Summary

1. Notes

2. Result Statistics

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

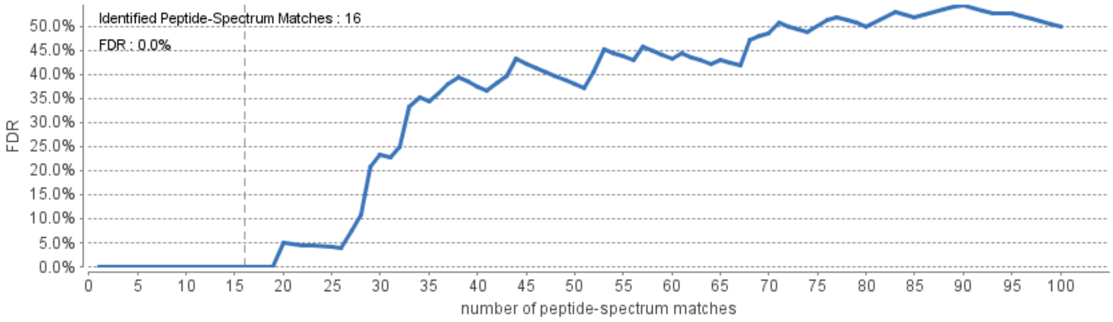
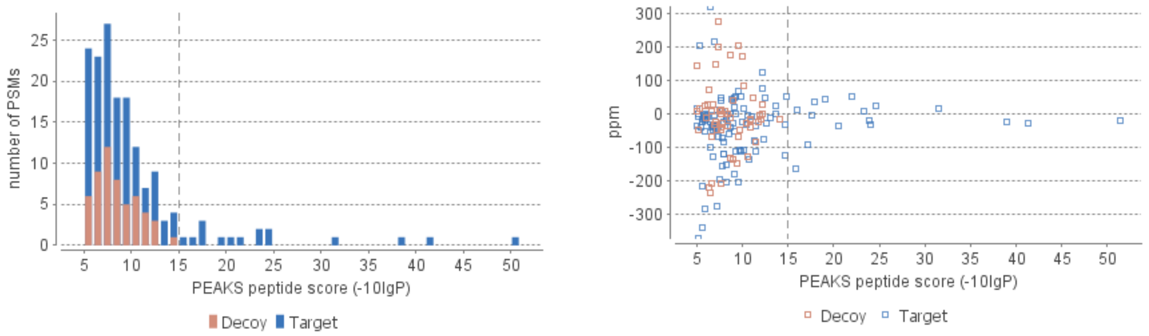
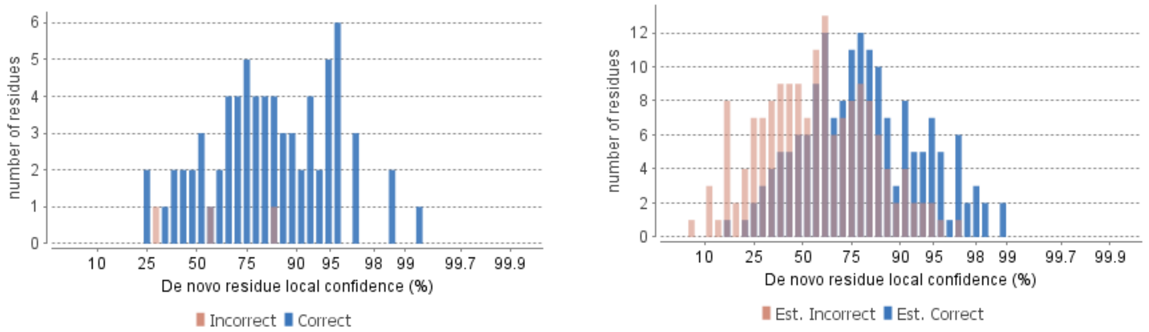


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

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


(a)

(b)

Table 1. Statistics of data.

# of MS Scans	1692
# of MS/MS Scans	810

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	16
Peptide Sequences	16

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	3	C

Protein Groups	9
Proteins	97
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 97 (=1);
FDR (Peptide-Spectrum Matches)	0.0%
FDR (Peptide Sequences)	0.0%
FDR (Protein)	1.0%
De Novo Only Spectra	49

3. Experiment Control

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

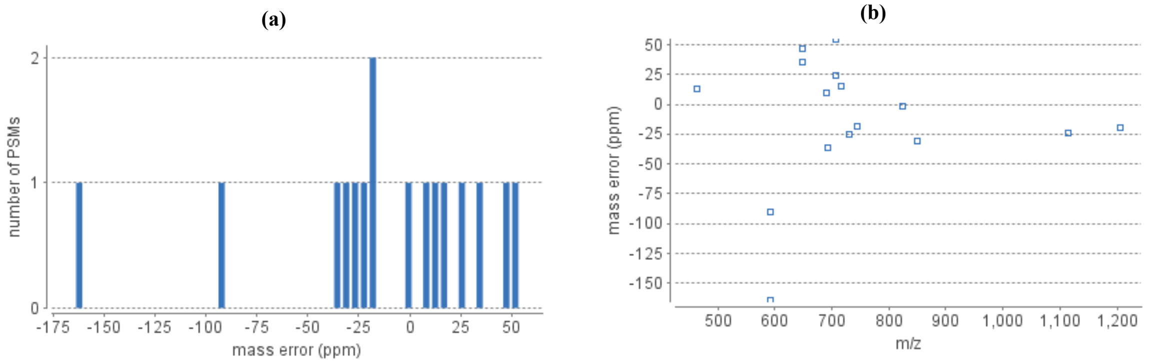


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Q-TOF	0	0	0	0	16

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: 0.1
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 57
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: D_2_180917.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: Quadrupole
MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
2	4567	tr|A0A1W7R9B8|A0A1W7R9B8_9SCOR	63.31	8	2	1	N	49805	Tubulin alpha chain OS=Hadrurus spadix PE=3 SV=1
2	4560	tr|T2BCS0|T2BCS0_9ORTH	63.31	31	2	1	N	12967	Tubulin-alpha I (Fragment) OS=Acanthodiphrus sp. OR584 PE=3 SV=1
2	4561	tr|T2BCU0|T2BCU0_9ORTH	63.31	31	2	1	N	12953	Tubulin-alpha I (Fragment) OS=Sasima sp. OR131 PE=3 SV=1
2	4559	tr|A0A166ASE2|A0A166ASE2_9NEOP	63.31	35	2	1	N	11265	Alpha tubulin (Fragment) OS=Chelisoches morio GN=TUBA PE=3 SV=1
2	4558	tr|T2BCQ2|T2BCQ2_9ORTH	63.31	42	2	1	N	9513	Tubulin-alpha I (Fragment) OS=Acanthoproctus vittatus PE=3 SV=1
2	4564	tr|A0A023GKQ6|A0A023GKQ6_9ACAR	63.31	11	2	1	N	36142	Tubulin alpha chain (Fragment) OS=Amblyomma triste PE=2 SV=1
2	4563	tr|A0A224Z8W6|A0A224Z8W6_9ACAR	63.31	14	2	1	N	27820	Tubulin alpha 1c OS=Rhipicephalus zambeziensis PE=3 SV=1
2	4562	tr|A0A224ZAW8|A0A224ZAW8_9ACAR	63.31	14	2	1	N	27554	Tubulin alpha chain (Fragment) OS=Rhipicephalus zambeziensis PE=3 SV=1
2	4577	tr|B7PGI8|B7PGI8_IXOSC	63.31	7	2	1	N	54955	Tubulin alpha chain OS=Ixodes scapularis GN=8052898 PE=3 SV=1
2	4576	tr|A0A023GNK0|A0A023GNK0_9ACAR	63.31	7	2	1	N	53649	Tubulin alpha chain (Fragment) OS=Amblyomma triste PE=2 SV=1
total 97 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
2	4575	tr|L7MD37|L7MD37_9ACAR	63.31	7	2	1	N	53220	Tubulin alpha chain (Fragment) OS=Rhipicephalus pulchellus PE=2 SV=1
2	4574	tr|G3MGN2|G3MGN2_9ACAR	63.31	7	2	1	N	52672	Tubulin alpha chain (Fragment) OS=Amblyomma maculatum PE=2 SV=1
2	4573	tr|A0A023FK91|A0A023FK91_9ACAR	63.31	8	2	1	N	50855	Tubulin alpha chain (Fragment) OS=Amblyomma cajennense PE=2 SV=1
2	4572	tr|A0A131XWB5|A0A131XWB5_IXORI	63.31	8	2	1	N	50311	Tubulin alpha chain (Fragment) OS=Ixodes ricinus PE=2 SV=1
2	4494	tr|A0A0P5ZYN7|A0A0P5ZYN7_9CRUS	63.31	8	2	1	N	50152	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
2	4571	tr|A0A1W7RAY3|A0A1W7RAY3_9SCOR	63.31	8	2	1	N	50120	Tubulin alpha chain OS=Hadrurus spadix PE=3 SV=1
2	4570	tr|A0A087TLA4|A0A087TLA4_9ARAC	63.31	8	2	1	N	49938	Tubulin alpha chain (Fragment) OS=Stegodyphus mimosarum GN=X975_18866 PE=3 SV=1
2	4568	tr|A0A293M7T6|A0A293M7T6_ORNER	63.31	8	2	1	N	49907	Tubulin alpha chain (Fragment) OS=Ornithodoros erraticus PE=4 SV=1
2	4569	tr|L7M1J3|L7M1J3_9ACAR	63.31	8	2	1	N	49942	Tubulin alpha chain OS=Rhipicephalus pulchellus PE=2 SV=1
2	4566	tr|A0A224YJ96|A0A224YJ96_9ACAR	63.31	8	2	1	N	48660	Tubulin alpha chain (Fragment) OS=Rhipicephalus zambeziensis PE=3 SV=1
2	4565	tr|A0A023FZA1|A0A023FZA1_9ACAR	63.31	9	2	1	N	42766	Tubulin alpha chain (Fragment) OS=Amblyomma parvum PE=2 SV=1
1	4613	tr|Q7PSI5|Q7PSI5_ANOGA	53.29	8	2	1	N	50865	Tubulin alpha chain (Fragment) OS=Anopheles gambiae GN=1270985 PE=3 SV=4
1	4579	tr|A0A0X9PE16|A0A0X9PE16_9ORTH	53.29	32	2	1	N	12316	Tubulin-alpha 1 (Fragment) OS=Tettigonia tsushimensis PE=3 SV=1
1	4580	tr|A0A0X9TMY8|A0A0X9TMY8_9ORTH	53.29	32	2	1	N	12316	Tubulin-alpha 1 (Fragment) OS=Tettigonia ussuriana PE=3 SV=1
1	4583	tr|A0A0P4Z4W3|A0A0P4Z4W3_9CRUS	53.29	12	2	1	N	32000	Tubulin alpha chain (Fragment) OS=Daphnia magna PE=3 SV=1
1	4581	tr|A0A185N6J1|A0A185N6J1_9ODON	53.29	23	2	1	N	17500	Tubulin-alpha I (Fragment) OS=Hetaerina cruentata PE=3 SV=1
1	4582	tr|A0A185N6J8|A0A185N6J8_9ODON	53.29	23	2	1	N	17500	Tubulin-alpha I (Fragment) OS=Hetaerina occisa PE=3 SV=1
1	4615	tr|A0A1B6INX8|A0A1B6INX8_9HEMI	53.29	8	2	1	N	51592	Tubulin alpha chain (Fragment) OS=Homalodisca liturata GN=g.17932 PE=3 SV=1
1	4612	tr|A0A1B6IMY7|A0A1B6IMY7_9HEMI	53.29	8	2	1	N	50785	Tubulin alpha chain OS=Homalodisca liturata GN=g.17933 PE=3 SV=1
1	4606	tr|A0A0K8RBU4|A0A0K8RBU4_IXORI	53.29	8	2	1	N	50016	Tubulin alpha chain OS=Ixodes ricinus PE=2 SV=1
1	4611	tr|B7PH43|B7PH43_IXOSC	53.29	8	2	1	N	50016	Tubulin alpha chain OS=Ixodes scapularis GN=8028862 PE=3 SV=1
1	4595	tr|A7UIK9|A7UIK9_MONAT	53.29	8	2	1	N	49908	Tubulin alpha chain OS=Monochamus alternatus PE=2 SV=1
1	4596	tr|A0A0N7ZFH6|A0A0N7ZFH6_9CRUS	53.29	8	2	1	N	49859	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4597	tr|A0A0K8TTW1|A0A0K8TTW1_TABBR	53.29	8	2	1	N	49937	Tubulin alpha chain OS=Tabanus bromius PE=2 SV=1
1	4598	tr|A0A0P5NHY4|A0A0P5NHY4_9CRUS	53.29	8	2	1	N	49770	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4599	tr|A0A182J1K8|A0A182J1K8_9DIPT	53.29	8	2	1	N	49908	Tubulin alpha chain OS=Anopheles atroparvus PE=3 SV=1
1	4600	tr|A0A131ZV00|A0A131ZV00_SARSC	53.29	8	2	1	N	50028	Tubulin alpha chain OS=Sarcoptes scabiei GN=QR98_0010090 PE=3 SV=1
1	4601	tr|Q7PUE2|Q7PUE2_ANOGA	53.29	8	2	1	N	49908	Tubulin alpha chain OS=Anopheles gambiae GN=1281950 PE=3 SV=5
1	4602	tr|A0A0P4YX17|A0A0P4YX17_9CRUS	53.29	8	2	1	N	49810	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4603	tr|A0A0P6A1J6|A0A0P6A1J6_9CRUS	53.29	8	2	1	N	49891	Tubulin alpha chain OS=Daphnia magna GN=APZ42_014287 PE=3 SV=1
1	4604	tr|A0A131ZUS5|A0A131ZUS5_SARSC	53.29	8	2	1	N	50083	Tubulin alpha chain OS=Sarcoptes scabiei GN=QR98_0009510 PE=3 SV=1
1	4605	tr|A0A0P5GV80|A0A0P5GV80_9CRUS	53.29	8	2	1	N	49839	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	6437	tr|A0A023F9U2|A0A023F9U2_TRIIF	53.29	8	2	1	N	50120	Tubulin alpha chain OS=Triatoma infestans PE=2 SV=1
1	4593	tr|A0A0X9H6Y0|A0A0X9H6Y0_NILLU	53.29	8	2	1	N	49824	Tubulin alpha chain OS=Nilaparvata lugens PE=2 SV=1
1	4592	tr|A0A0P5GQJ7|A0A0P5GQJ7_9CRUS	53.29	8	2	1	N	47024	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4591	tr|A0A0P5FTK3|A0A0P5FTK3_9CRUS	53.29	8	2	1	N	46077	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4590	tr|A0A0P5FQ62|A0A0P5FQ62_9CRUS	53.29	9	2	1	N	45682	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4589	tr|B7QP04|B7QP04_IXOSC	53.29	9	2	1	N	43524	Alpha tubulin, putative OS=Ixodes scapularis GN=8044135 PE=3 SV=1
1	4588	tr|A0A0P5NAD9|A0A0P5NAD9_9CRUS	53.29	9	2	1	N	43010	Tubulin alpha chain (Fragment) OS=Daphnia magna PE=3 SV=1
1	4587	tr|A0A0N8CYL8|A0A0N8CYL8_9CRUS	53.29	9	2	1	N	42559	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4586	tr|A0A0P5I692|A0A0P5I692_9CRUS	53.29	10	2	1	N	40534	Tubulin alpha chain OS=Daphnia magna PE=3 SV=1
1	4585	tr|A0A0P5Y6N4|A0A0P5Y6N4_9CRUS	53.29	10	2	1	N	37131	Tubulin alpha chain (Fragment) OS=Daphnia magna PE=3 SV=1
1	4584	tr|A0A0P5GEQ6|A0A0P5GEQ6_9CRUS	53.29	11	2	1	N	36445	Putative Tubulin alpha-1 chain OS=Daphnia magna PE=3 SV=1
1	6438	tr|A0A2A3EL84|A0A2A3EL84_APICC	53.29	7	2	1	N	52768	Tubulin alpha-1 chain OS=Apis cerana cerana GN=APICC_05992 PE=4 SV=1
5	4540	tr|E0W1G3|E0W1G3_PEDHC	38.97	5	1	1	N	58998	ATP synthase subunit beta OS=Pediculus humanus subsp. corporis GN=8239544 PE=3 SV=1
6	6443	tr|A0A224Y123|A0A224Y123_9ACAR	31.46	1	1	1	N	90149	7DB family member OS=Rhipicephalus zambeziensis PE=4 SV=1
3	6439	tr|A0A1B6CHY3|A0A1B6CHY3_9HEMI	24.65	2	1	1	N	45011	Uncharacterized protein (Fragment) OS=Clastoptera arizonana GN=g.30965 PE=4 SV=1
3	6440	tr|A0A1B6EG82|A0A1B6EG82_9HEMI	24.65	1	1	1	N	52410	Uncharacterized protein (Fragment) OS=Clastoptera arizonana GN=g.30971 PE=4 SV=1
3	6441	tr|Q173I4|Q173I4_AEDAE	24.65	1	1	1	N	121406	AAEL007127-PA (Fragment) OS=Aedes aegypti GN=AAEL007127 PE=4 SV=1
3	6442	tr|A0A0P6IU66|A0A0P6IU66_AEDAE	24.65	1	1	1	N	123498	Putative leucine-rich repeat-containing protein 49 (Fragment) OS=Aedes aegypti PE=2 SV=1
3	6444	tr|A0A1S4FFQ6|A0A1S4FFQ6_AEDAE	24.65	1	1	1	N	136121	Uncharacterized protein OS=Aedes aegypti PE=4 SV=1
3	6445	tr|A0A182GHL5|A0A182GHL5_AEDAL	24.65	1	1	1	N	136122	Uncharacterized protein OS=Aedes albopictus PE=4 SV=1
3	6448	tr|A0A1J1HJS3|A0A1J1HJS3_9DIPT	24.65	8	1	1	N	10376	CLUMA_CG001453, isoform A OS=Clunio marinus GN=CLUMA_CG001453 PE=4 SV=1
3	6450	tr|A0A182ST32|A0A182ST32_9DIPT	24.65	2	1	1	N	39779	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
total 97 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	6451	tr|R4N7H8|R4N7H8_LITVA	24.65	2	1	1	N	46639	Serine proteinase inhibitor OS=Litopenaeus vannamei GN=SERPIN PE=2 SV=1
3	6452	tr|A0A0Q9WK24|A0A0Q9WK24_DROVI	24.65	1	1	1	N	72237	Uncharacterized protein OS=Drosophila virilis GN=Dvir\GJ26009 PE=4 SV=1
3	6453	tr|A0A0J7P5Y5|A0A0J7P5Y5_LASNI	24.65	1	1	1	N	67228	Mothers against decapentaplegic homolog OS=Lasius niger GN=RF55_61 PE=3 SV=1
3	6456	tr|A0A088AF28|A0A088AF28_APIME	24.65	1	1	1	N	71575	Mothers against decapentaplegic homolog OS=Apis mellifera GN=Smad4 PE=3 SV=1
3	6457	tr|A0A151J4K9|A0A151J4K9_9HYME	24.65	1	1	1	N	71593	Mothers against decapentaplegic homolog OS=Trachymyrmex cornetzi GN=ALC57_10143 PE=3 SV=1
3	6458	tr|A0A151JWE9|A0A151JWE9_9HYME	24.65	1	1	1	N	71760	Mothers against decapentaplegic homolog OS=Trachymyrmex septentrionalis GN=ALC56_07567 PE=3 SV=1
3	6459	tr|A0A182MMM2|A0A182MMM2_9DIPT	24.65	1	1	1	N	92199	Uncharacterized protein OS=Anopheles culicifacies PE=4 SV=1
3	6464	tr|A0A0K2ULM4|A0A0K2ULM4_LEPSM	24.65	1	1	1	N	102645	Protein smoothenedlike [Apis florea] OS=Lepeophtheirus salmonis PE=3 SV=1
3	6465	tr|A0A182JTY0|A0A182JTY0_9DIPT	24.65	1	1	1	N	112299	Uncharacterized protein OS=Anopheles christyi PE=4 SV=1
3	6466	tr|A0A182XZ28|A0A182XZ28_ANOST	24.65	1	1	1	N	112587	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
3	6467	tr|W5J7J2|W5J7J2_ANODA	24.65	1	1	1	N	114344	Uncharacterized protein OS=Anopheles darlingi GN=AND_009649 PE=4 SV=1
3	6468	tr|A0A151X5F3|A0A151X5F3_9HYME	24.65	1	1	1	N	148441	Mothers against decapentaplegic homolog OS=Trachymyrmex zeteki GN=ALC60_05470 PE=3 SV=1
4	6449	tr|M9VSG2|M9VSG2_9ARAC	24.10	11	1	1	Y	22726	Actin (Fragment) OS=Tylogonus yanayacu PE=3 SV=1
9	6478	tr|A0A034VY87|A0A034VY87_BACDO	23.29	1	1	1	N	103437	Golgin subfamily A member 2 OS=Bactrocera dorsalis GN=GOGA2 PE=4 SV=1
9	6479	tr|W8BRA7|W8BRA7_CERCA	23.29	1	1	1	N	104076	Golgin subfamily A member 2 OS=Ceratitis capitata GN=GOGA2 PE=2 SV=1
9	6480	tr|A0A0A1WSG1|A0A0A1WSG1_ZEUCU	23.29	1	1	1	N	103532	Golgin subfamily A member 2 OS=Zeugodacus cucurbitae GN=Golga2_2 PE=4 SV=1
9	6537	tr|A0A1W4WI16|A0A1W4WI16_AGRPL	23.29	0	1	1	N	208801	eIF-2-alpha kinase activator GCN1 OS=Agrilus planipennis GN=LOC108733105 PE=4 SV=1
9	6589	tr|A0A0J7NUE4|A0A0J7NUE4_LASNI	23.29	0	1	1	N	285140	Translational activator gcn1 OS=Lasius niger GN=RF55_3722 PE=4 SV=1
9	6593	tr|A0A0M9ABE9|A0A0M9ABE9_9HYME	23.29	0	1	1	N	290199	Translational activator GCN1 OS=Melipona quadrifasciata GN=WN51_09965 PE=4 SV=1
9	6595	tr|A0A067RTH7|A0A067RTH7_ZOONE	23.29	0	1	1	N	290702	Translational activator GCN1 (Fragment) OS=Zootermopsis nevadensis GN=L798_15201 PE=4 SV=1
9	6597	tr|T1HJQ7|T1HJQ7_RHOPR	23.29	0	1	1	N	290116	Uncharacterized protein (Fragment) OS=Rhodnius prolixus PE=4 SV=1
9	6598	tr|A0A151WN86|A0A151WN86_9HYME	23.29	0	1	1	N	292488	Translational activator GCN1 (Fragment) OS=Trachymyrmex zeteki GN=ALC60_11607 PE=4 SV=1
9	6599	tr|A0A088ABA5|A0A088ABA5_APIME	23.29	0	1	1	N	293874	Uncharacterized protein OS=Apis mellifera GN=LOC409457 PE=4 SV=1
9	6600	tr|A0A224X4L0|A0A224X4L0_9HEMI	23.29	0	1	1	N	291128	Putative translational activator gcn1 OS=Panstrongylus lignarius PE=4 SV=1
9	6601	tr|R4WJK2|R4WJK2_RIPPE	23.29	0	1	1	N	290265	Translational activator gcn1 OS=Riptortus pedestris PE=2 SV=1
9	6602	tr|A0A069DYI0|A0A069DYI0_9HEMI	23.29	0	1	1	N	291122	Putative translational activator gcn1 OS=Panstrongylus megistus PE=2 SV=1
9	6603	tr|A0A232FBG6|A0A232FBG6_9HYME	23.29	0	1	1	N	293417	Uncharacterized protein OS=Trichomalopsis sarcophagae GN=TSAR_002295 PE=4 SV=1
7	6454	tr|A0A1Y9H1Z4|A0A1Y9H1Z4_9DIPT	21.96	1	1	1	N	86670	Microtubule-associated protein OS=Anopheles dirus PE=4 SV=1
7	6455	tr|A0A1Y9H2G1|A0A1Y9H2G1_9DIPT	21.96	1	1	1	N	95122	Microtubule-associated protein OS=Anopheles dirus PE=4 SV=1
8	6460	tr|A0A0P5ZW48|A0A0P5ZW48_9CRUS	20.57	5	1	1	N	17406	Uncharacterized protein (Fragment) OS=Daphnia magna PE=4 SV=1
8	6461	tr|A0A0P5AGV2|A0A0P5AGV2_9CRUS	20.57	5	1	1	N	17900	Uncharacterized protein (Fragment) OS=Daphnia magna PE=4 SV=1
8	6462	tr|A0A0P6AEJ7|A0A0P6AEJ7_9CRUS	20.57	5	1	1	N	18085	Uncharacterized protein (Fragment) OS=Daphnia magna PE=4 SV=1
8	6463	tr|Q16KV7|Q16KV7_AEDAE	20.57	4	1	1	N	18154	AAEL012853-PA OS=Aedes aegypti GN=AAEL012853 PE=4 SV=1
total 97 proteins									

tr|A0A1W7R9B8|A0A1W7R9B8_9SCOR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNAC WELYCVEHGI QPDGQMPSDK ALGVGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRG
81 GSYRQLYHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RVRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPSYANLNR**L ISQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSN DAGDEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|T2BCS0|T2BCS0_9ORTH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISAEK

81 AYHEQLSVAE ITNACFEPAN QMLKCDPRHG KYMA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	30	43	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	44	64	
total 2 peptides												

tr|T2BCU0|T2BCU0_9ORTH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISAEK

81 AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	30	43	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	44	64	
total 2 peptides												

tr|A0A166ASE2|A0A166ASE2_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RRNLDIERPT YTNLNR**LISQ IVSSITASLR FDGALNVDLT EFQTNLVPYP R**IHFPLATYA PVISAEKAYH EQLSVAEITN

81 ACFEPANQMV KCDPRHGKY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	17	30	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	31	51	
total 2 peptides												

tr|T2BCQ2|T2BCQ2_9ORTH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 CRRNLDIERP TYTNLNR**LIS QIVSSITASL RFDGALNVDL TEFQTNLVPY PR**IHFPLATY APVISAEKAY HEQLSVAEIT

81 NACF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	18	31	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	32	52	
total 2 peptides												

tr|A0A023GKQ6|A0A023GKQ6_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KVAEGCSGLQ GFLIFHSFGG GTGSGFKSLL MQRLSVDYGK KFKLEFSVYP APQVATAVVE PYNAILTTHT TLEHSDCSFM

81 VDNEAIYEIC RRNLDIDRPT YSNLNR**LISQ IVSSITASLR FDGALNVDLT EFQTNLVPYP R**IHYLLVAYS PVVSSERAHH

161 EQLTVAQMTS SCFEPANQMV KCDPRRGKYM ACCLLYRGDV VPKDVNAAIA AIKSKRSIQF VDWCPTGFKV GINYQPPTVV

241 PGGDLAKVPR AVCLLSNTTA IAEAWARLNH KFDLMYAKRA FVHWYVGEGM EEGEFSEARE DMAALEKDYE EVGADSVDGA

321 DASQEF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	107	120	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	121	141	
total 2 peptides												

tr|A0A224Z8W6|A0A224Z8W6_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVDNEAIYDI CRRNLDIERP TYANLNR**LIS QIVSSITASL RFDGALNVDL TEFQTNLVPY PR**IHFPLVTY APVISAEKAY

81 HEQLTVAEIT NACFEPANQM VKCDPRHGKY MACCMLYRGD VVPKDVNAAI AAIKTKRTIQ FVDWCPTGFK VGINYQPPTV
161 VPGGDLAKVP RAVCMLSNTT AIAEAWARLD HKFDLMYAKR AFVHWYVGEG MEEGEFSEAR EDMAALEKDY EEVGMDSNEV
241 ADEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	28	41	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	42	62	
total 2 peptides												

tr|A0A224ZAW8|A0A224ZAW8_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GAYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
81 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYANLNR**L ISQIVSSITA**

161 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

241 GDVVPK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	150	163	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	164	184	
total 2 peptides												

tr|B7PGI8|B7PGI8_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLKNRKLCPA GASIGGIAKK RAAVAPTSHL RSCEHLGSSA RSVGSSPSSI MRECISIHIG QAGVQIGNSC WELYCLEHGI
81 QQDGQMPSDK VSGGVDDSFN TFFAETGAGK HVPRAVFVDL EPTVVDEVRQ GAYRQLYHPE QLISGKEDAA NNYARGHYTI
161 GKEIVDLVLD RIRKLADACT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD YGKKSKLEFS IYPAPQVSTA VVEPYNSILT
241 THTTLEHSDC AFMVDNEAIY DICRRNLDID RPSYTNLNR**L ISQIVSSITA SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV

321 TYAPVISAEK AYHEQITVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG
401 FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA KRAFVHWYVG EGMEEGEFSE AREDMAALEK
481 DYEEVGMDSN EGVDDGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	280	293	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	294	314	
total 2 peptides												

tr|A0A023GNK0|A0A023GNK0_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ACWELYCLEH GLXLRARCSS VRRVRRIFVP TMRECISVHI GQAGVQIGNA CWELYCLEHG IQQDGQMPSD KVSGGIDDSF
81 NTFFAETGAG RHVPRAVFVD LEPTVVDEVR SGAYRQLYHP EQLISGKEDA ANNYARGHYT IGKEIVDLVL DRIRKLADQC
161 TGLQGFLVFH SFGGGTGSGF TSLLMERLSV DYGKKSKLEF SIYPAPQVST AVVEPYNSIL TTHTTLEHSD CAFMVDNEAI
241 YDICRRNLDI DRPTYTNLNR **LISQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL VTYAPVISSE KAYHEQITVA

321 EITNACFEPA NQMVKCDPRH GKYMACCMLY RGDVVPKDVN AAIAAIKTKR TIQFVDWCPT GFKVGINYQP PTVVPGGDLA
401 KVPRAVCMLS NTTAIAEAWA RLDHKFDLMY AKRAFVHWYV GEGMEEGEFS EAREDMAALE KDYEEVGMDS NEGADEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	261	274	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	275	295	
total 2 peptides												

tr|L7MD37|L7MD37_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GATHSYLRPL RARCCSVRXR RAVLPTPPNM RECISVHIGQ AGVQIGNACW ELYCLEHGIQ QDGQMPSDKV SGGIDDSFNT
81 FFAETGAGRH VPRAVFVDLE PTVVDEVRSG AYRQLYHPEQ LISGKEDAAN NYARGHYTIG KEIVDLVLDR IRKLADQCTG
161 LQGFLVFHSF GGGTGSGFTS LLMERLSVDY GKKSKLEFSI YPAPQVSTAV VEPYNSILTT HTTLEHSDCA FMVDNEAIYD
241 ICRRNLDIDR PTYTNLNR**LI SQIVSSITAS LRFDGALNVD LTEFQTNLVP YPR**IHFPLVT YAPVISAEKA YHEQITVAEI
321 TNACFEPANQ MVKCDPRHGK YMACCMLYRG DVVPKDVNAA IAAIKTKRTI QFVDWCPTGF KVGINYQPPT VVPGGDLAKV
401 PRAVCMLSNT TAIAEAWARL DHKFDLMYAK RAFVHWYVGE GMEEGEFSEA REDMAALEKD YEEVGMDSNE GADESEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	259	272	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	273	293	
total 2 peptides												

tr|G3MGN2|G3MGN2_9ACAR back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GHLRPLRARC SSVRRVRRIF VPTMRECISV HIGQAGVQIG NACWELYCLE HGIQQDGQMP SDKVSGGIDD SFNTFFAETG
81 AGRHVPRAVF VDLEPTVVDE VRSGAYRQLY HPEQLISGKE DAANNYARGH YTIGKEIVDL VLDRIRKLAD QCTGLQGFLV
161 FHSFGGGTGS GFTSLLMERL SVDYGKKSKL EFSIYPAPQV STAVVEPYNS ILTTHTTLEH SDCAFMVDNE AIYDICRRNL
241 DIDRPTYTNL NR**LISQIVSS ITASLRFDGA LNVDLTEFQT NLVPYPR**IHF PLVTYAPVIS SEKAYHEQIT VAEITNACFE
321 PANQMVKCDP RHGKYMACCM LYRGDVVPKD VNAAIAAIKT KRTIQFVDWC PTGFKVGINY QPPTVVPGGD LAKVPRAVCM
401 LSNTTAIAEA WARLDHKFDL MYAKRAFVHW YVGEGMEEGE FSEAREDMAA LEKDYEEVGM DSNEGADEGE EY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	253	266	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	267	287	
total 2 peptides												

tr|A0A023FK91|A0A023FK91_9ACAR back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GEPFLPTAAM RECISVHIGQ AGVQIGNACW ELYCLEHGIQ QDGQMPSDKV SGGIDDSFNT FFAETGAGRH VPRAVFVDLE
81 PTVVDEVRSG AYRQLYHPEQ LISGKEDAAN NYARGHYTIG KEIVDLVLDR IRKLADQCTG LQGFLVFHSF GGGTGSGFTS
161 LLMERLSVDY GKKSKLEFSI YPAPQVSTAV VEPYNSILTT HTTLEHSDCA FMVDNEAIYD ICRRNLDIDR PTYTNLNR**LI**
241 **SQIVSSITAS LRFDGALNVD LTEFQTNLVP YPR**IHFPLVT YAPVISAEKA YHEQITVAEI TNACFEPANQ MVKCDPRHGK
321 YMACCMLYRG DVVPKDVNAA IAAIKTKRTI QFVDWCPTGF KVGINYQPPT VVPGGDLAKV PRAVCMLSNT TAIAEAWARL
401 DHKFDLMYAK RAFVHWYVGE GMEEGEFSEA REDMAALEKD YEEVGMDSNE GADESEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	239	252	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	253	273	
total 2 peptides												

tr|A0A131XWB5|A0A131XWB5_IXORI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PSSIMRECIS IHIGQAGVQI GNSCWELYCL EHGIQQDGQM PSDKVSGGVD DSFNTFFAET GAGNHVPRAV FVDLEPTVVD
81 EVRQGAYRQL YHPEQLISGK EDAANNYARG HYTIGKEIVD LVLDRIRKLA DACTGLQGFL IFHSFGGGTG SGFTSLLMER
161 LSVDYGKKSK LEFSIYPAPQ VSTAVVEPYN SILTTHTTLE HSDCAFMVDN EAIYDICRRN LDIERPSYTN LNR**LISQIVS**
241 **SITASLRFDG ALNVDLTEFQ TNLVPYPR**IH FPLVTYAPVI SAEKAYHEQI TVAEITNACF EPANQMVKCD PRHGKYMACC
321 MLYRGDVVPK DVNAAIAAIK TKRTIQFVDW CPTGFKVGIN YQPPTVVPGG DLAKVPRAVC MLSNTTAIAE AWARLDHKFD
401 LMYAKRAFVH WYVGEGMEEG EFSEAREDMA ALEKDYEEVG MDSNEGVDDG EEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	234	247	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	248	268	
total 2 peptides												

tr|A0A0P5ZYN7|A0A0P5ZYN7_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVIDEVRT

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIIDLVLD RIRKLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD

161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA**

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCLLYR

321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGVDSV EGEGEEEGEE Y

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A1W7RAY3|A0A1W7RAY3_9SCOR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TMGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

81 GTYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RVRKLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD

161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPSYTNLNR**L ISQIVSSITA**

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVAE ITSACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIAAIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSM EGGEEDEGEE Y

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A087TLA4|A0A087TLA4_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNAC WELYCLEHGI QPDGNMPSDK AVGTGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

81 GGYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L ISQIVSSITA**

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGLDSN DGGEDEGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A293M7T6|A0A293M7T6_ORNER

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNAC WELYCLEHGI QADGQMPSDK VTGGVDDSFN TFFAETGAGK HVPRAVFVDL EPTVVDEVRT

81 GSYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADMCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

161 YGKKSKLEFS IYPAPQVATA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDID RPSYSNLNR**L ISQIVSSITA**

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISSEK AYHEQLTVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TAVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG ECMEEGEFSE AREDMAALEK DYEEVGMDSN DGVDEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|L7M1J3|L7M1J3_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNSC WELYCLEHGI QQDGRMPSDK ASGGVDDSFS TFFAETGAGR HVPRAVFVDL EPTVVDEVRS
81 GAYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYANLNR**L ISQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGMDSN EVADEGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A224YJ96|A0A224YJ96_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHIG QAGVQIGNAC WELYCLEHGI QQDGQMPSDK VSGGIDDSFN TFFAETGAGR HVPRAVFVDL EPTVVDEVRS
81 GAYRQLYHPE QLISGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLVFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDID RPTYTNLNR**L ISQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISSEK AYHEQITVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIAAIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VPRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDMAALEK DYEEVGM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A023FZA1|A0A023FZA1_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LRGSATRKAA NMRECISVHI GQAGVQIGNA CWELYCLEHG IQPDGKIPSD KVSGGVDDSF NTFFAQTGAG KHVPRAVFVD
81 LEPTVVDEVR TGSHKQLYHP EQLISGKEDA ANNYARGHYT IGKEIVDLVL DRIRKLADQC SGLQGFLVFH SFGGGTGSGF
161 TSLLMQRLSV DYGKKSKLEF SVYPAPQVAT AVVEPYNSIL TTHTTLEHSD CSFMVDNEAI YDICRRNLDI DRPTYSNLNR
241 **LISQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL VTYSPVISAE KAHHEQLTVA EITSSCFEPA NQMVKCDPRR
321 GKYMACCMLY RGDVVPKDVN AAIAAIKSKR SIQFVDWCPT GFKVGINYQP PTVVPGGDLA KVPRAVCML

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISQIVSSITASLR.F	Y	51.37	1486.8718	-17.9	744.4299	2	33.10	1223	1	241	254	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	255	275	
total 2 peptides												

tr|Q7PSI5|Q7PSI5_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LPFPGFFHQR ECISVHVGQA GVQIGNACWE LYCLEHGIQP DGQMPSDKTI GGGDDSFNTF FSETGAGKHV PRAVFVDLEP
81 TVVDEVRTGT YRQLFHPEQL ITGKEDAANN YARGHYTIGK EIVDLVLDRI RKLADQCTGL QGFLIFHSFG GGTGSGFTSL
161 LMERLSVDYG KKSKLEFAIY PAPQVSTAVV EPYNSILTTH TTLEHSDCAF MVDNEAIYDI CRRNLDIERP TYTNLNR**LIG**
241 **QIVSSITASL RFDGALNVDL TEFQTNLVPY PR**IHFPLVTY APVISAEKAY HEQLSVSEIT NACFEPANQM VKCDPRHGKY
321 MACCMLYRGD VVPKDVNAAI ATIKTKRTIQ FVDWCPTGFK VGINYQPPTV VPGGDLAKVQ RAVCMLSNTT AIAEAWARLD
401 HKFDLMYAKR AFVHWYVGEG MEEGEFSEAR EDLAALEKDY EEVGMDSGDG EGEGAEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	238	251	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	252	272	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
total 2 peptides												

tr|A0A0X9PE16|A0A0X9PE16_9ORTH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NEAIYDICRR NLDIERPTYT NLNR**LIGQIV SSITASLRFD GALNVDLTEF QTNLVPYPR**I HFPLVTYAPV ISAEKAYHEQ

81 LSVAEITNAC FEPANQMVKC DPRHGKYM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	25	38	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	39	59	
total 2 peptides												

tr|A0A0X9TMY8|A0A0X9TMY8_9ORTH

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NEAIYDICRR NLDIERPTYT NLNR**LIGQIV SSITASLRFD GALNVDLTEF QTNLVPYPR**I HFPLVTYAPV ISAEKAYHEQ

81 LSVAEITNAC FEPANQMVKC DPRHGKYM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	25	38	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	39	59	
total 2 peptides												

tr|A0A0P4Z4W3|A0A0P4Z4W3_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPSDKSVGGG DDSFNTFFSE TGSGKHVPRA VFVDLEPTVV DEVRTGTYRS LFHPEQLITG KEDAANNYAR GHYTIGKEIV
81 DLVLDRVRKL SDQCTGLQGF LIFHSFGGGT GSGFTSLLME RLSVDYGKKS KLEFAIYPAP QVSTAVVEPY NSILTTHTTL
161 EHSDCAFMVD NEAIYDICRR NLDIERPTYT NLNR**LIGQIV SSITASLRFD GALNVDLTEF QTNLVPYPR**I HFPLVTYAPV

241 ISAEKAYHEQ LTVGEITNAC FEPANQMVKC DPRHGKYMAC CMLYRGDV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	195	208	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	209	229	
total 2 peptides												

tr|A0A185N6J1|A0A185N6J1_9ODON

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TTHTTLEHSD CAFMVDNEAI YDICRRNLDI ERPTYTNLNR **LIGQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL

81 ATYAPVISAE KAYHEQLTVA EITNACFEPA NQMVKCDPRH GKYMACCMLY RGDVVPKDVN AAIATIKTKR TIQFV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	41	54	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	55	75	
total 2 peptides												

tr|A0A185N6J8|A0A185N6J8_9ODON

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TTHTTLEHSD CAFMVDNEAI YDICRRNLDI ERPTYTNLNR **LIGQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL

81 ATYAPVISAE KAYHEQLTVA EITNACFEPA NQMVKCDPRH GKYMACCMLY RGDVVPKDVN AAIATIKTKR TIQFV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	41	54	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	55	75	
total 2 peptides												

tr|A0A1B6INX8|A0A1B6INX8_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 CSVHYKHRSF TSNMRECISV HIGQAGVQIG NACWELYCLE HGIQPDGQMP SDKTIGGGDD SFNTFFSETG SGKHVPRAVF
81 VDLEPTVVDE VRTGTYRQLF HPEQLITGKE DAANNYARGH YTIGKEIVDI VLDRIRKLSD QCTGLQGFLV FHSFGGGTGS
161 GFTSLLMERL SVDYGKKSKL EFSIYPAPQV STAVVEPYNS ILTTHTTLEH SDCAFMVDNE AIYDICRRNL DIERPTYTNL
241 NR**LIGQIVSS ITASLRFDGA LNVDLTEFQT NLVPYPR**IHF PLATYAPVIS AEKAYHEQMT VAEITNACFE PANQMVKCDP
321 RHGKYMACCM LYRGDVVPKD VNAAIATIKT KRSIQFVDWC PTGFKVGINY QPPTVVPGGD LAKVQRAVCM LSNTTAIAEA
401 WARLDHKFDL MYAKRAFVHW YVGEGMEEGE FSEAREDLAA LEKDYEEVGV DSTEGEVEDG DEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	243	256	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	257	277	
total 2 peptides												

tr|A0A1B6IMY7|A0A1B6IMY7_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRAHMTSGRE CISVHIGQAG VQIGNACWEL YCLEHGIQPD GQMPSDKTIG GGDDSFNTFF SETGSGKHVP RAVFVDLEPT
81 VVDEVRTGTY RQLFHPEQLI TGKEDAANNY ARGHYTIGKE IVDIVLDRIR KLSDQCTGLQ GFLVFHSFGG GTGSGFTSLL
161 MERLSVDYGK KSKLEFSIYP APQVSTAVVE PYNSILTTHT TLEHSDCAFM VDNEAIYDIC RRNLDIERPT YTNLNR**LIGQ**
241 **IVSSITASLR FDGALNVDLT EFQTNLVPYP R**IHFPLATYA PVISAEKAYH EQMTVAEITN ACFEPANQMV KCDPRHGKYM
321 ACCMLYRGDV VPKDVNAAIA TIKTKRSIQF VDWCPTGFKV GINYQPPTVV PGGDLAKVQR AVCMLSNTTA IAEAWARLDH
401 KFDLMYAKRA FVHWYVGEGM EEGEFSEARE DLAALEKDYE EVGVDSTEGE VEDGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	237	250	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	251	271	
total 2 peptides												

tr|A0A0K8RBU4|A0A0K8RBU4_IXORI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPRAVYVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIF DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVSE ITNSCFEPVN QMVKCDPRHG KYMACCLLYR
321 GDVVPKDVNA AIAAIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGIDSA EGAEDDGGEE F

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|B7PH43|B7PH43_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGGGDDSFN TFFSETGAGK HVPRAVYVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIF DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVSE ITNSCFEPVN QMVKCDPRHG KYMACCLLYR
321 GDVVPKDVNA AIAAIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGIDSA EGAEDDGGEE F

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
total 2 peptides												

tr|A7UIK9|A7UIK9_MONAT back to list

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

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN 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.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0N7ZFH6|A0A0N7ZFH6_9CRUS back to list

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

Protein Coverage:

1 MRECISIHVG QAGIQIGNAC WELYCLEHGI QPDGRMPSDK VAGGVDDSFN TFFSECGSGK HVPRAVFVDL EPTVVDEVRT

81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDVVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQNSVGD ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEGEGGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0K8TTW1|A0A0K8TTW1_TABBR back to list

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

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETGAGK HVPRAVFIDL EPTVVDEVRT

81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSG EGEAEGAEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P5NHY4|A0A0P5NHY4_9CRUS back to list

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

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGRMPSDK VAGGIDDSFS TFFAECGSGK HVPRAIFVDL EPTVVDEVRT

81 GTYRSLFHPE QLITGKEAAA NNYARGHYTI GKEIVDIVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFA SLLMERLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQNSVGD ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR LDHKFDLMYA

401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEGEGGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 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 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN 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.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A131ZV00|A0A131ZV00_SARSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECLSIHLG QAGVQMGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETCSGK HVPRAVFVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVMD RIRKLADKCS GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFS IYPAPQVSTA VVEPYNSVLT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLA TYAPVISTEK AYHEQLTVGE ITNACFEPQN QMVKCDPRHG KYMAVCLLYR
321 GDVVPKDVNA AIAAIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVAIEST DADGDAGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 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 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVAE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN 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.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P4YX17|A0A0P4YX17_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGRMPSDK VAGGIDDSFS TFFAECGSGK HVPRAIFVDL EPTVVDEVRT
81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDIVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFA SLLMERLSVD
161 YGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPSYPNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQNSVGD ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEGEGGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P6A1J6|A0A0P6A1J6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGIQIGNAC WELYCLEHGI QPDGRMPSDK VAGGVDDSFN TFFSECGSGK HVPRAVFVDL EPTVVDEVRT
81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDVVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPSYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQMTVGD ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEGEGGDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A131ZUS5|A0A131ZUS5_SARSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TIGTGDDSFN TFFSETGSGK HVPRAVYVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFA VYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVAE ITNTCFEPAN QMVKCDPRHG KYMACCLLYR
321 GDVVPKDVNA AIASIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGLDST EADDTVGEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P5GV80|A0A0P5GV80_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK SVGGGDDSFN TFFSETGSGK HVPRAVFVDL EPTVVDEVRT
81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 SGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVGE ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEGEGNDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A023F9U2|A0A023F9U2_TRIIF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGGGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RIRKLADQCT GLQGFLIFHS CGGGTGSGFT SLLMERLSVD
161 FGKKSKLEFA IYPEPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVME ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWAR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSV EGEADPQEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0X9H6Y0|A0A0X9H6Y0_NILLU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISVHTG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK TVGSGDDSFN TFFSETGAGK HVPRAVFVDL EPTVVDEVRT
81 GTYRQLFHPE QLITGKEDAA NNYARGHYTA GKEIVDLVLD RIRKLADQCT GLQGFLIFHS FGGGTGSGFA SLLMERLSVD
161 YGKKSKLEYA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMADNEAIY DICRRNLDIE RPTYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPIVSAEK AYHEQLSVNE ITNSCFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNT AIATIKTKRT IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQRAVCMLSN TTAIAEAWSR LDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGMDSI VGEGEGEEA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P5GQJ7|A0A0P5GQJ7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSHPLRQMPS DKTIGGGDDS FNTFFSETGS GKHVPRAVFV DLEPTVVDEV RTGTYRQLFH PEQLITGKED AANNYARGHY
81 TIGKEIVDLV LDRIRKLSDQ CTGLQGFLIF HSFGGGTGSG FTSLLMERLS VDYGKKSKLE FAIYPAPQVS TAVVEPYNSI
161 LTTHTTLEHS DCAFMVDNEA IYDICRRNLD IERPTYTNLN R**LIGQIVSSI TASLRFDGAL NVDLTEFQTN LVPYPR**IHFP
241 LVTYAPVISA EKAYHEQLTV AEITNACFEP ANQMVKCDPR HGKYMACCML YRGDVVPKDV NAAIATIKTK RTIQFVDWCP
321 TGFKVGINYQ PPTVVPGGDL AKVSRAVCML SNTTAIAEAW ARLDHKFDLM YAKRAFVHWY VGEGMEEGEF SEAREDLAAL
401 EKDYEEVGMD SVEGEGEGND EY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	202	215	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	216	236	
total 2 peptides												

tr|A0A0P5FTK3|A0A0P5FTK3_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPSDKSVGGG DDSFNTFFSE TGSGKHVPRA VFVDLEPTVV DEVRTGTYRS LFHPEQLITG KEDAANNYAR GHYTIGKEIV
81 DLVLDRVRKL SDQCTGLQGF LIFHSFGGGT GSGFTSLLME RLSVDYGKKS KLEFAIYPAP QVSTAVVEPY NSILTTHTTL
161 EHSDCAFMVD NEAIYDICRR NLDIERPTYT NLNR**LIGQIV SSITASLRFD GALNVDLTEF QTNLVPYPR**I HFPLVTYAPV
241 ISAEKAYHEQ LTVGEITNAC FEPANQMVKC DPRHGKYMAC CMLYRGDVVP KDVNAAIATI KTKRTIQFVD WCPTGFKVGI
321 NYQPPTVVPG GDLAKVSRAV CMLSNTTAIA EAWARLDHKF DLMYAKRAFV HWYVGEGMEE GEFSEAREDL AALEKDYEEV
401 GMDSVEGEGE GNDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	195	208	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	209	229	
total 2 peptides												

tr|A0A0P5FQ62|A0A0P5FQ62_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAFGGGDDSF NTFFSETGSG KHVPRAVFVD LEPTVVDEVR TGTYRSLFHP EQLITGKEDA ANNYARGHYT IGKEIVDLVL
81 DRVRKLSDQC TGLQGFLIFH SFGGGTGSGF TSLLMERLSV DYGKKSKLEF AIYPAPQVST AVVEPYNSIL TTHTTLEHSD
161 CAFMVDNEAI YDICRRNLDI ERPTYTNLNR **LIGQIVSSIT ASLRFDGALN VDLTEFQTNL VPYPR**IHFPL VTYAPVISAE
241 KAYHEQLTVG EITNACFEPA NQMVKCDPRH GKYMACCMLY RGDVVPKDVN AAIATIKTKR TIQFVDWCPT GFKVGINYQP
321 PTVVPGGDLA KVSRAVCMLS NTTAIAEAWA RLDHKFDLMY AKRAFVHWYV GEGMEEGEFS EAREDLAALE KDYEEVGMDS
401 VEGEGEGNDE Y

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	191	204	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	205	225	
total 2 peptides												

tr|B7QP04|B7QP04_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MERLSVDYGK KSKLEFAIYP APQVSTAVVE PYNSILTTHT TLEHSDCAFM VDNEAIYDIC RRNLDIERPT YTNLNR**LIGQ**
81 **IVSSITASLR FDGALNVDLT EFQTNLVPYP R**IHFPLVTYA PVISAEKAYH EQLTVSEITN SCFEPANQMV KCDPRHGKYM
161 ACCLLYRGDV VPKDVNAAIA AIKTKRSIQF VDWCPTGFKV GINYQPPTVV PGGDLAKVQR AVCMLSNTTA IAEAWARLDH
241 KFDLMYAKRA FVHWYVGEGM EEGEFSEARE DLAALEKDYE EVGIDSAEGA EDDARSTAPP TGTCASASQC TWARRVCRSA
321 MPAGSFTASS MASSPTGRCQ TTGWWAAGRT PSTPSSWPPG RASMCPGLSS STWNPRWWTR CATDPTDSCS TRNR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	77	90	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	91	111	
total 2 peptides												

tr|A0A0P5NAD9|A0A0P5NAD9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRECISIHVG QAGIQIGNAC WELYCLEHGI QPDGRMPSDK VAGGVDDSFN TFFSECGSGK HVPRAVFVDL EPTVVDEVRT
81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDVVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD
161 YGKKSKLEFA IYPAPQVSTA VVEPYNSILT THTTLEHSDC AFMVDNEAIY DICRRNLDIE RPSYTNLNR**L IGQIVSSITA**
241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQNSVGD ITNACFEPAN QMVKCDPRHG KYMACCMLYR
321 GDVVPKDVNA AIATIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VSRAVCMLSN TTAIAEAWAR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0N8CYL8|A0A0N8CYL8_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRFNNNQQVK IGWENSASTE RRSYEVLYRV NNARGHYTIG KEIVDLVLDR VRKLSDQCTG LQGFLIFHSF GGGTGSGFTS
81 LLMERLSVDY GKKSKLEFAI YPAPQVSTAV VEPYNSILTT HTTLEHSDCA FMVDNEAIYD ICRRNLDIER PTYTNLNR**LI**
161 **GQIVSSITAS LRFDGALNVD LTEFQTNLVP YPR**IHFPLVT YAPVISAEKA YHEQLTVGEI TNACFEPANQ MVKCDPRHGK
241 YMACCMLYRG DVVPKDVNAA IATIKTKRTI QFVDWCPTGF KVGINYQPPT VVPGGDLAKV SRAVCMLSNT TAIAEAWARL
321 DHKFDLMYAK RAFVHWYVGE GMEEGEFSEA REDLAALEKD YEEVGMDSVE GEGEGNDEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	159	172	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	173	193	
total 2 peptides												

tr|A0A0P5I692|A0A0P5I692_9CRUS

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

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK SVGGGDDSFN TFFSETGSGK HVPRAVFVDL EPTVVDEVRT

81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMERLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLTVGE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIKTKRT IQFVDWCPTG FKVEIIFILI FTKF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P5Y6N4|A0A0P5Y6N4_9CRUS back to list

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

Protein Coverage:

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK SVGGGDDSFN TFFSETGSGK HVPRAVFVDL EPTVVNEVRT

81 GTYRSLFHPE QLITGKEDAA NNYARGHYTI GKEIVDLVLD RVRKLSDQCT GLQGFLIFHS FGGGTGSGFT SLLMDRLSVD

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

241 **SLRFDGALNV DLTEFQTNLV PYPR**IHFPLV TYAPVISAEK AYHEQLSVGE ITNACFEPAN QMVKCDPRHG KYMACCMLYR

321 GDVVPKDVNA AIATIK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	230	243	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	244	264	
total 2 peptides												

tr|A0A0P5GEQ6|A0A0P5GEQ6_9CRUS back to list

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

Protein Coverage:

1 MSGRSRILEV RYIGQRACEY DPEQGQQSPF RWYNGKKSKL EFAIYPAPQV STAVVEPYNS ILTTHTTLEH SDCAFMVDNE

81 AIYDICRRNL DIERPTYTNL NR**LIGQIVSS ITASLRFDGA LNVDLTEFQT NLVPYPR**IHF PLVTYAPVIS AEKAYHEQLT

161 VAEITNACFE PANQMVKCDP RHGKYMACCM LYRGDVVPKD VNAAIATIKT KRTIQFVDWC PTGFKVGINY QPPTVVPGGD

241 LAKVSRAVCM LSNTTAIAEA WARLDHKFDL MYAKRAFVHW YVGEGMEEGE FSEAREDLAA LEKDYEEVGM DSVEGEGEGN

321 DEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	103	116	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	117	137	
total 2 peptides												

tr|A0A2A3EL84|A0A2A3EL84_APICC back to list

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

Protein Coverage:

1 MSSAVKKRPI TKRNEAINNQ SVYADERECI SVHVGQAGVQ IGNACWELYC LEHGIQPDGQ MPSDKTIGGG DDSFNTFFSE

81 TGAGKHVPRA VFIDLEPTVV DEVRTGTYRQ LFHPEQLITG KEDAANNYAR GHYTIGKEIV DLVLDRIRKL ADQCTGLQGF

161 LIFHSFGGGT GSGFTSLLME RLSVDYGKKS KLEFAIYPAP QVSTAVVEPY NSILTTHTTL EHSDCAFMVD NEAIYDICRR

241 NLDIERPTYT NLNR**LIGQIV SSITASLRFD GALNVDLTEF QTNLVPYPR**I HFPLVTYAPV ISAEKAYHEQ LSVSEITNAC

321 FEPANQMVKC DPRHGKYMAC CMLYRGDVVP KDVNAAIATI KTKRTIQFVD WCPTGFKVGI NYQPPTVVPG GDLAKVQRAV

401 CMLSNTTAIA EAWARLDHKF DLMYAKRAFV HWYVGEGMEE GEFSEAREDL AALEKDYEEV GMDSAEGEGE GAEEY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LIGQIVSSITASLR.F	Y	41.35	1456.8613	-25.6	729.4193	2	31.98	1179	1	255	268	
R.FDGALNVDLTEFQTNLVPYPR.I	N	23.88	2408.2012	-19.3	1205.0846	2	32.06	1182	1	269	289	
total 2 peptides												

tr|E0W1G3|E0W1G3_PEDHC back to list

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

Protein Coverage:

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

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VALTGLTVAEYFRDQEGQDVLLFIDNIFR.F	Y	38.97	3341.7295	-24.5	1114.8898	3	44.24	1735	1	305	333	
total 1 peptides												

tr|A0A224Y123|A0A224Y123_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDTTARNVLA LSALILLPLL EAYCPRLAPD VISGKIIPCR YLCIRINFFE LPSIILSTER DGVLCSTLLL RRRGVCKNGG
81 CYPFESEGQK RRGMFRRVIT NIDKFASGSY KKPVEKPGAQ SGPIVSVIPS LLGGRSKDTA NGTSPPTSGL PPSSPASPSL
161 SAGTTSLVKS VGSTLTSIWA QAFPFNLKAG PPRRPTAANT AHSSNPQQAP GGMTAASSDG ASVAGIGGGP PVVPRLPTEG
241 SSNQSPPTGP SLGSNLFGRL PRLGSALTLS NRLMKLRDKS SASNAATGSS ISPVAGINAI NAGAIKDEVP GASGGTSGTH
321 AVKIGGGMPT AGPPAAPGNN DERPTPATPP ETASPRVMSG LLSTLGLGRT LARSQGEKTS TRLLGRLISS ATATNGRNAA
401 SINDGTTGST GKLSQPNANF VRGSPVGSPE TTQGSGNINV VSEAPPGLGS SPLISRLRTT AALRNAINKW KHGHSESAAA
481 PRIPSSPASQ GTAVTNTGAS KASSRTPQEN FPDANREVPT NPPVMAPGTS NEVSPSMAPR GRSSAGIIPG LSSAVALGGI
561 LSTSRGKNSG SSTVPNSINA SASEISAGNA KSNNELSVTA GSSVGTNGNY ASLPNATPVE TPGRSDNKNA ASGLHRVTLS
641 PEATPESSAV GAVNKIIRES QDVKAQSGVA PVNPISPVAA SGLVNPLVVR VSHEVPGVIL QEPGGEITGR PAAVSQSTKP
721 EKPRVPQTPT LSSL**TPGGSV TP**SATPPVPE SSSSAGSPKV ARPTIIKTPH ETHISSVEGE ARTQTPNATP SVGPPAGGAE
801 ATSVNAATRG TEETALEAPN GNAVLPPNNT LPGSKPEKIP TTTGKSERRS TFLSRLHNVR AAVTSPVTGG AETSRTFVRN
881 LLGGGLRRRL IN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPGGSVTP.S	Y	31.46	714.3548	15.3	715.3730	1	20.38	769	1	735	742	
total 1 peptides												

tr|A0A1B6CHY3|A0A1B6CHY3_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTKTYNDIEA VTRLLEEKEK DIELTARIGK ELLTHNNKLE TNVASLENEL RIANEKITQL THELQKKTEL IQILTSDYDD
81 SGSEAGTPTG QINFEVLQKR VCRLEEENIS LRKEASQLAA ATEDCELQEA RLVSDLASQL ALCR**TDLSGI T**LDAEQQREE
161 AITNKALAES LKQKLSAAEI KIITVTSEND ELVTMINLAR ETQCELATEL ADLKEKYAEV MNLLQDAQEG LRHQRKKAQP
241 RARGGLFPSL HTSLTTHNPD SIASELECSL FSELSLDSGI GVSSINVPSY KKVFETVRCA SRGSSLGSGS SSGSSPGHGP
321 RIISNSNYPS LNNTLPMSVS SSQKPRISSF STSSRPPLLR SNFTALDSAG ASDSESSEDF TYMSRGNPQT PAPADLEAAL
401 RRLTPGAVAA RRA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TDLSGIT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	145	151	
total 1 peptides												

tr|A0A1B6EG82|A0A1B6EG82_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNPAEAEELD RWLWQVKCQE ELEAAGEVPD CMYHVARGGT HGPHPRLRMF LPALNKVLCS NRVSQMTKTY NDIEAVTRLL
81 EEKEKDIELT ARIGKELLTH NNKLETNVAS LENELRIANE KITQLTHELQ KKTELIQILT SDYDDSGSEA GTPTGQINFE
161 VLQKRVCRLE EENISLRKEA SQLAAATEDC ELQEARLVSD LASQLALCR**T DLSGIT**LDAE QQREEAITNK ALAESLKQKL
241 SAAEIKIITV TSENDELVTM INLARETQCE LATELADLKE KYAEVMNLLQ DAQEGLRHQR KKAQPRARGG LFPSLHTSLT
321 THNPDSIASE LECSLFSELS LDSGIGVSSI NVPSYKKVFE TVRCASRGSS LGSGSSSGSS PGHGPRIISN SNYPSLNNTL
401 PMSVSSSQKP RISSFSTSSR PPLLRSNFTA LDSAGASDSE SSEDFTYMSR GNPQTPAPAD LEAALRRLTP GAVAARRA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TDLSGIT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	210	216	
total 1 peptides												

tr|Q173I4|Q173I4_AEDAE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NGVTTIKRTE KDRDKHPDRV NLDRKGLSSI PIIDDEPNLR LLSLQHNLIN TFHIPAETDT NNNEPKIPAS SPPSPKTSPT
81 GLQKSGANSS SNTTAKDSPA SSPTSNSASV TAASTNSSLY STNRNTKPLL RQKSTSRSQL YLNNNNNLYL AGKVTLSAKP
161 LNGQSPVCAT SPTNTAQHRN MLKKSNSFIS NATLFPSPPT HQQQSSNLLK LKNKLLLTPS FSIDNLNSAN ETTAVHESTS
241 NSNNNSGKTT PTSAAPPTNG VNHYVNPQTH ISPILSAAEP RYNLQNLVFL DLYDNQIEKI SCLDGLKCLT VLLLGKNRI**T**
321 **DISGLT**SLRQ TLRVLDLHGN KISNISSKIN QLQELKSLNL AGNQLRQIHS NDFNGLVNLK ELNLKRNRIK KIHGFDDLRS
401 LERLWLCHND LQCVEDMAAI AKAINLKEVT IENNPVSLAG DCVSFLVSYL PGLVSLSQMQ ITEQVRRAAS AWRKNKELSD
481 MNYSNLSTDV CQSIRREEII SNARTNWELL RSQQSTACRN VQRTAIVAKD VEMDLNNSNL SDINRNGKTK KSPANVNGNA
561 TSNNQRAPRA AVKKPPPNKK LIRSSSQDNS GSQLSEQGGE DYFRLPPILA PFLEQTPTTI ASSSKIESSE SSNGLHPDSS
641 ISSAISSDNE ELNVKEIEKD VMVDSTVVTE TIETPAKMNE SPPPQDFPSE NPEKIQENGN SNSDSGRGTS ETSSSTNQLD
721 ELNNDKVSTL STTSNKTTSD SVITTSSISE NDSNRATISQ KPKTVGPVKR TNTTRNNTVL NTVNNLANSS NLANTTTANS
801 NPSATSSISG TTTTNNSYVP PSKSKLNERE REQGGDYLIE ICGRYLNVYG MGALKFIDKQ WNMTKASDVH TVKFSYINFN
881 SITAILCRIK IRFVNAENFI FRETNITCLG QINALAESQG IASLTIDPEG NPITSKPWRN YAIYRLSHWG LKQINGIEIT
961 EEEVQDAEIM YAGLSDLVLW SLPEGLLQPL LQRLRLEETA HATKMTAKEW LMQADSSLKN IVGKEALQWK KHSTSQDDAI
1041 MRAKGKAYFA RMLDNTCNAV DKLQQLEHTW PTLLMELIRN TLIDYSQIDV YVRNMMLELL K

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.TDISGLT.S	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	320	326	
total 1 peptides												

tr|A0A0P6IU66|A0A0P6IU66_AEDAE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NGVTTIKRTE KDRDKHPDRV NLDRKGLSSI PIIDDEPNLR LLSLQHNLIN TFHIPAETDT NNNEPKIPAS SPPSPKTSPT
81 GLQKSGANSS SNTTAKDSPA SSPTSNSASV TAASTNSSLY STNRNTKPLL RQKSTSRSQL YLNNNNNLYL AGKVTLSAKP
161 LNGQSPVCAT SPTNTFLQKP SSILMSAQHR NMLKKSNSFI SNATLFPSPP THQQQSSNLL KLKNKLLLTP SFSIDNLNSA
241 NETTAVHEST SNSNNNSGKT TPTSAAPPTN GVNHYVNPQT HISPILSAAE PRYNLQNLVF LDLYDNQIEK ISCLDGLKCL
321 TVLLLGKNRI **TDISGLT**SLR QTLRVLDLHG NKISNISSKI NQLQELKSLN LAGNQLRQIH SNDFNGLVNL KELNLKRNRI
401 KKIHGFDDLR SLERLWLCHN DLQCVEDMAA IAKAINLKEV TIENNPVSLA GDCVSFLVSY LPGLVSLSQM QITEQVRRAA
481 SAWRKNKELS DMNYSNLSTD VCQSIRREEI ISNARTNWEL LRSQQSTACR NVQRTAIVAK DVEMDLNNSN LSDINRNGKT
561 KKSPANVNGN ATSNNQRAPR AAVKKPPPNK KLIRSSSQDN SGSQLSEQGG EDYFRLPPIL APFLEQTPTT IASSSKIESS
641 ESSNGLHPDS SISSAISSDN EELNVKEIEK DVMVDSTVVT ETIETPAKMN ESPPPQDFPS ENPEKIQENG NSNSDSGRGT
721 SETSSSTNQL DELNNDKVST LSTTSNKTTS DSVITTSSIS ENDSNRATIS QKPKTVGPVK RYGIGTLVRT NTTRNNTVLN
801 TVNNLANSSN LANTTTANSN PSATSSISGT TTTNNSYVPP SKSKLNERER EQGGDYLIEI CGRYLNVYGM GALKFIDKQW
881 NMTKASDVHT VKFSYINFNS ITAILCRIKI RFVNAENFIF RETNITCLGQ INALAESQGI ASLTIDPEGN PITSKPWRNY
961 AIYRLSHWGL KQINGIEITE EEVQDAEIMY AGLSDLVLWS LPEGLLQPLL QRLRLEETAH ATKMTAKEWL MQADSSLKNI
1041 VGKEALQWKK HSTSQDDAIM RAKGKAYFAR MLDNTCNAVD KLQQLEHTWP TLLMELIRNT LIDYSQIDVY VRNMMLELLK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.TDISGLT.S	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	331	337	
total 1 peptides												

tr|A0A1S4FFQ6|A0A1S4FFQ6_AEDAE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MSTSKLRGKS AIHINDSVIS SNSNNSHNTL LKIESVVPKL TTRGNNSNNF SHSSRLKTFH RSHSTLSTSY LKKVSEKRIF
  81  VPREAVGDKG RESPRDQQPN SQNDPQPDGS VLVQNGVTTI KRTEKDRDKH PDRVNLDRKG LSSIPIIDDE PNLRLLSLQH
 161  NLINTFHIPA ETDTNNNEPK IPASSPPSPK TSPTGLQKSG ANSSSNTTAK DSPASSPTSN SASVTAASTN SSLYSTNRNT
 241  KPLLRQKSTS RSQLYLNNNN LNYLAGKVTL SAKPLNGQSP VCATSPTNTF LQKPSSILMS AQHRNMLKKS NSFISNATLF
 321  PSPPTHQQQS SNLLKLKNKL LLTPSFSIDN LNSANETTAV HESTSNSNNN SGKTTPTSAA PPTNGVNHYV NPQTHISPIL
 401  SAAEPRYNLQ NLVFLDLYDN QIEKISCLDG LKCLTVLLLG KNRITDISGL TSLRQTLRVL DLHGNKISNI SSKINQLQEL

 481  KSLNLAGNQL RQIHSNDFNG LVNLKELNLK RNRIKKIHGF DDLRSLERLW LCHNDLQCVE DMAAIAKAIN LKEVTIENNP
 561  VSLAGDCVSF LVSYLPGLVS LSQMQITEQV RRAASAWRKN KELSDMNYSN LSTDVCQSIR REEIISNART NWELLRSQQS
 641  TACRNVQRTA IVAKDVEMDL NNSNLSDINR NGKTKKSPAN VNGNATSNNQ RAPRAAVKKP PPNKKLIRSS SQDNSGSQLS
 721  EQGGEDYFRL PPILAPFLEQ TPTTIASSSK IESSESSNGL HPDSSISSAI SSDNEELNVK EIEKDVMVDS TVVTETIETP
 801  AKMNESPPPQ DFPSENPEKI QENGNSNSDS GRGTSETSSS TNQLDELNND KVSTLSTTSN KTTSDSVITT SSISENDSNR
 881  ATISQKPKTV GPVKRYGIGT LVRTNTTRNN TVLNTVNNLA NSSNLANTTT ANSNPSATSS ISGTTTTNNS YVPPSKSKLN
 961  EREREQGGDY LIEICGRYLN VYGMGALKFI DKQWNMTKAS DVHTVKFSYI NFNSITAILC RIKIRFVNAE NFIFRETNIT
1041  CLGQINALAE SQGIASLTID PEGNPITSKP WRNYAIYRLS HWGLKQINGI EITEEEVQDA EIMYAGLSDL VLWSLPEGLL
1121  QPLLQRLRLE ETAHATKMTA KEWLMQADSS LKNIVGKEAL QWKKHSTSQD DAIMRAKGKA YFARMLDNTC NAVDKLQQLE
1201  HTWPTLLMEL IRNTLIDYSQ IDVYVRNMML ELLK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.TDISGLT.S	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	445	451	
total 1 peptides												

tr|A0A182GHL5|A0A182GHL5_AEDAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MSTSKLRGKS AIHINDSVIS SNSNNSHNTL LKIESVVPKL TTRGNNSNNF NHSSRLKTFH RSHSTLSTSY LKKVSEKRVF
  81  VPREAAGDRG RESPRDQQPQ SQNDAQPDGS VLVQNGVTTI KRTEKDRDKH PDRVNLDRKG LSSIPIIDDE PNLRLLSLQH
 161  NLINTFHIPA ETDTNNNEPK IPASPPPSPK TSPSGLQKSS ANPSSNTTTK DSPSSSPTSN STTVTAASTN NSLNITNRNT
 241  KQLLRQKSTS RSQLYLNNNN LNYLAGKVTL SAKPLNGQSP VCATSPTNTF LQKPSSILLS AQHRNMLKKS NSFISNATLF
 321  PSPPTHQQQS SNLLKLKNKL LLTPSFSIDN LNSANETTAV HESTSNSNNN SGKTTPTNVT PATNGVNHYV NPQTHISPIL
 401  SAAEPRYNLQ NLVFLDLYDN QIEKICCLDG LKCLTVLLLG KNRITDISGL TSLRQTLRVL DLHGNKISNI ASKINQLQEL

 481  KSLNLAGNQL RQIHSSDFNG LVNLKELNLK RNRIKKIHGF DDLRSLERLW LCHNDLQCVE DMAAIAKAIN LKEVTIENNP
 561  VSLAGDCVSF LVSYLPGLVS LSQMQITEQV RRAASAWRKN KELSDMNYSN LSTDVCQSIR REEIISNART NWELLRSQQS
 641  TACRNVQRTA VVAKDVEMDL NNSNLSDINR NGKTKKAPPN TNGNAVSNNQ RNPRAAAKKP PPSKKLIRSS SQDNSGSQLS
 721  EQGGEDYFRL PPILAPFLEQ TPTTIASTNK IESSESSNGQ NPDSSISSAL SSDNEELNVK EIEKDVETSN TAVNEAVEAP
 801  IKMIEPLSPK DIPSEIPEKI QENGNSNSDS GRGTSETSSS TNQLDELNND KVSTMSTVSN KTTSDSVITT SSISENDSNR
 881  ATISQKPKSV GPVKRYGIGT LVRTNTTRSN AVMNNVNSLA NSSNLASSTT VNTNPSAPSS IAGTATTNSN YVPPTKSKLN
 961  EREREQGGDY LIEICGRYLN VYGMGALKFI DKQWNMTKAS DVHTVKFSYI NFNSITAILC RIKIRFVNAE NFIFRETNIT
1041  CLGQINALAE SQGIASLTVD PEGNPITSKP WRNYAIYRLS HWGLKQINGI EITEDEVQDA ETMYAGLSDL VLWSLPEGLL
1121  QPLLQRLRLE ETAHATKMTA KEWLMQADSS LKNIVGKEAL QWKKHSTSQD DSVMRAKGKA YFARMLDNTC NAVDKLQQLE
1201  HTWPTLLMEL IRNTLIDYSQ IDVYVRNMML ELLK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.TDISGLT.S	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	445	451	
total 1 peptides												

tr|A0A1J1HJS3|A0A1J1HJS3_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MCWRTNQDNS KSMLDRYMIK LVIIQRSDHL GLGINVRGDE DWREKKSRKN CLRDLERKLL IAYRDTDLSG LTIVILDAFK

  81  MLRHVQK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.TDLSGLT.I	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	66	72	
total 1 peptides												

tr|A0A182ST32|A0A182ST32_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIAHCVSSTG QPQQEYQLTH PSYTDDTQNT SQIEHHTGSS TGRIESNFAV SDSGIEPLNE QEDVYDENDT SENDESDTDN
81 GRPVTVEESR YGVDDNSNGI IHDNRPVRIM SPSNGGPLAS TSAHDNVQTE LNNLEAVEVA FESDGSKRFL QHHFQSPRES
161 RKQLQHTEGA QLPSSLSDMT TNSASSSSSS FST**TDLSGLT** VSAAAAAAED VSQEQTISNL SLSTQRTIRR PSSSVQLTVN
241 VHNIKDASQP VRMETAPHND PPKSIQKHSQ GQQSMSDASR RNNPISISNF HSIASNDTLT SATTSSLQRH RTINSMNLNP
321 TTPAMVVKPV GEHRKLLKST GPILNYVFDH HPPYYKSTYY NTR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TDLSGLT.V	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	194	200	
total 1 peptides												

tr|R4N7H8|R4N7H8_LITVA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRLLVATAMA TAVLGFVRSQ CFSERDDFSV KVN**TDLSGIT** DFGFELYKQL APPESPENFF FSPYSIWTAF TLAYFGAGGE
81 TAAQLQRALR VDDKVATLRL WRALEAMYRT RQQNTTAYSF NIANRAYIDK SLPIRDCITN LLHSEVERVQ FFKVGAVAQE
161 INSFVSVATK GRIDQIINPS DLLDAIMVLV NAAYFKGTWQ FQFKASDTFP EPFYATSQNS DLVPMMHQTA SFRYNEFPEI
241 AAKVLELPYT GDAMSMFVFL PTEEGPLGFA RMVDRLSGNN LRAATHKGNL SFRTVDVKLP KFKMEVEIRE QFKPALKSMG
321 IRDIFDSEKV DLSTFGPLLN VTLEKVIHKA FVEVNEEGTE AAAATALIFA TRSGAARPLP IEFHCTRPFV FLIRDNDTHT
401 VLFMGSYKKP TKAKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.TDLSGIT.D	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	34	40	
total 1 peptides												

tr|A0A0Q9WK24|A0A0Q9WK24_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MANLEIYNLI VYNLLQIKLR NVVIFHCWQL PVLLPLAQLF SRNLIFSQFI SLSQSNESLA NFSKVYLDSE LTKIGVFLDL
81 GCEQSPFITN ESSRAQLYTH RYHWLIYDED GNMNTFVELF ERANLSINAD VTYVKPAKRT DPGSLFILHD VYNQGSQLGG
161 KLNITIDQSI YCNQTECEPV EYLSELHKRS RLQQR**TDLSG IT**FRQVALVT VIPLSSGEEK LLEFLNSEED YHLDWTSRVG
241 YRQNVHLQEL LRFNVRYIWR NQWSLNDSKG GALGEVTNAN ADLSTSAFVL SPERLRHIFP TAEVSEFRSI CIFRTPHNAG
321 IKAGVFLEPF KLSVWIVFGA VLMFSGILLW LTFRLEHRWM RHYLQYYVPS LLSSCLISFG AACIQGSHLI PCSTGGRLAF
401 IAVMFTSFLM YNYYTSIVVS SLLGSPVRSN IKTIQQLADS SLDVGFETIP FTRVYLNSSP RSDIRDLVKH KVEGRNPSNI
481 WLSAKEGVLR ARNQPGFVFV SEASFLYTFI EKYYLPHEIC ELNEIMFRPE NAVYTVIHIN STYKELLKQI QLRMMETGIT
561 QKHKFFYTKT KLHCYANNYV INVGMEYAAP LFIALLLSYF ASIFILMLEL AWAHLGRRHL QHFITAE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TDLSGIT.F	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	196	202	
total 1 peptides												

tr|A0A0J7P5Y5|A0A0J7P5Y5_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTGIAPSAPT SADACLSIVH SLMCHRQGGE SEGFSKRAIE SLVKKLKEKR DELDSLITAI TTNGAHPSKC VTIQRTLDGR
81 LQVAGRKGFP HVIYARIWRW PDLHKNELKH VKYCQFAFDL KCDSVCVNPY HYERVVSPGI ENAREQIIDC CGLLDVLMKW
161 VGFPRTDPFF **TDLSGLT**LQS SVGVGPGGRL VKDEYTVGGG GTAAAAAAAA VGSAMDVDGE MNQTIQHHPP APQPTASNNT
241 QQAQQGFIPG LPTPNPTVVH PMSHTVGSQQ QSLNAASSGT SGAQILSPAQ GQATADTFYG TNTPPQDINQ PSTVDALAAS
321 LGEGQSSPVS PVHLHHPNGF PVGTASYNSG APQWTGANTL TYTQSMQPPD PRHLHTASYW GGHGNDVSGN IGGLLSTQPA
401 PEYWCSVGYF ELDIQVGETF KVSSGCPTVT VDGYVDPSGG NRFCLGALSN VHRTEQSERA RLHIGKGVVL DLRGEGDVWL
481 RCQSEHSVFV QSYYLDREAG RAPGDAVHKI YPSAYIKVFD LRQCHKQMRG QAATAQAAAA AQAAAVAGHL THGGPIAKSI
561 SAAAGIGVDD LRRLCILRLS FVKGWGPDYP RQSIKETPCW IEVHLHRALQ LLDEVLHTMP IDGPRAIE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	171	177	
total 1 peptides												

tr|A0A088AF28|A0A088AF28_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVGLAGGGGH LYPSPPMQPN PELREMTGIA PSAPTSADAC LSIVHSLMCH RQGGESEGFS KRAIESLVKK LKEKRDELDS
81 LITAITTNGA HPSKCVTIQR TLDGRLQVAG RKGFPHVIYA RIWRWPDLHK NELKHVKYCQ FAFDLKCDSV CVNPYHYERV
161 VSPGIDPFF**T DLSGLT**LQSG VGVGPGGRLV KDEYSVGGGS SATAGAVGSA MDVDGEMNQT IQHHPPTQPT SSNNTQPSQQ

241 TFIPGLAPPN STSGEGVFGS NGGGNNGGNP HNKLDDNNCP RQTWIPTPHH PTTRNIHHPV VHPMSHTVGS QQQSLNTSSG
321 SSGTQMLSPS QGQSTETFYG TNTPPQDLNQ PPTVDALAAS LGEGQNSPVS PVHLHHSNGF PVGTAAYNSG APQWTGPNTL
401 TYTQSMQPPD HRHLHPTSYW GGHGGEVSGN IGGLLSTQPA PEYWCSVGYF ELDTQVGETF KVSSGCPTVT VDGYVDPSGG
481 NRFCLGALSN VHRTEQSEKA RLHIGKGVVL DLRGEGDVWL RCQSEHSVFV QSYYLDREAG RAPGDAVHKI YPSAYIKVFD
561 LRQCHKQMRG QAATAQAAAA AQAAAVAGHL THGAPITKSL SAAAGIGVDD LRRLCILRLS FVKGWGPDYP RQSIKETPCW
641 IEVHLHRALQ LLDEVLHTMP IDGPRGIE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	170	176	
total 1 peptides												

tr|A0A151J4K9|A0A151J4K9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVGLAGGGSH LYPSPPMQPN PELREMTGIA PSAPTSADAC LSIVHSLMCH RQGGESEGFS KRAIESLVKK LKEKRDELDS
81 LITAITTNGA HPSKCVTIQR TLDGRLQVAG RKGFPHVIYA RIWRWPDLHK NELKHVKYCQ FAFDLKCDSV CVNPYHYERV
161 VSPGIDPFF**T DLSGLT**LQSG VGVGPGGRLV KDEYTVGGGG TASAAAVGSA MDVDGEMNQT IQHHPPAQST ASNNAQQAQQ

241 GFIPGLPPPN STSTEGMFSA GGGGNNGNPH AKLDDNNCPR QTWIPTPHHS ASRNMHHPVV HPMSHTVGSQ QQSLNSASSG
321 TSSAQILSPA QGQSTADTFY NTTTPPQDIN QPPTVDALAA SLGEGQSSPV SPVHLHHPNG FPVGTAPYNS GAPQWTGANT
401 LTYTQSMQPP DPRHLHTTSY WGGHGNDVSG NIGGLLSTQP APEYWCSVGY FELDIQVGET FKVSSGCPTV TVDGYVDPSG
481 GNRFCLGALS NVHRTEQSER ARLHIGKGVV LDLRGEGDVW LRCQSEHSVF VQSYYLDREA GRAPGDAVHK IYPSAYIKVF
561 DLRQCHKQMR GQAATAQAAA AAQAAAVAGH LTHGAPITKS LSAAAGIGVD DLRRLCILRL SFVKGWGPDY PRQSIKETPC
641 WIEVHLHRAL QLLDEVLHTM PIDGPRAIE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	170	176	
total 1 peptides												

tr|A0A151JWE9|A0A151JWE9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVGLAGGGSH LYPSPPMQPN PELREMTGIA PSAPTSADAC LSIVHSLMCH RQGGESEGFS KRAIESLVKK LKEKRDELDS
81 LITAITTNGA HPSKCVTIQR TLDGRLQVAG RKGFPHVIYA RIWRWPDLHK NELKHVKYCQ FAFDLKCDSV CVNPYHYERV
161 VSPGIDPFF**T DLSGLT**LQSG VGVGPGGRLV KDEYTVGGGG TAAAAAAAAV GSAMDVDGEM NQTIQHHPPA QSTASNNAQQ

241 AQQGFIPGLP PPNSTSTEGM FSAGGGGNNG NPHAKLDDNN CPRQTWIPTP HHSASRNMHH PVVHPMSHTV GSQQQSLNSA
321 SSGTSGAQIL SPAQGQSTAD TFYNTTTPPQ DINQPPTVDA LAASLGEGQS SPVSPVHLHH PNGFPVGTAP YNSGAPQWTG
401 ANTLTYTQSM QPPDPRHLHT TSYWGGHGND VSGNIGGLLS TQPAPEYWCS VGYFELDIQV GETFKVSSGC PTVTVDGYVD
481 PSGGNRFCLG ALSNVHRTEQ SERARLHIGK GVVLDLRGEG DVWLRCQSEH SVFVQSYYLD REAGRAPGDA VHKIYPSAYI
561 KVFDLRQCHK QMRGQAATAQ AAAAAQAAAV AGHLTHGAPI TKSLSAAAGI GVDDLRRLCI LRLSFVKGWG PDYPRQSIKE
641 TPCWIEVHLH RALQLLDEVL HTMPIDGPRA IE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	170	176	
total 1 peptides												

tr|A0A182MMM2|A0A182MMM2_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MGDLENLHLI LLDNRTVRAS ESTAALKSCQ QLNVDVQKFL SLVMDGGKKL LAHLSDLHSA KSAVPQDLTD GKAQVERLLN
 81 TLDRKQTATN QAWTELERTV EVLQELATLE EGVSHVTSWI LTTAESMLNA QLRVGHDVNT ADQLRLEHEI LELQCWQTYG
161 CYAELLHKID HFPRRKDTPA YRDLQSQREW MDFVCRSFAQ RLERRRNILI TSVRFYRLVA EYFDRTSEVF QSLIMGERVE
241 DYALASTNLQ KLNENQRMLE MLEKEIIKEG EKLSDVLLMP VKDAVGRDID VDYSEDISNV RDILDATRSR SRIFADSVEL
321 QKLTLDQITH IFKYEQDART AVKWMSDLHQ VMLRSHAHVG ASVREIQAQK DEHQTLQETA KGTYNYGCQL LNASLALRQS
401 CKLETSQNIA MTKSLQRTWR SFQAVAQEQM TRLRVSAVFH RSVEEQCVKL RELHECVLRI GEISEQGRRR VRLRKYLATR
481 ERLLLEVGRM VRLGRLLKTR LREPFLLDDR LDAMASPENI ITESDNIMAC EAISSRLAEV AQVAEALDSV LSDVQGGFDD
561 EVEELTSAEA PEVTSKRNDS GNQSDDWSSS VKSTDDGSFV TASDCICTPQ SRSSSYHTAS ECRASPWWGV ESIERQSSLE
641 NDSAEDPDPE AFPSIKLLSG VVITSSANLS FDESEHSFPT VHGSASVDSH PDSDDTVPTV CSQTSPIATS SASSSALNSI
721 TRRENLALSL TPEELEQIEN DIRNNNLLAT VGTVDIVGKE LQSTQVTPTS EDSGNVSTSS VKLDVEDATR FEPVKGPTDI

801 SGLTYYYQNI ITKHTVKSCL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDISGLT.Y	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	798	804	
total 1 peptides												

tr|A0A0K2ULM4|A0A0K2ULM4_LEPSM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKEVSFGFLG SVTLVLLVEW IPGYADGVEQ DCWSQESKIC VPSNSSTCFG SPFPYSFIPE DAELGLLESW TYLKRIPKCW
 81 SSLRPLLCSL YAPECSPITN KTLGVPKALC KALKGPCRAL KQEYLPLSLQ SQWDRAFMCR GKSFCEREIA GGTRDILKFP
161 ESHEGVCYKP LVRAQNPANY FKFIDGCGLQ CFPPDKTPEQ YGKIQSLIGI GVLAALSTSS FATATLILDW KSSSYPNRII
241 FYINLCGLLF ISGWGLPFLQ GDNSFVCNPD NTRRVQEPGE GQDLACVALF VLIYYFGLSS ALWYAILTFS WNSLFSSMGL
321 LSAMSQREIL LKRTPYFHMI AWSVPAVLAI AIISLNGVEG DPLTGICFVS KSSPSFYFGF VIAPIAGICV ISTFFVVSSV
401 KSLVLAEKSA IEIAGISARS RRIRSTTVKI VIYSCIYFTC FFITVFSSVW IFSGYEEERN EAILKMYLGG EEFHKPLKYS
481 EIVILPTFLS VIASASWVWN KNTFKSWRKF FRRRFNSSEE RMKDIKVRKH ELITQAFAKR KDLALEGRLS LTFESSRFDP
561 VGVGNPSHFD DRGGVSSGDF SSTWAAALPR LVQRRGALVG GELINPQQQR RSSLDSEVSS VNRSRFSWME SRRQSFESQA
641 SSVPAFDMDR LQAIYDQAIS SSKKRPKKRS KKRKLIFSSS SRPESRMSSR RNSIGSSSFV CAKESSSATV ITLDPRKLMD
721 TRHSSKRFIS SPKEFFELKE KLKVLQTSSV DLDDSSKKMG NVTGTTTILS GGEEEEEGRE RRTVSIQTSF TDLSGLTQVV

801 HKSELGTQTT PPPGASDSSS QTIPHPIEPV VIQITDEHES SSFPSSAGGT GSGDGSGNQY ELFLKEDKHE HRGPPLHNRG
881 RRGAIIETSF KHLKDDLELY RLSSGVISRP LPASPLIDTS STS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.Q	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	791	797	
total 1 peptides												

tr|A0A182JTY0|A0A182JTY0_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEADVLNALN TQTAYMPGGR DRDGHPLVVI PVPFYDNLPW MKGFLETTVK YLLASLSPET VSSGLAVILD AQKCSWRSTR
 81 QYIRHVQQLL SEPMNSFLVI RPDAFWDKNR VENCARQHRK GEPTIIAKSR LVKYFDTSEL PEELGGIIAY NHEQWIQSRE
161 RIEEFRKSYD KAMGDLENLH LILLDNRTVR ASESTTALKS CQQLNVDVQK FLSLVMDGGK KLLAHLSDLH SAKSAVPQDL
241 TDGKTQVERL LNALDRKQTA TNQAWTELER TVEVLQELAT LEEGVSHVTS WILTKAESML NAQLRVGHDV STADQLRLEH
321 EILELQCWQT YGCYAELLHK IDHFPRRKDT PAYRDLQSQR EWMDFVCRSF AQRLERRRNV LITSVRFFRL VAEYFDRTSE
401 VFQSLIMGER VEDYALASAN LQKLNENQRM LEMMEKEIIK EGEKLSDVLL MPVKDAVGRD IDVDYSEDIS NVRDILDATR
481 SRSRIFADSV ELQKLTLDQI THIFKYEQDA RTAVKWMSDL HQVMVRSHAH VGATVREIQS QKDEHQTLQE TAKGTYNYGC
561 QLLNASLALR QSCKLETAQN IAMTKSLQRT WRSFQAIAQE QMTRLRVSAV FHRSVEEQCV KLRELHECVL RIGEISEQGR
641 RRVRLRKYLA TRERLLLEVG RMVRLGRLLK TRLKEPFLLD DRLDAMASPE NIITESDNIM ACEAISTRLA EVAQVAEALD
721 SVLSDVQGGF DDEVEELTSV DAPEVAGKRS DSGNQSDDWS SSVKSTDDGS FVTASDCICT PQSRSSSYHT ASECRASPWW
801 GVESIERQSS LENDSAEDPD PEAFPSIKLL SGVVMTSSAN LSFDESEHSF PTPAISHGSA SVDSHPDSDD TVPTVCSQTS
881 PIGNSSASSS ALNSINRREN LALSLTPEEL DQIENDIRNN NLLASVGTVD MVAKELQSTQ VTPTSEDSGN VSTSSVKLDA
961 EDTVRFEPLK GPTDISGLTY YYQNIITKHT VKSCL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDISGLT.Y	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	973	979	
total 1 peptides												

tr|A0A182XZ28|A0A182XZ28_ANOST

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

Protein Coverage:

1 MEADVLNALN TQTAYMPGGR DRDGHPLVVI PVPFYDNLPW MKRFLETTVK YLLASLSPET VNSGLAIILD AQKCSWRSTR
81 QYIRHVQQLL SEQMNSFLVI RPDAFWDKNR VENCARQHRK GEPTIISKSR LVKYFDTSEL PEELGGIIAY NHEQWIQSRE
161 RIEEFRKSYD KAMGDLENLH LILLDNRTVR ASESTAALKS CQQLNVDVQK FLSLVMDGGK KLLAHLSDLH SAKSAVPQDL
241 TDGKSQVERL LNILDRKQTA TNQAWTELER TVEVLQELAT LEEGVSHVTS WILTTAESML NAQLRVGHDV STADQLRLEH
321 EILELQCWQT YGCYAELLHK IDHFPRRKDT AAYRDLQSQR EWMDFVCRSF AQRLERRRNV LITSVRFFRL VAEYFDRTSE
401 VFQSLIMGER VEDYALASAN LQKLNENQRM LEMMEKEIIK EGEKLSDVLL MPVKDAVGRD IDVDYSEDIS NVRDILDATR
481 SRSRIFADSV ELQKLTLDQI THIFKYEQDA RTAVKWMSDL HQVMLRSHAH VGASVREIQS QKDEHQTLQE TAKGTYNYGC
561 QLLNASLALR QSCKLETSQN IAMTKSLQRT WRSFQAVAQE QMTRLRVSAV FHRSVEEQCV KLRELHECVL RIGEITEQGR
641 RRVRLRKYLA TRERLLLEVG RMVRLGRLLK TRLREPFLLD DRLDAMASPE NIITESDNIM ACEAISTRLA EVAQVAEALD
721 SVLSDVQGGF DDEVEELTSA EAPEVTTKRS DSGNQSDDWS SSVKSTDDGS FVTAGSDCIC TPQSRSSSYH TASECRASPW
801 WGVESIERQS SLENDSAEDP DPEAFPSIKL LSGVVITSSA NLSFDESEHS FPTPGISHGS ASVDSHPDSD DTVPTVCSQT
881 SPIATSSASS SALNSINRRE NLALSLTPEE LEQIENDIRN NNLLASVSSE DIVGKELQST QVTPTSEDSG NVSTSSVKLE
961 AEDPTRFEPV KGP**TDISGLT** YYYQNIITKH TVKSCL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDISGLT.Y	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	974	980	
total 1 peptides												

tr|W5J7J2|W5J7J2_ANODA

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

Protein Coverage:

1 MEADVLNALT TQTAWMPGGR DRDGHPLVVI PVPFYDSLPW MKGFLETTVR YLLASLSHDT VNSGLAILLD AQKCSWRVAR
81 QYIRHVQQLL GEHMNSFLVI RPDAFWDKNR VENCARQHRK GEPTIISKSR LMKYFEVSEL PEELGGLIAY NHDQWIQSRE
161 RIEEFRKSYE KAIGDLENLH LILLDNRSIR ASESSSALKS CLRLNLDVQK FLSLVMDNGK KLLAHLSDRH VSRSAVSQDL
241 TDSKCQVETM LNTLDRKQTA VNAARNELER TVEVLQELAN LEEGVSHVTN WILTTAESML NAQLKVGYDV NTADQLRLEH
321 EILELQCWKT YGYYAELIYK IDNLPRPKDT SAHQDLMSQR EWMDFVCRSF AQRLERRRNV LITSVRFFRL VAEYFDKTSE
401 VFQSLIIGER VEDFELASSN LQKLKENQIM LELVEKEIIK EGEKLSDVLL MPVKDAVGRD IDVDYSDDIS NVRDILDATK
481 SRSRIFAESV ELQKLTLDQI THIFKYEKDA RTAIQWMDDL HKVMLRSHTH VGSNVYEIQA QKDEHQAFQE TAKGTYNYGC
561 QLLNASLALR QSCKLDAEQN IAMTKSLQNT WKSFQAVSQE QMTRLRVSAV FHRSVEEHCM KLLELKDGVL KIGEIEDEGK
641 RKVRLSKHLA TRERLLVEVG RMVRLGRLLK TRLKEPFLLD DRVDTSVASF EHIITESDNI MACEAISTRL TEVARVAETL
721 DSVLSDVQGG FSDEVGELAS SDVNDGNFTL TKHNDSNNQS DDWTSSVKST DEGSFITASD CICTPQSRSS SYHTASECRA
801 SPWWGIESIE QQSSLDNDSS EDHDSEAYPS IKLLSGVVMS TSANISFDDS ENIFLTPADG QGAASVDSHP DSDDTVTSDN
881 SPRQQHQPSP LETSSASSSA LNSINRRENL ALSLTPEELE QIENDIRNNN LMGMDISSQD IKSTQVTPTS EDSGNVSTSS
961 VKLEEGEDGI LSPLQLTDPV RFEPVKGP**TD ISGLT**YYYQN IITKHTVKSC L

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDISGLT.Y	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	989	995	
total 1 peptides												

tr|A0A151X5F3|A0A151X5F3_9HYME

back to list

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

Protein Coverage:

1 MNERMAHFLT APYMSIYYNA GSAEISPRTE GETALSADVH PSPVSPAPTK QEPDVSIHRT DLFLTTRSTG SDLLTSKSLS
81 PFADSESRFS LLFLFSVNPS LPPSAVPLSN VGIVLPVQPD HLSSRKGTDV KDARKAQGRF YVLEDLRDEE QCTIEVLIVA
161 VDEVESQLRL IKSRFIETLA GISGQHQQET FQASGGGFIA ASRDLQAYLN GDWGIGIRYS SVLAEKKPEN GTEAKKSKIN
241 EKKCKPKRIA SCDYEAWDKY DIDTEINRID LQDEQRQAEM KRIQEQRKEL DKMNKMAHKT AVDKLSLTGT EINVMAEQER
321 EKGNEAFRAA DYGEALRHYN ASIDIDSNLN AYNNLIKLQR YEDALNDCNT VLTMDYRNIK ALLRRALSLE HLEKPHESLA
401 DYEAVLKLEP TNKTAISCVN KLRKPCESRK IRMKIEENMN DDENKSKYIK TKSTVKANSI ECPKLRVNSD ICYCDRAPGP
481 SRSIATKPHL KASYCVEIKS NKATAVAAAV ADIAANKSNE KTTRDSSSGD KLSPVARDFG AKNKTTRSQD ARNDDIFMIS
561 RESFPGPRGA KGRLEKSIFS CVSSPMSKTK PSTVIIEELP SDKLNIESPY EFLRLWQSLK DDVNLKLHAK LLRCIAHEDM
641 NKIIGNKLDA AMFSLILRCL DQQFCTPKDT ELLANLLYSL SRLSRFSIIS MFMDSGDKKG FRETRESNSQ PPMRPEKESA
721 RAEEKRDELD SLITAITTNG AHPSKCVTIQ RTLDGRLQVA GRKGFPHVIY ARIWRWPDLH KNELKHVKYC QFAFDLKCDS
801 VCVNPYHYER VVSPGIGMLR HNIRARKIID CCGLLGVLME WVGFPRTDPF F**TDLSGLT**LQ SGVGVGPGGR LVKDEYTVGG

881 GGTAVGSAMD VDGEMNQTIQ HHPPTQSTAS NNAQQAQQSF IPGLPPPNST STEGMFSAGG GGNNGNPHAK LDDNNCPRQT
961 WIPTPHHSAS RNMHHPVVHP MSHTVGSQQQ SLNAASSGTS GAQILSPAQG QSTADTFYNT TTPPQDINQS PTVDALAASL
1041 GEGQSSPVSP VHLHHPNGFP VGTAPYNSGA PQWTGANTLT YTQSMQPPDP RHLHTTSYWG GHGNDVSGNI GGLLSTQPAP
1121 EYWCSVGYFE LDIQVGETFK VSSGCPTVTV DGYVDPSGGN RFCLGALSNV HRTEQSERAR LHIGKGVVLD LRGEGDVWLR
1201 CQSEHSVFVQ SYYLDREAGR APGDAVHKIY PSAYIKVFDL RQCHKQMRGQ AATAQAAAAA QAAAVAGHLT HGAPITKSLS
1281 AAAGIGVDDL RRLCILRLSF VKGWGPDYPR QSIKETPCWI EVHLHRALQL LDEVLHTMPI DGPRAIE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.TDLSGLT.L	Y	24.65	705.3545	24.6	706.3792	1	10.96	475	1	852	858	
total 1 peptides												

tr|M9VSG2|M9VSG2_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 YVAIQAVLSL YASGRTTGIV LDSGDGVSHT VPIYEGYALP HAILRLDLAG RDLTDYLMKI LTERGYSFTT TAEREIVRDI
81 KEK**LCYVALD FEQEMATAAS SSSLEK**SYEL PDGQVITIGN ERFRCPEALF QPSFLGMESC GIHETTYNSI MKCDVDIRKD

161 LYANTVLSGG TTMYPGIADR MQKEITALAP STMKIKIIAP PERKY

C Carba

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LC(+57.02)YVALDFEQEMATAASSSSLEK.S	Y	24.10	2549.1665	-31.0	850.7031	3	31.26	1152	2	84	106	Carbamidomethylation
total 1 peptides												

tr|A0A034VY87|A0A034VY87_BACDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPGEEANESK AQKLAAARKK LREYQKRGAA ENANSAPTES HSNSIAGGSS ISSNISEASD YDISNNGHET TSTNMQISAN
81 NNIATDISAS AEIAVNTSEV IETPDFSLSA PAPSTAASYF QTTTQDIPAL TQDSFAAPTV ASPAIREYTT DQMQLQNINA
161 IQVLITEKAA LTTELNKCRS LCRGRELETE ELRTQLESTT QRQEELLQHY QVQQQSLEHL RNKNAELQHK LTQATAKQED
241 QAGHLDELKR LLDVMQQRAT EVEHQFKEKS NELEMAQLRI RQLSDEANVN QPDNRVETLT QTQFMYEQQI RDLQAMVQQL
321 TYDKEQASNQ YQSYVKHLNS ELSNLTEKNS ELLDEYTKQQ ERERQLVDHI GALEKDIQRN ISRQDQLRKE KEQESLTRSE
401 APVQEVEKLK EQIGDYEMER HEFQLKIKSQ EDRLEILSSE LQEKQTRLDQ LEEHVRNYAS EQPDQVKLLA TMESDKIAAS
481 RALAQNIELK KQLDELQLRF VQLTNDKADL MNKLDAEEHA NREMRANYNE MEERLHNTDE RFKYKDEEMI RLSHENMELT
561 NKAAALQWKL QRQGKKLDGH NHSYEPNDEL HEHQHNGCDD EHEHTHGDDH NEYEHDHHKH EHDHHEHEPD YHEHEHHYHE
641 HEHNQHGHEH DHHEHNHGHD EHSSDHEHNL NNENKNSQHH HQHVKQLSTS SSNTS**TPYLP T**EEAVERLEQ RFTRLMSQVA

721 DLTDEKQRLE HLVLQLQGET ETIGEYITLY QTQRRMLKQR EYEKAAQMQL LQREREQLRD RIAILNNLVN SLRADMPQSI
801 PNLQENFHTS VIANDDNIND TNTPLIVEAS EALEEQHDQP DSQLPANESR QILTKIQNII SEINENTQHI PDVATAQTVD
881 HINCCLGKIE VV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TPYLPT.E	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	696	701	
total 1 peptides												

tr|W8BRA7|W8BRA7_CERCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPVEEASESK AQKLAAARKK LREYQKRSAS ENVTAVVAHA APTESHGSSI TGGSSISSNI SEASDCEMTT NGNEATTASL
81 ENINENCSTT NAAATEFVQN TTSTAPVFQA PALPTAASYF STIAADGTAS ALDGIAMPTA ATNAVIKDAT ADQLQLQNVN
161 AIQVLISEKA ALTTDLNKYR SLSRERELEL EELRTQLESA LKRQDDLTQR YQTQQQGMEL LRKTNAELQH KLAQANAQQE
241 DQAGHLDELK RLLDNMQQRA VEIEHQFKEK SNELEMAQLR IRQLSDEASV NQVDNRVESL TQNQFMYEQQ IRDLQAMVQQ
321 LTYDKEQANN QYQSYVQHLN AEITNLSEKN TELMDESTKQ QERERQLVEH ISILEKDIQK NISRQDLLRK EKEKENAPDG
401 QQRAEELQKL KEQISDYELE RHEFQLKIKS QEDRLDMLNN ELLEKQTSLE ELYERMRHYA NIQPDQTKLL ATMESDKIAA
481 SRALSQNVEL KRQLDELEMR FVQLTNDKAD LMNKLDAEEH ANREMRTNYA DMEERLQSID ERFKFKDEEM IRLSHENMEL
561 KSKTEVLQRR LRQQGRSKNL TKTGEDEEND NQDEHTDDQD NNLQEHDDEK HEHKHNGCDD QHEHEHEHEH NHHEHEHEHE
641 HDYDHDHDHR EHEHEHDHGH HEHEHEHVHG AAHTHPTDLA HHHNHQHVKK TSSSS**TPYL PT**EEAVEKLE QRFTRLMSQV

721 ADLTDEKQRL EHLVLQLQGE TETIGEYITL YQTQRRMLKQ REYEKAAQMQ LLQREREQLR ERIAILNNLV HSLSTDLPHS
801 THRLPENFNT TLNTDNNAEA SINADTQPLI AVASEAQEDQ HLNQQQLAHS NAQQTANESR QILTKIQNII TEINENSQHI
881 PDVATAQTVD HLNCCLGKVE VV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TPYLPT.E	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	697	702	
total 1 peptides												

tr|A0A0A1WSG1|A0A0A1WSG1_ZEUCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPGEDPNDSK AQKLAAARKK LREYQKRGAA DNASQTGANS APTESHSSSI AGGSSISSNI SEASDYDVSS NGHEATSTNV
81 PVTNDNNIAT DNATTTEIPV ITSSDVIANT VSTVSAPAPP TAASYFQTTP LDVAAPALDS FTAPTVATTV LKETTTDQIQ
161 LQQVNAIQVL IAEKAALTTE LNKYRCLCRE RELETEELRT QLESTTQRQE ELTQRHQVQQ QNLEQMRNTN AELQHKLAQA
241 HAKQEDQAGH LDELKRLLDV MQQRATDVEH QFKEKANELE MAQLRIRQLS DEASVNQPDN RVETLTQTQF MYEQQIRDLQ
321 AMVQQLTYDK EQANNQYQSY VKHLNAELSS LSEKNSELLD ECTKQQERER QLVDHISTLE KDIQKNISRQ DQLRKEQEQV
401 NSPQSETPVK EVAQLKEQIS DFELERHEFQ LKIKSQEDRL ELLGNELQEK QTKLAQLEEH MRNYAAEQPD QTKLLATMES
481 DKIAASRALA QNIELKKQLD ELELRFVQLT NDKADLMNKL DAEEHANREM RANYNEMAER LRSIDERFKY KDEEMIRLSH
561 ENMELTNKAA ALQRKLKHHG RKLDEHDHEH EHGEHAHEHK QNGCGDGHEH SHEHEHIEHE HEHGNHEHEH GHHDHEHEHD
641 QYDHEHDHAH HEHVHDHSDQ EQYNEHEHEH GDHQHEHDHS QHHKHMKQLS TSSSNTS**TPY LPT**EEAVERL EQRFTRLMSQ

721 VADLTDEKQR LEHLVLQLQG ETETIGEYIT LYQTQRRMLK QREYEKAAQM QLLQHEREQL RDRIAVLNNL VNSLRADMPH
801 SITQLQENYH AAAAPDSAVT NDTSVAADAS TPLITEASEA FEEQQQHNHT DTQLTAQESR QILTKIQDII SEINENTQHI
881 PDVATAQTVD HINCCLGKIE VV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TPYLPT.E	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	698	703	
total 1 peptides												

tr|A0A1W4WI16|A0A1W4WI16_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NLQFSNALKD LPIKIQNSSL KQRREVFNKI QNVLSHSAIN ESIVKGICKA AQITLPRYHD SESQLLVKNL LISLIEIHPE

81 WSIKNLTPVL GDIASQYRNS VLFNIWKTIP NLIQLYMEQL QKLDQCQQVA VLGSVMIKYC ISNDKKETFQ GAVPLLMDIF

161 IKTVVSSKIK PLKEIVIGCY PLLQILSHDQ FKSILLPALQ KAMLRNPEVI IECVSYVLSG LSLDLSQYAV DIGKSLIANL

241 PSKDETVREH SVIACKQLAQ QCSDSGAIEK LVKDVFAVFH GSNGKLTLIE HKISVLRNGM NFKTSTAAVR TSYIQCMSVC

321 FNGNTIPQAT VLIPTLLKSI EKAIAQPSQY PIVIEGLSAT CLFLRIVTAQ GSNENAYQNI WNVIFDMDKQ LFVSEKFLSA

401 ATNEALVMVM EMSQILLLEF PERFNGKTGP LYRAILICVT SLSSETRRKC SIILKKMVSG LGGTAIARAL LKDLNVFLET

481 VKIQCKGDSA LKERNDYVNQ EISPHAIMEC VTTLCSAKDL PVDDAQLLAL DALLPASHPT ISKVTSDLWI KIVKHLHLNP

561 RDFVSQQSPQ LRKLLVEQYT KSKREENNTA MNMKRESKAY SYKEQLEEMQ LRRELEEKKR KEGKIKEPQY TPKQLEAIKN

641 QKIKESAIRS RLTEYNLIIE NCVSMVEACL RGNPKGLSCH FKDLLPTVLL ILRSPLAAPY ATKLYINLRR AVFPHHLDTL

721 GDLIAHVTLR LLKPACDLES NWEEEDLTKE MVRTIGLIHA TTLKRIEDDE VTRSGHLQNY FTASAMCYTF SLLKSALLSS

801 YAKTNENLIH DGLQIISEHA KLRASDEPDG DLYNSVYVNL LIIFFFLLEI IATAERTDIA PHVKDGYIMM FIYMPVVFQQ

881 EFTPYIGQII NPILKALADE NEYVRDTALK AGQRIVNLYA DSAILLLLPE LEKGLFDDNW RIRYSSVQLL GDLLYRISGV

961 TGKMSTETAS EDDNFGTEQS HQAIIRVLGA ERRNRVLAGL YMGRSDVALM VRQAALHVWK VVVTNTPRTL REIMPVLFGL

1041 LLGCLASESY DKRQVAARTL GDLVRKLGER VLPEIIPILE KGLQSERSDQ RQGVCIGLSE IMASTSKEMV LTFVNSLVPT

1121 VRKALCDPLP EVRQAAAKTF DSLHSTVGSR ALDDILPALL NQLNSDDANT VEWTLDGLRQ VMAIKSRVVL PYLVPQLTAP

1201 PANTKALSIL ASVAGEALNR YLPRILPALQ TVLASSKGTP EEAQQLEYCQ AVILSVVDET GIRTVVDTLL ENTRTDNTDQ

1281 RRAAAALLCA FCANSRAQYI AHVPQLLRGL IHLCTDNDKD VLQMAWEALN AITKNLEPKQ QAAYVSDVRQ AVRYALSDIK

1361 GIGTDLLLPG FCLPKGIAPI LPIFREAILN GDGDEKEQAA QGLGEVIRLT SAAALQPSVV AITGPLIRIL GDRFSSNVKS

1441 AVLETLATLL AKVGIMLKQF LPQLQTTFIK ALNDPNRTVR LKAAQALSYL IVIHQRPDPL FTELHNTIKN TDDSSVRETT

1521 LHALRGIISP AGDKMSEPVR KQIHSTLISL LNHPEEVTRN VAAGCLGALC KWLPPPQLDT TITEHILNDD TSADWTLRQG

1601 RGAALSVVLK ESPALLWDEQ YQLRLTLYYS KIFFLIEVLS DSHMKVQEAG TEALRVIGSV IRNPEIQAIV PVLLEALQDP

1681 SHKTSACLQT LLDTQFVHFI DAPSLALIMP VVQRAFQDRS TETRKMAAQI IGNMYSLTDQ KDL**TPYLPT**I IPGLKMSLLD

1761 PVPEVRSVSA RALGAMVRGM GESSFEDLLP WLLQTLTSES SSVDRSGAAQ GLSEVVGGLG VEKLHKLMPV YFFSKKYLNV

1841 LDVGARESLS DVISKVLRKI MHHAEGKEEE LDDTLLT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1744	1749	
total 1 peptides												

tr|A0A0J7NUE4|A0A0J7NUE4_LASNI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADVELAKAL KDLPNRVQTA SKKERREILQ NVVNVLSNPG INDKIVNGIC KVVSLTLHRY KDSASQSYVK NLIVELLKKQ
81 PEATIKHMTT VISEQATWHK NVVATLNTAL TAYTALKWSN LVILHGYNKM DNTEMNECLA KLIEAQANLS AAALASADRK
161 LANKVYALLA HEWTAIKNIE VIYVENLTKL ELGNGVIILA SLLTKYLVAT KRNDLVEQLK TNMIDIFIKV TISCKKKPDL
241 YVVDVAVPLL RRLTHEEFKT QLLPALQKAM LRNPEIIIES VGHILSGLSL DLSQYSQEIS KGLFANLHSK EDLVRDEAVG
321 ACRKLALQCS DTTALETLLS SAFAVFHGSE GKLTVATHKI SVLQGAGNLS YNVASGSSVQ KLAETACEHF VKVLETEVHE
401 KTLIQALEMM ALWSKKFSSA LPKIVVDAFK KGMAAKTSTA AVRTAYIKLF FSTPATPYSG IIAPILAQAI TRAMQQCAQP
481 AAVTEGLVAS YLLLKFVLAD QVENDKQNVL WNAIDEQIFF SEKFLSTCGD DILYHLMLLC ERLITEFSDR LNEKALTGIH
561 RAIVSCATAS NSATRQRCFP LVKKIMTGLS TYAPAQALLT EFNKFLENVK IKSESDKESK EESSMGEITG RCLADGLFAI
641 CSGSFLFEAP TYQMTRDALL PSHHPALLKA VPNLWFKIAK NYNLVPKDFL RSYSNEVRKM LIQNYKPVPN YENALVKIVS
721 LAPDAFLPAL VSNVTSKLDD PEILRVTKDE YFTYLTPDGE LYDKSVLPVN DENDILNSMN MKRESKVYSF KEQQEELQLR
801 RELYEKRKRE GKIKEPKLTP KQEETLKAQI AKENSIRKRL TELKAKIDNT VSLVTCSIRG NQQELSLHLK DLLPPILKNL
881 GSPLAAPEMS ELYVSLRQTV TMDNSVILRD LIAHVTLRQL QPQCDLDQAW EEENLDAAVK RTLNLIHAVT IKRKELFTAP
961 AFCYVFPFIR KTLLSYKDDG MIVQGLQLIQ EHAKQRGDSS TDLKDVRHPR LLPRKQMFDL LIELMETTTG RVQSHAVATL
1041 LDVAQSGSGH PGTAIATSED IDSLIGALQN SLSTVRDAAL RGLTVIRQAF PSQKEDQDQL DRLTRRVWIA RFDVNDENKI
1121 LATELWNAAD FTAHAEVLCE ELIRDIAHPV EPVQQAAAHA LAESLASVPH LTPSVLDSLL QLYQEKLAMI PPKLNDFGRV
1201 VEQPIDTWGP RRGVALSLAQ IAPLLTADTV HRLIQFFVLT GLGDRNQFVR TEMLTAAVAA VDLHGSANIT SLLPVFEDFM
1281 DKAPKIGSFD SIKQSVVILM GSLARHLDKN DPRIKPIVMR LIAALSTPSQ QVQEAVANCL PHLTDSIKED APKIVDNLMD
1361 QLLKSDKYGE RKGAAYGLAG LIKGMGILAL KQLDIMSKLT NAIQDKKNYR HREGALFAFE MLCTMLGRLF EPYIVHVLPH
1441 LLLCFGDSSQ YVRTATDDTA RVVMSKLSAH GVKLVLPSLL AALEEDSWRT KTGSVELLGA MAYCAPKQLS SCLPSIVPKL
1521 IEVLSDSHTK VQEAGAEALK VIGSVIRNPE IQAIVPVLLK ALQDPSHKTA TCLQTLLDTQ FVHFIDAPSL ALIMPVVQRA
1601 FLDRSTETRK MAAQIIGNMY SLTDQKDL**TP YLPT**IIPGLK TSLLDPVPEV RSVSARALGA MVRGMGESSF EDLLPWLMQT

1681 LTSETSSVDR SGAAQGLSEV VRGLGVEKLH KLMPEIISTA ERTDIAPHVK DGYIMMFIYM PSAFTTEFTP YIGQIINPIL
1761 KALADENEYV RETALRAGQR IVTLYADSAI MLLLPELEKG LFDDNWRIRY SSVQLLGDLL YRISGVSGKM STETASEDDN
1841 FGTEQSHYAI INALGAERRN RVLAGLYMGR SDVALMSDQA DQRQGVCIGL SEIMASTNKD MVLTFVISLV PTVRKALCDP
1921 LPEVRQAAAK TFDGLHSTVG VRALDDILPA MLTQLNSPDP AEAENTLDGL RQVMAIKSRV VLPYLVPQLA SPPVNTKALS
2001 ILASVAGEAL TRFLHRILPA LLTALSSAQG TANELQELEY CQAVVLSVTD EVGVRTVMDQ LMEATRAEDL SKRRSAATLL
2081 CAFCRDTRAD YSQYVPQLLR GLIHLFTDED RDVLQMSWEA LTAVTKTLSS EQQIAHVQDI RQAVRFAVSD LKGQELLPGF
2161 CLPKGITPIL PIFREAILNG LPEAKEHAAQ GLGEVIRLSS AAALQPSVVH ITGPLIRILG DRFNWSVKAA VLETLAILLG
2241 KVGVMLKQFL PQLQTTFLRA LNDSNRQVRL KAAYALSNLI IIHTRVDPLF TELHTGIKTG DDPAIRETML QALRGVLTPA
2321 GDKMTDPMKK QVFATLSSML SHPEDVTRNA VAGCFGALLR WLSPEQLAIA FNDHLLSNDV NVDWMLRHGR SAALFVVLKE
2401 SPITVYNPKE KDRVCAVILS YLAADRVQIV MNGVRACGYL FQYLMNESLP ISQQILSPFV RSMNNNSNDV KQLLARVCIH
2481 LARNIPPENM SAELLRGLLP MLVNGTKEKN GYVKANSELA LIAVLRLRQG EDEHQRCMAF LDVGAKESLS DVVSKVLRKV
2561 LSQPEGKIEE LDDTLLT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1629	1634	
total 1 peptides												

tr|A0A0M9ABE9|A0A0M9ABE9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MADVELTKAL KDLPNRIQTA SKNERRVLLQ NVVSVLSNPG INEKIVNGIC KTISSTLHRY KDTASQSYVK NLIEQLLKKQ
  81 PVPTIKHMTN VIVEQATWHK NVVPTINTSL TAYLALKWST LIILHGYKSN SDMNSELPKL IEAQANLSAA ALASMDKKLT
 161 NKVYVLLAHQ WSSVKNIDIV YLETLTKLEA GNGVIVLASL LTMYLVNTKK SDLVIKLKTN TIDAFIKLTI SCKKKPDLYV
 241 VHNAVPLLRR ISHDEFKSQL LPALQKAMLR NPEIIIESVG HILSGLSLDL SQYSQDISKG LFANLYSKED LVRDEAVGAC
 321 RRLALQCSDT VALENLLSSV FAVFHGSEGK LTVATHKISV LQGAGNLSYN AASGSSVERL AETACEHFIK VLETEVHEKT
 401 LIHALEMMAL WSNKFANNVP KCVIDAFKKG MTAKTSTAAV RTAYIKLFFS TPVVSYSEVI TPLLIQAISR AMQQSAQPVA
 481 VTEGLVASYL LLKFVLANQV ENDKQTVLWH AIDEQIFFSE KFLSTCGDDV LYHLMLLCKR LIIEFGDKLN EKTLNGVHRA
 561 IVTCATAPKY KIRKRCFPLI KKVLTGLSTY DPAQELLMEY NKFLENVKIK SENDSENKED SSSCEITGRC IADGLFAICS
 641 GSFLFELPAM QMTRDALIPS HHPAIYKAMP NLWFKIAKNF NLVPKKFLCT FNHEIKKILV QNYKPVASYE NALTKVISII
 721 PDIILPGIVF NITSKLDDPE ILKVTKDEYF TYLTPEGELY DKSVLPTNDE NDILNSMNMR RESKVYSFKE QQEELQLRRE
 801 LYEKRKKEGK IQEPKLTPKQ EEILKAQMTK ETAIRKRLTE LKFRIDIVVS LTMCSIRGNS QELSIYLKDF LPLILKNLGS
 881 PLAAPAMSDL YIHLKEIVKI NNPVLSDLVA HVTLRQLQPQ CDLNQAWEEE NLDTAVKRTL NLLHTTTIKH KKLFTAPTFC
 961 YIFPFIKKTL LSYRDDNMIV QGLQIIQEHA KQRGSSSDFR DMKHPQLLPR KHMFDLLIEL MEITSGRVQS HAVATLLDVA
1041 QSGSGQSGTA IATNEDIDSL IGALQNSLST IRDAALRALI VVRQAFPSQK EDSVQLSHLV RRIWIAKFDI CDENKILANE
1121 LWTAADLVMH ADKLADELIQ DIAHPVEPVQ QAAACALAQC LTEVLPLVPI ILDKLLQLYQ EKLTMIPPKL NDFGRVVEQP
1201 IDTWGPRRGV ALALAQMAPL LSADTILKLV QFFVSTGLGD RNQAVRTEML TAAVAVVDLH GKANITSLLP VFENFMDKAP
1281 KIGSFDSIKQ SVVILMGSLA RHLDKDDPRI KPIVMRLIAA LSTPSQQVQE AVANCLPHLV PSIKEDAPKI VDKLMDQLLK
1361 SDKYGERKGA AYGLAGIIKG MGILALKQLD IMTTLTNAIQ DKKNYRHREG ALFAFEMLCT MLGRLFEPYI VHVLPHLLLC
1441 FGDSSQYVRT ATDDTARVVM SKLSAHGVKL VLPSLLAALE EDSWRTKTGS VELLGAMAYC APKQLSSCLP SIVPKLIEVL
1521 SDSHTKVQEA GAEALKVIGS VIRNPEIQAI VPVLLKALQD PSHKTATCLQ TLLDTQFVHF IDAPSLALIM PVVQRAFLDR
1601 STETRKMAAQ IIGNMYSLTD QKDLTPYLPT IIPGLKTSLL DPVPEVRSVS ARALGAMVRG MGESSFEDLL PWLMQTLTSE

1681 TSSVDRSGAA QGLSEVVRGL GVEKLHKLMP EIISTAERTD IAPHVKDGYI MMFIYMPSAF TTEFTPYIGQ IINPILKALA
1761 DENEYVRETA LRAGQRIVNL YADSAIMLLL PELEKSLFDD NWRIRYSSVQ LLGDLLYRIS GVSGKMSTET ASEDDNFGTE
1841 QSHYAIINAL GAERRNRVLA GLYMGRSDVA LMVRQAALHV WKVVVTNTPR TLREILPTLF TLLLGCLAST SLQSDQADQR
1921 QGVCIGLSEI MTSTNKDMVI TFVISLVPTV RKALCDPLPE VRQAAAKTFD GLHSTVGVRA LDDILPAMLT QLNSPDSAEA
2001 ENTLDGLRQV MAIKSRVVLP YLVPQLTTPP VNTKALSILA SVAGEALTRF LHKILPGLLT ALSSAQGTPN EVQELEYCQT
2081 VILSVTDEVG IRTIMDQLME ATRADDLSRR RSAATLLCAF CRDTRADYSQ YVPQLLRGLI HLFTDNDKDV LQMSWEALTA
2161 VTKTLASDQQ IAHVQDIRQA VRFAVSDLKG QELLPGFCLP KGITPILPIF REAILNGLPE AKEQAAQGLG EVIKLTNASA
2241 LQPSVVHITG PLIRILGDRF NWSVKAAVLE TLAILLGKVG VMLKQFLPQL QTTFLKALND SNRQVRLKAA YAISNLIVIH
2321 TRVDPLFTDL HTGIKTGDDP AIRETMLQAL RGVLTPAGDR ITEPMKKQVF ATLSSMLGHP EDVTRNAVAG CFGALIRWLS
2401 PDQLNIALNE DLLCNDTSVD WMLRHGRSAA LFVALKESPT TIYNSKEKDR VCVVILSYLS ADRIQIIMNG IRACGYLFQY
2481 LMNEGQPIPQ QILPPFIRSM NNNNNDVKQL LAKVCIHLAR NIPPEKMSPE LLKSLLPMLV NGTKEKNGYV KANSELALIA
2561 VLRLKQGEEE YQRCMAFLDV GARESLSDVV SKVLRKVLSQ PEGKIEELDD TLLT
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1625	1630	
total 1 peptides												

tr|A0A067RTH7|A0A067RTH7_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 ITEGIIRGIC KVLQLALPRY RDSTSQFYIR NMIIALVKLH GDWTMKHLTS TLNDIAAAHK NLVSTKHTSQ SGLYALGWSC
  81 LLIEHGLSNC SDSAKAEFQR LVDTQGTLLS VVLAVGNKNK SAKAYRTLSA MWRSVKGSEE LYGNALTSSE PSTHIVVFGS
 161 YLIRYLTETK RVDLINKYKV TLLEMFIKVA ISCKTKPAVY AIRASDSLLK HVSHEEFKRQ LLPAMQKAML RNPEIILESV
 241 GHVIEGLFLD MSQYAQDVGR SLATNLHSKE DLAREESVSA CRCLALQCSD AGALEGLLQH LFDVFHGSEG KLTVATHKMS
 321 VLQGAGSLSC NAVTTGYSSQ RLATVAAHHF IKVLDVEVHE KTLIEALEML SLWCNKFNNE VPKDVMDWLK KGPGLKTSTA
 401 AVRTAYIECM SACLHGNTLA QGIELIPLLL KTVEKAVAQP AQVPLVTEAL YAACLLLKMA AADIGADKKL DNLWSVVLDM
 481 NKQLFVSEKF LTLASDEALY HVMQLCERLL LDHAHRLNGK ANPLHKGIIF CLTAPSSSLR LRCRPVVKKL VSVLGGTQLA
 561 RSLLKEFTRF LETAKIQSGE SVKENKDGPD TGSGGGGEIT AKVAVNCIIT FCSGSNLVPE DAQLLALDSL ISCHHPAIVA
 641 ASPNLWLKLL KYLKLDPYEF IRLSEENIKK IFIEEYSASP CMENSLQTVV RLNPDVVLPL LVTFVIKQLS DPSILLVTKD
 721 EYFTFLTPEG ELYDKSVLSG KDSENELNVK NVKRESKVYS YKEQLEELQL RRELEEKRRK QGKLKEPQLT PKQKETLRLQ
 801 LQRESAIRAR LTELNKRLEN VVSMIKAAAN DSGEELSLYF QDLLPHILKD LQSPLAAPYL SALYIDLRKC VSFTSRHKYL
 881 GDLIAHVTLR LQAPCCDLDA RWEDEDLSVA VTRTITALHK ATVRPRRTTS ADAPRTYLTA PAFCYVFPLI RFALLSAFAK
 961 ADDSLVISGL QIISEHVQMR GSADNTQEKD CYHPDLLPRK QMFELLIEMI SCTGGRIQQQ AGSALLDVAA SGCGAAGCAR
1041 ASVDEIDSLL AALQNPSAVV RDAALRGLIA MVGAFPTLKE DYNQALRLIR RIWVAQFDVC EENRVLAVVF DCHILSFTRY
1121 VISELLLTIV RTLPVVSTWT PLQMQVGVVS SCLIDHVLEQ LLVIYHEKLA ILPPKLDSFG RVVEQPVDMW EPRSGVALAL
1201 AQIAPLLTPK SVSHLITFFV SVGLGDRSPE VRKNMLAAAL AAVDLHGKET VNSLLPVFEE FLDKAPDSGS FDAIRQSVVI
1281 LMGSLARHLE RDDRKVKPIV GKLIDALSTP SQQVQEAVAN CLPPLVPAIK DDAPHLVQKL LHQLLESENY GERKGAAYGL
1361 AGLVKGMGIL ALKQLDIMNT LTTAIQNKKN FRHREGALFA FEMLCNMLGR LFEPYIVHVL PHLLLCFGDG SQYVRDATDD
1441 TARVVMSKLS AHGVKLVLPS LLAALEEDSW RTKTGSVELL GAMAYCAPKQ LSSCLPSIVP KLIEVLSDSH VKVQRAGAQA
1521 LKLIGSVIRN PEIQAIVPVL LEALQDPSNK TATCLQTLLD TQFVHFIDAP SLALIMPVVQ RAFMDRSTET RKMAAQIIGN
1601 MYSLTDQKDL TPYLPTIIPG LKTSLLDPVP EVRSVSARAL GAMVRGMGES SFEDLLPWLM QTLTSETSSV DRSGAAQGLS

1681 EVVGGLGVEK LHRLMPEIIS TAERTDIAPH VKDGYIMMFI YMPVVFTTEF TPYIGQIINP ILKALADENE YVRDTALKAG
1761 QRIVNLYADT AIMLLLPELE RGLFDDNWRI RYSSVQLLGD LLYRISGVSG KMSTETADED DNFGTEQSHH AIIDALGGGR
1841 RNRVLAGLYM GRSDVALMVR QAALHVWKVV VTNTPRTLRE ILPTLFSLLL GCLASTSYDK RQVAARTLGD LVRKLGERVL
1921 PEIIPILEKG LESDQPDQRQ GVCIGLSEIM ASTSKDMVLT FVNSLVPTVR RALCDPLPEV RQAAAKTFDS LHSTVGVRAL
2001 DDILPAMLNH LIDPHPKVAE SALEGLRQVM AIKSRVVLPY LVPQLIAPPR VNTKALSILA SVAGEALTKY LHKILPALLA
2081 ALSMAQGTPH EAQELEYCQA VVLSVTDEVG IRTIMDQLME STRSDKVELR RSAVTLLCAF CRHTHADYSQ YVPQLLRGLI
2161 HLFTDSNPDV LQMAWEALSA VTKVQNVEVT LDSSQQTTHV GDIRPAVRFA VSDLKGQDLL PGFCLPKGIT PILPIFREAI
2241 LNGLPEIKEQ AAQGLGEVIK LTSAQALQPS VVHITGPLIR ILGDRFKWNV KAAVLETLAL LLAKVGVMLK QFLPQLQTTF
2321 LKALNDSNRQ VRIKAATALS HLIVIHTRAD PLFTELHTGI RTADDPAETM LQAMRGVISP AGDKMTEPLR KAVYVTLTGM
2401 LGHPEDVTRA AAAGCLGSLC RWLSSEQLHA TLTDHLLYDD LPLDWTVRHG RSSALSVALK EASPQIYTDD YKDKICRVLL
2481 AYLTGDRVPI AMNGVRGCGY LFQHLMLTGQ PLPQQLLTPF VRSMNHSSNE VKQLLATVCS MLAKTVPPQH MAPELLRLLI
2561 PMLVNGTKEK NSYVKACSEF ALVSVLRLRQ GDETQQRCMN LLDIGARESL SDVISKVLRK VANQPEGKDE DIDDTLLT
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1611	1616	
total 1 peptides												

tr|T1HJQ7|T1HJQ7_RHOPR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 ICHVELSKVL KDLPLKVQTA SLAERKLIFE NVKSIIANPG FNENIVRGTC KVLQMTLPRY RDSDSQRYVV SIISSLTTIH
  81 PKWTLKHLSP ILNEVAAVYA SITATYSTAQ SCLHALSWSN LLIVNSLNKC EGNSSEEDFL KVVNAQSVLF SSILASGNGK
 161 LVENIFAFFN TMWKSNKDFL IPLYVKGTCK LPDCTHSIVF GAFFVKFLHE NKLNEYIEEV KAMEMLVKVV ISSKTRIPVY
 241 IAVACRPVLL LASHDDFSNV LLPALQKAML RNPELILYVL GKLLANVSLD LSKYSFNLGK TIAGSLCSND DDCRAQAADA
 321 IKSLSIQCSD PDAVGALTDH LFQLFNGSQG KITVSSHKIT ILQAIGNLSY NAVTGNSIQQ LTQNVAEQFI KILEVEVHEK
 401 TLIYCLEMMS LWCSKFTLSI PPKVISWFER GISLKTSTSL VRAAYIGVLS VCCQSATASQ TTQYIPLLVK CVEKAAAQPT
 481 QVAIVMEGLS AACLLLKMAT LDSVDSKLAP LYNIILDMDK QVFISEKFLL QASCDALCQV VSLCEKILME HVAQLMGNPK
 561 PLYRTLVICL TTRTVKAKCK PILHRMFSSL QGTQIATALL DEFTNLLISN KFQCTGKDNK ENSDTQTELK PRHLVDAITV
 641 MCSGTNLSKE DKKLLAFHSI LSCHHPLIET AQSKLWLKII KYFKLHPSKF ISHYNEKFIN LLVNDFTPHL SYEKSLSTIS
 721 ELNPNAVIPP VLDYVITLLS DPELLNVSAQ DYAIFKSPPG ELFDKSVLAS VSMLIYSFYL IYFLIKVVLE ESQDETTMNI
 801 KNMKRESKLA QPELTPKQKE IIRIQLEKEA AVRERLTKAE NKLIKAHHII VSVCNGSPLQ LALQFPTLIP LIVKGLNSPL
 881 CAGLLSKLYL YFRKPAFISV PVSNVTVERV ANTTLRLLKP KCELDPAWED QDIGKAMTWA VTELEKEGKM ITAPALSYVL
 961 PLIQCITKIV PSTSPLLTTC IQLLSKQCRL RASNIQPDLH NPQLLPRKQI MLLCIDLISS TAGRIQQQAS SCLLDVASAS
1041 SGGTGCSVAT PDEIGCLLTA LQHSSHHVRD AALRALYALV QVFPKPKKNA ELAFQIVKRV WVARWDVVVE NREIAHKLWE
1121 IANLDSHIPG LSEGLLVDIV HPVVEIQQAA ANALAALLQQ SKKQDTDVVL RMLLDIYNDK YNMVPARVDS LGRIVEKPID
1201 TWEPRSGVAL ALQQLAPLLT PNAVSDLAKF YVDKGLGDRS DTVRNNMLAA ALAAVDLHGK ECVNSLLSIF EPVLDKGPDC
1281 SSYDAVRQSV VILMGSLARH LDKDDKKVKP IVAKLIDALS TPSQQVQEAV ANCLPALVPS IKDEAPALVQ KLLNQLLSSE
1361 SYGQRKGAAY GLAGIVKGMG ILVLKQLDIM TTLTTAIQDK KNYRHREGAL FAFEMLCSVL GRLFEPYIVH VLPHLLLCFG
1441 DGNQYVRDAT DDCAKVVMSK LSAHGVKLVL PSLLAALEKD SWRTKTGSVE LLGAMAFCAP KQLSSCLPSI VPKLIEVLSD
1521 SHVKVQTAGT EALKQIGSVI RNPEIQAIVP VLLEALQDPS NKTAMCLQTL LDTQFVHFID APSLALIMPV VQRAFMDRST
1601 ETRKMAAQII GNMYSLTDQK DLTPYLPTII PGLKTSLLDP VPEVRSVSAR ALGAMVRGMG EASFEDLLPW LMKTLTSETS

1681 SVDRSGAAQG LSEVVGGLGV EKLHKLMPEI ITTAERSDIA PHVKDGYIMM FIYMPVVFTN EFTPYIGEII IPILKALADE
1761 NEYVRDTALK AGQRIVNLYA DSAITLLLPE LEKGLFDDNW RIRYSSVQLL GDLLYRISGV SGKMSTETAN EDDNFGTEQS
1841 HKAIIGALGA ERRNRVLAGL YMGRSDVALM VRQAALHVWK VVVTNTPRTL REILPTLFSL LLGCLASTSH DKRQVAAKTL
1921 GDLVRKLGER VLPEIIPILE QGLESDQPDQ RQGVCIGLSE MMTSTSRDMV LTFVNSLVPT VRKALCDPLP EVRQAAAKTF
2001 DSLHSTVGVR ALDDILPPML QQLNDPESEV AEWTLDGLRQ VMAIKSRVVL PYLIPQLTVT PINTKALSIL ASVAGEALTK
2081 YLHKILPALL TALASSEGST QEIEYCQAVV LSVTDEAGIR AIVDQLVEVG KCDNVETRKA AATLLCSFCT HSRADYSQHV
2161 SQLLRGLITN FTDHDPVVLQ MSWDALSAVT KSLDPSQQIQ YVGDIRQAIK FAASDLKSGN TLLPGLCLPK GITPILPIFR
2241 ESILNGSPEI KEAAAQGLGE VISLTTAQSL QPSVIHITGP LIRILGDRFP PSVKAAVLHT LATLLAKVGM MLKQFLPQLQ
2321 TTFLKALNDG NRLVRLKAAT ALSYLITIHT RPDPLFSELH NSVKSAEEPA VRETMMQALR GVVSAAGEKM SESVLKPIHL
2401 SLLSMLSHSE DATRSGAAGC VGALTRWLSP EQLAITLNDN LLVDDVTVEW TLRHGRSAAL FVALKEAPEK VYVPEYKDKI
2481 HKVILSFIAA DRIPIVMNGV RGCAYLFDYL FSNSETLPQP LLSPFVRSMN HPSNEVKQLL ARACSYLGRR EISSPEFLKS
2561 AIPMLVNGTK EKNGYVKANS ELSLVAVLRL RHGDEKLQWC MSLLDPGAAE ALSDVITKVL RKVAIQPEGK AEELDDTLLT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1623	1628	
total 1 peptides												

tr|A0A151WN86|A0A151WN86_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  LAKALKDLPN RVQTASKKER REILQNVASV LSNPGINDKI VNGICKVVSL TLHRYKDSAS QSYVRNLIVE LIKQQPDATV
  81  KHMTTVISEQ AAWHKNVVAT LNTALTAYIA LKWSNSLIFH GYHEHLTQMD ESLAKLIEAQ ANLSAAALAS ADKKLANKVY
 161  TLLAHEWEAI TDIETYVEHL IKLELGNGVI ILASLLTKYL VATKRNDLVE HLKTNMIDVF IKVTISCKKK PDLYIVDAAV
 241  PLLRRLTHEE FKTQLLPALQ KAMLRNPEII IESVGHILNG LSLDLSQYSQ EISKGLFANL HSKEDLVRDE AVEACRKLAI
 321  QCSDTTAVEM LLSSVFAVFH GSEGKLTVAT HKISVLQGAG NLSYNVASGS SVQKLAETAC EHFVKVLETE VHEKTLIHAL
 401  EMMALWSKKF SSNVPKIVVD AFKKGMAAKT STAAVRTAYI KLFFSTPASS YSGVIAPILA QAITRATQQC AQPTAVTEGL
 481  VASYLLLKFV LADQVENDKQ SVLWNAIDEQ IFFSEKFLST CSDDILYHLM LLCECLITEF SDKLNEKALT GIHRAIVSCA
 561  TAPNSATRQR CSPLVKKIMT GLSTYAPAQA LLTEFNKFLE NVKIRSESDK ENKEDTSMGE ITGRCLADGL FAICSGSFLF
 641  EAHTYQMTRD ALLPSHHPAL LKAVPNLWFK IVKNYNLVPK DFLRTYSNEV RKMLIQNYKP MPNYENALIK IVSLAPDAFL
 721  PALVSNVTSK LDDPEILRVT KDEYFTYLTP EGELYDKSVL PVNDENDILS SMNMKRESKV YSFKEQQEEL QLRRELYEKR
 801  KREGKIKEPK LTPKQEETIK AQIAKENGIR KRLTELKAKI DNTVSLVACS IRGNQQELSL YLKDLLPTIL KNLGSPLAAP
 881  EMSELYVSLR QTVTIDNSAI LGDLIAHVTL RQLQPQCDLD QSWEEENLDV AVKRTLNLIH AVTIKKKELF TAPAFCYVFP
 961  FIRKTLTSYK DEGMIVQGLQ LIQEHAKQRG STTDLKDLRH PRLLPRKQMF DLLIELMETT TSRVQSHAVA TLLDVAQSGS
1041  GQPGTAIATS EDIDSLIGAL QNSLSTVRDA ALRGLTVIRQ AFPSQKEDQD QLNRLTRRVW VAQFDVNDEN KILANELWNA
1121  ADFTAQAEVL CEELIQDIAH PVEPVQQAAA HALAKSLANV PHLTPTVLDN LLQLYQEKLA MIPPKLNDFG RVIEQPIDTW
1201  GPRRGVALAL AQIAPLLTAD TVHRLIQFFV LTGLGDRNQS VRTEMLTAAV AAVDLHGSAN ITSLLPVFEN FMDKAPKIGS
1281  FDSIKQSVVI LMGSLARHLD KNDPRIKPIV MRLIVALSTP SQQVQEAVAN CLPHLTDAIK EDAPKIVDNL MDQLLKSDKY
1361  GERKGAAYGL AGLIKGMGIL ALKQLDIMSK LTHAIQDKKN YRHREGALFA FEMLCTMLGR LFEPYIVHVL PHLLLCFGDS
1441  SQYVRTATDD TARVVMSKLS AHGVKLVLPS LLAALEEDSW RTKTGSVELL GAMAYCAPKQ LSSCLPSIVP KLIEVLSDSH
1521  TKVQEAGAEA LKVIGSVIRN PEIQAIVPVL LKALQDPSHK TATCLQTLLD TQFVHFIDAP SLALIMPVVQ RAFLDRSTET
1601  RKMAAQIIGN MYSLTDQKDL TPYLPTIIPG LKTSLLDPVP EVRSVSARAL GAMVRGMGES SFEDLLPWLM QTLTSETSSV

1681  DRSGAAQGLS EVVRGLGVEK LHKLMPEIIS TAERTDIAPH VKDGYIMMFI YMPSAFTTEF TPYIGQIINP ILKALADENE
1761  YVRETALRAG QRIVTLYADS AIMLLLPELE KGLFDDNWRI RYSSVQLLGD LLYRISGVSG KMSTETASED DNFGTEQSHY
1841  AIINALGAER RNRVLAGLYM GRSDVALMVR QAALHVWKVV VTNTPRTLRE ILPTLFTLLL GCLASTSYDK RQVAARTLGD
1921  LVRKLGERVL PEIIPILEKG LLSDQADQRQ GVCIGLSEIM ASTNKDMVLT FVISLVPTVR KALCDPLPEV RQAAAKTFDG
2001  LHSTVGVRAL DDILPAMLTQ LNSPDPAEAE NTLDGLRQVM AIKSRVVLPY LVPQLASPPV NTKALSILAS VAGEALTRFL
2081  HRILPALLTA LSSAQGTANE LQELEYCQAV VLSVTDEVGV RTVMDQLMEA TRAEDLSKRR SAATLLCAFC RDTRADYSQY
2161  VPQLLRGLIH LFTDEDRDVL QMSWEALTAV TKTLSSDQQI AHVQDIRQAV RFAVSDLKGQ ELLPGFCLPK GITPILPIFR
2241  EAILNGLPEA KEHAAQGLGE VIRLSSAAAL QPSVVHITGP LIRILGDRFN WSVKAAVLET LAILLGKVGV MLKQFLPQLQ
2321  TTFLRALNDS NRQVRLKAAY ALSNLIVIHT RVDPLFTELH TGIKTGDDPA IRETMLQALR GVLTPAGDKM TDPMKKQVFA
2401  TLSSMLGHSE DITRNAVAGC FGALLRWLTS EQLVVAFNDH LLCNDVNADW VLRHGRSAAL FVALKESPGT VYNPKEKDRV
2481  CSVILSYLAA DRVQIVMNGV RACGYLFQYL MNESQPIPQQ ILSPFVRSMN NNSNDVKQLL ARVCIHLARN IPPENMSPEL
2561  LRSLLPMLVN GTKEKNGYVK ANSELALIAV LRLRQGEEEH QRCMAFLDAG ARESLSDVVS KVLRKVLSQP EGKIEELDDT
2641  LLT
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1621	1626	
total 1 peptides												

tr|A0A088ABA5|A0A088ABA5_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADVELTKAL KDLPNRVQTA SKNERREILQ NVVNVLSNPG INEKIVHGIC KTISLTLHRY KDTASQSYVK NLIEELLKKQ
81 PEPSIKHMIN IVIEQAAWHK NVVPTLNTAL TAYLALKWST LIVLHGYKSN LNINSELPKL IEAQANLSAA ALASMDKKLT
161 EKVYVLLAHE WSSVKDIDIE YLETLTKLEV ENGVIVLASL LTKYLVTAKK NELVAKLKTN TIDPFIKLTI SCKKKPDLYV
241 VHNAVPLLRR ISHDEFKSQL LPALQKAMLR NPEIIIESVG YILSGLSLDL SQYSQDISKG LFANLHSKED LVRDEAVGAC
321 RRLALQCSDT IALENLLSSV FAVFHGSEGK LTVATHKISV LQGAGNLSYN AASGSSVERL AETACEHFIK VLETEVHEKT
401 LIHALEMMAL WTNKFANNVP KCVIDAFKKG MTAKTSTAIV RTAYIKLFFS APVASYSEAI TPLLLQSLTR AIQQSAQPAA
481 VTEGLIAAYL LLKFVLVNQV ENDKQIILWN AIDEQIFFSE KFLTTCADDI LYHLMLLCER LITEFGDRLN EKTLNGVHRA
561 IVACATAPKY KIRKRCFPLI KKILTGLSTY GPAQELLMEY NKFLERVKIK SENDENKEES FNYETTGRCL ADGLLAICSG
641 SFLFESPAMQ MTRDALIPSH HPAIYKAMPN LWFKIVKNFN LIPKHFLCSF NHEIKKILIQ NYKPIASYEN ALTNVISIIP
721 DIILPVIVSN ITSKLDDVEI LRVTKDEYFI YLTPEGELYD KSVLPTNDEN DILNSMNMKR ESKVYSFKEQ QEELQLRREL
801 YEKRKKEGKI KEPKLTPKQE EILKTQMAKE STIRKRLTEL KLKIDNVVSL TICSMHGNGQ ELSFYLKDLL PPILKNLGSP
881 LAAPAMSDLY IRLKEIIKIN NPVLSDVVAH VTLRQLQPQC DLNHAWEEEN LDSAVKRTLN LLHTTAIKQK KLFTAPTFCY
961 IFPFIKKTLL SYKDDNMIVQ GLQIIQEHAK QRGNSSDFRD MKHPQLLPRK HMFDLLIELM EITNGRVQTH AVATLLDVAQ
1041 SGSGQPGTAI ATNEDINSLI GALQNSLSTI RDAALRALTV VRQAFPSQKE DPDQLSYLIK RIWIARFDVC DENKILANEL
1121 WNAADLVMDA EKLSDELIQD TAHPVEPIQQ AAACALAQCL TEVPHLVPII LDKLLQMYQD KLAMIPPKLN DFGRIVEQPI
1201 DTWGPRRGVA LALAQLAPLL SADTVLKLVQ FFVSIGLGDR NQAVRTEMLT AAVAVVDLHG KANITSLLPV FEEFMDKAPK
1281 IGSFDSIKQS VVILMGSLAR HLDKDDSRIK PIVMRLIAAL STPSQQVQEA VANCLPHLVP SIKDDAPSIV DKLMDQLLKS
1361 DKYGERKGAA YGLAGIIKGM GILALKQLDI MTTLTNAIQD KKNYRHREGA LFAFEMLCTM LGRLFEPYIV HVLPHLLLCF
1441 GDSSQYVRTA TDDTARVVMS KLSAHGVKLV LPSLLAALEE DSWRTKTGSV ELLGAMAYCA PKQLSSCLPS IVPKLIEVLS
1521 DSHTKVQEAG AEALKVIGSV IRNPEIQAIV PVLLKALQDP SHKTATCLQT LLDTQFVHFI DAPSLALIMP VVQRAFLDRS
1601 TETRKMAAQI IGNMYSLTDQ KDL**TPYLPT**I IPGLKTSLLD PVPEVRSVSA RALGAMVRGM GESSFEDLLP WLMQTLTSET

1681 SSVDRSGAAQ GLSEVVRGLG VEKLHKLMPE IISTAERTDI APHVKDGYIM MFIYMPSAFT TEFTPYIGQI INPILKALAD
1761 ENEYVRETAL RAGQRIVNLY ADSAIMLLLP ELEKSLFDDN WRIRYSSVQL LGDLLYRISG VSGKMSTETA SEDDNFGTEQ
1841 SHFAIINALG AERRNRVLAG LYMGRSDVAL MVRQAALHVW KVVVTNTPRT LREILPTLFT LLLGCLASTS NDKRQVAART
1921 LGDLVRKLGE RVLPEIIPIL EKGLQSDQAD QRQGVCIGLS EIMTSTNKDM VITFVISLVP TVRKALCDPL PEVRQAAAKT
2001 FDGLHSTVGV RALDDILPAM LTQLNSPDPA EAENTLDGLR QVMAIKSRVV LPYLVPQLTT PPVNTKALSI LASVAGEALT
2081 RFLHKILPAL LTALSSAQGS PNEVQELEYC QAVILSVTDE VGIRTVMDQL MEATRADDPS RRRSAATLLC AFCRDTRADY
2161 SQYVPQLLRG LIHLFTDDDK DVLQMSWEAL TAVTKTLASD QQIAHVQDIR QAVRFAVSDL KGQELLPGFC LPKGITPILP
2241 IFREAILNGL PEAKEQAAQG LGEVIKLTSA SALQPSVVHI TGPLIRILGD RFNWSVKAAV LETLAILLGK VGVMLKQFLP
2321 QLQTTFLRAL NDSNRQVRLK AAYALSNLIV IHTRVDPLFT ELHAGIKTGD DPAIRETMLQ ALRGVLTPAG DKMTEPMKKQ
2401 VFATLSSMLG HSEDITRNAV AGCFGALIRW LTPDQLNVAF NENLLCNDST VDWMLRHGRS AALFVALKES PTTVYNNKEK
2481 DRVCSVILSY LSADRVQIVM NGVRACGYLF QYLMNEGQSI PQQILSPFVR SMNNNSNDIK QLLAKVCIHL ARNISPEKMS
2561 PELLKSLLPM LVNGTKEKNG YVKANSELAL IAVLRLRQGE EEHQRCMAFL DAGAKESLSD VVSKVLRKVL SQPEGKIEEL
2641 DDTLLT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1624	1629	
total 1 peptides												

tr|A0A224X4L0|A0A224X4L0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MTSTDDLSKV LKDLPLRVQT ASLSERKLIF ENVKSIVANP GFNENIVRGT CKVLQLTLPR YRDSDSQRYV LSIISSLSSV
  81 HPKWTFKHLS PILNEVAAVY VSITATKSTA QSCLHALSWS SLLIVNSLNK CEGNNTEEDF QKIVNAQSVL FSTILASGNG
 161 KKSEKGQHML STMWKSNKDF LIPLYVKGVC KLPECTHSIV FGSFFVKFLH ENKLNEHINE VKIKLMEMIV KVVISSKTRI
 241 PTYIAVACRP VLLLASHDDF SNVLLPALQK AMLRNPELIL YVLGKLLANV SLDLSKYSFN LGKTIAVSLC SNDDDCRAQA
 321 ADAIKSLSIQ CSDPDAVGAL ADYLFQLFNG SQGKITVSSH KITILQAIGN LSYNAVTGNS IQQLTQNVAE QFIKILEVEV
 401 HEKTLIYCLE MMSIWCTKFT LSIPPKVISW FDKGISLKTS TSLVRAAYIG VLSVCCQSAT ASQTTQYIPL LVKCVEKAAA
 481 QPTQVAIVME GLSAACLLLK MATLDSVDSK LAPLYNIILD MDKQVFISEK FLLQASCDAL CQVVSLCEKI LMEHVAQLLG
 561 NPKPLYRTLV ICLTTRTVKA KCKPILHRMF SSLQGTQIAT ALLDEFTNLL ISNKFQCTGK DNKENSDSQM ELKPRHLVDA
 641 ITVMCSGTNL SKEDKKLLAF HSILACHHPL IESAQSKLWL KIIKYFKLHP SKFIAHYNEK FINLLVNDFT PHLSYERSLS
 721 TITELNPNAV IPPVLDYVIT LLSDPELLNV SAQDYAIFKS PPGELFDKSV LANQDETTMN IKNMKRESKV YSYKEQQEEI
 801 ALRKELEEKK RKEGKLAQPE LTPKQKEIIR IQLEKEAAVR ERLTRAETKL IKAYHIIVSV CTGSSLQLAL QFPSLVPLVV
 881 KGLNSPLCAG LLSKLYLYFR KPAFICVPVS NITVDRVANT TLRLLKPKCE LDPAWEDQDI GKAMTWAVTE MEKEGKMITA
 961 PALSYILPMI QCITHIVPPT SPLLTNSIQL LSKQCRLRAS NIQPDLHSPQ LLPRKQIMLL CIDLISSTAG RIQQQASSCL
1041 LDVASASSGG TGCSVATPEE IGCLLTALQH SSHHVRDAAL RALYALVQVF PKSKKNADLA FQIVKRVWVA RWDVVVENRE
1121 IAHKLWEIAN LDSHIPGLSE GLLVDIVHPV VEIQQAAAYA LAALLQQSKK QDIDVVLRML LDIYNDKYNM VPARVDSLGR
1201 IVEKPIDTWE PRSGVALALQ QLAPLLTPNS VSDLAKFYVD KGLGDRSDTV RNNMLAAALA AVDLHGKECV NSLLSIFEPV
1281 LDKGPDCSSY DAVRQSVVIL MGSLARHLDK DDKKVKPIVA KLIDALSTPS QQVQEAVANC LPALVPSIKD EAPTLVQKLL
1361 NQLLSSESYG QRKGAAYGLA GIVKGMGILV LKQLDIMTTL TTAIQDKKNY RHREGALFAF EMLCSVLGRL FEPYIVHVLP
1441 HLLLCFGDGN QYVRDATDDC AKVVMSKLSA HGVKLVLPSL LAALEKDSWR TKTGSVELLG AMAFCAPKQL SSCLPSIVPK
1521 LIEVLSDSHV KVQTAGTEAL KQIGSVIRNP EIQAIVPVLL EALQDPSNKT AMCLQTLLDT QFVHFIDAPS LALIMPVVQR
1601 AFMDRSTETR KMAAQIIGNM YSLTDQKDLT PYLPTIIPGL KTSLLDPVPE VRSVSARALG AMVRGMGEAS FEDLLPWLMK

1681 TLTSETSSVD RSGAAQGLSE VVGGLGVEKL HKLMPEIIST AERSDIAPHV KDGYIMMFIY MPVVFTNEFT PYIGEIIIPI
1761 LKALADENEY VRDTALKAGQ RIVNLYADSA ITLLLPELEK GLFDDNWRIR YSSVQLLGDL LYRISGVSGK MSTETANEDD
1841 NFGTEQSHKA IIGALGAERR NRVLAGLYMG RSDVALMVRQ AALHVWKVVV TNTPRTLREI LPTLFSLLLG CLASTSHDKR
1921 QVAAKTLGDL VRKLGERVLP EIIPILEQGL ESDQPDQRQG VCIGLSEMMT STSRDMVLTF VNSLVPTVRK ALCDPLPEVR
2001 QAAAKTFDSL HSTVGVRALD DILPPMLNQL NDPESEVAEW TLDGLRQVMA IKSRVVLPYL IPQLTVTPIN TKALSILASV
2081 AGEALTKYLH KILPALLTAL ASSEGSSQEI EYCQAVVLSV TDEAGIRAIV DQLVEVGKCD NVETRKAAAT LLCSFCTHSR
2161 ADYSQHVSQL LRGLITNFTD HDPVVLQMSW DALSAVTKSL DPSQQIQYVG DIRQAIKFAA SDLKSGDTLL PGLCLPKGIT
2241 PILPIFRESI LNGSPEIKEA AAQGLGEVIS LTTAQSLQPS VIHITGPLIR ILGDRFPPSV KAAVLHTLAT LLAKVGMMLK
2321 QFLPQLQTTF LKALNDGNRL VRLKAATALS YLITIHTRPD PLFSELHNSV KSAEEPAVRE TMMQALRGVV SAAGEKMSEP
2401 VLKPIHLSLL SMLSHSEDAT RTGAAGCVGA LTRWLSPEQL ALTLNDNLLV DDVTVEWTLR HGRSAALFVA LKEAPEKVYV
2481 PEYKEKIHKV ILSFIAADRI PIVMNGVRGC GYLFDHLFSN SETLPQPLLS PFVRSMNHPS NEVKQLLARA CSYLGRREIS
2561 SPEFLKSAIP MLVNGTKEKN GYVKANSELS LVAVLRLRHG DDKLQWCMSL LDPGAAEALS DVITKVLRKV AIQPEGKAEE
2641 LDDTLLT
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1630	1635	
total 1 peptides												

tr|R4WJK2|R4WJK2_RIPPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MASNEELTKV LKDLPLKIQT SRKSERKLLF EKLRSAISNS GFSENIVRGL CRVLQMTLPR YCDSASQGYV RSLVKALANI
  81 HPNWTIKYLT PILAETANYN TSIIATKSTA QGSLQALSWS SILVSSALNK CSDENKQDFQ TILNAQSLLY SSVLASTNKK
 161 KISKANQMLT SLWNSNDLIL SLYEKGVLCL PDSTHSIVFG SFFIKYLCEK KSAEILEYKT KILDLIVKVV IMSKVQIDPY
 241 VVQACRPVLL LASHVDFSDT LLPSLQKAML RNPELALHVV GRILANLSLD LSQYAYTVGK IISASLYSND ENTRNQAASA
 321 CKFLSLQCSD PEAIWSLLEH LFQVFNGSQG KITVADHKIS ILQGIGNFSY NAVTGSSIQP LAKNAVEHFI KILETEVHEK
 401 TLVHCLEMMS LWCSKFVTEV PTTVLSWLEK GFALKTSTCP VRTAYIGVMS ACCQSGTAGQ ITQFIPILLK SVEKAAAQSS
 481 QVPVVTEGLS AACLLLKMST YTVVDSKLSF LYNIILDMEK QVFISERFLS QASCEALCQV MNLCEKILME DTIGGSVSTV
 561 RGPVHRALVT CIANHHVKTK CKPALLRMFS SLQGTQIAAM LLDELHALLV GNKFQSAKEN RDNQENHHEF KPRHLVDAIV
 641 LICSGTNLSK EDKNTLAFHA LLPCHHPLIL SSQGNVWLNI TKHLKLDPPK FVKHYKDKFI KLLIEDFQCH PSYERALKTI
 721 AEINSTLILP PLLNTVNEVF SDATLLNVSP MEYAIFKSPE GELFDKSILQ SKENETTMNI KNMKRESKVY SYKEQQEEIA
 801 LRKELEEKKR KEGKLSQPEL TPKQKEAVKI QLEKERAIRE RLKKDEERLN KAVQLLSCII AGAPLELALN LPTVIPPVVH
 881 GLSSALCADP LSDLFIALSQ PAFTGVSLQP VIVERVAYTA LRLLHPKCAI SSAWAEQDLG KAMRWMIQEM DKNVKDITSP
 961 VISYLLPSLK AALSSEPPND PIISTAIHLL STRVRLRGSS NRNPDLHSPV LLPRRQMMTL CIDIISSSGG RVQQQASACL
1041 LDLAQASSGA EGCAVASSEE IDTLLTALQQ SSSHVRDAAL RALLAITQVF PKPKQNAEQA FRLTKRIWVA KFDVVTENRD
1121 VADKVWANAN LSHDTKGLSE GLLDDVVHPV AEIQQAAASA LAALLQTGSS QTTVDVVLQL LLNIYNDKNN MVPARVDSLG
1201 RIVEKPIDTW EPRSGVALAL AQLAPLLTPD KVADLAKFYV EKGLGDRNET VRHNMLTAAL AAVDLHGKDT VNTLLPIFEP
1281 VLDKGPDCSS YDAVRQSVVI LMGSLARHLD KDDKKIKPIV AKLIDALSTP SQQVQEAVAN CLPALVPSIK DEAPILVNNL
1361 LERLLSSESY GERKGAAYGL AGIVKGMGIL VLKQLNIMST LTNAIQDKKN YKHREGALFA FEMLCSVLGR LFEPYIVHVL
1441 PHLLLCFGDG NSYVRDATDD CAKVVMSKLS AHGVKLVLPS LLAALEKDSW RTKTGSVELL GAMAYCAPKQ LSSCLPSIVP
1521 KLIEVLSDSH VKVQKAGTEA LKQIGSVIRN PEIQSIVPVL LEALQDPANK TATCLQTLLD TQFVHFIDAP SLALIMPVVQ
1601 RAFMDRSTET RKMAAQIIGN MYSLTDQKDL TPYLPTIIPG LKTSLLDPVP EVRSVSARAL GAMVRGMGEA SFEDLLPWLM

1681 KTLTSETSSV DRSGAAQGLS EVVGGLGVEK LHKLMPEIIS SAERSDIAPH VKDGYIMMFI YMPVVFTNEF TPYIGEIIVP
1761 ILKALADENE YVRDTALKAG QRIVNLYAES AITLLLPELE KGLFDDNWRI RYSSVQLLGD LLYRISGVSG KMSTETANED
1841 DNFGTEQSHK AIIGALGAER RNRVLAGLYM GRSDVSLMVR QAALHVWKVV VTNTPRTLRE ILPTLFSLLL GCLASTSHDK
1921 RQVAAKTLGD LVRKLGERVL PEIIPILEQG LESDQPDQRQ GVCIGLSEMM ASTSRDMVLT FVNSLVPTVR KALCDPLPEV
2001 RQAAAKTFDS LHSTVGVRAL DDILPPMLQQ LNNGDSGVSE WTLDGLRQVM AIKSRVVLPY LVPQLTATPI NTKALSILAS
2081 VAGEALTKYL NKILPALLTA LAASDGSPQE LEYCQAVVLS VNDEAGIRVI VDELLDASKS DKPECRRASA TLLCAFCTHT
2161 RADLSQHVAQ LLRGLILNFT DSDPVVLQMS WDALSAVTKT LDSSQQISYV GDIRQAIKFA ASDLKPGELL PGLCLPKGIT
2241 PILPIFRESI LNGSPETKEA AAQGLGEVIA LTTAQSLQPS VIHITGPLIR ILGDRFPPSV KAAVLHTLAG LLAKVGMMLK
2321 QFLPQLQTTF LKALNDGNRM VRLKAASALS YLITIHTRPD PLFSELHNSV KSAEEPAVRE TMMQALRGVI SAAGDKMSDA
2401 VVKQIHTSLL GLLGHAEDTT RTGAAGCLGA LTRSLTVDQL TVTLNDHLLQ DDLTSDWTLR HGRSTALFVA LKEAPERLYK
2481 DDFKEKVQKR LLVFLTADRV PIAMNGVRGC GYLFEYLMSN NEPVPQPLLS PFVRSMNHQS NEVKQLLARV CSYLARREIN
2561 SPEFLKAVIP MLVNGTKEKN SYVKANSELS LVSVLRLRNG DEKLQSCIAV LDPGAAEALT DVITKVLRKV ALQPEGKVEE
2641 LDDTLLT
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1631	1636	
total 1 peptides												

tr|A0A069DYI0|A0A069DYI0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTSTDDLSKV LKDLPLRVQT ASLSERKLIF ENVKSIVAKP GFNENIVRGT CKVLQLTLPR YRDSDSQRYV LSIISSLSSV
81 HPKWTFKHLS PILNEVAAVY ASITATKSTA QSCLHALSWS SLLIVNSLNK CEGNSTEEDF QKIVNAQSVL FSTILASGNG
161 KKSEKGQHML SNMWKSNKDF LIPLYVKGVC KLPDCTHSIV FGAFFVKFLH ENKLNEHINE VKIKLMEMMV KVVISSKTRI
241 PTYIAVACRP VLLLASHDDF SNVLLPTLQK AMLRNPELIL YVLGKLLANV SLDLSKYSLN LGKTIAASLC SNDDDCRAQA
321 ADAIKSLSIQ CSDPDAVGAL ADYLFQLFNG SQGKITVSSH KITILQAIGN LSYNAVTGSS IQQLTQNVAE QFIKILEVEV
401 HEKSLIYCLE MMSLWCSKFT LNIPPKVISW FDKGISLKTS TSLVRAAYIG VLSVCCQSAT ASQTTQYIPL LVKCVEKAAA
481 QPTQVAIVME GLSAACLLLK MATLDSVDSK LAPLYNIILD MDKQVFISEK FLLQASCDAL CQVVSLCEKI LMEHVAQLMG
561 NPKPLYRTLV ICLTTRAVKA KCKPILHRMF SSLQGTQIAT ALLDEFTNLL ISNKFQCTGK DNKENSDSQM ELKPRHLVDA
641 ITVMCSGTNL SKEDKKLLAF HSILACHHPL IESAQSKLWL KIIKYFKLHP SKFVAHYNEK FINLLVNDFT PHPSYERSLS
721 TITELNPNAV IPPVLDYVIT LLSDPELLNV SAQDYAIFKS PPGELFDKSV LAHQDETTMN IKNMKRESKV YSYKEQQEEI
801 ALRKELEEKK RKEGKLAQPE LTPKQKEIIR IQLEKEAAVR ERLTRAENKL IKAYHIIVSV CNGSSLQLAL QFPSLIPLVV
881 KGLNSPLCAG LLSKLYLYFR KPAFICVPVS NITVDRVANT TLRLLKPKCE LDPAWEDQDI GKAMTWAVTE MEKEGKMITA
961 PALSYILPMI QCITQIVPPT SPLLTNSIQL LSKQCRLRAS NIQPDLHSPQ LLPRKQIMLL CIDLISSTAG RIQQQASSCL
1041 LDVASASSGG TGCSVATPDE IGCLLTALQH SSHHVRDAAL RALYALVQVF PKSKKNADLA FQIVKRIWVA RWDVVVENRE
1121 IAHKLWEIAN LDSHIPGLSE GLLVDIVHPV VEIQQAAAYA LAALLQQSKK QDIDIILRML LDIYNDKYNM VPARVDSLGR
1201 IVEKPIDTWE PRSGVALALQ QLAPLLTPNS VSDLAKFYVD KGLGDRSDTV RNNMLAAALA AVDLHGKECV NSLLSIFEPV
1281 LDKGPDCSSY DAVRQSVVIL MGSLARHLDK DDKKVKPIVA KLIDALSTPS QQVQEAVANC LPALVPSIKD EAPTLVQKLL
1361 NQLLSSESYG QRKGAAYGLA GIVKGMGILV LKQLDIMTTL TTAIQDKKNY RHREGALFAF EMLCSVLGRL FEPYIVHVLP
1441 HLLLCFGDGN QYVRDATDDC AKVVMSKLSA HGVKLVLPSL LAALEKDSWR TKTGSVELLG AMAYCAPKQL SSCLPSIVPK
1521 LIEVLSDSHV KVQTAGTEAL KQIGSVIRNP EIQAIVPVLL EALQDPSNKT AMCLQTLLDT QFVHFIDAPS LALIMPVVQR
1601 AFMDRSTETR KMAAQIIGNM YSLTDQKDL**T PYLPT**IIPGL KTSLLDPVPE VRSVSARALG AMVRGMGEAS FEDLLPWLMK

1681 TLTSETSSVD RSGAAQGLSE VVGGLGVEKL HKLMPEIIST AERSDIAPHV KDGYIMMFIY MPVVFTNEFT PYIGEIIIPI
1761 LKALADENEY VRDTALKAGQ RIVNLYADSA ITLLLPELEK GLFDDNWRIR YSSVQLLGDL LYRISGVSGK MSTETANEDD
1841 NFGTEQSHKA IIGALGAERR NRVLAGLYMG RSDVALMVRQ AALHVWKVVV TNTPRTLREI LPTLFSLLLG CLASTSHDKR
1921 QVAAKTLGDL VRKLGERVLP EIIPILEQGL ESDQPDQRQG VCIGLSEMMT STSRDMVLTF VNSLVPTVRK ALCDPLPEVR
2001 QAAAKTFDSL HSTVGVRALD DILPPMLHQL NNPESEVAEW TLDGLRQVMA IKSRVVLPYL IPQLTVTPIN TKALSILASV
2081 AGEALTKYLH KILPALLTAL ASSEGSSQEI EYCQAVVLSV TDEAGIRAIV DQLVEVGKCD NVETRKAAAT LLCSFCTHSR
2161 ADYSQHVSQL LRGLITNFTD HDPVVLQMSW DALSAVTKSL DPSQQIQYVG DIRQAIKFAA SDLKSGDTLL PGLCLPKGIT
2241 PILPIFRESI LNGSPEIKEA AAQGLGEVIS LTTAQSLQPS VIHITGPLIR ILGDRFPPSV KAAVLHTLAT LLAKVGMMLK
2321 QFLPQLQTTF LKALNDGNRL VRLKAATALS YLITIHTRPD PLFSELHNSV KSAEEPAVRE TMMQALRGVV SAAGEKMSEP
2401 VLKPIHLSLL SMLSHSEDAT RTGAAGCVGA LTRWLSPEQL ALTLNDNLLV DDVTVEWTLR HGRSAALFVA LKEAPEKVYV
2481 PEYKEKIHKV ILSFIAADRI PIAMNGVRGC GYLFDHLFSN CETLPQPLLS PFVRSMNHPS NEVKQLLARA CSYLGRREIT
2561 SPEFLKSAIP MLVNGTKEKN GYVKANSELS LVAVLRLRHG DEKLQWCMSL LDPGAAEALS DVITKVLRKV AIQPEGKAEE
2641 LDDTLLT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1630	1635	
total 1 peptides												

tr|A0A232FBG6|A0A232FBG6_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MADAELTKAL KDLPNRIQTA SRNERREIFQ NVVDVLSNPG INEKIVGGIC KSVPITLHRY NDTASQSYVT NLIVALIKQH
  81 PQATLKNLTS VIAEQAVWHK SLIPTYNTAA SAYTVLRWSS LIFLHGAKEL DNLDNSDLSK LIEAQAVLSA AALAARDKKL
 161 TKKVELLFSH QWKTVKNNIE EKYVDVLIAA EPNEGVVALA GLLTTYLIAS DKADLIEKLK TSILSTFMKV CVSCKNKPDL
 241 YIIDAAAPFL KRISHDDFKN QLLPALQKAM LRNPEVIIET VGHILTSLSL DLSRYTDDIS KGLFANLHSK DDLVRDEAAD
 321 ACKRLSLQCS DSSAVEGLLK AIFAVFHGSE GKLTVATHKI SVLQGAGNLS FNAVSGSSVQ KLAEVACGYF IEVLKTEIHE
 401 KTLGHALEMM SLWCEKFANE APKNVIDAFK QGMASKNSTP AVRTAYIRLL FSIPPQPISS YTGTIVPILT QAITRATQQS
 481 AQPPVVTEGL YAAYLLLKLI ITGQVENDKQ GVLWSAVDDQ VFFTEKFLST CNDDTTHHLM LFCEKLIAEF TDKLNEKALS
 561 GIHRAIIVCV TTPRYATRSK CCAILKKILT AISTYEPVQS LFVEFNKFLE SVKFKVESDK ENAKEDANTE KVICGISLAD
 641 GLSAICSGSF LYEQHSYNLL RDALIPAHHP VIYKAVPNLW LTIAKQFCDN PSNFLRKFGS EIKKLFVQNY KPTPSYENAL
 721 QQVTSLAPDV ILPTLVAHVT AKLDDPEITK VTKDEYFTYL TPEGELYDKS VLPGNDENDI LNAMNMKRES KVYSFKEQQE
 801 ELQLRRELYE KRKKEGKIKE PKLTPKQEEA IKAQYTKENT IRNRLIEMNT NINNVVSMIN AAAEGNGFHL SFYFKDLLPS
 881 ILRNLASPLA APTMAELFVG LSKAVLISND PTLDQLVAHV TLRQHQPQCD LDPAWEEEEL SKAIKRTLNL IHTLTVKKKQ
 961 LFCAPAFCYV FHFIKKTLLT CKDDGMITQG LQIMQDHAKQ RGDSTNPEDA RHPRLLPRKQ MFDLLIELMS TTTGRVQTHA
1041 VATLLDVAQS GSGAEGAALA SSEEIDSLTG ALQNPLTAVR DAALRGLMVI KNAFPSEKED PVQLLNLTRR IWVAKFDVND
1121 ENKELANELW SSAGLTADPN ILCDELIQDI AHPVESVQQA AACALAELLS QDPELMPGIL DRLLHLYQTK LAMIPPKLND
1201 FGRIIEQPID TWGPRRGVAL ALAQFAPLLT PETIQTLIQF FVSTGLGDRN QTVRTEMFTA AVAAVDLHGK DNITSLLPVF
1281 EEFMDKAPKS GSFDCIKQSV VILMGSLARH LDKDDPRIKP IVTRLIAALS TPSQQVQEAV ANCLPHLVPS IKEDAPKIVE
1361 KLMHQLLNSD KYGERKGAAY GLAGLIKGMG ILALKQLDIM TTLTNAIQDK KNYRHREGAL FAFEMLCTML GRLFEPYIVH
1441 VLPHLLLCFG DSSQYVRAAT DDTARVVMSK LSAHGVKLVL PSLLAALEED SWRTKTGSVE LLGAMAYCAP KQLSSCLPSI
1521 VPKLIEVLSD SHTKVQEAGA EALKVIGSVI RNPEIQAIVP VLLKALQDPS KKTAMCLQTL LDTQFVHFID APSLALIMPV
1601 VQRAFMDRST ETRKMAAQII GNMYSLTDQK DLTPYLPTII PGLKTSLLDP VPEVRSVSAR ALGAMVRGMG ESSFEDLLPW

1681 LMMTLTSETS SVDRSGAAQG LSEVVRGLGV EKLHKLMPEI ISTAERTDIA PHVKDGYIMM FIYMPSAFTS EFTPYIGQII
1761 NPILKALADE NEYVRETALR AGQRIVTLYA DSAIMLLLPE LERGLFDDNW RIRYSSVQLL GDLLYRISGV SGKMSTETAS
1841 EDDNFGTEQS HYAIIKALGA ERRNRVLAGL YMGRSDVALM VRQAALHVWK VVVTNTPRTL REILPTLFSL LLGCLASTSF
1921 DKRQVAARTL GDLVRKLGER VLPEIIPILE RGLQSEQADQ RQGVCIGLSE IMASTSRDMV LSFVNSLVPT VRKALCDPLP
2001 EVRQAAAKTF DSLHSTVGVR ALDDILPAML TQLNSPDQAE AENTLDGLRQ VMAIKSRVVL PYLVPQLTSP PVNTKALSIL
2081 ASVAGEALTR FLHKILPALL TALSTAQGTP DEMQELEYCQ TVVLSITDET GVRTVMDQLM EATRSEDPSR RRSAATLLCA
2161 FCRDTRADYS QYVPQLLRGL IHLFTDDDKD VLQMSWEALT AVTKTLGSDQ QIAHVQDIRQ AVRFAVSDLK GQELLPGFCL
2241 PKGITPILPI FREAILNGMP EAKEHAAQGL GEVIRLTSAS ALQPSVVHIT GPLIRILGDR FNWSVKAAVL ETLAILLGKV
2321 GVMLKQFLPQ LQTTFLKALN DSNRQVRLKA AYALSNLIVI HTRADPLFAE LHTGVKNADD PAIRETMLHA LRGVITPAGD
2401 KMSEQMRKQV FVTLSGMLGH QEDITRNSVA GCYGALIKYL SPEQLNTAFN DHLLNSNVNE DWMLRHGRSA ALFVALKEAP
2481 GVVYNGKEKE RVCKVILSYL AADRTQIAMN GVRACGYLFQ YLMNNKEPVP QVILTPFVRS MNNNSNDVKQ LLARVCTHLA
2561 RNVNPENMSP DLLKSLLPML VNGTKEKNGY VKANSELALI AVLRLRVGDE EHQRCMSLLD VGARESLSDV VSKVLRKVIS
2641 QPEGKMEELD DTLLT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPYLPT.I	Y	23.29	690.3588	10.0	691.3730	1	16.19	637	1	1633	1638	
total 1 peptides												

tr|A0A1Y9H1Z4|A0A1Y9H1Z4_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MLGHTEPRAS EMDVRTVSYV SGGVEQAMEL GLQQARQTGV RNERSITGTE SPKPPPLSGP TFFPTSAVSS QQRPQPPVAV
  81 PAPFATPAPV PIAPVRSTVP PQHSIRFAPE PRTELKFVPP APLKTPLVRP LLSQHQPQRD ATVPQIIPAP IAHRQPVILQ
 161 QAPFAMDPAR VNPGMAAGAQ MMRPPANVGP PRTGTPTQQQ PPRPGGMFGG PHQPPGVPMP MRPQMVPGAG VPGMQPGMQP
 241 RPPPAQGMQR PPMMGQPPPI RPPNPMGGPR PTISPQNSNL GGMMPAGMGP RPPMPMQAGA GGGAGAGLPQ GMRPNFYSRP
 321 MGPGDASRPP SGTDMAGVGG GPPSATPSVD DDEDVVIGRL PADSSSALNS PNPARVPSRN FTMPPAMERE KSNPSRPPSV

 401 AGSYGKPGTA EHELDGSSGR PLHALKDFIS KDPTRPGQSP TQSPSPGSQQ SLSPANTDEN FSYRPGAKPA VGQQQQPQQQ
 481 QQFKMQPPPG PRPNAPSPMA TPGGRPDGDK VTFQIPNGGA GGREGSQEWN ARSRPPQPHM IRTGGPKQLT ADHKGDNDSG
 561 VDEYTQEKDR PNALASPASP LKSPSKIPGL ARRPENITSD QSRSRSTSKQ RANAKTPETP SEQPLIKKVP MNKIQVGGTP
 641 SPNLKVVKSK IGSLENASHK PGGGNVKIET KKIDIKAAPR IEAKNDAYMP KGGDKKIIST KLQWNAKPKI GSMDNASHKP
 721 GGGDKRIESI KTDFKERAKP KIGSKDNITY KPGGGDVKIV HQKIDIKAES KIGSLDNLKH KPGGGDKKIF DDKEYLKNIE
 801 HPITPSPSTQ EYLYKFY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.TDMAGVGG.G	Y	21.96	706.2956	54.0	707.3410	1	17.11	661	1	333	340	
total 1 peptides												

tr|A0A1Y9H2G1|A0A1Y9H2G1_9DIPT back to list

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

Protein Coverage:

1 MLGHTEPRAS EMDVRTVSYV SGGVEQAMEL GLQQARQTGV RNERSITGTE SPKPPPLSGP TFFPTSAVSS QQRPQPPVAV
81 PAPFATPAPV PIAPVRSTVP PQHSIRFAPE PRTELKFVPP APLKTPLVRP LLSQHQPQRD ATVPQIIPAP IAHRQPVILQ
161 QAPFAMDPAR VNPGMAAGAQ MMRPPANVGP PRTGTPTQQQ PPRPGGMFGG PHQPPGVPMP MRPQMVPGAG VPGMQPGMQP
241 RPPPAQGMQR PPMMGQPPPI RPPNPMGGPR PTISPQNSNL GGMMPAGMGP RPPMPMQAGA GGGAGAGLPQ GMRPNFYSRP
321 MGPGDASRPP SG**TDMAGVGG** GPPSATPSVD DDEDVVIGRL PADSSSALNS PNPARVPSRN FTMPPAMERE KSNPSRPPSV
401 AGSYGKPGTA EHELDGSSGR PLHALKDFIS KDPTRPGQSP TQSPSPGSQQ SLSPANTDEN FSYRPGAKPA VGQQQQPQQQ
481 QQFKMQPPPG PRPNAPSPMA TPGGRPDGDK VTFQIPNGGA GGREGSQEWN ARSRPPQPHM IRTGGPKQLT ADHKGDNDSG
561 VDEYTQEKDR PNALASPASP LKSPSKIPGL ARRPENITSD QSRSRSTSKQ RANAKTPETP SEQPLIKKVP MNKIQVGGTP
641 SPNLKVVKSK IGSLENASHK PGGGNVKIET KKIDIKAAPR IEAKNDAYMP KGGDKKIIST KLQWNAKPKI GSMDNASHKP
721 GGGDKRIESI KTDFKERAKP KIGSKDNITY KPGGGDVKIV HQKIDIKAES KIGSLDNLKH KPGGGDKKIF DDKEYLKNIE
801 HPITPSPSTQ RSSSMRRMTA SVSGVDLCRS IDYEPVRVPP LATASLTASL TIPSECIVLS VADEPSPERK VQKLESAPCY
881 IRKDGRAVHP KPFRTY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.TDMAGVGG.G	Y	21.96	706.2956	54.0	707.3410	1	17.11	661	1	333	340	
total 1 peptides												

tr|A0A0P5ZW48|A0A0P5ZW48_9CRUS back to list

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

Protein Coverage:

1 SWRQCHTVEL IDNSRSKALQ FQRLNYTDRY TYTGAQNVPF PSFWSERRRT TTIGTNHIQL FLYSVCMLHV YVPASRFSFV
81 FLFLFPVFVL FFSLPPPLFF ILLLFFLNRH LKFLKKEKRN GFVSLP**SGAF LPT**TPKLVYR HTTCHGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SGAFLPT.T	Y	20.57	691.3541	-36.4	692.3362	1	15.17	619	1	127	133	
total 1 peptides												

tr|A0A0P5AGV2|A0A0P5AGV2_9CRUS back to list

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

Protein Coverage:

1 RKSLLADEEF FFFQSISVDN SRSKALQFQR LNYTDRYTYT GAQNVPFPSF WSERRRTTTI GTNHIQLFLY SVCMLHVYVP
81 ASRFSFVFLF LFPVFVLFFS LQKEGKGTFC APLNRHLKFL KKEKRNGFVS LP**SGAFLPT**T PKLVYRHTTC HGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SGAFLPT.T	Y	20.57	691.3541	-36.4	692.3362	1	15.17	619	1	133	139	
total 1 peptides												

tr|A0A0P6AEJ7|A0A0P6AEJ7_9CRUS back to list

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

Protein Coverage:

1 RKSLLADEEF FFFQSISVDN SRSKALQFQR LNYTDRYTYT GAQNVPFPSF WSERRRTTTI GTNHIQLFLY SVCMLHVYVP
81 ASRFSFVFLF LFPVFVLFFS PPPLFFILLL FFLNRHLKFL KKEKRNGFVS LP**SGAFLPT**T PKLVYRHTTC HGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SGAFLPT.T	Y	20.57	691.3541	-36.4	692.3362	1	15.17	619	1	133	139	
total 1 peptides												

tr|Q16KV7|Q16KV7_AEDAE back to list

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

Protein Coverage:

1 MVTIKNDIES S**SGAFIPT**SS HQPVKDVNLK QEGARLSRRR SYRCVTIVSV VVLVLMGLGI GGVLYFGKTL KRTPTQVKDG
81 MPSTTTEAVP EEPTVSPPTF TDPYDGTETS VGPTDDDDEF DIDGPVDSST SSTPSTTTMT SRWKLWSDEG SGSEDDDYYD
161 SGSGDSLVI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.SGAFIPT.S	Y	20.57	691.3541	-36.4	692.3362	1	15.17	619	1	12	18	
total 1 peptides												