Summary

1. Notes

2. Result Statistics

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

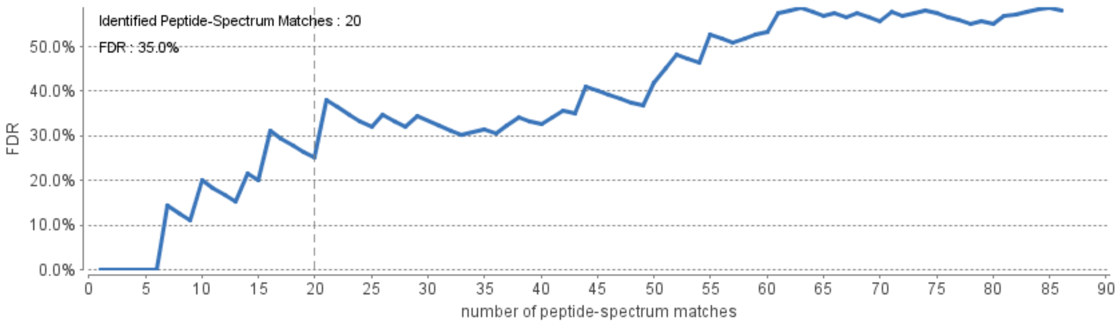

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

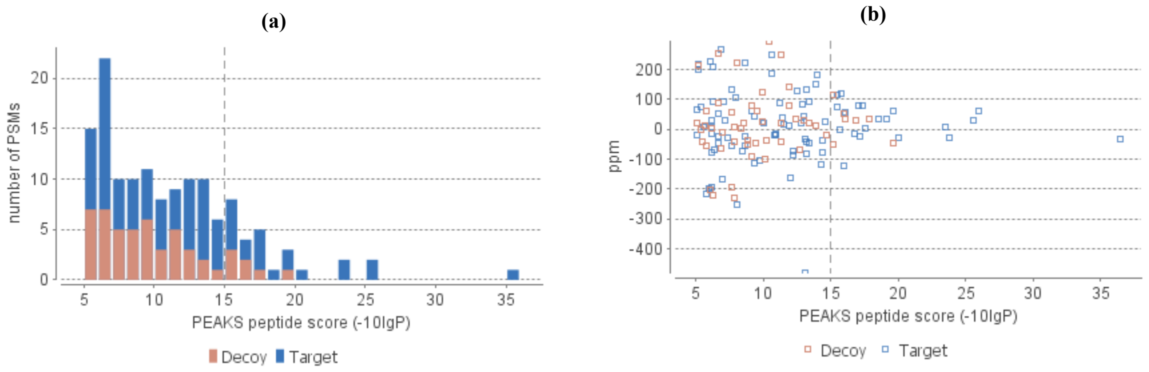

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

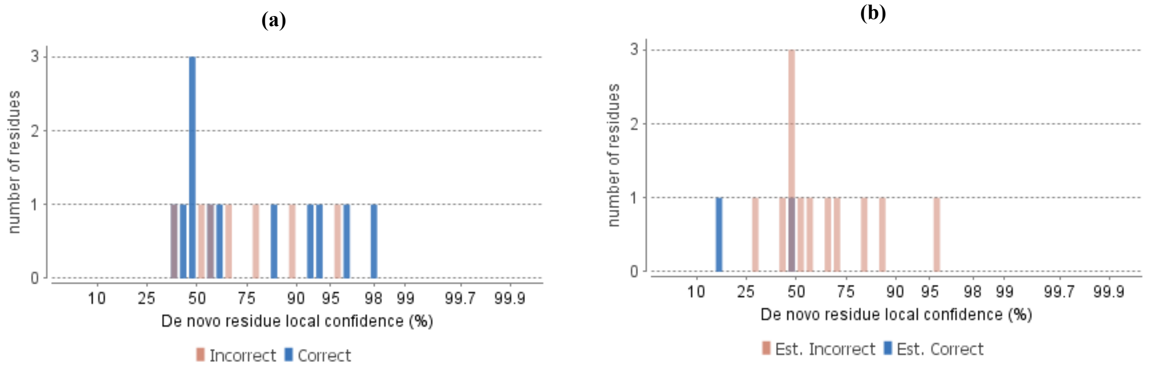

Table 1. Statistics of data.

# of MS Scans	0
# of MS/MS Scans	318

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	20
Peptide Sequences	20

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	1	C

Protein Groups	7
Proteins	32
Proteins (#Unique Peptides)	0 (>2); 1 (=2); 31 (=1);
FDR (Peptide-Spectrum Matches)	35.0%
FDR (Peptide Sequences)	35.0%
FDR (Protein)	21.9%
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.

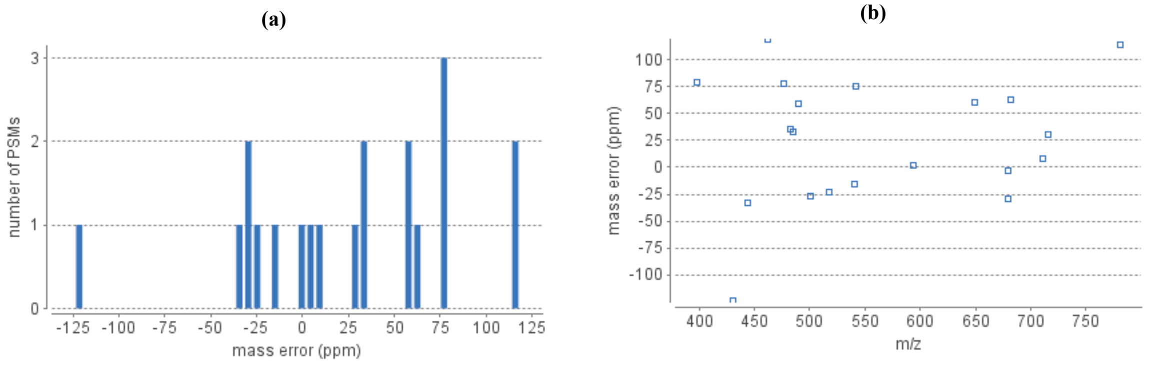

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
IT-TOF	0	0	0	0	20

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: 41
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: D_2.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
4	1166	tr|A0A1B0CWQ4|A0A1B0CWQ4_LUTLO	36.43	2	1	1	N	61318	Uncharacterized protein OS=Lutzomyia longipalpis PE=4 SV=1
6	12	tr|A0A2A3EFD7|A0A2A3EFD7_APICC	25.97	2	1	1	N	33838	Hemolymph protein OS=Apis cerana cerana GN=APICC_01024 PE=4 SV=1
6	13	tr|A0A0P5PCC8|A0A0P5PCC8_9CRUS	25.97	1	1	1	N	47674	Putative 116 kDa U5 small nuclear ribonucleoprotein component protein (Fragment) OS=Daphnia magna PE=4 SV=1
6	14	tr|A0A0P5UGL7|A0A0P5UGL7_9CRUS	25.97	1	1	1	N	48004	Putative 116 kDa U5 small nuclear ribonucleoprotein component protein (Fragment) OS=Daphnia magna PE=4 SV=1
6	15	tr|W5J9B5|W5J9B5_ANODA	25.97	1	1	1	N	47006	Uncharacterized protein OS=Anopheles darlingi GN=AND_009030 PE=4 SV=1
6	17	tr|A0A0A9WTJ7|A0A0A9WTJ7_LYGHE	25.97	1	1	1	N	57678	Homoserine kinase OS=Lygus hesperus GN=thrB_8 PE=4 SV=1
6	20	tr|A0A0P5AC35|A0A0P5AC35_9CRUS	25.97	1	1	1	N	74883	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	21	tr|A0A0P5SVT9|A0A0P5SVT9_9CRUS	25.97	1	1	1	N	80592	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	22	tr|A0A0P5Z225|A0A0P5Z225_9CRUS	25.97	1	1	1	N	91653	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	23	tr|A0A0P6GST7|A0A0P6GST7_9CRUS	25.97	1	1	1	N	94169	116 kDa U5 small nuclear ribonucleoprotein component protei
total 32 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
									n OS=Daphnia magna GN=APZ42_020697 PE=4 SV=1
6	24	tr|A0A0P4WTI5|A0A0P4WTI5_9CRUS	25.97	1	1	1	N	94065	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	25	tr|A0A0P5IVR0|A0A0P5IVR0_9CRUS	25.97	1	1	1	N	94184	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	26	tr|A0A0P5TSN9|A0A0P5TSN9_9CRUS	25.97	1	1	1	N	94277	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
6	67	tr|A0A2A3ERZ8|A0A2A3ERZ8_APICC	25.97	0	1	1	N	189462	Deleted in lung and esophageal cancer protein OS=Apis cerana cerana GN=APICC_07252 PE=4 SV=1
6	213	tr|Q7Q293|Q7Q293_ANOGA	25.97	0	1	1	N	475780	AGAP003967-PA OS=Anopheles gambiae GN=1278787 PE=3 SV=5
5	1182	tr|A0A0P5SWM5|A0A0P5SWM5_9CRUS	25.56	1	1	1	N	112653	Ubiquitin-associated protein OS=Daphnia magna PE=4 SV=1
5	1183	tr|A0A0P5E3J6|A0A0P5E3J6_9CRUS	25.56	1	1	1	N	113010	Ubiquitin-associated protein OS=Daphnia magna PE=4 SV=1
5	1184	tr|A0A0P5D183|A0A0P5D183_9CRUS	25.56	1	1	1	N	114611	Ubiquitin-associated protein OS=Daphnia magna PE=4 SV=1
10	1230	tr|A0A2A3EBV7|A0A2A3EBV7_APICC	25.55	2	2	1	N	74261	Cell division cycle protein OS=Apis cerana cerana GN=APICC_00245 PE=4 SV=1
2	1168	tr|W5JTY5|W5JTY5_ANODA	23.83	1	1	1	N	68668	Uncharacterized protein OS=Anopheles darlingi GN=AND_001991 PE=4 SV=1
2	1179	tr|A0A0L7KMQ9|A0A0L7KMQ9_9NEOP	23.83	4	1	1	N	15923	Acetyl-coA carboxylase (Fragment) OS=Operophtera brumata GN=OBRU01_24323 PE=4 SV=1
2	1199	tr|A0A182T4W9|A0A182T4W9_9DIPT	23.83	1	1	1	N	82068	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
1	1341	tr|A0A0A1X8U8|A0A0A1X8U8_ZEUCU	23.50	0	1	1	Y	169647	Serine/threonine-protein kinase SIK3 OS=Zeugodacus cucurbitae GN=SIK3_2 PE=4 SV=1
1	1470	tr|A0A131ZXT9|A0A131ZXT9_SARSC	38.13	0	3	2	Y	464657	Nipped-A-like protein OS=Sarcoptes scabiei GN=QR98_0013460 PE=3 SV=1
3	1204	tr|A0A0K8TQ34|A0A0K8TQ34_TABBR	20.04	3	1	1	N	19812	Putative alpha crystallins (Fragment) OS=Tabanus bromius PE=2 SV=1
3	1324	tr|A0A2A3EIL6|A0A2A3EIL6_APICC	20.04	1	1	1	N	93793	Leucine-rich repeat-containing protein OS=Apis cerana cerana GN=APICC_07668 PE=4 SV=1
3	1454	tr|A0A182XZ01|A0A182XZ01_ANOST	20.04	0	1	1	N	190500	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
3	1487	tr|A0A1I8NNI7|A0A1I8NNI7_STOCA	20.04	0	1	1	N	299077	Uncharacterized protein OS=Stomoxys calcitrans GN=106080961 PE=4 SV=1
3	1486	tr|A0A1I8NNI6|A0A1I8NNI6_STOCA	20.04	0	1	1	N	298042	Uncharacterized protein OS=Stomoxys calcitrans GN=106080961 PE=4 SV=1
3	1485	tr|A0A1I8NNI4|A0A1I8NNI4_STOCA	20.04	0	1	1	N	297712	Uncharacterized protein OS=Stomoxys calcitrans GN=106080961 PE=4 SV=1
3	1481	tr|A0A1I8NNI3|A0A1I8NNI3_STOCA	20.04	0	1	1	N	249529	Uncharacterized protein OS=Stomoxys calcitrans GN=106080961 PE=4 SV=1
3	1479	tr|A0A1I8NNI2|A0A1I8NNI2_STOCA	20.04	0	1	1	N	244584	Uncharacterized protein OS=Stomoxys calcitrans GN=106080961 PE=4 SV=1
total 32 proteins									

tr|A0A1B0CWQ4|A0A1B0CWQ4_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MDLAETMKAA LSSSKPGGGA SGNHPSGMNS NHTGAQGQDQ GVGAGAGYVT EKLYMLLQLY LQNKGWNPSV ELLQCFSELK
 81 DSALLPNAAY LQVLANRLAL DSQGRLVLRD TGKIVLPFEH FANAVMLKHM SGPHGLHLSL EATVRAVMDS YTIGRENFGM
161 EKEFIVEVVQ SCPNPACRFY KNHLGTPYID QQFPGPGMNP EFLTHMSQMA STGGASGTTD LPGMEKGTSG GAAAQSVVAQ
241 AAAAAAAKHA KQSQSQHQQQ ITAAIIQQQN RAIAQQSLEK FGNMTALEKQ RVLQQLDKKH YDAVQQQVAA AANICPPPPN
321 VPAVSGSSSI NVPTLIDTIQ LVQSLRNCLP APHIPVSSWK SEDRHRRSSK RRSNASADNK FLGMMQNNPA NVGNAGGGGG
401 SGGGMMGQQV LNMSTSAQNH LPPPPPPQGQ QQGVQHQSTG QQGQQQTSSG GGGGMEHNQQ AHKDFLRSNL DCLETLTSNK
481 DLLALHNGAW TNQEGRDGLA IGQDKIVRAF AELMRNMARM KTFIRPSMSL IDTIQLVQSL RNCLPAPHIP VSSWKSEDRH
561 RREPDLGNYE S
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
C.PPPPNVPAV.S	Y	36.43	886.4912	-32.5	444.2385	2	0.28	348	1	316	324	
total 1 peptides												

tr|A0A2A3EFD7|A0A2A3EFD7_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MFKYSTIFTA IIFLCAFLGC TISEDNLPNA EEALQKVSGI IDLNNLNVSG NPALDNVNAS VIKHALEESQ SVFKQKCDKN
 81 GGEGTFENAI NAMNDLEQCL KSFVNFTKLE KEMERHKPTG DLDTVFKTYC RKTPTLKKCV SNFTTAIEPC LEPQERENKK
161 IIQNITDSLL TFVCYKEGDR IALFISANGP ECLQSKQQEI QQCVNITLGS YIPQTDLNNG PGLNSLPLLV FGTKECTDIS
241 KVQSCIVREL EKCKDPVPAN IVDSIFNYII KVTPCQKVIN LQNTASSSTI NLLCMGLIFL LLILT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.TDSLLT.F	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	166	171	
total 1 peptides												

tr|A0A0P5PCC8|A0A0P5PCC8_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AAPRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEVSVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
241 IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEE**TDS LLT**KLGIKLS LEDRDKDGKN

321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401 RVFAGKVCTG MKARIMGPNY VPGNK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A0P5UGL7|A0A0P5UGL7_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEISVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
241 IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEE**TDS LLT**KLGIKLS LEDRDKDGKN

321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401 RVFAGKVCTG MKARIMGPNY VPGNKADL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|W5J9B5|W5J9B5_ANODA back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQILP**TDSLL T**MALLDEGAN ATQQLGLSAL RPRQTGGADD DTPTIAKVTS MVVLFSVSMV CGLVPFKLVR WFNINPTSPS

81 GGTHLFLIRL LLSFGGGALL STTFLHLLPE INHSIAALQD TGALPQPEDL PFPLGEFLLT SGFFMIYLLE EIVHWWMHRR
161 SARARRGTTG TASATNSKTH LHNNDTMMAE SKQSHAHGHS HLPVGNVTAV YPITDVDGTQ IVPEAGTGTD TTVASASSSS
241 LRGLLIVLAL SIHELFEGLA VGLERSPSAV WLLFGAVASH KFVIAFCVAF ELLVAAVRFR IAVAYIFVYS VVSPLGIGIG
321 IALSSVGTDT NQTIEVVSVI LQGLASGTLL YVIFFEILAK DSGHSHGGGS GEKTEPQEDH GGYNQPSTNG LWQFFAVLVG
401 FGLLFGIMVA TGHSHEHGHS HGGSGEHDHD HDHDHDHDDH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.TDSLLT.M	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	6	11	
total 1 peptides												

tr|A0A0A9WTJ7|A0A0A9WTJ7_LYGHE back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLSVLIGLLA FGVTIPGFEA YTNWEKTELD SNSTRHQSHA ENPERRQARN SFITQPTENS NNLKANVTLF DKMYGPKRNV
81 MSPSSTKIQD NKIPWHGFRA STFFRPRYKS LKTTCDCNVY KVYSNNEKSV MFRNNYELWS NVNYFPESRS VSLKIRRSEP
161 EEELSGDGRF IYDDDYSLIN YVDKGKWGND VTANQRGQTV KRTPKKKNSK REAEDREFSV MFHSRKDNEY RDKFSNNHDF
241 LKNGKKKSML HFEKKKYKHE SGSKPERKMT FLERRNNLRE SYNHVARTPL NLKSSKKKYP FWLSKKEKFG TKHETFSAIL
321 TSPKASASSL IPPRKVLHWA TTRSYVAAIS AQNNVTPATL SPNAHLVPPA LIPFLNLNL**T DSLLT**ARKSD VASYPSTPAT

401 MNRPAILVNQ SGSPQYLRVG NNNLDLRSLN LNPNLAFPFG FNMPIAKPME NNAGVYGPPA QVTTPVVFFF NAPTEGINPL
481 SNHLDKFKNT TTWNAKQGPP GNLNAV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TDSLLT.A	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	380	385	
total 1 peptides												

tr|A0A0P5AC35|A0A0P5AC35_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MRFTDTRKDE QERCITIKST AVTMYFELAE KDCLFITNPE QRETTEKGFL INLIDSPGHV DFSSEVTAAL RVTDGALVVV
 81  DCVSGVCVQT ETVLRQAIGE RIKPILFMNK MDRALLELQL DQEALYQTFQ RIVENVNVIV ATYADDDGPM GEVSVDPSKG
161  SVGFGSGLHG WAFTLKQFAE MYADKFKIDT IKLMNRLWGE NFFNPTTKKW SKTKDNDNKR SFNMYVLDPL YKVFDAIMNY
241  KKEETDSLLT KLGIKLSLED RDKDGKNLLK AVVRQWLPAG ETLLQMIAIH LPSPAVAQKY RTEMLYEGPL DDEAAVAMKN

321  CDPNGPLMMY VSKMVPTTDK GRFYAFGRVF AGKVCTGMKA RIMGPNYVPG NKADLYEKAI QRTVLMMGRF VEAIEDVPCG
401  NICGLVGVDQ FLVKTGTIST FKDAHNLRVM KFSVSPVVRV AVEPKNPADL PKLVEGLKRL AKSDPMVQCI IEESGEHIVA
481  GAGELHLEIC LKDLEEDHAC IPLKKSDPVV SYRETVSEES DQVCLSKSPN KHNRLYMKAV PMPDGLAEDI DKGEVNARDD
561  FKIRGRYLSD KYEYDVTEAR KIWCFGPDTT GPNLLIDVTK GVQYLNEIKD SVVAGFQWAT KEGVLCDENM RSVRFNIHDV
641  TLHADAIHRG GGQIIPTARR VFYASVTS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	245	250	
total 1 peptides												

tr|A0A0P5SVT9|A0A0P5SVT9_9CRUS

back to list

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

Protein Coverage:

```
  1  MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
 81  LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161  MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEVSVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
241  IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEETDS LLTKLGIKLS LEDRDKDGKN

321  LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401  RVFAGKVCTG MKARIMGPNY VPGNKADLYE KAIQRTVLMM GRFVEAIEDV PCGNICGLVG VDQFLVKTGT ISTFKDAHNL
481  RVMKFSVSPV VRVAVEPKNP ADLPKLVEGL KRLAKSDPMV QCIIEESGEH IVAGAGELHL EICLKDLEED HACIPLKKSD
561  PVVSYRETVS EESDQVCLSK SPNKHNRLYM KAVPMPDGLA EDIDKGEVNA RDDFKIRGRY LSDKYEYDVT EARKIWCFGP
641  DTTGPNLLID VTKGVQYLNE IKDSVVAGFQ WATKEGVLCD ENMRSVRFNI HDVTLHADAI HRGGGQIIPT ARRVFYASVT
721  S
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A0P5Z225|A0A0P5Z225_9CRUS

back to list

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

Protein Coverage:

```
  1  MSVIAHVDHG KSTLTDSLVG KAGIIAGAKA GEMRFTDTRK DEQERCITIK STAVTMYFEL AEKDCLFITN PEQRETTEKG
 81  FLINLIDSPG HVDFSSEVTA ALRVTDGALV VVDCVSGVCV QTETVLRQAI GERIKPILFM NKMDRALLEL QLDQEALYQT
161  FQRIVENVNV IVATYADDDG PMGEISVDPS KGSVGFGSGL HGWAFTLKQF AEMYADKFKI DTIKLMNRLW GENFFNPTTK
241  KWSKTKDNDN KRSFNMYVLD PLYKVFDAIM NYKKEETDSL LTKLGIKLRL EDRDKDGKNL LKAVVRQWLP AGETLLQMIA

321  IHLPSPAVAQ KYRTEMLYEG PLDDEAAVAM KNCDPNGPLM LYVSKMVPTT DKGRFYAFGR VFAGKVCTGM KARIMGPNYV
401  PGNKADLYEK AIQRTVLMMR AFIEAIEDVP CGNICGLVGV DQFLVKTGTI STFKDAHTLR VMKFSVSPVV RVAVEPKNPA
481  DLPKLVEGLK RLAKSDPMVQ CIIEESGEHI VAGAGELHLE ICLKDLEEDH ACIPLKKSDP VVSYRETVSE ESDQVCLSKS
561  PNKHNRLYMK AVPMPDGLAE DIDKGEVNAR DDFKIRGRYL SDKYEYDVTE ARKIWCFGPD TTGPNLLIDV TKGVQYLNEI
641  KDSVVAGFQW ATKEGVLCDE NMRSVRFNIH DVTLHADAIH RGGGHIIPTA RRVFYASVLT AAPRLMEPVY LCEIQCPENA
721  VGGIYGVLNR RRGHVFEESQ VAGTPMFVVK AYLPVNESFG FTADLRSNTG GQAFPQCVFD HWQILPGNPF ESTSKPAQVV
801  ADTRKRKGLK EGIPALDSYL DKL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	277	282	
total 1 peptides												

tr|A0A0P6GST7|A0A0P6GST7_9CRUS

back to list

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

Protein Coverage:

```
  1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
 81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEISVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
241 IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEETDS LLTKLGIKLS LEDRDKDGKN

321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401 RVFAGKVCTG MKARIMGPNY VPGNKADLYE KAIQRTVLMM GRFVEAIEDV PCGNICGLVG VDQFLVKTGT ISTFKDAHNL
481 RVMKFSVSPV VRVAVEPKNP ADLPKLVEGL KRLAKSDPMV QCIIEESGEH IVAGAGELHL EICLKDLEED HACIPLKKSD
561 PVVSYRETVS EESDQVCLSK SPNKHNRLYM KAVPMPDGLA EDIDKGEVNA RDDFKIRGRY LSDKYEYDVT EARKIWCFGP
641 DTTGPNLLID VTKGVQYLNE IKDSVVAGFQ WATKEGVLCD ENMRSVRFNI HDVTLHADAI HRGGGQIIPT ARRVFYASVL
721 TAAPRLMEPV YLCEIQCPEN AVGGIYGVLN RRRGHVFEES QVAGTPMFVV KAYLPVNESF GFTADLRSNT GGQAFPQCVF
801 DHWQILPGNP FESTSKPAQV VADTRKRKGL KEGIPALDSY LDKL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A0P4WTI5|A0A0P4WTI5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
 81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEVSVDP SKGSVGFGSG LHGWAFTLKQ FAEIYADKFK
241 IDTIKLMNRL WGGNFFNPTK KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEETDS LLTKLGIKLS LEDRDKDGKN

321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401 RVFAGKVCTG MKARIMGPNY VPGNKADLYE KAIQRTVLMM GRFVEAIEDV PCGNICGLVG VDQFLVKTGT ISTFKDAHNL
481 RVMKFSVSPV VRVAVEPKSP ADLPKLVEGL KRLAKSDPMV QCIIEESGEH IVAGAGELHL EICLKDLEED HACIPLKKSD
561 PVVSYRETVS EESDQVCLSK SPNKHNRLYM KAVPMPDGLA EDIDKGEVNA RDDFKIRGRY LSDKYEYDVT EARKIWCFGP
641 DTTGPNLLID VTKGVQYLNE IKDSVVAGFQ WATKEGVLCD ENMRSVRFNI HDVTLHADAI HRGGGQIIPT ARRVFYASVL
721 TAAPRLMEPV YLCEIQCPEN AVGGIYGVLN RRRGHVFEES QVAGTPMFVV KAYLPVNESF GFTADLRSNT GGQAFPQCVF
801 DHWQILPGNP FESTSKPAQV VADTRKRKGL KEGIPALDSY LDKL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A0P5IVR0|A0A0P5IVR0_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAGIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
 81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEVSVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
241 IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEETDS LLTKLGIKLS LEDRDKDGKN

321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
401 RVFAGKVCTG MKARIMGPNY VPGNKADLYE KAIQRTVLMM RAFIEAIEDV PCGNICGLVG VDQFLVKTGT ISTFKDAHNL
481 RVMKFSVSPV VRVAVEPKNP ADLPKLVEGL KRLAKSDPMV QCIIEESGEH IVAGAGELHL EICLKDLEED HACIPLKKSD
561 PVVSYRETVS EESDQVCLSK SPNKHNRLYM KAVPMPDGLA EDIDKGEVNA RDDFKIRGRY LSDKYEYDVT EARKIWCFGP
641 DTTGPNLLID VTKGVQYLNE IKDSVVAGFQ WATKEGVLCD ENMRSVRFNI HDVTLHADAI HRGGGQIIPT ARRVFYASVL
721 TAAPRLMEPV YLCEIQCPEN AVGGIYGVLN RRRGHVFEES QVAGTPMFVV KAYLPVNESF GFTADLRSNT GGQAFPQCVF
801 DHWQILPGNP FESTSKPAQV VADTRKRKGL KEGIPALDSY LDKL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A0P5TSN9|A0A0P5TSN9_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MVNFTVDEIR VMMDKKRNIR NMSVIAHVDH GKSTLTDSLV GKAVIIAGAK AGEMRFTDTR KDEQERCITI KSTAVTMYFE
  81 LAEKDCLFIT NPEQRETTEK GFLINLIDSP GHVDFSSEVT AALRVTDGAL VVVDCVSGVC VQTETVLRQA IGERIKPILF
 161 MNKMDRALLE LQLDQEALYQ TFQRIVENVN VIVATYADDD GPMGEISVDP SKGSVGFGSG LHGWAFTLKQ FAEMYADKFK
 241 IDTIKLMNRL WGENFFNPTT KKWSKTKDND NKRSFNMYVL DPLYKVFDAI MNYKKEETDS LLTKLGIKLS LEDRDKDGKN

 321 LLKAVVRQWL PAGETLLQMI AIHLPSPAVA QKYRTEMLYE GPLDDEAAVA MKNCDPNGPL MMYVSKMVPT TDKGRFYAFG
 401 RVFAGKVCTG MKARIMGPNY VPGNKADLYE KAIQRPVLMM GRFVEAIEDV PCGNICGLVG VDQFLVKTGT ISTFKDAHNL
 481 RVMKFSVSPV VRVAVEPKNP ADLPKLVEGL KRLAKSDPMV QCIIEESGEH IVAGAGELHL EICLKDLEED HACIPLKKSD
 561 PVVSYRETVS EESDQVCLSK SPNKHNRLYM KAVPMPDGLA EDIDKGEVNA RDDFKIRGRY LSDKYEYDVT EARKIWCFGP
 641 DTTGPNLLID VTKGVQYLNE IKDSVVAGFQ WATKEGVLCD ENMRRVRFNI HDVTLHADAI HRGGGQIIPT ARRVFYASVL
 721 TAAPRLMEPV YLCEIQCPEN AVGGIYGVLN RRRGHVFEES QVAGTPMFVV KAYLPVNESF GFTADLRSNT GGQAFPQCVF
 801 DHWQILPGNP FESTSKPAQV VADTRKRKGL KEGIPALDSY LDKL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TDSLLT.K	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	298	303	
total 1 peptides												

tr|A0A2A3ERZ8|A0A2A3ERZ8_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MTAFMKHILL RKKDKMNPES FTNMVSNVDK NKYAQFIQRR LQSMQSRNNN WKMSYTFVKT AQKNVVLRHK TNILLYSYKS
  81 KLKDVCPAQI QALKQHIQKD LEPKYDESKS TDIDFDEEEK EEDLDVHPSE LTVEVPKLKT WDMYKQLVEE SRLRPKVKYI
 161 PEQPVIDVST LSKIYFEYRI KKFIISRIVV KKKPQKSIIK LKKERILVAN KNYVEFKNFE LKKKIITIKN IGNMPVRYHL
 241 RKQPYHSKFW IMIKPVIENK NIIPPGLTVQ LIIFFRCDEI DTPDEILIIK VQYGSPLVIR MCGYKDSPHL IGICQSDEIP
 321 FKYSNMKLNQ DWQPEIEMSF DSLDTFYTES VKTDSLLTFM SNDDKFISMI FDCKRAFIGE EVYVTMKLKN IGGNGRFFII

 401 SEIDWFSMNI MDVTDKNILK LSCFTIWPAY FSLNKNEEMT FHMKFAPECF GIHVEKIYIL CTNCTLLTTE IIGDGLLYEP
 481 NFIQLSKHLK KIESSKRNID QYSKYYINLS TDTPDGVGQC IIPVNNVSEI SMYFSWKKRN VQTKNHKINE ENYFPLQLLH
 561 VEPDHGIFAP TSIHYFTVTA DYTNLQPNYY FAVLQLYVED IPIEAIPSEI EVITKKCTTK RRKCKKSVDI WVADVEIWLQ
 641 FMMDDKSEID QETEEISKYI IVSDYKYQRE YEEEEEEEEE EEEDEKEEKI SEIEFKEEYK STSQLINDEL FSHFDLINLK
 721 QFEPLWQEKI ISMEETYVLV LRNLANNPLN YLWGEVNGLD STKMKLCVCP EKGEILAGDA QKMEIIITPL KEGIVQSLFI
 801 PCFVGDLHKI IMLGIECFIE PLYVTFYFPL NDKMSLELKN NFVKIEWRTD SFKFAFDMAG KSKKYMKILN KYKNREEREI
 881 MNMDLDQGEI LKDASTDPLI QEIVAEESSE YFPNTSEINS FQTSNLRVQI DNNYSQNTIS SGNIIPFHQR YLPLITQPIV
 961 IEFLNLPLRT VRKKTFIIKN ETSIPTNFWL SIKNFYPIRC TCEWKSKKDL IKSIYKRVFG QKKGLVEETL YKAKQYGSGI
1041 VIYVDPLNSD IGPFKAISVD IYVFADTWGI YVDELEINII GLPKYTIGIC VQVVGSPITL SISNRNEFNI PVIKYGIEAI
1121 GMRLNDRKIL LTNTSVIPIV INWHTFLVKP VIKKMPFNII FSIQTPFTDK LASQLRLNNE KTESEIHLEE HTNFSSSKNL
1201 NTCDSIEIND IIESTTSSYM ESSFITSSGI SNNEILINKH SKNKCGNLKC KHDCKICLKH KNSKRSDIEL KILILPYYGL
1281 INTKICKVTP KEMFISPKSS VSLTINIQLD KYKFIKEINK LIEGEFFCKI LGFLRISPSD MYKDNYYARQ TEKYFSPIEI
1361 DVTANITKPR LYFNISKFDK TFICCANEVM QSKTKQIELT KKLLLYNNKN YTIEIFLETC DPFYIKSIAI HTESYQCKIG
1441 ILCINPNEYV EIKIICVVKE KLIKTILNTN QNFYYPKVTL KESLHIIYTD KYIEDIDLIL QIWFPILKLS SYTLDFGLIY
1521 VGDTKKLTLT IKNLSICNVN FEINKKFKID DFIIDQKCGT LSNRYNHEDG YFTITVSFQP KKPGQLVETL EILTDILHNI
1601 EECQLYGEGT LDEKYHSPGA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TDSLLT.F	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	353	358	
total 1 peptides												

tr|Q7Q293|Q7Q293_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MESDLSTCLR QLKTCLDTQQ IPQARSIIDR ITQLIVEKAE ESQAETDFNL ECMLTSANGL VAFLNKSFSS AKHFGKVIES
81 TFELFRKTIE KHSPLMGKRM VVIVPIALRY IQSSSVPARS RELAALVLQD SVAYGCLQNE TYAQLDQLPA ELLLVFQQGK
161 LPNRFQQNLY ELLGQLAQNF PASIPEPDRV RDIYLNAAEK QLLEENYPSL VSLAGAVRGL DLFLVHFAPS ENDRELRQRL
241 YLLVKKLSIW EENRSERAVF RNALHVVGNH APLFSWQLYA DHVHWQTMLA GRWIKSSSQE DRDAGLKALY AFHGEVARVL
321 STPELAAEGG REYPPKVDVL NQYVNYYRKL LSSATVDRLE IRIAIRGFGI MAGPCQQLAG ASSISLNELL TIVLQRIEGI
401 CERSASSTAD MLVYLPDFIQ ALSEILTHVQ QLSTVQLVSV QTMTVALVRD FYHISNAHHE LIVRSVVSML ENIGKLGGTT
481 RHQLLDSVLL QGIVWSCTHA LPFPAALPVP SSNVAAGDTA PKIDWKRDLV TYKNYLPLWQ GLLEKAQSAH DSSLLPALYR
561 ALMNTLFVIV EKLDLSTRKR TFQDDDGQEQ ELFFSDPNID LLPTKPKDYH IFLNLVELYR DMLHGPQTPA AVRELFADWI
641 RPYFERFVRQ SLNRPLVSGF VKLIEMGLAT AERIGYFRQQ EAPSEDFRTT QMLLAFYLEQ TIQRALYAIG ELQLACLRFV
721 LNAPVRLLVD FIEDKTRKQP LMVDVFRTAF RLGRSLLSIA RAALYSLQRI VRFRYPPLRR EIRERLLRQV LPLLEPFLRT
801 RDSTQPPAQS LRLAKFKRHR TANVPAVKIE RIKQQHRIEQ SVDTSELVTF QLRILNFFAD LQPNECCWLV VDELELECVH
881 ARENRGSSSS LTRWDGDSGR SLELRLLCES GTRPCIKLDS IVGRVCELAV ECSDRATKLA ACELLHTIVL YLLGISYQDQ
961 LAGLTQVCHH LLQLSCDTDL AVCQMFEPLL FQIIHFVTQP SKLGQQGTRA LLDCLLDATS NVQHSSTIRD LSVRCLREFL
1041 QWTNRQCGGT HLSNDRRKIK CTLLEQLKTH ALELNASHRY GSALAFNNLF RLLLQEDFHI VRYSFELMHS YAIGLIVTEQ
1121 EQIGLSSEAN GGSHGAIVEQ YLLALDHLGK LFEQRKALFN GCSSDESARS GRRQLIPTEL GGGEMEHLVR WLFRQCAARQ
1201 RLYRRKCMEL FARLSKTVRD VATAEQFLAK QFTHEQIVSI CLQADSLQGI ERASTLESLR NEQTNPPIMN ISLWLEYFLA
1281 TVDMYCWLRR EGLVVDELLQ TLLSRILPAF RYFLRSVVNF TVQEIMSNIE PVESFQQRSY EQRMSADKFV RFDALKSAVV
1361 VQVVDMLVLL LTRHSEDTVC SAVVLELWQD QATIEFLLAL LLKPHRLGQY CNFSIHHEVE GDRHLWAQLE TLVLQLIERS
1441 SEPIGQRFTI ALTEQLILVM EDVSERMRTL LIQRTIHAED QKLAKGLRFI AKHLRNRTLL AGTAKDRRIP LAACRLLQDC
1521 YEAIGQESVC LVLSPSATRF GTIVLEAIFG LADSTGHGDD MDGLVEFVIS CSLSEDMLQP NIRHGEHFLV CFGGAVYELF
1601 LQNPSNCLPM LLKALKPENF SFIVRFLCNL MDYSYRKQAA NTDSLKCLVE MLLAGGWSPL FECSRLQSNQ FGACDVQLIE
1681 LMSSVAMICP FPLNEIHHRV GPTYGRWLTE LIGSTRSELS IELKAKAIVL LPTLLGPNGA PEAESHWAEV ENALEALQTK
1761 HFPLRSAEFP PNSPERIGYL NCLERLLDAM VISRSPLLLK AIIQMTAPDG DGHIAETELR TAIERFFADQ PHEVQCKRLL
1841 ELWELFANHA YAPVVRETIL RRYLCTALWH CRYDSIVQFY TRIIRALSHN TMVEINGRTG WALEHALIDR AASYRLVEHY
1921 AALLPKQILT GDNCPVAQEL YGSAHDTLGA PVRGQRLIGD FSKRAHGVRR VALPTNDRTL AELFRKYQCA AYRALVALIS
2001 NTNEDARMYS VLLFRESREK GEFLWRHLID CSNEELYLEG TQEQEQLSRT FEKRVAIRRE GGGGGDPAQR KPALKDPGLS
2081 VVMESSLSQQ VFRFDMSHSV VLSAREVAQK DAAELAKRQQ GTLSNVSLER TKINRHEIMA TVCGCIRHMA ATKVPLDSVV
2161 HFLVGSLADA GQQKNVRLFL AKVIDNCRNE LQPHAALLIG PLMQLIVDGY IFRGLNPLVT DLIALVLEWN ASGEARRSLR
2241 EGATGEIASL ASVLLRFIMK HACPQQSARK MAVLRLNLEL IQEVIVQWHE ALTVPAELLF EMVSHRQPTE DRSQLQLIAG
2321 LQLGTIVLLK GRGKLVPWME STKQDYLRAV LRCLDLPDST SFKSAALLLG HSLAHIYPDG FPEPEQQTGE LETFHTECIA
2401 KLTSIQREYD RKFAEVLYET AKGFPSIADP FLSVLSYRFP SASGGEKRLY LELLLGGRLE KFNDELYREL ASMELTLLLQ
2481 DGELQLPTLH LLNRSLSLVR ELEHLQQLVE PIGRVATEPS TPNEARAVAF EILIYIHEHR SAELSEECRT SVWRNLIRGL
2561 CGSHETELGS GSIRGRILEY LTYSGKLPSD VKERFLFVLA QLYDPTVEGE FLGNAVALLL DPAIRCRESK DRLFLHEYLN
2641 ADVKFCEYTI ETAARQRHTM TLLTPMFAET SQQRQLQSFI TGRGSQMEQL IRATQLGGLD SAAQKQLPFE PTQDPGRLSK
2721 GNETFAMPTQ QHTLLFESSA LQLNRRSQRT GSSTDTAAQQ DRGFERLRKR ILKDSATNRQ QQTAWAVSRH YASQRQRTEQ
2801 RRDSTSKVTL YRRYRLADYP DLQINLLAFL LPLQALCRRD TTCARQTFVA IFNGLVECLL VGDSEGRTGR MVGDEWDRFV
2881 GRLDEALNPI LESTKACDPN LFGGLIELTL GKASGKFTLP PRTIASVAGT CNMLPMGALY LEAKLADGAD FDDEPVRTAG
2961 SVSSEADHWL QLSTLYHALH EHSVMVGIFG EKLDSDPQLR EAIELEALGR YGQAHRAYCE LVMRVSRARV DERNFCYKSA
3041 FNCLLQLGQW DVLLDEIGNQ VTNHEELWCD EWNQENLLPH YVHGNALLVL AGDEGGREFY RLLEQWLHMP QRERHIRQEF
3121 GEQLTALYLS AQDMVRARLF GEQTKRQFLD EWHCSGVLSE LVRTECLLSV RKVIELVAYS ELLERSTKEL EQAAGGLVVS
3201 WNNAQPTV**TD SLLT**WDTLLA YRRFLLEQLE TKCTREEEER EKSDSLTNVT QLSKLLFELE LNLLDVAFEQ DNVKFAGKII

3281 ARLRAFEACL REPQVDQVLR RKIARIRYDR VRVVEASAAN LTSALLRGFK QLVKLNSQLM PLEQEPGIRG VKQRAWTEFF
3361 HHSETVRTML KTSSDIIEQK DSSTLVELMQ TAMNTSSKQL TEEPLSMGDR LRKFSMQCLQ CGIDVLLDEG PSSSREGNSS
3441 ANDSSMEQLA DAHLRLARYC YDELDPARTA AEELPVERLL LTSLLPAIKY GSREARHLFP VLLQLRNLQN DVLGKEFHEN
3521 ACSVPSWNFL PWIPQLLSYM QIATPDRPLA PSGVEHFLDE VLMRLVQDYP MALYFPARLL LGELLQPGAS VRPFVNQFRA
3601 ALSFPVLDRF VAELYRVVMP ETRLSNMIAE LKRHLASVTD QPTYQTFIER LVPDVFPLDT NDLWRYGQAY RAALPLVERV
3681 RTLQSLHPVE DRGTILAKLQ ELETNLESLR PRSKTTRLQL EDLSPWLADY HSSGQRGSTT QLVEIPGQYG LDRGAPSPTQ
3761 HVTIVKVMPD VVVYGTLRLP IQLTFRGSDG NEYRFLAKFG EDLRQDQRIQ QLQREITHRL RWDQRCREQQ LQLRTYDVVP
3841 ILPNFGLFGW LEGTVAMSEI AKQAAPRYNP GDRGQAHVHH EFGRFLMSVS KQLDPSANDS FNLSSYNAPA LYGMAAAFCM
3921 PDRLQSKFVE LAQTIRGNTL KRALYDMAAT PEAYYRLRMN FAKSLATMNV TCWVLGIGDR HLSNIVLERA TGMLVGVDFG
4001 IAFGAGTRDL PIPELVPFRL TPQFVGVMEP MRLAGVLQKC HLYTLQCLRN CRTLLRACLE VFVREPTVDW LRAARQRMVE
4081 QPGESGRAEE RRSDREWNPQ VRVDTVLRKL NGANPKQLLT DELRFGVVAQ QRDFLVGYLA LVDAAAPACT EKVGRRATGT
4161 ISTELQTEML LEMAIDSRLL GITYSGWYPW F

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.TDSLLT.W	Y	25.97	648.3330	59.9	649.3792	1	0.44	442	1	3209	3214	
total 1 peptides												

tr|A0A0P5SWM5|A0A0P5SWM5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MRMSSTAKKG DKGKSSTNSS LPLSKDTAPH SSTKMANSKT VESKHDSSKA VEQLNPKLLP TAEQLRIAQM ISDSKKDDPE
  81  LPEKVNKLVE LTNCSADAAI IALHDSNNDL DHAIAALLDG ETEGDWEVSG KKKKPKQSAQ QLGPAGGDGP EGGSGVGSGR
 161  GRDRERDRPR SSRGGPPRLR GRGRGRDNKE NVEEGDGEHF GGSRGRGSRS GPRMSNGPGR EGSSGRGSGG GRGGRGGFRR
 241  GQRGPAPVTE TWEEGADYSA MTNVEPWGVD FPSAEDWDNE EYIGSLVETK VFTPSQSAAV NVPAPAAPIP EPAQLTNGSP
 321  SISNGGGGGN SSSSSSHVEP AVPVPAPPPQ VHYSTINNSA QQGIDLNALL QKTSGVTVAG SSMQQQFLQY SQQATDALKA
 401  AMGVGGGSSA NLKSAKPLRA KIPPPSKIPL SAVEMPDDPI VSGLDVKFGT LDFGIEPSGF DMGIDVAMTP SSTANINMGK
 481  QPDHHHQQQQ QQHQQQQHQQ HQQQQQQQQQ HQQSQHGLMS KIEQQYASSA PTPQPPAPST LPKPDSSLGG FSVSSASAPQ
 561  QSMATTSTQV KSTNSPASYP YGTSYAPPGV NSASTQATTT GVSQPAGAYP TNSQTSGVYS NNSSNSGYQG ASSQTAYGSY
 641  VQQQPHQQPQ QQQQQQQQQQ QASYQTYNNK MNSASSMNDA SSSVSSLRGD MPNATAASTS RQPNAVTSAT ATNKQAGTTL
 721  AASGSGLPNM PPGVPMLGPG SFIMGQAPGL PYYAAAAAAA GIQQHQVYSL EDMQYRYPHL AAAGYYDMGY QSPTSLGGGR
 801  DGTLASLAYA TGTDAKFSRN ETNSPVPTSL SQNAAQSHGG AFITPAAAAA TPLTPAYAYY YSGGVMPGGY QFGAPAALYP

 881  VSAATSGHAA SNAAQYGKGG LSGSGTGGAQ SGQTSGGATA GGPSNATASG YASYGSTYDD FSKAVYNSVG VGSAAGQTAK
 961  IGGVGASTGP SVGAAGSADL GPNVYGKTHN QLGKISTYDK TGGFHTGTPP PYGMAGNANA APLGVGVSVG VGGPSPYGTQ
1041  HMFIPTLAPH QSQHSHMMHQ QLHQDSASGP GQRSQSGGQQ NKQGSKSNYG GSYWGSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TNSPVPT.S	Y	25.56	714.3548	29.8	715.3834	1	0.46	483	1	822	828	
total 1 peptides												

tr|A0A0P5E3J6|A0A0P5E3J6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MRMSSTAKKG DKGKSSTNSS LPLSKDTAPH SSTKMANSKT VESKHDSSKA VEQLNPKLLP TAEQLRIAQM ISDSKKDDPE
  81  LPEKVNKLVE LTNCSADAAI IALHDSNNDL DHAIAALLDG ETEGDWEVSG KKKKPKQSAQ QLGPAGGDGP EGGSGVGSGR
 161  GRDRERDRPR SSRGGPPRLR GRGRGRDNKE NVEEGDGEHF GGSRGRGSRS GPRMSNGPGR EGSSGRGSGG GRGGRGGFRR
 241  GQRGPAPVTE TWEEGADYSA MTNVEPWGVD FPSAEDWDNE EYIGSLVETK VFTPSQSAAV NVPAPAAPIP EPAQLTNGSP
 321  SISNGGGGGN SSSSSSHVEP AVPVPAPPPQ VHYSTINNSA QQGIDLNALL QKTSGVTVAG SSMQQQFLQY SQQATDALKA
 401  AMGVGGGSSA NLKSAKPLRA KIPPPSKIPL SAVEMPDDPI VSGLDVKFGT LDFGIEPSGF DMGIDVAMTP SSTANINMGK
 481  QPDHHHQQQQ QQHQQQQHQQ HQQQQQQQQQ HQQSQHGLMS KIEQQYASSA PTPQPPAPST LPKPDSSLGG FSVSSASAPQ
 561  QSMATTSTQV KSTNSPASYP YGTSYAPPGV NSASTQATTT GVSQPAGAYP TNSQTSGVYS NNSSNSGYQG ASSQTAYGSY
 641  VQQQPHQQPQ QQQQQQQQQQ QQQQASYQTY NNKMNSASSM NDASSSVSSL RGDMPNATAA STSRQPNAVT SATATNKQAG
 721  TTLAASGSGL PNMPPGVPML GPGSFIMGQA PGLPYYAAAA AAAGIQQHQV YSLEDMQYRY PHLAAAGYYD MGYQSPTSLG
 801  GGRDGTLASL AYATGTDAKF SRNETNSPVP TSLSQNAAQS HGGAFITPAA AAATPLTPAY AYYYSGGVMP GGYQFGAPAA

 881  LYPVSAATSG HAASNAAQYG KGGLSGSGTG GAQSGQTSGG ATAGGPSNAT ASGYASYGST YDDFSKAVYN SVGVGSAAGQ
 961  TAKIGGVGAS TGPSVGAAGS ADLGPNVYGK THNQLGKIST YDKTGGFHTG TPPPYGMAGN ANAAPLGVGV SVGVGGPSPY
1041  GTQHMFIPTL APHQSQHSHM MHQQLHQDSA SGPGQRSQSG GQQNKQGSKS SYGGSYWGSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TNSPVPT.S	Y	25.56	714.3548	29.8	715.3834	1	0.46	483	1	825	831	
total 1 peptides												

tr|A0A0P5D183|A0A0P5D183_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRMSSTAKKG DKGKSSTNSS LPLSKDTAPH SSTKMANSKT VESKHDSSKA VEQLNPKLLP TAEQLRIAQM ISDSKKDDPE
81 LPEKVNKLVE LTNCSADAAI IALHDSNNDL DHAIAALLDG ETEGDWEVSG KKKKPKQSAQ QLGPAGGDGP EGGSGVGSGR
161 GRDRERDRPR SSRGGPPRLR GRGRGRDNKE NVEEGDGEHF GGSRGRGSRS GPRMSNGPGR EGSSGRGSGG GRGGRGGFRR
241 GQRGPAPVTE TWEEGADYSA MTNVEPWGVD FPSAEDWDNE EYIGSLVETK VFTPSQSAAV NVPAPAAPIP EPAQLTNGSP
321 SISNGGGGGN SSSSSSHVEP AVPVPAPPPQ VHYSTINNSA QQGIDLNALL QKTSGVTVAG SSMQQQFLQY SQQATDALKA
401 AMGVGGGSSA NLKSAKPLRA KIPPPSKIPL SAVEMPDDPI VSGLDVKFGT LDFGIEPSGF DMGIDVAMTP SSTANINMGK
481 QPDHHHQQQQ QQQQHQQQQH QQHQQQQHQQ HQQQQQQQQQ QQQQQHHQHQ QSQHGLMSKI EQQYASSAPT PQPPAPSTLP
561 KPDSSLGGFS VSSASAPQQS MATTSTQVKS TNSPASYPYG TSYAPPGVNS ASTQATTTGV SQPAGAYPTN SQTSGVYSNN
641 SSNSGYQGAS SQTAYGSYVQ QQPHQQPQQQ QQQQQQASYQ TYNNKMNSAS SMNDASSSVS SLRGDMPNAT AASTSRQPNA
721 VTSATATNKQ AGTTLAASGS GLPNMPPGVP MLGPGSFIMG QAPGLPYYAA AAAAAGIQQH QVYSLEDMQY RYPHLAAAGY
801 YDMGYQSPTS LGGGRDGTLA SLAYATGTDA KFSRNE**TNSP VPT**SLSQNAA QSHGGAFITP AAAAATPLTP AYAYYYSGGV

881 MPGGYQFGAP AALYPVSAAT SGHAASNAAQ YGKGGLSGSG TGGAQSGQTS GGATAGGPSN ATASGYASYG STYDDFSKAV
961 YNSVGVGSAA GQTAKIGGVG ASTGPSVGAA GSADLGPNVY GKTHNQLGKI STYDKTGGFH TGTPPPYGMA GNANAAPLGV
1041 GVSVGVGGPS PYGTQHMFIP TLAPHQSQHS HMMHQQLHQD SASGPGQRSQ SGGQQNKQGS KSNYGGSYWG SN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.TNSPVPT.S	Y	25.56	714.3548	29.8	715.3834	1	0.46	483	1	837	843	
total 1 peptides												

tr|A0A2A3EBV7|A0A2A3EBV7_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARQSGILDC EKMHNLSDNK NIDLDNCRKL IKSYIDLHLY SAALFWADKV VSLSNEDPKD VCTLAHCMYL MKQYHRAAHL
81 IRRGLEKTD VMCHYLTVRS LLEAKEYNEA LQVINESEIC TNITQSAFGD RADILEDAPK NVQSSILYVK GRVHEAMDNR
161 AVATDCYKQA LHCDVYSYQA FEALVQNQM**L SAAE**EKELLE SLPFGEQCTE AEAEFLRLLY ESKLKKYQEP YKKQVLATCS

241 VMGVLVTDKL LGNLDMEVTE AERLYYNCDY QKCFSLTERI LKKDPYHNSC LPVHIACLVE LKKTNALFYL AHKLVDLYPD
321 MALAWFAVGC YYYSIGKSDP ARRYLAKATA LDRLFGPAWL AYGHSFAVEN EHDQAMAAYF KASQLMKGCH LPLL**YIGLE**C

401 GLTNNLKLAD KFFQQAQSIA PNDPFVIHEM GVISFYNLDY KTAERQFKEA MKRIQGGLKD VILPSKWEAL LNNLGHTCRK
481 MKKYGEALEY HQQALMLNPL NASTYSAVGF IHALIGNTQE AVDAFHRALG LRRDDTFTTT MLTYVMEQLI EESPPYRDAP
561 IDIPKYKYPA NKHQETDNAE PLENTNNIAE SANQDIDKLR VNLFSGWGED SNKADDNTAD KVERNPQDVI VNYSSDISSE
641 VEMLDSSTAH IE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.YIGLE.C	Y	17.51	593.3060	2.0	594.3145	1	0.39	426	1	395	399	
M.LSAAE.E	N	16.08	489.2435	58.4	490.2793	1	0.36	377	1	190	194	
total 2 peptides												

tr|W5JTY5|W5JTY5_ANODA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASSMSSRNR IRRRLAAISF LSNISLDGTH RDTRLGPGHG AGAAAGLSLS GGRAALQLLN NNEQEGGGCG ASDQYEDGTE
81 DALDGPGIRS PLVDRDGDGA EDSSGRDTAS LNGAEREGTV AAQQPAGRAR ARTGTFSKSP ERQAGRRIDS EGNMVVPAAH
161 NGGLSTKSTP LKDRENWNPN DGRLNHTADK RLRANSATQR PSGAKRSLLM NTSAGPVLSS AADRSMDGQA GGGAGNHTHN
241 SSTESLMQGT KPASKSVIIN DTIVQREVRF YTMDRS**RAPA QH**GLQEDRIV LLSKKAPCHI FSVLPYCKGK ANGRTDTRQV

321 RRRHPSGARP LSSINDAPFD AFRLLGIERG GEAGQEVSYG YLLIPSRNYH REKKHTTEKG LKSAFEIPNF ASLENHAAAR
401 YYDTLNRNST ASPSQSMAVG GGATGGAAGA AGNAATSLML EGSKDYEDGY TSMSGLQYSA NILDDPELIA GKHRTLLTFT
481 SYVTSVIDYV RPSELKKELN DQFREKFPQI QLTLSKLRSI KREMKRINKL DSRIDFLTIS QAYVYFEKLI LSKLVNKENR
561 KLCAGACLLL SAKLNDIKGE ALKSLIEKTE SVFRLNRKEL IASEFAVLVA LEFSLHVSTS EIHPHYQRLM YES

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.RAPAQH.G	Y	23.83	678.3561	-29.6	679.3433	1	0.44	457	1	277	282	
total 1 peptides												

tr|A0A0L7KMQ9|A0A0L7KMQ9_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PGIEDEPAHE GRDSFPNALP PSIRRQHLSK AQQLALAEKR SKLSGTEESD PGMRRTSSRR AELQ**RAPAQH** QAASVQRGPA

81 HAGRDSNAPP PSIRRHLSKA QQLALAEKCS KLRPWHEEDQ LTQVATPTRP RPASGGICPK RSNSR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.RAPAQH.Q	Y	23.83	678.3561	-29.6	679.3433	1	0.44	457	1	65	70	
total 1 peptides												

tr|A0A182T4W9|A0A182T4W9_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSSLIIPIV RQPHSARERV TLSLSPCRRM AEQCTVSIED SKQQQQEQPA ISHDASHHHP ASRSPLISSI KSPTTCVVKA
81 EIAATIPNSD DDEYVVVKEE SGSTDETSTP RTTCDHRSTT TTTTPNSGVT PLSVAGDDDD GVKQKPYRLF SSTIASEEND
161 RTLHHQQHHH LLRMDSNGSD DIDGSLRHDE PADCPILLET PAMERVDEMG TDDVVVKLES TVDDADGIGI GKLTAISEKL
241 AAVKPKRLSD EFFSADDDND DEEEEEDEDD EEEREDEERK SNGGCSGAPD RSTMVDSEAQ ASLSEIKNLS ITCCGKLKDE
321 DDDVCEADEA EDEDENDGCR SSLNPSGSKD VQLNAKNSKK VTFSLVDVII EDPLEHAQQQ AEQHNAAAIA DGAAAAANDE
401 DEELLLDDVQ SMDAIERRDF EQEGGFLIRN RSLISGDRLN LEFLNNTHPR PPPNERTEPP PADPQPSSET GSGEAPALGS
481 ATSKPAVEVV PAPTSSSCSS SSTSVATCTA LNT**RAPAQH**T TTPTSSRYQH KKHHHHHHKK QHHREGKKGG GKSHVSSTGS
561 DSFSSSYNRE TENNCITRCA VYELTLALSA SLAKWSDINF DVNEPCNLSC SSTKTSPISS SFATTSSSSA SSLSAASSCS
641 SSTHYTSADT KTTKKECKPE KLADAFLNAN SNDSVSSERS LFGVHGAAED ETTLTVSDGQ TKDDDEPHTH HDDPCSSTSS
721 TASYSSSSSP SHSQTTTAQH NGDVSMMICS TAVLPPTASH SASSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.RAPAQH.T	Y	23.83	678.3561	-29.6	679.3433	1	0.44	457	1	514	519	
total 1 peptides												

tr|A0A0A1X8U8|A0A0A1X8U8_ZEUCU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

C Carba

1 MATSTSDNYK IPSTSKISVD KLLRVGYYEL EKTIGKGNFA VVKLASNIVT KSKVAIKIID KTCLNPEYLT KTFREISILK
81 SLRHPHITRL YEVMQSETMI YLVTEYASNG EIFDHLADNG PMKELEAARV FTQLVSAVQY CHSMGVVHRD LKAENVLLDK
161 DMNIKLADFG FSNRYEEGSP LTTWCGSPPY AAPEVFQGLE YDGPKADIWS LGVVLYALVC GALPFNGDTL LELKGRVVTG
241 KFRIPYFMSR DCEHLLRNML IVEPDRRYTL KQIIKHRWLS DWAAELNDIN DSVGGCSSGA NAAAYTQQSE NNSLIRSESN
321 CSFNMHGPVA IANLDTEVMR NMLQLPGLTA DMIADSVHNK RFDNIYAIYN LLADKLQQKR REHHRMQHQA AYSRLRKTSI
401 TTGVVDRSEP IKQESIDRLS PLTNTNALQG GLGFQWTDVS VDLEKFGELE LECLARTNEP QNQNQNHLCA NAGGNGGNTR
481 RHTVGPGDVA HEQALANPNV PPINFKCPPE NKNDTGPYLP MNLPMLQNQP LHNLTIKDQH LLKPPMVMGA SSFGRRASDG
561 GANLHIYYPS TGNNVHQVTG QTQQVEGNTY YINPNGSNTS GLSGASTDRH MVHGMRDQAH LPQLGASDTV SEENSEEIQK
641 YIQIRGKRHT VSCTEDLSIQ HQPGETCTVC GIYEPPLIQQ MPTIMSPQSG TSGASGGGGG MRMRRTGLLT VTERPPVISP
721 ELIREVESRM NRNYLPPALK MQQHQSHTHP PHGAPNPTLS QSPPTTSLMT YHSSSSSNIL PAQALSNAAL AGQQGPPSAT
801 GNNRRVHFKS TNKLPTVQEV GRYSPVRRAS EGSKAQFQGP LQE**CQYLQ**KV SAQRNFLIAP TPPLSENSIS LPGSPIHGKP
881 APHMMFRRGQ DLEVPPEAVR ALMPHLDRLV KEHRLNTDVA KRIISTGIVP LDLASHLGLT AHSGNVAVSG GHLDMTSPGM
961 QHQGAIYSLS VAPLSLPNNA NTSVIGAVSG PLTTQQPAFN HNMGTYSKQM LGKGPYQQQQ HFGLVHPQMQ HPGNGIVGQF
1041 SHITLSQGVA ALASGGHFSG SNSSSGCQSP IYSSFSGSSS PNPYIPGPGP FNSCTVSGNG GGGSSPLHQI TKGISVLSTG
1121 GGGSITRGTS AASEIASSAT CVPVAADAAS INQPLDLSMD ICTSDHTNTE MPTSTFAQQH VNWMIPQLSS FDLKPLNLSP
1201 AQPVRVVPTP PASPNLCIIQ EENANGQMYH TITTGTPHVG CTGGLINEDM SSPCQPSHPQ ICLTDVQGSE ITLVALSSEN
1281 SRDSECDSLE PPASLMSLQG LIITESSNDM PSITRCIGRK TSLECAVDSQ SSRLESDANA TNNVGESNRR GSDKSLGFSD
1361 DSLSNDSNNL SPCQEPSASS GFKSESHSEI GDQTEGHLSP DSICDSRRMS EEMCYEVPLP HECSNLDSTR ILELVKQTID
1441 QTMPPKGAVL HKGLPEEYSG AVGASDMNAE ARLSNASNAT SESSAISMDT SSSISGCYGN FGGIIGSSTS TNLSLEYSGG
1521 LQIELQVCEG RSRDNQAAGK GIKLRRISGD QFEYGKLCQQ LINKLTMQQV AG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.C(+57.02)QYLQ.K	Y	23.50	710.3058	7.4	711.3183	1	0.43	480	1	844	848	Carbamidomethylation
total 1 peptides												

tr|A0A131ZXT9|A0A131ZXT9_SARSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 METDNEDNAC LALRIVFDIH RRIPKMIDEA KKVFNLAKKF IMSCIQNSSK ILKQYKQYHV RSMEELDLEP ILQEIFVSTS  c Carba
  81 LEYKQDDSQK NINCFTLLPR GINSLKLMID LPLNVILLIQ IYRTALEPEY IDLLNLGFKL LAIQPSDEQK SHDQFNLDVY
 161 IDFLMIQIKH LSFISFLMRN QEEKLTQYID GEQLPLIVLS LLKNIPDDMI NLRKDLLLSC RYILSTKFRS YFVSHVTDFF
 241 DEKTLIGDSW NTRDLVRPLA YSVVFDLIHQ TRDSMSIKEL TIALNLYSKN FYEDNPPASV MIMTCRVIFN IVDSFSKSAN

 321 RENWTGVIQL LVKVLEMITD KIESMVEFMM PSMKSKILAA KSKSSPLTND IGKETLNFND KRSNYKSKTE YVCASFIETD
 401 DVRYQFSFPE SQNYFTDFRT LSKTLINGMK ILSTKLTDIH TRIQDCNIQQ NAISIVNYKT GYCRPRDIDI IVRFLKNGIK
 481 VLEVYNSNLF PTPPNRQIQT AAQMQQNLHI RAKEEKEIIE SFSAVFTCLP TQTFRVIIKD SIDFIINAII ENPNIQQLVN
 561 CFLSNKNTSS VFADTLTFYL VERMEVMGKN TELSNLYLKL FKSVFGSVSC FKYENEKMLQ SHLKKLVKNS MEMAINAQEP
 641 YNYFMLLRAL FRSIGGGTHD QLYREFLPML PTLLQGLNRF QTGIHRQNMK DLFVELCLTI PVRLSSLLPY LPWLMDPLVS
 721 ALNGTPSLIS QGLRTLELCV DNLQPDFLYA HFQPIRIELM QSLWRTLRQN ENIASVSLRI LGKLGGTNHR MMIEPQKLTY
 801 YDSHRESSMY EDESFLDKEN SEQSSSLNIP SHGSCAYIEI EFADSKFSLN MPVDRCIAAA YKYLRSPTTD PFYRQHCWEL
 881 VKGFLSANIQ RFISKDDQEH LEKLFSHPAF TSGTEFGYPS SIAPNLSSSF SKINFYKFCD EKLRKVHEQA LIAMLTASAI
 961 KELTVNVLKF MVSLTRTYTL VAICQQSGPI HTSGRIVKLH GMDPLVLIDA LTSTMGQEEQ ELGKPCRFLI CIIIDTAVTI
1041 LGSKERACQL PLFEYMLNKV CLLCYERAWY SKYGGCVTVR YIFDRMSLRW LLNHQLTIVK AMFFVMMDLA GDLSIGVIET
1121 AKDNLETMIK ICCPSPNTPK ESDLIDLQQK SMNEVTQELL RQVTHSNTTV RQQAMHLLSV MAKTSDCSVA DIIEPHKILL
1201 ADMVPFKKHK LFHQPFHVQI GILEGITFFI SLEPQLFVID LENVDHQCFF NDLISICEND DAQLGKLSCY KHYITQLPQL
1281 RKAALRMLSA CQYLQSMSNK IFDVLYKALT SSDIELQDCA YDCMKKYKYI QDINPDLIRK TVRGFLMTIS ELKVLTAKDH
           c
1361 LLILKLKNLA RLYTFLFNDK LCEHMLQQLN RLIENCGNIL RKHRDREYEM RMKAQQNQNV ENTASSLSFD VESILPANLN
1441 IAAEIIYLFC EISAAESTYV KVLLNLLNQT ELFLDIYVAK TFYKPIQCFM KRYTKISIAQ FQANLNTESI FRFFCYVFDD

1521 EKDGEPFRAI LYTSPSIIIE MLNTKLSSTP IQSIPLTTTA TQSPQNVPTP GMNIDVTSSS PNSPSFIASQ SSVNHSRYQA
1601 IKVISILIKH DPKWISSQGE LVKVLKTLWL SDSFHIGQDN FLIDYQQWEE PRLLAQCLLC YLEDNIDEIE FFFQMLKAFL
1681 HLYLCSFEFL KKFFITTIPE TYDIDWKKRS FLKYFELFPV TRTICPKSDC CLEWSQNLKA KILQLMIIPI FNQAIKSSKL
1761 KEFLQLPKDY EIPPFSPAYN FQPNLVSIFL NVLANDPKTS DGLQMFVIQL GCLIIEHASE YVRPLQKQEQ NENSSRVLMQ
1841 YDPVRILMQY AWPDVIQASK RQDSMKKFVC NLLFCHIISK NKIIKRLIKP VLCNLFKVCS SESRNVIFNA LEILIPVLPQ
1921 RLKEGYRTLR NLTKKLLFEE VHSTAQTNHL LQIIIRYYRI FYPTRHNYIQ YMISSIQRLA FSANGTFDHR KMALDLIEVI
2001 IRWEHERISS EQMDRSDDDS SGSECSYDSK QDQQSQSMQS SSKSSAGLQS QETQSNGPIA KEYSDTIILF LIRFICLVGE
2081 NASQQQQQQQ QQQLNSAQQV AQSNLAASNE FLSRRAQSLL KDILQNEFWP LKDIKLTLLE RILMTVKDNS SGNICQALEL
2161 IILFLDTMKR DVIIQLLSPL QRAISACCTS TNPKIVSTVH NLLTKLMAIV PPSGLSSTIF PESGQPVRAV NQTLETFEQL
2241 YTDIHSIILN GLASYNKIGQ PLNDQSIVTG PLQGPNAQNL QFQHQLMSNV LNRSSGGGTP GAPVHMMNST TTTLSQLFSV
2321 LMCLKAACVN KPMYIDRLAT PFSTMFQKLV KEHTGSANNS NQTSDFNVSL CADIINLCIE LIKNRIGALT NEIRRNILNN
2401 VFLTLIDKTT DVKVMRTLLK MVEDWIKQPS LSSAQCKANP SITTSAPGFR DKTMMIIRVG VNINQRFPNE IDLNIQFLEL
2481 VYYIYSDDQL KSSDIASKLE SAFMSGLRCS QPELRQKFFT LLDNCLRKSV ADRLLYIIIN QNWEAIGAHF WIKQAIELIL
2561 SVSDDSKIIS SPNKNALIPL PTALVPNNDH QDKSLLSGFV SNGIDYLSSM TIIDPSINLD LFGIGNTTNL QSSSTSSSSN
2641 GVDSLMEIDP SNEHVNDLFK DQNSTSNSAA NSESSKSTST TNSKQNICKI ACEFLNENAT YKSSTFYHAL SQLCHLDNDL
2721 AYHIWIQLFP RIYSILNDHQ RTIVSLELPG FLLSGAHAQQ RDIQQTKISV VGTFFEAISY CNPPIIFRPQ IIRYLSKYNY
2801 VWHRGCLILE EEIDSSNNMN PVTAIGGLVT NNIGQQANLN FSNYFSKQNR SFISNSEKNA LACNLPANLD DLFPSELPSS
2881 LSQPYYHECL SALADICETL KESDYWSGIW CKKAQYKETL MAIAYEQQGY FEQAKGAYEL AMSKASNDYS TAPSPPWLKE
2961 EFTLWEQHWI RCSKELNQWD FLLEYATNRE SLNPLLILES AWRIPDWNAM AQGLILVEHN LFKDFAWRLA LYKGYNAICN
3041 LNNRDFALAE RMIEFSSQFL VKEWRRLPHI VSSAHITILQ GAHQVIELQE ALNVHQILFN HNGMYSSERL NGDIRCLIKT
3121 WKNRLPDFTD DLSHWSDIFT WRQHHYQAIV TKSEQDNLLQ AQQQQSNASN VTSALALCGA HASAQSLIHL AKIARQNFLI
3201 NVALDQLSRI HTIPKVPIID CYHKIRQQLK CYLLKHSIQP TGDFKELHEA MSVVECTQLS FFQADTKAEF IALKGHILSK
3281 MKRTEEADKN LSIALQIHDQ SAKCWAMWAE FYYELFMDSV NESFSQRDLK HGSNAVIAYL QASRQMLETK VRKYLARVLW
3361 LLSYDKNDYF ADIIEKFNAG LSPSHWIPWV QQLLQCLVRS KSQTFLNIIS QMSKFYPEAV YYPTRTTYLA LKCEQRDIAF
3441 KIAYCRGSGP KAEMPVSNGL WRCTKIMHFQ RELHPTLLTS IEGIIDQFPW FRENSSEEIL RQLRQALAKC YTLAFENRKN
3521 VAETVATQPI LNYIRKMTNT FGTGIDGIVS GNSNVLNESK NLNATNAKRS QSSFTEKTTT AASETLARRA QSTVQDPDFQ
3601 KMKQQFANDF DFKMKGSKKL HQIIGKLKKW IKILEAKTRL LPKSWLLEEK CRYLSNFSQS ICNVSLPGEH YLPTNNTSGA
3681 VHIARFMPKV ELVSKHNTIA RRLYIRGENG KIYPYLVLSD SSITDLRNEE RFLHLLRLLN HYMTKHKETS RRVLNFTVPK
3761 ILAISTQMRL VEDNVSSLSL IEIYKQHMIR RGSDPDAPIA KYYDQLLSSQ TKGLQVSPAQ LKEIIEDIQS SMAPRTLLKE
3841 WALNTYASAT DFWHFRKLFT LQLGLAGLSE FVFHLTRLNP DMMYIHRDSG LMNIAYYRFD FIEEKAIFRD EIINWYKRTK
3921 INENLASLSS AIQAAKSVNA AAAAAAATAN DPNNEHCDEI KDQDQTQRLQ SMMDEKLLSI VEKNLDLREP PQIPEKELVT
4001 LTTKAVNSIM SRLQNLATFE GIDSNVAKLI DTAMSQENLC QMDPAWHPWL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.C(+57.02)QYLQ.S	Y	23.50	710.3058	7.4	711.3183	1	0.43	480	1	1291	1295	Carbamidomethylation
D.NPPAS.V	Y	18.54	484.2281	33.2	485.2515	1	0.31	373	1	295	299	
E.ISAAE.S	N	16.08	489.2435	58.4	490.2793	1	0.36	377	1	1452	1456	
total 3 peptides												

tr|A0A0K8TQ34|A0A0K8TQ34_TABBR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SIRLLLNLAE EMSAINRQIL RQMTPFGSFF PTTPRTGFPT SVFEQIKHKI DDPCYEV**TPS VP**IGKDGFKV SMDVSEFKPS

81 ELKVKAIDNA IIIEAKHKED RGDEGFISKE FVKKYVLPRG YDPKQIVSTL TAEGLLTVSV PKPPELEPKE HVVNIQHIGS

161 NSSSEKPKDE GSTDSAKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.TPSVP.I	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	58	62	
total 1 peptides												

tr|A0A2A3EIL6|A0A2A3EIL6_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKFPTLPWFE DSLSSIDNRR SAITRKYDMG LSLPFTQLGV LLFQRANIQS ESFSIAAGCH GLQRSKRLRY TICERGERVT

81 DGKVKWTTIF YTWPNERTMC CFLLLVYLFL SVTARDVSAE EVDCQVYNHL YVCLGNSVLH SVAFEDVNAV QTIEDIELHL

161 EGLGVQDIAK DAFLEVTNTS ALYIRDNQLS KIFKHYFADL DQLTYLDLKN NSIRDIEDGS FANLDSLETL ILDYNNMIAF

241 RPGMWKGLVD LHELYATNNK IALRRNMFKG LRNLETLALD CNEINEIPIG AFNGLPHIDL LYLSRNKISS LQLEVFRGLS

321 EINELDLGRN SLRSVSGGIF RYLRNLNSLW LNGNQIVMIK ADTFEGLDNL LLLFLNSNNL RFVDMSAFAR MKNVTVDPGF

401 KIAGRTMDNV SNVQGRFRCN NVAYQLPQAR RGYRLSWDRG QVYPIKDPIF AGVFKGYRQD ETPLPHPCYR STAMDYGWYA

481 PTIHTVPTSY YPRDNSFSTN QGRGGMYRNC SLNTFSLRIA VIVFQPEPSR ATQKYVPYIV VQLISNLTPR DPPVKFVDNT

561 FISPYAKGEL IFFENPIIHD FRRKKAVVEM PDLDGPIGQN GHLENDVAIK VLDLRAGGSD IIGAIILVRV KKMTNVNEFE

641 TAYNVKVNKF FKANKTTYPA LRKNILWTAS SDSMCGAQLK VGETYVVSGR VIYGDKAHIS SCGIAMPWRF VTSRQRKGFR

721 HLYHSSCMCK VRYTPWWIKG ITLENTDGTE CLWETRPGPE ECQKDFGICM YRESGCYW**TP SVP**YKNCIKN NGFNFNLPIE

801 SIKSIKRLLN NCATYKLLES I

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.TPSVP.Y	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	779	783	
total 1 peptides												

tr|A0A182XZ01|A0A182XZ01_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTTMMMVDNF ECAGYTFYSK FDSGNLGKVE LVRCCEGLGI VGNTVSNVVG AVSSSAPVVG SASNQTVPGT GITSASAIVA

81 ATLGIGLQQQ QQHHGLLSSA TGSGSTATTG VSSLGMPIPS PTPHATENPL VEVEFNLWTR PDCAGTPYEN QNRTWFHFAV

161 TGGRPNQIVK FNVMNLNKQA KLFSQGMHPV TKVGPNGRWE RIKDKPSYSI SNDVFFISFL HKVPEVGGDQ TRIYYAFTFP

241 FTYTELLEQL GTFDRKYGRH PFELNKMAYE ISQKYDKLPA AGMEETKNIS NLAPHRRKGK LAKMERVDRT SPESFDETAR

321 DGVGQQGVPL PSKETGPEAN KLQTAAPALG AGGGMIVDEN TSESMQQITN LVNKVKIELP TSSGAGALAG AEAKPTTAQS

401 SSSSACSTKL KLPSFHHQLS VASSSSTANP AQPEDDSKTD PRDEIYYCRE LLTHSIERRR IELLTISSFH KIQPAREVRL

481 RNLFPDEDAQ RCHTFKDKKI VFISSRVHPG ETPASFVLNG FLTMLLDRKS VVAQTLRRMY VFKIIPFLNP DGVYNGLYRS

561 DTRGHNLNRV YISPCHETQP AIYAARKLIR YYHLGVDEVE PYELEKEAPA PSLNVSVEGD QAGVAAPVEG SAPTLDVASG

641 SGNVALKKGT SSSTNPLAIA RRNSTHNAQV SQVNGVGATS STTATPITTT TTTTTTTTTN TTHSQKMKLP KLTAPSVDSA

721 KASNSSAVLA LSATTHPVKR LSSTMSLEGS TRKRRTPPLS S**TPSVP**TVPS ERRSVIAFVT PTAESAASLS NRPKATAPLA

801 TTWSDKIFAK ILRRRRAKAA TASSVDGATA AGGGKLSPIA QALPKPTLLL PAVEEEAAAA SPVSPATPTA NNRTTTASNA

881 SSPLTDESDS VEQDTPAASD SGFSEASSTS SSLTTTSKAV SVSSLPTQSS ADSSGCPPAE DTLPEVSSVP AVVQPPTLVA

961 AATTAAAQVF TEKLIPELNP IVSEGSAINV GPASVVRPGG RSGSSLSLKK SVHTVAARVD TGKGSTGSKG PHHKGGHALN

1041 KSHQFLGAPP GTLKFKEFLV HPHHHHHHHH HHHHHHHHLS GGAAAAAPSG GGGGGGVVQ GQVVATLHGG KMALGPFKKG

1121 AGSGKQHASS SSTSSLIGVS GTAGRTVAGG GSVLGEVGTT ASGGKTRPQT PQTNSAAQYS HYRSHRNEYL NPMTGPGGPG

1201 GGGGGVGSVG GPRSLNISVD FLAQLDERHD RAVYEDRSNL FMYIDLHGHA SKKGVFMYGN HLPNTVEAVE CMLLPRLMSL

1281 NSQHFHFDAC NFSERNMYYK GKRDGLSKEG SGRVAVYKTT GLIKSYTLEC NYNTGKCVNI LPPRGKEIVA KTTHTLVPPK

1361 YTPAVFEEVG KALGPSILDL TNSNPLSRLP NCEFRTLQGL RNALRIEIER GSSKARVTNK TQKSHTKRLA NQVSCTIDVA

1441 KENAIQWDPH HHHHHTLVG SPVGAGTGGQ SVGPTVVVPA SVVQGGTSLC KIVSDTENSP TLGTAGGNGN GNAGGTGGGT

1521 GSSSRQVLKT AGTTVVTLKT SSSTGGGKIC RKVGAFGKPK KSKVLCDVGG GGGGAGGGVV GGAMAGELML RSTKEQVPRK

1601 KIKVSPQQQC NAMQELCFKG GLGSGSLPNF LTVVPGTLSD LPGALVPGKK VKSESKLLDV NDIMQCDDSF DAAPCCSYTA

1681 VPLASGTIVT TAAGITKLIS TYTQASTTDL HTGTEELISL GCSGDVVASP VGPVASIEST GGSVGVAGGS IASASSGSSS

1761 GEGKSGKFGK STLKPSKQAK LAKSTKSGND TTGKKLLKKK RSLKTDSTSL KRKKTRVKPA LT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	762	766	
total 1 peptides												

tr|A0A1I8NNI7|A0A1I8NNI7_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNEKIKSPSG QGGAGSGPGP VGSGPQTTTA GNGGGGNGSA TSGGPAAPAA ATSGSGPPTP NNGNDTPAQM PPHPYGPPGG
81 GDPVMSHYHM HQQPPHPQHM PPHQQVGPPP SSSQNPGEHP QKDVGAEYGQ SPLGGPPPPI PGGHHPMYGR YHHGDPGMDP
161 YRYSHSPMQQ PPPGGKPQQS APGGGPGIGS PNRPPSQRYI PGQPQGPTPT LNSLLQSSHP PPPPQHRYTN SYDPQQPPQQ
241 QPPPPQSQPP PQGGAGGPQP PGGPAGQGGG GGPPPPQHGG PPPPSHQPHQ SPYGAQQTGW APPPRPYSPQ LGPSQQYRTP
321 PPTNTSRGQS PYPPSQGQNS GSYPSSPQQQ QPQPGQQQQQ QQPPQQQQPQ QQQQQQQSSS GSGGGSGGGP PPPPQSSNQG
401 TTPSQYSPYP QRYPTPPGPA TGPNHRTAYT THQYPEPNRP WPGGSSPAPS PGPGGHPLPP ASPHHTQHGG PPPSSSPSHA
481 PSPSPQPSQA SPSPHQVNQK KMDYITKSDK ELIGQNSNDS SSGGGHSGLG SGPPGTPNPQ QVMRPTPSPT GSSGSRSMSP
561 AVAQNHPISR PSSNQSSSGP MQQPSGGSGG GPPPPTQQAT QQQQQQQQQS QPVTGAANSS SSAGNSPQQG PPSSAAAGGP
641 QGGGQQPPPL PNQNSIGSQP PSQGPGGAQG YPLPPHMHGS YKMGGQSPGP QGMLSGYPPP PPQQAQQYSQ GSYPPRPQYP
721 PGGYGSTPPP TSQASSANSM PPGSGPQQYP GSRPMPNHSG QYPPYQNWVP PSPQQSGPVG PGPGGPGAPG APGMGNHIQG
801 KATPPPPQGS GSPRPLNYLK QHLQHKGGYP GGGPPGGPPQ GYGNGPGMHP GIPMGPPHHM GPPHGPTTMG PPPTTPPQSM
881 MPGVSVGEGG GPPPPPPEHI SQDNGLSSGS SGSASGPPHP VTSVVTTGPD GAPMDDASQQ STISNASAAS GEDPQCTTPK
961 SRKNDPYGQS HLAPPSTSPG GVGAGPHPGH PGEDYEINSP PNWARTPASP SFNSHVPQPE TFRTT**TPSVP** TVATTSAKKS
1041 DSLCKLYEMD DNPERRIWLD KLRAFMDERR TPITACPTIS KQPLDLYRLY LYVKERGGFV EVTKSKTWKD IAGLLGIGAS
1121 SSAAYTLRKH YTKNLLAYEC HFDRGDIDPL PIIQQIEAGT KKKSTKAASV PSPAGSSNSQ DSFPAPVGAA NTSMDGYPSY
1201 PGNYPGTGPQ PDYGAAGQMP RPPSQSNAQS PHPGPNNQTS AATPGGDNIS VNNPFDEPVG GVNSNAPNAG TTAHANSASS
1281 GAAGPPPPPP NVGPPPPQPP PTGRPPYPPG GPYPPPPVSR APGSPYPVQP GAYGQYGSGD QYNATGPPGQ FGQQQGQFPP
1361 QNRNMYPPYG PEGEAPPTGS NQYGPYGNRP YSQPPSGTSQ APSTPGAPSA PGGPPQPGGP PAPGSSPYPP PGAPGQQEYY
1441 RPPDQGPQPR RHPDFVKDSQ SYPGYNARPQ IYGWPGGANQ YRNQYPSSAS PQAWGVAPPR TQAPPGGQLG PSGQQQPPAS
1521 GAQWDQHRYP PQQQPPQPQQ QQQQPPYQQP GQQQPPPQWT QMGGAGTGAP GTPPSGAPGS PLRPPSAGQQ QRMPNSGPGG
1601 GMTGPNSAPV SGPQPGQPGA PPNSSSATGT MPTNSIGKPS FSMPPPPQAA GVSSGVQGIP PAQGGGMMPG TIGSGSQQKP
1681 MIGGVVGPPG APVMPPQPAT QQQQQPQQQQ QQQTPQQPQT QPSQQQQQQQ PPQQQQQQPQ PQPQQQPFAP PPVGPGPPLI
1761 KKEIVFPPDS VESTTPVLYR RKRLTKADVC PVDPWRIFMA MRSGQLTECT WALDVLNVLL FDDSTVQYFG LAHLPGLLTL
1841 LLEHFQKNLA EMFSDEGDEK ANQNDRISSD RKASNRRGIT TSTHNRRRLC DTVKPEKEEV EEEEKEDPQA RLHDHTVDGI
1921 EETYVEADIE GDFGIDSDED EGIDLGQVKQ IPHPEERVVL LAHTPNYTMM SRKGLPVRLQ PAEQDIFITD GLKEWDSEFS
2001 GNYEETAPIG SNAWTYGFTD RDINKGIIDV FKSEFVDIPF ARYIKTKPKD RKHKKGDNNV KIELEEDTSC EDLLNPKLES
2081 KESDREMEED EEVEARLQQN TFNKKRRLFN NSTASGNLVP QSEPTEAKKS KLQSDEHRPI EKSAFAIPLE IKRDDDCSEP
2161 LTTVTAAATT TTNTDSDCRE VDMELETITT KESSVTKAFD PKTTIRDPAL VLQRRRSSSS LEDECYTRDE ASLYLVNESQ
2241 DSLARRCICI SNIFRNMSFV PGNESILAKS QRFLAVLGRL LLLNHEHLPR TPKNRNYDRG TEEDTDFSDS CSSLQGEREW
2321 WWEYLISIRE NMLVIMANIA GHLDLSRYEE LIARPLIDGL LHWAVCPSAH GQDPFPSCGP ASSLSPQRLA LEALCKLCVT
2401 DNNVDLVIAT PPHSRLEKLC AVLTRHLCRN EDQVLREFSV NLLHYLAAAD SAMARTVALQ SPCISYLVAF IEQAEQTALG
2481 VANQHGINYL RENPDSMGTS LDMLRRAAGT LLHLAKHPDN RSLFMQQEQR LLGLVMSHIL DQQVALIISR VLFQVSRGPG
2561 AAVNSLEYRM QQKQLQQKLG MQERKNQVES KMDDEILNEK EQIVEPKDAT AAVATATTSD TAKCEARNEM APISTHANAV
2641 NEGTANSNNI EHMPSKNPSS SMIISADSEN SNSSSQITPT AAFNDVSNSS TNSNSCGTAA SSLSQNSTNS SMGSCSNMSS
2721 STTTAAMHHH LHINNNNNNN NSSSGGGSNS TLTTSEQLKS NMLGGAVSSS NTTPMATGST SGSGCSSINS NSMNNMTTNS
2801 SSSGSAAAQQ QLPISAPPPP PPATTAPPSQ APTANTSTTA AVA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	1026	1030	
total 1 peptides												

tr|A0A1I8NNI6|A0A1I8NNI6_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MNEKIKSPSG QGGAGSGPGP VGSGPQTTTA GNGGGGNGSA TSGGPAAPAA ATSGSGPPTP NNGNDTPAQM PPHPYGPPGG
  81 GDPVMSHYHM HQQPPHPQHM PPHQQVGPPP SSSQNPGEHP QKDVGAEYGQ SPLGGPPPPI PGGHHPMYGR YHHGDPGMDP
 161 YRYSHSPMQQ PPPGGKPQQS APGGGPGIGS PNRPPSQRYI PGQPQGPTPT LNSLLQSSHP PPPPQHRYTN SYDPQQPPQQ
 241 QPPPPQSQPP PQGGAGGPQP PGGPAGQGGG GGPPPPQHGG PPPPSHQPHQ SPYGAQQTGW APPPRPYSPQ LGPSQQYRTP
 321 PPTNTSRGQS PYPPSQGQNS GSYPSSPQQQ QPQPGQQQQQ QQPPQQQQPQ QQQQQQQSSS GSGGGSGGGP PPPPQSSNQG
 401 TTPSQYSPYP QRYPTPPGPA TGPNHRTAYT THQYPEPNRP WPGGSSPAPS PGPGGHPLPP ASPHHTQHGG PPPSSSPSHA
 481 PSPSPQPSQA SPSPHQELIG QNSNDSSSGG GHSGLGSGPP GTPNPQQVMR PTPSPTGSSG SRSMSPAVAQ NHPISRPSSN
 561 QSSSGPMQQP SGGSGGGPPP PTQQATQQQQ QQQQQSQPVT GAANSSSSAG NSPQQGPPSS AAAGGPQGGG QQPPPLPNQN
 641 SIGSQPPSQG PGGAQGYPLP PHMHGSYKMG GQSPGPQGML SGYPPPPPQQ AQQYSQGSYP PRPQYPPGGY GSTPPPTSQA
 721 SSANSMPPGS GPQQYPGSRP MPNHSGQYPP YQNWVPPSPQ QSGPVGPGPG GPGAPGAPGM GNHIQGKATP PPPQGSGSPR
 801 PLNYLKQHLQ HKGGYPGGGP PGGPPQGYGN GPGMHPGIPM GPPHHMGPPH GPTTMGPPPT TPPQSMMPGV SVGEGGGPPP
 881 PPPEHISQDN GLSSGSSGSA SGPPHPVTSV VTTGPDGAPM DDASQQSTIS NASAASGEDP QCTTPKSRKN DPYGQSHLAP
 961 PSTSPGGVGA GPHPGHPGED YEINSPPNWA RTPASPSFNS HVPQPETFRT TTPSVPTVAT TSAKKSDSLC KLYEMDDNPE

1041 RRIWLDKLRA FMDERRTPIT ACPTISKQPL DLYRLYLYVK ERGGFVEVCK VTKSKTWKDI AGLLGIGASS SAAYTLRKHY
1121 TKNLLAYECH FDRGDIDPLP IIQQIEAGTK KKSTKAASVP SPGNKSGSSN SQDSFPAPVG AANTSMDGYP SYPGNYPGTG
1201 PQPDYGAAGQ MPRPPSQSNA QSPHPGPNNQ TSAATPGGDN ISVNNPFDEP VGGVNSNAPN AGTTAHANSA SSGAAGPPPP
1281 PPNVGPPPPQ PPPTGRPPYP PGGPYPPPPV SRAPGSPYPV QPGAYGQYGS GDQYNATGPP GQFGQQQGQF PPQNRNMYPP
1361 YGPEGEAPPT GSNQYGPYGN RPYSQPPSGT SQAPSTPGAP SAPGGPPQPG GPPAPGSSPY PPPGAPGQQE YYRPPDQGPQ
1441 PRRHPDFVKD SQSYPGYNAR PQIYGWPGGA NQYRNQYPSS ASPQAWGVAP PRTQAPPGGQ LGPSGQQQPP ASGAQWDQHR
1521 YPPQQQPPQP QQQQQQPPYQ QPGQQQPPPQ WTQMGGAGTG APGTPPSGAP GSPLRPPSAG QQQRMPNSGP GGGMTGPNSA
1601 PVSGPQPGQP GAPPNSSSAT GTMPTNSIGK PSFSMPPPPQ AAGVSSGVQG IPPAQGGGMM PGTIGSGSQQ KPMIGGVVGP
1681 PGAPVMPPQP ATQQQQPQQ QQQQQTPQQP QTQPSQQQQQ QQPPQQQQQQ PQPQPQQQPF APPPVGPGPP LIKKEIVFPP
1761 DSVESTTPVL YRRKRLTKAD VCPVDPWRIF MAMRSGQLTE CTWALDVLNV LLFDDSTVQY FGLAHLPGLL TLLLEHFQKN
1841 LAEMFSDEGD EKANQNDRIS SDRKASNRRG ITTSTHNRRR LCDTVKPEKE EVEEEEKEDP QARLHDHTVD GIEETYVEAD
1921 IEGDFGIDSD EDEGIDLGQV KQIPHPEERV VLLAHTPNYT MMSRKGLPVR LQPAEQDIFI TDGLKEWDSE FSGNYEETAP
2001 IGSNAWTYGF TDRDINKGII DVFKSEFVDI PFARYIKTKP KDRKHKKGDN NVKIELEEDT SCEDLLNPKL ESKESDREME
2081 EDEEVEARLQ QNTFNKKRRL FNNSTASGNL VPQSEPTEAK KSKLQSDEHR PIEKSAFAIP LEIKRDDDCS EPLTTVTAAA
2161 TTTTNTDSDC REVDMELETI TTKESSVTKA FDPKTTIRDP ALVLQRRRSS SSLEDECYTR DEASLYLVNE SQDSLARRCI
2241 CISNIFRNMS FVPGNESILA KSQRFLAVLG RLLLLNHEHL PRTPKNRNYD RGTEEDTDFS DSCSSLQGER EWWWEYLISI
2321 RENMLVIMAN IAGHLDLSRY EELIARPLID GLLHWAVCPS AHGQDPFPSC GPASSLSPQR LALEALCKLC VTDNNVDLVI
2401 ATPPHSRLEK LCAVLTRHLC RNEDQVLREF SVNLLHYLAA ADSAMARTVA LQSPCISYLV AFIEQAEQTA LGVANQHGIN
2481 YLRENPDSMG TSLDMLRRAA GTLLHLAKHP DNRSLFMQQE QRLLGLVMSH ILDQQVALII SRVLFQVSRG PGAAVNSLEY
2561 RMQQKQLQQK LGMQERKNQV ESKMDDEILN EKEQIVEPKD ATAAVATATT SDTAKCEARN EMAPISTHAN AVNEGTANSN
2641 NIEHMPSKNP SSSMIISADS ENSNSSSQIT PTAAFNDVSN SSTNSNSCGT AASSLSQNST NSSMGSCSNM SSSTTTAAMH
2721 HHLHINNNNN NNNSSSGGGS NSTLTTSEQL KSNMLGGAVS SSNTTPMATG STSGSGCSSI NSNSMNNMTT NSSSSGSAAA
2801 QQQLPISAPP PPPPATTAPP SQAPTANTST TAAVA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	1012	1016	
total 1 peptides												

tr|A0A1I8NNI4|A0A1I8NNI4_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MNEKIKSPSG QGGAGSGPGP VGSGPQTTTA GNGGGGNGSA TSGGPAAPAA ATSGSGPPTP NNGNDTPAQM PPHPYGPPGG
  81 GDPVMSHYHM HQQPPHPQHM PPHQQVGPPP SSSQNPGEHP QKDVGAEYGQ SPLGGPPPPI PGGHHPMYGR YHHGDPGMDP
 161 YRYSHSPMQQ PPPGGKPQQS APGGGPGIGS PNRPPSQRYI PGQPQGPTPT LNSLLQSSHP PPPPQHRYTN SYDPQQPPQQ
 241 QPPPPQSQPP PQGGAGGPQP PGGPAGQGGG GGPPPPQHGG PPPPSHQPHQ SPYGAQQTGW APPPRPYSPQ LGPSQQYRTP
 321 PPTNTSRGQS PYPPSQGQNS GSYPSSPQQQ QPQPGQQQQQ QQPPQQQQPQ QQQQQQQSSS GSGGGSGGGP PPPPQSSNQG
 401 TTPSQYSPYP QRYPTPPGPA TGPNHRTAYT THQYPEPNRP WPGGSSPAPS PGPGGHPLPP ASPHHTQHGG PPPSSSPSHA
 481 PSPSPQPSQA SPSPHQELIG QNSNDSSSGG GHSGLGSGPP GTPNPQQVMR PTPSPTGSSG SRSMSPAVAQ NHPISRPSSN
 561 QSSSGPMQQP SGGSGGGPPP PTQQATQQQQ QQQQQSQPVT GAANSSSSAG NSPQQGPPSS AAAGGPQGGG QQPPPLPNQN
 641 SIGSQPPSQG PGGAQGYPLP PHMHGSYKMG GQSPGPQGML SGYPPPPPQQ AQQYSQGSYP PRPQYPPGGY GSTPPPTSQA
 721 SSANSMPPGS GPQQYPGSRP MPNHSGQYPP YQNWVPPSPQ QSGPVGPGPG GPGAPGAPGM GNHIQGKATP PPPQGSGSPR
 801 PLNYLKQHLQ HKGGYPGGGP PGGPPQGYGN GPGMHPGIPM GPPHHMGPPH GPTTMGPPPT TPPQSMMPGV SVGEGGGPPP
 881 PPPEHISQDN GLSSGSSGSA SGPPHPVTSV VTTGPDGAPM DDASQQSTIS NASAASGEDP QCTTPKSRKN DPYGQSHLAP
 961 PSTSPGGVGA GPHPGHPGED YEINSPPNWA RTPASPSFNS HVPQPETFRT TTPSVPTVAT TSAKKSDSLC KLYEMDDNPE

1041 RRIWLDKLRA FMDERRTPIT ACPTISKQPL DLYRLYLYVK ERGGFVEVTK SKTWKDIAGL LGIGASSSAA YTLRKHYTKN
1121 LLAYECHFDR GDIDPLPIIQ QIEAGTKKKS TKAASVPSPG NKSGSSNSQD SFPAPVGAAN TSMDGYPSYP GNYPGTGPQP
1201 DYGAAGQMPR PPSQSNAQSP HPGPNNQTSA ATPGGDNISV NNPFDEPVGG VNSNAPNAGT TAHANSASSG AAGPPPPPPN
1281 VGPPPPQPPP TGRPPYPPGG PYPPPPVSRA PGSPYPVQPG AYGQYGSGDQ YNATGPPGQF GQQQGQFPPQ NRNMYPPYGP
1361 EGEAPPTGSN QYGPYGNRPY SQPPSGTSQA PSTPGAPSAP GGPPQPGGPP APGSSPYPPP GAPGQQEYYR PPDQGPQPRR
1441 HPDFVKDSQS YPGYNARPQI YGWPGGANQY RNQYPSSASP QAWGVAPPRT QAPPGGQLGP SGQQQPPASG AQWDQHRYPP
1521 QQQPPQPQQQ QQQPPYQQPG QQQPPPQWTQ MGGAGTGAPG TPPSGAPGSP LRPPSAGQQQ RMPNSGPGGG MTGPNSAPVS
1601 GPQPGQPGAP PNSSSATGTM PTNSIGKPSF SMPPPPQAAG VSSGVQGIPP AQGGGMMPGT IGSGSQQKPM IGGVVGPPGA
1681 PVMPPQPATQ QQQQPQQQQQ QQTPQQPQTQ PSQQQQQQQP PQQQQQQPQP QPQQQPFAPP PVGPGPPLIK KEIVFPPDSV
1761 ESTTPVLYRR KRLTKADVCP VDPWRIFMAM RSGQLTECTW ALDVLNVLLF DDSTVQYFGL AHLPGLLTLL LEHFQKNLAE
1841 MFSDEGDEKA NQNDRISSDR KASNRRGITT STHNRRRLCD TVKPEKEEVE EEEKEDPQAR LHDHTVDGIE ETYVEADIEG
1921 DFGIDSDEDE GIDLGQVKQI PHPEERVVLL AHTPNYTMMS RKGLPVRLQP AEQDIFITDG LKEWDSEFSG NYEETAPIGS
2001 NAWTYGFTDR DINKGIIDVF KSEFVDIPFA RYIKTKPKDR KHKKGDNNVK IELEEDTSCE DLLNPKLESK ESDREMEEDE
2081 EVEARLQQNT FNKKRRLFNN STASGNLVPQ SEPTEAKKSK LQSDEHRPIE KSAFAIPLEI KRDDDCSEPL TTVTAAATTT
2161 TNTDSDCREV DMELETITTK ESSVTKAFDP KTTIRDPALV LQRRRSSSSL EDECYTRDEA SLYLVNESQD SLARRCICIS
2241 NIFRNMSFVP GNESILAKSQ RFLAVLGRLL LLNHEHLPRT PKNRNYDRGT EEDTDFSDSC SSLQGEREWW WEYLISIREN
2321 MLVIMANIAG HLDLSRYEEL IARPLIDGLL HWAVCPSAHG QDPFPSCGPA SSLSPQRLAL EALCKLCVTD NNVDLVIATP
2401 PHSRLEKLCA VLTRHLCRNE DQVLREFSVN LLHYLAAADS AMARTVALQS PCISYLVAFI EQAEQTALGV ANQHGINYLR
2481 ENPDSMGTSL DMLRRAAGTL LHLAKHPDNR SLFMQQEQRL LGLVMSHILD QQVALIISRV LFQVSRGPGA AVNSLEYRMQ
2561 QKQLQQKLGM QERKNQVESK MDDEILNEKE QIVEPKDATA AVATATTSDT AKCEARNEMA PISTHANAVN EGTANSNNIE
2641 HMPSKNPSSS MIISADSENS NSSSQITPTA AFNDVSNSST NSNSCGTAAS SLSQNSTNSS MGSCSNMSSS TTTAAMHHHL
2721 HINNNNNNNN SSSGGGSNST LTTSEQLKSN MLGGAVSSSN TTPMATGSTS GSGCSSINSN SMNNMTTNSS SSGSAAAQQQ
2801 LPISAPPPPP PATTAPPSQA PTANTSTTAA VA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	1012	1016	
total 1 peptides												

tr|A0A1I8NNI3|A0A1I8NNI3_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MNKVLPWEHF ENLYKELIGQ NSNDSSSGGG HSGLGSGPPG TPNPQQVMRP TPSPTGSSGS RSMSPAVAQN HPISRPSSNQ
  81 SSSGPMQQPS GGSGGGPPPP TQQATQQQQQ QQQQSQPVTG AANSSSSAGN SPQQGPPSSA AAGGPQGGGQ QPPPLPNQNS
 161 IGSQPPSQGP GGAQGYPLPP HMHGSYKMGG QSPGPQGMLS GYPPPPPQQA QQYSQGSYPP RPQYPPGGYG STPPPTSQAS
 241 SANSMPPGSG PQQYPGSRPM PNHSGQYPPY QNWVPPSPQQ SGPVGPGPGG PGAPGAPGMG NHIQGKATPP PPQGSGSPRP
 321 LNYLKQHLQH KGGYPGGGPP GGPPQGYGNG PGMHPGIPMG PPHHMGPPHG PTTMGPPPTT PPQSMMPGVS VGEGGGPPPP
 401 PPEHISQDNG LSSGSSGSAS GPPHPVTSVV TTGPDGAPMD DASQQSTISN ASAASGEDPQ CTTPKSRKND PYGQSHLAPP
 481 STSPGGVGAG PHPGHPGEDY EINSPPNWAR TPASPSFNSH VPQPETFRTT TPSVPTVATT SAKKSDSLCK LYEMDDNPER

 561 RIWLDKLRAF MDERRTPITA CPTISKQPLD LYRLYLYVKE RGGFVEVCKV TKSKTWKDIA GLLGIGASSS AAYTLRKHYT
 641 KNLLAYECHF DRGDIDPLPI IQQIEAGTKK KSTKAASVPS PGNKSGSSNS QDSFPAPVGA ANTSMDGYPS YPGNYPGTGP
 721 QPDYGAAGQM PRPPSQSNAQ SPHPGPNNQT SAATPGGDNI SVNNPFDEPV GGVNSNAPNA GTTAHANSAS SGAAGPPPPP
 801 PNVGPPPPQP PPTGRPPYPP GGPYPPPPVS RAPGSPYPVQ PGAYGQYGSG DQYNATGPPG QFGQQQGQFP PQNRNMYPPY
 881 GPEGEAPPTG SNQYGPYGNR PYSQPPSGTS QAPSTPGAPS APGGPPQPGG PPAPGSSPYP PPGAPGQQEY YRPPDQGPQP
 961 RRHPDFVKDS QSYPGYNARP QIYGWPGGAN QYRNQYPSSA SPQAWGVAPP RTQAPPGGQL GPSGQQQPPA SGAQWDQHRY
1041 PPQQQPPQPQ QQQQQPPYQQ PGQQQPPPQW TQMGGAGTGA PGTPPSGAPG SPLRPPSAGQ QQRMPNSGPG GGMTGPNSAP
1121 VSGPQPGQPG APPNSSSATG TMPTNSIGKP SFSMPPPPQA AGVSSGVQGI PPAQGGGMMP GTIGSGSQQK PMIGGVVGPP
1201 GAPVMPPQPA TQQQQQPQQQ QQQQTPQQPQ TQPSQQQQQQ QPPQQQQQQP QPQPQQQPFA PPPVGPGPPL IKKEIVFPPD
1281 SVESTTPVLY RRKRLTKADV CPVDPWRIFM AMRSGQLTEC TWALDVLNVL LFDDSTVQYF GLAHLPGLLT LLLEHFQKNL
1361 AEMFSDEGDE KANQNDRISS DRKASNRRGI TTSTHNRRRL CDTVKPEKEE VEEEEKEDPQ ARLHDHTVDG IEETYVEADI
1441 EGDFGIDSDE DEGIDLGQVK QIPHPEERVV LLAHTPNYTM MSRKGLPVRL QPAEQDIFIT DGLKEWDSEF SGNYEETAPI
1521 GSNAWTYGFT DRDINKGIID VFKSEFVDIP FARYIKTKPK DRKHKKGDNN VKIELEEDTS CEDLLNPKLE SKESDREMEE
1601 DEEVEARLQQ NTFNKKRRLF NNSTASGNLV PQSEPTEAKK SKLQSDEHRP IEKSAFAIPL EIKRDDDCSE PLTTVTAAAT
1681 TTTNTDSDCR EVDMELETIT TKESSVTKAF DPKTTIRDPA LVLQRRRSSS SLEDECYTRD EASLYLVNES QDSLARRCIC
1761 ISNIFRNMSF VPGNESILAK SQRFLAVLGR LLLLNHEHLP RTPKNRNYDR GTEEDTDFSD SCSSLQGERE WWWEYLISIR
1841 ENMLVIMANI AGHLDLSRYE ELIARPLIDG LLHWAVCPSA HGQDPFPSCG PASSLSPQRL ALEALCKLCV TDNNVDLVIA
1921 TPPHSRLEKL CAVLTRHLCR NEDQVLREFS VNLLHYLAAA DSAMARTVAL QSPCISYLVA FIEQAEQTAL GVANQHGINY
2001 LRENPDSMGT SLDMLRRAAG TLLHLAKHPD NRSLFMQQEQ RLLGLVMSHI LDQQVALIIS RVLFQVSRGP GAAVNSLEYR
2081 MQQKQLQQKL GMQERKNQVE SKMDDEILNE KEQIVEPKDA TAAVATATTS DTAKCEARNE MAPISTHANA VNEGTANSNN
2161 IEHMPSKNPS SSMIISADSE NSNSSSQITP TAAFNDVSNS STNSNSCGTA ASSLSQNSTN SSMGSCSNMS SSTTTAAMHH
2241 HLHINNNNNN NNSSSGGGSN STLTTSEQLK SNMLGGAVSS SNTTPMATGS TSGSGCSSIN SNSMNNMTTN SSSSGSAAAQ
2321 QQLPISAPPP PPPATTAPPS QAPTANTSTT AAVA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	531	535	
total 1 peptides												

tr|A0A1I8NNI2|A0A1I8NNI2_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MRPTPSPTGS SGSRSMSPAV AQNHPISRPS SNQSSSGPMQ QPSGGSGGGP PPPTQQATQQ QQQQQQQSQP VTGAANSSSS
  81 AGNSPQQGPP SSAAAGGPQG GGQQPPPLPN QNSIGSQPPS QGPGGAQGYP LPPHMHGSYK MGGQSPGPQG MLSGYPPPPP
 161 QQAQQYSQGS YPPRPQYPPG GYGSTPPPTS QASSANSMPP GSGPQQYPGS RPMPNHSGQY PPYQNWVPPS PQQSGPVGPG
 241 PGGPGAPGAP GMGNHIQGKA TPPPPQGSGS PRPLNYLKQH LQHKGGYPGG GPPGGPPQGY GNGPGMHPGI PMGPPHHMGP
 321 PHGPTTMGPP PTTPPQSMMP GVSVGEGGGP PPPPPEHISQ DNGLSSGSSG SASGPPHPVT SVVTTGPDGA PMDDASQQST
 401 ISNASAASGE DPQCTTPKSR KNDPYGQSHL APPSTSPGGV GAGPHPGHPG EDYEINSPPN WARTPASPSF NSHVPQPETF
 481 RTTTPSVPTV ATTSAKKSDS LCKLYEMDDN PERRIWLDKL RAFMDERRTP ITACPTISKQ PLDLYRLYLY VKERGGFVEV

 561 CKVTKSKTWK DIAGLLGIGA SSSAAYTLRK HYTKNLLAYE CHFDRGDIDP LPIIQQIEAG TKKKSTKAAS VPSPGNKSGS
 641 SNSQDSFPAP VGAANTSMDG YPSYPGNYPG TGPQPDYGAA GQMPRPPSQS NAQSPHPGPN NQTSAATPGG DNISVNNPFD
 721 EPVGGVNSNA PNAGTTAHAN SASSGAAGPP PPPPNVGPPP PQPPPTGRPP YPPGGPYPPP PVSRAPGSPY PVQPGAYGQY
 801 GSGDQYNATG PPGQFGQQQG QFPPQNRNMY PPYGPEGEAP PTGSNQYGPY GNRPYSQPPS GTSQAPSTPG APSAPGGPPQ
 881 PGGPPAPGSS PYPPPGAPGQ QEYYRPPDQG PQPRRHPDFV KDSQSYPGYN ARPQIYGWPG GANQYRNQYP SSASPQAWGV
 961 APPRTQAPPG GQLGPSGQQQ PPASGAQWDQ HRYPPQQQPP QPQQQQQQPP YQQPGQQQPP PQWTQMGGAG TGAPGTPPSG
1041 APGSPLRPPS AGQQQRMPNS GPGGGMTGPN SAPVSGPQPG QPGAPPNSSS ATGTMPTNSI GKPSFSMPPP PQAAGVSSGV
1121 QGIPPAQGGG MMPGTIGSGS QQKPMIGGVV GPPGAPVMPP QPATQQQQQP QQQQQQQTPQ QPQTQPSQQQ QQQQPPQQQQ
1201 QQPQPQPQQQ PFAPPPVGPG PPLIKKEIVF PPDSVESTTP VLYRRKRLTK ADVCPVDPWR IFMAMRSGQL TECTWALDVL
1281 NVLLFDDSTV QYFGLAHLPG LLTLLLEHFQ KNLAEMFSDE GDEKANQNDR ISSDRKASNR RGITTSTHNR RRLCDTVKPE
1361 KEEVEEEEKE DPQARLHDHT VDGIEETYVE ADIEGDFGID SDEDEGIDLG QVKQIPHPEE RVVLLAHTPN YTMMSRKGLP
1441 VRLQPAEQDI FITDGLKEWD SEFSGNYEET APIGSNAWTY GFTDRDINKG IIDVFKSEFV DIPFARYIKT KPKDRKHKKG
1521 DNNVKIELEE DTSCEDLLNP KLESKESDRE MEEDEEVEAR LQQNTFNKKR RLFNNSTASG NLVPQSEPTE AKKSKLQSDE
1601 HRPIEKSAFA IPLEIKRDDD CSEPLTTVTA AATTTTNTDS DCREVDMELE TITTKESSVT KAFDPKTTIR DPALVLQRRR
1681 SSSSLEDECY TRDEASLYLV NESQDSLARR CICISNIFRN MSFVPGNESI LAKSQRFLAV LGRLLLLNHE HLPRTPKNRN
1761 YDRGTEEDTD FSDSCSSLQG EREWWWEYLI SIRENMLVIM ANIAGHLDLS RYEELIARPL IDGLLHWAVC PSAHGQDPFP
1841 SCGPASSLSP QRLALEALCK LCVTDNNVDL VIATPPHSRL EKLCAVLTRH LCRNEDQVLR EFSVNLLHYL AAADSAMART
1921 VALQSPCISY LVAFIEQAEQ TALGVANQHG INYLRENPDS MGTSLDMLRR AAGTLLHLAK HPDNRSLFMQ QEQRLLGLVM
2001 SHILDQQVAL IISRVLFQVS RGPGAAVNSL EYRMQQKQLQ QKLGMQERKN QVESKMDDEI LNEKEQIVEP KDATAAVATA
2081 TTSDTAKCEA RNEMAPISTH ANAVNEGTAN SNNIEHMPSK NPSSSMIISA DSENSNSSSQ ITPTAAFNDV SNSSTNSNSC
2161 GTAASSLSQN STNSSMGSCS NMSSSTTTAA MHHHLHINNN NNNNNSSSGG GSNSTLTTSE QLKSNMLGGA VSSSNTTPMA
2241 TGSTSGSGCS SINSNSMNNM TTNSSSSGSA AAQQQLPISA PPPPPPATTA PPSQAPTANT STTAAVA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.TPSVP.T	Y	20.04	499.2642	-27.2	500.2579	1	0.26	379	1	484	488	
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)