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.

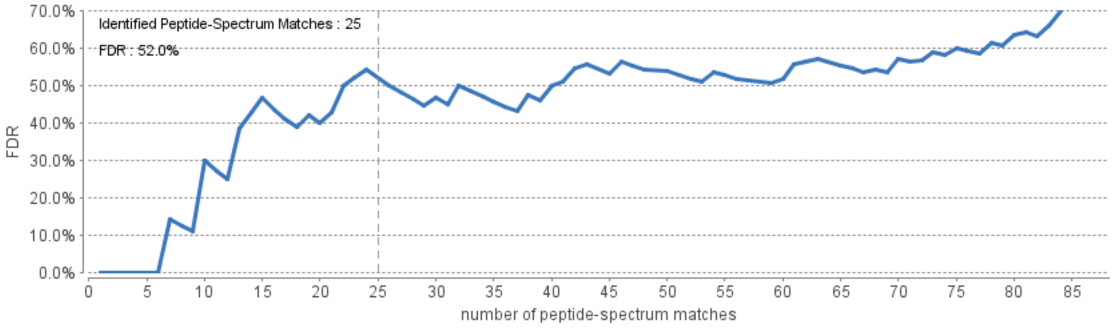

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

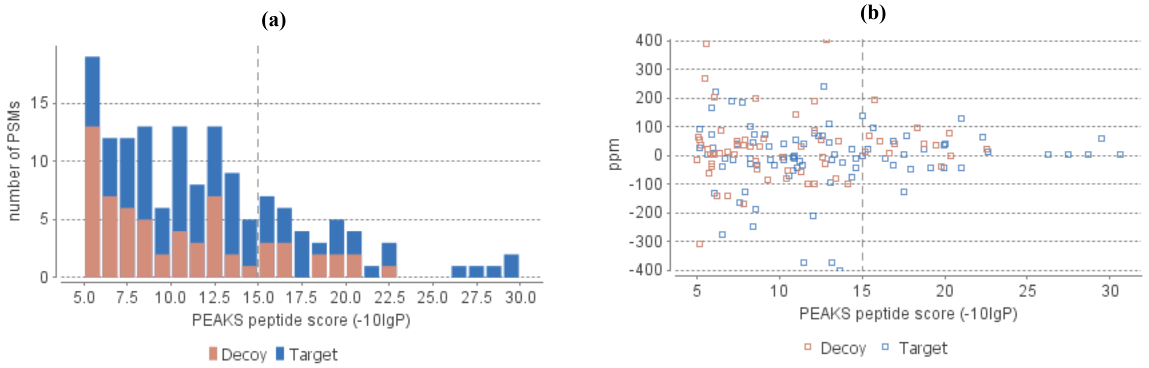
(a) **(b)**

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.

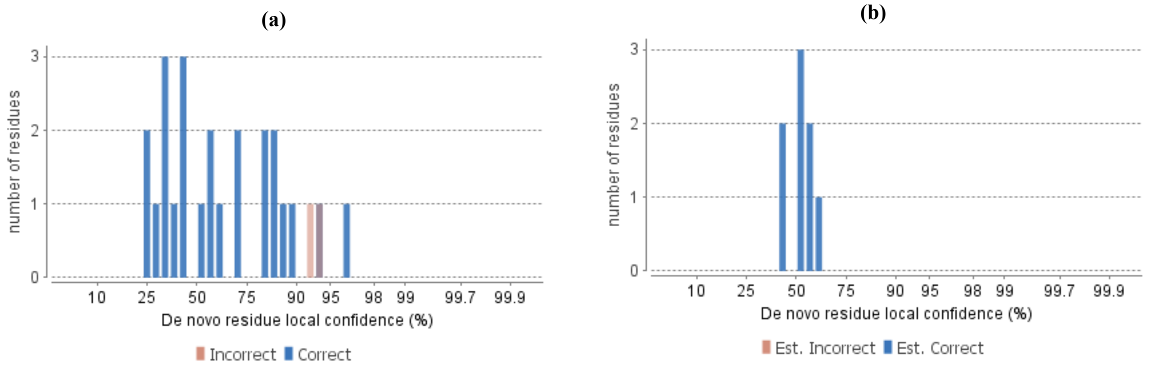
(a) **(b)**

Table 1. Statistics of data.

# of MS Scans	0
# of MS/MS Scans	331

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	25
Peptide Sequences	25

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

Protein Groups	9
Proteins	68
Proteins (#Unique Peptides)	0 (>2); 2 (=2); 66 (=1);
FDR (Peptide-Spectrum Matches)	52.0%
FDR (Peptide Sequences)	48.0%
FDR (Protein)	19.1%
De Novo Only Spectra	2

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.

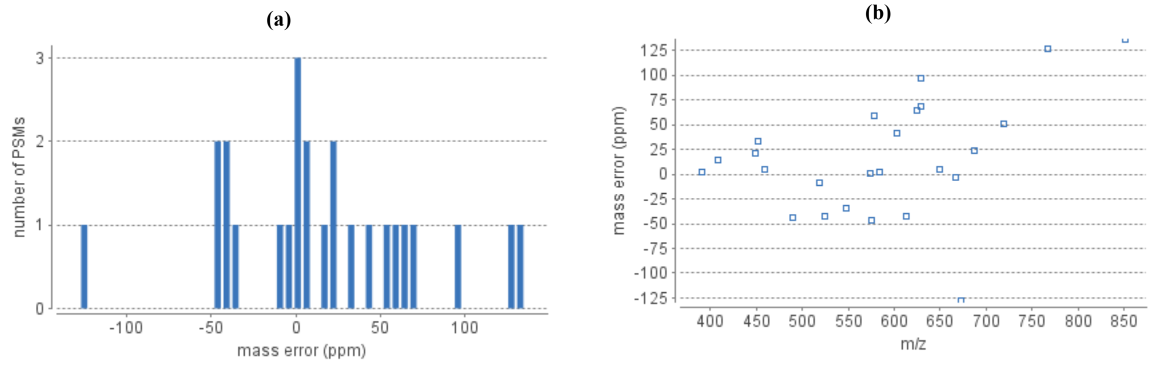

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
IT-TOF	14	9	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: 49
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_4.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
6	3395	tr|A0A1B6MB29|A0A1B6MB29_9HEMI	30.59	3	1	1	N	22895	Uncharacterized protein OS=Graphocephala atropunctata GN=g.33454 PE=4 SV=1
6	3400	tr|B8PUN0|B8PUN0_TRICA	30.59	1	1	1	N	54428	GPI mannosyltransferase 2 OS=Tribolium castaneum GN=Gr85 PE=3 SV=1
6	3401	tr|B7QJM5|B7QJM5_IXOSC	30.59	1	1	1	N	54996	General transcription factor 3C polypeptide, putative (Fragment) OS=Ixodes scapularis GN=8042230 PE=4 SV=1
6	3411	tr|A0A0R1ECC7|A0A0R1ECC7_DROYA	30.59	1	1	1	N	82539	Uncharacterized protein, isoform D OS=Drosophila yakuba GN=Dyak\GE14043 PE=4 SV=1
6	3412	tr|A0A0P5ESR9|A0A0P5ESR9_9CRUS	30.59	1	1	1	N	80778	Semaphorin-2A OS=Daphnia magna GN=APZ42_031771 PE=3 SV=1
6	3413	tr|A0A0P5BDT7|A0A0P5BDT7_9CRUS	30.59	1	1	1	N	82953	Semaphorin-2A OS=Daphnia magna PE=3 SV=1
6	3417	tr|N6TLU3|N6TLU3_DENPD	30.59	1	1	1	N	94422	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_02113 PE=4 SV=1
6	3419	tr|A0A2A3EQT3|A0A2A3EQT3_APICC	30.59	1	1	1	N	117446	COPII coat assembly protein OS=Apis cerana cerana GN=APICC_08588 PE=4 SV=1
6	3496	tr|A0A1I8PZD2|A0A1I8PZD2_STOCA	30.59	0	1	1	N	218816	Uncharacterized protein OS=Stomoxys calcitrans GN=106087545 PE=4 SV=1
6	3526	tr|B4P9U7|B4P9U7_DROYA	30.59	0	1	1	N	270520	Uncharacterized protein, isoform B OS=Drosophila yakuba GN=Dyak\GE12728 PE=4 SV=2
total 68 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
5	3441	tr|A0A0A9XY89|A0A0A9XY89_LYGHE	29.50	1	1	1	N	38853	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6-B OS=Lygus hesperus GN=jmjd6-b_1 PE=4 SV=1
5	3440	tr|Q7QIE1|Q7QIE1_ANOGA	29.50	1	1	1	N	38816	28S ribosomal protein S35, mitochondrial OS=Anopheles gambiae GN=1270264 PE=4 SV=4
5	3504	tr|A0A1I8NQQ3|A0A1I8NQQ3_STOCA	38.34	1	2	2	N	166401	Uncharacterized protein OS=Stomoxys calcitrans GN=106080743 PE=4 SV=1
5	3556	tr|A0A1B6DJE6|A0A1B6DJE6_9HEMI	29.50	1	1	1	N	74647	Uncharacterized protein OS=Clastoptera arizonana GN=g.14252 PE=3 SV=1
5	3563	tr|E9HT86|E9HT86_DAPPU	29.50	1	1	1	N	76941	Uncharacterized protein OS=Daphnia pulex GN=DAPPUDRAFT_265305 PE=3 SV=1
5	3579	tr|Q7Q069|Q7Q069_ANOGA	29.50	1	1	1	N	84077	AGAP012283-PA OS=Anopheles gambiae GN=1280406 PE=3 SV=2
5	3604	tr|B4PVD6|B4PVD6_DROYA	29.50	1	1	1	N	102751	Uncharacterized protein, isoform A OS=Drosophila yakuba GN=Dyak\GE24740 PE=4 SV=1
5	3747	tr|A0A132A3U2|A0A132A3U2_SARSC	29.50	0	1	1	N	539949	Dynein heavy chain, cytoplasmic-like protein OS=Sarcoptes scabiei GN=QR98_0040040 PE=4 SV=1
5	3728	tr|A0A0P5JZZ0|A0A0P5JZZ0_9CRUS	38.28	0	2	1	N	469891	Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
5	3726	tr|A0A0P5NK75|A0A0P5NK75_9CRUS	38.28	0	2	1	N	468656	Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
5	3723	tr|A0A0P5GP66|A0A0P5GP66_9CRUS	38.28	0	2	1	N	455844	Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
5	3718	tr|A0A0P5GPL7|A0A0P5GPL7_9CRUS	38.28	0	2	1	N	378728	Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
5	3717	tr|A0A0P5KVU5|A0A0P5KVU5_9CRUS	38.28	0	2	1	N	328044	Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
5	3716	tr|A0A0P5HCC7|A0A0P5HCC7_9CRUS	38.28	0	2	1	N	262220	Putative Vacuolar protein sorting-associated protein 13D OS=Daphnia magna PE=4 SV=1
1	3397	tr|T1J2W4|T1J2W4_STRMM	28.69	2	1	1	N	30268	Uncharacterized protein OS=Strigamia maritima PE=4 SV=1
1	3398	tr|A0A212FH02|A0A212FH02_DANPL	28.69	2	1	1	N	37765	Uncharacterized protein OS=Danaus plexippus plexippus GN=KGM_207528 PE=4 SV=1
1	3399	tr|A0A0L0CEB7|A0A0L0CEB7_LUCCU	28.69	0	1	1	N	284266	Papilin (Fragment) OS=Lucilia cuprina GN=FF38_11775 PE=4 SV=1
1	3402	tr|A0A0L0BYV5|A0A0L0BYV5_LUCCU	28.69	0	1	1	N	347170	Papilin (Fragment) OS=Lucilia cuprina GN=FF38_11191 PE=4 SV=1
1	3502	tr|A0A1A9X2L8|A0A1A9X2L8_9MUSC	28.69	0	1	1	N	316630	Uncharacterized protein OS=Glossina brevipalpis PE=4 SV=1
1	3525	tr|A0A1J1J7A5|A0A1J1J7A5_9DIPT	28.69	0	1	1	N	258284	CLUMA_CG020329, isoform A OS=Clunio marinus GN=putative Papilin PE=4 SV=1
1	3541	tr|A0A1J1J4N4|A0A1J1J4N4_9DIPT	28.69	0	1	1	N	283708	CLUMA_CG020329, isoform B OS=Clunio marinus GN=putative Papilin PE=4 SV=1
7	3396	tr|A0A0A9X7A0|A0A0A9X7A0_LYGHE	27.47	3	1	1	N	21979	Putative cytosol aminopeptidase OS=Lygus hesperus GN=pepA_6 PE=4 SV=1
7	3453	tr|A0A1B0CDL1|A0A1B0CDL1_LUTLO	27.47	0	1	1	N	173857	Uncharacterized protein OS=Lutzomyia longipalpis PE=4 SV=1
7	3543	tr|W5JJ28|W5JJ28_ANODA	27.47	0	1	1	N	293419	Translational activator gcn1 OS=Anopheles darlingi GN=AND_005505 PE=4 SV=1
2	3415	tr|N6U443|N6U443_DENPD	26.27	3	1	1	N	18247	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_07092 PE=4 SV=1
2	3420	tr|N6ULU5|N6ULU5_DENPD	26.27	2	1	1	N	24992	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=D910_06406 PE=4 SV=1
2	3425	tr|E9GXP3|E9GXP3_DAPPU	34.46	2	2	2	N	67915	Eyeless OS=Daphnia pulex GN=EYELESS PE=4 SV=1
2	3431	tr|N6TRL9|N6TRL9_DENPD	26.27	2	1	1	N	31364	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_00540 PE=4 SV=1
2	3457	tr|E0VSS2|E0VSS2_PEDHC	26.27	1	1	1	N	40411	Uncharacterized protein OS=Pediculus humanus subsp. corporis GN=8234546 PE=4 SV=1
2	3471	tr|E0VEY2|E0VEY2_PEDHC	26.27	1	1	1	N	43532	Endonuclease/reverse transcriptase, putative OS=Pediculus humanus subsp. corporis GN=8239485 PE=4 SV=1
2	3492	tr|A0A0A9YR59|A0A0A9YR59_LYGHE	26.27	1	1	1	N	48662	ATP-dependent RNA helicase WM6 OS=Lygus hesperus GN=Hel25E_3 PE=4 SV=1
2	3503	tr|N6THP3|N6THP3_DENPD	26.27	1	1	1	N	48758	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=YQE_03622 PE=4 SV=1
2	3510	tr|A0A2A3EK85|A0A2A3EK85_APICC	26.27	1	1	1	N	55291	Protein-tyrosine sulfotransferase OS=Apis cerana cerana GN=APICC_05518 PE=4 SV=1
2	3550	tr|E0VDU7|E0VDU7_PEDHC	26.27	1	1	1	N	73635	Uncharacterized protein OS=Pediculus humanus subsp. corporis GN=8239306 PE=4 SV=1
2	3572	tr|N6UT70|N6UT70_DENPD	26.27	1	1	1	N	82848	Uncharacterized protein (Fragment) OS=Dendroctonus ponderosae GN=109546223 PE=4 SV=1
2	3573	tr|T1K774|T1K774_TETUR	26.27	1	1	1	N	81480	DNA helicase OS=Tetranychus urticae GN=107361256 PE=3 SV=1
2	3580	tr|E9H0W5|E9H0W5_DAPPU	26.27	1	1	1	N	85435	Uncharacterized protein OS=Daphnia pulex GN=DAPPUDRAFT_307207 PE=4 SV=1
2	3582	tr|A0A132A9E2|A0A132A9E2_SARSC	26.27	1	1	1	N	87506	Uncharacterized protein OS=Sarcoptes scabiei GN=QR98_0060690 PE=4 SV=1
2	3590	tr|E0VGI0|E0VGI0_PEDHC	26.27	1	1	1	N	95972	Synaptonemal complex protein ZIP1, putative OS=Pediculus humanus subsp. corporis GN=8240008 PE=4 SV=1
2	3591	tr|A0A023F1X1|A0A023F1X1_TRIIF	26.27	1	1	1	N	91113	Putative ovo (Fragment) OS=Triatoma infestans PE=2 SV=1
2	3600	tr|A0A023F0I3|A0A023F0I3_TRIIF	26.27	1	1	1	N	102996	Putative reverse transcriptase (Fragment) OS=Triatoma infestans PE=2 SV=1
2	3608	tr|B4LPM7|B4LPM7_DROVI	26.27	1	1	1	N	104097	Kinase OS=Drosophila virilis GN=Dvir\GJ21386 PE=3 SV=2
2	3619	tr|A0A0C9RER1|A0A0C9RER1_9HYME	26.27	0	1	1	N	118054	PDCD11_0 protein OS=Fopius arisanus GN=PDCD11_0 PE=4 SV=1
2	3629	tr|A0A132AK64|A0A132AK64_SARSC	26.27	0	1	1	N	162918	DENN (AEX-3) domain containing protein OS=Sarcoptes scabiei GN=QR98_0098830 PE=4 SV=1
2	3642	tr|A0A2A3ESR1|A0A2A3ESR1_APICC	26.27	0	1	1	N	139357	WD repeat-containing protein OS=Apis cerana cerana GN=APICC_01216 PE=4 SV=1
9	3404	tr|A0A194PFM1|A0A194PFM1_PAPXU	22.61	4	1	1	N	20107	Protein-tyrosine phosphatase mitochondrial 1-like protein OS=Papilio xuthus GN=RR46_13303 PE=4 SV=1
9	3407	tr|A0A212F2V4|A0A212F2V4_DANPL	22.61	2	1	1	N	47226	Uncharacterized protein OS=Danaus plexippus plexippus GN=KGM_206731 PE=4 SV=1
total 68 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
9	3408	tr|A0A0L7LB71|A0A0L7LB71_9NEOP	22.61	2	1	1	N	53440	Uncharacterized protein OS=Operophtera brumata GN=OBRU01_11885 PE=4 SV=1
9	3409	tr|A0A2A4JH98|A0A2A4JH98_HELVI	22.61	2	1	1	N	53573	Uncharacterized protein OS=Heliothis virescens GN=B5V51_2186 PE=4 SV=1
9	3410	tr|H9IZZ0|H9IZZ0_BOMMO	22.61	1	1	1	N	54809	Uncharacterized protein OS=Bombyx mori PE=4 SV=2
8	3403	tr|Q4FEE6|Q4FEE6_9NEOP	21.04	3	1	1	N	35422	Cytochrome b (Fragment) OS=Tegeticula cassandra PE=3 SV=1
12	3469	tr|Q7PRK4|Q7PRK4_ANOGA	20.99	1	1	1	N	131961	AGAP010742-PA (Fragment) OS=Anopheles gambiae GN=1272555 PE=4 SV=4
12	3475	tr|A0A182WXT9|A0A182WXT9_ANOQN	20.99	0	1	1	N	136820	Uncharacterized protein OS=Anopheles quadriannulatus PE=4 SV=1
12	3481	tr|A0A1A9TG01|A0A1A9TG01_ANOST	20.99	0	1	1	N	141891	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
12	3482	tr|A0A182MKW5|A0A182MKW5_9DIPT	20.99	0	1	1	N	142163	Uncharacterized protein OS=Anopheles culicifacies PE=4 SV=1
12	3485	tr|W5JMT8|W5JMT8_ANODA	20.99	0	1	1	N	145096	Nephrin OS=Anopheles darlingi GN=AND_002529 PE=4 SV=1
12	3486	tr|A0A182Y6U2|A0A182Y6U2_ANOST	20.99	0	1	1	N	146008	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
13	3484	tr|A0A1B6DX46|A0A1B6DX46_9HEMI	20.04	2	1	1	N	33953	Uncharacterized protein (Fragment) OS=Clastoptera arizonana GN=g.41279 PE=4 SV=1
total 68 proteins									

tr|A0A1B6MB29|A0A1B6MB29_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWDTCVFIFI RRKIVLGIIF TLSLTYCIIS FVSVPVDHEV KEIDVLPARK LDESFIWHSG DENNGTVKVT TCRNSVQGQV
81 LIVDDKGYVC NRSEILANGC CDSSLASVVR YSCDTCKDNG CCRIYEYCIS CCLHPDKKDL LQNVLGKAPE TFRVLFASVT
161 DHFELCLAKC RTSSQSVQHE NSYKDPRAKH CYGDSPPS**TD SLTL**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TDSLTL	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	199	204	
total 1 peptides												

tr|B8PUN0|B8PUN0_TRICA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSEREVILKA ALTSRFFLIT IQYVSNLLIP DHEADAYTYP KNEDNGIFDK LVTHLLGGFV RWDAHHFMHI AIFGYTYEHT
81 LAFFPLFPYS AKPVVAILSY LLPFLS**TDSL TL**ITLITVNI FCFAQSALCL YQLSALIMNK DLALKAAILF CCNPASVFFT

161 APYSESLFCY LTFKSMLNSV LLYKKYKNQG YLLSDVAYII PICLSTCTRS NGVLNIGFLA YALICLFLEK IKLEKQICNL
241 LLCLAKFITL AAVLVLICLV PFICFQFYGY QTFCKNFKSY QVPLVLGHKN IDNFVLPGTF SQHNQSWCYK KMPLAYSYIQ
321 SHYWKVGFLQ YYELKQIPNF LLASPIILII LGHSLHFLKE FPKSISKLFN FDLISVKSVR TKKFFPVMAV FIVHASVLTL
401 FCVFNIHVQV TTRMLCSASP VIYWFCSYYV TDVNLFKNLI ARKCNWGELL VLSYFLGYYF VGTVMFCNFL PWT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TDSLTL.I	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	107	112	
total 1 peptides												

tr|B7QJM5|B7QJM5_IXOSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AAKTVFASSR RNMTEVTLKH RNLVLVEYPG IVRNVDKMLR TLGGIDEISE THSDPSRRLE LKFRPDDPYC KCVYANRFSA
81 SCLLLKVKRN RSKDGEPYSV SIEGTVSTVY KFRGMVDFQF LPMEKKADGG GYESLLDQLI PPTMPSLDWL KEETPVFILP
161 QVFSRLDTPA VQPLRDEPKR RVMPGRPSGR PDNVLGGTRH RRVKFACFLN HDDLKVPVEP KPEAWKQLEW RPQDPDVHKR
241 VKEAFEERPL WTRSALQVRL EEQPGRFKLI LPVVAYYVLS GPFRTSWVRL GFDPRKDPST KPYQILDFRL STCPRFPAPS
321 GLRHDVAPKR GLSAYLVPTK VLGTGCRRVV AQ**TDSLTL**AA QGDASSASSA SASTDPELVS TFKPGHLPPF RQLFYHLCDV

401 RLDEVQALVH ANDGKETGCH EKDGWCLEGT IAACRQIMLK DLRRTIKLLK AKSKLSQEND ESLPASDEED DDGEELDELL
481 DDDDDE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.TDSLTL.A	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	353	358	
total 1 peptides												

tr|A0A0R1ECC7|A0A0R1ECC7_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MDPESKAHIK RFVVGDDKLI LYERNLLKKL KPCELCSVEG SVLSICWHGN FIAWASHIGV RVYDLNERCS LGLIKWEVPS
 81 QERLENFRCH LRWSNNNTLL IGWVDTIRVC VIRKRNSIEA STGNLPVNIV DPISTFQTTF YVCGLAPLSE KQLVVLGYRK
161 EKCSSFKALR PVLCVIEYKM NNSEEICTDS LTLRGFEEYT VNDYSLGGLI EEKRFFIVAP KDIVVASLIE TDDRIEWLVK

241 HSKFEEAMEL IAANGSNVTV LSVAKLYINH LLALKKYDDA AKLCLRMLGN DKVLWEEEVF KFVKCQQLRS VSAYLPTSNE
321 CKLDPHVYEM VLYEFLKFDV FGFLNIIKEW PSHLYDGLAV INAIHDNFRK QHANQLLESL ALLYSYQGDF ESALRMYLKL
401 QNKDVFQLIR RYELYDVISK LIIPLIQLDR KCSFEILLDK NKIKTEIVVN QLEHNQEYLY WYLDSLLKKD PNNGFQKKLV
481 FLYANFDRKK LLPFLVRSKD YDIQEALVIC KQENFYPEMV YLLGRMGGVE AAEALNIIIH SIRDIEMAIE FCKEHDDNDL
561 WNALINEFSK HPEIVTKVLD GIVDYVNPAV VVEKIKMGQN IPNLRPSLIK MLWHYNIHGE VLSSAQQIQL NDYFEIHSEI
641 VTKQRRGHHV SYEQLCSMCQ RPVLMIGTHY NCIIRFECGH VYHKPCTQGK LQKNCTECYL WNLAVEKYV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.TDSLTL.R	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	188	193	
total 1 peptides												

tr|A0A0P5ESR9|A0A0P5ESR9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAGTRRWSCR PVMLCWLWMV AAVHLISAME QLNADHIKSF TCGKLYYRTS YLDAKRDVLY VGAMDRVIRI NLHNVSDTNC
 81 ETDSLTLDPS HVTNCISKGK SEFYDCRNHV RVIQPMGDGS RLYVCGTNAH NPKDWVINAN LTHLGRNEYV PGVGMGIAKC

161 PFDPSDNSTA VWVERGNPGD LPALYSGTNA EFTKADAVIF RTDLYNYTTG RREFTFKRTL KYDSKWLDKP NFVGSYDIGD
241 YVYFFFRETA VEYINCGKNV YSRVARVCKK DNGGKNILSQ NWATFLKARL NCSIPGEFPF YFNEIQSVYK VPGDDTRFYA
321 VFTTCQNGLT GSAICVFTTA DVHTAFLGKF KEQASSSSAW LPVLSSKVPE PRPGQCVNDT QTLPDTVLNF IRNHPLMDEA
401 VSHENGVPVF FKGDVAFSSL VVERLKIQGF PDDKHYTVYY AGTIDGKVYK VVQWFDESTQ QGKSELLDIF EVTSPEPIRM
481 MEISPKHKSI YATSDHRIRQ VNMVMCNGRY DNCLRCVRDP YCGWDKESNS CKPYAPGLLQ DVSSSSPGIC DACIAKKRLL
561 VTWGQAVHLS CAIKLPEPMS SMPVTWYYYS REKGQYQLSF RPDKYIQTAE QGMVIMGVTE QEAGRYDCRL GADTLCSYNI
641 TVDTQRCAAP SKSHDYQKVY SDWCHEFEKY KMAMKTWERR QLQCNSRQTN DTASSNQNAH PNEIYPRSPL V
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLTL.D	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	82	87	
total 1 peptides												

tr|A0A0P5BDT7|A0A0P5BDT7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MMRANNMPLL LLSLPLLFSS WASGSDQLVQ HPAVGATTPP ASHVDSDCCT HKSAHHKDHI KSFTCGKLYY RTSYLDAKRD
 81 VLYVGAMDRV IRINLHNVSD TNCETDSLTL DPSHVTNCIS KGKSEFYDCR NHVRVIQPMG DGSRLYVCGT NAHNPKDWVI

161 NANLTHLGRN EYVPGVGMGI AKCPFDPSDN STAVWVERGN PGDLPALYSG TNAEFTKADA VIFRTDLYNY TTGRREFTFK
241 RTLKYDSKWL DKPNFVGSYD IGDYVYFFFR ETAVEYINCG KNVYSRVARV CKKDNGGKNI LSQNWATFLK ARLNCSIPGE
321 FPFYFNEIQS VYKVPGDDTR FYAVFTTCQN GLTGSAICVF TTADVHTAFL GKFKEQASSS SAWLPVLSSK VPEPRPGQCV
401 NDTQTLPDTV LNFIRNHPLM DEAVSHENGV PVFFKGDVAF SSLVVERLKI QGFPDDKHYT VYYAGTIDGK VYKVVQWFDE
481 STQQGKSELL DIFEVTSPEP IRMMEISPKH KSIYATSDHR IRQVNMVMCN GRYDNCLRCV RDPYCGWDKE SNSCKPYAPG
561 LLQDVSSSSP GICDACIAKK RLLVTWGQAV HLSCAIKLPE PMSSMPVTWY YYSREKGQYQ LSFRPDKYIQ TAEQGMVIMG
641 VTEQEAGRYD CRLGADTLCS YNITVDTQRC AAPSKSHDYQ KVYSDWCHEF EKYKMAMKTW ERRQLQCNSR QTNDTASSNQ
721 NAHPNEIYPR SPLV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLTL.D	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	105	110	
total 1 peptides												

tr|N6TLU3|N6TLU3_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDSEYSEEE IEPKLKYVRL SNDLKVILNT TSATCIAVHT KFICLGTHRG VIYILDHEGN SDLSQKLKAH SVSVNQISID
81 KSGEYIATCS DDGRVFIHGL FSHENNFSLN VARLVKTVAV DPNFCKSPSN KRFIMGDDKL TLWERSFLGS LKSTVLLESE
161 GLVGSLSWGG NFLALSSNVG VRVYDMNARC SLGLIKWEEH PSMSIEKFRC NLRWANDRTL LIGWVDTVRV CIIRKRSNME
241 LAIRALPEYL VDPVSTFQTE FYISGIAPLD QQLVLLGVPK EHDENNKSLR PQLYIVEYKD NDYTDIC**TDS LTL**RGYQEYS

321 VNDYHLDVLL EENVFFIVAP KDVVIASPYD LDDRIQWFIQ HNKYKEALEI LQNNDSRSIY KHTIQSVGIE YLDFLLSRGM
401 YDDAGRLGLQ IFEKNHSLWE DQIYKFAMVH QLRAVSPYIP RTLETKLNPH IYEMILFEYL KFNAQGFLQL IKEWNHGLYN
481 VSAVINAVLD HALIDKSDIF VEALAILYSY EQKYDSSLSM YLKLNHKDVF TLIQNHNLHN VMEKMLTQLM DLDYAKTVAL
561 LLEKNSTPPE KIVEKLRSSP SHLYRYLDEY DKRNCKGEYH KELVELYAIF DRQKLLPFLK KSDHYPIQYA LDICQKNKFY
641 PEMVFLLGRI GDTKEALDLI IHELKDMQYA ISFCHEHDDS DLWDDLIDHC IDKPEFVTFL LQSIGNYIDP TTLIMKIKGN
721 MEIPGLRNSL VKMLNQYNLQ VSVQEGCKKI LVSDYFNLQK KLVHTRQKGT SVSSDVLCGA CHYKLIQNDI SRLSDLKMFN
801 CNHVFHRQCL EDDTTT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.TDSLTL.R	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	308	313	
total 1 peptides												

tr|A0A2A3EQT3|A0A2A3EQT3_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MICIVNNNAC KVEMNNSLDQ DFEEFRFSNQ NKICKDDAVD DLQKFDKHID DQNSIFSLRF SLFSCEICKK QFVTKKQLRI
81 HIHTHLGRPR IVLRRVTNLK SFKKKHSNTY WLDPEKKGSL KLTLKKQNFT DSLKLKLKKS SESEDFTVVK SNINLGIENH
161 SQRDVAGAKE NDQRHEKDTE NSINQPFENV MVEQQDEYGN IKFNTEEHNP LEENDRPPID VNEGDSGVGS DMANPSEKED
241 QNVDDLQSSD QYDNSDKRFS ETEDHEESDA LEATCRETIE NLKKLGEQSG SRSMNQLIEN SGIEEDDDRG HESNMIHNLE
321 ENPAISIISK STTFSNHTTD CTTVCEDEDK PEESTENTAS FNWSQLSTNI SNKNNESSKE NEEQSDHGGD NNIDNAGSLL
401 QNLIEHQRHN QNETLNNLPP ETEYVSLEKL AKLLILSRVC NEKFKDIAHL DEHRSKSGHY QCNIPECINL IFNSPLEVSM
481 HKAQMHGTPL SPSVSQLSPH LNTSSPHLNQ NSPHLSQTSP QLNTHSPHAV SMESPNTPNS QQINRNSPLT SPHQTNSPTY
561 NTVASTGQQI IPPVNFEQLP APVQQLAQQV QRMPLPQTQM PPSLPPGANT MIPGPNYFVQ PPGRPPLYRV PGPQGMHYPP
641 HIAHLYPQYG PGPYPQMTAP PQMHSQLPQQ ISRGRAPRVP QTGSTPRQRM KRPMQQSMQV QQNNSAIKQR RMDVLLPDRN
721 EDADCHVIAQ QKRNDGLPVI QNVQGATTQQ TSRNDSTIHL **TDSITL**SVRQ PGSAPAQVQN TSGASGKKSD AKAVANVLAA

801 RGITVTPAAN KNKSSEQNKQ QIPPQQQRTT SSQQPLNVTA LTLNSAISII PASSQKKQQE QGQFAVPHNK QNKTAVNEVE
881 RPPRPPTVDL TQDGPPQIPV VRRGRPPRAL LTCQVCDKNF QNQEMLTQHM ATHRAPSKLL HKCNLCPAQY PTVQALTTHK
961 QAYHKEVDTV AQNGGAELAL PVVDLKSPHV LNRLSNLGIQ SYIPLSQLSA QTGGYFGLPI ITIDGARNPN TCNLGALGAT
1041 SILSLGPLKH LSNR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TDSITL.S	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	761	766	
total 1 peptides												

tr|A0A1I8PZD2|A0A1I8PZD2_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFRNMKILVP SNSQESVPSP PPITAVNQQE FLQSAGGGNG SSASKDFTSN HGSLAQKANR RDQHQKHTGG PNKAKFTHGN
81 NGGRPMQLSQ HQQHKFHHNS NSGGNKGKKQ HYASNSNTTS SLNRKKFHQH QQNTLQQINY HNHHSQNTSQ HQQNQYMSAM
161 HSNQHKFQTT MNATATQTTA TTSSSNSSST SSNNNNCHLV KNQNYSNIVL SPKTNLCVDN NSSSTTPSAN SSNCTTTQSD
241 ISISSITSSE SSCKCSNQSH NCDKSSSFVE KTLQKYPQDL LCAISNDTTQ IAIAASTSSS PSFATHPTNI TSIPKTEALA
321 NCKCFPKFAK ITQSTASTLV NIKLNKKNKI DTAPKQQYFL ESESLSQCQC GLSSFAAAGH SLHTTTVSYQ PATATNNKKK
401 NWKIPNNNNC CGSRDVIDGG VCDICSVSLK PSNVQVTLTE NYEGKICNNL SSSCNSSGDV CNNSQRKQKD PLQSAGMSTG
481 FNLQKAAVPS VEANASNSVT EKSSFLSSSP TSIHKLSKAN QKSIDVTKPN KNETSKGISA ADNDINILES NNSRSVDTNA
561 KTRNYSCNNV SSPSSYSLDF LHSVGVQMSG ATKSSASNSS TEDNLRPLSS AKSANGTQGR ESSAACSGYP CSSVTSNQRQ
641 HHQQQQRYVN EGGISAGGGN NHNTYHHPQP TQLTIASFLK KDILGESIQT SSNSGSSTAC NSTRASNSSN LNNSTYNEQH
721 YVRSHQYGGR YYNNYYPTYY HQHHTSQHTM PHISACGYNG DVARFTSNGG NQRSFYGGYL NYQNNNSPNT NGSLQYTNQT
801 PPTQESSRTH FSHSIESHGV AVGDSTTTNK KGSVGSSRSS CSSSSSTSST SSSGSNRKLQ QQQNASVHNQ QKSLTQHLAI
881 ETLPSKLNSQ QGSSQRQGLH RGHNQHGQHH GHGGHHPHHH QNYYSHHHHH QHVVAHSTPT TPQHQNYYNL TYVCTDGNNG
961 TSSRSCSPAP VLPPTPSSSN PSPRSLDNCS VPGPSPAALA ANLQLNTAPL NYTQYSQNST SQQYHHYQQN HLFNKKLLAP
1041 LSLNVPSPSP SPTPTHLGGA SLQSHIPALV PQNIICCAQL DEASTAAAAA AANNGIIAGN DYDSDASSTH SSAQNRKYSS
1121 CRSALSSASS VASLCGGSKP HQLECKSQPG TPIDASASTT PLGSPIGYNT YAASLVHVFP KLQVSSTTGT TQQPHYNQSQ
1201 NDPKASSNSA QLPLIYHNGG VTSMLNLPGQ TTNIGEAATP NNYSDDDCHR QQTHFLLPLT STQSSAEHLN MPSFSAGTSR
1281 SNSSSGYWSP SQQCSFYNQL PLTGLMTTNL IVPNAASCGS SSSSISPSLP DRDDSKQSIQ HTQNKLPPSS GNTSPTASSS
1361 CSNEQLGISE ALLSSTNSSS TLSGRAGAIV RTCERNSSQL LGQQQQRLIV QQTQHPPSPT LPLSNNTSFS TAAQRARNCG
1441 SGGRNHQYTQ NNPTLISSVT ANCGAMTNNN QQTTAMIPQI FSHHQLQSMP PPPPPHNLLY NNPQTTNPLR PLGNSSVHDF
1521 FTHTPPDRFL ARAHLIEAKE APASLLNNSK WDNLSRDIWT KFISSQQTEE TFKQKMKLWR YLYLFIKNAY PRYGLYLVGS
1601 TISGFGSDTS DVDMCLVSRS ASNIDPRMEA LFNLTVLKDC LSKSGEFEYF NLIEAKVPIL RFRDRVHQLE VDLNFNNCVG
1681 IKNTHLLYCY SQLDWRLRPL VLVTKLWAQH HNINNAKNMT ISSYSLVLMV IHFLQYAVQP PVLPCLHQMF PHKFPLLRSN
1761 DFGFVDMNET IGPYESKNSQ TIGELFLNFL EYYSNFDYSQ HAISVRTGGI LPINACRTAK SLKNDIHQWK ELCIEEPFDL
1841 TNTARSVYDF ETFERVKGVF VSSWRVLKDT LDLNSIFLPD IEQTVQQVLS NFNAESEPNG IDDTIHLS**TD SITL**SWTEDC

1921 GTLESSSDDR ISSTSKQTTK YGGLKRAAHV KTNEDMLLEL NANVNESVCK PSPLILNTVS STPTTLSHSL TKSFNGKFLN
2001 RSHKTNAAMS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TDSITL.S	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	1909	1914	
total 1 peptides												

tr|B4P9U7|B4P9U7_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRLRGLRFG WLWLAWLAIL QLQTVAAMKV SLFGDGYVSM PLQETKMSTN IRVKFRTRQE NAFLFLAAGR TDYCLLRLES
81 GLISFTYKIE RDVVQLRSPK KQKLNDLEWH DVAVQRFENN ITLQVDGYIM RKQLPGDLAA LNIHFGTFLG GVGDFTAEFL
161 DGVIGFRGCI SDVFYNNINI IKRAKDRTSH TTSTGVSWTC STEFDGSIQD SISFMRNDSY SLMMKESHAM GETLSLQFRT
241 MASAGVIFFN GGFDFILLEI EDQHLKVTFN KAGSLVQFIT NEHISDGKWH RVLLRYNAAI AELILDDDTS GYRGTHANET
321 KASINLEKSV FFGGVQEEMR RRLISKGLRI NEISFKGCMR DIRVNDLPLG FAEMAISRSL ALNCLWKYPC VEFNPCLKSG
401 ICSQHGVDGF ICYCDQSYCI KADFQGPFKI FTETSPELEL LYVSPMQLLE GGTAFLSPHF IDIILDLRRY PSLNEQSIIF
481 HVVHQPKYGQ LLQYSAEKAI FVPCRTFNLV DLATDKLKYV HSGQENFNDH ATLDMQIFGD VHKIPENILG KHRFLLHANI
561 TPINDPPQLR LHSHKILRVI EGIERVLDVD LFNIDDPDSE PGNLIYTILP TQSPQETFGC FMVGGATTSA FSQAEVNVGK
641 VSYLYNSTTA ESFSYELQLQ VSDGIETSET VYLPVSVHPL ELRLVNNTGL IMIHKSSLPI SPANLSIGTN AVDDHIDIRY
721 DIVKAPQHGA LQRLRQIDGS WVNVDWFSDS QLLLGHIRYL HSSDFPWQDE FKFIASFGFV TTQTFDFRIT FTRLRITSTR
801 PSQISINGSR EILLTSDILS YETTPIGSFS RSVIYKITKP TRYGGIYVEG SRKAAKKLDS FTQQDIEKRR IRYQTHHTSY
881 SSFSDHLEFV VSVAECDDVT GALEISYRPP DELISKLGHQ NHEALQVQEG ERALITKNHF GIRFNIYESL QFQVSSSPEH
961 GVICKYNEQT SLTTPVEMFT LEQLFRNDIY YCHDDTESTR DTFELLILSE NETDLQFVAN MEVHIKLVND NEPYRTAIER
1041 VFHVVRNGIR TLNPSVLQYL DADVNTNHTD IHYIHVYSSN GAFYKSGHYI DSFTQDDIAN RRIMFQHTGA DSGTAAFIVT
1121 DREHEVNGLL EIRASDPFVS MMATNASIVQ EGKFVVLKNK DFILETNLDM KLDEIYYEVI KPPSYGILMY LSRANEGENG
1201 TTIYKATNYT SLSNFTHLDI ERERLVYWNT EIASMDKVRY RVHIKNITAE GEVMFRIYPS AYWEPLQVKQ NHTLYVEEST
1281 SVLISRDVLE VVHPNISPGD ITFLVTSSPM HGYLEMQSMS FDDEYNCKVF DQSSVNTEKM FYIQAGVNQS TDYFVFDVTN
1361 GITWLRQLMI KIVIIPEKLY MHSNIISVVE GKTVQLNPTD IQPYSEYYRG KILEYMVTIT PSSGHVLAGS SKVKRFTQKQ
1441 LEQGSIQYVH NGSENA**TDSI TL**VAMARNKE SVPFELEFSV VQVNDEEPMM VTNTGLQVWN GGRYVIKNTD LLAQDYDTPP

1521 ENLTFVVHHI YGGYLARNSA PHQKIEQFTQ AEINLEEIYF MHDSNSRRNE LSFVVTDGLF NTTTQMLNIE IKPIEILADH
1601 NENLHVFPLT KKQILRDYLH FKCSDEEREI RYNITVPPSL GRIVNEYIDN GFTKEVSEFT QNDVDNGYIF YEHTAVIMEF
1681 RTNDSFYFDV VAERSDRLLN QKFNIEISVS SGGLLRFLPV NKLNVDEGGS VPIRLDFSKI LEYLKTKAGI NNPELFIEAI
1761 QKPTHGSIGL GHDFKHMQRY HPSDFFTKKV YYIHDHSDTL EDTILMSVYL TQGNIFLCNL TIPVSINPIN DQPFRLITHL
1841 PQMTVVEGEN RTITRNDLLT EDADTPPEEI IYDVMSGPTL GVLKKITNDG HPEDLLSFSN QFTQADINND RIIYVHFGMP
1921 QSTTFCFTVS DGQSNPAYEI FTIKIDSINL KPSAVQAPVK VQQGATSTLM RLDHIGVSTN VHMDRLAYNV TNSPLYGILV
2001 YNHQITLGFT QQKLETSQIS YMQTTLDRSN DSFQISAYVP GTNYVAHVDV VMEVEPVIQI NGIVMKDAES SGGKIKLTTS
2081 LDNDNPLSLT LNQFNPKFVI TRMPSTGQIR KIIRSTGLTT DGQSDRSTNL FSYKELRSGV VYFVPYKSIE ETEADNDSFD
2161 YQLLIKTVQP AQATVSIEYR SRVEETETVH LGSAGLSINY LAIGCAIFIL LICLLIVLLI LKIRKLRKHK ADISKDQPPA
2241 LPCPPDLTSV SPQHHHHHHH GHHYASSEAD SVPATGNSTP LPGFSNIPHC KIIPVESYKH EYPDYDPDEE ETDDQCDPQQ
2321 MMLPQRYNPY HLEHDAWSSS CDMANDFAGY ASVPQSISGS VSSPPSAPPT NPLLRRNQYW V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.TDSITL.V	Y	30.59	648.3330	5.3	649.3438	1	0.29	1133	1	1457	1462	
total 1 peptides												

tr|A0A0A9XY89|A0A0A9XY89_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKIAVGEITT ANPVRPPETS SGTKSDLCDR FVALNESLLR KGVRLDELRG VAKCLDEPVE NCSHSTLGLW AITPLVAVIF
81 VVVVSDSSYY FDGMMKSALS VKCVLPNNYV FWEATRPVMD CRICSNLTAV KILNNLTRSD FKPFAYSYQP ILVKGAAAGW
161 PAVQEFDYAF FKRLFEA**VPE AY**KSVDEDCQ FLNFKSNFTS LQEVFSMPED RVRNSVDTHP WYIGWSNCHP EVLKEMRKYY

241 EKPHFLPEEA EHSHIEFVFM GYQQGAFMHL DYISRLMWQA QLKGHKVWRL TPTPECESVC SSISFTVSPG DILLLDTRQW
321 YHDTYILDGE FSITVSSEYG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.VPEAY.K	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	178	182	
total 1 peptides												

tr|Q7QIE1|Q7QIE1_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLARACGP WPLLWSRSVQ TVGIRLQSTR LQEDGARSGG LEEEEFRVLN LKQTKSQRLA RRKATRPEVP PPRSQQMATD
81 QDWGAVWPGP RTFNPSAVPL PIRQGYVTKR NQMSPGKFAN AELMKIPNFL HLTPPVIKRQ CEALKQFCTP WPKGLETEEK
161 MRAHYPVTCV TSDYCHALPT IRNPLSRIVT VQVELGALQL DRHARDKLLR LVGERYDPDT DLLTIVTDRC PLKKQNYDYA
241 IYLLTALYHE SNTVEPWEAT KCEADMEFFD YEQSRSKRNA EATLNWGRKE GDSGWQQ**VPE AY**GKAVSRLF NEGENEYNIA

321 KYKEQTLALL GLAEAEQVAQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.VPEAY.G	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	298	302	
total 1 peptides												

tr|A0A1I8NQQ3|A0A1I8NQQ3_STOCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKILQNETPN ATAPSDNITE KEKLQQHLPI VVEQKRKAKT LKNKILQNVA EQQQQEQDAL QQQQQQQPNV ATSLATTVIA

81 MTDQLSAAIT TATNTPSAIQ ATNNNNNNNN SSSSVTNDLV SKDLVFAANC NNTNSNKNKI QTNNNNSSSP TSNSDLIIAE

161 AAKILLKNGL NGTNAAAAAA VATATATLLT AAANFQIPQQ QQQQHLSKPQ LTTPASALSS LSSSTLTTSS TSSSSSSSTS

241 KPTLTESSST LAANAKTAAA AAHAQLVAIA AAAVNATNHK RLANTLTALN NSAASQFNSN NSSNSAKSTQ QQQLNNGLLV

321 GAISTPPPSS TVQAATTTAP SPTAHFAKPY KSSKGSNTTS TPPSSTSMST AASSIDMGVI DYTINSSSSL ASSTH**HTSAT**

401 **L**SSPPSSSSS TPIINLSVSA HTTNSHPKFV NSSPHHIRSD IGRPPISTLS STNNNHNQNNA VGSGGMGGFG GRLQFFKDGK

481 FILELARSKD GEKGGWVSVP RKVFRTPSAA TSSTVTPTAT ASTSAGIIPS PLTASPAAVI SGGGIGGGVS YPKNECSNSL

561 SFSDDNSSLQ SSPWQRDHCW KQAAPRKNVS KEMALFYHKP VCRKLTSSAR LLAQRKRRKP YDIQTLENCS FLFVLPHKTH

641 EQKEPNIEVE TKADGEDKIV EKKPKELDNN KQRLSTGEEI KTEIDETTKG ATNKDQCKEN KEAKIRLEQA EECNDVEMIK

721 ASPIKYESRE DDTTKKAIDP NGDEVEKMNT SDCDGVVETS KKSASLNGNV SNEDFPQHVP ETTDTIKTTA TATTKTEKEC

801 KNQGDEEKRL IKPENIKTRA KLTSIVQKLM DASASRLAAT AHLFKKSTQH SPSASATVPF IPSTSIPLSS ASASLSGGAG

881 GGGVGAKNQN SKASPPSNTA ASRLVEYHQQ HVSPRKRILR EFEKVSLEDN ATAAGGKRSR AKANHNSNVN STTSSTTHSQ

961 TSQASSMNKN NSLSTGCSAH GSNQSSKPSA GVATSQAPTK LYSSYSIHSL LGGGSSSSSS SVSPSSGSNK KPSDVPATIT

1041 SNSLAFNSYH QSSSIHNTTH QSPKSPDGNT SCGGKSPSTS ASKLKRSPPY SSPMREAHSR SPTVNSGVNA GFGYDYGRRS

1121 PRH**VPEAY**NK MKYPGMNENT GSPHHHQQQQ QYHHAPQGFY SPYMTSPHYI PPPTLASALS PSTSSSGAPS STSSTATSSS

1201 RSPRHHSSAF RATTPTSSTN MGGNTPNHNI PSTQRGDLSP QRSTTASPRE TTPRTVPKKT ASIRRQFASP TSANTTTNNS

1281 SCPSPTMENH RTEDNDRRTP VSHQQHILQR ASPGSANMQS SPLHPYSYMY AAGANSPHHP ASAVSPTANN PSTAAAAAAA

1361 AASYIPAVVG SPYYHPYIST LAAMRHPQMW MQHYQSAAAA AANPALLQAS RHPAMLSAAA VGAAAAAAAR LSPPYHGYQY

1441 NGVGNAAALA AAAAAAAGFG SASAATPPHH HSSSTIQPPP GSMFNAMVHG MTSSHPAAMH AAAAAGLVPA TGTAAAAALG

1521 SAQPMTDTTT DLSKASKNNY STSSSSSLAS SSPLQGTGNS AVSASTATTL NSMYQTNNKD EQSSDVPLNL SKH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.VPEAY.N	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	1124	1128	
H.HTSATL.S	Y	17.67	628.3181	69.0	629.3687	1	0.21	1118	1	396	401	
total 2 peptides												

tr|A0A1B6DJE6|A0A1B6DJE6_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSKRSQPKWS VEKSDSPAAL KLYNSLTRQK EVFIPRNGRQ VMWYSCGPTV YDASHMGHAR SYISFDILRR VLSDYFGYNV

81 LYVMNITDID DKIIKRARQK YLYAKYISES HDLSQTLTDT YAAMELLTLK AKGAADPDQR NMLMNMTKRV TEAIECLEKA

161 VKSKEQDKIQ IAQKGLLEVS QDSLSDWLDK HQGHTVEDNA IFCELPRYWE AEYHKDMDAL NVLRPNVLTR VSEYVPEIVT

241 YIQKIISNGL AYESNGSVYF DVKSFDDRNN HYYAKL**VPEA Y**GDQASLQTG EGDLRGEDAE KHSPNDFALW KASKPGEPWW

321 ESPWGKGRPG WHIECSAMAS AICGDCLDIH TGGVDLKFPH HDNELAQSEA YYDNDQWVRY FLHSGHLTIA GCKMSKSLKN

401 FVSISDALKR NTSRQLRLAF LLHSWRDTLD YSDNTMEMAV GYEKMLNEFF LTVKDVTRPI STNTKLDNFS KWGTKELELE

481 TKFSNTKESV HLALCDNVDT RTVLDIIRDC ISACNIYIRD GEVNCLLLRD IAAYITNIMK IFGTIQEDDH IGFPIANIGA

561 GINVEQTVMP YLSILAEFRD NVRGLARSHK ATDILQECDR LRDDVLPSVG VRLEDHEGRT AAVKLVDKET LLKERDAKKK

641 AEHDRALDKE KKT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.VPEAY.G	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	277	281	
total 1 peptides												

tr|E9HT86|E9HT86_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSEATSLNNS GTKLMIYNSL TRKKEVFTPQ NGNNITWYSC GPTVYDASHM GHARSYMSFD ILRRVLRDYF GYDITYVMNI
81 TDIDDKIIKR ARQNYLYEKY AAESSELETL RKDVEESVGR LAKQMAVTTD PDKKVMQETM LAKVTAAINK SAEITSKAAD
161 GLCHDAKSFL MAEAKDVLSD WLDSIKHGMD VSDNAIFASL PRYWEEEFYK DMAALNVLPA DVITRVSQYV PEIVDYIAKI
241 MERGFAYSAN GSVYFDVAKF DSQKNHKYAK L**VPEAY**GDSK ALQEGEGDLS VSEDRLSEKK SPNDFALWKN SKSGEPSWDS

321 PWGKGRPGWH IECSVMASAI LGSSMDFHTG GVDLKFPHHD NELAQSEAYY DNDEWVSYFL HTGHLTIQGC KMSKSLKNFI
401 TIQDALSRNS SRELRIFFLL HQWKETLDYS HSAMEEASSY EKMLREFFLN AKDLLRSGPT AAAITAQQQQ QHFQKWSDAE
481 RELNQRFVQA KNRVRQAVCD NIDTKTSLEA IKSLISDCNK YLARMKRSAN RVLIKSVAEY VTRLFQIFGV IEGKQTLGFP
561 STESSAGGPG NNDISAEEIV MPVLEALAEF REEVRKEARQ LGAKSVLELC DRFRDDVLPS LGVRLEDREG HPPALKLVPR
641 DELLKEKLLK EKILKEKLLK EKEERRKTEL NRQTDK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.VPEAY.G	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	272	276	
total 1 peptides												

tr|Q7Q069|Q7Q069_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAKRVQPTWQ APEEKPAPKL YLYNSLTRRK ELFVPRDGRN VHWYSCGPTV YDASHMGHAR SYISFDILRR VLSDYFGYNV
81 LYVMNITDID DKIIKRARQN HLYERYLQQS KDMPLERLLD DSKEVMATFR ENLARTTDAD KKTMMDRMLE KLTAAVDNLS
161 LAVKEGDEGR IQQAQDQFLQ DSKDPLADLL DSKQGSSVTE NAIFETLPRY WEDAFHKDMA ALNVLQPDVL TRVSEYVPQI
241 VTYIEKIIAN GLAYEANGSV YFDVAGFDRR EQHHYAKL**VP EAY**GDAKQLQ EGEGDLSIGA DRLTEKRSAN DFALWKSSKA

321 GEPWWDSPWG RGRPGWHIEC SAMASDICGD YLDIHTGGVD LKFPHHDNEL AQSEAHDGSA EWVKYFLHTG HLTIAGCKMS
401 KSLKNFVTIQ QVLEKHTATQ LRLAFLLHSW KDTLDYSDNT MEMAVQYERF LNEFFLNVKD LTRHVQTGPA RDAFDRWRPV
481 EAELERKFAD ARAAIHEALC DNVDTRTALD VMRGLVSACN VYIKEHRSAG FNALLLRRVA AYCTDLLHIF GAISGPRGGI
561 GFPISAGAAG DGTGMAGDLE QTVMPYLQAL AEFRNAVREQ ARGLKATEIL QLCDQLRDDV LPGLGVRLED REGAPSALKL
641 VPAEVLLRER EAKRAEENRK AAEKERKKAE AAAAQAAKDA QRKINPLDMF RSETDKYSAF DDATGLPTHD LEGKEISKGQ
721 LKKLQKLQQA QEKRYQEYLA SQA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.VPEAY.G	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	279	283	
total 1 peptides												

tr|B4PVD6|B4PVD6_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MELLLLFMLA LQLIESSIGS KDVPIHQIES IVGENIYLPC NVTTFDGDEP VLVLWYRDDK GTPIYSIDIR AGVSKAPKRW
81 SDDSVFGDRA YFIFDKEPGK LSIQNTQASD SGTYRCRVDF LKAQTINSLI RLNVISPPKQ VIIRDSSNVE RSTVVGPYSE
161 GDIVSLKCQV IGGYPTPTIS WYRDGLEMPC ELSHLAGGKI IECEITLPSL GREDLNSRLT CRALSHPRAP IVEAVVQIDM
241 NFAPLNIRLL GAHQPLSAGR RYDLLCQSAG SRPPAVITWW QNGIRLEKTT ETTSSDGNQT TSTLSISLSK SDAGKYLSCK
321 AYNHAVPSEP LEDGWKLDIQ Y**VPEAY**VRLG TSLDPGTLRE GTDVYFDCLV MAHPNVFRIE WRHNEQPLSH NISQGVIISN

401 HSLVLQGVTR ATAGNYSCVG FNAEGEGISA PFALNILYAP TCAQNQKKVY GIAKQEDAKV MCTVDANPRE VEFSWTFNNS
481 AESIDVATNH IIGSGTTSIV TYTPVNELDY GTLLCLASNK IGKQRVPCVF HIIAAGRPEK VHNCTVNNIS MTSLTVTCSD
561 GFNGGLPQSF NLELLDSYTQ EIKANITSTV PKFTVPGLSP GSIYRLNIYA FNTKGRSDPA IVNAAMLRMP EKQLTSEQTH
641 NLRAELLFSP VMSLTIGLTL AVLVAVLAII LALRIPCTAS SRRRQKELSN ENISRDESPG PSDKSSGSKE VDDCDEKNPD
721 VVPESIEPDE QVESIRKRQQ ISTIDTNRSP NRGIFVNEQQ HLTAAEISLR ASHGIGYCTL RSGMHAQAQS SVGEISINVT
801 PHVYSNSISQ CTLPRQSSQN VWNNYNCNIT GARPTSTFHQ LTFPQGRVNV GGHNPVQPMH GHAPSPSQAS NSSMASSTNT
881 LPQPHPHGRT IALHHMNQAQ CGRVCIGIAS DGIHTAEQNL SDDEVTVQTP LMIKRDSTV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VPEAY.V	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	342	346	
total 1 peptides												

tr|A0A132A3U2|A0A132A3U2_SARSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDSLPNPID SGQDTISGQF HDASSNPQSS TASHLDLSLL LSYIKRVVSA LMEDDGSVPI SLKQLLANDS THEILKKFIQ
81 EPQTKSILIQ RLILKDDDDD GTVGASSSTD ENIIYCISSE VKYDDPKISS LVLIKQGSIL EAEKPLSHQL RLMNLNDSFP
161 YETLHSYVSA AVAPYFKSFV KETGRAERDG DKMAPNVEKK IAELEMGLLH LQQNIDIPEI TLQIHPVVQQ VINKCREESV
241 KVSMEHFGDR CHDSVFLNQL QAGVNRWIRE IQKVTNLDRD PSSGTALQEI SFWLNLERAL LRIQEKRESL EVITTLDILK
321 NGKRFHATVS FDADTRLKEA LATVADYNPL MKDFPLNDLL AATDLEKIKI SLQFLFQHLR KIRNTKYPMK RALKLMEAIS
401 RDLMAQMLKV LGTRRMMHIA YEEFDRIIAQ CFEVFHTWDD EYEKFQTLLR DIVKKKRDEH LKMIWRINFA HKKLQIRMEQ
481 MRKFRRQHEQ LRAVILRVLR PSSKSQKESV DSLKGDDYAN EKTAGFESSL TDINEIEEVR IAYELVKEVD ALDMTKEGTE
561 CWEASIKRYE EQIDRVEARI TAKLRDQLGI AKNANEMFRI FSHFNALFVR PHISGAIREY QTQLIQRVKD DIETLHEKFK
641 VQYPQNKACK MSKVYDLPLV SGSIIWARQI ERKLSVYMKR VEDVLGKGWE THIEGQKLKN DAESFRLKLN TQSIYDDWCR
721 NIQQKQMNVS GRIFTIESAR SHQKSGFRLR VNFTPDIIIL AKEVRNLRSL GFRVPLAIVN KAHQANQHFP FAVSLIETVK
801 AYGRTCEKIE KKSSLTLLIA GLKSEVQELF SEGATMVWES YKRDSYVQKL GESVLNFQEK VDELLDIVEQ IDIEVKSLED
881 CSYCSTIFKE ILNRIQKAVD DLSLHRYSNL SEWVSRLDKE VESKLVIRLE AGIQAWTRAL EGTSTKKIDS DIDTDSPITA
961 TMSKLGGDPK ISILNHEIRI TNQVMYVSPS VEEARFNLLQ ELFAWQNVIL TLNRIESSRY QVNLEQSESK NYQDLLNKMP
1041 GKGPDVLNAA YEAIESRISQ MRDYIQQWLT YQSLWDLQPD MLYAKLGEDV PKWMNTLIEI KKSRTTFDTA DTRKEIGPIS
1121 IDYAKVQSKV TLKYDSWHKE VLSKFGILLG QEMTSLHSSI LNSRMELEKQ SIDTANTKDA VTFITYVQSL KTKILQWGKQ
1201 VEIFKEGQRI LERQRFQFPN NWLHVDNIEG EWSAFNEIMK RKDASIQQQI TSLQVKIVAE DKLVESKSVD FLNEWDRGKP
1281 VQGSINPKEA LNRLTIFETK FNHLHEDRDN IMRAKEALEL LEPNVSSTSP NDDKLMVALE ELQDLKFVWT ELAKVWEQID
1361 SLKEMAWLSV QPRKLRQHLD GLLAQLKAMP ARLRQYASYD YIKRVLQSLT KSNVLIVELK SDALKERHWR SLCKQLRVTW
1441 ILSELTLGQV WDIDLQRNET IVKEIIQVAQ GEMALEEFLK QVREFWQTYQ LELVNYHHEC RIIRCWDDLF SKVKEHINSI
1521 SAMKLSPYFK EFEEDATTWE EKLNRINSIF DIWIDVQRRW VYLEGIFNGS SDIQALLPVE TSRFQSISSE FLQLMRKVSK
1601 NPMIIDVINI PGVQRSLERL SDLLGKIQKA LGEYLERERS SFPRFYFVGD EDLLEIIGNS NNILRLQKHF KKMFAGVSSI
1681 ILNEDQSKVI GLCSKEGEEV HFFNPVSIVD HPKINKWLSL LEREMRSTLA KLLTQAVSDQ ISIQDDRIDL NKFVEWIDKY
1761 QAQIVVLAVQ ISWSESVESA LIQSNQSENR LQEVLNSVES TLQILADLVL QEQPPLRRKK LEHLITEYVH KRDVIRDLLR
1841 KHIQSHKSFE WLSKMRFYFD SKQADILQKL TIHMANAKFF YGFEYLGVQD KLVQTPLTDR CYLTMTQALE ARLGGSPFGP
1921 AGTGKTESVK ALGNQLGRFV LVFNCDETFD FQAMGRIFVG LCQVGAWGCF DEFNRLEERM LSAVSQQIQQ IQESLRNCSN
2001 KSELMVELVG KQVRINTDMA IFITMNPGYA GRSNLPDNLK KLFRSLAMNK PDRQLIAQVM LFSQGFRMAE KLATKIVPFF
2081 KLCDEQLSNQ PHYDFGLRAL KSVLISAGNI KRDRIQRIKQ LNSSSDEASI AEHLPEQEIL IQSICETMVP KLIAEDIPLL
2161 FSLLSDVFPG IKYSKTEMNQ LKAHIKNVCN EMYLACDDYG EDCPSESSTQ SNSSTIVHQQ DESSWLAKVL QLYQISLLNH
2241 GLMMVGPSGS GKSTAWKVLL NALERLDGME GVAHVINPKA ISKEALYGTL DPNTREWTDG LFTHILRKII DNVRGEINKR
2321 QWIIFDGDVD PEWVENLNSV LDDNKLLTLP NGERLSIPPN VRIMFEVQDL KYATLATVSR CGMIWFSEDV LSTEMIFENF
2401 FARLRNIPLE DVDEDFTSSA YIQTASRSKQ LKSTKAMEEK RNSDEPISDS LLLQHNFAQT LRNYFTSDGL VKRCYEFATK
2481 QEHIMDFTRL RAFSSLFSLL NQCCRNVLLY NQNHPDFQID QDVLEKYVPG ALVYCILWAF AGDAKSKVRQ DLGEFIRSIT
2561 TIPLPNPNPS YTLIDYEINL TGEWSLWQNK VPQIEIENHR VASPDVVVPT VDTVRHESLL NTWLKEHKPL VLCGPPGSGK
2641 TMTLFNSLRS LPDMEVVGLN FSSATTPELL LKTFDHYCEC RKTSNGFVMS PIQISKWLIL FCDEINLPQI DKYGTIRVIS
2721 FLRQLVEYGG FYRDSDHAWV KLERIQFVGA CNPPTDPGRK PLSHRFLRHV PIIYVDYPGE SSLKQIYGTF NRAMLKIMPS
2801 IRVYADPLTS AMVEFYLISQ EHFTQDMQPH YVYSPRELTR WVRGIVEAIR PLDSLSVEAL VRLWAHEALR LFQDRLVEDH
2881 ERQWTDENID LIALKHFPNI NRNQALARPI LFSNWLSKDY LPVEREELRE FVKARLKVFY EEELDVQLVL FNEVLDHVLR
2961 IDRIFRQPQG HLLLIGVSGA GKTTLSRFVA WMNGLSIFQI KVHNKYSGSD FDEDLRSVLR RAGCKNEKIC FILDESNVLD
3041 SGFLERMNTL LANGEVPGLF EGDEYTTLIT QIKDASQREG LMLDSNEELY KWFTQQVIKN LHVVFTMNPS SKELKDRAAT
3121 SPALFNRCVL NWFGDWTPEA QFQVGFEFTS KLDLDNSRYV PPEDFPAAFT SFKSPPVHRD AVINSLVYIH STLHHANERL
3201 IRRGARTTTI TPRHYLDLIN HYVKLFYEKC SELEDEQLHL NVGLAKIRET VEQVEELQIS LASKSNDLAA KNLAANAKLK
3281 EMLEDQQEAE REKAKSQELQ LMLKEQETAI AEKTSAVMAD LAKVKPAVEE ARQAVQSIKK QNLVEVKSMT NPPPAVKLAL
3361 ESICLLLGES TTDWKVIRSI LIRENFISTI VNFQTDNITE EIRHKMITKY LQNPDYNFEK IKHASLACEP LVKWAIAQVN
3441 YADMLKKIEP LRNELKNLET EAAANKTKAE EIDRLVAQLE KSIASYKEEY ANLVSQAQAI KSDLSSVQSK VDRSIALLKS
3521 LSSERQRWEH SSETFKNQMQ TIAGDCILSA AFLAYAGYFD QQYRQSLFSS WCSHLTKARI QFRPDLALTE YLSTADERLR
3601 WQANNLPSDD LCVENAIMLK RFNRFPLIID PSGQATKFLL SEFEAKRITK TSFLDDSFRK NLESALRFGN PLLVQDVENY
3681 DPILNPVLNR EVRKTGGRVL ITLGDQEIDL SPSFCIFLST RDPTVEFPSD ICSRVTFVNF TVTRSSLQAQ CLNQVLKCER
3761 PDIDEKRSDL LKLQGEFHVK LRRLEKSLLQ ALNDVKGRIL DDDSIISTLE NLKHEAADIS KKVEETDRVI AEVDAVSQQY
3841 NPLAQACSSI FFTLEGFNQV HFLYQYSLQF FLDIFTDVLS NSVQNHISDH NQRLTAITRK LFEVVYLRVT RGTLHQDWLV
3921 FALLLGKIYI RGFTSEKNFE IEFDHLLRGL DGILPGQPLI SIKDVQPDRL ESATALTKLR CFKNLQKIID STPKFHDWLS
4001 CDLPENHIPT LWEDDKELSD IGRVMRQLLV IHTFRPDRII SMVNRVVDCI FGQKFSQNVE NEYDFATTVD KLIKASTPIL
4081 LCSVSGYDAS SRVDDLAAEM NRSITSIAIG SAEGFSQAEK VINSASKSGK WVMLKNVHLA LQWLVQLEKK LHALQPNPSF
4161 RLFLTMEIHP KIPVNLLRAG RIFVFEPPPG IRANLLRTFS AIPAARMMKT PNERSRLYFL VAWCHAILQE RLRYSPLGWS
4241 KRYEFNESDL KVSFDTLDTW IDAVSLGRTN LPPDKVPFDA IRTLLGQCIY GGKIDNDFDQ RLLTTFLKKL FTPKSFDSEF
4321 ILAFDHQDSE QITKINIPEG IIRRDEFLNW IESLPDRQTP SWLGLPNQAE SVLSTNHGID LIAKLLKLQL IEDDDDIVVI
4401 GSDNSDRSQF NSIKSSSNED GRPVWMRTLL TSATNWLKLM PSNLETMRRT SENIKEPLYR YFEREVNGAA KLLSIVRQDL
4481 LDVISICKSE KKQTNYHRDV NESLAKGMVP NHWKSYFKSP ESFTVIQWIT DFVDRIKQMQ QISSTSMSSL KNLNIWLGGL
4561 F**VPEAY**ITAT RQFVAQANGW SLEELALEIS VSDSAATTDK SSFSINGLKL QGGEVINNKL YVSKRIVTPL PFTSFKWLKS

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4641  SGVAEESESK SSITIPVYLN STRSELLFSV DMELGENQEE YMFYERGVAL VCSSNA
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VPEAY.I	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	4562	4566	
total 1 peptides												

tr|A0A0P5JZZ0|A0A0P5JZZ0_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLERLVAWFC NNYLGRYLEN LNTDQLSVAL LQGEVELENV PLKRDILDQL GLPLQIHAGF VGKISFQIPL RKIRSEPWVI

81 SFEQLYLVAG PKDKNEPYNE ESEENGALER KMAALDLMEA EWRSENDPQG LSSSSLYSLT YSSWLSYGAS LVTNIVQNIQ

161 LRIKDIHIRY EDGISCPGKV FACGVRVDSL TAQTCDESWV PKFMPATSQG LMYKLLELDG LAVYWDTNTE LFANLPLDVL

241 SSKLMQPCSI ERNEFLLAPV SGYAHLKRNC NVKPLRSLNQ PRVACDFQLD RVNIEIRDVQ YHQLVQCCRS LELLARGLQF

321 RRWRVDSEVQ SHPHPRRQWR FSVNCIIAEI RKKNQSRNWP FVIRRAKEIV LYVQSFKEHL LNPIGMTAES KLQRERIESE

401 LELQELQVLR SIAMQQIAKS QSKNESVFND AATGNSSLFQ RWFSSWWSAE ESTNGNEQSA NEDRVEHEIL ETLEDAMRDN

481 TVRQRDILPL QFSSTLKQGL IRLSTCHRTE TGQSWSTLLE IEFDNVLQEW ESRPRLKSNK FHLSLGNVWV RDCSTAASLF

561 PLIVSPQRKD ARPFKSFAGM GSLLPGFNLP FFRSSPSSPN LNVSQDEAPL FDFVYERHPP GSNWDHRLKI TSLAIECVYN

641 HSLFQKIIEL YSVPHNTTEE RSVLGQRLRQ AALSGFEAVK QKTKESLTQS LTPSSVNLPS KQQSWDLLIN ISAPHILIPE

721 SVVSRDSLLM IIDFGHFHVT RSIVNCIAAE LETTTRNGNE DDDDEQYITP CSTPPNESAV TTPLDDAHDM NSFMSGNKEC

801 NDLSDKYNVH FSDLQLLVCR VKDNWKQAHL KGTSALHLLD RFSILIHVEK YGRLVPGLEK PFLTLTASLP HLVAHINEPK

881 IHALLSVSKQ FRSNVVPTPV YETASEDGDT DETDASLAET EKSEEHWFMA QFNIEQLSVE VQSRGRSVAE LQVGGVQASY

961 SMRPTDSSVH LAVHSLLLVD AMQTLGSDYE LLIASHKHVS MDSMSGSLKE SEPTSPVSPS SPDPSSHKGQ RATSPVSLAQ

1041 ALTSLQTDPS WRKDGLSPPM ARHRMATSAL KSEALILIDI VTVEPTWVDG KAEGRIRIIK VHFNSLDVIA NQDTVVELAS

1121 FFQRVMPKKT MPSNPDESNF STGLPSNHSR FPPFALVPDG STDITFDFHR LTILLLRSVV KEEMLIGRKV ATLTVTEAHI

1201 SGNLASDVLV QGSLGGLQVL DLTPEGQKHQ RVVSVGHDPL VEQHQNLYML VSQGLYDTTK DKNEVKAFSF KFLQPGLEAP

1281 GEEEEGYKLS LEIRMASLCY SHSVHFLAEV AACVSEFKQS VSNMAMSLKL TAAEMAVDLL HRGTEGLAQS IYISGSTSVT

1361 EGLSLNAMKE ANDEEQPSPP SRVRLSALLE SPILVLPKSA KSPQVLVAHL GQIEISNDIK VETEHPPQLS EELSGGTHKE

1441 HFEVEVRDMS LYSLNVDEKW KSSFSHFYTG PSAFLRITAQ ELYSCASPHG RPILHDTLLK FSLHRIVDRP ILSDADPFLF

1521 PLTDFYPKLE VCDVFQVHGC VVSPLQVSLS KDQYQQIIQS LDNLNWNKVD ASSNFEAGPD PSTKNRAPAR VKQRELILNL

1601 KFQLPRFSMQ LLDNSNRAIV SLSFEDFLVA YEQNCTFSAT VQTSLKSLIL EDLMVKEDSK YRRLVASNDR QSDRIAGRLN

1681 LSSFMSSSCP DLRAQGLYNP GSRSLPARLE SDKSQWKSSV RAKAPQKKPI AKCPSTPPSS SSMMYHQRFT RSGVGDNNLV

1761 FIKILLVDPD SPDFALKYNS THRFIEINFN ALDVIINLES WVMVLDFFGT STTKVSRQQK KKVAASSPGY QDWSKMANAH

1841 TVNARWEVEV RSFSLLLNRK DYEVAEATIS NLTWEMASMR GNLDVTGKLG SITVQDLTSA GKMYRERFIT SGNEALDFQF

1921 FCFSADDPQL ARDYDIRLNL NMASVLYVHT QRFYTECFSM LEQFQELRRV AGTFGATGQS GAASVSRKPW RHGTRILLNV

2001 EAGSPVILVP ICSTSEHLLV IDLGRISVSN KFVVTDGSVC LPTINKSRKA GLKGLPVVPI TANPETVLVD VIQVELSNMD

2081 LCTGQRQKAN RSQVGDLILG SYLIRRSGQS LLKDTCEMKL EVRRNLDSHL KHPVPDMDLC GLLSTVQCSV DEHQYKLVRG

2161 LLAFNLGEPV DFLHSDQPPP TSPIQLPDDS KPPMWAKLKI HIDLVDVMLE VKDSRIGAFS TIKFIDSRLV YESNSDGSKD

2241 VDLVSQQVVI RDTRYDASSA THSATKKNVF TQILEPVTKA RREGSLQAEV HYRSTEDFTR FTVVLNNMRL LAVVDWWTLF

2321 REFLLHSPDE YRGTNNDKGR NSEESDVKPH AKWTATSTRP SPIIVSTGVI SKRAALIDTR KVPVEFKINI SDSEVVIIED

2401 TSVRESSAVI LKGTALLTYR PQIHSKPLSC QLNRVEIFSS QLNLEEETAL SIVDPATISI EIVDKSSATD VKGILDATSS

2481 DLHQILEVQA QQIILRLSYN DMKLFMRILD SLPHQARLTS AESTIVNEIN KLKALGFSTD DCQTALRSCN DNLEEAALWL

2561 TQNASTVTGQ RQPEMAEIQI RGIEIRTGCV SLCVIDDCRD ADLPLAEITT SQLLLRQSID VAQMTGEGTL TCQFAIDYYN

2641 RVLSGWEPFV EPFKCHVHWN FLAFNGSIAN RPSQSIFFDT EDVVNLTCTR ALLELFGTVK RNWMEDYYGQ NNKELSSLGD

2721 GSSVVRQRSP FVPFALHNAT GSKIKFRTLT ASLLTEGAPS AASTKSSRWI HCEAGDVVAF SFENRGKLRH HDSHQTQTHQ

2801 LSIELDGWME FGPVSVDRVG VYFRYASVHS SPSRRNTAAV ERDLERVLVV IAVTLEGSAR RLVTVRSALQ VTNNLEETVE

2881 LRLEPPAFNL HPSKTVRVPP CTTYPIPMSY LMSQIFVRPM AEKLPHAFSF CKDPIEWHAP TQTTANIRQC NPVISNQDLT

2961 YRFAVDIHRE NFPPEKINTD DSEWTAQPAH TITLLSPLVV VNLLPYELLW ELKAVGQSGI IKPGKSTSIH TVNVSAGFQI

3041 AFRTENFVHS SDLVIGTSPH NFSTRLRLYD SANRLLLLQV KISSKAPGSV KLSISAPYWL VNKAGIPLIF RQEGVQQEAA

3121 GQFDEHEMAR SLSPMLFSFT DREASHSLTA RIGTGLHLGC KPHWCQHFPL QKGVRVRSFL VSPRDGRPEL VYLVGISIRS

3201 GRGRYRDTQI VTLAPCYQLY NQSSWTLEVS QAYFATTFTD PGAQSTYLNL VPGCHLPFHW PRLDKDQLLC VRLLDVKNCH

3281 WSGGFAIQNI SSFHINIRDG ESRANFLRVE IFQQECTFCV VFSDATGFPP PLRVDNLALV PIIFHQSD**VP EAY**LHTTVRP

3361 GSSMPYVFDE PTKPARLNII APGGASSSYD MTTLKEGSQL TYENFIYVCL TVTFNGDDMS TGNALDPNNV ELVLDVPEGT

3441 RVVLSGKETG KRSQLWRMTG SGMLQHEGSS PPRDPSNPQI DPSRILVLDI AGPALQPSEF VHLMLRKPDP RRQLTQTWHF

3521 TEDGRLCCGH SNVFVQAKDG FYGIRQGLSC KTWRMWNDVV LGPAQSVTYY RLPSGIPAEQ AIHWQRLRPG SGCLSVKTIM

3601 DGPTRVLQVA DFLNKPSHCH SNENSVTAST DAEKTSNKQL KVEMKFKGGL GLSIVNHSPP EELAYCRLSN ISLELITGDG

3681 TLSIDASVQS IQIDDSLQDP HCPVVVYVSP SVNQDESKDM PALRLTVHRQ LTSRLNADIF KNLIVTFKNL TINIEENQLF

3761 KLLAFAGFNQ SDLELERIDE SEYESQRSLN AATSIDAKRY YFGILKLVLE QVRLSVYTSS KLPPELKAIK RKLGLTLIKF

3841 EDANIELHPF IRSHPFETAQ LIIDSVVKHY KDELKSQAAR ILGSTDFLGN PLGFVNDVSE GVSGFLYEG**N VGGL**VQNVTF

3921 GLSNSAAKVT GSLSDGLGRV TMDERHEEVR QRLLKHTGQS SDHLVAGLKG FGFGILGGMT SIFTQTYEGI SNEGLGGLFT

4001 GFGKGLVGTV TKPAVGVLDL ATGAASAVRD SSRSSSREIP RRIRPPRLVI GPGGIVPRYS EKQGRGQELL FQLNRHEYRE

4081 TFIAYEALGS LPESLHMLIS SEHIRVFSMN SPNKEVVLDI HLSELQSCKS VVIKDFGTQS TAHYYVELSL LLEPDNPLGA

4161 RRPQVRCDSE SLAKRVTQEI NYAKSVYEEN RHSLISSPKF SP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	3349	3353	
total 2 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	3910	3914	
total 2 peptides												

tr|A0A0P5NK75|A0A0P5NK75_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MLERLVAWFC NNYLGRYLEN LNTDQLSVAL LQGEVELENV PLKRDILDQL GLPLQIHAGF VGKISFQIPL RKIRSEPWVI
  81 SFEQLYLVAG PKDKNEPYNE ESEENGALER KMAALDLMEA EWRSENDPQG LSSSSLYSLT YSSWLSYGAS LVTNIVQNIQ
 161 LRIKDIHIRY EDGISCPGKV FACGVRVDSL TAQTCDESWV PKFMPATSQG LMYKLLELDG LAVYWDTNTE LFANLPLDVL
 241 SSKLMQPCSI ERNEFLLAPV SGYAHLKRNC NVKPLRSLNQ PRVACDFQLD RVNIEIRDVQ YHQLVQCCRS LELLARGLQF
 321 RRWRVDSEVQ SHPHPRRQWR FSVNCIIAEI RKKNQSRNWP FVIRRAKEIV LYVQSFKEHL LNPIGMTAES KLQRERIESE
 401 LELQELQVLR SIAMQQIAKS QSKNESVFND AATGNSSLFQ RWFSSWWSAE ESTNGNEQSA NEDRVEHEIL ETLEDAMRDN
 481 TVRQRDILPL QFSSTLKQGL IRLSTCHRTE TGQSWSTLLE IEFDNVLQEW ESRPRLKSNK FHLSLGNVWV RDCSTAASLF
 561 PLIVSPQRKD ARPFKSFAGM GSLLPGFNLP FFRSSPSSPN LNVSQDEAPL FDFVYERHPP GSNWDHRLKI TSLAIECVYN
 641 HSLFQKIIEL YSVPHNTTEE RSVLGQRLRQ AALSGFEAVK QKTKESLTQS LTPSSVNLSS KQQSWDLLIN ISAPHILIPE
 721 SVVSRDSLLM IIDFGHFHVT RSIVNCIAAE LETTTRNGNE DDDDEQYITP CSTPPNESAV TTPLDDAHDM NSFMSGNKEC
 801 NDLSDKYNVH FSDLQLLVCR VKDNWKQAHL KGTSALHLLD RFSILIHVEK YGRLVPGLEK PFLTLTASLP HLVAHINEPK
 881 IHALLSVSKQ FRSNVVPTPV YETASEDGDT DETDASLAET EKSEEHWFMA QFNIEQLSVE VQSRGRSVAE LQVGGVQASY
 961 SMRPTDSSVH LAVHSLLLVD AMQTLGSDYE LLIASHKHVS MDSMSGSLKE SEPTSPVSPS SPDPSSHKGQ RATSPVSLAQ
1041 ALTSLQTDPS WRKDGLSPPM ARHRMATSAL KSEALILIDI VTVEPTWVDG KAEGRIRIIK VHFNSLDVIA NQDTVVELAS
1121 FFQRVMPKKT MPSNPDESNF STGLPSNHSR FPPFALVPDG STDITFDFHR LTILLLRSVV KEEMLIGRKV ATLTVTEAHI
1201 SGNLASDVLV QGSLGGLQVL DLTPEGQKHQ RVVSVGHDPL VEQHQNLYML VSQGLYDTTK DKNEVKAFSF KFLQPGLEAP
1281 GEEEEGYKLS LEIRMASLCY SHSVHFLAEV AACVSEFKQS VSNMAMSLKL TAAEMAVDLL HRGTEGLAQS IYISGSTSVT
1361 EGLSLNAMKE ANDEEQPSPP SRVRLSALLE SPILVLPKSA KSPQVLVAHL GQIEISNDIK VETEHPPQLS EELSGGTHKE
1441 HFEVEVRDMS LYSLNVDEKW KSSFSHFYTG PSAFLRITAQ ELYSCASPHG RPILHDTLLK FSLHRIVDRP ILSDADPFLF
1521 PLTDFYPKLE VCDVFQVHGC VVSPLQVSLS KDQYQQIIQS LDNLNWNKVD ASSNFEAGPD PSTKNRAPAR VKQRELILNL
1601 KFQLPRFSMQ LLDNSNRAIV SLSFEDFLVA YEQNCTFSAT VQTSLKSLIL EDLMVKEDSK YRRLVASNDR QSDRIAGRLN
1681 LSSFMSSSCP DLRAQGLYNP GSRSLPARLE SDKSQWKSSV RAKAPQKKPI AKCPSTPPSS SSMMYHQRFT RSGVGDNNLV
1761 FIKILLVDPD SPDFALKYNS THRFIEINFN ALDVIINLES WVMVLDFFGT STTKVSRQQK KKVAASSPGY QDWSKMANAH
1841 TVNARWEVEV RSFSLLLNRK DYEVAEATIS NLTWEMASMR GNLDVTGKLG SITVQDLTSA GKMYRERFIT SGNEALDFQF
1921 FCFSADDPQL ARDYDIRLNL NMASVLYVHT QRFYTECFSM LEQFQELRRV AGTFGATGQS GAASVSRKPW RHGTRILLNV
2001 EAGSPVILVP ICSTSEHLLV IDLGRISVSN KFVVTDGSVC VPTINKSRKA GLKGLPVVPI TANPETVLVD VIQVELSNMD
2081 LCTGQRQKAN RSQVGDLILG SYLIRRSGQS LLKDTCEMKL EVRRNLDSHL KHPVPDMDLC GLLSTVQCSV DEHQYKLVRG
2161 LLAFNLGEPV DFLHSDQPPP TSPIQLPDDS KPPMWAKLKI HIDLVDVMLE VKDSRIGAFS TIKFIDSRLV YESNSDGSKD
2241 VDLVSQQVVI RDTRYDASSA THSATKKNVF TQILEPVTKA RREGSLQAEV HYRSTEDFTR FTVVLNNMRL LAVVDWWTLF
2321 REFLLHSPDE YRGTNNDKGR NSEESDVKPH AKWTATSTRP SPIIVSTGVI SKRAALIDTR KVPVEFKINI SDSEVVIIED
2401 TSVRESSAVI LKGTALLTYR PQIHSKPLSC QLNRVEIFSS QLNLEEETAL SIVDPATISI EIVDKSSATD VKGILDATSS
2481 DLHQILEVQA QQIILRLSYN DMKLFMRILD SLPHQARLIS AESTIANEIN KLKALGFSTD DCQTALRSCN DNLEEAALWL
2561 TQNASTVTGQ RQPEMAEIQI RGIEIRTGCV SLCVIDDCRD ADLPLAEITT SQLLLRQSID VAQMTGEGTL TCQFAIDYYN
2641 RVLSGWEPFV EPFKCHVHWN FLAFNGSIAN RPSQSIFFDT EDVVNLTCTR ALLELFGTVK RNWMEDYYGQ NNKELSSLGD
2721 GSSVVRQRSP FVPFALHNAT GSKIKFRTLT ASLLTEGAPS AASTKSSRWI HCEAGDVVAF SFENRGKLRH HDSHQTQTHQ
2801 LSIELDGWME FGPVSVDRVG VYFRYASVHS SPSRRNTAAV ERDLERVLVV IAVTLEGSAR RLVTVRSALQ VTNNLEETVE
2881 LRLEPPAFNL HPSKTVRVPP CTTYPIPMSY LMSQIFVRPM AEKLPHAFSF CKDPIEWHAP TQTTANIRQC NPVISNQDLT
2961 YRFAVDIHRE NFPPEKINTN DSEWNAQPAH TITLLSPLVV VNLLPYELLW ELKAVGQSGI IKPGKSTSIH TVNVSAGFQI
3041 AFRTENFVHS SDLVIGTSPH NFSTRLRLYD SANRLLLLQV KISSKAPGSV KLSISAPYWL VNKAGIPLIF RQEGVQQEAA
3121 GQFDEHEMAR SLSPMLFSFT DREASHSLTA RIGTGLHLGC KPHWCQHFPL QKGVRVRSFL VSPRDGRPEL VYLVGISIRS
3201 GRGRYRDTQI VTLAPCYQLY NQSSWTLEVS QAYFATTFTD PGAQSTYLNL VPGCHLPFHW PRLDKDQLLC VRLLDVKNCH
3281 WSGGFAIQNI SSFHINIRDG ESRANFLRVE IFQQECTFCV VFSDATGFPP PLRVDNLALV PIIFHQSDVP EAYLHTTVRP

3361 GSSMPYVFDE PTKPARLNII APGGASSSYD MTTLKEGSQL TYENFIYVCL TVTFNGDDMS TGNALDPNNV ELVLDVPEGT
3441 RVVLSGKETG KRSQLWRMTG SGMLQHEGSS PPRDPSNPQV DPSRILVLDI AGPALQPSEF VHLMLRKPDP RRQLTQTWHF
3521 TEDGRLCCGH SNVFVQAKDG FYGIRQGNDV VLGPAQSVTY YRLPSGIPAE QAIHWQRLRP GSGCLSVKTI MDGPTRVLQV
3601 ADFLNKPSHC HSNENSVTAS TDAEKTSNKQ LKVEMKFKGG LGLSIVNHSP PEELAYCRLS NISLELITGD GTLSIDASVQ
3681 SIQIDDSLQD PHCPVVVYVS PSVNQDESKD MPALRLTVHR QLTSRLNADI FKNLIVTFKN LTINIEENQL FKLLAFAGFN
3761 QSDLELERID ESEYESQRSL NAATSIDAKR YYFGILKLVL EQVRLSVYTS SKLPPELKAI KRKLGLTLIK FEDANIELHP
3841 FIRSHPFETA QLIIDSVVKH YKDELKSQAA RILGSTDFLG NPLGFVNDVS EGVSGFLYEG NVGGLVQNVT FGLSNSAAKV

3921 TGSLSDGLGR VTMDERHEEV RQRLLKHTGQ SSDHLVAGLK GFGFGILGGM TSIFTQTYEG ISNEGLGGLF TGFGKGLVGT
4001 VTKPAVGVLD LATGAASAVR DSSRSSSREI PRRIRPPRLV IGPGGIVPRY SEKQGRGQEL LFQLNRHEYR ETFIAYEALG
4081 SLPESLHMLI SSEHIRVFSM NSPNKEVVLD IHLSELQSCK SVVIKDFGTQ STAHYYVELS LLLEPDNPLG ARRPQVRCDS
4161 ESLAKRVTQE INYAKSVYEE NRHSLISSPK FSP
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	3349	3353	
total 2 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	3901	3905	
total 2 peptides												

tr|A0A0P5GP66|A0A0P5GP66_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MAALDLMEAE WRSENDPQGL SSSSLYSLTY SSWLSYGASL VTNIVQNIQL RIKDIHIRYE DGISCPGKVF ACGVRVDSLT
  81 AQTCDESWVP KFMPATSQGL MYKLLELDGL AVYWDTNTEL FANLPLDVLS SKLMQPCSIE RNEFLLAPVS GYAHLKRNCN
 161 VKPLRSLNQP RVACDFQLDR VNIEIRDVQY HQLVQCCRSL ELLARGLQFR RWRVDSEVQS HPHPRRQWRF SVNCIIAEIR
 241 KKNQSRNWPF VIRRAKEIVL YVQSFKEHLL NPIGSTAESK LQRERIESEL ELQELQVLRS IAMQQIAKSQ SKNESVFNDA
 321 ATGNSSLFQR WFSSWWSAEE STNGNEQSAN EDRVEHEILE TLEDAMRDNT VRQRDILPLQ FSSTLKQGLI RLSTCHRTET
 401 GQSWSTLLEI EFDNVLQEWE SRPRLKSNKF HLSLGNVWVR DCSTAASLFP LIVSPQRKDA RPFKSFAGMG SLLPGFNLPF
 481 FRSSPSSPNL NVSQDEAPLF DFVYERHPPG SNWDHRLKIT SLAIECVYNH SLFQKIIELY SVPHNTTEER SVLGQRLRQA
 561 ALSGFEAVKQ KTKESLTQSL TPSSVNLPSK QQSWDLLINI SAPHILIPES VVSRDSLLMI IDFGHFHVTR SIVNCIAAEL
 641 ETTTRNGNED DDDEQYITPC STPPNESAVT TPLDDAHDMN SFMSGNKECN DLSDKYNVHF SDLQLLVCRV KDNWKQAHLK
 721 GTSALHLLDR FSILIHVEKY GRLVPGLEKP FLTLTASLPH LVAHINEPKI HALLSVSKQF RSNVVPTPVY ETASEDGDTD
 801 ETDASLAETE KSEEHWFMAQ FNIEQLSVEV QSRGRSVAEL QVGGVQASYS MRPTDSSVHL AVHSLLLVDA MQTLGSDYEL
 881 LIASHKHVSM DSMSGSLKES EPTSPVSPSS PDPSSHKGQR ATSPVSLAQA LTSLQTDPSW RKDGLSPPMA RHRMATSALK
 961 SEALILIDIV TVEPTWVDGK AEGRIRIIKV HFNSLDVIAN QDTVVELASF FQRVMPKKTM PSNPDESNFS TGLPSNHSRF
1041 PPFALVPDGS TDITFDFHRL TILLLRSVVK EEMLIGRKVA TLTVTEAHIS GNLASDVLVQ GSLGGLQVLD LTPEGQKHQR
1121 VVSVGHDPLV EQHQNLYMLV SQGLYDTTKD KNEVKAFSFK FLQPGLEAPG EEEEGYKLSL EIRMASLCYS HSVHFLAEVA
1201 ACVSEFKQSV SNMAMSLKLT AAEMAVDLLH RGTEGLAQSI YISGSTSVTE GLSLNAMKEA NDEEQPSPPS RVRLSALLES
1281 PILVLPKSAK SPQVLVAHLG QIEISNDIKV ETEHPPQLSE ELSGGTHKEH FEVEVRDMSL YSLNVDEKWK SSFSHFYTGP
1361 SAFLRITAQE LYSCASPHGR PILHDTLLKF SLHRIVDRPI LSDADPFLFP LTDFYPKLEV CDVFQVHGCV VSPLQVSLSK
1441 DQYQQIIQSL DNLNWNKVDA SSNFEAGPDP STKNRAPARV KQRELILNLK FQLPRFSMQL LDNSNRAIVS LSFEDFLVAY
1521 EQNCTFSATV QTSLKSLILE DLMVKEDSKY RRLVASNDRQ SDRIAGRLNL SSFMSSSCPD LRAQGLYNPG SRSLPARLES
1601 DKSQWKSSVR AKAPQKKPIA KCPSTPPSSS SMMYHQRFTR SGVGDNNLVF IKILLVDPDS PDFALKYNST HRFIEINFNA
1681 LDVIINLESW VMVLDFFGTS TTKVSRQQKK KVAASSPGYQ DWSKMANAHT VNARWEVEVR SFSLLLNRKD YEVAEATISN
1761 LTWEMASMRG NLDVTGKLGS ITVQDLTSAG KMYRERFITS GNEALDFQFF CFSADDPQLA RDYDIRLNLN MASVLYVHTQ
1841 RFYTECFSML EQFQELRRVA GTFGATGQSG AASVSRKPWR HGTRILLNVE AGSPVILVPI CSTSEHLLVI DLGRISVSNK
1921 FVVTDGSVCV PTINKSRKAG LKGLPVVPIT ANPETVLVDV IQVELSNMDL CTGQRQKANR SQVGDLILGS YLIRRSGQSL
2001 LKDTCEMKLE VRRNLDSHLK HPVPDMDLCG LLSTVQCSVD EHQYKLVRGL LAFNLGEPVD FLHSDQPPPT SPIQLPDDSK
2081 PPMWAKLKIH IDLVDVMLEV KDSRIGAFST IKFIDSRLVY ESNSDGSKDV DLVSQQVVIR DTRYDASSAT HSATKKNVFT
2161 QILEPVTKAR REGSLQAEVH YRSTEDFTRF TVVLNNMRLL AVVDWWTLFR EFLLHSPDEY RGTNNDKGRN SEESDVKPHA
2241 KWTATSTRPS PIIVSTGVIS KRAALIDTRK VPVEFKINIS DSEVVIIEDT SVRESSAVIL KGTALLTYRP QIHSKPLSCQ
2321 LNRVEIFSSQ LNLEEETALS IVDPATISIE IVDKSSATDV KGILDATSSD LHQILEVQAQ QIILRLSYND MKLFMRILDS
2401 LPHQARLTSA ESTIVNEINK LKALGFSTDD CQTALRSCND NLEEAALWLT QNASTVTGQR QPEMAEIQIR GIEIRTGCVS
2481 LCVIDDCRDA DLPLAEITTS QLLLRQSIDV AQMTGEGTLT CQFAIDYYNR VLSGWEPFVE PFKCHVHWNF LAFNGSIANR
2561 PSQSIFFDTE DVVNLTCTRA LLELFGTVKR NWMEDYYGQN NKELSSLGDG SSVVRQRSPF VPFALHNATG SKIKFRTLTA
2641 SLLTEGAPSA ASTKSSRWIH CEAGDVVAFS FENRGKLRHH DSHQTQTHQL SIELDGWMEF GPVSVDRVGV YFRYASVHSS
2721 PSRRNTAAVE RDLERVLVVI AVTLEGSARR LVTVRSALQV TNNLEETVEL RLEPPAFNLH PSKTVRVPPC TTYPIPMSYL
2801 MSQIFVRPMA EKLPHAFSFC KDPIEWHAPT QTTANIRQCN PVISNQDLTY RFAVDIHREN FPPEKINTDD SEWTAQPAHT
2881 ITLLSPLVVV NLLPYELLWE LKAVGQSGII KPGKSTSIHT VNVSAGFQIA FRTENFVHSS DLVIGTSPHN FSTRLRLYDS
2961 ANRLLLLQVK ISSKAPGSVK LSISAPYWLV NKAGIPLIFR QEGVQQEAAG QFDEHEMARS LSPMLFSFTD REASHSLTAR
3041 IGTGLHLGCK PHWCQHFPLQ KGVRVRSFLV SPRDGRPELV YLVGISIRSG RGRYRDTQIV TLAPCYQLYN QSSWTLEVSQ
3121 AYFATTFTDP GAQSTYLNLV PGCHLPFHWP RLDKDQLLCV RLLDVKNCHW SGGFAIQNIS SFHINIRDGE SRANFLRVEI
3201 FQQECTFCVV FSDATGFPPP LRVDNLALVP IIFHQSDVPE AYLHTTVRPG SSMPYVFDEP TKPARLNIIA PGGASSSYDM

3281 TTLKEGSQLT YENFIYVCLT VTFNGDDMST GNALDPNNVE LVLDVPEGTR VVLSGKETGK RSQLWRMTGS GMLQHEGSSP
3361 PRDPSNPQID PSRILVLDIA GPALQPSEFV HLMLRKPDPR RQLTQTWHFT EDGRLCCGHS NVFVQAKDGF YGIRQGNDVV
3441 LGPAQSVTYY RLPSGIPAEQ AIHWQRLRPG SGCLSVKTIM DGPTRVLQVA DFLNKPSHCH SNENSVTAST DAEKTSNKQL
3521 KVEMKFKGGL GLSIVNHSPP EELAYCRLSN ISLELITGDG TLSIDASVQS IQIDDSLQDP HCPVVVYVSP SVNQDESKDM
3601 PALRLTVHRQ LTSRLNADIF KNLIVTFKNL TINIEENQLF KLLAFAGFNQ SDLELERIDE SEYESQRSLN AATSIDAKRY
3681 YFGILKLVLE QVRLSVYTSS KLPPELKAIK RKLGLTLIKF EDANIELHPF IRSHPFETAQ LIIDSVVKHY KDELKSQAAR
3761 ILGSTDFLGN PLGFVNDVSE GVSGFLYEGN VGGLVQNVTF GLSNSAAKVT GSLSDGLGRV TMDERHEEVR QRLLKHTGQS

3841 SDHLVAGLKG FGFGILGGMT SIFTQTYEGI SNEGLGGLFT GFGKGLVGTV TKPAVGVLDL ATGAASAVRD SSRSSSREIP
3921 RRIRPPRLVI GPGGIVPRYS EKQGRGQELL FQLNRHEYRE TFIAYEALGS LPESLHMLIS SEHIRVFSMN SPNKEVVLDI
4001 HLSELQSCKS VVIKDFGTQS TAHYYVELSL LLEPDNPLGA RRPQVRCDSE SLAKRVTQEI NYAKSVYEEN RHSLISSPKF
4081 SP
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	3238	3242	
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	3790	3794	
total 2 peptides												

tr|A0A0P5GPL7|A0A0P5GPL7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MNSFMSGNKE CNDLSDKYNV HFSDLQLLVC RVKDNWKQAH LKGTSALHLL DRFSILIHVE KYGRLVPGLE KPFLTLTASL
  81 PHLVAHINEP KIHALLSVSK QFRSNVVPTP VYETASEDGD TDETDASLAE TEKSEEHWFM AQFNIEQLSV EVQSRGRSVA
 161 ELQVGGVQAS YSMRPTDSSV HLAVHSLLLV DAMQTLGSDY ELLIASHKHV SMDSMSGSLK ESEPTSPVSP SSPDPSSHKG
 241 QRATSPVSLA QALTSLQTDP SWRKDGLSPP MARHRMATSA LKSEALILID IVTVEPTWVD GKAEGRIRII KVHFNSLDVI
 321 ANQDTVVELA SFFQRVMPKK TMPSNPDESN FSTGLPSNHS RFPPFALVPD GSTDITFDFH RLTILLLRSV VKEEMLIGRK
 401 VATLTVTEAH ISGNLASDVL VQGSLGGLQV LDLTPEGQKH QRVVSVGHDP LVEQHQNLYM LVSQGLYDTT KDKNEVKAFS
 481 FKFLQPGLEA PGEEEEGYKL SLEIRMASLC YSHSVHFLAE VAACVSEFKQ SVSNMAMSLK LTAAEMAVDL LHRGTEGLAQ
 561 SIYISGSTSV TEGLSLNAMK EANDEEQPSP PSRVRLSALL ESPILVLPKS AKSPQVLVAH LGQIEISNDI KVETEPPPQL
 641 SEELSGGTHK EHFEVEVRDM SLYSLNVDEK WKSSFSHFYT GPSAFLRITA QELYSCASPH GRPILHDTLL KFSLHRIVDR
 721 PILSDADPFL FPLTDFYPKL EVCDVFQVHG CVVSPLQVSL SKDQYQQIIQ SLDNLNWNKV DASSNFEAGP DPSTKNRAPA
 801 RVKQRELILN LKFQLPRFSM QLLDNSNRAI VSLSFEDFLV AYEQNCTFSA TVQTSLKSLI LEDLMVKEDS KYRRLVASND
 881 RQSDRIAGRL NLSSFMSSSC PDLRAQGLYN PGSRSLPARL ESDKSQWKSS VRAKAPQKKP IAKCPSTPPS SSSMMYHQRF
 961 TRSGVGDNNL VFIKILLVDP DSPDFALKYN STHRFIEINF NALDVIINLE SWVMVLDFFG TSTTKVSRQQ KKKVAASSPG
1041 YQDWSKMANA HTVNARWEVE VRSFSLLLNR KDYEVAEATI SNLTWEMASM RGNLDVTGKL GSITVQDLTS AGKMYRERFI
1121 TSGNEALDFQ FFCFSADDPQ LARDYDIRLN LNMASVLYVH TQRFYTECFS MLEQFQELRR VAGTFGATGQ SGAASVSRKP
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1361 VDEHQYKLVR GLLAFNLGEP VDFLHSDQPP PTSPIQLPDD SKPPMWAKLK IHIDLVDVML EVKDSRIGAF STIKFIDSRL
1441 VYESNSDGSK DVDLVSQQVV IRDTRYDASS ATHSATKKNV FTQILEPVTK ARREGSLQAE VHYRSTEDFT RFTVVLNNMR
1521 LLAVVDWWTL FREFLLHSPD EYRGTNNDKG RNSEESDVKP HAKWTATSTR PSPIIVSTGV ISKRAALIDT RKVPVEFKIN
1601 ISDSEVVIIE DTSVRESSAV ILKGTALLTY RPQIHSKPLS CQLNRVEIFS SQLNLEEETA LSIVDPATIS IEIVDKSSAT
1681 DVKGILDATS SDLHQILEVQ AQQIILRLSY NDMKLFMRIL DSLPHQARLI SAESESTIVN EINKLKALGF STDDCQTALR
1761 SCNDNLEEAA LWLTQNASTV TGQRQPEMAE IQIRGIEIRT GCVSLCVIDD CRDADLPLAE ITTSQLLLRQ SIDVAQMTGE
1841 GTLTCQFAID YYNRVLSGWE PFVEPFKCHV HWNFLAFNGS IANRPSQSIF FDTEDVVNLT CTRALLELFG TVKRNWMEDY
1921 YGQNNKELSS LGDGSSVVRQ RSPFVPFALH NATGSKIKFR TLTASLLTEG APSAASTKSS RWIHCEAGDV VAFSFENRGK
2001 LRHHDSHQTQ THQLSIELDG WMEFGPVSVD RVGVYFRYAS VHSSPSRRNT AAVERDLERV LVVIAVTLEG SARRLVTVRS
2081 ALQVTNNLEE TVELRLEPPA FNLHPSKTVR VPPCTTYPIP MSYLMSQIFV RPMAEKLPHA FSFCKDPIEW HAPTQTTANI
2161 RQCNPVISNQ DLTYRFAVDI HRENFPPEKI NTNDSEWNAQ PAHTITLLSP LVVVNLLPYE LLWELKAVGQ SGIIKPGKST
2241 SIHTVNVSAG FQIAFRTENF VHSSDLVIGT SPHNFSTRLR LYDSANRLLL LQVKISSKAP GSVKLSISAP YWLVNKAGIP
2321 LIFRQEGVQQ EAAGQFDEHE MARSLSPMLF SFTDREASHS LTARIGTGLH LGCKPHWCQH FPLQKGVRVR SFLVSPRDGR
2401 PELVYLVGIS IRSGRGRYRD TQIVTLAPCY QLYNQSSWTL EVSQAYFATT FTDPGAQSTY LNLVPGCHLP FHWPRLDKDQ
2481 LLCVRLLDVK NCHWSGGFAI QNISSFHINI RDGESRANFL RVEIFQQECT FCVVFSDATG FPPPLRVDNL ALVPIIFHQS
2561 DVPEAYLHTT VRPGSSMPYV FDEPTKPARL NIIAPGGASS SYDMTTLKEG SQLTYENFIY VCLTVTFNGD DMSTGNALDP
2641 NNVELVLDVP EGTRVVLSGK ETGKRSQLWR MTGSGMLQHE GSSPPRDPSN PQIDPSRILV LDIAGPALQP SEFVHLMLRK
2721 PDPRRQLTQT WHFTEDGRLC CGHSNVFVQA KDGFYGIRQG NDVVLGPAQS VTYYRLPSGI PAEQAIHWQR LRPGSGCLSV
2801 KTIMDGPTRV LQVADFLNKP SHCHSNENSV TASTDAEKTS NKQLKVEMKF KGGLGLSIVN HSPPEELAYC RLSNISLELI
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2961 NQLFKLLAFA GFNQSDLELE RIDESEYESQ RSLNAATSID AKRYYFGILK LVLEQVRLSV YTSSKLPPEL KAIKRKLGLT
3041 LIKFEDANIE LHPFIRSHPF ETAQLIIDSV VKHYKDELKS QAARILGSTD FLGNPLGFVN DVSEGVSGFL YEGNVGGLVQ
3121 NVTFGLSNSA AKVTGSLSDG LGRVTMDERH EEVRQRLLKH TGQSSDHLVA GLKGFGFGIL GGMTSIFTQT YEGISNEGLG
3201 GLFTGFGKGL VGTVTKPAVG VLDLATGAAS AVRDSSRSSS REIPRRIRPP RLVIGPGGIV PRYSEKQGRG QELLFQLNRH
3281 EYRETFIAYE ALGSLPESLH MLISSEHIRV FSMNSPNKEV VLDIHLSELQ SCKSVVIKDF GTQSTAHYYV ELSLLLEPDN
3361 PLGARRPQVR CDSESLAKRV TQEINYAKSV YEENRHSLIS SPKFSP
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	2562	2566	
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	3114	3118	
total 2 peptides												

tr|A0A0P5KVU5|A0A0P5KVU5_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MLVSQGLYDT TKDKNEVKAF SFKFLQPGLE APGEEEEGYK LSLEIRMASL CYSHSVHFLA EVAACVSEFK QSVSNMAMSL
  81 KLTAAEMAVD LLHRGTEGLA QSIYISGSTS VTEGLSLNAM KEANDEEQPS PPSRVRLSAL LESPILVLPK SAKSPQVLVA
 161 HLGQIEISND IKVETEHPPQ LSEELSGGTH KEHFEVEVRD MSLYSLNVDE KWKSSFSHFY TGPSAFLRIT AQELYSCASP
 241 HGRPILHDTL LKFSLHRIVD RPILSDADPF LFPLTDFYPK LEVCDVFQVH GCVVSPLQVS LSKDQYQQII QSLDNLNWNK
 321 VDASSNFEAG PDPSTKNRAP ARVKQRELIL NLKFQLPRFS MQLLDNSNRA IVSLSFEDFL VAYEQNCTFS ATVQTSLKSL
 401 ILEDLMVKED SKYRRLVASN DRQSDRIAGR LNLSSFMSSS CPDLRAQGLY NPGSRSLPAR LESDKSQWKS SVRAKAPQKK
 481 PIAKCPSTPP SSSSMMYHQR FTRSGVGDNN LVFIKILLVD PDSPDFALKY NSTHRFIEIN FNALDVIINL ESWVMVLDFF
 561 GTSTTKVSRQ QKKKVAASSP GYQDWSKMAN AHTVNARWEV EVRSFSLLLN RKDYEVAEAT ISNLTWEMAS MRGNLDVTGK
 641 LGSITVQDLT SAGKMYRERF ITSGNEALDF QFFCFSADDP QLARDYDIRL NLNMASVLYV HTQRFYTECF SMLEQFQELR
 721 RVAGTFGATG QSGAASVSRK PWRHGTRILL NVEAGSPVIL VPICSTSEHL LVIDLGRISV SNKFVVTDGS VCLPTINKSR
 801 KAGLKGLPVV PITANPETVL VDVIQVELSN MDLCTGQRQK ANRSQVGDLI LGSYLIRRSG QSLLKDTCEM KLEVRRNLDS
 881 HLKHPVPDMD LCGLLSTVQC SVDEHQYKLV RGLLAFNLGE PVDFLHSDQP PPTSPIQLPD DSKPPMWAKL KIHIDLVDVM
 961 LEVKDSRIGA FSTIKFIDSR LVYESNSDGS KDVDLVSQQV VIRDTRYDAS SATHSATKKN VFTQILEPVT KARREGSLQA
1041 EVHYRSTEDF TRFTVVLNNM RLLAVVDWWT LFREFLLHSP DEYRGTNNDK GRNSEESDVK PHAKWTATST RPSPIIVSTG
1121 VISKRAALID TRKVPVEFKI NISDSEVVII EDTSVRESSA VILKGTALLT YRPQIHSKPL SCQLNRVEIF SSQLNLEEET
1201 ALSIVDPATI SIEIVDKSSA TDVKGILDAT SSDLHQILEV QAQQIILRLS YNDMKLFMRI LDSLPHQARL ISAESTIANE
1281 INKLKALGFS TDDCQTALRS CNDNLEEAAL WLTQNASTVT GQRQPEMAEI QIRGIEIRTG CVSLCVIDDC RDADLPLAEI
1361 TTSQLLLRQS IDVAQMTGEG TLTCQFAIDY YNRVLSGWEP FVEPFKCHVH WNFLAFNGSI ANRPSQSIFF DTEDVVNLTC
1441 TRALLELFGT VKRNWMEDYY GQNNKELSSL GDGSSVVRQR SPFVPFALHN ATGSKIKFRT LTASLLTEGA PSAASTKSSR
1521 WIHCEAGDVV AFSFENRGKL RHHDSHQTQT HQLSIELDGW MEFGPVSVDR VGVYFRYASV HSSPSRRNTA AVERDLERVL
1601 VVIAVTLEGS ARRLVTVRSA LQVTNNLEET VELRLEPPAF NLHPSKTVRV PPCTTYPIPM SYLMSQIFVR PMAEKLPHAF
1681 SFCKDPIEWH APTQTTANIR QCNPVISNQD LTYRFAVDIH RENFPPEKIN TNDSEWNAQP AHTITLLSPL VVVNLLPYEL
1761 LWELKAVGQS GIIKPGKSTS IHTVNVSAGF QIAFRTENFV HSSDLVIGTS PHNFSTRLRL YDSANRLLLL QVKISSKAPG
1841 SVKLSISAPY WLVNKAGIPL IFRQEGVQQE AAGQFDEHEM ARSLSPMLFS FTDREASHSL TARIGTGLHL GCKPHWCQHF
1921 PLQKGVRVRS FLVSPRDGRP ELVYLVGISI RSGRGRYRDT QIVTLAPCYQ LYNQSSWTLE VSQAYFATTF TDPGAQSTYL
2001 NLVPGCHLPF HWPRLDKDQL LCVRLLDVKN CHWSGGFAIQ NISSFHINIR DGESRANFLR VEIFQQECTF CVVFSDATGF
2081 PPPLRVDNLA LVPIIFHQSD VPEAYLHTTV RPGSSMPYVF DEPTKPARLN IIAPGGASSS YDMTTLKEGS QLTYENFIYV

2161 CLTVTFNGDD MSTGNALDPN NVELVLDVPE GTRVVLSGKE TGKRSQLWRM TGSGMLQHEG SSPPRDPSNP QIDPSRILVL
2241 DIAGPALQPS EFVHLMLRKP DPRRQLTQTW HFTEDGRLCC GHSNVFVQAK DGFYGIRQGN DVVLGPAQSV TYYRLPSGIP
2321 AEQAIHWQRL RPGSGCLSVK TIMDGPTRVL QVADFLNKPS HCHSNENSVT ASTDAEKTSN KQLKVEMKFK GGLGLSIVNH
2401 SPPEELAYCR LSNISLELIT GDGTLSIDAS VQSIQIDDSL QDPHCPVVVY VSPSVNQDES KDMPALRLTV HRQLTSRLNA
2481 DIFKNLIVTF KNLTINIEEN QLFKLLAFAG FNQSDLELER IDESEYESQR SLNAATSIDA KRYYFGILKL VLEQVRLSVY
2561 TSSKLPPELK AIKRKLGLTL IKFEDANIEL HPFIRSHPFE TAQLIIDSVV KHYKDELKSQ AARILGSTDF LGNPLGFVND
2641 VSEGVSGFLY EGNVGGLVQN VTFGLSNSAA KVTGSLSDGL GRVTMDERHE EVRQRLLKHT GQSSDHLVAG LKGFGFGILG

2721 GMTSIFTQTY EGISNEGLGG LFTGFGKGLV GTVTKPAVGV LDLATGAASA VRDSSRSSSR EIPRRIRPPR LVIGPGGIVP
2801 RYSEKQGRGQ ELLFQLNRHE YRETFIAYEA LGSLPESLHM LISSEHIRVF SMNSPNKEVV LDIHLSELQS CKSVVIKDFG
2881 TQSTAHYYVE LSLLLEPDNP LGARRPQVRC DSESLAKRVT QEINYAKSVY EENRHSLISS PKFSP
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	2101	2105	
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	2653	2657	
total 2 peptides												

tr|A0A0P5HCC7|A0A0P5HCC7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MANAHTVNAR WEVEVRSFSL LLNRKDYEVA EATISNLTWE MASMRGNLDV TGKLGSITVQ DLTSAGKMYR ERFITSGNEA

81 LDFQFFCFSA DDPQLARDYD IRLNLNMASV LYVHTQRFYT ECFSMLEQFQ ELRRVAGTFG ATGQSGAASV SRKPWRHGTR

161 ILLNVEAGSP VILVPICSTS EHLLVIDLGR ISVSNKFVVT DGSVCVPTIN KSRKAGLKGL PVVPITANPE TVLVDVIQVE

241 LSNMDLCTGQ RQKANRSQVG DLILGSYLIR RSGQSLLKDT CEMKLEVRRN LDSHLKHPVP DMDLCGLLST VQCSVDEHQY

321 KLVRGLLAFN LGEPVDFLHS DQPPPTSPIQ LPDDSKPPMW AKLKIHIDLV DVMLEVKDSR IGAFSTIKFI DSRLVYESNS

401 DGSKDVDLVS QQVVIRDTRY DASSATHSAT KKNVFTQILE PVTKARREGS LQAEVHYRST EDFTRFTVVL NNMRLLAVVD

481 WWTLFREFLL HSPDEYRGTN NDKGRNSEES DVKPHAKWTA TSTRPSPIIV STGVISKRAA LIDTRKVPVE FKINISDSEV

561 VIIEDTSVRE SSAVILKGTA LLTYRPQIHS KPLSCQLNRV EIFSSQLNLE EETALSIVDP ATISIEIVDK SSATDVKGIL

641 DATSSDLHQI LEVQAQQIIL RLSYNDMKLF MRILDSLPHQ ARLISAESVN EINKLKALGF STDDCQTALR SCNDNLEEAA

721 LWLTQNASTV TGQRQPEMAE IQIRGIEIRT GCVSLCVIDD CRDADLPLAE ITTSQLLLRQ SIDVAQMTGE GTLTCQFAID

801 YYNRVLSGWE PFVEPFKCHV HWNFLAFNGS IANRPSQSIF FDTEDVVNLT CTRALLELFG TVKRNWMEDY YGQNNKELSS

881 LGDGSSVVRQ RSPFVPFALH NATGSKIKFR TLTASLLTEG APSAASTKSS RWIHCEAGDV VAFSFENRGK LRHHDSHQTQ

961 THQLSIELDG WMEFGPVSVD RVGVYFRYAS VHSSPSRRNT AAVERDLERV LVVIAVTLEG SARRLVTVRS ALQVTNNLEE

1041 TVELRLEPPA FNLHPSKTVR VPPCTTYPIP MSYLMSQIFV RPMAEKLPHA FSFCKDPIEW HAPTQTTANI RQCNPVISNQ

1121 DLTYRFAVDI HRENFPPEKI NTNDSEWNAQ PAHTITLLSP LVVVNLLPYE LLWELKAVGQ SGIIKPGKST SIHTVNVSAG

1201 FQIAFRTENF VHSSDLVIGT SPHNFSTRLR LYDSANRLLL LQVKISSKAP GSVKLSISAP YWLVNKAGIP LIFRQEGVQQ

1281 EAAGQFDEHE MARSLSPMLF SFTDREASHS LTARIGTGLH LGCKPHWCQH FPLQKGVRVR SFLVSPRDGR PELVYLVGIS

1361 IRSGRGRYRD TQIVTLAPCY QLYNQSSWTL EVSQAYFATT FTDPGAQSTY LNLVPGCHLP FHWPRLDKDQ LLCVRLLDVK

1441 NCHWSGGFAI QNISSFHINI RDGESRANFL RVEIFQQECT FCVVFSDATG FPPPLRVDNL ALVPIIFHQS D**VPEAY**LHTT

1521 VRPGSSMPYV FDEPTKPARL NIIAPGGASS SYDMTTLKEG SQLTYENFIY VCLTVTFNGD DMSTGNALDP NNVELVLDVP

1601 EGTRVVLSGK ETGKRSQLWR MTGSGMLQHE GSSPPRDPSN PQIDPSRILV LDIAGPALQP SEFVHLMLRK PDPRRQLTQT

1681 WHFTEDGRLC CGHSNVFVQA KDGFYGIRQG NDVVLGPAQS VTYYRLPSGI PAEQAIHWQR LRPGSGCLSV KTIMDGPTRV

1761 LQVADFLNKP SHCHSNENSV TASTDAEKTS NKQLKVEMKF KGGLGLSIVN HSPPEELAYC RLSNISLELI TGDGTLSIDA

1841 SVQSIQIDDS LQDPHCPVVV YVSPSVNQDE SKDMPALRLT VHRQLTSRLN ADIFKNLIVT FKNLTINIEE NQLFKLLAFA

1921 GFNQSDLELE RIDESEYESQ RSLNAATSID AKRYYFGILK LVLEQVRLSV YTSSKLPPEL KAIKRKLGLT LIKFEDANIE

2001 LHPFIRSHPF ETAQLIIDSV VKHYKDELKS QAARILGSTD FLGNPLGFVN DVSEGVSGFL YEG**NVGGL**VQ NVTFGLSNSA

2081 AKVTGSLSDG LGRVTMDERH EEVRQRLLKH TGQSSDHLVA GLKGFGFGIL GGMTSIFTQT YEGISNEGLG GLFTGFGKGL

2161 VGTVTKPAVG VLDLATGAAS AVRDSSRSSS REIPRRIRPP RLVIGPGGIV PRYSEKQGRG QELLFQLNRH EYRETFIAYE

2241 ALGSLPESLH MLISSEHIRV FSMNSPNKEV VLDIHLSELQ SCKSVVIKDF GTQSTAHYYV ELSLLLEPDN PLGARRPQVR

2321 CDSESLAKRV TQEINYAKSV YEENRHSLIS SPKFSP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.VPEAY.L	Y	29.50	577.2748	59.2	578.3162	1	0.52	1082	1	1512	1516	
G.NVGGL.V	N	17.54	458.2489	5.1	459.2585	1	0.43	999	1	2064	2068	
total 2 peptides												

tr|T1J2W4|T1J2W4_STRMM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAPDYKKTIN QKAMLGSLQK INMLSSVDVE KQLIDQAVQV NLCDIANNPK QTEEKTTNTA PWVGFLERER KLMLVHNISQ

81 GMKRYHEDFI RFSRNNYPRL AVVVTDFHII ITRPVLFDLL FPGDSVVKLV VTLNTDQCNF VITFGATVPV PIWNKNNLDT

161 EAAKKYLNFL DPKNRFVYCS GINSKTCTSG HFNEIVKYRL **GSFERW**QSKK CRVWFKAGAS VSYVVILSGL SKCQHCRNLT

241 LKMKQVSSTV VAMKNRMPVV IPQVD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GSFERW.Q	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	201	206	
total 1 peptides												

tr|A0A212FH02|A0A212FH02_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSEKCITAVI VVVLTVLICE ERADYCGCKT VRPCYKRMLD ELLGEDEDAC IENVAIGAST VTIFLKAIST YCDKFIKLYD

81 IATTYEGKIL YEVAMSRYVN EEIEKVTNGS KIKPVILLDA GQDAGSETVG FALYIIEQLA ACVENKDMIR NFLWIILPST

161 NPDGQEYSR**G SFERW**QKNYR SIMDYEATGV DITRNFDDFF TECFRVENKF SQNYQGPHPN SENETKFITN VMKKYKSGIK

241 TYISFRRNGH AILYPFASRN VSLDNMQKTK MKSDEIAKKE SLFHFSVGCW SCAVMVAERA CARGGARGRT ARYHSVVSRG

321 GGDASSANSS QHLQS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.GSFERW.Q	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	170	175	
total 1 peptides												

tr|A0A0L0CEB7|A0A0L0CEB7_LUCCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1	STEYSSSTES	SLSTDSSLSS	DAYSSTESSS	STESSLSTES	SSTSDIDTTS	SDIYSSTDVS	ESTFVTKIST	DITKSTDSSD
81	TTSSDFTDKY	TVSLATDSSE	TTDISKSTDS	ESTTVSLHTD	TSESYSSTEI	STESSGATGS	SESTSFKDES	ETTVSEDISS
161	SSDSSTYSSS	VTDTSTESSS	ATDKIDSTEI	STGSTDSSTE	KTESTETTES	TESTETTDST	SLDSTESSIS	TETITESSVS
241	TTNLPTDSSV	TDSTESSEST	ETTDSTSLGS	TESSLSTETI	TESSVSTTNL	PTDSSVTDST	ESTVTTESTD	STDLSNSDST
321	ESTISTEPTT	ESSVYTTVQS	TGSTASDSTN	FSEASEYTDF	TDSSTSDLRD	STLQTDTTTE	SPVSTTDQST	DSTDFASTDS
401	SAATESSETT	DLTSSTDIFT	STELLASTES	SIWTSSSTKL	YETTVSSETS	STSTDVTLSS	DSTTVISSTD	IITSLKSSTD
481	VSESTDTSYT	SESSDELTET	SSTLGISDTT	DFSTETIGQE	SSGDTTLETE	STVIFDSTTD	TSGDSSLSTN	EFTTVDIWTT
561	EEDYEKSTPN	TLEAAITKES	KVKKCKAKKL	KDCKKTEHGC	CPDGKHIAKG	PFDKGCPIAK	TCAETEFGCC	HDGVSPAGGK
641	NFEGCPQSQC	AETLFGCCPD	KFTAAEGEDY	EGCPEPTTLP	PTTTTEIPEE	TTELLESESA	ETYSTNIPET	TDVFSTDSTD
721	IQETTDIFDT	TDISETTDAT	QTKVTVQSCS	FSEFGCCPDG	KTVASGKNFA	GCEDVFDEKN	CRNSLFGCCN	DGRTSATGPD
801	NEGCPACTYE	PYGCCPDNET	PAHGPLGEGC	CLNSPFGCCP	DNINSARGPN	FEDCECQYAP	YGCCPDKKTA	ARGPNSEGCG
881	CETLEFGCCP	DKLTPALGPK	FEGCSCHTLQ	FGCCPDGITV	AQGPHHYGCH	CSQTEFKCCP	DEKTPAKGPN	NEGCTCLESK
961	YGCCPDGVTS	AQGDKFDGCE	NVKEPPQMSC	KLPKETGTCG	NFSIKFFFDT	SYGACAKFWY	GGCGGNGNRF	DSESECKETC
1041	QEFKGKDACL	LPKSQGPCTG	YITKWYFDSD	RGRCEEFKYG	GCYGTNNRFD	SLEECQSLCT	VSESIPTCEQ	PMDEGPCE**GS**
1121	**FERW**YYDNAT	DVCRPFRYGG	CKGNKNNYPT	EHACNYHCRQ	PGVHKDYCSL	PKKTGDCGEK	HARWHYSEAD	KKCMPFYYTG
1201	CGGNKNNFQS	LESCEDHCPK	QVAKDICEIP	AEVGECTNYE	PMWYYDTKDQ	RCRQFYYGGC	GGNENKFTSE	DACNQRCEKK
1281	SEPQPEPQPE	PQPEVVQPPT	DINVCDEKPA	QGECDNYTMV	WHFDKEHSVC	RQFYYGGCGG	NGNRFESQAD	CERQCIGESQ
1361	AVPEPVPVQP	EQPTNENVCL	LPQDTGDCDD	YMPYWYFDST	ISQCSSFYYG	GCGGNGNRFT	SEEECLKHCS	AEPGFQTRFE
1441	PDLEASPEID	DTRKCFLPVA	TGNCLDNQVR	WYYNSVDGVC	DEFVYTGCGG	NANSYASEDE	CENECFPAQE	TCVLPPLRGN
1521	GTESMIRWHF	NEEIGRCSEF	EFTGGRGNRN	NFVTEQECMS	RCGSGEQPAS	TYSVCDQPLE	AGECDNSTTA	WYYDNESMIC
1601	VAFTYTGCGG	NGNRFQSREQ	CERQCGEFKG	VDVCNEEVAT	GPCRQWQTRY	YFNKTSRICE	PFTYGGCQGT	GNRFENRGEC
1681	ESVCLIGQEP	TFPHNKGTKT	IYFLLQDKPN	HSIMSPDICK	QEVDVGRCRG	RSETQRRWYY	DDARGNCISF	IYSGCAGNQN
1761	NFRSYESCYD	FCSKTDITNE	VLPNRCESYE	NECNSMSCPY	GVRRIPVDDN	ECQRCECNNP	CADHTCNDGQ	QCAIEVSPNV
1841	PGQFIPVCRL	SNKPGLCPQL	SADDGICGRE	CYTDADCRDD	NKCCSNGCGF	VCVRPTPPTV	RTTAPTTAAP	VVVYPGEVRA
1921	SLAPKEKQEL	DVQTPMGGIA	VLRCFATGNP	APNVTWSRNN	VVVDTNQGRY	VLTSSGDLTI	VQVRQTDSGS	YVCVASNGLG
2001	EPVRREVELQ	VTEPVNLPAY	VYGDRNVTQV	VTLNRPAVVR	CPAGGHPAPM	VHWWRNRSRL	PLVSQRYELA	RDYSLTFRSV
2081	KLSDLGPYTC	DAWNRLSRRP	ASIKVTLVAV	GPARAVTNED	AQYLQYIVEP	PKAPVTQRPS	FPYRPTRPPA	IPPPYVPAIP
2161	VSAVVGMDPN	NNYTPGSTIA	IGCSVQGYPK	PNVTWIKDGL	PLLPSERIQI	SVGEPYRLVI	NNINSADSGK	YGCKAANAVS
2241	YSISEESVNV	ESKYNYFFNS	TMPFLEDSGI	ESEDKSSLLA	EEHDLNYLLR	NNTEEHMANL	EVKFSGPTSI	ITKSQASSLK
2321	ATSSSQTNIS	NEPEESLKPP	NTCEPYRLVI	NNINSADSGK	YGCKAANAVS	YSISEESVNV	ESKYNYFFNS	TMPFLEDSGI
2401	ESEDKSSLLA	EEHDLNYLLR	NNTEEHMANL	DVKFSGPTSI	ITKSQASSLK	ATSSSQTNIS	NEPEESLKPP	NTCRILQRKL
2481	ELKVERAKRN	YSHYQETNKR	KSQSATLIPI	SRLSIPGDLE	QKPLVDYKSE	SDDCEEISFF	PNEHHKVRSK	RQAELSDTFS
2561	IQEMTIDSDL	ESNDSQNLEL	LTPHLKRSFI	DYLAMCLCFH	QSS			

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.GSFERW.Y	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	1119	1124	
total 1 peptides												

tr|A0A0L0BYV5|A0A0L0BYV5_LUCCU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MDLSRRSRLP PLIGFILLLC IQTSQSRFFG ERLKRQNGAH MYLPASSIIP GGEGDDSTEW SDWSSASECS RSCGGGVSFQ
  81 TRECLRTAPN GAPICKGGNR KYFSCNTQDC PEGEPDFRSQ QCSRFNHQPF DGIFYEWIPY KNAPNPCELN CMPNGERFYY
 161 KHKAKVIDGT RCNDKDLDVC VDGQCQPVGC DMMLGSDAKE DICRKCGGDG TTCRTIADRF TTNNLAAGYN DLLLIPSGAT
 241 NIRIQETSPS NNYLACRNLS SHYYLNGNFR IDFPRSMEFA GSWWNYQRKP MGFAAPDQLT CLGPINEPIF IVMLVQDKNV
 321 SIEYEYSIPQ SVSSSTPDVY TWTHMEYGPC TASCGGGTQT RTVTCNNRLN LKEVDVSFCD ERAKPAESQE CGMEPCAPHW
 401 VTSEWGKCSK GCGSDGMQNR TVTCERTSAT GENTIEEDSV CLEEVGNKPA NQQECNRDIE NCPKYHLGPW TPCDKLCGEG
 481 KQKRKVTCYI EENGRKKVLN DDDCIEEKPE TEKVCMLTPC EGVDWIISPW SGCDACGQTT ETRTAICASK SGKVYDDEFC
 561 APETPSLSRP CESKKCKTLW FTSEWSKCSS PCGKGIQSRV VLCGEYDGKT ITKVTDDSQC DVTSKPEAEQ ECEGDDKECP
 641 GQWFTGPWES CTKPCGGGER QREVLCLTNG TKSNNCDESK IQSLSEKCNT QACTEDEVMP VESTDKQVTD EEYEEDCEEE
 721 DDDNIKYVTD KMSEDLKTSD GIDFDEESTM SSLITDDLML SDSTPSVDTT DEEISTDTPL TTVDGSGDEA ESTEFSSIAT
 801 EGSGDGKQKR KVTCYIEENG RKKVLNDDDC IEEKPETEKV CMLTPCEGVD WIISPWSGCD ACGQTTETRT AICASKSGKV
 881 YDDEFCAPET PSLSRPCESK KCKTLWFTSE WSKCSSPCGK GIQSRVVLCG EYDGKTITKV TDDSQCDVTS KPEAEQECEG
 961 DDKECPGQWF TGPWESCTKP CGGGERQREV LCLTNGTKSN NCDESKIQSL SEKCNTQACT EDEVMPVEST DKQVTDEEYE
1041 EDCEEEDDDN IKYVTDKMSE DLKTSDGIDF DEESTMSSLI TDDLMLSDST PSVDTTDEEI STDTPLTTVD GSGDEAESTE
1121 FSSIATEGSG DGIETTSETT DRSQSTDPSE STGSDYTEST ISSTEESSST EYSSSTESSL STDSSLSSDA YSSTESSSST
1201 ESSLSTESSS TSDIDTTSSD IYSSTDVSES TFVTKISTDI TKSTDSSDTT SSDFTDKYTV SLATDSSETT DISKSTDSES
1281 TTVSLHTDTS ESYSSTEIST ESSGATGSSE STSFKDESET TVSEDISSSS DSSTYSSSVT DTSTESSSAT DKIDSTEIST
1361 GSTDSSTEKT ESTETTESTE STETTDSTSL DSTESSISTE TITESSVSTT NLPTDSSVTD STESSESTET TDSTSLGSTE
1441 SSLSTETITE SSVSTTNLPT DSSVTDSTES TVTTESTDST DLSNSDSTES TISTEPTTES SVYTTVQSTG STASDSTNFS
1521 EASEYTDFTD SSTSDLRDST LQTDTTTESP VSTTDQSTDS TDFASTDSSA ATESSETTDL TSSTDIFTST ELLASTESSI
1601 WTSSSTKLYE TTVSSETSST STDVTLSSDS TTVISSTDII TSLKSSTDVS ESTDTSYTSE SSDELTETSS TLGISDTTDF
1681 STETIGQESS GDTTLETEST VIFDSTTDTS GDSSLSTNEF TTVDIWTTEE DYEKSTPNTL EAAITKESKV KKCKAKKLKD
1761 CKKTEHGCCP DGKHIAKGPF DKGCPIAKTC AETEFGCCHD GVSPAGGKNF EGCPQSQCAE TLFGCCPDKF TAAEGEDYEG
1841 CPEPTTLPPT TTTEIPEETT ELLESESAET YSTNIPETTD VFSTDSTDIQ ETTDIFDTTD ISETTDATQT KVTVQSCSFS
1921 EFGCCPDGKT VASGKNFAGC EDVFDEKNCR NSLFGCCNDG RTSATGPDNE GCPACTYEPY GCCPDNETPA HGPLGEGCCL
2001 NSPFGCCPDN INSARGPNFE DCECQYAPYG CCPDKKTAAR GPNSEGCGCE TLEFGCCPDK LTPALGPKFE GCSCHTLQFG
2081 CCPDGITVAQ GPHHYGCHCS QTEFKCCPDE KTPAKGPNNE GCTCLESKYG CCPDGVTSAQ GDKFDGCENV KEPPQMSCKL
2161 PKETGTCGNF SIKFFFDTSY GACAKFWYGG CGGNGNRFDS ESECKETCQE FKGKDACLLP KSQGPCTGYI TKWYFDSDRG
2241 RCEEFKYGGC YGTNNRFDSL EECQSLCTVS ESIPTCEQPM DEGPCEGSFE RWYYDNATDV CRPFRYGGCK GNKNNYPTEH

2321 ACNYHCRQPG VHKDYCSLPK KTGDCGEKHA RWHYSEADKK CMPFYYTGCG GNKNNFQSLE SCEDHCPKQV AKDICEIPAE
2401 VGECTNYEPM WYYDTKDQRC RQFYYGGCGG NENKFTSEDA CNQRCEKKSE PQPEPQPEPQ PEVVQPPTDI NVCDEKPAQG
2481 ECDNYTMVWH FDKEHSVCRQ FYYGGCGGNG NRFESQADCE RQCIGESQAV PEPVPVQPEQ PTNENVCLLP QDTGDCDDYM
2561 PYWYFDSTIS QCSSFYYGGC GGNGNRFTSE EECLKHCSAE PGFQTRFEPD LEASPEIDDT RKCFLPVATG NCLDNQVRWY
2641 YNSVDGVCDE FVYTGCGGNA NSYASEDECE NECFPAQETC VLPPLRGNGT ESMIRWHFNE EIGRCSEFEF TGGRGNRNNF
2721 VTEQECMSRC GSGEQPASTY SVCDQPLEAG ECDNSTTAWY YDNESMICVA FTYTGCGGNG NRFQSREQCE RQCGEFKGVD
2801 VCNEEVATGP CRQWQTRYYF NKTSRICEPF TYGGCQGTGN RFENRGECES VCLIGQEPTF PHNKGTKTIY FLLQDKPNHS
2881 IMSPDICKQE VDVGRCRGRS ETQRRWYYDD ARGNCISFIY SGCAGNQNNF RSYESCYDFC SKTDITNEVL PNRCESYENE
2961 CNSMSCPYGV RRIPVDDNEC QRCECNNPCA DHTCNDGQQC AIEVSPNVPG QFIPVCRLSN KPGLCPQLSA DDGICGRECY
3041 TDADCRDDNK CCSNGCGFVC VRPTPPTVRT TAPTTAAPVV VYPGEVRASL APKEKQELDV QTPMGGIAVL RCFATGNPAP
3121 NVTWSRNNVV VDTNQGRYVL TSSGDLTIVQ VRQTDSGSYV CVASNGLGEP VRREVELQVT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.GSFERW.Y	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	2287	2292	
total 1 peptides												

tr|A0A1A9X2L8|A0A1A9X2L8_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MYLSASYIVP GGEGDDPYEW TDWSSPSECS RSCGGGVSYQ MRECRRLAPS GAPLCSGGNR KYFSCNTQDC PEEETDFRAQ
  81 QCSRFNHVPF DGIYYEWVPY MGSPNPCQLS CMPKGERFYY VHKAKVIDGT RCNDQSLDVC VDGQCQSVGC DMMLGSDARE
 161 DKCRKCGGDG STCKTVGDKF TINNLSAGYN DILLIPTGAT NIRVMETAPS NNYIACRNLS SHYYLNGNWR IDFPRPMFFA
 241 GAWWNYQRRP TGFAAPDQLT CHGPIIESIY IVMLVQDKNV SIDYEYSIPT TVSSSTPDVY TWTHMEYGQC SATCGGGTQW
 321 RVVTCNNRLN LEQVDPSLCD QEAKPTEAQE CATDPCPPQW VSSDWSKCSK GCGSDGIQNR NVTCERSSSK GESIVEDDTI
 401 CLDKVGNKPA TQQECNRDVK NCPKYHLGPW SPCDKLCGEG AQKRKVTCFI EENGRKRVLS DDDCVEEKPE TEKSCILAPC
 481 EGVDWIISEW SGCGDCGQTT ETRFAICASK AGKVYPEEFC APEVPLLSRP CESKKCQIQW FTSEWSKCSS ACGKGVQSRT
 561 VLCGEYDGES ITKVVDASQC DEATKPDSEQ ECEGEEKECP GQWFTGPWGP CSKQCGGGER QREVLCLANG TKSTNCDESK
 641 IESLSEKCNV HACTEDEVMP VDSTDKQLTD DEDEEEEEEC DEDEEDEDEV EVVTGKMSED LRISDGIDLD QEITTISSLI
 721 TDELMLSDAP SDEPTPEDGS TLITPEGSGD EVDDSTLVTE GSGETDVTGS SVEVTTNTES SISSESTSLF STESITRSST
 801 LGSASTDLTS ETSTTMSTFT AVSTDSTSEF STDTSALPES GSTEVSGTTD LTSESSTEVS ISTSRSSESS TDLASESSTE
 881 HSASTGGSSE SSIDTSALTD STSEESTTSE SSTEFSKSFT DSTESTEASS ESSTEYSLST EASSHSSADS TETITDSSES
 961 TSESSTESTE STSESSTDST ESTSTDITSS TESTTQDSAE SSTESSTADS TESSTESTES STETPVSTES SVSTETSLST
1041 ESSVFTETSA STESSTSTDS SVFTESSAES TSESSTELST ESSTDSALST ESTSESSTET SIGTESTGSS SSTDIKTESS
1121 TEIFASTDSS LSTELTSEVS TDITASTTDS ATEFSTSTET AETVTESSDL TESTDSLVST VEISSTLSSA STESIDSSTI
1201 SSYESTDSSE TTVIDSTKSG STVSSSKIYD FSTTDSTESE YTDSSTSAYK STTVDIWSTE EEVQQSTPYT LETIVTKAVK
1281 PKKCKPKTCE KSPYGCCPDH KTKAKGPFDE GCPIPKTCDE TEFGCCHDGV SAAEGKNFEG CPKSQCAETL FGCCPDKFTP
1361 ADGEENEGCP EPTTLPPTTT TEMSTTEETA SEEQATDITD STSFEITETT DSAMPPYVPS CSFNEFGCCP DGQTNAIGEN
1441 FAGCEKGDCR ESIYGCCRDG RTLASGPNEE GCPQCTFEPY GCCPDNETPA HGPLGEGCCL ASVYGCCPDN INSAHGPNFE
1521 NCECQYSPYG CCPNNQTSAR GPSYEGCSCE SAKFGCCPDK LTAAKGPKFE GCACHTLQFG CCPDGITVAQ GPHHYGCHCS
1601 QTEFKCCPDE NTPAKGPDNE GCSCVESKFG CCPDGITSAQ GEKFEECKNV KESPQKSCGL PKESGPCTNY TIKYFFDTSY
1681 GACARFWYGG CEGNGNRFES EDDCKQTCQD YIGKDACLLP KSSGPCTGYN KKWYFNADLD RCEEFNYGGC YGTNNRFDSR
1761 EECQTLCAVS ESLPPCEQPM DEGPCEGSFE RWHYDNQTDT CRPFTYGGCK GNKNNYPTEH ACNYHCRQPG IHKDYCSLPK

1841 QTGDCSAKQP RWYYSENDKK CMPFYYTGCG GNRNNFPSLQ SCEDHCPKEV AKNVCEIAAE VGDCRNYEPM WYYDVNDERC
1921 RQFYYGGCGG NDNKFSTEDA CKQRCEEPSQ PETPLVAPQP EPEPQPERPP LLGEACEQNF EVGECTNYTL SWYYDYDQSI
2001 CRQFYYGGCG GNDNRFETEI ECQQRCILPP PDNSTEYSGE GSQESSKCFL PVASGNCLGY QMRWYYNSID GVCEEFTYTE
2081 CEGNANNFAS EDECESECFA AQPTCSLPPV RGNCSDAMIR WHFEPQSGKC LEFEFSGCRP NRNNFKTEEE CMVFCGERPP
2161 TPVYSVCDLP LEAGECDNQT TAWYYDGESM TCVAFTYTGC GGNGNRFQTR EQCERQCGDF KGVDVCNEDV MTGPCRQWQT
2241 RYYFNKITRT CEPFTYGGCQ GTGNRFEDRA ECESVCIIGQ EPTYPVHKGK LLNSIHNCHH SYLCPSMLSS DICKQNVDIG
2321 RCLGPSVNER RWYYDDARGT CVAFIYSGCA GNQNNFRTFE SCYDFCAREL APPSPPVADN EVFIPCEEYE AECQTLRCPY
2401 GQRRVPVDNC HRCECVNPCA EYSCPEGQKC AIEIPAARSS QFLPVCRAIT KPGECPLLTA TGGSCSRECY DDADCRAHNK
2481 CCATGCSFVC VRPTPPTVPT TPSPPTATPA VIYPGEFAVK LEPKNKPELD VKTPVGGIAV LRCFATGNPA PNITWFFNNI
2561 LIDTHHGRYV LTSTGDLTIV QVRQTDTGSY VCVAGNGLGD PLRREIELQV TEPVNMPAYV YGNKNATQIV TLNRPAVVRC
2641 PAGGHPAPMV YWWRNRERLP LVHQRYEFTR DYSLRFHSMQ LSDLGPYTCH VWNRVSTRPA SIKITLKAFG PARAISNDEA
2721 QYLQYIIDPA QAPTTQRPSY PYRPARPVAV PPPAVYEVPT RPPVRANAVI GMDPNNSYIP GSTITIGCAV QGYPKPNVTW
2801 IKDDLTIVPS ERIQTTQSEP YRLIISDVNA GDSGKYGCKA ANNVSYSISE ETVTIESTIP LSNDCIDNAH FANCKLIVAG
2881 RYCKNKYYAK FCCRSCALAG QL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.GSFERW.H	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	1787	1792	
total 1 peptides												

tr|A0A1J1J7A5|A0A1J1J7A5_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MRIIKYCNST GGSLALLFFM LTQQISLAHS KHRHIVHRHK RQHGANLYLP ETYIIPGGEG TESEWGQWST PSECSRTCGG
  81 GVAYQSRECL IIGRDGEPSC QGGNKKYFSC NTQDCPDDEA DFRHQQCSYF DRTPFEDVYY NWVPYTKAPN PCELNCMPRG
 161 ERFYYRHKSK VIDGTRCNDH SVDVCVDGQC QPVGCNLMLG SPAREDKCRK CQGDGSSCKT VTGLLDMNNL QVGYNDILLI
 241 PQGATNIAIQ ERSPSNNYIA IRNLTGHYYL NGNYRIDFPR PMTFAGSLWT YERKPNGFAA PDKITCLGPI DEAVYLVLLS
 321 QDQNVGVNYE YSVPRAAAAP EEPEIYSWAF TKFEVCSKSC GGGHQARNVT CTKQRTSEEV DESLCDSSQK PAEWQKCGLL
 401 DCAPQWIEGE WGKCSAPCGQ SGKKERKVHC EKINANGAVT VVDDEVCLEL VGNKPATESS CNEGKICPSW FTGKWQPCNK
 481 LCGEGKKTRQ VICYRKEENG DITVLDDKDC SDEKPEEEMD CMIVPCEGVE YITSSWSGCD VCGATVETRS VQCASKAGKI
 561 YNETFCNKKP KPELSRPCNA TPCDYAWFTS QWTKCSAECG KGLENRVVVC GKLEGDVIKK ADESKCEEIE KPEDERECDG
 641 PKECPAQWFA GPWTKCSKRC GGGIRTRKVI CLGIDGATET NKCQEDKILF ASDDCNMDAC VDDELLPVDT TSQPVEEDDE
 721 SEEWCDEDYE EMTTDQNGVL KVTSDYTDLS SGIDFSSMAS TESSPLTEEL MLSDATGFET DVTDETTDMS IEGSGSSTSD
 801 MDLESRFDGS GTDESTSVTS DKTMMTSSGL SSISEESTSA SSDDTTESLS SLDSTKDSTE ESDITTESDS DSSTSSPTSE
 881 SSSETSKSSV DGSSSSISTE SSSSSDSTDS SISSDSTDSS SSSDSTDSSI SSDSTTDSSS TSDDTTTESD SSTSESITTE
 961 SSSSESSTDQ DTIIQSTTRD LADYEIQTSS FDYSTELSTE EVSEESSSEV TTVSSETSNS ETTESDGTSD STDSTDTSDF
1041 TDTTDSTDKS DSTDNTESTD TSDSTDTTDS AETTETTETT EEFTGSTDST DFTSTTENSS TEATESTQTD ESSTTGDEST
1121 ETSDTSTSSD FDSSTVDIWS TTDSSDYDDS STMTSAFEKA VRAELKPKKC KPRPKKPAAC FVSEYGCCPD NKTAAIGPFN
1201 EGCEIPETCK ETKFNCCSDG LTPAKGTNGK GCPSEDCKDT LFGCCPDAVS VSKGNNNEEC PEPTTTPVPT TKPTTTKTTA
1281 KTKSGDTTTA AGTTKVPEVE SRLQGCFASE FGCCQDNSTE ATGPNYGGCS SCINTQFGCC PDNETPAHGP LREGCCLLSP
1361 FGCCPNNINE ARGPSLEGCG CEYSPYGCCP DGTTSAKGHD NEGCGCKDTP HGCCPDEITP AAGEEYSGCP CHSYQFGCCS
1441 DGETISTGPH SQGCHCSSTP FKCCSDNVTP AKGPDFEGCD CSTSQFGCCP DGVTEAKGNS FEGCEDKVPD SPQKACSLKR
1521 DMGTCSDNYT VKYFFDSEYG GCSRFWYGGC GGNENRFDSE IECKEICVEP TGKDSCLLPK IHGPCTGYYP MWHYDSDRNT
1601 CTQFIYGGCL GNANRFEKIE DCQAQCVVDE KIPSCDQPIE QGSCSGSFER WGYDKERDIC VPFNYGGCKG NKNNFATENA

1681 CNYQCKTPGV GKIKDTCQLP ADIGNCQTYV AQWYYDTKIK RCRQFYYGGC GGNDNRFATD SECEQRCSTR EQEKPRTRHP
1761 ETQRPPEQPT RQTSRPMIER QKDICLLPYQ SGTCREQHRR FYYDRGYGIC SQFLYTGWDG NENNFETLDE CETLCDDAVG
1841 LCDLAPLYGR CSENITRWYF DAYTQECQEF EFSGCYGNKN NFEDKRSCEY ACRRPDETRT SEAQTIQTAR PTSRPAPQPE
1921 ERVSEDVCSQ PEDPGSCDEY VILYTFNSTS RQCKRFYYGG CDGNDNRFNS QDECESTCLS PEVDSRVQPE RERDCDQYIR
2001 HCESLRCPYG LLKSYDAGCE QCECEDPCAE YECPIDSKCS VDVSDQEGVT VFVPVCRRFT KPGQCPRLEQ RTAACEVECH
2081 DDADCRGDYK CCSAGCSNIC TPPIDNRVRP TTQAPYHPEA QAPSLQEVSE EDLQPVAREG GVATLRCFAT GFPPPSITWK
2161 RGGLELKTNH GRFVLTSNGD LQIVQLHRTD AGTYVCVAYN GIGNSIEREV TLTVDVPVTA NIMLPKGRVY SVGTDILLNC
2241 NVTGEPTPEI TWYKDNRQLD PSDHIEMPEP NRVIIVGAHP SDSGNYRCVA RNNYSQAFAA EVISVEGFHI PSDCTDHQKF
2321 ANCALIVKGN YCNHKYYAKF CCRSCTLAGQ LQSHPNQI
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GSFERW.G	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	1646	1651	
total 1 peptides												

tr|A0A1J1J4N4|A0A1J1J4N4_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRIIKYCNST GGSLALLFFM LTQQISLAHS KHRHIVHRHK RQHGANLYLP ETYIIPGGEG TESEWGQWST PSECSRTCGG

81 GVAYQSRECL IIGRDGEPSC QGGNKKYFSC NTQDCPDDEA DFRHQQCSYF DRTPFEDVYY NWVPYTKAPN PCELNCMPRG

161 ERFYYRHKSK VIDGTRCNDH SVDVCVDGQC QPVGCNLMLG SPAREDKCRK CQGDGSSCKT VTGLLDMNNL QVGYNDILLI

241 PQGATNIAIQ ERSPSNNYIA IRNLTGHYYL NGNYRIDFPR PMTFAGSLWT YERKPNGFAA PDKITCLGPI DEAVYLVLLS

321 QDQNVGVNYE YSVPRAAAAP EEPEIYSWAF TKFEVCSKSC GGGHQARNVT CTKQRTSEEV DESLCDSSQK PAEWQKCGLL

401 DCAPQWIEGE WGKCSAPCGQ SGKKERKVHC EKINANGAVT VVDDEVCLEL VGNKPATESS CNEGKICPSW FTGKWQPCNK

481 LCGEGKKTRQ VICYRKEENG DITVLDDKDC SDEKPEEEMD CMIVPCEGVE YITSSWSGCD VCGATVETRS VQCASKAGKI

561 YNETFCNKKP KPELSRPCNA TPCDYAWFTS QWTKCSAECG KGLENRVVVC GKLEGDVIKK ADESKCEEIE KPEDERECDG

641 PKECPAQWFA GPWTKCSKRC GGGIRTRKVI CLGIDGATET NKCQEDKILF ASDDCNMDAC VDDELLPVDT TSQPVEEDDE

721 SEEWCDEDYE EMTTDQNGVL KVTSDYTDLS SGIDFSSMAS TESSPLTEEL MLSDATGFET DVTDETTDMS IEGSGSSTSD

801 MDLESRFDGS GTDESTSVTS DKTMMTSSGL SSISEESTSA SSDDTTESLS SLDSTKDSTE ESDITTESDS DSSTSSPTSE

881 SSSETSKSSV DGSSSSISTE SSSSSDSTDS SISSDSTDSS SSSDSTDSSI SSDSTDSSIS SDSTDSSSSS FSTDSSSTSD

961 DTTTESDSST SESITTESSS SESSTDQDTI IQSTTRDLAD YEIQTSSFDY STELSTEEVS EESSSEVTTV SSETSNSETT

1041 ESDGTSDSTD STDTSDFTDT TDSTDKSDST DNTESTDTSD STDTTDSAET TETTETTEEF TGSTDSTDFT STTENSSTEA

1121 TESTQTDESS TTGDESTETS DTSTSSDFDS STVDIWSTTD SSDYDDSSTM TSAFEKAVRA ELKPKKCKPR PKKPAACFVS

1201 EYGCCPDNKT AAIGPFNEGC EIPETCKETK FNCCSDGLTP AKGTNGKGCP SEDCKDTLFG CCPDAVSVSK GNNNEECPEP

1281 TTTPVPTTKP TTTKTTAKTK SGDTTTAAGT TKVPEVESRL QGCFASEFGC CQDNSTEATG PNYGGCSSCI NTQFGCCPDN

1361 ETPAHGPLRE GCCLLSPFGC CPNNINEARG PSLEGCGCEY SPYGCCPDGT TSAKGHDNEG CGCKDTPHGC CPDEITPAAG

1441 EEYSGCPCHS YQFGCCSDGE TISTGPHSQG CHCSSTPFKC CSDNVTPAKG PDFEGCDCST SQFGCCPDGV TEAKGNSFEG

1521 CEDKVPDSPQ KACSLKRDMG TCSDNYTVKY FFDSEYGGCS RFWYGGCGGN ENRFDSEIEC KEICVEPTGK DSCLLPKIHG

1601 PCTGYYPMWH YDSDRNTCTQ FIYGGCLGNA NRFEKIEDCQ AQCVVDEKIP SCDQPIEQGS CS**GSFERW**GY DKERDICVPF

1681 NYGGCKGNKN NFATENACNY QCKTPGVGKK SCNLPKESGD CEEKHARWYF SQNDNKCMPY YYSGCGGNDN NYDSEYSCAD

1761 QCPPTVVKDT CQLPADIGNC QTYVAQWYYD TKIKRCRQFY YGGCGGNDNR FATDSECEQR CSTREQEKPR TRHPETQRPP

1841 EQPTRQTSRP MIERQKDICL LPYQSGTCRE QHRRFYYDRG YGICSQFLYT GWDGNENNFE TLDECETLCD DAVGLCDLAP

1921 LYGRCSENIT RWYFDAYTQE CQEFEFSGCY GNKNNFEDKR SCEYACRRPD ETRTSEAQTI QTARPTSRPA PQPEERVSED

2001 VCSQPEDPGS CDEYVILYTF NSTSRQCKRF YYGGCDGNDN RFNSQDECES TCLSPEVDSR VQPERERDCD QYIRHCESLR

2081 CPYGLLKSYD AGCEQCECED PCAEYECPID SKCSVDVSDQ EGVTVFVPVC RRFTKPGQCP RLEQRTAACE VECHDDADCR

2161 GDYKCCSAGC SNICTPPIDN RVRPTTQAPY HPEAQAPSLQ EVSEEDLQPV AREGGVATLR CFATGFPPPS ITWKRGGLEL

2241 KTNHGRFVLT SNGDLQIVQL HRTDAGTYVC VAYNGIGNSI EREVTLTVDE PVDGSAYILG DTNSTVLAII SEPATLRCLA

2321 GGYPKPFVTW WRGDKILPLK DDRIEITRDY SLNLNSVDLY DLGPYVCQAY NSIGRPVSIQ VTLRTHGPVN PHSEEDYKYL

2401 QYVDNYPLTT APPRIPNPSP TPRTRPSYVQ STPPHITSAP RISLVPVTAN IMLPKGRVYS VGTDILLNCN VTGEPTPEIT

2481 WYKDNRQLDP SDHIEMPEPN RVIIVGAHPS DSGNYRCVAR NNYSQAFAAE VISVEGFHIP SDCTDHQKFA NCALIVKGNY

2561 CNHKYYAKFC CRSCTLAGQL QSHPNQI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GSFERW.G	Y	28.69	780.3555	2.5	391.1860	2	0.37	956	1	1663	1668	
total 1 peptides												

tr|A0A0A9X7A0|A0A0A9X7A0_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 METMHTDMMG AATALCTL**KA** **AATL**ELPVNL TVAVGFVENA IGPDAYCPSS ILTSLNGRSV EIRNTDAEGR LVLADLLTFV

81 QRDAPLSKPP HTIIDLATLT GAIVIGLGER RAGLFSNHLP LTQQLMRCGM GCGEEVWPMP IGDEHTQKMK RNLADLTNAA

161 VGRAGGSCTA AAFLSEFIEP LRLHKTTKTI VTKTSRGGAS KRRKHS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.KAAATL.E	Y	27.47	573.3486	1.1	574.3565	1	0.18	1076	1	19	24	
total 1 peptides												

tr|A0A1B0CDL1|A0A1B0CDL1_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMSTNSPGSG GNSTNNKNKI QQQQYSFVVQ QANPLSTQKN PIGATTTFGI ISGADGFHAP PTSAAFTGQT VPGQQQAQQS
81 APNTIRAMNQ ATPTLPQQQS SQQSELQKMQ PQQTLQPLSY GQQQRQGAQP PAIYSRNNGS NPATNRTRAP MMSSPMYASP
161 HIPQHLVMAQ YPTIPTAFNS QQRQTQNQIY QQHNQVQFNQ ATHIQPPGFT YYPNIFSNPP YMQQRPNATA PIGITQGTPT
241 LAPASSQPGM TLPPTVLPPS AMAAAAAVGP PSSTPKTTTA NRRQHALQII DPNSGMDILD EFLHTKSSSR TQSPAAAVQP
321 PAEAPPEAVV VAPAPEYGAN TVELQVGDMG AMTPVVSAIS DGPAVDITPK QTQNKKKKPV EIEKPPPPVK GEQAPPPQQQ
401 QQQQQQQQQV SEVPTPIIPT TAAVTVVSSP IIDTTTTTTT VTETSIIPDN SGTCISTSVS VSNDQVSANA NISNNNVVAV
481 EAQECESTQA EEVGAIINNN SKAPPSVVEE TNVQNNNEAI REPEVADTNE NVTPQSTDET DEVAAPIEET IIPPANVKVA
561 VSDEIPEKVT AAVAAEVPEE KPAAAE**KAAA TL**INYDEGQW SPANPDGRKY YTVEQLRKLS EDPRSKIKPD VKFEPILKKA

641 RGEQGLNYGG QMVERKLPAG RGGDSNLLPR FAQNLMQGSP GGNQLTGGYK RVSQQGNKSS GASGGGSSQG KNPQNSGMIR
721 VSLSLREDVK LNETENAWRP SHMKASESSS EEDRITEELY KNFRCILNKL TPEKFNVLVG QVKALKIDTS ERLNGCIELI
801 FEKAVSEPNF SVAYAQLCKQ ISTISVSEPQ PPPENGADGA TKPPPQSHEQ YMFRKTLLNR CQTEFQTISA QTDAQKVRTK
881 RLEEFKDDPE KHEEYKFLVE EEERKLRWRA LGTVRFIGEL FKSDMLTSNI MNNCIAILMN NRHEDSLECL CKLLTTIGQR
961 LDQNMLVDYF VKLQEIVDNR KQHKISSRVR FMIQDLIDLK KNKWVPRRPD LKPKTIVQIQ KEAEAEYNNQ AIGGGGGGGG
1041 GGGGGGGGSG GGYREQVRDQ RDRHNRGGGG GGGSGGYNKS SNHGSGSGGK SNDDGWTMQN TKSNRSTAVD TKKLTVKATN
1121 IDQNTPLGTA QMYKWQPQST NMYQALSDMD TSRPDSGANA NKGKGFGGFG KGSTERERYE GRGSQHKSSR ENSSTRSAAS
1201 RSLQAPARPQ GPSRLPYASM ASTSQGGVGG ASRSIEKIVP EKLPQREPPP PPQLSEEELK ELGEKIRRRW MEMIMEVVEG
1281 YTNVEQCTEF IEKVPEEHHY LGIREIYDHI LEQKSKQREA AGEIFAHAIR NARSISLEAY LHGLRLHMEN TLAKVSENLI
1361 QANMGGQLLA HMLRYFVSKR GPGAAVELWE KSQVKWTDFM QSSKVDEFIA KNNFNFLVNK DFSTYQSTSS NNTSLDGVQE
1441 RLKELITTNA SSDTIFEWIS ANVGTIDKNF IRILTTVVIE SCLYPNYKIN APLLETQCGL LTKYIENKEE FEMQCLYAIQ
1521 KLIFKLEHPS GLMSNIFGTL YDLEVLSTDS FKNWLNSTEE PEGKGVAVKS LHSFFTNLFI NDGSDENE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.KAAATL.I	Y	27.47	573.3486	1.1	574.3565	1	0.18	1076	1	587	592	
total 1 peptides												

tr|W5JJ28|W5JJ28_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADAELAKAL KDLPNRVLNV PVEERAELFQ NVIAVLPNPG INATVVRGIC KVIGTTLTKY KDPESQALVK ELLVAVLKQH
81 PDLAYEHFNA VLKALLTKDL AAAPPLKGAQ AAVLALGWAN TVALNADHES AVGKKEFPKL LEVQAGLYQL ALTSGIQKIS
161 DKAFSFLCQF FGHQEGLERS YFDKLIALEP SSGVIVMLCA ILRYCQQQEH DSVALLQQHK AKLLDHVVKG LVTVKTKPHA
241 SDIAGCAILL RAITKDEFRT IIVPALQRSM LRSAEVILRA VGAIVNELEL DISDYALDLG KPLVQNLASK EETVRQEAVE
321 SLKQVALKCS GATAIEALLK EVFAVLNGSG GKITVAEFRI NLLQGAGNLS YNKISTEKIQ TILPSVCDQF AKVIESEIQE
401 KVVCHALEMF GLWTENYRGE ISPKIVQLFK KGLEAKAQPI RTSYLQWFLS CLHYGKLPGG SDFTLALSKV VEKAAQNPTQ
481 TPLVSEGVGA ACIILLTNRT VEDKLKDFWN VVLDMSRPVF LGEKFLATTN AETLCYVMVI CEQLLLHHRS ELKGGGSTDP
561 LFRAAIVCVM SAQQKVRRYC LPLIRRIVNS EDGVALAKSL LAEMTRYAEN VKILNEGDPH EDGVAPAQAL VDAIWTICDV
641 ELLASANAQS LALSALLCSH HPAALSVRSD LWESILARYK LDGKHFIALN TAQIGDVFFA VYKAKPMYES TLATLSRISP
721 EQILPVLVKN VCDQLTNSRM SDVTDEEYFT YLTPDGELYD KSVLPSSDEP IQTAHLKREN KAYSYKEQLE ELQLRRELEE
801 KRRKEGKWKP PQLTPKQKEL IDKQREKENA IKLRLRALND TITTLVSQIE GAAKGTPKQL SLFFPTLLPA ILRVFSSPLA
881 APAMVKLYIR LRDCCFTSEQ VELGRDISIA TVRMSKPHCD LEEGWCTANI VELVSDILVS LYDETIDMYN VHREEPGSKN
961 YLLNAPTFSY TFEFLKRALT LSEADRDESL LINGIQLIAY HAQLKGDTVD GKDFDDLYHP VFMPRLEMIR LLLRLIQKHR
1041 GRVQTQAVAA LLDVADSSSG REYRARADER EIECLLVALQ DDLEAVRDVA LRALAIMIDV LPSIADDYEL GLRLTRRIWV
1121 AKHDVAEDTK QLADTVWVQG NYELPIVMAD ELMKDIVHPE LCIQKAAAGA LVSILMEDAS TVDGVQEQLL EIYREKLTMI
1201 PARLDQFDRE IEPAIDPWGP RRGVAIAFCH IAPFLTPELV KSLIEFMVRH GLRDRSEIVQ KEMLAASLGI VEHHGKDSVA
1281 YLLPTFEQFL DKAPSHSSYD NIRQAVVILM GSLARHLDRE DPRIKPIVDR LLTALSTPSQ QVQEAVANCI PHLIPSVKEE
1361 APAMVKKLMQ QLVKSEKYGV RRGSAYGIAG IVKGLGILSL KQLDIMSKLT AHIQDKKNFK CREGALFAFE MLCSTLGRLF
1441 EPYIVHVLPH LLQCFGDSSS YVRQAADECA KTVMAKLSAH GVKLVLPSLL NALDEDSWRT KTASVELLGA MAFCAPKQLS
1521 SCLPSIVPKL MEVLGDSHIK VQEAGADALR VIGSVIKNPE IQAIVPVLLK ALEDPSGKTS ACLQSLLETK FVHFIDAPSL
1601 ALIMPVVQRA FMDRSTETRK MAAQIIGNMY SLTDQKDLTP YLPNIIPGLK TSLLDPVPEV RAVSARALGA MVRGMGESSF
1681 EDLLPWLMQT LTSESSSVDR SGAAQGLSEV VGGLGVEKLH KLMPEIIATA ERNDIAPHVK DGYIMMFIYM PSAFPNDFTP
1761 YIGQIINPIL KALADENEYV RDTALKAGQR IVNLYAESAI ALLLPELEKG LFDDNWRIRY SSVQLLGDLL YKISGVSGKM
1841 TTQTASEDDN FGTEQSHKAI IRSLGGDRRN RVLAGLYMGR SDVSLMVRQA ALHVWKVVVT NTPRTLREIL PTLFSLLLGC
1921 LASTSYDKRQ VAARTLGDLV RKLGERVLPE IIPILERGLN SDQADQRQGV CIGLSEIMAS TSRDMVLTFV NSLVPTVRKA
2001 LADPLPEVRQ AAAKTFDSLH TTVGSRALED ILPSMLESLS DPDPDVAEWT LDGLRQVMAI KSRVVLPYLI PQLTATPVNT
2081 KALSILASVA GEALTKYLPK ILPALMSALA AAQGTPEEVL ELEYCQAVIL SVSDEVGIRT IMDTVMESTK SDKAETR**KAA**

2161 **ATL**LCAFCTH SPGDYSQYVP QLFRGLLRLL ADSDRDVLQR SWDALNAVTK TLDSAQQIAH VTDVRQAVKF ASSDLPKGSE

2241 LPGFCLPKGI TPLLPVFREA ILNGLPEEKE NAAQGLGEVI KLTSPTSLQP SVVHITGPLI RILGDRFNAG VKASVLETLA
2321 ILLHKVGIML KQFLPQLQTT FLKALHDPSR VVRIKAGHAL AELILIHTRP DPLFIEMHNG VRNADDATVR ETMLQALRGI
2401 MTPAGDKMTE PLRKQIYATL AGMLGHSEDV TRAAAAGCFG ALVRWLPSDL LDDALASHLL NEDYGDDATL RHGRTAALFV
2481 ALKEHPATIV TSKYETKIAK VINGAIVSDK VPVAQNGVRA AGYLLQYCMT DAEGVKLPMT VIGPFVKSMN HSSHEVKQLL
2561 AKTCTYLARV VPPAKTAPEY LKLAIPMLVN GTKEKNGYVK SNSEIALVHV LRLRDGEEFH QRCLTLLEPG ARESLSEVVS
2641 RALRKVAMQS VIGKDEELDD TILT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KAAATL.L	Y	27.47	573.3486	1.1	574.3565	1	0.18	1076	1	2158	2163	
total 1 peptides												

tr|N6U443|N6U443_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 CTVIGIAGSN EKGKWLTEEL GFDYFINYKT QNVEEELRKA APKGVDCYFD NVGGDISVTV INQMKPFGRV AICG**DISSY**N

81 ATEPAKIISP IRSILFNELK VQGFRVSSWN ERWLEGIHKN LRWIIDGKLK YRETITEGFD NIFKAFTEML QGGNIGKASV
161 KV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.DISSY.N	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	75	79	
total 1 peptides												

tr|N6ULU5|N6ULU5_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSKKFCEND VRALFSGVGT IEECTVLRDP AGNSRGCAFV TFSNKQAALL AIKSLHQSQT MEGCSAPLVV KFADTQKEKE
81 LKRHQQMQAS VWNALATPTL ASPPQQYSPV LPSEATSLQL LQAMGGSALL QQQFLSNSEN LLAPIGVQNL VTLAAMTQPA
161 TAATAPLCMA NLLGKGAGVE RTLTAAGLQA GLQSGLGTTT **DLSSY**GSLIT NATLNAAAVA AAGKQIEGKA LWVLDFSLSP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.DLSSY.G	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	201	205	
total 1 peptides												

tr|E9GXP3|E9GXP3_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLMEDVGLDS GAMMDSHSGV NQLGGVFVSG RPLPDQTRQK IVELAHSGAR PCDISRILQV SNGCVSKILG RYYETGSIRP
81 RAIGGSKPRV ATNDVVGKIS QFKRECPSIF AWEIRDRLLQ EAICNNDNIP SVSSINRVLR NLAAQKEHQQ QHQHPHQHAT
161 IPSPDSVYDK LRMLNGQSQW PRTNTNTWYP NGNGAGLGLT TGVGAGSPPY TPLPGATSPD QTPLCHQISS NDGSYNHKKG
241 GDDVMSEDGG VSSGENSRSA PPTPTTTTPS DDDQARLRLK RKLQRNRTSF TNEQIESLEK EFERTHYPDV FARERLAAKI
321 GLPEARIQVW FSNRRAKWRR EEKLRNQRRG PDQQQSSSQQ PDQVNPQQQQ QQQQQQPQQQ QQQQQQQQQI NVVEPPPSSP
401 RSVSHSANYP GGIYSSLATS MMTDTYSSAF NGMNSMTGFS AMGHHPGGHG AVGPVAAAAM TPVTPSMSHI AAVPPIGTGP
481 CSLQQQQQQP HQQQQQQQQP PHQTQQPRDH HSAHSVHSSG GYSCMSRMSG GY**DISSY**NRH HPHLSHAMGQ VSGPIGPTAT

561 S**VSNSL**AHNY HQSVNSQYGM HHNSHNSTTG LISPGVSVPV AVPGQPTAEM HHQYWTRLQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.DISSY.N	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	533	537	
S.VSNSL.A	Y	16.36	518.2700	-8.9	519.2727	1	0.16	1051	1	562	566	
total 2 peptides												

tr|N6TRL9|N6TRL9_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGDDTSDAIM SSAAFNDLIS **DISSY**NGDLM KDFDFEAKPS EAANSLKLEE KDLQPAQVSS ESLKTTQSPS EQSNQANYSL

81 PVFEKNPSAS VSNRLSYPNM DFAKTELSPA AQTLKQMAEQ HQHKNQMGLN FNPNSRVPNA RSPYSDFQFQ GDYGSPSANQ
161 NYHKNSPSFP QPDMIKQEMI YQGNEYDMKR KQIPAAGVYP KQKQYSPYGS PGPGGSPGFL PSGRGSCPPP NAGQYNAGTP
241 PRPPSGSGNG NPQGPSGTSV QINQAQQLNI NQHGPIQSVL SLSRKALPID

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.DISSY.N	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	21	25	
total 1 peptides												

tr|E0VSS2|E0VSS2_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTSENFKTLY VSDTGNNADS VEWCPISPYK NSFACGTYHL IESNEKPDEE NDNNACTRSG GVIIYTICKD RLEKNCRVDC
81 PAVLDMKWCN EKVNDDIVLA VANASGEVVT YTFKNYILKF LSKCSIKTQK DYLILALDWT KKNDENLICC SDSKGNISII
161 KFLNNTLTII KEWNGHSLEA WAVCFDSFQN NIIYSDEGVF KMWDTRKDNS GEIMTSKTHG AGVTVLNSNP FDEFSLVSGG
241 YDENVFFWDT RNWKSPLKTI TAGGGLWRLK WHPSGKQKFL LAACIYGGFQ IY**DLSSY**KSI SEYKEHESMA YGADWSYLNQ

321 KEMEELLGCS QSSLIATCSF YDRKLCVSTW SQNSNK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.DLSSY.K	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	293	297	
total 1 peptides												

tr|E0VEY2|E0VEY2_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRTHLRGDGG TKIRADLPIA IMWNVVVQGQ LRFGYRKRRC DGAGDPGRFA SHLGFVHEEG RFKIERAQTA EILETGIPPS
81 RRRSRRHRRG RSSAGFESGV AGVAGSSSPR DMEFKGGELE EAPERSEFGS VGFFVPHRDK KLRSSSGPLT DGTTRDFLAE
161 VIAELFPRVA PYAFRPPDFA FVRKRDRVTE GEIRTLLDAT SKRRTALGPN GVHYWILGKF AEVMCARLSA LYTARFRRAS
241 FPKQWKCANL VLLENREEIR RRQAHIDRFA FSTWRLVLLP KSGRDPSSRS SYRPICRLDV DGKSFERIVA SRIIAHLKNG
321 DKRH**DLSSY**Q FEFRTGRSTA DALIRVRDLV QAALKKRGVA IAISIEERVK NALSSVPKRG DLDEP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
H.DLSSY.Q	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	325	329	
total 1 peptides												

tr|A0A0A9YR59|A0A0A9YR59_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADNDDLLDY EDEEQAEQPA IDGAAEGAQR KDVKGAYVSI HSSGFRDFLL KPEILRAIVD CGFEHPSEVQ HECIPQAVLG

81 MDILCQAKSG MGKTAVFVLA TLQQMEQLND NQVTVLVMCH TRELAFQISK EYERFSKYMP QVKVAVFFGG LPIAKDEEVL

161 KSNCPHIVVG TPGRVLALVR SKKLVLKNLK HFVLDECDKM LEQLDMRRDV QEIFRNTPHS KQVMMFSATL SKDIRPVCKK

241 FMQDPMEVYV DDEAKLTLHG LQQHYVKLKE NEKNKKLFDL LDILEFNQVV IFVKSVQRCI ALAQLLCDQN FPAVAIHRAM

321 NQEERLSKYQ EFKDFQKRIL VATNLFGRGM DIERVNIVFN YDMPEDTDTY LHRVARAGRF GTKGLAITFA SDENDAKILN

401 SVQDRFDVNI TELPDEI**DLS SY**IDGR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.DLSSY.I	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	418	422	
total 1 peptides												

tr|N6THP3|N6THP3_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSEEDDDEF IEQQQKFLKR SADELETGNP IDNFEQPVKL QCTAQQHGTN QNEGLTKFSV EIVQQLEFTT SAANSQPQQI

81 STNVTVKTHA NASVKSDISS PKAATPGTPG HASKANIGLD VGTLVECVKQ EPDNDFADLD QCAAALEKDA ANGGAGFGDF

161 PDLMGDDTSD AIMSSAAFND LIS**DISSY**NG DLMKDFDFEA KPSEAANSLK LEEKDLQPAQ VSSESLKTTQ SPSEQSNQAN

241 YSLPVFEKNP SASVSNRLSY PNMDFAKTEL SPAAQTLKQM AEQHQHKNQM GLNFNPNSRV PNARSPYSDF QFQGDYGSPS

321 ANQNYHKNSP SFPQPDMIKQ EMIYQGNEYD MKRKQIPAAG VYPKQKQYSP YGSPGPGGSP GFLPSGRGSC PPPNAGQYNA

401 GTPPRPPSGS GNGNPQGPSG TSVQINQAQQ LNINQHGPIQ SVLSLSRKAL PID

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.DISSY.N	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	184	188	
total 1 peptides												

tr|A0A2A3EK85|A0A2A3EK85_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAYTSTSNCF LLISLKLTYN ISVRYHDTRA RVIRELDSDK RNDRVPLDPF QIVQLIRMRS MLKHCIQFSV FYKVLTIFCL

81 RNSMMEDTLN ILIGKHKERV TMEIDGHTDG VTKLRIIIKF GFVHRALMKG IGQHLLIIMQ NASTIPSNDK KYVVGPFDHK

161 RYTYDRYMPL IFIGGVPRSG TTLVRAMLDA HPDVRCGQET RVIPRILQMR MHWLKSEREN LRLSEAGISK EVMDSAIAAF

241 CLEIIARHAE PAPRLCNKDP LTLKMGSYIL DLFPNAKFIF MIRDGRATVH SIISRKVTIT GF**DLSSY**RQS LIKWNHAISI

321 MYGQCKEIGS DKCLMVPYEQ LVLHPRQWMK KILNFLDVPW NESVMHHEEF INKPGGVPLS KVERSSDQII KPVNLEALTK

401 WVGHIPDDVV REMPDIAPML SVLGYDPYAN PPVYGAPDRL VSENTRRVLA NGEVWAARAR QFSLEKLIEL SKEDEATNAP

481 NA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.DLSSY.R	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	303	307	
total 1 peptides												

tr|E0VDU7|E0VDU7_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MELGRYLERI QKNFKQAYKS CHDKKKER**DL SSY**SFKTIKW THSIWLGEPV RSPRLFWNPK ENSIEFKIEA NTIGCILIQF

81 NDNDFIILWI DDTSGKPHIE DCHLGNDSKI LFRDEEENYK LLGGYQNLTH TQISFERKWN TCDVNDTVLG SDTVLVGWSI

161 YPNDEFDKNI SKLYTEEEEG GGGGDVFDG VFKGEKFILL QSPSQLDIPK GHNVHKWDIL MRNVVISNKT TTRYWCKVFR

241 TPSLPKKSHI IAYEPMILSN YTQLIHHMFL YECEAPPGFL DSYSSSNQNG YPCYGSEMPE DWEKCITPVH HIGLPIGPRQ

321 SYFMLEIHYK DPGTTSVIDN SGFRIYYTED LRPFDAGVMM TGVKVTPLHL VPPQQNEYKS IGLCNDVCTN KLFPLMGIKV

401 VSVLLHSHVP TSSMRLRHIR GDNEINNIVE NNKYQYEYQV NQRLKKEVTV FPSDHLITEC DYITTNMESP EFGKKFSREE

481 MCSSFVTYYP KTNLSSCHSM IPVRYFFKTI GIKSFYNVTM DDIEKYIMKI SSNKIYKFSM LSPYLGGYNS ELNNFSTLLK

561 MFSDENSLLK LKINEPNEFK GKNLSAYIES LPWNDTSFTK SFENSLAKGL QIVFCRIRNN KLAIVSTEYR KFSKI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DLSSY.S	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	29	33	
total 1 peptides												

tr|N6UT70|N6UT70_DENPD

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MYLVKPMAKS LLRQSYCRFP ARVHCARHFQ NQATESAEEN SHLFDLLKKY EYRLLYSSIL EQHRIRYGYH QQRAFIKKTE
81 MADFKLKTAI RSLRPLPVSL KYFTDYNLDD IEKSAAEEAE SEIVEEADSL TNFPYKVNAT VEDEGFVDEP KKPDPHSIKK
161 QIEARKEALD NDKENWMTHY ENYEDDLEEH NERLLFGDGD DWKVNYGTPD PRCAISNVPC GGCGAYLHCQ DSSIPGYIPS
241 EIFKNSFKRH AGAPLSSLLC QRCHFLKEYN IALQVRVSPD DYPKILQNIA FNSGLALLMV DLTDFPCSIW PGIADILGPK
321 ASIVVVGNKV DLLPKDDYDH LKKIKEAMFN SVKLHGFGTA NIKSIELISA KTGFGVERLI DSLLRVWKWR GDVYIIGCTN
401 VGKSSLFNLL LQSDFCKIQA ADLIQRSTTS PWPGTTLNLL KFPITRFGGH RMFARRKRLE MLQKIEKQEL KLNREMLSKE
481 NVPSYATLIG RVERSQQPRP SKDEIPDNFS VGGTRNVSGI TCMGINEELP EFVHGKWCYD TPGVMHPDQI LHLLTTEELV
561 RTLPKELIRP ETFCVKPGSS LFIAGLARLD YVNGRNSVRL TVFRANTLPI TICKTTEADR LYEELLGTEL LAVPILKSDR
641 KEKWPGLELA KSFKVFGKCE **DLSSY**DVVLS SAGWVAINCN FDNYEFSAWT PEKRGVHLRD ALLPKAVTMR GRRVRDSVAY

721 GQHKLII

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.DLSSY.D	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	661	665	
total 1 peptides												

tr|T1K774|T1K774_TETUR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDGFDDPGVY FSNVSSLQDE GEGRQINLTG IKRKFKDFLK QYHEGNLLYK YRDMLRRQYN IGQFWIEVAL E**DISSY**DEDL

81 ATQITKYPIE SLPLFEEAAK EVGDEVTRPR PEGEEEARDF QVLISSDGHC VSLRDLKSDY ISKLVRVSGI VIAASSVRAK
161 ATEVAIQCRG CREIVSSLHV RPGLEGFLMP RKCNSDQAGR TAKCPLDPYF IIPDKCKCID FQTLKLQEAP EAVPQGEMPR
241 HLQMYCDRYL CERVVPGNRV TVVGIYSIKK ISAMKHDRKA NTGVRNPYIR VIGIQIQSEN FGHRAVIPYT SEEEEYFINL
321 AASPNVYDRI VKSIAPSVYG CTDMKKAIAC LLFSGSRKRL PDGLTRRGDI NVLFLGDPGT AKSQLLKFVE KVAPIGVYTS
401 GKGSSAAGLT ASVTRDPATR NFIMEGGAMV LADGGCVCID EFDKMREDDR VAIHEAMEQQ TISIAKAGIT TTLNSRCAVL
481 AAANSVFGRW DDTKADQNIE FMPTILARFD MIFVIKDEHN ERKDATLARH VMDVHMNAQT TIEDSIEGEL SLNTLKKYVS
561 YCRSKCGPRL SADAGRKLIE SYVNMRNGGD DPDASRRSTI PITVRQLEAV VRISESLAKM ELKPFVEDRH VEEAKRLFSA
641 STLKAASSGD LAGAEGFTSE EDHQALVKVE KQIKKRFPVG TQLTETSIVQ DLVQRDIPEK TVHKVLNCMI RRGEISYRVS
721 RKILYRVK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.DISSY.D	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	72	76	
total 1 peptides												

tr|E9H0W5|E9H0W5_DAPPU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSKELNENDK RKRNNLLSQY YGITEEKDVE NLFDVDGKHF NADAYVDKLV QETSLKQLID KEQELVREIQ SLDSEMQTLV
81 YENYNKFILA TDTIRQMKSD FKTMEDEMEK LVQDMSHIAT FANNISSNLQ DRRQQITKLS NIHELLKNLQ FLFDLPNKLK
161 TCVEENNYSL AVKYYAKSEQ VLQDFGDHPS FSGIQSDCKE IVETLRKCLK VQFSRAEVTS QELEESASLL CKLGESSTDL
241 AREFLEINKV RLEKDLE**DLS SY**VWSGENNG EVVLIFIEKC CNTALNNVAL TIATFNNIFP STILKHNEGM NSMATDVINQ

321 LCPIVESKIV EIIGFEISEA CCLSVVAALD KFHRRLLAVQ RLLLVDKQWS FTLITEIARI ISYRSANALV IKWTSELQGW
401 RDSWNNDNQP HGSVKFIEGA LVEHIHRAFV ALTAFVGNHV TFSQDSQFRQ TFGRRYVREE VLVLSLRKLS TMLANLSNVT
481 GKDSASPTLI LVLSRVAIDF SQNLAQSLLS LIEEQFDIPV GFQGDHLTPI SVITLDFKQT SQSLLQSYVQ SESHVLVQMI
561 RKSMDSRDWL TASEPRSVRP VIKRVLEEIS RVDSHAAQLY EEGSRKERSS DSSRRTHHSS SRMQQKSSWS SLGPSQLDSS
641 LLNNIQKLFS ERIDLSGTVE PNKGSVVMAI IKICLKGFLE CVRLKTFGKY GIQQIQVDCY YLQLFLWRFT FDENLVHSLL
721 DEILSSAVQR CLEPVLMEPG VVELICER

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.DLSSY.V	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	258	262	
total 1 peptides												

tr|A0A132A9E2|A0A132A9E2_SARSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFEKRTKSKL KSNPSNTSRK NDPFNKPKKS NKNNNRIKND NEKTNYFVTN RDAKTISTIE ESDGRHSNPL DNELRDPRPN
81 IFINSDADPF SSHSLNDEDF DILRKALPKL NTIAEEDGGE AASIVSPISS QQLRRSIPQI FNVSNVYQNP MHFRSQSNFF
161 ANDFGRPASK PSYHWSFNPN AILNLTSRFT TTTSPPLLHS GTRVQSSSSS SSVSLPTSTT PKTITRQRPT AEPKSHKTNN
241 NNFIELPQSN LYSNHYSELH FDQISQQNLP KTSKSTPTPS SPTLITSV**DL SSY**ERPIIRS STFSFPTSTT SAPMFRFESN

321 QSNNLTSRFP STTAKATTPE HRSIEYHFVD DYPRQSVPTN PSSPSPSISR SSSAIPIVVV NDEDRKPQPR RRNKARQKNQ
401 KESQRQNQQQ QSRCDENKCQ LPYCRCGSSS IPGGFDAKEI PQMVMITFDD SINDLNWDLY QEIFSNRYNP NGCPILGTFY
481 LSHEWTDYSQ VQNLYAAGHE MASHTITHSF GSKFSKEKWL NEVNGEREIM SLYGGVKYED VRGMRAPFLQ PGGNKQFEML
561 YEANFTYDSS LPVFDNNPPF WPYTFDYPIN HECMIEPCPT RTFPGLWEVG MVMLIDHRGG RCSMVDACSH PSTEDEVFEV
641 LLRNFNRHYR KNKAPFGLYF HSAWFNTQHH KRGFLKLIDH IGKNPDVWFV TKWQLIQWMQ QPTPNRHLNS FRPFHCDYSD
721 REPCPRPKVC STKFRDGPRY LKTCQKCPKY YPWVGKTGFS R

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.DLSSY.E	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	289	293	
total 1 peptides												

tr|E0VGI0|E0VGI0_PEDHC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPSPDDVNDQ INGEGQKKSH DNYFAKNFDE CMKRLHILEK EHELVETNDN KVQLFYIFDE SKTDEEKPLN RLSSSSSSTP
81 KIIENDVNNK NNDTSQQPGN KNLKTNQVLG VKSEFEEHSV NSCDSNVIEN GSSCSTIKPG ENETADNISN ENADKIAKNN
161 KEIISEWYSN LKQRFEPNEK NNKKENAKEM SCRIMGATLK NSNDPPNSDE HEANTRHYFN TLVKPNKLLI DEELPDPDTV
241 RNIRAKFQEN LNATLDRKLN GKLSGSMNNI SYRKPENRHV PRPLSIQCDR DDVMRHINGN LGHTTKRFSG NQMEFSESIK
321 DSENEQSSPI IKKKFIDKYE KSPKNYLSNK VFHSKWTDTG SVSSGVSS**DL SSY**DMDLENY SKEANETEPD FATVSDDDLL

401 NEIKDKHYVQ NEILEKIRSF GTSVTYYGGE MLTCSIGPLL SPTAQAIMEE ISEKYEKESN ISLSFADIYS KYVEANEQNK
481 TKKVGRTRSF GHTDMFQRPN VLNNREIDMY KYDLEVEIGI RKPKGLYVIN PKKSKIRNNT ENKTLQEVVD CPPSTVLTDD
561 AKGKKYETPL SIQVDNNDNV EKTDSEVNKK RFQQPSLQII VGNNQQNYDE EKYNESPTIR KNSEEIIKMR LENAKNALFQ
641 RSVSVPHHIM NVTSRFEPEE KKKGILFGYD KKLLDENKKN NNCDIVFEEF EISENFSDKS DELKSSTGKK YSKDDMSILK
721 ETNKKFHFEE EEENNNNNIE LKKIGEETVA DIENRMTAID ENSSDVVNKN DNNNNNNNYQ RKSNGDIFIA NESITGKKYD
801 DNDKIKETET VEENNNNIIA ERPFESRILV DKRQP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.DLSSY.D	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	369	373	
total 1 peptides												

tr|A0A023F1X1|A0A023F1X1_TRIIF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HNFDKMPKIF LIKNRLLQQQ LKLLEAQKSR EELSPPGSPC SPEPLSLIVN KPPDGDPLKK EDDQRECGSP PNLDIQPQSP
81 TEGETKKEPP ERPKTPPRRF FSSILGGDVP YGSSRGHHVL TSAEKKEYLP VDKPEEPKQH PKCQQVSVIQ RTPSSLPAKP
161 ESQMVIIQEP EQEAPIDYHV PKKDTEKDFS DINKSKLALA IKRGQILIAG RRISGGNQIL MAAAGHSRSG GGGHTGGQQ
241 SGGSSGGSRN SSGGNSYTVS GGGGMSSGGS GGAVGGTGGG GGPGKSNYGP SSPPTGSLPP FYESLKGGGL HGYQQYSSSY
321 QNLMSGNVGS NDLAMDCDTG QELPNHYPPN GGDGPPKQYS LLQNVCATYG ICVKEED**DLS SY**VKDQNFLQ YDDALMVDSV

401 TGAVVDPLQF TATLTFSSPA DHTALLESLS DAADLFLREQ PNETIPPPVE PSVNPFPEHR VNGNFQETSP TPPTYPARLP
481 PGYQEVAKER SEMNINESER PNNLQLQVQV PQPKQPKWES NGSSQQGSLL SPGLSSLELD SSTSMSLPSP TSCSLDGTGS
561 LSPPPQAPPA DISAIPSLQV RVGVLQHRPQ QYEWQSSYKA GTPSSSPVPN SRNVYFGADD EGIREKCMHS RVPQVCVDKL
641 GLPGDAALEF VNGGHGIKNP LANSEAASIP RPPDNDKDEK TNISHNGRFT CHLCSKSFSL QRLLNRHMKC HSDVKRYLCT
721 FCGKGFNDTF DLKRHTRTHT GVRPYKCNLC EKSFTQRCSL ESHCLKVHGV QHQYAYKERR TKMYVCEDCG HTTNEPEVHY
801 LHLKENHPYS PALLKFYDKR HFKFTNSNFA NMLLVRS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.DLSSY.V	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	378	382	
total 1 peptides												

tr|A0A023F0I3|A0A023F0I3_TRIIF

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 LTVLLWNSNG LLTHKHELEI LLNDRNIDIA LITETHLTDR HHFHITGYTT YRTDHAAQRA QGGTAILASH SLQHNLQSLQ
  81 SSDSYQSTSI SLKFFPFPIT ISAVYCSPTF PIYYPQMKSL FQSFGRRFIA GGDFNAKHPQ WGSRLANSRG RLLNNLIHTE
 161 RYSFISPDHP TYWPSDPNRA PDIVDFFVAS GVRSVFSSAQ TLNELSSDHS PVLLTLNITP ILKPTRPCLI QSPVNWNYFK
 241 IFLENSLNLK ISLKSADEVE NAVQLLTNSI QQAIQQSSST PKIRSSLPKQ QLPNHIRSLI AAKRRARRRW QRTRYPSDRR
 321 TFNQLTNFLR EQLISYRSSQ YDKYLESLST DDNSLWSATR KILKYHTIPT PIRSEDGSWV RCDKEKSALF ANHLEKTFTP
 401 HPDQNNPAHM NQVIENLIVP HPLEPPPKPF HPSEVKSLID HIPLKKSPGH DLITSEIIRH LPRKAIVFLT SIYNSVLRTT
 481 HFPIQWKYSL ITLIPKPHKN PSDISSYRPI SLLPVLSKIL EKLLLKRIIP TLESQNIIPY HQFGFRSQHS TIQQCFRVVD

 561 KISSTLEKKS FCLGAFLDVT QAFDRVWHPG LLYKLKQFLP TPYYQILQSY LTDRYFRVRC GIEFSDIKPI HAGVPQGSIL
 641 GPVLYTVFTA DIPTHPETLI TTYADDTAIL STNPNPAQTS SHIQEHLDLI SSXXXXXKIR LNEDKCQQIT FTLRRQTCPP
 721 VRINNKEIPT STQVRYLGLY LDSRLTWNPH TRLKRQELNR RYGQLRRLLG RRSTIKVQNK LTLYKTLLRP VWTYGAELWG
 801 SAKQSNIQRI QSFQSKVLRH IVNAPYYVSN STLHKDLNIP FVNKLIRTRF LNFHTNLQIH PNPTAQTLSS STHPDNPPRR
 881 LKRRWPRDLL NT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.DISSY.R	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	503	507	
total 1 peptides												

tr|B4LPM7|B4LPM7_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MVYFLGDWGM GDSDLSSYQQ HVPNIQQQQQ QQHQRIHGHQ QQQQQQHQQ QQQQQQQQQQ HQLVAQISTS LSLLQSQLQF

  81 ASGSSFLQQQ QQQQQHVAGP RSSSSSLVTA NLQQLSVSSG GNNNNNNSTC NTPSKSQQQQ QQQQQQLQQI DSHPGTGAAL
 161 KVHSSWLRQC SESNTSQPTA DSCVGKPKST QLSKDLLDNE DEVALHPLSN QVGGHTRLLL LNQSTVIKPL NLRELDFYQN
 241 IPQDVQKFVP KYKGVMQATT MGGVKLDKRY SPSFRDDAAA VPVRKMSASK RKRDEVLRMK VHKNGNAADV IKSISQLDNS
 321 NKQYFLMLEN ITSQFRNPCI LDLKMGTRQH GDDASAEKRS KQMAKCAAST SGSLGVRLCG MQTYQADLEQ YAKRDKYWGR
 401 ELNEAGFKTA LHDFFYNGYR LRIRVIRKIL QRLMQLRRVI EKQSSYRFYS CSLLIVYEGY EENPMAHPPS MDLDDWLEAP
 481 KSATLQPSGA FDYHPENSID EDDIEDDEAG HEAGDELEPH DTDEDLQLVA AVDSGNASAT NSSTGADGCN YDADASNDSN
 561 SRLNLATRRH LHKRGFAEAA ARGVKQTATS STTTTDEEED EEEDNVNNKA QHKHLSAMPP PRTCGVLPAK TPTGGKGSAN
 641 GNATPAFIPI SEETVFLDPE PALPSVTTSS PHSGDSWMNY SSNSSDDFSG LSEQIKAVAS GRQTCNNSSD DGSSDYESSI
 721 MGPTEAMFKR YKSQQSFDAS AAAGSLEPTS PPHTASNSNA TIKSLVSPNS SSASSLKSVK GAVKRLRCKD DDEHYAAHDD
 801 PREAKKSTIT STPVSAVSSP SKSRVQCSCE NISNSLLGGI LLDSLERRAS AEGSDNNTSS EPKANTAATR NSALMHGSKS
 881 LDMSAPPTDD SACFVDVRLI DFAHTAFVPR NGSMLPTPTA AAPVHHGPDG GFLTGLDSLN RLLNEILGEE SI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.DLSSY.Q	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	14	18	
total 1 peptides												

tr|A0A0C9RER1|A0A0C9RER1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MVQQNFPRGG KKPLKKNLPN YALLQASKLK SQKSKMKKRK GEDAQLKTGI IARAALNLTY GTLTQGMILL GRVQRSSQYD
  81 VTISLPGRLS GLLQITDISE AYTNLLQNLV SSQLPPPDFK PLSDLYKRGN YLVCYVKVID VQSKHRVILS VQPEMINLNF
 161 DSGKLAPGSR IACSISCVED HGYVVDTGNK NLRGFLSKND VKVGVKYYVG QQVFCVVRST TTTEGITTLK LTTDPKFTNS
 241 PLSSEDQHLN SLIPGTKLSV VIKKLLPDGL HISFNKDNIG YINRLYLENP LDTYEEGSQL FATFLYTLPT VKFSYFTEIA
 321 LEPECATLTI GEMEKAKILF HDRKGIALRI KKNFRGYMPL KRTGVEFDQI RDKFPPNSVH KCRILTYDNF DRVYICSALK
 401 HELTLEYKIP ETVTAGDLMP VQIIRESPNK FLFVKSGRIL GDVPPEQIRD IDDAVVPLIG KKVLARVLSR DKNGERFNFT
 481 LKRSLVESNR PILSEFTQAQ VGSTYLGTVI NKSGKGLLIK FYEDLKGVIP SKALRNIPGG IKAFREGQVI EVKVANVIIQ
 561 ERRLILELAT ADKKRMICPF EIGETVEGKV IDSSVEGVHI RILNPSGNDA ITAYLPAGHM SPCEKTGKQM AALSVPGDTM
 641 SALVFSTTPE FILTTTLNPQ KWYTDIKNLS VSDCIPCSIT QINTTGIEVL LPVKDLKCYG IVSLNKIDNI KLLFKHQILF
 721 GKITQINKKT QVIHLTTIFH EVWSSAVEND TDLIASVDVL ALYLSKLKQL ASFSYYSTHK ISKMKLGQKV SGVVETITEN
 801 GTVIKLNDGV PAIARKSHAE KSLKIGDKVN GSILWINYVD ELVEITLDPI LMNAIKPKQN EIPEDALKKK LKGEIVLINR
 881 WFVLVVLKGC GKGNLVALPT KAHVNDLTPD LSSYKIGAKI KCYVIMKDNE SEIIPIVYRN AGFVTPKLHK SGMVDCQVKM

 961 DDNITPGDEF VVSETIQKKR KRHLENVTEK NRAMKKLKTD PITNSSSHKT KSIKTKREIA LIKSKNEEQQ EMFTCANESE
1041 GLVTFALAED AEDANKKN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.DLSSY.K	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	910	914	
total 1 peptides												

tr|A0A132AK64|A0A132AK64_SARSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNENRISDYF VISGVSEIDR HPQDEYHTDF EPITDITVIN RSNHEPIPAG YKCIERTPQN FEANLNHGSI KGSKFFICYK
81 RGRNKPPLLD VGVFQNDHSQ LVSQDCEIIK YTPSGFTANL NAGSTEIYLT YRRSTKSTPY NQLVVSDICV ILSGKESPPH
161 AFCLIDKNLN KGYFGFGSNA YLCYKKTMDR PPHLIYQPVI IDRYPKN**DLS SY**SLPQNLPM FCLPKGASIE CWPRDDSNLT

241 SLSTFILTTN VGTKIYATLL NYYEKIDHTV LTDDELLKIK FIENINDEEL LQKALTKNL RRIKSLCLLS QWPFFEQFKN
321 FLNFIYVNFV DKPSSIPIEH YVFHFMNSIP FPSPDRQNIL VNLSPSYEDL MFTQTFDDFP IPSNGASFKK LLQNLGPENC
401 IHLLLFMLTE QKILLHSLRL SILTELAEAL VAMIFPLNWN CPYIPLCPLN LAGVVNAPLP FILGFYSQYF DYFEPPNDVI
481 SIDIDTKAIY LSDNKRNLNI KLLPKKELRL LKERLEEVYK RIEMNIKIRD LQTRRKFDKQ IELEILEAFL QFMASILKDF
561 RRFLKPITAA PKIKATDPTT LFDFEGFIQS KEPYVQFYRL LTNTQMFTKF IEERSLVSNK NISFAFFDDC CEKVEKYERL
641 NLHRYSKLNL LMNQEQQTKS SKTVFISIPF LISENDHHAE SLKFDGHLDD DLLTKLQTKF GQSNLIGLKS VQSAADFTDS
721 VRFESELECY AFVKRAKHEV LKAQKIAHQS HKSDCEWSRC LLINAYALWF THFPVFSYEM FQLKPSILSN EDNSNDGQQL
801 INETHPLSIA YQALQRMQTM NFSVPDEFCY RILMILCCIH NRPALAVKIF LDMKKYEVRL NAITYGYYNK AVLDGDWPNV
881 SNSRWTKLCN VIRVVLHFQK HITATADAIN DCDHQNEMVA TEFIDKDLFE KSKKQSTSSM TIVDHCSAGI LFLRKDLENR
961 PNRTKKLLEN RNDTSCRKRY KSCDDTGDSV AEDFKKILPT LNDRAEKTFD EIESSKKFPS SLSKTHLESG NDDLLEMDTG
1041 KRFSANSFVS PLKATFGNMD FSKSPMADKL RSSFRIAKRL TKTKYNFAHR SLQEPDKNTN KISSLFSKAD FLSEETHNST
1121 KGINESKSSS LSKNFDGTKQ FLVPLSSTPT QSVAEFQSLR SQFQTYASPS EYFYSTVKSI GGRINEFKLS LGAVNAQSPV
1201 KFNMMNAVTS RFNPRPDDYY INQSIDNLLD AFDENSFQME KYQKILDEYY RKPLLDLNES SSILWRIEIM SCTVCRQCQS
1281 IIYDEEIMCK WFADDSNLNT ECIHCSSKFV PSLTIYIKDF RQSEDKEGHQ LEPISVPYLS TLVLRKEFEN ILNTETYSTL
1361 MRSQFVDEHP IVYWNLIWYF DRLNLPTHIT GLALVASTLN SAQMIEVSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.DLSSY.S	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	208	212	
total 1 peptides												

tr|A0A2A3ESR1|A0A2A3ESR1_APICC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFTLLGEVNL WTFDDNINIK STDFGAFRYH DKRIDHIHEE GKKSYCQKRG MIYVPTNKKG NKLKDSIKYL EEQLKDNSIV
81 YCQWYNDCAL QLMLNNALLI QIQTNIDTGD ICKITFDKYL IGKLLDHISD VIITKNYILC TYNDNQITIV HFTRSKRHVF
161 DKINKLEPKL STIDLFGPNG RRLDKKVQTN KCGDLILIWW KSTMNEVYPW SPAVKEHDRA NIHLYRLIGV KLELICYIRS
241 EFDPLCIMFD ICNDNIIHSV EQKVSRKGEV TIEWRTYEVS QQDKLQRIAV VSISLPTHTS CVKFSPTQEL LLLCCIDGSI
321 IIYDQTRATT TSVKAVFIPT LASWHSDGII FVVGNDKGQL QHFDIALNCI KSQTLSEEAV QANIL**DLSSY** FRIQPALLRM

401 EWNKKNDLNC YINLYNHGNS LLLIIFQRGP LGVIKMLEGN SFTGDVLVKR YLSLSQVEQA TSLLLAMNWD THSRACMHAL
481 NQIVNYLFKL PLTTERENLI QNALGSFHVP IKPISQAIEE EYGDEIRDLT RRFFHHLLRY HMFEKAFRLA IDLNDHDLFM
561 DIHFYALVVN DTAMATAAKE NAERILSRSN SCNSSHSTCS RASCSICSYS ISDKGEESCS DESENFSKEN QTDTKQSKNH
641 NYKKESNNQI PPLPILHPHP LHKNLLSTSF TDVSSDAKTD CNLETSFNMP NSTLVTTSFN HSSHLSLSNT FLTSTSFNKP
721 LYKIHTNSIP VSTMSSNSQS FNNISDDLMT TSFGSLSLNE RKTGISNRFN ENSVDTALNK VLCGEMQFSL DDVSNNATTA
801 NLIQENSFMS TPFNNPTYES VTSDVSSDLL RSSLDNIDNN IMSTSFSTVG IDTSNSYDNS FNDLVTTKSD SNIASSPLKS
881 IRSSVIMNDI VSKALPDSIV INKSISNFHN NHSNLASTSF NFLENQIQDS GNSNLKNFNS EDNSNMKLQQ SILAKKVDFN
961 IPPPPSLTNS FTNYFQGLPK KNLRLSRSTS GLADIDESVR KFSFTKTRNV NSYLLQKQNS TSNILQDQFK YNNIKSSRYR
1041 FNYDFDCISL HGSCDNLDMH SSTNNLRLSN SQFSAPYSIQ NKFERHSKLV LSQNGTNTSV NKESKISSNI PPLPVISAPI
1121 SNSISCTPFS TFTDTTLATN EKPKVKFSDT VTHILVPGTG QSHKQKRSTI SQVHLTDPKR ELAESLPLCL GNEDYLKDFQ
1201 PLSKEDINDK IKESSRSEES SKIKVVHFGL L

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.DLSSY.F	Y	26.27	583.2490	2.4	584.2576	1	0.11	1085	1	386	390	
total 1 peptides												

tr|A0A194PFM1|A0A194PFM1_PAPXU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFARVTFYPT LLYNVVMEKL IEEENIKGVV SMNETYELKI FSNDAEKW**RE HGVAF**LQLAT TDIFEAPDQD KLYDGVTFIN

81 RFLPHGGKLR GVPERDHEHV GSGTVYVHCK AGRTRSATLV GCYLMMKNGW SPEQAVEHMR SKRAHILLHT KQWQALHIFH
161 SRHLLTHTNT NTDL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.REHGVAF.L	Y	22.61	814.4086	14.6	408.2175	2	0.33	966	1	49	55	
total 1 peptides												

tr|A0A212F2V4|A0A212F2V4_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNLFVIDGCP ELVARQILLL SLALEKTTRF GLLEKSRRFL EIYGNLLLRP PTSRYLIAKA QQLVSMITNP DYMSCLLPCV
81 SVDQMKYRER DYMETLMNFW TTGNTNQFNA CELWEHRLRH TLGLRYDNRM GVYDWDYHMR LKELASQICF PEYKHF**REHG**
161 **VAF**TWLETEV CRPNVSLAAG VCKCGDRYLH RGYLGDLVTS PYIAYGLDCE DKDMLKSSHG VNYKRATDVS ERNVMRMLYE
241 IENRKAFDAN LMSLDTEQNL GMAVLSQFDA KISESGPEAP LLLREDRDSY IEVDYGKVHF LSLTALDHYP HKPQFQGLFH
321 GVFVGHNVLP RLKPSVWSMA RDDAVVIMET RKYMAELKRD DVKSYGEQIL QAATAAQCEK IRPFDPERDD FAKFLIRRKS
401 ESTDLLA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.REHGVAF.T	Y	22.61	814.4086	14.6	408.2175	2	0.33	966	1	157	163	
total 1 peptides												

tr|A0A0L7LB71|A0A0L7LB71_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFWGFSPALD LQEEYLKHGD ENAFELNFLV IGGCDARHLL KTLAQAYRHT RRYMNIFVID GCTELVARQL LLMSLALEKT
81 SRCGLLEKTR RFLEVYGNIL LRPPTSRYVI AKARQLTGMV TNPDFMNCLL PCISIEQMKY RERDYMENLM NFWTTGNTNQ
161 FNACELWEHR IRRSLGFRYD TRVGVYDWDF HMRMKEIAGQ ICFPEYKHF**R EHGVAF**TWLE TEVCRPNVTL AAGVYKCGDR
241 YLHRGYLGDM VTSPFISYGL ECVDKDMLIS SHGVCHKRAT DVSERNVMRM LYELENHREF DVSAMNLDKG MDLGMVVLSE
321 FDAKLSESHP EAPLLLREDR DTYINMDFGK VHFLSLSALD HYPHKPHFQG LFHGVFVGTN MLPRVKPSVW SMARDNALVL
401 MESRKYMVEL KRDDVKAYGD QIQQAAAAAQ CERICPFDPE KDDFARFIIR RSSGSIDIPN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.REHGVAF.T	Y	22.61	814.4086	14.6	408.2175	2	0.33	966	1	210	216	
total 1 peptides												

tr|A0A2A4JH98|A0A2A4JH98_HELVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFWGISPALD LQEEYLKYGD KNAYELNFLV IGGCDGRHLL KTLAQAYRHT RRYMNLFVVD GCPELVARQL LLTSLALEKT
81 TRCGLLEKTR RYLEIYGNLL LRPSTSRYLI AKARQLVGMV TNPDYMNCLL PCVSIEQMKY RERDYMENLI NFWTTGNTNQ
161 FNACELWEHR IRHSLGVRYD SRMGVYDWDY HMRMKEIGSQ ICYPEYKHF**R EHGVAF**TWLE TEVCRPNVSF AAGVYKCGDR
241 YLHRGYLGDI VTSPYIGYGL TCEDSDMLKS SHGVNYKRAT DIAERNVMRM LYEVENRQEF DAAALNLETE KNLGMVVLAQ
321 IDAKISESGP EAPLLLREDR DTYINVDYGK VHFLSLSALE HYPHKPHFQG LFHGVFVGHN MLPRVKPSVW SMARDDAVVL
401 MESRKYMVEQ KRDDVKAFGE QITQAATAAQ CERIATFDAE KDDFARFLIK RRSESTDTNI SF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.REHGVAF.T	Y	22.61	814.4086	14.6	408.2175	2	0.33	966	1	210	216	
total 1 peptides												

tr|H9IZZ0|H9IZZ0_BOMMO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFWGVSPALD LQQEYLKYGD EHAYELNFLV IGGCDGRHLL KTLAQAYRHN RRYMNLFVID GCPELIARQL LLMSLALEKT
81 TRCGLLEKTR RYLEVYGNLL LRPPTSRYVM AKARQLVGMI TNPDYMSCLL PSVSLEHIKD KERDYLENLM NFWTTGNTNQ
161 YNPCELWEYR LRNSLGVRYD NRHGVYDWDY HMRLKEIASA VCFQEYKHF**R EHGVAF**TWLE TEVCRPNVTF AAGVYKCGDR
241 YLHRGYLGDL VTSPYXGDLV TSPYICLGLD CEDKDMLKST HGVNYKRSTD ISERNVMRMM YEMENHKKFD VAEMEIENER
321 NLGMVVLSEF DAKISECGPE IPLVLREDRE TYIDVDYGKV HFLSVSALDH YPHKPQFQGL FHGVFVGQNM VSRIKPSLWS
401 MARDDAVVIM ESRKYMIELK RDDVKAFADQ IQEAAAAGHC EKIKAFDPEK DDYARFVIRR KRSEGTDFSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.REHGVAF.T	Y	22.61	814.4086	14.6	408.2175	2	0.33	966	1	210	216	
total 1 peptides												

tr|Q4FEE6|Q4FEE6_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HICRDVNYGW LIRTLHANGA SFFFICIYLH IGRGIYYESF IYKNTWMVGT LILFLLMATA FMGYVLPWGQ MSFWGATVIT
81 NLLSAIPYLG LTLVNWIWGG FAVDNATLTR FYTFHFLLPF ILSMMVMIHL LFLHQTGSNN PLGINSNLDK IPFHPYFSFK
161 DMIGFIIMLF LLIMLTLSNP YLLGDPDNFI PANPLVTPIH IQPEWYFLFA YAILRSIPNK LGGVIALIMS IAILFILPFT
241 FYKKIQGNQF YPINQILFWS LLVIVILLTW IGARPVEDPY ILIGQILTIL YFSYY**MFNPI IANK**WD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.MFNPIIANK.W	Y	21.04	1046.5582	-42.4	524.2642	2	0.57	1054	1	296	304	
total 1 peptides												

tr|Q7PRK4|Q7PRK4_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLCNAQQKF RIVPRDLQVL EGTEALLRCE IYNLVGAVQW TKDGFALGFS HTIPGYPRYS VLADRNLGIY NLRISNASIE
81 DDAEYQCQVG PAKFNSAIRA NARLTVISPP SSIEIQGHSR NAKVEVREGQ DLTLTCVVSN AKPVAQIVWY RGKTEYKSDT
161 IENKVTETEG KRYTVSSQLR IKPTSDDDYM EYTCQAKHKA LQPDRPMQTK VQLSVLYPPG EPQIEGFTAG EVLRRGQNVE
241 LICRSRGGNP PAQLIW**YKND VQ**VRMAYRTT DRLSENIYSF VAEEGDNKAR LRCEANNIMI AAPLKTEITL SVLFAPTQVT
321 ISGASEARTG DVVSLQCQTA PSNPPAEIKW SVSGHHVKNT TSRTIENPDG GWITLSNISV PVEANKRSLV VICHGLNMQL
401 TENVIATHTV NVLLPPSQPV ITGYTEGTII AAGSVQRLQC TSSGGNPLAT LTWYKNDKKL NTPTKTTDKS VSSEISILVN
481 ATDNQAKYRC EAHNSATEIP MSASRTLAVN FPPETVKIKI IPPELKPGIE ATLICDSSSS NPPATISWWR DGIAVDGMNN
561 SSKPGLWGGT VSSLELKVNI SQDMDGNVYT CQSANEALQR NVHEAIKLQV LYPPKFKPPP SSTVVGAEGE PLTVAMVATG
641 NPMSISYTWT KDGLPILSSA GAQRIVSEGP ILNITRLNRN DTGIYTCEAV NSQGSAMINI SVVVEYGASI QSISENVTVN
721 PGEEAMLSCT VEGKPLTEEH IRWERIGYDM TIKTSTTFAN GTSYLHVKNA RREDVGNFRC IADNRVANPT SRDVLLIVKF
801 APEIDKSPVM LRAAAGFGER ARLPCRAQAA PRPKFYWSRS GQVLNVNQSA KFYVEHKQID ALTYESILVV ERVASNDYGL
881 YECIARNELG NVKEKVRLDV TSPPDPPVSL NVLNVTHDSV TLAWTPGFDG GMKANYRIRY RELNSDRYWY EDSQPNSYKL
961 TIGGLRMNTL YVFSIMASNG LGSSRYLPDV TRAHTKGKER QARLFMVQSA EIPSFVIFCI ALAALCLLAV NAGLVIWCII
1041 RKRAKGKQQS SRVPTLFFLL VPPFLVLNIR HFVTGETLSS VSEKSDAYST DANRPDYTDD TTSKSASTYL VENGDMPPPR
1121 YQKEGTLPPY PNNINGAYAR TLPHPRHNPV NYQQRSHDDQ MIERSSYVTA PSPGPPFDGS YYNMNSDRYL SYPPM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	257	262	
total 1 peptides												

tr|A0A182WXT9|A0A182WXT9_ANOQN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PPSSIEIQGH SRNAKVEVRE GQDLTLTCVV SNAKPVAQIV WYRGKTEYKS DTIENKVTET EGKRYTVSSQ LRIKPTSEDD
81 YMEYTCQAKH KALQPDRPMQ TKVQLSVLYP PGEPQIEGFT AGEVLRRGQN VELICRSRGG NPPAQLIW**YK NDVQ**VRMAYR
161 TTDRLSENIY SFVAEEGDNK ARLRCEANNI MIAAPLKTEI TLSVLFAPTQ VTISGASEAR TGDVVSLQCQ TAPSNPPAEI
241 KWSVSGHHVK NTTSRTIENP DGGWITLSNI SVPVEANKRS LVVICHGLNM QLTENVIATH TVNVLLPPSQ PVITGYTEGT
321 IIAAGSVQRL QCTSTGGNPL ATLTWYKNDK KLNTPTKTTD KSVSSEISIL VNATDNQAKY RCEAHNSATE IPMSASRTLA
401 VNFPPETVKI KIIPPELKPG IEATLICDSS SSNPPATISW WRDGIAVDGM NNSSKPGLWG GTVSSLELKV NISQDMDGNV
481 YTCQSANEAL QRNVHEAIKL QVLYPPKFKP PPSSTVVGAE GEPLTVAMVA TGNPMSISYT WTKDGLPILS SAGAQRIVSE
561 GPILNITRLN RNDTGIYTCE AVNSQGSAMI NISVVVEYGA SIQSISENVT VNPGEEAMLS CTVEGKPLTE EHIRWERIGY
641 DMTIKTSTTF ANGTSYLHVK NARREDVGNF RCIADNRVAN PTSRDVLLIV KFAPEIDKSP VMLRAAAGFG ERARLPCRAQ
721 AAPRPKFYWS RSGQVLNVNQ SAKFYVEHKQ IDALTYESIL VVERVASNDY GLYECIARNE LGNVKEKVRL DVTSPPDPPV
801 SLNVLNVTHD SVTLAWTPGF DGGMKANYRI RYRELNSDRY WYEDSQPNSY KLTIGGLRMN TLYVFSIMAS NGLGSSRYLP
881 DVTRAHTKDT PPSQPASSLG SKTATSQSTG GTIGASGIVL LIGVAAGICL VLLNIILIGC CIHRRTVHKR IKRGETLSSV
961 SEKSDAYSTD ANRPDYTDDT TSKSASTYLV ENGDMPPPRY QKEGTLPPYP NNINGAYART LPHPRHNPVN YQQRSHDDQM
1041 IERSSYVTAP SPGPPFDGSY YNMNSDRYLS YPPMQQDYSA MEMSTPPPPV IPALPKNTGT LTRTSRPMVP PPDVTYHAQS
1121 VVNESSSSPQ HMSSSLSNTV LGPSQAPVPA PKPLQGILKD PKRNSSASNS SQHQQLQHGA QLIAVQNPSP VPLVGGVPGL
1201 PLVGSTFLGA AVAGNGPNGG TGGTSSLGNS LLIGTYDPSS TNLSSFNASF GFTDADGHLR V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	149	154	

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

tr|A0A1A9TG01|A0A1A9TG01_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  PPSSIEIQGY NRNAKVEVRE GQDLTLTCVV SNAKPVAQIV WYRGKTEYKS DTIENKVTET EGKRYTVSSQ LRIKPTSEDD
  81  YMEYTCQAKH KALQPDRPMQ TKVQLSVLYP PGEPQIEGFT AGEVLRRGQN VELICRSRGG NPPAQLIWYK NDVQVRMAYR
 161  TTDRLSENVY SFVAEEGDNK ARLRCEANNI MIPAPLKTEI TLSVLFAPTQ VTISGASEAR TGDVVSLQCQ TAPSNPPAEI
 241  KWSVSGHHVK NTTSRTIENP DGGWITISNI SVPVEANKRS LVVICHGLNM QLTENVIATH TVNVLLPPNQ PVITGYTEGT
 321  IIAAGSVQRL QCSSTGGNPL ATLTWYKNDK KLNSPSKATD KSVSSEISIL VNATDNQAKY RCEAHNSATE IPMSASRTLA
 401  VNFPPETVKI KIIPPELKPG IEATLICDSS SSNPPATISW WRDGIAVDGM NNSSKPGLWG GYVSSLELKV NISQDMDGNV
 481  YTCQSANEAL QRNVHEAIKL QVLYPPKFKP PPSSTVVGAE GEPLTVAMVA TGNPMSISYT WTKDGLPILS STGAQRIVSE
 561  GPILNITRLN RNDTGIYTCE AVNSQGSAMI NISVVVEYGA SIQSISENVT VSPGEEAMLS CTVEGKPLTE EHIRWERIGY
 641  DMTIKTSTTF ANGTSYLHVK NARREDVGNF RCIADNRVAN PTSRDVLLIV KFAPEIDKSP VMLRAAAGFG ERARLPCRAQ
 721  AAPRPKFYWS RSGQVLNVNQ SAKFYVEHKQ IDALTYESIL VVERVASNDY GLYECIARNE LGNVKEKVRL DVTSPPDPPV
 801  SLNVLNVTHD SVTLAWTPGF DGGMKANYRI RYREVNSDRY WYEDSQPNSY KLTIGGLRMN TLYVFSIMAS NGLGSSRYLP
 881  DVTRAHTKDT PPSQPASSLG SKTATSQSAG GTIGASGIVL LIGVAAGICL VLLNIILIGC CIHRRTVHKR IKRGPAGDVP
 961  EMVQSAEIPS FVIFCIALAA LCLLAVNAGL VIWCIVRKRA KGETLSSVSE KSDAYSTDAN RPDYTDDTTS KSASTYLVEN
1041  GDMPPPRYQK EGTLPPYPNN INGAYARTLP HPRHNPVNYQ QRSHDDQMIE RSSYVTAPSP GPPFDGSYYN MNSDRYLSYP
1121  PMQDYSAMEM STPPPPVIPA LPKNTGTLTR TTRPMVPPPD VTYHAQSVVN ESSSSPQHMS SSLSNTIIGS GAPSQAPVPA
1201  PKPLQGILKD PKRNSSASNS SQHQQLQHGA QLIAVQNPSP VPLVGGVPGL PLVGSSFLGA TGGNGANGVT TGGTSSLGNS
1281  LLIGTYDPTS TNLSSFNASF GFTDADGHLV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	149	154	
total 1 peptides												

tr|A0A182MKW5|A0A182MKW5_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1  MTPPSSIEIQ GYSRNAKVEV REGQDLTLTC VVSNAKPAAQ IVWYRGKTEY KSDTVENKVT ETEGKRYTVS SQLRIKPTSE
  81  DDYMEYTCQA KHKALQPDRP MQTKVQLSVL YPPGEPHIEG FTAGEVLRRG QNVELICRSR GGNPPAQLIW YKNDVQVRMA
 161  YRTTDRLSEN VYSFVAEEGD NKARLRCEAN NIMIPAPLKT EIKLSVLFAP TQVTISGASE ARTGDVVSLQ CQTAPSNPPA
 241  EIKWSVSGHH VKNTTSRTIE NPDGGWITIS NISVPVEANK RSLVVICHGL NMQLTENVIS THTVNVLLPP NQPVITGYTE
 321  GTIIAAGSVQ RLQCTSTGGN PLATLTWYKN DKKLNSPIKS TEKSVSSEIS ILVNATDNQA KYRCEAHNSA TEIPMSASRT
 401  LAVNFPPETV KIKIIPPELK PGIEATLICD SSSSNPPATI SWWRDGIAVD GMNNSSKPGL WGGYVSSLEL KVNISQDMDG
 481  NVYTCQSANE ALQRNVHEAI KLQVLYPPKF KPPPSSTVVG AEGEPLTVAM VATGNPMSIS YTWTKDGLPI LSATGAQRIV
 561  SEGPILNITR LNRNDTGIYT CEAVNSQGSA MINISVVVEY GASIQSISEN VTVSPGEEAM LSCTVEGKPL TEEHIRWERI
 641  GYDMTIKTST TFANGTSYLH VKNARREDVG NFRCIADNRV ANPTSRDVLL IVKFAPEIDK SPVMLRAAAG FGERARLPCR
 721  AQAAPRPKFY WSRSGQVLNV NQSAKFYVEH KQIDALTYES ILVVERVASN DYGLYECIAR NELGNVKEKV RLDVTSPPDP
 801  PVSLNVLNVT HDSVTLAWTP GFDGGMKANY RIRYREVNSD RYWYEDSQPN SYKLTVGGLR MNTLYVFSIM ASNGLGSSRY
 881  LPDVTRAHTK DTPPSQPASS LGSKTATAQS TGGTIGASGI VLLIGVAAGI CLVLLNIILI GCCIHRRTVH KRIKRGLGVD
 961  APEMVQSAEI PSFVIFCIAL AALCLLAVNA GLVIWCILRK RAKGETLSSV SEKSDAYSTD ANRPDYTDDT TSKSASTYLV
1041  ENGDMPPPRY QKEGTLPPYP NNINGAYART LPHPRHNPVN YQQRSHDDQM IERSSYVTAP SPGPPFDGSY YNMNSDRYLS
1121  YPPMQDYSAM EMSTPPPPVI PALPKNTGTL TRTTRPMVPP PDVTYHAQSV VNESSSSPQH MSSSLSSTVI GNSLPSQAPV
1201  PAPKPLQGIL KDPKRNSSAS NSSQHQQLQH GAQLIAVQNP SPVPLVGGVP GLPLVGSTFL GTAGGNGTNV GTGGSSSLGN
1281  SLLIGTYDPS STNLSSFNAS FGFTDADGHL V
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	151	156	
total 1 peptides												

tr|W5JMT8|W5JMT8_ANODA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MPSAFCDTIE NKVTETEGKR YTVTSQLRIK PGSEDDYMEY TCQAKHKALQ PDRPMQTKVQ LSVLYPPGEP QIVGFAAGEV
  81 LRRGQKVELI CRSRGGNPPA QLIWYKNDVQ VQMAYRTTDR LSENTYTFVA EESDNKARLR CEANNIMIQA PLKKEIALSV

 161 LFAPTHVTIS GASEARTGDV VSLQCQTAPS NPPAEIKWSV NGHHMKNTTS RTIENQDGGW ATVSNISVPV EANKRSLVVI
 241 CHGLNMKLTE NVISTHTVNV LLPPSQPTIT GYTEGTIIPA GSVQRLQCTS TGGNPLATLT WYKNDKKLNS ATKTTDKSVS
 321 SELSILVNAT DNQAKYRCEA QNSATEIPLS ADRTLAVNFP PETVKIKIIP PELKPGIEAT LICDSSSSNP PATISWWRDG
 401 IAVDGLNNAT KPGLWGGWVS SLELKVNISQ DMDGNVYTCQ SANEALQRNV HEAIKLQVLY PPKFKPPPSS TVVGAEGEPL
 481 TVAMVATGNP MSISYTWTKD GLPILSSAGA QRIVSEGPIL NITRLNRNDT GIYTCEAVNS QGSAMINISV VVEYGASIQS
 561 ISENVTVSPG EEAMLSCTVE GKPLTEEHIR WERIGYDMTI KTSTTFANGT SYLHVKNALR EDVGNFRCIA DNRVANPTSR
 641 DVLLIVKFAP EIDKSPVMLR AAAGFGERAR LPCRAQSAPR PKFYWSRSGQ VLNVNQTAKF YVENKQIDAL TYESILVVER
 721 VAANDYGLYE CIVRNELGNV KEKVRLDVTS PPDPPVSLNV LNVTHDSVTV AWTPGFDGGM KANYRVRYRE VNSDRYWYED
 801 SQPNSYKLTI GGLRMNTLYV FSIMASNGLG SSRYLPDVTR AHTKDTPPSQ PASSLGSKTA SSQSTGGSIG ASGIVLLVGV
 881 AAGICLVLLN IILIGCCIHR RTVHKRIKRD SKHQMAPSDS SLPSEGKKIH EHHDTQKVES NLSGLKHALH GTSYQLKLGI
 961 VVSMANAKKA LDSANSPDME TPEMAQKAEI PSFVIFCIAL AALCLLAVNA GLVTWFMMRK RAKGETLSSV SEKSDAYSTD
1041 ANRPDYTDDT TSKSASTYLV ENGDMPPPRY QKEGTLPPYP NNINGAYART LPHPRHNPVN YQQRSHDDQM IERSSYVTAP
1121 SPGPPFDGSY YNMNSDRYLS YPPMDYSAME MSTPPPPIIP ALPKNTGTLT RMTSRPMVPP PDVTYHAQSI ISESSSSPQH
1201 GMGNMASTAL TGVPGTTTSS IPPQPAPKPL QGILKDPKRN SSASNSSAHA QALQQQLNSG AQLIAVQNPS PVPLGSVPGI
1281 PLVGSTFLGP AAGVPGPANV SQAGTSSLGN SLLIGTYDPS STNLSSFNAS FGFTDADGHL V
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	105	110	
total 1 peptides												

tr|A0A182Y6U2|A0A182Y6U2_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MDSAPPSSIE IQGYNRNAKV EVREGQDLTL TCVVSNAKPV AQIVWYRGKT EYKSDTIENK VTETEGKRYT VSSQLRIKPT
  81 SEDDYMEYTC QAKHKALQPD RPMQTKVQLS VLYPPGEPQI EGFTAGEVLR RGQNVELICR SRGGNPPAQL IWYKNDVQVR

 161 MAYRTTDRLS ENVYSFVAEE GDNKARLRCE ANNIMIPAPL KTEITLSVLF APTQVTISGA SEARTGDVVS LQCQTAPSNP
 241 PAEIKWSVSG HHVKNTTSRT IENPDGGWIT ISNISVPVEA NKRSLVVICH GLNMQLTENV IATHTVNVLL PPNQPVITGY
 321 TEGTIIAAGS VQRLQCSSTG GNPLATLTWY KNDKKLNSPS KATDKSVSSE ISILVNATDN QAKYRCEAHN SATEIPMSAS
 401 RTLAVNFPPE TVKIKIIPPE LKPGIEATLI CDSSSSNPPA TISWWRDGIA VDGMNNSSKP GLWGGYVSSL ELKVNISQDM
 481 DGNVYTCQSA NEALQRNVHE AIKLQVLYPP KFKPPPSSTV VGAEGEPLTV AMVATGNPMS ISYTWTKDGL PILSSTAKLF
 561 SSATRNTALP GAQRIVSEGP ILNITRLNRN DTGIYTCEAV NSQGSAMINI SVVVEYGASI QSISENVTVS PGEEAMLSCT
 641 VEGKPLTEEH IRWERIGYDM TIKTSTTFAN GTSYLHVKNA RREDVGNFRC IADNRVANPT SRDVLLIVKF APEIDKSPVM
 721 LRAAAGFGER ARLPCRAQAA PRPKFYWSRS GQVLNVNQSA KFYVEHKQID ALTYESILVV ERVASNDYGL YECIARNELG
 801 NVKEKVRLDV TSPPDPPVSL NVLNVTHDSV TLAWTPGFDG GMKANYRIRY REVNSDRYWY EDSQPNSYKL TIGGLRMNTL
 881 YVFSIMASNG LGSSRYLPDV TRAHTKDTPP SQPASSLGSK TATSQSAGGT IGASGIVLLI GVAAGICLVL LNIILIGCCI
 961 HRRTVHKRIK RGKCPGGRIA TGTLWALWFY AGCPAGDVPE MVQSAEIPSF VIFCIALAAL CLLAVNAGLV IWCIVRKRAK
1041 GETLSSVSEK SDAYSTDANR PDYTDDTTSK SASTYLVENG DMPPPRYQKE GTLPPYPNNI NGAYARTLPH PRHNPVNYQQ
1121 RSHDDQMIER SSYVTAPSPG PPFDGSYYNM NSDRYLSYPP MQDYSAMEMS TPPPPVIPAL PKNTGTLTRT TRPMVPPPDV
1201 TYHAQSVVNE SSSSPQHMSS SLSNTIIGSG APSQAPVPAP KPLQGILKDP KRNSSASNSS QHQQLQHGAQ LIAVQNPSPV
1281 PLVGGVPGLP LVGSSFLGAT GGNGANGVTT GGTSSLGNSL LIGTYDPTST NLSSFNASFG FTDADGHLV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.YKNDVQ.V	Y	20.99	765.3657	126.7	766.4700	1	0.28	1210	1	153	158	
total 1 peptides												

tr|A0A1B6DX46|A0A1B6DX46_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 NVEDSTQLTV ECLRDIPPYI LTQLMQELKG FGNEPRVLFP PAVEMKNITD SFSSVDPWAH SSSTPWLTGI TADNGMDGSA

  81 IFMKGKENEE LLSELNDQFE GIAPLVLGFR ETAVNPQRIA RSIRKFYFGP NEIWNETMNE LTEMFTDANY LHCSEEAVRR
 161 HSGPTYKYYY NYLGSKTLFP STSGVRHFDE MFHLFPFPTL NKENTTVEEE LFGEIFLEFI TNFATVGNPT PKGSKIKWEP
 241 VTSAANEYLY IDNETQMMQK KLKSKRDKFW QNLEFRNKPK SLFRRPPEKN YEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.SVDPW.A	Y	20.04	602.2700	41.2	603.3021	1	0.14	1102	1	54	58	
total 1 peptides												
