Summary

1. Notes

2. Result Statistics

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

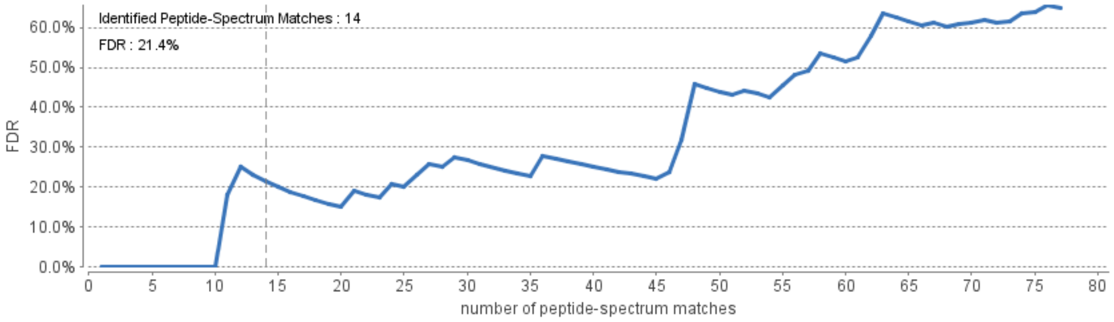
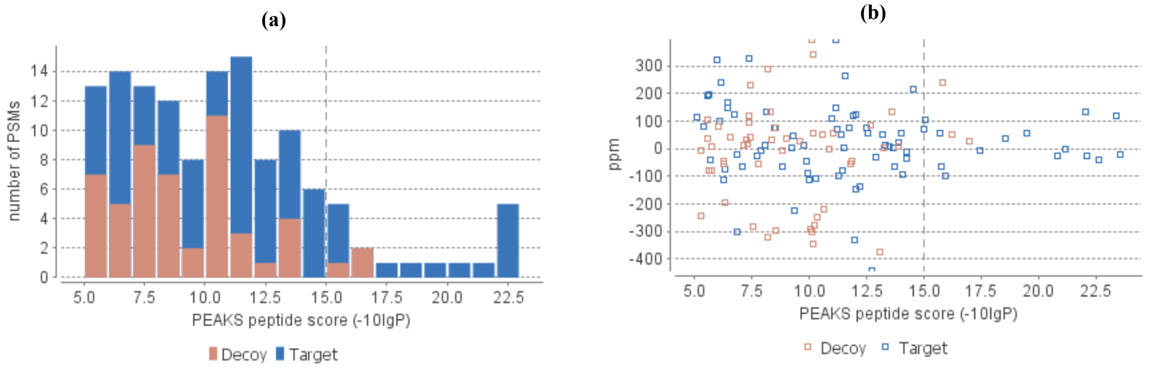
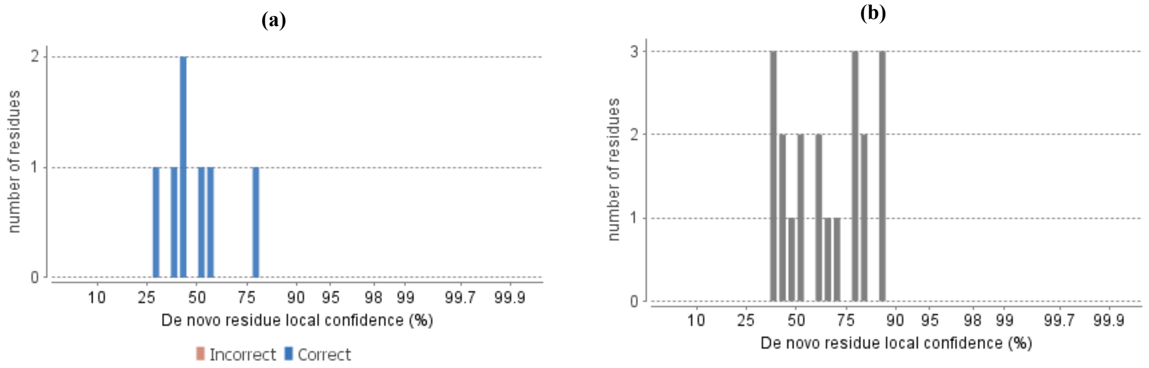


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(a)

(b)

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


(a)

(b)

Table 1. Statistics of data.

# of MS Scans	0
# of MS/MS Scans	307

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	14
Peptide Sequences	13

Table 4. PTM profile.

Name	ΔMass	#PSM	Position

Protein Groups	6
Proteins	39
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 39 (=1);
FDR (Peptide-Spectrum Matches)	21.4%
FDR (Peptide Sequences)	23.1%
FDR (Protein)	2.6%
De Novo Only Spectra	4

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.

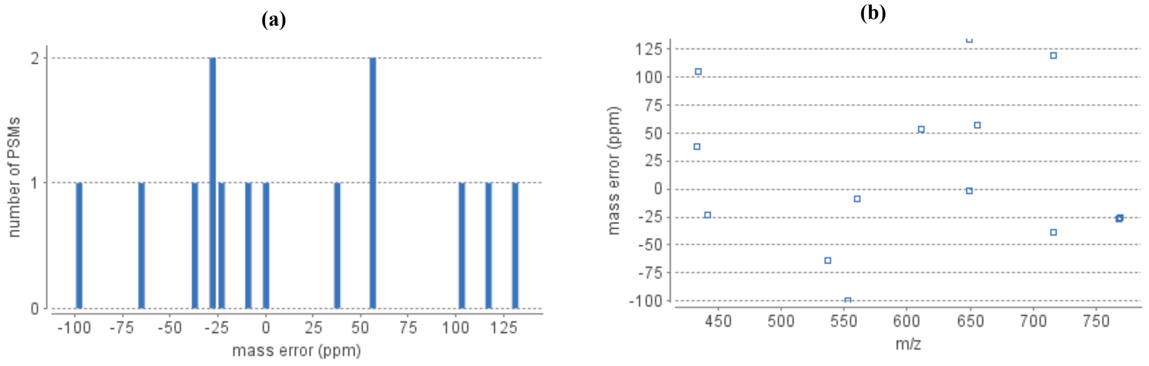


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
IT-TOF	0	0	0	0	13

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
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: 37
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_1.mgf
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: 3D Ion Trap
MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	4	tr|A0A0L7LEM8|A0A0L7LEM8_9NEOP	23.54	1	1	1	N	105320	Sterile alpha and TIR motif-containing protein 1 OS=Operophtera brumata GN=OBRU01_09756 PE=4 SV=1
2	2	tr|A0A0M8ZN23|A0A0M8ZN23_9HYME	23.40	2	1	1	N	35683	Cysteine and histidine-rich domain-containing protein OS=Melipona quadrifasciata GN=WN51_08722 PE=4 SV=1
2	3	tr|A0A0K2UTD0|A0A0K2UTD0_LEPSM	23.40	1	1	1	N	61169	Bestrophin homolog OS=Lepeophtheirus salmonis PE=3 SV=1
4	5	tr|K7J505|K7J505_NASVI	22.61	1	1	1	N	141606	Uncharacterized protein OS=Nasonia vitripennis PE=4 SV=1
5	6	tr|A0A0P5PMM1|A0A0P5PMM1_9CRUS	22.09	7	1	1	N	10537	Uncharacterized protein OS=Daphnia magna PE=4 SV=1
5	7	tr|A0A0P6HUU9|A0A0P6HUU9_9CRUS	22.09	4	1	1	N	16290	Uncharacterized protein OS=Daphnia magna PE=4 SV=1
5	8	tr|A0A0P5ZY29|A0A0P5ZY29_9CRUS	22.09	4	1	1	N	19499	Uncharacterized protein (Fragment) OS=Daphnia magna PE=4 SV=1
5	9	tr|A0A0P6CN45|A0A0P6CN45_9CRUS	22.09	3	1	1	N	20689	Uncharacterized protein (Fragment) OS=Daphnia magna PE=4 SV=1
5	10	tr|A0A1Y1MQ48|A0A1Y1MQ48_PHOPY	22.09	3	1	1	N	23985	Uncharacterized protein OS=Photinus pyralis PE=4 SV=1
5	11	tr|A0A1Y1MNG8|A0A1Y1MNG8_PHOPY	22.09	3	1	1	N	27379	Uncharacterized protein OS=Photinus pyralis PE=4 SV=1
5	16	tr|T1L0D8|T1L0D8_TETUR	22.09	1	1	1	N	53600	Uncharacterized protein OS=Tetranychus urticae GN=107369126 PE=4 SV=1
5	18	tr|A0A195EUT9|A0A195EUT9_9HYME	22.09	1	1	1	N	64817	Ecdysteroid UDP-glucosyltransferase OS=Trachymyrmex septentrionalis GN=ALC56_13778 PE=4 SV=1
5	41	tr|A0A151WPW6|A0A151WPW6_9HYME	22.09	0	1	1	N	148791	Ecdysteroid UDP-glucosyltransferase (Fragment) OS=Trachymyrmex zeteki GN=ALC60_11023 PE=4 SV=1
1	12	tr|A0A2A3EFD7|A0A2A3EFD7_APICC	22.04	2	1	1	N	33838	Hemolymph protein OS=Apis cerana cerana GN=APICC_01024 PE=4 SV=1
total 39 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	13	tr|A0A0P5PCC8|A0A0P5PCC8_9CRUS	22.04	1	1	1	N	47674	Putative 116 kDa U5 small nuclear ribonucleoprotein component protein (Fragment) OS=Daphnia magna PE=4 SV=1
1	14	tr|A0A0P5UGL7|A0A0P5UGL7_9CRUS	22.04	1	1	1	N	48004	Putative 116 kDa U5 small nuclear ribonucleoprotein component protein (Fragment) OS=Daphnia magna PE=4 SV=1
1	15	tr|W5J9B5|W5J9B5_ANODA	22.04	1	1	1	N	47006	Uncharacterized protein OS=Anopheles darlingi GN=AND_009030 PE=4 SV=1
1	17	tr|A0A0A9WTJ7|A0A0A9WTJ7_LYGHE	22.04	1	1	1	N	57678	Homoserine kinase OS=Lygus hesperus GN=thrB_8 PE=4 SV=1
1	20	tr|A0A0P5AC35|A0A0P5AC35_9CRUS	22.04	1	1	1	N	74883	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	21	tr|A0A0P5SVT9|A0A0P5SVT9_9CRUS	22.04	1	1	1	N	80592	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	22	tr|A0A0P5Z225|A0A0P5Z225_9CRUS	22.04	1	1	1	N	91653	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	23	tr|A0A0P6GST7|A0A0P6GST7_9CRUS	22.04	1	1	1	N	94169	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna GN=APZ42_020697 PE=4 SV=1
1	24	tr|A0A0P4WTI5|A0A0P4WTI5_9CRUS	22.04	1	1	1	N	94065	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	25	tr|A0A0P5IVR0|A0A0P5IVR0_9CRUS	22.04	1	1	1	N	94184	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	26	tr|A0A0P5TSN9|A0A0P5TSN9_9CRUS	22.04	1	1	1	N	94277	116 kDa U5 small nuclear ribonucleoprotein component protein OS=Daphnia magna PE=4 SV=1
1	67	tr|A0A2A3ERZ8|A0A2A3ERZ8_APICC	22.04	0	1	1	N	189462	Deleted in lung and esophageal cancer protein OS=Apis cerana cerana GN=APICC_07252 PE=4 SV=1
1	213	tr|Q7Q293|Q7Q293_ANOGA	22.04	0	1	1	N	475780	AGAP003967-PA OS=Anopheles gambiae GN=1278787 PE=3 SV=5
6	32	tr|A0A0C9QED2|A0A0C9QED2_9HYME	20.81	2	1	1	N	34481	ZNF512B_1 protein OS=Fopius arisanus GN=ZNF512B_1 PE=4 SV=1
6	34	tr|A0A1D2MGM0|A0A1D2MGM0_ORCCI	20.81	2	1	1	N	45605	Putative zinc finger protein OS=Orchesella cincta GN=Ocin01_14551 PE=4 SV=1
6	36	tr|A0A0C9RGU6|A0A0C9RGU6_9HYME	20.81	1	1	1	N	44691	ZNF512B_4 protein (Fragment) OS=Fopius arisanus GN=ZNF512B_4 PE=4 SV=1
6	37	tr|E9IFI6|E9IFI6_SOLIN	20.81	1	1	1	N	44260	Uncharacterized protein (Fragment) OS=Solenopsis invicta GN=SINV_16067 PE=4 SV=1
6	49	tr|A0A0P4ZHG8|A0A0P4ZHG8_9CRUS	20.81	1	1	1	N	75254	Clip-domain serine protease OS=Daphnia magna PE=3 SV=1
6	54	tr|A0A0N7ZRG5|A0A0N7ZRG5_9CRUS	20.81	1	1	1	N	79723	Clip-domain serine protease OS=Daphnia magna PE=3 SV=1
6	55	tr|A0A0P5TVI3|A0A0P5TVI3_9CRUS	20.81	1	1	1	N	80185	Clip-domain serine protease OS=Daphnia magna PE=3 SV=1
6	56	tr|A0A0P6E702|A0A0P6E702_9CRUS	20.81	1	1	1	N	80167	Clip-domain serine protease OS=Daphnia magna PE=3 SV=1
6	59	tr|A0A0P6C0G6|A0A0P6C0G6_9CRUS	20.81	1	1	1	N	86960	Clip-domain serine protease OS=Daphnia magna PE=3 SV=1
6	60	tr|A0A212ESI2|A0A212ESI2_DANPL	20.81	1	1	1	N	93715	V-type proton ATPase subunit a OS=Danaus plexippus plexippus GN=KGM_208959 PE=3 SV=1
6	99	tr|A0A0Q9WN59|A0A0Q9WN59_DROVI	20.81	0	1	1	N	178848	Uncharacterized protein, isoform B OS=Drosophila virilis GN=Dvir\GJ20346 PE=4 SV=1
6	107	tr|B4LSM1|B4LSM1_DROVI	20.81	0	1	1	N	188625	Uncharacterized protein, isoform A OS=Drosophila virilis GN=Dvir\GJ20346 PE=4 SV=1
total 39 proteins									

tr|A0A0L7LEM8|A0A0L7LEM8_9NEOP

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVIVLLQMVS STTSSSAASS QRIHNSSQRL QHMATSEMKA SSMKSDLTEL KSSISEMKNL SNTAAKNFGQ RLRSSMENIV
81 DQDDMGDRHL PDIRDLSDMG DMGDISDMNE LQGDGPLVTF PESDTPPPIS DKPSLMSGSS AVVGSNAANE LKYSAARVTS
161 ASSTRVVADG YSASRSAANS ARMRRLQHGD LQYAERSAAG ASHRLLQAEG LTAEQNAAYL QEQRSLKAGE VTAQEANNMT
241 SSSSRLQTEA FSAEKKAMAS AQARQTVTST GMFSHKEHSS VAHSNMTISS KNLSTKSTLL SSQMSQLLNG TIKPGDEDLT
321 NLTFEDLDKL NANSNQKDVD MAIQKYSSRM NAFITSIKNN QIDMKNASIH FNKLNEMLRR AWAVPTYGHE LGYSLCSTLR
401 TTGGLDILMA NCLESGNPDL QFSSAKLLEQ CLTTENRAHV VENGLEKVVN VACVCTRQAN SVDHSRIGTG ILEHLFKHSE
481 STCGDVIKLG GLDAVLFECR KNDVETLRHC ATALANLSLY GGAENQEAMI KRKVPMWLFP LAFHNDDNIK YYACLAIAVL
561 VANKEIEAAV LKSGTLDLVE PFVTSHNPSE FAKSNLAHAH GQSKNWLKRL VPVLSSKREE ARNLAAFHFC MEAGIKKQQG
641 NTEIFREIGA IESLKKVASC PNAVASRYAA QALRHIGEEV PHKLSQQVPL WSIEDVREWT IGPEYTSYTY SMLNAGVDKE
721 SIRGLSDEQL ENECRIGNSI HRLRILNAIR AYESSLPSKG EENMEKNLDV FVSYRRSNGS QLASLLKVHL QLRGFTVFID
801 VERLEAGKFD NNLLQSIRQA KHFLLVLTPS ALDR**CKMDTE R**KDWVHREIV AALQSKCNIV PIIDNFEWPK AEELPEDMRA

881 VCHFNGVRWI HDYQDACVEK LESFLRGKSN LANRLEGPLR GRDVQTPGTA TIGRGPPNYQ RMASCESRGS DKAD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.CKMDTER.K	Y	23.54	881.3735	-23.2	441.6838	2	0.15	29	1	835	841	
total 1 peptides												

tr|A0A0M8ZN23|A0A0M8ZN23_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSQEENLLCY NRGCGKKFDP NNNKEGDCIY HPGYPIFHDA YKGWSCCNKK CTDFTEFLNI KGCAKSCHSN IKPAEPEKPV
81 IDKSKSNEVI QMIAQPCNNE PALPRPPLET LQVVL**TPNVS PT**LLEQIKGL TCNISENICE SKVQIGQSCK NNSCKATYSG

161 FASDDEICNH HPGTPIFHEG MKYWSCCQKK TTDFSTFLEQ PGCTQGKHTW ISKNTGKRVK CRMDWHQTGS FVVVSIYAKK
241 YQPDQSSIKL NPIRLTVDLL FIEGNSRYNL DLELRGKAEP GSWAKLDFPR ITEEIEENGQ NDENISAQVE AVDLSDL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.TPNVSPT.L	Y	23.40	714.3548	119.4	715.4474	1	0.42	217	1	116	122	
total 1 peptides												

tr|A0A0K2UTD0|A0A0K2UTD0_LEPSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTVSYAAKIS TVKVGVFFKL LFTWTGSVYK LIWFEFMAYL VLYFSISILY RFGLGEDGKK IFETLSIFCN THTTLIPLTF
81 VLAFYVSHVV SRWWDQYKTI PWPDGVAFKV NAYCRGKNKH QNDEIRSIRR NVVRYTCAAI IETLRMVSCK VKKRFPTMNH
161 LVEAGILTDK EVKMIENAHK KTTYLEYSYW VPLYWASELI NQAYQKGYIQ QSKYVMDIHG ELTKIRTECG LILSYDWISF
241 PLVYTQVVTL ALNIYFGATL VGRQYLDPNK NLDGVGPDFI FPFFTSFEFF FYNGWCKVAE ALLNPFGEDD EDFDTNWMVD
321 RNIQLAYVMV DEIGRNPPDV EKDPYWDVGI PPELPYTVAS LDVRGAKQLE TGAHKLNVPL DLQETVDPAN LPDISFSGNK
401 LQRRISCVMD EVLSWASTPL TDRKCVHGLK RNNSQRSGTS FLSRRRRNSS INNNHLSSFR SVSLKSFDSF VN**TPNVSPT**S

481 SRKKSIIESR KLSTITTGSG LETVLEGKEI SLVNDDIRQN PNIEIIISEP NEN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.TPNVSPT.S	Y	23.40	714.3548	119.4	715.4474	1	0.42	217	1	473	479	
total 1 peptides												

tr|K7J505|K7J505_NASVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGQAQSMSSG ADGCDGCLGY DRLVPPAIPG IIESQPGLST GGVPGTYPGG TRPGTVTYPG GTPGTQTTGG GTITGGTGTG
81 PAVQIPGRMY IPGFIPGTQV GGTIPGTYPG GVQPATPPVG GGPGSQTTGG VQYPPGYYGG TVPGNQAGPG VPGTQIITSG
161 PSGQMPGGVV YQPGTQGGGD GPGAQLPGGL LYPSGTQVVG SGGPGTQTPG GVVYQPGIQV GPRGPGTQPS GGVLYPPGTQ
241 LGGGGPGTQF PGGVVYQPGT QVGGGGPGTQ PSGGVLYPPG TQVGGGGPGT QFPDGVVYQP GTQVGGGGPG AQLPGAVLYP
321 PGTQVIGGGG PGTQTPGGVV YQPGIQAGGG GPGAQAPGIV YQPGTQVGGG PGAPGGIVYQ PGTKTVGGGP GAQAPGVVYQ
401 PGTQVGGGPG APGGIVYQPG TQTGGGGPGA QAPGLIYQPG TQAGGVSGSE YPGGVTYPPG TQVVGGGGPG TQIPGIAYQP
481 ETQVGVGPGA QTPGGVVYQP GIQTGGAVLY PPGTQIGGGG VPGAQTPGIV YQPGTQAGVV GPGVQTPGGV YYPPGTPITG
561 SGGPGTQTGS VYQPGTQVGA VTPGTQSPGS GQGTVIGGTY PPGTQLVRGG TPGTSVYQPG MQLPGGTYLP GTQITGGVYP
641 PGKQVGGGTQ VPGGTVYQPG AQMPGGVVYT PGTQVSAGGS PGTQTGVSYQ PGAQIPGGGT YPPGTQVIGG TPYPPGKQII
721 DGVPYPPGTV IPGGGVYPPG TQVGGGVYSP GTQVGGGVYP PGTQVGGGVY PPGTQVGGGV YPPGTQVGGG IYPPGTQVGG
801 DIYPPGTQVG GGVYPPGTQI GGVAYPPSVV PSGQVTQPGI TPGLHVPGGV LIPGVTPGTQ FPGGVIPGTQ TGGVYPPGTS
881 GTGTTTYPGQ VPAGVTGPPV TGGEQKPIMR GDIPGTVLYP APQLETG**TPG GSVPT**IVPGG YPGLIPGQYP GGGTVLIPGQ

961 GPVVGVPGTT GVVGGGGQTV VTGQQAGGGT INAAADDGSD SQAISSVTQG EAGTQASATA EGRHGQGSAK SQVTGTYTGS
1041 GSFSAQAGTS DNTKSAQTQV SGGKDGAKSS AQGSGGLGKS QTQVELDSNS GATSTNAQSS GWNHGTNSQV QASSKGGMAD
1121 AQANGEGQTS SQAQIGFQPY VSDRKENPAQ ERRDKPFRGG GTASAQSGTF RGQSQSQLQG SFHYGITYTG AAQAGSGSGA
1201 AALRKPFNFS NTDPELFKPF KLEITTEAPR EQLQGESSNS RQTVIAITQR NAQAEKKNNN RPDRPPYEAN VDDYEEYEDE
1281 EYGERQTTAP SARQTMRVVT DGEYDVSVRQ EESTEESTSR SLPGYIAPAT HRAKVTSVAG RKTIAQGDGR SQSQTVTIVP
1361 VSRTSTTSRA SSDTRSLKPA VSSTPKTNYV SVANSVAGKI DDKNPPGKKY EHRYYTKSST CGYFTFSCNV VYGANGRRKI
1441 CKPKMPTYAD GTPKC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.TPGGSVPT.I	Y	22.61	714.3548	-38.6	715.3345	1	0.42	216	1	928	935	
total 1 peptides												

tr|A0A0P5PMM1|A0A0P5PMM1_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQKKGGDKAV P**FYPPPF**RQK RKHLPACQQF FSFKKKKKEI EKEMKHFHSM QMFENVLWSV LLCVGSSPPP PFSIFIYSRW

81 TINMDSLSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.FYPPPF.R	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	12	17	
total 1 peptides												

tr|A0A0P6HUU9|A0A0P6HUU9_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQKKGGDKAV P**FYPPPF**RQK RKHLPACQQF FSFKKKKKXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
81 XKKKKKEIEK EMKHFHSMQM FENVLWSVLL CVGSSPPPPF SIFIYSRWTI NMDSLSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.FYPPPF.R	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	12	17	
total 1 peptides												

tr|A0A0P5ZY29|A0A0P5ZY29_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDNFPGPEA KKAPHVCSKM LSCLAKEKEK RWMRTHRAHK TPTSCIPTAA YSEQGEGKRG TFKVLSHLCN SLTTCSFVML
81 RKIKRMGRHA HTKVSETERK KEXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXRLNW GGISQLFKTI INPSRPIASH
161 S**FYPPPF**FLG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.FYPPPF.F	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	162	167	
total 1 peptides												

tr|A0A0P6CN45|A0A0P6CN45_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSDNFPGPEA KKAPHVCSKM LSCLAKEKEK RWMRTHRAHK TPTSCIPTAA YSEQGEGKRG TFKVLSHLCN SLTTCSFVML
81 RKIKRMGRHA HTKVSETERK KERXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXPTIRLNW GGISQLFKTI INPSRPIASH
161 S**FYPPPF**FLG VQVKRSEGGK K

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.FYPPPF.F	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	162	167	
total 1 peptides												

tr|A0A1Y1MQ48|A0A1Y1MQ48_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGVTSKILFF VIVFGLLNCG LSKPHHKRHA RSSHHANDPS KNPYQSLPGY PSQ**FYPPPF**S SPYGYQPMQM PPVYAPYPNP
81 YYMNMQYNPY MPMYQPYPAY FPNPYIQPYP YQHQFPTYPD PFAHIPAEII DVDSDFTIEN HKPKVEVESS QHVELPDSLQ
161 QPIKTSQVEE SATKVEVKST DETVKESGNK SEEIEKKNED KSIFNLFG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.FYPPPF.S	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	54	59	
total 1 peptides												

tr|A0A1Y1MNG8|A0A1Y1MNG8_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGVTSKILFF VIVFGLLNCG LSKPHHKRHA RSSHHANDPS KNPYQSLPGY PSQ**FYPPPF**S SPYGYQPMQM PPVYAPYPNP
81 YYMNMQYNPY MPMYQPYPAY FPNPYIQPYP YQHQFPTYPD PFAHIPAEII DVDSDFTIEN HKPKVEVESS QHVELPDSLQ
161 QPIKTSQVVT TKPLQTLITR TFNKNSKPVV NIQQSNLQEE SATKVEVKST DETVKESGNK SEEIEKKNED KSIFNLFG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.FYPPPF.S	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	54	59	
total 1 peptides												

tr|T1L0D8|T1L0D8_TETUR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMRPMFTQCL NSSMCPPQCP PGPNSGPPGP GPGSGPVLGP GSDP**FYPPPF** SPYNRRLNHN CTDLRIHELN KRLQNKPEEC

81 DNVFWDNLTT DFFEEDATLT LILCLEDGIK RFTIGRTLIP RYFRSLFEGG VTDLSFNLRN PKESYHNSLI TLDCEQCSMI

161 TYHGKFNVNK TPMGNFPPGV DSQQVKDQMH ITKETSVVVN TEGRLTLEFT NDDLMRIKSW LFNTRSYQEL VPRNLINMYA

241 QDPSALERFS KDITRQGFTN ATLNYLRLCL ILEPMQELMA SHKKFGLDPR DSLKQTLYAK WQKTVTDRPD SQRPVNKRRK

321 RKSSASNNAN GGGATGKKKN NTSISPGPPS FSLASQDVMV VGEPSMMGGE FGDEDERTIT RLENSQYDPN ASGVSNGLED

401 GDDFNSLSRA PGSGQGPVQG PNSGSGPGPG QQGNLGQPHG ANIPPTGWSG PGGPGSNSGP VSSNQDNRGN NQGGSGPQSS

481 QVDKKPSPLN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.FYPPPF.S	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	45	50	
total 1 peptides												

tr|A0A195EUT9|A0A195EUT9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKPVVEMIFW IACFVCTATP IETARILAII AIPSYSHHIA YQLLWTTLSR RGHKIVVLTT DPINDPSLTN LTEINFKSNY

81 NVVTKINFIE NMETHTWLST VNEQLWPVCN QITENIYKHP EVRKMYELNS DTKFDVVIVE TIKSPSLYAL AYRFNAPLIG

161 VSTLGLYNSN YYLLGAPVLP SHPSAWEMGD TTDFNLSLWQ RIKNFIRLWY HIYCTLNHFY SEQQAIAEKY LGKNIPDIRD

241 MERNISFVFQ NQQKVLSFVR PQTSNVLSFG NFQISKKLAA LPENLTEFIT DAPNGFIYMS LGTNVRISSL SKHVQSIFRD

321 VFASLPYKIL WKHDSELPNK PDNIYIAKWF PQQSILAHPN IKLFIYQGGI QSTEEAVYYT VPLLGLPVLA DQYTQVKKMV

401 SLGVAKHLNI MKLSRENLNE SIIDILYDEG YKKRMLKVKE LNEDKPYDVL EHVIWWIEFV IRHKGASHLR TSIAYDPCLF

481 LRLVPLSERL LFIIKTTLPG DYQKAIEKDI FSSSSALLCF LSFLHETRVS RGVIVFVPDN V**FYPPPF**PRS FLPRFTKGDS

561 L

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.FYPPPF.P	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	542	547	
total 1 peptides												

tr|A0A151WPW6|A0A151WPW6_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 NQPVYKTRLA LPEDYDNVMT FMCDAFYKDD PTMVNIGLNE EEPAPSLLQI MYDEIREGMT LIAEGEDECI VGAVVNAGSC

81 PWDPDKFVEF ARCCECGPTR DVIEFEAYVT GKPNLWERYC VLKIFECSYL AVRPDFRNQG IARKLVLDSW YLARDCGYRL

161 FRVDCNNRYI ARVADGFGWK RVCTIPFHKY VREDGGLVFK HIKEPHTEVQ IYIDRVKFCK DYCPPYKTCD KITSAPNNLT

241 CSKRLLIITP TPSYSHQIVF RVLCLALNKR GHEIVTLTPN ILNDTTITNY TEIDFGFIYE KIDDTDMSQT RWNLTQLAGL

321 KTRLLTLGHN IAEDALSHPD LTKYYANRTD MQFDAVIAEM IMTPAIYMLA HRFSAPLIGI MSMDLQNCHR FSLGSPVLPS

401 HSSNWELENL TGLNLPFWRR LMNFINTWWS IHSWFNSFAI KQQKIAEKYF GNNVPHITDV AKNMSLVLIN QEPLLAYARP

481 EIPNIVHFSG LHITKTPPSL PKNLKAFLDS ATNGFIYLSL GSNTKSKLLP KEILEIFANT FANLSYKVLW KFENDSFHVP

561 PNVFISKWTP QQGVLAHPNI KLFIYQGGLQ STEEAVHYAV PLIGIPFVFD QVYQVMKMVS LRVARYLDIV RLTRSELHDA

641 IIEVIDDKGY KDRMLALRAL TKDKPYDSLE NVIWWIEFVM RHNGAPHLRF NGVDIAWYQQ FDLDVIVFLT ITLFLVLCAI

721 LAIVGCVMKH KMKPVAEMTF WIACFVYIAT PIETARILAI IAIPSYSHQI PYRPLWTTLS QRGHEIVVLT TDPINDPSLT

801 NLTEINFKSH YELIGRLNFV KNIETFINWL SAVRTQMWSL CNEITENIYK HPEVRKMYEP NSDTKFDAVI VETVKSPGLY

881 ALAYRFNAPL IGVSTLGLYS GNYYLLGAPV LPSHPSAWEM ENTTDFNLSL WQRIKNFIRQ WYHIYCTLNH FYSEQQAIAE

961 KYLGKNIPDI TDMERNISFV FHNQQETLSF VRPQTSNVLS FGNFHILRKL AALPENLKEF ITDAPNGFIY VSLGTNVRIS

1041 SLQHVQSIFL DVFASLPYKI LWKHDSELSN KPDNIYIAKW FPQQSILAHP NIKLFIYQGG LQSTEEAVYY TVPLLGLPVL

1121 ADQNGQVNKM VSLGVAKRLN MMELSRENLN ASIIDILYDE GYKKRMLEVK ALNEDKPYDL LEHVIWWIEF VIRHKGASHL

1201 RTSIAHDSCL FLRLVPLSER LLFIIKTTFP GDYQKAIEKD IFSSSSALLR FLSFLHETRA SRSVIVFVPD NV**FYPPPF**PR

1281 SFLPRFTKSG SL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.FYPPPF.P	Y	22.09	766.3690	-26.8	767.3557	1	0.30	259	1	1273	1278	
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 IIQNI**TDSLL T**FVCYKEGDR 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	6	11	
total 1 peptides												

tr|A0A0A9WTJ7|A0A0A9WTJ7_LYGHE

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| 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	380	385	
total 1 peptides												

tr|A0A0P5AC35|A0A0P5AC35_9CRUS

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| 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 KKEE**TDSLLT** 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	245	250	
total 1 peptides												

tr|A0A0P5SVT9|A0A0P5SVT9_9CRUS

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| 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 MNYKKEE**TDS LLT**KLGIKLS 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	298	303	
total 1 peptides												

tr|A0A0P5Z225|A0A0P5Z225_9CRUS

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| 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 NYKKEE**TDSL LT**KLGIKLRL 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	277	282	
total 1 peptides												

tr|A0A0P6GST7|A0A0P6GST7_9CRUS

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| 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 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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 MNYKKEE**TDS LLT**KLGIKLS 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	353	358	
total 1 peptides												

tr|Q7Q293|Q7Q293_ANOGA

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| 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 WNNAQPTVTD SLLTWDTLLA 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	22.04	648.3330	133.6	649.4269	1	0.27	158	2	3209	3214	
total 1 peptides												

tr|A0A0C9QED2|A0A0C9QED2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKILFVFALL VAVAFAEEAE KKDAATESKA DETESSKKTE KRGILGLGYG YGYDIGGYDI GGGHGQSLHS SDYDVDSIGS
81 YGGGYHGDHH VKTVTVVKNV AVPYPVEKHI PYPVEKHVPY PVKVKIPVPA PYPVEKPVPY EVKVPVDRPY PVHVPKPYPV
161 TVEKPYPVPV DKPVPYEVKV PVDRPYPVPV EKPYPVPVKV PVPQPYTVHK HVPVPVEKPV PVPVKVP**VDK PYF**IEKEVPV

241 PVEKEVPVPV KVPYPVPVHV HHEEHHGHYG GEQHGDFGGG DLGGDHTGGY GGGYGGGYGG GHAGFQPSYG SEGGEYHH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.I	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	228	233	
total 1 peptides												

tr|A0A1D2MGM0|A0A1D2MGM0_ORCCI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDQNQPQLLH PCKFCDHKSA SKCNLYTHIK MMHE**VDKPYF** CKFCKTRFKT KTELDNHTEI HADKNPFPCD FCGKRYPRLV

81 ELNSHRLIHQ EKQLKCPVCS KMFRHKSSLN THILGHTGEK GFRCIICDKA FSQVGTLNHH YHSHTNEKPH FCTLCDESFA
161 RTTGLISHTK SKHPDFAKSK LNWKGPEKCQ LCGKECSNKG NLKIHMETHS NLKKFECQLC PRKFSQKASY HTHLRRHTGE
241 TPYKCVQCNK RFTELSGLRK HQFVHTGNKP FSCKYCKKAF IKPGILTTHL FKWHEKPIKC ALCKERFRDN DCFHAHLGDK
321 HSNQFLHFCV FCEKVFQSWI GFRNHMTTHT REKPEWCEFC DDCFDSNWRL KTHMQKKHSQ NFRKD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.VDKPYF.C	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	35	40	
total 1 peptides												

tr|A0A0C9RGU6|A0A0C9RGU6_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SQWLSATLKT HVSSRMKTKI ELALVALLAL SQSTWVYSEE ASASKKMDES SVEGESTVKK TEKRGLGHSY GDLGGGFGGG
81 YESHGHEEHV KTVTIEKKIP VPVEVTKHVP YLVEKHVPYE VKVGVPQPYT VEKHVPYPVK VFVKVPVHVP QPYTVEKKVP
161 YEVKVPVDRP YEVKVHVPQP YVVEKHVPVP VKVPVPQPYT VEKHVPYPVK VKIPVPAPYP VEKPVPYEVK VPVDRPYPVH
241 VPKPYPVTVE KPYPVPVDKP VPYEVKVPVD RPYPVPVEKP YPVPVKVPVP QPYTVHKHVP VPVEKPVPVP VKVP**VDKPYF**

321 IEKEVPVPVE KEVPVPVKVP YPVPVHVHHE EHHGHYGGEQ HGDFGGGDLG GDHTGGYGGG YGGGYGGGHA GFQPSYGSEG
401 GEYHH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.I	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	315	320	
total 1 peptides												

tr|E9IFI6|E9IFI6_SOLIN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LQIAIILVAV ATQVICAKDS SKVDSNKSSQ DVEAESTEKK TEKRGLQHSF GDLGGGGIEL HGGGGGGGGG GGGGYDSHEH
81 VKTVTVVKKV PVPYEVTKHV PYLVEKHVPY EVKVGVPQPY TVEKHVPYPV KVFVKVPVHV PQPYTVEKKV PYEVKVPVDK
161 PYEVKVYVPQ PYTVEKHIPV PVKVPVPQPY TVEKHVPFPV KVKVPVPQPY PVEKPVPYEV KVPVDKPYPV PVPKPYPVTV
241 EKPYPVPVEK PVPYEVKVPV DKPYPVPVEK PYPVPVKVPI PAPYHVHKPV PVPVEKPVPV PVKVP**VDKPY F**VEKEVPVPV

321 EKHIPVPVKV PVAVPVHIPK HHGDLGGYGG GGGGGGYGG GGGYGGGGGY GGYGGGGEGG DYGGGYSDGG GIDLHGGFSG
401 SSGGGGGGGG GGGGGGGGGG GYDSIHG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.V	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	306	311	
total 1 peptides												

tr|A0A0P4ZHG8|A0A0P4ZHG8_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFVWECVKTE GTPLGMCMER FMFGSCCAHD LDNNVVPKPS LSSMIATMAS NYPPPIVPKN ISSAATPSPP SILTTLITSV

81 VPARANSTNK TELETETTKP SSGQPLTMPT DTPTDATLSN ELAPTTSSGS STVTSSPSDG TTLLIDSKTS TTIATSSTQT

161 HVVESTTKPS GSQLTLGYIK LRPKPYRRTT TPRAAIPTVA TGITNQPLVS STVTKPINPT LATAPPIAPT INLLIPNNIV

241 NLVAVPVATS PTTAQSLITT IQLLTTLQHP DALVALTVPS SHLSLVTSTQ PNSSAPLIEL PDSSVNELNS TSDIESTIPS

321 ATNKP**VDKPY F**HHVTTGVLP TTEAESTEPQ STQSDSSTPS TVSPITTSFV TKPNIDVTEF IAVSASSTET VEVTSTSTES

401 SSRKPESNVT PTSHKNTTST ESTRKPTLAV TSLPSSYNIE CGVPPMLAEA TREERIVGGN NSKFGSWPWQ VSVRRTSFFG

481 FSSTHRCGGA LLNELWVITA GHCVEDLLVS QIRMRMGEFD FSSVQEPYPF VERGVNKKIV HPKYNFFTYE YDLALVRLEE

561 PITFQPNIAP ICLPATDESL IGQNGTVTGW GRLSEGGTLP SMLQQVTVPI VSNDKCKDMF LKAGRHEYIP DIFMCAGFEE

641 GGRDSCQGDI QIYQLDSRKR DVKNFTRTVN VIYEILGRVQ SMASKPKGTV CFKSFSIMLP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.H	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	326	331	
total 1 peptides												

tr|A0A0N7ZRG5|A0A0N7ZRG5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDFRFGMGLL LLSFLPLVFS ASQTQNNLTT PSYQISRKPC YVKGQEGTCM FVWECVKTEG TPLGMCMERF MFGSCCAHDL

81 DNNVVPKPSL SSMIATMASN YPPPIVPKNI SSAATPSPPS ILTTLITSVV PARANSTNKT ELETETTKPS SGQPLTMPTD

161 TPTDATLSNE LAPTTSSGSS TVTSSPSDGT TLLIDSKTST TIATSSTQTH VVESTTKPSG SQLTLGYIKL RPKPYRRTTT

241 PRAAIPTVAT GITNQPLVSS TVTKPINPTL ATAPPIAPTI NLLIPNNIVN LVAVPVATSP TTAQSLITTI QLLTTLQHPD

321 ALVALTVPSS HLSLVTSTQP NSSAPLIELP DSSVNELNST SDIESTIPSA TNKP**VDKPYF** HHVTTGVLPT TEAESTEPQS

401 TQSDSSTPST VSPITTSFVT KPNIDVTEFI AVSASSTETV EVTSTSTESS SRKPESNVTP TSHKNTTSTE STRKPTLAVT

481 SLPSSYNIEC GVPPMLAEAT REERIVGGNN SKFGSWPWQV SVRRTSFFGF SSTHRCGGAL LNELWVITAG HCVEDLLVSQ

561 IRMRMGEFDF SSVQEPYPFV ERGVNKKIVH PKYNFFTYEY DLALVRLEEP ITFQPNIAPI CLPATDESLI GQNGTVTGWG

641 RLSEGGTLPS MLQQVTVPIV SNDKCKDMFL KAGRHEYIPD IFMCAGFEEG GRDSCQGDSG GPLQIRGRDG KYFLGGIISW

721 GIDALRPISL EFVPEYPNLP TGF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.H	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	375	380	
total 1 peptides												

tr|A0A0P5TVI3|A0A0P5TVI3_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDFRFGMGLL LLSFLPLVFS ASQTQNNLTT PSYQISRKPC YVKGQEGTCM FVWECVKTEG TPLGMCMERF MFGSCCAHDL

81 DNNVVPKPSL SSMIATMASN YPPPIVPKNI SSAATPSPPS ILTTLITSVV PARANSTNKT ELETETTKPS SGQPLTMPTD

161 TPTDATLSNE LAPTTSSGSS TVTSSPSDGT TLLIDSKTST TIATSSTQTH VVESTTKPSG SQLTLGYIKL RPKPYRRTTT

241 PRAAIPTVAT GITNQPLVSS TVTKPINPTL ATAPPIAPTI NLLIPNNIVN LVAVPVATSP TTAQSLITTI QLLTTLQHPD

321 ALVALTVPSS HLSLVTSTQP NSSAPLIELP DSSVNELNST SDIESTIPSA TNKP**VDKPYF** HHVTTGVLPT TEAESTEPQS

401 TQSDSSTPST VSPITTSFVT KPNIDVTEFI AVSASSTETV EVTSTSTESS SRKPESNVTP TSHKNTTSTE STRKPTLAVT

481 SLPSSYNIEC GVPPMLAEAT REERIVGGNN SKFGSWPWQV SVRRTSFFGF SSTHRCGGAL LNELWVITAG HCVEDLLVSQ

561 IRMRMGEFDF SSVQEPYPFV ERGVNKKIVH PKYNFFTYEY DLALVRLEEP ITFQPNIAPI CLPATDESLI GQNGTVTGWG

641 RLSEGGTLPS MLQQVTVPIV SNDKCKDMFL KAGRHEYIPD IFMCAGFEEG GRDSCQGDSG GPLQIRGRDG KYFLGGIISW

721 GIGCAEANLP GVCTRISKFT NWILENVT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.H	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	375	380	
total 1 peptides												

tr|A0A0P6E702|A0A0P6E702_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDFRFGMGLL LLSFLPLVFS ASQTQNNLTT PSYQISRKPC YVKGQEGTCM FVWECVKTEG TPLGMCMERF MFGSCCAHDL
81 DNNVVPKPSL SSMIATMASN YPPPIVPKNI SSAATPSPPS ILTTLITSVV PARANSTNKT ELETETTKPS SGQPLTIPTD
161 TPTDATLSNE LAPTTSSGSS TVTSSPSDGT TLLIDSKTST TIATSSTQTH VVESTTKPSG SQLTLGYIKL RPKPYRRTTT
241 PRAAIPTVAT GITNQPLVSS TVTKPINPTL ATAPPIAPTI NLLIPNNIVN LVAVPVATSP TTAQSLITTI QLLTTLQHPD
321 ALVALTVPSS HLSLVTSTQP NSSAPLIELP DSSVNELNST SDIESTIPSA TNKP**VDKPYF** HHVTTGVLPT TEAESTEPQS

401 TQSDSSTPST VSPITTSFVT KPNIDVTEFI AVSASSTETV EVTSTSTESS SRKPESNVTP TSHKNTTSTE STRKPTLAVT
481 SLPSSYNIEC GVPPMLAEAT REERIVGGNN SKFGSWPWQV SVRRTSFFGF SSTHRCGGAL LNELWVITAG HCVEDLLVSQ
561 IRMRMGEFDF SSVQEPYPFV ERGVNKKIVH PKYNFFTYEY DLALVRLEEP ITFQPNIAPI CLPATDESLI GQNGTVTGWG
641 RLSEGGTLPS MLQQVTVPIV SNDKCKDMFL KAGRHEYIPD IFMCAGFEEG GRDSCQGDSG GPLQIRGRDG KYFLGGIISW
721 GIGCAEANLP GVCTRISKFT NWILENVT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.H	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	375	380	
total 1 peptides												

tr|A0A0P6C0G6|A0A0P6C0G6_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDFRFGMGLL LLSFLPLVFS ASQTQNNLTT PSYQISRKPC YVKGQEGTCM FVWECVKTEG TPLGMCMERF MFGSCCAHDL
81 DNNVVPKPSL SSMIATMASN YPPPIVPKNI SSAATPSPPS ILTTLITSVV PARANSTNKT ELETETTKPS SGQPLTMPTD
161 TPTDATLSNE LAPTTSSGSS TVTSSPSDGT TLLIDSKTST TIATSSTQTH VVESTTKPSG SQLTLGYIKL RPKPYRRTTT
241 PRAAIPTVAT GITNQPLVSS TVTKPINPTL ATAPPIAPTI NLLIPNNIVN LVAVPVATSP TTAQSLITTI QLLTTLQHPD
321 ALVALTVPSS HLSLVTSTQP NSSAPLIELP DSSVNELNST SDIESTIPSA TNKP**VDKPYF** HHVTTGVLPT TEAESTEPQS

401 TQSDSSTPST VSPITTSFVT KPNIDVTEFI AVSASSTETV EVTSTSTESS SRKPESNVTP TSHKNTTSTE STRKPTLAVT
481 SLPSSYNIEC GVPPMXXXXX XXSTRKPTLA VTSLPSSYNI ECGVPPMLAE ATREERIVGG NNSKFGSWPW QVSVRRTSFF
561 GFSSTHRCGG ALLNELWVIT AGHCVEDLLV SQIRMRMGEF DFSSVQEPYP FVERGVNKKI VHPKYNFFTY EYDLALVRLE
641 EPITFQPNIA PICLPATDES LIGQNGTVTG WGRLSEGGTL PSMLQQVTVP IVSNDKCKDM FLKAGRHEYI PDIFMCAGFE
721 EGGRDSCQGD SGGPLQIRGR DGKYFLGGII SWGIGCAEAN LPGVCTRXXX XXXXYFLGGI ISWGIGCAEA NLPGVCTRIS
801 KFTNWILENV T

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.H	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	375	380	
total 1 peptides												

tr|A0A212ESI2|A0A212ESI2_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGAMFRSEEM ALCQLFIQPE AAYTSVSELG EAGSVQFRDL NPDVNAFQRK FVNEVRRCDE MERKLRYIEV EVHKDKVNVP
81 AVKDMPRAPN PREIIDLEAH LEKTENEILE LSHNAINLKQ NYLELTELKH VLEKTEAFFA AQEEIGMDSL TKSLISDEAG
161 QQAATRGRLG FVAGVVQRER VPAFERMLWR ISRGNVFLRR AELDKPLEDP NTGNEIYKTV FVAFFQGEQL KSRIKKVCTG
241 FHASLYPCPP SNTERLDMVK GVRTRLEDLN MVLNQTQDHR QRVLVSVAKE LGSWSIMVRK MKAIYHTLNL FNMDVTNKCL
321 IGECWVPTAD LPNVQKALVD GSSDEVPPTF NRTNKFTRGF QTLIDAYGVA SYRECNPALY TIITFPFLFA VMFGDLGHGL
401 IMALFGLWMV VKEVSLAAKK SNNEIWNIFF AGRYIILLMG CFSMYTGLVY NDIFSKSMNI FGSAWFNPYD NQTLERFEAF
481 TLDPKASY**VD KPYF**FGIDPI WQTAENKIIF LNSYKMKLSI IFGVIHMIFG VCMSVVNYNF FKRRYSIFLE FLPQIIFLFL

561 LFAYMVFMMF YKWVAYSTLA TDEAYTQGCA PSVLILFINM MLFSSTEPEG GCKEYMFEGQ ETLQRAFVLV ALCCIPVMLL
641 GKPLYLLCAA KKKHDKPQSN GSVNQGIEMQ EQTDIEQAPK PAAGGHDHDD EPFSEIMIHQ GIHTIEYVLS TISHTASYLR
721 LWALSLAHAE LSEVLWNMVL QLGLKDHNWV GSIKLYVAFM FWSLFTLAIL VMMEGLSAFL HTLRLHWVEF MSKFYAGLGY
801 IFQPFCFKTI LEQEDED

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VDKPYF.F	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	489	494	
total 1 peptides												

tr|A0A0Q9WN59|A0A0Q9WN59_DROVI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMQRLITQQV VDQKGALYIT NALWTLMEHN IEEVKVLQTV TLLLTTNLVV HGDTLAKALV LCFRLHYTKN PTIVNTAGAT
81 IRQLVSLVSA RVYLEKDSVH SLQQQQQQQQ QQLQQSGTSS PDTDGNGTQD GQTFAMDAFH LFQDLVQLVN AEQPFWLLGM
161 TEMTRTFGLE LLEAVLSNFS AVFHENQEFR LLLKERVCAL VIKLFSPNVK HRQLPAPSNG TAAVP**VDKPY F**PISMRLLRL
241 VAILIQKYHT ILVTECEIFL SLIIKFLDPD KPHWQRALAL EVIHKLVTRS TLIAFFCKSY DLKNHATHIV HDMIAAMGSY
321 VRYSLINASA VLSNGGQQAV GAAGQPPSTL SALASGGNNQ CGFMFRGAYL PLVASFAPGL PKAVYLEMLD KLDAPNIPDS
401 YGISLAYAIL LDMTRSIGGV IQRTPELHPT HNMAVITEEE HKPLCLQLIN SSWSGLLSAF IPLVETSIDE GTTENILKAM
481 QNYAALCGML DQLQPRDAFI MAMCRASFPP HYAMSIFANA AQLDADLRCH TRSGSQDLSS QFINSCNADG GDFRPQIVAV
561 GTPLPSASLP HSVMQAPVML TNKNLQCMRA ILLLAHNNGS ILGTSWHIVL QTLQHLVWIL GLKPSTGGSL QAIPKPAVEA
641 NVGIQTAVMA DLPVLSQMIG QLFESSQYLD DVALHHLIDA LCKLSHEAME LAYANREPSL FAVAKLMETG LVNMPRIEVL
721 WRPLTNHLLE VCQHRHIRMR EWGVEAITYL VKSALQFKHK QPLKENLELQ TMLLSPLSEL STVLHADVRQ RQLDCVLQIL
801 NTAGEILSFG WPAIIEIIGA VNDHHGEPLI RTAFQCLQLV ITDFLTVMPW RCLPLCISTA AKFGSQTQEL NISLTAIGLM
881 WNISDFFNQN QDKLTSTQLE DVAILPDFPG TLKMPQFDKL WMCLYAKLGE LCVDLRPAVR KSAGQTLFST IAAHGSLLNP
961 PTWQALVWQV LFPLLDNVRA LSSSASNEKV DASGNILIHH SRNTAQKQWA ETQVLTLSGV CRVFNTKRDL LQMLGDFERA
1041 WSLILEFIQN AALSKNGEVS LAALKSLQEI MYHTSTERGL KDGQTAQQQD EEIWNIAWNI WLSIGMESTK MSATTRLLPG
1121 VTGGDSQEDF YIPSQAFLTA LIQIFPAIFQ HIQVRFSASD FDKFCTVLTN AVCIPVQTDA VPYIMSTVSD TLLTPLHDGI
1201 LECMELIQKE AIRPDSESSI RQLIPAIFRQ LLIFSKFACA PPTFQQSVEH NKYGKSGNHY ANNAAVEVVS MNYIPFGEKS
1281 ISICVKLYQS TATEESVVQE QILHDIIKAL RTPLAMKYKC LSSSTWKLAI SSLISVLHTG LKVARTKPQH FASQWDDLAD
1361 TLDKFLFPIS VCTIEDRGLE EIVLDETIDC QVIELLRDEV LPYAHELPHQ FIMQIVVLLN KGSIHSASDS NICYESDWKL
1441 REIFAKTCFE TLLQFSLLED QATATACNNN RLNANLLTAG GAGAVNKDFA GRLAVTALLH RFQEVLKRFN DDERQSGKCP
1521 LPRFRLSEIS FVLKAIATLV VSMKKAPASK VNKPAWDLLI GLYPYLVDCT TTTSPEVSRS LREALLQYTD LLQAPSYVKD
1601 NAIQSNGQQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.P	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	226	231	
total 1 peptides												

tr|B4LSM1|B4LSM1_DROVI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFVGGGVVG GGTDVHKFVE ALQADFKTLS LETKKKYPQI KEACEEAISK LCTAGSSQQN SVYYTVNQIL YPLVQGCETK
81 DLKIIKFCLG MMQRLITQQV VDQKGALYIT NALWTLMEHN IEEVKVLQTV TLLLTTNLVV HGDTLAKALV LCFRLHYTKN
161 PTIVNTAGAT IRQLVSLVSA RVYLEKDSVH SLQQQQQQQQ QQLQQSGTSS PDTDGNGTQD GQTFAMDAFH LFQDLVQLVN
241 AEQPFWLLGM TEMTRTFGLE LLEAVLSNFS AVFHENQEFR LLLKERVCAL VIKLFSPNVK HRQLPAPSNG TAAVP**VDKPY**
321 **F**PISMRLLRL VAILIQKYHT ILVTECEIFL SLIIKFLDPD KPHWQRALAL EVIHKLVTRS TLIAFFCKSY DLKNHATHIV
401 HDMIAAMGSY VRYSLINASA VLSNGGQQAV GAAGQPPSTL SALASGGNNQ CGFMFRGAYL PLVASFAPGL PKAVYLEMLD
481 KLDAPNIPDS YGISLAYAIL LDMTRSIGGV IQRTPELHPT HNMAVITEEE HKPLCLQLIN SSWSGLLSAF IPLVETSIDE
561 GTTENILKAM QNYAALCGML DQLQPRDAFI MAMCRASFPP HYAMSIFANA AQLDADLRCH TRSGSQDLSS QFINSCNADG
641 GDFRPQIVAV GTPLPSASLP HSVMQAPVML TNKNLQCMRA ILLLAHNNGS ILGTSWHIVL QTLQHLVWIL GLKPSTGGSL
721 QAIPKPAVEA NVGIQTAVMA DLPVLSQMIG QLFESSQYLD DVALHHLIDA LCKLSHEAME LAYANREPSL FAVAKLMETG
801 LVNMPRIEVL WRPLTNHLLE VCQHRHIRMR EWGVEAITYL VKSALQFKHK QPLKENLELQ TMLLSPLSEL STVLHADVRQ
881 RQLDCVLQIL NTAGEILSFG WPAIIEIIGA VNDHHGEPLI RTAFQCLQLV ITDFLTVMPW RCLPLCISTA AKFGSQTQEL
961 NISLTAIGLM WNISDFFNQN QDKLTSTQLE DVAILPDFPG TLKMPQFDKL WMCLYAKLGE LCVDLRPAVR KSAGQTLFST
1041 IAAHGSLLNP PTWQALVWQV LFPLLDNVRA LSSSASNEKV DASGNILIHH SRNTAQKQWA ETQVLTLSGV CRVFNTKRDL
1121 LQMLGDFERA WSLILEFIQN AALSKNGEVS LAALKSLQEI MYHTSTERGL KDGQTAQQQD EEIWNIAWNI WLSIGMESTK
1201 MSATTRLLPG VTGGDSQEDF YIPSQAFLTA LIQIFPAIFQ HIQVRFSASD FDKFCTVLTN AVCIPVQTDA VPYIMSTVSD
1281 TLLTPLHDGI LECMELIQKE AIRPDSESSI RQLIPAIFRQ LLIFSKFACA PPTFQQSVEH NKYGKSGNHY ANNAAVEVVS
1361 MNYIPFGEKS ISICVKLYQS TATEESVVQE QILHDIIKAL RTPLAMKYKC LSSSTWKLAI SSLISVLHTG LKVARTKPQH
1441 FASQWDDLAD TLDKFLFPIS VCTIEDRGLE EIVLDETIDC QVIELLRDEV LPYAHELPHQ FIMQIVVLLN KGSIHSASDS
1521 NICYESDWKL REIFAKTCFE TLLQFSLLED QATATACNNN RLNANLLTAG GAGAVNKDFA GRLAVTALLH RFQEVLKRFN
1601 DDERQSGKCP LPRFRLSEIS FVLKAIATLV VSMKKAPASK VNKPAWDLLI GLYPYLVDCT TTTSPEVSRS LREALLQYTD
1681 LLQAPSYVKD NAIQSNGQQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.VDKPYF.P	Y	20.81	767.3854	-26.1	768.3726	1	0.29	260	1	316	321	
total 1 peptides												
