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.

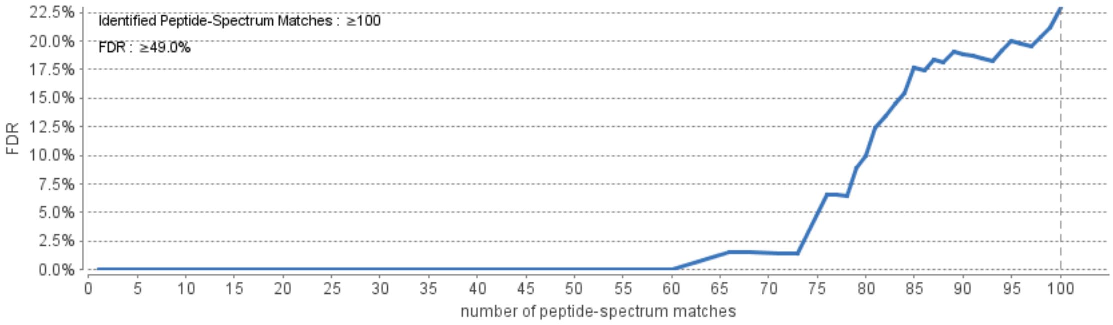
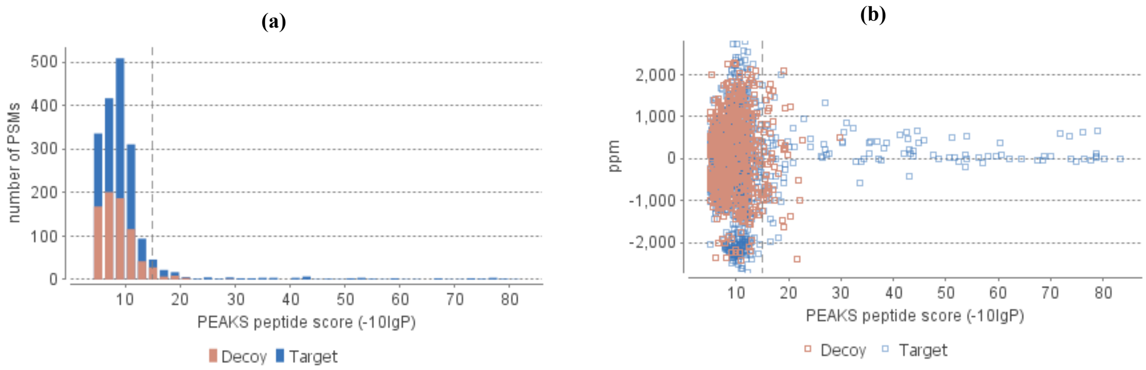


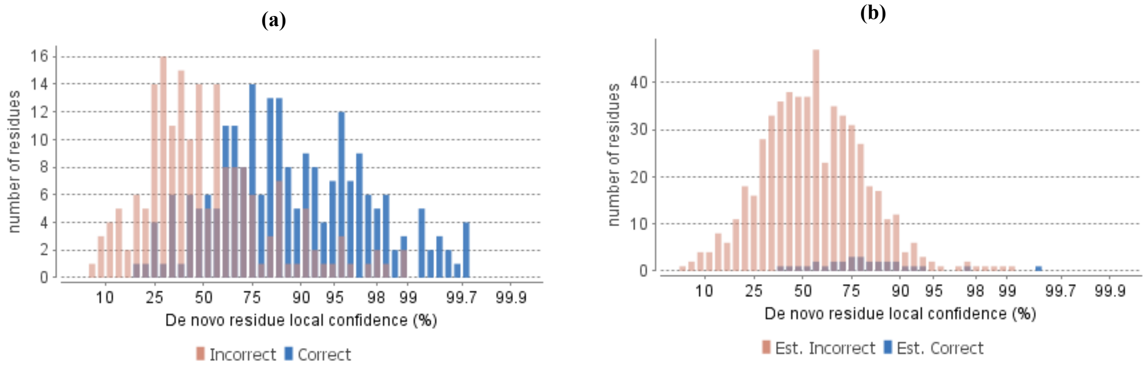
Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.



(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	1718
# of MS/MS Scans	3696

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	117
Peptide Sequences	109

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	4	C
Carbamylation	43.01	2	N-term
Deamidation	.98	2	N
Hydroxylation	15.99	1	P
Oxidation	15.99	1	M
Carbamidomethyl	57.02	1	N-term
Ubiquitin	114.04	1	C
Phosphorylation	79.97	1	T

Protein Groups	32
Proteins	218
Proteins (#Unique Peptides)	53 (>2); 11 (=2); 154 (=1);
FDR (Peptide-Spectrum Matches)	41.9%
FDR (Peptide Sequences)	44.0%
FDR (Protein)	3.2%
De Novo Only Spectra	52

CarbamidomethylDTT	209.02	1	C

3. Experiment Control

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

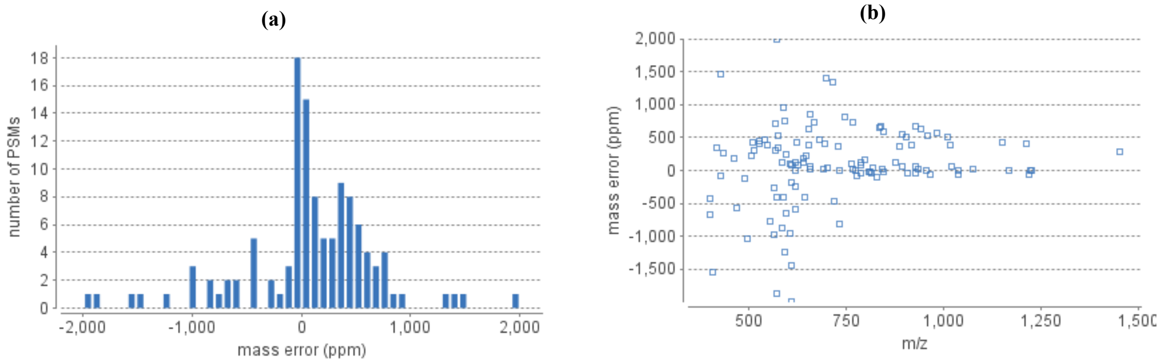


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
LTQ	0	0	0	0	109

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fragment ion tolerance: 0.5
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 85
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: IT_douglas_1_20170921_01.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: Linear Ion Trap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	11608	tr|A0A087ZTA6|A0A087ZTA6_APIME	195.71	14	9	9	Y	115302	Sodium/potassium-transporting ATPase subunit alpha OS=Apis mellifera PE=3 SV=1
1	11607	tr|V9I6A9|V9I6A9_APICE	195.71	14	9	9	Y	112642	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.11 PE=2 SV=1
1	11606	tr|V9I6B8|V9I6B8_APICE	195.71	14	9	9	Y	112686	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.12 PE=2 SV=1
1	11605	tr|V9I7I5|V9I7I5_APICE	195.71	15	9	9	Y	107666	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.17 PE=2 SV=1
1	11604	tr|V9I7X6|V9I7X6_APICE	195.71	15	9	9	Y	107710	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.20 PE=2 SV=1
3	4600	tr|A0A131ZV00|A0A131ZV00_SARSC	138.70	17	5	5	Y	50028	Tubulin alpha chain OS=Sarcoptes scabiei GN=QR98_0010090 PE=3 SV=1
2	4505	tr|T1GUQ6|T1GUQ6_MEGSC	117.75	16	6	6	Y	42846	Tubulin beta chain OS=Megaselia scalaris PE=3 SV=1
2	4516	tr|A0A0J7L622|A0A0J7L622_LASNI	117.75	8	6	6	Y	88812	Tubulin beta-1 chain OS=Lasius niger GN=RF55_1586 PE=3 SV=1
2	11640	tr|A0A1B1LYT4|A0A1B1LYT4_9NEOP	117.75	15	6	6	Y	48507	Tubulin beta chain (Fragment) OS=Thitarodes armoricanus PE=2 SV=1
2	4508	tr|A0A023FK66|A0A023FK66_9ACAR	117.75	14	6	6	Y	49838	Tubulin beta chain OS=Amblyomma cajennense PE=2 SV=1
2	4511	tr|B4QE31|B4QE31_DROSI	117.75	14	6	6	Y	50147	Tubulin beta chain OS=Drosophila simulans GN=Dsim\GD25319 PE=3 SV=1
2	4510	tr|V9IK78|V9IK78_APICE	117.75	14	6	6	Y	50175	Tubulin beta chain OS=Apis cerana GN=ACCB10461 PE=2 SV=1
total 218 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
2	11641	tr|A0A0M4EEV8|A0A0M4EEV8_DROBS	117.75	14	6	6	Y	50147	Tubulin beta chain OS=Drosophila busckii GN=Dbus_chr2Rg2269 PE=3 SV=1
2	11642	tr|A0A1A9WAB8|A0A1A9WAB8_9MUSC	117.75	14	6	6	Y	50161	Tubulin beta chain OS=Glossina brevipalpis PE=3 SV=1
2	11643	tr|C7SAW9|C7SAW9_9MUSC	117.75	14	6	6	Y	50136	Tubulin beta chain OS=Anastrepha suspensa PE=3 SV=1
2	4513	tr|A0A0P5E5N2|A0A0P5E5N2_9CRUS	117.75	14	6	6	Y	50179	Tubulin beta chain OS=Daphnia magna GN=APZ42_016801 PE=3 SV=1
2	11644	tr|A0A151X2S9|A0A151X2S9_9HYME	117.75	7	6	6	Y	97182	Tubulin beta-1 chain OS=Trachymyrmex zeteki GN=ALC60_06337 PE=3 SV=1
6	11661	tr|A0A088A5I8|A0A088A5I8_APIME	117.06	13	4	4	Y	66565	Pyruvate kinase OS=Apis mellifera PE=3 SV=1
4	11712	tr|V9IK50|V9IK50_APICE	115.31	24	4	4	Y	35840	Glyceraldehyde-3-phosphate dehydrogenase OS=Apis cerana GN=ACCB10847 PE=2 SV=1
4	11711	tr|A0A088AHC8|A0A088AHC8_APIME	115.31	24	4	4	Y	35883	Glyceraldehyde-3-phosphate dehydrogenase OS=Apis mellifera GN=Gapdh PE=3 SV=1
4	11713	tr|A0A2A3E509|A0A2A3E509_APICC	115.31	22	4	4	Y	39233	Glyceraldehyde-3-phosphate dehydrogenase OS=Apis cerana cerana GN=APICC_00732 PE=4 SV=1
5	11646	tr|V9I8Q3|V9I8Q3_APICE	115.02	23	4	4	Y	28076	2014-3-3 protein zeta OS=Apis cerana GN=ACCB00245.3 PE=2 SV=1
5	11645	tr|G9I551|G9I551_9HYME	115.02	23	4	4	Y	28092	14-3-3 zeta (Fragment) OS=Megachile rotundata PE=3 SV=1
5	11647	tr|G9I553|G9I553_9HYME	115.02	23	4	4	Y	28083	14-3-3 zeta OS=Megachile rotundata PE=3 SV=1
5	11648	tr|G9I552|G9I552_9HYME	115.02	23	4	4	Y	28090	14-3-3 zeta OS=Megachile rotundata PE=3 SV=1
5	11649	tr|A0A088AHG5|A0A088AHG5_APIME	115.02	14	4	4	Y	45145	Uncharacterized protein OS=Apis mellifera PE=3 SV=1
14	11669	tr|A0A088AST9|A0A088AST9_APIME	110.18	10	2	2	N	39789	Enolase OS=Apis mellifera PE=4 SV=1
12	11666	tr|A0A2A3E8V4|A0A2A3E8V4_APICC	109.14	7	2	2	N	53334	Synaptic vesicle membrane protein VAT-1 OS=Apis cerana cerana GN=APICC_08337 PE=4 SV=1
12	11664	tr|V9IAR8|V9IAR8_APICE	109.14	7	2	2	N	51304	Synaptic vesicle membrane protein VAT-1-like OS=Apis cerana GN=ACCB00697.1 PE=2 SV=1
12	11665	tr|A0A088A347|A0A088A347_APIME	109.14	7	2	2	N	51304	Uncharacterized protein OS=Apis mellifera GN=LOC409207 PE=4 SV=1
12	11663	tr|A0A026WY44|A0A026WY44_OOCBI	109.14	9	2	2	N	40240	Synaptic vesicle membrane protein VAT-1-like protein-like protein (Fragment) OS=Ooceraea biroi GN=X777_08174 PE=4 SV=1
9	11657	tr|A0A232ETH5|A0A232ETH5_9HYME	101.64	4	3	3	N	105753	Delta-aminolevulinic acid dehydratase OS=Trichomalopsis sarcophagae GN=TSAR_003676 PE=3 SV=1
9	11678	tr|F5BYH9|F5BYH9_HELAM	101.64	7	3	3	N	73030	Heat shock protein OS=Helicoverpa armigera PE=2 SV=1
9	11679	tr|I4DIU0|I4DIU0_PAPXU	101.64	7	3	3	N	72996	Heat shock protein cognate 3 OS=Papilio xuthus PE=2 SV=1
9	11677	tr|V9IGA1|V9IGA1_APICE	101.64	7	3	3	N	72866	Glucose-regulated protein OS=Apis cerana GN=ACCB02326 PE=2 SV=1
9	11676	tr|A0A1A9WZF3|A0A1A9WZF3_9MUSC	101.64	7	3	3	N	72720	Uncharacterized protein OS=Glossina brevipalpis PE=3 SV=1
9	11675	tr|A0A212FBA7|A0A212FBA7_DANPL	101.64	7	3	3	N	72732	Heat shock cognate 70 protein OS=Danaus plexippus plexippus GN=KGM_208844 PE=3 SV=1
9	11674	tr|A0A194PQY8|A0A194PQY8_PAPXU	101.64	7	3	3	N	72637	Heat shock 70 kDa protein cognate 3 OS=Papilio xuthus GN=RR46_08832 PE=3 SV=1
9	11672	tr|A0A0M9A8F3|A0A0M9A8F3_9HYME	101.64	7	3	3	N	72650	Heat shock 70 kDa protein cognate 3 OS=Melipona quadrifasciata GN=WN51_09203 PE=3 SV=1
9	11673	tr|A0A088ACF4|A0A088ACF4_APIME	101.64	7	3	3	N	72478	Uncharacterized protein OS=Apis mellifera PE=3 SV=1
13	11786	tr|E4W6B4|E4W6B4_PROCL	98.77	9	3	3	Y	55914	ATP synthase subunit beta OS=Procambarus clarkii PE=2 SV=1
13	4519	tr|D8VIP0|D8VIP0_HELME	98.77	14	3	3	Y	37534	ATP synthase subunit beta (Fragment) OS=Heliconius melpomene melpomene PE=4 SV=1
13	4517	tr|G3KAY5|G3KAY5_HELNM	98.77	14	3	3	Y	36677	ATP synthase subunit beta (Fragment) OS=Heliconius numata silvana GN=ATPs PE=4 SV=1
13	4518	tr|G3KAV3|G3KAV3_HELNM	98.77	14	3	3	Y	36677	ATP synthase subunit beta (Fragment) OS=Heliconius numata arcuella GN=ATPs PE=4 SV=1
13	11781	tr|A0A182YSV3|A0A182YSV3_ANOST	98.77	11	3	3	Y	47035	ATP synthase subunit beta OS=Anopheles stephensi PE=3 SV=1
13	11787	tr|E0W6V9|E0W6V9_MARJA	98.77	9	3	3	Y	55854	ATP synthase subunit beta OS=Marsupenaeus japonicus PE=2 SV=1
13	4533	tr|Q1HPT1|Q1HPT1_BOMMO	98.77	9	3	3	Y	54988	ATP synthase subunit beta OS=Bombyx mori GN=Atpsyn-beta PE=2 SV=1
13	11785	tr|V9IJZ2|V9IJZ2_APICE	98.77	9	3	3	Y	55130	ATP synthase subunit beta OS=Apis cerana GN=ACCB10178 PE=2 SV=1
13	4532	tr|I4DIU5|I4DIU5_PAPXU	98.77	10	3	3	Y	54872	ATP synthase subunit beta OS=Papilio xuthus GN=RR46_14819 PE=2 SV=1
13	4531	tr|A0A1B0CLT6|A0A1B0CLT6_LUTLO	98.77	10	3	3	Y	54969	ATP synthase subunit beta OS=Lutzomyia longipalpis PE=3 SV=1
13	11783	tr|A0A0M4F807|A0A0M4F807_DROBS	98.77	10	3	3	Y	54273	ATP synthase subunit beta OS=Drosophila busckii GN=Dbus_chr4g20 PE=3 SV=1
13	11782	tr|A0A182T1X0|A0A182T1X0_9DIPT	98.77	10	3	3	Y	53945	ATP synthase subunit beta OS=Anopheles maculatus PE=3 SV=1
13	4528	tr|E3XEC7|E3XEC7_ANODA	98.77	10	3	3	Y	53768	ATP synthase subunit beta OS=Anopheles darlingi GN=AND_006288 PE=3 SV=1
13	4529	tr|A0A182FTY6|A0A182FTY6_ANOAL	98.77	10	3	3	Y	53768	ATP synthase subunit beta OS=Anopheles albimanus PE=3 SV=1
13	4530	tr|A0A1I8NT76|A0A1I8NT76_STOCA	98.77	10	3	3	Y	54485	ATP synthase subunit beta OS=Stomoxys calcitrans GN=106084826 PE=3 SV=1
13	4740	tr|Q7PZV3|Q7PZV3_ANOGA	92.38	13	2	2	N	23962	AGAP012106-PA (Fragment) OS=Anopheles gambiae GN=1280570 PE=4 SV=4
13	4739	tr|Q7PKD7|Q7PKD7_ANOGA	92.38	13	2	2	N	22698	AGAP012081-PA (Fragment) OS=Anopheles gambiae GN=1280592 PE=4 SV=2
13	4541	tr|A0A023FND3|A0A023FND3_9ACAR	92.38	6	2	2	N	56225	ATP synthase subunit beta (Fragment) OS=Amblyomma cajennense PE=2 SV=1
11	11698	tr|A0A088ACZ3|A0A088ACZ3_APIME	95.47	17	3	3	Y	30482	Uncharacterized protein OS=Apis mellifera GN=porin PE=4 SV=1
11	11699	tr|V9IK96|V9IK96_APICE	95.47	17	3	3	Y	30482	Voltage-dependent anion-selective channel OS=Apis cerana GN=ACCB10957 PE=2 SV=1
7	11680	tr|A0A087ZPQ8|A0A087ZPQ8_APIME	91.89	14	3	3	Y	41713	Fructose-bisphosphate aldolase OS=Apis mellifera PE=3 SV=1
10	11709	O18330|MRJP1_APIME	90.77	6	2	2	N	48886	Major royal jelly protein 1 OS=Apis mellifera GN=MRJP1 PE=1 SV=1
10	11710	tr|C6K481|C6K481_APIME	90.77	6	2	2	N	48886	Major royal jelly protein 1 OS=Apis mellifera PE=2 SV=1
total 218 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
26	50841	tr|A0A1W4WYG0|A0A1W4WYG0_AGRPL	76.10	3	1	1	N	60897	arginine kinase isoform X1 OS=Agrilus planipennis GN=LOC108737292 PE=3 SV=1
26	50840	tr|A0A1B6I0G0|A0A1B6I0G0_9HEMI	76.10	3	1	1	N	58337	Uncharacterized protein OS=Homalodisca liturata GN=g.14479 PE=3 SV=1
26	50839	tr|A0A084W9Z4|A0A084W9Z4_ANOSI	76.10	4	1	1	N	45177	AGAP005627-PB-like protein OS=Anopheles sinensis GN=ZHAS_00015056 PE=3 SV=1
26	50838	tr|Q7PIQ5|Q7PIQ5_ANOGA	76.10	4	1	1	N	43773	AGAP005627-PA OS=Anopheles gambiae GN=1276313 PE=3 SV=3
26	50837	tr|A0A1B6K7L4|A0A1B6K7L4_9HEMI	76.10	4	1	1	N	41972	Uncharacterized protein OS=Homalodisca liturata GN=g.14477 PE=3 SV=1
26	50836	tr|A0A1B6IHK2|A0A1B6IHK2_9HEMI	76.10	4	1	1	N	39981	Uncharacterized protein OS=Homalodisca liturata GN=g.14486 PE=3 SV=1
26	50835	tr|A7UTS9|A7UTS9_ANOGA	76.10	4	1	1	N	39775	AGAP005627-PC OS=Anopheles gambiae GN=1276313 PE=3 SV=1
26	50834	tr|B3GCX2|B3GCX2_9COLE	76.10	6	1	1	N	28108	Arginine kinase (Fragment) OS=Tenomerga cinerea PE=3 SV=1
26	50833	tr|B3GCX8|B3GCX8_9COLE	76.10	6	1	1	N	28141	Arginine kinase (Fragment) OS=Dineutus sublineatus PE=3 SV=1
26	50831	tr|J4H7X4|J4H7X4_9DYTI	76.10	6	1	1	N	27476	Ark (Fragment) OS=Sternopriscus wehnckei GN=arginine kinase PE=3 SV=1
26	50832	tr|J4H166|J4H166_9DYTI	76.10	6	1	1	N	27462	Ark (Fragment) OS=Sternopriscus mundanus GN=arginine kinase PE=3 SV=1
26	50829	tr|B3GCX9|B3GCX9_METCO	76.10	6	1	1	N	27379	Arginine kinase (Fragment) OS=Metrius contractus PE=3 SV=1
26	50830	tr|B3GCY8|B3GCY8_9CARA	76.10	6	1	1	N	27302	Arginine kinase (Fragment) OS=Bembidion inaequale PE=3 SV=1
26	50828	tr|F4YJL0|F4YJL0_9CUCU	76.10	6	1	1	N	27078	Arginine kinase (Fragment) OS=Xyleborus artespinulosus PE=3 SV=1
26	50826	tr|A0A0A0RI03|A0A0A0RI03_9CARA	76.10	6	1	1	N	26714	Arginine kinase (Fragment) OS=Paussus damarinus PE=3 SV=1
26	50827	tr|A0A0A0RPF2|A0A0A0RPF2_9CARA	76.10	6	1	1	N	26772	Arginine kinase (Fragment) OS=Paussus dohrni PE=3 SV=1
26	50823	tr|B3FA28|B3FA28_9CARA	76.10	7	1	1	N	25167	Arginine kinase (Fragment) OS=Bembidion rothfelsi GN=ArgK PE=3 SV=1
26	50824	tr|B3F9Z8|B3F9Z8_9CARA	76.10	7	1	1	N	25167	Arginine kinase (Fragment) OS=Bembidion chalceum GN=ArgK PE=3 SV=1
26	50825	tr|B3F9Y1|B3F9Y1_9CARA	76.10	7	1	1	N	25167	Arginine kinase (Fragment) OS=Bembidion arenobilis GN=ArgK PE=3 SV=1
26	50819	tr|J7EQ35|J7EQ35_9COLE	76.10	7	1	1	N	25234	Arginine kinase (Fragment) OS=Chrysobothris shawnee PE=3 SV=1
26	50820	tr|J7EPA5|J7EPA5_9COLE	76.10	7	1	1	N	25188	Arginine kinase (Fragment) OS=Chrysobothris rugosiceps PE=3 SV=1
26	50821	tr|J7EN85|J7EN85_9COLE	76.10	7	1	1	N	25220	Arginine kinase (Fragment) OS=Chrysobothris femorata PE=3 SV=1
26	50822	tr|J7EQ70|J7EQ70_9COLE	76.10	7	1	1	N	25220	Arginine kinase (Fragment) OS=Chrysobothris wintu PE=3 SV=1
26	50818	tr|F4YJL3|F4YJL3_9CUCU	76.10	7	1	1	N	24965	Arginine kinase (Fragment) OS=Xyleborus aff. impexus AIC-2011 PE=3 SV=1
26	50817	tr|M1XFD9|M1XFD9_9DYTI	76.10	7	1	1	N	24816	Arginine kinase (Fragment) OS=Carabdytes upin GN=ark PE=3 SV=1
26	50816	tr|A0A0A0QTY4|A0A0A0QTY4_IPSTY	76.10	8	1	1	N	22343	Arginine kinase (Fragment) OS=Ips typographus GN=ArgK PE=3 SV=1
26	50813	tr|A0A0U3BYR0|A0A0U3BYR0_9SCAR	76.10	8	1	1	N	21627	Arginine kinase (Fragment) OS=Dynastes hercules hercules GN=argK PE=3 SV=1
26	50814	tr|A0A0U2RDA7|A0A0U2RDA7_9SCAR	76.10	8	1	1	N	21627	Arginine kinase (Fragment) OS=Dynastes hercules paschoali GN=argK PE=3 SV=1
26	50815	tr|A0A0U3CB64|A0A0U3CB64_9SCAR	76.10	8	1	1	N	21627	Arginine kinase (Fragment) OS=Dynastes hercules GN=argK PE=3 SV=1
26	50812	tr|A0A0U3BCD2|A0A0U3BCD2_9SCAR	76.10	8	1	1	N	21555	Arginine kinase (Fragment) OS=Dynastes hercules occidentalis GN=argK PE=3 SV=1
19	11818	tr|A0A067QJP9|A0A067QJP9_ZOONE	62.08	3	1	1	N	66600	Protein ROP OS=Zootermopsis nevadensis GN=L798_02248 PE=3 SV=1
19	11806	tr|A0A1B6GVI9|A0A1B6GVI9_9HEMI	62.08	3	1	1	N	50526	Uncharacterized protein (Fragment) OS=Cuerna arida GN=g.36277 PE=3 SV=1
19	11835	tr|A0A0N0BCK0|A0A0N0BCK0_9HYME	62.08	2	1	1	N	77801	Protein ROP OS=Melipona quadrifasciata GN=WN51_06176 PE=3 SV=1
19	11834	tr|E2AA52|E2AA52_CAMFO	62.08	2	1	1	N	73998	Protein ROP OS=Camponotus floridanus GN=EAG_11820 PE=3 SV=1
19	11833	tr|A0A195DWY9|A0A195DWY9_9HYME	62.08	2	1	1	N	73738	Protein ROP OS=Trachymyrmex cornetzi GN=ALC57_10375 PE=3 SV=1
19	11832	tr|A0A195FYQ4|A0A195FYQ4_9HYME	62.08	2	1	1	N	73246	Protein ROP (Fragment) OS=Trachymyrmex septentrionalis GN=ALC56_00126 PE=3 SV=1
19	11831	tr|F4WGN1|F4WGN1_ACREC	62.08	2	1	1	N	72621	Protein ROP OS=Acromyrmex echinatior GN=G5I_04816 PE=3 SV=1
19	11830	tr|A0A151IBC5|A0A151IBC5_9HYME	62.08	2	1	1	N	72469	Protein ROP OS=Cyphomyrmex costatus GN=ALC62_12408 PE=3 SV=1
19	11829	tr|A0A154PJE5|A0A154PJE5_9HYME	62.08	2	1	1	N	72016	Protein ROP (Fragment) OS=Dufourea novaeangliae GN=WN55_03479 PE=3 SV=1
19	11828	tr|A0A195BXB7|A0A195BXB7_9HYME	62.08	2	1	1	N	72023	Protein ROP OS=Atta colombica GN=ALC53_00225 PE=3 SV=1
19	11827	tr|A0A232FGS2|A0A232FGS2_9HYME	62.08	2	1	1	N	70865	Uncharacterized protein OS=Trichomalopsis sarcophagae GN=TSAR_001702 PE=3 SV=1
19	11826	tr|A0A088ACI1|A0A088ACI1_APIME	62.08	2	1	1	N	70236	Uncharacterized protein OS=Apis mellifera PE=3 SV=1
19	11825	tr|A0A0A9Z3R2|A0A0A9Z3R2_LYGHE	62.08	3	1	1	N	67587	Protein ROP (Fragment) OS=Lygus hesperus GN=Rop_0 PE=3 SV=1
19	11823	tr|A0A1Y1LDV6|A0A1Y1LDV6_PHOPY	62.08	3	1	1	N	67451	Uncharacterized protein OS=Photinus pyralis PE=3 SV=1
19	11824	tr|K7IZP4|K7IZP4_NASVI	62.08	3	1	1	N	67690	Uncharacterized protein OS=Nasonia vitripennis GN=LOC100119538 PE=3 SV=1
19	11822	tr|A0A0J7KU67|A0A0J7KU67_LASNI	62.08	3	1	1	N	67157	Protein rop OS=Lasius niger GN=RF55_6075 PE=3 SV=1
19	11820	tr|A0A069DW98|A0A069DW98_9HEMI	62.08	3	1	1	N	66762	Putative vesicle trafficking protein sec1 OS=Panstrongylus megistus PE=2 SV=1

total 218 proteins

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
19	11819	tr|A0A1B6DP73|A0A1B6DP73_9HEMI	62.08	3	1	1	N	66957	Uncharacterized protein OS=Clastoptera arizonana GN=g.37966 PE=3 SV=1
19	11821	tr|A0A0P4VMN7|A0A0P4VMN7_9HEMI	62.08	3	1	1	N	66849	Putative vesicle trafficking protein sec1 OS=Rhodnius neglectus PE=2 SV=1
19	11817	tr|E0VWU1|E0VWU1_PEDHC	62.08	3	1	1	N	66833	Protein ROP, putative OS=Pediculus humanus subsp. corporis GN=8235768 PE=3 SV=1
19	11814	tr|R4WS90|R4WS90_RIPPE	62.08	3	1	1	N	66745	Syntaxin binding protein-1,2,3 OS=Riptortus pedestris PE=2 SV=1
19	11815	tr|A0A158NNZ9|A0A158NNZ9_ATTCE	62.08	3	1	1	N	66826	Uncharacterized protein OS=Atta cephalotes GN=105622449 PE=3 SV=1
19	11816	tr|A0A151X8A1|A0A151X8A1_9HYME	62.08	3	1	1	N	66806	Protein ROP OS=Trachymyrmex zeteki GN=ALC60_04448 PE=3 SV=1
19	11813	tr|A0A0C9Q2F2|A0A0C9Q2F2_9HYME	62.08	3	1	1	N	66218	Rop_0 protein (Fragment) OS=Fopius arisanus GN=Rop_1 PE=3 SV=1
19	11812	tr|T1IAP1|T1IAP1_RHOPR	62.08	3	1	1	N	66519	Uncharacterized protein (Fragment) OS=Rhodnius prolixus PE=3 SV=1
19	11811	tr|A0A0L7QPT2|A0A0L7QPT2_9HYME	62.08	3	1	1	N	65885	Protein ROP (Fragment) OS=Habropoda laboriosa GN=WH47_07849 PE=3 SV=1
19	11810	tr|V9IAQ1|V9IAQ1_APICE	62.08	3	1	1	N	65423	Syntaxin-binding protein 1 OS=Apis cerana GN=ACCB00715.1 PE=2 SV=1
19	11809	tr|V9ID17|V9ID17_APICE	62.08	3	1	1	N	65502	Syntaxin-binding protein 1 OS=Apis cerana GN=ACCB00715.2 PE=2 SV=1
19	11808	tr|E2B6A3|E2B6A3_HARSA	62.08	3	1	1	N	65634	Protein ROP OS=Harpegnathos saltator GN=EAI_13038 PE=3 SV=1
19	11807	tr|A0A0C9RMG4|A0A0C9RMG4_9HYME	62.08	3	1	1	N	64355	Rop_2 protein (Fragment) OS=Fopius arisanus GN=Rop_2 PE=3 SV=1
8	11771	tr|A0A0A0VC07|A0A0A0VC07_9ARAC	60.72	7	1	1	N	21477	ATP/ADP translocase OS=Scytodes thoracica PE=2 SV=1
8	11772	tr|A0A0P6CE35|A0A0P6CE35_9CRUS	60.72	4	1	1	N	32931	ADP/ATP translocase OS=Daphnia magna PE=3 SV=1
8	11773	tr|A0A1W7R9C9|A0A1W7R9C9_9SCOR	60.72	4	1	1	N	33220	ADP/ATP translocase 3 OS=Hadrurus spadix PE=3 SV=1
8	11774	tr|V9IK47|V9IK47_APICE	60.72	4	1	1	N	33013	ADP,ATP carrier protein 2 OS=Apis cerana GN=ACCB10355 PE=2 SV=1
8	11776	tr|M9NYU2|M9NYU2_APICC	60.72	4	1	1	N	32983	Adenine nucleotide translocase OS=Apis cerana cerana GN=ANT PE=2 SV=1
8	11777	tr|A0A087U5M6|A0A087U5M6_9ARAC	60.72	4	1	1	N	33367	ADP/ATP translocase 1 (Fragment) OS=Stegodyphus mimosarum GN=X975_20222 PE=3 SV=1
8	11778	tr|Q6VQ13|Q6VQ13_APIME	60.72	4	1	1	N	32986	ADP/ATP translocase OS=Apis mellifera GN=Ant PE=2 SV=1
8	11775	tr|A0A2A3ELD5|A0A2A3ELD5_APICC	60.72	4	1	1	N	33013	ADP,ATP carrier protein OS=Apis cerana cerana GN=APICC_04827 PE=4 SV=1
16	11800	tr|A0A0J7L3Z2|A0A0J7L3Z2_LASNI	59.67	11	1	1	N	15503	Myelin p2 OS=Lasius niger GN=RF55_2486 PE=3 SV=1
16	11798	tr|A0A2A3ERN5|A0A2A3ERN5_APICC	59.67	11	1	1	N	15194	Fatty acid-binding protein, muscle OS=Apis cerana cerana GN=APICC_00057 PE=4 SV=1
16	11799	tr|A0A088AE74|A0A088AE74_APIME	59.67	11	1	1	N	15223	Uncharacterized protein OS=Apis mellifera GN=Fabp PE=3 SV=1
16	11794	tr|Q76LA4|Q76LA4_APIME	59.67	11	1	1	N	15035	Fatty acid binding protein OS=Apis mellifera GN=FABP PE=2 SV=1
16	11795	tr|A0A023EFS1|A0A023EFS1_AEDAL	59.67	11	1	1	N	14795	Putative fatty acid-binding protein fabp OS=Aedes albopictus GN=109402823 PE=2 SV=1
16	11796	tr|A0A1L8DZ33|A0A1L8DZ33_9DIPT	59.67	11	1	1	N	14879	Putative fatty acid-binding protein fabp OS=Nyssomyia neivai PE=3 SV=1
16	11797	tr|V9IIS4|V9IIS4_APICE	59.67	11	1	1	N	15007	Fatty acid binding protein OS=Apis cerana GN=ACCB10883 PE=2 SV=1
16	11791	tr|Q177Y4|Q177Y4_AEDAE	59.67	11	1	1	N	14803	AAEL005997-PA OS=Aedes aegypti GN=AAEL005997 PE=3 SV=1
16	11792	tr|T1E383|T1E383_9DIPT	59.67	11	1	1	N	14770	Putative fatty acid bindin protein OS=Psorophora albipes PE=2 SV=1
16	11793	tr|A0A1B0EX54|A0A1B0EX54_LUTLO	59.67	11	1	1	N	14909	Uncharacterized protein OS=Lutzomyia longipalpis PE=3 SV=1
27	11916	tr|A0A1B6MNR0|A0A1B6MNR0_9HEMI	56.39	9	1	1	N	18875	Uncharacterized protein (Fragment) OS=Graphocephala atropunctata GN=g.39446 PE=4 SV=1
27	11915	tr|A0A0K8TZW2|A0A0K8TZW2_BACLA	56.39	14	1	1	N	12050	Phosphatidylinositol transfer protein beta isoform OS=Bactrocera latifrons GN=Pitpnb_3 PE=4 SV=1
27	11944	tr|A0A1A9WJA5|A0A1A9WJA5_9MUSC	56.39	5	1	1	N	35003	Uncharacterized protein OS=Glossina brevipalpis PE=4 SV=1
27	11943	tr|A0A1B0G7Y9|A0A1B0G7Y9_GLOMM	56.39	5	1	1	N	34467	Uncharacterized protein OS=Glossina morsitans morsitans PE=4 SV=1
27	11942	tr|A0A067R8Y0|A0A067R8Y0_ZOONE	56.39	5	1	1	N	34477	Phosphatidylinositol transfer protein alpha isoform OS=Zootermopsis nevadensis GN=L798_05574 PE=4 SV=1
27	11941	tr|A0A0N7Z9V5|A0A0N7Z9V5_9EUCA	56.39	5	1	1	N	34580	Uncharacterized protein OS=Scylla olivacea PE=4 SV=1
27	11939	tr|L7M5S1|L7M5S1_9ACAR	56.39	5	1	1	N	32599	Putative phosphatidylinositol transfer protein OS=Rhipicephalus pulchellus PE=2 SV=1
27	11940	tr|A0A224YXR0|A0A224YXR0_9ACAR	56.39	5	1	1	N	32599	Phosphatidylinositol transfer protein OS=Rhipicephalus zambeziensis PE=4 SV=1
27	11938	tr|L7M5B6|L7M5B6_9ACAR	56.39	5	1	1	N	32562	Putative phosphatidylinositol transfer protein OS=Rhipicephalus pulchellus PE=2 SV=1
27	11937	tr|A0A0L7QKW7|A0A0L7QKW7_9HYME	56.39	5	1	1	N	32076	Phosphatidylinositol transfer protein alpha isoform OS=Habropoda laboriosa GN=WH47_11448 PE=4 SV=1
27	11935	tr|W8BHP2|W8BHP2_CERCA	56.39	5	1	1	N	31555	Phosphatidylinositol transfer protein beta isoform OS=Ceratitis capitata GN=PIPNB PE=2 SV=1
27	11936	tr|A0A034W637|A0A034W637_BACDO	56.39	5	1	1	N	31632	Phosphatidylinositol transfer protein alpha isoform OS=Bactrocera dorsalis GN=PIPNA PE=4 SV=1
27	11931	tr|A0A224XUC6|A0A224XUC6_9HEMI	56.39	6	1	1	N	31728	Putative phosphatidylinositol transfer protein OS=Panstrongylus lignarius PE=4 SV=1
27	11932	tr|T1PCP0|T1PCP0_MUSDO	56.39	6	1	1	N	31296	Phosphatidylinositol transfer protein OS=Musca domestica GN=101889625 PE=2 SV=1
27	11933	tr|D3TN38|D3TN38_GLOMM	56.39	6	1	1	N	31511	Phosphatidylinositol transfer protein OS=Glossina morsitans morsitans PE=2 SV=1
27	11934	tr|R4G5F6|R4G5F6_RHOPR	56.39	6	1	1	N	31762	Putative phosphatidylinositol transfer protein OS=Rhodnius prolixus PE=2 SV=1
27	11930	tr|A0A1I8MLN0|A0A1I8MLN0_MUSDO	56.39	6	1	1	N	31362	Uncharacterized protein OS=Musca domestica GN=101889625 PE=4 SV=1
27	11927	tr|A0A088AUP1|A0A088AUP1_APIME	56.39	6	1	1	N	31549	Uncharacterized protein OS=Apis mellifera GN=vib PE=4 SV=1
total 218 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
27	11928	tr|A0A1B6IDS7|A0A1B6IDS7_9HEMI	56.39	6	1	1	N	31376	Uncharacterized protein OS=Homalodisca liturata GN=g.41929 PE=4 SV=1
27	11924	tr|A0A0J7L2C9|A0A0J7L2C9_LASNI	56.39	6	1	1	N	31356	Phosphatidylinositol transfer protein alpha isoform OS=Lasius niger GN=RF55_2913 PE=4 SV=1
27	11925	tr|A0A0A9YWM3|A0A0A9YWM3_LYGHE	56.39	6	1	1	N	31362	Phosphatidylinositol transfer protein alpha isoform OS=Lygus hesperus GN=PITPNA_1 PE=4 SV=1
27	11926	tr|A0A1B6FGX0|A0A1B6FGX0_9HEMI	56.39	6	1	1	N	31436	Uncharacterized protein OS=Cuerna arida GN=g.40960 PE=4 SV=1
27	11929	tr|V9IGA9|V9IGA9_APICE	56.39	6	1	1	N	31549	Phosphatidylinositol transfer protein alpha isoform OS=Apis cerana GN=ACCB04141 PE=2 SV=1
27	11922	tr|D3PIG7|D3PIG7_LEPSM	56.39	6	1	1	N	31382	Phosphatidylinositol transfer protein beta isoform OS=Lepeophtheirus salmonis GN=PIPNB PE=2 SV=1
27	11921	tr|A0A0P4VQ48|A0A0P4VQ48_9EUCA	56.39	6	1	1	N	31557	Uncharacterized protein OS=Scylla olivacea PE=4 SV=1
27	11923	tr|A0A224Z5P9|A0A224Z5P9_9ACAR	56.39	6	1	1	N	31276	Phosphatidylinositol transfer protein OS=Rhipicephalus zambeziensis PE=4 SV=1
27	11920	tr|C1C1G0|C1C1G0_CALCM	56.39	6	1	1	N	31212	Phosphatidylinositol transfer protein alpha isoform OS=Caligus clemensi GN=PIPNA PE=2 SV=1
27	11919	tr|A0A1I8PUA1|A0A1I8PUA1_STOCA	56.39	6	1	1	N	30551	Uncharacterized protein OS=Stomoxys calcitrans GN=106084712 PE=4 SV=1
27	11918	tr|A0A232FH25|A0A232FH25_9HYME	56.39	6	1	1	N	30760	Uncharacterized protein (Fragment) OS=Trichomalopsis sarcophagae GN=TSAR_017055 PE=4 SV=1
27	11917	tr|A0A0K8VNQ1|A0A0K8VNQ1_BACLA	56.39	7	1	1	N	26186	Phosphatidylinositol transfer protein beta isoform OS=Bactrocera latifrons GN=Pitpnb_1 PE=4 SV=1
20	50799	tr|I1ZEB5|I1ZEB5_9ACAR	51.22	3	1	1	N	62273	Heat shock protein cognate 5 (Fragment) OS=Trochilodectes sp. AD1236 GN=Hsc70-5 PE=3 SV=1
28	11998	tr|D9IFR6|D9IFR6_9DIPT	48.68	2	1	1	N	69844	Heat shock protein 70-p1 OS=Oxycera pardalina PE=3 SV=1
15	12710	tr|A0A026W3N3|A0A026W3N3_OOCBI	46.11	1	2	2	N	278590	Spectrin alpha chain OS=Ooceraea biroi GN=X777_12199 PE=4 SV=1
29	50843	tr|A0A1B6ENV6|A0A1B6ENV6_9HEMI	44.82	3	1	1	N	43714	Uncharacterized protein OS=Cuerna arida GN=g.43130 PE=4 SV=1
18	11865	tr|A0A1C9FPZ6|A0A1C9FPZ6_9HYME	43.82	6	1	1	N	23638	Triosephosphate isomerase (Fragment) OS=Pristiphora staudingeri PE=3 SV=1
18	11868	tr|A0A1C9FPZ7|A0A1C9FPZ7_9HYME	43.82	6	1	1	N	23652	Triosephosphate isomerase (Fragment) OS=Pristiphora ruficornis PE=3 SV=1
18	11869	tr|A0A289YXQ1|A0A289YXQ1_9HYME	43.82	6	1	1	N	23680	Triosephosphate isomerase (Fragment) OS=Pristiphora brevis PE=4 SV=1
18	11863	tr|A0A1C9FQ23|A0A1C9FQ23_9HYME	43.82	6	1	1	N	23682	Triosephosphate isomerase (Fragment) OS=Pristiphora abietina PE=3 SV=1
18	11864	tr|A0A1C9FPY5|A0A1C9FPY5_9HYME	43.82	6	1	1	N	23638	Triosephosphate isomerase (Fragment) OS=Pristiphora albitibia PE=3 SV=1
18	11866	tr|A0A1C9FPY7|A0A1C9FPY7_9HYME	43.82	6	1	1	N	23638	Triosephosphate isomerase (Fragment) OS=Pristiphora luteipes PE=3 SV=1
18	11867	tr|A0A1C9FQ28|A0A1C9FQ28_9HYME	43.82	6	1	1	N	23724	Triosephosphate isomerase (Fragment) OS=Pristiphora mollis PE=3 SV=1
18	11871	tr|A0A289Z694|A0A289Z694_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora conjugata PE=4 SV=1
18	11873	tr|A0A289ZSG2|A0A289ZSG2_9HYME	43.82	6	1	1	N	24211	Triosephosphate isomerase (Fragment) OS=Pristiphora appendiculata PE=4 SV=1
18	11875	tr|A0A289Z5U6|A0A289Z5U6_9HYME	43.82	6	1	1	N	24255	Triosephosphate isomerase (Fragment) OS=Pristiphora staudingeri PE=4 SV=1
18	11876	tr|A0A289ZUV1|A0A289ZUV1_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora condei PE=4 SV=1
18	11882	tr|A0A289YU85|A0A289YU85_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora carinata PE=4 SV=1
18	11883	tr|A0A289ZSB5|A0A289ZSB5_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora angulata PE=4 SV=1
18	11885	tr|A0A289YUJ3|A0A289YUJ3_9HYME	43.82	6	1	1	N	24281	Triosephosphate isomerase (Fragment) OS=Cladius compressicornis PE=4 SV=1
18	11887	tr|A0A289Z121|A0A289Z121_9HYME	43.82	6	1	1	N	24255	Triosephosphate isomerase (Fragment) OS=Pristiphora caraganae PE=4 SV=1
18	11888	tr|A0A289ZGX1|A0A289ZGX1_9HYME	43.82	6	1	1	N	24255	Triosephosphate isomerase (Fragment) OS=Pristiphora subopaca PE=4 SV=1
18	11870	tr|A0A289ZUT5|A0A289ZUT5_9HYME	43.82	6	1	1	N	24327	Triosephosphate isomerase (Fragment) OS=Pristiphora punctifrons PE=4 SV=1
18	11872	tr|A0A289YXV8|A0A289YXV8_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora compressa PE=4 SV=1
18	11874	tr|A0A289ZSB4|A0A289ZSB4_9HYME	43.82	6	1	1	N	24255	Triosephosphate isomerase (Fragment) OS=Pristiphora bifida PE=4 SV=1
18	11877	tr|A0A289ZSL8|A0A289ZSL8_9HYME	43.82	6	1	1	N	24299	Triosephosphate isomerase (Fragment) OS=Pristiphora testacea PE=4 SV=1
18	11878	tr|A0A289ZSJ3|A0A289ZSJ3_9HYME	43.82	6	1	1	N	24227	Triosephosphate isomerase (Fragment) OS=Pristiphora amphibola PE=4 SV=1
18	11879	tr|A0A289YU32|A0A289YU32_9HYME	43.82	6	1	1	N	24269	Triosephosphate isomerase (Fragment) OS=Pristiphora melanocarpa PE=4 SV=1
18	11880	tr|A0A289ZS39|A0A289ZS39_9HYME	43.82	6	1	1	N	24297	Triosephosphate isomerase (Fragment) OS=Pristiphora rufipes PE=4 SV=1
18	11881	tr|A0A289YFQ4|A0A289YFQ4_9HYME	43.82	6	1	1	N	24239	Triosephosphate isomerase (Fragment) OS=Pristiphora dedeara PE=4 SV=1
18	11884	tr|A0A289ZGZ1|A0A289ZGZ1_9HYME	43.82	6	1	1	N	24269	Triosephosphate isomerase (Fragment) OS=Pristiphora ruficornis PE=4 SV=1
18	11886	tr|A0A289YU53|A0A289YU53_9HYME	43.82	6	1	1	N	24297	Triosephosphate isomerase (Fragment) OS=Pristiphora cincta PE=4 SV=1
18	11891	tr|V9IKD3|V9IKD3_APICE	43.82	5	1	1	N	26885	Triosephosphate isomerase OS=Apis cerana GN=ACCB10042 PE=2 SV=1
18	11892	tr|A0A1L1ZLV2|A0A1L1ZLV2_APICC	43.82	5	1	1	N	26885	Triosephosphate isomerase OS=Apis cerana cerana GN=Tpi PE=2 SV=1
18	11889	tr|A0A0J7KLG9|A0A0J7KLG9_LASNI	43.82	5	1	1	N	26774	Triosephosphate isomerase OS=Lasius niger GN=RF55_8905 PE=3 SV=1
18	11890	tr|A4ZXC4|A4ZXC4_APIME	43.82	5	1	1	N	26899	Triosephosphate isomerase OS=Apis mellifera GN=Tpi PE=2 SV=1
total 218 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
25	53070	tr|A0A0L7R8Y4|A0A0L7R8Y4_9HYME	37.12	7	1	1	Y	33611	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Fragment) OS=Habropoda laboriosa GN=WH47_00158 PE=4 SV=1
25	53076	tr|A0A088AR98|A0A088AR98_APIME	37.12	7	1	1	Y	37370	Uncharacterized protein OS=Apis mellifera GN=LOC410497 PE=4 SV=1
25	53077	tr|V9IJ30|V9IJ30_APICE	37.12	7	1	1	Y	37370	Guanine nucleotide-binding protein subunit beta OS=Apis cerana GN=ACCB10939 PE=2 SV=1
30	12021	tr|B4KM55|B4KM55_DROMO	26.91	1	1	1	N	105928	Uncharacterized protein OS=Drosophila mojavensis GN=Dmoj\GI19404 PE=4 SV=2
38	51134	tr|A0A151ILK1|A0A151ILK1_9HYME	26.89	0	1	1	N	585668	Midasin OS=Cyphomyrmex costatus GN=ALC62_03318 PE=3 SV=1
21	50875	tr|A0A1B6HTR0|A0A1B6HTR0_9HEMI	26.62	2	1	1	N	43480	Uncharacterized protein (Fragment) OS=Homalodisca liturata GN=g.4415 PE=4 SV=1
31	51019	tr|A0A212F2D3|A0A212F2D3_DANPL	26.37	4	1	1	N	18076	Pheromone-binding protein OS=Danaus plexippus plexippus GN=KGM_210513 PE=4 SV=1
31	51025	tr|A0A0L7KX54|A0A0L7KX54_9NEOP	26.37	2	1	1	N	45697	Uncharacterized protein OS=Operophtera brumata GN=OBRU01_19449 PE=4 SV=1
23	51098	tr|A0NE24|A0NE24_ANOGA	24.14	0	1	1	N	430596	AGAP008807-PA (Fragment) OS=Anopheles gambiae GN=AgaP_AGAP008807 PE=4 SV=2
32	51020	tr|A0A1J1IXA2|A0A1J1IXA2_9DIPT	22.83	5	1	1	N	26709	CLUMA_CG016452, isoform A OS=Clunio marinus GN=CLUMA_CG016452 PE=4 SV=1
36	12067	tr|A0A067QWN1|A0A067QWN1_ZOONE	20.97	4	1	1	N	21591	Diuretic hormone OS=Zootermopsis nevadensis GN=L798_11499 PE=4 SV=1
35	12003	tr|A0A182XX22|A0A182XX22_ANOST	20.96	1	1	1	N	111336	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
35	12004	tr|A0A1A9U6X3|A0A1A9U6X3_ANOST	20.96	1	1	1	N	149137	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
total 218 proteins									

tr|A0A087ZTA6|A0A087ZTA6_APIME

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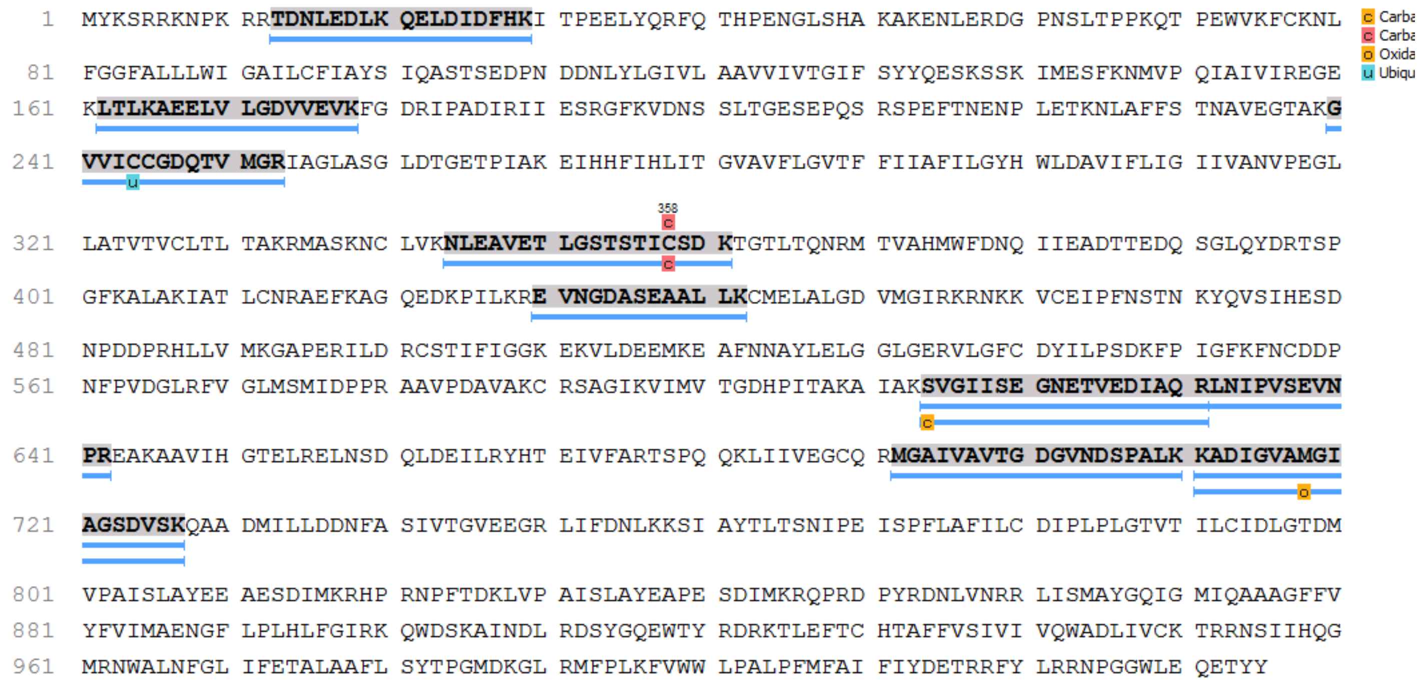
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MYKSRRKNPK RR**TDNLEDLK QELDIDFHK**I TPEELYQRFQ THPENGLSHA KAKENLERDG PNSLTPPKQT PEWVKFCKNL

81 FGGFALLLWI GAILCFIAYS IQASTSEDPN DDNLYLGIVL AAVVIVTGIF SYYQESKSSK IMESFKNMVP QIAIVIREGE

161 K**LTLKAEELV LGDVVEVK**FG DRIPADIRII ESRGFKVDNS SLTGESEPQS RSPEFTNENP LETKNLAFFS TNAVEGTAK**G**

241 **VVICCGDQTV MGR**IAGLASG LDTGETPIAK EIHHFIHLIT GVAVFLGVTF FIIAFILGYH WLDAVIFLIG IIVANVPEGL

321 LATVTVCLTL TAKRMASKNC LVK**NLEAVET LGSTSTICSD K**TGTLTQNRM TVAHMWFDNQ IIEADTTEDQ SGLQYDRTSP

401 GFKALAKIAT LCNRAEFKAG QEDKPILKR**E VNGDASEAAL LK**CMELALGD VMGIRKRNKK VCEIPFNSTN KYQVSIHESD

481 NPDDPRHLLV MKGAPERILD RCSTIFIGGK EKVLDEEMKE AFNNAYLELG GLGERVLGFC DYILPSDKFP IGFKFNCDDP

561 NFPVDGLRFV GLMSMIDPPR AAVPDAVAKC RSAGIKVIMV TGDHPITAKA IAK**SVGIISE GNETVEDIAQ RLNIPVSEVN**

641 **PR**EAKAAVIH GTELRELNSD QLDEILRYHT EIVFARTSPQ QKLIIVEGCQ R**MGAIVAVTG DGVNDSPALK KADIGVAMGI**

721 **AGSDVSK**QAA DMILLDDNFA SIVTGVEEGR LIFDNLKKSI AYTLTSNIPE ISPFLAFILC DIPLPLGTVT ILCIDLGTDM

801 VPAISLAYEE AESDIMKRHP RNPFTDKLVP AISLAYEAPE SDIMKRQPRD PYRDNLVNRR LISMAYGQIG MIQAAAGFFV

881 YFVIMAENGF LPLHLFGIRK QWDSKAINDL RDSYGQEWTY RDRKTLEFTC HTAFFVSIVI VQWADLIVCK TRRNSIIHQG

961 MRNWALNFGL IFETALAAFL SYTPGMDKGL RMFPLKFVWW LPALPFMFAI FIYDETRRFY LRRNPGGWLE QETYY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KADIGVAMGIAGSDVSK.Q	Y	83.33	1617.8396	-15.4	809.9146	2	31.50	2414	1	711	727	
K.LTLKAEELVLGDVVEVK.F	Y	79.02	1854.0713	661.7	928.6564	2	37.32	3067	2	162	178	
K.KADIGVAM(+15.99)GIAGSDVSK.Q	Y	78.72	1633.8345	47.7	817.9635	2	31.62	2428	1	711	727	Oxidation (M)
R.MGAIVAVTGDGVNDSPALK.K	Y	77.71	1813.9243	-48.5	907.9255	2	33.41	2628	1	692	710	
K.SVGIISEGNETVEDIAQR.L	Y	73.56	1915.9486	525.9	959.4854	2	34.39	2738	2	614	631	
R.TDNLEDLKQELDIDFHK.I	Y	54.10	2072.0061	7.8	1037.0184	2	36.08	2928	1	13	29	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	Y	41.97	1923.9095	117.0	642.3855	3	33.20	2604	1	344	361	Carbamidomethylation
K.S(+43.01)VGIISEGNETVEDIAQR.L	Y	41.36	1958.9545	561.7	981.0347	2	36.91	3020	1	614	631	Carbamylation
K.GVVIC(+114.04)CGDQTVMGR.I	Y	33.79	1550.7003	-72.9	776.3009	2	30.63	2321	1	240	253	Ubiquitin
R.EVNGDASEAALLK.C	Y	31.11	1315.6619	856.3	659.4015	2	30.12	2268	1	430	442	
R.LNIPVSEVNPR.E	Y	18.31	1236.6826	-237.8	619.2015	2	31.77	2444	1	632	642	
total 11 peptides												

tr|V9I6A9|V9I6A9_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

c Carba
c Carba
o Oxida
u Ubiqu

1 MASKGKLATE SRRKNPKRR**T DNLEDLKQEL DIDFHK**ITPE ELYQRFQTHP ENGLSHAKAK ENLERDGPNS LTPPKQTPEW
81 VKFCKNLFGG FALLLWIGAI LCFIAYSIQA STSEDPNDDN LYLGIVLAAV VIVTGIFSYY QESKSSKIME SFKNMVPQIA
161 IVIREGEK**LT LKAEELVLGD VVEVK**FGDRI PADIRIIESR GFKVDNSSLT GESEPQSRSP EFTNENPLET KNLAFFSTNA
241 VEGTAK**GVVI CCGDQTVMGR** IAGLASGLDT GETPIAKEIH HFIHLITGVA VFLGVTFFII AFILGYHWLD AVIFLIGIIV
365
321 ANVPEGLLAT VTVCLTLTAK RMASKNCLVK **NLEAVETLGS TSTICSDK**TG TLTQNRMTVA HMWFDNQIIE ADTTEDQSGL
401 QYDRTSPGFK ALAKIATLCN RAEFKAGQED KPILKR**EVNG DASEAALLK**C MELALGDVMG IRKRNKKVCE IPFNSTNKYQ
481 VSIHESDNPD DPRHLLVMKG APERILDRCS TIFIGGKEKV LDEEMKEAFN NAYLELGGLG ERVLGFCDYI LPSDKFPIGF
561 KFNCDDPNFP VDGLRFVGLM SMIDPPRAAV PDAVAKCRSA GIKVIMVTGD HPITAKAIAK **SVGIISEGNE TVEDIAQRLN**
641 **IPVSEVNPR**E AKAAVIHGTE LRELNSDQLD EILRYHTEIV FARTSPQQKL IIVEGCQR**MG AIVAVTGDGV NDSPALKKAD**
721 **IGVAMGIAGS DVSK**QAADMI LLDDNFASIV TGVEEGRLIF DNLKKSIAYT LTSNIPEISP FLAFILCDIP LPLGTVTILC
801 IDLGTDMVPA ISLAYEEAES DIMKRHPRNP FTDKLVNERL ISMAYGQIGM IQAAAGFFVY FVIMAENGFL PLHLFGIRKQ
881 WDSKAINDLR DSYGQEWTYR DRKTLEFTCH TAFFVSIVIV QWADLIVCKT RRNSIIHQGM RNWALNFGLI FETALAAFLS
961 YTPGMDKGLR MFPLKFVWWL PALPFMFAIF IYDETRRFYL RRNPGGWLEQ ETYY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KADIGVAMGIAGSDVSK.Q	Y	83.33	1617.8396	-15.4	809.9146	2	31.50	2414	1	718	734	
K.LTLKAEELVLGDVVEVK.F	Y	79.02	1854.0713	661.7	928.6564	2	37.32	3067	2	169	185	
K.KADIGVAM(+15.99)GIAGSDVSK.Q	Y	78.72	1633.8345	47.7	817.9635	2	31.62	2428	1	718	734	Oxidation (M)
R.MGAIVAVTGDGVNDSPALK.K	Y	77.71	1813.9243	-48.5	907.9255	2	33.41	2628	1	699	717	
K.SVGIISEGNETVEDIAQR.L	Y	73.56	1915.9486	525.9	959.4854	2	34.39	2738	2	621	638	
R.TDNLEDLKQELDIDFHK.I	Y	54.10	2072.0061	7.8	1037.0184	2	36.08	2928	1	20	36	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	Y	41.97	1923.9095	117.0	642.3855	3	33.20	2604	1	351	368	Carbamidomethylation
K.S(+43.01)VGIISEGNETVEDIAQR.L	Y	41.36	1958.9545	561.7	981.0347	2	36.91	3020	1	621	638	Carbamylation
K.GVVIC(+114.04)CGDQTVMGR.I	Y	33.79	1550.7003	-72.9	776.3009	2	30.63	2321	1	247	260	Ubiquitin
R.EVNGDASEAALLK.C	Y	31.11	1315.6619	856.3	659.4015	2	30.12	2268	1	437	449	
R.LNIPVSEVNPR.E	Y	18.31	1236.6826	-237.8	619.2015	2	31.77	2444	1	639	649	
total 11 peptides												

tr|V9I6B8|V9I6B8_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

c Carba
c Carba
o Oxida
u Ubiqu

1 MASKGKLATE SRRKNPKRR**T DNLEDLKQEL DIDFHK**ITPE ELYQRFQTHP ENGLSHAKAK ENLERDGPNS LTPPKQTPEW
81 VKFCKNLFGG FALLLWIGAI LCFIAYSIQA STSEDPNDDN LYLGIVLAAV VIVTGIFSYY QESKSSKIME SFKNMVPQIA
161 IVIREGEK**LT LKAEELVLGD VVEVK**FGDRI PADIRIIESR GFKVDNSSLT GESEPQSRSP EFTNENPLET KNLAFFSTNA
241 VEGTAK**GVVI CCGDQTVMGR** IAGLASGLDT GETPIAKEIH HFIHLITGVA VFLGVTFFII AFILGYHWLD AVIFLIGIIV
365
321 ANVPEGLLAT VTVCLTLTAK RMASKNCLVK **NLEAVETLGS TSTICSDK**TG TLTQNRMTVA HMWFDNQIIE ADTTEDQSGL
401 QYDRTSPGFK ALAKIATLCN RAEFKAGQED KPILKR**EVNG DASEAALLK**C MELALGDVMG IRKRNKKVCE IPFNSTNKYQ
481 VSIHESDNPD DPRHLLVMKG APERILDRCS TIFIGGKEKV LDEEMKEAFN NAYLELGGLG ERVLGFCDYI LPSDKFPIGF
561 KFNCDDPNFP VDGLRFVGLM SMIDPPRAAV PDAVAKCRSA GIKVIMVTGD HPITAKAIAK **SVGIISEGNE TVEDIAQRLN**
641 **IPVSEVNPR**E AKAAVIHGTE LRELNSDQLD EILRYHTEIV FARTSPQQKL IIVEGCQR**MG AIVAVTGDGV NDSPALKKAD**
721 **IGVAMGIAGS DVSK**QAADMI LLDDNFASIV TGVEEGRLIF DNLKKSIAYT LTSNIPEISP FLAFILCDIP LPLGTVTILC
801 IDLGTDMVPA ISLAYEAPES DIMKRQPRDP YRDNLVNRRL ISMAYGQIGM IQAAAGFFVY FVIMAENGFL PLHLFGIRKQ
881 WDSKAINDLR DSYGQEWTYR DRKTLEFTCH TAFFVSIVIV QWADLIVCKT RRNSIIHQGM RNWALNFGLI FETALAAFLS
961 YTPGMDKGLR MFPLKFVWWL PALPFMFAIF IYDETRRFYL RRNPGGWLEQ ETYY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KADIGVAMGIAGSDVSK.Q	Y	83.33	1617.8396	-15.4	809.9146	2	31.50	2414	1	718	734	
K.LTLKAEELVLGDVVEVK.F	Y	79.02	1854.0713	661.7	928.6564	2	37.32	3067	2	169	185	
K.KADIGVAM(+15.99)GIAGSDVSK.Q	Y	78.72	1633.8345	47.7	817.9635	2	31.62	2428	1	718	734	Oxidation (M)
total 11 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.MGAIVAVTGDGVNDSPALK.K	Y	77.71	1813.9243	-48.5	907.9255	2	33.41	2628	1	699	717	
K.SVGIISEGNETVEDIAQR.L	Y	73.56	1915.9486	525.9	959.4854	2	34.39	2738	2	621	638	
R.TDNLEDLKQELDIDFHK.I	Y	54.10	2072.0061	7.8	1037.0184	2	36.08	2928	1	20	36	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	Y	41.97	1923.9095	117.0	642.3855	3	33.20	2604	1	351	368	Carbamidomethylation
K.S(+43.01)VGIISEGNETVEDIAQR.L	Y	41.36	1958.9545	561.7	981.0347	2	36.91	3020	1	621	638	Carbamylation
K.GVVIC(+114.04)CGDQTVMGR.I	Y	33.79	1550.7003	-72.9	776.3009	2	30.63	2321	1	247	260	Ubiquitin
R.EVNGDASEAALLK.C	Y	31.11	1315.6619	856.3	659.4015	2	30.12	2268	1	437	449	
R.LNIPVSEVNPR.E	Y	18.31	1236.6826	-237.8	619.2015	2	31.77	2444	1	639	649	
total 11 peptides												

tr|V9I7I5|V9I7I5_APICE

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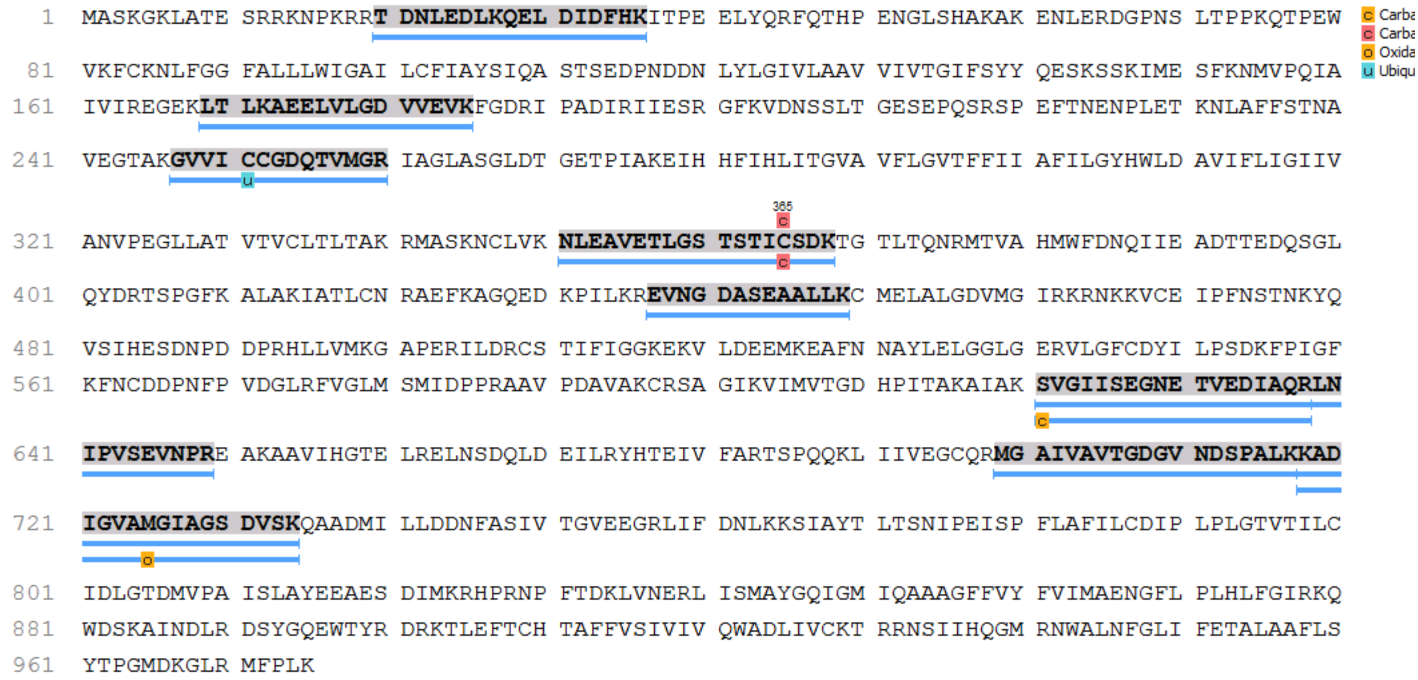
| Protein Coverage | Supporting Peptides |

Protein Coverage:



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81 VKFCKNLFGG FALLLWIGAI LCFIAYSIQA STSEDPNDDN LYLGIVLAAV VIVTGIFSYY QESKSSKIME SFKNMVPQIA
161 IVIREGEK**LT LKAEELVLGD VVEVK**FGDRI PADIRIIESR GFKVDNSSLT GESEPQSRSP EFTNENPLET KNLAFFSTNA
241 VEGTAK**GVVI CCGDQTVMGR** IAGLASGLDT GETPIAKEIH HFIHLITGVA VFLGVTFFII AFILGYHWLD AVIFLIGIIV
321 ANVPEGLLAT VTVCLTLTAK RMASKNCLVK **NLEAVETLGS TSTICSDK**TG TLTQNRMTVA HMWFDNQIIE ADTTEDQSGL
401 QYDRTSPGFK ALAKIATLCN RAEFKAGQED KPILKR**EVNG DASEAALLK**C MELALGDVMG IRKRNKKVCE IPFNSTNKYQ
481 VSIHESDNPD DPRHLLVMKG APERILDRCS TIFIGGKEKV LDEEMKEAFN NAYLELGGLG ERVLGFCDYI LPSDKFPIGF
561 KFNCDDPNFP VDGLRFVGLM SMIDPPRAAV PDAVAKCRSA GIKVIMVTGD HPITAKAIAK **SVGIISEGNE TVEDIAQRLN**
641 **IPVSEVNPR**E AKAAVIHGTE LRELNSDQLD EILRYHTEIV FARTSPQQKL IIVEGCQR**MG AIVAVTGDGV NDSPALKKAD**
721 **IGVAMGIAGS DVSK**QAADMI LLDDNFASIV TGVEEGRLIF DNLKKSIAYT LTSNIPEISP FLAFILCDIP LPLGTVTILC
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881 WDSKAINDLR DSYGQEWTYR DRKTLEFTCH TAFFVSIVIV QWADLIVCKT RRNSIIHQGM RNWALNFGLI FETALAAFLS
961 YTPGMDKGLR MFPLK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KADIGVAMGIAGSDVSK.Q	Y	83.33	1617.8396	-15.4	809.9146	2	31.50	2414	1	718	734	
K.LTLKAEELVLGDVVEVK.F	Y	79.02	1854.0713	661.7	928.6564	2	37.32	3067	2	169	185	
K.KADIGVAM(+15.99)GIAGSDVSK.Q	Y	78.72	1633.8345	47.7	817.9635	2	31.62	2428	1	718	734	Oxidation (M)
R.MGAIVAVTGDGVNDSPALK.K	Y	77.71	1813.9243	-48.5	907.9255	2	33.41	2628	1	699	717	
K.SVGIISEGNETVEDIAQR.L	Y	73.56	1915.9486	525.9	959.4854	2	34.39	2738	2	621	638	
R.TDNLEDLKQELDIDFHK.I	Y	54.10	2072.0061	7.8	1037.0184	2	36.08	2928	1	20	36	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	Y	41.97	1923.9095	117.0	642.3855	3	33.20	2604	1	351	368	Carbamidomethylation
K.S(+43.01)VGIISEGNETVEDIAQR.L	Y	41.36	1958.9545	561.7	981.0347	2	36.91	3020	1	621	638	Carbamylation
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R.EVNGDASEAALLK.C	Y	31.11	1315.6619	856.3	659.4015	2	30.12	2268	1	437	449	
R.LNIPVSEVNPR.E	Y	18.31	1236.6826	-237.8	619.2015	2	31.77	2444	1	639	649	
total 11 peptides												

tr|V9I7X6|V9I7X6_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASKGKLATE SRRKNPKRR**T DNLEDLKQEL DIDFHK**ITPE ELYQRFQTHP ENGLSHAKAK ENLERDGPNS LTPPKQTPEW

81 VKFCKNLFGG FALLLWIGAI LCFIAYSIQA STSEDPNDDN LYLGIVLAAV VIVTGIFSYY QESKSSKIME SFKNMVPQIA

161 IVIREGEK**LT LKAEELVLGD VVEVK**FGDRI PADIRIIESR GFKVDNSSLT GESEPQSRSP EFTNENPLET KNLAFFSTNA

241 VEGTAK**GVVI CCGDQTVMGR** IAGLASGLDT GETPIAKEIH HFIHLITGVA VFLGVTFFII AFILGYHWLD AVIFLIGIIV

321 ANVPEGLLAT VTVCLTLTAK RMASKNCLVK **NLEAVETLGS TSTICSDK**TG TLTQNRMTVA HMWFDNQIIE ADTTEDQSGL

401 QYDRTSPGFK ALAKIATLCN RAEFKAGQED KPILKR**EVNG DASEAALLK**C MELALGDVMG IRKRNKKVCE IPFNSTNKYQ

481 VSIHESDNPD DPRHLLVMKG APERILDRCS TIFIGGKEKV LDEEMKEAFN NAYLELGGLG ERVLGFCDYI LPSDKFPIGF

561 KFNCDDPNFP VDGLRFVGLM SMIDPPRAAV PDAVAKCRSA GIKVIMVTGD HPITAKAIAK **SVGIISEGNE TVEDIAQRLN**

641 **IPVSEVNPR**E AKAAVIHGTE LRELNSDQLD EILRYHTEIV FARTSPQQKL IIVEGCQR**MG AIVAVTGDGV NDSPALKKAD**

721 **IGVAMGIAGS DVSK**QAADMI LLDDNFASIV TGVEEGRLIF DNLKKSIAYT LTSNIPEISP FLAFILCDIP LPLGTVTILC

801 IDLGTDMVPA ISLAYEAPES DIMKRQPRDP YRDNLVNRRL ISMAYGQIGM IQAAAGFFVY FVIMAENGFL PLHLFGIRKQ

881 WDSKAINDLR DSYGQEWTYR DRKTLEFTCH TAFFVSIVIV QWADLIVCKT RRNSIIHQGM RNWALNFGLI FETALAAFLS

961 YTPGMDKGLR MFPLK

C Carba
C Carba
O Oxida
U Ubiqu

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.KADIGVAMGIAGSDVSK.Q	Y	83.33	1617.8396	-15.4	809.9146	2	31.50	2414	1	718	734	
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K.SVGIISEGNETVEDIAQR.L	Y	73.56	1915.9486	525.9	959.4854	2	34.39	2738	2	621	638	
R.TDNLEDLKQELDIDFHK.I	Y	54.10	2072.0061	7.8	1037.0184	2	36.08	2928	1	20	36	
K.NLEAVETLGSTSTIC(+57.02)SDK.T	Y	41.97	1923.9095	117.0	642.3855	3	33.20	2604	1	351	368	Carbamidomethylation
K.S(+43.01)VGIISEGNETVEDIAQR.L	Y	41.36	1958.9545	561.7	981.0347	2	36.91	3020	1	621	638	Carbamylation
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R.EVNGDASEAALLK.C	Y	31.11	1315.6619	856.3	659.4015	2	30.12	2268	1	437	449	
R.LNIPVSEVNPR.E	Y	18.31	1236.6826	-237.8	619.2015	2	31.77	2444	1	639	649	
total 11 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 **SLR**FDGALNV DLTEFQTNLV PYPRIHFPLA TYAPVISTEK **AYHEQLTVGE ITNACFEPQN QMVK**CDPRHG KYMAVCLLYR

321 GDVVPKDVNA AIAAIKTKRS IQFVDWCPTG FKVGINYQPP TVVPGGDLAK VQR**AVCMLSN TTAIAEAWAR** LDHKFDLMYA

401 KR**AFVHWYVG EGMEEGEFSE AR**EDLAALEK DYEEVAIEST DADGDAGDEY

C Carba
C Carba
C Carba
☒ Mutat

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AFVHWYVGEGMEEGEFSEAR.E	Y	73.99	2329.0110	2.2	1165.5154	2	35.96	2914	1	403	422	
R.LIGQIVSSITASLR.F	Y	60.25	1456.8613	372.6	729.7094	2	40.36	3407	1	230	243	
R.AVC(+57.02)MLSNTTAIAEAWAR.L	Y	50.61	1863.8971	17.0	932.9717	2	37.77	3117	1	374	390	Carbamidomethylation
R.AVCMW(sub L)SNTTAIAEAWAR.L	Y	42.44	1879.8710	629.3	941.5343	2	37.84	3124	1	374	390	Mutation
K.AYHEQLTVGEITNACFEPQNQMVK.C	Y	35.49	2749.2839	392.3	917.7948	3	35.40	2851	2	281	304	
R.A(+57.02)VCMLSNTTAIAEAWAR.L	Y	19.84	1863.8971	423.1	622.5692	3	37.76	3115	1	374	390	Carbamidomethylation (DHKE, X@N-term)
R.AVC(+209.02)MLSNTTAIAEAWAR.L	Y	16.76	2015.8937	509.9	1009.4680	2	37.89	3130	1	374	390	Carbamidomethylated DTT modification
total 7 peptides												

tr|T1GUQ6|T1GUQ6_MEGSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FWEIISDEHG IDATGAYHGD SDLQLER**INV YYNEASGGK**Y VPRAVLVDLE PGTMDSVRSG PFGQIFRPDN FVFGQSGAGN P Phosp

124

81 NWAK**GHYTEG AELVDSVLDV VRK**EAESCDC LQGFQLTH**SL GGGT**GSGMGT LLISKIREEY PDRIMNTYSV VPSPKVSDTV

161 VEPYNATLSV HQLVENTDET YCIDNEALYD ICFRTLKLTT PTYGDLNHLV SLTMSGVTTC LRFPGQLNAD LRKLAVNMVP

241 FPRLHFFMPG FAPLTSRGSQ QYRALTVPEL TQQMFDAKNM MAACDPRHGR **YLTVAAIFR**G QQLIFVEWIP NNVKTAVCDI

321 PPRGLK**MSAT FIGNSTAIQE LFK**RISEQFT AMFRRKAFLH WYTGEGMDEM EFTEAESNMN DLVS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	327	343	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	291	299	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	85	102	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	85	103	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	28	39	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	119	124	Phosphorylation (STY)
total 6 peptides												

tr|A0A0J7L622|A0A0J7L622_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAQNVNPFSS TQNTPTKAAE EKQSLPKDNH AVSKRLQKEL MVLMMNTEQG VSAFPEGENL FKWIGTITGP RDTVYAGLTY P Phosp

81 KLTLEFPHSY PYSAPIVRFA TPCFHPNVDT GGNICLDILK DKWSALYDVR TILLSIQSLL SGTIWTDFKP QIENLNTDKL

161 TIVAWDPPGY GKSRPPDRTF PDDFFQRDAA WAHSLMQTLG YSKFSLIGWS NGGITSLLLA STYPESIRRM VVFGANAYIH

241 PDEAKIYENI RDIDKWSERM RTSMIQVYGE DYFRKTWSNW IDAKLRLYEK QNGNVCKEVL SKIKCPTLII HGAKDAIVFP

321 EHPTYLKQNI ANSNLHILEK GAHNLHLRYF EEFNNLFWEI ISDEHGIDPT GTYHGDSDLQ LER**INVYYNE ASGGK**YVPRA

480

401 ILVDLEPGTM DSVRSGPFGQ IFRPDNFVFG QSGAGNNWAK **GHYTEGAELV DSVLDVVRK**E AESCDCLQGF QLTH**SLGGGT**

481 GSGMGTLLIS KIREEYPDRI MNTYSVVPSP KVSDTVVEPY NATLSVHQLV ENTDETYCID NEALYDICFR TLKLSTPTYG

561 DLNHLVSLTM SGVTTCLRFP GQLNADLRKL AVNMVPFPRL HFFMPGFAPL TSRGSQQYRA LSVPELTQQM FDAKNMMAAC

641 DPRHGR**YLTV AAIFR**GRMSM KEVDEQMLNI QNKNSSYFVE WIPNNVKTAV CDIPPRGLK**M SATFIGNSTA IQELFK**RISE

721 QFTAMFRRKA FLHWYTGEGM DEMEFTEAES NMNDLSEYQ QYQEATADED AEFDEEQEAE VDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	700	716	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	647	655	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	441	458	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	441	459	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	384	395	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	475	480	Phosphorylation (STY)
total 6 peptides												

tr|A0A1B1LYT4|A0A1B1LYT4_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LLQFWEIISD EHGIDPTGAY HGDSDLQLER **INVYYNEASG GK**YVPRAILV DLEPGTMDSV RSGPFGQIFR PDNFVFGQSG P Phosp

127

81 AGNNWAK**GHY TEGAELVDSV LDVVRK**EAES CDCLQGFQLT H**SLGGGT**GSG MGTLLISKIR EEYPDRIMNT YSVVPSPKVS

161 DTVVEPYNAT LSVHQLVENT DETYCIDNEA LYDICFRTLK LSTPTYGDLN HLVSLTMSGV TTCLRFPGQL NADLRKLAVN

241 MVPFPRLHFF MPGFAPLTSR GSQQYRALTV PELTQQMFDA KNMMAACDPR HGR**YLTVAAI FR**GRMSMKEV DEQMLNIQNK

321 NSSYFVEWIP NNVKTAVCDI PPRGLK**MSAT FIGNSTAIQE LFK**RISEQFT AMFRRKAFLH WYTGEGMDEM EFTEAESNMN

401 DLVSEYQQYQ EATADEDAEF EEEEQEGEIE N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	347	363	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	294	302	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	88	105	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	88	106	
total 6 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	31	42	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	122	127	Phosphorylation (STY)
total 6 peptides												

tr|A0A023FK66|A0A023FK66_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEVISDEHGI DPTGSYHGDS DLQLER**INVY YNEASGGK**YV PRAILVDLEP GTMDSVRSGP P Phosp

143

81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAEGCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTFSVV PSPKVSDTVV EPYNATLSVH QLVENTDETF CIDNEALYDI CFRTLKLTTP TYGDLNHLVS ATMSGVTTCL

241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTARGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMREVDEQM LNVQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEEGEFEDEP EADAEA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|B4QE31|B4QE31_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DATGAYHGDS DLQLER**INVY YNEASGGK**YV PRAVLVDLEP GTMDSVRSGP P Phosp

143

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL

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

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFEEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|V9IK78|V9IK78_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DPTGTYHGDS DLQLER**INVY YNEASGGK**YV PRAILVDLEP GTMDSVRSGP P Phosp

143

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLSTP TYGDLNHLVS LTMSGVTTCL

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

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFDEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|A0A0M4EEV8|A0A0M4EEV8_DROBS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DATGAYHGDS DLQLER**INVY YNEASGGK**YV PRAVLVDLEP GTMDSVRSGP P Phosp

143
P

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL

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

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFEEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|A0A1A9WAB8|A0A1A9WAB8_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DATGAYHGDS DLQLER**INVY YNEASGGK**YV PRAVLVDLEP GTMDSVRSGP P Phosp

143
P

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL

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

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DEDAEFEEEQ EAEVEEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|C7SAW9|C7SAW9_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI DATGAYHGDS DLQLER**INVY YNEASGGK**YV PRAVLVDLEP GTMDSVRSGP P Phosp

143 P

81 FGQIFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL

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

321 MSMKEVDEQM LNIQNKNCSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMSDLVS EYQQYQEATA DEDAEFEEEQ EAEVDEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
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R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|A0A0P5E5N2|A0A0P5E5N2_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MREIVHIQAG QCGNQIGAKF WEIISDEHGI QPNGTYHGES ELQLER**INVY YNEASGGK**YV PRAVLVDLEP GTMDSVRSGP P Phosp

143 P

81 FGQLFRPDNF VFGQSGAGNN WAK**GHYTEGA ELVDSVLDVV RK**EAESCDCL QGFQLTH**SLG GGT**GSGMGTL LISKIREEYP

161 DRIMNTYSVV PSPKVSDTVV EPYNATLSVH QLVENTDETY CIDNEALYDI CFRTLKLTTP TYGDLNHLVS LTMSGVTTCL

241 RFPGQLNADL RKLAVNMVPF PRLHFFMPGF APLTARGSQQ YRALTVPELT QQMFDAKNMM AACDPRHGR**Y LTVAAIFR**GR

321 MSMKEVDEQM LNIQNKNSSY FVEWIPNNVK TAVCDIPPRG LK**MSATFIGN STAIQELFK**R ISEQFTAMFR RKAFLHWYTG

401 EGMDEMEFTE AESNMNDLVS EYQQYQEATA DDEADFEEDG DHADQDAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	363	379	
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	310	318	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	104	121	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	104	122	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	47	58	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	138	143	Phosphorylation (STY)
total 6 peptides												

tr|A0A151X2S9|A0A151X2S9_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLQFWEIISD EHGIDPTGTY HGDSDLQLER **INVYYNEASG GK**YVPRAILV DLEPGTMDSV RSGPFGQIFR PDNFVFGQSG P Phosp

127 P

81 AGNNWAK**GHY TEGAELVDSV LDVVRK**EAES CDCLQGFQLT H**SLGGGT**GSG MGTLLISKIR EEYPDRIMNT YSVVPSPKVS

161 DTVVEPYNAT LSVHQLVENT DETYCIDNEA LYDICFRTLK LSTPTYGDLN HLVSLTMSGV TTCLRFPGQL NADLRKLAVN

241 MVPFPRLHFF MPGFAPLTSR GSQQYRALSV PELTQQMFDA KNMMAACDPR HGR**YLTVAAI FR**GRMSMKEV DEQMLNIQNK

321 NSSYFVEWIP NNVKTAVCDI PPRGLK**MSAT FIGNSTAIQE LFK**RISEQFT AMFRRKAFLH WYTGEGMDEM EFTEAESNMN

401 DLVSEYQQYQ EATADEDAEF DEEQEAEFWE VISEEHGIDQ SGIYHGDSDL QLERISVYYN EASVATSTNG GKYVPRAILL

481 DLEPGTMDAV RSGAYGKLFR PDNFVFGQSG AGNNWAKGHY TEGAELVDMV LDVVRKECEN CDCLQGFQLT HSLGGGTGSG

561 MGTLLISKIR EEYPDRIMNT YSVMPSPKVS DTVVEPYNAT LSVHQLVENT DETYCIDNEA LYDICFRTLK VSNPSYGDLN

641 HLVSLTMSGV TTCLRFPGQL NADLRKLAVN MVPFPRLHFF MPGFAPLTSR SMQQYSALSV PELTQQMFDA KNMMAACDPR

721 HGRYLTVAAV FRGRMSMKEV DEQMLSVQNK NSSYFVEWIP NNVKTAVCDI PPKGLKMSST FIGNTTAIQE LFKRISEQFT

801 AMFRRKAFLH WYTGEGMDEM EFTEAESNMN DLVSEYQQYQ EATAEEDFEA EECADDFETC EQEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.MSATFIGNSTAIQELFK.R	Y	68.73	1856.9342	53.0	929.5236	2	39.45	3304	1	347	363	
total 6 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.YLTVAAIFR.G	Y	45.92	1052.6018	449.0	527.5445	2	37.51	3088	1	294	302	
K.GHYTEGAELVDSVLDVVR.K	Y	30.47	1957.9745	628.1	654.0754	3	39.24	3281	1	88	105	
K.GHYTEGAELVDSVLDVVRK.E	Y	30.25	2086.0693	407.1	696.6468	3	38.14	3158	1	88	106	
R.INVYYNEASGGK.Y	Y	26.20	1313.6251	59.7	657.8591	2	28.85	2158	1	31	42	
H.SLGGGT(+79.97).G	Y	18.60	570.2051	2000.2	572.3529	1	50.38	4546	1	122	127	Phosphorylation (STY)
total 6 peptides												

tr|A0A088A5I8|A0A088A5I8_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

74 c
1 MSLKPQFLLK CERISLRISV SALFVDLLLI KFDFNFKNFK KPAKMVWVTV YDKMVSGK**TI SHALYAQTQL DHVCALDIDA** c Carba
81 **PIGAVR**LSGI ICTIGPASRS IDMLEKMIDT GMNIARLNFS HGTHEYHAET IANVRQAQKN VSSKAGLSIP VGIALDTKGP
161 EIR**TGLLEGG GAAEVELKK**D QLFKLSTDKA YAEK**GTSSIV YVDYENITK**V LKPNSRVFVD DGLISLKVTA ILSLFYVLCV
241 SNPELVVTVV ENGGMLGSRK GVNLPGTPVD LPAVSEKDKS DLIFGVEHEV DMIFASFIRD AHALTEIRTI LGEKGKNIKV
321 ISKIENHQGV VNIDEIIDAS DGIMVARGDL GIEIPPEKVF LAQKSAISKC NKVGKPIICA TQMLESMVKK PRATRAESSD
401 VANAILDGAD CVMLSGETAK GDYPLECVLT MANICKEAES AIWQTQLFHE LSMK**AIPPID ATHAVAIAVV EASVK**CLASA
481 IIVITTTGHS AYLISKYRPR CPIITVTRHS QTARQSHLYR GILPLHFEEP RLADWVKDVD VRVQFGMKFG KNQGFIKPGD
561 AVIVVTGWRK GAGFTNSLRI VYVDIEIPEE QTASVRATSD TDSYEYMNI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.GTSSIVYVDYENITK.V	Y	71.73	1687.8304	596.8	845.4261	2	34.45	2745	1	195	209	
R.TGLLEGGGAAEVELKK.D	Y	53.71	1570.8566	85.9	786.5031	2	31.36	2399	1	164	179	
K.AIPPIDATHAVAIAVVEASVK.C	Y	32.74	2071.1677	-58.4	1036.5306	2	39.10	3265	1	455	475	
K.TISHALYAQTQLDHVC(+57.02)ALDIDAPIGAVR.L	Y	30.21	3047.5498	391.8	1017.2552	3	35.85	2902	1	59	86	Carbamidomethylation
total 4 peptides												

tr|V9IK50|V9IK50_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSKIGINGFG RIGRLVFRAS IEFGAQVVAI NDPFIGLEYM AYMLKYDSTH GKFKGDVKIE NDQLIVNGNA IAVFSEREAK d Deam
81 NIPWTK**AGAE YIVESTGVYT TK**EKASGHLQ AGAKKVVITA PSADAPMFVC GVNLDAYDPS YTIVSNASCT TNCLAPLAK**V**
236 d
161 **IHDNFEIVEG LMTTVHAVTA TQK**VVDAPSA KLWRDGRGAC QNIIPAATGA AKAVGKVIPA LDGKLTGMAF R**VPVHNVSVV**
d
241 **DLTVR**LGKGA DYKTIKAKVK EASEGPLK**GI LGYTEDEVVS SDFIGDDHAS IFDAK**AGIAL NNNFVKLISW YDNEYGYSCR
321 VIDLIKYMQS KEK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGAEYIVESTGVYTTK.E	Y	80.18	1687.8304	-14.2	844.9105	2	32.73	2552	1	87	102	
K.VIHDNFEIVEGLMTTVHAVTATQK.V	Y	38.63	2652.3582	367.9	885.4519	3	40.43	3415	1	160	183	
R.VPVHN(+.98)VSVVDLTVR.L	Y	32.30	1533.8514	729.7	768.4926	2	32.53	2530	1	232	245	Deamidation (NQ)
R.VPVHNVSVVDLTVR.L	Y	30.21	1532.8674	420.3	512.1779	3	32.64	2542	1	232	245	
K.GILGYTEDEVVSSDFIGDDHASIFDAK.A	Y	20.19	2899.3398	289.0	1451.0962	2	38.63	3212	1	269	295	
total 5 peptides												

tr|A0A088AHC8|A0A088AHC8_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSKIGINGFG RIGRLVFRAS IEFGAQVVAI NDPFIGLEYM AYMLKYDSTH GKFKGDVKIE NDQLVVNGNK IAVFSEREAK d Deam
81 NIPWTK**AGAE YIVESTGVYT TK**EKASGHLQ AGAKKVVITA PSADAPMFVC GVNLDAYDPS YTIVSNASCT TNCLAPLAK**V**
236 d
161 **IHDNFEIVEG LMTTVHAVTA TQK**VVDAPSA KLWRDGRGAC QNIIPAATGA AKAVGKVIPA LDGKLTGMAF R**VPVHNVSVV**
d
241 **DLTVR**LGKGA DYKTIKAKVK EASEGPLK**GI LGYTEDEVVS SDFIGDDHAS IFDAK**AGIAL NNNFVKLISW YDNEYGYSCR
321 VIDLIKYMQS KEK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGAEYIVESTGVYTTK.E	Y	80.18	1687.8304	-14.2	844.9105	2	32.73	2552	1	87	102	
K.VIHDNFEIVEGLMTTVHAVTATQK.V	Y	38.63	2652.3582	367.9	885.4519	3	40.43	3415	1	160	183	
R.VPVHN(+.98)VSVVDLTVR.L	Y	32.30	1533.8514	729.7	768.4926	2	32.53	2530	1	232	245	Deamidation (NQ)
R.VPVHNVSVVDLTVR.L	Y	30.21	1532.8674	420.3	512.1779	3	32.64	2542	1	232	245	
K.GILGYTEDEVVSSDFIGDDHASIFDAK.A	Y	20.19	2899.3398	289.0	1451.0962	2	38.63	3212	1	269	295	
total 5 peptides												

tr|A0A2A3E509|A0A2A3E509_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSKIGINGFG RIGRLVFRAS IEFGAQVVAI NDPFIGLEYM AYMLKYDSTH GKFKGDVKIE NDQLIVNGNA IAVFSEREAK d Deam

81 NIPWTK**AGAE YIVESTGVYT TK**EKASGHLQ AGAKKVVITA PSADAPMFVC GVNLDAYDPS YTIVSNASCT TNCLAPLAK**V**

236
d

161 **IHDNFEIVEG LMTTVHAVTA TQK**VVDAPSA KLWRDGRGAC QNIIPAATGA AKAVGKVIPA LDGKLTGMAF R**VPVHNVSVV**

d

241 **DLTVR**LGKGA DYKTIKAKVK EASEGPLK**GI LGYTEDEVVS SDFIGDDHAS IFDAK**AGIAL NNNFVKLISW YDNEYGYSCR

321 VIDLIKYMQS KEKYQSEEVQ KKTVFKLHIE YAKIILVLYI N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AGAEYIVESTGVYTTK.E	Y	80.18	1687.8304	-14.2	844.9105	2	32.73	2552	1	87	102	
K.VIHDNFEIVEGLMTTVHAVTATQK.V	Y	38.63	2652.3582	367.9	885.4519	3	40.43	3415	1	160	183	
R.VPVHN(+.98)VSVVDLTVR.L	Y	32.30	1533.8514	729.7	768.4926	2	32.53	2530	1	232	245	Deamidation (NQ)
R.VPVHNVSVVDLTVR.L	Y	30.21	1532.8674	420.3	512.1779	3	32.64	2542	1	232	245	
K.GILGYTEDEVVSSDFIGDDHASIFDAK.A	Y	20.19	2899.3398	289.0	1451.0962	2	38.63	3212	1	269	295	
total 5 peptides												

tr|V9I8Q3|V9I8Q3_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVDKEELVQ RAKLAEQAER YDDMAAAMK**A VTETGVELSN EERNLLSVAY K**NVVGARRSS WRVISSIEQK TEGSERKQQM c Carba

c

81 AKEYREKVEK ELREICYDVL GLLDKYLIPK ASNAESKVFY LKMKGDYYR**Y LAEVATGETR** NAVVDDSQKA YQDAFEISKS

161 KMQPTHPIRL GLALNFSVFY YEILNSPDKA CQLAKQAFDD AIAELDTLNE DSYKDSTLIM QLLR**DNLTLW TSDTQGDADE**

241 **AQEGGDN**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNLTLWTSDTQGDADEAQEGGDN	Y	64.42	2450.9946	4.3	1226.5099	2	35.53	2866	1	225	247	
K.AVTETGVELSNEER.N	Y	51.66	1532.7318	11.6	767.3821	2	28.40	2113	2	30	43	
R.YLAEVATGETR.N	Y	47.53	1208.6036	104.2	605.3721	2	28.49	2121	1	130	140	
K.A(+43.01)VTETGVELSNEER.N	Y	37.75	1575.7375	-44.4	788.8411	2	32.51	2528	1	30	43	Carbamylation
K.AVTETGVELSNEERNLLSVAYK.N	Y	35.69	2421.2388	398.8	1212.1095	2	36.66	2992	1	30	51	
total 5 peptides												

tr|G9I551|G9I551_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVDKEELVQ RAKLAEQAER YDDMAASMK**A VTETGVELSN EERNLLSVAY K**NVVGARRSS WRVISSIEQK TEGSERKQQM c Carba

c

81 AKEYREKVEK ELREICYDVL GLLDKYLIPK ASNAESKVFY LKMKGDYYR**Y LAEVATGETR** NAVVDDSQKA YQDAFEISKS

161 KMQPTHPIRL GLALNFSVFY YEILNSPDKA CQLAKQAFDD AIAELDTLNE DSYKDSTLIM QLLR**DNLTLW TSDTQGDADE**

241 **AQEGGDN**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNLTLWTSDTQGDADEAQEGGDN	Y	64.42	2450.9946	4.3	1226.5099	2	35.53	2866	1	225	247	
K.AVTETGVELSNEER.N	Y	51.66	1532.7318	11.6	767.3821	2	28.40	2113	2	30	43	
R.YLAEVATGETR.N	Y	47.53	1208.6036	104.2	605.3721	2	28.49	2121	1	130	140	
K.A(+43.01)VTETGVELSNEER.N	Y	37.75	1575.7375	-44.4	788.8411	2	32.51	2528	1	30	43	Carbamylation
K.AVTETGVELSNEERNLLSVAYK.N	Y	35.69	2421.2388	398.8	1212.1095	2	36.66	2992	1	30	51	
total 5 peptides												

tr|G9I553|G9I553_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVDKEELVQ RAKLAEQAER YDDMAASMK**A VTETGVELSN EERNLLSVAY K**NVVGARRSS WRVISSIEQK TEGSERKQQM C Carba

C

81 AKEYREKVEK ELREICYDVL GLLDKYLIPK ASNAESKVFY LKMKGDYYR**Y LAEVATGETR** NAVVEDSQKA YQEAFDIAKS

161 KMQPTHPIRL GLALNFSVFY YEIINSPARA CHLAKQAFDD AIAELDTLNE DSYKDSTLIM QLLR**DNLTLW TSDTQGDADE**

241 **AQEGGDN**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNLTLWTSDTQGDADEAQEGGDN	Y	64.42	2450.9946	4.3	1226.5099	2	35.53	2866	1	225	247	
K.AVTETGVELSNEER.N	Y	51.66	1532.7318	11.6	767.3821	2	28.40	2113	2	30	43	
R.YLAEVATGETR.N	Y	47.53	1208.6036	104.2	605.3721	2	28.49	2121	1	130	140	
K.A(+43.01)VTETGVELSNEER.N	Y	37.75	1575.7375	-44.4	788.8411	2	32.51	2528	1	30	43	Carbamylation
K.AVTETGVELSNEERNLLSVAYK.N	Y	35.69	2421.2388	398.8	1212.1095	2	36.66	2992	1	30	51	
total 5 peptides												

tr|G9I552|G9I552_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVDKEELVQ RAKLAEQAER YDDMAASMK**A VTETGVELSN EERNLLSVAY K**NVVGARRSS WRVISSIEQK TEGSERKQQM C Carba

C

81 AKEYREKVEK ELREICYDVL GLLDKYLIPK ASNAESKVFY LKMKGDYYR**Y LAEVATGETR** NAVVEDSQKA YQEAFDIAKS

161 KMQPTHPIRL GLALNFSVFY YEILNSPDKA CQLAKQAFDD AIAELDTLNE DSYKDSTLIM QLLR**DNLTLW TSDTQGDADE**

241 **AQEGGDN**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNLTLWTSDTQGDADEAQEGGDN	Y	64.42	2450.9946	4.3	1226.5099	2	35.53	2866	1	225	247	
K.AVTETGVELSNEER.N	Y	51.66	1532.7318	11.6	767.3821	2	28.40	2113	2	30	43	
R.YLAEVATGETR.N	Y	47.53	1208.6036	104.2	605.3721	2	28.49	2121	1	130	140	
K.A(+43.01)VTETGVELSNEER.N	Y	37.75	1575.7375	-44.4	788.8411	2	32.51	2528	1	30	43	Carbamylation
K.AVTETGVELSNEERNLLSVAYK.N	Y	35.69	2421.2388	398.8	1212.1095	2	36.66	2992	1	30	51	
total 5 peptides												

tr|A0A088AHG5|A0A088AHG5_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVDKEELVQ RAKLAEQAER YDDMAAAMK**A VTETGVELSN EERNLLSVAY K**NVVGARRSS WRVISSIEQK TEGSERKQQM C Carba

C

81 AKEYREKVEK ELREICYDVL GLLDKYLIPK ASNAESKVFY LKMKGDYYR**Y LAEVATGETR** NAVVDDSQKA YQDAFEISKS

161 KMQPTHPIRL GLALNFSVFY YEILNSPDKA CQLAKQKRHF CSLYSCSGGS FCFHDRIVHT FTNTVTTEFS VVEDSQKAYQ
241 EAFDIAKSKM QPTHPIRLGL ALNFSVFYYE IINSPDKACQ LAKQKRCSSE ETVVEDSQKA YQEAFDIAKS KMQPTHPIRL
321 GLALNFSVFY YEIINSPARA CHLAKQAFDD AIAELDTLNE DSYKDSTLIM QLLR**DNLTLW TSDTQGDADE AQEGGDN**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNLTLWTSDTQGDADEAQEGGDN	Y	64.42	2450.9946	4.3	1226.5099	2	35.53	2866	1	375	397	
K.AVTETGVELSNEER.N	Y	51.66	1532.7318	11.6	767.3821	2	28.40	2113	2	30	43	
R.YLAEVATGETR.N	Y	47.53	1208.6036	104.2	605.3721	2	28.49	2121	1	130	140	
K.A(+43.01)VTETGVELSNEER.N	Y	37.75	1575.7375	-44.4	788.8411	2	32.51	2528	1	30	43	Carbamylation
K.AVTETGVELSNEERNLLSVAYK.N	Y	35.69	2421.2388	398.8	1212.1095	2	36.66	2992	1	30	51	
total 5 peptides												

tr|A0A088AST9|A0A088AST9_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKKILTSLFL ISKYSTRSTT SSTTTSSTTS FTRTSSRMSS IKSIKARQIF DSRGNPTVEV DLVTDDGLFR **SEVPSGASTG**
81 **IHEALELR**DN DKSKYHGKSV FKAISNINNT IGPELIK**SNL DVTSQSDIDN FLLK**LDGTPN KSNLGANAIL GVSLAVCKAG
161 AAKKKKPLYR YIADLAGNTN IILPVPAFNV INGGSHAGNK LAMQEFMILP TGASSFSDAM KMGTEIYHHL KNGIKSRFGL
241 DATSVGDEGG FAPNILDNKE ALNLIIDSIK TAGYDGKVKI GMDVAASEFY KNGKYDLNFK NEKSDPSTYL DSDSLKNLYL
321 QFIKEFPIVS IEDPFDQDDW SSWTTLTSST DIQIVGDDVT VTNPNR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SNLDVTSQSDIDNFLLK.L	Y	76.36	1907.9476	-0.7	954.9805	2	37.29	3063	1	118	134	
R.SEVPSGASTGIHEALELR.D	Y	67.63	1851.9326	-45.8	926.9312	2	33.17	2601	1	71	88	
total 2 peptides												

tr|A0A2A3E8V4|A0A2A3E8V4_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNRQYDKIQH FLITGLNFQD LMARQGAIDS PPKTPFIMGS ECAGDIEQVG EGVENFKIFI HKHHHTRYKK KPSKEKISKP
81 PVSIIGQRKK DCSTLRQKIS CGVGDRVVAL PDHKAWAELV AVPATSVFAL PAGMSYLDAA AITMNYTVAY ILLFELANLT
161 PGK**NLLLHSA GGGVGQAVVQ LAK**TVKDVTI FGVCSKSKHE ALKATGTIDH ILERGADYSN EVRKISPEGV DIVLDCLCGE
241 ECNKGYALLK PMGK**YILYGS SNVVTGETK**S FFSAARSWWQ VDKVSPIKLF DENKTLSGLN LRHLMYQHGS HAFVRRAVER
321 VFALWNEGKI KPVVDSTWAL EDVPEAMQKM HDRKNIGKIV LDPSLEPKPK PATPAKGKTK DKKAASQESQ EKKASSVESE
401 EGEKKKEPEL TNGTSEDKSD SECKTVKIKN FADKDLHLLR YTTLDYYVLM SANYRVDNEL IWKTKTKNYM KQQDMNKN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLLLHSAGGGVGQAVVQLAK.T	Y	74.90	1931.0952	-69.1	966.4882	2	34.70	2773	2	164	183	
K.YILYGSSNVVTGETK.S	Y	68.46	1629.8250	-44.1	815.8838	2	32.54	2531	1	255	269	
total 2 peptides												

tr|V9IAR8|V9IAR8_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAEDKNETSP SAEGEKPPQE AAPSKQEKEE PKENKEEEKK VEENGDGDKP KENGEEKPTP EPKDMRAIVL NGFGGLKSVK
81 ALRKPEPTLS EGEVLIRVKA CGLNFQDLMA RQGAIDSPPK TPFIMGSECA GDIEQVGEGV ENFKVGDRVV ALPDHKAWAE
161 LVAVPATSVF ALPAGMSYLD AAAITMNYTV AYILLFELAN LTPGK**NLLLH SAGGGVGQAV VQLAK**TVKDV TIFGVCSKSK
241 HEALKATGTI DHILERGADY SNEVRKISPE GVDIVLDCLC GEECNKGYAL LKPMGK**YILY GSSNVVTGET K**SFFSAARSW
321 WQVDKVSPIK LFDENKTLSG LNLRHLMYQH GSHAFVRRAV ERVFALWNEG KIKPVVDSTW ALEDVPEAMQ KMHDRKNIGK
401 IVLDPSLEPK PKPATPAKGK TKDKKAASQE SQEKKASSVE SEEGEKKKEP ELTNGTSEDK SDSDSKEKES S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLLLHSAGGGVGQAVVQLAK.T	Y	74.90	1931.0952	-69.1	966.4882	2	34.70	2773	2	206	225	
K.YILYGSSNVVTGETK.S	Y	68.46	1629.8250	-44.1	815.8838	2	32.54	2531	1	297	311	
total 2 peptides												

tr|A0A088A347|A0A088A347_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAEDKNETSP SAEGEKPPQE AAPSKQEKEE PKENKEEEKK VEENGDGDKP KENGEEKPTP EPKDMRAIVL NGFGGLKSVK
81 ALRKPEPTLS EGEVLIRVKA CGLNFQDLMA RQGAIDSPPK TPFIMGSECA GDIEQVGEGV ENFKVGDRVV ALPDHKAWAE
161 LVAVPATSVF ALPAGMSYLD AAAITMNYTV AYILLFELAN LTPGK**NLLLH SAGGGVGQAV VQLAK**TVKDV TIFGVCSKSK
241 HEALKATGTI DHILERGADY SNEVRKISPE GVDIVLDCLC GEECNKGYAL LKPMGK**YILY GSSNVVTGET K**SFFSAARSW
321 WQVDKVSPIK LFDENKTLSG LNLRHLMYQH GSHAFVRRAV ERVFALWNEG KIKPVVDSTW ALEDVPEAMQ KMHDRKNIGK
401 IVLDPSLEPK PKPATPAKGK TKDKKAASQE SQEKKASSVE SEEGEKKKEP ELTNGTSEDK SDSDSKEKES S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLLLHSAGGGVGQAVVQLAK.T	Y	74.90	1931.0952	-69.1	966.4882	2	34.70	2773	2	206	225	
K.YILYGSSNVVTGETK.S	Y	68.46	1629.8250	-44.1	815.8838	2	32.54	2531	1	297	311	
total 2 peptides												

tr|A0A026WY44|A0A026WY44_OOCBI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SGLNFQDLMA RQGAIDSPPK TPFIMGSECA GDIEQVGEGV ENFKVGDRVV ALPDHKAWAE QVAVPATSVF ALPNGMSYLD
81 AAAITMNYTV AYILLFELAH LTPGK**NLLLH SAGGGVGQAV VQLAK**TVKDV TIFGVCSKSK HESLKATGSI DHLLERGTDY
161 TNEVRKISPE GVDIVLDCLC GEECNKGYAL LKPMGK**YILY GSSNVVTGET K**SFFSAARSW WQVDKVSPIK LFDENKTLSG
241 LNLRHLMYQH GSHAFVRRAV NQVYTLWSEG KIKPVVDSTW ALEDVPEAMQ KMHDRKNIGK IVLDPNLEPK PKPATPAKGK
321 AKDKKSANQE EKKASSVESE EGEKKKEPEL TNGTSEDKSD SDSKEKESS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLLLHSAGGGVGQAVVQLAK.T	Y	74.90	1931.0952	-69.1	966.4882	2	34.70	2773	2	106	125	
K.YILYGSSNVVTGETK.S	Y	68.46	1629.8250	-44.1	815.8838	2	32.54	2531	1	197	211	
total 2 peptides												

tr|A0A232ETH5|A0A232ETH5_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEIESKNILH SGYFHPVLRQ WQAPNVGITA ENLMFPIFVL DEPNAVTEIQ SMPGVNRYGI NKLKGLLEPL IAKGLKSILL
81 FGVANNLPKD EIASAADSPA NPIIQALPLL RKWFPSLIIA CDVCLCPYSS HGHCGMLNDD GTIDNKPSIK RIADIAVAYA
161 KAGAHIVAPS DMMDGRIKAI KHGLAAAGLS NKVAVLSYSV KFASGFYGPF RDASKSAPKF GDRQCYQLPS GSNGLAARAA
241 ARDIEEGADM LMVKPGLAYL DIVKETKNAH PEYPMFIYQV SGEYAMLYHG AQNGAINLEA VLKETKMKGA TALLLLGLVA
321 AIAASKEEKK DKDDIGTVIG IDLGTTYSCV GVYKNGRVEI IANDQGNR**IT PSYVAFTADG ER**LIGDAAKN QLTTNPENTV
401 FDAKRLIGRE WTDATVQHDV KFFPFKVIEK NSKPHIKVST SQGDKIFAPE EISAMVLGK**M KETAEAYLGK** KVTHAVVTVP
481 AYFNDAQRQA TKDAGIISGL QVMRIINEPT AAAIAYGLDK KDGEKNVLVF DLGGGTFDVS LLTIDNGVFE VVATNGDTHL
561 GGEDFDQRVM DHFIKLYKKK KGKDIRKDNR AVQKLRREVE KAKRALSASH QVR**IEIESFF EGEDFSETLT R**AKFEELNMD
641 LFRSTMKPVQ KVLEDADMSK KDVDEIVLVG GSTRIPKVQQ LVKEFFGGKE PSRGINPDEA VAYGAAVQAG VLSGEQDTDA
721 IVLLDVNPLT MGIETVGGVM TKLIPRNTVI PTKKSQIFST ASDNQHTVTI QVYEGERPMT KDNHLLGKFD LTGIPPAPRG
801 VPQIEVTFEI DANGILQVSA EDKGTGNREK IVITNDQNRL TPDDIERMIK DAEKFADEDK KLKERVEARN ELESYAYSLK
881 NQLQDKEKLG SKVSDSDKAK MEEAIDEKIK WLEENQDTDP EEYKKQKKEL SDIVQPIISK LYQGAGGGVP PTGGEESDDD
961 LKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	614	631	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	460	470	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	369	382	
total 3 peptides												

tr|F5BYH9|F5BYH9_HELAM back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLKMRWSILA LACVVVAVCA DDKKDKEKDI GTVIGIDLGT TYSCVGVYKN GRVEIIANDQ GNR**ITPSYVA FTADGER**LIG
81 DAAKNQLTTN PENTVFDAKR LIGREWGDAT VQHDVKFFPF KVVEKNSKPH VSVMTSQGDK IFAPEEISAM VLIK**MKETAE**
161 **AYLGK**KVTHA VVTVPAYFND AQRQATKDAG AIAGLQVMRI INEPTAAAIA YGLDKKEGEK NVLVFDLGGG TFDVSLLTID
241 NGVFEVVATN GDTHLGGEDF DQRVMEHFIK LYKKKKGKDI RKDNRAVQKL RREVEKAKRA LSSSHQVK**IE IESFFEGEDF**
321 **SETLTR**AKFE ELNMDLFRST LKPVQKVLED ADMNKKDVDE IVLVGGSTRI PKVQQLVKEF FNGKEPSRGI NPDEAVAYGA
401 AVQAGVLSGE QDTDAIVLLD VNPLTMGIET VGGVMTKLIP RNTVIPTKKS QIFSTASDNQ HTVTIQVYEG ERPMTKDNHL
481 LGKFDLTGIP PAPRGIPQIE VTFEIDANGI LQVSAEDKGT GNREKIVITN DQNRLTPEDI ERMIKDAERF ADEDKRLKER
561 VEARNELESY AYSIKNQLQD KEKLGAKLSD DEKTKMEEAI DAAIKWLEDN QDVDSEEYKK QKKSLEDVVQ PIIAKLYQGQ
641 GGVPPPGAGG DEEDFKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	309	326	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	155	165	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	64	77	
total 3 peptides												

tr|I4DIU0|I4DIU0_PAPXU back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVKMRWYLLG LVCAVALVCA EDKKEKDKDI GTVIGIDLGT TYSCVGVYKN GRVEIIANDQ GNR**ITPSYVA FTADGER**LIG

81 DAAKNQLTTN PENTVFDAKR LIGREWTDST VQHDVKFFPF KVVEKNSKPH VSVMTAQGDK IFAPEEISAM VLTK**MKETAE**

161 **AYLGK**KVTHA VVTVPAYFND AQRQATKDAG VIAGLNVMRI INEPTAAAIA YGLDKKEGEK NVLVFDLGGG TFDVSLLTID

241 NGVFEVVATN GDTHLGGEDF DQRVMEHFIK LYKKKKGKDI RKDNRAVQKL RREVEKAKRA LSSGHQVK**IE IESFFEGEDF**

321 **SETLTR**AKFE ELNMDLFRST LKPVQKVLED ADMNKKDVDE IVLVGGSTRI PKVQQLVKEF FNGKEPSRGI NPDEAVAYGA

401 AVQAGVLSGE QDTDAIVLLD VNPLTMGIET VGGVMTKLIP RNTVIPTKKS QIFSTASDNQ HTVTIQVYEG ERPMTKDNHL
481 LGKFDLTGIP PAPRGIPQIE VTFEIDANGI LQVSAEDKGT GNREKIVITN DQNRLTPEDI ERMIKDAEKF ADDDKKLKER
561 VESRNELESY AYSIKNQLQD KEKLGAKVSD DDKAKMEEAI DAAIKWLEDN QDTDAEEYKK QKKSLEDVVQ PIIAKLYQGQ
641 GGVPPPGAGG EDEDFKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	309	326	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	155	165	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	64	77	
total 3 peptides												

tr|V9IGA1|V9IGA1_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKKMKGVKAL FLLGLITFAF AKEEKQKEDI GTVIGIDLGT TYSCVGVYKN GRAEIIANDQ GNR**ITPSYVA FTADGER**LIG

81 DAAKNQLTTN PENTVFDAKR LIGREWSDPT VQRDIKSFPF KVIEKNSKPH IRMVINGEEK VFAPEEISAM VLGK**MKETAE**

161 **AYLGK**KVTHA VVTVPAYFND AQRQATKDAG TISGLVVMRI INEPTAAAIA YGLDKKDGEK NVLVFDLGGG TFDVSLLTID

241 NGVFEVVATN GDTHLGGEDF DLRVMDHFTK LYKKKKGKDI RKDSRTLQKL RREVEKAKRA LSVSHQVR**IE IESFFEGEDF**

321 **SETLTR**AKFE ELNMDLFRST LKPVQKVLED SDMNKKDVDE IVLVGGSTRI PKVQQLVKEF FGGKEPSRGI NPDEAVAYGA

401 AVQAGVLSGE QDTDAIVLLD VNPLTMGIET VGGVMTKLIP RNTVIPTKKS QIFSTASDNQ HTVTIQVYEG ERPMTKDNHP
481 LGKFDLTGIP PAPRGIPQIE VTFEIDANGI LQVSAEDKGT GNREKIVITN DQNRLTPDDI ERMIKDAEKF ADDDKKLKER
561 VEARNELESY AYSLKNQLAD KEKLGSKVSD SDKAKMEEAI DEKIKWLEEN ADTDPEEYKK QKKELTDIVQ PIIAKLYQGA
641 GGGVPPTGGD DEDLKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	309	326	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	155	165	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	64	77	
total 3 peptides												

tr|A0A1A9WZF3|A0A1A9WZF3_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRLFLILAVM AFVGCTRGEE KKDKEKEIGT VIGIDLGTTY SCVGVYKNGR VEIIANDQGN R**ITPSYVAFT ADGER**LIGDA

81 AKNQLTTNPE NTVFDAKRLI GREWSDTNVQ HDIKFFPFKV IEKNSKPHIN VATSQGNKVF APEEISAMVL GK**MKETAEAY**

161 **LGK**KVTHAVV TVPAYFNDAQ RQATKDAGVI AGLNVMRIIN EPTAAAIAYG LDKKEGEKNV LVFDLGGGTF DVSLLTIDNG

241 VFEVVATNGD THLGGEDFDQ RVMDHFIKLH KKKKGKDIRK DNRAVQKLRR EVEKAKRALS SAHHVR**LEIE SFFEGEDFSE**

321 **TLTR**AKFEEL NMDLFRSTLK PVQKVLEDAD MNKKDVHEIV LVGGSTRIPK VQQLVKDFFG GKEPSRGINP DEAVAYGAAV

401 QAGVLSGEQD TDAIVLLDVN PLTLGIETVG GVMTKLIPRN TVIPTKKSQI FSTASDNQHT VTIQVYEGER PMTKDNHLLG
481 KFDLTGIPPA PRGIPQIEVS FEIDANGILQ VSAEDKGTGN KEKIVITNDQ NRLTPEDIER MIRDAEKFAD EDKKLKEKVE
561 SRNELESYSY SLKNQIGDKD KLGAKLSEED KIKMEAAIEE TIKWLEQNSD ADPEEYKKQK KDLETIVQPI IAKLYQGAGG
641 VPPTEGGEDS DDLKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	307	324	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	153	163	
total 3 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	62	75	
total 3 peptides												

tr|A0A212FBA7|A0A212FBA7_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRWCILALAC VLAAVYADEK KEKDKDIGTV IGIDLGTTYS CVGVYKNGRV EIIANDQGNR **ITPSYVAFTA DGER**LIGDAA

81 KNQLTTNPEN TVFDAKRLIG REWSDSTVQH DVKFFPFKVV EKNSKPHVSV MTSQGDKIFA PEEISAMVLT K**MKETAEAYL**

161 **GK**KVTHAVVT VPAYFNDAQR QATKDAGVIA GLNVMRIINE PTAAAIAYGL DKKEGEKNVL VFDLGGGTFD VSLLTIDNGV

241 FEVVATNGDT HLGGEDFDQR VMEHFIKLYK KKKGKDIRKD NRAVQKLRRE VEKAKRALSS SHQVK**IEIES FFEGEDFSET**

321 **LTR**AKFEELN MDLFRSTLKP VQKVLEDADM NKKDVDEIVL VGGSTRIPKV QQLVKEFFNG KEPSRGINPD EAVAYGAAVQ

401 AGVLSGEQDT DAIVLLDVNP LTMGIETVGG VMTKLIPRNT VIPTKKSQIF STASDNQHTV TIQVYEGERP MTKDNHLLGK
481 FDLTGIPPAP RGIPQIEVTF EIDANGILQV SAEDKGTGNR EKIVITNDQN RLTPEDIERM IKDAEKFADD DKKLKERVES
561 RNELESYAYS IKNQLQDKEK LGSKLSDDEK SKMEEAIDAS IKWLEDNQDA DAEDYKKQKK SLEDVVQPII AKLYQGQGGV
641 PPQGAGGEDE EFKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	306	323	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	152	162	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	61	74	
total 3 peptides												

tr|A0A194PQY8|A0A194PQY8_PAPXU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRWYLLGLVC AVALVCAEDK KEKDKDIGTV IGIDLGTTYS CVGVYKNGRV EIIANDQGNR **ITPSYVAFTA DGER**LIGDAA

81 KNQLTTNPEN TVFDAKRLIG REWTDSTVQH DVKFFPFKVV EKNSKPHVSV MTAQGDKIFA PEEISAMVLT K**MKETAEAYL**

161 **GK**KVTHAVVT VPAYFNDAQR QATKDAGVIA GLNVMRIINE PTAAAIAYGL DKKEGEKNVL VFDLGGGTFD VSLLTIDNGV

241 FEVVATNGDT HLGGEDFDQR VMEHFIKLYK KKKGKDIRKD NRAVQKLRRE VEKAKRALSS GHQVK**IEIES FFEGEDFSET**

321 **LTR**AKFEELN MDLFRSTLKP VQKVLEDADM NKKDVDEIVL VGGSTRIPKV QQLVKEFFNG KEPSRGINPD EAVAYGAAVQ

401 AGVLSGEQDT DAIVLLDVNP LTMGIETVGG VMTKLIPRNT VIPTKKSQIF STASDNQHTV TIQVYEGERP MTKDNHLLGK
481 FDLTGIPPAP RGIPQIEVTF EIDANGILQV SAEDKGTGNR EKIVITNDQN RLTPEDIERM IKDAEKFADD DKKLKERVES
561 RNELESYAYS IKNQLQDKEK LGAKVSDDDK AKMEEAIDAA IKWLEDNQDT DAEEYKKQKK SLEDVVQPII AKLYQGQGGV
641 PPPGAGGEDE DFKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	306	323	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	152	162	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	61	74	
total 3 peptides												

tr|A0A0M9A8F3|A0A0M9A8F3_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKEIKALILL SLVTFAFAKE EKQKEDIGTV IGIDLGTTYS CVGVYKNGRA EIIANDQGNR **ITPSYVAFTA DGER**LIGDAA

81 KNQLTTNPEN TVFDAKRLIG REWSDPTVQR DIKFFPFKVI EKNSKPHIRM VINGEEKVFA PEEISAMVLG K**MKETAEAYL**

161 **GK**KVTHAVVT VPAYFNDAQR QATKDAGTIS GLIVMRIINE PTAAAIAYGL DKKDGEKNVL VFDLGGGTFD VSLLTIDNGV

241 FEVVATNGDT HLGGEDFDQR VMDHFTKLYK KKKGKDIRKD SRALQKLRRE VEKAKRALSV SHQVR**IEIES FFEGEDFSET**

321 **LTR**AKFEELN MDLFRSTLKP VQKVLEDSDM NKKDVDEIVL VGGSTRIPKV QQLVKEFFGG KEPSRGINPD EAVAYGAAVQ

401 AGVLSGEQDT DAIVLLDVNP LTMGIETVGG VMTKLIPRNT VIPTKKSQIF STASDNQHTV TIQVYEGERP MTKDNHLLGK
481 FDLTGIPPAP RGIPQIEVTF EIDANGILQV SAEDKGTGNR EKIVITNDQN RLTPDDIERM IKDAEKFADD DKKLKERVEA
561 RNELESYAYS LKNQLADKEK LGSKVSDSDK AKMEEAIEEK IKWLEENADT DPEEYKKQKK ELTDIVQPII AKLYQGAGGG
641 VPPTGGDEED LKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	306	323	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	152	162	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	61	74	
total 3 peptides												

tr|A0A088ACF4|A0A088ACF4_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKGVKALFLL GLITFAFAKE EKQKEDIGTV IGIDLGTTYS CVGVYKNGRA EIIANDQGNR **ITPSYVAFTA DGER**LIGDAA

81 KNQLTTNPEN TVFDAKRLIG REWSDPTVQR DIKSFPFKVI EKNSKPHIRM VINGEEKVFA PEEISAMVLG K**MKETAEAYL**

161 **GK**KVTHAVVT VPAYFNDAQR QATKDAGTIS GLVVMRIINE PTAAAIAYGL DKKDGEKNVL VFDLGGGTFD VSLLTIDNGV

241 FEVVATNGDT HLGGEDFDLR VMDHFTKLYK KKKGKDIRKD SRTLQKLRRE VEKAKRALSV SHQVR**IEIES FFEGEDFSET**

321 **LTR**AKFEELN MDLFRSTLKP VQKVLEDSDM NKKDVDEIVL VGGSTRIPKV QQLVKEFFGG KEPSRGINPD EAVAYGAAVQ

401 AGVLSGEQDT DAIVLLDVNP LTMGIETVGG VMTKLIPRNT VIPTKKSQIF STASDNQHTV TIQVYEGERP MTKDNHPLGK

481 FDLTGIPPAP RGIPQIEVTF EIDANGILQV SAEDKGTGNR EKIVITNDQN RLTPDDIERM IKDAEKFADD DKKLKERVEA

561 RNELESYAYS LKNQLADKEK LGSKVSDSDK AKMEEAIDEK IKWLEENADT DPEEYKKQKK ELTDIVQPII AKLYQGAGGG

641 VPPTGGDDED LKDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IEIESFFEGEDFSETLTR.A	Y	78.68	2147.9897	17.7	1075.0211	2	40.04	3371	1	306	323	
K.MKETAEAYLGK.K	Y	27.81	1239.6169	126.9	620.8944	2	27.91	2068	1	152	162	
R.ITPSYVAFTADGER.L	Y	27.14	1525.7412	93.5	763.9492	2	33.16	2600	1	61	74	
total 3 peptides												

tr|E4W6B4|E4W6B4_PROCL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLGAAARACS SVLKAAKPAV ASLSLQHGGA RTIPAVYAAQ RNYAAKAEAA TQTGVANGKV VAVIGAVVDV QFDGELPPIL h Hydr

81 NSLEVENRTP R**LVLEVAQHL GENTVR**TIAM DGTEGLVRGN VVRDTGGPIS IPVGPGTLGR IINVIGEPID ERGPVPTEFY

161 STIHAEAPDF VDMSVEQEIL VTGIKVVDLL APYSKGGKIG LFGGAGVGKT VLIMELINNA AK**AHGGYSVF AGVGER**TREG

241 NDLYHEMIES GVISLKDDTS KVSLVYGQMN E**PPGARARVA LTGLTVAEYF R**DQEGQDVLL FIDNIFRFTQ AGSEVSALLG

321 RIPSAVGYQP TLATDMGTMQ ERITTTKKGS ITSVQAIYVP ADDLTDPAPA TTFAHLDATT VLSRGIAELG IYPAVDPLDS

401 ISRIMDPNII GAEHYNVARA VQKILQDHKS LQDIIAILGM DELSEEDKLT VARARKIQKF LSQPFQVAEV FTGYSGKFVS

481 LEKTIASFKE ILAGKYDYLP EAAFYMQGDI QDVLEKAEQL ATQGS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	223	236	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	92	106	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	272	291	Hydroxylation
total 3 peptides												

tr|D8VIP0|D8VIP0_HELME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VQFEDSLPPI LNALEVQNRS PR**LVLEVAQH LGENTVR**TIA MDGTEGLVRG QPVHDCGSPI RIPVGAETLG RIINVIGEPI h Hydr

81 DERGPIPTDK TAAIHAEAPE FVDMSVQQEI LVTGIKVVDL LAPYAKGGKI GLFGGAGVGK TVLIMELINN VAK**AHGGYSV**

161 **FAGVGER**TRE GNDLYHEMIE SGVISLKDKT SKVALVYGQM NE**PPGARARV ALTGLTVAEY FR**DQEGQDVL LFIDNIFRFT

241 QAGSEVSALL GRIPSAVGYQ PTLATDMGTM QERITTTKKG SITSVQAIYV PADDLTDPAP ATTFAHLDAT TVLSRAIAEL

321 GIYPAVDPLD STSRIMDPNI IGAEHYNVAR GV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	154	167	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	23	37	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	203	222	Hydroxylation
total 3 peptides												

tr|G3KAY5|G3KAY5_HELNM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EDSLPPILNA LEVQNRSPR**L VLEVAQHLGE NTVR**TIAMDG TEGLVRGQPV HDCGSPIRIP VGAETLGRII NVIGEPIDER h Hydr
81 GPIPTDKTAA IHAEAPEFVD MSVQQEILVT GIKVVDLLAP YAKGGKIGLF GGAGVGKTVL IMELINNVAK **AHGGYSVFAG**
161 **VGER**TREGND LYHEMIESGV ISLKDKTSKV ALVYGQMNE**P PGARARVALT GLTVAEYFR**D QEGQDVLLFI DNIFRFTQAG
241 SEVSALLGRI PSAVGYQPTL ATDMGTMQER ITTTKKGSIT SVQAIYVPAD DLTDPAPATT FAHLDATTVL SRAIAELGIY
321 PAVDPLDSTS RIMDPNIIGA EHYN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	151	164	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	20	34	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	200	219	Hydroxylation
total 3 peptides												

tr|G3KAV3|G3KAV3_HELNM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EDSLPPILNA LEVQNRSPR**L VLEVAQHLGE NTVR**TIAMDG TEGLVRGQPV HDCGSPIRIP VGAETLGRII NVIGEPIDER h Hydr
81 GPIPTDKTAA IHAEAPEFVD MSVQQEILVT GIKVVDLLAP YAKGGKIGLF GGAGVGKTVL IMELINNVAK **AHGGYSVFAG**
161 **VGER**TREGND LYHEMIESGV ISLKDKTSKV ALVYGQMNE**P PGARARVALT GLTVAEYFR**D QEGQDVLLFI DNIFRFTQAG
241 SEVSALLGRI PSAVGYQPTL ATDMGTMQER ITTTKKGSIT SVQAIYVPAD DLTDPAPATT FAHLDATTVL SRAIAELGIY
321 PAVDPLDSTS RIMDPNIIGA EHYN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	151	164	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	20	34	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	200	219	Hydroxylation
total 3 peptides												

tr|A0A182YSV3|A0A182YSV3_ANOST

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LPPILNALEV QGRSAR**LVLE VAQHLGENTV R**TIAMDGTEG LVRGQRVLDT GSPIRIPVGA ETLGRIINVI GEPIDERGPI h Hydr
81 NTNLSAPIHA EAPEFIEMSV EQEILVTGIK VVDLLAPYAK GGKIGLFGGA GVGKTVLIME LINNVAK**AHG GYSVFAGVGE**
161 **R**TREGNDLYN EMIEGGVISL KDKSSKVALV YGQMNE**PPGA RARVALTGLT VAEYFR**DQEG QDVLLFIDNI FRFTQAGSEV
241 SALLGRIPSA VGYQPTLATD MGSMQERITT TKKGSITSVQ AIYVPADDLT DPAPATTFAH LDATTVLSRA IAELGIYPAV
321 DPLDSTSRIM DPNIIGAEHY NIARGVQKIL QDYKSLQDII AILGMDELSE EDKLTVARAR KIQRFLSQPF QVAEVFTGHA
401 GKLVPLEETI KGFTKILNGE LDHLPEVAFY MVGPIEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	148	161	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	17	31	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	197	216	Hydroxylation
total 3 peptides												

tr|E0W6V9|E0W6V9_MARJA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLGAAQRACS TILKAAKPAV VSKGLQNVGS KTLPALYTSQ RNYAAKAEAA TQTGVPNGSV VAVIGAVVDV QFDGELPPIL h Hydr
81 NALEVANRSP R**LVLEVAQHL GENTVR**TIAM DGTEGLIRGN AVVDTGSPIS IPVGPGTLGR IINVIGEPID ERGPIPTEHF
161 SAIHAEAPDF VEMSVEQEIL VTGIKVVDLL APYSKGGKIG LFGGAGVGKT VLIMELINNV AK**AHGGYSVF AGVGER**TREG
241 NDLYHEMIES GVISLKDDTS KVSLVYGQMN E**PPGARARVA LTGLTVAEYF R**DQEGQDVLL FIDNIFRFAQ AGSEVSALLG
321 RIPSAVGYQP TLATDMGSMQ ERITTTKKGS ITSVQAIYVP ADDLTDPAPA TTFAHLDATT VLSRGIAELG IYPAVDPLDS
401 ISRIMDANII GHEHYNVARS VQKILQDHKS LQDIIAILGM DELSEEDKLT VARARKIQKF LSQPFQVAEV FTGYSGKFVS
481 LPDTIKSFKE ILAGKYDDLP EAAFYMQGSI EDVVEKAEQL AAQAS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	223	236	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	92	106	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	272	291	Hydroxylation
total 3 peptides												

tr|Q1HPT1|Q1HPT1_BOMMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLGAISRVGS GILAVKSVAE KSLSECGKIV AVNAVNKRDY AAKSAGKGQG KVVAVIGAVV DVQFEDNLPP ILNALEVQNR h Hydr
81 SPR**LVLEVAQ HLGENTVR**TI AMDGTEGLVR GQPVLDSGSP IRIPVGAETL GRIINVIGEP IDERGPIPTD KTAAIHAEAP
161 EFVDMSVQQE ILVTGIKVVD LLAPYAKGGK IGLFGGAGVG KTVLIMELIN NVAK**AHGGYS VFAGVGER**TR EGNDLYHEMI
241 ESGVISLKDK TSKVALVYGQ MNE**PPGARAR VALTGLTVAE YFR**DQEGQDV LLFIDNIFRF TQAGSEVSAL LGRIPSAVGY
321 QPTLATDMGT MQERITTTKK GSITSVQAIY VPADDLTDPA PATTFAHLDA TTVLSRAIAE LGIYPAVDPL DSTSRIMDPN
401 IIGAEHYNVA RGVQKILQDY KSLQDIIAIL GMDELSEEDK LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPLEETIKGF
481 SKILAGDYDH LPEVAFYMVG PIEEVVAKAD TLAKNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	215	228	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	84	98	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	264	283	Hydroxylation
total 3 peptides												

tr|V9IJZ2|V9IJZ2_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLNVVSKAAA GALRAVKPSI LQNEITKISG ALSVNSRDYA KAASSKGGAQ GKIVAVIGAV VDVQFDDALP PILNALEVQN h Hydr
81 RTPR**LVLEVA QHLGENTVR**T IAMDGTEGLV RGQSVLDSGY PIRIPVGAET LGRIINVIGE PIDERGPIPT DKLAPIHADA
161 PEFVDMSVEQ EILVTGIKVV DLLAPYAKGG KIGLFGGAGV GKTVLIMELI NNVAK**AHGGY SVFAGVGER**T REGNDLYHEM
241 IESGVISLKD KTSKVALVYG QMNE**PPGARA RVALTGLTVA EYFR**DQEGQD VLLFIDNIFR FTQAGSEVSA LLGRIPSAVG
321 YQPTLATDMG SMQERITTTK KGSITSVQAI YVPADDLTDP APATTFAHLD ATTVLSRAIA ELGIYPAVDP LDSTSRIMDP
401 NIIGAEHYNV ARGVQKILQD YKSLQDIIAI LGMDELSEED KLTVARARKI QRFLSQPFQV AEVFTGHAGK LVPLEETIKG
481 FKKILAGDYD HLPEVAFYMV GPIEEVVAKA ESLAKQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	216	229	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	85	99	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	265	284	Hydroxylation
total 3 peptides												

tr|I4DIU5|I4DIU5_PAPXU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSTAGRAGL LAARTVVNNS LAEKTPLVAG ALANKRDYAA KAAGKGQGKV VAVIGAVVDV QFEDNLPPIL NALEVQNRSP h Hydrc
81 R**LVLEVAQHL GENTVR**TIAM DGTEGLVRGQ PVLDSGSPIR IPVGAETLGR IINVIGEPID ERGPIPTDKT AAIHAEAPEF
161 VDMSVEQEIL VTGIKVVDLL APYAKGGKIG LFGGAGVGKT VLIMELINNV AK**AHGGYSVF AGVGER**TREG NDLYHEMIES
241 GVISLKDKTS KVALVYGQMN E**PPGARARVA LTGLTVAEYF R**DQEGQDVLL FIDNIFRFTQ AGSEVSALLG RIPSAVGYQP
h
321 TLATDMGTMQ ERITTTKKGS ITSVQAIYVP ADDLTDPAPA TTFAHLDATT VLSRAIAELG IYPAVDPLDS TSRIMDPNII
401 GAEHYNVARG VQKILQDYKS LQDIIAILGM DELSEEDKLT VARARKIQRF LSQPFQVAEV FTGHAGKLVP LEETIKGFSK
481 ILQGEYDHLP EVAFYMVGPI EEVVAKAETL AKNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	213	226	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	82	96	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	262	281	Hydroxylation
total 3 peptides												

tr|A0A1B0CLT6|A0A1B0CLT6_LUTLO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSAINNAVR VATKRETGKF ISGLVQFNRQ YAAKTAAKAG ASNGRVVAVI GAVVDVQFDE NLPPILNALE VEGRKPR**LVL** h Hydrc
81 **EVAQHLGENT VR**TIAMDGTE GLVRGNKVLD TGSPIKIPVG AETLGRIINV IGEPIDERGP IETNKFAAIH AEAPEFVEMS
161 VEQEILVTGI KVVDLLAPYA KGGKIGLFGG AGVGKTVLIM ELINNVAK**AH GGYSVFAGVG ER**TREGNDLY NEMIESGVIS
241 LKDKTSKVAL VYGQMNE**PPG ARARVALTGL TVAEYFR**DQE GQDVLLFIDN IFRFTQAGSE VSALLGRIPS AVGYQPTLAT
h
321 DMGSMQERIT TTKKGSITSV QAIYVPADDL TDPAPATTFA HLDATTVLSR AIAELGIYPA VDPLDSTSRI MDPNVIGQEH
401 YNVARGVQKI LQDYKSLQDI IAILGMDELS EEDKLTVARA RKIQRFLSQP FQVAEVFTGH AGKLVPLEET IKGFSKILIG
481 EYDHLPEVAF YMVGPIEEVV AKAERLAKEA A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	209	222	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	78	92	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	258	277	Hydroxylation
total 3 peptides												

tr|A0A0M4F807|A0A0M4F807_DROBS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFALRAAAKA DKNLLPFLGQ LTRGHAAKAS AKAAAGANGK IVAVIGAVVD VQFDENLPPI LNALEVDNRS PR**LVLEVAQH** h Hydrc
81 **LGENTVR**TIA MDGTEGLVRG QKVLDTGYPI RIPVGAETLG RIINVIGEPI DERGPIPTDK TAPIHAEAPE FVEMSVEQEI
161 LVTGIKVVDL LAPYAKGGKI GLFGGAGVGK TVLIMELINN VAK**AHGGYSV FAGVGER**TRE GNDLYNEMIE SGVISLKDKT
241 SKVALVYGQM NE**PPGARARV ALTGLTVAEY FR**DQEGQDVL LFIDNIFRFT QAGSEVSALL GRIPSAVGYQ PTLATDMGSM
h
321 QERITTTKKG SITSVQAIYV PADDLTDPAP ATTFAHLDAT TVLSRAIAEL GIYPAVDPLD STSRIMDPNI IGQEHYNVAR
401 GVQKILQDYK SLQDIIAILG MDELSEEDKL TVARARKIQR FLSQPFQVAE VFTGHAGKLV PLEQTIKGFS QILAGEYDHL
481 PEVAFYMVGP IEEVVEKADR LAKEAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	204	217	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	73	87	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	253	272	Hydroxylation
total 3 peptides												

tr|A0A182T1X0|A0A182T1X0_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSSMKTLMT AAIRADQIMA RSYAAKAAAK AAAGAQGKVV AVIGAVVDVQ FDEQLPPILN ALEVQGRSAR **LVLEVAQHLG** h Hydr

81 **ENTVR**TIAMD GTEGLVRGQQ VLDTGSPIRI PVGAETLGRI INVIGEPIDE RGPINTNLSA PIHAEAPEFI EMSVEQEILV

161 TGIKVVDLLA PYAKGGKIGL FGGAGVGKTV LIMELINNVA K**AHGGYSVFA GVGER**TREGN DLYNEMIEGG VISLKDKSSK

241 VALVYGQMNE **PPGARARVAL TGLTVAEYFR** DQEGQDVLLF IDNIFRFTQA GSEVSALLGR IPSAVGYQPT LATDMGSMQE

321 RITTTKKGSI TSVQAIYVPA DDLTDPAPAT TFAHLDATTV LSRAIAELGI YPAVDPLDST SRIMDPNIIG AEHYNIARGV
401 QKILQDYKSL QDIIAILGMD ELSEEDKLTV ARARKIQRFL SQPFQVAEVF TGHAGKLVPL EETIKGFTKI LNGELDHLPE
481 VAFYMVGPIE EVVEKAERLA KEAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	202	215	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	71	85	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	251	270	Hydroxylation
total 3 peptides												

tr|E3XEC7|E3XEC7_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSSMKTLVS AAVRADQVLA RTYAAKAAAA AAGAQGKVVA VIGAVVDVQF DDNLPPILNA LEVQGRTAR**L VLEVAQHLGE** h Hydr

81 **NTVR**TIAMDG TEGLVRGQRV LDTGSPIRIP VGAETLGRII NVIGEPIDER GPIETNLSAP IHAEAPEFIE MSVEQEILVT

161 GIKVVDLLAP YAKGGKIGLF GGAGVGKTVL IMELINNVAK **AHGGYSVFAG VGER**TREGND LYNEMIEGGV ISLKDKSSKV

241 ALVYGQMNE**P PGARARVALT GLTVAEYFR**D QEGQDVLLFI DNIFRFTQAG SEVSALLGRI PSAVGYQPTL ATDMGSMQER

321 ITTTKKGSIT SVQAIYVPAD DLTDPAPATT FAHLDATTVL SRAIAELGIY PAVDPLDSTS RIMDPNIIGA EHYNIARGVQ
401 KILQDYKSLQ DIIAILGMDE LSEEDKLTVA RARKIQRFLS QPFQVAEVFT GHAGKLVPLE ETIKGFTKIL NGELDHLPEV
481 AFYMVGPIEE VVEKAERLAK EAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	201	214	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	70	84	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	250	269	Hydroxylation
total 3 peptides												

tr|A0A182FTY6|A0A182FTY6_ANOAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSSMKTLVS AAVRADQVLA RTYAAKAAAA AAGAQGKVVA VIGAVVDVQF DDNLPPILNA LEVQGRTAR**L VLEVAQHLGE** h Hydr

81 **NTVR**TIAMDG TEGLVRGQRV LDTGSPIRIP VGAETLGRII NVIGEPIDER GPIETNLSAP IHAEAPEFIE MSVEQEILVT

161 GIKVVDLLAP YAKGGKIGLF GGAGVGKTVL IMELINNVAK **AHGGYSVFAG VGER**TREGND LYNEMIEGGV ISLKDKSSKV

241 ALVYGQMNE**P PGARARVALT GLTVAEYFR**D QEGQDVLLFI DNIFRFTQAG SEVSALLGRI PSAVGYQPTL ATDMGSMQER

321 ITTTKKGSIT SVQAIYVPAD DLTDPAPATT FAHLDATTVL SRAIAELGIY PAVDPLDSTS RIMDPNIIGA EHYNIARGVQ
401 KILQDYKSLQ DIIAILGMDE LSEEDKLTVA RARKIQRFLS QPFQVAEVFT GHAGKLVPLE ETIKGFTKIL NGELDHLPEV
481 AFYMVGPIEE VVEKAERLAK EAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	201	214	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	70	84	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	250	269	Hydroxylation
total 3 peptides												

tr|A0A1I8NT76|A0A1I8NT76_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSAARSALS RSDKKVISLL AQSQREYAKA AAKAAAVGNG KIVAVIGAVV DVQFEDQLPP ILNALEVDNR TPR**LVLEVAQ** h Hydr

81 **HLGENTVR**TI AMDGTEGLVR GHKVIDTGFP IRIPVGAETL GRIINVIGEP IDERGPIPTD KTAPIHAEAP EFVDMSVEQE

161 ILVTGIKVVD LLAPYAKGGK IGLFGGAGVG KTVLIMELIN NVAK**AHGGYS VFAGVGER**TR EGNDLYNEMI ESGVISLKDK

241 TSKVALVYGQ MNE**PPGARAR VALTGLTVAE YFR**DQEGQDV LLFIDNIFRF TQAGSEVSAL LGRIPSAVGY QPTLATDMGS
h

321 MQERITTTKK GSITSVQAIY VPADDLTDPA PATTFAHLDA TTVLSRAIAE LGIYPAVDPL DSTSRIMDPN IIGSTHYNVA
401 RGVQKILQDY KSLQDIIAIL GMDELSEEDK LTVARARKIQ RFLSQPFQVA EVFTGHAGKL VPLEETIKGF TQILAGEYDH
481 LPEVAFYMVG PIEEVVEKAE RLAKEAA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	205	218	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	74	88	
E.P(+15.99)PGARARVALTGLTVAEYFR.D	Y	19.15	2160.1802	-466.0	720.7318	3	38.28	3173	1	254	273	Hydroxylation
total 3 peptides												

tr|Q7PZV3|Q7PZV3_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFSTMKSLMT TAVRAEQMMA RSYAAKAAAK AAAGAQGKVV AVIGAVVDVQ FDEQLPPILN ALEVQGRSAR **LVLEVAQHLG**

81 **ENTVR**TIAMD GTEGLVRGQR VLDTGSPIRI PVGAETLGRI INVIGEPIDE RGPIDTNLSA PIHAEAPEFI EMSVEQEILV

161 TGIKVVDLLA PYAKGGKIGL FGGAGVGKTV LIMELINNVA K**AHGGYSVFA GVGER**TREVN DLYNEMI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	202	215	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	71	85	
total 2 peptides												

tr|Q7PKD7|Q7PKD7_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSAATRPILA RSYAAKAAVN AAAGAQGKVV AVIGAVVDVQ FDEQLPPILN ALEVQGRSAR **LVLEVAQHLG ENTVR**TIAMD

81 GTEGLVRGQR VLDTGSPIRI PVGAETLGRI INVIGEPIDE RGPIDTNLSA PIHAEAPEFI EMSVEQEILV TGIKVVDLLA
161 PYAKGGKIGL FGGAGVGKTV LIMELINNVA K**AHGGYSVFA GVGER**TREGN DLYNEMI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	192	205	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	61	75	
total 2 peptides												

tr|A0A023FND3|A0A023FND3_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TMLSVVGRAC SSVLKAAKPA ASLVKVNGAN SKLLPALCAT HPSSRRHAAA QAGAKAGNGH IVAVIGAVVD VQFDDNLPPI
81 LNALEVEGRK PR**LVLEVAQH LGENTVR**TIA MDGTEGLVRG QKVKDTQSPI KIPVGPETLG RIMNVIGEPI DERGPIPSDK

161 FLAIHQEAPE FVEMSVEQEI LVTGIKVVDL LAPYSKGGKI GLFGGAGVGK TVLIMELINN VAK**AHGGYSV FAGVGER**TRE

241 GNDLYHEMIE GGVISLKDKS SKVSLVYGQM NEPPGARARV ALTGLSVAEY FRDQEGQDVL LFIDNIFRFT QAGSEVSALL
321 GRIPSAVGYQ PTLATDMGTM QERITTTKKG SITSVQAIYV PADDLTDPAP ATTFAHLDAT TVLSRGIAEL GIYPAVDPLD
401 STSRIMDPNV VGQEHYDIAR GVQKILQDYK SLQDIIAILG MDELSEEDKL TVSRARKIQR FLSQPFQVAE VFTGQAGKFV
481 PIADTISGFK SILNGEMDHL PEVAFYMVGP IEEVREKAEK LAAEAT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AHGGYSVFAGVGER.T	Y	70.14	1405.6738	43.2	703.8746	2	30.94	2354	2	224	237	
R.LVLEVAQHLGENTVR.T	Y	44.48	1676.9209	672.1	840.0312	2	33.56	2645	1	93	107	
total 2 peptides												

tr|A0A088ACZ3|A0A088ACZ3_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAPPSYNDLG KSARDLFSSG YHFGLIKLDV KTKTK**SGVEF SSGGVSNQDT GK**VFGSLETK YNIDDYGLKF SEKWNTDNTL c Carba

100 c

81 ATDITFADKL LK**GLTLGYGC TFSPQTGTK**T GKLKTAYKHD NVSAAADFDL SLSTGPLVNA STVVGYQGWL AGYQACFDTQ

161 RNKLTKNNFA LGYTASDFTL HAAVNNGCDF SGLIYHKVKP ELEGAINLEW NSSNNVTQFG IATKYNLDND ASIRAK**VNSN**

241 **LQVGLGYQQK** LRDGVTLTLS TNIDGKNFGS GGHKIGLALD LQA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SGVEFSSGGVSNQDTGK.V	Y	56.97	1654.7434	-111.5	828.2867	2	28.03	2080	1	36	52	
K.GLTLGYGC(+57.02)TFSPQTGTK.T	Y	54.01	1786.8560	547.5	894.9244	2	33.78	2669	1	93	109	Carbamidomethylation
K.VNSNLQVGLGYQQK.L	Y	34.50	1546.8103	2.6	774.4144	2	30.57	2316	1	237	250	
total 3 peptides												

tr|V9IK96|V9IK96_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAPPSYNDLG KSARDLFSSG YHFGLIKLDV KTKTK**SGVEF SSGGVSNQDT GK**VFGSLETK YNIDDYGLKF SEKWNTDNTL c Carba

100 c

81 ATDITFADKL LK**GLTLGYGC TFSPQTGTK**T GKLKTAYKHD NVSAAADFDL SLSTGPLVNA STVVGYQGWL AGYQACFDTQ

161 RNKLTKNNFA LGYTASDFTL HAAVNNGCDF SGLIYHKVKP ELEGAINLEW NSSNNVTQFG IATKYNLDND ASIRAK**VNSN**

241 **LQVGLGYQQK** LRDGVTLTLS TNIDGKNFGS GGHKIGLALD LQA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SGVEFSSGGVSNQDTGK.V	Y	56.97	1654.7434	-111.5	828.2867	2	28.03	2080	1	36	52	
K.GLTLGYGC(+57.02)TFSPQTGTK.T	Y	54.01	1786.8560	547.5	894.9244	2	33.78	2669	1	93	109	Carbamidomethylation
K.VNSNLQVGLGYQQK.L	Y	34.50	1546.8103	2.6	774.4144	2	30.57	2316	1	237	250	
total 3 peptides												

tr|A0A087ZPQ8|A0A087ZPQ8_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAEKYDKLT PELKQELKSI AQQIVAPGKG ILAADESTAT IGKRLKDINV ENTEDNRRAY RQLLFTSAK**D AISQHISGVI** d Deam

81 **LFHETLYQK**A DDGTPFVELL KQRNILPGIK VDTGVVTLFG TEEETTTQGL DNLQARCIQY KKDGCQFAKW RCVLKIRKDC

161 PSK**LAILENA NVLAR**YASIC QSARIVPIVE PEILPDGDHD LARCQQVTEE VLAAVYKALS DHHVYLEGTL LKPNMVTPGQ

241 SCPNKASPQE IAAATVTALL RTVPPAVPGI TFLSGGQSEE EASVNLDAIN KFPANKPWAL TFSYGRALQA SVLRAWGGKK

321 EQISAGQEEL IKRAKANGLA SLGKYKAGSI TGKAAHDANS ESALGK**YSGG VVGAAGNATL FVANHAY**

d

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.YSGGVVGAAGNATLFVANHAY	Y	58.05	2037.9908	64.9	1020.0688	2	37.04	3035	1	367	387	
K.LAILENANVLAR.Y	Y	43.02	1295.7561	231.3	649.0352	2	35.20	2829	1	164	175	
K.YSGGVVGAAGN(+.98)ATLFVANHAY	Y	42.77	2038.9749	469.4	680.9846	3	36.78	3006	1	367	387	Deamidation (NQ)
K.DAISQHISGVILFHETLYQK.A	Y	36.99	2298.2007	419.0	1150.5891	2	36.79	3007	1	70	89	
total 4 peptides												

O18330|MRJP1_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTRLFMLVCL GIVCQGTTGN ILRGESLNKS LPILHEWKFF DYDFGSDERR QDAILSGEYD YKNNYPSDID QWHDKIFVTM

81 LRYNGVPSSL NVISKKVGDG GPLLQPYPDW SFAKYDDCSG IVSASKLAID KCDRLWVLDS GLVNNTQPMC SPKLLTFDLT

161 TSQLLKQVEI PHDVAVNATT GKGRLSSLAV QSLDCNTNSD TMVYIADEKG EGLIVYHNSD DSFHRLTSNT FDYDPKFTKM

241 TIDGESYTAQ DGISGMALSP MTNNLYYSPV ASTSLYYVNT EQFRTSDYQQ NDIHYEGVQN ILDTQSSAKV VSKSGVLFFG

321 LVGDSALGCW NEHRTLERHN IR**TVAQSDET LQMIASMK**IK EALPHVPIFD RYINR**EYILV LSNK**MQKMVN NDFNFDDVNF

401 RIMNANVNEL ILNTRCENPD NDRTPFKISI HL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TVAQSDETLQMIASMK.I	Y	78.68	1751.8434	113.3	877.0282	2	35.84	2901	2	343	358	
total 2 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.EYILVLSNK.M	Y	24.16	1077.6069	468.2	540.0630	2	33.82	2674	1	376	384	
total 2 peptides												

tr|C6K481|C6K481_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTRLFMLVCL GIVCQGTTGN ILRGESLNKS LPILHEWKFF DYDFGSDERR QDAILSGEYD YKNNYPSDID QWHDKIFVTM
81 LRYNGVPSSL NVISKKVGDG GPLLQPYPDW SFAKYDDCSG IVSASKLAID KCDRLWVLDS GLVNNTQPMC SPKLLTFDLT
161 TSQLLKQVEI PHDVAVNATT GKGRLSSLAV QSLDCNTNSD TMVYIADEKG EGLIVYHNSD DSFHRLTSNT FDYDPKFTKM
241 TIDGESYTAQ DGISGMALSP MTNNLYYSPV ASTSLYYVNT EQFRTSDYQQ NDIHYEGVQN ILDTQSSAKV VSKSGVLFFG
321 LVGDSALGCW NEHRTLERHN IR**TVAQSDET LQMIASMK**IK EALPHVPIFD RYINR**EYILV LSNK**MQKMVN NDFNFDDVNF

401 RIMNANVNEL ILNTRCENPD NDRTPFKISI HL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.TVAQSDETLQMIASMK.I	Y	78.68	1751.8434	113.3	877.0282	2	35.84	2901	2	343	358	
R.EYILVLSNK.M	Y	24.16	1077.6069	468.2	540.0630	2	33.82	2674	1	376	384	
total 2 peptides												

tr|A0A1W4WYG0|A0A1W4WYG0_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFTLWYTILG YKEYKAKNQR CLTCKRDGKE SSGNSSNIVK NTSPQTPKSS PLKVPTSLPP PPPPPPLNKS PIGLQRPSHT
81 HIPQPAPIRK PARSPSPHPI RSEAIDMPSE EESDEGSSEE EEEEEDDEEE EEDYDDDINE HSVIDSSALK TKKLLQDTIT
161 NDPRNSVKDF ISIEKNSPHN QRKSNEMVDA AVLDKLESGF KKLEASDSKS LLKKYLTREV FDKLKTKKTS FGSTLLDVIQ
241 SGLENHDSGI GIYAPDAEAY TVFADLFDPI IEDYHGGFKK TDKHPPKNWG DVSVFGNLDP AGEFVVSTRV RCGRSLEGYP
321 FNPCLTEEQY KEMEQKVSST LSGLEGELKG TFYPLTGMSK EVQQKLIDDH FLFKEGDRFL QAANACRFWP TGRGIFHNDN
401 KTFLVWVNEE DHLR**IISMQM GGDLGQVYR**R LVTAVNDIEK RLPFSHHDRL GFLTFCPTNL GTTVRASVHI KVPKLASNKA

481 KLDEVASKFN LQVRGTRGEH TEAEGGIYDI SNKRRMGLTE FDAVKEMYDG IAELIKIEKE L

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	415	429	
total 1 peptides												

tr|A0A1B6I0G0|A0A1B6I0G0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFALWYLYYG YKELRVVAEQ RGGNVPGSSA PTPVLFQKEP PVPAPPAQPV IRPPPPDVKP APPPPDVKPA PPPVVKPAPP
81 PEPKPQFTPG PPPQAPTPSP PAQPPPQPKP QPAKPIDIQR PRIPQQSPED RLMRPDNRPD PPSWNPVPTN PEDQLMNPEV
161 YQRRTPKMVD AATLEKLEAG FKKLAASDSK SLLKKYLTQE VFDKLKTLKT PSFGSTLLDV IQSGLENHDS GVGIYAPDAE
241 AYTTFADLFD PIIEDYHGGF KKTDKHPAKD WGDVDTFQNL DPAGEFIIST RVRCGRSMEG YPFNPCLTEA QYKEMEEKVS
321 STLSGLEGEL KGAFYPLTGM TKEVQQKLID DHFLFKEGDR FLQAANACRF WPTGRGIYHN DNKTFLVWCN EEDHLR**LISM**

401 **QMGGDLGQVY R**RLVTAVNDI EKRVPFSHND RLGFLTFCPT NLGTTIRASV HIKVPKLAAN KAKLEEVAGK FNLQVRGTRG

481 EHTEAEGGVY DISNKRRMGL TEYQAVKEMN DGIAELIKIE REL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	397	411	
total 1 peptides												

tr|A0A084W9Z4|A0A084W9Z4_ANOSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGGCASKDKK DSKVVENDTA GGTAGGTTDA DAANAGEGCV SNSMVFLSRN KSDTMVDAAV LEKMEAGFAK LAASDSKSLL
81 KKYLTREVFD ALKNKKTSFG STLLDCVQSG FENPDSGVGI YAPDAEAYTL FSDLFDPIIE DYHKGFKKTD KHPARDFGDV
161 AAFGNVDPTG EFVVSTRVRC GRSMEGYPFN PCLTEAQYKE MEDKVSATLS GLEGELKGKF YPLTGMDKAV QQQLIDDHFL
241 FKEGDRFLQA ANACRFWPTG RGIYHNDNKT FLVWCNEEDH LR**IISMQMGG DLGQVYR**RLV TAVNDIEKRI PFSHHDRLGF

321 LTFCPTNLGT TIRASVHIKV PKLAKDYAKL EATADKYNLQ VRGTRGEHSE AEGGIYDISN KRRMGLTEFQ AVKEMYDGIS
401 EIIKIEKSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	283	297	
total 1 peptides												

tr|Q7PIQ5|Q7PIQ5_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGGCASKDKK DSKVVENETA AGTGGGTDAE AANGGEGNKS DTMVDAAVME KMEAGFAKLA ASDSKSLLKK YLTKEVFDAL

81 KNKKTSFGST LLDCVQSGFE NPDSGVGIYA PDAEAYSLFA DLFDPIIEDY HKGFKKTDKH PASDFGDVNA FGNVDPTGEF

161 VVSTRVRCGR SMEGYPFNPC LTEAQYKEME GKVSTTLSGL EGELKGKFYP LTGMDKAVQQ QLIDDHFLFK EGDRFLQAAN

241 ACRYWPSGRG IYHNDNKTFL VWCNEEDHLR **IISMQMGGDL GQVYR**RLVTA VNDIEKRIPF SHHDRLGFLT FCPTNLGTTI

321 RASVHIKVPK LAKDYAKLEA TADKYNLQVR GTRGEHSEAE GGIYDISNKR RMGLTEFQAV KEMYDGISEI IKIEKSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	271	285	
total 1 peptides												

tr|A0A1B6K7L4|A0A1B6K7L4_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTGKSCARCG KQMIRIPKMV DAATLEKLEA GFKKLAASDS KSLLKKYLTQ EVFDKLKTLK TPSFGSTLLD VIQSGLENHD

81 SGVGIYAPDA EAYTTFADLF DPIIEDYHGG FKKTDKHPAK DWGDVDTFQN LDPAGEFIIS TRVRCGRSME GYPFNPCLTE

161 AQYKEMEEKV SSTLSGLEGE LKGAFYPLTG MTKEVQQKLI DDHFLFKEGD RFLQAANACR FWPTGRGIYH NDNKTFLVWC

241 NEEDHLR**LIS MQMGGDLGQV YR**RLVTAVND IEKRVPFSHN DRLGFLTFCP TNLGTTIRAS VHIKVPKLAA NKAKLEEVAG

321 KFNLQVRGTR GEHTEAEGGV YDISNKRRMG LTEYQAVKEM NDGIAELIKI EREL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	248	262	
total 1 peptides												

tr|A0A1B6IHK2|A0A1B6IHK2_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVDAATLEKL EAGFKKLAAS DSKSLLKKYL TQEVFDKLKT LKTPSFGSTL LDVIQSGLEN HDSGVGIYAP DAEAYTTFAD

81 LFDPIIEDYH GGFKKTDKHP AKDWGDVDTF QNLDPAGEFI ISTRVRCGRS MEGYPFNPCL TEAQYKEMEE KVSSTLSGLE

161 GELKGAFYPL TGMTKEVQQK LIDDHFLFKE GDRFLQAANA CRFWPTGRGI YHNDNKTFLV WCNEEDHLR**L ISMQMGGDLG**

241 **QVYR**RLVTAV NDIEKRVPFS HNDRLGFLTF CPTNLGTTIR ASVHIKVPKL AANKAKLEEV AGKFNLQVRG TRGEHTEAEG

321 GVYDISNKRR MGLTEYQAVK EMNDGIAELI KIEREL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	230	244	
total 1 peptides												

tr|A7UTS9|A7UTS9_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVDAAVMEKM EAGFAKLAAS DSKSLLKKYL TKEVFDALKN KKTSFGSTLL DCVQSGFENP DSGVGIYAPD AEAYSLFADL

81 FDPIIEDYHK GFKKTDKHPA SDFGDVNAFG NVDPTGEFVV STRVRCGRSM EGYPFNPCLT EAQYKEMEGK VSTTLSGLEG

161 ELKGKFYPLT GMDKAVQQQL IDDHFLFKEG DRFLQAANAC RYWPSGRGIY HNDNKTFLVW CNEEDHLR**II SMQMGGDLGQ**

241 **VYR**RLVTAVN DIEKRIPFSH HDRLGFLTFC PTNLGTTIRA SVHIKVPKLA KDYAKLEATA DKYNLQVRGT RGEHSEAEGG

321 IYDISNKRRM GLTEFQAVKE MYDGISEIIK IEKSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	229	243	
total 1 peptides												

tr|B3GCX2|B3GCX2_9COLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VGIYAPDAES YSVFADLFDP IIEDYHGGFK KTDKHPPKNW GDVDTLGNLD PTGEYIVSTR VRCGRSLEGY PFNPCLTEEQ
81 YKEMEQKVSS TLSGLEGELK GTFYPLTGMA KDVQQKLIDD HFLFKEGDRF LQAANACRFW PTGRGIYHND NKTFLVWCNE
161 EDHLR**IISMQ MGGDLGQVYR** RLVTAVNDIE KRLPFSHHDR LGFLTFCPTN LGTTVRASVH IKVPKLAANK AKLDEVAGKF

241 NLQVRGTRG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	166	180	
total 1 peptides												

tr|B3GCX8|B3GCX8_9COLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EAYSVFSDLF DPIIEDYHTG FKKTDKHPPK NWGDVDSLGN LDPTGEYVVS TRVRCGRSME GYPFNPCLTE EQYKEMEQKV
81 SSTLSGLEGE LKGTFYPLTG MSKDVQQKLI DDHFLFKEGD RFLQTANACR FWPSGRGIYH NENKTFLVWC NEEDHLR**IIS**

161 **MQMGGDLGQV YR**RLVTAVND IEKRVPFSHH DRLGFLTFCP TNLGTTVRAS VHIKVPKLAA NKAKLDEVAG KFNLQVRGTR

241 GEHTEAEG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	158	172	
total 1 peptides												

tr|J4H7X4|J4H7X4_9DYTI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AEAYTLFADI FDPIIEDYHG GFKKTDKHPP KNWGDVDSLG NLDPNGEYVV STRVRCGRSM EGYPFNPCLT EEQYKEMEQK
81 VSTTLSGMEG ELKGTFYPLT GMSKEVQQKL IDDHFLFKEG DRFLQAANAC RFWPSGRGIY HNENKTFLVW CNEEDHLR**LI**

161 **SMQMGGDLGQ VYR**RLVTAVN DVEKRVPFSH NDRLGFLTFC PSNLGTTVRA SVHIKVPKLA ANRAKLEEIA GKYNLQVRGT

241 RG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	159	173	
total 1 peptides												

tr|J4H166|J4H166_9DYTI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AEAYTVFADI FDPIIEDYHG GFKKTDKHPP KNWGDVDSLG NLDPNGEYVV STRVRCGRSM EGYPFNPCLT EEQYKEMEQK
81 VSTTLSGMEG ELKGTFYPLT GMSKEVQQKL IDDHFLFKEG DRFLQAANAC RFWPSGRGIY HNENKTFLVW CNEEDHLR**LI**

161 **SMQMGGDLGQ VYR**RLVTAVN DVEKRVPFSH NDRLGFLTFC PSNLGTTVRA SVHIKVPKLA ANRAKLEEIA GKYNLQVRGT

241 RG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	159	173	
total 1 peptides												

tr|B3GCX9|B3GCX9_METCO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AYTVFSDLFD PIIEDYHAGF KKTDKHPPKN WGDVDTFGNL DPAGEYIVST RVRCGRSMEG YPFNPCLTEE QYKEMEQKVS
81 STLCGLEDEL KGTFYPLTGM SKDVQQKLID DHFLFKEGDR FLQAANACRF WPTGRGIYHN ENKTFLVWCN EEDHLR**LISM**

161 **QMGGDLGQVY R**RLVTAVNDV EKRIPFSHHD RLGFLTFCPT NLGTTVRASV HIKVPKLAAN KAKLEEIASK YSLQVRGTRG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	157	171	
total 1 peptides												

tr|B3GCY8|B3GCY8_9CARA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AYSVFAELFD PIIEDYHTGF KKTDKHPPKN WGDVDTFGNL DPTGEYVVST RVRCGRSMEG YPFNPCLTEE QYKEMEQKVS
81 TTLNGLEGEL KGTFYPLTGM SKDVQQKLID DHFLFKEGDR FLQAANACRF WPSGRGIFHN DTKTFLVWCN EEDHLR**LISM**
161 **QMGGDLGQVY R**RLVTAVNDI EKRVPFSHHD RLGFLTFCPT NLGTTVRASV HIKVPKLAAN KAKLEEVAGK YNLQVRGTRG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	157	171	
total 1 peptides												

tr|F4YJL0|F4YJL0_9CUCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 YAPDAEAYTV FADLFDPIIE DYHKGFGRGD KHPPKNWGDV SVFGNLDPNN EFVVSTRVRC GRSLEGYPFN PCLTEEQYKE
81 MEQKVSSTLS GLESELKGTF YPLTGMSKDV QQKLIDDHFL FKEGDRFLQA ANACRFWPTG RGIFHNENKT FLVWCNEEDH
161 LR**IISMQMGG DLGQVYR**RLV TAVNDIEKRI PFSHNDRLGF LTFCPTNLGT TVRASVHIKV PKLAANKAKL EEVASKYN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	163	177	
total 1 peptides												

tr|A0A0A0RI03|A0A0A0RI03_9CARA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PDADSYTVFA DLFDPIIEDY HGGFKKTDKH PPKNWGEVDT FGNLDPAGEF IVSTRVRCGR SLQGYPFNPC LTEEQYKEME
81 QKVSSTLCGL EGELKGTFYP LTGMSKDVQQ KLIDDHFLFK EGDRFLQAAN ACRFWPSGRG IYHNEAKTFL VWCNEEDHLR
161 **LISMQMGGDL GQVYR**RLVTA VNDIEKRLPF SHHDRLGFLT FCPTNLGTTV RASVHIKVPK LAANRAKLEE IASKY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	161	175	
total 1 peptides												

tr|A0A0A0RPF2|A0A0A0RPF2_9CARA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PDADSYTVFA DLFDPIIEDY HGGFKKTDKH PPKNWGEVDT FGNLDPTGEF IVSTRVRCGR SLQGYPFNPC LTEEQYKEME
81 QKVSTTLCGL EGELKGTFYP LTGMSKDVQQ KLIDDHFLFK EGDRFLQAAN ACRFWPTGRG IYHNEAKTFL VWCNEEDHLR
161 **LISMQMGGDL GQVYR**RLVTA VNDIEKRLPF SHHDRLGFLT FCPTNLGTTV RASVHIKVPK LAANRAKLEE IASKY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	161	175	
total 1 peptides												

tr|B3FA28|B3FA28_9CARA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HPPKNWGDVD TFGNLDPTGE YVVSTRVRCG RSMEGYPFNP CLTEEQYKEM EQKVSTTLNG LEGELKGTFY PLTGMSKDVQ
81 QKLIDDHFLF KEGDRFLQAA NACRFWPSGR GIFHNDTKTF LVWCNEEDHL R**LISMQMGGD LGQVYR**RLVT AVNDIEKRIP
161 FSHHDRLGFL TFCPTNLGTT VRASVHIKVP KLAANKAKLE EVAAKYNLQV RGTRGEHTEA EG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	132	146	
total 1 peptides												

tr|B3F9Z8|B3F9Z8_9CARA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HPPKNWGDVD TFGNLDPTGE YVVSTRVRCG RSMEGYPFNP CLTEEQYKEM EQKVSTTLNG LEGELKGTFY PLTGMSKDVQ
81 QKLIDDHFLF KEGDRFLQAA NACRFWPSGR GIFHNDTKTF LVWCNEEDHL R**LISMQMGGD LGQVYR**RLVT AVNDIEKRIP
161 FSHHDRLGFL TFCPTNLGTT VRASVHIKVP KLAANKAKLE EVAAKYNLQV RGTRGEHTEA EG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	132	146	
total 1 peptides												

tr|B3F9Y1|B3F9Y1_9CARA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HPPKNWGDVD TFGNLDPTGE YVVSTRVRCG RSMEGYPFNP CLTEEQYKEM EQKVSTTLNG LEGELKGTFY PLTGMSKDVQ
81 QKLIDDHFLF KEGDRFLQAA NACRFWPSGR GIFHNDTKTF LVWCNEEDHL R**LISMQMGGD LGQVYR**RLVT AVNDIEKRIP
161 FSHHDRLGFL TFCPTNLGTT VRASVHIKVP KLAANKAKLE EVAAKYNLQV RGTRGEHTEA EG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	132	146	
total 1 peptides												

tr|J7EQ35|J7EQ35_9COLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DPIIEDYHGG FKKTDKHPPK NWGDVNVFGN LDPCGDYIVS TRVRCGRSLE GYPFNPCLTE EQYKEMEQKV SCVLSAFEGE
81 HKGTFYPLTG MSKEVQQKLI DDHFLFKEGD RFLQAANACR FWPTGRGIFH NDNKTFLIWV NEEDHLR**IIS MQMGGDLGQV**
161 **YR**RLVCGVNE IEKRLPFSHH ERLGFLTFCP TNLGTTVRAS VHIKVPKLAA NKAKLEEVAA R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	148	162	
total 1 peptides												

tr|J7EPA5|J7EPA5_9COLE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DPVIEDYHGG FKKTDKHPPK NWGDVNVFGN LDPCGDYIVS TRVRCGRSLE GYPFNPCLTE EQYKEMEQKV SCVLSAFEGE
81 HKGTFYPLTG MSKEVQQKLI DDHFLFKEGD RFLQAANACR FWPTGRGIFH NDNKTFLIWV NEEDHLR**IIS MQMGGDLGQV**
161 **YR**RLVAGVNE IEKRLPFSHH ERLGFLTFCP TNLGTTVRAS VHIKVPKLAA NKAKLEEVAA R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	148	162	
total 1 peptides												

tr|J7EN85|J7EN85_9COLE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DPVIEDYHGG FKKTDKHPPK NWGDVNVFGN LDPCGDYIVS TRVRCGRSLE GYPFNPCLTE EQYKEMEQKV SCVLSAFEGE
81 HKGTFYPLTG MSKEVQQKLI DDHFLFKEGD RFLQAANACR FWPTGRGIFH NDNKTFLIWV NEEDHLR**IIS MQMGGDLGQV**
161 **YR**RLVCGVNE IEKRLPFSHH ERLGFLTFCP TNLGTTVRAS VHIKVPKLAA NKAKLEEVAA R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	148	162	
total 1 peptides												

tr|J7EQ70|J7EQ70_9COLE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DPVIEDYHGG FKKTDKHPPK NWGDVNVFGN LDPCGDYIVS TRVRCGRSLE GYPFNPCLTE EQYKEMEQKV SCVLSAFEGE
81 HKGTFYPLTG MSKEVQQKLI DDHFLFKEGD RFLQAANACR FWPTGRGIFH NDNKTFLIWV NEEDHLR**IIS MQMGGDLGQV**
161 **YR**RLVCGVNE IEKRLPFSHH ERLGFLTFCP TNLGTTVRAS VHIKVPKLAA NKAKLEEVAA R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	148	162	
total 1 peptides												

tr|F4YJL3|F4YJL3_9CUCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FADLFDPIIE DYHKGFGRND KHPPKNWGDV SVFGNLDPNN EFVVSTRVRC GRSMEGYPFN PCLTEEQYKE MEQKVSSTLS
81 GLDGELKGTF YPLTGMSKDV QQKLIDDHFL FKEGDRFLQA ANACRFWPSG RGIFHNENKT FLVWCNEEDH LR**IISMQMGG**
161 **DLGQVYR**RLV TAVNDIEKRV PFSHNDRLGF LTFCPTNLGT TVRASVHIKV PKLAANKAK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	153	167	
total 1 peptides												

tr|M1XFD9|M1XFD9_9DYTI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 YHTGFKKTDK HPPKNWGDVD TLGNLDPTGE FVVSTRVRCG RSMEGYPFNP CLTEEQYKEM ENKVSTTLSG LEGELKGTFF
81 PLTGMSKDVQ QKLIDDHFLF KEGDRFLQAA NACRFWPSGR GIYHNENKTF LIWCNEEDHL R**IISMQMGGD LGQVYR**RLVT
161 AVNDIEKRIP FSHHDRLGFL TFCPSNLGTT VRASVHIKVP KLAANKAKLE EVASKYNL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	142	156	
total 1 peptides												

tr|A0A0A0QTY4|A0A0A0QTY4_IPSTY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PKNWGDVSVF GNLDPAGEYV VSTRVRCGRS LEGYPFNPCL TEEQYKEMEQ KVSSTLSGLD GELKGTFYPL TGMSKEVQQK
81 LIDDHFLFKE GDRFLQAANA CRFWPTGRGI YHNENKTFLV WCNEEDHLR**L ISMQMGGDLG QVYR**RLVTAV NDIEKRLPFS
161 HHDRLGFLTF CPTNLGTTVR ASVHIKVPKL AANKAKL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	130	144	
total 1 peptides												

tr|A0A0U3BYR0|A0A0U3BYR0_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GDVSVFGNLD PANEYIVSTR VRCGRSLEGY PFNPCLTEEQ YKEMEQKVSS TLSGLEGELK GTFYPLTGMS KDVQQKLIDD
81 HFLFKEGDRF LQAANACRFW PTGRGIYHND NKTFLVWCNE EDHLR**IISMQ MGGDLGQVYR** RLVTAVNDIE KRIPFSHNDR
161 LGFLTFCPTN LGTTVRASVH IKVPKLASNK A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	126	140	
total 1 peptides												

tr|A0A0U2RDA7|A0A0U2RDA7_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GDVSVFGNLD PANEYIVSTR VRCGRSLEGY PFNPCLTEEQ YKEMEQKVSS TLSGLEGELK GTFYPLTGMS KDVQQKLIDD
81 HFLFKEGDRF LQAANACRFW PTGRGIYHND NKTFLVWCNE EDHLR**IISMQ MGGDLGQVYR** RLVTAVNDIE KRIPFSHNDR
161 LGFLTFCPTN LGTTVRASVH IKVPKLASNK A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	126	140	
total 1 peptides												

tr|A0A0U3CB64|A0A0U3CB64_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GDVSVFGNLD PANEYIVSTR VRCGRSLEGY PFNPCLTEEQ YKEMEQKVSS TLSGLEGELK GTFYPLTGMS KDVQQKLIDD
81 HFLFKEGDRF LQAANACRFW PTGRGIYHND NKTFLVWCNE EDHLR**IISMQ MGGDLGQVYR** RLVTAVNDIE KRIPFSHNDR
161 LGFLTFCPTN LGTTVRASVH IKVPKLASNK A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	126	140	
total 1 peptides												

tr|A0A0U3BCD2|A0A0U3BCD2_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GDVSVFGNLD PANEYIVSTR VRCGRSLEGY PFNPCLTEEQ YKEMEQKVSS TLSGLEGELK GTFYPLTGMS KDVQQKLIDD
81 HFLFKEGDRF LQAANACRFW PTGRGIYHND NKTFLVWCNE EDHLR**IISMQ MGGDLGQVYR** RLVTAVNDIE KRIPFSHNDR
161 LGFLTFCPTN LGTTVRASVH IKVPKLASNK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IISMQMGGDLGQVYR.R	Y	76.10	1666.8171	642.2	834.9510	2	35.12	2820	1	126	140	
total 1 peptides												

tr|A0A067QJP9|A0A067QJP9_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKALVGQK IMNEAIKNKR KPGQGMEWRV LVVDQLAMRM VSACCKMHDI SAEGITIVED IHKKREPLST MEAVYLITPC
81 DSSVKALMAD FPNSNHCMYR AAHVYFTEAC PGEVFNQLCR STAAKYLKTV KEINIAFIAY EEQVFSLDSP NTFQYFYNPM
161 LSGNRTANME RMAEQIATLC ATLGEYPSVR YRSDFDKNVE LAQLVQQKLD AYKADEPTMG EGPEKARSQL IILDRGFDCV
241 SPLLHELTLQ AMAYDLLPIE NDVYKYEATA GAPEKEVLLD ENDELWVELR HQHIAVVSQS VTKNLKKFIE SKRMPQGDKQ
321 SMRDLSQMIK KMPQYQKELS KYSTHLHLAE DCMKAYQGYV DKLCK**VEQDL AMGTDAEGER** IKDHMRNIVP ILLDQAVSAT
401 DKMRIIALYI ISKNGISDEN LTKLVQHAQI SPQDKQTIIN MANLGLNVVV DGNRKKIYHG TRKERITEQT YQMSRWTPVI
481 KDIMEECIED KLELKHFPFL AGRAASSGYH APTSARYGHW HKDKGQQTVK NVPRLIVFVV GGVCFSEIRC AYEVTQAAKN
561 WEVICGSSHI LTPEDFLSNL QKLSNQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	366	380	
total 1 peptides												

tr|A0A1B6GVI9|A0A1B6GVI9_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSLKALVGQK IMNEVIKQKK KTGKEVEWRV LVVDQLAMRM VSACCKMHEI SAEGITIVED INKKREPLST MEGVYLITPC
81 EKSVHALMQD FNSPNRTMYR AAHVYFTEAC PVGLFETLKK AKVAKYIQSL MEINVSFIAY ESQVFSLDSP ETFQCVYNPS
161 FAGSRVANLE RIAEQIATLC ATLGEYPSVR FRFDFEKNAE LAQLVQQKLD AYKADEPTMG EGPEKARSQL IILDRGFDCV
241 SPLLHELTLQ AMAYDLLPIE NDVYKYEATA GSPEKEVLLD ENDELWVDLR HQHIAVVSQN VTKNLKKFIE SKRVPQGDKQ
321 SMRDLSQMIK KMPQYQKELS KYATHLHLAE DCMKAYQGYV DKLCK**VEQDL AMGTDAEGER** IKDHMRNIVP ILLDQAVSNY
401 DKMRIILLYI LSRNGISEEN LNKLVQHAQI LPQEKQAIIN MAN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	366	380	

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

tr|A0A0N0BCK0|A0A0N0BCK0_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MEIGRTRSYA GRESAEKKVM LAVSKRGRSA VNPGSSFTIA LTAGSAAISF TSNTNAITQW SKIMNEVIKQ KKTGTSGVQW
81 RILVVDQLAM RMVSACCKMH DISAQGITLV EDINKKREPL PTMEAIYLIT PCNSSVQKLI EDFSNPTRTI YKVAHVYFTE
161 ACPDELFKEL CHSLVAKRIK TLKEINIAFI PYEEQHVLTM ECIHACTLPV CPEELFNELC KSLAAKKIKT LKEINIAFLP
241 YESQVFSLDS RETFACFYNA SFSNLRTANM ERIAEQIATL CATLGEYPSV RYRSDFDRNI ELAHMVQQKL DAYKADEPTM
321 GEGPEKARSQ LLILDRGFDC VSPLLHELTL QAMAYDLLDI DNDVYRFEAS AGVQKEVLLD ENDDLWVDLR HQHIAVVSQN
401 VTKNLKKFTE SKRMPQGDKQ SMRDLSQMIK KMPQYQKELS KYATHLQLAE DCMKRYQGNV DKLCK**VEQDL AMGTDAEGER**

481 IKDQMKNITP ILLDQTVNHL DKLRIIALYV ISKNGISEEN LNRLVHHAQI SADDKQTIVN MANLGINIVV DGGNRRKLYT
561 VQRKERITEQ TYQMSRWTPI MKDIMEDAIE DKLDSKHFPF LAGRAASSGY HAPTSARYGH WHKDKGSQTI KNVPRLIVFV
641 VGGVCFSEIR CAYEVTNALK NWEVIMGSSH IITPKSFLDD LSKLHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	466	480	
total 1 peptides												

tr|E2AA52|E2AA52_CAMFO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKAQVGQK IMNEVIKQKK KTTGGVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC
81 NSSVQKLIDD FSNPARTTYK VAHVYFTEAC PDELFKELCH SLVSKHIKTL KEINIAFIPY EEQHILIIRM HSCLHSMPVC
161 PEELFNEICK SLAAKKVKTL KEINIAFLPY ESQVTKQTKI INAIVVALER KLYNLQVFSL DSRETFACFY NPSFSNLRAA
241 NMERIAEQIA TLCATLGEYP SVRYRSDFDR NVELAQLVQQ KLDAYKADEP TMGEGPEKAR SQLLILDRGF DCVSPLLHEL
321 TLQAMAYDLF EATAGQEKEV LLDENDDLWV ELRHQHIAVV SQNVTKNLKK FTESKRMPQG DKQSMRDLSQ MIKKMPQYQK
401 ELSKYATHLQ LAEDCMKRYQ GNVDKLCK**VE QDLAMGTDAE GER**IKDHMRN ITPILLDQTV NHLDKLRIIA LYVISKNGIT

481 DENLNRLVHH AQVSVDDKQT IVNIANLGIN VVVDSNRKKL YTVPRKERIT EQTYQMSRWT PIIKDVMEDS IEDKLDSKHF
561 PFLAGRAASS GYHAPTSARY GHWHKDKGQQ TIKNVPRLIV FIVGGVCFSE IRCAYEVTNA LKNWEVIIGS SHIITPKSFL
641 NDLSKVHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	429	443	
total 1 peptides												

tr|A0A195DWY9|A0A195DWY9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNEVIKQKKK STGGVEWRIL VVDQLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN PSVQKLIDDF
81 SNPTRTTYKV AHVYFTEACP DELFKELCHS LVAKHIKTLK EINIAFIPYE EQPFTLFINK HILIIRMHSC LQLMPVCPEE
161 LFNEICKSLA AKKIKTLKEI NIAFLPYESQ VVALEREIYL QVFSLDSRET FACFYNPSFF NLRSANMERI AEQIATLCAT
241 LGEYPSVRYR SDFDRNVELA QLVQQKLDAY KADEPTMGEG PEKARSQLLI LDRGFDCVSP LLHELTLQAM AYDLLDIDND
321 VYRFEATAGQ EKEVLLDEND DLWVELRHQH IAVVSQNVTK NLKKFTESKR MPQGDKQSMR DLSQMIKKMP QYQKELSKYA
401 THLQLAEDCM KRYQGNVDKL CK**VEQDLAMG TDAEGER**IKD HMRNITPILL DQTVNHLDKL RIIALYVISK NGITDENLNR

481 LVHHAQVSVD DKQTIVNMAN LGINVVVDSN RKKLYTVPRK ERITEQTYQM SRWTPVIKDV MEDSIEDKLD SKHFPFLAGR
561 AASSGYHAPT SARYGHWHKD KGQQTIKNVP RLIVFIVGGM CFSEIRCAYE VTNALKNWEV IIGSSHIITP KSFLNDLSKL
641 HV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	423	437	
total 1 peptides												

tr|A0A195FYQ4|A0A195FYQ4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 FSHVTEIMNE VIKQKKKSTG GVEWRILVVD QLAMRMVSAC CKMHDISAQG ITLVEDINKK REPLPTMEAV YLITPCNSSV
 81 QKLIDDFSNP TRTTYKVAHV YFTEACPDEL FKELCHSLVA KHIKTLKEIN IAFIPYEEQP FTLFINKHIL IIRMHSCLQL
161 MPVCPEELFN EICKSLAAKK IKTLKEINIA FLPYESQVFS LDSRETFACF YNPSFFNLRS ANMERIAEQI ATLCATLGEY
241 PSVRYRSDFD RNVELAQLVQ QKLDAYKADE PTMGEGPEKA RSQLLILDRG FDCVSPLLHE LTLQAMAYDL LDIDNDVYRF
321 EATAGQEKEV LLDENDDLWV ELRHQHIAVV SQNVTKNLKK FTESKRMPQG DKQSMRDLSQ MIKKMPQYQK ELSKYATHLQ
401 LAEDCMKRYQ GNVDKLCKVE QDLAMGTDAE GERIKDHMRN ITPILLDQTV NHLDKLRIIA LYVISKNGIT DENLNRLVHH

481 AQVSIDDKQT IVNMANLGIN VVVDSNRKKL YTVPRKERIT EQTYQMSRWT PVIKDVMEDS IEDKLDSKHF PFLAGRAASS
561 GYHAPTSARY GHWHKDKGQQ TIKNVPRLIV FIVGGMCFSE IRCAYEVTNA LKNWEVIIGS SHIITPKSFM NDLSKLHV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	419	433	
total 1 peptides												

tr|F4WGN1|F4WGN1_ACREC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MALKGQVGQK IMNEVIKQKK KSTGGVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC
 81 NSSVQKLIDD FSNPTRTTYK VAHVYFTEAC PDELFKELCH SLVAKHIKTL KEINIAFIPY EEQHILIIRM HSCLQLMPVC
161 PEELFNEICK SLAAKKIKTL KEINIAFLPY ESQVFSLDSR ETFACFYNPS FFNLRSANME RIAEQIATLC ATLGEYPSVR
241 YRSDFDRNVE LAQLVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV SPLLHELTLQ AMAYDLLDID NDVYRFEATA
321 GQEKEVLLDE NDDLWVELRH QHIAVVSQNV TKNLKKFTES KRMPQGDKQS MRDLSQMIKK MPQYQKELSK YATHLQLAED
401 CMKRYQGNVD KLCKVEQDLA MGTDAEGERI KDHMRNITPI LLDQTVNHLD KLRIIALYVI SKNGITDENL NRLVHHAQVS

481 VDDKQTIVNM ANLGINVVVD SNRKKLYTVP RKERITEQTY QMSRWTPIIK DVMEDSIEDK LDSKHFPFLA GRAASSGYHA
561 PTSARYGHWH KDKGQQTIKN VPRLIVFIVG GMCFSEIRCA YEVTNALKNW EVIIGSSHII TPKSFLNDLS KLHV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	415	429	
total 1 peptides												

tr|A0A151IBC5|A0A151IBC5_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MNEVIKQKKK STGGVEWRIL VVDQLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN SSVQKLIDDF
 81 SNPTRTIYKV AHVYFTEACP DELFKDLCHS LVAKHIKTLK EINIAFIPYE EQPFTLFINK HILIIRMHSC LRLMPVCPEE
161 LFNEICKSLA AKKIKTLKEI NIAFLPYESQ VFSLDSRETF ACFYNASFFN LRSANMERIA EQIATLCATL GEYPSVRYRS
241 DFDRNVELAQ LVQQKLDAYK ADEPTMGEGP EKARSQLLIL DRGFDCVSPL LHELTLQAMA YDLLDIDNDV YRFEVTAGQE
321 KEVLLDENDD LWVELRHQHI AVVSQNVTKN LKKFTESKRM PQGDKQNMRD LSQMIKKMPQ YQKELSKYAT HLQLAEDCMK
401 RYQGNVDKLC KVEQDLAMGT DAEGERIKDH MRNITPILLD QTVNHLDKLR IIALYVISKN GITDENLNRL VHHAQVTVDD

481 KQTIVNMANL GINVVVDSNR KKLYTVPRKE RITEQTYQMS RWTPVIKDVM EDSIEDKLDS KHFPFLAGRA ASSGYHAPTS
561 ARYGHWHKDK GQQTIKNVPR LIVFIVGGMC FSEIRCAYEV TNALKNWEVI IGSSHIITPK SFLNDLSKVH V
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	412	426	
total 1 peptides												

tr|A0A154PJE5|A0A154PJE5_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 VLFFAEIMNE VIKQKKASGT GVQWRILVVD QLAMRMVSAC CKMHDISAQG ITLVEDINKK REPLPTMEAI YLITPCNNSV
 81 QKLIEDFSNP TRTIYKVAHV YFTEACPEEL FKVLCQSLVA KRIKTLKELN TAFIPYEEQH VLTTECIHAC TRTVCPEELF
161 NEICKSLAAK KIKTLKEINI AFLPYESQVF SLDSRETFAC FYNASFANLR TANMERIAEQ IATLCATLGE YPSVRYRSDF
241 DRNVELAHMV QQKLDAYKAD EPTMGEGPEK ARSQLLILDR GFDCVSPLLH ELTLQAMAYD LLDIENDVYR FEASAGVQKE
321 VLLDENDDLW VELRHQHIAV VSQNVTKNLK KFTESKRMPQ GDKQSMRDLS QMIKKMPQYQ KELSKYATHL QLAEDCMKRY
401 QGSVDKLCKV EQDLAMGTDA EGERIKDQMK NITPILLDQT VHHLDKLRII ALYVISKNGI TDENLNRLVH HAQISVDDKQ

481 TIVNMANLGI NIVVDGGNRK KLYTVQRKER ITEQTYQMSR WTPIMKDIME DAIEDKLDSK HFPFLAGRAA SSGYHAPTSA
561 RYGHWHKDKG QQTIKNVPRL IVFVVGGVCF SEIRCAYEVT NTLKNWEVIM GSSHIITPKS FLDDLSKLHV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	410	424	
total 1 peptides												

tr|A0A195BXB7|A0A195BXB7_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MNEVIKQKKK STGGVEWRIL VVDQLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN SSVQKLIDDF
 81  SNPTRTTYKV AHVYFTEACP DELFKELCHS LVAKHIKTLK EINIAFIPYE EQVKQRTLWQ EKMFDRFILH VCPEELFNEI
161  CKSLAAKKIK TLKEINIAFL PYESQVFSLD SRETFACFYN PSFFNLRSAN MERIAEQIAT LCATLGEYPS VRYRSDFDRN
241  VELAQLVQQK LDAYKADEPT MGEGPEKARS QLLILDRGFD CVSPLLHELT LQAMAYDLLD IDNDVYRFEA TAGQEKEVLL
321  DENDDLWVEL RHQHIAVVSQ NVTKNLKKFT ESKRMPQGDK QSMRDLSQMI KKMPQYQKEL SKYATHLQLA EDCMKRYQGN
401  VDKLCKVEQD LAMGTDAEGE RIKDHMRNIT PILLDQTVNH LDKLRIIALY VISKNGITDE NLNRLVHHAQ VSVDDKQTIV

481  NMANLGINVV VDSNRKKLYT VPRKERITEQ TYQMSRWTPV IKDVMEDSIE DKLDSKHFPF LAGRAASSGY HAPTSARYGH
561  WHKDKGQQTI KNVPRLIVFI VGGMCFSEIR CAYEVTNALK NWEVIIGSSH IITPKSFLND LSKLHV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	407	421	
total 1 peptides												

tr|A0A232FGS2|A0A232FGS2_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MNEVINQKKK NTGGTEWRIL VVDQLAMRMV SACCKMHDIS AQGITLVEDI HKKREPLPTM EAIYLITPSN QSVTKLIDDF
 81  SNPTRTMYKA AHVYFTEACP DKTFTDLCHS TAAKYIKTLK EINIAFIPYQ EQVNLMCPEE MFNDICKSLA AKKVKTLKEI
161  NIAFLPYESQ VFSLDCRETF ACFYNPSLIN VRNANMERIA EQIATLCATL GEYPSVRYRS DFDRNVELAQ MVQQKLDAYK
241  ADEPTMGEGP EKARSQLLIL DRGFDCVSPL LHELTLQAMA YDLLEIENDV YKYEVAVGDG RQEKEVLLDE NDDLWVDLRH
321  QHIAVVSTNV TKNLKKFTES KRMPQTSEKQ NMRDLSQMIK KMPQYQKELS KYATHLHLAE DCMKHYQGNV DKLCKVEQDL

401  AMGTDAEGER IKDHMRNITP ILLDQNINNM DKLRIIALYV LSKNGIPDDN LNRLIHHAQM SPEDRQTIVN MANLGLNVVV

481  EGNRKKIYTV PRKERITEQT YQMSRWTPVV KDIMEDAIED KLEQKHFPFL GGRTASSGYH APTSARYGHW HKEKGQQTIK
561  NVPRLIVFIV GGVCFSEIRC AYEVTNAQKN WEVIIGSSHI ITPKSFLSEL SKLHINVA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	396	410	
total 1 peptides												

tr|A0A088ACI1|A0A088ACI1_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MALKAQVGQK IMNEVIKQKK TGSSGVQWRI LVVDKLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC
 81  NSSVQKLIED FSNPTRTSYK VAHVYFTEAC PDELFKELCH SLVAKRIKTL KEINIAFIPY EEQELFNELC KSLAAKKIKT
161  LKEINIAFLP YESQVFSLDS AETFACFYNA SFSNLRTANM ERIAEQIATL CATLGEYPSV RYRSDFDRNL ELAHMVQQKL
241  DAYKADEPTM GEGPEKARSQ LLILDRGFDC VSPLLHELTL QAMAYDLLDI ENDVYRFEAS AGVQKEVLLD ENDDLWVDLR
321  HQHIAVVSQN VTKNLKKFTE SKRMPQGDKQ SMRDLSQMIK KMPQYQKELS KYATHLQLAE DCMKRYQGNV DKLCKVEQDL

401  AMGTDAEGER IKDQMKNITP ILLDQTVHHL DKLRIIALYV ISKNGISEEN LNRLVHHAQI SPDDKQTIVN MANLGINIVV

481  DGGNRKKLYT VQRKERITEQ TYQMSRWTPV MKDIMEDAIE DKLDSKHFPF LAGRAASSGY HAPTSARYGH WHKDKGSQTI
561  KNVPRLIVFV VGGVCFSEIR CAYEVTNALK NWEVIIGSSH IITPKSFLDD LSKLHI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	396	410	
total 1 peptides												

tr|A0A0A9Z3R2|A0A0A9Z3R2_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VSKMALKALV GQKIMNDAIK MKGVKKNTKD VEWRVLVVDQ LAMRMVSACC KMHEISAEGL TIVEDIHKKR EPLPTMEAVY
81 LITPSEKSVH ALINDFASPN RQMYLGAHVY FTEACPEKLF DTLCHSTVAK YIKTLKEINI AFIPYEQQVF SLDAPETFQC
161 FYNPTLISSR TANMERIAEQ IATLCATLGE YPSVRYRSDY ERNVELAQII QQKLDAYKAD EPTMGEGPEK ARSQLLILDR
241 GFDCVSPLLH ELTLQAMAYD LLPIENDVYK YEATQGNPEK EVLLDENDEL WVEMRHQHIA VVSQNVTKNL KKFIDSKRMP
321 AGDQKSMKDL STMIKKMPQY QKELSKYSTH LHLAEDCMKS YQGYVDKLCK **VEQDLAMGTD AEGER**IKDHM RNIVPILLDQ

401 AVSNYDKMRI ILLYVLVKNG ISDESLNKLV QHAQIQPHEK QAIVNLGNLG LNVVVDGNNV RKKIWTPPRK ERITEQTYQM
481 SRWTPVIKDL MEDCIDDKMD LKHFPYLAGR TASSGYHAPS SARYGHWHKD KGQQAVKNVP RLLVFVIGGM TFSEIRCAYE
561 VTNNVKNWEV IIGSSHIMTP EDFLSNLSNL SN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	371	385	
total 1 peptides												

tr|A0A1Y1LDV6|A0A1Y1LDV6_PHOPY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKAQVGHK IMQEVIKHKG PKKNGPIKHG TTEWRVLVVD QLAMRMVSAC CKMHDISAEG ITLVEDIAKK REPLPSMEAI
81 YLITPCEKSI HLLMNDFETP RPMYRGAHVF FTEACPDTLF NELSHAHVAK YIKTLKEINI AFIPTEQQVF SLDSPGTFQC
161 FYDPSLAAAR NANMERMAEQ IATLCATLGE YPSVRYRSDW ERNVELAQLI QQKLDAYKAD EPTMGEGPEK ARSQLLILDR
241 GFDCVSPLLH ELTFQSMAYD LLPIENDVYR YEASAGAVEK KEVLLDENDE LWVELRHQHI AVVSQSVTKN LKKFTDSKRM
321 TQTDKQSLKD LSQMIKKMPQ YQKELSKYST HLHLAEDCMK AYQGYVDKLC K**VEQDLAMGT DAEGER**IRDH MRNIVPILLD

401 PKITNEYDKM RIIALYALAK NGITEENLSK LATHAQIKDK QKIANLQYLG VNVITDGSNR RKQYTVPRKE RITEQTYQMS
481 RWTPIIKDIM EDCIEDKLDH KHFPFLAGRA QTSGYHAPTS VRYGHWHKDK GQQTVKNVPR LLVFVVGGIC FSEIRCAYEV
561 TNAVKNWEVI IGSSHILTPE LFLSDLATLG G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	372	386	
total 1 peptides												

tr|K7IZP4|K7IZP4_NASVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKAQVGQK IMNEVINQKK KNTGGTEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED IHKKREPLPT MEAIYLITPS
81 NQSVTKLIDD FSNPTRTMYK AAHVYFTEVC PEEMFNDICK SLAAKKVKTL KEINIAFLPY ESQVFSLDCR ETFACFYNPS
161 LINVRNANME RIAEQIATLC ATLGEYPSVR YRSDFDRNVE LAQMVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV
241 SPLLHELTLQ AMAYDLLEIE NDVYKYEVAV GDGRQEKEVL LDENDDLWVD LRHQHIAVVS TNVTKNLKKF TESKRMPQTS
321 EKQNMRDLSQ MIKKMPQYQK ELSKYATHLH LAEDCMKHYQ GNVDKLCK**VE QDLAMGTDAE GER**IKDHMRN ITPILLDQNI

401 NNMDKLRIIA LYVLSKNGIP DDNLNRLIHH AQMSPEDRQT IVNMANLGLN VVVEGNRKKI YTVPRKERIT EQTYQMSRWT
481 PVVKDIMEDA IEDKLEQKHF PFLGGRTASS GYHAPTSARY GHWHKEKGQQ TIKNVPRLIV FIVGGVCFSE IRCAYEVTNA
561 QKNWEVIIGS SHIITPKSFL SELSKLHINV A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	369	383	
total 1 peptides												

tr|A0A0J7KU67|A0A0J7KU67_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKAQVGQK IMNEVIKQKK KTTGGVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC
81 NPSVQKLIDD FSNPTRTTYK VAHVYFTEVC PEELFNEICK SLAAKKIKTL KEINIAFLPY ESQVFSLDSR ETFACFYNPS
161 FFNLRAANME RIAEQIATLC ATLGEYPSVR YRSDFDRNVE LAQLVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV
241 SPLLHELTLQ AMAYDLLDID NDVYRQAKFE ATVGQEKEVL LDENDDLWVE LRHQHIAVVS QNVTKNLKKF TESKRMPQGD
321 KQSMRDLSQM IKKMPQYQKE LSKYATHLQL AEDCMKRYQG NVDKLCK**VEQ DLAMGTDAEG ER**IKDHMRNI TPILLDQTVN

401 HLDKLRIIAL YVISKNGITD ENLNRLVHHA QVTVDDKQTI VNMANLGINV VVDSNRKKLY TVPRKERITE QTYQMSRWTP
481 IIKDIMEDSI EDKLDAKHFP FLAGRAASSG YHAPTSARYG HWHKDKGQQT IKNVPRLLVF IVGGVCYSEI RCAYEVTNAL
561 KNWEVIIGSS HIITPKSFLN DMSKVHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	368	382	
total 1 peptides												

tr|A0A069DW98|A0A069DW98_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKALVGQK IMNDAIKQKK KGKEVEWRVL VVDQLATRMV SACCKMHEIS AEGLTIVEDI SKKREPLPTM EAVYLITPSE
81 KSVHALMQDF ASPNRTMYRA AHVYFTEACP EVLFEELCHH QVVKFIKTLK EINVAFIAYE QQVFSLDAPE TFQCFYNPSL
161 MSSRMANMER IAEQIATLCA TLGEYPSVRY RSDFDRNVEL AQIVQQKLDA YKADEPTMGE GPEKARSQLL ILDRGFDCVS
241 PLLHELTLQA MAYDLLPIEN DVYKYEATSG QPDKEVLLDE NDELWVELRH QHIAVVSQNV TKNLKKFIDS KRVPQGDKQS
321 MRDLSQMIKK MPQYQKELSK YSTHLHLAED CMKAYQGYVD KLCK**VEQDLA MGTDAEGER**I KDQMRNIVPI LLDQAVSNYD
401 KMRIILLYTL SKNGISEENL NKLVQHAQIQ SSEKQAIVNL GNLGLNVVVD GNRKKIYQPP RKERITEQTY QMSRWTPIIK
481 DLMEDCIDDK LDPKHFPFLL GGRASSSGYA HAPASARYGH WHKDKGQQTV KNVPRLIVFV IGGVTFSEIR CAYEVTCAVK
561 NWEVIIGSSH ILTPEDFLSN LANLST

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|A0A1B6DP73|A0A1B6DP73_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKALVGQK IMNEAIKQKK PKSGKEVEWR VLVVDQLAMR MVSACCKMHE ISAEGITIVE DIHKKREPLP SMDSVYLITP
81 SEKSVHALMQ DFSSPNRTMY RAAHVYFTEA CPDELFYSLG KAPVAKKIKT LKEINISFIA YEQQVFSLDS PETFQCFYNP
161 TFASSRVPNL ERIAEQIATL CATLGEYPSV RYRYDFDKNV ELAQIVQQKL DAYKADEPTM GEGPEKARSQ LLILDRGFDC
241 VSPLLHELTL QAMAYDLLPI ENDVYKYEAT AGQPEKEVLL DENDELWVEL RHQHIAVVSQ NVTKNLKKFI DSKRMPQGDK
321 QSMRDLSQMI KKMPQYQKEL SKYSTHLHLA EDCMKAYQGY VDKLCK**VEQD LAMGTDAEGE R**IKDHMRNIV PILLDQAVSN
401 YDKMRIILLY ILSRNGISEE NLNKLIQHAQ ILPQDKQAII NMANLGMNVV VEGNRKKIYQ VPRKERITEQ TYQMSRWTPV
481 IKDLMEECIE DKLDPKHFPF LAGRAASSGY HAPTSARYGH WHKDKGQPTV KNVPRIIVFI VGGVSFSEIR CAYEVTNANK
561 NWEVIVGSSH VLTPEDFLSN LANLNN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	367	381	
total 1 peptides												

tr|A0A0P4VMN7|A0A0P4VMN7_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKALVGQK IMNDAIKQKK KAKEVEWRVL VVDQLAMRMV SACCKMHEIS AEGLTIVEDI HKKREPLPTM EAVYLITPSE
81 KSVHALMQDF ASPNRTMYRA AHVYFTEACP EVLFEELCHH QVVKYIKTLK EINVAFIAYE QQVFSLDAPE TFQCFYNPSL
161 ISSRVANMER IAEQIATLCA TLGEYPSVRY RSDFDRNVEL AQIVQQKLDA YKADEPTMGE GPEKARSQLI ILDRGFDCVS
241 PLLHELTLQA MAYDLLPIEN DVYKYEATSG QPDKEVLLDE NDELWVELRH QHIAVVSQNV TKNLKKFIDS KRVPQGDKQS
321 MRDLSQMIKK MPQYQKELSK YSTHLHLAED CMKAYQGYVD KLCK**VEQDLA MGTDAEGER**I KDQMRNIVPI LLDQAVSNYD
401 KMRIILLYTL SKNGISEENL NKLVQHAQIQ PHEKQAIVNL GNLGLNVVVD GNRKKLYQPP RKERITEQTY QMSRWTPILK
481 DLMEDCIDDK LDPKHFPFLL GGRAASSGYA HAPASARYGH WHKDKGQQTV KNVPRLLVFI IGGVTFSEIR CAYEVTSAAK
561 NWEVIIGSSH ILTPEDFLSN LANLSN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|E0VWU1|E0VWU1_PEDHC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKAMVGQK IMNEAIKNKS KTGKGVDWRV LVVDQLAMRM VSACCKMHEI SAEGITLVED INKKREPLST MEAIYLITPC

81 EKSVHSLIND FASPNRSMYR AAHVYFTEVC PEELFNELCK SCAAKKIKTL KEINIAFLPY ESQVFSLDSP ETFQCFYNPS

161 FAKSRIANME RIAEQIATLC ATLGEYPSVR YRFDYDKNVE LAQLIQQKLD AYKADEPTMG ESPEKARSQL LILDRGFDCV

241 SPLLHELTLQ AMAYDLLPID NDVYKYEASA GAPEKEVLLD ENDELWVELR HQHIAVVSQN VTKNLKKFID SKRMPAGDKQ

321 SMKDLSQMIK RMPQYQKELS KYSTHLHLAE DCMKAYQGYV DKLCK**VEQDL AMGTDAEGER** IKDHMRNIVP ILLDQGVTHY

401 DKMRIILLYI LSKNGISEEN LTKLIQHAQI LPQEKQTIIN MANLGVNIVV DGNRKKIYQV PRKERITEQT YQMSRWTPVV

481 KDIMEECIED KLDVKHFPFL SGRATSSGYH APTSVRYGHW HKDKAQQTVK NVPRLIVFII GGVCFSEIRC AYEVTNAVKN

561 WEVIIGSSHI MTPEDFLSNL CNLSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	366	380	
total 1 peptides												

tr|R4WS90|R4WS90_RIPPE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKALVGQK IMNDAIKQKR KAKEVEWRVL VVDQLAMRMI SACCKMHEIS AEGLTIVEDI NKKREPLPTM EAVYLITPSE

81 KSVHALMNDF SSPNRTMYRA AHVYFTEACP EQLFETLCHA RVAKYIKTLK EINIAFIPYE QQVFSLDAPE TFQCFYNQSL

161 ANSRLANMER IAEQVATLCA TLGEYPSVRY RSDFPKNVEL AQIIQQKLDA YKADEPTMGE GPEKSRSQLL ILDRGFDAVS

241 PLLHELTLQA MAYDLLPIEN DVYKYEATAG APEKEVLLDE NDELWVELRH QHIAVVSQNV TKNLKKFIES KRMPQGDKQS

321 MRDLSQMIKK MPQYQKELSK YSTHLHLAED CMKVYQGYVD KLCK**VEQDLA MGTDAEGER**I KDHMRNIVPI LLDQAVSNYD

401 KMRIILLYAL SKNGISEENL NKLVQHAQIQ PHEKQAITNL GNLGLNVVVN GNRLKIHQPT RKERITEQTY QMSRWTPVVK

481 DLMEDCIDDK LDIKHFPFLA GRAATSGYQA PSSVRYGHWH KDKGQQTVKN VPRLIVFIIG GMSFSEIRCA YEVTNAVKNW

561 EVIMGSSHIL TPEDFLSNLS NLSN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|A0A158NNZ9|A0A158NNZ9_ATTCE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKGQVGQK IMNEVIKQKK KSTGGVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC

81 NSSVQKLIDD FSNPTRTTYK VAHVYFTEAC PDELFKELCH SLVAKHIKTL KEINIAFIPY EEQVFSLDSR ETFACFYNPS

161 FFNLRSANME RIAEQIATLC ATLGEYPSVR YRSDFDRNVE LAQLVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV

241 SPLLHELTLQ AMAYDLLDID NDVYRFEATA GQEKEVLLDE NDDLWVELRH QHIAVVSQNV TKNLKKFTES KRMPQGDKQS

321 MRDLSQMIKK MPQYQKELSK YATHLQLAED CMKRYQGNVD KLCK**VEQDLA MGTDAEGER**I KDHMRNITPI LLDQTVNHLD

401 KLRIIALYVI SKNGITDENL NRLVHHAQVS VDDKQTIVNM ANLGINVVVD SNRKKLYTVP RKERITEQTY QMSRWTPVIK

481 DVMEDSIEDK LDSKHFPFLA GRAASSGYHA PTSARYGHWH KDKGQQTIKN VPRLIVFIVG GMCFSEIRCA YEVTNALKNW

561 EVIIGSSHII TPKSFLNDLS KLHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|A0A151X8A1|A0A151X8A1_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALKGQVGQK IMNEVIKQKK KSTGGVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAIYLITPC

81 NPSVQKLIDD FSNPTRTTYK VAHVYFTEAC PDELFKELCH SLVAKHTKTL KEINIAFIPY EEQVFSLDSR ETFACFYNPS

161 FFNLRSANME RIAEQIATLC ATLGEYPSVR YRSDFDRNVE LAQLVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV

241 SPLLHELTLQ AMAYDLLDID NDVYRFEATA GQEKEVLLDE NDDLWVELRH QHIAVVSQNV TKNLKKFTES KRMPQGDKQS

321 MRDLSQMIKK MPQYQKELSK YATHLQLAED CMKRYQGNVD KLCK**VEQDLA MGTDAEGER**I KDHMRNITPI LLDQTVNHLD

401 KIRIIALYVI SKNGITDENL NRLVHHAQVS VDDKQTIVNI ANLGINVVVD SNRKKLYTVP RKERITEQTY QMSRWTPIIK

481 DVMEDSIEDK LDSKHFPFLA GRAASSGYHA PTSARYGHWH KDKGQQTIKN VPRLIVFVVG GMCFSEIRCA YEVTNALKNW

561 EVIIGSSHII TPKSFLNDLS KLHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|A0A0C9Q2F2|A0A0C9Q2F2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ALKAQVGQKI MNEVIKQKKT AKAGAVEWRI LVVDQLAMRM VSACCKMHDI SAQGITLVED INKKREPLPT MEAVYLITPC

81 NSSVQKLIDD FSNPGRIIYK AAHVYFTEAC PDDIFNQLCN SLGPKQIKTL KEINIAFIPY EEQVFSLDSR ETFACFYNPS

161 FINLRNANME RIAEQIATLC ATLGEYPSVR YRSDFDRNVE LAQIVQQKLD AYKADEPTMG EGPEKARSQL LILDRGFDCV

241 SPLLHELTLQ AMAYDLLDIE NDVYRYEATQ GQEKEVLLDE NDELWLELRH EHIAVVSNKV TKNLKKFTES KRMPQGDKQS

321 MRDLSQMIKK MPQYQKELSK YATHLHLAED CMKRYQGSVD KLCK**VEQDLA MGTDAEGER**I KDQMRNITPV LLDQTVADID

401 KLRIISLYVL SKNGISEENL SRLIGHAGVS GDDKQTILNM ANLGINVDGK GRKPYQVSRK ERITEQTYQM SRWTPVVKDI

481 MEDAIEERLD SKHFPFLAGR AASSGYAHAP TSVRYGHWHK DKGQATIKNV PRLIIFIVGG LCFSEIRCAY EVTNAIKNWE

561 VIVGSSHIIT PKSFLTDLSK LHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	365	379	
total 1 peptides												

tr|T1IAP1|T1IAP1_RHOPR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ILFHFTEIMN DAIKQKKKAK EVEWRVLVVD QLAMRMVSAC CKMHEISAEG LTIVEDIHKK REPLPTMEAV YLITPSEKSV

81 HALMQDFASP NRTMYRAAHV YFTEVCQEEL FNELCKSLAA RKIKTLKEIN IAFLPYESQV FSLDAPETFQ CFYNPSLISS

161 RVANMERIAE QIATLCATLG EYPSVRYRSD FDRNVELAQI VQQKLDAYKA DEPTMGEGPE KARSQLIILD RGFDCVSPLL

241 HELTLQAMAY DLLPIENDVY KYEATSGQPD KEVLLDENDE LWVELRHQHI AVVSQNVTKN LKKFIDSKRV PQGDKQSMRD

321 LSQMIKKMPQ YQKELSKYST HLHLAEDCMK AYQGYVDKLC K**VEQDLAMGT DAEGER**IKDQ MRNIVPILLD QAVSNYDKMR

401 IILLYTLSKN GISEENLNKL VQHAQIQPHE KQAIVNLGNL GLNVVVDGNR KKLYQPPRKE RITEQTYQMS RWTPILKDLM

481 EDCIDDKLDP KHFPFLLGGR AASSGYAHAP ASARYGHWHK DKGQQTVKNV PRLLVFIIGG VTFSEIRCAY EVTSAAKNWE

561 VIIGSSHILT PEDFLSNLAN LS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	362	376	
total 1 peptides												

tr|A0A0L7QPT2|A0A0L7QPT2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EIMNEVILQK KTATSGAQWR ILVVDQLAMR MVSACCKMHD ISAQGITLVE DINKKREPLP TMEAIYLITP CNSSVQKLIE

81 DFNNPTRTTY RVAHVYFTEV CPEELFNELC KSLAAKKIKT LKEINIAFLP YESQVFSLDS RETFACFYNP SFSNMRTANM

161 ERIAEQIATL CATLGEYPSV RYRSDFDRNV ELAHMVQQKL DAYKADEPTM GEGPEKARSQ LLILDRGFDC VSPLLHELTL

241 QAMAYDLLDI DNDVYRFEAS AGVQKEVLLD ENDDLWVELR HQHIAVVSQN VTKNLKKFTE SKRMPQGDKQ SMRDLSQMIK

321 KMPQYQKELS KYATHLQLAE DCMKRYQEKV DKLCK**VEQDL AMGTDAEGER** IKDQMKNITP ILLDQTVHHL DKLRIIALYV

401 ISKNGISEEN LNRLVNHAQI SADDKQTIVN MANLSINIVV DGGNRRKLYT VPRKERITEQ TYQMSRWTPV MKDIMEDAIE

481 DKLDSKHFPF LAGRAASSGY HAPTSARYGH WHKDKGSQTI KNVPRLIVFV VGGVCFSEIR CAYEVTNALK NWEVIIGSSH

561 IITPKSFLDD LSKLHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	356	370	
total 1 peptides												

tr|V9IAQ1|V9IAQ1_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNEVIKQKKT GSSGVQWRIL VVDKLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN SSVQKLIEDF

81 SNPTRTSYKV AHVYFTEVCP EELFNELCKS LAAKKIKTLK EINIAFLPYE SQVFSLDSAE TFACFYNASF SNLRTANMER

161 IAEQIATLCA TLGEYPSVRY RSDFDRNLEL AHMVQQKLDA YKADEPTMGE GPEKARSQLL ILDRGFDCVS PLLHELTLQA

241 MAYDLLDIEN DVYRFEASAG VQKEVLLDEN DDLWVDLRHQ HIAVVSQNVT KNLKKFTESK RMPQGDKQSM RDLSQMIKKM

321 PQYQKELSKY ATHLQLAEDC MKRYQGNVDK LCK**VEQDLAM GTDAEGER**IK DQMKNITPIL LDQTVHHLDK LRIIALYVIS

401 KNGISEENLN RLVHHAQISP DDKQTIVNMA NLGINIVVDG GNRKKLYTVQ RKERITEQTY QMSRWTPVMK DIMEDAIEDK

481 LDSKHFPFLA GRAASSGYHA PTSARYGHWH KDKGSQTIKN VPRLIVFVVG GVCFSEIRCA YEVTNALKNW EVIIGSSHII

561 TPKSFLDDLS KLHI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	354	368	
total 1 peptides												

tr|V9ID17|V9ID17_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNEVIKQKKT GSSGVQWRIL VVDKLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN SSVQKLIEDF

81 SNPTRTSYKV AHVYFTEACP DELFKELCHS LVAKRIKTLK EINIAFIPYE EQVFSLDSAE TFACFYNASF SNLRTANMER

161 IAEQIATLCA TLGEYPSVRY RSDFDRNLEL AHMVQQKLDA YKADEPTMGE GPEKARSQLL ILDRGFDCVS PLLHELTLQA

241 MAYDLLDIEN DVYRFEASAG VQKEVLLDEN DDLWVDLRHQ HIAVVSQNVT KNLKKFTESK RMPQGDKQSM RDLSQMIKKM

321 PQYQKELSKY ATHLQLAEDC MKRYQGNVDK LCK**VEQDLAM GTDAEGER**IK DQMKNITPIL LDQTVHHLDK LRIIALYVIS

401 KNGISEENLN RLVHHAQISP DDKQTIVNMA NLGINIVVDG GNRKKLYTVQ RKERITEQTY QMSRWTPVMK DIMEDAIEDK

481 LDSKHFPFLA GRAASSGYHA PTSARYGHWH KDKGSQTIKN VPRLIVFVVG GVCFSEIRCA YEVTNALKNW EVIIGSSHII

561 TPKSFLDDLS KLHI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	354	368	
total 1 peptides												

tr|E2B6A3|E2B6A3_HARSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNEVIKQKKK TTGGVEWRIL VVDQLAMRMV SACCKMHDIS AQGITLVEDI NKKREPLPTM EAIYLITPCN SSVQKLIDDF

81 SNPTRTTYKV AHVYFTEACP DELFKELCHS LVAKHIKTLK EINIAFIPYE EQVFSLDSRE TFACFYNPSF FNLRPANMER

161 IAEQIATLCA TLGEYPSVRY RSDFDRNVEL AQLVQQKLDA YKADEPTMGE GPEKARSQLL ILDRGFDCVS PLLHELTLQA

241 MAYDLLDIDN DVYRFEATAG QEKEVLLDEN DDLWVELRHQ HIAVVSQNVT KNLKKFTESK RMPQGDKQSM RDLSQMIKKM

321 PQYQKELSKY ATHLQLAEDC MKRYQGNVDK LCK**VEQDLAM GTDAEGER**IK DHMKNITPIL LDQTVNHLDK LRIISLYVIS

401 KNGISDENLN RLVHHAQVSV DDKQTIVNIA NLGINVVVEG NRKKLYTVQR KERITEQTYQ MSRWTPIIKD VMEDSIEDKL

481 DSKHFPFLAG RAASSGYHAP TSARYGHWHK DKGQQTIKNV PRLIVFIVGG VCFSEIRCAY EVTNALKNWE VIIGSSHVIT

561 PKSFLNDLSK LHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	354	368	
total 1 peptides												

tr|A0A0C9RMG4|A0A0C9RMG4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KKTAKAGAVE WRILVVDQLA MRMVSACCKM HDISAQGITL VEDINKKREP LPTMEAVYLI TPCNSSVQKL IDDFSNPGRI

81 IYKAAHVYFT EVCPEELFND LCKSIGARKI KTLKEINIAF LPYESQVFSL DSRETFACFY NPSFINLRNA NMERIAEQIA

161 TLCATLGEYP SVRYRSDFDR NVELAQIVQQ KLDAYKADEP TMGEGPEKAR SQLLILDRGF DCVSPLLHEL TLQAMAYDLL

241 DIENDVYRYE ATQGQEKEVL LDENDELWLE LRHEHIAVVS NKVTKNLKKF TESKRMPQGD KQSMRDLSQM IKKMPQYQKE

321 LSKYATHLHL AEDCMKRYQG SVDKLCK**VEQ DLAMGTDAEG ER**IKDQMRNI TPVLLDQTVA DIDKLRIISL YVLSKNGISE

401 ENLSRLIGHA GVSGDDKQTI LNMANLGINV DGKGRKPYQV SRKERITEQT YQMSRWTPVV KDIMEDAIEE RLDSKHFPFL

481 AGRAASSGYA HAPTSVRYGH WHKDKGQATI KNVPRLIIFI VGGLCFSEIR CAYEVTNAIK NWEVIVGSSH IITPKSFLTD

561 LSKLHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.VEQDLAMGTDAEGER.I	Y	62.08	1619.7097	-19.2	810.8466	2	28.66	2138	1	348	362	
total 1 peptides												

tr|A0A0A0VC07|A0A0A0VC07_9ARAC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASFDPVSFA K**DFLAGGVAA AISK**TAVAPI ERVKLLLQVQ HVSKQIAVDK QYKGMIDCFV RIPREQGFLS YWRGNLANVI
81 RYFPTQALNF AFKDKYKQVF LGGVDKRTQF WRYFLGNLAS GGAAGATSLC FVCPLDFART RLAADVGKAA GEREFAGLGN
161 CLVKIFKSGG IAGLYRGFNV SVQGIIIYRA AYFGFL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	12	24	
total 1 peptides												

tr|A0A0P6CE35|A0A0P6CE35_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTDAAVSFAK **DFLAGGVAAA ISK**TAVAPIE RVKLLLQVQH ASKQITADKQ YKGIIDCVVR IPKEQGVLSF WRGNLANVIR
81 YFPTQALNFA FKDKYKQIFL GGVDKRTQFW RYFAGNLASG GAAGATSLCF VYPLDFARTR LAADVGKAGA EREFKGLGDC
161 LVKIYKSDGI KGLYQGFNVS VQGIIIYRAA YFGIYDTAKG MLPDPKNTHI FISWMIAQSV TAVAGLTSYP FDTVRRRMMM
241 QSGRKGTDIM YTGTLDCWRK IARDEGSKAF FKGAWSNVLR GMGGAFVLVL YDEIKKYT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	11	23	
total 1 peptides												

tr|A0A1W7R9C9|A0A1W7R9C9_9SCOR back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTFDAVSFLK **DFLAGGVAAA ISK**TAVAPIE RVKLLLQVQH ASQQISVEKQ YKGIIDCFVR IPKEQGFLSY WRGNLANVIR
81 YFPTQALNFA FKDKYKQLFL GGIDKKTHFW RHFLGNLASG GAAGATSLCF VYPLDFARTR LAADIGKVGA DREFAGLFHC
161 LAKIFKHDGI IGLYRGFNVS VQGIIIYRAA YFGFFDTAKG MLPNPKNTPI LLSWLIAQTV TTVAGIMSYP FDTVRRRMMM
241 QSGRPVAERM YKNTIDCWGK IYKSEGGGAF FKGALSNVIR GTGGALVLVI YDEIKNYIV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	11	23	
total 1 peptides												

tr|V9IK47|V9IK47_APICE back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV
81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLRYFVGNLA SGGAAGATSL CFVYPLDFAR TRLAADVGKA GGEREFTGLG
161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM
241 MMQSGRAKSE ILYKNTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	13	25	
total 1 peptides												

tr|M9NYU2|M9NYU2_APICC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV
81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLRYFVGNLA SGGAAGATSL CFVYPLDFAR TRLAADVGKA GGEREFTGLG
161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKA PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM
241 MMQSGRAKSE ILYKNTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	13	25	
total 1 peptides												

tr|A0A087U5M6|A0A087U5M6_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPVDVLSFAK **DFLAGGVAAA ISK**TAVAPIE RVKLLLQVQH VSKQISVDKQ YKGIVDCFVR IPKEQGILSF WRGNLANVIR
81 YFPTQALNFA FKDKYKQIFL GGVDKRTQFW RYFMGNLASG GAAGATSLCF VYPLDFARTR LAADVGKGPA NREFSGLINC
161 LTKIFKTDGL FGLYRGFSVS VQGIIIYRAA YFGFYDTTKG MLKTDPKNTP IIVSWVIAQC VTMVSGIISY PFDTVRRRMM
241 MQSGRAKADM QYKNTLDCWI KIGRQEGPTA FFKGALSNII RGSGGALVLV LYDEIRNFLV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	11	23	
total 1 peptides												

tr|Q6VQ13|Q6VQ13_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV
81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLRYFVGNLA SGGAAGATSL CFVYPLDFAR TRLAADVGKA GGEREFTGLG
161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM
241 MMQSGRAKSE ILYKSTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	13	25	
total 1 peptides												

tr|A0A2A3ELD5|A0A2A3ELD5_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV
81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLRYFVGNLA SGGAAGATSL CFVYPLDFAR TRLAADVGKA GGEREFTGLG
161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM
241 MMQSGRAKSE ILYKNTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	60.72	1218.6608	81.3	610.3872	2	50.99	4616	4	13	25	
total 1 peptides												

tr|A0A0J7L3Z2|A0A0J7L3Z2_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSEILTGIL GKRYKLQTSE KFDEYMKALG VGMVTRKMGA TVSPVVELTE KDGVYTLKTT STFKNTEIK**F KLGEEFEEET**
81 **VDGR**KVKSIC TLDGNKLVQV QKGDKNTTID REFTPTEMKA IMKVDDIVCT RVYKLQE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	70	84	
total 1 peptides												

tr|A0A2A3ERN5|A0A2A3ERN5_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSAFYRKRY KLQSSENFDE FMKALGVGIM TRKVGSSVSP VVELSENNGL YTLKTTSPFK NTEIK**FKLGE EFEEETVDGR**
81 KVKSVCTLDG NKLIQVQKGE KQTTIEREFS STEMKAIMKV DDIICTRVYK VQD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	66	80	
total 1 peptides												

tr|A0A088AE74|A0A088AE74_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSAFYRKRY KLQSSENFDE FMKALGVGIM TRKVGSSVSP VVELTENNGL YTLKTTSPFK NTEIK**FKLGE EFEEETVDGR**

81 KVKSVCTLDG NKLIQVQKGE KQTTIEREFS STEMKAIMKV DDIICTRVYK IQD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	66	80	
total 1 peptides												

tr|Q76LA4|Q76LA4_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPDFLGKRYK LYSSENFDDF MKALGVGIMT RKVGSSVSPV VELTENNGLY TLKTTSPFKN TEIK**FKLGEE FEEETVDGR**K

81 VKSVCTLDGN KLIQVQKGEK QTTIEREFSS TEMKAIMKVD DIICTRVYKI QD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|A0A023EFS1|A0A023EFS1_AEDAL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAWVGKKYK MEKSEGFDDY MKALGVGMVL RKLGNSISPT VELVKEGDEY TFNTTSTFKN TTIK**FKLGEE FEEETVDGR**K

81 VKSVCTLEGD NKLVHEQKGE KPTTIIREFT ATDLTATMTA GNAKCVRYYK AV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|A0A1L8DZ33|A0A1L8DZ33_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAWEGKKYK LEKSDNFDEY MKALGVGMVL RKMGNTVTPT VELVKNGDEY TFNTTSTFKS TAIK**FKLGEE FEEETVDGR**K

81 VKSVCTMDGP NKLIHDQKGE KPTVITREFT PTELTASMTA GDVKCVRYYK VV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|V9IIS4|V9IIS4_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPDFLGKRYK LYSSENFDDF MKALGVGIMT RKVGSSVSPV VELSENNGLY TLKTTSPFKN TEIK**FKLGEE FEEETVDGR**K

81 VKSVCTLDGN KLIQVQKGEK QTTIEREFSS TEMKAIMKVD DIICTRVYKV QD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|Q177Y4|Q177Y4_AEDAE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAWVGKKYK MEKSEGFDDY MKALGVGMVL RKLGNSISPT VELVKEGDEY TFNTTSTFKN TTIK**FKLGEE FEEETVDGR**K

81 VKSVCTLEGD NKLIHEQKGE KPTTIIREFT DTDLIATMTA GNAKCVRTYK AV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	

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

tr|T1E383|T1E383_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAWVGKKYK MEKSEGFDDY MKALGVGLVL RKLGNSISPT VELVKDGDEY TFNTTSTFKN TTIK**FKLGEE FEEETVDGR**K

81 VKSVCTFEGD NKLVHEQKGD KPTTIIREFT DSELTATMTA GGAKCVRYYK VA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|A0A1B0EX54|A0A1B0EX54_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSAWEGKKYK LEKSENFDEY MKALGVGMVL RKMGNTVTPT VELVKNGDEY TFNTTSTFKS TTIK**FKLGEE FEEETVDGR**K

81 VKSVCTMDGP NKLVHDQKGE KPTVIIREFT PTDLTATMTA GDVKCVRYYK AV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.FKLGEEFEEETVDGR.K	Y	59.67	1783.8264	52.5	892.9673	2	33.50	2638	2	65	79	
total 1 peptides												

tr|A0A1B6MNR0|A0A1B6MNR0_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VHNATDMLIK EYRVTLPLTV E**EYQVAQLYS VAEASK**NETG GGEGIEVLKN EPFDNYPLLG GKYSKGQYTY KIYHLQSKVP

81 GFIKLIAPKG SLEIHEEAWN AYPYCKTVIS NPGYMKENFV IVIESYHIGD RGTKDNVHEL PPEKLKHREV VKIDIGNDPV

161 SSSDYKP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	22	36	
total 1 peptides												

tr|A0A0K8TZW2|A0A0K8TZW2_BACLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYNAG QYTYKIYHLA SKVPAFIRLL

81 APKGSLEIHE EAWNAYPYCR TVITVCT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A1A9WJA5|A0A1A9WJA5_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDKGQPVGAH HHRVTLPLTV E**EYQVAQLYS VAEASK**NETG GGEGIEVLKN EPFTNHPLLG GKYSSGQYTY KIYHLASKVP

81 AFIRLLAPKG SLEIHEEAWN AYPYCKTVIT NPKFMKNDFI LQIDSLHMAD YGDSNNNPGY MRDNFIIIIE SLHLADVGDQ

161 ENVHELPPEK LKIREVVHID IAHDPVTPAD YKLDEDPTKF QSKKTGRGPL IESDWKLKVK PVMTCYKLVT CEFKWFGLQG

241 RIENFIQKSE RRLFTNFHRQ VFCWMDRWHG LTMDDIRAIE EKVKEELDKQ RNEGEVRGTR ADSD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	22	36	
total 1 peptides												

tr|A0A1B0G7Y9|A0A1B0G7Y9_GLOMM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFTNH PLLGGKYSSG QYTYKIYHLA SKVPAFIRLL

81 APRGSLEIHE EAWNAYPYCK TVITNPGFMK ERFLVQIDSL HTADYGDFDN NPGYMRDNFI IIIESLHLAD VGDQENVHEL
161 PPEKLKIREV VHIDIAHDPV TPADYKLDED PTKFHSTKTG RGPLVESDWK LKVKPVMTCY KLVTCEFKWF GLQGRIENFI
241 QKSERRLFTN FHRQVFCWMD RWHGLTMDDI RAIEEKVKEE LDKQRNEGEV RGTRADSD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A067R8Y0|A0A067R8Y0_ZOONE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFEDH PLLGGKYRKG QYTYKIYHLA SKVPSFIRLL

81 APRGSLEVHE EAWNAYPYCK TVISNPYMKE KFVLVIESLH VADNGQQDNN PGYMKENFFI MIESLHLADT GMQQNVHELP
161 PEKLRNRDVV HIDIANDSVT AADYKPDEDP TKFKSEKTGR GPLRGQWMDK VKPVMTCYKL VTVEFKWFGL QTKIEHFIQK
241 SERRLFTNFH RQVFCWIDRW HGLTMEDIRA IEEKTKEELD KQRMIGEVRG MKAETE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A0N7Z9V5|A0A0N7Z9V5_9EUCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFVKEFRVIL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFENY PLLGDEYSKG QYTYKIYHLK SKVPAFIRLL

81 APEGSLEMHE EAWNAYPYCR TIISNPGYMK ENFYITIESL HVLDNGESEN NPSYMKRNFT VMIETLHLAD MGTQENAHRL
161 TGEKLNMREV VTIDIANDPV KPSDYKADED PTKFKSEKTG RGPLQGPQWW KKCDPVMTCY KLVTCEFKWF GFQTRIEKFI
241 MDAERRLFTN FHRQVFCWMD QWHGMDMNDI RRLEDTTKDE LDEQRKVGTV RGTKGE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|L7M5S1|L7M5S1_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVVL PITVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFEGK QLLGGKYNKG QYTYKIYHLE SKVPPFIRML

81 MPKGSLAVHE EAWNAYPYCR TVLTNPDYMA GNFTLCIETM HAPDNGTQEN VHELPPEKLK IREVDVIDIA SDPVLPKNGR
161 RPQTENGAGE DYKEDEDPST FVSKKTGRGP LKGDWMKTCK PVMCAYKLVT VEFKWFGLQN RVEAFIQKTE RRIFLNFHRQ
241 VFCWMDRWYG MTMADIRKLE EQTKKELDEQ LKKGTVRGTK GEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A224YXR0|A0A224YXR0_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVVL PITVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFEGK ELLGGKYNKG QYTYKIYHLE SKVPPFIRML

81 MPKGSLAVHE EAWNAYPYCR TVLTNPDYMA ANFSLCIETM HAPDNGTQEN VHELPPEKLK IREVDVIDIA SDPVLPKDGR
161 RRHAGCGAGE DYKEDEDPST FVSKKTGRGP LKGDWMKTCK PVMCAYKLVT VEFKWFGLQN RVEAFIQKTE RRIFLNFHRQ
241 VFCWMDRWYG MTMADIRKLE EQTKKELDEQ RKKGTVRGTK GEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|L7M5B6|L7M5B6_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVVL PITVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFEGK QLLGGKYNKG QYTYKIYHLE SKVPPFIRML

81 MPKGSLAVHE EAWNAYPYCR TVLTNPDYMA GNFTLCIETM HAPDNGTQEN VHELPPEKLK IREVDVIDIA SDPVLPKNRR

161 SQRENCEGDY KEDEDPSTFV SKKTGRGPLK GDWMKTCKPV MCAYKLVTVE FKWFGLQNRV EAFIQKTERR IFLNFHRQVF

241 CWMDRWYGMT MADIRKLEEQ TKKELDEQLK KGTVRGTKGE E

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A0L7QKW7|A0A0L7QKW7_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNASFFIFML SVERKLFRGI **EYQVAQLYSV AEASK**NNTGG GEGIEVLKNE PFTDYPLLGG KYSSGQYTYK IYHLASKVPG

81 FIRIMLPKNS LEIHEEAWNA YPYCKTVITN PGYMKENFVI MIESFHIDDV GNQHNVHELS SDKLKIREVI HIDIANDPIG

161 SADYKEDEDP TKFKSVKTGR GPLVGKDWKN KVQPVMTCYK LVTCEFKWFG LQTRVESFIQ KAERRLFTNF HRQVFCWIDR

241 WYGLTMDDIR AIEESTKEEL DRQRHQGEVR GMRADD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	21	35	
total 1 peptides												

tr|W8BHP2|W8BHP2_CERCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYNAG QYTYKIYHLA SKVPAFIRLL

81 APKGSLEIHE EAWNAYPYCR TVITNPKFMK DGFRITIDSL HVPNDSGDLP NVHELPPEKL KTREVVHIDI ANDTVLPADY

161 KPTEDPTKFK SEKTGRGPLV GPNWKKNVDP VMTCYKLVTC EFKWFGLQTR IENFIQKSER RLFTNFHRQV FCWMDRWHGL

241 TMEDIRAIEE KVKEELDRQR QVGEVRGMRA DSD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A034W637|A0A034W637_BACDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYNAG QYTYKIYHLA SKVPAFIRLL

81 APKGSLEIHE EAWNAYPYCR TVITNPKFMK DGFRITIDSM HVRDDAGNIP NVHELPPEKL KTREVVHIDI ANDTVLPADY

161 KPTEDPTKFK SEKTGRGPLV GPNWKKNVDP VMTCYKLVTC EFKWFGLQTR IENFIQKSER RLFTNFHRQV FCWMDRWHGL

241 TMEDIRAIEE KVKEELDRQR QVGEVRGMRA DSD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A224XUC6|A0A224XUC6_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDDF PLLGGKYSKG QYTYKIYHLQ SKVPAFIRLL

81 APKGSLEIHE EAWNAYPYCR TVLTNPNYMK DKFVIIVETL HVGDRGKSPN VHELNEEKLK LREVVMIDIG SDPVSPADYK

161 EDEDPRKFKS QKTGRGPLDS AVWREKVDPV MTCYKLVTVE FKWFGLQSRI ENFIQKSERR LFTTFHRQLF CWMDRWYGLT

241 MEDIRKIEET TKEELDQQRN VGQVRGMHAD CE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|T1PCP0|T1PCP0_MUSDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFTDH PLLGGKYSSG QYTYKIYHLA SKVPAFIRIL

81 APKGSLEIHE EAWNAYPYCK TVITNPKFMK DGFKVIIDSL HLADLGESEN VHQLPPEKLK QREVVHIDIA NDPVTPADYK

161 PDEDPTKFKS EKTGRGPLVG ADWKKKVDPV MTCYKLVTCE FKWFGLQSRI ENFIQKSERR LFTNFHRQVF CWMDRWHGLT

241 MEDIRAIEDK VKEELDKQRQ EGEVRGTKAD SD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|D3TN38|D3TN38_GLOMM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFTNH PLLGGKYSSG QYTYKIYHLA SKVPAFIRLL

81 APRGSLEIHE EAWNAYPYCK TVITNPGFMK ERFLVQIDSL HTADYGDFDN VHELPPEKLK IREVVHIDIA HDPVTPADYK

161 LDEDPTKFHS TKTGRGPLVE SDWKLKVKPV MTCYKLVTCE FKWFGLQGRI ENFIQKSERR LFTNFHRQVF CWMDRWHGLT

241 MDDIRAIEEK VKEELDKQRN EGEVRGTRAD SD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|R4G5F6|R4G5F6_RHOPR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDDF PLLGGKYSKG QYTYKIYHLQ SKVPAFIRLL

81 APKGSLEIHE EAWNAYPYCR TVLTNPNYMK DKFVIIVETL HVGDRGMSTN VHELNEEKLK MREIVMIDIG CDPVAPADYK

161 ESEDPKKFKS QKTGRGPLDS AVWREKVEPV MTCYKLVTVE FKWFGLQSRI ENFIHKSERR LFTTFHRQLF CWMDRWYGLT

241 MEDIRRIEET TKEELDKQRN VGQVRGMHAD CE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A1I8MLN0|A0A1I8MLN0_MUSDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFTDH PLLGGKYSSG QYTYKIYHLA SKVPAFIRIL

81 APKGSLEIHE EAWNAYPYCK TVITNPGYMK DNFIIIIESH HIADIGDQEN VHQLPPEKLK QREVVHIDIA NDPVTPADYK

161 PDEDPTKFKS EKTGRGPLVG ADWKKKVDPV MTCYKLVTCE FKWFGLQSRI ENFIQKSERR LFTNFHRQVF CWMDRWHGLT

241 MEDIRAIEDK VKEELDKQRQ EGEVRGTKAD SD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A088AUP1|A0A088AUP1_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLNVK**EYQVA QLYSVAEASK** NNTGGGEGIQ VLKNEPFTDY PLLGGKYSSG QYTYKIYHLA SKVPAFIRIM

81 LPKNSLEIHE EAWNAYPYCK TVITNPGYMK ENFVIMIESF HIDDVGNQHN VHELPPDKLK IREVIHIDIA NDPIANADYK

161 EDEDPTKFKS VKTGRGPLIG KDWKNNVQPV MTCYKLVTCE FKWFGLQNRV ESFIQKAERR LFTNFHRQVF CWIDRWYGLT

241 MEDIRAIEES TKEELDRQRD QGEVRGMRAD D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A1B6IDS7|A0A1B6IDS7_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYSKG QYTYKIYHLQ SKVPGFIKLI

81 APKGSLEIHE EAWNAYPYCK TVISNPGYMK ENFVIVIESY HIGDRGTKDN VHELPPDKLK QREVVKIDIG NDPVSSSDYK

161 PTEDPTKFKS EKTGRGPLTN SWTESVEPVM TCYKLVTVEF KWFGLQTRVE NFIQKSERRL FTVFHRQLFC WMDRWHGLTM

241 EDIRALEEKT KEELDRQRKT GEVRGMKADT D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A0J7L2C9|A0A0J7L2C9_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLTVE**EYQVA QLYSVAEASK** NNTGGGEGIE VLKNEPFTDY PLLGGKYSSG QYTYKIYHLA SKVPAFIRIL

81 LPKNSLEIHE EAWNAYPYCK TVISNPGYMK DNFVIMIESF HIGDVGNQHN VHELPPDKLK IREVVHIDIA NDPVGSADFK

161 EDEDPTKFKS QKTGRGPLVG KDWKNNVQPV MTCYKLVTCE FKWFGLQTRV EGFIQKAERR LFTNFHRQVF CWIDRWYGLT

241 MEDIRAIEDN TKEELDRQRH QGEVRGMRAD D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A0A9YWM3|A0A0A9YWM3_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NNTGGGEGIE VLKNEPFENY PLLGGKYDKG QYTYKIYHLQ SKVPGFIRLL

81 APKGSLEIHE EAWNAYPYCR TIISNPGYMK DNFSIVIESY HIGDRGKQDN VHELAPEKLK DREVVMIDVG NDPVTSADYK

161 ASEDPTKFSS QKTGRGPLTG NWKDTVDPVM TCYKLVSVEF KWFGLQNRVE NFIHKSERRL FTTFHRQVFC WMDRWHGMTM

241 DDIRAIEEKT KEELDRQRNQ GEVRGMKADN D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A1B6FGX0|A0A1B6FGX0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYSKG QYTYKIYHLQ SKVPGFIKLI

81 APKGSLEIHE EAWNAYPYCK TVITNPGYMK ENFMIVIESY HIGDRGTKEN VHELPPDKLK QREVVKIDIG NDPVSSSDYK

161 PTEDPTKFKS EKTGRGPLTN SWTESVEPVM TCYKLVTVEF KWFGLQTRVE NFIQKSERRL FTVFHRQLFC WMDRWHGLTM

241 EDIRALEEKT KEELDRQRKT GEVRGMKADT D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|V9IGA9|V9IGA9_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PLNVK**EYQVA QLYSVAEASK** NNTGGGEGIQ VLKNEPFTDY PLLGGKYSSG QYTYKIYHLA SKVPAFIRIM

81 LPKNSLEIHE EAWNAYPYCK TVITNPGYMK ENFVIMIESF HIDDVGNQHN VHELPPDKLK IREVIHIDIA NDPIANADYK

161 EDEDPTKFKS VKTGRGPLIG KDWKNNVQPV MTCYKLVTCE FKWFGLQNRV ESFIQKAERR LFTNFHRQVF CWIDRWYGLT

241 MEDIRAIEES TKEELDRQRD QGEVRGMRAD D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|D3PIG7|D3PIG7_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PMTVD**EYQVA QLYSVAEASK** NETGGGEGVE VIKNEPYDNV PLLGGKFTKG QYTYKIYHMA SKVPSIIRYI

81 VPKGALEIHE EAWNAYPYCK TVLTNPGYME DKFYIKVETY HIADRGDSEN VHELEADKLK MREVVKIDIA NDDVSRGDYK

161 EDEDPVKYKS QKTGRGPLSD PQWIKSVEPV MTAYKLVTVQ FKWFGIQGKV ENFIQQTERR LFLNFHRQVF CWTDKWHGLT

241 MEDIRAIEDK TKEELEEQRK HGEVRGTKPI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A0P4VQ48|A0A0P4VQ48_9EUCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFVKEFRVIL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFENY PLLGDEYSKG QYTYKIYHLK SKVPAFIRLL

81 APEGSLEMHE EAWNAYPYCR TIISNPGYMK ENFYITIESL HVLDNGESEN AHRLTGEKLN MREVVTIDIA NDPVKPSDYK

161 ADEDPTKFKS EKTGRGPLQG PQWWKKCDPV MTCYKLVTCE FKWFGFQTRI EKFIMDAERR LFTNFHRQVF CWMDQWHGMD

241 MNDIRRLEDT TKDELDEQRK VGTVRGTKGE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A224Z5P9|A0A224Z5P9_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVVL PITVE**EYQVA QLYSVAEASK** NETGGGEGIE VIKNEPFEGK ELLGGKYNKG QYTYKIYHLE SKVPPFIRML

81 MPKGSLAVHE EAWNAYPYCR TVLTNPDYMA ANFSLCIETM HAPDNGTQEN VHELPPEKLK IREVDVIDIA SDPVLPKDYK

161 EDEDPSTFVS KKTGRGPLKG DWMKTCKPVM CAYKLVTVEF KWFGLQNRVE AFIQKTERRI FLNFHRQVFC WMDRWYGMTM

241 ADIRKLEEQT KKELDEQRKK GTVRGTKGEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|C1C1G0|C1C1G0_CALCM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEFRVTL PMTVD**EYQVA QLYSVAEASK** NETGGGEGVE VIKNEPYDNV PLLGGKFTKG QYTYKIYHLA SKVPSLIRYI

81 VPKGALEIHE EAWNAYPYCK TVLTNPGYMD DKFYIKVETY HLADRGDSEN VHELEADKLK NREVIKIDIA KDDVTRGDYK

161 ENEDPSKYKS EKTGRGPLGE NWIKSVDPVM TAYKLVTVQF KWFGLQGKVE NFIQQTERRL FLNFHRQVFC WTDRWHGLTM

241 DDIRAIEDKT KEDLEKQRKE GEVRGTKPI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|A0A1I8PUA1|A0A1I8PUA1_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RVTLPLTVD**E YQVAQLYSVA EASK**NETGGG EGIEVLKNEP FTDHPLLGGK YSSGQYTYKI YHLASKVPAF IRLLAPKGSL

81 EIHEEAWNAY PYCKTVITNP KFMKDNFKVI IDSLHLADGG DSDNVHQLPP EKLKQREVVH IDIANDPVTP ADYKDDEDPI

161 KFKSEKTGRG PLVGADWKKK VDPVMTCYKL VTCEFKWFGL QSRIENFIQK SERRLFTNFH RQVFCWMDRW HGLTMEDIRA

241 IEDKVKEELD KQRQEGEVRG TRADSD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	10	24	
total 1 peptides												

tr|A0A232FH25|A0A232FH25_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RVTLPLTVE**E YQVAQLYSVA EASK**NNTGGG EGIEVLKNEP FTDYPLLGGK YSSGQYTYKI YHLASKVPGF IRILLPKNSL
81 EIHEEAWNAY PYCKTVISNP GYMKDNFIIV IESYHIGDVG DQENVHELPP DKLKIREVVH IDIANDPITN ADYKEDEDPI
161 KFKSEKTGRG PLVGKDWKHH VDPVMTCYKL VTCEFKWFGL QTRVESFIQK AERRLFTNFH RQVFCWMDRW HGLTMEDIRA
241 IEEKTKEELD RQREKGEVRG MRADD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	10	24	
total 1 peptides												

tr|A0A0K8VNQ1|A0A0K8VNQ1_BACLA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLIKEYRVTL PLTVE**EYQVA QLYSVAEASK** NETGGGEGIE VLKNEPFDNY PLLGGKYNAG QYTYKIYHLA SKVPAFIRLL
81 APKGSLEIHE EAWNAYPYCR TVITNPKFMK DGFRITIDSM HVRDDAGNIP NVHELPPEKL KTREVVHIDI ANDTVLPADY
161 KPTDDPTKFK SEKTGRGPLV GPNWKKNVDP VMTCYKLVTC EFKWFGLQTR IENFIQKSER RLFTNFHR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.EYQVAQLYSVAEASK.N	Y	56.39	1684.8308	26.7	843.4452	2	34.43	2742	1	16	30	
total 1 peptides												

tr|I1ZEB5|I1ZEB5_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KVIENAEGSR TTPSVVAFTK DGERLVGMPA KRQAVTNAAN TFYATKRLIG RRFDDPEVQK DMKIVSYKIV KASNGDAWVE
81 AHGKMYSPSQ IGAFILMKMK ETAEAYLNQP VKNAVVTVPA YFNDSQRQAT KDAGQISGLN VLRVINEPTA AAIAYGMDKS
161 EDKIVAVYDL GGGTFDISIL EIQKGVFEVK STNGDTFLGG EDFDNALVNF LSAEFKKDQG IDVTKDIMAM QRLKEAAEKA
241 KIELSSALQT DINLPYLTMD ANGPKHMNLK LTRSKFESLV ADLIKRTIEP CKKAISDAEV SKSDIKEVIL VGGMTRMPKV
321 QEIVQETFGR APSKSVNPDE AVAVGAAVQG GVLSGNVTEI LLLDVTPLSL GIETLGGVMT KLINRNTTIP TKK**SQVFSTA**
401 **ADGQTQVEIK** VYQGEREMAS NNKLLGQFSL VGIPPAPRGV PQIEVTFDID ANGIVNVSAR DKGTGKEQQI IIQSSGGLSK
481 DDIENMIKAA EKFAEEDKKK REIVETVNQA EGIIHDTESK MEEFKDQLPS EEYEKLKEKI AKTREVLANK DNETPEKIKE
561 VCNDLQQSSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.SQVFSTAADGQTQVEIK.V	Y	51.22	1807.8951	505.9	905.4121	2	31.30	2392	1	394	410	
total 1 peptides												

tr|D9IFR6|D9IFR6_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPAVGIDLGT TFSCVGVFQH GKVEIIANDQ GNRTTPSYVA FTESERLIGD AAKNQVAMNP KNTVFDAKRL IGRKYDDPKI
81 QEDLRNWPFT VKSDSGKPKI CVEFKGEQKR FAPEEISSMV LTKMKETAEA YLGETVSDAV ITVPAYFNDS QRQATKDAGA
161 IAGLNVLRII NEPTAAALAY GLDKNLSGER NVLIFDLGGG TFDISILTID EGSLFEVRAT AGDTHLGGED FDNRLVSHLA
241 DEFKRKFKKD LRSNPRALRR LRTAAERAKR TLSSSTEATI EIDALFEGAD FYTKVSRARF EELCADLFRS TLQPVEKALC
321 DAKMDK**AQIH DIVLVGGSTR** IPKVQSLLQN FFNGKSLNLS INPDEAVAYG AAVQAAILSG DKSSKIQDVL LVDVAPLSLG
401 IETAGGVMTK IVERNSRIPC KQSQTFTTYS DNQPAVTIQV FEGERAMTKD NNLLGTFNLT GIPPAPRGVP KIDVTFDLDA
481 NGILNVSAKD TSTGNSKNIT IKNDKGRLSQ SDIDRMLAEA ERYAEEDEKQ RQRVAARNQL EGYVFNLKQS VEDAGSKLSP
561 EDKDTVLKSC DDTIKWLDNN NLAEKEEFEH RFQELTRKCS PIMTKLHSGS GAGQQGPSCG QQTGGFGGAR SGPTVEEVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AQIHDIVLVGGSTR.I	Y	48.68	1464.8048	-2.0	733.4082	2	31.02	2362	1	327	340	

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

tr|A0A026W3N3|A0A026W3N3_OOCBI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDQITPKEVK ILENPEDIQE RREQVLGRYA NFKSEARNKR DKLEDSRRFQ YFKRDADELE GWIYEKLQAA SDESYKDPTN
81 LQAKIQKHQA FEAEVAAHSN AIVLLDNTGS EMITQHHFAS DIIRKRLEEL HRLWELLLSR LADKGLKLQQ ALVLVQFIRH
161 CDEVMFWIHD KEAFVTTDEF GHDLEHVEVL QRKFDEFQKD MASQEYRVTE VNELADKLLL DGHPERDTIL RRKEELNESW
241 QRLKQLATLR QEKLFGAHEI QRFNRDADET MAWIAEKDVV LSSDDFGRDL ASVQTLQRKH EGIERDLAAL EDKVYTLGAE
321 ADRLAAIHEA DHSRQIQAKR AEILQSWESL TAKAKERRLK LDESYYLHRF LADYRDLVSW MNDMRAIISA DELAKDVAGA
401 EALVDRHQEH KGEIDARADS FDATTLAGNK LLEKKHYAAE EVARKLNSLA DDKSSLLSLW EKRRILYEQC VDLQLFYRDT
481 EQADAWMAKQ EAFLANEDLG DSLDSVEALI KKHEDFDKSL AAQEEKIKVL DDFAGKLIEG EHYAADDVAQ RRQLLLERRA
561 ILLEKSAQRR RRLEDAYKLQ QFERDCDETK GWVNEKLKFA TDDSYLDPTN LNGKVQKHQN FEQELNANRT RMEEMVATGQ
641 ELIDGDHYAS DRIRTRTEEI VTLWESLARA TEKKGAKLQE ASQQQFNRT VEDIELWLSE VEGQLMSEDC GKDLTSVQNL
721 QKKHALLEAD VTSHADRIDS ITQAAEQFVK SGHFDADNIK TKQEQLQTRY AALQRPMSSR KQRLLDSLQV QQLFRDIEDE
801 EAWIREKEPV AASTNRGRDL IGVQNLQKKH QAVLAEINNH EPRVAAVCQA GSTMLQEGHF AAEEINNRLT ALDEHWGQLK
881 DKARQRKNDL DDSLQAHQYF ADANEAESWM KEKRPIVMNG DYGKDEDSSE ALLKKHEALV SDLEAFASTI AALRDQAAAC
961 RQQETPTVDI TGKECVVALY DYTEKSPREV SMKKGDTLTL LNSNNKDWWK VEVNDRQGFV PAAYVKRVEP EAGLSASQQN
1041 LAREQSSIAA RQAQIEGQYD DLLRLARERQ NKLNETAKAY VLVREAAELA TWIKDKENHA QVQDVGEDLE QVEVMQKKFD
1121 DFQADLKANE VR**LAEMNEIA VQLMSLGQTE AALK**IQTQIQ DLNEKWTSLQ TLTAERANQL GSAHEVQRFH RDVDETKDWI
1201 REKDAALNND DLGKDLRSVQ ALQRKHEGLE RDLAALGDKI KQLDETANRL MQSHPETAEQ TYAKQKEINE EWTQLTAKAN
1281 SRKEKLLDSY DLQRFLSDYR DLMAWINSMM GLVASEELAS DVTGAEALLE RHQEHRMEID ARASTFQTFE MFGQQLLQSS
1361 HYASVEIMEK LDSMTEARQE LEKAWIQRRM QLDQNLELQL FCRDCEQAEN WMSAREAFLS SADAVDSSDN VEALIKKHED
1441 FDKAINAHEE KIATLQTLAD QLIAAEHYAA KPIDERRCQV LDRWRHLKDA LIEKRSRLGE SQTLQQFSRD ADEMENWIAE
1521 KLQLATEENY KDPANIQSKH QK**HQAFEAEL AANADR**IQAV LAMGGNLIDK HQCAGSEDAV QKRLASIADQ WEYLTQKTTE
1601 KSMKLKEANK QRTYIAAVKD LDFWLGEVES LLTSEDAGKD LASVQNLMKK HQLVEADIQA HEERIKDMNA QADSLIESGQ
1681 FDAAGIQEKR QSINERYERI RNLAAHRQAR LNEANTLHQF FRDIADEESW IKEKKLLVGS DDYGRDLTGV QNLKKKHKRL
1761 EAELGSHEPA IQAVQEAGEK LMDVSNLGVP EIEQRLKLLN QAWAELKQLA ATRGQKLDES LTYQQFLAKV EEEEAWITEK
1841 QQLLSVEDYG DTMAAVQGLL KKHDAFETDF AAHGERCKDI CEAGETLIKA GNHRADAIGQ RCAQLRNKLE QLGALAARRK
1921 TRLNDNSAYL QFMWKADVVE SWIADKETHV RSEEFGRDLS TVQTLLTKQE TFDAGLHAFE HEGIQNITSL KEMLVESGHD
2001 QTPNIQKRHA DVIARWQKLL ADSDARKQRL LRMQDQFRQI EELYLTFAKK ASAFNSWFEN AEEDLTDPVR CNSIEEIRAL
2081 REAHAQFQAS LSSAEADFQA LAALDRQIKS FNVGPNPYTW FTMEALEDTW RNLQKIIKER DVELAKEAQR QEENDKLRKE
2161 FAKHANAFHQ WLAETRTAMM EGSGSLEQQL EATKRKTQEV RARRQDLKKI EDLGAILEEH LILDNRYTEH STVGLAQQWD
2241 QLDQLGMRMQ HNLEQQIQAR NQSGVSEDAL KEFSMMFKHF DKDKSGRLNH QEFKSCLRAL GYDLPMMEEG QPDPEFENIL
2321 DIVDPNRDGY VSLQEYMAFM ISKETENVQS SEEIENAFRA ITAADRPYVT KEELYANLTK EMADYCVARM KPYVDPKSER
2401 PITAALDYIE FTRTLFQN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LAEMNEIAVQLMSLGQTEAALK.I	Y	35.52	2359.2126	120.2	787.5060	3	42.08	3600	1	1133	1154	
K.HQAFEAELAANADR.I	Y	21.17	1541.7222	297.2	515.0674	3	29.89	2247	1	1543	1556	
total 2 peptides												

tr|A0A1B6ENV6|A0A1B6ENV6_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNRQPSAKNN VPDELRDVLL EFTISYLLEQ PPDVLDYAVE FFTKLRDNRT TIVRPPPRAA SPDDSVISNE EDDEPPVPRF
81 NTRRKSVFAE AYDPEADDDD TQKVVFPKSD EQRQGLAESV KKILLFRSLD KEQMHEVLDA MFEKRVKEGD YIIKQGDDGD
161 NFYVIQTGTY HAYVKLDDGN QKLIHTYHDK GSFGELALLY NQPRAATIQA GSEGSLWALD RQTFRRIILK SAFKKRKMYE
241 TLIDCVPMLK TLQSYERLNL ADALIPRTYE DGDLIIKQGD AADGMYFVEA GTIKITIFNE DGKEIQVKEI KKGGYFGELA
321 LVTHKPRAAS AYAVGTTK**LA FLDVEAFER**L LGPCMEIMKR NIDDYESQLE KIFGSKHNIT DVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LAFLDVEAFER.L	Y	44.82	1308.6714	392.4	655.5997	2	38.65	3214	1	339	349	
total 1 peptides												

tr|A0A1C9FPZ6|A0A1C9FPZ6_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYTKSVLP ATVQVSAQNS YKVAKGAFTG EISPAMLLDS GIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLAKNV NPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A1C9FPZ7|A0A1C9FPZ7_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYTKSVLP ATIQVSAQNS YKVAKGAFTG EISPAMLLDS GIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLAKNV NPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A289YXQ1|A0A289YXQ1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYAKSVLP ANVQVSAQNS YKVAKGAFTG EISPAMLLDS EIPWVILGHS
81 ERRNVFGETD ELIAEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKIKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLSKNV SPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A1C9FQ23|A0A1C9FQ23_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYAKSVLP ANVQVSAQNS YKVAKGAFTG EISPAMLLDS EIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLSKNV SPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A1C9FPY5|A0A1C9FPY5_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYTKSVLP ATVQVSAQNS YKVAKGAFTG EISPAMLLDS GIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLAKNV NPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A1C9FPY7|A0A1C9FPY7_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYTKSVLP ATVQVSAQNS YKVAKGAFTG EISPAMLLDS GIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLAKNV NPAVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A1C9FQ28|A0A1C9FQ28_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VKKEIDEIVA FLKAGPLDPN VEVVVGVPAL YLTYAKSILP ANVQVSAQNS YKVAKGAFTG EISPAMLLDS EIPWVILGHS
81 ERRNVFGETD ELISEKVAHA LEAGLKVIAC IGEKLDEREA GKTEEVVFKQ TKAIADKVKS WDNVVLAYEP VWAIGTGKTA
161 TPQQAQEVHD KLRQWLSKNV SPVVSESLR**I IYGGSVTAGN AK**ELAKEKDI DGFLVGGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	190	202	
total 1 peptides												

tr|A0A289Z694|A0A289Z694_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZSG2|A0A289ZSG2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPATVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELVSE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289Z5U6|A0A289Z5U6_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZUV1|A0A289ZUV1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YU85|A0A289YU85_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZSB5|A0A289ZSB5_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YUJ3|A0A289YUJ3_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEIVV GVPALYLTYA KSVLPPNVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGESDELISE KIAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKIKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289Z121|A0A289Z121_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZGX1|A0A289ZGX1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZUT5|A0A289ZUT5_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFRQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YXV8|A0A289YXV8_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZSB4|A0A289ZSB4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZSL8|A0A289ZSL8_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZSJ3|A0A289ZSJ3_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YU32|A0A289YU32_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATIQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZS39|A0A289ZS39_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELIAE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKIKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YFQ4|A0A289YFQ4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPPNVQV SAQNSYKVAK GAFTGEISPA MLLDSGVPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289ZGZ1|A0A289ZGZ1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYT KSVLPATIQV SAQNSYKVAK GAFTGEISPA MLLDSGIPWV
81 ILGHSERRNV FGETDELISE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKVKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LAKNVNPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|A0A289YU53|A0A289YU53_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 WKMNGVKKEI DEIVAFLKAG PLDPNVEVVV GVPALYLTYA KSVLPANVQV SAQNSYKVAK GAFTGEISPA MLLDSEIPWV
81 ILGHSERRNV FGETDELIAE KVAHALEAGL KVIACIGEKL DEREAGKTEE VVFKQTKAIA DKIKSWDNVV LAYEPVWAIG
161 TGKTATPQQA QEVHDKLRQW LSKNVSPAVS ESLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	195	207	
total 1 peptides												

tr|V9IKD3|V9IKD3_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGRKFFVGGN WKMNGTKSEI NDIVGFLKKG PLDSNVEVVV GVPSIYLTYA KNILPNNISI AGQNTYKVAK GAFTGEISPA
81 MLLDNGIPWV ILGHSERRNI FGENDELIAE KVAHALDSGL KVIACIGEKL EEREAGKTDE VVFRQTKAIA NKINSWDNVV
161 VAYEPVWAIG TGKTATPQQA QEVHEKLRNW FSKNVNQTVA ETVR**IIYGGS VTAGNAK**DLA KEKDIDGFLV GGASLKPDFV

241 QIVNAKQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.D	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	205	217	
total 1 peptides												

tr|A0A1L1ZLV2|A0A1L1ZLV2_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGRKFFVGGN WKMNGTKSEI NDIVGFLKKG PLDSNVEVVV GVPSIYLTYA KNILPNNISI AGQNTYKVAK GAFTGEISPA

81 MLLDNGIPWV ILGHSERRNI FGENDELIAE KVAHALDSGL KVIACIGEKL EEREAGKTDE VVFRQTKAIA NKINSWDNVV

161 VAYEPVWAIG TGKTATPQQA QEVHEKLRNW FSKNVNQTVA ETVR**IIYGGS VTAGNAK**DLA KEKDIDGFLV GGASLKPDFV

241 QIVNAKQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.D	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	205	217	
total 1 peptides												

tr|A0A0J7KLG9|A0A0J7KLG9_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARKFFVGGN WKMNGTKSEI GDIVAFLKTG PLDPNVEVVV GVPSIYLTHV TSIVPNNVSV SAQNTYKVSK GAFTGEISPA

81 MLLDNGIPWV ILGHSERRNV FGETDELIAE KVAHALEAGL KVIACIGEKL EEREAGKTEE VVYRQTKAIA DKIKSWDNVV

161 LAYEPVWAIG TGKTATPQQA QEVHEKLREW LSKNVDPAVS NTLR**IIYGGS VTAGNAK**ELA KEKDIDGFLV GGASLKPDFV

241 QIVNARC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.E	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	205	217	
total 1 peptides												

tr|A4ZXC4|A4ZXC4_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGRKFFVGGN WKMNGTKSEI NDIVGFLKKG PLDSNVEVVV GVPSIYLTYA KNILPNNISI AGQNTYKVAK GAFTGEISPA

81 MLLDNGIPWV ILGHSERRNI FGENDELIAE KVAHALESGL KVIACIGEKL EEREAGKTDE VVFRQTKAIA NKINSWDNVV

161 VAYEPVWAIG TGKTATPQQA QEVHEKLRNW FSKNVNQTVA ETVR**IIYGGS VTAGNAK**DLA KEKDIDGFLV GGASLKPDFV

241 QIVNAKQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IIYGGSVTAGNAK.D	Y	43.82	1249.6666	71.9	625.8855	2	28.07	2084	1	205	217	
total 1 peptides												

tr|A0A0L7R8Y4|A0A0L7R8Y4_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TSGMEPIGRI QMRTRRTLRG HLAKIYAMHW GSDSRNLVSA SQDGKLIVWD SYTTNKVHAI PLRSSWVMTC AYAPSGSYVA

81 CGGLDNICSI YSLKTREGNV RVSRELPGHT GYLSCCRFYD DNQIVTSSGD MTCALWDIET GQQCTSFIGH TGDVMSLSLA

161 PDTRTFVSGA CDASAKLWDL REGSCKQTFP GHESDINAVT FFPNGYAFAT GSDDATCRLF DIRADQELAM YSHDNIICGI

241 TSVAFSKSGR LLLAGYDDFN CNVWDSMKAE RAGILAGHDN R**VSCLGVTED GMAVGTGSWD SFLR**IWN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VSCLN(sub G)VTEDGMAVGTGSWDSFLR.I	Y	37.12	2443.1147	-8.4	1222.5544	2	38.94	3247	1	282	304	Mutation
total 1 peptides												

tr|A0A088AR98|A0A088AR98_APIME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSELESLRQ ESDKLKNAIR DARKAACDTT LVQATSGMEP IGRIQMRTRR TLRGHLAKIY AMHWGSDSRN LVSASQDGKL
81 IVWDSYTTNK VHAIPLRSSW VMTCAYAPSG SFVACGGLDN ICSIYSLKTR EGNVRVSREL PGHTGYLSCC RFYDDNQIVT
161 SSGDMTCALW DIETGQQCTS FIGHTGDVMS LSLAPDTRTF VSGACDASAK LWDIREGTCK QTFPGHESDI NAVTFFPNGY
241 AFATGSDDAT CRLFDIRADQ ELAMYSHDNI ICGITSVAFS KSGRLLLAGY DDFNCNVWDS MKAERAGILA GHDNR**VSCLG**
321 **VTEDGMAVGT GSWDSFLR**IW N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VSCLN(sub G)VTEDGMAVGTGSWDSFLR.I	Y	37.12	2443.1147	-8.4	1222.5544	2	38.94	3247	1	316	338	Mutation
total 1 peptides												

tr|V9IJ30|V9IJ30_APICE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSELESLRQ ESDKLKNAIR DARKAACDTT LVQATSGMEP IGRIQMRTRR TLRGHLAKIY AMHWGSDSRN LVSASQDGKL
81 IVWDSYTTNK VHAIPLRSSW VMTCAYAPSG SFVACGGLDN ICSIYSLKTR EGNVRVSREL PGHTGYLSCC RFYDDNQIVT
161 SSGDMTCALW DIETGQQCTS FIGHTGDVMS LSLAPDTRTF VSGACDASAK LWDIREGTCK QTFPGHESDI NAVTFFPNGY
241 AFATGSDDAT CRLFDIRADQ ELAMYSHDNI ICGITSVAFS KSGRLLLAGY DDFNCNVWDS MKAERAGILA GHDNR**VSCLG**
321 **VTEDGMAVGT GSWDSFLR**IW N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.VSCLN(sub G)VTEDGMAVGTGSWDSFLR.I	Y	37.12	2443.1147	-8.4	1222.5544	2	38.94	3247	1	316	338	Mutation
total 1 peptides												

tr|B4KM55|B4KM55_DROMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNSKADVNRR VLAIQAKKKR HRNNKKRGKQ NGANGAPVQE NQQQQQQPQQ QHHQQPLQQQ QEQPEQQQYE EPETQAPENA
81 NNSHIEGASK FELHVGNASG AINSKSTASF SNATASTSSG GSANTPDAQS KSKSQNNMQH SQSQSQQYQQ QARSSSNESD
161 ESELVSENEE QELKEDYCKG GYHPVNIGDL FQGRYHVIRK LGWGHFSTVW LCWDLQEKRY VAIKIVKSAQ HFAETAKDEI
241 KILRAVRETD PTNPRRHKTV QMFDDFKITG VNGTHICMVF EVLGDNLLKL IRKSNYRGIP LENVKSITRQ VLEGLDYLHS
321 CCKIIHTDIK PENVLLCVDE PHVRSLAVEA TQLYCMNSKM YPSLVSRAPK EYREPPITGK MSKNKKKKLK KKAKKRMELF
401 KKQRDYLEQA GGDEQHEQPE QLEQPVPE**AH ALNGDAGVS**D NEQDVDGEDG NAGCEDVEPV VQPIKPELDG TEKAKKKRKR
481 KNKNKFSQQQ SQAQDQKPPQ ENSTSSGDSS SVALKSSNTN GSNSNSSHST STLKGQSNGA AGGNKKASRP KQELQQPQQR
561 QQVNNNNSNS KQNSNSNSKI SNNSMEGSSS TNGGPYSEPL LPPPPPPPLA KQRVKRDPAL EPCNVQVKIA DLGNACWVDR
641 HFTEDIQTRQ YRSLEVILGA GYDTSADIWS TACMVFELAT GDYLFEPHSG DTYTRDEDHI AHIIELLGPI PRHIVFRGTY
721 PTYTFNRNGE LRNITGLKPW GLMDVLVEKY EWSKREAEAF TAFLKPMLEF DPAKRATAAE CLQHEWLRXD TMQPGCWLPA
801 SQPAGAAVAV AIEAAAATAA GAGADVASSD YVQSTASVAT LASISSIAST SASAMAALAQ ARPYSATTSA PPTPQSHAIH
881 HAMSSVRTAP ATPTRTPKHT DDVDGVQDIG LTVAISEMLP PAPPPPPPLP SMSAPYSKSK SQRFFWRKAL RRVFQRRK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.AHALNGDAGVS.D	Y	26.91	1010.4781	227.8	506.3614	2	47.56	4220	1	429	439	
total 1 peptides												

tr|A0A151ILK1|A0A151ILK1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQPECTKDVV ECFPELLLAL ISIAIPIKNI QSSASRDKDI IHKLNCVILG KLLDVNQDLL IYVLHYFDVN PAPFELFDDS
81 LDTLIPVKRQ NRRKFSRISE VSDHDIVIAC HSILQSAVSH FKHKWNWSKF YKYLTNADDR VKWVALKCIA IVLNMSESTR
161 LSWLKTLILN FGKFLIDYED KSVDTSIICV SFESMEDTVK NISSIISVGG ILLPTLGKTH STYNLVPVSS MKKNLQSLAI
241 AIGSRKCICL QGPVGCGKTA LVEYLARVTG HDSSNFIKVQ LGDQTDSKML LGMYRCTDVP GEFVWQPGVL TQAVIAGKWL
321 LLEDVDSAAL DVASVLSNLM ETGTLCVPGY RDTIYVNSGF QLFVTQRLMM SVTGIQKHVT GSSSLLQKHW LCLNMEPLST
401 DELVIVVQTL FPVLNSIATK IIDVFLLFSV GDYDSGSNAC DATLSLKIGR QMSTRDLIKW CSRAIVDFVV SSPDSLLKIF
481 QDALDVFCCS VSNQEQRLNL AKKITDKLGI IREKAEHFCN KHKPFIDLLP DLLVAGRAKL TRKKAEYARI DIEKINFSFT
561 RPSACLLERI AICIKQKEPV LLVGETGTGK TSSIQYLARS TGHKLVVINM NQQSESADLL GGYKPVDLKF LISPIREEFE
641 ILFRSYFIIE PNKEFLKRIA SCHKQQKKDI LERFGQNKKA QKKSDQDDDL NMLKKWEKML EKLDKLRAQV KSQYALAFSF
721 IEGSLVRALR DGYWVLLDEI NLANAETLEC LSGLLEGSSE SLSLLERGDG EPVKRHPDFT VFACMNPATD VGKRDLPVGL
801 RNRFTEFYVD ELTEQSDLEL LVSSYLAELN LPEKHKAIVK FYLNVRKEAM STLFDGTAHK PHYSLRTLCR ALYISASNPC
881 SNVLRSLYES FSLSFLTQLD YNSYPIVQKM IAKAILNNKN IKEILGIPIP KPKCSPGEDY IYIEGYWVLQ GSLTPEIPTN
961 YILTDSVRRN LKDLVRVVSI GKIPILLQGD TSVGKTSLIT YLAKTTGHVC VRINNHEHTD LQEYVGSYIA DETGKLVFKE
1041 GILVDAMRKG YWIILDELNL APSDVLEALN RVLDDNRELF IPETQQVVKA HEHFMLFATQ NPPGLYGGRK VLSRAFRNRF
1121 IELHFDEIPP NELQIILNQR CSMPESYCKQ VINVMTDLQI RRKSTAAFAG KRGFITLRDL FRWGERYRLA PDVGNKLYDW
1201 SQHLADEGYL VLAAKVRKAE EADEIRQVIK KHLKRDVDPD NLFTLNDKTS PVTRHILEEI LKNGISGFRH IVWTYHMRRI
1281 AVLMKKSCQF KEPVLLVGET GGGKTTVCQL IAAINGQAMR GVNCHMHTES SDFLGNLRPV RDHVENNQKL FEWMDGPLID
1361 AMRNGDLFLA DEISLADDSV LERLNSLLEP ERSLLLAEKG IESLHGEENT VITADEKFIF VGTMNPGGDY GKKELSPALR
1441 NRFTEVWCEG CMARNDLRDI IIHNLRTDLE TTKEPIANAI LRFTEWLQAT EVGKKLTVSI RDVLTWVNFI NVSTASTLSK
1521 LSIGKAYYHG ACLTYIDSLG CSSTGSESIN KLQDFTEAAL RFIKLEIENT IKPELDMETP VINEDVVNAS DKFGILPFYI
1601 KKGPHTCENH AFTFTPTTKL NTLKLLRALQ LNKPIL**LEGS PGVG**KTSLVS ALAKATGHTL LRINLSDQTD VSDLFGADLP

1681 VEGGKGGEFA WRDGPFLRAL RAGYWILLDE LNLASQSVLE GLNACFDHRG EIYIPELGKT FLVKPGTKLF GCQNPLRQGG
1761 ARRGLPRSFL NRFTQISVAT LMEDDLKFIL RMQFPSLPIE LINHMVQFNS KLASEAGIVW GHTGSPWEMN LRDVIRWCEI
1841 TIKAASNEFC NNKQYFNPGD GVELIYVNRM RTYEDRQKVY QIYQEMFSLE KYPLPPNQLP TYITADKFSI GDVVLSRKNC
1921 SEPQDFNLLV LRDQKRALKS LVQCVEMNWM SILVGTSGSG KSSVVRLLAA LTGQKLRSIT VNSAMDTTEI LGSFEQTDYN
2001 RHLEQLFEDV TTLLIESLQT KITDDKLEQV TELHEHLEQV RHLFDENVAG RTMAAETKLF LHKIEELSKL VSSMKLWESS
2081 RELELLDIES KLRNLSIFVE QDKCLNAGGK FEWVDSVLVK CLQDGTWLLI DQVNLCSPAV LDRLNGLLEP NGVLSIGERG
2161 IDSNGNVVTI KPHKNFRLFL TMNPRYGEIS RAMRNRGVEI YMLGSKENID KNLIDFNSLL FNAGIMKSAH RDALLDIYDR
2241 MSEEIVWDQF NMVDLLHTAF LVKQRLLRGF SAKQSIKNAC IDVYIKPRPL RDSRFREHLT SLIDEIVEQR VTCDEEISVI
2321 DLDAATWSVK NLQDNSRLVL IRQQGLLLNA ALKMYESLLK SDSGNIGRNI ITTKSLNDFC GLKEDEKFML NVDVTDILSY
2401 LLLNFYEQSS QDDAPLRKEL VSKMLRGNAI FDNLEHKSEL MEKVIAQYCS ESTNARRSLP LDLWQLVGRT TCDNDTTGRD
2481 TNKLLLLLYA DSMILNRDIS LKKTENKDLI SIKLYCSAVK NGKLFPQLKN QPLITFFVQF LEQASFYIKT ILQDINIEKY
2561 IDLRKDLRWF SRFERLGELT LIDKAGKSKG LFTNLDQISL LLSVHYKWLL KFLRKLKSLS NKTMSKSKLW NIVDRINHQL
2641 ESPYDSIKKI SKRIKKFLIL PSPHSTEVNM EVQSKLMRIT KDLDERDEGG STLKQKLKII SVQLKDALAM RKEIILLWRD
2721 VYSRKSFDET TLENIHNVEQ FCDKSLRDLA VHSLPKREMM QSNARICLWP IYEYVFLSLA CTLQGKMCRE ETISSVTLTE
2801 CLAKFEDVTS IPSDLMGLLR AMVGVERKVE LLLLPELFCC LAQFIQRSHA FKDTSRLLHW RGITEEDIEE SITSYVESKI
2881 ECHVGGPVLL NLVLQLMLNK TNREKEKNVL PAVALGTYKE QVNQLQLLND ILWKNSISLT NKRCDSSSND LATLKFYLHL
2961 YSSTIDKMER DIQDLISMEK QDENFTHIKS KLSDYYESVK ELRKAYKSSI DDENEEESFS KTLRRGKGWM ILGYIQLMLF
3041 GNLELIDPVH KVELKLEYLE EDIADFRKTI YVTMLQDRIL GISAANEHPR FVAMRDCEKR LLKTRDDLNC LRAFRPASAN
3121 FASLSKDCAD FRKRVGSYTL VKKHMNLYMI ADNISRDCES TDLTKTVSEA ETWGLSVQLF AEKIKTKYLP AYPDVVLPLL
3201 TALAQLSHGV FILINEIRRL ISLRKSRVTD LESFIYNLIR FPTIGWQQEN LLNLSGLCVS TDMKSLIGSC STDTFVRMQE
3281 QFRIFKLGLH ELHNHVILNR GLTKSLWRDM NELLQQIVLI WKQQQLEEEK RAAEKDSLYK NKIESHNDTL TEEEELALEV
3361 RKLFPSYREK DFNDIENESQ LSFTEKTPTQ LDKTESNFSG LITKDDIREI QQTHSNIVTS FIATKWICNS STLTSSTNYI
3441 ESLIQRYNMV YGMLDNILPS LSEGLAIKLY NSLNFLTTLG LQASQEKSAD QILRENTKDE SKGRKRAYDF YKDCKVEEVR
3521 QCLPLCENIL NRVNNLLQEW PEHSTLKSIQ NIIERIYTFS ITSPVSRFLT GLELLLVKIH QWEENAHSGV SMTDYVLKLM
3601 QQIICWRNLE LSCWKDCLDA TYENLRSDTS KWWFFLYALI ESYIMRSEKD NVQETNDEPI TKHKLVESLE HFMNQSCLVE
3681 FESRLDLLLT FHCHVYYFDD SDNKNELLAI LWNVYNYYKQ FVDDVKARID VLKAPIEKKL KDFVKIARWN DNNYWAVKET
3761 VEKTHRTLHK LVKEFQNALK QTVSTCLIVN PKDFIVTKSL QSVDVKAQFI SELNTLLKKA RKAPCRCEEI IRRNSYPSVR
3841 RKLEDFIESY MEQSVRLREK NIDRSLPKNK QKSQAKSILQ QKKMMLANYF KDLYQMGINY RTGTQTLNNN ADEVIDFTVS
3921 PLDLSTIRQY FEAKKVDEYM LAHWEGCEKY YYKSLIRLNA LNAMLDTNRT TDLGQKNIER CRGHSAHLML IAHKQKMTIV
4001 QSFDRFSSLR AQILNLSEAR EQDPNMLRQN RNVNYSIKKL AENLKTLLIT LEIGFEQLLL FLRCCPAESS SDPNGATLTL
4081 DANALPIIAA SQNDEIWKNA NRVLKENLNL VKSTAKRFHS LFMPFEVLSI DIHNSFVTFL DTKMEHFLQN NSMLFEKLRA
4161 STDIENGEQL QKENHTIKRY ELNLKNLINM ILLVIQEKFK DIKEDILYIN KEPNEMNDVN IEKEAKEKLN VKLLERDIKE
4241 LKLSDIYSLF SNLLLLIHEF DDLQSANHCI RLLLKCLPLL EQYILLVQFY LNEQVASFRI TCKILYLQLN VFLDLAANGF
4321 CVPKDLDLEE SEMNESEEKT EKGGMGLADG EGTKDVSDRI ESEDQLEDAR PADQEQEKQD DKACKEEEKG IDMSENFDNE
4401 LQDMKKNDEE QSDDDDDEEN DLDKEMGETE KGAEQLDKEI WGDDQEESEE DNQQSENESE EEGTGEQIGE KEMGARDDNG
4481 KRKQNDDDDM DHDENQEKNK KEINELDEPK IDEDHINPYH GKFQPQPEPE PLDLPEDMNL DEDGKEDNGG DDENPFDIDE
4561 MKKPPPEKQD IKLEKESEEI KENDSEENSS EDEDDNNNTG QSQSAQQESG HSGSSKQETV SAPQSNAMTK PIEKRNNPGE

4641 SNEDRSLLNR FESTLKKLKT TYTQDEVSRD ENEDDANNTD GNKAEMAQHI KDFEKFDDYT LDAATEDQNE EETKDDTMDV
4721 EMHEDKENDV TDDKVNEHKP EKVSETTDNQ CKKNSDGKRN MENNQTETTV ELEGETAETM KVERGNESTF HTMEWNIEEN
4801 DLSSDHVERK RFEMERMLGE WTQVPSTEEA TAAWNCLCSV TDAAARDLSE KLRLVLEPTQ ASRLKGDYKT GKRINMRKII
5041 FTIVDNPINK DSTEDIRMPV FEKGKLLGIR SYMDNFPFPF YMILRDINTL PGVLSDALRQ WFEVVGKIDT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.LEGSPGVG.K	Y	26.89	714.3548	1334.0	716.3150	1	48.57	4338	1	1637	1644	
total 1 peptides												

tr|A0A1B6HTR0|A0A1B6HTR0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GMAANLQNIF VAKATSM**VAL GSAAFV**VTMV PVLIGRRISS KHPPQIETRN TRMDFILSLF LSFGGGVLLC TTFLHLLPEV
81 TKNIEHLQRK GKIPEDFPLP LPELIMCCGF FIMYIVEEVA HKILHSHHAK QGGTQDRDIT LNISSAVLVD SEATLSEDYG
161 HIIKQDLITV TFTPPREEDT KNISRDTKTH RSSCVSKREE DIHSHKHCHN REHEEQSRDL HYDHDHQHHD HETGDHHTLV
241 TTSPPSLREL LIVLALTVHE GFEGLAIGLE SSVAAVWYLL AAVATHKCVL AFCIGIELVS GHISLPLSIF YAFIYSCASP
321 FGIGMGLLMS TSDNDHLTEL LSVLLQGVAT GTLLYVVFFE ILKRDNHGEA KLAQLIVVIV GFAGMAALTV LLNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.VALGSAAFV.V	Y	26.62	833.4647	348.1	417.8847	2	32.32	2506	1	18	26	
total 1 peptides												

tr|A0A212F2D3|A0A212F2D3_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAIMMFAIFI LSIFIPSVNL NQDVMKSLSY KFGTKLFECG ERTNYTRAMA RDILHIWEES YDLNHDETGC LVLCAMVRLE
81 LLDQQGNMIV ENTEGFIRAN GGDDSMVSFL IQLYSMCREK TSS**ISNGCKA** AIELSKCFRA AIQQIGWVPD TTSLLVISYD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.ISNGCKA.A	Y	26.37	691.3323	12.4	692.3481	1	47.60	4225	1	124	130	
total 1 peptides												

tr|A0A0L7KX54|A0A0L7KX54_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MERGGGHSAR PAGQTAATRL RSAVRATSIP AMDDQQTITV CLQNIASIDN KTVHYVTLEC GGVLLLYRGH KFEILSRAHD
81 GGARYTCSSR **LSNGCKA**VVH VNKHDAVVYA AAHHNHEPDN YFINLERGTK LLMYRGYTYS KNGMFRGGGD RFVCSSRLSM
161 NCKAIVHVGK HGTIVSATSY HTHDPTKYIQ GSAQFINLER GSKLLIYEGY SFARNGMFRK GGDRYTCSSR QSMKCKATVH
241 VDKDGNIVSA ASYHTHDPTK YIRVSGGRYI KYINLERGTK LLMYQGYSFA KNGIGRKGGE RYTCSSRLTM KCKAIVRVDR
321 YGTIYITLER GSKLLMYQGY SFAKNGMFRK SCERYICSSR ISMKCKAIVR VGKDGNIVSA VADHNHDPIS IWDDKKPASQ
401 LPIQIITLSN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LSNGCKA.V	Y	26.37	691.3323	12.4	692.3481	1	47.60	4225	1	91	97	
total 1 peptides												

tr|A0NE24|A0NE24_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 DPLKDPQICG RPVCSKTSKF RYNVGHLYKY DHSMYVKTAL VGSGDNTSEL HISSVVEIDF YAPCQGILRL YSIEVRERAA
  81 QAAEEEFFEY GEEPEHTETS DVDETGGVHP KSDVIAEELM RFELRFAFHD GAIGEICHED SESVWTLNLK RGILSALQNT
 161 MPRFDIDYDT TETDVSGICD VQYKTNGRNG TSLLFRKTKD LVSCKRRYKT TSFIQTVPYD FRTNYVAWPI LNSNSYCDFS
 241 IDNSIYKSVA CYERHQLVPF SNGLAGAVTE TYNRLELADE ETYVHEGNNE IDIQRRSSLL YDHTPSVHES HDEIKASREL
 321 LMELCVHGFP NIRRDFPDVF LKFLTAARAL SSNALYQLLT RSRAICDNGH KHILESLPYI GSAASVTLMK DQIVENNLMK
 401 HGKESGDQTY LLSGSTVVNT FCKIHSNCGE SEAVQAIVQY LEEELLDTIQ SAESKLQHDR RKRERVIVLL MSLGNMGVVN
 481 KRLNFELRTI IESERYPTEV RVEAVNVFRR SDCTRTKDYF LKLYSTFLLD VEVRIAAYLQ AMRCPDHLSV RLIKNVLKTE
 561 EVKQVGSFVW SHLTNLAKSA SPVRVQAQGL LAENDLDSKF NLDIRKFSRN YEQTLFFDEY NFGMTVDSNV IFSTESYVPR
 641 SLRLNLTTDL FGESINFLEL NVRLEGLEQS VHHLFGPNGT YSAKKVGERV DTYMKFLRQY VPTKVLELFD GESSWRDELQ
 721 DAEENGRGKR AAVQRLPVLI ARQIQEDVDR LGFHLKGNFD KPQVTIGVKI FGNDLNYYTD GLEIFSKVNQ RKKLASLFDG
 801 KESSYTKSSV FLDTSYDVPL SSGMPLALGL VGASSVDLRL TGKIRAFDYT RWLIDIEGKL KPSITMDITA SMRSDLMHAS
 881 TAIKEKTNLY SNSAWAAHLK LRGTDQAVLQ VSLPQERNDI FSIRSEMFVL TERRELQQAG IERRYSNSTC TWPFIDQAIG
 961 LKMCTNYSLP DVSNTGKDVE VPSLILSGPV NFDVSLEKTD PTAKMFVLKY SWAERQNQTI VGVVFETPNS QIPRIFRANI
1041 TNEVQRKTAS MSFVNGNISH KAIGMYINNP NQQRVEMSLN VNDRKYLALE MGYNKTDTRN GRMYYPSFYL SVNNERIAGL
1121 GGQVNQTAKN NISQWDYMIM FETKRVRTKT IGYVSVSHNM TYMIHNSMEY RFIGSTTERL VINALAEMAL KEVLMYRANF
1201 DLRSSAYPHF DVALNGTLLD GMGHLDFTLL HNNAPDLRDE KYRTTLKMIF ARDNPYRSQL ILTPNSQQLI GGSAEQTDPT
1281 ERTTFHENML QKGVDHTVRL LVRYAPKREV IGVGSFSMPR SQRFWLESRF NLTVPGFHPC TATLRLTENS TKDHQFDFKG
1361 VWFTEHAANV SGWYKDRSSN VKYYHYAKLA AQIGLTNSTR ELFGVMKYIQ DEHDNRLSMN AMFEKKPYGI ILQHTQQIAN
1441 GTKSYAMVQW KDERYWFSAL MKSAPIKQLD LELHIDKIRD ISATLRGYKT PLKREVGVEF KWDANRDPTQ RIALTGELNT
1521 PTDRIYDGLF LLSYPNRTFS GTFDLKATHP RYLANARISW NTTEAIVIHF DAGTHEEMLS KMWLLLHLNT TFHGWRRNAL
1601 SGAFSFKDNV LYTDLIANWA EDQRLGVELN GTYRSNKEIF NCELGTQLKS SLRNIPAVTM YFNQTLVTDR VETTVLLNYE
1681 TTDQPVQEFS VRSNWQHKAD KRHSNITGSL RLISPYENYR MGALVAKVSV SDNRTITGAA DLQLDDNTYD LLLEGHIRNL
1761 VDCMLTANIT SSNINYRSIN GRFGISEKNR HLVAEIITPK TELGIELLYA VVSPQNFDVK FHLATPLKEL EKVILRAKLQ
1841 KDNVDFRAGM NNMVLGCTGV WRKAHLKDFE YSYRIYTPLQ KFEESALIVK VVINSERAQY VDVELSGKFS EYKLGVKAMS
1921 KPKPDIKRVM LPQTASSLVE ENLWNNEVDD EQEDEDYDEE EDEENLLNFI GEIELYTIVM PTIEGTLELT EQNSQYRAIG
2001 KLKVSQGDID FRDRFYLRDL LNMHNSLQLK TPFPVAQQIT SEFVMKFSHE TTDITVGMNV KFNNRSEWVN TGFHVNYKKS
2081 VDEAEVHKHQ ALVDLMTPMK NLQKVFLNGT LELEDHSYKG NLTAKTMTTD ASLALSFEAE DQFIDTFMSV WVRAPLMPYY
2161 ACRVFYKQDF SRTENTMDLG FTVNDGDLYS NFRMDGAWSF AKPHYIKGAG KYQSNFLPIN LINTDFLITR SPLPRAHCNV
2241 KFHDKNGVVE EIKARAERNR ELFMVDLSVP MEDYRNFSIH GRLQHRQGSE YAVSGQLYRN EHIFQVEGSA TIAEDIPYRA
2321 ELAFQPLTPE GSIGSIRYDC RNSSTSTEFN LEVESGNKVA KLDGSFKLLA MSDWFLKLGL ESSEPGLKSV DFYMGINPEA
2401 NGKALGKFNL HSPWVQYGID QADVEMMFDV QPISGSVVAR YGIRDVSGNA SCLWNWALKS NTQFALENRV LRNSVERYFR
2481 TGVRYVSPDL ENNHNLTFGG DLNLNNIWIF SANSSVDFIS IRDMSAVLKV LLPKPVGDVH TLALAMNGNL PFLEPVKSFN
2561 METSYETDES RKRYAYHSEY SGIGDIRALV RFDWGPDVRK ERIQSILNVF RIGDRQELMM TLRGPWYLED AFVTHGTYDT
2641 IENLYLVSGN ISMPASTKVM SANVIFNDLS NMKADVNCTT PFLNVSWIHG QLEFIESPIE SIRYVKGSWP ESSAIFDAKA
2721 TYRNNNQDRE QQGTVKMEVP LQTRHFAEIK YGLSERPAIT TGYAEVEYNS KNVLSGQYTS KEESRPGFDK ETIEVMLKNE
2801 YKPIGVHYVH SVNKQDPTVE SLDFKRAEIF ELDNKEDNKF NVTGELHVLS KEKGREYIVR AIQTNRTVEL TANIEEDNIV
2881 SKKQSRLELA PTVWIAYDFE RTNRSRDDVE AQNFTLKISY PNRNISADGW YSYTSSAFDS DITLSYSPNR TNAEDESEMP
2961 KQRTVRGGVV WRDLANSSTD GQQIRVFLGH PSFQRDVTVD ARYFTDPKHW FTSKAELRYN DDNEHLLAMG LDLNDMQPIV
3041 GFWNYSYHLF STHEASDLDL DSIGSIGLRP GLWGVSSNSH YKRAYLSQMH GHVLGWMNLH QKEMHYERIT SQSKYRIWTK
3121 ATGAYPVYLI NGTLLDGPEL DATGFFYLNI DDKMVQMKIN MTPDGSENVY MYGIIPDTRS AYFDLWRDYD KAREVDVTYY
3201 LKMNHSRLIT GHLLWRPEIK SDVQKLVRDY VNQMHQALLE YTEFWIKHVY LETKDSTMGI YEAAVPYIEG FLNDAAGLSV
3281 LQHDFEELQH FLNASYAADD FYIRSITNIT MTVLDELALK NKITSLPKIL TELWQVMGES GQALGKSIAW LLERVKQSYQ
3361 KFIDIVGSIF HGDAMRYLSL TLEDSLERYD KVVKEVHLQF IKHIQELWDK AIMMTTTFWH KMLQNIEPTI IRLAHYGESL
3441 GWFVGNEIFT FLYNKTQEIA DSPYFNTVTN FTQDLDLLYK DLITNDVFTN LKKYSSVWWE FMRKKYFQVV PFARELYQVG
3521 NELLEEIKQL RKIEFVHFLI QRYEEVKAKA EWLAEEFQVV SRLSQMWKVV SKKFMHLAQT ALQAEDNYRE AKTKFIFDPE
3601 RGVMELEQKL PMSWHAFNET PKFEEIPEFK YISKIQDLFA GSNTTIWTVY NDICPYVDLE VWLPPFKSTA LLIGSRHYMS
3681 FDKRFISLDL SDSNRCQYLL AHDYYNRTIT LLLESSDLRY GQTSRQITLI IDGNTLAIDV FNI
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.AIGEICHE.D	Y	24.14	870.3905	270.9	436.3204	2	31.53	2418	1	132	139	
total 1 peptides												

tr|A0A1J1IXA2|A0A1J1IXA2_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVESKFIAS IVTLLFS**TFL LGNGLILD**CQ YTNVTAVTHN HIAGRNNSDV LGLLVENSGL MFLPQNIDNF FPNLESLNFR

81 SASIQSLKSS DLNVFPNLIQ IDFFSNLITQ LDFHIFEENL KLRAIRFQSN PLNHIGHGVF DHLNELTSIH TQGTCHPLTI

161 TNNRNQVVSG IFNFFRQCPP TLEMMEREIL TGRNFGRIVD EQIADQMNPL TLQVFQLRQE LIQLEHRIAV LERN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TFLLGNGLILD.C	Y	22.83	1174.6598	948.7	588.8943	2	35.48	2860	1	18	28	
total 1 peptides												

tr|A0A067QWN1|A0A067QWN1_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLAAVLTLLL SALVSCGTAS IEPPLLEAL**A APSADH**ETTS YLLPRLSAKF RPHGDWDSAP DPRFYVLTEL QRESSQAARR

81 MKRTGAVPSL SIVNPLDVLR QRLLLEIARR RMRQSQDQIQ ANREMLQTIG KRDADQSQQR SSDDDDEDDE MDSEFMVSST

161 DEKSGSNRPR DTPDWSPSSG PRWDDEFASQ HH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AAPSADH.E	Y	20.97	667.2925	737.0	668.7916	1	4.79	348	1	30	36	
total 1 peptides												

tr|A0A182XX22|A0A182XX22_ANOST

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGPVEEPTTK QAPPARSTTP PASSRSADSQ QATNAKKRSV LDRLGTKASS TSSAEREKTV HIESRSTARD PAGTKDVSKG

81 SDTAANASGA GTKSTIISLS AHRREEREIY VPLFRRKEAT VSQEQSAGGA AAAAAAAAK NRARQDITMR GDNRHRERSR

161 ERSNRETRSP ISRLPPQHSA RTDPHSIRGR SRENNFRRPE RDRAVDRVER IDDHQSMGGR KSRPRERSRS REWVRDGHR**E**

241 **RSGSGGAH**PK NGTDTVRGRI GSRVIVLPPK PEYNEDVIEV PVASVIKVQP RPVVPKAKQP SKNLLLKAMA EAQRSTVANL

321 KKTINNTIDS SNHSSMHRGE LKRKLVIEIP GAASSHSVPV DVQYERLQPD TQYALHEGIS YHGLREDHHH ARVHDDQEDE

401 EEEDVAEEE EVHEVDITHQ VLMEDCDVDE EFKEILQSEW NPAPKRDYQT DHMEMAEDDA AAAAGTEQE PAATTESKDT

481 KFVVTLDGAF KASVADREVS PSHTPPPPLP PPPSTSAISS EHPKGRMSVK DRIGFKARTE PTARSPTRKD SKEMEETLKK

561 RKERFSEKLV VAPPATTKPS AKKASSPPAP SNVAPSTRSS NRASPKTTNS RSSTQSHSGS SASRRRTTPS LSPERPPRPR

641 NSSPNRSKRV EGSRNVSASP NQLNELLLQR TKELMDDSVS SSPIYMSKSD YDKMEPASRK RKRVSPIQFD LTDEDERHDS

721 DDDYHHHHHH HHHHHHHRNE RRARSREEHR ARRSPSRDSD ERSVTRKESR REWEREGEGR DDRESERAKS PGRKFKKLES

801 SRKFDDIPPL LSAVALTGAE GKTSKLTSGG GAGSGAIKER CKYFPNCRQR DACEFLHPTT PCKAFPNCKF GDKCLYLHPM

881 CKYDQTCHRL DCNFMHSKSA SAVVASSGLT APPLASSVVP VQNYKTISAK PLPPVCRFYP NCVNSQCQYL HPKMCHFGKH

961 CVNRAECNFY HYDIAAKDLH DASSKDKFRW ISPFSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.ERSGSGGAH.P	Y	20.96	856.3787	-88.1	429.1589	2	25.79	1873	1	240	248	
total 1 peptides												

tr|A0A1A9U6X3|A0A1A9U6X3_ANOST

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HVDLSTFRLF TCAFRTATHI APFDRFTQPN SMDTLGTEIG QKMRSAVKAK LIELGTGSAT GYIDDELPDY VMIMVANKRS

81 RQQMVDDLSL FLGAQTEIFV NWLHQVLQKL QEVTLPASAA AAASASTKSK EPTKRKSSEV EDKKKDKKRK DKKTKRRDRS

161 TDGEEAADAS GRMSGTEDNT PPRPAVVLPA TSITEVFAHQ YIEKAKKSLE TDGLPVAKKS SGERSESQDR SKQTKSKTPP

241 AATSKEPSNS GLPSIADLAS ASVVQKHHKE LCELKEIEER ISAAKRHLRS LGTDISDEDS EDLLLLKANE DDLFPPRARS

321 KEVTAARSAA SKPPESTVSK QRQRITMGPV EEPTTKQAPP ARSTTPPASS RSADSQQATN AKKRSVLDRL GTKASSTSSA

401 EREKTVHIES RSTARDPAGT KDVSKGSDTA ANASGAGTKS TIISLSAHRR EEREIYVPLF RRKEATVSQE QSAGGAAAAA

481 AAAAAKNRAR QDITIRGDNR HRERSRERSN RETRSPISRL PPQHSARTDP HSIRGRSREN NFRRPERDRA VDRVERIDDH

561 QPMGGRKSRP RERSRSREWV RDGHR**ERSGS GGAH**PKNGTD TVRGRIGSRV IVLPPKPEYN EDVIEVPVAS VIKVQPRPVV

641 PKAKQPSKNL LLKAMAEAQR STVANLKKTI NNTIDSSNHS SMHRGELKRK LVIEIPGAAS SHSVDVQYER MQPNAQYALH

721 EGISYHGLRE DHHHARVHDD QEDEEEEEDV AEEEEVHEVD ITHQVLMEDC DVDEEFKEIL QSEYNPAPKR DYQTDHMEMA

801 EDDAAAAAAG PEQEPAATTE SKDTKFVVTL DGAFKASVAD REVSPSHTPP PPLPPPPSTS AISSEHPKGR MSVKDRIGFK

881 ARTEPTARSP TRKDSKEMEE TLKKRKERFS EKLVVAPPAT TKPSAKKASS PPAPSNVAPS TRSSNRASPK TTNSRSSTQS

961 HSGSSASRRR TTPSLSPERP PRPRNSSPNR SKRVEGSRNV SASPNQLNEL LLQRTKELMD DSVSSSPIYM SKSDYDKMEP

1041 ASRKRKRVSP IQFDLTDEDE RHDSDDDYHH HHHHHHHHHH HRNERRARSR EEHRARRSPS RDSDERSVTR KESRREWERE

1121 GEGRDDRESE RAKSPGRKFK KLESSRKFDD IPPLLSAVAL TGAEGKTSKL TSGGGAGSGA IKERCKYFPN CRQRDACEFL

1201 HPTTPCKAFP NCKFGDKCLY LHPMCKYDQT CHRLDCNFMH SKSASAVVAS SGLTAPPLAS SVVPVQNYKT ISAKPLPPVC

1281 RFYPNCVNSQ CQYLHPKMCH FGKHCVNRAE CNFYHYDTAA KDLHDASSKD KFRWISPFSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.ERSGSGGAH.P	Y	20.96	856.3787	-88.1	429.1589	2	25.79	1873	1	586	594	
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)