKH FSVEGQLEFR
81 ALLFVPKRAP FDLFENRKQK NNIKLYVRRV FIMDNCEDLI PEYLNFIKGV VDSEDLPLNI SREMLQQNKI LKVIRKNLVK
161 KCLELFDSIA EDRDMYKKFY EQFSKNIKLG IHEDSQNRKK LAEFLRYYTS ASGDEMCSLK DYASRMKENQ KHIYFITGES
241 KDQVANSAFV ERVRERGLEV IYMIEPIDEY CVQQLKEYDG KTLVSVTKEG LELPEDEAEK KRQEENKTKF ENLCKVMKDI

321 LDKKVEKVIV SNRLVKSPCC IVTSQYGWTA NMERIMKAQA LRDSSTMGYM AAKKHLEVNP DHPIMENLRV KADADRNDKA
401 VKDLVMLLFE TALLCSGFAL EDPQLHADRI YRMIKLGLGI DEDEVAGAGD NTSTGPTADE MPPLEGDDED ASRMEEVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	242	252	
total 1 peptides												

tr|A0A023FKD7|A0A023FKD7_9ACAR

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 GTVLLVPVSC AGSKCHVKMP EEARMEESGE VETFAFQAEI AQLMSLIINT FYSNKEIFLR ELISNSSDAL DKIRYESLTD
81 PSKLDAQKEL FIKIIPNRDD RTLTIIDTGI GMTKADLINN LGTIAKSGTK AFMEALQAGA DISMIGQFGV GFYSAYLVAD
161 KVTVTSKHND DEQYTWESSA GGSFTIRTDN TEPLGRGTKI VLHLKEDQTE YLEERRVKDV VKKHSQFIGY PIRLLVQKER
241 EKEVSDDEEE EKEEKAEEEK PDEEGKPKIE DVEDDDESEN KDKKKKKKIK EKYSEDEELN KTKPIWMRNP DDISQEEYGE
321 FYKSLTNDWE DHLAVKHFSV EGQLEFRALL FVPKRAPFDL FENRKQKNNI KLYVRRVFIM DNCEDLIPEY LNFIKGVVDS
401 EDLPLNISRE MLQQNKILKV IRKNLVKKCL ELFDSIAEDR DMYKKFYEQF SKNIKLGIHE DSQNRKKLAE FLRYYTSASG
481 DETCSLKDYA SRMKENQKHI YFITGESKDQ VANSAFVERV RERGLEVIYM IEPIDEYCVQ QLKEYDGKTL VSVTKEGLEL

561 PEDEAEKKRQ EENKAKFENL CKVMKDILDK KVEKVIVSNR LVKSPCCIVT SQYGWTANME RIMKAQALRD SSTMGYMAAK
641 KHLEVNPDHP VMETLRQKAD ADRNDKAVKD LVMLLFETAL LCSGFALEDP QLHADRIYRM IKLGLGIDDD EVAGAGDTSA
721 APAADEMPPL EGDDEDASRM EEVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	509	519	
total 1 peptides												

tr|B5TGR4|B5TGR4_TRIVP

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| **Protein Coverage** | **Supporting Peptides** |

Protein Coverage:

1 MPEDVAMEQA ETFVFQAEIA QLMSLIVNTF YSNKEIFLRE LISNSSDALD KIRYESLTDP SRLESGKELF IKIVPNKNDR
81 TLTIIDSGIG MTKADLVNNL GTIAKSGTKA FMEALSAGAD ISMIGQFGVG FYSAFLVADT VTVVSKHNDD EQYLWESSAG
161 GSFTVKVDVG GEPLGRGTKI VMHMKEDMTE FLEERKIKEI VKKHSQFIGY PIKLLVEKER DKELSDDEAE EEEEKKEDKE
241 DKEEDKDTPK IEDVEDDEEG KEKKKKKKTV KEKYTEDEEL NKTKPIWTRN PEDITTEEYG EFYKSLTNDW EDHLAVKHFS
321 VEGQLEFKAL LFAPRRAPFD LFENKKKKNN IKLYVRRVFI MDNCEDLIPE YLNFMKGVVD SEDLPLNISR EMLQQNKILK
401 VIRKNLVKKC LDLFEELAED KENYKKFYEQ FSKNLKLGIH EDSQNRKKLS DLLRYQTSAS GDEVCSLKDY VARMKENQKH
481 IYYITGESK**D QVANSAFVER** VRKRGFEVLY VTEPIDEYVV QQMKDYDGKN LVSVTKEGLE LPEDEEEKKK REEDKAKFET

561 LCKVMKDILD KKVEKVVDSN RLVESPCCIV TSQYGWTANM ERIMKAQALR DSSTMDYMAA KKHLEINPDH PVMDALRVKA
641 EAEKNDKAVK DLVMSLFETA LLSSGFALED PQVRAARIYR MIKLGLGIDE DEPLLVEEEK PDSAMPAADG DTEDASRMEE
721 VD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	490	500	
total 1 peptides												

tr|A0A0P6CIM3|A0A0P6CIM3_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KNIKLGIHED SQNRKKLSEL LRYYTSASGD EMVSLKDYCT RMKENQKHIY FITGETK**DQV ANSAFVER**LR KHGLEVIYMI

81 EPIDEYCVQQ LKEFEGKTLV SVTKEGLELP EDEEEKKKQE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.L	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	58	68	
total 1 peptides												

tr|A0A1P8LG21|A0A1P8LG21_9CUCU back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DHLAVKHFSV EGQLEFRALL FVPRRMPFDL FENKKRKNNI KLYVRRVFIM DNCEEIIPEY LNFIKGVVDS EDLPLNISRE
81 MLQQNKILKV IRKNLVKKCL ELFEELSEDK DGYKKFYEQF SKNLKLGIHE DSQNRTKIAD LLRFTTSASG DEACALKEYV
161 SRMKENQKSI YYITGESK**DQ VANSAFVER**V KKRGFEVESS T

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	179	189	
total 1 peptides												

tr|E2ILN7|E2ILN7_9CUCU back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WEDHFAVKHF SVEGQLEFRA LLFVPRRMPF DLFENKKRKN NIKLYVRRVF IMDNCEELIP EYLNFIKGVV DSEDLPLNIS
81 REMLQQNKIL KVIRKNLVKK CLELFEELTE CKDSFKKFYE QFSKNIKLGI HEDSANRSKL ADPLRYHTSA SGDEVCSLKD
161 YVSRMKQNQK NIYYIAGESK **DQVANSAFVE R**VKKRGFEVV YMTEPIDEYV VQQLKEYDGK TLVSVTKEGL ELPEDEDEKK

241 KREEDKAKFE GLCKVMKSIL DNKVEKVVVS NRLVESPCCI VTSQYGWTAN M

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	181	191	
total 1 peptides												

tr|A0A087UN67|A0A087UN67_9ARAC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MQEDYDDAET FAFQAEIAQL MSLIINTFYS NKEIFLRELI SNSSDALDKI RYESLTDPSK LDSCKDLYIK IIPNKEDRTL
 81 TIIDTGIGMT KADLVNNLGT IAKSGTKAFM EALQAGADIS MIGQFGVGFY SAYLVADKVT VTSKHNDDEQ YTWESSAGGS
161 FIVRPDHGEP LGRGTKIVLY LKDDQQEYVE ERRIKEVIKK HSQFIGYPIK LVVQKEREKE VSDDEAEEEK DEEKKEEEDE
241 KPKIEDVGED EDEDKEKDKK KKKKIKEKYT EDEELNKTKP IWMRNPDDIS QEEYGEFYKS LTNDWEDHLA VKHFSVEGQL
321 EFRALLFVPK RAPFDLFENR KQKNNIKLYV RRVFIMDNCE DLIPDYLNFI KGVVDSEDLP LNISREMLQQ NKILKVIRKN
401 LVKKCLELFD EIAEDKDMYK KFYEQFSKNL KLGIHEDSTN RKKLAEFLRY YTSLSGDEYC SLKDYVSRMK ENQKSIYFIT
481 GESKDQVANS AFVERVRKRG FEVIYMTEPI DEYCVQQLKE YDGKTLVSVT KEGLELPEDE EEKKKREEDK AKFENLCKII

561 KDILDKRVEK VVVSNRLVTS PCCIVTSQYG WSANMERIMK AQALRDSSTM GYMAAKKHLE INPDHPIIEN LRQKAEVDKN
641 DKSVKDLVML LFETSLLCSG FALENPQTHA SRIYRMIKLG LGIDEEEIA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	485	495	
total 1 peptides												

tr|A0A0B4L0J0|A0A0B4L0J0_9CUCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MPEETQGDVE TFAFQAEIAQ LMSLIINTFY SNKEIFLREL ISNSSDALDK IRYESLTNPS KLESGKDLFI KIVPNKSEGT
 81 LTIIDTGIGM TKADLVNNLG TIAKSGTKAF MEALQAGADI SMIGQFGVGF YSAYLVADKV TVVSKHNDDE QYIWESSAGG
161 SFTIRPDHGE PLGRGTKIVL HIKEDQTEFL EEHKVKEVVK KHSQFIGYPI KMVVEKEREK ELSEDEAEEE KKEGEEEDKE
241 KPKIEDVGED EDEDKKKEDK KKKKTIKEKY TEDEELNKTK PIWTRNPDDI SQEEYGEFYK SLTNDWEDHL AVKHFSVEGQ
321 LEFRALLFVP RRVPFDLFEN KKRKNNIKLY VRRVFIMDNC EELIPEYLNF IKGVVDSEDL PLNISREMLQ QNKILKVIRK
401 NLVKKCLELF EELSEDKDGY KKFYEQFSKN LKLGIHEDSQ NRSKLADLLR YHTSASGDEA CSLKDYVSRM KENQKSIYFI
481 TGESKDQVAN SAFVERVKKR GFEVVYMTEP IDEYVVQQMK EYDGKALVSV TKEGLELPED EEEKKKREED KAKFEGLCKV

561 MKSILDNKVE KVVVSNRLVE SPCCIVTSQY GWTANMERIM KAQALRDTST MGYMAAKKHL EINPDHPIVE NLRQKAEADK
641 NDKAVKDLVI LLFETALLSS GFTLEEPQVH ASRIYRMIKL GLGIDEEEAM LTEEAPAADA PVEGGDAEDA SRMEEVD
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	486	496	
total 1 peptides												

tr|A0A1W4X044|A0A1W4X044_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MPEEQDVETF AFQAEIAQLM SLIINTFYSN KEIFLRELIS NSSDALDKIR YESLTDPSKL NSGKELYIKI IPNKSEGTLT
 81 IIDTGIGMTK ADLVNNLGTI AKSGTKAFME ALQAGADISM IGQFGVGFYS AYLVADKVTV VSKHNDDEQY IWESSAGGSF
161 TIRPDHGEPL GRGTKLVLHI KEDQTEFLEE HKIKEIVKKH SQFIGYPIKL QVEKEREKEL SDDEMEEEKK EEEEKKEEDK
241 PKVEDVGEDE EEDTDKEKKK KKKTIKEKYT EDEELNKTKP IWTRNPDDIS QEEYGEFYKS LTNDWEDHLA VKHFSVEGQL
321 EFRALLFVPR RAPFDLFENR KRKNNIKLYV RRVFIMDNCE ELIPEYLNFV RGVVDSEDLP LNISREMLQQ NKILKVIRKN
401 LVKKCLELFE ELAEDKDNYK KYYEQFSKNL KLGIHEDTQN RAKLADLLRY HTSASGDEAC SLKEYVSRMK PNQKQIYYIT
481 GESKDQVANS AFVERVKKRG FEVVYMTEPI DEYVVQQLKE YDGKQLVSVT KEGLELPEDE EEKKKREEAK AKFEGLCKVM

561 KSILDNKVEK VVVSNRLVDS PCCIVTSQYG WTANMERIMK AQALRDTSTM GYMAAKKHLE INPDHPIIEN LRQKAEADKN
641 DKAVKDLVIL LFETALLSSG FTLDEPQVHA SRIYRMIKLG LGIDEEEPMS TEETAEGADV PVPTEGESED ASRMEEVD
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	485	495	
total 1 peptides												

tr|A0A1Z2RU91|A0A1Z2RU91_HERIL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEETQEVET FAFQAEIAQL MSLIINTFYS NKEIFLRELI SNSSDALDKI RYESLTDPSK LDSGKELYIK IIPNKAAGTL

81 TIIDTGIGMT KADLVNNLGT IAKSGTKAFM EALQAGADIS MIGQFGVGFY SAYLVADKVT VTSKHNDDEQ YTWESAAGGS

161 FTVSNDHSEP LGRGTKIVLH IKEDQMEYLE EAKINSIVTK YSQFIRYPIK LLVKKEREKE VSDDEAEGED KEKEEKKEGE

241 GDEPKLEDVG EDEDADSADK KKKKKTVKVK YTEDEELNKT KPIWTRNADE ITKEEYGEFY KSLTNDWEDH LAVKHFSVEG

321 QLEFRALLFV PRRVPFDLFE NNKKRNNIKL YVRRVFIMDN CQDLIPDHLK FIKDVVDYED LSLNLSLEML QQNKFLKVIR

401 ENLVKKCLEL FERLAEDKAL YKKFYDQFSK NLKLGVHEDS RNRAKLADFL RFHTSASGDE YCSLNDYVSR MKENQKHIYF

481 ITGESK**DQVA NSAFVER**VKK RGFEVVYMTE PIDEYVIQHL KDYQGKSLVS VTKEGLELPE DEAEKKKREE DKAKFEGLCK

561 VMKSILDNKV EKVVVSNRLV DSPCCIVTSQ YDWFANMERI MKAQALRDSS TMGYMASKKH LEINPDHPII ENLRQKTEAD

641 KNDKSVKDLV ILLFETSLLS SGFSLDDPQV HASRIYRMIK LGLGIDEDEP MATEEAPAST NSEMPPLVDD SEDASHMEEV

721 D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	487	497	
total 1 peptides												

tr|H9B0B8|H9B0B8_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEDVAMEQG DVETFAFQAE IAQLMSLIIN TFYPNKEIFI RELISNSSDA LDKIRYESLT DPSKLDSCKD LHIKIIPNKN

81 DKTLTFIDSG IGMTKADLVN NLGTIAKSGT KAFMEALQAG ADISMIGQFG VGFYSAYLVA DKVTVVSKHN DDEQYIWESS

161 AGGSFTIRSD KGEPLGRGTK IILHIKEDQA EYLEESKIKE IVKKHSQFIG YPIKLLLEKE RDKELSEDED EDEKKDEEKE

241 EDKDKPKIED VGEDEDEGKP KEEKKKKKTV KEKYTDEEEL NKTKPIWTRN PDDITQEEYG EFYKSLTNDW EDHLAVKHFS

321 VEGQLEFRAL LFIPRRAPFD LFENKKRKNN IKLYVRRVFI MDNCEDLIPE YLNFIRDVVD SEDLPLNISR EMLQQNKILK

401 VIRKNLVKKC LELFEELAED KENYKKCYEQ FSKNLKLGIH EDSTNRKKIS DLLRYHTSAS GDEQCSLKEY VGRMKENQKH

481 IYYITGESR**D QVANSAFVER** VRKRGYEVIY MTEPIDEYVV QQLEEYDGKQ LVSVTKEGLE LPVDEDEKKK MEEDKTKYEN

561 LCKIMKDILD KRVEKVTVSN RLVDSPCCIV TSQYGWTANM ERIMKAQALR DTSTMGYMAA KKHLEINPDH SIMENLRLKA

641 EADKHDKSVK DLVMLLFETA LLSSGFSLED PGVHASRIHR MIKLGLGLDD DEMPVEEEKV DNDVPQLEGD AEEASRMEEV

721 D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	490	500	
total 1 peptides												

tr|A0A131Z059|A0A131Z059_RHIAP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEETRMDDS GEVETFAFQA EIAQLMSLII NTFYSNKEIF LRELISNSSD ALDKIRYESL TDPSKLDAQK ELFIKIIPNK

81 DDRTLTIIDT GIGMTKADLI NNLGTIAKSG TKAFMEALQA GADISMIGQF GVGFYSAYLV ADRVTVTSKH NDDEQYTWES

161 SAGGSFTIRT DNTEPLGRGT KIVLHLKEDQ AEYLEERRIK DVVKKHSQFI GYPIRLLVQK EREKEVSDDE EEEKEKEEKT

241 EEEKPDEEGK PKIEDVEDDD ESADKDKKKK KKIKEKYSED EELNKTKPIW MRNPDDISQE EYGEFYKSLT NDWEDHLAVK

321 HFSVEGQLEF RALLFVPKRA PFDLFENRKQ KNNIKLYVRR VFIMDNCEDL IPEYLNFIKG VVDSEDLPLN ISREMLQQNK

401 ILKVIRKNLV KKCLELFDSI AEDRDMYKKF YEQFSKNIKL GIHEDSQNRK KLAEFLRYYT SASGDEVCSL KDYTSRMKEN

481 QKHIYFITGE SK**DQVANSAF VER**VRERGLE VIYMIEPIDE YCVQQLKEYD GKTLVSVTKE GLELPEDEAE KKRQEENKAK

561 FENLCKVMKD ILDKKVEKVI VSNRLVKSPC CIVTSQYGWT ANMERIMKAQ ALRDSSTMGY MAAKKHLEVN PDHPIMENLR

641 VKADADRNDK AVKDLVMLLF ETALLCSGFA LEDPQLHADR IYRMIKLGLG IDEDEVAGAG DNTSAGPTAD EMPPLEGDDE

721 DASRMEEVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	493	503	
total 1 peptides												

tr|A0A224YTX2|A0A224YTX2_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEETRMDDS GEVETFAFQA EIAQLMSLII NTFYSNKEIF LRELISNSSD ALDKIRYESL TDPSKLDAQK ELFIKIIPNK
81 DDRTLTIIDT GIGMTKADLI NNLGTIAKSG TKAFMEALQA GADISMIGQF GVGFYSAYLV ADKVTVTSKH NDDEQYTWES
161 SAGGSFTIRT DNTEPLGRGT KIVLHLKEDQ AEYLEERRIK DVVKKHSQFI GYPIRLLVQK EREKEVSDDE EEEKEKEEKT
241 EEEKPDEEGK PKIEDVEDDD ESADKDKKKK KKIKEKYSED EELNKTKPIW MRNPDDISQE EYGEFYKSLT NDWEDHLAVK
321 HFSVEGQLEF RALLFVPKRA PFDLFENRKQ KNNIKLYVRR VFIMDNCEDL IPEYLNFIKG VVDSEDLPLN ISREMLQQNK
401 ILKVIRKNLV KKCLELFDSI AEDRDMYKKF YEQFSKNIKL GIHEDSQNRK KLAEFLRYYT SASGDEVCSL KDYTSRMKEN
481 QKHIYFITGE SK**DQVANSAF VER**VRERGLE VIYMIEPIDE YCVQQLKEYD GKTLVSVTKE GLELPEDEAE KKRQEENKAK
561 FENLCKVMKD ILDKKVEKVI VSNRLVKSPC CIVTSQYGWT ANMERIMKAQ ALRDSSTMGY MAAKKHLEVN PDHPIMENLR
641 VKADADRNDK AVKDLVMLLF ETALLCSGFA LEDPQLHADR IYRMIKLGLG IDEDEVAGAG DNTSAGPTAD EMPPLEGDDE
721 DASRMEEVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	493	503	
total 1 peptides												

tr|A0A0K8R8N9|A0A0K8R8N9_IXORI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEEVRMEDA AGEAETFAFQ AEIAQLMSLI INTFYSNKEI FLRELISNSS DALDKIRYES LTDPTKLDAQ KELFIKIIPN
81 RDDRTLTLID TGIGMTKADL INNLGTIAKS GTKAFMEALQ AGADISMIGQ FGVGFYSAYL VADKVTVTSK HNDDEQYTWE
161 SSAGGSFTIR TDNCEPLGRG TKIVLHLKED QTEYLEERRI KDVVKKHSQF IGYPIKLLVQ KEREKEVSDD EEEEEKEKKE
241 DKEKEDEAVD EEGKPKIEDV DDEEEDKDKK KKKKIKEKYS EDEELNKTKP IWMRNPDDIS QEEYGEFYKS LTNDWEDHLA
321 VKHFSVEGQL EFRALLFVPK RAPFDLFENR KQKNNIKLYV RRVFIMDNCE DLIPEYLNFV KGVVDSEDLP LNISREMLQQ
401 NKILKVIRKN LVKKCLELFD SVSEDKEMYK KFYEQFSKNI KLGIHEDSQN RKKLAEFLRY YTSASGDETC SLKDYVSRMK
481 ENQKHIYFIT GESK**DQVANS AFVER**VRERG LEVIYMIEPI DEYCVQQLKE YDGKTLVSVT KEGLELPEDE AEKKRQEENK
561 NKFENLCKLM KDILDKKVEK VIVSNRLVKS PCCIVTSQYG WTANMERIMK AQALRDSSTM GYMAAKKHLE VNPDHPVMET
641 LRQKADADRN DKAVKDLVML LFETALLCSG FALEDPQLHA DRIYRMIKLG LGIDEDEVAG AGDNTAAAPA GEDMPPLEGD
721 EEDASRMEEV D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	495	505	
total 1 peptides												

tr|B7QI01|B7QI01_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEEVRMEDA AGEAETFAFQ AEIAQLMSLI INTFYSNKEI FLRELISNSS DALDKIRYES LTDPTKLDAQ KELFIKIIPN
81 RDDRTLTLID TGIGMTKADL INNLGTIAKS GTKAFMEALQ AGADISMIGQ FGVGFYSAYL VADKVTVTSK HNDDEQYTWE
161 SSAGGSFTIR TDNCEPLGRG TKIVLHLKED QTEYLEERRI KDVVKKHSQF IGYPIKLLVQ KEREKEVSDD EEEEEKEKKE
241 DKEKEDEAVD EEGKPKIEDV DEEEEEKDKK KKKKIKEKYS EDEELNKTKP IWMRNPDDIS QEEYGEFYKS LTNDWEDHLA
321 VKHFSVEGQL EFRALLFVPK RAPFDLFENR KQKNNIKLYV RRVFIMDNCE DLIPEYLNFV KGVVDSEDLP LNISREMLQQ
401 NKILKVIRKN LVKKCLELFD SVSEDKEMYK KFYEQFSKNI KLGIHEDSQN RKKLAEFLRY YTSASGDETC SLKDYVSRMK
481 ENQKHIYFIT GESK**DQVANS AFVER**VRERG LEVIYMIEPI DEYCVQQLKE YDGKTLVSVT KEGLELPEDE AEKKRQELNK
561 NKFENLCKLM KDILDKKVEK VIVSNRLVKS PCCIVTSQYG WTANMERIMK AQALRDSSTM GYMAAKKHLE VNPDHPVMET
641 LRQKADADRN DKAVKDLVML LFETALLCSG FALEDPQLHA DRIYRMIKLG LGIDEDEVAG AGDNTAAAPA SEDMPPLEGD
721 EEDASRMEEV D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	495	505	
total 1 peptides												

tr|L7MEG0|L7MEG0_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KPAPAACTAD SSIRCSLSLV PVLSSGCKRR SLFKMPEETR MDDSGEVETF AFQAEIAQLM SLIINTFYSN KEIFLRELIS
81 NSSDALDKIR YESLTDPSKL DAQKELFIKI IPNKDDRTLT IIDTGIGMTK ADLINNLGTI AKSGTKAFME ALQAGADISM
161 IGQFGVGFYS AYLVADKVTV TSKHNDDEQY TWESSAGGSF TIRTDNTEPL GRGTKIVLHL KEDQAEYLEE RRIKDVVKKH
241 SQFIGYPIRL LVQKEREKEV SDDEEEEKEK EEKAEEEKPD EEGKPKIEDV EDDDESADKD KKKKKKIKEK YSEDEELNKT
321 KPIWMRNPDD ISQEEYGEFY KSLTNDWEDH LAVKHFSVEG QLEFRALLFV PKRAPFDLFE NRKQKNNIKL YVRRVFIMDN
401 CEDLIPEYLN FIKGVVDSED LPLNISREML QQNKILKVIR KNLVKKCLEL FDSIAEDRDM YKKFYEQFSK NIKLGIHEDS
481 QNRKKLAEFL RYYTSASGDE MCSLKDYTSR MKENQKHIYF ITGESK**DQVA NSAFVER**VRE RGLEVIYMIE PIDEYCVQQL

561 KEYDGKTLVS VTKEGLELPE DEAEKKRQEE NKAKFENLCK VMKDILDKKV EKVIVSNRLV KSPCCIVTSQ YGWTANMERI
641 MKAQALRDSS TMGYMAAKKH LEVNPDHPIM ENLRQKADAD RNDKAVKDLV MLLFETALLC SGFALEDPQL HADRIYRMIK
721 LGLGIDEDEV AGAGDNTSAG PTAEEMPPLE GDDEDASRME EVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DQVANSAFVER.V	Y	36.78	1234.5942	12.3	618.3120	2	29.14	2316	1	527	537	
total 1 peptides												

tr|A0A2A3EHN0|A0A2A3EHN0_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLNLCRQALI VNNQKVSTRC LGTIIPVSNT IEFPLENEPI LSYKKGSPER AELEKVLDKM SNECEEVPLV IGNEEIKTDL
81 CKYQVMPHNH KVKIAKYYWA TADLVKKAID VSVKAQREWE KYPFEKRLEI WLRAADLMAT KYRQQLNAAT MLGQSKTVIQ
161 AEIDSAAELI DFFRMHGYFA KEAMKYQPIS PNKETLNSMR YRGMDGFVAA VSPFNFTAIG GNLSYTPALM GNAVLWKPSD
241 TALLSNWWIF KICKEAGVPS GVVNFIPCEG PVFGDTITSS PYLSGINFTG SVPTFNRLWI QVGKNLGKYK NYPKLIGECG
321 GK**NYHFVHAS ADVESVVNGT IK**SAFEFNGQ KCSACSRMYV PESLWPQIKE GLLSIRDTLK IGDVRDFTVF TGAVIDAIAF

401 KRISSYIEHA KKSSNLEIIG GGKYDDSIGY FINPTIVVTK NPKDKIMTEE IFGPVLTIYV YKDSNLDETM KLVESSTPYA
481 LTGSIFSQDE KWARRALEEF KYTAGNFYVN DKSTGSVVGQ QPFGGSRMSG TNDKAGGPHY ALRWASPQNT YSDVITSLYY
561 TLQTEKYRFF WVVQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NYHFVHASADVESVVNGTIK.S	Y	34.98	2186.0757	485.7	730.0531	3	33.96	2856	1	323	342	
total 1 peptides												

tr|V9IL90|V9IL90_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLNLCRQALI VNNQKVSTRC LGTIIPVSNT IEFPLENEPI LSYKKGSPER AELEKVLDKM SNECEEVPLV IGNEEIKTDL
81 CKYQVMPHNH KVKIAKYYWA TADLVKKAID VSVKAQREWE KYPFEKRLEI WLRAADLMAT KYRQQLNAAT MLGQSKTVIQ
161 AEIDSAAELI DFFRMHGYFA KEAMKYQPIS PNKETLNSMR YRGMDGFVAA VSPFNFTAIG GNLSYTPALM GNAVLWKPSD
241 TALLSNWWIF KICKEAGVPS GVVNFIPCEG PVFGDTITSS PYLSGINFTG SVPTFNRLWI QVGKNLGKYK NYPKLIGECG
321 GK**NYHFVHAS ADVESVVNGT IK**SAFEFNGQ KCSACSRMYV PESLWPQIKE GLLSIRDTLK IGDVRDFTVF TGAVIDAIAF

401 KRISSYIEHA KKSSNLEIIG GGKYDDSIGY FINPTIVVTK NPKDKIMTEE IFGPVLTIYV YKDSNLDETM KLVESSTPYA
481 LTGSIFSQDE KWARRALEEF KYTAGNFYVN DKSTGSVVGQ QPFGGSRMSG TNDKAGGPHY ALRWASPQSI KETFVPLREH
561 DYAYMRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NYHFVHASADVESVVNGTIK.S	Y	34.98	2186.0757	485.7	730.0531	3	33.96	2856	1	323	342	
total 1 peptides												

tr|A0A088A1I8|A0A088A1I8_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLNLCRQALI VNNQKVSTRC LGTIIPVSNT IEFPLENEPV LSYKKGSPER AELEKVLNKM SNECEEVPLV IGNEEIKTDL
81 CKYQVMPHNH KVKIAKYYWA TADLVKKAID VSVKAQREWE KCPFEKRLEI WLRAADLMAT KYRQQLNAAT MLGQSKTVIQ
161 AEIDSAAELI DFFRMHGYFA KEAMKYQPIS PNKETLNSMR YRGMDGFVAA VSPFNFTAIG GNLSYTPALM GNAVLWKPSD
241 TALLSNWWIF KICKEAGVPP GVVNFIPCEG PVFGDTITAS PYLSGINFTG SVPTFNRLWI QVGKNLGKYK NYPKLIGECG
321 GK**NYHFVHAS ADVESVVNGT IK**SAFEFNGQ KCSACSRMYV PESLWPQIKE GLLSIRETLK IGDVRDFTVF TGAVIDAIAF

401 KRITSYIEHA KKSSNLEIIG GGEYDNSIGY FINPTIVITK NPKDKIMTEE IFGPVLTIYV YKDSNLDETM KLVESSTPYA
481 LTGSIFSQDE KWARRALEEF KYTAGNFYVN DKSTGSVVGQ QPFGGSRMSG TNDKAGGPHY ALRWASPQSI KETFVPLREH
561 DYAYMRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NYHFVHASADVESVVNGTIK.S	Y	34.98	2186.0757	485.7	730.0531	3	33.96	2856	1	323	342	
total 1 peptides												

tr|A0A0Q9XTW1|A0A0Q9XTW1_DROMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQKFARDNWV ARAAHENIET QHQKQCDGFL GNFLSKGLKS NQLIVNTDEK TLKPIARLKE PRDLFALPKD KDNDCSQQAP
81 RWPVECQVIG ERIIHIPYVP VQPEPLNVPT GNELKPRPVG EENGIVVFSY CPISAVNYGS THTKIKTEEK SSEDSDDSSD
161 SRNEFISVNR RMTLQSGKTH LNRVSKLFNR LDDHSTSNSQ DDDDDYNVSV DGKETREKPV IQSIIDAKKK RFETTTLQHS
241 TDGKIKGTSK VDDIWKNNSS EYKPASPHYV LSQFGKKVSK AIIKKIIDYD EKPSTGTSSL TSEKVQNKYA VTPFKLPKTN
321 IPRLEVAFQG NSQQSFEKVS HSRKCNMIGD RDEDINSSDD CSIEMNDIVN DDVISGCDGK VSVGRLVGGA DKCPRTSSSS
401 VSDSETLVGE ESMCRIASAP DKMPKDLPLI PAPLCTRAVT MAAAVAAVAR GRRRGFESIP GSNIGVPHMS TSINTSTYDQ
481 ANDRHNPELN NVTDRTTFQS QHISYDIPQM QFSRSSVGGA KYVSNCHPMN AEEYESLEFE SRFESGNLAK AVQITPTYYE
561 LYLRPDLYTS RSKQWFYFRV RHTRRNMLYR FSIVNLVKSD SLYNDGMRPV MYSTLGAKEK NEGWRRCGNN ISYYRNDDES
641 NNNTNEEDED NSSYTLTFTI EFEHDNDTVF FAHSYPYTYS DLQDYLMEIQ RHPVKSKFCK LRLLCRTLAG NNVYYLTVTA
721 PSNNDDTMRR KKSIVVSARV HPSETPSSWM MKGLMDFITG DSTVAKRLRH KFIFKLVPML NPDGVIVGNT RNSLTGKDLN
801 RQYRTVIRET YPSIWYTKAM IRRLIEECGV AMYCDMHAHS RKHNIFIYGC ENKRNPEKRL TEQVFPLMLH KNSADRFSFE
881 SCKFKIQRSK EGTGRIVVWM LGITNSYTIE ASFGGSSLGS RKGTHFNIQD YEHMGRAFCE TLLDYCDENP NKVKRHAKLF
961 KQIKKIRKRE KREQKALKLQ KMADQERLRS KIIERLMREG SSADEPLNIP LSDYSSDEGN CSSSSDNEGK HSITASDLEG
1041 PCCAPIRAPP SSPEIMHEIR KFRVRRMHKV MHVLDQIYFS PVLQRKFKAL ARLKRRRHKL GCKAVGSKRA TGGGGGPSSP
1121 NGNASERLIS SESPQITVKT ARQSPDSESS ESNGSQSSDL LTDASNEINQ TGKQSTRKRN KKKKHMPTEK CKTKATNRKM
1201 RIDRNLRLWL ANRRIFIFRR KKNRRQRIRN KPLKKRGEVI RTALDLPTTD PGSDLHFSTD DEELFPTGNV TFGAVAPLRH
1281 TLLQSELQRR YIEEIGDLVV QKPKPAHMPP ELIVTAPSKN CGPGGVKKLE VYKLIPSTAP EQQAQMQAQT SGTGARRTYS
1361 WHNLNQDSGR AKPSFFMNES KPDPKIQK**SP PRR**IPNNFIP LNLQRHGHSN HAEDLHVKLS IKKKIWAGAH GDSDVRPLGW

1441 YKGQSQAHAH MATVMATAAA TAALRSAEGS QARSMYTAAS NKEPLISAAE SKTGSATLPP AYVGAPRRSR KLEQVDLFNA
1521 CSEKLLLWQQ SHKKAQPSNT RLLGGTTTKL ENPQIFIRGR KPKKIIRTTG GNDAHSNVSG VTGKGKRKTS IIKLADTTQF
1601 VTRFSRTHTS TGGSATGNLQ QHQITQMQRL ILKTQSGSGS ESIQNASVSG IQNPGGRITS KFKTGGIVVT AVQQSLGSHA
1681 GGVNVSKRFP HTGGLPIKNS SNSLASDTQN MFQCRIENKQ VAGISLDTVN LVRKVKTKLK KRKSRTLAND ASTSAK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SPPRR.I	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1389	1393	
total 1 peptides												

tr|A0A0P5C1N7|A0A0P5C1N7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MTTQSYYKDR LGFDPNDPRE MSSLDPTLHG YEENLSKFKD ERDAIQKKTF TKWVNKHLRK IGRRVDDLFE DLRDGHNLVS
  81 LLEVLSGDHL PRERGQMRFH MLQNVQTSLD YLRYRKIKLV NIRAEDIVDS NPKLTLGLIW TIILHFQISD IMVGQDESLT
 161 AREALLRWAQ RTTAKYPGVR VKDFTSSWKD GLAFSAIIHR NRPDLVDWRS LKNRGIRDRL DSAFNVVERE YGVTRLLDPE
 241 DVDTPEPDEK SLITYISSLY DVFPNPPALH PLYDPETQRK YSDYRELSSS LHVWIRESTL LMQDRNFPNT LIEVKKLALE
 321 SNRFRTDEVP PRLREKQHIG RLYKDIEKFL EETEEKLEPE LRPDVLERNW NQLLLLHQER DAAIHKEMER LERLQRIAEK
 401 VHREAKQSDA RLDEVEARID EEAKRLDRLH PRDAMKNCEV LNAELASIEE TIKIMFTDVQ ALKDGRYNQT ADLHKRVQRI
 481 HQRWQSIRAV FQTRLVEVLP SLTSPDAGRS SRSSLEARLF ETNEHFRFLR ECSEWVRSKL TQMEKAAYGS DLPSVQIELE
 561 SHLKEHKSVD KFQSNVEKCI SNKIKFQSEE SAIYVHHVTI LQKSYTELTV TSKKRLSDLE MLQDFIQSAT TELIWLNEKE
 641 EIEISRDWSS KSLNVTEIER YYEALMSELE KREIQVSAVQ DRGEALVLQH HPASKCVEAY MTALSTQWKW LLQLTLCLET
 721 HLRHAAVYHN FFSEVEKCEQ WCILQDQLLN STYSQSEFTL DEGEKLLKEM QDLREDLSHY SSVVEALYER SREVVPLKQR
 801 RTSLRQPIAV TSICIYKQVE VAIGKDEVCK LVSNSSKTKW KVVTNNGVEC QVPSVCLLIP PPDPEAAEAA ERLKRQYDRC
 881 EALWLKKQMR MSQNMIFATI KVVKSWDLSQ FMAMGKDQRD AIRKALNEDA EKLLQQGDPN DPQLRRLQRE IDEVNQLFDE
 961 FERRAAMGNR PELSQRAIGD QLTTLLVQLE ESERTLISRI TAPLPRDLDQ LEQLVVEHKH FETELQLLQP ELESAKENVE
1041 ACPRKTPSMQ TKLDTCITKW NNIWQNSNLY IERLKGTEIV LNGLDESTKF VSRLEIQLAS CENMPSEPES LRKVHDDLVD
1121 MQSNIQMQQG VIDQLAEEAG TVRQLVVRSR TSVNATIRKH PDVDRLEAEV KTVITRWSNI CTQVVERLQS CETTFEHLER
1201 YSAMSQVNHT WIDATSETVS KMPPVENGVQ AKAQLDSTAK LYNGVAAKKP SMDEANILGA RLIREAKIYD IRLKSYRTAL
1281 EEFQPSWDGI VQTRRTSRGS ATAMEYVARD LDDLNGRYEE LVDALQRRLQ LLCDMAQQEL DEFEFDVGCL AERPVVHTYL
1361 NELHVCSNNS DNDESHDDAD MPSIPYSPKT SMSSSPPRRS SITTVYIDSE QQMSTRVSTT TLIQRRDSGS NGRMSAESSR

1441 RQSQSIVSSS MSSATSTTSS SMTQSLSNTP HFANRKTGQQ LTLTEAIQTG LLDVERGAFI DPLTGNALTL SEAASQGLVD
1521 STVASALTRP SLGLRNPRTG QGISLMQAIQ LGLYDASRGG FVHPQTREPV TAEEALLMGI LLREKQAMEE RYKLCDDGMA
1601 RLLVWISNIE AQLANQDTVR EDVAELKNQI NVIRGVRDDM ESHSRPVNAC LDQVRQIVSQ GGEYLSADEI NTMESKGQEL
1681 KKRYDTGTDQ TDKLLRKVSV ALDELHKFRT EISNFKTWIV KSNKLAEEKE RQLANLSRVQ ANAETTREFV SDVIAHQADL
1761 RFITMAAQKF VDESMEYLAV LNDFRDKLPQ RMRHIEPSEL LVKAEVVEVT EDYQTLMKRA NRLSDKMTDI NSKNKDYQEI
1841 VTKAKAWLKE VEPKATKIVS EPLGAEPKAV EDQLGRAKAL NNDVMANERL VNHTVQAATS LLTALDGDVS EVERSNLESV
1921 PADIQDRYRK LLNALTDKCQ FLDNALVQSQ GVQEALDSLA NWLSQAENQL KNMTKPTSLN KDRLDEQLRE HRVLVADIDS
2001 HRAGFESINE AAAALVANPD NARVARKIEA KMKDMNSRYE KLQDKVYKRG YVLEEIYKSL DTFTTSVTQF DDWYQQVWEI
2081 LDASDQEEAE QLSSRIEDIS QQKDQRRENF DNMLQIGRTL VVKKDIADAT PVREKIKTLE MQWKDLSTII EQSLKDGKAR
2161 TDQLHTYEKL RDQVLEWLTK NEGRVDALEP VAVDADILKR QTDELRPIMK EYRDYETTIS RVADLGTAYE NMSRPAGDTS
2241 RKPSIVSPSK RSSITTLRRS SQDSRRPSQD LRRQSQDLRT PSPNKVGMGA LPVNQLLSSV ASSGFSGRRS SQDFYGMEDS
2321 SVVQKQIADI YDRYGQLGSK LHDRKAELEL MTEEAKKHTD ALKTLAAFLD KVERQLPRDS AVPQTRDDAE KQLRSVKNVL
2401 EDMYDKQPQL DGLKTQVTEL LRRKSGVPGA DALQDQLVTV SGRWKDLQDR CKARSKFLED VKDFHDTHDQ LSAWLTAKDR
2481 MMSVLGPISS DPRLVHHQLQ QVQVLREEFK AHEPQVQHLE RLADLILEIA EPNSNDGRKV NDKVVSISAK WSDLIGRLEE
2561 RKQNLDAASG TSRQFYANLG QLQDALQKIS DNLEELAVEN VYPEEILKHL EDLQDQLESQ RPLIAGLETV GEQLCAVLSD
2641 ASSKAEVAQK LSQIDKMHAQ LQKKLDNRRA ELENLLKDNR EFEDQCGQLQ EWLGDCASLL VEALQVSADR DVLRRQLQHN
2721 EPAYKDVMDR EHEVIMMLDK GQELANQSPN KNEAKAFNKL LEKIRGDWNK VRQETVSRHR RLQTCMELCR KYDGSQEMFL
2801 PWLDQAEAKL NQMQPVAFKK SDLDAQVKDL QSFRNDISRH SATFETNRSL GESFLSACDV NKEGVKNELT ITKERWDQIN
2881 AAVLERSQSL EDIAQRLAEF IELLRDSQHA MQRCEDRLSS HDALGPAARD SRLLDRIRTL LDEAVQLEKG VDRVQQYAAG
2961 LVADAASHDS NASHIQDQAE DLARRYSELR AHLEDRCNML ETASVAVLQF NEHVKAVLGD LSTLETELDS MSPAGRDLDT
3041 LNNQLDQTHH FLAKLEARQT EVEAIATDGQ NLVSEGHAPD AQGLRDQLDS LRKQTTRLED RGKNRLDELE KTLVRVESFY
3121 DLHSNIMQHI DEASNEERAF KPIVGDVELV RQQQEEFRSF KQDLIIPLGQ NVEEANRSGQ GLVQSAANGV STTALESDLE
3201 KMNDRWNNLK EKLNDRERRL DVAFLQSGKF QEALQGLSKW LSDTEEMVAN QKPPSADYKV VKAQLQEQKF LKKLLLDRQQ
3281 SMSSLLDMGQ DIANHAHPEE QAEIEEQLQE LVARFDALTN GADDRMEALE KAMAVAKEFQ DKFSPIADWL EKMERKIKDM
3361 EIVPTDEEKI QQRIEEHDLL HDDILSKKPA FDSLTDIATN LMSLVGEEEA SVLADRLTEL TDRYGALVEN SEALGRLLSD
3441 AKTGLRHLVL SYEDLLAWME SMESKLFKYR ILSVHVEKLQ EQMEELMYLT EEVAGHQPQV ESVVDTGLEL MRHITNEEAL
3521 QLKEKLDSVQ RRYTDLTGRA DDLLKHAQET LPLVEQFHVS HNRLANWLLD AEDRLQALDS SSAASGGSAG LDVQESIIAR
3601 LESELSEVRP FLDMVNQSGP QLCQRCPGEG SAYIESLITR DNRRFDAICE QIQRKAERLH LSKQRSMEVV GDLDELLDWF
3681 RETEQQLRES EPPSSDPEVI RVQLKEHKVI GDEISTQKGR VRDILSAAQK VLRESPQTED SAFIREKMED LKETRDRVSE
3761 LSADRLSILE QALPLAEHFY EAHSDLSNWL GEIEEALSNL DDPAIRPEQI VRQQEGTKLL MAEVAEHKPL FDKLNKTGTT
3841 LAKLCIEEEG VKVHDILESD NARYAALRSG LRERQQALEE ALQETSQFSD KLDGMLAALA TAFEQVKSAE PVAAHPDKIQ
3921 EQMQENQSVV EDLEKRESAF EAVKRAADEV IVKNPSDPAV KDIEGKLKKL SKLWDTVVSA TGERGKSLEE ALAVAERFWE
4001 ELQAVMRALK ELQETLVTQE PPAVEPAKIH QQQATLQDIK TDIEHTKPEV EHCRQVGQEL INLCGEPDKP EVKKHIEELD
4081 SAWDNITALY AKREENLIDA MEKAMEYHDT LNSLAEFLEK AEKKFHDMRP LGTDIETVKE QIEQLKAFKA DVDPQMVKVE
4161 TLNRQAADLA DRSSPDQAAR LKEPLAKVNR RWEDLLRGVV DRQRELEHAL LRLGQFQHAL NELLVWIQRT DSTLDELKPV
4241 FGDPSVIEVE LAKLKVLIND IQAHQTSVDT LNDAGRQLVE TDKGSDDSNK TQQRLVLLNK KWGDLVEKAS SRQKELEDAL
4321 REAQQFTAEI QDLLLWLNDI DGALSMSKPV GGLPETASDQ LQRFMEVYHE LEKNRPLVES CLQRGAEYLK RSTDGAAVSL
4401 QHNLRTLKQR WDNVMNRAND KKIKLEIALK EATEFHDALQ AFIDWLTNAE KTLGGLKPAS RVMETVLSQI EEHKSFQKDI
4481 AAQREVMLSL DKKGTHLKYF SQKQDVILIK NLLISVQHRW ERVLSRAAER TRALDHAYKE AKEYHDSWHE LYSWLDEAEK
4561 GFDDAVLQLG KDPEKIKQLL AKHKEFQRTL GAKQPTYDGI VRLGKLVKDR APKTDEPTLK QMMSDLKAKW QSVCNKSVDR
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4641 QRKLEEGLLF SGQFKDAIQA LVDWLCKTNP AQMMEGPVHG DLDTVMALRE QHKNFEEELN SRLAQTKQVR KMAVDVMANA
4721 SEDDRAAIQK QVSELDVIWE NVSKAASTRS ANIDDALVQA ETLHKAVNML LEWLSDAEMK LRFAGALPDE EPETKQQLAD
4801 HHKFLEEVIK KETDKDDTLA LAQDILGKAH PDAVSVIRHW ITIIQARWEE VMAWANQREH RLNEHLRNLR EMASMLEELL
5041 EMLPRNPRAR QLWDRWRNVW MMAWDRQRRL HDKLNYLQEL EKVKNFSWDD WRRRFMKYMN NKKSRVTDLF RKMDKNNEGF
5121 IPREDFIEGI MKTKFPTSRM EMNAVANMFD RNNEGYIDWK EFLAALRPDW EERPTTEDEI IHDEVKRAVN QCTCRNRFKV
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.SPPRR.S	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1395	1399	
total 1 peptides												

tr|A0A1B6LCG7|A0A1B6LCG7_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MHCSRIEDGV EVFVQLGTLI VEGRLPAEGT DRGYKEGPHC PQTSTATTHS RAHQCDPSGF LCMRGERLRK HMSLLCNNAV
 81 PMCVEVLLCP VCHCGSERAQ SPEIANIPSS SDLLLEQWTV SVIHMSGEPC NMSVRGLFQA VRSQLHFSQL SAWLSSSKGT
161 RPINVCYRVT LPEQAFASQF SRPPQHHSFP PAAVGPNTQL KVSVNTLPRG EGLPEVKCAA CTPETNLRKR STGLEQPLLG
241 ESLLDPPGPS SSSRAHAGLC KWHTGSPPSP PRRRPSRQVM ARRCDKHTVA SLQILPGPVD DRMQTDCNQH GKHDCRC
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5521 TTPSQRGRTA SGSSGAGTPG TPGMMRREGT SDSMTGIARK TTSTGIRKPS GTPLSRPSPK
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SPPRR.R	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	269	273	
total 1 peptides												

tr|A0A0Q5VMA2|A0A0Q5VMA2_DROER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MMDRESLSEW AKDKPLSILQ LDPADRAVLR IADERDAIQK KTFTKWVNKH LKKHWKYAKT YTMLHVCVTT NGIPCCSQSA
  81 NRRVVDLFED LRDGHNLLSL LEVLSGEHLP REKGKMRFHM LQNAQMALDF LRYKKIKLVN IRAEDIVDGN PKLTLGLIWT
 161 IILHFQISDI VVGKEDNVSA REALLRWARR STARYPGVRV NDFTSSWRDG LAFSALVHRN RPDLLDWRKA RNDRPRERLE
 241 TAFHIVEKEY GVTRLLDPED VDTNEPDEKS LITYISSLYD VFPEPPSIHP LFDMESQRRV HEYRDLAQQF IYWCREKTAY
 321 LQERSFPPTL IEMKRLLSDL QRFRSEEVSA RKREKSKLIQ IYKELERYFE TVGEVDVEAE LRPDAIEKAW YRMNTALQDR
 401 EVILQQEIER LERLQRLADK VQREIKHVDQ KLSDLETRIG EEGRRIERLH PVDAKSIVEA LETEIRHLEE PIQDMNQDCH
 481 VLNEGRYPHV SELHKKVNKL HQRWAQLRTN FHTNLVQKLS GLKYPVHETT VTRQTRMVVE SRQIDTNPHF RDLQEHIEWC
 561 QNKLKQLLAA DYGSDLPSVK EELDRQQHEH KIIDQFHTKI LNDERQQTKF SGDELALYQQ RLNQLQKVYA ELLSTSTKRL
 641 SDLDSLQHFL GQASAELQWL NEKEQVEITR DWADKQLDLP SVHTYYENLM SELEKREMHF ATILDRGEAL LNQQHPASKC
 721 IEAHLTALQQ QWAWLLQLTL CLEVHLKHAT EYHQFFGEIK DAEQWLAKRD EILNSKFSQS DFGLDQGETL LRGMQDLREE
 801 LNAFGETVAT LQRRAQTVVP LNKRRQPVNR QGPVQAICAY KQQGQLQIEK GETVTLLDNS GRVKWRVRTA KGQEGPIPGA
 881 CLLLPPPDQE AIDAAERLKR LFDRSVALWQ KKHLRLRQNM IFATIRVVKG WDFDQFLAMG PEQRTAIRRA LNDDADKLLS
 961 EGDPNDPQLR RLRREMDEVN RLFDEFEKRA RAEEESKQAS RIFTEECIAI KSKLEDMARE LDQIILAPLP RDLDSLEHVL
1041 EIHSDYERRL HLLEPELKHL QETFRTIALK TPVLKKSLDN LMELWKELNT QSGLHKDRLK LLEASLAGLE DNEHVISELE
1121 NELARHQDLP STAEGLQQVF KQLNHMQDII TQQQPQMDKM NDAADQLGRM GVPTKVLGDL KRLHSNVERL NTRWSAVCNQ
1201 LGERMRSCET AIGLMKNLQS SVQVEESWVD GTTEGLSAMP TATSAYELDK LLGAAIERKP KIENVNVAGG RLIREAKIYD
1281 SKCLRFVDWL VEARPSFSPP RRDLRPADSD PGATQYYSQR LDNLNTKYDR LLEQLSQRLK TAIEVNGSDG LQYAESLQKP

1361 LKTFRVDFSA GSVPTGDGYA ARPEDLYTTT YSTTQISSTK TTKSSTKSVY SSDGLDAASQ EVSTASLPQS QIQFNEIRTL
1441 KRAQQLGGHS VLDIAGIRDP STGRVLTIGE AIQLRILDVR TGEMLVGDRR ITLEQASDQG LIDLQLAKQL LEPGAGRDAN
1521 GRELSLLEVI QREISEAESG YETAEKRIKQ AVFEKFNMCE ENVNDLLKWV TTVEQKISSV GGPREKIDEL RNQINALKQI
1601 KDEIESQQRP VATCLEQIRQ IVLTGGDVLS APEVTTLENS GRELRSRVDR VNDRTVRLLR RLEAGRDELT KLRSELDVFS
1681 DWLQVARRTL EDKERSLSDL TRLPSQADSV REFVSDVIGH QADLRFITMA AQKFVDESKE FLAILNDFRT SLPERLPHVE
1761 PLSSAESPIR QEVSLVSAQY KDLLNRVNAL QDRVSGLGGR QREYQDALDK ANEWLRSVHP RVSRIISEPI AGDPKGVQDQ
1841 MNEAKALHNE MLSSGRLVDN AQQALDNLLR SLGGQLSPME INQLELPIAD LKNNYQQLLD NLGEHCKTLD KTLVQSQGVQ
1921 DALDSLVGWV NQAEDKFKLN LRPASLIKER LQEQIREHKV LLADLQSHQA SIDSVQVSAK HLLGSASNAR IAKKVESNLN
2001 DVTVKFEKLY EKANKRGEFL DDVYNRLSRY LDEISTVEQR MANLQEALDS RETSLLSTEE LARRMNELSR DKDQLAPQFE
2081 DCVRSGKDLI SLRDVTDTGV LRDRIKALES QWRNINISID ERAKLSKQKA EQQLAYEGLK DQVLSWLAST EARVNGLPPV
2161 AIDLDRIKQQ HDELKPICKD YRDYAPTIDK INDIGAQYDA LIRPESPARK RSTYSPIKRA SPLRRMSGDA RSPSPTKGGI
2241 LSPLSTGSSG FGSRRSSQDG FQLSELSPVQ QQLSEINNRY GLIGVRLNDR QHELDNLNEE LRKQYENLKG LAQFLERIQR
2321 QLPKESISNK DEAERCIKQA RKILEDMYEK QSLLDTTKAQ VKDILRRKSD VPGAEQLRQE NDSIQEKWKN LNDICKNRIA
2401 FSEKLRDFLD THGNLKSWLD SKERMLTVLG PISSDPRMVQ SQVQQVQVLR EEFRTQQPQL KHFQELGHDV VDHLAGTPDA
2481 QAVENKLKDI LGKWDDLVGK LDDRANSLGG AADSSKEFDA AVNRLREALQ NISDNLDALP TDGDHQENLR KIENLERQLE
2561 GQRPLLADVE HSATTLCNIL GDPASRADVN SRVAALEKQY LALQKKLDTK KAETEASLRD GRHFAENCSK TLGWLGGELS
2641 NLTDRLLVSA HKPTLQHQID THEPIYREVM AREHEVIMLI NKGKDLTDRQ QDRGVKRDLD RIQQQWEKLR REAVDRHTRL
2721 QTCMEHCKKY SQTSETFLAW LRTAEDKLAD LTPGVLSKAK LETRLRDLQT FRSEVWKHSG EFENTKGLGE TFLTSCDIDK
2801 EPIKAELQDI RDRWERLNND LIARAHEIEN CSRRLGDFND ELRNLDHSLG RCEDRLAAHD ALGGAAKDPK LLERVKAIRE
2881 ELTNLSKPLQ SLKALAKDIS AEARAAGGDA DHLTSEVDGL ADRMSELQGR LDDRCGELQS AATAVSQFNE QMKSLGIDLN
2961 DLETEIEKLS PPGREIKIVQ VQIDDVGKIQ NKLDRLVGRL EDAERAADVL VDAGFAADTT QTREQISTLR KTLGRLDNRV
3041 RDHEDNLQAT LKALREFYDN QSQTLDDIQD VSDEFKRMKP VGSELDQIRR QQEDFRNFRE RKVEPLAINV DKVNVAGRDL
3121 VRSAGSGVST TAIEKDLEKL NDRWNDLKER MNERDRRLDV ALLQSGKFQE ALAGLSKWLS DTEEMVANQK PPSSDYKVVK
3201 AQLQEQKFLK KMLLDRQNSM GSLANLGKEV ANHCEPAERA SIEKQLNDLM KRFDALTDGA EQRELDLEEA MEVAKRFHDK
3281 ISPLELWLDN TERSVKAMEL IPTDEEKIQQ RIREHDRLHD EILGKKPDFS DLADVAAQLM HLVSDEEAVN LGEKVRGVTE
3361 RYTGLVDASD NIGALLAESR QGLRHLVLSY QDLVAWMESM EAELKRFKSV PVYAEKLLEQ MDHLLELNEN IAGHASNVES
3441 TVESGAELMK HISNDEAIQL KDKLDSLQRR YGDLTNRGGD LLKSAQNALP LVQQFHEAHN RLVEWMQSAE AALAPSEPRQ
3521 ADVLRLEGEL ADMRPILDSI NQVGPQLCQL SPGEGAATIE SIVTRDNRRF DSIVEQIQRK AERLHLSNQR AKEVTGDIDE
3601 LLEWFREMDT TLREADLPAM EPKLVRAQLQ EHRSINDDIS SQKGRVRDVT AASKKVLRES PQSENTATLR EKLDDLKEIV
3681 DTVAQLCSER LGILEQALPL SEHFADSHQG LTAWLDDMEQ QISRLSMPAL RPDQITLQQD KNERLLQSIA EHKPLLDKLN
3761 KTGEALGALV ADDDSAKINE ILDTDNARYA ALRLELRERQ QALESALQES SQFSDKLEGM LRALANTVDQ VNQLDPLSAL
3841 PQKIREQIED NDALMDDLDK RQDAFSAVQR AANDVIAKAG NKADPAVRDI KAKLEKLNNL WNDVQNATKK RGSSLDDILS
3921 VAEPFWKQLN SVMKTLKDLE ETLSCQEPPA AQPQDIKKQQ VALQEIRHEI DQTKPEVEQV RRHGSNLMNM CGEPDKPEVK
4001 KHIEDLDNAW DNITALYAKR EENLIDAMEK AMEFHETLQN LLKFLTKAED KFAHLGAVGS DIDAVKRQIE QLKSFKDEVD
4081 PHMVEVEALN RQAVELTERT SPEQAASIRE PLSVVNRRWE ALLRGMVDRQ KQLEHALLHL GQFQHALNEL LVWINKTDST
4161 LDQLKPIPGD PQLLEVELAK LKVLANDIQA HQNSVDTLND AGRQLIETEK GSVEASTTQE KLRKLNNEWK QLLQKASDRQ
4241 HELEEALREA HGYIAEVQDI LGWLGDVDAV IGASKPVGGL PETATEQLER FMEVYNELDE NRPKVETIQA QGQEYIKRQN
4321 QMKVSSSNLQ HTLRTLKQRW DAVVSRASDK KIKLEIALKE ATEFHDTLQA FVEWLTQAEK LLSNAEPVSR VLETIQAQME
4401 EHKVLQKDVS THREAMLLLD KKGTHLKYFS QKQDVILIKN LLVSVQHRWE RVVSKAAERT RALDHGYKEA REFNDAWSGM
4481 MQYLQETEQV LDQIIEEATA SKEPQKIKKY IGKLKETHRQ LGAKQSAYDG TMRTGKNLLE RAPKGDRPVL DKMLIELKEQ
4561 WTRVWSKSID RQRKLEEALL LSGQESDALG ELLEWLKKAK SRLNENGPVH GDLETVQGLC EHHKHIEQDL QKRAAQMQGV
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4641 EKTGRDLERS GNNPEVGRQL DEMQSIWEEV KSAVAKRGER LQVALVDAEK LNARVQALFD WLDHAEHKLR YAKNAPDDEK
4721 VSREMMDIHM EFMKDLRVRE REKSEIPEYA EDIINKAYPD AIPIIKNWLS IIQQRWEEVR QWAINRESKL EQHLQSLKDL
4801 DDTIEELLAW LSGLEGTLLN LKHEQLPDEI PPVEKLIEDH KEFMENTARR QNEVDRACKP RQLPPGARKP SRSGKTPVRG
5041 LEMKAVADLF DRNGEGLIDW QEFIAALRPD WQERKPANDS DKIHDEVKRL VMLCTCRQKF RVFQVGEGKY RFGDSQKLRL
5121 VRILRSTVMV RVGGGWVALD EFLQKNDPCR AKGRTNIELR EQFILADGVS QSMAAFTPRR STPNAAATAS SSPHAHNGGS
5201 SNLPPYMSGQ GPIIKVRERS VRSIPMSRPS RSSLSASTPD SLSDNEGSHG GPSGRYTPRK VTYTSTRTGL TPGGSRAGSK
5281 PNSRPLSRQG SKPPSRHGST LSLDSTDDHT PSRIPQRKPS TGSTASGATP RPARLSVTTI TTPGSRLNGT STITRKTASG
5361 SASPAPTRRN ISGSSTPSGM QTPRKSSAEP TFSSTMRRTS RGTTPTEKRE PFRL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1298	1302	
total 1 peptides												

tr|A0A1I8PMC0|A0A1I8PMC0_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MTSHSYYKNR LGFDPNEAQY ESSTTTTRRS GSRSSSSHNQ NVNSHHLHAS QHYEHSHTQH RSQHASPTHH SSASPARISI
  81 SPGGASLDHY ADISPAKKAK HSPASASSSI QQPLGGYEDA LTQFKDERDA IQKKTFTKWV NKHLKKANRR VEDLFEDLRD
 161 GHNLLSLLEV LSGEHLPREK GKMRFHMLQN AQMALDFLRY KKIKLVNIRA EDIVDGNPKL TLGLIWTIIL HFQISDIVVG
 241 KEDNVSAREA LLRWARRSTA RYPGVRVNDF TSSWRDGLAF SALVHRNRPD LLDWRKARND RPRERLENAF HIVEKEYGVT
 321 RLLDPEDVDT NEPDEKSLIT YISSLYDVFP EPPSIHPLYD MESQRRVHEY RDLAKQFISW CREKTAYLQD RSFPPNLIEL
 401 KRLLGDLHSF GSDEVSARKR EKSKLVQIYK ELERYFEIVG EIDVEAELRP EAIEKAWYRM QTALQDRDMI LQQEIERLER
 481 LQRLADKVQR EIKHVDMKIT DLETRITEEA RHIETLHPVN AKNIVESLET EIRHLEEPIQ EMNQDCHILN EGRYTHAAEL
 561 HKKVNKLHQR WAQLRTTFHT VLVQKLSGLK YPVHEKTTTR QQRVVVESRQ IETNPYFRDL QEHIEWCQNK LKQLLAADYG
 641 SDLPSVKKEL DRQQHEHKDI DQFHSKILKD EHQQTKFSGD ELTLYQQRLN QLQKVYAELL STSTKRLSDL DTLQHFLAQA
 721 SAELQWLNEK EQIEITRDWA DKNLDLSSVH RYYENLMSEL EKRELHFGTI LDRGETLLNQ HHPASKCIEA HLTALQQQWA
 801 WLLQLTLCLE VHLKHATEYH QFFAEIKDAE QWLSKRDEIL NSEYSKSEFG LDQGETLLRG MQDLREELNA FGDTVATLQL
 881 RAQTIVPLNK RRQPVNRQSP VQAICAYNQQ GQIPVEKGET CTLMDNSGRV KWRVRTTKGQ EGLVPSACLL MPPPDKEAID
 961 AAERLKRLFD RSVSLWQKKH LRLRQNMIFA TIRVVKDWDF EQFLAMGPEQ RTAIRRALND DADKLLSEGD PNDPQLRRLK
1041 REMDEVNRLF DEFEKRARAE EESKQASRIF TEECITIKGK LEDMARELEQ IISAPLPRDL DSLEHVLEIH SDYERRLQLL
1121 EPELQHLQET FRTIALKTPA LKKSLDNLMI LWKELNTLSN LHKDRLKLLE ASLAGLEDNE HFISEIENQL AKHQDLPSTP
1201 ERLEMVFKQL THMQDLITQQ QPQMDKMTDA ADQLGRMGVP TKVLGDLKRL HANVERLNTR WSSICNQLAE RMRSCENAIG
1281 LMKNLQSSVQ VEESWVDGTT ERLSAMPTAT SAYELDKLLG AAIERKPKIE NVNLAGGKLI REAKIYDGKC MRFIDWLLEV
1361 RPSFSPPRRD LRPADSDPGA TQYYSQRLDI LNTKYDRLLE QLSQRLKTAI EVNGSDGLQY AESLQKPLKT FRVDFSNANN

1441 VPTGEGYVAR DADLFTTTYS TTQFSTTKTT KSVYDATDYV HTTTTTNGTA GPVPATTSKQ SQIQFNEIHS LKRVQTKNEN
1521 VGTTTTTEFV GGTNVKHLLD MTGIRDPRTG RVLTIGDAIQ MRLLDVRTGE MLVGDKRISL EEAVKQGLID AKLAHQLLQP
1601 GAARDGRDGR ELSLLEVIQR EITEAETGYE TAEKRIKVTV DESPDAENPK NIADAISAGN VDTKTGLYRV KSGKTITLAE
1681 AYERGYLIRH ESVTIKSNAL CLSDAIAHGL VDTAGWIADR NSGDKFRLDS AIANQLIDPN IREVVDAKRD IKITLTEALN
1761 SGILNPKTGR YWNEVTKEKL TFIEAKNRQL IVKPYTLKDI CDLNLLDKQS MITSPMRREK LSIMQAIESG VLDGNNLKCI
1841 TKRKGELVTL QEAIADGIVL PAESRYRDYM TSEVLSIPEA VERGLISSVS QKSIFDIDGF KDMRSNDFVS FNVALSRGIL
1921 RRKSNGFALE TSRDTQVPLE VALNEGLIRP EVYEMFNKGI GVHNASGKEL SVFDLCYHSL IDPKTGYLLD PKAEETVPLD
2001 LAIERKFITP EGALLLSSLL NITLTTETVT RTINRYVTIR ASSQEPLETT IVLTFTEALR QGFIDEERQL FKDPKTGNIY
2081 SVQQALSYGL LQPDANETVP EPTNRKKTKS TITIVTKQIV PESEPIKLNT QNFIEKSVEI PIAEEVRKPG KISTDFIQSE
2161 KTSYVQQNVR ERQIIEFPPG GWPLKDAIEQ QLFNPDTGVF HIKNTERAVT FEECINKYII NSLSVSVIDP RTGEKLSIRN
2241 AFERDIIDSY GSYTNTNDDV ETMRSAIGQG KIILEHVPST KTSAREQCIL RVSKINNLPE IVEISTPLLS GSSQKFVEVR
2321 TVQRELTSPE PLQIAPGAIY DPSTALVIFT HNGQTENIFD AARHGLIDES LIRIVDPQTK EVISISEALA RNIYDPQNGT
2401 ILTDDTYAVD ILTAIQKGLI VVAGAPLVAA EGALRTIRFV TDPRTGEQIP VEVAYERGIV SRDQLRKTKS VESDASEDKV
2481 VVLQKMRKMI LKPDDAFKKG IIDVVARDIL ENKDNFLGDN NEVLNITEAL QRGQIDGSKG KIADPQRNRF LNISEAVKER
2561 VIDPEETNHI LIPLAQSLSI PKLMEQGLVD TKTQTIVHPE SGYGLNIREA IVCDVLDQYS KLKRPIKCTL EEAIEKHIVD
2641 PDESTFNVNG KVLTLAQAVN ADIFEKTSDK VKPLVPIPPV GMTFPVVVEK GLLKPENVSV IHPESRKEIP LKKAIEEGFI
2721 MSIPYPPQAD AMEVHHAVQQ GLINIVDQTF RHPKDNGQAT PLRPALETGR LVVKPISDFV VTQQPVARTE IMETITAVHT
2801 VTTKTIELVQ GYVLISNNEV QNIKTGEVWT IEEAKAKGIL KEEETSKESR SVTGNKDNIE ELLQQPNTED QTTISERVIQ
2881 NTTKNKNLIV TQQGTIQMEG HPMPTPGQPM PGQETPKQDS KLSATLNNVK EAAKMGALGI VAAPVLAGGA LVSGIKQLVK
2961 TSTTTTTTTE FNDETQKVIS TSATLGAVET NDKFPRETAP SPHNPNGSHA SSSMTTTITS TVPQQPGITK DAPKPPTQDS
3041 AQSDDVLPHL KDSKTKATDV HTIDNLMKDT ENFINTTTAN FINQEKNVEG QHLPKTGVHS PADATRSLEG NDNLQVKPSD
3121 QITSALSHEE PNKKSKDRTP SDKDRTVDKD RPLQEASDNA TNKGVSSNVI ITTEMSATTT DPINEIVEVS ETTGQPKDRK
3201 PSSGDLESSK GNQTTTTTTT TITTSKITKG EGFEPSEGVP SLTEASLKGI VDDKHPQKYG VVTDFIKHET NVLHRPEESL
3281 ASPSGLKSQL VDGSLQSDKP ESDKPQLIGQ TTRTTTTTTI TTTTEQVGQF NAPLQPFSED VETDLESFGG DKSQQDSPNN
3361 KQGEKPKDGS LPANLLKSGQ TPPSSILTEE TTQKHPSTMD KSENDESQQF NNASTAPQVA SGEKSPVSAT DVSTIVKSTH
3441 GEDPQTFTPL DTKDKPSLAA RKSTDKLGDL TQPQNATDDP HRRVVDFIQA EKGDHTAGNV LQNVKDAAKF GAMALVGAPV
3521 LAGKAIVDAL KSEGKPSDEN ISATTTKTTT VTTISSTTTK PVDSTTISEY SSEGGPQRLT PPKTLALGDA ISQNLISPDE
3601 CKVVVDGEEQ DQSVSELLKE EQLSPLDEVQ VLDDKLVVLQ PMTYVIDAGD ELTPEHLSEL NIYDPENQYF IDPSTGMKIS
3681 FQTLVFDMNV FNPETILVKN FSTGKYETLT DALERPLLDR HTGHMVDPKT GKKIPFFECV NRNWIIRANP EKEKPAAIEN
3761 VIDPATGKVI LGDGRICSIV DAINNGLLDI QSISVRDPVS GEVIPLRMAI ELGVVDMQAG TVIDIQTLKE IPMEDAFKLG
3841 FLVPGARKPI SLEAAVRKGL YDPDTGKLYD SESDNQVDVQ KSIEIGLVDP KISLIVDSKS QKAIKLDCAI EDELVVAETG
3921 QVKDTKTNTL VPFNVGVEKK LVKTDSITWS LPEVLQREYY SPKTGKILNP TTGEEILLQQ AIELGFVEID SCLVKDDDKN
4001 SIVSGKQAAK EGLLDTVRGC LNSPNIKLDE AFVKGYLIST KKPLSLVDCL LRGLYDPETS KFTIDDKTVD LKTAITLKLI
4081 NADELVLLDP KTESIISLTE AIAKGYIDPV NGYVINPYTG TKLSLNEALE NRVLIPPKRK RSLPDAVYRG LYDPKTGEFS
4161 NTVTREKLST ERAIRRGILD PDSTIVSVAG EVIPFEKAAQ VGIVDSQRGT VRDDNDKEID FKEAFDRGVL LEAKKPLRLI
4241 EAVIKNVYDE SDGTFMDPKS GLKLSFAQAV DNHLLDEDSV QIRDFNTGLY KQLNLAHASE SGVIDGKNAK LVYNNQKITI
4321 KHAFDVGILM DTQAPLSLQR ALHQGLFDEK TGKLTDAKTG RKITLLESIR SFVINPQLPC YFDEINEQMH NLHETCRMGI
4401 INRREGVFRE PGSNTFISLN EALNLGLIVD IENASFGLYE LLAMRFYDMD TRKVIHPVTG RKFNLNEACV EDVVSLSSSL
4481 VKNHKTGKYI RLAQAIKENI IDDTNGCYNL SPTEQIDLQE ARARGLIVSN RRLMSLELVM RMHLFRPETG KFCDPTTGEF
4561 YDLAEAIQNG EIDPATTAEK NHVTGKELPL NEAIANGDID VTKGRVFDPK TKSAYNYEVA LGRGILVTVA KPLTERSEVI
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1365	1369	
total 1 peptides												

tr|A0A0P9C0Q5|A0A0P9C0Q5_DROAN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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4561 [illegible]
4641 NRQDSVELLG QTPMSIVVSK PREMSLEEAI KYNIIDPKTA LVRDFDTFKF VPFEVAQNNG IIDLSKRTIV DPKALYFVFD
4721 [illegible] QTSTADDSTQ PPEPVVYTLK DATTLGIIDP DSALVKDLAK
4801 SKLVRLPEAF RKGLMDANKA NVLNTKTSKL CTLNEAYESG LIVTPRRSFG LLEGISFNLY NPTNGCFVDP FQMNPDIIKR
4881 [illegible]
4961 [illegible]
5041 ITLENAGREE RSRVDRVNDR TVRLLRRLEV GRDELTKLRS ELDVFSDWLQ SARRTLEDKE RALSDLTRLS SQSESVREFV
5121 SDVIGHQADL RFITMAAQKF VDESKEFLAI LNEFRTSLPE RLPHVEPLAS AESPIRQEVS LVSAQYKDLM NRVNALQDRI
5201 SGLGGRQREY QDALDKANEW LRSTQPRVSR LIAEPIAGDP KSVQEQMNEA KALHNELLSN GRLVDNAQQA LDSLLYSLGG
5281 QLSPMEINQL EVPISDLKDK YQKLLDTLGE HCKTLDKTLV QSQGVQEALD NLGSWVNQAE DKFKLQLRPA SLIKERLQEQ
5361 IREHKSLLAD MQSHQASIDS VESSAKHLMS TASNARIAKK VETNLNDVIT KFDKLFDKVV KRGEFLDDVS NRLGKYLDEI
5441 SGIEQDIVTL QDALDSRDTN LLSAEELARR MQELSRHKES LTPSYEDCIR NGKDLISIRD VTDTSTLRDR IKALESQWRN
5521 INISLDEKAK LSKQKAEHQV AYESLKDQVL SWLASTETRI SGLAPVAIDL DKIRQQNDEL KPIYKDYRDY ASTIDKINDI
5601 GSQYDALIRP ESPGRKRSTF SPIKRVSPLR RMSGDARSPS PTKGGILSPL STGSSGFGSR RSSQDGFQIS ELSPVQQQLS
5681 EINNRYSLIG VRINDRQNEL DNMSEEVRKQ FENLKNLATF LERIQRQLPK ESVSNKDDAD RCIKQARKIL EDMYEKQSLL
5761 DTTKTQIKDI LRRKSDVPGA EQLRVENDNI VEKWKQLSDI CKSRINFSEK LRDFLDTHNN LKNWLDSKER MFTVLGPISS
5841 DPRMVQSQVQ QVQVLREEFR TQQPQLKHFQ EIGHDVLEHL DADTPDASAV DKKLQDINKR WEDLVSRLDE RANSLGGAAD
5921 SSKEFDAAVN RLREALQQIS DNLDSLPSDG DHQENLRKIE NLERQLEGQR PLLADAEQSA AALCNILGDP ASRADVNSRV
6001 AALEKQYQAL QKKLDTKKAE TEATLRDGRH FAENCSKTLG WLSGELSNLA ERLLVSAHKP TLQHQIDTHE PIYREVMARE
6081 HEIIMLINKG KDLSDRQQDR TVKRDLERIQ QQWEKLRREA VDRHTRLQTC MEHCKKYATT SEVFLAWLRT AEDKLTDLTP
6161 GVLSKSKLDT RLKDLQTFRS EVWKHSGEFE NTKGLGETFL TSCDVDKEPI KGELQDIRER WERLNNDLIA RAHEIENCSR
6241 RLGDFNDELR NLDHAVGRCE DRLAAHDALG GAAKDPKLLD RVKAIREELT NLQKPLQSLK GMAKDICAEA RAAGGDADHL
6321 TDDVDGISDR IGELQSRLDD RLGELQSAAT AVSQFNEQIK NLGIDLNEIE NEIEKLTPPA REIKRVQGQI DDTFKLQAKL
6401 ERLVERIEDG ERAADALVDA GFSPDTAQTR DQISTLRKTL VRLDNRVRDH SQNLEDTLRL LQEFYDMESH TMDDIQDITE
6481 EFRRMKPVGS ELEQIRRQQE DFCNFRENKI EPLAQNVEKV NVAGRDLVRS AASGVSTTQI EKDLEKLNDR WNDLKERMNE
6561 RDRRLDVALL QSGKFQEALA GLSKWLSDTE EMVANQKAPS SDYKVVKAQL QEQKFLKRML LDRQNSMSSL SSLGKEVANH
6641 CEPSERTAIE KQLHDLMKRF DALTDGAEKR EQDLEEAMEV AKRFHDKITP LELWLDNTER AVKGMELIPT DEEKIQQRIR
6721 EHGRLHDEIL GKKPDFSDLT DVASQLMHLV SDEEAVNLSE KVSTITDRYT GLVDASDNIG ALLADSRQGL RHLVLTYQEL
6801 VAWMERMENE LKRFRSVPVY AEKLLEQMDV LVELNENIAN HAPNVESTVE SGAELMKHIS NDEAIQLKDK LDSLQRRYGE
6881 LTNRGGDLLK SAQNALPLVK QFHEAHNRLI EWMQVAEAAL STSEPRQSDV LRLEAELVEM RPTLDTVNLV GPKLCQLSPG
6961 EGASTIETIV TRDNRRFDAI VEQIQRKAER LHLSNQRAKE VTNDIDELLE WFREMDTNLR EADPPAIEPK LVRAQLQEHR
7041 SVNDDISSQK GRVRDVTAAS KKVLRESPQS ENTTTLREKL DDLKEIVDTV AQLCSERLGV LEQALPLSEH FADSHAGLTT
7121 WLDDMEQQIS RLSMPALRPD QITQQQDKNE RLLQSIVEHK PLLDKLNKTG EALGALVAED DSARINEILD SDNARYAALR
7201 LELRERQQAL DNALQESSQF SDKLEGMLRA LANTVDQVNQ LDPLSALPQK IREQIDDNDA IMEDLDKRTD AFSAVQRAAS
7281 DVIAKAGNKS DPAVRDIKSK LEKLNNLWND VQKATKKRGS SLDDILNVAE PFWNQLQSVM KTLKDLEETL SSQEPPAAQP
7361 QEIQKQQVAL QEIRHEIDQT KPEVEQVRRH GSNLMNLCGE PDKPEVKKHI EDLDHAWDNI TALYAKREEN LIDAMEKAME
7441 FHETLQNLLK FLTKAEDKFV HLGPVGSDID AVKKQIEQLK SFKDEVDPHM VEVEALNRQA VELTERTSPE QAASIREPLT
7521 IVNRRWESLL RGMVERQKQL EHALLHLGQF QHALNELLVW INKTDGTLDQ LKPIPGDPQL LEVELAKLKV LANDIQAHQN
7601 SVDTLNDAGR QLIESEKGSV EASTTQEKLR KLNQEWKMLL QKAADRQHDL EESLRDAQSY IAEVQDILGW LGDVDAIIGA
7681 SKPVGGLPET ATEQLERFME VYNELEENRV KVETIQAQGQ EYIKRQNQMK VSSNNLTHTL RTLKQRWDAV VSRASDKKIK
7761 LEIALKEATE FHDTLQAFVE WLNQAEKQLA NAQPVSRVLE TIQAQMEEHK ILQKDVSTHR EAMLLLDKKG THLKYFSQKQ
7841 DVILIKNLLV SVQHRWERIV SKAAERTRAL DHGYKEAREF NDAWNNMMQY LQETETVLDQ IIEEATSSKD PQKIKKCIAR
7921 LKDTHRQLTG KQSLYDSIMR NGKNLMERAP KSDEAVIGKM LCELKDQWTR VLSKSIERQR KLEEALLLSG QFSDALGELL
8001 EWLKKAKQRL NEDGPVHGDL ETVQGLCDHH KHIEQDLQKR ATQMQGVLKT GRDLERSGNN PDVGRQLDEL QTVWDEVKSA
8081 TAKRGERLQY ALKDAEQLNG SIQALFDWLD HAEHKLRYAK NAPDDEKISR EMMDMHIEFM KDLHIRETQK HETFEFAETI
8161 IGKAYPDAIP IIKNWLSIIE ERWEEVKQWA INREAKLEQH LQSLKDLDET IEELLAWLSG LEATLLNLER ESLPDEIPPL
8241 EKLIEDHKEF MENTARRQTE VDRACKPKQL PPGARKMSRT GKTPVRGSSH DIREQSPDGT LRRQSFKGSR DQGLNNRKSS
8321 SRMTPNRDTP DRDRLPHYGP RFSPSSVGPE LEFRSTRAKL LWDKWRHVWM LSWERQRRLN DHLMYLKDLE RVRNFSWDDW
8401 RKRFLKHMNH KKSRLTDLFR KMDKDNNGLV PRGEFIDGIL NTKFDTSRME MGAVADLFDR NGEGLIDWQE FIAALRPDWQ
8481 ERKPQTDSDK IHDEVKRLVM LCTCRQKFRV FQVGEGKYRF GDSQKLRLVR ILRSTVMVRV GGGWVALDEF LTKNDPCRAK
8561 GRTNIELREQ FILADGVSQS MASFTPKRPP TNAAQNGNNS NTPPYMSSQG PIIKVRERSG RSMPMKPTTR SSHSASTPDS
8641 LSDNEGSHGN VSGRYTPRKV TYTSTRTGLT PGGSRAGSKP NSRPLSRQGS KPPSRHGSTL SLDSTDEHTP SRIPQRKQSG
8721 ASTVSGTGTT PRPSRLSVTS TTTRTNGTTT ITRKTASGSA SPAPTRRNVS GTSTPSGMQT PRKSSAEPTF SSTMRSRTSR
8801 GTTPVEKREP FRL
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   1 MHSSSQSTLK RTQQLVRQTN GGRGDVLSSG SEVVHSSRGP AITTNIDDSS LRYRHETKRE RTVEAVITDY PGVSPLGSVP
  81 HERTNIERTV TFQDPAGNSR RISETRALVP SSGSGSSSTA HYQQVTRNKR ISTEVLGSSV ESTKTSQRAP NGHRRVTTHI
 161 VRKVTTLSRA EENAQPAEDL LPPAKMIRSS ELEYRRALPP AIESSTHRRE ISDIVVGKED NVSAREALLR WARRSTARYP
 241 GVRVNDFTSS WRDGLAFSAL VHRNRPDLLD WRKARNDRPR DRLETAFHIV EKEYGVTRLL DPEDVDTNEP DEKSLITYIS
 321 SLYDVFPEPP SIHPLFDMES QRRVHEYRDL AQQFIYWCRE KTAYLQERSF PPTLIEMKRL LSDLQRFRSE EVSARKREKS
 401 KLIQIYKELE RYFETVGEVD VEAELRPDAI EKAWYRMNTA LQDREVILQQ EIERLERLQR LADKVQREIK HVDQKLTDLE
 481 TRIVEEGRRI ERLHPVDAKS IVEALETEIR HLEEPIQDMN QDCHVLNEGR YPHVSELHKK VNKLHQRWAQ LRTNFHTNLV
 561 QKLSGLKYPV HETTVTRQTR MVVESRQIDT NPHFRDLQEH IEWCQNKLKQ LLAADYGSDL PSVKEELDRQ QHEHKIIDQF
 641 HSKILNDERQ QTKFSGDELA LYQQRLNQLQ KVYAELLSTS TKRLSDLDSL QHFLGQASAE LQWLNEKEQV EISRDWADKQ
 721 LDLPSVHRYY ERAFGNGDEN LMSELEKREM HFATILDRGE ALLNQQHPAS KCIEAHLTAL QQQWAWLLQL TLCLEVHLKH
 801 ATEYHQFFGE IKDAEQWLAK RDEILNSKFS QSDFGLDQGE TLLRGMQDLR EELNAFGETV ATLQRRAQTV VPLNKRRQPV
 881 NRQGPVQAIC AYKQQGQLQI EKGETVTLLD NSGRVKWRVR TSKGQEGSIP GACLLLPPPD QEAIDAAERL KRLFDRSVAL
 961 WQKKHLRLRQ NMIFATIRVV KGWDFDQFLA MGPEQRTAIR RALNDDADKL LSEGDPNDPQ LRRLRREMDE VNRLFDEFEK
1041 RARAEEESKQ ASRIFTEECI AIKSKLEDMA RELDQIILAP LPRDLDSLEH VLEIHADYER RLHLLEPELK HLQETFRTIA
1121 LKTPVLKKSL DNLMELWKEL NTQSGLHKDR LKLLEASLAG LEDNEHVISE LENELAKHQD LPSTAEGLQQ VFKQLTHMQD
1201 VITQQQPQMD KMNDAADQLG RMGVPTKVLG DLKRLHSNVE RLNTRWSAVC NQLAERMRSC ETAIGLMKNL QSSVQVEESW
1281 VDGTTERLSA MPTATSAYEL DKLLGAAIER KPKIENVNVA GGRLIREAKI YDSKCLRFVD WLLEARPSFS PPRRDLRPAD

1361 SDPGATQYYS QRLDNLNTKY DRLLEQLSQR LKTAIEVNGS DGLQYAESLQ KPLKTFRVDF SAGSVPTGDG YAARPEDLYT
1441 TTYSTTQFSS TKTTKSSTKS VYSSDGLDAA SQEVITSNLP PSQIQFNEIR TLKRSQQLGG NSVLDIAGIR DPRTGRVLTI
1521 GEAIQLRILD VRTGEMLVGD RRISLEQAAE QGLIDAQLAR QLLQPGAGRD ASGRELSLLE VIQREINEAE SGYETAEKRI
1601 KVNSTVTVES TGSPENPRNI ADAITAGSVD TKTGLYRVKS GQTISLAEAY ERGYLIRHES VTIKSNALCL SDAIAHGLVD
1681 GAGWIADRNS GDKFRLDSAI ANQLIDAGVR EVVDAKRDTK ITLQEALQSG VLNAKTGRYV NEVTKEKLTF AEARNRQLIV
1761 KPYTLKDICD LNLLDKQAQI TSPMRREKLS IMQAIEAGVL DGNNLKCITK RKGELVTLQE AIADGIVLPA ECKYRDFMTG
1841 ELISIPEAVE RGLISSVAQR SIFDIDGFKD LRSSDYVSFN VALSRDLLRR KSTGFALETG RDSLVPLEVA VGEGLVRQEV
1921 YEMFNRGIGV QNASGQELSV FDLVYHNLID PKTGYLLDPK TGETVPLDTA IERKFITAEG ALLLSSLLNI TLTTETVTRT
2001 INRYVTIRAG SQEPGDQVLL TFTEAVRQGF IDEERQLFKD PKTGNIYSVQ QALNYGLLVP DSNQTVPEPT NRKKTKSTIT
2081 IVTKQIIPEA EPIKLNTQHT KYVEKSVEIP ISQELIKPQR VVSDFINMEK SSYIEQNVTE RQIMELPPGG WRLKDAIEQR
2161 IFNPDTGVFH VQGTDRLVNF EECINKQIIN NLSVSIIDPS TGDKISVQSA FERDILDSYG NYTNSRKQVL GMRSAIDEGK
2241 IILETVPATR GSSQKTILRI TRVNNMPDVL EVSTPLKDAP PKFVEVSTCQ RELASPEPLQ IAPGAIYDPS TALVIFTQSG
2321 ETENIFDAAR QGLIDEQLIK IVDPRTKQPI SVTEAIARSI YDPKTETILD AEGQPVDLIT ATKLGLLSVV GAPLVAAEGA
2401 LRTVRFVTDP RTGEQIPVEV AYERGIVSRD QLQRGRSFDS EPSTTTVEEK VVVLQRMRKI ILKPKDALRK GIIDEETCKI
2481 LEDTNNFTNP QGEVVNITEA LNTGMIDGRR GKIIDPQSNR VLNLRQAVEQ KILDPEQTNH ILMPLAKSLS VPRLAAQGLV
2561 DPKTQTIVHP ESGYPLSIHE AIVCEVLDPH STLRKPEKCT LEAAIKKGIV DADESIFKYK NKNLNISEAI EARLFDPSYD
2641 QQKSKVDIPP VGMIFPVAVE KSLVEPSKRV VLHPSTKNAL PIKQAIDENF IMSIPYAPKK DAIEVVAAME RDLIDVAAQT
2721 ITVPTTGERL PLRQAMENGV LVVKQLSDFV VTQKPIPKTE IMETVRAVHT VTTKTIELMQ GYVLISNNEV QNVNTGEVVS
2801 LEEAKELGIL REESTTRETK AAAGESPEAV QNLPTSSDQT VVVEERTQTV VVSSDTHKQE MQVISTTQST KENPAIPTVS
2881 EAETKVGKEP SKTLQNVKDA AKMGALGVIA APVLAGGALV SGVKSLIKSV KSPAEDAKTT TQKPEKPQSS FIEQERRNVP
2961 EPQQVPSEVD NLLNETENFI SSTTANFIIN EQQQEKPQEV SRQEVESTNT LTTTTVTTIT TSKTTTETGD AEPVVVEDVK
3041 TTTTVETTPV EPEIAKKPED KPVDVQVTET ITTVTREETI SEPEKPTTKE PTPEKIVEKK PVEKPAKKET TPAPVTKETT
3121 PAPVTKEPTP EPIQKEKTPE PAPREAAQVP TKPEPQPRTA VKEEVPAFEP PFTAPLAPFE EPKAETKITE VTTEVQEPVS
3201 STETITTITT TVTTIDQQPK EVTEVDKSEP AKITEVEVEK PAVQEPIKDD KPSEILDEVS EEPTSSIVVE ERVITVEEPT
3281 ITESTVTTTI TTTTTTTSSE EQQPQETVVT EIVKEEPKKD TPQPEKTVVT EELVKEEPAK DASQPITEPT QTTETVTTTT
3361 TIIQEEKPQQ PGDLEQIVQP PTSTNKHQSV VDFIQAEKNT QPSEGSKVLQ NVKDAAKLGA LAIVGAPVLA GKALVDALTS
3441 DKATKTGQPT THVVTEIVEE LPADISRTTS TIVTKVTTTT TTTTTTGEGS PEDEARDVVE LPISSAEPTI KREVPKTLPI
3521 GDAISQKLIS PDECQVIVDG EQQSQTVSTL LKEEQLSPLD EVQIIDDKLI ILQQISYLVD VDTELTPEKL SELNIYDPEN
3601 QYFIDPTTGQ KISFQTLVFD MNIFNPETIL VKNFSTGKYE TLTAALERPL LDRHTGHMVD PKTGKKIPFF ECIERQWIIR
3681 ADPEEQKPTG MENVTIDPQT GQVILDDGRV CSIVEAINSG KLDIQSISVR DPVSGEVIPL RMAIELGVVD MQAGTVIDIQ
3761 TLKEIPMELA FQLGFLVPGA RKPISLEAAV RKGLYDPETG KLFDSESQNQ VDVQKSIEIG LVDPKISLIV DTVTKKEVKL
3841 DCAIEDELVV PSTGQIKDNK NNTLVPFDVG VQQRLVKTDS VTWSLPEVLQ REYYTPSTGK VLNPVTGEEI LLQQAIEMGF
3921 VELDTTLVKD ADHDKIVPGK EAAKVGLLDT VRGTLSSPNI SLDEAFVKGY LISTKKPLSL VDCLLRGLYD PSTAKFTIDD
4001 KQLDLKSAIA QKLINPEELV LLDPKTESII SLTEAIAKGY LDPIGGYVIN PYTSTKLSLH EALENRILIP PKRKRSLPDA
4081 VYRGLYDPKT GQFSNTVTRE KLTTERAIRR GILDPDSTVV NVGSGQIIPF GVATETGIVD SRQGTVKDQD DKSIDFKEAF
4161 DRGVLVEAKK PLRLIEAVVK NVYDEVDGHF VDPKSGEKLN FAEALNTNLL DEHSVQIRDF KTGLYKQLNL THAKDSGVID
4241 AQNSKLLYNN QTMTLKHAFD IGILMDVNAP ISIQRAIHQG LFDDKTGKLS DPRSGRQITL LEGMRSFVIN PHLSCYFDEQ
4321 TETMYSLSET CRNGIINRRE GVFREPGSSS FVPLGEALSL GLIVDIENAG FGLYELLSMG FYDTPTRKVL HPVTNRKLNL
4401 NEACVEDVVS LSSSLVKHHE TGKYLRLANA IKEQLIDDNR GCYNLGNEQL DLQAARARGF IVSNRRLLSL ELVLRQQLYR
4481 PETGKFCDPT TGEYLDLIEA IHSGFIDPAT TVFKNQLTGK ELPLGEAIEN GDIDVSKGRV FDPKSKSAYN YDVALARGIL
4561 VTVARPLTDR SEVVRRQDSV ELLGQTPVSV VISKPREMSL EEAIRYNIID PKTALVRDED SEKELPYSVA VERGLVDTTK
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1350	1354	
total 1 peptides												

tr|A0A0Q9WS80|A0A0Q9WS80_DROWI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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4641  RTLVDPKALY FAFDPTLIVY VREPITFDQA AESKCLDLQT GILTYVPVSS ATGNESAPAG DDSANDSLTV IETPKVYTLK
4721  [illegible] [illegible] [illegible] [illegible] NVLNTQTSKL CTLQEAYESG LICTPKRSFG LLEAITFNLY
4801  NPTNGCLVDP FQMHPDIIRR RKFTLAEAIG SGLVDPSSTV VRDPSSGVIV PLTAAIGSGL IDAAEGRLTD ASDPKNNIDL
5041  RSLSDLTRLP SQADSVREFV SDVIGHQADL RFITMAAQKF VDESKEFLAI LNDFRTSLPE RLPHVEPLSS AESPIRQEVS
5121  LVSAQYKDLL NRVNALQDRV SGLGGRQREY QDALDKANEW LRSIAPRVSR IIAEPIAGDP KGVQDQMNEA KALHNELLSS
5201  GRLVDNAQQA LDNLLRSLGG QLSPMEINQL ELPIADLKNN YQQLLDNLGE HCKNLDKTLV QSQGVQDALD SLVGWVNQAE
5281  DKFKLNLRPA SLIKERLQEQ IREHKVLLAD LQSHQASIDS VQISAKHLLA SASNARIAKK VESNLNDVTG KFEKLYEKAN
5361  KRGEFLDDVY NRLGRYLDDI SNVEQRMASL QEALDSRETS LLSTEELARR MNDLSREKDH LAPQFEDCVR NGKDLIGLRD
5441  VTDTGVLRDR IKALESQWRN INISIDERAK LSKQKAEQQL AYEGLKDQVL SWLASTEARV NGLPPVAIDL DRIKQQHDEL
5521  KPICKDYRDY APTIDKINDI GAQYDALIRP ESPARKRSTY SPIKRASPLR RMSGDARSPS PTKGGILSPL STGSSGFGSR
5601  RSSQDGFQLS ELSPVQQQLS EINNRYGLIG VRLNDRQHEL DNLSEELRKQ YDNLKGLAQF LERIQRQVPK ESVSNKDEAE
5681  RCIKQARKIL EDMYEKQSLL DTTKAQIKDI LRRKSDVPGA EQLRLENENI QEKWKNLNDI CKNRIAFSEK LRDFLDTHGN
5761  LKSWLDSKER MLTVLGPISS DPRMVQSQVQ QVQVLREEFR TQQPQLKHFQ ELGHDVVDHL AGTPDAQAVE VKLKDILGKW
5841  EDLVGKLDDR ANSLGGAADS SKEFDAAVNR LREALQNISD NLDALPTDGD HQENLRKIEN LERQLEGQRP LLADVEQSAA
5921  TLCNILGDPA SRADVNSRVA ALEKQYLALQ KKLDTKKAET EASLRDGRHF AENCSKTLGW LGGELSNLTD RLLVSAHKPT
6001  LQHQIDTHEP IYREVMAREH EVIMLINKGK DLSDRQQDRG VKRDLDRIQQ QWEKLRREAV DRHTRLQTCM EHCKKYSQTS
6081  EQFLAWLRTA EDKLSDLTPG VLSKAKLETR LRDLQTFRSE VWKHSGEFEN TKGLGETFLT SCDIDKEPIK AELQDIRDRW
6161  ERLNNDLIAR AHEIENCSRR LGDFNDELRN LDHSLGRCED RLAAHDALGG AAKDPKLLER VKAIREELTN LSKPLQSLKA
6241  LAKDISAEAR AAGGDADHLT SEVDGLADRM SELQGRLDDR CGELQSAATA VSQFNEQMKS LGIDLNDLET EIEKLSPPAR
6321  EIKIVQQQLD DVGKIQHKLD RLVGRLEDAE RAADVLVDAG FAADTTQTRE QISTLRKTLG RLDNRVRDHE DNLQATLKAL
6401  REFYDNQSTT LDDIQDVSEE FKRMKPVGSE LDQIRRQQED FRNFRERKVE PLAVNVDKVN VAGRDLVRSA GSGVSTTAIE
6481  KDLEKLNDRW NDLKERMNER DRRLDVALLQ SGKFQEALAG LSKWLSDTEE MVANQKPPSS DYKVVKAQLQ EQKFLKKMLL
6561  DRQNSMGSLA NLGKEVANHC EPAERASIEK QLNDLMKRFD ALTDGAEQRE LDLEEAMEVA KRFHDKISPL ELWLDNTERA
6641  VKSMELIPTD EEKIQQRIRE HDRLHDEILG KKPDFTDLAD VAAQLMHLVS DEEAVNLGEK VRGVTERYTG LVDASDNIGA
6721  LLSESRQGLR HLVLSYQDLV AWMESMEAEL KRFKSVPVYA EKLLEQMDHL LELNENIAGH ASNVESTVES GAELMKHISN
6801  DEAIQLKDKL DSLQRRYGDL TNRGGDLLKS AQNALPLVQQ FHEAHNRLVE WMQSAEAALA PSEPRQSDVL RLEGELADMR
6881  PILDTINLIG PQLCQLSPGE GAATIESIVT RDNRRFDSIV EQIQRKAERL HLSNQRAKEV TGDIDELLEW FREMDTTLRE
6961  ADPPAMEPKL VRAQLQEHRS INDDISSQKG RVRDVTAASK KVLRESPQSE NTATLREKLD DLKEIVDTVA QLCSERLGIL
7041  EQALPLSEHF ADSHQGLTAW LDDMEQQISR LSMPALRPDQ ITLQQDKNER LLQSIAEHKP LLDKLNKTGE ALGALVADED
7121  SAKINEILDT DNARYAALRL ELRERQQALE SALQESSQFS DKLEGMLRAL ANTVDQVNQL DPLSALPQKI REQIEDNDAL
7201  MDDLDKRQDA FSAVQRAAND VIAKAGNKSD PAVRDIKAKL EKLNNLWNDV QNATKKRGSS LDDILSVAEP FWKQLNSVMK
7281  TLKDLEETLS CQEPPAAQPQ DIKKQQVALQ EIRHEIDQTK PEVEQVRRHG SNLMNMCGEP DKPEVKKHIE DLDNAWDNIT
7361  ALYAKREENL IDAMEKAMEF HETLQNLLKF LTKAEDKFAH LGAVGSDIDA VKRQIEQLKS FKDEVDPHMV EVEALNRGLQ
7441  RQAVELTERT SPEQAASIRE PLSVVNRRWE ALLRGMVERQ KQLEHALLHL GQFQHALNEL LVWINKTDGT LDQLKPIPGD
7521  PQLLEVELAK LKVLANDIQA HQNSVDTLND AGRQLIETEK GSLEASTTQE KLRKLNNEWK QLLQKASDRQ HELEEALREA
7601  HGYIAEVQDI LGWLGDVDAV IGASKPVGGL PETATEQLER FMEVYNELEE NRPKVETIQA QGQEYIKRQN QMKVSSSNLQ
7681  HTLRTLKQRW DAVVSRASDK KIKLEIALKE ATEFHDTLQA FVEWLTQAEK LLSNAEPVSR VLETIQAQME EHKVLQKDVS
7761  THREAMLLLD KKGTHLKYFS QKQDVILIKN LLVSVQHRWE RVVSKAAERT RALDHGYKEA REFNDAWSGM MQYLQETEQV
7841  LDQIIEEATA SKEPQKIKKY IGKLKETHRQ LGAKQSVYDG TMRTGKNLME RAPKGDRPVL DKMLLELKEQ WTRVWSKSIE
7921  RQRKLEEALL LSGQFSDALG ELLDWLKKAK SRLNENGPVH GDLETVQGLC EHHKHIEQDL QKRAAQMQGV LKTGRDLERS
8001  GNNPEVGRQL DEMQSIWEEV KNAVAKRGDR LQVALVDAEK LNARVQALFD WLDHAEHKLR YAKNAPDDEK VSREMMDIHM
8081  EFMKDLRVRE REKTETFEYA EDIIGKAYPD AIPIIKNWLS IIQQRWEEVR QWAINRESKL EQHLQSLKDL DDTIEELLAW
8161  LSGLEGTLLN LKHERLPDEI PPVEKLIEDH KEFMENTARR QNEVDRACKP RQLPPGARKP SRSGKTPVRG SSHDLRETSP
8241  DGTLRRQSFK GSRDQGLNAR KGSRVTPTRD TPDRDRLPHY GPRFSPSTAG PELEFRSPRA KLLWTKWRDV WMLSWERQRL
8321  LYDHLLYLKD VERARNFSWD DWRKRFLKYM NHKKSRLTDL FRKMDKDNNG MIPRDVFIDG ILNTKFDTSG LEMKAVADLF
8401  DRNGEGLIDW QEFIAALRPD WQERKPATDS DKIHDEVKRL VMLCTCRQKF RVFQVGEGKY RFGDSQKLRL VRILRSTVMV
8481  RVGGGWVALD EFLQKNDPCR AKGRTNIELR EQFILADGVS QSMAAFTPRR STPNAAATAS SSPNAQNGGS SNLPPYMSGQ
8561  GPIIKVRERS VRSIPMSRPS RSSLSASTPD SLSDNEGSHG GPSGRYTPRK VTYTSTRTGL TPGGSRAGSK PNSRPLSRQG
8641  SKPPSRQGST LSLDSTDDHT PSRIPQRKPS TASTTSGTTP RPARLSVTST TPGSRLNGTS TITRKTASGS ASPAPTSRPS
8721  RIPIKIPSFD SKSTSPTSST TNPTSLGRNI SGSSTPSGMQ TPRKSSAEPT FSSTMRRTSR GTTPTEKREP FRL
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   1 MQHSSSSQST LKRTQQLVRQ TRNGTGGVGG AGDVLSSGSE VIHMSRGPAI TTQIDDTNLR YRHETKRERH VEAVITDYPA
  81 GVAHPLGNVP HERTNFERTV TFQDESGARR PSDGGRALVP ASSVGSSSYQ QVTRNKRIST EVLGSSVEST KTSQRAPNGH
 161 RRVTTHIVRK VTTLSRAEEN QLPAEDLLPP AKMIRSSELE YRRGLPAIES SSMQRKEISD IVIGKEDNVS AREALLRWAR
 241 RSTARYPGVR VNDFTSSWRD GLAFSALVHR NRPDLLDWRK ARNDRPRERL ETAFHIVEKE YGVTRLLDPE DVDTNEPDEK
 321 SLITYISSLY DVFPEPPSIH PLFDMESQRR VHEYRDLAQQ FIYWCREKTA YLQERSFPPT LIEMKRLLSD LQRFRSDEVS
 401 ARKREKSKLI QIYKELERYF ETVGEVDVEA DLRPDAIEKA WYRMNTALQD REVILQQEIE RLERLQRLAD KVQREIKHVD
 481 HKLDELEKRI SEEGRRIERL HPMDAKSIVE ALETEIRHLE EPIQDMNQDC HVLNEGRYPH ASELHKKVNK LHQRWAQLRT
 561 NFHTNLVQKL SGLKYPVHET TVTRQTRMVV ESRQIDTNPH FRDLQEHIEW CQNKLKQLLA ADYGSDLPSV KDELDRQQHE
 641 HKIIDQFHSK ILNDERQQTK FSGDELNLYQ QRLNQLQKVY AELLSTSTKR LSDLDSLQHF LTQASAELQW LNEKEQVEIT
 721 RDWADKQLDL PSVHRYYENL MSELEKREMH FATILDRGEA LLNQQHPAAK CIEAHLTALQ QQWAWLLQLT LCLEVHLKHA
 801 TEYHQFFAEI KDAEQWLAKR DEILNSKFSQ SDFGLDQGES LLRGMQDLRE ELNAFGETVS TLQRTAQTIV PLNKRRQPVN
 881 RQGPVQAICA YKQQGQLQIE KGETVTLLDN SGRVKWRVRT SKGQEGSIPG ACLLLPPPDQ EAIEAAERLK RLFDRSVALW
 961 QKKHLRLRQN MIFATIRVVK GWDFDQFLAM GPEQRTAIRR ALNDDADKLL SEGDPNDPQL RRLRREMDEV NRLFDEFEKR
1041 ARAEEESKQA SRIFTEECIA IKSKLEDMAR ELDQIILAPL PRDLDSLEHV LEIHSDYERR LHLLEPELKH LQETFRTIAL
1121 KTPVLKKSLD NLLELWKELN TQSGLHKDRL KLLEASLAGL DDNEHVISEL ENELSKHQDL PSTAEGLQQV FKQLTHMQDI
1201 ITQQQPQMDK MNDAADQLGR MGVPTKVLGD LKRLHSNVER LNTRWSAVCN QLGERMRSCE TAIGLMKNLQ SSVQVEESWV
1281 DGTTERLSAM PTATSAYELD KLLGAAIERK PKIENVNVAG GRLIREAKIY DSKCLRFVDW LLEVRPSFSP PRRDLRPADS

1361 DPGATQYYSQ RLDNLNTKYD RLLEQLSQRL KTAIEVNGSD GLQYAESLQK PLKTFRVDFS AGSVPTGDGN AARQEDLYTT
1441 TYSTTQFSST KTTKSSSKSI YSSDNLDAAS QQDNTALPTH QSQIQFNEIR TLKRSQQLGG PNSVLDIAGI RDPRSGRILT
1521 IGEAIQLRIL DVRTGEMLVG DRRITLEEAA EQGLIDAQLA RQLLQPGAGR DASGRELSLL EVIQREITEA ETGYETAEKR
1601 IKVNNTVTVE QKTLDEAIGS PENPRNIADA ISAGSVDTRT GLYRVKSGQT ISLAEAYERG YLIRHESVTI KSNALCLSDA
1681 IAHGLVDGPG WIADRNSGDK FRLDSAIANQ LIDASVREVV DAKRDVKITL QEALQSGVLN AKTGRYVNEV TKEKLSFAEA
1761 RNRQLIVKPY TLKDICDLNL LDKQSQITSP MRREKLSIMQ AIEAGVLDGN QLKCITKRKG ELITLQEAIA DGIVLPAECK
1841 YRDFMTGELI SIPEAVERGL ISSVAQRSIF DIDGFKDLRS NDFVSFNVAL SRDLLRRKST GFALETGRDS LVPLEVAVGE
1921 DLVRQEVYEM FNRGIGVHNA SGKELSVFDL VYHNLIDPKT GYLLDPKTGE TVPLDTAIER KFITTEGALL LSSLLNITLT
2001 TETVTRTINR YVTIRAGSQE PGDSVLLTFT EAVRQGFIDE ERQLFKDPKT GNVYSVQQAL NYGLLVPDSN QTVPEPTNRK
2081 KTKSTITIVT KQIIPEAEPI KLNTQHTKYV EKSVEIPITT ELVKPQRVVS DFINMEKSSY IEQNVTERQI MELPPGGWRL
2161 KDAIEQGLFN PDTGVFHVQG TDRLVSFEES IDKQIINNLS VAVIEPNTGD KISVKSAFER DILYSYGNYT NNRQQVLGMR
2241 RAIADGKIVL ETVPATRGAS QKTILRITRV NNMPDVLEVS TPLKDSPPKF LEVVTCQREL ASPEPLQIAP GAIYDPSTAL
2321 VIFTQSGETE NIFDAARHGL IDEQLIKIID PSTKQTISVT EAIARSIYDP RTGTILNAEN QPVDLITATK LGLLTVVGAP
2401 LVAAEGALRT VRFVTDPRTG EQIPVEVAYE RGIVSRDQLQ RGRSFDDNKS VVEEKVVVLQ KMRKIILKPK DALRKGIIDE
2481 ETCHILEDTA NFTNGQGEVV NISEALNTGL IDGRRGKVID PQSNRVLNLR QAVEQKIIDP EQTNHILMPL AKSLSVPKLG
2561 SQGLIDPQSQ TIVHPESGYP LSIHEAIICE VLDPQSKLQK PSKCTIEEAI EKGIINADDS TFKYKDKTLN LTEAIEAKLF
2641 DSNYDQQKSK VEIPPVGMIF PVAVEKSLVE PTKRVVLHPT NKKQLPIKQA IEKNFIMSIP YAPKPDAIEV VPAMERGLID
2721 VAAQTFTHPT TGERLPLRVA FETGVLVVKQ LSQFVVTQKP IPKTEIMETV RAVHTVTTKT IELMQGYVLI SNNEVQNVNT
2801 GEVCSLEEAK ELGILREEST TRETNTAAGD SPEQVATAIT STLPTTSDQT VIVEERTQTV VVSSDTHKQE LQVVSTTQST
2881 KETSPLQSQV IDEVKPTKEP SKTLQNVKDA AKLGALGVIA APVLAGGAIV SGVKSLINSA KTTSSEKSET KQPEKPQDSK
2961 LKPQQVPTNE VDDLLQETEN FISSTTANFI ANEQQQQVPQ EKPVKEQPQP STELATSTLT STTTVTTITT SKTTQEVQGE
3041 PEPEIITSTT TVESKPVEEQ IVKPQELNFP PQDEITQVTE TVTTVTEKQV EPILDTQKEP TSKLALQKEP TPEPTPPQKT
3121 EKQPSPEPTT KPEPKPRASL KEEVVEFEPP YTAPLAPFEE TTVTKTTTEI KEVPVSSSET VTTTITTTVT TATPDEPTKE
3201 VIEKIVTKET TPQKVEEIKP VETSPQPEPE IPKVEDKKPV EPTAQTEEPS KIIEKTETVE TPGGNTIVTE ERVVTVEEPT
3281 ITESTTTTTT ITTTTSTTTT GDEEGPKENV TVTETIKKVE QPEEVKEEPI ETTKVTETIT TKTTVTEEKP QQPGDLEQIG
3361 GPKVVTEKHQ SVVDFIAKER EQQPSKESGG SSNILQNVKD AAKLGALAVV GAPILAGKAL VDALSTDKVT KPGQVVVTET
3441 SEELVPHDDG LSTATIITKV TTTTTTTTSS STTETTPTDD EARDTVEEPA IIQETIGKRE VPKTLPIGDA ISQKLISPDE
3521 CQIIVDGEQQ ADTVSTLLRD EQLSPLDEVQ IIDDKLIILQ QVTYVVDADT ELTPEKLSEL NIYDVDHQYF IDPSTGQKIS
3601 FQTLVFDMNI FNPETILVKN FSTGKYETLT AALERPLLDR HTGHMVDPKT GKKIPFFECI DRQWIIRANP EVQRPAAIEN
3681 VVIDSQTGQV ILDDGRVCSI VEAINSGKLD IQSISVRDPV SGEVIPLRMA IELGVVDMQA GTVIDIQTLK EIPMELAFQL
3761 GFLVPGARKP ISLEAAVRKG LYDPETGKLF DSESQNQVDV QKSIEIGLVD PKISLIVDTV TKKEVKLDCA IEDDLVLPAT
3841 GQIKDNKNNT LVSFDVGVQQ HLVKTDNVTW SLPEVLQREF YEPQTGKVLN PVTGEEILLQ QAIEMGFVEL DSTLVKDVDH
3921 NKILPGKEAA KVGLLDTVRG TLSSPNITLD EAFVKGYLIS TKKPWSLVDC LLRGLYDSAT AKFTIDGKQL DLKSAISQKL
4001 INPDELVLLD PKTESIISIT EAIAKGYLDP IGGFVINPYA STKLSLPEAL ENRILIPPKR KRSLPDAVYR GLYDPKTGQF
4081 SNTITREKLT TERAIRRGIL DPDSTVVNVS GQVIPFSIAT ETGIVDSQQG TVRDADDKPI DFKEAFDRGV LVEAKKPLRL
4161 IEAVVKNVYD EIDGHFVDPK SGEKLNFAEA LNTNLLDEHS VQIRDFKTGL YKQLNLTHAK DEGIIDAQNS KLLYNNQTMT
4241 LKHAFDIGIL MDVNAPISIQ RAIHQGLFDD KTGKLSDPKT GRKITLLESM RSFVINPHLP CYFDEQTEQM YTLSETCRNG
4321 IINRREGVFR EPESSSFVPL GEALSLGLIV DIENAGFGLY ELLAMGFYDE ATRKVLHPVT NRKLNLNEAC VEDVVSLSSS
4401 LVKHHETGKY LRLANAIKEH LIDDTKGCYN LGKEQIDLQT ARSRGLIVSN RRLLSLELVL RQQLYRPETG KFCDPTTGEY
4481 LDLIEAIHSG FIDPATTVFK NQLTGKELPL TEAIENGNID VSKGRVFDPK SKSAYNYDVA LSRGILVTVV RPLTDRGEVV
4561 RRQDSVELLG QTPVSVVISK PREMSLDEAI RYNIIDPKTA LVRDFDSFKE LPYSVAQERG LVDTSKRTLV DPKALYFAFD
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1349	1353	

total 1 peptides

tr|A0A0R1DVJ7|A0A0R1DVJ7_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

4641 PTLLIYVREP ISFDQAAESK CLDLQTGMLT YVPPTTVSTA SIAATSDNDS ANDSLTVLET PKIYTLKDAA GSGIIDPDSA
4721 LVKDLAKAKL VRQPPAFKKG LMDANKANVL NTQTSKLCTL QEAYESGLIC TPKRSFGLLE AITFNLYNPT NGCLVDPFQM
4801 HPDIIKRKKY TLAEAITAGL VDPSSTVVRD PSTGVIHPLA SAIANGLIDA TEGRLIDAQE PKNNIDLVKA AEKGLLLPAE
5041 DSTREFVSDV IGHQADLRFT TMAAQKFVDE SKEFLAVLND FRTSLPERLP HVEPLSSAES PIRQEVSLVS AQYKDLLNRV
5121 NALQDRVSGL GGRQREYQDA LDKANDWLRS VQPRVSRVIS EPIAGDPKAV QDQMNEAKAL HNEILSSGRL VDNAQQALDN
5201 LLRSLGGQLS PMEINQLELP IADLKNNYQQ LLDTLGEHCK TLDKTLVQSQ GVQDALDSLV SWVNQAEDKY KLNLRPASLI
5281 KERLQEQIRE HKVLLADLQS HQASIDSMQI SAKHLLASAS NARIAKKVES NLNDVTGKFE KLYEKVTKRG EFLDDVYNRL
5361 SKYLDDISTV EQRMASLQEA LDSRETSLLS TEELARRMQD LSREKDHLAP LFEDCVRNGK DLISLRDVTD TGALRDRIKA
5441 LESQWRNINI SIDERAKLSK QKAEQQLAYE GLKDQVLSWL ASTEARVNGL APVAIDLDKI RQQHDELKPI CKDYRDYAPT
5521 IDKINDIGSQ YDALIRPESP ARKRSTYSPI KRTSPLRRMS GDARSPSPTK GGILSPLSTG SSGFGSRRSS QDGFQLSELS
5601 PVQQQLSEIN NRYGLIGVRL NDRQNELDNL SEELRKQYEN LKGLAQFLDR IQRQVPKESV SNKDEAERCI KQARKILEDM
5681 YEKQSLLDTT KAQIKEILRR KSDVPGAEQL RLENENIQEK WKNLNDICKN RIAFSEKLRD FLDTHGNLKS WLDSKERMLT
5761 VLGPISSDPR MVQSQVQQVQ VLREEFRTQQ PQLKHFQELG HDVVDHLAGT PDAQAVETKL KDVLSKWEDL VGKLDDRANS
5841 LGGAADSSKE FDAAVNRLRE ALQNISDNLD TLPLDGDHQE NLRKIENLER QLEGQRPLLA DVEQSAATLC NILGDPASRA
5921 DVNSRVAALE KQYLALQKKL DTKKAETEAS LRDGRHFAEN CSKTLGWLSG ELSNLTDRLL VSAHKPTLQH QIDTHEPIYR
6001 EVMAREHEII MLINKGKDLS DRQQDRGVKR DLDRIQQQWD KLRREAVDRH TRLQTCLEHC KKYSQTSETF LAWLRTAEDK
6081 LADLTPGVLS KSKLETRLRD LQTFRSEVWK HSGEFENTKG LGETFLTSCD IDKEPIKAEL QDIRDRWERL NNDLIARAHE
6161 IENCSRRLGD FNDELRNLDH SLGRCEDRLA AHDALGGAAK DPKLLERVKA IREELTNLSK PLQSLKALAK DISAEARAAG
6241 GDADHLTNEV DGLADRMSEL QGRLDDRCGE LQSAATAVSQ FNEQMKSLGI DLNDLETEIE KLSPPGREIK IVQQQLDDNG
6321 KLQNKLDRLV GRLEDAERAA DVLVDAGFAA DTTQTREQIS TLRKTLGRLD NRVRDHEESL QNTLKNLREF YDIQSQTLDD
6401 IQDVSDEFKR LKPVGSELDQ IRRQQEDFRN FRERKVEPLA VNVDKVNVAG RDLVRSAATG VSTNVIEKDL EKLNDRWNDL
6481 KERMNERDRR LDVALLQSGK FQEALAGLSK WLSDTEEMVA NQKPPSSDYK VVKAQLQEQK FLKKMLLDRQ NSMGSLANLG
6561 KEVANHCEPA ERASIEKQLN DLMKRFDALT DGAEQREQDL EEAMEVAKRF HDKISPLELW LDNAERSVKA MELIPTDEEK
6641 IQQRIREHDN LHDEILGKKP DFTDLADVAA QLMHLVSDEE AVNLGEKVRG VTERYTNLVD ASDNIGALLS ESRQGLRHLV
6721 LSYQDLVAWM ESIENEMKRF KSVPVYTEKL LEQLDDLLEL NQDVADHAAN VESTVESGAE LMKHISNDEA IQLKDKLDSL
6801 QRRYGDLTNR GIELINSLHK AQPLVQQFHE AHNRLVEWMQ SAETALAPSE PRQADVLRLE GELAEIRPVL DTINLIGPQL
6881 CQLSPGEGAA TIESIVTRDN RRFDAIVEQI QRKAERLHLS NQRAKEVTGD IDELLEWFRE MDTTLREADL PAIDPKLVRA
6961 QLQEHRSIND DISSQKGRVR DVTAASKKVL RESPQSENTA TLREKLDDLK EIVDTVAQLC SERLGILEQA LPLSEHFADS
7041 HQGLTTWLDD MEQQISRLSM PALRPDQITL QQDKNERLLQ SIAEHKPLLD KLNKTGEALG ALVAEEDSAK INEILDTDNA
7121 RYAALRLELR ERQQALESAL QESSQFSDKL EGMLRALANT VDQVNQLDPL SALPQKIREQ IEDNDALMDD LDKRQDAFSA
7201 VQRAANDVIA KAGNKSDPAV RDIKAKLEKL NNLWNDVQKA TKKRGGSLED ILRVAEPFWK QLNSVMKTLK DLEETLSCQE
7281 PPAAQPQDIK KQQVALQEIR HEIDQTKPEV EQVRRHGSNL MNMCGEPDKP EVKKHIEDLD NAWDNITALY AKREENLIDA
7361 MEKAMEFHET LQNLLKFLTK AEDKFAHLGP VGSDIDAVKR QIEQLKSFKD EVDPHMVEVE ALNRQAVELT ERTSPEQAAS
7441 IREPLSVVNR RWDSLLRGMV DRQKQLEHAL LHLGQFQHAL NELLVWINKT DGTLDQLKPI PGDPQLLEVE LAKLKVLAND
7521 IQAHQNSVDT LNDAGRQLIE TEKGSLEAST TQEKLRKLNN EWKQLLQKAS DRQHELEEAL REAQGYIAEV QDILGWLGDV
7601 DAVIGASKPV GGLPETATEQ LERFMEVYNE LEENRPKVET IQAQGQEYIK RQNQMKVSSS NLQHTLRTLK QRWDAVVSRA
7681 SDKKIKLEIA LKEATEFHET LQAFVEWLTQ AEKQLSNAEP VSRVLETIQA QMEEHKVLQK DVSTHREAML LLDKKGTHLK
7761 YFSQKQDVIL IKNLLVSVQH RWERVVSKAA ERTRALDHGY KEAREFNDAW SGMMQYLQET EQVLDQIIEE ATASKEPQKI
7841 KKYIGKLKET HRQLGAKQSV YDGTMRTGKN LMERAPKGDR PVLDKMLLEL KEQWTRVWSK SIERQRKLEE ALLLSGQFSD
7921 ALGELFDWLK KAKGRLNENG PVHGDLETVQ GLCEHHKHIE QDLQKRAGQM QGVLKTGRDL ERSGNNPEVG RQLDELQSIW
8001 EEVKSAVAKR GDRLQVALVD AEKLNARVQA LFDWLDHAEH KLRYAKNAPD DEKVSREMMD IHMEFMKDLR IREREKTETF
8081 DYAEEIINKA YPDAIPIIKN WLSIIQQRWE EVRQWAINRE SKLEQHLQSL KDLDDTIEEL LAWLSGLEGT LLNLKHEQLP
8161 DEIPPVEKLI EDHKEFMENT ARRQNEVDRA CKPRQLPPGA RKPSRSGKTP VFKGSRDQGL NARKGSRVTP TRDTPDRDRL
8241 PHYGPRFSPS STGPDPEFRS PRAKLLWNKW RDVWMLSWER QRLLHEHLMY LKDVERARNF SWDDWRKRFL KYMNHKKSRL
8321 TDLFRKMDKD NNGMIPRDVF IDGILNTKFD TSGLEMKAVA DLFDRNGEGL IDWQEFIAAL RPDWQERKPA TDNDKIHDEV
8401 KRLVMLCTCR QKFRVFQVGE GKYRFGDSQK LRLVRILRST VMVRVGGGWV ALDEFLQKND PCRAKGRTNI ELREQFILAD
8481 GVSQSMAAFT SKRGSSAATA ASSPNSGQNG GSGNLPPYMS GQGPIIKVRE RSVRSIPMSR PSRSSLSAST PDSLSDNEGS
8561 HGGPSGRYTP RKVTYTSTRT GLTPGGSRAG SKPNSRPLSR QGSKPPSRHG STLSLDSTDD HTPSRIPQRK PSITSTASGT
8641 TPRPARLSVT TSTTPGSRLN GGTSTITRKT ASGSASPAPT SNGGMSRSSS IPALTGFGFK PVRRNISGSS TPSGMQTPRK
8721 SSAEPTFSST MRRTSRGTTP TEKREPFRL

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   1 MTSHSYYKDR LGFDPNEQQP GSNNSMKRSS SRQTTHHHQS YHHATTSSSQ SPARISVSPG GNNGTLEYQQ VQREQRDREL
  81 YSSNGSHHHH HQPHHQQQHH HHRHSATGSA SSLYENSSSS PAAPKKAKHS STQAQPQGGY EDALTQFKDE RDAIQKKTFT
 161 KWVNKHLKKH WKYAKTYTML HVCVTTNGIP CCSQSANRRV VDLFEDLRDG HNLLSLLEVL SGEHLPREKG KMRFHMLQNA
 241 QMALDFLRYK KIKLVNIRAE DIVDGNPKLT LGLIWTIILH FQISDIVVGK EDNVSAREAL LRWARRSTAR YPGVRVNDFT
 321 SSWRDGLAFS ALVHRNRPDL LDWRKARNDR PRERLETAFH IVEKEYGVTR LLDPEDVDTN EPDEKSLITY ISSLYDVFPE
 401 PPSIHPLFDM ESQRRVHEYR DLAQQFIYWC REKTAYLQER SFPPTLIEMK RLLSDLQRFR SEEVSARKRE KSKLIQIYKE
 481 LERYFETVGE VDVEAELRPD AIEKAWYRMN TALQDREIIL QQEIERLERL QRLADKVQRE IKHVDQKLTD LETRIGEEGR
 561 RIERLHPVDA KSIVEALETE IRHLEEPIQD MNQDCHVLNE GRYPHVSELH KKVNKLHQRW AQLRTNFHTN LVQKLSGLKY
 641 PVHETTVTRQ TRMVVESRQI DTNPHFRDLQ EHIEWCQNKL KQLLAADYGS DLPSVKEELD RQQHEHKIID QFHTKILNDE
 721 RQQTKFSGDE LALYQQRLNQ LQKVYAELLS TSTKRLSDLD SLQHFLGQAS AELQWLNEKE QVEITRDWAD KQLDLPSVHK
 801 YYERAFGNGD ENLMSELEKR EMHFATILDR GEALLNQQHP ASKCIEAHLT ALQQQWAWLL QLTLCLEVHL KHATEYHQFF
 881 GEIKDAEQWL AKRDEILNSK FSQSDFGLDQ GETLLRGMQD LREELNAFGE TVATLQRRAQ TVVPLNKRRQ PVNRQGPVQA
 961 ICAYKQQGQL QIEKGETVTL LDNSGRVKWR VRTANGQEGP IPGACLLLPP PDQEAIDAAE RLKRLFDRSV ALWQKKHLRL
1041 RQNMIFATIR VVKGWDFDQF LAMGPEQRTA IRRALNDDAD KLLSEGDPND PQLRRLRREM DEVNRLFDEF EKRARAEEES
1121 KQASRIFTEE CIAIKSKLED MARELDQIIL APLPRDLDSL EHVLEIHSDY ERRLHLLEPE LKHLQETFRT IALKTPVLKK
1201 SLDNLMELWK ELNTQSGLHK DRLKLLEASL AGLEDNEHVI SELENELARH QDLPSTTEGL QQVFKQLNHM QDIITQQQPQ
1281 MDKMNDAADQ LGRMGVPTKV LGDLKRLHSN VERLNTRWSA VCNQLGERMR SCETAIGLMK NLQSSVQVEE SWVDGTTQGL
1361 SAMPTATSAY ELDKLLGAAI ERKPKIENVN VAGGRLIREA KIYDGKCLRF VDWLVEARPS FSPPRRDLRP ADSDPGATQY

1441 YSQRLDNLNT KYDRLLEQLS QRLKTAIEVN GSDGLQYAES LQKPLKTFRV DFSAGSVPTG DGYAARQEDL YTTTYSTTQI
1521 SSTKTTKSST KSVYGSDGLD AASQDVSTAI LPQSQIQFNE IRTLKRSQQL GGHSVLDIAG IRDPRTGRVL TIGEAIQLRI
1601 LDVRTGEMLV GDRRITLEQA ADQGLIDVQL AKQLLEPGAG RDANGRELSL LEVIQREISE AESGYETAEK RIKVNNTITV
1681 EQASGELGSP ENPRNIADAI TAGSVDTKTG LYRVKSGQTI SLAEAYERGY LIRHESVTIK SNALCLSDAI AHGLVDGAGW
1761 IADRNSGDKF RLDSAIANQL IDASVREVVD AKRDTKITLQ EALQSGVLNA KTGRYVNEVT KEKLTFAEAR NRQLIVKPYT
1841 LKDICDLNLL DKQAQITSPM RREKLSIMQA IEAGVLDGNL LKCITKRKGE LVTLQEAIAD GIVLPAECKY RDFMTGELIS
1921 IPEAVERGLI SSVAQRSIFD IDGFKDLRSN DYVSFNVALS RDLLRRKSTG FALETGRDSL VPLEVAVSEG LVRQEVYEMF
2001 SRGIGVQNAS GTELSVFDLV YHNLIDPKTG YLLDPKTGET VPLDTAIERK FITPEGALLL SSLLNITLTT ETVTRTINRY
2081 VTIRAGSQEP VDSVLLTFTE AVRQGFIDEE RQLFKDPKTG NIYSVQQALN YGLLVPDSNQ TVPEPTNRKK TKSTITIVTK
2161 QIIPEAEPIK LNTQHTKYVE KSVEIPISQE LVKPHRVVSE FINLEKSSYI EQNVTERQIM ELPPGGWRLK DAIEQRLFNP
2241 DTGVFHVQGT DRLVNFGECI NKQIINKLSL SVIDPSTGDK ISVQSAFERD ILDSYGNYTN SRKQVQGMRS AIDESKIILE
2321 TVPATRGANQ KTILRITKVN NIPDVLEVST PLKDAPPKFV EVLTCQRELA SPEPLQIAPG AIYDPSTALV IFTQTGETEN
2401 IFEAARQGLV DEQLIKIVDP TTKQPISVTE AIARSIYDPK TATILDSEGQ PVDLITATKL GLLSVVGAPL VAAEGALRTV
2481 RFVTDPRTGE QIPVEVAYER GIVSRDQLHR GRSFDSEPTT VEDKVVVLQR MRKVILKPKD ALRKGIIDEE TCEILENTSN
2561 FTNPKGEVVN ITEALNTGLI DGRRGQVIDP QNNRVLNLRQ AVEQKIIDSE QTNHILMPLA KSLSVPRLAG QGLIDPQTQT
2641 IVHPESGYPL SIHEAIVCEV LDPHSKLHKP EKCTLEEAIT KGIINADDST FSYKNKTLNI TEAIEEKLFD PSYDQQKSKV
2721 EIPPVGMIFP VAVEKSLVEP SKRVVLHPST KKALPIKQAI EENFIMSIPY SPKPDAIEVV TALERDLIDV ASQTLTVPST
2801 GERIPLRQAM ENGILVVKNL SDFVITQKPI PKTEIMETVR AVHTVTTKTI ELMQGYVLIS NNEVQYVSTG EVCSLEEAKE
2881 LGILREESTT RETKAAAGES PESIGAVVTS GDQTVIVEER TQTVVVSSDT RKQEMQVVST TQSTKDTSVP IVSEIETKAS
2961 KEPSKTLQNV KDAAKLGALG VIAAPVLAGG AIVSGVKSLI KSVKSPTEDA KTTAKPNEPQ TSFIEPERRK ELQPQQVPSE
3041 VDSLLSETEN FISSTTANFI ANEKQQDKPD TLPQKRDPFE VESTSTLTTT TVTTITTSST TTETGNQEPV VVEDVSTTVK
3121 ENTVVVEPSK VPEDKTEVSK TTETITTVIT NKTDTVPENI SQEQTSEESA KNEPEVPKDT SSRPAETEAS PKPVQKELTP
3201 EPAPNAEFTE SVKKDLTPKP EYKENTTQLA QITSKDISPA PTSENEHSAE PTSKPEPMPR AAKKEDISEI EPPFTAPLAP
3281 FVDQVSDTKI TEIKTEIEEP VTSSQTITTI TTTVKTVDEH PTVEEVSGIN KSENIVDVQA KEPAVQKPVK VNETSDDTTR
3361 PEPTSEIVLE ERVVTVEKPT ITETTVTTTT ITTTTSLGSA EALPQAESTP TVKETPLNEP VPSSLVQPTE IKQITQGDDK
3441 KPVEIVDTAR KTPEQEPVKT IPAEPFSTSE TTETITTKTT IVEEEKLHQP SDLEQIIQPQ TNPEKHQSIV DFIEQEKSTQ
3521 PAESGSKILQ NVKDAAKLGA LAIVGAPVLA GKALVDALTT EKTVKPEHST TQVVTETVEE LPTEIISTST ATLVTKVTTT
3601 TTTTTTSTSE GTPDDEARDV VTLPTELVDS SVKREVPRTL AIGDAISQKL ISPDECQVIV DGEQQSQTVS TLLKEEQLSP
3681 LDEVQIIDDK LIVLQQVSYL VDADTELTPQ NLYELNIYDP ENQYFIDPST GQKISFHTLV FDMNVFNPET ILVKNFSTGK
3761 YETLTAALER PLLDRHTGHM VDPKTGKKIP FFECIDRQWI IRANPEEQKP SGIENVTIDT QTGQVVLDDG RVCSIVEAIN
3841 SGKLDIQSIS VRDPVSGEVI PLRMAIELGV VDMQAGTVID IQTLKEIPME LAFQLGFLVP GARKPISLEA AVRKGLYDPE
3921 TGKLFDSESQ NQVDVQKSIE IGLVDPKISL IVDTVTKKEV KLDCAIEDDL VLPATGQIKD NKNNTLVPFD VGVQQRLLKT
4001 DNVTWSLPEL LQREYYTPST GKVLNPVTGE EILLQQAIEM GFVELETTLV KDVDHDKILP GKEAAKVGLL DTVRGTLSSP
4081 NISLDEAFVK GYLISTKKPL SLVDCLLRGL YDPSTAKFTI DDKQLDLKTA IAQKLINPEE LVLLDPKTES IISITEAIAK
4161 GYLDPIEGYV INPYASTKLS LHEALENRIL IPPKRKRSLP DAVYRGLYDP KTGQFSNTVT REKLTTERAI RRGILDPDST
4241 VVNVGSGQII PFGVATETGI VDSKHGTVRD TDDHSIDFKE AFDRGILVEA KKPLRLIEAV VKNVYDEVDG HFVDPKSGEK
4321 LNFAEALNTN LLDEHSVQIR DFKTGLYKQL NLTHAKDNGI IDAQNSKLLY NNQTMTLKHA FDIGILMDVN APISIQRAIH
4401 QGLFDDKTGK LSDPRTGRQI TLLESMRSFV VNPHLPCYFD EQTEQMYTLS ETCRNGIINR REGVFREPGS NSFVPLGEAL
4481 SLGLIVDIEN AGFGLYELLS MGFYETSTRK VLHPVTNRKL NLNEACVEDV VSLSSSLVKH HETGKYLRLA NAIKEQLIDD
4561 SSGCYNLGKE QLDLQAARAK GEIVSNRRLL SLELVLRQQL YRPETGKFCD PTTGEYLDLT EAIHSGFIDP ATTVEKNQLT
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4561 [illegible]

Supporting Peptides:

4641 GKELPLTEAI ENGDIDVTKG RVFDPKSKSA YNYDVALSRG ILVTISRPLT DRNDVVRRQD SVELLSQTPV SVVISKPREM

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1422	1426	

total 1 peptides

4721 SLEEATRYNT IDPKIALVRD FDSFKFLPYS VAVERGLVDT TKRTLVDPKA LFFAFDPTLI VYVREPVTFD QAAESKCLDL

4801 QTGMLTYVPA SGPGSAPAAS ASDDSANDSL TVIETPKVYT LKEAASAGVV DPDSALVKDL AKAKLVRLPE AFRKGLMDAN

4881 [illegible]

tr|A0A1I8MXA4|A0A1I8MXA4_MUSDO

back to list

4961 [illegible]

| Protein Coverage | Supporting Peptides |

5041 VEQKISSVGG PREKIDELRN QINALKQIKD EIESQQRPVA TCLEQIRQIV LTGGDVLSAP EVTTLENSGR ELRSRVDRVN

Protein Coverage:

5121 DRTVRLLRRL EAGRDELTKL RSELDVFSDW LQVARRTLED KERSLSDLTR LPSQADSVRE FVSDVIGHQA DLRFITMAAQ

5201 KFVDESKEFL AILNDFRTSL PERLPHVEPL SSAESPIRQE VSLVSAQYKD LLNRVNALQD RVSGLGGRQR EYQDALEKAN

5281 EWLRSVHPRV SRIISEPIAG DPKGVQDQMN EAKALHNELL SSGRLVDNAQ QALDNLLRSL GGQLSPMEIN QLELPIADLK

5361 NNYQQLLDNL GEHCKTLDKT LVQSQGVQDA LDSLVGWVNQ AEDKFKLNLR PASLIKERLQ EQIREHKVLL ADLQSHQASI

5441 DSVQVSAKHL LASASNARIA KKVESNLNDV TVKFEKLYEK ANKRGEFLDD VYNRLSRYLD EISTVEQRMA SLQEALDSRE

5521 TSLLSTEELA RRMNELSREK DQLAPQFEDC VRSGKDLISL RDVTDTGVLR DRIKALESQW RNINISIDER AKLSKQKAEQ

5601 QLAYEGLKDQ VLSWLASTEA RVNGLPPVAI DLDKIKQQHD ELKPICKDYR DYAPTIDKIN DIGAQYDALI RPESPARKRS

5681 TYSPIKRASP LRRMSGDARS PSPTKGGILS PLSTGSSGFG SRRSSQDGFQ LSELSPVQQQ LSEINNRYGL IGVRLNDRQH

5761 ELDNLNEELR KQYENLKGLA QFLERIQRQL PKESVSNKDE AERCIKQARK ILEDMYEKQS LLDTTKAQVK DILRRKSDVP

5841 GAEQLRQEND SIQEKWKNLN DICKNRIAFS EKLRDFLDTH GNLKSWLDSK ERMLTVLGPI SSDPRMVQSQ VQQVQVLREE

5921 FRTQQPQLKH FQELGHDVVD HLAGTPDAQA VETKLKDILG KWDDLVGKLD DRANSLGGAA DSSKEFDAAV NRLREALQNI

6001 SDNLDSLPTD GDHQENLRKI ENLERQLEGQ RPLLADVEQS AATLCNILGD PASRADVNSR VAALEKQYLA LQKKLDTKKA

6081 ETEASLRDGR HFAENCSKTL GWLGGELSNL TDRLLVSAHK PTLQHQIDTH EPIYREVMAR EHEVIMLINK GKDLTDRQQD

6161 RGVKRDLDRI QQQWEKLRRE AVDRHTRLQT CMEHCKKYSQ TSETFLAWLR TAEDKLADLT PGVLSKAKLE TRLRDLQTFR

6241 SEVWKHSGEF ENTKGLGETF LTSCDIDKEP IKAELQDIRD RWERLNNDLI ARAHEIENCS RRLGDFNDEL RNLDHSLGRC

6321 EDRLAAHDAL GGAAKDPKLL ERVKAIREEL TNLSKPLQSL KALAKDISAE ARAAGGDADH LTSEVDGLAD RMSELQGRLD

6401 DRCGELQSAA TAVSQFNEQM KSLGIDLNDL ETEIEKLSPP GREIKIVQVQ IDDVGKIQNK LDRLVGRLED AERAADVLVD

6481 AGFAADTTQT REQISTLRKT LGRLDNRVRD HEDNLQATLK ALREFYDNQS QTLDDIQDVS DEFKRMKPVG SELDQIRRQQ

6561 EDFRNFRERK VEPLAINVDK VNVAGRDLVR SAGSGVSTTA IEKDLEKLND RWNDLKERMN ERDRRLDVAL LQSGKFQEAL

6641 AGLSKWLSDT EEMVANQKPP SSDYKVVKAQ LQEQKFLKKM LLDRQNSMGS LANLGKEVAN HCEPSERASI EKQLNDLMKR

6721 FDALTDGAEQ RELDLEEAME VAKRFHDKIS PLELWLDNTE RSVKAMELIP TDEEKIQQRI REHDRLHDEI LGKKPDFSDL

6801 ADVAAQLMHL VSDEEAVNLG EKVRGVTERY TGLVDASDNI GALLAESRQG LRHLVLSYQD LVAWMESMEA ELKRFKSVPV

6881 YAEKLLEQMD HLLELNENIA GHASNVESTV ESGAELMKHI SNDEAIQLKD KLDSLQRRYG DLTNRGGDLL KSAQNALPLV

6961 QQFHEAHNRL VEWMQSAEAA LAPSEPRQAD VLRLEGELAD MRPILDSINQ VGPQLCQLSP GEGAATIESI VTRDNRRFDS

7041 IVEQIQRKAE RLHLSNQRAK EVTGDIDELL EWFREMDTTL READLPAMEP KLVRAQLQEH RSINDDISSQ KGRVRDVTAA

7121 SKKVLRESPQ SENTATLREK LDDLKEIVDT VAQLCSERLG ILEQALPLSE HFADSHQGLT SWLDDMEQQI SRLSMPALRP

7201 DQITLQQDKN ERLLQSIAEH KPLLDKLNKT GEALGALVAD DDSAKINEIL DTDNARYAAL RLELRERQQA LESALQESSQ

7281 FSDKLEGMLR ALANTVDQVN QLDPLSALPQ KIREQIEDND ALMDDLDKRQ DAFSAVQRAA NDVIAKAGNK ADPAVRDIKA

7361 KLEKLNNLWN DVQNATKKRG SSLDDILNVA EPFWKQLNSV MKTLKDLEET LSCQEPPAAQ PQDIKKQQVA LQEIRHEIDQ

7441 TKPEVEQVRR HGSNLMNMCG EPDKPEVKKH IEDLDNAWDN ITALYAKREE NLIDAMEKAM EFHETLQNLL KFLTKAEDKF

7521 AHLGAVGSDI DAVKRQIEQL KSFKDEVDPH MVEVEALNRG LKRQAVELTE RTSPEQAASI REPLSVVNRR WEALLRGMVE

7601 RQKQLEHALL HLGQFQHALN ELLVWINKTD STLDQLKPIP GDPQLLEVEL AKLKVLANDI QAHQNSVDTL NDAGRQLIET

7681 EKGSVEASTT QEKLRKLNNE WKQLLQKASD RQHELEEALR EAHGYIAEVQ DILGWLGDVD AVIGASKPVG GLPETATEQL

7761 ERFMEVYNEL DENRPKVETI QAQGQEYIKR QNQMKVSSSN LQHTLRTLKQ RWDAVVSRAS DKKIKLEIAL KEATEFHDTL

7841 QAFVEWLTQA EKLLSNAEPV SRVLETIQAQ MEEHKVLQKD VSTHREAMLL LDKKGTHLKY FSQKQDVILI KNLLVSVQHR

7921 WERVVSKAAE RTRALDHGYK EAREFNDAWS GMMQYLQETE QVLDQIIEEA TASKEPQKIK KYISKLKETH RQLGAKQSVY

8001 DGTMRTGKNL LERAPKGDRP VLDKMLIELK EQWTRVWSKS IDRQRKLEEA LLLSGQFSDA LGELLDWLKK AKSRLNENGP

8081 VHGDLETVQG LCEHHKHIEQ DLQKRAAQMQ GVLKTGRDLE RSGNNPEVGR QLDEMQSIWE EVKSAVAKRG ERLQVALVDA

8161 EKLNARVQAL FDWLDHAEHK LRYAKNAPDD EKVSREMMDI HMEFMKDLRV REREKSETFE YAEDIINKAY PDAIPIIKNW

8241 LSIIQQRWEE VRQWAINRES KLEQHLQSLK DLDDTIEELL AWLSGLEGTL LNLKHEQLPD EIPPVEKLIE DHKEFMENTA

8321 RRQNEVDRAC KPRQLPPGAR KPSRSGKTPV RGSSHDLREQ SPDGTLRRQS FKGSRDQGLN ARKGSRITPT RDTPDRDRLP

8401 HYGPRFSPST SGPELEFRSS RAKLLWTKWR DVWMLSWERQ RLLNDHLLYL KDVERARNFS WDDWRKRFLK YMNHKKSRLT

8481 DLFRKMDKDN NGMIPRDVFI DGILNTKFDT SGLEMKAVAD LFDRNGEGLI DWQEFIAALR PDWQERKPAN DSDKIHDEVK

8561 RLVMLCTCRQ KFRVFQVGEG KYRFGDSQKL RLVRILRSTV MVRVGGGWVA LDEFLQKNDP CRAKGRTNIE LREQFILADG

8641 VSQSMAAFTP RRSTPNAAAT ASSSPHAHNG GSSNLPPYMS GQGPIIKVRE RSVRSIPMSR PSRSSLSAST PDSLSDNEGS

8721 HGGPSGRYTP RKVTYTSTRT GLTPGGSRAG SKPNSRPLSR QGSKPPSRHG STLSLDSTDD HTPSRIPQRK PSTGSTASGA

8801 TPRPARLSVT TTTTPGSRLN GTSTITRKTA SGSASPAPTS RPSRIPIKIP SFDSKSTSPS STTNPTSLGR NISGSSTPSG

8881 MQTPRKSSAE PTFSSTMRRT SRGTTPTEKR EPFRL

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   1 MYRIDKEFGT GQNKGFSLKG GTIAATSTTT GCQDREATMH STKTSTASSS LMKKRGSGYS GNSTTAIVPS RGPAITTNID
  81 EQSAQYQHQF KHEKTIEAVI TDYPGVAPAS ATPHERLSYD RSLVVRKSFR NGGGDPIPVT QTVVAVTTTS PGHDRHDLQE
 161 SYQQVTRNKR ISTEILGSSV ESTKTSQRGP SGHRRITTHI VRKVTTLSRA EEQQLPPEDL LPPAKMVRSS ELEYRHTLPR
 241 TTALPAIEPA SSTSTTIRRT KISDIVVGKE DNVSAREALL RWARRSTARY PGVRVNDFTS SWRDGLAFSA LVHRNRPDLL
 321 DWRKARNDRP RERLETAFHI VEKEYGVTRL LDPEDVDTNE PDEKSLITYI SSLYDVFPEP PAIHPLFDME SQRRVHEYRD
 401 LAQQFIYWCR EKTAYLQDRS FPPSLIELKR LLNDLHTFRN EEVSARKREK SKLIQIYKEL ERYFESIGEI DVEADLRPEA
 481 IEKAWYRMQT AMQDRDMILQ QEIERLERLQ RLADKVQREI KHVDMKITDL ETRITEEARH IETLHPVNAK NIVESLETEI
 561 RLLEEPLHDM NQDCHVLNEG RYPHAAELHK KVTKLHQRWA QLQTTFHTVL LPKLSGLKYP VHEKTTTRQH RIVVESRQIE
 641 TNPLFKDLLE HIEWCQNKLK QMLAADYGSD LPSVKEERDR QQHAHKVIDQ FHAKILNDER QQSKFSGDEL NLYQQRLNQL
 721 QKVYAELLST STKRLSDLDT LENFLAQASA ELQWLNEKEQ IEITRDWADK NLDLASVHRY YENLMSELEK RELHFGTILD
 801 RGETLLRQQH PASKCIEAHL TALQQQWAWL LQLTLCLEVH LKHSTEYHQF FAEIKDAEQW LSKRDEILNS EYSKSEFGLD
 881 QGEALLRGMQ DLREELNAFG ETVAQLQHRA QTIVPLNKRR QPVNRQSPVQ AICAYNQQGQ IPVEKGETCT LLDNSGRVKW
 961 RVRTTKGQEG LVPSACLLMP PPDKEAIDAA ERLKRLFDRS VSLWQKKHLR LRQNMIFATI RVVKDWDFDQ FLAMGPEQRT
1041 AIRRALNDDA DKLLSEGDPN DPQLRRLRRE MDEVNRLFDE FEKRARAEEE SKQASRIFTE ECIAIKGKLE DMARELEQII
1121 SAPLPRDLDS LEHVLEIHAD YERRLQLLEP ELQHLQETFR TIALKTPALK KSLDNLMVLW KELNTLSNLH KDRLKLLEAS
1201 LAGLEDNEHF ISEIENQLAK HQDLPSTPER LEMVFKQLTH MQDLITQQQP QMDKMTDAAD QLGRMGVPTK VLGDLKRLHA
1281 NVERLNTRWS AICNQLAERM RSCENAIGLM KNLQSSVQVE ESWVDGTTER LSAMPTATSA YELDKLLGAA IERKPKIENV
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1521 AGSVPSTSKQ SQIQFNEIHS LKRVQTRNEN VGTGGDTTNI KHLLDITGIR DPRTGRVLTI GDAIQMRLLD VRTGEMIVGD
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1761 IDPNVREVVD AKKDTKITLT EALKSGILNP KTGRYWNEVT KEKLTFIEAK NRQLIVKPYT LKDICDLNLL DKQSKITSPM
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2241 KYIINSLSVS VIDPNTGEKL STRNAFERDI IDSYGSYTNK NGDVETMRSA INEGKIILEP VPITKSSARE QCILRISKLN
2321 NLAEVVEIST PLAADASPKF VEVNTVQREL TSPEPLQIAP GAIYDPSTAL VIFTHNGQTE NIFDAARHGL IDESLIRIVD
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2721 KVSVVHPENR KEIPLQKAIE EGFVMSIPYP PQADAVDVHH AVEQGLINVV DQTFKHPKDV GPPTPIRQAL ETGRLVVKPI
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2881 EHVEDILQQQ PITQAQPQVQ PQTTTTSTIT SDGTQRQIIQ TSVIKTEVQT PMETIDSTTN QQIPTKDTKL SSALNNVKEA
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3121 NLVKDTENFI NTTTANFIRQ EKAGELRSNI AEAKQPGSQT IDTKITTVTT SQVVPPTPTP TTSVTVETNA SGEPVPVAGT
3201 QNANDSKVPS QVVITTETAK KTTDPINEIV EVNETGDQPQ YVVSFEDSDT EVNTTSTVST TTVITTTTST VLTNTPLGDI
3281 TEAEEPQKPA EPTHQVPGAN KNVHEIETAP EDKLPEKYGV ITDFMKHEIS TSTKPKVLEG LPAGQVNSSE APVDNVVVNE
3361 QQEPKDANNT HSTMETVNNQ ETTTGAIDPK SKPVIDNMDD VNSVPPKTVD EATRTKETKV EKSPVEHDDV AKVKETTDTP
3441 KPAERKSLDN LTTDLSHPQT GVTDHQDKHQ NVVDFIEAEK GAAVNPTERE SNILQNVKDA AKLGAMALVG APVLAGKAIV
3521 DALKPDEKPK DSSVTTTITT VLTSTTTKTT TAAATSTTQP DESTQGETPR ETQNQNQQRG VTPPKTLALG DAISQKLISP
3601 DECKVLVDGE EQDQSVTELL KDEQLSPLDE VQVLDDKLVV LQPMTYLIDA SDDLTPEHLS ELNIYDTANQ YFTDPSTGLK
3681 ISFQTLVFDM NVFNPETILV KNFSTGKYET LTDALERPLL DRHTGHMVDP KSGKKIPFFE CVSRNWIIRA NPEKEKPAAI
3761 ENVIDPESGK VILGDGRVCS IVDAINNGLL DIQSISVRDP VSGEVIPLRM AIELGVVDMQ AGTVIDIQTL KEIPMEDAFK
3841 LGFLVPGSRK PISLEAAVRK GLYDPETGKL YDSESDNQVD VQKSIEIGLV DPKISLIVDA KSQKAIKLDC AIEDELVVTE
3921 TGQIKDTQTN TLVPFDIGVE KNLVKTDSIT WSLPEVLQRE YYSPKTGKIL NPSTGEEILL QQAIELGFVE LDSCLVKDDD
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4081 LINSDELVLL DPKTESIISL TEAISKGYID PIHGYVINPY TGTKLSLNEA LENRVLIPPK RKRSLPDAVY RGLYDPKTGE
4161 FSNTITREKL STERAIRRGI LDPDSTIVSV AGEVIPFEKA AQVGIVDSHR GTVKDDDDKE IDFKEAFDRG VLLEAKKPLR
4241 LIEAVIKNVY DEVDGSFMDP KTGQKLSFAQ AVDSNLLDED SVQIRDFNTG LYKQLNLAHA ADTGVIDGSN AKLVYNNQKI
4321 TIKHAFDVGI LMDTQAPISL QRALHQGLFD EKTGKLTDPK SGRKITLLES IRSFVINPQL PCYFDEIQEQ MHSLTDTCRM
4401 GIINRREGVF REPGSNTFVS LNEALNLGLI VDIENASFGL YELLAMGFYD KHTGKVLHPV TGRKLNLNEA CVEDVVSLSS
4481 SLIKSNKTGK YIRLAQAIKE QVIDDTKGCY NLSPTDQIDL QEARARGLIV SNRRLLCLEL VMRMQLFRPE TGKFCDPTTG
4561 EYYDLAESIQ NGEIDPATTV EKNQVTGKET PLNEAIANGD VDVSKGRVED PKSQSAYNYD VALSRGILIT VAKPLTERTA
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4641  EVVKDSVDLL GQTPVSIVVS KPREMSLEEA IKYNIIDPKT ALVRDFDTFK FIPFEVAQQK GIVDLNKRTV VDPKALYFVF
4721  [illegible] QSPEQHDVDE NSEGPTTTNE PVVYTLKDAT TLGIIDPDSA
4801  LVKDLVKSKL VRLPEAFRKG LMDANKANVL NTKTSKLCTL KEAYESGLIV TPKRSFGLLE AIAFNLYNPT NGCFVDPFQM
5041  VLSAPEVTTL ENAGRELRSR VDRVNDRTVR LLRRLEAGRD ELTKLRSELD VFSEWLQSAR RTLEDKERAL SDLTRLSSQS
5121  ESVREFVSDV IGHQADLRFI TMAAQKFVDE GKEFLAILND FRTSLPERLP HVEPLASSES PIRQEVSLVS AQYKDLMNRV
5201  NALQDRISGL GGRQREYQDA LDKANEWLRS TQPRVGRVIA EPIAGDPKSV QEQMNEAKAL HNELLSNGRL VDNAQQALDS
5281  LLYTLGGQLS PMEINQLEVP IADLKDKYQK LLDSLGEHCK TLDKTLVQSQ GVQEALDNLG NWVNQAEDKF KLQLRPASLI
5361  KERLQEQIRE HKALLADMQS HQASIDSVES SAKHLMNTAS NARIAKKVET NLNDVTTKFD KLYDKVVKRG EFLDDVFNRL
5441  CKYLDEFSGV EQEIVTLQDA LDSRDTSLLS AEELAHRMQE LSNRKESLSP AYEDCIRNGK DLISIRDVTD TSTLRDRIKA
5521  LESQWRNINV SLDEKTKLSK QKAEHQVAYE SLKDQVLSWL ASTETRITGL APVAIDLEKI RQQNDELKPI YKDYRDYAST
5601  IDKINDIGSQ YDALIRPESP GRKRSTFSPI KRVSPLRRMS GDARSPSPTK GGILSPLSTG SSGFGSRRSS QDGFQLSELS
5681  PVQQQLSEIN NRYTLIGVRI NDRQNELDNM NEEVRKQFEN LKNLAAFLER IQRQLPKESV SNKDEADRCI KQARKILEDM
5761  YEKQSLLDTT KTQIKDILRR KSDVPGAEQL RVENDNIVEK WKQLSDICKN RINFSEKLRD FLDTHNNLKN WLDSKERMLT
5841  VLGPISSDPR MVQSQVQQVQ VLREEFRTQQ PQLKHFQEIG HDVLDHLEAD SPDASAVNKK LQDVNSKWED LVGRLDERAN
5921  SLGGAADSSK EFDAAVNRLR EALQQISDNL DSLPSDGDHQ DNLRKIENLE RQLEGQRPLL ADAEQSAAAL CNILGDPASR
6001  ADVNSRVAAL EKQYQALQKK LDTKKAETEA TLRDGRHFAE NCSKTLGWLS AELSNLAERL LVSAHKPTLQ HQIDTHEPIY
6081  REVMAREHEV IMLINKGKDL TDRQQDRGVK RDLERIQQQW EKLRREAVDR HTRLQTCMEH CKKYVSTSEV FLAWLRTAED
6161  KLVDLNPGVL SKSKLDTRLH DLHTFRSEVW KHSGEYENTK GLGETFLSSC DVDKDPIKSE LQDIRERWER LNNDLIARAQ
6241  EIENCSRRLG DFNDELRNLD HAVGRCEDRL AAHDALGGAA KDPKLLDRVK AIREELTNLQ KPLQTLKGMA KDICAEARAA
6321  GGDAEHLTDD VDGIADRIGE LQSRLDDRLG ELQSAATAVS QFNEQIKNLG IDLNDIENEV EKLSPPAREI KRVQGQIDDT
6401  YKLQTKLERI VERIEDGERA ADALVDAGFS PDTAQTREQI STLRKTLARL DNRVRDHSQL LEETLRSLQE FYDMESQTMD
6481  DIQDISEEFR RMKPVGSELE QIRRQQEDFR NFRENKIEPL AQNIDKVNMA GRDLVRSAAS GVSTTQIEKD LEKLNDRWND
6561  LKERMNERDR RLDVALLQSG KFQEALAGLS KWLSDTEEMV ANQKAPSSDY KVVKAQLQEQ KFLKRMLLDR QNSMSSLSSL
6641  GKEVANHCEP SERNAIEKQL HDLMKRFDAL TDGAEQREKD LEEAMEVAKL FHDKITPLEL WLDNTERAVK GMELIPTDEE
6721  KIQQRIREHG RLHDEILGKK PDFSDLADVA GQLMHLVSDE EAGNLGEKVR TITDRYTGLV DASDNIGALL ADSRQGLRHL
6801  VLTYQELVAW MERMETELKR FRSVPVFAEK LLEQMDVLVE LNENIANHAP NVESTVDSGA ELMKHISNDE AIQLKDKLDS
6881  LQRRYGELTN RGGDLLNSAQ NALPLVKQFH EAHTRLIDWM QVAESALSTS EPRQSDVLRL EAELVEMRPT LDCVNLVGPK
6961  LCQISPGEGA STIETIVTRD NRRFDAIVEQ IQRKAERLHL SNQRAKEVTN DIDELLEWFR EMDANLREAD PPAIEPKLVR
7041  AQLQEHRSVN DDISSQKGRV RDVTAASKKV LRESPQSENT ATLREKLDDL KEIVDTVAQL CSERLGVLEQ ALPLSEHFAD
7121  SHAGLTTWLD DMEQQLSRLS MPALRPDQIT QQQDKNERLL QSIAEHKPLL DKLNKTGEAL GALVADDDSA RINEILDSDN
7201  ARYAALRLEL RERQQALDNA LQESSQFSDK LEGMLRALAN TVDQVNQLDP LSALPQKIRE QIEDNDAIMD DLDKRTDAFS
7281  AVQRAASDVI AKAGNKSDPA VRDIKSKLEK LNNLWNDVQK ATKKRGSSLD DILNVAEPFW NQLQSVMKTL KDLEETLSSQ
7361  EPPAAQPQEI QKQQVALQEI RHEIDQTKPE VEQVRRHGSN LMNLCGEPDK PEVKKHIEDL DNAWDNITAL YAKREENLID
7441  AMEKAMEFHE TLQNLLKFLT KAEDKFAHLG PVGSDIDAVK KQIEQLKSFK DEVDPHMVEV EALNRQAVEL TERTSPEQAA
7521  SIREPLAVVN RRWEALLRGM VERQKQLEHA LLHLGQFQHA LNELLVWISK TDGTLDQLKP IPGDPQLLEV ELAKLKVLAN
7601  DIQAHQNSVD TLNDAGRQLI ESEKGSLEAS TTQEKLRKLN QEWKMLLQKA SDRQHELEES LREAQGYIAE VQDILGWLGD
7681  VDAIIGASKP VGGLPETATE QLERFMEVYN ELEENRPKVE TIQAQGQEYI KRQNQMKVSS SNLQHTLRTL KQRWDAVVSR
7761  ASDKKIKLEI ALKEATEFHD TLQAFVEWLN QAEKQLANAQ PVSRVLETIQ VQMEEHKVLQ KDVSTHREAM LLLDKKGTHL
7841  KYFSQKQDVI LIKNLLVSVQ HRWERIVSKA AERTRALDHG YKEAREFNDA WNNMMQYLQE TETVLDQIIE EATSSKDPQK
7921  IKKCIARLKD THRQLTGKQT LYDSTMRNGK NLMERAPKTD EAVLGKMLCE LKDQWTRVLS KSIERQRKLE EALLLSGQFS
8001  DALGELLEWL KKAKQRLNED GPVHGDLETV QGLCEHHKHI EQDLQKRAAQ MQGVLKTGRD LERSGNNPDV GRQLDELQTV
8081  WDEVKSATAK RGDRLQVALK DAEKLNGSIQ ALFDWLDHAE HKLRYAKNAP DDEKISREMM DMHIEFMKDL HVREQQKHET
8161  FEFAEDIIGK AYPDAIPIIK NWLSIIEERW EEVKQWAINR EAKLEQHLQS LKDLDDTIEE LLAWLSGLEA TLLNLERESL
8241  PDEIPPLEKL IEDHKEFMEN TARRQTEVDR ACKPKQLPPG ARKMSRTAKT PVFKGSRDHG LNNRKSSSRM TPSRDTPDRD
8321  RLPHYGPRFS PSSVGPELEF RSTRAKLLWD KWRHVWMLSW ERQRRLNDHL MYLKDLERVR NFSWDDWRKR FLKHMNHKKS
8401  RLTDLFRKMD KDNNGLVPRG EFIDGILSTK FDTSRMEMGA VADLFDRNGE GLIDWQEFIA ALRPDWQERK PQTDSDKIHD
8481  EVKRLVMLCT CRQKFRVFQV GEGKYRFGDS QKLRLVRILR STVMVRVGGG WVALDEFLQK NDPCRADEHL AELMPIFERI
8561  RAQEQVPCAF PIHMGAGGTV FVRCNSSRSV PLSPHVMHCH PTTHWVRERS GRSIPMTKQT RSSLSASTPD SLSDNEGSHG
8641  NASGRYTPRK VTYTSTRTGL TPSGSRAGSK PNSRPLSRQG SKPPSRHGST LSLDSTDEHT PSRIPQRKQS AASTISGTGT
8721  TPRPSRLSVT STTTTRTNGT TTITRKTASG SASPAPTRNG GMSRSSSIPA LTGYGYKPRR NISGTSTPSG MQTPRKSSAE
8801  PTFSSTMRSR TSRGTTPVEK REPFRL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1393	1397	
total 1 peptides												

tr|A0A0J9U1A2|A0A0J9U1A2_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MMDRESLSEW AKDKPLSILQ LDPADRAVLR IADERDAIQK KTFTKWVNKH LKKANRRVVD LFEDLRDGHN LLSLLEVLSG
  81 EHLPREKGKM RFHMLQNAQM ALDFLRYKKI KLVNIRAEDI VDGNPKLTLG LIWTIILHFQ ISDIVVGKED NVSAREALLR
 161 WARRSTARYP GVRVNDFTSS WRDGLAFSAL VHRNRPDLLD WRKARNDRPR ERLETAFHIV EKEYGVTRLL DPEDVDTNEP
 241 DEKSLITYIS SLYDVFPEPP SIHPLFDMES QRRVHEYRDL AQQFIYWCRE KTAYLQERSF PPTLIEMKRL LSDLQRFRSD
 321 EVSARKREKS KLIQIYKELE RYFETVGEVD VEAELRPDAI EKAWYRMNTA LQDREVILQQ EIERLERLQR LADKVQREIK
 401 HVDQKLTDLE TRIGEEGRRI ERLHPVDAKS IVEALETEIR HLEEPIQDMN QDCHVLNEGR YPHVSELHKK VNKLHQRWAQ
 481 LRTNFHTNLV QKLSGLKYPV HETTVTRQTR MVVESRQIDT NPHFRDLQEH IEWCQNKLKQ LLAADYGSDL PSVKEELDRQ
 561 QHEHKIIDQF HTKILNDERQ QTKFSGDELA LYQQRLNQLQ KVYAELLSTS TKRLSDLDSL QHFLGQASAE LQWLNEKEQV
 641 EITRDWADKQ LDLPSVHRYY ENLMSELEKR EMHFATILDR GEALLNQQHP ASKCIEAHLT ALQQQWAWLL QLTLCLEVHL
 721 KHATEYHQFF GEIKDAEQWL AKRDEILNSK FSQSDFGLDQ GETLLRGMQD LREELNAFGE TVATLQRRAQ TVVPLNKRRQ
 801 PVNRQGPVQA ICAYKQQGQL QIEKGETVTL LDNSGRVKWR VRTAKGQEGP IPGACLLLPP PDQEAIDAAE RLKRLFDRSV
 881 ALWQKKHLRL RQNMIFATIR VVKGWDFDQF LAMGPEQRTA IRRALNDDAD KLLSEGDPND PQLRRLRREM DEVNRLFDEF
 961 EKRARAEEES KQASRIFTEE CLAIKSKLED MARELDQIIL APLPRDLDSL EHVLEIHSDY ERRLHLLEPE LKHLQETFRT
1041 IALKTPVLKK SLDNLMELWK ELNTQSGLHK DRLKLLEASL AGLEDNEHVI SELENELARH QDLPSTAEGL QQVFKQLNHM
1121 QDIITQQQPQ MDKMNDAADQ LGRMGVPTKV LGDLKRLHSN VERLNTRWSA VCNQLGERMR SCETAIGLMK NLQSSVQVEE
1201 SWVDGTTERL SAMPTATSAY ELDKLLGAAI ERKPKIENVN VAGGRLIREA KIYDSKCLRF VDWLVEARPS FSPPRRDLRP

1281 ADSDPGATQY YSQRLDNLNT KYDRLLEQLS QRLKTAIEVN GSDGLQYAES LQKPLKTFRV DFSAGSVPTG DGYAARQEDL
1361 YTTTYSTTQI SSTKTTKSST KSVYSSDGLD AASQEVSTAS LPQSQIQFNE IRTLKRSQQL GGHSVLDIAG IRDPRTGRVL
1441 TIGEAIQLRI LDVRTGEMLV GDRRITLEQA ADQGLIDLQL AKQLLEPGAG RDASGRELSL LEVIQREISE AESGYETAEK
1521 RIKVNNTVTV EQTSGELGSP ENPRNIADAI TAGSVDTKTG LYRVKSGQTI SLAEAYERGY LIRHESVTIK SNALCLSDAI
1601 AHGLVDGAGW IADRNSGDKF RLDSAIANQL IDASVREVVD AKRDTKITLQ EALQSGVLNA KTGRYVNEVT KEKLTFAEAR
1681 NRQLIVKPYT LKDICDLNLL DKQAQITSPM RREKLSIMQA IEAGVLDGNL LKCITKRKGE LVTLQEAIAD GIVLPAECKY
1761 RDFMTGELIS IPEAVERGLI SSVAQRSIFD IDGFKDLRSN DYVSFNVALS RDLLRRKSTG FALETGRDSL VPLEVAVSEG
1841 LVRQEVYEMF SRGIGVQNAS GKELSVFDLV YHNLIDPKTG YLLDPKTGET VPLDTAIERK FITPEGALLL SSLLNITLTT
1921 ETVTRTINRY VTIRAGSQEP VDSVLLTFTE AVRQGFIDEE RQLFKDPKTG NIYSVQQALN YGLLVPDSNQ TVPEPTNRKK
2001 TKSTITIVTK QIIPEAEPIK LNTQHTKYVE KSVEIPISQE LVKPHRVVSE FINMEKSSYI EQNVTERQIM ELPPGGWRLK
2081 DAIEQRLFNP DTGVFHVQGT DRLVNFEECI NKQIINNLSL SVIDPSTGDK ISVQSAFERD ILDSYGNYTN SRKQVQGMRS
2161 AIDEGKIILE TVPTTRGANQ KTILRITKVN NIPDVLEVST PLKDAPPKFV EVLTCQRELA SPEPLQIAPG AIYDPSTALV
2241 IFTQTGETEN IFDAARQGLV DEHLIKIVDP TTKQPISVTE AIARSIYDPK TATILDSEGQ PVDLITATKL GLLSVVGAPL
2321 VAAEGALRTV RFVTDPRTGE QIPVEVAYER GIVSRDQLHR GRSFDSEPST VEDKVVVLQR MRKVILKPKD ALRKGIIDEE
2401 TCEILENTRN FTNPKGEVVN ITEALNTGLI DGRRGQVIDP QNNRVLNLRQ AVEQKIIDSE QTNHILMPLA KSLSVPRLAD
2481 QGLIDPQTQT IVHPESGYPL SIHEAIVCEV LDPHSKLHKP EKCTLEEAIT KGIINADDST FSYKNKTLNI TEAIEAKLFD
2561 PSYDQQKSKV EIPPVGMIFP VAVEKSLVEP SKRVVLHPST KKALPIKQAI EENFIMSIPY SPKPDAIEVV TAMERDLIDV
2641 AAQTLTVPST GERIPLRQAM ENGVLVVKNL SDFVITQKPI PKTEIMETVR AVHTVTTKTI ELMQGYVLIS NNEVQNVNTG
2721 EVCSLEEAKE LGILREESTT RETKAAAGES PESIPAVVTS GDQTVVVEER TQTVVVSSDT RKQEMQVVST TQSTKDTSVP
2801 SVSEIDTKGS KEPSKTLQNV KDAAKLGALG VIAAPVLAGG AIVSGVKSLI KSVKSPTEDA KTTAKPKEPQ TSFIEQERRN
2881 ELQPQQVPSE VDNLLSETEN FISSTTANFI ANEKQQDKPD TLPQESNLPL EVESTSTLTT TTVTTITTSS TTTETGNLEP
2961 VVVEDVSTTV KEDAVVVKPS KVPEDKTEVS KITETITTVT SNEKDTVPEK ISPETASEES AKKDPVVTKD TSSRPAETES
3041 SPKPAQKELT PEPAQNAEFV ESVKKDPTPE PDYKENITEP AQITPKEPSP APASQNEQSS EPTSKPEPMP RTAKKEEISE
3121 IEPPFTAPLA PFVDQVEKTK ITEIKTEIKE PVTSSQTITT ITTTVKTVDE QPIVEEITEV SKSENIVDVQ VKEPTAQEPI
3201 KEKKTSEDTT RTEPTNEIVI EERVVTVEEP TITETTVTTT TITTTTSSTE ETLPQENTAT VKETPLNEPV PSSPAQLRDI
3281 EQTTNDQKKP EEIVDTEKKT TEPKPVETIP TEPVSTSETT VTVTTKTTIV DEGKLHQPSD LVQIAQPHST SDKHQSLVDF
3361 IEQEKGTQPA ESGSKILQNV KDAAKLGALA IVGAPVLAGK ALVDALTTEK TIKPEPSTTQ VVTQTVEELP TEIITTSTAT
3441 LVTEVTTTTT TTTTSTSEGT PDDEARDVVK LPTELVESSV KREVPRTLAI GDAISQKLIS PDECQVIVDG EQQSQTVSTL
3521 LKEEQLSPLD EVQIIDDKLI VLQQVSYLVD ADTELTPQNL YELNIYDPEN QYFIDPSTGQ KISFHTLVFD MNVFNPETIL
3601 VKNFSTGKYE TLTAALERPL LDRHTGHMVD PKTGKKIPFF ECVDRQWIIR ANPEEQKPSG IENVTIDTQT GQVVLDDGRV
3681 CSIVEAINSG KLDIQSISVR DPVSGEVIPL RMAIELGVVD MQAGTVIDIQ TLKEIPMELA FQLGFLVPGA RKPISLEAAV
3761 RKGLYDPETG KLFDSESQNQ VDVQKSIEIG LVDPKISLIV DTVTKKEVKL DCAIEDDLVL PATGQIKDNK NNTLVPFDVG
3841 VQQRLLKTDN VTWSLPELLQ REYYTPSTGK VLNPVTGEEI LLQQAIEMGF VELETTLVKD VDHDKILPGK EAAKVGLLDT
3921 VRGTLSSPNI SLDEAFVKGY LISTKKPLSL VDCLLRGLYD PSTAKFTIDD KQLDLKTAIA QKLINPEELV LLDPKTESII
4001 SITEAIAKGY LDPIEGYVIN PYASTKLSLH EALENRILIP PKRKRSLPDA VYRGLYDPKT GQFSNTVTRE KLTTERAIRR
4081 GILDPDSTVV NVGSGQIIPF GVATETGIVD SKHGTVRDAD DHPIDFKEAF DRGILVEAKK PLRLIEAVVK NVYDEVDGHF
4161 VDPKSGEKLN FAEALNTNLL DEHSVQIRDF KTGLYKQLNL THAKDTGIID AQNSKLLYNN QTMTLKHAFD IGILMDVNAP
4241 ISIQRAIHQG LFDDKTGKLS DPRTGRQITL LESMRSFVVN PHLPCYFDEQ TEQMYTLSET CRNGIINRRE GVFREPGSNS
4321 FVPLGEALSL GLIVDIENAG FGLYELLSMG FYDPSTRKVL HPVTNRKLNL NEACVEDVVS LSSSLVKHHE TGKYLRLANA
4401 IKEQLVDDSR GCYNLGNEQL DLQAARARGL IVSNRRLLSL ELVLRQQLYR PETGKFCDPT TGEYLDLIEA IHSGFIDPAT
4481 TVFKNQLTGK ELPLTEAIEN GDIDVSKGRV FDPKSKSAYN YDVALSRGIL VTITRPLTDR NDVVRRQDSV ELLNQTPVSV
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1272	1276	
total 1 peptides												

tr|A0A1W4VPU6|A0A1W4VPU6_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

4641 AESKCLDLQT GLLTYVPASV PGSAAAASAS DDSANDSLTV IETPKVYTLK EAASAGVVDP DSALVKDLAK AKLVRLPEAF
LLEAITFNLY NPTNGCLVDP FQMHPDIIRR RKFTLAEAIG
4801 SGLVDPSSTV VRDPSTGVIV PLTAAISSGL IDASEGRLTD ANEPKNNIDL VKAAEKGLLL PAEQRQAVFE KFNMCEENVN
LNDFRTSLPE RLPHVEPLSS AESPIRQEVS LVSAQYKDLL NRVNALQDRV SGLGGRQREY
5121 QDALDKANEW MRSVHPRVSR IISEPIAGDP KGVQDQMNEA KALHNELLSS GRLVDNAQQA LDNLLRSLGG QLSPMEVNQL
5201 ELPIADLKNN YQQLLDNLGE HCKTLDKTLV QSQGVQDALD SLVGWVNQAE DKFKMNLRPA SLIKERLQEQ IREHKVLLAD
5281 LQSHQASIDS VQVSAKHLLA SASNARIAKK VESNLNDVTV KFEKLYEKAN KRGEFLDDVY NRLSRYLDEI STVEQRMASL
5361 QEALDSRETS LLSTEELARR MNELSRDKDQ LTPQFEDCVR SGKDLISLRD VTDTGVLRDR IKALESQWRN INISIDERAK
5441 LSKQKAEQQL AYEGLKDQVL SWLASTEARV NGLPPVAIDL DRIKQQHDEL KPICKDYRDY APTIDKINDI GAQYDALIRP
5521 ESPARKRSTY SPIKRASPLR RMSGDARSPS PTKGGILSPL STGSSGFGSR RSSQDGFQLS ELSPVQQQLS EINNRYGLIG
5601 VRLNDRQHEL DNLSEELRKQ YENLKGLAQF LERIQRQLPK ESVSNKDEAE RCIKQARKIL EDMYEKQSLL DTTKAQVKDI
5681 LRRKSDVPGA EQLRQENDSI QEKWKNLNDI CKNRIAFSEK LRDFLDTHGN LKSWLDSKER MLTVLGPISS DPRMVQSQVQ
5761 QVQVLREEFR TQQPQLKHFQ ELGHDVVDHL AGTPDAQAVE IKLKDILGKW DDLVGKLDDR ANSLGGAADS SKEFDAAVNR
5841 LREALQNISD NLDTLPTDGD HQENLRKIEN LERQLEGQRP LLADVEQSAA TLCNILGDPA SRADVNSRVA ALEKQYLALQ
5921 KKLDTKKAET EASLRDGRHF AENCSKTLGW LGGELSNLTD RLLVSAHKPT LQHQIDTHEP IYREVMAREH EVIMLINKGK
6001 DLTDRQQDRG VKRDLDRIQQ QWEKLRREAV DRHTRLQTCM EHCKKYSQTS ETFLAWLRTA EDKLADLTPG LLSKAKLETR
6081 LRDLQTFRSE VWKHSGEFEN TKGLGETFLT SCDIDKEPIK AELQDIRDRW ERLNNDLIAR AHEIENCSRR LGDFNDELRN
6161 LDHSLGRCED RLAAHDALGG AAKDPKLLER VKAIREELTN LSKPLQSLKA LAKDISAEAR AAGGDADHLT SEVDGLADRM
6241 SELQGRLDDR CGELQSAATA VSQFNEQMKS LGIDLNDLET EIEKLSPPGR EIKIVQVQID DVGKIQNKLD RLVGRLEDAE
6321 RAADVLVDAG FAADTTQTRE QISTLRKTLG RLDNRVRDHE DNLHSTLKAL REFYDNQSQT LDDIQDVSDE FKRMKPVGSE
6401 LDQIRRQQED FRNFRERKVE PLAINVDKVN VAGRDLVRSA GSGVSTTAIE KDLEKLNDRW NDLKERMNER DRRLDVALLQ
6481 SGKFQEALAG LSKWLSDTEE MVANQKPPSS DYKVVKAQLQ EQKFLKKMLL DRQNSMGSLA NLGKEVANHC EPGERASIEK
6561 QLNDLMKRFD ALTDGAEQRE LDLEEAMEVA KRFHDKISPL ELWLDNTERS VKAMELIPTD EEKIQQRIRE HDRLHDEILG
6641 KKPDFSDLAD VAAQLMHLVS DEEAVNLGEK VRGVTERYTG LVDASDNIGA LLAESRQGLR HLVLSYQDLV AWMESMEAEL
6721 KRFKSVPVYA EKLLEQMDHL LELNENIAGH ASNVESTVES GAELMKHISN DEAIQLKDKL DSLQRRYGDL TNRGGDLLKS
6801 AQNALPLVQQ FHEAHNRLVE WMQSAEAALA PSEPRQADVL RLEGELADMR PILDSINQVG PQLCQLSPGE GAATIESIVT
6881 RDNRRFDSIV EQIQRKAERL HLSNQRAKEV TGDIDELLEW FREMDTTLRE ADLPAMEPKL VRAQLQEHRS INDDISSQKG
6961 RVRDVTAASK KVLRESPQSE NTATLREKLD DLKEIVDTVA QLCSERLGIL EQALPLSEHF ADSHQGLTAW LDDMEQQISR
7041 LSMPALRPDQ ITLQQDKNER LLQSIAEHKP LLDKLNKTGE ALGALVADDD GAKINEILDT DNARYAALRL ELRERQQALE
7121 SALQESSQFS DKLEGMLRAL ANTVDQVNQL DPLSALPQKI REQIEDNDAL MDDLDKRQDA FSAVQRAAND VIAKAGNKAD
7201 PAVRDIKAKL EKLNNLWNDV QNATKKRGSS LDDILSVAEP FWKQLNSVMK TLKDLEETLS CQEPPAAQPQ DIKKQQVALQ
7281 EIRHEIDQTK PEVEQVRRHG SNLMNMCGEP DKPEVKKHIE DLDNAWDNIT ALYAKREENL IDAMEKAMEF HETLQNLLKF
7361 LTKAEDKFAH LGAVGSDIDA VKRQIEQLKS FKDEVDPHMV EVEALNRQAV ELTERTSPEQ AASIREPLSV VNRRWEALLR
7441 GMVERQKQLE HALLHLGQFQ HALNELLVWI NKTDSTLDQL KPIPGDPQLL EVELAKLKVL ANDIQAHQNS VDTLNDAGRQ
7521 LIETEKGSVE ASTTQEKLRK LNNEWKQLLQ KASDRQHELE EALREAHGYI AEVQDILGWL GDVDAVIGAS KPVGGLPETA
7601 TEQLERFMEV YNELDENRPK VETIQAQGQE YIKRQNQMKV SSSNLQHTLR TLKQRWDAVV SRASDKKIKL EIALKEATEF
7681 HDTLQAFVEW LTQAEKLLSN AEPVSRVLET IQAQMEEHKV LQKDVSTHRE AMLLLDKKGT HLKYFSQKQD VILIKNLLVS
7761 VQHRWERVVS KAAERTRALD HGYKEAREFN DAWSGMMQYL QETEQVLDQI IEEATASKEP QKIKKYIGKL KETHRQLGAK
7841 QSVYDGTMRT GKNLLERAPK GDRPVLDKML IELKEQWTRV WSKSIDRQRK LEEALLLSGQ FSDALGELLE WLKKAKSRLN
7921 ENGPVHGDLE TVQGLCEHHK HIEQDLQKRA AQMQGVLKTG RDLERSGNNP EVGRQLDEMQ SIWEEVKSAV AKRGERLQVA
8001 LVDAEKLNAR VQALFDWLDH AEHKLRYAKN APDDEKVSRE MMDIHMDFMK DLRVREREKT ETFEYAEDII NKAYPDAIPI
8081 IKNWLSIIQQ RWEEVRQWAI NRESKLEQHL QSLKDLDDTI EELLAWLSGL EGTLLNLKHE QLPDEIPPVE KLIEDHKEFM
8161 ENTARRQNEV DRACKPRQLP PGARKPSRSG KTPVFKGSRD QGLNARKGSR ITPTRDTPDR DRLPHYGPRF SPSTSGPELE
8241 FRSPRAKLLW TKWRDVWMLS WERQRLLNDH LLYLKDVERA RNFSWDDWRK RFLKYMNHKK SRLTDLFRKM DKDNNGMIPR
8321 DVFIDGILNT KFDTSGLEMK AVADLFDRNG EGLIDWQEFI AALRPDWQER KPANDSDKIH DEVKRLVMLC TCRQKFRVFQ
8401 VGEGKYRFGD SQKLRLVRIL RSTVMVRVGG GWVALDEFLQ KNDPCRAKGR TNIELREQFI LADGVSQSMA AFTPRRSTPN
8481 AAATASSSPH AHNGGSSNLP PYMSGQGPII KVRERSVRSI PMSRPSRSSL SASTPDSLSD NEGSHGGPSG RYTPRKVTYT
8561 STRTGLTPGG SRAGSKPNSR PLSRQGSKPP SRHGSTLSLD STDDHTPSRI PQRKPSTGST ASGTTPRPAR LSVTTTTTPG
8641 SRLNGTSTIT RKTASGSASP APTSNGGMSR SSSIPALTGF GFKPIRRNIS GSSTPSGMQT PRKSSAEPTF SSTMRRTSRG
8721 TTPTEKREPF RL

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   1 MTSHSYYKDR LGFDPNEQQP GGSNSMKRSS SRQTTHHHQS YHHATTSSSQ SPARISVSPG VAGLSANNGT LEYQQVQREQ
  81 RDRELYSTSS NNNNSHHHHQ QQHHHHQHHH HRHSVGSASS PLYENSNNSP AAPKKAKHSS TQAQPQGGYE DALTQFKDER
 161 DAIQKKTFTK WVNKHLKKHW KYAKTYTMLH VCVTTNGIPC CSQSANRRVV DLFEDLRDGH NLLSLLEVLS GEHLPREKGK
 241 MRFHMLQNAQ MALDFLRYKK IKLVNIRAED IVDGNPKLTL GLIWTIILHF QISDIVVGKE DNVSAREALL RWARRSTARY
 321 PGVRVNDFTS SWRDGLAFSA LVHRNRPDLL DWRKARNDRP RERLETAFHI VEKEYGVTRL LDPEDVDTNE PDEKSLITYI
 401 SSLYDVFPEP PSIHPLFDME SQRRVHEYRD LAQQFIYWCR EKTAYLQERS FPPTLIEMKR LLSDLQRFRS EEVSVRKREK
 481 SKLIQIYKEL ERYFETVGEV DVEAELRPDA IEKAWYRMNT ALQDREVILQ QEIERLERLQ RLADKVQREI KHVDQKLTDL
 561 ETRIGEEGRR IERLHPVDAK SIVEALETEI RHLEEPIQDM NQDCHVLNEG RYPHVSELHK KVNKLHQRWA QLRTNFHTNL
 641 VQKLSGLKYP VHETTVTRQT RMVVESRQID TNPHFRDLQE HIEWCQNKLK QLLAADYGSD LPSVKEELDR QQHEHKIIDQ
 721 FHSKILNDER QQTKFSGDEL ALYQQRLNQL QKVYAELLST STKRLSDLDS LQHFLGQASA ELQWLNEKEQ VEITRDWADK
 801 QLDLPSVHRY YERAFGNGDE NLMSELEKRE MHFATILDRG EALLNQQHPA SKCIEAHLTA LQQQWAWLLQ LTLCLEVHLK
 881 HATEYHQFFG EIKDAEQWLA KRDEILNSKF SQSDFGLDQG ETLLRGMQDL REELNAFGET VATLQRRAQT VVPLNKRRQP
 961 VNRQGPVQAI CAYKQQGQLQ IEKGETVTLL DNSGRVKWRV RTAKGQEGPI SGACLLLPPP DQEAIDAAER LKRLFDRSVA
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1121 KRARAEEESK QASRIFTEEC IAIKSKLEDM ARELDQIILA PLPRDLDSLE HVLEIHADYE RRLHLLEPEL KHLQETFRTI
1201 ALKTPVLKKS LDNLMELWKE LNTQSGLHKD RLKLLEASLA GLEDNEHVIS ELENELARHQ DLPSTAEGLQ QVFKQLNHMQ
1281 DIITQQQPQM DKMNDAADQL GRMGVPTKVL GDLKRLHSNV ERLNTRWSAV CNQLGERMRS CETAIGLMKN LQSSVQVEES
1361 WVDGTTERLS AMPTATSAYE LDKLLGAAIE RKPKIENVNV AGGRLIREAK IYDSKCLRFV DWLLEARPSF SPPRRDLRPA

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1521 TTTYSTTQFS STKTTKSSTK SVYSSDGLDA ASQEVSTTNL PQSQIQFNEI RTLKRSQQLG GQSVLDIAGI RDPRTGRVLT
1601 IGEAIQLRIL DVRTGEMLVG DRRITLEQAA DQGLIDAQLA RQLLQPGAGR DASGRELSLL EVIQREISEA ESGFETAEKR
1681 IKVNNTVTVE QQSSTAEIVS PENPRNIADA ISAGSVDTKT GLYRVKSGQT ISLAEAYERG YLIRHESVTI KSNALCLSDA
1761 IAHGLVDGAG WIADRNSGDK FRLDSAIANQ LIDASVREVV DAKRDTKITL QEALQSGVLN AKTGRYVNEV TKEKLTFAEA
1841 RNRQLIVKPY TLKDICDLNL LDKQAQITSP MRREKLSIMQ AIEAGVLDGN LLKCITKRKG ELVTLQEAIA DGIVLPAECK
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2081 TETVTRTINR YVTIRAGSQE PGDSVLLTFT EAVRQGFIDE ERQLFKDPKT GNIYSVQQAL NYGLLVPDSN QTVPEPTNRK
2161 KTKSTITIVT KQIIPEAEPI KLNTQHTKYV EKSVEIPITQ ELVKPQRVVS EFINMEKSSY IEQNVTERQI MELPPGGWRL
2241 KDAIEQKLFN PDTGVFHVQG TDRLVNFEEC INKQIINNLS VSVIDPSTGD KISVQSAFER DILDSYGNYT NSRKQVQGMR
2321 SAIDESKIIL ETVPATRGAN QKTILRITRV NNMPDVLEVS TPLKDAPPKF VEVLTCQREL ASPEPLQIAP GAIYDPSTAL
2401 VIFTQTGETE NIFDAARQGL IDEQLIKIVD PTTKQPISVT EAIARSIYDP RTATILDSEG QPVDLITATK LGLLSVVGAP
2481 LVAAEGALRT VRFVTDPRTG EQIPVEVAYE RGIVSRDQLQ RGRSFDTEPV TVEEKVVVLQ RMRKVILKPK DALRKGIIDE
2561 ETCEILENTN NFTNPKGEVV NISEALNTGL IDGRRGQVID PQSNRSLNLR QAVEQKILDP EQTNHILMPL AKSLSVPRLA
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2721 DPSYDKQKSK VEIPPVGMIF PVAVEKSLVE PSKRVVLHPS TKKALPIKQA IEENFIMSIP YSPKADAIEV VTAMERDLID
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2881 GEVCSLEEAK ELGILREEST TRETKAAAGE SPESVAALAT STNDQTVVVE ERTQTVVVSS DTRKQEMQVV STTQSTKEIP
2961 VSSVSEVETK SSKEPSKTLK NVKDAAKMGA LGVIAAPVLA GGAIVSGVKS LFNSGKSPTE DAKTTAKPEK PQSSFIDQER
3041 SNVPKPQQVP SEVDNLLSET ENFISSTTAN FIANEKQQEN PKELTRGEVQ PTVVESTSTL TTTTVTTITT SKTTTETENQ
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3281 IAEIEPPFTA PLAPFVDPVS ETKITEITTE IQEPITSSQT ITTITKTVKT IEEQPTTEDV TVIGESEPEK IVDVQVKEPT
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3521 VVDFIEREKG PQPADGSGSN ILKNVKDAAK LGALAIVGAP VLAGKALVDA LTTEKAVKPG QSTTQVVTET VEELPTEEIS
3601 TSTSTLITKV TTTTTTTTTS TVEGTPEDES RDVVEMPAEI VETTIKREVP RTLPIGDAIS QKLISPDECQ VIVDGEQQSQ
3681 TVATLLKEEQ LSPLDEVQII DDKLIVLQQV TYLVDVDTEL TPESLSELNI YDPENQYFID PSSGQKVSFH TLVFEMNVFN
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3841 DDGRVCSIVE AINSGKLDIQ SISVRDPVSG EVIPLRMAIE LGVVDMQAGT VIDIQTLKEI PMERAFQLGF LVPGARKPIS
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4001 PFDVGVQQRL VKTDSVTWSL PELLQREYYT PSTGKVLNPV TGEEILLQQA IEMGFVELET TLVKDADHDK ILPGKEAAKV
4081 GLLDTVRGTL SSPNISLDEA FVKGYLISTK KPLSLVDCLL RGLYDPSTAK FTIDDKQLDL KSAIAQKLIN PEELVLLDPK
4161 TESIISITEA IAKGYLDPIA GYVINPYAST KLSLHEALEN RILIPPKRKR SLPDAVYRGL YDPKTGQFSN TVTREKLTTE
4241 RAIRRGILDP DSTVVNLGSG QIVPFGVATE SGIVDSKQGT VRDADDNPID FKEAFDRGVL VEAKKPLRLI EAVVKNVYDE
4321 VDGHFVDPKS GEKLNFAEAL NTNLLDEHSV QIRDFKTGLY KQLNLTHAKD NGIIDAQNSK LLYNNQTMTL KHAFDIGILM
4401 DVNAPISIQR AIHQGLFDDK TGKLSDPRTG RQITLLESMR SFVINPHLPC YFDEQTEQMY TLSETCRNGI INRREGVFRE
4481 PGSNNFVPLG EALSLGLIVD IENAGFGLYE LLSMGFYDVN TRKVLHPVTN RKLNLNEACV EDVVSLSSSL VKHHETGKYL
4561 RLANAIKEQL IDDTRGCYNL GNEQLDLQAA RARGLIVSNR RLLSLELVLR QQLYRPETGK FCDPTTGEYL DLIEAIHSGF
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1431	1435	
total 1 peptides												

tr|A0A1W4VBG9|A0A1W4VBG9_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

4641 IDFATTVFKN QLTGKELPLT EAIENGDIDV SKGRVFDPKS KSAYNYDVAL SRGILVTITR PLTDRNDVVR RQDSVELLGQ
PYSLAVERGL VDTTKRTLVD PKALYFAFDP TLIVYVREPV
4801 TFDQAAESKC LDLQTGMLTY VPASAPGSAP AASASDDSAN DSLTVIETPR VYTLKEAASA GVVDPDSALV KDLAKAKLVR
5041 EENVNDLLKW VTTVEQKISS VGGPREKIDE LRNQINALKQ IKDEIESQQR PVATCLEQIR QIVLTGGDVL SAPEVTTLEN
5121 SGRELRSRVD RVNDRTVRLL RRLEAGRDEL TKLRSELDVF SDWLQVARRT LEDKERSLSD LTRLPSQADS VREFVSDVIG
5201 HQADLRFITM AAQKFVDESK EFLAILNDFR TSLPERLPHV EPLSTAESPI RQEVSLVSAQ YKDLLNRVNA LQDRVSGLGG
5281 RQREYQDALD KANEWLRSVH PRVSRIISEP IAGDPKGVQD QMNEAKALHN ELLSNGRLVD NAQQALDNLL RSLGGQLSPM
5361 EINQLELPIA DLKNNYQQLL DNLGEHCKTL DKTLVQSQGV QDALDSLVGW VNQAEDKYNL NLRPASLIKE RLQEQIREHK
5441 VLLADLQSHQ ASIDSVQISA KHLLASASNA RIAKKVESNL NDVTGKFEKL YEKANKRGEF LDDVYNRLGR YLDEISTVEQ
5521 RMANLQEALD GRETSLLSTE ELARRMNELS RDKDQLAPQF EDCVRNGKDL ISLRDVTDTG VLRDRIKALE SQWRNINISI
5601 DERAKLSKQK AEQQLAYEGL KDQVLSWLAS TEARVNGLAP VAIDLDRIKQ QHDELKPICK DYRDYAPTID KINDIGSQYD
5681 ALIRPESPAR KRSTYSPIKR ASPLRRMSGD ARSPSPTKGG ILSPLSTGSS GFGSRRSSQD GFQLSEMSPV QQQLSEINNR
5761 YGLIGVRLND RQHELDNLSE ELRKQYENLK GLAQFLERIQ RQLPKESVSN KDEAERCIKQ ARKILEDMYE KQSLLDTTKA
5841 QVKDILRRKS DVPGAEQLRQ ENDNIQERWK NLNDICKNRI AFSEKLRDFL DTHGNLKSWL DSKERMLTVL GPISSDPRMV
5921 QSQVQQVQVL REEFRTQQPQ LKHFQELGHD VVDHLAGTPD AQAVEVKLKD ILGKWEDLVG KLDDRANSLG GAADSSKEFD
6001 AAVNRLREAL QNISDNLDAL PSDGDHQENL RKIENLERQL EGQRPLLADV EQSAATLCNI LGDPASRADV NSRVAALEKQ
6081 YLALQKKLDT KKAETEASLR DGRHFAENCS KTLGWLGGEL SNLTDRLLVS AHKPTLQHQI DTHEPIYREV MAREHEVIML
6161 INKGKDLSDR QQDRGVKRDL DRIQQQWEKL RREAVDRHTR LQTCMEHCKK YSQTSETFLA WLRTAEDKLA DLTPGVLSKA
6241 KLETRLRDLQ TFRSEVWKHS GEFENTKGLG ETFLTSCDID KEPIKAELQD IRDRWERLNN DLIARAHEIE NCSRRLGDFN
6321 DELRNLDHSL GRCEDRLAAH DALGGAAKDP KLLERVKAIR EELTNLSKPL QSLKALAKDI SAEARAAGGD ADHLTNEVDG
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6481 LEDAERAADV LVDAGFAADT TQTREQISTL RKTLGRLDNR VRDHEDNLQA TLKALREFYD SQSQTLDDIQ DVSDEFKRMK
6561 PVGSELDQIR RQQEDFRNFR ERKVEPLAIN VDKVNVAGRD LVRSAGSGVS TTAIEKDLER LNDRWNDLKE RMNERDRRLD
6641 VALLQSGKFQ EALAGLSKWL SDTEEMVANQ KPPSSDYKVV KAQLQEQKFL KKMLLDRQNS MGSLANLGKE VANHCEPAER
6721 ASIEKQLNDL MKRFDALTDG AEQRELDLEE AMEVAKRFHD KISPLELWLD NTERSVKAME LIPTDEEKIQ QRIREHDRLH
6801 DEILGKKPDF TDLADVAAQL MHLVSDEEAV NLGEKVRGVT ERYTGLVDAS DNIGALLAES RQGLRHLVLS YQDLVAWMES
6881 MEAELKRFKS VPVYAEKLLE QMDHLLELNE NIAGHASNVE STVESGAELM KHISNDEAIQ LKDKLDSLQR RYGDLTNRGG
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7121 SSQKGRVRDV TAASKKVLRE SPQSENTATL REKLDDLKEI VDTVAQLCSE RLGVLEQALP LSEHFADSHQ GLTAWLDDME
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3601 TSTSTLITKV TTTTTTTTTS TVEGTPEDES RDVVEMPAEI VETTIKREVP RTLPIGDAIS QKLISPDECQ VIVDGEQQSQ
3681 TVATLLKEEQ LSPLDEVQII DDKLIVLQQV TYLVDVDTEL TPESLSELNI YDPENQYFID PSSGQKVSFH TLVFEMNVFN
3761 PETILVKNFN TGKYENLTTA LERPLLDRHT GHMVDPKTGK KIPFFECIAR QWIIRANPEE QRPSGMENVT IDTQTGQVVL
3841 DDGRVCSIVE AINSGKLDIQ SISVRDPVSG EVIPLRMAIE LGVVDMQAGT VIDIQTLKEI PMERAFQLGF LVPGARKPIS
3921 LEAAVRKGLY DPETGKLFDS ESQNQVDVQK SIEIGLVDPK ISLIVDTVTK KEVKLDCAIE DDLVLPATGQ IKDNKNNTLV
4001 PFDVGVQQRL VKTDSVTWSL PELLQREYYT PSTGKVLNPV TGEEILLQQA IEMGFVELET TLVKDADHDK ILPGKEAAKV
4081 GLLDTVRGTL SSPNISLDEA FVKGYLISTK KPLSLVDCLL RGLYDPSTAK FTIDDKQLDL KSAIAQKLIN PEELVLLDPK
4161 TESIISITEA IAKGYLDPIA GYVINPYAST KLSLHEALEN RILIPPKRKR SLPDAVYRGL YDPKTGQFSN TVTREKLTTE
4241 RAIRRGILDP DSTVVNLGSG QIVPFGVATE SGIVDSKQGT VRDADDNPID FKEAFDRGVL VEAKKPLRLI EAVVKNVYDE
4321 VDGHFVDPKS GEKLNFAEAL NTNLLDEHSV QIRDFKTGLY KQLNLTHAKD NGIIDAQNSK LLYNNQTMTL KHAFDIGILM
4401 DVNAPISIQR AIHQGLFDDK TGKLSDPRTG RQITLLESMR SFVINPHLPC YFDEQTEQMY TLSETCRNGI INRREGVFRE
4481 PGSNNFVPLG EALSLGLIVD IENAGFGLYE LLSMGFYDVN TRKVLHPVTN RKLNLNEACV EDVVSLSSSL VKHHETGKYL
4561 RLANAIKEQL IDDTRGCYNL GNEQLDLQAA RARGLIVSNR RLLSLELVLR QQLYRPETGK FCDPTTGEYL DLIEAIHSGF
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Supporting Peptides:

4641 ...FKN QLTGKELPLT EAIENGDIDV SKGRVFDPKS KSAYNYDVAL SRGILVTITR PLTDRNDVVR RQDSVELLGQ

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SPPRR.D	Y	24.15	611.3503	26.1	612.3736	1	50.03	4673	1	1431	1435	
total 1 peptides												

4721 ... PYSLAVERGL VDTTKRTLVD PKALYFAFDP TLIVYVREPV

4801 TFDQAAESKC LDLQTGMLTY VPASAPGSAP AASASDDSAN DSLTVIETPR VYTLKEAASA GVVDPDSALV KDLAKAKLVR

tr|B4LHD0|B4LHD0_DROVI

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| Protein Coverage | Supporting Peptides |

5041 EENVNDLLKW VTTVEQKISS VGGPREKIDE LRNQINALKQ IKDEIESQQR PVATCLEQIR QIVLTGGDVL SAPEVTTLEN

Protein Coverage:

5121 SGRELRSRVD RVNDRTVRLL RRLEAGRDEL TKLRSELDVF SDWLQVARRT LEDKERSLSD LTRLPSQADS VREFVSDVIG

1 MSQRGKRGNQ QQLQQQPPQ QQLRQDVEPQ PPPTKRRKGR PPNGAPATAA AAAASTTATA TVAAATTTVQ SNNNSNNNSS
81 NNNNNNSSSS STWQARSVAD IKMSSIYNRS STEAPAELYR KDLISAMKLP DSEPLANYEY LIVTDQWKQE WEKGVQVPVN
161 PDSLPEPCVY VLSEPIVSPA HDFKLPKNRF LRITKDEHYS PDLHCLTNVV ALAENTCAYD IDPIDEAWLR LYNGDRALCG
241 AFPINETQFE RVIEELEVRC WEQIQVILKQ EEGLGIEFDE NVICDVCRSP DSEEANEMVF CDNCNICVHQ ACYGITAIPS
321 GQWLCRTCSM GIKPECVLCP NKGGAMKSNK SGKHWAHVSC ALWIPEVSIG CVDRMEPITK ISSIPQSRWA LICVLCRERV
401 GSCIQCSVKT CKTAYHVTCA FQHGLEMRAI IEEGNAEDGV KLRSYCQKHS MSKGKKEGAA SSHHTAASSC MQKHNNKFSS
481 SGTAAGDDAG HTTTGAKGED HRRRKNHRKN DMTSEERNQA RALRLQEVEA EFDKHVNIND ISCHLFDVDE DAIEAIYNYW
561 KLKRKSRHNR ELIPPKSEDV EMLARKQEQQ DLENHKLVVH LRQDLERVRN LCYMVSRREK LSRSLFKLRE QVFYKQLGVL
641 DEAVQQQQQQ QLVPTEQQQP QQAQRPALDT DAIIYANDGP TLYDSFYSST DQLTVPAQYR SLDYILEQLM GRKQARGRAS
721 QSPNKRKQAA AAALKSSPKK KLNNGAITTN TTTATTLAQK AAKPRGSPRA PTTTASTAMP CAGRRASKSG PATAATSSQQ
801 HKSHKSTAAA SAATSSGSSS SADSSSARSS SASSSSSSDS GSASGSGSES NSDSRGYHGN KSQPAAGAVK KQSYARSVEQ
881 RQRQRQRRQS EAAACASAAS AGARTSCSSS SSDDDDDDRA RARARARERE RERERERERV KRQHKSTAVP AKSQATKSKH
961 SEGARPTGAG TGAGSGAARR KQAASNGGGA SAAPTGATRG LAQMDKEMRQ QEPGSMSSDE SEELLPVKHA RSTTNSRNTS
1041 ATAGNLAAAA ATGATATSAM RKMGQHIYSD SDSSTTSTPE REAAGQHHRT ETEAEQAATE SNVSDSQNQQ TIRTKAAMKE
1121 FVPGTTPTAA TGTQNKSKAN AKSNSSKGSA APVFPPVDLL VVPQRQAAKK ASENMRNSTN LATALLPDAS ERLREPEPSP
1201 ANANASSGSS KAKDEAEKTR PKELPKAAAK TTGEARAERG KRGRPPKQQK EKEKEKEREK EKEREKEKEQ EKEREREKPK
1281 EKEKPTPAVT PKNNELAKLG NFAVSYVPQR QAAKKAAEQL KSSGAALAKA TQETIASEDA VGAAAGTSTG AAAANTTTPP
1361 SRATASTTTT TTTPPSRAAA SKQQQQTTPL RRGSQLRRSK EEQTPVKRRI AAPNLSSSSS GESNSSSSGE SNSSSSASSN
1441 AATAAAPAPA PAPAGASITS SSSSSVPKRS PRKSLDKPAA AAVPPPPPPP PLASRTRQNS TNKSPKRTPQ KTAPAPTQEL
1521 VTPPAPPKAS TQRRKSSLDD ASPALSKRAT RNSKSRPPSP APAPTPEKLT SSRRKSRAES PKKTPPNLEH EIAQRKAATG
1601 GRASSALDKL LDKKQQQLNN ATPAPTASTA TTATTTPTIT RVPTPTPTPT PPPQTQRSPP PEPAAEDRLV QRSPTPPAAQ
1681 EAGEQPMDID EELTTAPTHT QLSANASKLA ELSADIDERP PAAPLPASPT PTPSNDELSD EDRSGSDRSR SDRRRGNRWR
1761 RRRRRTRDED EEEQEHTHHT QHLLNEMEMA RELEEERKNE LLANASKYSA STSSPAVTVI PPEPPEIIEL DSNSNSGEQQ
1841 QVQQAQQVQA HDSLLPVVPS VPSVPATPSC SALELDAAHQ PIVDAILELE DSKYANSYAS SLASSVANVL NPPNSGRLTS
1921 LLGTSLVGGG SKQIFEEDST LATRNLVEKL RKTKRKAQLD ECKDTMDLLP PTPAIPSVFP FHNAADPEDV IHVQKELQQA
2001 QQQAAQHQNL VLFGSSAPNS VASQLTIKDS PLTANSGGSY ANSLTNTPNA TPTTNANNNL GGYSSMVNYQ TAQAALSCYL
2081 NKSSVSPQLQ QQQQKSSNGQ GAGGGGGAGM GAAAGGAGMG ATGAPQSTPD FVDLAAAAVK NSLGSYPGAG GATVPSVQPN
2161 SGLVAATNSQ ANNNNNKLSD YDENTRMQSP FGRMQRWNEN DLIAARRSSS PSSVSESNDQ PPSLDKSYFN SYAGAGTGAP
2241 G**IGATA**ACNN NNNNNNNNNN SAAGSGTGSG SGSGSGAFGS HTPLVNGIDA MSMYNNQTQQ PVQPVQATTT PTHQQAQPQR
2321 TPNSQQYNGG IYPQLAAIIQ AQQSTPAESQ TIYGNSSQSQ PSTPYVSTPY ATPNMTLTPN HQYQLTPPYA AALLPAIMQQ
2401 QQQQQQQLEQ QQQQQQQLEP VQLETVPVPV AVPVPVPQSL PQSLPLTVPV PVPSKELISP SKRSSSSSSS ASAKREQQKK
2481 SPQLPPGKSP GKSPRQAAVA ALQPPPPLPV PSTVPTATPT PPAKYDPLTH TLAGKLRQRA PRGSSSGSGA AGTRGRGRGR
2561 GRGRGGSSGN AMLPLPPPMA DYGSNTHIVN NLVGTPYEFN NYDDELSGSG VENLQSLRDR RRSFELRTPG AAPSTTSYAS
2641 CKLRGQNKTA AGTTSATATS AATSSATSSS AAPANPLLQP VLPGPVDMRT YNLGFEAPHS SASQEAYQNN LLGAFDSGTA
2721 DQTLSEFDEE DERQFQSALR ATGTTSSNSN NHNNNNNNNH NGNKTAGGGG GGVSVPSLQP SLLQGALLHS SEANQSAPTL
2801 LTELLPAAAA AAAALEASLE ATSEEVSIDS DTTTMLNTKA SLSDARNQLK IKGPLAYPDL HYSSSVTQTS CQLSTGAGGA
2881 SSLVQTQVQV QTTVTASSVA TGSSSSAAAL SVSGNSRRMR KKELLSLYVV QKDTLNDDSS CGLPAASDSL PLEKLDKLDE
2961 EQPATTATSG NAKRFKKNSS NRELRALDAA NACLEEQEEG AGASAGGAAG AAAGDGRRRS ACSSGSATDN GKTGAASSAG
3041 KRRGRSKTLE SSEDDHHQAA AALAAATAPK LKIKIRGLPS EAQELERSGG SGTSYSYEMT RRACPPKKRL TSNYSTPTLE
3121 EIKRDSMNYR KKVMQDFDKG DDNNSRRELA GGANESQQQV LKPKKDKKDK PKKDKKEKKR LKQQLLLQQQ QQQQQQLFSL
3201 NSCGGNILTS TMTTTLIENR LSASPGEKPK LILRINKRKA ETTTTISLDQ QQQDKPQQEK QQQEKPEQQQ QQQQMEAPLR
3281 LKIARISAGG VYVIGAKTET KEIAKEPAPA P**APASS**PAEL PLVAASPLTN NSSFTPHSQN ANASPALLGK DASTPSPPCL
3361 IIDSSKSADV HDSTSLPESG GAGPGAGVGA GGGSGAAVAA VAVVGAALSS SSPLCVNVGN YDNSNNSLPS ASGSGSSNSC
3441 NSNSNNNNNN NNNNNNNNNG NNNNNSRGGG ALLPLKKDCE VR

Supporting Peptides:

...TTP RPARLSVTST TTPGSRLNGT STITRKTASG SASPAPTSNG GMSRSSSIPA LTGFGFKPIR RNISGSSTPS

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.APASS.P	Y	15.15	431.2016	-2258.5	431.2350	1	39.71	3502	2	3312	3316	
G.IGATA.A	N	15.02	431.2380	2589.0	433.3617	1	14.06	998	2	2242	2246	
total 2 peptides												

tr|A0A293N017|A0A293N017_ORNER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRNLFTSLGF KVTLTDGFVR TQRIIDVLQG VRDQIGHSDQ IFVAVIMAHG ARGKIKSCDK DVELKKILEI FNNSNCPTLR
81 GKPRLFFIQA CQVERHDERE PQRTASDENI YWNCDVDLYK DCLLSLATPP GFVAWRHRDK VTYLSALRS**V FTQNINDR**KD

161 GSSPPDITEL LSTVASKVAY ELEALDTEES EKKMKQMPYF MSALTKKLIL TPGKAS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VFTQNINDR.K	Y	22.09	1105.5516	49.4	553.8104	2	24.22	1771	1	150	158	
total 1 peptides												

tr|A0A293N044|A0A293N044_ORNER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDSYHIERDN KGHCAIINIT DYQGLCPNRD VNDGRLMRNL FTSLGFKVTL TDGFVRTQRI IDVLQGVRDQ IGHSDQIFVA
81 VIMAHGARGK IKSCDKDVEL KKILEIFNNS NCPTLRGKPR LFFIQACQVE RHDEREPQRT ASDENIYWNC DVDLYKDCLL
161 SLATPPGFVA WRHRDKVTYL SALRS**VFTQN INDR**KDGSSP PDITELLSTV ASKVAYELEA LDTEESEKKM KQMPYFMSAL

241 TKKLILTPGK AS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.VFTQNINDR.K	Y	22.09	1105.5516	49.4	553.8104	2	24.22	1771	1	186	194	
total 1 peptides												

tr|A0A0L0C4S2|A0A0L0C4S2_LUCCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MVNIIWGSPP LTGTGIVKVI VQDMNDHSPE FERQSYHATV QENQAIGTKV IQPIANDKDA GLNAKIRFTL LGEKLERFHC
  81 NAETGEITTA AILDREETAV YFLTLMAQDS SATEPRATAV NLTISVQDVN DNMPRFEANQ YHINIPDKTG QNEFVFGAWA
 161 RDNDEGLNAL VMYNISGKDV EYFTINAKTG VIKTKRNLGS DLNRQYSLVI HAYDQGIPSK SSQSDLMISM KPSSSFPSFN
 241 YMANTQFMLS EDVAPGKKIT TITASSPKKG SAGNIKYSIA GGNLGEAVRI DSTTGVVTIG KDGLDYELSS QYEIWLEALD
 321 SDRLPLRSVM LLTINVTDAN DNAPVMEKLI YNAEVMEEES PPQTIVKVKA NDRDSGDNGE VTYRLLDDFE GTFEIDADSG
 401 EIYTTMRLDR EEMSHYELTV EAVDQGMPQL TGSATVLLNL LDKNDNPPKF TRLFSVNVTE NAEIGSFVIQ VTSMDLDEGP

 481 NANAIYTLTE NPGEKFKLDS ISGNITVDGH IDREEQDEYI LKITASDGAW RSDTPITITI QDQNDNAPEF ERGFYSFNFP
 561 ELQRAVAFVG QVVANDRDKH GPNSVISFSL QHPSDIFTID PATGEIFSKK SIKYKHSQYE ASPENVYTLT VIATDNGKPP
 641 LYSECMININ IVDANNHAPK FEKSLYLSPV PEHARVGQRV VRVQAHDSLD TGVNAEVEYS FKQGNGTEFF SISHQDGWIS
 721 LSKTLEVTPN TLFYLNVKAS DHGVPSKSDE TRVHIIVTGE NRYSPEFTVL SYQVIVPENE PVGSTILTVS ASDRDEGLNG
 801 MLRYAIAGGN ERSEFKVDAE TGAVIILQPL DYDSIQEYHL NISVQDLGFK PKTAVAQLTV ILTDINDNPP LFNQSEYHAF
 881 ISENKPANSY VFRAQAKDKD SPKNAIIRYS ITSGSGKNFF AINANTGVIT SSVSFDYEER NEYLLQVMAA NPDSQMHSMC
 961 KIIVHIRGVN EFYPQFVQPV FHFDVSESAE VGTPVGSIQA TDKDAGEDGN VYYLLVGSSN DKGFSINPST GFIYVSRHLD
1041 RETQSRAVLT VMAKNYGSIR GNDTDEAQVI ISIQDGNDPP EFLKSLYMAK ISEAAAVGSK VVNVKAVDKD VRPQNNQFSY
1121 SIINGNINQT FKVDPQTGEI ATSKKLDREQ VPEYNLVVGA IDTGLPPQTG TTMVRIELLD VNDNGPTFSN DGLIGYISEN
1201 EPAGTSIMTL SATDPDLPPN GGPFMYYLIG GKHKAFITID KHSGLVKSTR SFDREQTPEL EAIIEVEDNG QPKQKAQHKL
1281 IIKVLDQNDS PSSTRTVHVL LNVFNDNMPI GKIADVHPND ADVTGNYRCR IIPSSQSSPM GLLIIPNACD LHTTYQTSVN
1361 NGYSYSISGN DGKHGDVVST VTVGFQNFDN STIANSITVL IRNMTAENFL ASYYRNFVDL MKSAVDSSEN LLVYSVRNTT
1441 YNSTDLEVMI ALKMANQGYR LPHYLVDRLS KKREAVTRLL KTATNVVIGY DPCSLSQACD NGGLCTSERR LHDSETLNIV
1521 DSESLIFSGP LVTHDFICKC PDGFMGQQCD KRQDPCAPNP CHGNAQCRRL GYDFQCNCPA NREGKYCQQE RGDVCSGNPC
1601 SNGGSCRSSP DGSSFFCLCR PGYRGNQCEH VADSCRPNPC LHGGVCVAIK PGYKCTCSEG RYGRHCEKTT FGFGDLSFMT
1681 FPPLDAATND ISVVFATTKP DALLMYNYGI QSGGRSDFVA IEVVRGKAFF SFGGARTAIT TVVVGGSNNL NLADGNWHKV
1761 TATRNGRVMS LSVANCVENG DVCEECRPGD TTCYADDVGP IGTLNFNKQP LLLGGLISAD PVLERPGQLH TDDLVGCVHS
1841 VSVNGRALNL SQPLKQRSIS ITCNRNLNGG PCIQSTNTDL TANLCGPFGS CMDRWDTAMC QCGGSLLSPD CQNSLEPISI
1921 TDGAFIEFKI TEKHRRMQLL DNLYAGNSIW SYDISRQRRF TIDHDNLTAL AQTNELPKTL SLMFRTYKEN GLLLFAASNN
2001 HYTSLELQNG KMVYYSNQDS IVNMTISNPA KLNDGKWHNI TLHSVNRILR IIIDDARAGE ELDFAGVHDY LDPYLTVLSV
2081 GGVRREYLLQ EHMPTNYEGC FANFTINNEI QPFNGSGSVF SEVLSRGKIT HGCAGVMGIG AAQVADPISI GVTLVIVFFV
2161 ILVVAILGSY VIYRFRGKQE KIGSLSCGVP GFKIKHNPPS TMLGGAGVSQ NPADHVLSRG MHGNEAQVGY HNDNGDLIRS
2241 VPGHHMVGPE LISKKFKERE INPGEHQQQR PQRPDIIERE VVSKSPPLRD EHHPPIPPPS QSHHPHDHAS SVDMGSEYPE
2321 HYDLENASSI APSDIDIVYH YKGYREAGGV RKYKATPAPV ASYTHHKHQS AASQQQHRHS PRHGVGGPFV PRGVPPQANQ
2401 PPPPSSTPRQ HQSTPLARLS PSSELSSQQP RILTLHDISG KPLQSALLAT TSSSGGVGKD ALHSNSERSL NSPVMSQLSG
2481 QSSSASRQKP VVSAQTASQA PMGLTAEEIE RLNARPRTSS LVSTLDAVSS SSEAPRGPVG AHHLSLSGGL HSTDVDAHSS
2561 TSTDESGNDS FTCSEIEYDN NSINGDAKFS TSKSIPDERN PVGRAMSGDG SRGSAVAKAP PMPPHSFDGF DSSFRGSLST
2641 LVASDDDVST HMGALYRQVN SAASPTAPPP MGWEYLLNWG PNFESLVGVF KDIAELPDNV GSDQRATGSL RMNQGQNKQS
2721 EEYV
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.NLLDKNDNPPK.F	Y	21.66	1266.6567	4.7	634.3386	2	27.99	2188	1	439	449	
total 1 peptides												

tr|A0A1A9W0E4|A0A1A9W0E4_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MITKRTDRNK PTWNLLLKRV RSPPLTGTGI VKVIVQDMND HRPEFERQSY HTSVAENLPI GTKVLQPKAT DRDTGLNAKL
  81 RFTLLGEKLE RFHCHSETGE ITTAAVLDRE ETAMYFLTLM AQDSSTTEPH ATAVNLTINV IDANDNMPRF EASNFNVNIP
 161 DKTSGGEFVF GAQAEDMDED LNALVMYNIS GKDAEHFTIN HKTGVIKTRF SLKSELSTVY KVVIHAYDQG VPSKSSVTDL
 241 SISLKPLTAF PSFNYIANTQ FLLPEDVPEG KVITTVMATS PKKGSASNIR YSIAGGNLRE AVRVDQSTGM VSIGKDGLDY
 321 ELSPQYDIWL EASDSDRTPL RSVMLLSINV TDANDNSPIM EKLIYNVEIT EEETPPQTVI KVKGHDRDSG DNAEISYRLV
 401 DDYEGTFEID ADSGEIFTNL RLDREELEHY ELLIEAVDQG MPQLTGSATI LLNLLDKNDN PPKFTRLFSV NVTENAEVGS

 481 FVIQVTSIDL DEGDNANASY SLTENPGEKF KLDAVSGNVT VAGHIDREEQ DEYILKITAS DGAWRSDTPI TITIQDQNDN
 561 APEFERPIYN FNFPELQRSV AFVGHVTAID RDKHGPNSVI SYSLQYPSDL FAIDPASGEI FSKRSIKYKN SQFEASPENI
 641 YTMTVIATDN GKPPLYSECI VNINIVDTNN HPPKFEKSQY LSPVPEHARV GQRVAKVHAF DALDSGVNAE IEYSVTKGNG
 721 SDYFTINKMD GWITLIRSLE VQPNTLFTLV VTASDHGVPS KMDQSRVSIV VTGENRFTPE FTALSYQVIV PENEPIGSTI
 801 LTVSASDRDE GPNGMLRYSI SGGNERSEFK VNVETGAITI HQPLDYDLIQ EYHLNISVED LGFKPKSTMA MLTVILTDIN
 881 DNPPLFNQTQ YHAFIPENRP PHTPIFKASA TDRDSPKNAM IRYSVVSGSG KGLFIINSNT GIIYSSASFD YEERHEYALQ
 961 IMAANPDSPM HSTAIITVHI TGVNEFYPQF VQPVFHFDIS ESADVGTPVG SIQATDKDAG EDGNVYYLLV GSSNDKGFSI
1041 NPSTGFIYVS RHLDRETQSR AVLTVLAKNY GSIRGNDTDE AQVIISIQDG NDPPEFLKTL YSEKISESVL PGTKVITVKA
1121 VDKDVRPQNN QFSYSIINGN LNQTFKIDPQ NGDIETSRKL DRETIPEYNL IVGAIDIGSP PQTGTTTVKI KLLDVNDNGP
1201 TFSESGLIGY IYENEPPGTT IMTLSATDPD LPPNGGPFTY HLIGGRHKTS ISIDQHTGLV KSTRSFDREL TPILEAIIDV
1281 EDNGQPKQRA QHKLIIKVLD QNDSPSSPRT VHIILNVFNN DIPVGKIADV HPNDDDISGN YRCRIIPSTQ SSPTGLLIIP
1361 NACELHTTYQ TIMNGGYSYS VSGNDGKHGD VISTVTLGFQ TFNNNTITNS ITILIRNMTS EEFLSIHFRN FMDLIKSLID
1441 ANDELILYSF RNVTRLKSTD LEVMLAVKMS THGFRLPHYV SERLAKKHDA MQRLLKSSEP IIIGYDPCSS SETCENGGLC
1521 VSARTLHDMH SLNIIDSESL IFSAPLISHD FLCKCPEGFT GQQCDKRQDP CTPNPCHSNA QCRRINFEFQ CVCPPNREGK
1601 YCQQERGDVC LINSCSNGGS CRSSPDGATF FCLCRPGYRG NHCEHVADSC RPNPCLHGGL CMALKTGYKC SCSDGRYGRH
1681 CEKTTYGFGE LSYMALPSLD TATNDISIVF ATTKPDGLLL YNYGIQSGGR SDFVALEVVR GKAFFSFGGA RSAMTTVIVG
1761 ANSGINLADG NWYKITATRN GRVMSLAVAK CTENGDNCEE CRPGEVSCYS DDVGPIGTLN FNKQLLLLGG LSSADPVLER
1841 PGQLHTDDFV GCIHSISING RLLNMSQPLK QRAISATCTR TTNGGPCSQS FHNDPNLSLC GNFGTCMDRW HSAMCECGGG
1921 LLSPDCFNSL DPISISEGGF IEFKISEKHR RMQLLDNLYG GNNIWSYDIN RRRRFTFAYD NLTALAQMND PPKTMSLLFR
2001 TLKENGLVLY AATNNHYTAL ELQKGRLTYY SIRDSVVNMT ISSTDNLNDG KWHNITLHTT GRIFRIIIDG SRAGEELDFA
2081 GVHDYLDPYL TVLSLGGVRK EFYTQEYTFI NYEGCIANFT INNEIQPFNG SGSVFHEVVT RGKITPGCVG ALGIGAAQVA
2161 DPISIGVTLV IVFFVILVVA ILGSYVIYRF RGKQEKIGGL SCGVPGFKIK HNPASTMLGG PGVSQNQADH VLTRGVHSNE
2241 VQVGYHNDNG DLIRSVPGHH IVGPELISKK FKEREINPAE HQQQRPQRPD IIEREVVSKS PPLRDDHHPP IPPPTQTHHP
2321 HDHASSVDMG SEYPEHYDLE NASSIAPSDI DIVYHYKGYR EAGGVRKYKA TPAPVASYTH HKHQPTASQQ QHRHSPRHGV
2401 AAPFVPRGVP PQASQPPPPA SAPRQHQSTP LARLSPSSEL SSQQPRILTL HDISGKPLQS ALLATTSSSG GVGKDALHSN
2481 SERSLNSPVM SQLSGQSSSA SRQKPVVSGQ TAPQTSMGLT AEEIERLNAR PRTSSLVSTL DAVSSSSEAP RVSGGPHHLS
2561 LGGGLHSADV DARSSTSTDE SGNDSFTCSE IEYDNNSING DTKFSTSKSI SDERNVVGRA LSGDGGIASS VGKTPPMPSH
2641 SYDGFDSSFR GSLSTLVASD DDLSTNMGGL YRQANSAASP SAPPIGWEYL LNWGPNFESL VGVFKDIAEL PDSVANEQHV
2721 TGSLRMSQTG QKTSEEYV
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.NLLDKNDNPPK.F	Y	21.66	1266.6567	4.7	634.3386	2	27.99	2188	1	453	463	
total 1 peptides												

tr|A0A1I8MA30|A0A1I8MA30_MUSDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LKVMILDKND SPPVFRDLPL SFNVSEDLTA GHLIATIRAS DPDTLGTLTF SLMGGDNGKF LLEPETGKLR LKDALDRELK

81 DNYKLRVRVS DGVQHTETVV EIEVTDTNDN PPAFDVPVYS FDIPENAPRG YQVGIITATD PDLGNNAVVT YTVISEWAND

161 VFSLNPQTGV LTLTARLDYE EIQHYILLVQ AQDNGQPSLS NAITVYCNVM DLNDNPPVFD PMSYSMEIYE NVSIGTPVVT

241 VMATDIDSGD NGRIEYTITS GDDNNDFEIF SNGTIRTKRM LDRETKSSYN LIVTARDCAK EFPMMYDDYH DDDDDGYDGD

321 HYQDDDYDGA PASHQYRLRS QQQQQQQKQQ RYPSMPYNLP RQRRQYLQYQ QQQQQLLQNQ QQIAGLSPEP QQRLSSTVQV

401 TIILKDVNDE APIFVSSNYT EILENIPLNT VVMVVKAVDR DEGKNGYIEY SLDGSGSGES HVPFSLGPVD GLLRVSGKLD

481 RETQTSYLLN ITARDRGEPP KMTQSQLYVR VLDENDNAPI FDPKQYTASV AENASIGAMV LQVSATDIDD GANGRVRYSI

561 VAGDENRDFM ISEDSGIVRV SKNLNYERKS RYVLSVKAED SAADLGLAYE NEKGRQKLTH LFENRYDLAE MVIVITDIND

641 NPPTFLDSPY VAYVMENVVP PNGGYVLSVQ AYDADTPPFN SLVRYFLKEG DTDLFRINAS TGEISLLRSL DREAKAEYTL

721 TLVAMDTGSP PLTGTGVVQV IVQDVNDHSP EFERQSYYAT IQENLAIGTK VLQPHAFDKD AGLNAKIRFT LLGEKLERFH

801 CNSETGEITT ASVLDREETA VYFLTLMAQD SSATEPRATA VNLTITVSDV NDNMPRFEAN QFHVNIPDKT GLNEFVFGAW

881 ARDADEGLNS LVMYNISGKD VQYFQINAKT GVIKSQKSLG SDLNRQYSLT IHAYDQGVPS KSSQAELMIS LKPAASFPTF

961 NYMANTQFML SEDIEPGKRI TTIMGSSPKK GAAGSIRYSI AGGNLGEAVR IDASSGVVTI GKDGLDYELA SQYEIWLEAL

1041 DSDRIPLRSV MLLTINVTDA NDNAPVMEKL IYNTEIMEEE SPPQTIVRLK AHDRDSGVNG EVSYRLLDDF EGTFEIDADS

1121 GEIYTTMRLD REEISRYELS VVAVDQGMPQ LTGSATVII**N LLDKNDNPPK** FTRLFSVNVT ENAEIGSFVI QVTSMDLDQG

1201 INANALYTLT ENPGEKFHLD SLSGNITVAG HIDREEQDEY ILKITASDGA WRSDTPITIT IQDQNDNAPE FDHTFYSFNF

1281 PELQRSVAFV GQVVANDRDK HGPNSVISYS LQQPSDVFTI DPATGEIFSK KSIKYKHSQY EASPENTYTL TVLATDNGKP

1361 PLYSECMVNI NIVDANNHPP KFEKDLYLSP VPEHARVGQR VVRVQAHDSL DTGVNAEIHY SFTSGNGTEY FSIGQHDGWI

1441 SLAKSLEVAP NTHFSLTIKA ADHGVPSKSD EAQVQIIVTG ENHFAPEFTA LSYQVIVPEN EPIGSTILTV TASDRDEGPN

1521 GMLRYAIAGG NERSEFKVDP ESGAVIILEP LDYDSIQEYH LNISVQDLGF KPKTAIAQLT VILTDINDNP PLFNQREYHA

1601 FISENRPPQS FVFKAQAKDR DSPKNAIIRY SINGGSGKNY FAINPSTGVI TSSVSFDYEE RREYTLEIMA ANPDSPMHSM

1681 CRILVHIRGV NEFYPQFIQP VFHFDVSESA EMGTAVGSIQ ATDKDAGEDG NVYYLLVGSS NDKGFAINPN TGFIYVSRHL

1761 DRETQSRAVL TVLAKNYGSI RGNDTDEAQV IISIQDGNDP PEFLKSLYTA KISEAVNVGT KVTTVKAVDK DVRPQNNQFS

1841 YSIIGGNINQ TFKVDPQSGE IETARHLDRE QIPEYNLVVG AIDTGLPAQT GTTLVRVELL DVNDNGPTFP PEGLVGYIQE

1921 NEPAGSSIMT LSATDPDLPP NGGPFTYQLI GGKHKSFITV DKHSGLVKST RSFDREQTPE LEAIIEVEDN GQPKQKAQHK

2001 LQIRVLDQND SPSSSRTVHV ILNVFNDDMP VGKIADVHPN DPDISGNYRC RIIPNSQSSP MGLLTIPQAC DLHTTYQTSV

2081 NNGYSYSVSG NDGKHGDVVS TVTVGFQSFD NSTIANSITI LVRNMTAENF LATHYRQFVE TLKSAIDSSD DLMVYSVHNT

2161 TSSMNSTDLE VLVALKMSNQ GYRLPHYVVE RLAKKREVLQ RLMQTTSSSS VVIGFDPCSM AKACDNGGLC TSERRLHDVH

2241 SLNIVDSESL IFSGPLVTHD FVCKCPDGFM GQQCDKRQDP CSPNPCHGNS QCRRLGFDFQ CVCPVNREGR YCQQERGDVC

2321 SGNPCGNGGS CRSSPDGSSF FCLCRPGYRG NQCEHATDSC RPNPCHYGGV CVALKPGYKC NCPEGRYGRH CERTTYGFGD

2401 LSYMTFPSLD AATNDISIVF ATTKPDALLM YNYGIQSGGR SDFVAIEVVR GKAFFSFGGV RTAITTVVVG GNTHLNLADG

2481 NWHKVTATRN GRVMSLSVAK CTENGDSCDE CRLGDSTCYA DDVGPIGTLN FNKQPLLLGG LISADPVLER PGQIHSDDLV

2561 GCVHSVSING RALNLSQPLK QRGISSSCKH NLQGGLCSVG PYSDPATSMC GFLGTCVDRW DAAMCECGAE LMAPNCQNAL

2641 EPISLADGGF VEFQISEKHR RMQLLDNLYA GNSIWSYDVT RQRRFTIERN NFTALAQVSE TPKSLSLMFR TFKENGLILF

2721 AATNNQYTSL ELLNGKISYY SNQDSVVNIT INNSNKLNDG KWHNLTLHTS NRILRFIIDG SRAGEELDYA GVHDYLDPYL

2801 TVLSVGGARK EYLQADHMAT SYEGCLANFT INNEIQPFNG TGSVFGDVHV HGKVSHGCVG VMGIGAAQVA DPISIGVTLV

2881 IVFFVILVVA ILGSYIIYRF RGKQEKIGSL SCGVPGFKIK HNSPATMLGG SGGSQNQADH VLSRGMHSEA QVGYHNDGGD

2961 LIRGVPGHHM VGPELISKKF KEREINPGDH QQQRPQRPDI IEREVVSKSP MRDEHHPPIP PPSQTHHPHD HVGSVDMNSE

3041 YLEHYDLENA SSIAPSDIDI VYHYKGYREA GGVRKYKATP APVASYTHHK HQSAAQQQQH RHSPRHGVGG PFAPRGVPPQ

3121 AAQPPPPSST PRQHQSTPLA RLSPSSELSS QQPRILTLHD ISGKPLQSAL LATTSSSGGV GKDALHSNSE RSLNSPVMSQ

3201 LSGQSSSASR QKPVVSAQTT AQTSMGLTAE EIERLNGRPR TSSLVSTLDA VSSSSEAPRG TVGAHHLSLG GGLHSTDVDA

3281 HSSTSTDESG NDSFTCSEIE YDNNSINGDA KYSTSKSISD ERNPVSRAMS GDGSRGPSVA KPPPMPPHSF DGFDSSFRGS

3361 LSTLVASDDD MSTHMGALYR QANSAASPSA PPPIGWEYLV NWGPNIQSIV GVFKDIAEMP DSVRGDQRPT GSLRMQQQQQ

3441 QKQSEEYV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.NLLDKNDNPPK.F	Y	21.66	1266.6567	4.7	634.3386	2	27.99	2188	1	1160	1170	
total 1 peptides												

tr|B4N084|B4N084_DROWI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKYLGGIALL VALLAINIKD AQAVCGYESC PATQPNMINI HMVPHSHDDV GWLKTVDQYF YGHRSNIQHA GVQYIIDTVV
81 AELIKDPKRR FIQVETSFFH KWWSEQSETS KQVVHKLVEE GRLEFTGGAW AMNDEAAVHY QSVVDQFTLG LKFLDDTFGT
161 CGRPRVGWQI DPFGHSREQA SIFAQMGYDG EFFARMDHND KDKRLDDLAM EMIWDASESL SNDELFTGML YRHYSAPPGY
241 CFDVHCGDDP IIDTKSY**DNN VK**SRVDDFLS YVSAVAENYR SNHVMIPMGD DFQYEDAQVN FKNMDKLIKY VNERQSEGST
321 YNLFYSTPGC YLHSLHESLQ SWPNKTEDFF PYGSDTNSFW TGYFTSRPTQ KRFERDGNHM LQVAKQLSTL AHLTGEQQKE
401 DLLYLRKIMG VMQHHDAITG TEKQHVSDDY DRLLYDGILG AANTARDALR ELTNLPEGEF ESCLQLNISV CAFTKDSADN
481 VVVTLFNPLA HSATEYVRIP VKKESYEVTD EQGRTVASEV VPVAWQILDL DFRSNDTQHD LVFKASVDKI AHFYIKKVDS
561 GDSDSKTLVK INGHKSEVPK RFKKVHAMQN VETYDDDDSG ETVVQNSLIK LVIDNSSGRL KTIEMNGVSE SVEQKFAVYE
641 TKDSGAYVFR QNGDIKEVDD DVEFSVYDGT LVKEVHQQVS EYISQVIRIY EGVNRVEFEW LVGPIPTDSD TAREIVSLFK
721 TGISSDGVFY TDSNGREMLK RQKNKRENYD PDLGQQPTSG NYYPITSRIA LEDSKKRFAV LNDRAQGGSS MQNGELEIML
801 HRRLIRDDGY GVGEALNEEK FGNPLIARGK LHVILNTAGS KATAAERKAE KEIHLPFAKF FSKKPSTTST AVAKALPSFD
881 DFPQSVHLFS LEPFSDNEIL FRVENFLDHN EGNVVSFNIR PIFDSLNGLE IRETSLDGNL PLSDMKRFKF HHDGSGVRPT
961 SVEYTYPTHK PLAADKSQDA SDFSVTLNPM QIRTFIIKYE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.DNNVK.S	Y	21.61	588.2867	1822.9	590.3664	1	23.96	1744	1	258	262	
total 1 peptides												

tr|A0A1I8NPG9|A0A1I8NPG9_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MVGLLNPIKY GGNFYDLYTL TTRRKVQNER KQGKRKNKDK KSPIAILDGN PELRVLNPLD PPLIKEQLLL CPAFPVAHIE
  81 LQSNASQFAV FSAIRSTVLE AETRRLLFYE LSGNVRHLPN INSTCCLLCG SCLASNQSIE CSCHTLNALQ QVGGANGAGV
 161 VAPAPGGVGG GKRSRQDSAN SDVESDSEEC IEKETKIVSV PLIVGAGLRS LFELISEARH IQPMLCSKAL KALLDVIQGQ
 241 QPESFKHEPE ELINPLYDLL LDLATMSTGT TTESSAGVAG NEGDWSAVAC SALVGLCIAR GDTGKMLKAI AALIMSPRHL
 321 SIQRIQMPAV LGMLQRTVIS AALAKPTCPE FYTKGVPVNS LVDEFNIKAP FGGFTEPALA SDGTYLYLLL GGALLKIGTG
 401 YNGSYKGHIY MQNDEFTKEK TGWLGYSNGQ LYYRRNSKRN ADHLHLVNTE LLTIKSMNPV NMLPIREGFN YTLFTDEDSL
 481 NAICTNRDDS LVVRRLNIGH QNRTADRDNS LPVELPLQLS RKRFRTLGYA TFEEEVLNQN QILKIQASYN IFEPKIPNDV
 561 DLQEIVCGKE FGLVCANGKV YYYGKSSSLG LKSVGRTPIM KLTELIISKI SRIIHIAVGH DGIHALLVND DGTVYFAGTA
 641 RRGEDGDISK NRRQPKAVKP KKMTKIEGHV IVQAACNNGT SAFVTKTGKL IMFGKDTVHC DSQGFVSDFS DQHIQKVSLG
 721 KAHCVALNAK GQVFTFGLNN KGQCGHVYNK SKENSSSPSV NVDGSANGGG KSQSLKKLKF DFSNLCDYDD HSVVQGQCRV
 801 CVVCRECTGY NVSCVSSLNV PLEERVGGAI CACGHGDAGC SKCGLCATCI AVQEAENVSD TKDSNKQLNR QRSKSLIMRR
 881 KDKKSIDDTS SHAEENPPRV APLAPQLLQM PSTSPVVQVS CGLHHTVLLT LSGEVYAFGS NQFGQLGTGD MQPVSGPVRV
 961 NVPGNVCQVA AGSNHTVLLT YKGLVYTFGN FQKGQLGRLP HDFQQKGSNS RGDGEKASSA AQFREALVNS ESLPEKATVA
1041 QLISQRQKIL WHCTPGVVFG IGPSFGKKAT WIGASGDQTF IKLDESLITT QMLPKMNVAA NKKTILMIPT IPLTFSAISI
1121 NRRDGNCTAH YYNQVDFAKM EHSNKPKVVP EVNQNVDQNT MVQLGPSSSN AINEQMSRSM HEARNQMFDL QDNHMHNPSS
1201 SIQRKERNRE YAKGSLKSPS SPKAAASSST AAINDKTYTK LAFAMDPMYN ILWVYDCNQK KVLSYNVLAS EIQQSGMNSS
1281 NYRALLTPEL SLPNKLDSKI SRLHASLNLL ACLDVLTSAQ DFIPACFEDI SPKEDNQSKE QKDNQYQICN RFDNFGGGWG
1361 YSGHSVEAIR FSADTDVMIY GFGMFGGRGE YSCKLKLYDM GCDGGGYEKE GTLISETKEI PFECPARSKY HILLPKAVSI
1441 TAGRWYLVWA RIAGPSSDCG SCGQATVTTE DQVVFTFKSS KKANNGTDVN SGQIPAILYR LITQESKQPP APVDIDPVKR
1521 VTKEFANSVT KECFESLVLM LNWSWEAFKG YLREQRDMSH QLQVKQSLEY LIHVNKSCLR LLRKYTNEIY PQYGTSDEIA
1601 EYISTASTHK TMGNRTEKDV TKFTKPSNSL LTKYFNDNIG GAGGGGSGSG LGNQSPMKKS NMENIQLAEC IGNVRAMLIG
1681 IFCDDIFQDI SSDEALSMAL EILDECHISF VACFGVFYPT STLKWNCLCD LLSEMDKQGT LHSRLLSAIL AGLCSPTVKL
1761 RSTFALLNHG NDRHSIVSPS DNSGLPMLSS TDSHQYPILV EQMIYRTQQE KRDFLSNSWT FKDVLMRLLD IIANPIRDRL
1841 ENIYNRSVPY TYSSSSYCSK DFNQGLIDNC CHLLARVLAE IVYQTAIGDY DKMFVPPRTL HSSGSRFARC DQSRTWNTGS
1921 FGPDAIAFSV DRSGIAVAGC MVYTGSGSYE YQLELLCDTS GDLQQQQPLQ QQQHKWETLE SVSGTYDQTV VQNDMAEVKF
2001 ERSVLIKENS RYALRFCSQG HRTCSGDGGL PSVRGPCGTT FQFYACDLSF NGTNAHRGQI PCILYYSTPI KSETNGCNGG
2081 TFGSNGSTSN DVSLTNETTM RDTALQIASD ITKKCSELLV LARNTLAASL SPSDNSSNHS QTIDSEHNIT PIEEHMDINW
2161 ANNSRTSHLP AEAGGLSAAR DLSKRLESFS KGIIETLKFE KRSTNPFEME IEIGATEIHP KDLMIEESSS IHDLNFRNGQ
2241 ITKFNGNERV GAEAVESLMG ASSQFHPVAM ARADSEDTPA HMAASQILDV FNYGSSNLFH TLLPLVYAHI ANLACNDAKS
2321 SVQILGLIKD ILPHIAALNQ LSLNKETGVQ GNLPRLRPSF DLFHKKLDLV NEACSNALVA AASSNPPNDH SPTSDIPTTS
2401 NHYCIVESEH PYRNASINCY RVEFPPCVQW LTIEFDAQCG TAQLEDYLLV SVPMRPLISS EMCHANEDYY DILDNNVKSH

2481 RSAEGTQCKN ASLLTSCYKT TAQKEAEHKS EPDWFVVKKF NTSSNWLQNV MILPGNCVEF SLETSSLYAQ DPRVNRFGFK
2561 CLVVGYDNPV LLNSNNSCLV RIEQELSYLG GMCSGNLMKK NLSLPDDKDV EDLSTISETI STHFTLLSKG LALAEPDLTI
2641 HQALESYLPI GSQSNERQFL KDFISGAPGS SGARLAAWLQ PEPRLDPNKC ELNTITEALR YGWPTQITVT IRDQYGDAIV
2721 VPELKVEIKA IPTGSGGNGN VKVRRASQTD TYFGGVAPPP RQNYEPTIKE KMCFKAITFM KPYTNYSFEE LRYNSPIQTR
2801 VTETLFAQDM EDGTFSVHWT PNAVGSYCLT VTIDGILLEE VYRVEVKEGS IPPPAHKRVM KNHHTPNKLR KFYTENTAGL
2881 RIRSHPTLQS EQVGIIKLNG VISFIDEIEN DDGVWLRLST ESIRQHCAMG WYPTEAWCLQ YNQHLAKTLL HPVIENTPGP
2961 RETTTTDMNM DSQPMSPVPV TSAMPAEARN RQRDILENLE PVSASIESPS STTKSESPNK KMFDFPNNAL KPVEFPHVST
3041 NPFICADTES KNSLGEHQTH PFGGGAIEDE PKEDPFGAGN SGGSNAIGSA IAGVVGGGAI KLQALQKWFK GDNEPHSGGR
3121 DYSFKPSDVG EIASVSVREL VRVMGGQDTR TVNGNGSQRS CSPIKIPADD KAGDSPNNSG RSADTSAENS ILQDSSNSGR
3201 SAKDEATQLD VGNFDVANMR KTHFTPSQTA ALLSTPKHSP RRVGAAAKSA AGSGASCLAN EAAALKESDI SNLEEEMSLM
3281 QITTTSTAVG GGGCTVQDQI LFGDARNTNS TASTDNSSPP IWPEPIASAG SNATQNAFFK SMPAAKKTTM GPIKRAMPPS
3361 FAESIRAVFA AFLWHEGIVH DAMACASFLK FHPNLPKEGT TVVTRRDHGE GRQQLSKEQK AQQRHSVEVA NAGNYLNIRP
3441 STLETLTKSG NFSVNNRKYR KGLSNDGGDG NTADIGEKQK LHALPEVVTV LPPALRSLVY LWEHICSNCV HIVQSNSLNQ
3521 EKFNSREANG DSKEKPTPKD KENKKAKKKK DDGSWCEICQ VFLPIPVTYH MRIVHPGCGK SAKGKGYNSV GIFCEGWAGN
3601 CGEGGKGASS WFLMCDTCRD KYISTNKNTN NLNNTNAAGP CNELNLFGIK TTTLIANSDI YNTMRENATF LLELSSNVSN
3681 LPTDSGNVTS GLGSSKRSPQ QMPVVAEHQH FNMSEMNKPS TSRGDGAQQR HSRVGLRING KLGGNVLLRK SFTAGACSPE
3761 QPWLAPETFA CLETFGPANK DDLPYEIFGM GPNESGFDRP LSEISYESAD LANFDQPNPP SCMTSSTGTL SKFHRSYSMG
3841 QGWGAVQQQS NTNFREEPYY PKVVFRKRNN STTDSDGSLL ICYPSENLRR LVPDHMLIAT SVVQKTHHGP EVGADSITSA
3921 DGKDAKFEFE GSKQQNQRNN SEAESANQVN ALLQRPSMAF MTQKHDLKKL RSAMKRSLRI ATCRNYSLQA LNWLLRSVTQ
4001 SVCLHDLMWW FVSSLSITGP ANSDPMDGKF DELEPALEHP VSYTQISGRL SHMITESLHT FLQSVADLTL HLPLGSPLQR
4081 IAIQCFGIRF RQTDHQFLHS SHVFGNISKI LSKSDEQNES PGVFGLPEDA EAKEPSTKDL YAVPDAGGKI IYYSDLNGHF
4161 DVTVSSRQAM AESLTDNSTE TFWESDEEDR NKSKIVEISM NKLTYCCKIL LIHIDNSRDI QNKVSTVAFY GGQSLGDTSL
4241 IKSVEVDAKA CIWISTKIND DNFTHFRLEF TGPENTLRVR QIKILGLPAA MCGSGDQLTN PYDLAGTSSS QGHAFKYNMK
4321 LTNAVRIQQQ ICEAETLRVF RLITGQVFGK LISLEPANDE SAGVIGKSLS QNALGMDTSA NSILADSLDL REHMVGILFS
4401 RSKLSHLQKQ VIVHIVHAIK KEARRAREDW DAVNLANSLR DPNGTGSNGQ ESKTDATSER GRTADTYCFE MLSMVLALSG
4481 SVVGRSYLSH QHGLIKDLLS LLHTGSDRVQ RQVTSLLRRI LPEISPATFA DILGVHRLPP SDYNIAHQIA IDFDMDSLGL
4561 LDIFLAVIAK SLQLQMKVKS AGGKSNMEKT PSEIRLYNSL DLSVHLLKPV KMHMSAEHVT AEAEDSFSRT EYGFEYFRAM
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4641  EMKTSRSIHR EVKKETTKNL NQRWFLNGVI PTKQAESIIS LIRDLATGKL GEKWSQMTKA AIAEAVLNLT RLDEIFRCPE
4721  NCVKIAILWL ALASLCVLDN DHVEKLSSGQ WTISDIRPMC SNHDDGETSA IIQCESCGSL CGDCDRFLHL NRKTRTHKRT
4801  VCKEEEEAIR VELHESCGRT KLFWLLALAD SKTLKGMVEF RDGSHTIISG AQDSVGRCRF CGITGNSGLL EIGNVCADAQ
4881  CQEYAANSCL KTKPCGHVCG GVVNEKKCLP CLQHVCHARE NNVADGLNDP KLTQDADDMC MICFVEALAC APSIQLECGH
4961  VFHFHCCKAV LEKRWSGPRI TFGFSLCPIC KADIKHPMLA EILEPINALK QDVKRKAQMR IKYEGIVKDT ESRDLTNLAM
5041  DRYAYYVCFK CQKAYYGGEA RCDVEIGEKF NPEELVCGGC SDVARAQMCP KHGTDFLEYK CRYCCSVAVF FCFGTTHFCD
5121  TCHDDFQRLT NIPKNKLPQC PAGPKAKQLM GEECPLHVIH PPTGEEFALG CGVCRNAQTF
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.DNNVK.S	Y	21.61	588.2867	1822.9	590.3664	1	23.96	1744	1	2474	2478	
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)