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.

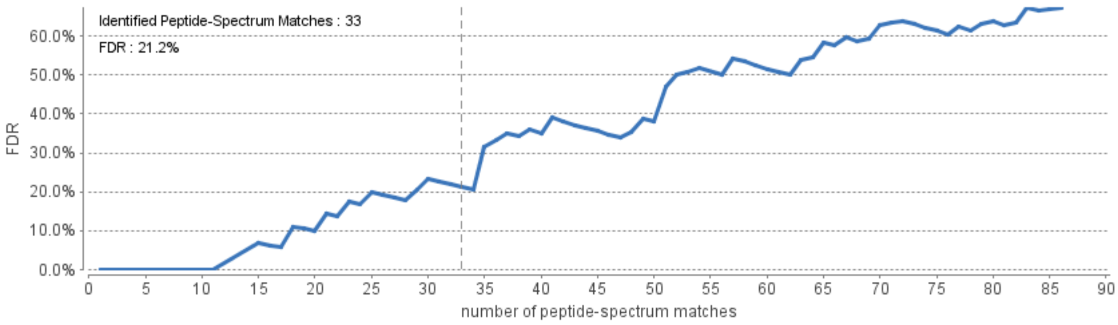
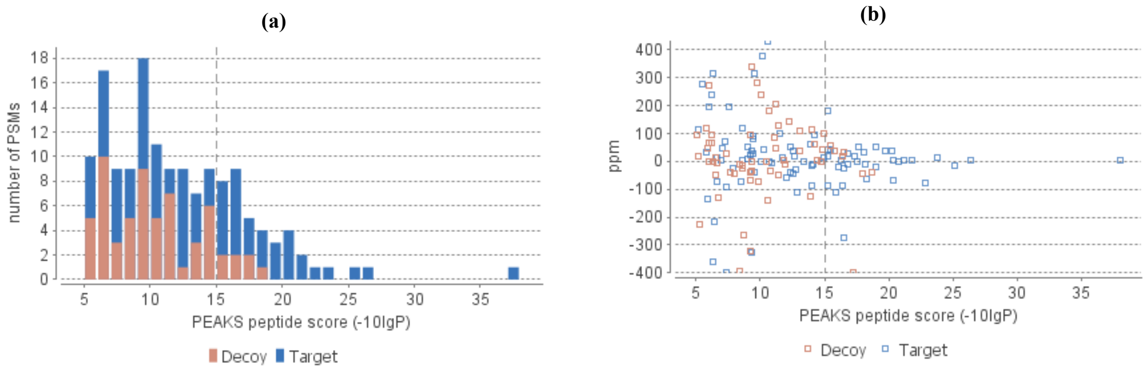
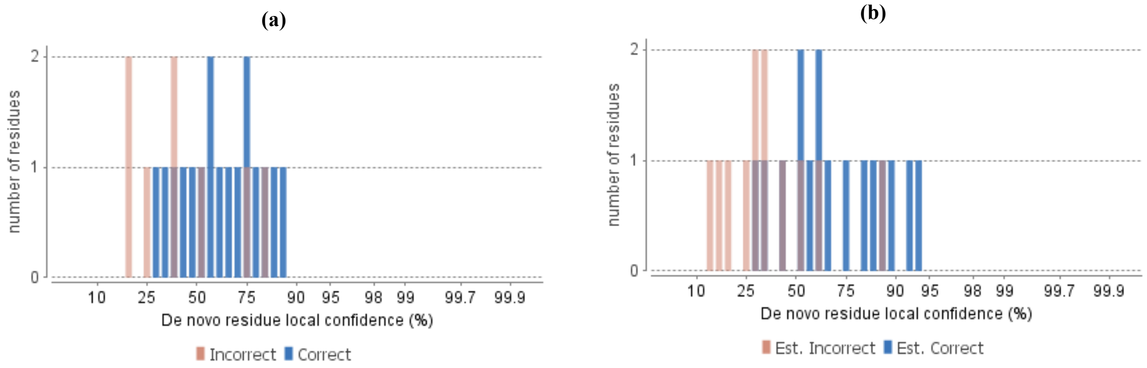


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(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	0
# of MS/MS Scans	322

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	33
Peptide Sequences	33

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	3	C

Protein Groups	10
Proteins	74
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 74 (=1);
FDR (Peptide-Spectrum Matches)	21.2%
FDR (Peptide Sequences)	21.2%
FDR (Protein)	27.0%
De Novo Only Spectra	3

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.

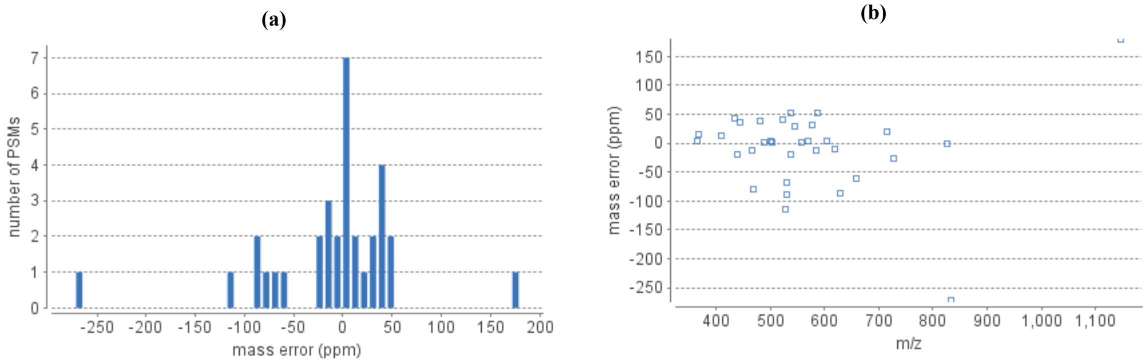


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
IT-TOF	26	5	2	0	0

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fixed Modifications:
Carbamidomethylation: 57.02
Variable Modifications:
Oxidation (M): 15.99
Fragment ion tolerance: 0.1
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 45
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: D_3.mgf
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: 3D Ion Trap
MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	2221	tr|A0A1W6EVV2|A0A1W6EVV2_9HYME	38.01	3	1	1	N	44539	Hyaluronidase OS=Ampulex compressa PE=2 SV=1
7	2248	tr|A0A182SXW9|A0A182SXW9_9DIPT	26.37	4	1	1	N	18534	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
7	2255	tr|A0A0N8DDY6|A0A0N8DDY6_9CRUS	26.37	3	1	1	N	21674	Apolipoprotein d OS=Daphnia magna PE=4 SV=1
7	2259	tr|A0A182N890|A0A182N890_9DIPT	26.37	3	1	1	N	22968	Uncharacterized protein OS=Anopheles dirus PE=4 SV=1
7	2266	tr|A0A182YFN2|A0A182YFN2_ANOST	26.37	3	1	1	N	26461	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
7	2267	tr|A0A1A9U4E8|A0A1A9U4E8_ANOST	26.37	3	1	1	N	26953	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
7	2269	tr|A0A1D2NEM6|A0A1D2NEM6_ORCCI	26.37	2	1	1	N	30507	Uncharacterized protein OS=Orchesella cincta GN=Ocin01_02999 PE=4 SV=1
7	2270	tr|A0A1D2MIF2|A0A1D2MIF2_ORCCI	26.37	2	1	1	N	31559	Uncharacterized protein OS=Orchesella cincta GN=Ocin01_13905 PE=4 SV=1
7	2274	tr|A0A151X2F2|A0A151X2F2_9HYME	26.37	2	1	1	N	34481	Uncharacterized protein OS=Trachymyrmex zeteki GN=ALC60_06533 PE=4 SV=1
7	2291	tr|A0A1A9WR47|A0A1A9WR47_9MUSC	26.37	1	1	1	N	65223	Uncharacterized protein OS=Glossina brevipalpis PE=4 SV=1
7	2300	tr|A0A1L8DSR7|A0A1L8DSR7_9DIPT	26.37	1	1	1	N	74696	Putative e3 ubiquitin ligase OS=Nyssomyia neivai PE=4 SV=1
7	2301	tr|A0A1L8DSL4|A0A1L8DSL4_9DIPT	26.37	1	1	1	N	74682	Putative e3 ubiquitin ligase OS=Nyssomyia neivai PE=4 SV=1
7	2325	tr|A0A0J7KID5|A0A0J7KID5_LASNI	26.37	0	1	1	N	146071	Zinc finger protein 687 OS=Lasius niger GN=RF55_10078 PE=4 SV=1
total 74 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
7	2343	tr|A0A1Y1N3M1|A0A1Y1N3M1_PHOPY	26.37	0	1	1	N	178802	Uncharacterized protein (Fragment) OS=Photinus pyralis PE=4 SV=1
4	2223	tr|A0A182N577|A0A182N577_9DIPT	25.11	1	1	1	N	174669	Uncharacterized protein OS=Anopheles dirus PE=4 SV=2
9	2250	tr|A0A1A9Y4N1|A0A1A9Y4N1_GLOFF	23.84	4	1	1	N	16154	Uncharacterized protein OS=Glossina fuscipes fuscipes PE=4 SV=1
9	2256	tr|V5GJC8|V5GJC8_ANOGL	23.84	4	1	1	N	18131	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase (Fragment) OS=Anoplophora glabripennis GN=NDST PE=4 SV=1
9	2284	tr|A0A212FE53|A0A212FE53_DANPL	23.84	2	1	1	N	38803	Uncharacterized protein OS=Danaus plexippus plexippus GN=KGM_208095 PE=4 SV=1
9	2290	tr|A0A087UES5|A0A087UES5_9ARAC	23.84	1	1	1	N	50662	Vacuolar protein sorting-associated protein 54 (Fragment) OS=Stegodyphus mimosarum GN=X975_19258 PE=4 SV=1
9	2292	tr|A0A0C9RF26|A0A0C9RF26_9HYME	23.84	1	1	1	N	65441	ZFP112_1 protein OS=Fopius arisanus GN=ZFP112_1 PE=4 SV=1
9	2293	tr|A0A067QZW3|A0A067QZW3_ZOONE	23.84	1	1	1	N	65808	Uncharacterized protein OS=Zootermopsis nevadensis GN=L798_10090 PE=4 SV=1
9	2299	tr|A0A0K8VIY6|A0A0K8VIY6_BACLA	23.84	1	1	1	N	69464	Rho-related GTP-binding protein RhoU OS=Bactrocera latifrons GN=RHOU_1 PE=3 SV=1
9	2302	tr|A0A0K8UPX9|A0A0K8UPX9_BACLA	23.84	1	1	1	N	69976	Rho-related GTP-binding protein RhoU OS=Bactrocera latifrons GN=RHOU_0 PE=3 SV=1
9	2303	tr|W8BC92|W8BC92_CERCA	23.84	1	1	1	N	71192	Rho-related GTP-binding protein RhoU OS=Ceratitis capitata GN=RHOU PE=2 SV=1
9	2310	tr|N6ULE5|N6ULE5_DENPD	23.84	1	1	1	N	94598	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=D910_04077 PE=4 SV=1
9	2317	tr|A0A0T6AVT5|A0A0T6AVT5_9SCAR	23.84	1	1	1	N	117347	Zinc finger protein OS=Oryctes borbonicus GN=AMK59_6750 PE=4 SV=1
9	2332	tr|A0A1Y1M7P2|A0A1Y1M7P2_PHOPY	23.84	0	1	1	N	160823	Uncharacterized protein (Fragment) OS=Photinus pyralis PE=4 SV=1
8	2249	tr|A0A0M8ZQP9|A0A0M8ZQP9_9HYME	22.87	1	1	1	Y	61059	Uncharacterized protein OS=Melipona quadrifasciata GN=WN51_06333 PE=4 SV=1
1	2535	tr|Q7QJM3|Q7QJM3_ANOGA	21.15	0	1	1	N	142404	AGAP007578-PA OS=Anopheles gambiae GN=1269651 PE=4 SV=3
10	2321	tr|A0A2A3EPU8|A0A2A3EPU8_APICC	20.74	2	1	1	N	28565	Viral IAP-associated factor OS=Apis cerana cerana GN=APICC_01694 PE=4 SV=1
10	2342	tr|A0A2A3EAV6|A0A2A3EAV6_APICC	20.74	2	1	1	N	37045	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase OS=Apis cerana cerana GN=APICC_03559 PE=4 SV=1
10	2409	tr|A0A2A3EKU2|A0A2A3EKU2_APICC	20.74	1	1	1	N	58571	Glucosylceramidase OS=Apis cerana cerana GN=APICC_06000 PE=4 SV=1
10	2410	tr|A0A0J7KFW6|A0A0J7KFW6_LASNI	20.74	1	1	1	N	60746	Maltase 1-like protein OS=Lasius niger GN=RF55_11254 PE=4 SV=1
10	2432	tr|A0A023EZA0|A0A023EZA0_TRIIF	20.74	1	1	1	N	73996	Putative solute carrier family 22 member 15-like protein (Fragment) OS=Triatoma infestans PE=2 SV=1
10	2472	tr|E9GCX6|E9GCX6_DAPPU	20.74	1	1	1	N	104908	Uncharacterized protein OS=Daphnia pulex GN=DAPPUDRAFT_101288 PE=4 SV=1
10	2484	tr|A0A2A3E979|A0A2A3E979_APICC	20.74	0	1	1	N	116999	ATP-dependent RNA helicase OS=Apis cerana cerana GN=APICC_00734 PE=4 SV=1
10	2486	tr|A0A182SQ67|A0A182SQ67_9DIPT	20.74	0	1	1	N	119293	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
10	2499	tr|A0A084VFC9|A0A084VFC9_ANOSI	20.74	0	1	1	N	129190	AGAP007628-PA-like protein OS=Anopheles sinensis GN=ZHAS_00003734 PE=4 SV=1
10	2508	tr|A0A023EWX6|A0A023EWX6_TRIIF	20.74	0	1	1	N	144274	Putative titin isoform x6 (Fragment) OS=Triatoma infestans PE=2 SV=1
10	2522	tr|A0A2A3EGN6|A0A2A3EGN6_APICC	20.74	0	1	1	N	159596	UHRF1-binding OS=Apis cerana cerana GN=APICC_02690 PE=4 SV=1
10	2525	tr|T1KS98|T1KS98_TETUR	20.74	0	1	1	N	163863	Uncharacterized protein OS=Tetranychus urticae PE=4 SV=1
10	2528	tr|A0A0A7AS86|A0A0A7AS86_TIGJA	20.74	0	1	1	N	169783	ATP-binding cassette transporter sub-family C member 1 isoform X2 OS=Tigriopus japonicus PE=2 SV=1
10	2597	tr|E0VC08|E0VC08_PEDHC	20.74	0	1	1	N	296517	Ubiquitin specific protease 9/faf, putative OS=Pediculus humanus subsp. corporis GN=8231313 PE=3 SV=1
10	2589	tr|A0A2A3E5A8|A0A2A3E5A8_APICC	20.74	0	1	1	N	249631	Proteasome-associated protein ECM29 OS=Apis cerana cerana GN=APICC_01357 PE=4 SV=1
10	2587	tr|T1K7Q5|T1K7Q5_TETUR	20.74	0	1	1	N	238023	Uncharacterized protein OS=Tetranychus urticae PE=3 SV=1
10	2584	tr|E9FZS9|E9FZS9_DAPPU	20.74	0	1	1	N	223312	Myosin heavy chain isoform 1 OS=Daphnia pulex GN=DAPPUDRAFT_347733 PE=3 SV=1
5	2224	tr|E0VZX2|E0VZX2_PEDHC	20.36	1	1	1	N	105199	Uncharacterized protein OS=Pediculus humanus subsp. corporis GN=8235626 PE=4 SV=1
11	2322	tr|A0A2A3E8Z7|A0A2A3E8Z7_APICC	20.34	2	1	1	N	28120	Proteasome subunit alpha type-7-1 OS=Apis cerana cerana GN=APICC_03835 PE=4 SV=1
11	2323	tr|E9GMZ8|E9GMZ8_DAPPU	20.34	2	1	1	N	28310	Proteasome subunit alpha type OS=Daphnia pulex GN=DAPPUDRAFT_231056 PE=3 SV=1
11	2419	tr|A0A212EXZ1|A0A212EXZ1_DANPL	20.34	1	1	1	N	60902	Synaptic vesicle glycoprotein 2B OS=Danaus plexippus plexippus GN=KGM_204443 PE=4 SV=1
11	2430	tr|A0A2A3EM41|A0A2A3EM41_APICC	20.34	1	1	1	N	69624	Glucose dehydrogenase [acceptor] OS=Apis cerana cerana GN=APICC_01842 PE=4 SV=1
6	2228	tr|F0J9M9|F0J9M9_AMBVA	20.22	4	1	1	N	20114	Uncharacterized protein (Fragment) OS=Amblyomma variegatum PE=2 SV=1
6	2230	tr|A0A1B0EV99|A0A1B0EV99_LUTLO	20.22	3	1	1	N	24306	Uncharacterized protein OS=Lutzomyia longipalpis PE=4 SV=1
6	2232	tr|A0A0L7RI67|A0A0L7RI67_9HYME	20.22	3	1	1	N	24979	Uncharacterized protein OS=Habropoda laboriosa GN=WH47_06722 PE=4 SV=1
6	2234	tr|A0A0T6AV86|A0A0T6AV86_9SCAR	20.22	3	1	1	N	28593	Uncharacterized protein (Fragment) OS=Oryctes borbonicus GN=AMK59_6699 PE=4 SV=1
6	2235	tr|A0A023FFQ7|A0A023FFQ7_9ACAR	20.22	3	1	1	N	28680	Putative growth arrest and dna-damage-inducible protein-interacting protein 1 (Fragment) OS=Amblyomma cajennense PE=2 SV=1
6	2236	tr|A0A023FRY2|A0A023FRY2_9ACAR	20.22	3	1	1	N	29876	Putative growth arrest and dna-damage-inducible protein-interacting protein 1 OS=Amblyomma cajennense PE=2 SV=1
6	2237	tr|A0A023FSZ9|A0A023FSZ9_9ACAR	20.22	3	1	1	N	30593	Putative growth arrest and dna-damage-inducible protein-interacting protein 1 (Fragment) OS=Amblyomma parvum PE=2 SV=1
6	2238	tr|N6TQ66|N6TQ66_DENPD	20.22	3	1	1	N	30426	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=109533987 PE=4 SV=1
total 74 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
6	2239	tr|J3JZE4|J3JZE4_DENPD	20.22	2	1	1	N	32293	Uncharacterized protein OS=Dendroctonus ponderosae PE=2 SV=1
6	2242	tr|A0A0J7KQT0|A0A0J7KQT0_LASNI	20.22	2	1	1	N	36343	Dehydrogenase reductase sdr family protein 7-like protein OS =Lasius niger GN=RF55_7395 PE=3 SV=1
6	2251	tr|N6UK05|N6UK05_DENPD	20.22	2	1	1	N	43871	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_04530 PE=4 SV=1
6	2257	tr|A0A1B6LM09|A0A1B6LM09_9HEMI	20.22	1	1	1	N	57345	Uncharacterized protein OS=Graphocephala atropunctata GN=g.18369 PE=3 SV=1
6	2260	tr|A0A1B0DP54|A0A1B0DP54_PHLPP	20.22	1	1	1	N	66079	Uncharacterized protein OS=Phlebotomus papatasi PE=4 SV=1
6	2262	tr|A0A1L8DV31|A0A1L8DV31_9DIPT	20.22	1	1	1	N	66940	Putative pleckstrin similarity domain protein OS=Nyssomyia neivai PE=4 SV=1
6	2263	tr|A0A1L8DV35|A0A1L8DV35_9DIPT	20.22	1	1	1	N	66906	Putative pleckstrin similarity domain protein OS=Nyssomyia neivai PE=4 SV=1
6	2271	tr|N6UIT9|N6UIT9_DENPD	20.22	1	1	1	N	114888	Eukaryotic translation initiation factor 3 subunit A (Fragment) OS=Dendroctonus ponderosae GN=YQE_01948 PE=3 SV=1
6	2273	tr|V5GT97|V5GT97_ANOGL	20.22	1	1	1	N	114359	Eukaryotic translation initiation factor 3 subunit A OS=Anoplophora glabripennis GN=EIF3A PE=3 SV=1
6	2275	tr|A0A1B0CIX4|A0A1B0CIX4_LUTLO	20.22	1	1	1	N	122202	Uncharacterized protein OS=Lutzomyia longipalpis PE=4 SV=1
6	2276	tr|U4U4N7|U4U4N7_DENPD	20.22	1	1	1	N	130159	Eukaryotic translation initiation factor 3 subunit A (Fragment) OS=Dendroctonus ponderosae GN=D910_02348 PE=3 SV=1
6	2278	tr|A0A1W4W4T7|A0A1W4W4T7_AGRPL	20.22	1	1	1	N	141423	Eukaryotic translation initiation factor 3 subunit A OS=Agrilus planipennis GN=LOC108732709 PE=3 SV=1
6	2281	tr|A0A0T6BCR8|A0A0T6BCR8_9SCAR	20.22	1	1	1	N	146282	Eukaryotic translation initiation factor 3 subunit A OS=Oryctes borbonicus GN=AMK59_2130 PE=3 SV=1
6	2285	tr|A0A1B0GE32|A0A1B0GE32_GLOMM	20.22	1	1	1	N	152953	Uncharacterized protein OS=Glossina morsitans morsitans PE=4 SV=1
6	2295	tr|A0A1D2NI72|A0A1D2NI72_ORCCI	20.22	0	1	1	N	283067	Uncharacterized protein OS=Orchesella cincta GN=Ocin01_01792 PE=4 SV=1
total 74 proteins									

tr|A0A1W6EVV2|A0A1W6EVV2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMLRVQSLLV FAFAAMASAK FLGFDPATLG DGKSREFNAY WNIPTFMCHK YGLNFTEVSS EFGIRQNTGD TFRGNEIAIL
81 YDPGMFPALL KDENGKFIKR NGGVPQRGNL EEHLKLFEKH LIEQVPDEKF DGVGVIDFES WRPIYR**QNWA SLTPYK**DLSV
161 SLVRKEHPSW SNRQVEQEAK EEFEKSGKLF MEKTLKLAQK LRPLAAWGYY AYPYCYNLTP KQPTTQCNRE TIKENDKMTP
241 WLFMNEDMLF PSVYMGKKLS QQQRVGLVEG RVREARRIST HMKGTHKILP YFWYRLNDEK DYYLNGNELE AILREMSTLG
321 ANGVILWGSS DDFKTREKCE NFWGYLMQIF GPAVKSVVER ARNGYDNQIL YNEEMGNDVN ALR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.QNWASLTPYK.D	Y	38.01	1206.6033	3.4	604.3110	2	0.43	774	1	147	156	
total 1 peptides												

tr|A0A182SXW9|A0A182SXW9_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLAIALFVC LAATPTVTSD ATFQQYVELM FQFDSVFETL CLVQTNDSVQ ARRMVEANQD LQTCVNLHHD PQNFTNALDS
81 **LTVENR**KDFI SYNCDQFEEI KKCYHPFTRQ LEICFTERDV SMIKTLIMLE EEFAYICEQD GANVQTVARS NYSYCAAFSK
161 V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.LTVENR.K	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	81	86	
total 1 peptides												

tr|A0A0N8DDY6|A0A0N8DDY6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVNYFPIWLL IAATCYQTFI QAQLFERGNC PDVNAVPDFK LSEYTGKWYE NRKTISRFQN SMAQSCASVV FKETDGK**LTV**
81 **ENR**GLQRLTR RNIVLNGKAR HPDPSKGEFV VNFFGNASYG DETLMILGTD YDSYSVSWSC IGAGPMHLYT LWVHTRDPNP
161 TPETIDLALD VVKRNALDET KLLMTNRRNC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTVENR.G	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	78	83	
total 1 peptides												

tr|A0A182N890|A0A182N890_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFQFDAVFET LCLEKTNDSS EAQRMVEANQ DLQRCVNLHH DPQNFTNTLD A**LTVENR**KAA DLRFVCSNCD QFEEIKKCYL
81 PFTRQLETCF NVRDVAMAKT LIMLEEEFAF ICENDGSNVI AVEQSNYSYC AGNLKELLQN CSLLDWAELR SKTINTMTDR
161 DCSIFRQLAT CFKNNITTCG APLFAQLFNI RFQAIVKQTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LTVENR.K	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	52	57	
total 1 peptides												

tr|A0A182YFN2|A0A182YFN2_ANOST back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLAIALFVA TTPTVTSDAT FQQYVELMFQ FDSVFETLCL EHTNDSVQAR RMVEANQELQ TCVNLHHDPQ NFTNALDT**LT**
81 **VENR**KDFISY NCDQFEEIKK CYLPFTRQLE ICFTGRDVSM VKTLIMLEEE FAYICEQDGA NVLSVPRSNY SYCAGNLQEL
161 LQNCSMQDWA ELRSKTIDTM TERDCSIFQR LATCFQNNIT KCGAPLFAQL FNIRYRAIVK QTYCNKDTP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.LTVENR.K	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	79	84	
total 1 peptides												

tr|A0A1A9U4E8|A0A1A9U4E8_ANOST back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKMLLAIALF FALATTPTVT SDATFQQYVE LMFQFDSVFE TLCLEHTNDS VQARRMVEAN QELQTCVNLH HDPQNFTNAL
81 DT**LTVENR**KD FISYNCDQFE EIKKCYLPFT RQLEICFTGR DVSMVKTLIM LEEEFAYICE QDGANVLSVP RSNYSYCAGN
161 LQELLQNCSM QDWAELRSKT IDTMTERDCS IFQRLATCFQ NNITKCGAPL FAQLFNIRYR AIVKQTYCNK DTP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.LTVENR.K	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	83	88	
total 1 peptides												

tr|A0A1D2NEM6|A0A1D2NEM6_ORCCI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPRQSFFRSS AVALLILLLV SVFADYRVQI ETTENPTTSE SIDSTEDEQS KPWESPLQEL LRIAESCTMK DPEFIQKTHT
81 AKIIWENCMD SINPGVSTSE HSISSNEKGD STGRSFPEIP ICVNTSAFKG CWISVIAALN ECEAGVGDVV GAIYFALYDD
161 TCREGGR**LTV ENR**RKVAEEG EPCSRNYSTP ECDINTMLRN SNDLCLRFYS ITACDLSSID PNCSNEYDKR LHADIFERVG
241 NDLQCFPSSQ SNGGTDLIIG QLSTFIITVL LTAFM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LTVENR.R	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	168	173	
total 1 peptides												

tr|A0A1D2MIF2|A0A1D2MIF2_ORCCI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIAKSFSCCF YTAALVHILC VFPGEGAEVT DTTGEYSDAS DPWETPVQEL QRVTQSCEFK IPDFAHIAYN AEAEWQRCID
81 TIHPKFPILE STRSRSNAPL NDTVIREIDR QLYMAICRNT TAYRGCWLSV IGALNKCEQG AGDISDKIYF ALYEDICRDG
161 GR**ITVENR**RR AAAEGSPCLR NYATKECSMI KLKEKMRHSS DLCIRFQSNT ACDLSSIDRN CSNKVDKQLH AEIFERVGQV
241 LNCTSSPSED ESNGANRLTG YSYMFIAIIL IFVSNINKFN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.ITVENR.R	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	163	168	
total 1 peptides												

tr|A0A151X2F2|A0A151X2F2_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVGNVTEEKR G**ITVENR**RSG KDSQWGFGGE SAVTSRNAVA PPTGESEKVV VWKGGYHAYT SKGMERHAPR KWGQGLRGNV

81 AWEAPCLTVG RGAFPGMRRG VWYRESFQGS LRGWKRGGME WNGVERSARR CLEDKARSSD GCVRASGTTS NVFRWYGRSR

161 LVEVEHVFDA QGGLHIVGLL VGGSRKITSG ALGWSTQLSS WQRTKLKSSD AATEQEGRGI PSVLAYGSSR ISKTELNTPR

241 GHREFPPHQP HPRNPRHPIA PNLSLSFRIV AFRYTFLSRF RLHPPYHHHA LGSLSPPLWI SFFPLNLRL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.ITVENR.R	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	12	17	
total 1 peptides												

tr|A0A1A9WR47|A0A1A9WR47_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKLPLISSAI TLKEIDQILD LVLSADLLLV TNSSSLM**LTV ENR**ETKRTFH VHYIPADLLL SVQDENIYYG LGRQALNKCH

81 HFTRDLHVDV QKGLVLDDPK KSPIRVKRAD LRILSISFLG VEIEREVYRV KHALSIVNFE INIEHRMASA ERAIPKWIKV

161 ELFQQVFEEI ISGYRQTKEF EVKEALPPGE NYATIMLRIK AGIELMDGSI KSCNFMLKTA HSSEMLREMM DRFDMFDTET

241 DMYRFIIPEL EQMYTQVGVN VKFSCKFYKL PDIDESYVLL EDLKCRGFKN ANRLEGLDIN HTKHVLKKLA QWHAASATRV

321 TTKGPYDEKY MKSYFKPEGF EAMKSMFANV TKYFISCVSS YNGYEEYYED LCKIEKLLMD ELYKLNEIDE NDFNALNHGD

401 AWCNNIMFQT DDNDDVLETY LVDYQLPKYG TVAQDLYYFL LSSTKYEIKL KHFDYLISYY HENLVKHLRL LNYPNKLPTL

481 KGIHMQLLKH GVWGLTSTCG ILAAVLLDPT EKANLDNFMS ANDVAVDFKM QMFSNPRYRK HAEALLPWLY YRGALEISSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.LTVENR.E	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	38	43	
total 1 peptides												

tr|A0A1L8DSR7|A0A1L8DSR7_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVRTRLLGL IDVLMRVPPL FVIDEILKIQ MGLATSSMSS PVSTIVENVD N**ITVENR**TDD MQRLVHEEIE FYKVISITTI

81 KFFMCLLGCI VAACIFMLWT RHLVIVYKYI LSVGLIFLSY WSNVSAINLI RENPNLLENI LLDPGGIAFA IIPHSMAQWM

161 MGAIFAYIHS GPRYDLIQKI LPFSFLMPLI LASLPFMPRA LVKHSPAFAA ILPLVLSKIA LWSSSFDVIK TIFNGYQHAK

241 NFATSFGLSA LVENEWQRLN VPCVLRAFWI IRLCEELVTL VMSSEVPLAF MATIQSLLVS GCETVTAVLG MTSIVSLICH

321 YVGKLFQLFL MSEDYDEDKS IGTVSAILFY ILALQTGLTS LSPDKRFIRL CRNLCLLVTA LLHFLHNIVA PLLMSLSAAR

401 NPSRKRHVRA LTVCLFLLVA PVFLLSILWS RHTPSTWLLA VTAFSVEVIV KVLVSLATYT LFLLDARRQT FWEKLDDYVY

481 YIRAFGNSVE FCFGIFLFFN GAWILLFESG GAIRALMMCI HAYFNIWCEA RAGWAVFMKR RTAVHKISSL PEATTEQLVA

561 FEDVCAICYQ EMTSAKITRC KHYFHGVCLR KWLYVQDRCP LCHEIIMNPD PKQGEKCPEE QPADERPAPI ADQSASTSSA

641 DRPNTSADAS IERTLNSSVN HL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.ITVENR.T	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	52	57	
total 1 peptides												

tr|A0A1L8DSL4|A0A1L8DSL4_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSVRTRLLGL IDVLMRVPPL FVIDEILKIQ MGLATSSMSS PVSTIVENVD N**ITVENR**TDD MQRLVHEEIE FYKVISITTI

81 KFFMCLLGCV VAACIFMLWT RHLVIVYKYI LSVGLIFLSY WSNVSAINLI RENPNLLENI LLDPGGIAFA IIPHSMAQWM

161 MGAIFAYIHS GPRYDLIQKI LPFSFLMPLI LASLPFMPRA LVKHSPAFAA ILPLVLSKIA LWSSSFDVIK TIFNGYQHAK

241 NFATSFGLSA LVENEWQRLN VPCVLRAFWI IRLCEELVTL VMSSEVPLAF MATIQSLLVS GCETVTAVLG MTSIVSLICH

321 YVGKLFQLFL MSEDYDEDKS IGTVSAILFY ILALQTGLTS LSPDKRFIRL CRNLCLLVTA LLHFLHNIVA PLLMSLSAAR

401 NPSRKRHVRA LTVCLFLLVA PVFLLSILWS RHTPSTWLLA VTAFSVEVIV KVLVSLATYT LFLLDARRQT FWEKLDDYVY

481 YIRAFGNSVE FCFGIFLFFN GAWILLFESG GAIRALMMCI HAYFNIWCEA RAGWAVFMKR RTAVHKISSL PEATTEQLVA

561 FEDVCAICYQ EMTSAKITRC KHYFHGVCLR KWLYVQDRCP LCHEIIMNPD PKQGEKCPEE QPADERPAPI ADQSASTSSA

641 DRPNTSADAS IERTLNSSVN HL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.ITVENR.T	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	52	57	
total 1 peptides												

tr|A0A0J7KID5|A0A0J7KID5_LASNI

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

Protein Coverage:

```
   1  MSSENTTTVK ADKSPNKNFV RQSKVQQCKI AEPFVKKVAK DSISKPIIET DINKILNNPV KIPISGKKIL PKILPKINSN
  81  HLEQGQTSNS NSKILPKTKS DHLEQGQASN SNSKILSVQS SQNAGKKIIL SKTISDHLKQ GLQTSITNNN SKILNVQSSE
 161  NTDITSIIDQ LSSHLISNKK LVVIGQDSNN VACDKNEVST EKRSSTLVLD NSEDTDNMSS QKKVCNSANI KKQEKILIKN
 241  GKKYLIKHQN NVTKENPSIL PIVSSTTKVI KQLASEHNTS MSTSTNSSKA ENISVEQVAP FSNDIFILTP SPSPSESSSS
 321  SGWIGDSYIK KTAITSKLRN APPQIITVQS ASGIIQKKYL FETISLNEKN GDVYMNIKIV DRISKEGFRD TCEVIPKYRE
 401  QMINEFDQLH SLELKERINH LQLVSEEMRK VLDFLSSNVL WEKSRSINTL QRLLEKCLHK CNQDITDNKD DDVILNEWES
 481  KISKITDLHK CISCNKLIKP KSYIPGFSRL SKNDNIYCSC YKLVCHECLS YQDTLSRFTA HQNYHKNCKP YVCPNCDSKF
 561  TSVRSLEVHT WTVCFHTLKK FILSCKICEI DGFRDMESIT RHIVIMHSTT KIACEECGKV LSSYSEYVKH STETHPSMLN
 641  PNPIRLVKCR LGNVIIRFEN FMSYADMHPA IQKKIWFKCP FCHLITVENR HTTAILNDHL RNKHLHRLSE ILSKEALLDI

 721  FGTDFVKADV NEVSETSVDM FTNEAAKHTI IPRIVNARTI SSEIFEHGTE DEVPLWKYDD SNVAWSRIEI KPSAIENVDD
 801  GQKITSMPKI LNVKSMSDLK SSKPKEAVTK TSTEAKEKPN SQSPQAEIII DEKDDPLAGK DTKKMKLNDS KSDNKEETGK
 881  TKEPDKINNE SIVSTDINNV RVNSPIESCK GILDSEFTSK TSIDGRIKVV DIREICKPNI EPFVAVEPNG TPTKDENTSY
 961  MTSIPQPPPL AKIPQHLLES MEVYKPDDGS KNVARTKKFL ARRMNDKTKG RIAIHGTTDT QEVNVDYLCH LCGEQINTST
1041  SVVKAHFHEK HSDECKLAII TPRLIRISPD FINGGYKQFI NSRKRKADSA LLASKRKRRW TPKKHTETKD ASAPVGLCVE
1121  QETAEDGEGN FKCKKCDQRC TDMSDLREHI AANHRLKGRY LVCLECGENF VVAPSLQMHL KAFHGIEDPI NYMNQNPSYA
1201  PGVDGDSEAE GKTTVANQCY VCMAVFENKA AVDKHLRVHG MAFLNRKRIE ARNALKSPEK KANMEEDKQN VAKDSPKETV
1281  KQDKPAEIIL EKLNVAM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ITVENR.H	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	685	690	
total 1 peptides												

tr|A0A1Y1N3M1|A0A1Y1N3M1_PHOPY

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

Protein Coverage:

```
   1  CLKGPAAEVL KSLEISQRNY PIAWKLLEER FENEKLIVNH HVQALFDMPS LIKDNFSSLR RLIDDFNKHI GALQQLKQPV
  81  STWDTILIYM VVNKLDTNLR KAWEDSLESN DLPKLSDLMQ FLVNKCRVLE TIQGSKGDKF AEKTDKGVRS KVVMNVASDR
 161  SEARNDCLIC NDSHFIYKCP ELVKLTVENR INKIRELRLC LNCLKRGHAA RFCKASRCRI CKRAHNSVLH LQRASTETDV

 241  IQDSSTAGND IEERLNAHCN TRNAHVFLTT AIVKVRNSQG KNIPLRALLD SGSDSNFIGK GVYRMLGLKQ QRTNVSVSGI
 321  GHVVSNIHNQ AQVTIGSMYN DFSRTLKFLI INEITATIPS VRFDKINFQI PADINLADVD FNVPGRVDML IGAEVFYDIL
 401  LSRKLELGKN KPILRESQLG WLVTGKITHE DFVQKRNCNT CVRDVKLLGQ LQKFWEVENF EIPREYASEN EECEVNFINT
 481  SSRDVDGRFI VQLPLKGCEL GESGATALKR FLSLERRLAR DVVLKNNYSD FMTEYHNLGH MELVKSIDHR SDIDEGELIY
 561  YIPHHAIVKE GSSTTKLRVV FDASAQTTNG KSLNDILRVG PVIQNDLLSI MMRFRKHNVV LVGDIEKMYR QVWVQRDFQN
 641  LQRIIWRDED KLNLYRLKTV TYGTAPASFL STRCLRQLAN ENKIKYEHAC RVITDDFYID DLITGGHDVA EVVALRLQIT
 721  SILRQGGFNL RKFGSNEISV LESIQGVGDK HVIKDDKDTK TLGIIWESKA DIIKFEIDNE ELDTLTKRNI LRAISKIFDP
 801  LGLVSPVVIS AKILIQGLWA LQLGWDEEIS ENVGEIWTKF WGELQKVRAL KIPRHVVLER FDYVELHGFC DASEKAYGCA
 881  VYVRSVYGSE VRVALLCAKS RVAPTKRITL PRLELCGAVL LVQLVETVKK NIKLAFAREH YWTDSNIVLC WVNKPANSWK
 961  TFVSNRVGKI QELTEASQWS HVSGILNPAD LVTRGVSVET LQQNRWFEGP EFLESIEITY SSKVKNETSE TLEMRSSSTV
1041  FTAVVNISYE LFERFSTLTK LIRVLAWCRR FFKNCAKIKT KGVLTCRELA EAGLVVVKAV QGEAFQAELK NMKVGNASAA
1121  GRLLKLNPFL DDNNVIRVGG RLKNSQLSYN SKHPIVLPKN HKYVELLIKQ EHARLLHAGA QAVLATIRTR YWILGGRDVV
1201  RRVLRKCIIC FRTKPLNYSP LMGDLPAMRS NAVRPFYTSS VDYGGPFLIK DSKLRNRKFI KCYLCVFVCG VSKAVHLELA
1281  TDLTASTFLL VLKRFIARRG IPKELYSDNG TNFVGAYNQL KNIRHELALL TKNEELQNFI TKNNIEWHFM PANSPHMGGL
1361  HEAAVKSAKC LLYKLINNVH FTYEDFYTLL CQIEGVLNSR PLTTMSTDPN DYSVLTPGHF LIGEALVTIP EKEVTQRAFN
1441  SLKSYEKICR IRHQFWERWN LEYLTSLQER SKWRSSKGVQ PKVGDPVLLM EEHRPPQMWT LGRITHLHPG SDGSVRVVSV
1521  KTPNSEVTRA VRKVCPLPLD VEQPFQGGED VESDPGNQRR SLLRRSKNE
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTVENR.I	Y	26.37	730.3973	3.1	366.2071	2	0.24	627	1	185	190	
total 1 peptides												

tr|A0A182N577|A0A182N577_9DIPT

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

Protein Coverage:

1 MLGFRAVGIL LLVQTSLSVA QLFGDSQNAL VPSAG**GRNVL RQGDR**TPGHD HTHIETIDVK CDQRNGMLVT VQFEDDFRGV

81 IYSQGYHNDP KCRYVQANQG GRQFTFTVPY DRCGSKPSCA VCASVDNILV IQTDEEVQEA WDTARRISCS QSEQQQNTII

161 FKPFVVDQLE VINVPTSTGG VECWMDIQRG LYPSISPIPS VIKIGEALSV LVYLRDPKGE YDVSVKDCYA YDSPDYDAST

241 TARLQLSDKN GCSRKKKLFG LWQKTTQTGG SGATLVVHNS IKAFKFPDRM QVFLKCDIEI CRGGCGPQVC AEENLISTVE

321 TTTRRLPGPT RGRPAQTTTL APVVPTRGRR PTVTPAPAQP EYTVPTTQPP RRGTRPPRPP VEATPATAPP RRTRPPNTRP

401 PTQTPTTEFV CQPGSTDDRC NDVIVTQRPD CSRGSRDPRC RSRGTRPTPT TTVATPAPLR CFPGSTDPRC PTTFRPSVRP

481 TRPPPSPTAI RFATTTEATE DEDSVPDCFL RLGDPRCDEV SIYLPVIPQD QVTTRQPIVP TVPSVTPSTA LNCFPGSNDP

561 RCRTPVLRCS PGTTDPRCPG FVRPQPPTTS SPARCYPGSP DPRCPQPTSP PKDTATYLPP VDKPNCYPGS TDPRCPQTTP

641 APRCYPGSND PRCPQTTPRP VPTTTPAPAC YPGSTDLRCP KPTPTTQPPL RCYPGSADPR CPQTTTPRPV PTTTPAPRCY

721 PGSTDLRCPQ TTTRPAPTTT AAPRCYPGSN DPRCPTTPRQ TTTTQPPLRC YPGSTDLRCP QTTPRPVPTT TPAPACYPGS

801 TDPRCPTTPR PTTQPPLRCY PGSNDPRCPQ TTPRPVPTTT PAPRCYPGST DLRCPQTTPR PTTTTTSAPR CYPGSTDPRC

881 PQTTPRPVPT TTPAPVCYPG STDPRCPKPT QTTQPPLRCY PGSTDLRCPQ TTTRPVPTTT PAPRCYPGSN DPRCPTTPRP

961 TPSTTSAPRC YPGSTDLRCP QTTTPRPVPT TTRGPSCYPG STDPRCPQTT PRPVPTTTPA PRCFPGSTDL RCPQTTPRPV

1041 PKCYPGSRDP QCSDKQDSET YLPPVEVPRP TTTQRPACYP GSTDPRCPQT TTRPAPTTTP APRCYPGSND PRCPTTPRPT

1121 PTTTSAPRCY PGSTDLRCPQ TTPRPVPTTT PAPRCYPGSN DPRCPTSPRP TTTTQPPLRC YPGSTDLRCP QTTPRPVPTT

1201 TPAPRCYPGS NDPRCPTTPR PSPTTTSAPR CYPGSTDLRC PQTTPRPVPT TTPAPVCYPG SSDPRCPKPT PTTQPPLRCY

1281 PGSSDPRCPQ TTPRPVPTTT PAPRCYPGST DLRCPQTTPR SVPTTTPAPR CYPGSNDPRC PTTPRPTTTT PPPLRCYPGS

1361 TDLRCPQTTP RPVPTTTPAP RCYPGSNDPR CPTTPKPTTT TQPPLRCYPG STDLRCPQTT PRPVPTTTPA PRCYPGSSDP

1441 RCPQTTPRPT PTTQPPLRCY PGSNDLRCPQ TTTRPPVPTT RKPCYPGSPD PACPRPFLTT TPSACYPGSP DPNCPQPYRP

1521 SSTNPPATYL PPFPESSGRS ARHLSPETLS DINALADSDA AEPAAAGSVS SAAGESSVDS TAAGGATRTK REASVSNDLD

1601 GEPTKEIVSI TLNIKGYQFG A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.GRNVLRQGDR.T	Y	25.11	1169.6377	-13.2	585.8184	2	0.47	759	1	36	45	
total 1 peptides												

tr|A0A1A9Y4N1|A0A1A9Y4N1_GLOFF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFNKQHSDWI IVKKRLVGAR RFEIRLLNKN ILHCSPQGLL EQKMSPIFPF LIAHIAVGHS ARLLDYNCIR LIHRFDWLDL

81 SIFRLASLPY FGCFGFSLLN FTFQQQSPTM **YTEHLR**TRLR ATKSQRSREQ VLKTLY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.YTEHLR.T	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	111	116	
total 1 peptides												

tr|V5GJC8|V5GJC8_ANOGL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GELVPKRVHA LLPHAKLITI LISPAKRAYS WYQHTKAHGD IIANNYSFHQ VITASDTAPK PLRDLRNRCL NPGKYAQHLE

81 RWMTYFLPQA LHIIDGEELK SNPIEVMNEV QKFLKITPVF N**YTEHLR**FDP KKGFFCQVVN GDHTKCLGRS KGRQYPP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.YTEHLR.F	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	122	127	
total 1 peptides												

tr|A0A212FE53|A0A212FE53_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDVKSMFFVF YYFSTVFCGY PPTGDEVQLG SVLLPATRRG RYLANIIRRQ AVDGTGIKFN KDADRMNAEA KKKVDVLSEE

81 LLPYIIAEQE RRTTLYKRIM TAIQNGEKGV TIAEIRNKPP LIIRKGLLYR CPSNRAPKEP DGSGSLMCED DLEPTQVMYD

161 SCLSAEDKEL YVAENKYFFC NRHKVEGPDL PRNGTTVIGC APIERTSLNY TTSKCALEDT DDVVVHYRYY PDRVSHKVEG

241 PDLPRNGTTV IGCAPIERTS LNYTTSKCAL EDTDDVVVHY RYYPDRSYKF VTELDPDREV CDHWNPCQIG YIYSLPSPDQ

321 ALLANELWRE **YTEHIR**HTP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.YTEHIR.H	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	331	336	
total 1 peptides												

tr|A0A087UES5|A0A087UES5_9ARAC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKNLHFLLQR IQALYQVMDD TLEVAAGHIS NVSTEENLHR CHPLHLLESE NELMVLEQDY VKLKTNLKDV LCSVCDHAHD

81 CCAKILTAKA KDGSLDKLIM SEFLILAKSI EEFQHQSEMI SGTQSTALRL VLQNQATRFV TRFHEERKTK LGLILENEQW

161 KQADVPMEFQ ELVNNIISTG CITSLKSKED KIYRDPQPYL IVNGENFAVC GTALMLLKMV IEYCQCAEEL PMLAQDLASR

241 LVELLKAFNS RTCQLVLGAG ALQVVGLKTI TTKHLALTSR CLHLILYFIP YVKNHFQSKI PGKQQILDKN FDQVTKI**YTE**

321 **HIR**EISHKLE SIISDMFEAQ LKKWEVKAPV PSPSFSAISK QLNKVHELIH NMLSPEELNN IFLRVNNSFK NKLRDHLLRL

401 QVNNDGGPQH GLVTQELTFY TQNLKKLQVP CDFNMNDLWQ SR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.YTEHIR.E	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	318	323	
total 1 peptides												

tr|A0A0C9RF26|A0A0C9RF26_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFIVTKQIDS ENISKLCRTC LREDGEKMVC LFVGPAGSSL AAKLRSLSCL EVWQGDGLPE KLCDRCITRA ESALLFREQC

81 RAADKALRQA ATKVSGPSKY SPVPGSKGYE ENPGFTPVET SEKSVKCTEC EAVLMNYQEL CFHNRPQAPF ANESTSMQHM

161 HIVESNNHYF SSESSINDPV ITTNRNLQVA VLEPPKNDRP ACALHCSLCN HTFPNRNQLI SHNFSHSNNH IDNSCDDSIQ

241 IGEDSTEIAE NLSFHQYPRD HENIISMTYP QNLTIPENQR IQPKVIDSQS DIEIATSNRV LKYPTMTDEK IHSCSTCEKK

321 FSQKSKLKIH EFRHTGQRPY KCDDCNKAYT SKSKLNAHVR LHTKTNLHEC KICDKIFSYP SYLKEHQKVH IVGEKKEIKM

401 KSKGFECSVC CKQFRLKKNL KAHLRLHSGE GLYHCEICSK IFSQKYNLKI HMRTHKGIKL HKCEYCAKSF TEKGN**YTEHL**

481 **R**IHTKVKPFD CKICGKSFSQ SSHLKSHEVT HESTRRHQCT LCGKRFKLLS HLKRHANLHS SVKRFKCNQC DQMFSQAFSL

561 KRHLKRHCET

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.YTEHLR.I	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	476	481	
total 1 peptides												

tr|A0A067QZW3|A0A067QZW3_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLFTCLRVAD NVNQTKLWSS NGIHLTVYSL DQDVDPKMLM TQYHHLAVIL DLSCSGSGYL LAQASKEKHF SSLHHWLLLS

81 EKTLSLSVDP LITTLEPFDL QLDSHVTIAH IGSSLKQVLL QDVYRIGRQD PLIITPPRDW TSGQLISPGS QIDNYNGIHL

161 RTSVLVVDGT WDTHTDLNYR HLNTESKINY VLMTYVSEML NFRMNITLTD TWGYPEEGPD CFSGIVGTLQ CGECEISATG

241 VMWKMERMDV IDYVTEITKF RGAFMFLKPS LSEVSIIYEL PFSSSVWATY ILTVAFLTIV LVFVQHVERH VRPLSSPDHP

321 VSWSDAVLDT VGIVCQQGTE NIPKNLASRM VFIFMMLLSL FLLTSYSAII VSLIQTTSSS ISTLTDLMQS AMKLSMNDKL

401 ANEITDPAVE KVFKEKLYTQ PFHEAFITDE VGVERIRRGL NAFHGINGAY KIISDTYEEH EKCRFKEIKM FEANHVGFPI

481 RKGSP**YTEHI R**QRTHWLREA GMVGREETRW YYPKPRCETS GQNFVSVGIQ EFYPTLVILT YGIFLSIVML VVEVVYNKYQ

561 HILLVTSFKS CTRKIRN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.YTEHIR.Q	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	486	491	
total 1 peptides												

tr|A0A0K8VIY6|A0A0K8VIY6_BACLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVKLTKFFS SAAAIPTMTT ASPSSETAAT SYHHQQQHMQ FMQQQSSLTY NPYIAGGMDS DELYDDDNMS LYSSATAGSG

81 IMTQRGHSCN NSQRPLLGER KPPKMLLSSN ATKKNKKSTG FNQPQRHLHL QQQQQHEGKP QLLPHQKSYI SPYVQQQKRD

161 SAKGLHGFND FDILSQQ**YTE HLR**SSPHIGY PYGSPPSPSA KSNDFVFDPL PQQHTLYGND VVHQQQNANQ YRIQQTGNDI

241 NETDYSYYER NAYNVSGSGS GSPDGASNGV PAAVHYMGKS SRFDDDFCTR RNATFSEPQP VLLSEQTWTP PVPAVTDDMT

321 GPFIFGSVPP ERFNHHRPQN GDNTLSKLPN ELAYTSSPTA GESLSECVID VADKHPPYND QVTVLSSDTS SSSRNSSGKG

401 MKFLLRKSKS KRSAKGKKFD TSSVQTKSQP KQLKTPSIKC VLVGDGAVGK TNLILTYLKN RFNTEHVPTA SDIYNADVLV

481 NDNPVHLTIC DTAGQDTLDN LRQLCYPDSD VFVLCFSVVR PETFHAVKTK WAPKFSKSKA SLILVGTQAD LRKNTKVLKN

561 LQLNGESPIS HADAWDLAAS VGATYIETSS ATQDKVKEVF DTAIWEGLTP TILPPTPRPP LWKKMLCLA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.YTEHLR.S	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	178	183	
total 1 peptides												

tr|A0A0K8UPX9|A0A0K8UPX9_BACLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVKLTKFFS SAAAIPTMTT ASPSSETAAT SYHHQQQHMQ FMQQQSSLTY NPYIAGGMDS DELYDDDNMS LYSSATAGSG

81 IMTQRGHSCN NSQRPLLGER KPPKMLLSSN ATKKNKKSTG FNQPQRHLQL QQHQQQQQQH EGKPQLLPHQ KSYISPYVQQ

161 QKRDSAKGLH GFNDFDILSQ Q**YTEHLR**SSP HIGYPYGSPP SPSAKSNDFV FDPLPQQHTL YGNDVVHQQQ NANQYRIQQT

241 GNDINETDYS YYERNAYNVS GSGSGSPDGA SNGVPAAVHY MGKSSRFDDD FCTRRNATFS EPQPVLLSEQ TWTPPVPAVT

321 DDMTGPFIFG SVPPERFNHH RPQNGDNTLS KLPNELAYTS SPTAGESLSE CVIDVADKHP PYNDQVTVLS SDTSSSSRNS

401 SGKGMKFLLR KSKSKRSAKG KKFDTSSVQT KSQPKQLKTP SIKCVLVGDG AVGKTNLILT YLKNRFNTEH VPTASDIYNA

481 DVLVNDNPVH LTICDTAGQD TLDNLRQLCY PDSDVFVLCF SVVRPETFHA VKTKWAPKFS KSKASLILVG TQADLRKNTK

561 VLKNLQLNGE SPISHADAWD LAASVGATYI ETSSATQDKV KEVFDTAIWE GLTPTILPPT PRPPLWKKML CLA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.YTEHLR.S	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	182	187	
total 1 peptides												

tr|W8BC92|W8BC92_CERCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVKLANFFS NVASMPTTAA VSPPITSATS TTTSTTGYHQ QQQHIPFMQQ QTQQQSSLLY PYIAGDMDGD GLYDDDNMSL

81 YSNVTTANDI MMQRSHSCNN SQRPLLGERK PPKMLSSETT KKNKKSTGIN QPQRNLQQQQ QQGKPQLLQQ QKSYISPYVQ

161 QQKRDSAKGL HGFNDFDVLS QQ**YTEHLR**SS PHIGYPYGSP PSPTAKSNDF VFDTLTMRQQ LPLCGDPIYS NTGLMRKQQM

241 NPQQQTGNDI NETTDYHSFY GSNAGTVSGS GGDSNGLVTS TNNTPSSHYM GKSSRFEDDF CNRRNAKFAA PQPLSTIGKG

321 RMPLLLDDAE DVGGPFIFGG VPHEQPRQQN QYYGDSSLSK EVQQEELNKI PRAAISSVDS VIDEAEKCSP FEGQVTVSSS

401 DTSASSRDSG SNKGAKFLLR KGKSKRGAKV IEKKSGANAA MQRKTQQKDL KTPSIKCVLV GDGAVGKTNL ILSYLKNRFN

481 TEHVPTASDI YRADVMVNES LVHLTICDTA GQDTLDKLRQ LCYPDSDVFV LCFSVVKPET FHSVKTKWAP KFAKTKAALI

561 LVGTQADLRN DTHVLNRLKL TGERPISYAD AWDLAASVDA KYIETSSATQ DKVKEVFDTA IWEALSPTTL PPTPKPPLWK

641 KLLCLA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.YTEHLR.S	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	183	188	
total 1 peptides												

tr|N6ULE5|N6ULE5_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FIKSNTRPEP NIRCGVEHGL RILQNHDHKT DARLKSDPKV LVFVETIFSK LGKDIAELLV HTRIKYKVEV TGKSLPVLTN

81 LDKGRYGVII FENYNKYLQM DNWNRELLDK YCREYSVGII GFIPAEDETY VGSQLKGFPL FIHTNLKLKD ATLNAASEIL

161 RLTRAGETAW GDLPGNDWTI FKANHSTYEP LEWAHRNDFF PINESGVKTP LPTVIQDHGL FDNIQRIIFG SGLKFWLHRL

241 LFLDSLSYLS HGHLSLSLER SILVDVDDIF VGDIGTRLKP DDVEALINTQ KRQVKLTEDK GDDLILENVE KFMWFSHMWN

321 HQQPHLYDNL SLLMDDMVLN KNFAKQHRIP IDSGYSISPH HSGVYPVHDL LYIAWKKVWK IRVTSTEEYP HLRPARLRRG

401 FIHRNIMVLP RQTCGLFTHT MFIDKYPGGR EKLDESIQGG ELFQTIVYNP INIFMTHMSN YGNDRLGLYT FESVIKFVQC

481 WTNIRLTSAP PLQLAENYFK LYPRESDPIW GNPCDDVRHQ KIWSKNKSCD SLPKFLVIGP QKTGTTALST FLSLHPSIAS

561 NVPSPTTFEE IQFFNAQNYL RGLDWYMSFF PSDTNSLTRY FFEKSATYFD GELVPRRVHA LLPYAKLITI LISPAKRAYS

641 WYQHTKAHRD NVANNFSFHQ VITASDAATK DLRDLRNRCL NPGKYAQHLE RWMSYFPQAS IHIIDGDQLK SNPIEVMNEL

721 QKFLKITPFL N**YTEHLR**FDK RKGFFCQVKE GSTKCLGRNK GRQYPPMEER SLKYLQRYYL SHNTALVKLF NKNGIRLIPK

801 WLKEDLSDQN DTDS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.YTEHLR.F	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	732	737	
total 1 peptides												

tr|A0A0T6AVT5|A0A0T6AVT5_9SCAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MNSLQKNTEM DSENIVCPVC TLFLRPGITL KAHLSSHPKQ KVIEALVRIS SSENETKTQA TTSDQNENLI GSTNTITSNS
 81 QAWNSPSMPV NTVYPNFSAM PGNHSFIYQQ FMSSSTPPPN VLNVNPLTQQ IVTIPTVFNS QMMCPPYVYQ QQQVIMSSGP
161 SVMSIVPKPL PIELPTLPNQ ESRASTSEID GDDQDDLTDE PDLVAIEISE LNTNEEENLR EKEGNIVELD KVETEISEIK
241 ANSDYKVDVM PNKIMQGNTV IACSNIQREI SENSIVDCMK SAECEDSLTI DQDAEQEYPV ECNVELNKSC QTQTVNNFGE
321 VAVSEEEEVI QIPNEPENKP NCYYAEVQES ITNTNYTILQ NSFEQAESTY TSTHTESLFA SRSHEQNTTS VIDMDGMNLF
401 INSDFLNNQL VSQVDEFECV NNERSRIILN LGGLETNFIN RDNNDESLSR ESANIRTDEH MPPRGELSGQ ESNGGTSDVN
481 WNRVQYQEVC STYDLIAREN WNDDISDTEP NSAPNQSHSQ ILSNCEDDTP TVSGFREPPI TYKCPTCGES FNCPKERRVH
561 QREHHSISEK KEKEIGGQIG GKRVKKLTIK PKKTDIKTEN NFDNVFTNKL KLESNNEGDK CNVIPQNNEI EVQKKEDVTI
641 NNPNICTVCD MVVADNNALK QHQLEAHNLS SDVRHKCKTC EQTFPNESKY TEHLRTHPLE CRLCGKYFYR KQNMQLHMKR

721 HLGIKPYKCN ICEKAFLTKQ KHDEHKNIHT GDTPIKCNMC DETFRRHSNL VQHRNRHHFN MKRKMKDYVC SCGEIFHSKR
801 KLAWHKEIHD PKPKGCSHCS EKFIHMSSLT RHIRRAHNER FLPNKERVSE NVECPICKGV YLRSYLEVHI RNHSGHKPFS
881 CLICNKSFTT KWNLKLHKWT HASRTAKPFK CDLCKGAFIR QSDYTAHMNA HKSVKPYTCN YCGAQFIRKY NCQRHVKEHE
961 KVKTFSCQVC GKSFHRSYYL KDHIRVHSGV RPYACHICGK TSTTKSNHNK HVRIHHAREP VSTEN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.YTEHLR.T	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	690	695	
total 1 peptides												

tr|A0A1Y1M7P2|A0A1Y1M7P2_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MSADLETVFA EAIKGIKAVK PFPYDDYANR LHNKVRFTFQ NNVMQPNIDR APTYPEDDPD PDNWFIDIFG VWDLLYKASF
  81 PSVSGGIASV DNQYDPKNLK QYVSNENSKI RYLEVLTNLM GFCLGEHINR ELKSQRTRTI DDLWHYDGFQ DFCLDAVTKQ
 161 SFIMNEIRTD MARDDHFFSI AWLMIADYMQ DRDHVYRTAP SAGIDFQNKA SYKTLNQWSY TLWANRDKGD PTQMDDIVKF
 241 CGRVATIGLC PPNATTNIQQ PAPTWSVTKA FYDMGINAVE DDDYNRDLQD SLSRLQDQEE IVNEWRSYCL ALTSAWENEI
 321 LPYWNTGVYR SFAAKKFEYI QSWEHIAFTE EGDELGWADY LPVTDQPPAA PKQSLNNIVL PGTPITLSNG TLRPCSAVCS
 401 GDEVLVCPDN SISAPAHCRR IRQATKADLV GFNGEVPWAL KSQVFHTTTG PRALDPEAAQ SFNPYRRIGK LAIGHVVLRL
 481 QENEYQYVEI KSIEKAAECP LANAYTLLLS GTHQTYHAHG YLVDTNATSH TLRETVESLR KVPGDQRLGL LYHFQEIRGM
 561 FGKFDAEAIY QRLNWELFGQ YKSPDGQGPS MSKSANPLNY TEHLRTTKSM SVSKGIPIDR LARGFRLKSH EPDRLPAGYE

 641 LPTLSLVDGY LLIDGEVQLR SKHDARKRSF RWTRQVLQTK MFEHGVVEIC PRVISGKGVI YLSSEAEPRE VPTRDQIHAF
 721 EAKAYSLDDL KAGNTRSVAD DESWTSFGKW NVTLDKSVWP PNTERTEPED PMDGGTFEDG YWAQQVQVPA VRLNLVDSLQ
 801 DQINQKYSQG LGDFYDVTSQ MKDGEQTYSV QFKRAPMVPF VSDAKPDINK TFGVGFQSDL DIDITLPSLF QEMTFTMDAL
 881 YESFTGYFFE YDPTMRGYKG NRHLVQGTVS DSDAVKACRS KISHAYAAIS KPGEVHIISN QQLQPSALTE SLLPLSAPSL
 961 EDLVRFTGYE EKSLHNDSQL LIRSMMYYHM DETQREKILQ IPKPTVPDEL PAALADNLPD NLKTFFKDKY GPGFICRYVG
1041 RTQKHMKSFT DQEMKKLWYW WQGNSKDCLS QSEEYNDINR LSSREAMKRR YESNLQPYLD DNPDDWATKL FTEVTNNTRL
1121 LLNWVHFPIG DDGNNVVNKQ CNILDALSPS SDWSQKFFDK FLAFATTHGS SAADIEPDGG QDQKYNWLHD SMRDLIVAVL
1201 NDDPSISDEV KKGLQADIEQ FEKENNLNQQ ADAQQRAAAI LEKSTVFMQE LAGWFTYIGK GLAAGFSGTA LWKWVGKAFD
1281 TVAEKLSSSL PALGNLKGLS SLCMVGVGLA TAAVSIWGLV NSWSTMPDAQ RAVVIFEVVR MVVGGVDKAI NAFNSFKSKP
1361 ASTAADEFNM EALNDGLAEE ISENGTKLGD VAQEVAGDED YRTAIADGIH GEGIATTTDG QESWNE
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.YTEHLR.T	Y	23.84	817.4082	13.3	409.7168	2	0.24	639	1	600	605	
total 1 peptides												

tr|A0A0M8ZQP9|A0A0M8ZQP9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MQQSKLLECT YTVYAQTKTC QTLGFQKFTK RLKHAQIVSG RYRNGAKMES DIEMKFSNKI LYNGGNSDSK FVIINNSFWR   C Carba
 81 NGLKITKNDL LLSNREKIER EGRQRVISKN FNARADHDNS DLDRTVQLDK LSEKVCGALG IKGGQTQAEI YATSRSNIFK
161 GTVPGTVPGQ TVPQYRGICG STRQQAPLST YTPYFEDCYD GVKFKSCFQH HEQRKQELLP LKRWKGAAPN AAVRNAVFRI
241 LLKLGATSLF PHLERTFAGS FSIHIFTVLD YYDTYVNEIT QIDLRPNLNR KLPINILLLG YSIESCRVSI YANEILPITW
321 ERETHVTTQT ADSTEHLNDK KQKEYLNLGV RNLSKSNSKN ATELRTNRLV TIINSRLKVG YFWRLINARF NELESYMNGA
401 AHCEERWTED VLMSHREIYE TVEMWKKFVR LEDKVSESCR SQILRNKFKV MREKCLIFQS IISESDETDN FLDNAKCNVK
                                                                                      C
481 FNRDFATDEL REFASWKHTV GTGSRDVKNE LRGNSELLDR VYSSYKTK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.C(+57.02)NVKFNR.D	Y	22.87	936.4600	-80.0	469.1998	2	0.15	671	1	477	483	Carbamidomethylation
total 1 peptides												

tr|Q7QJM3|Q7QJM3_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNTLKAPSLH SLLDSDHGSN DSLLAESLQL DIEELDDEEY AIPAVDTLPT LESVLSEIDS DLDSVSALGV RQSNGNGTGT
81 QTSIADDDLI RGGTTPTPSL EEQLKLESIL RHVVLHGVTA QLTSAVDRVD AGLATSCAVS MMIAVGTSHG HILAFDCTQT
161 LKWCCQEGIT QGAVSAMAFN EDSSRLLAGF ARGAILMIDT QTGDVIRTLN EVITPNTGVL HLKWTNRPAL ALCSDSGGSV
241 WSLNFTRRLG IRGCDSRCLF SGARGEVCTV EPLLLGDEEH PLKTYTIVAL ATLSKFFVVL IRPRLKVIKF HPMAGYPDCL
321 PLLAWQMVLI QAADSTRSID PVLAAARGSD LFFHQIIYNS GRISLLFLRH IQLSYNLLAI HWLGPKSIAC LDTKEVLHLS
401 DVRTNRELEV IDLSNVGLMY NSAQFKGLAT GGNVSPALAL AGAAACYNTV VSQGNQLYLL GGKSLHGISA RAWSDRISYL
481 TSMQRWDEAI ELAIEGYRAA AGRHRRLVSS KDRILRMYEE YLSVTKKTPE LCLEAIVGCL IEIQEKQLLW EELYDRLPTT
561 DHYLQIIAKH IECDHLDAVA PSVAQVMCEY FWKKGETTRL ENLILKLNWQ CLDLHQVLTI CRKERLYRAQ MYLNTKALGD
641 YTVSLTDLIP QIELATDDLH LGNCVLVYIS SCLAGRGYPT GEIAPETIPT VKHEVLRCLT VIHSNKAPED ELPYPYLRRL
721 LQFDTRETLN VISLAFQEKE FNGELGLSQR QRIINILLEI LTPEHATWSQ IGALLNFIAQ QIASRELPEN ELLLEKVVAY
801 LTAPTDVPLS RREHFEREQT WLELLCSNCL DHMPTEQLLD IARQNRCYHV AEHLLERLGR YEEIFDCYLL DEFRRMQIFS
881 YISQHASDTR RQIYQLVVQN LCQLVDINCE QAVRVLVDGF MRYLSHFLQL LEQA**AVPER**L FRFLEALLKQ SVQLETTDLE

961 RYLELLCQYR PEEVIEFLKS NDSYRLDNAV RTIKRYELNA PLIYLYEKQG DYQSAYAVAV ETLKDAPESS AEMCALQVSA
1041 LCTRASSVLT ESDREQLWFS LLHIVLARSD LTTVTKNILH SASEFVDLSK LVQLVLTSSG STSTGNFGDI KHLLIGMLSN
1121 SAYETLLLQT TSRILGNDLH AMLARERKIA MRGLAVKSIK CIVCRARLYN SERQPIVVMG DCGHAMHQQC AANFCTVPVE
1201 TPNGTDGNGG AAQSVETGTG KAPVMKRLKC PRCDAVVVEE CSIRTPECYV ESGPYANDSS TDKGPSTLKL SAPPRVG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.AVPER.L	Y	21.15	570.3125	4.5	571.3223	1	0.13	748	1	935	939	
total 1 peptides												

tr|A0A2A3EPU8|A0A2A3EPU8_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFQNFNMVLT EQDPNEDTEW NDILRKKGII PEKPKEVTEE QIVDIVENTI NEKTGRAPND LENKTLDELD ELEDEEDEKV
81 LLEYRRKRIA EMKELANKSK YGEVKEISAE DYVQEVNNAG DDIWVILHLY KSGIPLCTLI NQHL**INLAK**K FPTTKFLKSI

161 STTCIPNWPD SNLPTIFIYH NGNMVKQIIG PIELRGMKLT EAELEWMLGQ AEAIPTKITK DPKPKIRDVL FSSLRHENDD
241 VADSNDW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.INLAK.K	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	145	149	
total 1 peptides												

tr|A0A2A3EAV6|A0A2A3EAV6_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAIHWGIAGA GKISHDFVSS LQTLPESEHI VVAVAARELS RAQNFSSLHK IKKAFDSYTK LAEDNDIDVV YIGTLHPQHF
81 EIAKLMLNHG KHVLCEKPLT MNLKQTTEL**I NLAK**EKKLFL MEGIWSRCFP IYEILKKEIE SGSIGEIYQV LVSFGFKMPD

161 VERLNIKNLG GGTILDLGVY GIQFACLIFD NEMPHTVQAT GCLNEEGVDQ STSISFLYKG NHTATILTHS RVDLPNEAYI
241 IGTKGMIKVP KFWCPTTLEL PNEIVNVSLP ETKSKFNFIN SVGLSYEANE VRNCILKGMI ESPKVPHNLS LLIAQLEDEI
321 RKQIGVTYLE D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.INLAK.E	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	110	114	
total 1 peptides												

tr|A0A2A3EKU2|A0A2A3EKU2_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNTKDVWTTL LFIISFFFKQ SIANDCVPYR VDDEIIACVC NATYCDGIPD NSPEVPTEGN SYWYVSNKQG LRMKVSEIKF
81 DSCENFDADT TITVDSKKKY QKIIGFGGAF TDATG**INIAK** LSRATQNQLI RAYYDPKKGS RYTLGRVPIG CTDFSTRIYT
161 YDDVLGDTLL KNFSLAPEDY NYKIPYAKLA IELNPEVLLF AAAWSAPLWM KQFDNNITYL KEEHYETYVN YLIKFLDKYK
241 RNGLDIWGIT PSNEPLLGFM INDSNISMTW IPETQANWIA NYFGPTLASS PFNKTLLLTY DDNRSKIIEY VETAIKIGGK
321 YIAGIGVHWY QDLIYPVTVV DYIHEKFPDK FILMTEASIF DSIWTSSSKL KSEAWQRGEK YILSIIDYMN HWSVGWVDWN
401 MVLDKTGGPT VTNNKLDAPI IVNPETDEFY KQPLYYAIKH VSRFVDRGSF RISITDNNSV NSTAFLTPSG ETVVVLYNGA
481 TSTKRIILKD LQKDNKLCLE LSPQSMNTLK YK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.INIAK.L	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	116	120	
total 1 peptides												

tr|A0A0J7KFW6|A0A0J7KFW6_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDSNNDGVGD LKGISSKLQH FVDSGITGIW LSPIYASPMI DFGYDISDFK DIDPTFGTMQ DLEELTAQAK KLGIKVILDL
81 VPNHTSDKHE WFRKSLIGEG KYKDYYVWKT GKNNNQSPPN NWISVFSGPA WSFNTSRNQW YFHQFEYRQP DLNYSNSEVR
161 DEMEDVIRFW LRKGIDGFRV DAVPHLFEDA NLPDEPRSYA PGATERDYTY LEHIYTKDDP RTYDLVASWR KVLDDYADYH
241 NEDEKVMMTE AYTSLENTTR YYKFGSHVPF NFKFITDVNN DSKAADFKRI IDDWISQTPN GEIPNWVMGN HDRSRTASRY
321 PGRGDQMTML EMILPGIAVT YNGEEIGMLD KRDISWEDTQ DPQACNAGKD KYQSQSRDPN RTPFQWDSTK NAGFSKANRT
401 WLPIHENYIE **LNLAK**QKIAN ESHYKIYTSL IKMRQRETAL QQGNLKTLVQ NNGQVLIVIR QHNEQSVVLL INFNDKIAQI
481 VNLTGQGLAN ELVVEVATIG SPVKKGTTVN TREINLPAKA ALVFASKKS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LNLAK.Q	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	411	415	
total 1 peptides												

tr|A0A023EZA0|A0A023EZA0_TRIIF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DEMNIDVTSV ELEFEEAERS YCNDKDDGSK VEVGVQDQDG EILPENIESQ DLLVSHKAER TKRVFGSNKK KLNRELRMKG
81 QSYLGYRRPP NQCLTYHDSQ RLARVMGPPC NSAFCKSSNN KRKCGNIPHH LREEIFTNFW DNLNWAQRKI YVCNLVVRTA
161 TKSKKNGEIP SRRAATLKYF IKVGENVIYP VCKTMFLSTF GLREWQVSNW VKNVKHGIKE QHLRTRLLPD RVSCKDTFMR
241 SFLEKLNKLP SHYCRKNSDL LYLEQTFVTK KDLYNTYLVK CKESGESPKS QNTLTKLMKK MNISPYKPKK DQCNVCCGHE
321 ENNITEEEWH KHQEEKERAR EEKNKDKSMA LNGEKHVLTM DLQALKTCPS IFASALYYKT KLTVHNFTVF NIGTKHCKCY
401 WFDETSSDLQ ASTFASIIVH YIEQYLCDGK SIVIFSDGCT YQNRNCVLSN AL**LNLAK**EKK MLIEQKFLTK GHTQMECDSV
481 HANIEKKLRN QKIFLPSDYV RKTEEARQHP QPYETTLLDH EFFYNYNVNL VYSSIRPGRK PGDPNVTDIR ALKYTPEGVI
561 YYKTDFNEPY LELPKRRTSK NQPEQNENFE FPRLYQGRLK IKKNKFDHLQ QIKSVLPKDC WDFFDNIPHL P

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.LNLAK.E	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	453	457	
total 1 peptides												

tr|E9GCX6|E9GCX6_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVTTSMRCIL VMCFAAVCCQ CQSDNNPGGS SSWEKLQISP DTLSSIEYGN FLVEIYEHAN NYKATTTASE KKYFYSPLAL
81 LDHKSAFVTY NKFTKQTEMR FRIEMWNDKV QNEVVKHLNE MQMDGHEIKS NKVRVIPLEK VILASKRPTV DYSLSPEWTN
161 YDKSKILWLS LSCNDQKICD ELANEMRSVP KHLDHFKLLY SLSSQTSQTK HTTISIDSVT SGQMVSTLLQ KFGDKKEIFL
241 TADDEKKMLA ETVTNIRMDT FDDYEVLSPD TESQILSILK DLLVTSRTTI KEQRDKMWDS VFWNDDNYRP DKTTKTLNEI
321 INKLDTETQK KLADMFKTRE NKERIQHNFD SNNWADVDRI SSVISGKLSN DSDSSRRDEI LKEDVEKLIQ ESRNQVEWDG
401 ERFVPKPMQL SR**INLAK**FRD SQSFQDRNLR VRYTSAELSA PIKFVEHAEL TVTGEWNNLK DELKATTELL NITVNNLVKI
481 NAELSNVKSD LTNKLEGTKK ELEKTKINLE ETRANLSTQL NETKQELLKT RPDFLKTFDD LSTKLNGTKR ELGKTKIELE
561 ETKTSVKNLS TQLNGTKKEL GKTKIDLEET RINVKNLSTQ LNETKQDLLK TRTDLTKKED DLSTKLKGTK KELGETKIDL
641 EETRANVKNL STQLNETKQD LLKTRSDLTN KDDDLSTKMK EHELKVAEEI LSTVKEIFYV LGITTNLSTT RAVVGQMPTS
721 CADLERNGQK VNGFFLVKGS KKMETVYCNF YPNQTEKQKW IGYADVKSAP VHFYVQRNSS FDAKSTPLPF DLVRVNEGNA
801 MNLTSGIFTA PQPGTYFFSF AAVVRLSSSS SFVDFYSHLH LNGNPIGSSK VYEHKSPGDQ WNPLTLQSTL KLKKGDQLWV
881 QIWYRDDSSS TLYDGGNRYT HFTGLLLEEE IWATL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.INLAK.F	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	413	417	
total 1 peptides												

tr|A0A2A3E979|A0A2A3E979_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MVRSSDKDRH HRRRSRSRSR SRSATPEKKR RRSRSRDRDR ERDKGRHRER RSRSRDRDRD RRDRSERDRD RDRKRGDSKE
  81  KRLTGSKSSR SGKDRSNRSR SRERKEKEKG DSDELPFDHT KLDKEEEQKR LELEMQKRRE RIERWRAERK KKELEATKKD
 161  GKASILANLQ LPMKKWSLED DSDEETPVVQ NSNKEVKEDG ETKEEVEEVK EEAKDDEEEV DPLDAFMAEV QEEVRKVNKL
 241  DNKGGKNANN GTGTGGTQSG GVVIVTGVAK KKVQKQKGEL IEQNQDGLEY SSEEEGENLH ETAAGIANKQ KRELAKVDHA
 321  TTEYQPFRKS FYVEVPEIAR MTPEEVEAYK EELEGIRVKG KGCPKPIKSW AQCGVTKKEL EVLKKLGYEK PTPIQCQAIP
 401  AIMSGRDLIG IAKTGSGKTL AFLLPMFRHI LDQPPLADGD GPIALIMTPT RELCMQIGRD SKKFTKSLGL SHVCVYGGTG
 481  ISEQIAELKR GAEIIVCTPG RMIDMLAANS GRVTNLRRVT YVVLDEADRM FDMGFEPQVM RIMENVRPDR QTVLFSATFP
 561  RQMEALARRI LTRPVEVQVG GRSIVCKDVE QHVVVLEEDQ KFYKLLEILG HYQDKGSAII FVDKQENADT LLKDLMKASY
 641  SCMSLHGGID QCDRDSTILD FKAGRTKLLV ATSVAARGLD VKHLILVVNY DCPNHYEDYV HRCGRTGRAG NKGYAYTFIT
 721  SEQERYAGDI LRAHELAGVP VPEPLRQLWE GYKARQAADG KKVHTGGGFS GKGFKFDESE AALANEKKKF QKAALGLQDS
 801  DDEDIENDID QQIESMLAPK RTVREIARPS ATNIAVPGQP VPSATDKLEL ARRLASKINI AKNLGAEAKG ATQQAAEAIL

 881  KGAGPTNLIT AKTVAEQLAA KLNTKLNYQP REEDLVESDV EAGEQTFRKY EEELEINDFP QQARWRVTSK EALAQISEYS
 961  EAGLTVRGTY IAPGKAPPEG ERKLYLAIES TSELAVSKAK AEVSRLIKEE LIKLQASGAH TASRGRYKII VSAENICIM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.INIAK.N	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	858	862	
total 1 peptides												

tr|A0A182SQ67|A0A182SQ67_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  IFDQFDEEVF HRCRFYVDSL PSQQIVAVYR IRLLWIAYIL DCSRQQFDEA LDHLYLLSEI LDTSGEANIE LNLPNQCANT
  81  SISKSSVREL ISETERKLRI TRVKRHYDSG EHEPVVTILK DTLQYYTSVG NPDESILSLT IQTQMLLESL WSMAEMEQFM
 161  TAPVQHDSRK SRMWANNINF TLLYIESIIK QEGVAIIDVL GKNLSRLIQS LHRMLTHQLD PSGEKNYTAQ LCLIEFWRAW
 241  IVLYYVLERQ DDMDSSVKLN RPPALADQCG ALKLEPERLC NSIMMCFVAH ELLGKKNWCS KGDSGLLFHT LDVVVPKIRS
 321  PMLEPFRETL NEYLEQVTYC LYGYPQKRPR LRHIQDHCAV QVSLTWERAI QLFDLYRPDS LPEFNSYKLE SISTDMEALL
 401  QRIILLIPRE INIAKLSRPI SEFIDGKGNT LPEAANILQS EVKPIFYLLA DFYFKSRDFT RAIRYYVMDL ALEPSRFDSW

 481  AGISLSKASK VETKLNSTET IPLQEFLDET DNGMKCFDQC LQLNEEDSQL WIEYGSFAYN IHSFCSRSLK LLSDTLSMES
 561  FALVETHKER CLDIAFTCFN KVSLSKLCYN NATGDAIDEQ QQQVQSTEEN GQNHEDEIWL HHYMLGKIAE KKKEHPAVYL
 641  THYLKSAKYL YECNATYPIK INHSSPSQLA IEALEIFYRI NAAIIKYVEQ HSPINKKTSR LFLRTLKELS TSPFAVNRAK
 721  INENMLKRKI SPNAGGNGNN SGNAGGTTDM DGAVGSPKAA KPGEQTASEA GTAGSAPAET EPAGEENTVR EQPESVAAAA
 801  VNSPKQPQES KPGESDVQVV EDVDAVPSPV SGASQMVAGR ALEHLRVEEI KQLGDLQHPS IRRGSQESAI TSTTTTTTTT
 881  TSTSSSSSDS SDSDSDTSSD SDSDSTSTDD ELINQQPINP TQRDTIFKLC IKNLEECITR FPEHYKSMYR LIHHFMHAPG
 961  STKSFESARQ LLLGTYRTTL GNQIPGLFTE RKTTNFFNGL WRIPASDIDR PGNFASHISK CVIVLMETLK EFSEYDVLLD
1041  LAMQLQRTPE PDK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.INIAK.L	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	411	415	
total 1 peptides												

tr|A0A084VFC9|A0A084VFC9_ANOSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGAGMTSPGV SIHARSIGTA QCLSPPTSVS PQLSVTWAFP TVGHSRLDLS DDDDEEGEVL SSEQQHPAAA GSVPRRPFHA
81 PASDGSTSVL PEAAGSNPSG TLAKPNDPKK RTVKVLPANR TGNVMKSPDV VGAGGSFFGG DPAAALVAGA RCETDDDEDY
161 SASLNAIIQR KASVKKKRAG YKGHRRASSP ISQMMGLPDG VGGGGGGGRR RSSVYTTSSG ETGITLPGDE QSLGGGREEA
241 TGRQDKLFDT IRLHKEVLQT VKLQPISMKR KLKLVQQAKS YITRHEGALQ EHFTSRTARS LVAQFNIFLT TKWQQLLREL
321 ANLVTYLIPW ESRIKEIESH FGSVVASYFT FLRWLFWVNV VISVMLVVFI MVPEEIYVDP EKAKCDIRKS MSQQERALTR
401 NFSTIWEFEG HLKYSPLFYG YYSTFSGAIA WGYNLPLAYF FTGLVVYIYS FVATLKKMAE NSRMSKLSSK DDEYVFSWKL
481 FTGWDYMIGH METAQNRMAS IILGFKEALL EEAEKKKDTR NWKIILLRIL VNFLILGLLV VSAYKVIQVV RNSMDFKDSD
561 SWWRRNETTI VMSLISFFFP MIFEALGIME YYHPRKQLRI QLARIMVLNM LNLYSLIFAL FDKIAHMTRE LRRMKPLNFT
641 SSASQCFVPQ EGSRWNVSSF LTDGSTQTLD AQDNKYRNAD IRTLCWETMF GQELAKLTVM DLIVTIVSTL ILDFCRALFV
721 RFMNGCWCWD LEKKFPKYGD FKIAENILHL VNNQGMVWMG MFFSPGLAV**L NIAK**LVIILY LRSWTVLTCN VPHEVVFRAS

801 RSNNFYFALL LTMLFLCVLP VSYAIVFLEP SWHCGPFSNS NRIYHLLTNA TERIVPEMVT KYIVSPAAVI PLLVLLILII
881 YYLLSLTGSL REANQDLKLQ LRKERTEERR KMFKIATSTQ QQTPGTDMAG INGLSSSWHK VLDSTQLRLQ STTDNATDSE
961 NSTTKRKELL QRMMKKALQK EHVEGGESSV GPTQTLSAAP PVLVSPPLMG TVTVNEKQRA VGKSNRAGQN TEDVFRFDRR
1041 AVEQMGRGSK ASEATDDDNG RKKFERTRPS TAERFRLAAQ AERRRIHNLR MAGKAAEQTT ADWIEQIPVI TISKTSSDEC
1121 IIESDLDDPH DRKEANVTEA VLSKTTRQS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.LNIAK.L	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	770	774	
total 1 peptides												

tr|A0A023EWX6|A0A023EWX6_TRIIF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EELTREKLIQ KYKTLMALTN KIKIARNEAL SDNESLKNEI KAANEKIKIL SQQNVTAEEM LAALTEQKLK MAMEIDDMKK
81 EKQNYYKTVK EDASKQTESY QIENERLKKE NNDLLLKLNE KEKNELQLQN DVKKLNENNE NVIILCNNIR KEKIDLQSKL
161 EEMEVTLNKV QDEKKSVFEL LSKQFNKHFE NINCLKQFLE QELKSFCNYQ CAEEINVLLD QNLSLKNNVV ELNDSINTFL
241 KERESSETNM FNLTNKLEKL KSELEIVTSD RDQIMNNLES VRLETKHLIE NSEKLVDELE ILKAEKIQKE HEMNTLLNSK
321 NDEIELLHSR LLDLQQFSEE LKANLLSYSE YVNTLERKQC DCFKENLQYS IIRESKKGEA INEFTNEFLT KIDNLSKIKN
401 TFSTISESVQ NISLKLLQNE VHASELELIK AINKLDSIIT NEEDYKCPNI KCSCFLLKNV GTKLNESMTN YEKILTDMKH
481 DLELLQEQPT IISNKEKFNE KVKEEFKLNI IRNKKKHSEY QISQDVHMDN ILSKMEEYEV LNDLLEKKII ICKEELGFAL
561 VQLHNAEELG KLMQHEIQSL QSHLYEAIAE RERLNDMVNE KVQVIIKLDE ELSVEQSKAH KLISDLENSQ IELNAARTAL
641 DTEQTKSTDL FSEMKCSQNE HPEAKQELNL EQSTSNQSVN NIENELVLSR QVLDAELLKS KKLITDLQSS QIEFNEAKYA
721 LDAEKTKSKK LIDDLERSQS ELNIVKYALD TEQSKTNQLI GELKNAHLEI NAAKHALQIE QLKSIKLLDD LSNSQSNLGE
801 VQHALDAELS NSSRLINDQE NFQSELNNVK QILDLEQSKS QKLIDDLKHS HCE**LNIAK**DA LLAEQTESNI LKNKLKKSEC

881 ELNNTRQALQ LTESRCNTLN TELKKSHAEL NKVKNLLEEK CNSINDLKKE STSAVSKMSE LSEANLKLKQ ENDSLKLNIN
961 ETVKQIEITK LREAQDKNEI MDLKLSNEQL NIKLIKLEET NNKLNQKLPS YKMNVYDLRK EILTLKEYCK NLHEDHYCSL
1041 QNTHQEIVRS MNIHVAVWLA RENLLKENLC DHLRPEKEVQ FRSDTRKNML SQEIISKDKN ADVECHRPDK KHLVDNACQV
1121 NMQQNENNAI LIQEMRKESD SRKEEISKSG ELELLSEHNS AKIQSLETNL ALSKQELATT QLEINQLREE FYSYRLRAQA
1201 LLSKQKGELE SQREKEAKEQ IEKLNNELES IRGKMEVILT E

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LNIAK.D	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	854	858	
total 1 peptides												

tr|A0A2A3EGN6|A0A2A3EGN6_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSLIKKQLL KHLSRFTKNL SADKINLSTF KGEGELTNLE LDEIVLTDLL ELPSWLRLTN AWCNKVSFRI QWTKLRSVPI

81 FLSLDEVHIE VETCEDLRDL SSSQGLSSYT GPAKYSFIHK VIDGITVTVN TVSVTFKSPA FIASVQMNRI IVESKSATWQ

161 RCDLRTTRVK DPDRGQLLIF KELEWQTVRI EAQSTKDKNL TPLRLLTNQA RCRITIKKRI SDCFVMGSRL ILILDDLLWV

241 LTDSQLKAAL HFIDSLGGLI EKATILERKT KAARKLEVLP EYQAQISQQS RTKSQYNTAI SKIFTRYDVV ETSYHFLCQR

321 IDLHLCDDAG NGRSSHPDLK DGGALQISLV SFQIDYYPYH LAMSDRKHWA KYKENATPHS QWLQQSLSSF RSQFMDLIDS

401 GRTQHSPLIR SQGNVTVNNT KGIGENLEKN NQSQNINATT HEQKKSQHPS GNPVKNYILE QLAKLMTTCI IIRIDDFTLY

481 KVTTTSRNPI PKEFVTGDRD KFCLPEDVTI VHAEFTYYYY PGDITFPLPP PKFYVQLNPI QVNFDVSSCL WFNSFALNLY

561 YSLMNKDKQT TYTSTTLMYF DVKIEAILPR IVFESPQDYP NQKDRPKSLH IQTSRASITN VRCTERSSRA DLAQCVNAFQ

641 MGQMFFSTEF PNRSNDFHVL TDKFLAHCAG TDNIRYPPPN FSSNSVNELI RQLHRELLWT EAKDVWCCNL EPVWGDFLGA

721 RAVGQNRPVP FLDAFPLTLW CYMTMNSLDK DSSEKKSTGD IHGLAYISNL VSVQINHYQY LFLLRLSEVL SEMATYLTID

801 SNKILKVDSG SSLVIGALIP QVEVTFVMPS HTPGKENSGG DLESVMPDSS SIADDIAGSS IPWQSTERIE SNAKKININN

881 DIITPQSDVS SMLSMDFMHS TNPTQTVVTF KHNDTNKHDQ QTKNIMHNRQ SIGVEEEKVL PPLRYALDTT HKHNKGDSSS

961 NTPFIPNNFN VGLSSMKKGL SNLMTSIDSA LKASPEDGSS DTVSIRSDVS SDSENYVLVS LQDQEKLDTM FSVDNSIRVA

1041 AVEEASEVVE ETPDTQSEKS MDSVCKRKDI VSMITFKLSK VEFIQQSFGY ASSIKIQISN IGNDECSSIP WDEFQTKFSA

1121 RSRGWVELPS DSNCGSCIKL RLDHDLKCKS DSWKLSQASR TINNKNLYLS RNENQNNITE QDVDVCNIDV HNKQSVLDLF

1201 EDKLEVIITN ISMALSMSSV SGLTDLTEDE IIPRPIPLQV YLESISLRLN EDRPPNNITS PGPIPID**LNI AK**LKIIRDAN

1281 GVFHIEPVVN LLSRSNSLVT LTSNDTQIAQ NINHEMELNV LRQSSKQLKL DNEQLRSRLN ALEKISEENA KLIRIKEESN

1361 VIKSHLSAAQ EDIQLLLKEK RALQETITQL ENRIIGSGLG SGTRASWSSK R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.LNIAK.L	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	1268	1272	
total 1 peptides												

tr|T1KS98|T1KS98_TETUR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGDFTFFCAS ILFNLILLVH THGHHGHHGH SHHTKELISS STLPPRPAFT SPTSPPSIPD HLDPKVFTFT QNNSFLLINS

81 TDCWPPHITR SLNFKFRTHR SNSLLLFHSV NSAPPGYPLY EFHMILNRGA VEIVHEFGLA LDKFTIGKGF NDDRWHQVNL

161 TIIASEAKLK IIIDGQIGSI FVLRSFLSLH PNGYQPYGQY NPKQPSIYGN IPSSLYFGGL DPNLRYVHKH HHSPRFIGCL

241 GNIQFTHSSI LFVDVPLITS VGLKTGCINL CRSSIQCSLG SSCVNHYTHS TCDCFGTEFE DTWCSVSPVT ALTLRGTSFI

321 TYTAFNWTER TETLMNRISL HFRTRFDDSM LLYAYGLYPD FNHVFLDLIE GKLRFEIDFG EGPLRVTTTG SKLSDGAWHN

401 VTVIHAKRDV HIIVDGITHR LHVNGQRFYL HLEPYIYVAG LPKSVEVRSL YPKSLVRSKF VGCLKSVYFN REDIFLGLRK

481 NQPNIRFTGL FGPEFGCSPV PSLPITFQTS RSYLNVTKTF SNVLDLFMEF KTPQRDVILS SGRFRFVEEP TSHLLWILHL

561 KNSIPHFSII DYDNDNSEIQ PISKTWSSGK PVRFLAGQWQ MIGLYGQSSN LTIEINNEYT VKYQFEGEMS FNSYIIVGAL

641 NATFNNSNAY GYGIMGCIRN LGVDHETVDS RILLNNRALH SGRVALDQCS YINPCDYPGA CEHGGKCTVN KEGDADCDCT

721 DTGYAGKTCH FALYKRTCEE YYLLGHRKNG TYMIDIDRNG PLPPARVECT MSFKRTETTV NHNLPVEYIV RKKDFPSYYI

801 DIEYREFNKE MLKALIGHTK GCTQEIKYGC RKAP**LNLAK**E AWMISASDWR LDSVGSNISG RCPCSTAMNC QDPQRYCNCD

881 FLDERENEDS GVIVEPAKLA ITRAFFLASP NLTEASEGRF TLSPLKCIDL STQEHIVTFK TRQSYLELDG WVSGDLAFSF

961 RTTVSYGVIL YQAPLFPHHG RFLVTLISPF EILFEYSVNG VPRQSKLISR SKLNNGQWQQ VWVDYETRHM RFTVNLDSLM

1041 IDLDRNEMFD LFEGPLYIGG APESKLKDKS SLGFIGCFRG LLIAERIIPL SIPERATDIE SRCQESCQPN PCQNNGHCIE

1121 MWGNYECICA NPFAHSGRNC QDDANLNGLT ISSDNAFVHM MVHGNETHPV LNKRISLSFR TYEDSGLVFY ANDHLNNFIQ

1201 IHLFNLSVIF TTNNYRTIVS GRVRVGPELI SGNLIQVSIE RRRNSTVLSV YTGCERNCSL PISATINSSL GLLQEYYQKP

1281 WQYGGSMELV RPIRSFIALP PHTQFFIGGV DPIVDHSLPT FIGCISGLLI NHTLFDLEQA IEESSEKREE KHVSINGNVT

1361 GGCQRVCDKK PCENGGKCRE NMRIGSIEGV KCQCEQTSYQ GHFCEQDIGV RFDGSSVLTY NITTIDVEPK NGICLEFAFS

1441 AEPEMIGRCL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.LNLAK.E	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	835	839	
total 1 peptides												

tr|A0A0A7AS86|A0A0A7AS86_TIGJA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MSSFEEFCGG PIWDVNVTWN TKDPDFTTCF HQTILLYIPT GFLVLFSPLE VYFRIYRGSN KPVPWTLLNI AKLILNGILV

  81 ILPVIDLGYA INEDARTVHV VAAIVKIVTY VCALCLAVAS QRRGVVTSGL LVIFWFLAAI GGAITFASVL STPYLSGDHF
 161 MLPFLSYTLQ FPLILVLFFL NCWADAPSKY KKLEEDVPNL TPEKHASFFS RAIFAWFDPF AWKGWRRTLE YTDLWDLKKS
 241 ERCSGIVPEW DRQWEKNVIK TIQNSKAPSQ VSITSTLMKS FGPAYAISAL YQLGTSVLQF ASPQIVNLII DFVESDQPVW
 321 KGYLYTGLIC LSTLFNTILN NQCFYQEYTV GLRIKTALIS AIYRKSVKLS NSGRKVMTVG ETTNLMSIDT QKFMDLTLYL
 401 NMIWASPLQI ALAMYFLWDI LGPSSLAGLA VMVLMIPLNA VVAQQMKKYQ HAQMKDKDRR TRLMDEILNG IKVLKLYAWE
 481 PSFEKHVVDI RAREISALKK SAYLNSFTTF LWTCAPVLVA LASFATYVLS DSANILDANT AFVSLTLFNL LRVPLNMLPM
 561 LLVFLVQCEV SLTRINTFMN SDELRVNAVD RNPNAKGAIV VKKATFAWDK DAEPVLRDIN LTVKEGELVA VVGTVGAGKS
 641 SLLSAFLGEM ERLGGSIKTN GKVAYVPQQA WMKNASLKDN ILFSKSYKSN LYDRVLNSCA LVTDLEMLPG GDETEIGEKG
 721 INLSGGQKQR VSIARAVYSN RDLYLLDDPL SAVDSHVGKH IFENVIGPHG LLKKKTRVLV THGVSFLPQV DNILVMKDGR
 801 ISERGTYEEL LNKQGDFASF LIQYLTEEGD KEKGLEEESE LEDLKQELEK TLGKEAVQRQ LMASKSVLTS LTDLISESSE
 881 KGQHFNQKGK KRSSLMSTSR IHPFSSNSNI PPSERGLDEI KVGQNLIEKE KAEIGGVKWS IYRYYAKSIG TKWSLVTILF
 961 YVIYQGFQLG ANVWLSEWST DPRATTDTSV RDMYLGVYGV LGLLQSLAIM TGTCFVMVGT LNAAAKLHST MLHRILRSPM
1041 SFFDTTPLGR ILNRFSKDID IIDVTIPMNI RMLLNQSFNV LGTLVVICFA NPIFIAVVIP IILMYYFLQK FYVTTARQVK
1121 RMESITRSPI YSHFGETISG APTIRAYEMV QDFITENEKK IDYNQKCYYP TYVSSRWLSV RLELIGNLVI LFASLFAVLF
1201 RDTMDPGKVG LSLSYALNIT GPMNMLVRMT SEVETNMVSV ERISEYQETP QEAPLEIPEQ DPPPEWPQYG VVKFDNYQTR
1281 YREGLDLVLK GISVQIESGE KIGIVGRTGA GKSSLTLALF RIIESAGGSI YIDNENIGLL GLSKLRSRLT IIPQDPVLFS
1361 GSMRLNLDPF EQYSDREIWR ALSHAHLKSY VSNLPGGLSF DVNEGGENLS VGQRQLVCLA RALLRKTKVL VLDEATAAVD
1441 LETDDLIQTT IRAEFSDCTV LTIAHRLNTI MDSSKVLVLD AGQIKEFDTP ENLMAQRDSI FYGMANDAGL INNLD
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.LNIAK.L	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	68	72	
total 1 peptides												

tr|E0VC08|E0VC08_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTISTRGVNE PTECNDQVTN TEVVEEIIED EPISEIGEPD FPHDKLAELD TKISSPRWVV PVLPDQELEC LLQASIDLCK
81 KGIDTRSEAC QRFFREGLTI SFTKILTDDA VNSWKPNIQL YIYQNCQRLV ELCVIKLNQD WFPLLDLLAM LFNPNCKFHV
161 FNNSRPPESI PPGMHISDEE VYCRPVPDSR LPRGWLVDLI NKFGNLGGFK ILLERFQTGE NLSVAVMYSL IRPFGLCYEL
241 LTVNTIVKYF MPVIEIILQV LDGLTDEELK KEAKNELKND SISCIIKAAK CLVSRVPGKE ETSKDLEIFR LRMILRLLQI
321 SSFNGKMNAL NEVNKVIASV AYYPHRHTPV EEDEWLTPER MAKWIKDNQV LEIVLRDSLH QPQYVEKLEK ILRFIIKERC
401 LTLSDLDAIW AAQAGKHEAI VKNVHDLLAK LAWDFSPEQL DHLFECFQSS WTNANKKQRE KLLELIRHLA EDDKDGVMAH
481 KVLTLFWNLA HSDDVPTEIM DQALAAHVKI LDYSCSQKKD AQKTSWLAKC VEELKSGDKW VLPALKQIRE ICCLYEQSPN
561 LNHSQRSQHI YYRQQIIDRL QNNHSLVILV SDSLENYIEK VKKLVSHHPE LDSQNFCIDG RYCHELQVQE RLNFLRFLLK
641 DGRLWLCDSQ AKQIWKCLAE DGVFPSDREA CFKWFSKLMG EEPDLDPTKN REFFEDNILQ LDPTLLTESG MKCFERFFKT
721 VNKKEGKLIQ KHRSIVMEDP DLIGMDYLWR VITNSGEEIA NRAIEIMREV CTNLGSQLTS NIYEFHETYI AECLDRLRTH
801 YDNVTLLMKE DIMKNRLKDE AVRMCRVMKV LHEYISECDN TFVNERKILP LHRAYRGKCI ILTIRFTHPQ RALDDMDIYT
881 HTNETLASFR RSILRRIKAG TSVKVELVVN GDSREPIILA DDRKLLSQLP IRDKMIITAK LCQTNINAAS SPETSSDSST
961 SSPQHPYDGP NLEAENVLPG VLMSRKSIYA KFLFQLSDLG CELHYPPLRD GARNLLQLVP PDQSTVEKLK QLFEIYPNSE
1041 HSQDNNITVE NIFFDNSCTK VLYNVEVMYS LLMPASDPMS AEAFEFQYNF VKSGHAPIVL EMLTKNNFLP NADVATKRSA
1121 YVTILKMCKL LLTVIGHVLG RVPFDDSSQP HDQGGSDGNP INSHSPTSHA SPSGLLRTLN SVFNQGVELM IRNVAKKLAA
1201 YIDEQPQIIM ESKAGQMFLS ARSWELPDTN TVRAVMRLAW AASTGSLSCL HSPHEMHNSH LLGKIPDPDD VVLCREALQV
1281 LTVSLVLNYK VMDNFIKDPL WHTFIIDLLL LAKNRVVRSS ASDQFLLILY DSAQQPLLFC ISLLFSQLNT TVIANCKNSS
1361 EYFLLLCRLI NYALMTDCPV PNAEILLDNE IAWLKKIKEN VKETGETQVE EAVLEGH**LNI AK**ELMGFLSP EKKYLLGSSE

1441 KKGLCFIKEI LEDFIFPASK LMLQFLKTGD LVCENAIPVC NTPCTENAAF DLLVALCMGC VPNMKLLVHM LTEMFYSERE
1521 KPLTEWDYMP PIGPRPPKGF CGLKNAGATC YMNSVLQQLY MVESIRVGLL AAEGAATDLN EDFSGEERLE TENTDVEHID
1601 GDSNDDKGGV DESRKEYNIG ILKQVQAIFG HLAYSELQYY VPRGLWKHFK LQGKPVNLRE QQDAVEFYLR LVESLDEALK
1681 ALGQEQIMSK VLVGSFSDQK ICKGCPHRYF KEELFSVINV DIRNHSSLLD SLEQYVKGEL LEGADAYHCD KCNKKVVTVK
1761 RPCIKKLPPV LAFQLKRFDY DYERECAIKF NDYFEFPRDL DMDPYTVSGL AKLEGELIDC DYDELSKEMC TKYQLTGIVV
1841 HSGQASGGHY YSYILHRQSD GTSKWYKFDD GDVSECRMEE DEEMKSQCFG GDYTGEVFDH IMKRLSYRKQ KRWWNAYMLY
1921 YTRLDVRSSN TSFCEYNNNN INVYLNYNYI IYLLIVILLF LADLKKNTMK MPLVIEQGVR RQNIVFMHNR NQFSAEYFQF
2001 IKKIVSCNSS LLRLHNDKLT LDSEELSMLS VQLASRFLFH TGFHTKKSLR GAAYDWYEVL SQHLRHSASV RLWFAKEIIF
2081 QHPYRLSEYL LNSPSTEVRA AFMKIILFLA HFSLHDGPCD SLIYNGKSKN IDSNFSLSDH LLHALILLLD KDIADHGKHS
2161 VHYFTLFQMY AQLGLEEKAQ LLRLNVAKIF INVALEEGPI PAIKSQYFDC TKLHQVVSML VRCCDLSTST QNSNASVQPL
2241 PNPYCDPQCS SSYLMPIQPD VAELLFGKVG YAKKLIDNPS PSEDIVKLIQ FCTWENPIFS KNLLSETLRQ IACTIYQDLK
2321 HYLDWLLHLL LIEDSWQTHR IHNALQGMAD SDAKEGLFEI VIKSKTHYQK KAYQCIKYMT TLFSKCRAAH VLLTSTEEIR
2401 RKWLHCNECF PFPANVQYSC DNWLLSTKTN DSANGYFPER SNSARKLLVH SVELCPQDEP EVEEVSEEGE GLQSLEWKGL
2481 VVSKYFGNQS KDRRKNRVQI RKMDETSEDG IASIVEMQQR SFKPIRRENN QRRSDPNAAD SGDEEFAWFC GMNKRMSSPS
2561 DLPQSLSRHS LTDVALVQET QVS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.LNIAK.E	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	1418	1422	
total 1 peptides												

tr|A0A2A3E5A8|A0A2A3E5A8_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MKIQWLSNFI LAGTIRFLLM NSEYQKIISD RVEVSTALNS WKRVTEGVYL YNFGIDPYTG DLFHETPIGL YVFNFIQQHL
  81 PQSILFCLFV FTDLLTALFL GLTAKQYATE LVFKKKEKEK LWHTTTVFTN LLYSVALISM IKSSIFWTCL SISLLTLQGF
 161 YPISLIVPAI IYIARSDSIK QKRNILNFII VFISILIGLF YISYYIMGNW SFIWNTFGFI LTVPDLRPNI GLYWYFFTEV
 241 FEHFRWLFIA SFQINVSLLY IVPLALRLRH DPMLLAFSYL AVIAIFKSYP CIGDVGFYMS LLPLWKHLFQ YTQQGFIVGC
 321 FMLFCTIFAP TVWYQWIYSR SANANFYFGV TLAFAIAQIF LVTDILFASV KHEFAVRHGI NKDINGILLE RVFFRLGSAD
 401 TDEQLQASVC KFLPPVLLKL SSAQEGVRKK VMELLIHINK RIKSRPQVQL PVETLLLQYQ DPAASSFVIN FTIIYIKLGY
 481 PRMEMQKQAE LIPSILNAIE GKPLSHQDSL LFIIMPALGH VNIPVDSDKR AFFLGLHDKP YVSKQLLNFM LDVLLLPYGS
 561 VGQMQNQQSD QAIDWSCFRV PPGLSEYAFK RVIGENPPTA EQLEQTKLGI VKFLAGGFFP DSDILIHLIV AAADTRFSVA
 641 NLADLELKKI VNTLDWSSMQ LAAPLYSLFL GTDTLGIQKE IKPEMKRLPA GIRIRLKLLH YLCRVTKAGF IIPPCIQVVF
 721 HSLQEGDGKT TNAKLKSMAL QFTLNIVQQC SLAPLSRIAG IILNGMIKLI FEGEDIHKMM AYTVIGQLGQ RIPSVIDKNS
 801 NLLCHLFDTL VSTEGDLRRT VRDTLISITS AFILNKDDEA NISLMNGLLS TYIESSESNV RHVYITMHYA ATVFPSDDVP
 881 SRYLLLLASG DDKHEIRTEA MKVLYGTMHK NECDKQNCNH ISLPDFKKLV TYIYSKMQAR MSIGNEKMNI ENKILPYNIT
 961 VFTEIITYLR ICLARNAHVT KYNELLQHPC ESTPLITRYL KNLYEDKIEI LHHYLDIILI FSHASADQTS LQALLEMIGS
1041 IPQFITRIYE NNLSWLRTLL ISTKPDIRQL AAKIYGLITA QLSNNEFEAQ ISEIMGIIDK NNLEAQHGSL LTLTYMMERR
1121 LVFKRSNINN DCFNWDLYIN VVRMICNFLH NNTILLLDAA IQSIGILGKT CELPLSNEGK EEPNKKEIVE ILFSVLNNVK
1201 LNTKIKEKAA LSLGYLCVGE NFPHTSYIVN KIITTVKETK DIEIHLIMGE TLVCCVQAEA SPEKRDAWTI LPSEHTVPYS
1281 DTSTELLIRT LDELLHIYKD PHPNLRQAVC VWLLALLKYN IQRECIKEKF SSLHYAFMDF LSDDSDIVQD MAAKGLSLIH
1361 INSNKEQKEF FVSNILDQFT QGRKTVQQVT LDTKLFEEGQ LGKSPTSGNL STYREICSLA TELQKPDLVY YFMHLANHNA
1441 VWTSKKGAAF GFAAIAEIAN EELNKYLPNI IPRLYRYQFD PTPKIQHSMS SIWRAIVPST SKAIEQYHKE ILNDITDNLT
1521 NYEWRVRISC CNALADLLRV NVRLNLAKCA PELLKILFRV MDDIHEGTRL AATNTTKALS KVCVRYCDSS YGKEGEEVLQ

1601 AILPVLLDIG VVNVVSSVRI VSLQTISQLV SRAGVLLKPS LVILIPALLS TIGESENPNL SYLSNVCGTM SEARDAIDNI
1681 RASAAKEHYA TETMTKCIQY IDADILKELM PKIIELIKSS IGFGTKITCL HFIILLSTHF KQELQPYSGK LLNVLMNGLL
1761 DRNSVVRKNN AIAIGHIVGS AKESSLEKLF KMLNTWYMER DDSTKLAIGQ TLQAINNYNQ EILRNFSNIV IPLTFFAMHE
1841 QKAQENENVI DLWTELWNEI TPGTETGIRQ NIESITNILR TSLESSSWNT KAQAANAIHT LAEKLGSNID ATIRDILLKV
1921 LMDGLRGRTW DGKDRLLNAL ATLTCNSKMA LKENSEMSMN IVQILYRESK KEALEYRRHA LYAFGTILHE LNIDKFKEVY
2001 EIVQEIWTML ARKDADESLV SEEKIKRNDV IKLYETVYEI LGKAWPLYKE TQDKYCVEFI THYDKMLPIQ STTIQISMLS
2081 SLNLFVDKLA LLKINISDLS VEDKTMLDLI CDIFNKILKY SMGISYTRIR KEALNIALSL GRKLRYTKNN EKFDKMILII
2161 QETLPELTKD NEPEIRTRII DIKEMLKI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LNLAK.C	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	1544	1548	
total 1 peptides												

tr|T1K7Q5|T1K7Q5_TETUR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MAEDPDPTQY LFISLEQKRK DQTKPYDGKK MVWVPDEKEC FILGNISSTK GDIVTVDCGK GDERQVKKDL LQQVNPPKFE
  81 KCEDMSNLTY LNDASVLHNL KERYTAQLIY TYSGLFCVAI NPYKRFPIYT GRVIKMYQGK RRSEMPPHLF AICDGAYTDM
 161 LTNRENQSML ITGESGAGKT ENTKKVIAYF AQVGASSKKE EAKDKKKGSL EDQIVQTNPV LEAYGNAKTV RNDNSSRFGK
 241 FIRIHFGPMG KLAGGDIETY LLEKARVISQ QAAERSYHIF YQIISGSVAG VSEMCLLSND VCDYHFVSQG KTTIPGMDDG
 321 AEFALTDEAF DILGFSLEEK HNIYKITAAV MHLGELKFKQ RPREEQAEAD GTEEGERVAH LLGLNAADLY KNLCKPRIKV
 401 GNEFVNQGKS KEQVSYSIGA LAKAIFDRLF KWMVKKINET LDTKQKRQYF IGVLDIAGFE IFEYNSFEQF CINFTNEKLQ
 481 QFFNHHMFVL EQEEYKREGI EWEWVDFGMD LQACIDLIEK FNGFEQICIN FTNEKLQQFF NHHMFVLEQE EYKREGIDWE
 561 FIDFGMDLQA CIELIEKPMG ILSILEEESM FPKASDKTFL DKLNTNHLGK SPNFQKPKPP KPGQSEAHFA LVHYAGTVPY
 641 NITGWLEKNK DPLNDCVVDQ FKHSSNNLLV EIFADHPGLG ADDSTASKGA GGKGGGGRKK GSGFQTVSGL YRHKRKINFP
 721 KEEITDFLRY LQEQLNKLMT TLRSTQPHFI RCIIPNETKT PGQKRFTEQL NKLMTTLKST HPHFIRCIIP NELKKPGFID
 801 SHLVMHQLTC NGVLEGIRIC RKGFPNRMGY PDFKQRYTIL APTAVPKGFV DAKQVAAKVT EAIQLEPENF RLGHTKIFFR
 881 AGILGRLEEM RDERLSKIVT WLQAWCRWWF VKKTFKRLQE QRIALLVIQR NLRKFLTLRN WLWWKLYSKV KPLLTMAKVE
 961 DEIKALEEKL KKETEEKEKE AKLRKELEVQ NVKLLQEKND LFLQLEAERS GAGDVEERLQ KTMSQKHDLE QQLQELQDRL
1041 SHEEDAHTQL SGSKKKLEQD ISHLKKEIED LELSLQKAEQ DKATKDHQIR NLNDEIAHQD EMINKLNKEK KHLQESVQKT
1121 SEDLQGAEDK INHLNKVKAK LEQTLDELED NLEREKKLRA DVEKNKRKIE SDLKLAQEAV ADLEKNKKEL EGAIQRKEKE
1201 MASLSAKLED EQSLVAKLQK QIKEIQSRIE ELEEELEAER QARAKAEKQR ADLAREIEEL SERLEEAGGA TTSQIELNKR
1281 REAELAKLRR DLEESNLQHE QAMAALRKKH NDAVAELSEQ LDNVVKIKAK LEKERATLAA ENQDLQAVVD NSTKNQANLE
1361 KQNKQLEMQL GELQHKIDEQ NRTLGDFDAS KKKLAVENGE LQRQLEEAES QVNQLGKLKA SLQSQLEEAK RTADEESRER
1441 AAIMGKYRNL EHDLDGLREQ LEEEAEGKAD LQRQLSKANA EITAWRTKFE SEGLARLEEL EESKKKLQIK LQESEEHIEQ
1521 LNAKCSGLEK TKQRLQGEIE DMSIEVEKAN SLAASLEKKQ KHFDKIVADW KHKVDDLAAE LDASQKECRN YSTELFKLRA
1601 LYEESQEHYE AVKRENKNLQ DEIKDLMDQL GEGGRSVHEL EKMRKRLEME KEELQAALEE AEAALEQEEN KVLRAQLELS
1681 QVRQEIDRRL QEKEEEFENT RKNHQRALDS MQASLEAEAR GKAEALRMKK KLESDINELE IALDHANKAN AEAQKTIKKY
1761 QQMIKDLQTS LEEEQRARDE AREQYAMAER RCNALHGELE ESRQLLEQAD RARRNAEQEN GELHEANNEL SAQNASLSMA
1841 KRKLEGEMQA LQADLDEMLN EAKQSEEKAK KAMVDAARLA DELRAEQEHA QQQEKMRKAM EQQIKELQVR LDEAEQAALK
1921 GGKKVIQKLE QKVRELEQEL ESEQRRHGDA AKNLRKAERR LKELQFQSEE DRKNQERMQD LVDKLQQKIK TYKRQIEEAE
2001 EIAALNLAKF RKVQQELEDA EERADMAENA LAKLRARNRS SASASRAMSP GPGLPKARAQ QHAE
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LNLAK.F	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	2005	2009	
total 1 peptides												

tr|E9FZS9|E9FZS9_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPPKKDMGPD PDPAQYLFVS LEMKRADQTK PYDGKKATWV PCEKDSYQLG EITGTKGDLV VVKVADGNEK MVKKDQCFPV

81 NPPKFEKVED MADLTYLNDA AVLHNLRQRY YHKLIYTYSG LFCVAINPYK RFPIYTQRVI KMYIGKRRNE VPPHIFCISD

161 GAYMDMLTNH ENQSMLITGE SGAGKTENTK KVIAYMASVG ASTKKPKEGE VKKGNLEDQI VQTNPVLEAF GNAKTTRNDN

241 SSRFGKFIRI HFGNSGKLAG ADIETYLLEK ARVISQQALE RSYHIFYQIM SGKLPTLKAM CSLSDNIYDY PFVSQGKVTV

321 PSIDDSEEMQ MADEAFEILG MGEQRPEIWK ITAAVMHFGT MKFKQRGREE QADPDGTQEG ENVAKMMGVD GPQLYMNFLK

401 PRIKVGNEFV TQGRNVNQVV YSIGAMAKAI FDRLFKWLVK RVNETLETGQ KRVTFIGVLD IAGFEIFDYN GFEQLCINFT

481 NEKLQQFFNH HMFVLEQEEY KKEGIDWVFM DFGMDLQACI ELMEKPMGVL SILEEESMFP KATDQTFAEK LNNNHLGKSA

561 SFVKPKPAKA GCKEAHFAIA HYAGTVPYNI TGWLEKNKDP LNDTVVDQFK KGSSKLVQEI FADHPGQSGG KEEAKGGKRG

641 KGGGFSTVSS AYREQLNGLM KTLNATSPHF IRCIIPNETK SPGVIDSHLV MHQLTCNGVL EGIRICRKGF PNRMVYPDFK

721 HRYMILAPNE MKAEPDERKA AKICLEKIAL DPEWYRIGHT KVFFKAGVLG QLEEMRDDKL AKIITWMQSF IRGYHTRKQY

801 KQLQDQRVAL CVVQRNLRSY LQMRTWAWYR LWQKVKPLLN VTRVEDEIKA LEDKAAAAQA NFEKEEKLRK ELETNLAKLT

881 KEKEDLLNRL QAESGTVADF HDKQNKLMSQ KADLESQLSD TQERLQQEED ARNQLFQNKK KLEQEASGLK KDIEDLELAL

961 QKTETDKATK DHQIRNLNDE IAHQDELINK LNKEKKHMQE VNQKTAEDLQ ASEDKVNHLN KVKAKLEQTL DELEDSLERE

1041 KKLRADIEKN KRKTEGDLKL TQEAVADLER NKKELEQTIQ RKDKEIASLN AKLEDEQSLV GKLQKQIKEL QSRIEELEEE

1121 VEAERQARAK AEKQRADLAR ELEELGERLE EAGGATAAQI ELNKKREAEL SKLRRDLEES NIQHESVLSN LRKKHNDAVS

1201 EMSEQIDQLN KMKAKAEKDR SQFAGENNDL RAAMDHVSSD KAAAEKMTKM LQQQLNEIQS KLDEANRSLN DFDVQKKKLT

1281 IENSDYLRQL EDAESQVSQL QKLKISLTTQ LEDSKRMADE EGRERATLLG KFRNLEHDID NIREQLDEES EAKADLQRQL

1361 SKSNADCQMW RHKYESEGVA KAEELEDAKR KLQARLGEAE EAIESLNQKN VALEKIKMRL SGELDDMHVE VERATVLANQ

1441 MEKRGKNFDK VVSEWKAKVD DLAAELDASQ KECRNYSTEL FRLKAGYDES QEHLEAVRRE NKNLADEIKD LMDQIGEGGR

1521 NVHEIDKQRK RLEVEKEELQ AALEEAESAL EQEENKVLRA QLELSQVRQE IDRRIQEKEE EFENTRKNHQ RAIDSMQASL

1601 EAEAKGKAEA LRMKKKLESD INELEIALDH ANKANAEAQK SIKRYQQSIK ETQSALEEEQ RNRDDLREQY GIAERRANAL

1681 QGELEESRTL LEQADRARRQ AETELADAHE QLHDLTAQAA SSSAAKRKME SELQTLHADL DDMINETKNS EEKAKKAMVD

1761 AARLADELRA EQEHAQAEK QRKALELQVK ELQVRLDESE NNALKGGKKA IQKLEERVRG LETELDGEQR RHADAQKNLR

1841 KSERRIKELT FQSDEDRKNH ERMQDLVDKL QQKIKTYKRQ IEEAEEIAA**L NLAK**FRKAQQ ELEEADERAE LADQAVSKLR

1921 AKGRGGSASR LSPPPQMKPR SKRDFE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.LNLAK.F	Y	20.74	557.3537	0.6	558.3613	1	0.26	742	1	1890	1894	
total 1 peptides												

tr|E0VZX2|E0VZX2_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARSKKKTKP DEKFVFLSSW VLNENDKKKG KNEGGGGEDS DDYNAEITGR ESSMENGKNS ESMDKNNKKE NNGKMDDGNE

81 SYPPTPPEPD KELLFLIEFL VDTLTLFPDK MMLDFIDPCS LQGPLSVVLT FLHFPPMKLG ETDVDPTRRT GDNVVQYNSG

161 KSLMFALTES LFEEPPPIYL EISAEREMPH AFLFSQLPIG KTKIQLTELF KRVFVLYDEK PGKTVSKSIK DTYQLIDNEN

241 KNVAEVSVYI RLTCMGENIV TEFEKNEDPE LPLLYKNMDS KKIYECVEKD AREDQSGYRT VPLEVKKYCE YEKEKKKKN

321 YVPPDPADEN YEEIYAEING SVIRINFEKN RRKDPPKPFH VTDFCDCNIP LPRDLVAGMS DLSLSLEPRD GCQIQGQSDK

401 NLTTDDNVDN DPNRVGLDRA NQLIFTVPPP QKLTAPNAKT ILYNVSTCQN GQLHNHSKEN FLVEKVKTPE NTSAKMLNDP

481 EKDVFILRII KRGRRGGPHE KGHFSKDAKR EKMKKNNNHK NAKEPGGDEG DGNVPPEEEK EMLFLIE**FLV DTLLLK**QDKT

561 EFSHMDPCLL QGQTCVVLTF LHFPPMCICE TDFNPCEQTG KNCIKFNSGK SLMFALSESD FENPERIFLE IGAQKVLPHG

641 SVPNRLNMGV TKICLTELFK QVFEKVDKNP NKFPISKSIK DNYRLFASNT KWPSAEVTIY IRLSCLGQNV VTEFQRGNDD

721 CEPLMFKNKE SRKAYECTAK DLRMEDEAED LCPPVPGWGE ISGRDCGDDA PANGTDDLDD DDEFDEFGTE AHGHALTIKI

801 QKSQKKMMEN SKSTNSDDGY PGHKIGFQIP ESQHICKKGK AENKARVYRV NQPGSGKNGE CGNEPIQIVQ GVDSPDKDIF

881 FLRIGKKGES YGKGKLELEL RTPKIKIDRP IDVPRKFDKM PLFTSRD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.FLVDTLLLK.Q	Y	20.36	1060.6532	-68.2	531.2977	2	0.46	717	1	548	556	
total 1 peptides												

tr|A0A2A3E8Z7|A0A2A3E8Z7_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTARYDRAIT VFSPDGHLLQ VEYAQEAVRK GSS**AVGVR**GN DVVVLGVEKK SIAKLQEERT VRKICLLDEH VVMAFAGLTA

81 DARVLINRAQ VECQSHRLTV EDPVTLEYIT RYIAGLKQKY TQSNGRRPFG ISCLLAGFDY DGVPHLYQTE PSGIYYEWKA

161 NATGRNAKTV HEFLQKYYTP EEVATEKGTI KLAIRALLEV VQSGRKNLEI AVMRRGQPLQ MLDLDTIGEY VTEIEREKEA

241 EAEKKKQKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.AVGVR.G	Y	20.34	500.3071	4.5	501.3166	1	0.19	689	1	34	38	
total 1 peptides												

tr|E9GMZ8|E9GMZ8_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGSARYDRAI TVFSPDGHLF QVEYAQEAVK KGST**AVGVR**G KNLVILGVEK KSVAKLQEER TVRKICLLDD HVVMAFAGLT

81 ADARILINRA RIECQSHKLT VEDPVTLEYI TRYIAGLKQR YTQSNGRRPF GISCLLAGFD FDGTPHLYQT DPSGTYHEWK

161 ANATGRNAKT VREFLEKNYN VEEMEDEEKV IKLAIRALLE VVQSGSKNLE LAIMRRGQPM KMLEVDEIEK HVAAVEKEKE

241 EEAEKKKQKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AVGVR.G	Y	20.34	500.3071	4.5	501.3166	1	0.19	689	1	35	39	
total 1 peptides												

tr|A0A212EXZ1|A0A212EXZ1_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVCRVAPKET PSQRDGAQEQ QVADYETALD AAGYGRFSRS VLGACACAFF TTGVENCVMS YVLPAARCEL NLTTYHTGLI

81 NMAFMSGGVA SAFFWGIVAD VFGRKNILSM TLIVDSTILL AQSTVSDYRL LIAARGINGF LIGGPSTLVF TYLSDLVGFK

161 RRQFYLDLIG MSFVVAWLFL PAIAWLVIPI KLTYTTILPI YSWRLFLALG SIPGFMAGIW VLILPESPRL LSDTNRSDKA

241 LKIIGKIHKS NKEMTEFKIK KLIQDNILMT KSMNGEQNRS KVLFMGVMKD LKMFVSKMYA KKSTLILFVF FANMAAGFGL

321 NFWIPELLLR TKGKSCSSNI SVPENAKLLN ASIPWDDLPK VLELRGGTDD EYNATVFDAT GGDCSEDIDD SIYTSGLIVG

401 ACCVIGNAAC ALISSRG**AVG VR**RAAVLCAL ACAAACVVLA ACVCACAATE HIAVAAAAAL NAASLNGNVL LIRLLLHALP

481 AKLSGLGVCW GAWWGRAGGV ATNFAVGALL DYSCPAPFIA VAALLALSIG GIMMIKIDQD KTADEDKNGS ESSGKNIYID

561 RYISTHM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.AVGVR.R	Y	20.34	500.3071	4.5	501.3166	1	0.19	689	1	418	422	
total 1 peptides												

tr|A0A2A3EM41|A0A2A3EM41_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MESCMRGTCS SALQSSPASI FAMLIQTLIA SRCELSDTSE YPRDRKEEIL NSKMEFDFVI VGAGSAGSVL ARRLTEVEDW

81 NVLLIERGEN PLPETVPPGL FFSILNGSQD YRYALEQQES ACLGMRDKRC AWSKGKALGG SSDINGMIYI IGNQKDFDDW

161 ANEGNPGWSY EEVLPHFRKS SSCSPEFTAK HGDKYCGTDG PLKIRYYNYT VTNFEDIILE AAREAGHHIL DPVNGDYYLG

241 FGRTMGNLDQ GKRQSCSKTY LTPVKDRKNL YVMTSSRVDK ILFEGKR**AVG VR**ITLSNNET VEVRATKEVI LSAGSIASPQ

321 ILMLSGIGPK EHLKEFGIPV LADLPVGKNL QDHVIWFGMY YSFVNESVTS APTEKDQLNS AYEYLEARKG PLATLANDLI

401 GYVNVEDSDS PYPDIQILFS QIQRLDTGSM KMAMASYNTN DEITRIMLDE IKRKDLITIY SSLMKPKSRG EVKLRNADPA

481 DPVKIYSNYY TVADDWKKMT KVLPILKNLL NTTALKKYGM EFNIYDVPEC RHLTPDTEER YECVIRHVSA SNYHACCTCK

561 MGPAGDPRTV VDHRLNVHNV KNLRVIDASI IPNIMSGNIH ASVVMIAEKG ADLIKQDWGI NV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AVGVR.I	Y	20.34	500.3071	4.5	501.3166	1	0.19	689	1	288	292	
total 1 peptides												

tr|F0J9M9|F0J9M9_AMBVA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FAFLLSSSDE MLVALRSAVS SSPKLASKSL RRCTASSSEA SAIASTSTAL RTLSKEEIDR KRDVSRLPPR EYARVVKLQY

81 TSPTMEFEYT IKNMRKDYAK FGSATGINPG IMWPSKEELQ DLVHIEKKFY PTLQQLFDED SAKQQAEVEA RRL**REEEIER**

161 NMAKLANARI AMLEREA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.REEEIER.N	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	154	160	
total 1 peptides												

tr|A0A1B0EV99|A0A1B0EV99_LUTLO

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

Protein Coverage:

1 MMRLSLEMFS NTANESYKEV ASVSFHGDYL RIHREYHTLP SGFTEIEGDL SRKAMLLKRI NTYSWQQLRK YSALYLTGDK
81 AREEYASVHP FLDFKGILGD RKGLQENLAK RKSQINLSKL YEQWDKYRKL QEEKSTLEKK RIDIAENLKN QAL**REEEIER**
161 LKAEGKALRN TLKDLKENSY NFEEEFINKS SKSQWNSSSY AGRDNL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.REEEIER.L	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	154	160	
total 1 peptides												

tr|A0A0L7RI67|A0A0L7RI67_9HYME

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

Protein Coverage:

1 MKGRRAKRNT LRIDWKQSER K**REEEIER**TG TRRKREQVEE DEDAWLLLRM VRVPLVVRAE RGPPELPRCS ECNEKEEEEE
81 EERGSSTLKN FGTGRYTGEW ANFIKLPVLG RLLRATSSSA NYTEPSCTRR LVLTIWSRSL DWMEEEGGTA SWRKTGREAV
161 CSEEEQAAAA AAAAQAQARE KKQKKQEKKK KKKTKKQERI TRAVPRLLGR RYTGS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.REEEIER.T	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	22	28	
total 1 peptides												

tr|A0A0T6AV86|A0A0T6AV86_9SCAR

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

Protein Coverage:

1 VEMIRNLIFS KVTQGNAHKI KVLANRCASN KVLDIEKLEQ EASTVDVIDS EAAA**REEELE R**KRNKSRLYE DHRNFLHGKP
81 PHTESMHPSH DTLKYKRKLY GRYGAVSGVD ARLCWPTREE LADVIEYERV EYPHTIPEMI EIAKKTRTEN QAKILKREEE
161 ISNKMLKLDI WIKELNSRIA KKEGEALEAK QRKEKLIEEV RRHFGYTVDP RDDRFKEMLQ KKEKEQKKAM KEARKKAKEE
241 QV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.REEELER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	55	61	
total 1 peptides												

tr|A0A023FFQ7|A0A023FFQ7_9ACAR

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

Protein Coverage:

1 MLVAFRSAVL SSPKLVPNSL RRCTGSTSEA SAIASTSTAV RTLSKEEIDR KRDVSRLTRR VYARGVKLEY TSPTLEFEYN
81 ISNMRKDYAK FGSATGINPG IMWPSKEELQ DLVYIEKKFY PTLQQLFDED RAKQQAEVET RRL**REEEIER** NMAKLASARI
161 AMLEREAARK AKADEERLHR EQMILEVREY IGYNVEPSDP KFKEVMEMKE EERKKAQKEA RKKAKQEKML AKLMAVGAAG
241 TDEGKATDAS G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.REEEIER.N	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	144	150	
total 1 peptides												

tr|A0A023FRY2|A0A023FRY2_9ACAR

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

Protein Coverage:

1 MLVAFRNTVL SSPKLVPSSL RRCTGSTSEA SAIASTSTAV RTLSKEEIDR KRDVSRLSRR VYARGVKLEY TSPTMEFEYN
81 IPNMRKDYAK FGSATGINPG IMWPSKEELQ DLVYIEKKFY PTLQQLFDED RAKQQAEVEA RRL**REEEIER** NMAKLASARI
161 AMLEREAARK AKADEERLQR EQMILEVREY IGYNVEPSDP KFKEVMEMKE EERKKAQKEA KKKAKQEKML AKLMAVGAAG
241 TDEGKATDAS GKTTEESGDG EGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.REEEIER.N	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	144	150	
total 1 peptides												

tr|A0A023FSZ9|A0A023FSZ9_9ACAR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ISTNMLAAFR SAVLSSPKLV PNSLRRCTAS ASETSAIAST STAVRTLSKE EIDRKRDVSR LSPRAYSRGV KQEYTSPTME
81 FEYNINNMRK DYARFGSATG INPGIMWPSK EELQDLVYIE KKFYPPLQQL LDEDRAKQQA EVEERRR**REE EIER**NMTKLA

161 SARIAMLERE AEMKAKADEQ RLQREQMILE VREYIGYNVE PSDPKFKEVM EMKEEERKKA QKEARKKAKQ EKMLAKLMAI
241 GATGADESKA AAESGTTTES EDTQKADS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEEIER.N	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	148	154	
total 1 peptides												

tr|N6TQ66|N6TQ66_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPSTRTVHKC EVEPNNPQDE PTVAPSDHKE SKNIINVKDV GFLHGFVASL SVILVSEIGD KTFFIAAIMA MRHPRLTVFG
81 GAISALVLMT ILSALFGWLV TIIPRAYTFY ISTALFAIFG LKMLKEGCAM SPTEGQEEME EVQMELRN**RE EELER**TSNQD

161 VEVASTNRRP KSTNPLAVTL RIFLQAFTLT FLAEWGDRSQ LTTILLGARE NVYGVILGGV IGHSVCTGVA VLGGRMIAQK
241 ISVRTVTIIG GVVFLVFALS ALFFDPNMGE EDQSKSAN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.REEELER.T	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	149	155	
total 1 peptides												

tr|J3JZE4|J3JZE4_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFAMKNRQSI VFICTFLMCL YFSKCEVEPN NPQDEPTVAP SDHKESKNII NVKDVGFLHG FVASLSVILV SEIGDKTFFI
81 AAIMAMRHPR LTVFGGAISA LVLMTILSAL FGWLVTIIPR AYTFYISTAL FAIFGLKMLK EGCAMSPTEG QEEMEEVQME
161 LRN**REEELER** TSNQDVEVAS TNRRPKSTNP LAVTLRIFLQ AFTLTFLAEW GDRSQLTTIL LGARENVYGV ILGGVIGHSV

241 CTGVAVLGGR MIAQKISVRT VTIIGGVVFL VFALSALFFD PNMGEEDQSK SAN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.REEELER.T	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	164	170	
total 1 peptides												

tr|A0A0J7KQT0|A0A0J7KQT0_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKRQEETLMG WNIIWLFFKL FGLPITFPWL VYHFYNIMQQ RRKITALRSK VVMITGASSG LGEALAHTFY RCGCRIILVA
81 R**REEELER**VK NDLINTHQTV PITHPPIVLP LDLTDINNMK DEVSKAIMVH GRIDILINNA GISFRGEVIN TNVDVDIKIM

161 LTNYFSQVAL SKIVLPFMME QQSGHIVGIS SVQGRIAIPF RSAYAASKHA LQAWYDTTRA ELFDKNIKFT IVNPGYIKTS
241 LSLNALTGNG KIYGLMDKAT ENGYQPGYVA ECVLKSVLKQ EKEVTIAPFT SKAAIVIRTL FPSLFFWIMQ KRARKLAKNK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEELER.V	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	82	88	
total 1 peptides												

tr|N6UK05|N6UK05_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVNAEKSSKT FLQSFGLPSL KAKPCQPSEY GFDQGQFGVP DVMKSGLGSA KSTLENVHPL TQSEKNYRQN VDMMNMQILR
81 NIQGMHAPLK LAMEIRAANK IGHLPCLQSS WVMFDSLTGR DLEISPEDVF NTGEFLEVVG QPHAIAPSDH KESKNIINVK
161 DVGFLHGFVA SLSVILVSEI GDKTFFIAAI MAMRHPRLTV FGGAISALVL MTILSALFGW LVTIIPRAYT FYISTALFAI
241 FGLKMLKEGC AMSPTEGQEE MEEVQMELRN **REEELER**TSN QDVEVASTNR RPKSTNPLAV TLRIFLQAFT LTFLAEWGDR

321 SQLTTILLGA RENVYGVILG GVIGHSVCTG VAVLGGRMIA QKISVRTVTI IGGVVFLVFA LSALFFDPNM GEEDQSKSAN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.REEELER.T	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	271	277	
total 1 peptides												

tr|A0A1B6LM09|A0A1B6LM09_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MNLFQNKLYA TSTSLRVINA AIKHCRANTV WATKRKPKTS ADLALEYFDN IYRPIFGKQW PSIRLALLSP HKYCAVVNNY
 81 GDSDSLSTQL QNEGAINMRE MFESYQNVLS EKKGSSKRKK EFNHVYELNK KMEKIVARQR EEELERIYPQ GVERLQSETS

161 TGKISDKNKA DLETGELVKQ AKTPLDKSLS EASIDTDRQI DAGEGLASSK LNEFVPVSRL IGKEQFVSEA EHFTFYNETQ
241 NFPVTVEPET SLHFPAHLQV FAFDQGNISS FNPSKPGASG VLGYYLLDAG SVLPVLALGL RPGDTVLDMC AAPGGKSLLC
321 LQTLYPDMLV CNDISRSRLN RLSLVMRQYL TDWEQRVTIT QEPGANILDT NKYSKILVDV PCTTDRVSVM ECDNNIFKPS
401 RNKERILLPQ LQVELLFQAL KLVKKGGAVV YSTCSLNPAQ NDGVVQMALR KVWEETSMKI VVKDLSKALE PAKIVFKFAE
481 PSCVKYGSLV VPYLPSNFGP MYFCKLEKEE
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.REEELER.I	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	140	146	
total 1 peptides												

tr|A0A1B0DP54|A0A1B0DP54_PHLPP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAVLLRNVTN SIWHAFAALH QEQDGLVNKT KLKVLTANIA TLVDLYGVER GLDHFRSTAT LNFEHFKFYL AQEVFSCLPN
 81 TLTLAELRNH EAKIDEICWL VCRQKYTSQR ESSIYPEESI YKLFRIFCMF SDLVVRSDGN CQVLMHSSEA VQIVQQLLNL
161 LGLDYEAEKK YEYLVNSDLT YRFEQFLSLV EFREVREGTF ECIESLYEAI YIKDIIKKGY LLRRGYLLPT LREYWFVLQP
241 CELSYYKTPH LKELCGSICL DSNCMVKPFM SPSGKHDKVQ RFIITSGERN FELAAHDHRS RMQWIAALQL AITYSAGKEG
321 FQRDLTARRR QQRDATKQKR REEELERSTH MQEVEEAKVQ LAREKMARVA AETQAKELEA IAREDSRRVA ELEDMKLTLE

401 KLLMEETQAK RDEEIVRALQ ARVLSDEWEK RSELEQLQEE QRVLLEQERQ KRMEFEVKQK EKELQLKEAE KRLKELEDER
481 QKLDIELKLS RCKIKQSEET KEMLEARLQT MQPPSREGSR VRRALSFMPS TRERQTTGAD TEKRGSSIRR SDKIISTKIN
561 H
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEELER.S	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	341	347	
total 1 peptides												

tr|A0A1L8DV31|A0A1L8DV31_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAVLLRNVTN SIWHAFSALH QEQDGMVNKT KLKVLTANLA TLLDLYGVER GLDHFRSTAT LNFEHFKFYL AQEVFSCLPN
 81 TLTLSELRNH EAKIDEICWL VCRQTYTIQR ESSIYPEEVI YKLFRIFCMF SDLVVRNDGN CHVLMHSSEA VQIVQQLLNL
161 LGLDYEAEKK YEYLVNSDLT YRFDQFLSLV EFREVREGTF GCIESFYEAV DEIYQIYIKD IIKKGYLLRR GYLLPTLREY
241 WFVLQPCELS YYKTPHLKEL CGSICLDSNC MVKPFMSPSG KHEKVQRFII TSGERNFELA AHDHRSRMQW IAALQLAITY
321 SAGKEGFQRD LTARRRQQRD ATKQKRREEE LERSTHIQEV EEAKVQLARE KMARVAAETQ AKEFEAIARE DSRRVAELED

401 MKLTLEKLLM EETQAKRDEE IVRALQARVL SDEWEKRTEL EQLQEEQRML LEQERQKRME FEVKQKEKEN QLKEAEKRLK
481 ELEDERQKLD IELNQSRCKI KQSEETKEML EARLQSMQPP TREGSRVRRA LSFMPSTRER PTGADMAEKK AAAIRRSDKI
561 ISTKFNR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEELER.S	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	347	353	
total 1 peptides												

tr|A0A1L8DV35|A0A1L8DV35_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAVLLRNVTN SIWHAFSALH QEQDGMVNKT KLKVLTANLA TLLDLYGVER GLDHFRSTAT LNFEHFKFYL AQEVFSCLPN
 81  TLTLSELRNH EAKIDEICWL VCRQTYTIQR ESSIYPEEVI YKLFRIFCMF SDLVVRNDGN CHVLMHSSEA VQIVQQLLNL
161  LGLDYEAEKK YEYLVNSDLT YRFDQFLSLV EFREVREGTF GCIESLYEAV DEIYQIYIKD IIKKGYLLRR GYLLPTLREY
241  WFVLQPCELS YYKTPHLKEL CGSICLDSNC MVKPFMSPSG KHEKVQRFII TSGERNFELA AHDHRSRMQW IAALQLAITY
321  SAGKEGFQRD LTARRRQQRD ATKQKRREEE LERSTHIQEV EEAKVQLARE KMARVAAETQ AKEFEAIARE DSRRVAELED

401  MKLTLEKLLM EETQAKRDEE IVRALQARVL SDEWEKRTEL EQLQEEQRML LEQERQKRME FEVKQKEKEN QLKEAEKRLK
481  ELEDERQKLD IELNQSRCKI KQSEETKEML EARLQSMQPP TREGSRVRRA LSFMPSTRER PTGADMAEKK AAAIRRSDKI
561  ISTKFNR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEELER.S	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	347	353	
total 1 peptides												

tr|N6UIT9|N6UIT9_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MARYGQRPEN ALKRANEFIE VGKPARALDT LQEVFRNKKW AYNWSESVLE PIMFKYLDLC VELKKSHIAK EGLFQYRNMF
 81  QSVNVGSLEN VIRGYLRMAE EKTENAREQS AQAVIDIDDL DNLATPESLL LSAVSGEDAQ DRSDRTILTP WVKFLWESYC
161  QCLELLRTNA HVENLYHDIA RMAFQFCLKY NRKTEFRKLC DKLRKHLEDI CKLPTQVANV SMSKPETQQL NLETRLHQLD
241  FAIQMELWQE AYKAIEDINN LMNLSKKMPV PKTMANYYQK LAMVFWKAGN YLFHAAALFK LLQLSKEMKK NITQEELQKM
321  ACRVLIATLA IPLPSAHPEF DRFIETDKSP LEKAQRLAVL LGLMQPPSRA SLLKDLVRVN VVNLATPQLQ EVYRWLEVDF
401  DPLNLCSHMN TIMEQLRAEE SGAALQQYIS ALQDVTLVRL VRQVAQVYQT IEFARLIELA KFTTIFHMER LLVDCVRHND
481  MQIRIDHGKQ CIHFGIDLSE SQREDKPEGP TLQVMPSEQV RNQLVNMSNV LIQSAAIINP NKKKAEREKL RSIMVQNYHE
561  NKVKEHERIL ERHKIIEDRK EYIERLNTVR EEEEQKRLED IQRQQLMAEQ KRLEEERQER ERRRHQNEIE QIKHRHLQEK
641  LQQISQTGHG QKILKKMDEE DIKKLDADQI AAKEAEELQK ERRELQAKLK SHEKKVDYFE RAKRLEEIPL LQESLKERQL
721  QDQTFWEEQE KERIAAAIEG RKLAVATRDR LCRMKADRDE FLNKLTSERN ALYSEKLGAF EKMLAEERRK RLNERKEKRK
801  EARRVKWLKE KQEAEEEERK RQQQLLEERE REAKEEKERQ ERLEKERIEK EQKEREAAEK LEKLEMNDRV AAKQKAREEE

881  LERKLREQNE KMDRDAPAPW RRGGGDKEIK RSEPLRRGGG VGESRDRDES KKFEPYVPKS RAAGSDNFWR RSAAEKEREP

961  SRERDRPDT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.REEELER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	877	883	
total 1 peptides												

tr|V5GT97|V5GT97_ANOGL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MLRIVLTVPS SPLRVKFLWE SYCQCLELLR TNAHVENLYH DIARMAFQFC LKYNRKTEFR KLCDKLRKHL EDICKLPAQV
 81  ANVSMSKPET QQLNLETRLH QLDFAIQMEL WQEAYKAIED IHNLMNLSKK MPVPKTMANY YQKLAMVFWK AGNYLFHAAA
161  LFKLFQLSKE MKKNITPEEL QRMACRVLIA TLGIPLPSAH PEFDRFIETD KSPLEKAQRL AVLLGLFQPP TRVSLLKDLV
241  RVNVINLASP QLQDLYNWLE VEFHPLLLCN RVHDVIVSLQ SEENSPLQQY IPALQDVTLV RLVRQIAQVY QTIEFAKLLQ
321  LAKFTTAFHL ERLLVDCVRH NDMQIRIDHG KQCIHFGMDL SESQREDKPE GPTLQVMPSE QVRNQLVNMS TVLNQAIQVI
401  NPNKKKVERE KLRVSMVQNY HETKVREHQK ILQRHKIIED RKEYIERLNT VREEEEQKRL EEMQRQHVLA EQKRLEQERE
481  ERERKRALNE IQQIKDRHRK EKLQQISQTE HGQKILKKLD EDVIKKLDAD QIAAKEAEEL QKERRELQAK LKSQEKKVDY
561  FERAKRLEEI PLLQANMKER QLQDQNFWEQ QEKERIAAAI EERKLAVATR DRLARMKPDK DEFLAKLKKE RNIVYEDKLK
641  EFEKLLAEER KKRLQERKAK RKEERRTKWL KEKEEEAERK AAELRRREEE ERQRAEEAAR KEREEKERIE REEREKKMKE
721  QQEMLDRVAA RQRQREEEIE RKLQEEKESR DKVKESSWRR GELGGGGGGG GGGGNFWRGG DKSEEAPKKT EAWRPARFRG

801  NPDDPPPEAA TVGEPWKTRR RTGGRINVTT EGKNVAMREK TNAAMTEETI DATTEGRTVA KIGEMTAVTT GERIAVRSLA
881  AASTEANETA TGSPIEKEEP VSLETTGSAE VEKIEIVEMT GTAETIGIEG EGMTEVVRGV PLGRRRTTDR PAGRLCREAV
961  GMEVRTHGGL VKRAVGGRNP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.REEEIER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	735	741	
total 1 peptides												

tr|A0A1B0CIX4|A0A1B0CIX4_LUTLO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAVLLRNVTN SIWHAFSALH QEQDGMVNKT KLKVLTANLA TLLDLYGVER GLDHFRSTAT LNFEHFKFYL AQEVFSCLPN
81 TLTLSQLRNH EAKIDEICWL VCRQKYTSQR ESSIYPEEAI YKLFRIFCMF SDLVVRSDGN CQVLMHSSEA IQIVHQLLNL
161 LGLDYEAEKK YEYLVNSDLT YRFEQFLSLV EFREVREGTF ECIESLYEAV DEIYQIYIKD IIKKGYLLRR GYLLPTLREY
241 WFVLQPCELS YYKTPHLKEL CGSICLDSNC MVKPFMSPSG KHDKVQRFII TSGERNFELA AHDHRSRMQW IAALQLAITY
321 SAGKEGFQRD LTTRRRQQRE ATKQKR**REEE LER**STHIQEV EEAKVQLARE KMARVAAETQ AKELEAIARE DSRRVAELED

401 MKLTLEKLLM EETQAKRDEE IVRALQARVL SDEWEKRSEL EQLQEEQQLL LEQERQKRME FEIKQKEKEQ QLKEAEKRLK
481 ELEEERQRLD IELNLSRCKI KQSEETKEML EARLQNMQPP TTREGSRSRN PAKMGKRQHQ KDKMYLTYTE WSQFYGGKKE
561 DSKDDENLKF KRLPFDHCCL SMVPFEHPYC DKNGNIFELQ AIVDFLRKYK INPITGEPLD AKSLIKLNFQ KNHEDLYHCP
641 TLFKPFTKNS HIVAIATTGN VFSYEAIDQL NIKTKNWKDL IDDTPFTRKD IIVLQDPGNL EKFNISTFHH IRKNLRVETE
721 EEIAEKKDPK GRLKTISMET KDILEQLEKD YKPAETVVQE KKVADKFNAA HYSTGAVAAS FTSTAMETAL NHEAAIIAED
801 DVRYERVKKK GYVRLQTNFG PLNLELHCDL VPKTCENFIK LTTQGYYDNT KFHRSIRNFM IQGGDPTGTG TGGKSFWGKK
881 FDDEFKPNLS HTGRGVLSMA NSGPNTNGSQ FFITFRSCRH LDGKHTVFGK LVGGLDTLNE MEKIEVDNKD RPIEDIIIQR
961 AQVFVDPFQE VDEQLAKDRA EEAEKLQKER EEKEKKKQQQ TLVAYREGVG KYLKIQPYKN EGPSTEPAVP AKKKKNISYE
1041 FGDFSSW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.REEELER.S	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	347	353	
total 1 peptides												

tr|U4U4N7|U4U4N7_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARYGQRPEN ALKRANEFIE VGKPARALDT LQEVFRNKKW AYNWSESVLE PIMFKYLDLC VELKKSHIAK EGLFQYRNMF
81 QSVNVGSLEN VIRGYLRMAE EKTENAREQS AQAVIDIDDL DNLATPESLL LSAVSGEDAQ DRSDRTILTP WVKFLWESYC
161 QCLELLRTNA HVENLYHDIA RMAFQFCLKY NRKTEFRKLC DKLRKHLEDI CKLPTQVANV SMSKPETQQL NLETRLHQLD
241 FAIQMELWQE AYKAIEDINN LMNLSKKMPV PKTMANYYQK LAMVFWKAGN YLFHAAALFK LLQLSKEMKK NITQEELQKM
321 ACRVLIATLA IPLPSAHPEF DRFIETDKSP LEKAQRLAVL LGLMQPPSRA SLLKDLVRVN VVNLATPQLQ EVYRWLEVDF
401 DPLNLCSHMN TIMEQLRAEE SGAALQQYIS ALQDVTLVRL VRQVAQVYQT IEFARLIELA KFTTIFHMER LLVDCVRHND
481 MQIRIDHGKQ CIHFGIDLSE SQREDKPEGP TLQVMPSEQV RNQLVNMSNV LIQSAAIINP NKKKAEREKL RSIMVQNYHE
561 NKVKEHERIL ERHKIIEDRK EYIERLNTVR EEEEQKRLED IQRQQLMAEQ KRLEEERQER ERRRHQNEIE QIKHRHLQEK
641 LQQISQTGHG QKILKKMDEE DIKKLDADQI AAKEAEELQK ERRELQAKLK SHEKKVDYFE RAKRLEEIPL LQESLKERQL
721 QDQTFWEEQE KERIAAAIEG RKLAVATRDR LCRMKADRDE FLNKLTSERN ALYSEKLGAF EKMLAEERRK RLNERKEKRK
801 EARRVKWLKE KQEAEEEERK RQQQLLEEKE REAKEEKERQ ERLEKERIEK EQKEREAAEK LEKLEMNDRV AAKQKA**REEE**

881 **LER**KLREQNE KMDRDAPAPW RRGGGDKEIK RSEPLRRGGG VGESRDRDES KKFEPYVPKS RAAGSDNFWR RSAAEKEREP

961 SRERDRPDTR DRADTRYDRD RRDTREIGRR DERDSGRSYE RDRGSERPRF YDSSRYDRKT DSRTDERDRK PENGGSTWRS
1041 SKTSDDTLRR GPPPSSRSGP SRREEPIRRG GDDGTADDDR RGGEDRKVVE EKRPAPKEK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.REEELER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	877	883	
total 1 peptides												

tr|A0A1W4W4T7|A0A1W4W4T7_AGRPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARYGQRPEN ALKRAHEFIE VGKPARALDT LQEVFRNKKW AYNNWSESVL EPIMFKYLDL CVELKKSHIA KEGLFQYRNM
81 FQSVNVGSLE NVIRGYLRMA EEKTEYAREQ SAQAVVDIDD LDNLATPESI LLSAVSGEDA QDRSDRTILT PWVKFLWESY
161 CQCLELLRTN AHVETLYHDI ARMAFQFCLK YNRKTEFRKL CDKLRKHLED ICKLPAQVAN VSIAKPETQQ LNLETRLYQL
241 DSAIQMELWQ EAYKAIEDIH GLMNMSKKLP VPKTMANYYQ KLAMVFWKAG NYLFHASALF KLFQLSKEMK KNITQEELQR
321 MACRVLIATL SIPLPSAHPE FDRFIETDKS PLEKAQKLAV LLGLMQPPTR ASLLKDLVRV NVINLATPQL QELYNWLEVD
401 FHPLLLCSRV QSVINFLKSD EGSPLVQYIP ALQDVTLVRL VRQVAQVYQT IEFGRLIELA QFTTPFHMER LLVDCVRHND
481 MQIRIDHGKQ CIHFGIDLSE SQREDIPEGP TLQAMPSEMI RNQLINMSTV LHQAVNVINP NKKKVEREAL KHAMVKNYHE
561 TKVQEHQRIL ERHQIIEDRK EYIERMNTVR EEEEQRRLEE MQRQQALAEQ KRLEQEREER ERKRALNEIQ QIKDRHLKEK
641 MQQISQTTHG QRVLKKLEED DIKKMDADQI AAREAEELQK ERRELQAKLK SQEKRVDYFE RAKRLEEIPL LQAYLKERQQ
721 QDQAFWEQQE KERIAAAIEE RKLAVATCER LARMKPDKDA FLEMLLKKRN SIYEEKLRKF EERLAEERKK RLAERKATRK
801 EERRARWLKE KQEEEERKRE EEKRREEEER ARLEEIARKE REERERQERE ERERKQKEQQ EMLERAAAKQ RA**REEEIER**K

881 LQEEREALKE STPASSWRSK GETMSSSDVS DSWRRPEKGD ESKKPEAWRS PALSQKPRDQ DRDKDRERED ADKERDREPT
961 SWRNKESRDG PREIGRGGGE RYRKDDRDRG DDLYPREDRY DRDRDRRDNR DRDIDRDRDR DRDRRDDRDR RDDKDRYRDD
1041 YRDRRGDDRD HRRDDRRRDD RDRDRDRYIR DDYPDRRGER FRERRDDRRD DKDRDRKDDR RFDRDRRDGD KGKDTRITRG
1121 PGGGSGSVRE STGNSWRAGG VRKDDLRRDD KEDRKIKSEK PEQVSANKDG WTSVGSKRR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.REEEIER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	873	879	
total 1 peptides												

tr|A0A0T6BCR8|A0A0T6BCR8_9SCAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARYGQRPEN ALKRANEFID VGKPARALDT LQEVFRNKKW AYNWSESVLE PIMFKYLDLC VELKKSHIAK EGLFQYRNMF
81 QSVNVGSLEN VIRGYLRMAE EKTENAREQS AQAVVDIDDL DNVATPESIL LSAVSGEDAQ DRSDRTILTP WVKFLWESYC
161 QCLELLRTNA HVETLYHDIA RMAFQFCLKY NRKTEFRKLC DKLRKHLEDI CKLPVQVANV SISKPETQQL NLETRLYQLE
241 SAIQMELWQE AYKAIEDIHG LMNMSKKMPV PKTMANYYHK LAMVFWKAGN YLFHAAALFK LFQLSKEMKK NITPEELQRM
321 ACNVLIATLA IPLPSAHPEF DRFIETDKSP LEKAQRLAIL LGLFQPPTRA SLLKDIVRVN VVNLASPQLQ DLYNWLEVDF
401 HPLMLCSRVQ TVIETLQAEE NTALVQYVPA LQDVTLVRLV RQVAQVYQTI EFSRLIELAK FTTPFHMERL LVDCVRHNDM
481 QIRIDHKKQC VHFGIDLSES QREDNPEGPT LQSMPSEQIR NQLVNMATVL HQAISIINPN KKKLEREKLR SQMVTNYHEH
561 KVQDHQRILQ RRRIIEDRKE YIERLNTARE EEEQRRLEEM ARQQALAEQR RLEQEREERE RKRALNEIQQ IKDRHLKEKM
641 HQISQTSHGQ KILKKLDEDD IKKMDADQIA VREAEELQKE RRELQAKLKS QEKKVDYFER AKRLEEIPLL QASMKERQLQ
721 DQAFWEQQEQ ERINAAIEER KLAVANQERL IRMKTDKLAF LDKLMKDRNI VYEDKLRDFE KLLAEERKKR LAQRKEQRKQ
801 ERRAAYLKQK EEEEERKRTE QRIKEEKEKE RLEELARQQQ EEKEKAEREE KEREYRLKQE MLERAAAKQK A**REEEIER**KL

881 EEENQRLKEL AGTANVTPVG SGAGGVGGWR GGKGGERERE RERDREPERV REPPGRRDDT WRKVGDRREE QGEKKPEAWR
961 SPRIREMERG SDSRGGESSW RTDRFDRRGP EDRRGVEDRD RFEDRRRGDD RREDRDRDRS DRDRERDRDD RDRRTDDRDR
1041 RGGDEERPER RGGEERRGMD RYGDRGERDR ERRGIEDRDR GRDDRYNSRD DRRDDRDRDR REERDRDRGR DKDDRRDDRS
1121 SWRSAMKDDE APMRRPMPSG RGGRDTVSDW RSGGGKDMRR AEDGPRRGGD DRREDRDRDR RDDRDRRDDR ERRGEDRRGP
1201 ARSEKPREQP QETEDGWSQV SKRR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.REEEIER.K	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	872	878	
total 1 peptides												

tr|A0A1B0GE32|A0A1B0GE32_GLOMM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIKQVVDNIV TVFEQLFKCV MELIISYIVH FVVQVCKFFL ALVLIFGIGY GIFYLFTPRK IVEKVYGRHG PRALARRTHD
81 DDEEIWDMEK EYARIL**REEE LER**EFATMLQ MDEQEEDSFD RYGLYPKFGS REYAEYAEYA EQDEPIPTQM TSARVREVII

161 PPAVSKFKEP VDRVVLEQRK PQALPVLETA PAGTTAHPTP AAHPTPAAHP TPAAHPTPAA HTTPAAPRVP RSWSNMEDQW
241 ARIVKRIIDE QDKLAAQIWG QAHQQEVQAG SKGPGLDRIS PKSMPEREEE RGIWLDREES DEVLNVVDQE MDYSQIYMKG
321 TPRVRRITSE GSPSVRESFT FPASEKLQTQ RVQKSYLPRR LLDEFESEEK DEFSLSPLAP PATSTRPPAG LLDESTEYVI
401 DGEMDKSVLK ADKSSSKRTG EGRPPLQTGQ RMNEIESDEM GVSKPSTATR RREGRPSLQR RQQMDDIESD ETDVPKSAFA
481 PPIVSTAEQQ SVHVSHNVVT PRRPHEDRGV LRRRNLLDEF ESDANDIAVP ITTVTPIRPL PLSRFRADDK IKLKNKYEDE
561 DRYEDEDDDS DMDVDDGEMW DIEKGYAKML RREAQEEYLK MMTRGALERQ FAESWKKIGK QEDKPVSTDA PRQKPTLARH
641 DEPTQEEIGD KLAIPDVTTL EKGRRLGSLV DWWKKKTRHT SPRRRIHKEE IGDMGAKETK NLKTEKGQQP QERYLPFSIP
721 IERREDGLTE SEELLSENDL TPSKMRRSRF SPTRKDAYKK YRWSNMEEEW ARMVKKKQEE QDKNYVDKLK DSQQKHGPQR
801 PEKEAEAVAS ERVRPNTAQG GQDNHKERRS ELSSSESPIA QSAHRRKGEN DKDIGQMKEE LVKTPRIKAL EKAFEILLET
881 EARKREQHGE QNIDDVARVW KRLMKRDALE KAFTTILERE QKNETKAYTT LRARSTSDEY ISDMSRSAFT RKCSKQTVDA
961 RLERYPNDVH LQGTPKVRRL GSDMRSHSVP PYETPRRPQA KGSHLPRRKL LNEFGSEISA LQDKSTAYVL SSDEIAKSIP
1041 KASKKETFLP HRRSSSKRPR EDRFPLQRIK RIGEFESDEI DQSISIFAPA AERQREDTSN FQNESAAYRI DPYEINKSAY
1121 SVEKRQIIIP SSKRPRESRP PLKRSRRVEE FEIDESTSTS NSRREDTSPL QRQSTLHDET AESRKWTTRQ RPREDREPIR
1201 GRKLLDEFDS HNMEKSNSSS TESTPRCRSI WCGRCLAQKK TIIPRSERPR EVRPEEEFEA NEIDESMSTS APASSSTPKR
1281 PKYEDTPNIP HEDKKRIQRR KLLDEFDLEE SDQSNPKTRN N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.REEELER.E	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	97	103	
total 1 peptides												

tr|A0A1D2NI72|A0A1D2NI72_ORCCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDVDSEASL PLPASPSENG NDGRERKLSV GSDSGIEKIP APQLESSSHL DEIPYPVEME KEDIEQDIPL PPDSSKYSPS
81 QAIAGEDETE INMSPAQSSE VVNSASVTET NKPRIHVLGK EQAKKRLAAF SAAKMASAAA ASSKKTSAGK GVTVFHQSSK
161 SKTNQESLAI ASIKQEEEKM KEVMALNSIL SEKLKQVSVI STSIPKPPPV IATVNPTVVN PDSVRSDISS LDVPVLEARM
241 SSSSDAFVKK SQSSGSSRNI RVKRDSSSSR SRSRSHSKSE SSVDARKPRD RRSRSRDRRS RSKERRSRSR EPKRSKDRRS
321 RSKSIERPSR SRDKRSRSKE RISKSRDRTK RSRSRDKKSR DLVRRRSRSR DKDKSRNKRD KRRDSAERDK TDIKKTTSRR
401 SRSRSETPPL LLKKKDKRRS RSKSPPLKSK KKDKHSKSRS SRSRSRSREI RERKKEREQR EKERKEKEAT ERERKERERK
481 EAQKKRE**REE EIER**ELDKIR RSRMPTDWQE FGKYQFKFEH IHRLWGQLST EEKRTRSSSR TSEDSESRSP SRPKETAQPT

561 PLTRTLQRSL KSVATIPVEL KNGEKGEFPV EFLKKTSVLP SINYGFNPFS FAGYYKSREQ ILKVETSDIS REMHDVIVRK
641 DPVIDIASTE SQKSQQWFAT NEMAFCPSDG SKGVLISHLY SDDMEDSPSD SSKPVQLTEL PKKAAINSSS RSDSNNKSSE
721 ETEHEQDSMD SAPSPLLKKK YDEEKSKRES EGKNGDKRQR GSSESDPESD VEKQQYISRS TKPVLKKTEE KEIEKRPKRD
801 TSDARAGSSK NEKSKSQPES DDEYIEDMDV DFQLEKENLQ RVAQIAVKAS PKLNSPVVPS KEAAKNSTDI KVKEKDKKHK
881 DKDKKEKKHK KKKRHHKVSK KKARDSSLED DGDSSSDEEH EKSEKSKKVK DSDKHSHKKL EEAAKEKETN LPDPKEKHAS
961 KKKRGRLEKT SEDSDKSSED DSDDSAKKQP KRKRSKVSTK EVEKPEKEPE KVEVPKSSST KRERSRSRSV ERKHKKSKDK
1041 KTKRKKQDSK LKHKKKHSKR SRANSTSSGS TGSERDTSSP TSSSSSSSDE SDAETKRKSK KKKDGDNEPS DKKPDDKHKK
1121 DRNGGGGASG RGRGNDAGGG GSSGGTSHHG RDRDHREHSR KDSNDHRRDR GKDGRHSGGR KRNNTYEELM AELTNTPIGT
1201 NGDTISDEVC GIHDEQDPEK VVASLIQNIH APIMPNHLDF GANAILSELD DDEILKSIMN QEDINISDIL LKKSFTEEIE
1281 KSPKGENKVS RREKVLSNQT FTSWSDDSQE NFEFPRGASS GAPSSGYETE KSVGTTEGEK LNTHLSTVKS LNSGSESGSG
1361 SSSSSSSSSG SSSSDSSSSS DTEESDTEPT VPKNCEDLTG PSDPSVPVKL YDPFKESSES DGDESKKKSE LATSIDFPKV
1441 LDVSQVQKDI SKITDLHLEI GNRETFKTDQ SHQPASSEKS GAVIISEALP IPTLLSRGTV PSYTPKDTRL PMSIVAVKAS
1521 TTENEPESKV VVGGVNAVSQ DDTKTVERRR SRSRSLSGSS RSRSRSYSPR DSSRRDSFDP RSRHRPRSGS YDRSGREDED
1601 RRRRSPSPRG RSYNSRSRHG HSREHRHRDR EDRHRRRRSH SRSRSRSRSR SRSRSVSPRG SIRYHPRNSR WRDDFSRDGR
1681 RFRHRDERGR RFDREFDKIS PEFLSPREEY RGRLRRDFEE ILHKEGYYGA GPSVIKTDSP PVQLNVADST ISDSELAAGG
1761 MIPGGILPTT GEIFGGISKE ALFEHNQHMH ANSHSMYFYP PHPVQSDASA GANPDFHDQA HPQSNNPDGY EYNSSPKRLS
1841 LDERLEKEMG IQLREEPPQP EPQTRPPVFG PILSKTSGED SSKMKPPVQW TTPQNQSQVI RVGNMVQVVP ADLPCAVTIT
1921 AADVAAFGDK AKLKPAEVES IEQKEDGSSD KQVKIVKIKV PVVPFKVPYW EAPEIEPPVV NPHHISRRSK KLKRKKKSTS
2001 TKRKVVADGK EIGGIEAEKE TGEDDESKSQ EQSAEKSITK VQAHVPFQYS SEINYTLHML GQFLCQEFMP IYVSMLASFV
2081 ELFKTLFGLG YLSTTPVFRL VVSRMADTDV PSGCDLEETT LSGESKCISE STDVSKRQDE LEDMKEADES EPDPTDVKKS
2161 VETLVVESES VVVDVKPLAL DKPLDKIDFP PPARGILVSA GFRERTEDRL KVKARGVTFK DGINPGDGTS SSGGEEMPSP
2241 PPPTTAPSQG LKVKVKRKKK VKVKGPKKNE NVASGDTSEQ PPSPPPVPSV PYPYCPPGIL YQVCLRYAVH YAQAVAEKGF
2321 DIVFQPSDQM PVVLDQTAEA VQPTTPDIET STGEFLNGPQ FSLTAPVINM PMSNNVDTFS KPYASGVHPV PIVSTRNEHT
2401 QGISLPTEGC RIPTIVRNEV TSDISYNDCS YINHHMNYDM PINELHNSTP PLSMPKEEGC DNNKIIPIIG HGTSPSVTIR
2481 HKTKNMYPVN KNIVEVPTVD FSEQPMLHMR GNELNISENS VPELM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.REEEIER.E	Y	20.22	959.4672	38.2	480.7592	2	0.34	679	1	488	494	
total 1 peptides												
