Summary

1. Notes

2. Result Statistics

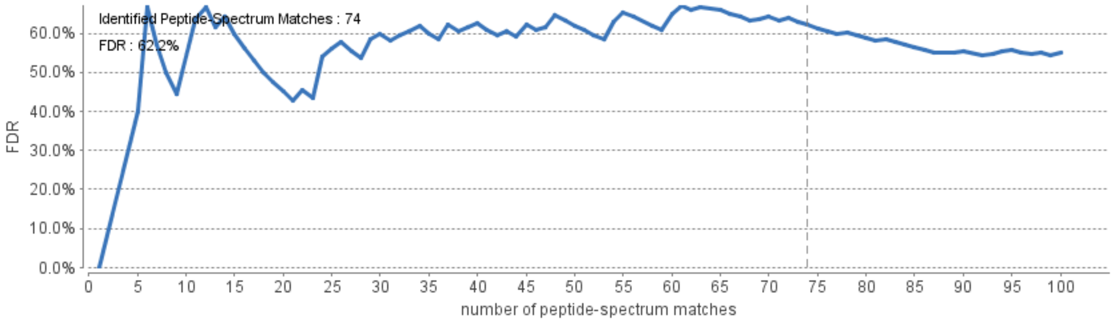

Figure 1. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corresponding FDR.

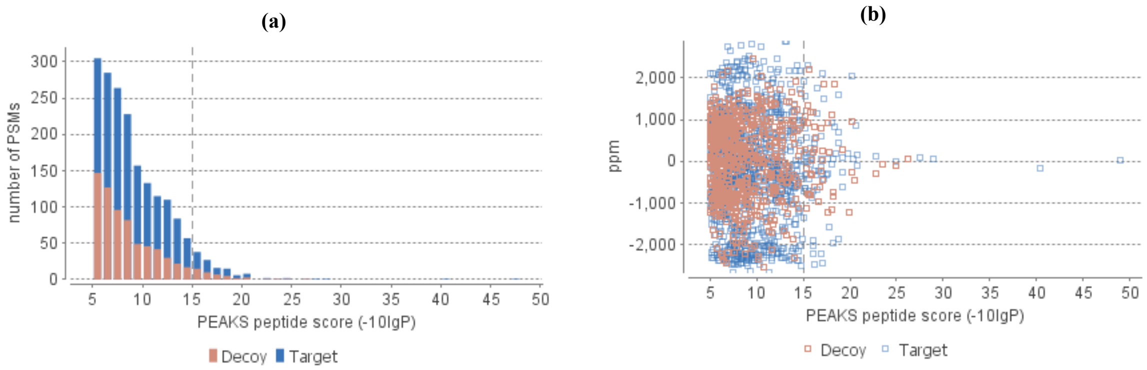

Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

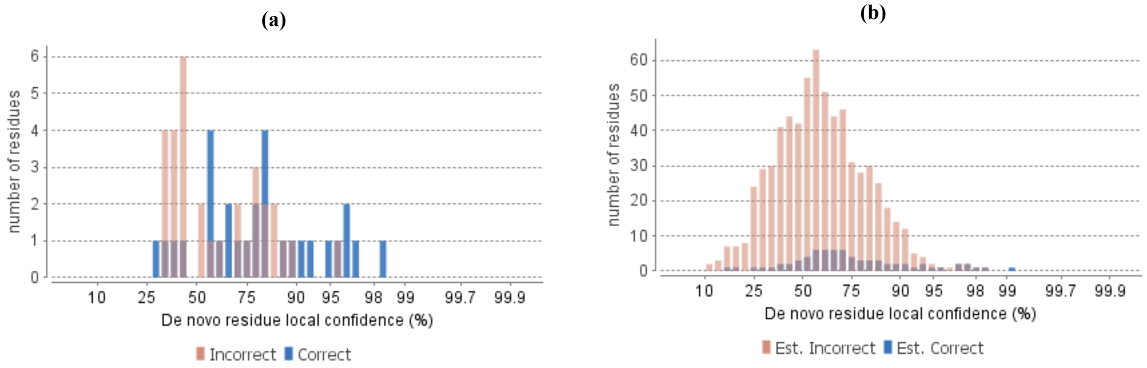

Figure 3. De novo result validation. Distribution of residue local confidence: **(a)** Residues in de novo sequences validated by confident database peptide assignment; **(b)** Residues in "de novo only" sequences.

Table 1. Statistics of data.

# of MS Scans	1552
# of MS/MS Scans	4087

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	74
Peptide Sequences	67

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	5	C
Oxidation	15.99	2	M

Protein Groups	17
Proteins	32
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 19 (=1);
FDR (Peptide-Spectrum Matches)	62.2%
FDR (Peptide Sequences)	68.7%
FDR (Protein)	46.9%
De Novo Only Spectra	78

3. Experiment Control

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

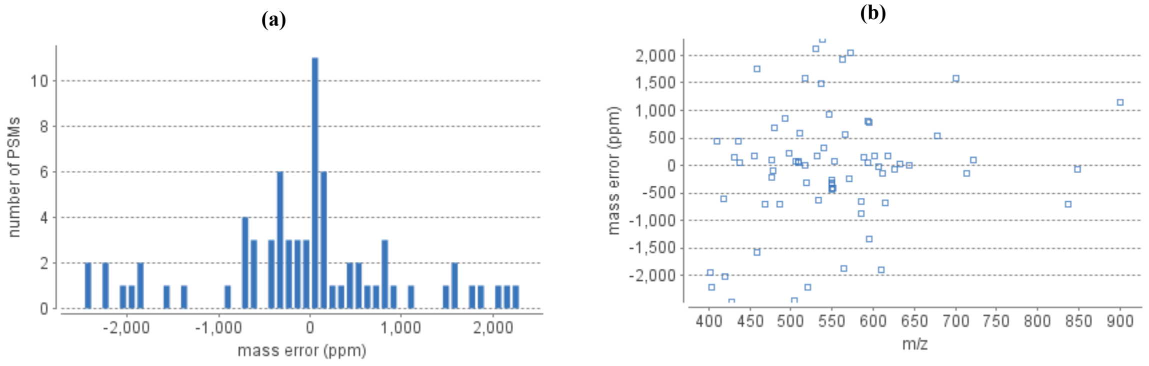

Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
LTQ	47	13	5	2	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: 0.5
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 104
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: IT_douglas_4_20170921_04.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: Linear Ion Trap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
10	109997	tr|L7M2G6|L7M2G6_9ACAR	48.98	4	1	1	N	36559	Putative pseudouridine synthase OS=Rhipicephalus pulchellus PE=2 SV=1
12	110537	tr|A0A0L7LF47|A0A0L7LF47_9NEOP	40.41	1	1	1	N	106594	Putative ribosomal RNA methyltransferase NOP2 OS=Operophtera brumata GN=OBRU01_09760 PE=3 SV=1
3	111172	tr|A0A0J7L789|A0A0J7L789_LASNI	28.97	0	1	0	N	147499	La-related protein OS=Lasius niger GN=RF55_1235 PE=4 SV=1
3	111685	tr|A0A069DZQ6|A0A069DZQ6_9HEMI	28.97	0	1	0	N	125251	Putative rna-binding protein (Fragment) OS=Panstrongylus megistus PE=2 SV=1
3	114665	tr|A0A067R4G0|A0A067R4G0_ZOONE	28.97	0	1	0	N	162159	Down syndrome cell adhesion molecule-like protein CG42256 (Fragment) OS=Zootermopsis nevadensis GN=L798_07641 PE=4 SV=1
3	114801	tr|B4QNL9|B4QNL9_DROSI	28.97	0	1	0	N	187523	GD13707 OS=Drosophila simulans GN=Dsim\GD13707 PE=4 SV=1
3	115224	tr|A0A1W4VP26|A0A1W4VP26_DROFC	28.97	0	1	0	N	215687	autophagy-related protein 2 homolog A OS=Drosophila ficusphila GN=LOC108099165 PE=4 SV=1
3	115212	tr|A0A0J9RP88|A0A0J9RP88_DROSI	28.97	0	1	0	N	215010	Uncharacterized protein, isoform A OS=Drosophila simulans GN=Dsim\GD13707 PE=4 SV=1
3	115200	tr|Q2XXT5|Q2XXT5_DROSI	28.97	0	1	0	N	210932	CG1241 (Fragment) OS=Drosophila simulans GN=GD13707 PE=4 SV=1
total 32 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	115201	tr|Q2XXT4|Q2XXT4_DROSI	28.97	0	1	0	N	210764	CG1241 (Fragment) OS=Drosophila simulans GN=GD13707 PE=4 SV=1
3	114958	tr|A0A182VIR2|A0A182VIR2_ANOME	28.97	0	1	0	N	195336	Uncharacterized protein OS=Anopheles merus PE=4 SV=1
32	115008	tr|A0A0P5PN82|A0A0P5PN82_9CRUS	27.72	0	2	1	N	216261	FERM and PDZ domain-containing protein OS=Daphnia magna PE=4 SV=1
16	113461	tr|A0A1D2MK27|A0A1D2MK27_ORCCI	27.57	1	1	1	Y	91660	Alanine aminotransferase 2 OS=Orchesella cincta GN=Ocin01_13348 PE=4 SV=1
33	110166	tr|A0A1A9TCY8|A0A1A9TCY8_ANOST	26.29	0	2	0	N	212333	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
64	110640	tr|A0A0P4ZIA8|A0A0P4ZIA8_9CRUS	26.26	0	2	1	N	429011	Protein SZT2 OS=Daphnia magna PE=4 SV=1
284	114961	tr|A0A0J9R316|A0A0J9R316_DROSI	25.56	0	2	0	N	224359	Voltage-dependent L-type calcium channel subunit alpha OS=Drosophila simulans GN=Dsim\GD24041 PE=3 SV=1
14	113138	tr|A0A0A9Z5R4|A0A0A9Z5R4_LYGHE	24.90	2	1	1	N	34477	Metaxin-1 OS=Lygus hesperus GN=Mtx1 PE=4 SV=1
40	110107	tr|B4P0S9|B4P0S9_DROYA	24.07	1	2	0	N	76211	Uncharacterized protein (Fragment) OS=Drosophila yakuba GN=Dyak\GE13439 PE=4 SV=2
135	110890	tr|A0A0N8CGV4|A0A0N8CGV4_9CRUS	23.78	0	2	0	N	376553	Transformation/transcription domain-associated protein OS=Daphnia magna PE=3 SV=1
11	110378	tr|D6N9W7|D6N9W7_BOMMO	22.74	1	1	1	N	142101	Regulatory-associated protein of TOR OS=Bombyx mori PE=2 SV=1
5	111006	tr|A0A224XHB0|A0A224XHB0_9HEMI	20.81	0	1	1	N	429567	Putative dyneins heavy chain (Fragment) OS=Panstrongylus lignarius PE=4 SV=1
5	115331	tr|T1HU69|T1HU69_RHOPR	20.81	0	1	1	N	261011	Uncharacterized protein (Fragment) OS=Rhodnius prolixus PE=4 SV=1
15	113337	tr|A0A224XPX1|A0A224XPX1_9HEMI	20.79	2	1	1	N	45853	Putative catalytic domain of phosphatidylinositol-specific phospholipase c x domain protein (Fragment) OS=Panstrongylus lignarius PE=4 SV=1
2	110031	tr|W5J800|W5J800_ANODA	20.57	1	1	1	N	109703	Uncharacterized protein OS=Anopheles darlingi GN=AND_008288 PE=4 SV=1
4	110043	tr|B4QZJ2|B4QZJ2_DROSI	20.31	1	1	1	N	92885	Aminopeptidase OS=Drosophila simulans GN=Dsim\GD17884 PE=3 SV=1
4	110237	tr|A0A0K2SZ75|A0A0K2SZ75_LEPSM	20.31	1	1	1	N	87088	Uncharacterized protein OS=Lepeophtheirus salmonis PE=4 SV=1
4	110274	tr|Q9VAM2|Q9VAM2_DROME	20.31	1	1	1	N	93563	Aminopeptidase OS=Drosophila melanogaster GN=Dmel\CG11951 PE=3 SV=1
4	110608	tr|A0A1S3D1G5|A0A1S3D1G5_DIACI	20.31	2	1	1	N	46888	dnaJ homolog subfamily C member 13-like OS=Diaphorina citri GN=LOC103508576 PE=4 SV=1
4	110617	tr|A0A182RGI7|A0A182RGI7_ANOFN	20.31	1	1	1	N	66258	O-acyltransferase OS=Anopheles funestus PE=3 SV=1
4	110650	tr|B4QZJ4|B4QZJ4_DROSI	20.31	1	1	1	N	107096	Aminopeptidase OS=Drosophila simulans GN=Dsim\GD17862 PE=3 SV=1
4	110651	tr|B4HZ86|B4HZ86_DROSE	20.31	1	1	1	N	107383	Aminopeptidase OS=Drosophila sechellia GN=Dsec\GM12249 PE=3 SV=1
9	113521	tr|A0A1I8MW53|A0A1I8MW53_MUSDO	20.19	0	1	1	Y	153143	Uncharacterized protein OS=Musca domestica GN=101891633 PE=4 SV=1
total 32 proteins									

tr|L7M2G6|L7M2G6_9ACAR

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

Protein Coverage:

```
  1  MANASLQTVA HASEAFQLLR GIFCVYKPAN ISCAAVRRTV IGNLCRDLNE MEVRPPADFV TIEGSVSSGV DLTVKSSPSF
 81  ADHPLVVGPR YQPEDFKMAH GVNLGKYTSG VLLMRVNGGY HKMKRLCDSN QLRTYELRGE FGKASDTHTP LSRIVEKATY
161  RHITAARLER LLGSIQSSYQ VQAFKYAGVP LNSQAAFEMA AKDTVRPADK SPPLVYNIRC VELDLPYFTL ELSCIHETED
241  YLLQLVHEIG LHLHSCAICH RVRLIRYGLF NTNLALLRKH WTLEYILRNI QDCRQLVRQE LLEPHSPHFT DLNEADKSSC
321  SPTDS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VTIEGSVSSGVDL.T	Y	48.98	1261.6401	20.5	631.8403	2	27.89	2163	1	60	72	
total 1 peptides												

tr|A0A0L7LF47|A0A0L7LF47_9NEOP

back to list

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

Protein Coverage:

```
  1  MGRKAKFDET KKVKKGPGRK ARKQPDPIFR KELLDDDEPK KLSHKQKQRA AKRVKKRTEL AEKRKALKEA KKNVAKKTEV
 81  EVEAGSDEEN VKGFTDDNKE WLKPKKAQKA KKGKPKQEES ESEDENQGSD DENEVSDEEN EGSDEGVSDE EVDSDADVEP
161  APKKGKENYK YTVKMFMKSV FETNNHYSDD LFQDSDAEPE TGDASSDEEG DSSSKIEYNS DSDEKSEADD DEDDDMLPIE
241  KANLKLKKRQ KQDKKLADEE MQINIAKQDV FAFPSEEELE NPTSLQDIHQ RIKDVVTVLG DLNRLKAEGR SRCEYTELLL
321  KDLCMYYSYN EFLMEVLMQI FPVLELVEFL EASETARPVT IRTNSLKTRR RDLAQALINR GVNLDPVGKW SKVGLVVYSS
401  TVPIGATPEY LAGHYILQGA SSYLPVMALA PQENERILDM AAAPGGKASH IAAIMKNTGA LFANDANKDR TKAIVGNFHR
481  LGVVNAVVCN YDGREFPQVI KGFDRVLLDA PCTGTGVIAK DPSVKTTKDQ KDIQRCFNLQ RQLLLAAIDC CNAKSSSGGY
561  IVYSTCSILP EENEWVVNYA LKRRNVKLVP TSLDFGTEGF TKYRQHRFHP SLKLTRRFYP HTHNMDGFFV AKLKKFSNPE
641  PVADEDEEGE KKETEESQEN GDAEPEGNSE GSDTEKKAPV KRPAQTKESG PQKKKNKQEQ QKLQQKENQA ATANNKKKKQ
721  KNKKNKQNKD TQPQPTSGQP EGENVNQFKQ SKKTKGSNDK NEQKTQESVK KTQKQNAQST ISDKDTLKKN IQSPVNDTQS
801  PGRKNKKKNK KRNAPPQSNP AQVTESKPVA SPVNSNQGTP NKNKKNKKGN VSRQASQSND KAQLTESKTV ASPVKSNPVT
881  PNLNKKDKKV NASTSKVSQT KAFVKITETL EKKVAHKLKN KNKKKQIGQL NANKGKQTKP GQGVGKKFKK N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.QGASSY.L	Y	40.41	611.2551	-151.0	612.1700	1	49.54	4692	1	418	423	
total 1 peptides												

tr|A0A0J7L789|A0A0J7L789_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAKLASNQG GARSNGERQE AGPCQSYASV LNPKSTSQSR ASSFKSNNKE NIGEQVTVSQ QQHQQQSQQQ QIQQQQQAAT
81 MVERLMPSMI KDKSSCQRIP ARCQTTRTTI QPVSDNFPEK DKDRYESSLS RTLADAHQDN SQRDVAGQLN NGDVANDGEF
161 QTVANKGARR KEKMREQHRE SHRERHRLRE NNNRHQQPPR GPIGVGGGGV ARRGSDERSH RERGDRNGVA EHGPKEAHHH
241 RDDQIVEAEA QPVSLVTPPV KYVEAPLPTV NAWTKNRTSS SSSSSTPQPQ PQPQPQPQPQ PQQTAKTSSP LDVVPAAATS
321 TCADRPSDRE RRVLQPQPQQ QQQQQQQRQQ QQQQQQQQQH EDTIENGVED SAQPTIVRAP RDRRRFNQNA SDFTNIGDWP
401 TLGTQAERKA AISPSKQNGV VNDEPSTFKG NSTIESRGKE NKEQNHCQDD SDEHTDNGEK KKKANKQKWV PLEIDLPQNR
481 GTMRSPRFQN HRERNGEAND GESWRERDYD RSSGYNQRGR AGRSYRGRGR GGRGRAGFRH RHDHEYTNYA TTDYIQTHKY
561 EHADTGYMIP FMGTCYFNNA NYVDIPTLKE CIRQQIEYYF CEENLVKDFF LRRKMNAQGF LPLTLIASFQ RVQNLTMDID
641 LVINAVMESD KLEVLEFEDG YKIRTKLDPL KWPITDIASN MVISSLSQQS SSSQNEVIHP TSETFCPAAK PLLAIPIPAV
721 PRVFESYSVL NSVPMANEIL NPDVPEFVPM DLTEKTNGFT AINESNETKN EIQFEKIKEE IYKLTNSITV PHFSLNNNSP
801 IKIDDTLPAM VDSSTSDSLP EERINGELDT SSDNAWKEVR RRVKQPHKDR SEEKEKFENT RNKTREELNF QFDEELDSPP
881 PTGRHNAFSE WSEDDEDYEL SDRDINKIVI FTQTHPPASG SRIPKHEGHD RTGDWITRVK MTQDLEQLIN DGLNYYEDEL
961 WRQNNQRYGS SSSIGSYKTI NMISQEDFEK MAPKVPRKAN PEVPPPPPSC IEDLEIPQSA SSLQLPSISL EKKDHRPEKS
1041 RWNEKSQARE GRRASRFFAV VKEPSVDPTT PRKRKTRHSN NPPVEHHVGW IMDVREHRPR THSVGSSAGT SPNEGYLASS
1121 YGSVGIISEH PSHALLKESG FTQQAYHKYR SRCLKERKRL GIGQSQEMNT LFRFWSFFLR ENFNRTMYEE FKIIAKEDAC
1201 EGYRYGVECL FRFYSYGLEK KFRHVLYKDF EIETIYDYES GQLY**GLEKF**W AFLKYYKNSD QLHVDSKLEE YLSKFKSIED

1281 FRVVK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.GLEKF.W	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	1245	1249	
total 1 peptides												

tr|A0A069DZQ6|A0A069DZQ6_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NNNNEKTKEI VEVGEQDTNE KKKFIEAPLP KYNPWSVNKN AAQVIKGKVN KDNITKVQNN QQNGSEKRVL QPHTVENGTS
81 GQANQQNQSP SVVFASWDKK RVNKKASDFS YTEDWPSLDK INNSQRKASV DLETQDDADR SMPPPCSSNN SGSLAQNRKD
161 LTVLKEESSV SDKSSGGRLS DSEPNTFHDI DNKKKGRNKG VARHKWVPLD LDITKTRNKR ERSPKNFSKD KSVDDNKVEC
241 GHCGNARAKD QGNAFRGRGN NKSGRGRGRA SRGGLKSRFT ETEYSDYPTD YTQLNKFLGG SEFVVPYFGT FYYNSSNYSN
321 LDDPTLREYL RKQIEYYFSE ENLMKDLFIR RKMDREGYLP VTLIASFHRV RALTTDINKI ISAIISSDQL DLVDNFKVRT
401 KIEPLKWPIP DTVGNPLYIS SGHPLAMHPL GPNATLVPMA GIQSIVNPSS SNPESTSATT TVPPNRSVNY TAGGFPLPVV
481 APPPLSFSPS LVDNLNPDVP EFIPSVILKE NVDSDDKQTG AKEEEHPNDS QKENIVHEGK IIKSNAKILK TENANNEAIG
561 KSVNVISARQ ALLKSPKSPV KPVEESWKEV SHVRRKSKSF TGKKSEQMLN QNPIEEQEVL DFQFDEELNV PVGRLNQFTD
641 WSEDEGEDYE LSDSEINKLL IVTQTSQSSR GIKHEGYDRT GDWTTRVKMS QDLEQAINLG LQYYEESLWN EWPPISNTYK
721 TVKIISQEDF DIMVPKAPKK PLQDVPPPPP PSLSALEVAD EDIVQEEVAT IEEPEKPKDW TEDRRTGRIK PTTPRFYAVV
801 KGPTRPEKGY KRKTKHSNNP PVEHHVGWIM DVREHRPRTS STGSSTGTSP NEGYLSGSTP SSLPTFQHPS HSLLKENNFT
881 HQVYHKYHSR CLKERKLLGS GQSQEMNTLF RFWSFFLRQH FNQTMYKEFK TLALEDAKLG FRYGLECLFR YYSYGLEKVF
961 RPQLYQDFQQ ETINDYENGQ LY**GLEKF**WAF LKYYKHSSKL TVDSKLRKYL SRFKSIEDFR VCDDNEEKGA CGRLASEKRR

1041 GRCVSESGTA DKEKFLHIRS RTGSIGSPRM TRHRNDSLPT NHEHTKTQSR SRNNSHYDPQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.GLEKF.W	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	983	987	
total 1 peptides												

tr|A0A067R4G0|A0A067R4G0_ZOONE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SAGSLYDTQG PVFVSEPSSK VEFTNSSGGR VDCSAHGNPA PSVEWLGSDN LAVSSIPAIR IVLGNGSIYF PPFEAEVFRQ
81 DVHWAVYRCF VSNSVGAILS RDVTVRAVVI QRYEPEVQGP GGFLGNDVII RCNVPAFVKE HVTVTSWLQE PSFNIYPSTV
161 SDYIDYSREL NSVQTQACRS VVVVNGKYHM LPSGELMILN VTASDAMRSY RCRTHHQLTQ EVVVSRNVGR IQLTDIRGRV
241 PPVLNERLMI LTAKVDETIV VPCVAYANPR PQYRWVYHQQ NGHETSLDGT ERHIVRDGTL VITTVRESDA GTYLCNASNK
321 EGSETLEVQL SVSSPLQVLV HPSRQRVDLG KSATFRCSIS GFPRSSIHWL KDGHPLRTGA RIRQSSDDRV HISAVSKEDR
401 GMYQCFVKNQ LEVAQGSAEL RLGEVYPQLA YKFIEQTLQP GSSVSLKCSA SGNPTPRISW TLDGFALPHN ERLMIGQYVT
481 VFGDVISHVN ISSVKPEDGG EYECVAENRA GRTSHSARLN VYGLPYVRPM PPIPAVAGKQ LVVKCPVAGY PIDTIIWEKD
561 GVRLPTNIRQ RVTNGTLALE NVQRASDQGT YSCTARNKQN YTAQRSVDVR VLVPPKITPF SFARDLNVGD RTSIQCVVVT
641 GDLPLSFVWL KDHYSSLSPT TSTSISTSST GTTTSTDITT RQYDDFTSTL SIGSITRAHS GNYTCRVSNA AATITHTAQL
721 RVNVPPRISP FYFEDGVTEG MRTQIMCTAS QGDRPFNITW RKDLQPLGHE NGSDAPWINV SDYAPFSSIL TINTVTSSHS
801 GNYTCVVTNK AGSAEYTAQL SVTVPPRWLV EPTDHSVVQG NPVSLHCQVD GFPKPTVTWK QAVGTEPGEY RDLSYHNQRI
881 HSLENGSLVI SKAAQEHEGY YLCQAGNGIG PGLSKVILLT VHAGPRFKVR SRQERARKGE TVHLRCEADG DQPMDVTWKA
961 KGSPIESDYE MRYTVKTTSL SHGSLSKLTI MDVLPVDRGD FICIASNLYG QDRATIQLIV QEPPNFPRNL HVAEQTGRSV
1041 LLSWSPGAES DSPVTSYILQ YKEASDVWHE HNPQLSVAGD RSVVLVAGLH PATTYHFRLY AENALGTSSP SDTLHVMTES
1121 EIPGGPPRQV SVEAASPQEL HVTWQPPEQQ LWNGELLGYK IGFRKIGPGP EDEGPYNFTR IGAGIIDNEV RLS**GLEKF**TK

1201 YSVTVQAFNS RGDGPASDAV IIQTLEDVPS APPQDVICTP VSAHDLQVSW LPPDRAHLHG IVQGYRLFFE PVEERYELGI
1281 RENRAIAATT TVLHGLKPFT NYSIQLLAYT RAGDGVISPV TFCTTEETVP DAPEKVKAVS SSENAAYIGW LPPRHPNGMI
1361 TKYTVYLRVL EQGKELKIVK TTVAAHQLHY EVSGLLTSKM YEAWVTATTR VGQGAGTPVV HLSPATSAGV PASVVSFGQL
1441 VTVPWKVTVK LACLCVGVPR PKAQWRLGDL TLHHQPK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GLEKF.T	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	1194	1198	
total 1 peptides												

tr|B4QNL9|B4QNL9_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSWFNPWDGL KTKMCRYLLQ RYLGQFFENN LNLEQLKVDL YNGKAVVEDI FLKVNAFNDL FEDQGWAFEV VSGHIGRLTV
81 VVPWNALMTN DSSLEIHNLT ITLRPVTRYQ SGTTMLESMW SSVSSSMQMA EECMKQVDDD VPFLNHNNAL I**GLEKF**AETI

161 DNVLNRIRAK LTNTTLNIEY LLPRSDRKLV LSFQASHVEY KNKTGYEMPM STSQDTETEE DPNSSFNALP MIAKHNLVIE
241 GLSLHTSEVL DVMDHQFGPT PYEQLCKIVE LKGAQNIQIN IKQTENIVGP KVSLELSLDD IYFMLTPRQI HLLIEFSKGF
321 NCGGQQERPK KGRSLKSAPP SEYQMQSLQQ PTRMTGILGQ NADWCTGMSE ADPSEYSAYG NPPRSGYARS RKMSESTNSM
401 VTSCTNTLQQ ELGYTEKSGE ILKFKVQISK IYGIALHQDI LIQNTANIDS CSTVFDHASY LRYSDTASGF FLGTVLENHM
481 PLPNQQYLLL RAAPIIVSGS QQRYFQELTS RTTLSATAVD LIEVLDNSME HLLQFDRQRN CPDGYHIRPE IVLTQSSSFM
561 FKQNHNRCSN KIECSLDECT AELDISIYDR LGALFGSSPF SGDSDSSTPY PDDPNQTEFV VKSENLRLHL RFPVVDGRAA
641 NDPQKIPWWK KNVRRDFLAV EFRSLVVSSR SQISIVSDEL DVFYCDADKQ SAVHLLKCQQ RMQPNKKIQI DVLQLKDTTD
721 GQKKPRKSPF SSKCTFGYTS HVEGLDCSVD KTDSLLPGET EEINEFCDSC TQSSKLKIFT FIPHVKVVLE SKSMYELIYN
801 RLNGDLFMWE PRSPHYENNT DNEVPESKDL YAEPQLEEFK RNLLLSTSAM ESSIYFSMAE PTVSAPPAPP VRNEAFSFEL
881 FVEQGSLILF SHLLDPETNQ RSKECGKFQV NLKELRLFTV NGLDNDSNRS FFCIQLGEIE ALHCGNTLQD LELAWSDLAD
961 EKLLPTIYNF AHVHQQQDRK RMEVLSLVAE IKKQPEQRIK RMKMSFGISG AILQHHSCHS EHSWLNQLID FMDVADFPIE
1041 EYEPFALVSE LQLHVWNAGI DYRPKFFPQR AFLDLGYCTL SSNIISSMSG CTLRLLAEDC VLHLGLVKES NDSLIPVLNL
1121 GLLNISFRLN AEGSGQPRVD LRSSIHDMHL KTCYDSAAAL AQLIAYVAND RDLCPPEEPI LNEDTKPAEP KPNEEHEVSD
1201 HTQNHVSKLM ADAVIDVECS PNLRATKSPG GREEGIEIFY FPDEPKEKRK STPAKLQTTS LMVESPSVIG DILDFESNVI
1281 LQSYYHQSQV QPQTSLGSQV QQELGSLGNA SLEERDFDII HDEEISRMDK FGVKQIYISD DPLQIVDNHF ELPHEKVDLL
1361 RPPANFPVAE STYTLCEMTF TWHLYGGRDF PDEPLKKSSS SATSGFGMSD TYKYGVSQAQ EQDKQDKKGS KKSLPKQPKG
1441 SQRNLEVLVE MQLSKIRFSY ETYPLTSMYS SRQVLLVSEI EIRDRLRSSD INKFLYHPTG NNLSHKPDEN MVIVKALNVR
1521 PNPQKSSAEE CSLRVSILPI KLNIDQDTLL FLEDFFSGMF RNSASAAGGT KTEVSSSSAT DMPVMSVSKM PDEFSDELPD
1601 SEVKEMVERN LNVLIEENSL DVELEEDTAT ASPVFFREVI FSPALPICFV LSWKAD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GLEKF.A	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	152	156	
total 1 peptides												

tr|A0A1W4VP26|A0A1W4VP26_DROFC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MSWFNPWDGL KTKMCRYLLQ RYLGQFFENN LNLEQLKVDL YNGKAVVEDI FLKVNAFNDL FEDQGWAFEV VSGHIGCLTV
  81 VVPWNALMTN DSSLEISNLT ITLRPVTRFQ SGTTMLESMW SSVSSSMQMA EECMKQVDDD VPFLNHNNAL IGLEKFAETI

 161 DNVLNRIRAK LTNTTLNIEY LLPRSDRKLV LSFQASQVEY KNKTGYEMTM STSQDTETET DPSSSFNALP MIAKHNLVIE
 241 GLSLHTSEVL DVMDPRFGPT PYEQLCKIVE LKGAQNIQIS IKQTENIAGP KVSLELSLDD IYFMLTPRQI HLLVELSKGF
 321 NSGGQQERPK KGRSLKSAPP SEYQMQGHQQ PTRMTGILGQ NADWCTGMSE PEPSEYSGYG AGNAPRSVYS RSRKMSESTN
 401 SMLTSCTNTL QQELGYTEKS GEILKFKVQI SKLYGVALHR DILVQNTASI DSGSSVFDRA SYLRYADTAS GFFAGTLLEN
 481 HMPLQQQHYL LLRAAPIIVG GSQQRYFQEL TSRTTLSATA VDLCEVLDNS MEHLLQFDRQ RNCPDGYHIR PEIVVTQSSS
 561 SMFKQNHNRC ANKIECSLDE CTAELDISIY DRLGALFGCS PFAGDSAPPN PYPEDPSQTE FSVKCENLRL HLRFPVVDGR
 641 AANDPQKVPW WQKNVRRDFL ALEFRALVVS SRTQISILAD ELDAFYCDAD KQSAVRLAKC QQSQNQKKIQ IDILQLQDGQ
 721 SAGDSQKKPA RKSPFSSKCT FGYTSHVEGL DGGGDKTDSL LPGDTEEINE FCDSCTQSSK LKVFAFIPHV KVVLESKSMY
 801 ELIYNRLNGD LFMWEPRSPH YESPREEESA GSRGLSMDAE PQLEEFRRNL LLSTSAMESS IYFSMAEPPA STSAAPPPPV
 881 RNEAFSFEMF VEQGSLVLFS HLLDPESNQR TSECGKFQVN LKELRLFTVN GLDNDATRSF FCIQLGEIEA LHCGSTQQDL
 961 VLAWSDLPDE SLLPTIYNLA AVHQQRERKR AEVLSLVAEI KKQPEQRIKR IKMSFGISGA VLEHHSCHSE HSWLTQLIDF
1041 MDVADFPIEA YEPFALVSEL QLHVWNAGID YRPRFFPQRA FLDLGYCTLS SNIISSMSGC TLRLLAEDCV LQLGPLKEPN
1121 DSLIPVLNLG LLNISFRLGA EGSGRPKVDL RASIHDMHLK TCFDSAAALA QLIAYVANDR DLCPPEEPVL FPNEEARPAE
1201 PKASEEQEVS EHAQNHVSKL MADAVMDVEC APSPKTNRTP GGREEGIEIF YFPDEPKERR KNLATPVKLQ SKSLMVESPS
1281 VIGDILDFES NVILQSYYHQ SQNQDHQVPA SLGSQVQQEL GSLGNATLEE RDFDFIHGEE VSRMDKFGVK QIYVSEEPLQ
1361 IVDNHFELPH EKVDLLRPPA NFPVAESSYT LCEMTFTWHL YGGRDFPLDE PPRRSSPSAS SSAGGFGMSD TYKYGVSQPL
1441 DKLDKQERKG LSKQPKGSQR NPEVLVEIQL SKIRFSYESY PLSSMYSSRQ VLLVSEIEVR DRLRSSDINK FLYHPTGHSL
1521 VHKPDENMVI VKALNVRPNP QKSSAEECSL RVSILPIKLN IDQDTLLFLE DFFSGMFRNS GGTSAGGGAP KAEGSGSSSA
1601 PADMPVMSVS KLPEELADEL ADELPDSEVK EMVERNLNVL IEENSSEADL EEDPATAPPV FFREVIFSPA LPICFDYHGR
1681 RIELSRGPVT GLIMGLAQLQ GSGISLREIV NRRGILGWNK LCEFLAKEWL KDIKRNQLPN ILSGIGPANA VLQLFQGVYD
1761 LFRLPIEQYN KDGRIIRGFQ LGAQSFTART ALAALEITSR IIHLLQFTAE TTFDMLSAGP SLKKRKGGRQ GRRRRQGRPK
1841 DLREGVANAY SIVRDGINES ASTLIEAAIT EHDQKGYSGA VGAVVRQIPQ LVVCPAVLAT QATTNILGGA KSSLVPEAKL
1921 EARDKWKQEI H
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GLEKF.A	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	152	156	
total 1 peptides												

tr|A0A0J9RP88|A0A0J9RP88_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MSWFNPWDGL KTKMCRYLLQ RYLGQFFENN LNLEQLKVDL YNGKAVVEDI FLKVNAFNDL FEDQGWAFEV VSGHIGRLTV
  81 VVPWNALMTN DSSLEIHNLT ITLRPVTRYQ SGTTMLESMW SSVSSSMQMA EECMKQVDDD VPFLNHNNAL IGLEKFAETI

 161 DNVLNRIRAK LTNTTLNIEY LLPRSDRKLV LSFQASHVEY KNKTGYEMPM STSQDTETEE DPNSSFNALP MIAKHNLVIE
 241 GLSLHTSEVL DVMDHQFGPT PYEQLCKIVE LKGAQNIQIN IKQTENIVGP KVSLELSLDD IYFMLTPRQI HLLIEFSKGF
 321 NCGGQQERPK KGRSLKSAPP SEYQMQSLQQ PTRMTGILGQ NADWCTGMSE ADPSEYSAYG NPPRSGYARS RKMSESTNSM
 401 VTSCTNTLQQ ELGYTEKSGE ILKFKVQISK IYGIALHQDI LIQNTANIDS CSTVFDHASY LRYSDTASGF FLGTVLENHM
 481 PLPNQQYLLL RAAPIIVSGS QQRYFQELTS RTTLSATAVD LIEVLDNSME HLLQFDRQRN CPDGYHIRPE IVLTQSSSFM
 561 FKQNHNRCSN KIECSLDECT AELDISIYDR LGALFGSSPF SGDSDSSTPY PDDPNQTEFV VKSENLRLHL RFPVVDGRAA
 641 NDPQKIPWWK KNVRRDFLAV EFRSLVVSSR SQISIVSDEL DVFYCDADKQ SAVHLLKCQQ RMQPNKKIQI DVLQLKDTTD
 721 GQKKPRKSPF SSKCTFGYTS HVEGLDCSVD KTDSLLPGET EEINEFCDSC TQSSKLKIFT FIPHVKVVLE SKSMYELIYN
 801 RLNGDLFMWE PRSPHYENNT DNEVPESKDL YAEPQLEEFK RNLLLSTSAM ESSIYFSMAE PTVSAPPAPP VRNEAFSFEL
 881 FVEQGSLILF SHLLDPETNQ RSKECGKFQV NLKELRLFTV NGLDNDSNRS FFCIQLGEIE ALHCGNTLQD LELAWSDLAD
 961 EKLLPTIYNF AHVHQQQDRK RMEVLSLVAE IKKQPEQRIK RMKMSFGISG AILQHHSCHS EHSWLNQLID FMDVADFPIE
1041 EYEPFALVSE LQLHVWNAGI DYRPKFFPQR AFLDLGYCTL SSNIISSMSG CTLRLLAEDC VLHLGLVKES NDSLIPVLNL
1121 GLLNISFRLN AEGSGQPRVD LRSSIHDMHL KTCYDSAAAL AQLIAYVAND RDLCPPEEPI LNEDTKPAEP KPNEEHEVSD
1201 HTQNHVSKLM ADAVIDVECS PNLRATKSPG GREEGIEIFY FPDEPKEKRK STPAKLQTTS LMVESPSVIG DILDFESNVI
1281 LQSYYHQSQV QPQTSLGSQV QQELGSLGNA SLEERDFDII HDEEISRMDK FGVKQIYISD DPLQIVDNHF ELPHEKVDLL
1361 RPPANFPVAE STYTLCEMTF TWHLYGGRDF PDEPLKKSSS SATSGFGMSD TYKYGVSQAQ EQDKQDKKGS KKSLPKQPKG
1441 SQRNLEVLVE MQLSKIRFSY ETYPLTSMYS SRQVLLVSEI EIRDRLRSSD INKFLYHPTG NNLSHKPDEN MVIVKALNVR
1521 PNPQKSSAEE CSLRVSILPI KLNIDQDTLL FLEDFFSGMF RNSASAAGGT KTEVSSSSAT DMPVMSVSKM PDEFSDELPD
1601 SEVKEMVERN LNVLIEENSL DVELEEDTAT ASPVFFREVI FSPALPICFD YHGRRIELSR GPVTGLIMGL AQLQGSGINL
1681 REIVNRRGIL GWNKLCEFLA KEWLKDIKRN QLPNILSGIG PTNAVLQLFQ GIYDLFRLPI EQYNKDGRII RGFQLGAQSF
1761 TARTALAALE ITSRIIHLLQ FTAETTFDML SAGPSMKKRK GGRQGKRRRQ GRPKDLREGV ANAYTIVREG INESANTLIE
1841 AAITEHDQKG YSGAVGAVVR QIPQLVVCPA VLATQATTNI LGGAKSSLVP EAKLEARDKW KQEIH
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GLEKF.A	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	152	156	
total 1 peptides												

tr|Q2XXT5|Q2XXT5_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QRYLGQFFEN NLNLEQLKVD LYNGKAVVED IFLKVNAFND LFEDQGWAFE VVSGHIGRLT VVVPWNALMT NDSSLEIHNL
81 TITLRPVTRY QSGTTMLESM WSSVSSSMQM AEECMKQVDD DVPFLNHNNA LI**GLEKF**AET IDNVLNRIRA KLTNTTLNIE

161 YLLPRSDRKL VLSFQASHVE YKNKTGYEMP MSTSQDTETE EDPNSSFNAL PMIAKHNLVI EGLSLHTSEV LDVMDHQFGP
241 TPYEQLCKIV ELKGAQNIQI NIKQTENIVG PKVSLELSLD DIYFMLTPRQ IHLLIEFSKG FNCGGQQERP KKGRSLKSAP
321 PSEYQMQSLQ QPTRMTGILG QNADWCTGMS EADPSEYSAY GNPPRSGYAR SRKMSESTNS MVTSCTNTLQ QELGYTEKSG
401 EILKFKVQIS KIYGIALHQD ILIQNTANID SCSTVFDHAS YLRYSDTASG FFLGTVLENH MPLPNQQYLL LRAAPIIVSG
481 SQQRYFQELT SRTTLSATAV DLIEVLDNSM EHLLQFDRQR NCPDGYHIRP EIVLTQSSSF MFKQNHNRCS NKIECSLDEC
561 TAELDISIYD RLGALFGSSP FSGDSDSSTP YPDDPNQTEF VVKSENLRLH LRFPVVDGRA ANDPQKIPWW KKNVRRDFLA
641 VEFRSLVVSS RSQISIVSDE LDVFYCDADK QSAVHLLKCQ QRMQPNKKIQ IDVLQLKDTT DGQKKPRKSP FSSKCTFGYT
721 SHVEGLDGSV DKTDSLLPGE TEEINEFCDS CTQSSKLKIF TFIPHVKVVL ESKSMYELIY NRLNGDLFMW EPRSPHYENN
801 TDNEVPESKD LYAEPQLEEF RRNLLLSTSA MESSIYFSMA EPTVSAPPAP PVRNEAFSFE LFVEQGSLIL FSHLLDPETN
881 QRSKECGKFQ VNLKELRLFT VNGLDNDSNR SFFCIQLGEI EALHCGNTLQ DLELAWSDLA DEKLLPTIYN FAHVHQQQDR
961 KRMEVLSLVA EIKKQPEQRI KRMKMSFGIS GAILQHHSCH SEHSWLNQLI DFMDVADFPI EEYEPFALVS ELQLHVWNAG
1041 IDYRPKFFPQ RAFLDLGYCT LSSNIISSMS GCTLRLLAED CVLHLGLVNE SNDSLIPVLN LGLLNISFRL NAEGSGQPRV
1121 DLRSSIHDMH LKTCYDSAAA LAQLIAYVAN DRDLCPPEEP ILNEDTKPAE PKPNEEHEVS DHTQNHVSKL MADAVIDVEC
1201 SPNLRATKSP GGREEGIEIF YFPDEPKEKR KSTPAKLQTT SLMVESPSVI GDILDFESNV ILQSYYHQSQ VQPQTSLGSQ
1281 VQQELGSLGN ASLEERDFDI IHDEEISRMD KFGVKQIYIS DDPLQIVDNH FELPHEKVDL LRPPANFPVA ESTYTLCEMT
1361 FTWHLYGGRD FPDEPLKKSS SSATSGFGMS DTYKYGVSQA QEQDKQDKKG SKKSLPKQPK GSQRNLEVLV EMQLSKIRFS
1441 YETYPLTSMY SSRQVLLVSE IEIRDRLRSS DINKFLYHPT GNNLSHKPDE NMVIVKALNV RPNPQKSFAE ECSLRVSILP
1521 IKLNIDQDTL LFLEDFFSGM FRNSASAAGG TKTEVSSSSA TDMPVMSVSK MPDEFSDELP DSEVKEMVER NLNVLIEENS
1601 LDVELEEDTA TASPVFFREV IFSPALPICF DYHGRRIELS RGPVTGLIMG LAQLQGSGIN LREIVNRRGI LGWNKLCEFL
1681 AKEWLKDIKR NQLPNILSGI GPTNAVLQLF QGIYDLFRLP IEQYNKDGRI IRGFQLGAQS FTARTALAAL EITSRIIHLL
1761 QFTAETTFDM LSAGPSMKKR KGGRQGKRRR QGRPKDLREG VANAYTIVRE GINESANTLI EAAITEHDQK GYSGAVGAVV
1841 RQIPQLVVCP AVLATQATTN ILGGAKSSLV PE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GLEKF.A	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	133	137	
total 1 peptides												

tr|Q2XXT4|Q2XXT4_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 QRYLGQFFEN NLNLEQLKVD LYNGKAVVED IFLKVNAFND LFEDQGWAFE VVSGHIGRLT VVVPWNALMT NDSSLEIHNL
  81 TITLRPVTRY QSGTTMLESM WSSVSSSMQM AEECMKQVDD DVPFLNHNNA LIGLEKFAET IDNVLNRIRA KLTNTTLNIE

 161 YLLPRSDRKL VLSFQASHVE YKNKTGYEMP MSTSQDTETE EDPNSSFNAL PMIAKHNLVI EGLSLHTSEV LDVMDHQFGP
 241 TPYEQLCKIV ELKGAQNIQI NIKQTENIVG PKVSLELSLD DIYFMLTPRQ IHLLIEFSKG FNCGGQQEGP KKGRSLKSAP
 321 PSEYQMQSLQ QPTRMTGILG QNADWCTGMS EADPSEYSAY GNPPRSGYAR SRKMSESTNS MVTSCTNTLQ QELGYTEKSG
 401 EILKFKVQIS KIYGIALHQD ILIQNTANID SCSTVFDHAS YLRYSDTASG FFLGTVLENH MPLPNQQYLL LRAAPIIVSG
 481 SQQRYFQELT SRTTLSATAV DLIEVLDNSM EHLLQFDRQR NCPDGYHIRP EIVLTQSSSF MFKQNHNRCS NKIECSLDEC
 561 TAELDISIYD RLGALFGSSP FSGDSDSSTP YPDDPNQTEF VVKSENLRLH LRFPVVDGRA ANDPQKIPWW KKNVRRDFLA
 641 VEFRSLVVSS RSQISIVSDE LDVFYCDADK QSAVHLLKCQ QRMQPNKKIQ IDVLQLKDTT DGQKKPRKSP FSSKCTFGYT
 721 SHVEGLDGSV DKTDSLLPGE TEEINEFCDS CTQSSKLKIF TFIPHVKVVL ESKSMYELIY NRLNGDLFMW EPRSPHYENN
 801 TDNEVPESKD LYAEPQLEEF RRNLLLSTSA MESSIYFSMA EPTVSAPPAP PVRNEAFSFE LFVEQGSLIL FSHLLDPETN
 881 QRSKECGKFQ VNLKELRLFT VNGLDNDSNR SFFCIQLGEI EALHCGNTLQ DLELAWSDLA DEKLLPTIYN FANVHQQQDR
 961 KRMEVLSLVA EIKKQPEQRI KRMKMSFGIS GAILQHHSCH SEHSWLNQLI DFMDVADFPI EEYEPFALVS ELQLHVWNAG
1041 IDYRPKFFPQ RAFLDLGYCT LSSNIISSMS GCTLRLLAED CVLHLGLVKE SNDSLIPVLN LGLLNISFRL NAEGSGQPRV
1121 DLRSSIHDMH LKTCYDSAAA LAQLIAYVAN DRDLCPPEEP ILNEDTKPAE PKPNEEHEVS DHTQNHVSKL MADAVIDVEC
1201 SPNLRATKSP GGREEGIEIF YFPDEPKEKR KSTPAKLQTT SLMVESPSVI GDILDFESNV ILQSYYHQSQ VQPQTSLGSQ
1281 VQQELGSLGN ASLEERDFDI IHDEEISRMD KFGVKQIYIS DDPLQIVDNH FELPHEKVDL LRPPANFPVA ESTYTLCEMT
1361 FTWHLYGGRD FPDEPLKKSS SSATSGFGMS DTYKYGVSQA QEQDKQDKKG SKKSLPKQPK GSQRNLEVLV EMQLSKIRFS
1441 YETYPLTSMY SSRQVLLVSE IEIRDRLRSS DINKFLYHPT GNNLSHKPDE NMVIVKALNV RPNPQKSSAE ECSLRVSILP
1521 IKLNIDQDTL LFLEDFFSGM FRNSASAAGG TKTEVSSSSA TDMPVMSVSK MPDEFSDELP DSEVKEMVER NLNVLIEENS
1601 LDVELEEDTA TASPVFFREV IFSPALPICF DYHGRRIELS RGPVTGLIMG LAQLQGSGIN LREIVNRRGI LGWNKLCEFL
1681 AKEWLKDIKR NQLPNILSGI GPTNAVLQLF QGIYDLFRLP IEQYNKDGRI IRGFQLGAQS FTARTALAAL EITSRIIHLL
1761 QFTAETTFDM LSAGPSMKKR KGGRQGKRRR QGRPKDLREG VANAYTIVRE GINESANTLI EAAITEHDQK GYSGAVGAVV
1841 RQIPQLVVCP AVLATQATTN ILGGAKSSLV PE
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GLEKF.A	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	133	137	
total 1 peptides												

tr|A0A182VIR2|A0A182VIR2_ANOME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MASTQVSHGT SVSNAANNNN NNNNNTNSSN NNNNNNNNNN NNNNNSSSSY ANVLLNLKEQ QGKDVSHQAD NNKENIGSER
  81 PGSGAPPNSS SSKGKSVAGK ESVTLGTATA HNPTNTAATG TAATSTAPMA DEAKVPLSNE LDVKNNTPDE LEDDANFVPV
 161 VSHHKRDRKA KAAAAAAAAA AAGASTPHGG PKSSGEKQSA AGAARGSGRR PAAPGTQTHA GKQGKLSHER GGGPDEKGGS
 241 YRKDFGKRKS SDRSRNLANA AGESAKDEKL HDATAEGGSA GGASSTSGAP GKQLQQAAAP GGAVAGPAGS PSDEEDRGKE
 321 DAKKFVEAPL PKVNAWKVTP SIEPAPIPAN DTRAQTKSNT AKVAPAAAPS SAAAAAAPAV PSPASAVAAV EKSDVSSATG
 401 SNEKRNVQPK QPTKAQGNGN QKAMPNDPNG SKPAAPAGGK SDKKRNNAKA ADFTANSGDW PTLGEKKNTP ADGPKKGGSS
 481 EASAEKQNAA SKTTGSAVSS TSTAGVQPKS SEPMNAPPAQ SSSSSPKKHQ QPADVPVPES GPSTSKSTSS TNTSNNSAVV
 561 KDNATKTADG TSARASTARA NNQTGPKSTN EEGGKNAAAP SSTAAAAAPP KQPATAPSTT SKQANSDGAT TDTAASEQAT
 641 ATTSQSRPHS RGRGTAAEGE VNGSAASASN NTRKGPKPKW VPLEIELPKA RERRARTPRH RRYDDYEESG WHQHQDSSTG
 721 GQQSAGQTQH ANQQPQAQQQ QQQPPQQQQQ QQAQHQQHQP QSHRGNGAPP GGRMPRGRTT RGGGGGPPAY RGGRGGSGRI
 801 ATGRGGMNFG YRRGAPMRGG ANRHMNDRTT ATTGAAAGVE NGVVGGIPLG TGQDFQDFTA VNTKIGTDQA AFIMPYLSTF
 881 YYNGAPLIGM DQLSIKECIK KQIEYYFSEE NLNRDFYLRR KMDPEGFLPV TLIASFHRVQ ALTDDIDIIT EAIKESEKLE
 961 LIEDYKVRTR VNPTMWPIDH SVTIVNGAMN FGVTFADQQQ QQLDRTSALP SQAVQGEQQA PDAKPAGPEQ QQQGAAVSAA
1041 VPAPTSVPVA GDGADVAAVP QLQVASKILS SIPPPPLPRN IRNPVSKASK TVPLLIPCVN VAPMVKPCSV KEVAQKTNAA
1121 PATQPPPAES GKSAEENLNP DVPEFVPAAA QVENKPPKSK ANEKKQPNPP PTAAGGGKKG KAAQQHGGGS EGGKEGKTVK
1201 VDEKPATATA QPEEESAEQQ QQQPQPEAAL WKEVKRRSRS SQSHPQQAPA QQQQQQQQAK QQTKNSSATS SVSGPLSNDI
1281 AGSKKAASME QLAKQSSSQQ AKPQQGGSNA TTQQLKQDNL GTAPAAAAAA GANAASTTEE REELDFQFDE ELDIPRSCGG
1361 RVNHFTDNWS EDDDESDYEI PDTEINKLLI VTQITNRLPK HDGYDRTGDF TTRTKITQDL ERIINDGLYN YEEDLLTSKS
1441 DGRRGGGYHG YRTVNLISQE EYDKLVTKPT KLATLEVASP QPSAPMAPPS VTIASPPAAS SPPSSAALND NSMVDDQSLL
1521 DVSGLNVSTA STTTGNRHKA RFYAVNKDEF VDPITPRKRK TRHLNNPPVE SHVGWVLDAV EHRPRTTSIG SSAGTSPTAS
1601 SYGSLPHSLP VFQHPSHALL KENGFTQQVY HKYHSRCLKE RKRMGPGQSQ EMNTLFRFWS FFLRENFNKN MYNEFRQLAI
1681 EDAAEGFRYG LECLFRFYSY GLEKKFRAQL YEDFQHETVS DYENGQLYGL EKFWAFQKYY KNASKLTVNP KLKEYLDKFN

1761 SIEDFRVLEP QINEMLEGVG TLKPCQTKRR PRSVSESEGV AVVVGSAPGP SHAGSHAYQA GVSRRGGSSG SGAGSSSHSN
1841 TGHYTSRNR
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.GLEKF.W	N	28.97	592.3220	53.3	593.3608	1	25.88	1938	1	1729	1733	
total 1 peptides												

tr|A0A0P5PN82|A0A0P5PN82_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFLNPWYGQI GAGPAAEDAP TTTDKEAPDA VANETAVKGD GTDIQETPPT VSLNVAAGVA AKPENDDTKA DVATLPSGQQ

81 TEPFKNRLKC GWTAHMTQEG RLFYCNHINQ TSSWLPPIDN WNGSIQAGAS GGTSLPYGWE AATDREGKAY FINHLNKTTT

161 YEDPRKDWGE EPPQPREVEL SRHPELGFGF VAGSEKPVIV RFVTEGGPSV DKXXXXXXXG SEKPVIVRFV TEGGPSVDKL

241 LPGDQIWRIN GEDVKHAPRD HVIQLVRSCK ETVHLAVCQP PLDNSTRKSA LLSAAKKAKL RNNPSRVRFA EGVVINGTTL

321 PLSQSLGKEE PCPPLMPNVM KVYLENGQTK SFKYDSATTV SDVLNSLQQK LGFKSMDNFS LCVEHVKSIR KNKLTLLDPA

401 ESLAWIAARP GAHNLRCMLR IAFLPKDAYD LLRKDTGSFE YLFTQCCNDV VQERFAPELK YDIALRIAAL HMHQHALTNK

481 MQGKLTIKNI EREYGLERFV PTSLVEAMKR KELRKLLSHF FKVNQQLTAP GQKQLTVLQA KLHYLKIIAE LPSYGAKCFS

561 TNFKSDSNVE TVILVSPKFG VSQISGMRSS APLTLCNVED ITSLNVRRED ELIQYVEIRL KDPDKETLLL SLEERDAEEI

641 ILVLRGYHKL ATDRVLPVHR ERSRWTQDSA PPYHTRHTVL PSPWSFVEQP PASCGASEPE EKLVRYADLS VPPPYHPPPQ

721 GFQIPNNRYP CAGEHDEGAI GEREFDDPFD PTATYDSPRA LRGVSLALCP QQNNKVDSNM NKPLPNNNVD AAGATAAMKN

801 RMPVLTSVSS REMPAARRVS TLETAVPSHK LGFDMPSVVS MEILESQQQQ TELLVQQLAD CSEARNDAVI QRVSELKRLV

881 EDAEQYLTGG GDRASRVSDV ET**SSLLS**DMS QLSKTESDQS GSGAGAGYGR LRHSDSLLLL TQGQKQLSLP DNSTILLDAA

961 DHASSSDTDS VSTTPNQTPT HSPSQRPKSA EGLKHGTPSR PPSMLKPSDS SFGLHSPDVI PSVAGHEEKD LEGLLRRLQD

1041 DLPLAEGSLI YLDPDIIDLT MIPPPITPEE DGLKMKFPAT INEPPTPFAD RDSLENELAA MKSTPSGVAR GRPSPSDLGE

1121 LQDLTDLAQW SDVVSDSSCL NSSQERDFHD SEDKFSLSGV STRSVSSLAS SVRAGSTSSL SVQTLTESKR RWIADEKRKH

1201 LTANPDLDKF LSTVAVPLPP VGGNKSSSQA GSGDFSNDDL SAYIIPPPPA NASTSSNNGL VILQKLYAAR EGIFQVMREE

1281 PPSGVNSAKQ SAKNFDEKDR VMVEMKVRFE QREPNHGVSS KIGEMHRLLA SSNNASAVTE TVTVTTASSN ITSTKGTTPD

1361 LSPASS**HSSG Y**GSLKSIADC SSNPPPELPA RQPAGQFSPR KNGFANFKMP ALNPLNGALK APGYGPNFRS TFIDDDDEDD

1441 EAIPPPPPPP RNPIPRMIIA AAAAANARLS TPGKGSESAT VPPPGPLTKS SSQGDLLGRI SVKTPSSGRM SDTHRLRMEE

1521 MGPSGVAGVK GMSASTESIS TVHKNGQSGT SSPSKLSMAS SSDSIGSNAS VATVKNAPGN FVTGISVTSV KESDSTPPLP

1601 PRNSPTRVVI PKLPVTPQIE STTKSVIVNR VTRPSVDSRS APTTANVLPS QRPPALPSRL RKPPVTSSVT SPQKPTPPAI

1681 QMVTPSANGP SGARTTVTKA AAPPPPPITS TPPPSPSHYA VPGVMKPLNE SPAKHSEYQI PVVSRVPRTT MAPPPPSDSS

1761 RVSQPGAPLS TSSPKLGART NASIGNNVIS LNIRVEGKGT PGQDLPTWTN NSPTHRKSGN SGVVLPERDN GSLDSGSFEQ

1841 DSLDGSTDFD LTTLISQSEQ AVSRVISRLA VSPVAKAEQA HFQGDEDLSQ VEAARDRLIN ESRQFVTASK MFVKSVTDSP

1921 QAMAICLSQC VVLIERMGIA VGDVSQREQN RDLPPKVRDV ARAFLHTLKA AAEASGQGVS DPSMGRLMGK ATALAGVLTI

2001 LMRSLRP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.HSSGY.G	Y	19.20	549.2183	-263.0	550.0812	1	22.00	1553	9	1367	1371	
T.SSLLS.D	N	17.03	505.2748	-2450.2	505.0440	1	9.20	652	2	903	907	
total 2 peptides												

tr|A0A1D2MK27|A0A1D2MK27_ORCCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQFPVILYQS AAFCWEMPQP FQKSNNSFPF LFKTVPAELC NPTNSHLMEG VCVSRERCLA FGGTSFGDCQ QGSAIGTCCK

81 FDKQCSVPKR SVVAFQVVEN LMSSGFGGAL ILSYGTSKTI SVIIESKEGI HFNIRATQIP CDSTNKAPDD CLQYFTSSTA

161 AVKSFGFPRQ LNNQRYTICV KPSTGGSLLS WSICTDEDAE GLQLSRFKVS ENSVPCLTDW IAVDSEKRCG QNFTSLTTNT

241 GTNSRIRVNF DENESGDDIF TVELPDTVPE PMLECSNIGN PQGEQVYPSS TPRQLCEYTP ATNSCLCRFS NMPNPMAQTL

321 SLHLPMMAPS HGEHYCPTIQ GYTASPPMIF GGECKYFANI RVTDTANTDF GLLITQVRLR SGATLVLASP AVLSTVFSLV

401 LALISCPELM ELSGFNEDVK RKARDILSSC RGGSAGSYSD SRGMQIIRKH VAKYIEKRDG GIAAHPDDII LSAGASEGIR

481 ACLKLLKSGE NVEKESYTNG DAVKRNQNMK QKAAVL**IPVP EYPL**YSATLE EYNMKKVPYY LDEHEDGWDV NVQELETIVE

561 KAREENCEPR AVVVINPGNP TGHILPRENM EAIIRFAYQQ RLVLLADEVY QDNVYGTKKF LSFKKVLSEM EAPYNSTELI

641 SVHSCSKGFV CECGLRAGYF EVVNMDPDVK SVLTASVAAN LCPTVLGQAV VDCLVDPPKE TDPSYELFMK EKSTILNNLA

721 ERAELAHREF NAIPGISCAQ LDGAMYAFPR IYLPEKAIRV AKEAGYQPDV FYSLSLLDTT GICVVPGSGM GQMPGTYHFR

801 TTILASTEKM KMMLDKFRTF HLEFVRKYSE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.H(sub I)PVPEYPL.Y	Y	27.57	950.4861	95.3	476.2956	2	29.01	2291	1	517	524	Mutation
total 1 peptides												

tr|A0A1A9TCY8|A0A1A9TCY8_ANOST

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

Protein Coverage:

1 MGDAINFGPA WLRKVSSDSN TASNHHSTNS SASSSHHTSS SHTMLNSNSG GGGGGSTTIV NNAGGG**GGVG L**HHQHHHQPP

81 SSHSSAYHSL HSLSQSGSGS SVAGGGNGGT GGGGLSNSSF AGGSVLANNG GTGPGTANSA TATTTTATAI RYPLAEFRYG
161 REEMLALFDG RTVKAPEILV QYKRLFVEKP QPPLALTPCP EEELIVEPES RRPWPSRSVS LGIPGRGARG GSVDRGRGRG
241 RGLYTSYQRS SSFYEDESRG VGRGERPWLE RNGTGGIGGD IEWNNSSSSP RKEYGTRVIR TGGSTMESWR RSRTDEESVG
321 GVISNGGVGD WRSGGGAPGS ITGLVREKWT RSTSWRDEDS GAAHHGLDRG LNSGGGGDRM IPPYKSRLSS GSGLGSGGVV
401 GGIGDLSSGG HSMGGPGGMR RPNWDTDELP EWATENPSDF GGSFDATGAF HDSDNDGESG GNGANRYGGD ASNETNGGTK
481 TTNHAKDDDR LKDMRRRAED GEAIESRRGG SDEALGRNRS EGAAVASGKG RGETPGKGMN HVGGGGGGSG SSRAEEESLA
561 DRNEPNDDEN LPSTGAIDSS QQQKQQRIKR QAGGGKDGGN QVSGVVPSES TVAPSEPAPN AQSNSTKGIS SSRESIESSV
641 SSTVSGTAAG NAAAATASDG GDGRQNSPSW QKGNEVSASS KNTPDHQHRV PSAPGERRET GNEIIDPNDG AKHHHPAQHE
721 KRNEPKKSPS STSVDRMQEV ADDMVAQLIM DDEFLATDGD PSVISSIAAS GTGGLVGKSP VFGMSAAGGG GPSGPAATSM
801 TSAGGLPMNM VLPKALQPMQ QLFGNGNMSR VNPLLLSDPV AANRAAMAAA AAAAAAGVNP MAQLHHLMGP PRGMDIWYYC
881 DPQGKVQGPF QAAEMTEWYR AGYFDESLSV RRECDEVYNT LGTLVALCGG MPFLNSSVIQ PFKAPANGAK HSPQQQQQQQ
961 LQQQTPQPNA SASQGGQQKQ QIAPGANGNT VMPSPNQQQQ QQPAGQQGPG QQSGQASAGA SGGGGGPNVV PSIHLLRQQS
1041 IVLQKLQNSE GWNLLSPEQQ NMIITQQMNQ LLSSEAATRL GMISPSAGSS SAGGTNQHHQ QQQQQQAGAG IFSGGGSAAG
1121 GMPSGPDALV NLKLREMQQQ QQQGQPQQQQ PPPAHVMMEQ LQKSVPGNQH SNAFLKLHLP EFNQVSQAPA AGVRPMLGNM
1201 NVDPSTAAAV AAAASSQLMH GIGFNHQAAG QNIGPLGPNN LLLNRGGLLG AGGPAQQQPL PQQPHPAAGK PGGEDPIQSL
1281 FMQLSLHKNQ QASQQQQLPN HQPKSDMMGG GAPAGWMQTG QPQGANAGTA TAGGLAGLVP RGPMVGAASG WGDLPPPTSA
1361 SFASIMQQQQ QQQQPHMALA GHHPLLLGGS GPMNDGSNEP QAPSVVSLFK HHQQAEKQQQ IEKEQQQQQQ QQQQLLQQQQ
1441 LQQQMHQENV LAQQKQQQLQ QQSQHVQENQ GQKAAKKQQK NSQAGTGGSS NSSNGQATTI TSEEESEFII VKKEMEEKKR
1521 QKELKKQQQE EQKRKLAEEK KVLEELEAQK RAKLLESQRR EAMKIQEQQQ QQQQQRSVPK AVPAPWSAAM AEIANSKLSL
1601 TEIQKTERAL LARREHSLRE QQEQQQLLEM QSQLLDGRLK WNAQNLMPAK VKPLAEIQAE EAAAAERARE KHANASGLTV
1681 AAIAAQGTVK GGGAKKEDSL ASLLGGGGSG SAAGSAVWQV RGGGSSSSST SNMLYFNSTK AWDGDTSGIL GG**GSAGL**SNS

1761 VSSGGFWEEP TQPSVVTAAS IVAAAGKASA AGARKQSSGV TASSGGKQQQ QQQQQLLSKS KTMGSISTSS SSTVTAAKQQ
1841 KQQQGATKGG SASNAAGGKS AGKNGNATGN NDRKDERKHP NEQQQPTNEF TDWCTRALSS LNSNVDIPTF VGFLQDIESP
1921 FEVKDYIRLY LGENKECSEF AKQFLERRSK YKNQQRQKNA HIDDMCKPAP AINPSSNDFQ ETKGKNKKVK KNKMMKLDSR
2001 ILGFSVTAAP DRLNVGERDY GDNV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.GGVGL.H	N	18.26	401.2274	-1954.1	401.4507	1	50.80	4837	1	67	71	
G.GSAGL.S	N	16.06	403.2067	-2204.6	403.3250	1	49.11	4643	1	1753	1757	
total 2 peptides												

tr|A0A0P4ZIA8|A0A0P4ZIA8_9CRUS

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

Protein Coverage:

```
   1 MGSENEETME LEAEHLFLLM KKDYRISRNA RAEWYFNHLN HTVQIPKADK VENFKGEIEI VSAIPQETPI EWDWDTSHLY
  81 QYVISLSTVV TFLSHTYRLV LCLDLSPSAA TVDCVEGVTL LDEILTSFKN CVQGLARPFI VPGSQLLFCP KIYVTVIAHT
 161 PFLVSKGQQV LVAGWLLQQD NVNAFVDLVQ FKLSSIEVRL SCWTNFVEEQ RDAHLADAER IVGGLFETVS DRTTNSSCST
 241 ISIATPEVSF ISILRYGMLA LELLPEKSSA GIIIFTDGVF GTTDAGWSEA LLSQLRHNTI ACSFVQVGSR TCHPASSEGF
 321 LPNNDLMEFV ASTTFGTCLS GAPHVDGGYD YQMNVYHQYF LTWGFEKYLL RPTQTVKDTK IWNLSNRCFE SSAIHRVKKK
 401 VSDYPVNCSL HSVLSCRLRE GFTIKEVHLD DDVVEVHLAL PWRPSIQVEY SIRGQWPITQ GTVRCGISVQ GPYDFLHDVT
 481 CKKIQSLCSR YRQLVVQSYW ALVKNLSETD QLLVHLHSFS SNPAFYTVPE AIKSGVPLFY LPPNESSLVN ASSDLSYPHF
 561 DAFWKPICVL DIGYWQRWLH CHRIGILLQH DRPLPKHLHL PSTSGRYHSI QCRQAATALN AALRDFTSFV LLENHSYIGL
 641 VCTDSEKPVS FYLVRLTHKP PCVILRIAFL GGTAGSIRQK VVADLKNAVQ SLNFPQRSLP QDFSKTIAAI PCCKVLQKPA
 721 EKILLRYENF QVVPHDPFVG QNNNIQMKRP SASPGTQWST LSHYLHHRRW IWCIQGSPGL ALSLNSVARI LSIITKMRLQ
 801 EGFSFAHSSS GIFTFLLEVD MERQHGQLLP GSTDDESQDQ AQNCSCVVQY VLFPPHRTGS FGLKDSEDEA TEESDILDSS
 881 DAQLEIVTEC WVEPQAGIVG DSPDERGFFQ GLDYHALAES FHPMDLDCIS SLVTFEHLNL MCRQADRVGV TCEQEKSVPS
 961 SPAIPGRRDV LSPLTGNGSS YNFTPPSGWD RRTEEALKDD TVSCVPFCFQ LPRLLPKCSR AKLLFSTFVQ EFKAPIRYIP
1041 NPADTVNELL FDLLTRQLSQ LGLREVILQE GDCRQLLENL NLQAAADCPH KEEDFPNNSV DADTEVESFA TAREANSTPR
1121 SPRDINISNP PSRPSLLTPL NISYRSGINS HDDRAESAAN KNEPLTPMWR CFVKSVSSSH ILLVLLPASF QDLKLLMLNE
1201 EHLQMPRSAH LTKVKPDFIP HAEPYSNNDG SVESKSTNEE VAKHMTTDDD QMTSCSQSQS TSQPCSLGPT RTNSFAGQQR
1281 PRLASHSSVQ AARIRAGSLD TAPLPHGQQQ QSHPQQFQHH HVHASCSVGS ADRRHNSKTS SSLFGSGASY FRPVTSLPSF
1361 SSPVRSAPVH ASLSLPVYVF DCPLTNLVSQ LLSRGANPKV TIYRDHTFPN DEDISASTGE EEANEEDRQA ESQSIPEDPV
1441 SAGSINILSQ YCAVVEALYC KCLGQALFTS LQLGRQIHSR DVDAAMNLCK ETLLEIDITA FLQNICGHLK DFKMKAGLEI
1521 LRQRKQSSSS GEPLVEDDAK WDFPLSLLRL HQPCANLKHL HKLIRTRFQE ILCLSFKPVP SLFDYYFYCP PDHPLSPAPD
1601 GGLAIHDLSI GHDDTELVEF RRSSDTDNSV SQTCSVTGGR SDSASEPIDD VEWEEDGEDE TEATSVPLFL HLTATVRSKK
1681 NVTSQSLNAL PTCLGDLMTS ISGSSAVLDL KGLKITLDFL CLTFRSDLED LVPGPHNQRT TSFCSSSSGI LDANNPCPTL
1761 TSQSELSEDE DGLPMDEDDR TESISRQLLH IPEGQRRRIK AALADIEWML RDEIVAFMLD SFPITEATLA AVVQHVQSSP
1841 HRPSCRRKNV PLHFVLNPQE SSRRFLVEFT KLPIQGHLLR EEGSFYYLTE NTCQAKFQGS LDPPLGSSRY RKTDADLTSE
1921 ASASRSLVAQ TSTDSCATAG LGVEEQPGEG EADRIDYQME NTVGESESEA TKDAAVMMDS TITLVSNGEG DAVGEPEASD
2001 VRPDDVQSDS LFKKTSKRRF ESGTTSIPGT RHSDSSSVVD SIRNTEDGYE GGSSNSEDEF EWLKELDMEK PKMPPFWLVL
2081 KVNEEAVVTY FHCRFELARP EEIQQWKQIH EDLINSITAL GKLINQQMLL KDLHDTRSCN GLLEPETNDD IWHQDDLAHI
2161 KPTCHRINSD HLHTYGSQEQ PGYLEATLKL QPGSFQCRQV WETHFPLHPR LKTGPGKLGS SKGVQQLRIV LNAFSVNNRN
2241 NMFVYQENSG NVFYLRLNES SCVSHRNPSD SVSISRYNAD EADGASYSCS RRSSNWNVSD RGGLDEDSID SQRRSGSFSE
2321 RDSVGGDQMS LGSVSLNRSL HYQSQQHLLR KEDCIQLKVH GITEAGPAIK IDLVRVLQNK LDDAVLEVLH SLLSRNPACK
2401 LTSDDVHFIQ KPNEPPHIIL QSTVQACALP YLPALAYYLR QNLLDSVVYT PKYMDNFVGH HFQDYSPFFP APTSDVYLYN
2481 RPQASGNRGI ACIAFALVDG VGNPVSQLEW PRPATAVKMD GGIGPSSLSE FEEFIRADLC VKATDRKGPG PMAAMEFRIW
2561 ERGHVNEDTL REKLELAIQH ALWDVVLEYR LLPFPLCAVT DQNGVLVPQN LGDGLPCSEP TTPVRRKWQL IQPIVHEEDI
2641 PVDPRSRSVS FSGLPPNRSC VASGTTNPLA TSSAIDPKWK VRHTSGTSSI SIERPLSPVT SIQLRSSGPI SPVERFCERS
2721 VSTSSVTSSL TTGTLPELDK LELGERGVLH PVYSKLLEKW FNLGLQKNVA SIKFQKASLL APLTVPTLLK AVNHICSSSV
2801 TPELSMKIFS SSEPGAPYIP YLPASRCPKQ GSVDRSVLDK THILIGRNMA QWKESLSGEI NLSDSTQQEN NGQVALKVQR
2881 AHQRFVSYVH DSPVNPCPEA VRLVQSQSGN FGSDVDKANT SGDHSSVVSL LIPRQRLLWA TVSRDQEWTM WLYNFNKDNY
2961 ESLTKQCHNL VQWHNARWAL LSSIVAQKLG LFHNQQCSGR THAHQTIRHN PFLVLSEMEA LVKLHVPPAS RDYNVSTTRK
3041 PSQSSLPHFA YLETYRDSKP NRLLSNTPYG NQGDLVTRHG QQWIEKRYSE RREEMQRLLV LCPARSSGNN ILVTEDIIQL
3121 FKQVARIIHY CFTPLLFLPK WRIQVARTRD PNMATASLTS EFRPRHESGN SVNSGRNSPS NSPPRQPRRP TDDHWHQSLC
3201 SAYLQEYVQY LHTLGFLQME IKPLATKRGP KSALKSQRIV GEEAGRVRHV SHPTRVNGGP SPSSPSSTSS SDANTLYFHK
3281 SHQGGILVCE VAIQEPFFYT KVYALEMSRL LHVGMGGAFP NVGHIASAQA HYTDRFLNEC DHIKVLLHLH SFTYDFHLRS
3361 LNSFVSGRQY LLKPGFHLVS FLDDFTKYYN KAPNFARNQV VSNSLTLKDP ATTGEQLFNY LLTRERRYGF QVLRMASSSN
3441 SDNDKVTTEF VLAKQWSFKT IQREYGDLRH ADDYDVTLLV SHESVVEDPM TIFIKFYVIM TSKREYYPRL LVEKKPGKFR
3521 TVSTATPVKA ASAPPLETVD RVAEDSDATA SSTQDVQQMP APGNGQGKIS KSDADLQLAD KERNTPTPEL LSVSNPEVSF
3601 IQRKGSIMVN AALPEENRTS PAGPAVVAAA AAAFIRQEVI NYLGYYTKHE QDMQSMMSEQ AKKAEDLIRA IVNQAKVHCR
3681 RDTLWQRLQQ SPASSSTNLT YLEFRELLTL SHTEPISSGE PQLVPLLAQP VSWYQGLAKL LLSRYPENHR HYSSADGKIQ
3761 YVIVLNQRLP GTAMMLSCDV HADKAELSSL CQEIPSTEME VSTVFSMDNG FHSRPMIMQG FIEDFVNLCA FHIWSGLLG
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GPSSL.S	N	17.78	459.2329	-1577.6	459.5157	1	48.81	4609	1	2524	2528	
L.SPAPDGGL.A	Y	16.96	712.3391	-131.4	713.2528	1	49.05	4636	1	1596	1603	
total 2 peptides												

tr|A0A0J9R316|A0A0J9R316_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDFERGASGG GGFSPNGNGG PGSGDVSRTA RYDSGEGDLG GGNNIMGIDS MGIANIPETM NGTTIGPSGA GGQKGGAAAG
81 AAGQKRQQRR GKPQPDRPQR ALFCLSVKNP LRALCIRIVE WKPFEFLILL TIFANCI**ALA VY**TPYPGSDS NVTNQTLEKV

161 EYVFLVIFTA ECVMKILAYG FVLHNGAYLR NGWNLLDFTI VVIGAISTAL SQLMKDAFDV KALRAFRVLR PLRLVSGVPS
241 LQVVLNSILK AMVPLFHIAL LVLFVIIIYA IIGLELFSGK LHKACRDEIT GEYEENIRPC GVGYQCPPGY KCYGGWDGPN
321 DGITNFDNFG LAMLTVFQCV TLEGWTDVLY SIQDAMGSDW QWMYFISMVI LGAFFVMNLI LGVLSGEFSK ERNKAKNRGD
401 FQKLREKQQI EEDLRGYLDW ITQAEDIEPD AVGGLISDGK GKQPNEMDST ENLGEEMPEV QMTESRWRKM KKDFDRVNRR
481 MRRACRKAVK SQAFYWLIIV LVFLNTGVLA TEHYGQLDWL DNFQEYTNVF FIGLFTCEML LKMYSLGFQG YFVSLFNRFD
561 CFVVIGSITE TLLTNTGMMP PLGVSVLRCV RLLRVFKVTK YWRSLSNLVA SLLNSIQSIA SLLLLLFLFI VIFALLGMQV
641 FGGKFNFDGK EEKYRMNFDC FWQALLTVFQ IMTGEDWNAV MYVGINAYGG VSSYGALACI YFIILFICGN YILLNVFLAI
721 AVDNLADADS LSEVEKEEEP HDESAQKKSH SPTPTIDGMD DHLSIDIDME QQELDDEDKM DHETLSDEEV REMCEEEEEV
801 DEEGMITARP RRMSEVNTAT KILPIPPGTS FFLFSQTNRF RVFCHWLCNH SNFGNIILCC IMFSSAMLAA ENPLKANDDL
881 NKVLNKFDYF FTAVFTIELI LKLISYGFVL HDGAFCRSAF NLLDLLVVCV SLISLVSSSN AISVVKILRV LRVLRPLRAI
961 NRAKGLKYVV KCVVVAIKTI GNIMLVTYLL QFMFAVIGVQ LFKGKFFKCT DGSKMTQDEC YGTYLVYDDG DVHKPRLRER
1041 EWSNNRFHFD DVAKGMLTLF TVSTFEGWPG LLYVSIDSNK ENGGPIHNFR PIVAAYYIIY IIIIAFFMVN IFVGFVIVTF
1121 QNEGEQEYKN CDLDKNQRNC IEFALKAKPV RRYIPKHGIQ YKVWWFVTSS SFEYTIFILI MINTVTLAMK FYNQPLWYTE
1201 LLDALNMIFT AVFALEFVFK LAAFRFKNYF GDAWNVFDFI IVLGSFIDIV YSEIKSKDTS QIAECDIVEG CKSTKKSAGS
1281 NLISINFFRL FRVMRLVKLL SKGEGIRTLL WTFIKSFQAL PYVALLIVLL FFIYAVVGMQ VFGKIALDGN NAITANNNFQ
1361 TFQQAVLVLF RSATGEAWQE IMMSCSAQPD VKCDMNSDTP GEPCGSSIAY PYFISFYVLC SFLIINLFVA VIMDNFDYLT
1441 RDWSILGPHH LDEFIRLWSE YDPDAKGRIK HLDVVTLLRK ISPPLGFGKL CPHRMACKRL VSMNMPLNSD GTVLFNATLF
1521 AVVRTSLSIK TDGNIDDANS ELRATIKQIW KRTNPKLLDQ VVPPPGNDDE VTVGKFYATY LIQDYFRRFK KRKEQEGKEG
1601 HPDSNTVTLQ AGLRTLHEVS PALKRAISGN LDELDQEPEP MHRRHHTLFG SVWSSIRRHG NGTFRRSAKA TASQSNGALA
1681 IGGSASAALG VGGSSLVLGS VDPAGGDYLY DTLNRSVADG VNNITRNIMQ ARLAAAGKLQ DELQGAGSGG ELRTFGESIS
1761 MRPLAKNGGG AATVAGTLPP EANAINYDNR NRGILLHPYN NVYAPNGALP GHERMIQSTP ASPYDQRRLP TSSDMNGLAE
1841 SLIGGVLAAE GLGKYCDSEF VGTAAREMRE ALDMTPEEMN LAAHQILSNE HSLSLIGSSN GSIFGGSAGG LGGAGSGGGL
1921 GGSSSIRNAF GGSGS**GPSSL** SPQHQPYSGT LNSPPIPDNR LRRVATVTTT NNNNKSQVSQ NNSSSLNVRA NANSQMNMSP

2001 TAQPVQQQSP QRGQGNPTYS S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GPSSL.S	N	17.78	459.2329	-1577.6	459.5157	1	48.81	4609	1	1936	1940	
I.ALAVY.T	N	15.56	535.3006	2301.4	537.5398	1	48.28	4548	1	138	142	
total 2 peptides												

tr|A0A0A9Z5R4|A0A0A9Z5R4_LYGHE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIRGPIRID VWKGDWGLPS VDLECLQFLA YIKINAIDMK ITN**VNNPY**FT PEGKLPVIRL KDRNISRFED LVKYMEDKNM

81 NPDYGLNRKQ QAEAQAYRTL LKEKLFPALQ YVWWLDQNNE TGVTTPWYSR ILPIPFNFYY PGKFKREAEG MLTALFDNYE
161 NDKDIESKVI GDAEKCLTAI SIRLGSSDFI FGSHPTSIDA TLYAYLAPLL KAPLRSTGLQ NHLKACTNLN KYVSRMSQRY
241 FSQDYNEYEA KRKKEMKAQK EQVEQDPTLR RNQFIAVFVA LAAMYGYAVS TGALQKLH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.VNNPY.F	Y	24.90	605.2809	-19.1	606.2766	1	32.04	2642	1	44	48	
total 1 peptides												

tr|B4P0S9|B4P0S9_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAPAGLYILL SACCVSLASA GFGFGFGGGS LGLGGGNGGG SAQASLPGLS LGGEYNRGSS GSVLNQAANG ILGAASTGAN
 81 VIHSAGSAAA SHGAQAANGV LGAAGSGADA VHSAGSTAAA HGAQAINGVL GVAATGANVI HSAGSAAASH GAQAANGVLG
161 AAGSGVDAAH SAGSTAANHG AQAINGILGV AATGANAVHS AGSTAASHGA HDAHAVLGAA ATGVNAVHSA GSTAADQLHK
241 ASEHSGSSSV SIGAGHLNIQ SSDNSGAKPN AAHLTIGSSG VTGSSGLHHS TGSATVDAAN AVLNAAGAGA TGSSGAAHGA
321 QVVNGVLGVA GAGANVVHSA GSIAAAHGAQ AANKVASGIA NGASTGSGAS SGHLSIGSSG ISGSSSGSHG NGHLSVGTSG
401 ANTAQITGSS SAGAHHTGSV QAGSAKITAG HGKIEASGSN SGAAGAGHLD VGATGASAMK TSSTYHKAES SKVSAGHAST
481 GGATSGSTSG QLSIGASGGS GSAGSHGVGN FNIKSSETTY SSKTEESKFS AGHAHISSGS STIGASGTQA GSAHIKTEHK
561 KVESSGSSSS LTGSGSASIG AGHLNIQSAG STGSSQTASN SASIGVGHLS IGATDSTSKE SSAHASSGHL SIGSAGISGS
641 AGSGAGSSKI NAGHLSIGTS GISGSAGSGA AAGSSKINAG HLSIGSSGIS GSAGSGAGSS KINAGHLSIG TSGISGSAGS
721 GAGSAKINAG HLSIGSSGIS GSAGSGAAAG SSKINAGHLS IGSSGISGSA GSGAGSAKIN AGHLSIGSSG NAGSASLGSN
801 GLSVGANGHK SSTVGSIGLA GAHDAASLDH GVASGILTSE CFEMGNQSI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
I.GSAGI.S	N	16.06	403.2067	-2204.6	403.3250	1	49.11	4643	1	633	637	
T.GSSGL.H	N	16.00	419.2016	-2022.7	419.3610	1	3.18	234	1	283	287	
total 2 peptides												

tr|A0A0N8CGV4|A0A0N8CGV4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MKALDVYALN IPSAVVAETT GSLNSTLTGF PAAGVTANRQ TVPAQTIRSK EEKEVLEHFA GVFAMMNPQT FKEVFATTIE
  81 YVVERIYRNS ALQVVANSFL ANPSTSAVFA TILVEYLLNH MEEMGLNVER SNLYLKLFKL VFGSVSLFAA ENEQMLKPHL
 161 PHIVNKSMEL ALSAKEPYNY FLLLRALFRS IGGGSHDLLY QEFLPLLPNL LQSLNSLQSG LHKQHMKDLF VELCLTVPVR
 241 LSSLLPYLPM LMDPLVSSLN GSQTLVSQGL RTLELCVDNL QPDFLYEHIQ PVRAELMQAL WRTLRNPNDQ IAHVAFRVLG
 321 KFGGGNRKMM VEPQRLDYWD KDSGPCVVIH FQELKQPVSL PVEKIMETAF SALKSSSTEP FYRTQCWEVV RCFLLSSLHL
 401 DDDRLVMQRL LSHHSFLEGD VHPVQSPSFQ CSDKQARHVH QTAVTAMFVA AAIKELRQAV LPTMVSLVRH YTLVAVVQQA
 481 GPFPMLVPGR SAQRILGMDP LVLVDALATI MGHEEKELCK PGHLALVLML DTASIVLGSK ERACKLPLME YLAERMCSLC
 561 YDRAWYAKLG GCIAIKFLFE RMAFKWVLDH QYVFLKALLF VMMDLTGEVS SGAIDMAKAN LEKMLLLCAT PLPELLPSPE
 641 IVSAQKKSLH DVTHELVRQV TSPNSTVREQ AMHLLQVLAR ITNQTPTAIM EPHKEVLADM IPPKKHLLRH QPVNAQIGLM
 721 DGNTFCTTLK PRLFTIDLNV VEHKVFFHEL LSLCEVDDTV LLKLPCYKSV SNLTPLRKSA LQALAACHYI TQCRDKILNV
 801 IFKALSCNNA ELQETAFSCM KKILVGTQIE METVHAAVRP LLLLLGDYRS LSTNVILRLS HTTQLFPHVF NEKLCEQLLQ
 881 HLRKWLEVVI VAFKTGGNRP VATHSSHGPF SSSTSSSSSL CSNEVKVAIG IIGLFHQIPA ASARFLEILC KLVLQTERAL
 961 GLEPGSPFRE PLIKFLLRYP TETIDLLLRD DIIADADWNR FLEHFVRHSD GKPFRGAIKG NTTRLINFVL GGISSESATA
1041 KPHALQVTVR ILRIIICKDD QWISEQPELI NVLTKAWCXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXIICKD
1121 DQWISEQPEL INVLTKAWCS GRYDEKKTSD LSIAERKEQR QLAKILLHYF QQHPEEVELL FHLMRALCDR TIPDFYFLKE
1201 FLEKTVGQSY GADWKRASFF KFVELFRNPN LGQELKAKIL QHIIIPGFSV SFERGEGELL IGTPPTPDQD NNESVVSVFI
1281 NKVIDPDNPF GTSDAVRILL LQLSCLLVEQ ASQHIHDAAN KRQGNKLRRL MTFAWPCLLS KNCVDPTTRY HGHLLLSHII
1361 AKFAIHKRIV LQVFHSLLKA HAVEARSVVR QALEILTPAM PLRMEDGNTM LTHWTKKIIV EEGHTIAQLV HILQLLVRHY
1441 KVYYPVRHHL VQYMITSIQR LGFTPTATLE HKKLAVELAE VVLKWELQRM KDEADSGGES CDETLPSGSQ KRAGNDGQPE
1521 LKKPRLASSS SSGKTLEVSK PIEKTHCDAI ANFLLRLACQ VNDATSTANS SGEQLSKRCV ALLKMALKPD VWPNCELKLA
1601 WFDRLFQTAD NTPAAATASA ATVSAPNFTN ICTALDLLTF LLSILRKEQI LAGFKPLQRG LSSLMNCVNP KVVRCLHGLL
1681 SRLMSVFPTE PTNSNVASKH EELEGLYAAV TKAIYEGLGA YERNTTAPST SLLGTLMLLK AACTNNPCYI DRLITSFMRA
1761 LQRMAREHSA PATGDRQTTA ASTTTESGFS SCELLILSLD LVKNRVGVMG VEMRKAFIGS ILVGLLEKSN EPKVVRSIVR
1841 MLDEWMKTKT PIAINQGPSL REKSILLVKM MQCLEKRFPD DVELNIAFLE LINFVYCEES LKGSELVSKL EPAFLAGLRC
1921 PQPSTRAKFF HVLDTSMRRR LHDRLLYIVC SQNWEAISAH YWIKQCLELI LVTSVSGAPI HTAPASALLP GVTSVIATAD
2001 ASERENFSVA GNIKEEPEEL LDVFAHVKED DIDMDLSNAP NDPLTPSGVN KTGLATLVNR QVKFLESGRE ITSAQFLEAV
2081 AQLAHMDTSL AEVLWLDLFP RIWKVLGERQ QQALSVELVP FLCSGAHVVQ RDCQPSAINT FAEALSLCVP PIRIKPCLLK
2161 YLGKSHNLWH RTTLMLEQLA FDSGNSTAHT KVKQKEAGND FDLDPGAVSH HETLDALSEM YSTLKEEDLW SGLWQRRAHL
2241 PETIIAVAYE QQGFFEQAQG TYELAMTKVR QEFANTPAPI SLQSEYRLLE DHWMRCGKEL NQWELLQEFG CSPECLNYQL

2321 VLESAWRTPN WVVVRDALTQ LEQACPKEYA WKVNLYRGFL AMCHPEEQHT NMVERYVELA SSLCIREWRR LPAIVSHVHL
2401 TTLQAAQQVV ELQEAAQIHQ GLLQSRPGTL HDVKAIVKTW RNRLPVIADD LSHWSDVFTW RQHHYQFIVS HYDQQSDQQA
2481 SAQSMLGVHA SAQAIIHFGK VARKHNLTGV CLDSLARIYS IPSVPIVDCF QKIRQQVKCY LQAANVLGKN ELQEGLEVIE
2561 STNLKYFAKE MTAELYALKG MLLAQIGRPD DANKAFSAAV QMHDTLVKAW ALWGDHLEQV FTKDSRNIGI GISAITCFLH
2641 ACRHQNESKS RKYLAKVLWL LTYDDDKLSL AEALDKYCVG VPPVQWLPWI PQLLVCLVRD EGKLVLNLLS QVGRMFPQAV
2721 YFPIRTLYLT LKIEQRERYK SAELAATQAT ADSGSTVGNG TPQASTPVAA GAEAAGPIKA TEPMWRCSRI MHMQRDLHPT

2801 VLSSLEGIVD QMVWFRENWY EEVLRQLRQG LAKCYAIAFE NRGSVAEATI TPHTLSFVKK LVATFGIGIE NIANSASGSF
2881 SSAASESLAR RAQATAQDPV FQRMKTQFST DFDFTLPGAM KLHNLIHKLK KWIKILEAKT KLLPRSFLIE EKCRFLSNFN
2961 LQTAEVELPG EFLLPKHTHY YVRIARFLPR VEIVQKHNTA ARRLYIRGHN GKIYPYLVVN DAGLGDARRE ERVLQLLRML
3041 NNYLNKHKET SKRFLNFTVP RVVAVSPQMR LVEDNPSSAT LLDIYRLRCV KRNIEHDMPI AKYYERLATI QARGCQASHQ
3121 VLRDIHKDVQ QIMVPRTLLR EWANVTFPTA TFYWTFRKML TLQMALVNLA EYVLHLTRLN ADMLYIHQDS GLLSVSYFKF
3201 DVEDSNGELD ANRPVPFRLT PNLADFLTMI GVAGPLTASM IAAARCLVQP SVKVSAILKA ILRDEMIAWH KKKTADEKEK
3281 EGGGSVQVEG DILIGLVNKA VTAIINRLQS LSTFDGNESK VSTLVAAANS NDNLCRMDPA WHPWL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.AAGPI.K	N	16.18	427.2430	-2476.4	427.1923	1	59.58	5608	1	2774	2778	
N.TPAPI.S	N	15.20	497.2849	214.7	498.3990	1	47.42	4448	1	2276	2280	
total 2 peptides												

tr|D6N9W7|D6N9W7_BOMMO back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTEMPPYHAV KDEEKTSGQS DSDSSSDTDD WDLSQCFDKP QHLEPIKGAE RVEHSWRVKE KYKTHCVALV LCLNVGVDPP

81 DVVKTQPCAR LECWIDPLSL SPSKALESIG HALQSQYERW QPRARYKQSL DPTSEEVKKL CCSLRRNAKD ERVLFHYNGH

161 GVPKPTAQGE IWVFNRTYTQ YIPLSMYDLQ TWMGAPSLYV YDCSNAGIIV DSFKLFADQH EREYEAQKNE EGTSSIPQVS

241 YKNCIQLAAC AAGQSLPMNP ELPANLFTAC HTTPVKTAMK WFVLRTRTRY ADRDLHDLID KIPGQVTDRR TMLGELNWIF

321 TAITDTIAWS SLPADLFQQL FRADLLTASL CRNFLLADRI MRSYNCTPVS SPALPSLAAH PLWAAWEQTL DSALAQLVTL

401 SSAPHPLDYS HSPFFRDQLT AFQVWLDLGC GGRGVPEQLP MVLQVLLSTL HRVRALQLLC RFLAL**GAWAV RAM**LAVGIFP

481 YMLKLLQASA PVLRASMVYI WARIIAVDPS CQADLVNAKG HTYFLSVLQD PTVDSEHRTL AAYVLAGIVD GYPAGQEAAL

561 QGSMISICLE QLGDREPVLA QWICISLGRL WRGFEAARWT GVRDLAHEKL FPLLEHSEPE VRAACAFALG SFVWWCGGAG

641 RCEQANALDL QVGVQLAARL PLDASPLVRA EILAALQWLV LIFEQHFIAV YIQERVRRND RGGPSGRAEA GQEALAGGGG

721 GAAGGRSRPP HYSLPAIGFG SVPVRLFSTL CAMAREPHPR VAQMATDILN YISNQSAQVD SVAEPARNSA SLPPSPGTRH

801 HEHARTLPGH GHRRGKSGLP HTISEESVAN RDRDSGGDRE RHKDSLSSNS SQTCTSKKAI VSTEFVEWAG GAFSRPEPAR

881 PDCESREHHQ RRWTLARNRE LRREARAACR VSRLETQALH SRCPLPPAVV LFHPYDQHLA VASKDNFGIW DWGTAAKLCV

961 GSWRPAWGRI SSLAYLNEHQ HALLAVASHT GNLAVYRPSG SSTEPALVSA WRALDVSPPP QYTPPRAQPI YSIAQLVSDQ

1041 FSSNEDKLAT NKNKQQADPN LGGGTVVRWV AARRWVAAGG RARGVRPWDA RRELRVGDLA APGDAALTAL GAARPDVLAA

1121 GFQDGAVRLW DQRTLAPTHD LRRHAAPVLA AAHSLRADLL VTGCANGEIC IYDTRKMAVL EEIRAPGPLA AVDVHPLCDL

1201 VACGSPNQCI SLYDLRGNAL NTIKFHEGFM GPRIGPVSCL AFHPLRWAPT ARRLTWRSWT HLHSYFCDVL SRNWAKYSLM

1281 KLNSI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.GAWAVRAM.L	Y	22.74	860.4327	137.2	431.2826	2	25.10	1857	1	466	473	
total 1 peptides												

tr|A0A224XHB0|A0A224XHB0_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 KSEGEEEMKT PVAPPDEKAE TKMKAPDKKE KEKQMKQIRK SIGELQRDIE HLEEESSTGL FEKVPDGENI MDEPCDLEDM
  81 EGRPILSAPS TYVSTAESTM KTVSLCEILR TFATNPEKRG VWDRYLEMID EFVKEGLKHA VGASISYLIS EMNNDHNNGP
 161 LFEVKLKVID NKLSHEPSLV DDENLEGTFL CEIVSIINNI NAIALLIPRI SYFQKDRTYK DELLTEEKIV DLQQMIILNA
 241 RMVMMTARNY SSNFDRFSYL WTDNKDLTLK QFLKFSRRLT PEEMDMENAE DEFGRRLIPF LSPTLDDFRT KIDYYEEIYK
 321 DLLRLKEEEI IDEWFCLSYK VFKKQVLNYS ASWAMLYKQH LIDEVMNTVT TFDKFVTEAT AGLHKNLEEG DYEGLVKIMG
 401 YLREVEVYKV KATDLFKPVE ESMDMLKSYG HVFPLEIYRM LKTLPDRWEK LKKRAAKYQV LVEPLIAAET DTIRKRLSLF
 481 DVRMDLYLVE FKKKPFWLWE CDAYYELDKT NTEIKRLEDL KANLDNQATL FYIETGATPI IEQLRKEVTL MKVVWDYLYV
 561 VTSMISTWEN TRWRTIDSES MDMDLKRLLK ELRTLDRTVR NWDIFNIIEN MVKNLITALR AITELQNPAI KPRHWEELMA
 641 EVKISLEITD ETTLKDLLSL SLHKYEDEVK TIVDKSVKEQ QIEKMLTELT ATWAHVEFEY EPHLRTGLKT LRVSEENVEM
 721 LEENQVQVQN MLSSKFVGFY LKEVTTWQKK LSSAEQMITT WSEVQRIWRY LESIFTESED IRKTLPEDTK LFDQSDKLFR
 801 SMLKSMEATP NVVLAASQPS ILDNLNMLLA NLQKCEKALT SYLDTKKLIF PRFYFLSNND LMDILANSMQ PDLVCRHLTK
 881 LYDAISNLRF AKVDGKMTKT ATGMHAKDGE FVDMFWPCEC VGAVEDWLNS LTRAMVRTVR EYFRLALLAY DGKPRHEWVF
 961 DFPAQPVMVI IQIMWAAEVT VAFRFLEEGH ENSMKDYQKK QIFMLSQLIN VMLGDLSDDS RLMITAICTI EVHSRDIVAK
1041 MIASKVGSAK EFQWQSQLRH RWDHGVGDCF INICDAQFEY QYEYFGNQPR LVITPLTDRC YITLTQSLHL IMGGAPAGPA
1121 GTGKTETTKD LSKGLGIMIY VFNCSEQMDY RSIGNIYKGL SQTGAWGCFD EFNRISVEVL SVVAVQVKTV LDAIKGKKSI
1201 FNFQGEVIRM IPTVGMFITM NPGYAGRAEL PENLKALFRP CAMVVPDFDL ICENMLIGEA FQEARVLGKK FITLYELCKE
1281 LLSKQDHYDW GLRAIKSVLR VAGSLRRGDK ERPENQVLMR ALRDFNIPKI VTEDRPIFMG LIGDLFPALD VPRKRDMAFE
1361 KLVHQAALDM KLQPEDGFIL KVVQLVELFA VRHSVFIIGD AGTGKSMVWK TLHKTYANMK MKPHYNDLEP KAVTNNELFG
1441 IINPSTREWK DGLFSVLLRD QANMSGDGPK WMVMDGDIDP MWIESLNTVM DDNKVLTLAS NERIALTPAM RLLFEISNLR
1521 TATPATVSRA GILYINPTDL GWTPYVRSWL QKNKDENIRN TLESYFEKYI PNTLKASKSA WKIITPIPEN AHIHVLCTLL
1601 ELLLTPVNVP RECPKEWYEI YFVFCCVWAF GSACHQDQVE DHRVKFTQWW TGEFKSVRFP DAVMKNEATV FHYYVDEETK
1681 KFFPWTDKII PFILDYDIPL QSTLVNTAET TRVRYFIDLL IEKKKPVMLV APAGCGKSVI IGSKMRALSE DYAVTNIAFN
1761 FYTTSEMLQK ILEKPLEKKS GRNFGPPGNK TMIYFIDDMN MPEVDKYGTV QPHTLIRQHM DYQHWYDRQK LSLKDIHNIM
1841 FVSCMNPTAG SFTIDSRLQR HFAVFALSFP TADALKHIYT SLLSQHVHNP QHKFKLNVIQ FIDKLLATAL SVHGRMQAEF
1921 LPTAIKFHYI FNLRDLSNIF QAILMTSSEC ITSPVTFIRV YLHEASRVYG DKLITLAEQD VFQELLKQQA IQFTQDLPEA
2001 EYTREPRIYC HFADGIGDPR YNEIPSWDYL KRILTEAMQQ YNDLIANMNL VLFEDAMAHI CRINRVMEMP RGNALLVGVG
2081 GSGKQSLSRL SAFISSLESF QIQLTKGYTS NDLRADLAGI YIKAGLKNVG IMFLMTDSQV PDERFLVLIN DMLSSGEIPE
2161 LFGDDEVENI VQTIAPEVKG AGINDTRENC WRFFIDRARK NIKTMLCFSP VGSTLRIRAR KFPALVSCTT IDWFMEWPQV
2241 ALENVSLRFL ADLEDLEDNL HLPVSLLMAY MHTSVNHMSE IYRNNEKRYN YTTPKSFLEL INLYSKLLIQ KNREINTKIE
2321 RLENGLEKLV SCAEQVSGLQ EQLAGQSVIV AEKNKNASDL IAVVAKETQI VSREKIIAKD EERKCQIIEE DVRVKQKMCE
2401 EDLAKAMPAL EAAQAALNTL NKTNLTEMKS FGTPPEAVAK VAAAVMVLLS KKGKIPRDRS WKAAKAMMGS ADGFLYTLVH
2481 YNKENIHPEI VKAIIPYIKD SEFTPENVIT KSSAAAGLCA WVINIMKFHE VWMVVLPKKK AEAAAKAELA ASRAQLAALD

2561 RKISALEAKL SELTEKYELA LEEKNICQAE EDKTRQAIDL ANRLVNGLAS ENVRWRETVN SLKVQLGTLP GNVILITAFI
2641 SYVGCFTRRY REELMEKIWK PRLDVYKPPI PYTEGVDPLL MLTDDAQIAA WNNEGLPNDR MSSENATILT NSERWPLMID
2721 PQLQGIKWIK NKYGTTLQVI RLGQKHYLDK IEQAVSEGRV MLIENIGEAM EPVLDNLLGR NLIRKGKVVK IGDREIDFNP
2801 RFRLIIQTKL ANPHYLPEIQ AQTTLINFTV TKDGLEDQLL AEVVKAERPD LESQKSTLTK QQNNFKIQLK ILEDELLQRL
2881 SAAGPDILSD RDLVEKLEST KKTAENINIK VEEAKITSVK IDTAREGYRT IATRGSLMYF IMNDLYKINL LYQFSLKAFS
2961 TVFHHAIATS LPATTAELRV ENLMENITFC VFMYTSRGLF ECDKLIFLSQ MSLQILVHSQ EIVMNELDFL LKFPYNPHVT
3041 SPVSFLTHTA WGGIHTLCEM EDFSNLDKDI ISAADRWRKF VNGETPEREK FPQEWSNKTH FQQLLILRTL RPDRMSYALK
3121 LYIQAKLGDK YVSARTVEFE KSYQETTAST AVFFILSAGV DPTYDVEKLG KQLGFTFDKK NFHNVSLGQG QEPVAEHAIE
3201 FGSRHGHWVI LQNLHLVANW LPELDKKMEK AQENPHQTFR LFLSSEPSSD PQFCVIPQGV LESSIKITNE PPTGMMANLH
3281 KALENFNQAT LDMCTKETEF KSILFALCYF HAVVAERRKF GPQGWNRSYP FNVGDLTISV MVLYNYLESN VTIPWVDLRY
3361 LFGEIMYGGH ITDDRDRRLC RTFLEVYLEP SLIEGELEFA PGFPSPPNSD YEGYHKYIDA MLPPESPLLY GLHLNAEIGF
3441 LTTQVQNLFK TLIELQPREA GEAALGGVSK EEQVFTMIDS ILKVAHHEFI MVEMLARMEE RTPYNIVALQ ECERMNMLTA
3521 EIRRTLNELS LGLKGELTIT SDMEALQESL VMDVVPGGWA AKAYPSQLGL TAWYADLELR IRELEGWTNT FRLPTAVWLG
3601 GLFNPSSFLT AIMQMTARKN EWPLDKMCLQ CEVLKQKSRD QVNVPKEGAN ISNLYMEGAR WDVATNSIAE ARLKEMFPLM
3681 PVIFVKAITQ DKQDLRGTYE CPVYKTRMRG PTYVQSFHLR TRDKPSKWIL RGVGLLLSV
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.VINIM.K	Y	20.81	588.3305	156.4	589.4298	1	32.22	2664	1	2522	2526	
total 1 peptides												

tr|T1HU69|T1HU69_RHOPR

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LRAITELQNP AIKPRHWEEL MEEVKISLVI KDDTTLKDLL SLNLHKYVEE VKTIVDKSVK ELQIEKMLTE LAATWAHVEF
81 EYEPHLRTGL KTLRVSEENV EMLEENQVQV QNMLSSKFVG IYLKEVTSWQ KKLSNAEQVI ATWAEVQRIW RYLESIFSES
161 EDIRKTLPED TKLFDQSDSL FRSMLKSVEA MPNVVLAASQ PSVLDNLNML LANLQKCEKA LSSYLDTKKI IFPRFYFLSN
241 NDLMDILSNS MLPELVCRHL TKLYDSISNL KFAKMPDGKL TKSAIGMHAK DGEFVDMFWP CECVGAVSLI VEDWLNALTL
321 AMVRTVREYF RRALLAYGDK PRHEWVFDFP AQTVMVIVQV MWSAEVTVAF KFLEEGYENS MKDYQKKQVS QLINVMLGEL
401 SDATRLMITA ICTIEVHSRD IVAKMIASKV GSAREFQWQS QLRHRWDHDL GDCFINICDA QFKYQYEYFG NQPRLVITPL
481 TDRCYITLTQ SLHLIMGGAP AGPAGTGKTE TTKDLSKGLG IMIYVFNCSE QMDYRSIGNI YKGLSQTGAW GCFDEFNRIS
561 VEVLSVVAVQ VKTVLDAIKG KKSMFNFQGE MIRLIPTVGM FITMNPGYAG RAELPENLKA LFRPCAMVVP DFDLICENML
641 IGEAFQEARV LGKKFITLYE LCKELLSKQD HYDWGLRAIK SVLSVAGSLR VSDKERPENQ VLMRALRDFN IPKIVTEDRP
721 IFMGLIGDLF PALDVPRKRD LAFEKFVHTA AVEMKLQPED GFILKVVQLV ELFAVRHSVF IIGNAGTGKS MVWKTLHKTY
801 ANMKLKPHYN DLEPKAVTNN ELFGIIHPAT REWKDGLFSV LLRDQANMAG TGPKWMVMDG DIDPMWIESL NTVMDDNKVL
881 TLASNERIAL TPSMRLLFEI SNLRTATPAT VSRAGILYIN PTDLGWTPYV RSWLQKNKDE RIRNLIDSYF EKYVPIILKA
961 SKSVWKIVTP IPETAHIHVL CSLLELLLTP TNVPRDCPRE WYEIYFVFCC CWAFGSACHQ DQVHDNRIKF SNWWVNEFKT
1041 VRFPIAVTKG ETTVFHYYVD EETKRFYPGF NYNYAIKVPQ LERWHLWFEI PLTEKPLNSS LNFYQQTLVN TAETTRIRYF
1121 LDLLIEHKKP VMLIASAGCG KSVIIKAKIG NLSDDYAVTN IAFNYYTSSE MLQKVLEKPL EKLSGRNFGP PGNKTMIYFI
1201 DDLNMPEVDK YGTVQPHTLI RQHMDYQHWY DRQKLTLKDI HNIMFVTCMN PTAGSFTIDS RLQRHFAVFA LSFPSIDDLK
1281 HIYSSLLGQH LHNPNQKFKL AVIQFADKLL ATALSVHIRM QAEFLPTAIK FHYIFNLRDM SNLFQAVLMA SSDCISSPAV
1361 FLRVYMHEAS RVYGDKLISL AEQEAFQRIL KEQALQHAQV RNYFWRDDFC MYQVTVFLKL KPRIYCHFAE GIGDPKYNEI
1441 TNWEYLKRLL TEAMQQYNDL IANMNLVLFE DAMSHICRIN RVMEMPRGNA LLVGVGGSGK QSLSRLSAFI SSLEAFQIQL
1521 TKGYTSNDLR ADLATIYLKA GLKNIGSMFL MTDSQVPDER FLVLINDMLS SGEIPELFGD EEVENLIQSI APEVKGEGRV
1601 DTKENCWKFF IERARKNIKT MLCFSPVGST LRIRARKFPA LVNCTTIDWF MEWPQVALEN VSLRFISDLE DLEYRLPMSL
1681 LMAYIHTSVN HMSEVFKNNE KRFNYTTPKS FLELINLYSK LLMEKNQEVH LKIERLENGL EKLVSCAEKV TGLQDQLALQ
1761 SIIVAEKNKK ASDLILVVTK ETQIVSKEKI IAKDEERKCQ IIEEDVRVKQ QMCEEDLKRA MPALEAAQAA LNTLNKTNLT
1841 EMKSFGTPPP AVAKVAAAVM VLLAKKGKIP KDRSWKAAKV SATGYVNAMM GTADVFLHTL VHYNKENIHQ EIVKAVQPYI
1921 KDPEFTPETV ITKSSAAAGL CAW**VINIM**KF HEVWMVVLPK KKAEAAAKAE LAASRAQLAA LDRKITALEV KLQELTEKYE

2001 KAVEEKNICQ AQEEKTRETI DLANRLVNGL ASENIRWRET VHNLKMQLIT LPGNVILITA FISYVGCFTR KYREELMERI
2081 WIPRLSYYKP RIPYTEGIDP LLLMTDDAQI AVWNNEGLPT DRMSSENATI LTNSDRWPLI IDPQLQGIKW IKNRYGASLQ
2161 VIRLGQKHYL DKLEQAISDG RIMLIENIGE TMEPVLDNLL GRNLIRKGKV VKIGDREIDF HPRFRLIIQT KLANPHYLPE
2241 IQAQTTLINF TVTRDGLEDQ LLAEVVKAER PDLENQK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.VINIM.K	Y	20.81	588.3305	156.4	589.4298	1	32.22	2664	1	1944	1948	
total 1 peptides												

tr|A0A224XPX1|A0A224XPX1_9HEMI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PIVEIIVSPV ISRSSLRLLD INWDVGEQWS KGDWVALYNV PPDLRINPLF KTEVRNSEGW TRTGVPEGRR FPENPNFNKV
81 CLGFWAAYWK AHLNTPVATS CLGTNPKWMG ESKKVMRNLK LKDMFIPGTH DSAAFHLAYS PFRETRYHKY VFAQDENILE
161 QLIHGARYLD FRIGNYNGVW WLNHGIVKVH PLQHVLEEIK LFLNNTQEII VMDLHAFPVG FRERETHQQL VNYLRKELGA
241 YMAPPWLSWN ANLGQLWDRN KRLVVAYNDR SIVAEHFDIL WWPVMQKWPD VRSLNAL**HSY FVGVF**NMFER KSRSSSLAWA

321 AMAELTPDVW GVISDKYGGL RNLAYAVNHN VTQWFRDDWG SLCNAVAVDF IRSTGIVDAA IRWNVRKATR SNCDP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.HSYFVGVF.N	Y	20.79	954.4599	-88.5	478.1950	2	29.10	2301	1	298	305	
total 1 peptides												

tr|W5J800|W5J800_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFGSHSECVK EEWQSWWSGS GSAGGYSFMH PNYERPATSG GHTSVEDANR ITEGIPKKLY VPQHKEKCPS LTHRGGTPVQ
81 KTSFRAKDIT REFTAGIKER CMIPVINCQA VTSVLDPVTG HISTVLTTTA SPSQQAPASQ QQQQQQQPLL GGDTVTSQTS
161 KKPSYLNLAC CVNGYSNLTT YDSKLRQDIN KSREVSPSRP IIATLHYNRT ESSGTGGGTG HLLTAPTLSY VSMNNTINNN
241 YSGSTVGGTG QLSLAGSRMF KLNGSATSNG VGRLRGMNGT ANGVGGGGAV DVTDNAACAL FNGNGSFAGS GLRSKVISSQ
321 SQISSITRDD PSQMTPKKSF IQQRVEKLYG ATEGVVINKQ IYSNSERKYL YNIANENNGT TTNGLNSTTT SAHTGKGHVP
401 VLNGSACGAK NGSTNLTNGG THSRIVDENN KLIEGDEQSQ DDADVEALPV LRHLRPEFRA QLQIFSPKKI PKPSPSRSST
481 TTAAVNSGSV VHHTNGSHCG SSVEETLYSQ TQSNTTTTGQ YSSLESNLSD KRQEEYSLEQ LSGETVRLSI TTNGTMSTTT
561 TTTEKSIESS SSEYHHYQET ISHHGNDTST LQHTVTDPSE KIVSSLPVVV PSPSAAGAAD VDVSSRQQAE SLVSVATANS
641 ATVPVDIVGQ QQEETPTASV SCGVLENDIQ QNSVAEQQEG IYGNDSRYIE SKVSASDKKE ASADGSVNGG DILNCDIPSV
721 EQKRTVEENS MHTAMNGVGG VNTTMAADLE GITSSGKDIT AKTTTAVATS NGNSVSSHNN INNNNNHELD GNYFLQILRN
801 EQNRLQTMAT EVENEMQQLK SNGVVLCEDI NGYLLVAIGK ARLLCSQKMK QFEGLCYTNL NQSPDEKFQT TGEDLRGFWD
881 MVMLQVNDVD ATYAEIDTFR KNGWKKPVIK SPPVSVRNGA NRTTKLVKRP YKTATATTNG STNGASTGST TSAVNDGESK
961 KASAALAAAK REAQRKQLLE MKRKQKLANG QNGLQAVEIF TPTVLTSDDG EAAGL**SSSAG ASTTTL**VDTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.SSSAGASTTTL.V	Y	20.57	981.4615	852.3	492.1562	2	30.36	2444	1	1016	1026	
total 1 peptides												

tr|B4QZJ2|B4QZJ2_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKCVFLILAA LGLSVAEGST YDHFRLPTAL RPQRYDVRLL TQLENPDDFR FNGTVKIQIE VLQNTHNITV HSKDLTIDDT
81 DVTLSQIGGE ATTENCITST AVNPTHDFYI LNTCKELLAG QVYELSLPFS AKLQDQLAGY YRSSYVDTVA NETRWISVTQ
161 FEPASARLAF PCFDEPGYKA SFAITLGYHK KYTGLSNMPV KETRPHESIP DYVWTAFEES LPMSTYLVAY SLNDFSHKPS
241 TLPNGTLFRT WARPNAIDQC GYAAEFGPKV LNYYEELFGI KFPLPKVDQI AVPDFNAGAM ENWGLVTFAE NALLYSPEYS
321 ALEAKQATAN IVAHELAHQW FGNLVTMKWW TDLWLNEGFA TYVASLCVED IHPEWRTLQL ESMSNLLTIF RKDSLESSHP
401 ISRPIEMTSQ ISESFDEISY QKGSSVIRMM HLFLGEEAFR TGLNHPKTIQ DLPGPDQWVI FNNQLSAPYK VNYDAQNWKL
481 LIETLNSEDY QSIHVVNRAQ LIDDVMYFAW TGEQNYEIAL QVISYLERER ELLPWKSAFD NLKFVNGILR QSSNFKFFKS
561 FTR**RLITPIY** EHLNGINDTV ASEQQQDKTI LKAMVADWAC LFEVSDCIAQ ALSYYRSWRS EANPDEVNPV PLGFRDVVYC
641 TAIKHGSVED WDFLWTRYQK ANVATEKQII LDSLGCSQEV WVQQRYLERN FDGMGDIRKQ DSTSVFQAIA TSEVGFLLAK
721 KYLMDNVDSI SKFYHPQSES LSELLPPLCE QIFTRRDYDE FMNFLASSKE QLKDIEQTIS QSLETMLINV QWKERNYERF
801 TRAIKKYV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.RLITPIY.E	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	564	570	
total 1 peptides												

tr|A0A0K2SZ75|A0A0K2SZ75_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDNDPLYQYF EFDNPELSLG LEDSFFDFSN EIHGESDEFY SDDEDDLGSY HYDDHYWRCG DGKQLFLKVK DSNVAESSVF
81 SQLENPESKE WHYEALFFLL EELETFFLTW KRRTTHSFTI HLKSDNENTT GSDTDEERPQ KSLITNAALS KRKYCESTRI
161 FYSIFPKYDQ FYQVYREIQG IKNRILDIRF ALFLSSIPSD IVRQLPDELW LKIWRFSANP RDTIALNYQP YFQETTVLVE
241 KNRLSQLFLS VFRLHKIMYK ILFTFLLKHP PMQEMQMYSD TSMNIIAGLL WCHFYDIKRN LSRLNDLDST LKKRNEVMDL
321 KTKMNHGIFA FETVNLHGNF LCDVEQVGIG DSFFMPESQS PVWNASNVFF PNQHLNGTFL FLQKYISGTD IFIRFVVWNA
401 LSNSLEAIIY THILLVDYIS CCEYGYNLIS FCGQDVAITL PSLTSDNLIF FTYKWNLSLT NEEQQELQPD SSPVIKEFRV
481 EPNSFKYKPN SVSQAIISAN GAQLTVIMYA IDNEFSKLFV YKDSKKVYFT ESFPQKSCIK DAKGDKILII SKGGDHGNVI
561 QLFDLSQRKI LYTYVADNVA DLCRSSVSAL FDDDPDLHRF IIYTHNKRYY LVIDYSKSGD PIIVREGYIS SEVDDCLHES
641 LTFYKDMLFF IEKGTQLQDQ YQYYIMFFDF KST**RILTPIY** HEESSSVYPR VETYFAETKL IFFIAKDKLS FCKNRKTFVY
721 LDFTADRASS VLKELEYLNS AN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.RILTPIY.H	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	674	680	
total 1 peptides												

tr|Q9VAM2|Q9VAM2_DROME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKCVFLILAA LGLSFAGEGS TYDHFRLPTA LRPQSYDVRI LTQLENPDDF HFNGTVKIQI EVLQNTHNIT LHSKDLTIDD
 81 TEITLSQIGG EETTENCITS TAVNPTHDFY ILNTCKELLA GQFYELSLPF SAKLQDQLAG YYRSSYVNTV ANETRWISVT
161 QFEPAAARLA FPCFDEPGYK ASFAITLGYH KKYTGLSNMP VNETRPHESI PDYVWTSFEE SLPMSTYLVA YSLNDFSHKP
241 STLPNGTLFR TWARPNAIDQ CDYAAELGPK VLKYYEELFG IKFPLPKVDQ IAVPDFSAGA MENWGLVTFA ESTLLYSPEY
321 SSQEAKQETA NIVAHELAHQ WFGNLVTMKW WTDLWLNEGF ATYVASLCVE DIHPQWRTLQ LESMSNLLTI FRKDSLESSH
401 PISRPIEMTS QISESFDEIS YQKGSSVIRM MHLFLGEEAF RTGLKLVLES VPKTIHDLPG PDQWVIFNNQ LSAPYKVNYD
481 AQNWKLLIET LNSEDYHSIH VVNRAQLIDD VLYFAWTGEQ DYEIALQVIS YLERERELLP WKSAFDNLQF VSGILRQTPN
561 FRFFKNFTRR LITPIYEHLN GINDTVASEE QQDKTILKAI VADWACSFEV SDCVTQALSF YRSWRSEANP DEVNPVPLGI

641 RGVVYCTAIK HGCDEDWDFL WTRYQKANVA TEKQIILDSL GCSQEVWVLQ RYLERNFDGM GDIRKQDSTS VFQAIADSEV
721 GFLLAKKYLM DNVDSISKFY HPQSESMSEL LPPLSEQIFT QRDYDEFMNF MASSKDQLKD IEQTISQSLE TMLINVQWKE
801 RNYERFTRAI SKHF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.RLITPIY.E	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	570	576	
total 1 peptides												

tr|A0A1S3D1G5|A0A1S3D1G5_DIACI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAATPGLLSH LLLTLHATSG DVANVEVLLE ALMSLVSHAT TVKEMLAKGG YLFLLDLLCN SSQYQLRVRA AELLARLCND
 81 KLSGPRVKLA LDHFLPPTLT DSLREAPASS IGLFDSEQEN PELLWNQNQR VQLMSNVRVM CQQLYQSIRA NPLAQTTPLP
161 PPPPIMNTRE IIVGGVYLRL FALNTGWNLR KPKHFLSGLL DEGLRVMGAT PLDTPLLDLI SKCLLGLLQA QPNLIDLVPS
241 LGHIPRLCCQ LSSSPLPVSK SIVATLHILS LSEACVGSMS QVDCIGPIKY VLTSHQSLLS LTAETLARIF AAKKDKIVKQ
321 AIDADLISTL LNLLSGQGGL ESCDNASTVK AHIVKALKSM AQSAMYGGFV SATLDKSSVW SAYKSQNHDL FIGSSQSNAY
401 LTGVPATAGY LTQGNTSMPS SKKWRLLTPL YLSL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
W.RLLTPLY.L	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	425	431	
total 1 peptides												

tr|A0A182RGI7|A0A182RGI7_ANOFN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MNDAGSENES SSIAGYNDRV PGTTVQNAIN SHVQREYHVE IVKDMAIEKM KQKMHEIVDR MGKDVEKELN FAMDDMFSEV
 81 KQCNLNNYER KQLYNGKSSN GTDAQRQNST LNGKLPIKVF RARNSLLTDM LEIRHIKTIY HIFIVMLIIL FLNTVVHDFV
161 GTGSINLGLR PIIAGFGKFH IAVMLWCCMQ TSNFLLYPCF RMWAAKRNNY NPGSAGQKCW DWTAIVLFIL YQWGFFFAAI
241 ASHVWFDLPP ATGVAYLMEM VRFMMKSHAF VRSSAPKALT SDKNEADFES IHADTSCRLP PFSKYVYFMF APTLVYRDDY
321 PRTRTIRWRV VARHALEMVG TVFFLSFILE RLLTPLYENF GTAQISSGNF VNSLFCSLLP GTLFSLCFFY CSLHSCMNIV

401 AELTRFADRM FYRDWWNEST FNEYIRSWNI VVSDWLYTYL YKDCVEYVFR NCRLLAMVIV FTVSAAFHEI ILSFTFRFFY
481 PVMFVQFEFV GILLLVITQR MGKDTGNFLL WLALAIGNGL HLSLYSMEYY ARRNCPDVGK SLVDYLVPVS WFCNGISHNP
561 NWTITAPWNL Q
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.RLLTPLY.E	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	351	357	
total 1 peptides												

tr|B4QZJ4|B4QZJ4_DROSI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MKCFLLLVLV IGLDLSSANS IPSYNHYRLP TALRPQKYYL RILTLLESPD DLRFVGNVQI VIEALKNTRN ITLHSKNLTI
 81  DESRITLRQI SGASNKDNCV SSTSVNPTHD YYIMHTCEEL LAGNVYKLGL PFSADLTRQL FGYYLSSYKN PVTNKTRWLS
161  ATQFEPSFAR KAFPCFDEPG FKASFVVTLG YHKQFKAISN MPVREIRKHE SLQNYIWCEF QESVPMSTYL VAYSVNDFTF
241  KPSTLPNGAL FRTWARPNAI DQCNYAAEFG PKVLQYYEEF FGIRYPLPKI DQMAVPDFSA GAMENWGLVK YRESTLLYSP
321  NHSSLADKQD LANVIAHELA HQWFGNLVTM KWWTDLWLNE GFATYVAGLG VQKIHPEWDS RDKSSLVALM ASFRLDSLVS
401  SHPISRPIRM VAEIEESFDA ISYQKGSAVL RMMHLFMGEE SFRTGLKEYL KLYAYKNAEQ NNLWESLTTA AHQNGALAGH
481  YDINTIMDSW TLQTGYPVLN ITRDYSAGTA EITQERYLRN SQIPQADRVG CWWVPLSYTS REENDFNTTA PKAWMECSST
561  DEGVPTIIDH QAGPDEWLIL NIQLSTPYKA NYDARNWKLL IDALNSKEFE SIHVINRAQL LDDVLYFAWT GEQDYETALQ
641  VTNYLRRERD LIPWKSALDN LKLLNRILRQ TPNFGSFKRY MKRLLTPIYE HLHGMNDTFS SMPQQDEVLL KTTVVNVACQ

721  YDVSDCVTQA QAYFRRWRAE ANPDENNPVP LNLRSTVYCT AIGQGTEEDW NFLWTRYRKS NVGSERQTIL STLGCSKEVW
801  ILQRYMEKSF DPKSAIRKQD SSLCFQAVAS GQVGFLLAKQ YFIENVELIH KYYYPQTRTM SRLLTPLSEQ VSTLSDLKKF
881  RSFANDSRQL LKGIRQAMQQ SLETMLTNVQ WMDWNYHQFS RTIRRHL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.RLLTPIY.E	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	683	689	
total 1 peptides												

tr|B4HZ86|B4HZ86_DROSE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MKWFLLVVLV ISLDLSSANS ISSYNHYRLP TALKPQKYYL RILTLLESPD DLRFAGNVQI VIEALKNTRN ITLHSKNLTI
 81  DESRITLRQI SGASNKDNCV SSTSVNPTHD YYIMHTCEEL LAGNVYKLGL PFSAHLTRQL FGYYLSSYKN PVTNKTRWLS
161  ATQFEPSFAR KAFPCFDEPG IKASFVVILG YHKQYKAISN MPVREIRKHE SLPNYIWCEF EESVPMSTYL VAYSVNDFTF
241  KPSTLPNGAL FRTWARPNAI DQCNYAAEFG PKVLQYYEEF FGIRYPLPKI DQMAVPDFSA GAMENWGLVK YRESTLLYSP
321  THSSLADKQD LANVIAHELA HQWFGNLVTM KWWTDLWLNE GFATYVAGLG VQKIHPEWDS RDKSSLVALM TSFRLDSLVS
401  SHPISRPIRM VAEIEESFDA ISYQKGSAVL RMMHLFMGEE SFRSGLKEYL KVYAYKNAEQ NNLWESLTTA AHQNGALAGH
481  YDINTIMDSW TLQTGYPVLN ITRDYSAGTA EITQERYLRN SQIPKADRVG CWWVPLSYTS REENDFNTTA PKAWMECSST
561  DEDVPTIIDH QAGPEEWLIL NIQLSTPYKA NYDAKNWKLL IDTLNSKEFE SIHVINRAQL LDDVLYFAWT GEQDYETALQ
641  VTNYLRRERD LIPWKSALDN LKLLNRILRQ TPNFGSFKRY MKRLLTPIYE HLHGMNDTFS SMPQQDEILL KTTVVNVACQ

721  YDVSDCVTQA QAYFRRWRAE ANPDENNPVP LNFRSTVYCT AISQGTEEDW NFLWTRYRKS NVGSERQTIL STLGCSKEVW
801  ILQRYMEKSF DPKSAIRKQD SSLCFQAVAS RQVGFLLAKR YFIENVELIH KYYYPQTRTM SRLLTPLSEQ VSTLSDLKKF
881  RSFANDSRQL LKGIRQAMQQ SLETMLTNVQ WMDWNYHQFS RTIRRHL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.RLLTPIY.E	Y	20.31	874.5276	62.9	438.2986	2	28.71	2256	1	683	689	
total 1 peptides												

tr|A0A1I8MW53|A0A1I8MW53_MUSDO

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 PERIRLRDSH YKNALHYCAA QSVARTGDLV AAASIAVAAP ELLESADEDG FTPLHLAVIQ GNLAMVNLLL ANKADVNAVD   C Carba
                                                  127
                                                   C
  81 KEGHSVVHWA TVCGEVAALR AVLAAGANVT TPDINGGSPL HYAAQMCGAT YEGKLSQASS HKLALEILGI LLAHPQCSVD
                                                   C
 161 VEDKDGRQPL LWAASAGSAK AILALVKAGA RVETADKDGL TALHCAASRG HTECIDTLIS LCGAPTDLID SNGCTALHYA
 241 VTLGHADATS RLLDFEADPN RQDRKGRTPA HCGCAKGQFE TVKLLKERNA NLWLRNAKGD LPLHEAAASG RRELVEWLLE
 321 QRPKQVNTTS NDGRSLLHIA AYNDYTDMCK LLIDYGADIN AVYRNSKGIV ITPLDCSLQK GHRSTAKFLQ SHGCLPAGKL
 401 KLAARRPNPF TQPPMEAVKP LQYVEKEEIH DLSNSKKYVV YLKRSESDGA EDGNCSCSEQ TYRREQRYAH ICHRHRKGKG
 481 RHLRRRTSSC GDPKESDHEC SGMCRSKSNI EIRRRKSRER YLSSSEWEDD EDDSDSCENC CYHKRQKQRV LHKKRSISNK
 561 RSKDAIDSDG KHEGGGIEEA QAKAAQKSGD LEVRESDQSP EALIVPEDAA KQNTAEARGK GEEQPESTEQ VFSRSASPTK
 641 PSVPSTPTTA VKEGTFIKTP PAPEEEADTS ALISGAEFTD DDENASKSIV TEVQVHHPAE DEGNTSEKPE RIAIDAQEKE
 721 ESTEKAPLEE EVAKQVEEIV DTATAIAETA TAPPLAPETS TDAEEQQKAM EEKAIEAEES QPQEQKVGTT GQTDGVQPQE
 801 TSEDLGKPSK ENMETNLETP VQANQTSASP LPQTSEAHEI HDIPPQPEQP NQEEEKETHT EAAADKPSET TASNPQTTSN
 881 DLPPQSNAAN AEEAHKISSK QKTNEEERDD EDLDERPHPV REQESRRSFT LLPSDSAEDE PAMEVQKEAL RRKSSFQVLK
 961 SDDSVIEVDD SNSARDEVEM SDSTVFKVLT SPQTQLFEAD SNRSEEVTLQ DDEHEDEDET QTQKRFRPQD EPISPYDYAT
1041 GRKRRLKKRV KSGTKSRSNW QRTEAEAAEM QQNTRDQDSG FEPSPRTLKT KIPTPRNIYT AHLPRRPLYT TLDGRSCSSR
1121 LENRKAGDKG ACDMTAVTRS IQRNIRRYYM ERKIFQHLLE LKSLQIRSNK LNEAVLVKRA VDDYHKSCAA LGGETGTRLR
1201 RYNFSEYTFK NFELFLYETL KALQKPGTYN FQNINEVYDE AERRLSPDYN SYEKALQCTT RTHRCLHAAH AYTGIPCAAY
1281 IPMMNHHTMP KFGFGPYKKT GVGSFYLPKI LTTGTGCGGK VSLELSHGKS KQLISLPSDK LDSNKRYFVT FTVKETEKAA
1361 ASAAAGVGAG NCEGKNTADG CSGDVAGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
M.C(+57.02)GATY.E	Y	20.19	570.2108	2039.4	572.3810	1	32.60	2708	1	127	131	Carbamidomethylation
total 1 peptides												