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.

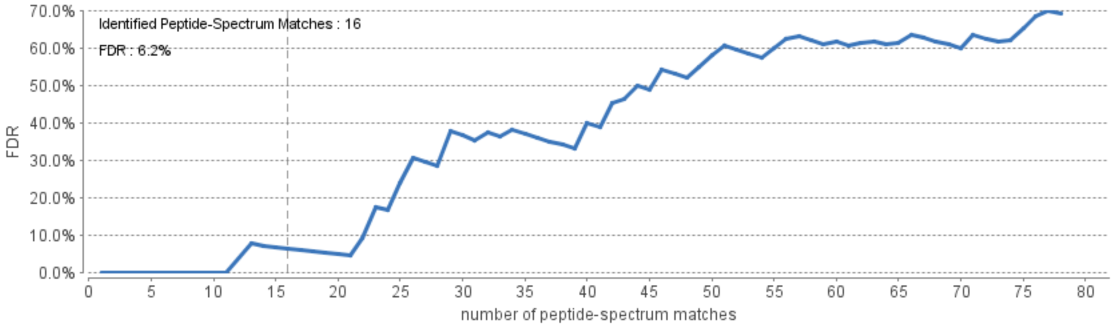
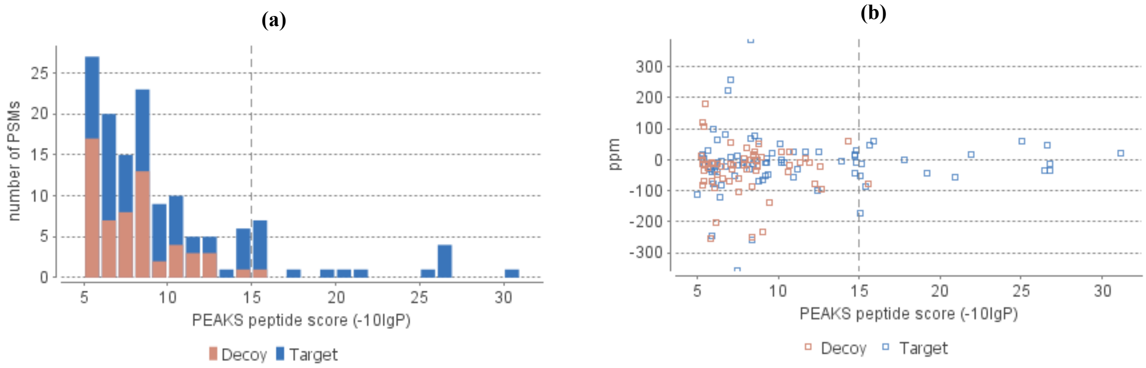
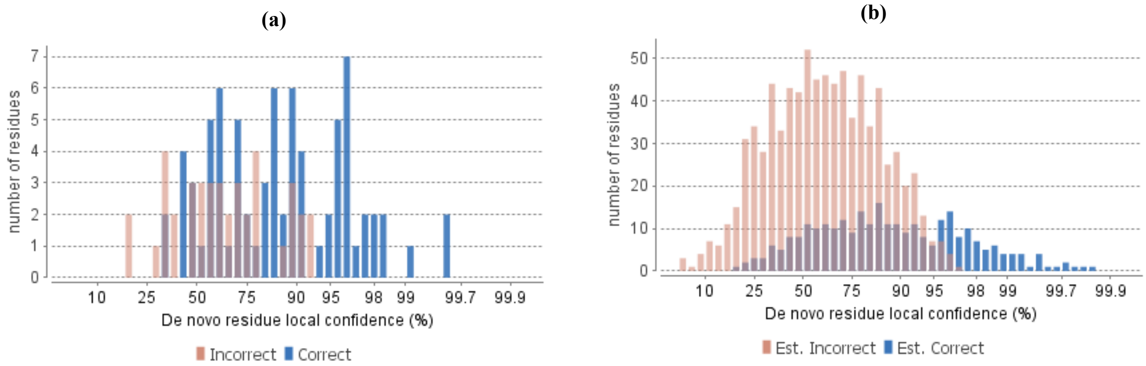


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(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	1332
# of MS/MS Scans	1035

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	16
Peptide Sequences	14

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Oxidation	15.99	4	M
Carbamidomethyl	57.02	1	C

Protein Groups	6
Proteins	34
Proteins (#Unique Peptides)	0 (>2); 0 (=2); 34 (=1);
FDR (Peptide-Spectrum Matches)	6.2%
FDR (Peptide Sequences)	7.1%
FDR (Protein)	5.9%
De Novo Only Spectra	100

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.

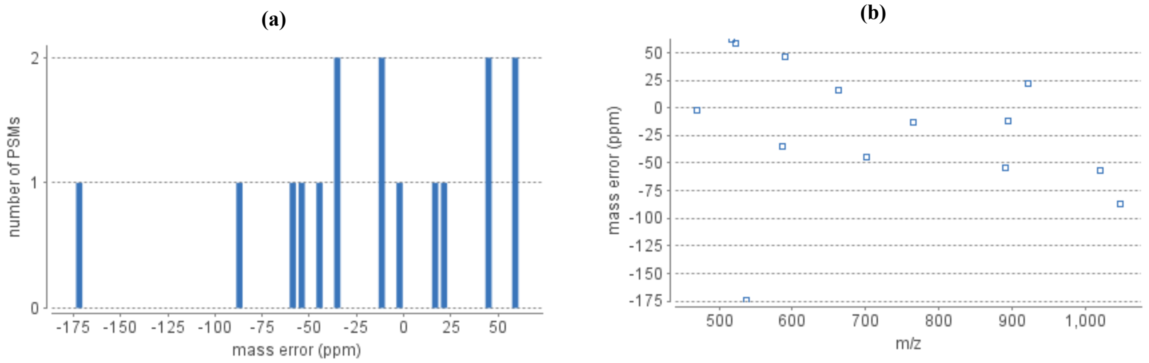


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Q-TOF	8	2	4	0	0

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fixed Modifications:
  Carbamidomethylation: 57.02
Variable Modifications:
  Oxidation (M): 15.99
Fragment ion tolerance: 0.1
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 68
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: D_4_180917.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: Quadrupole
MS/MS Scan Mode: Time of Flight (TOF)

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	10729	tr|A0A1V9X4S6|A0A1V9X4S6_9ACAR	31.12	3	1	1	Y	32264	Rhomboid-like protein (Fragment) OS=Tropilaelaps mercedesae GN=BIW11_01988 PE=3 SV=1
1	10727	tr|A0A0J7K0B6|A0A0J7K0B6_LASNI	26.74	10	1	1	N	12413	Tigger transposable element-derived protein 6-like protein OS=Lasius niger GN=RF55_19627 PE=4 SV=1
1	10728	tr|A0A0J7KCY6|A0A0J7KCY6_LASNI	26.74	7	1	1	N	16856	Kinesin family member 21a OS=Lasius niger GN=RF55_12207 PE=4 SV=1
2	10726	tr|A0A0M9A8V0|A0A0M9A8V0_9HYME	26.73	3	1	1	N	25334	Hyaluronidase (Fragment) OS=Melipona quadrifasciata GN=WN51_02856 PE=3 SV=1
2	10730	tr|E3PQY2|E3PQY2_9HYME	26.73	4	1	1	N	20652	Hyaluronidase (Fragment) OS=Chelonus inanitus PE=2 SV=1
2	10731	tr|E3PQY4|E3PQY4_9HYME	26.73	3	1	1	N	27954	Hyaluronidase (Fragment) OS=Chelonus inanitus PE=2 SV=1
2	10732	P49370|HUGAA_VESVU	26.73	2	1	1	N	38933	Hyaluronidase A OS=Vespula vulgaris PE=1 SV=1
2	10733	tr|Q05FZ2|Q05FZ2_VESGE	26.73	2	1	1	N	38923	Hyaluronidase (Fragment) OS=Vespula germanica GN=Ves g2a PE=2 SV=1
2	10734	P49371|HUGA_DOLMA	26.73	2	1	1	N	38929	Hyaluronidase OS=Dolichovespula maculata PE=1 SV=1
2	10735	tr|S6CWF7|S6CWF7_COTCN	26.73	2	1	1	N	39498	Hyaluronidase OS=Cotesia congregata GN=hyal PE=3 SV=1
2	10736	tr|E0AD89|E0AD89_POLPI	26.73	2	1	1	N	40482	Hyaluronidase (Fragment) OS=Polybia paulista GN=hyal PE=2 SV=1
2	10737	P86875|HUGA_VESMG	26.73	2	1	1	N	41948	Hyaluronidase OS=Vespa magnifica PE=1 SV=2
total 34 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
2	10738	tr|A0JCZ2|A0JCZ2_GLYIN	26.73	2	1	1	N	41662	Hyaluronidase OS=Glyptapanteles indiensis GN=GIP_L1_00710 PE=3 SV=1
2	10739	tr|A0A158NRG0|A0A158NRG0_ATTCE	26.73	2	1	1	N	41770	Hyaluronidase OS=Atta cephalotes GN=105623333 PE=3 SV=1
2	10740	tr|A0A151I2G6|A0A151I2G6_9HYME	26.73	2	1	1	N	41738	Hyaluronidase OS=Atta colombica GN=ALC53_08652 PE=3 SV=1
2	10741	tr|A0A0L7RCK4|A0A0L7RCK4_9HYME	26.73	2	1	1	N	42396	Hyaluronidase (Fragment) OS=Habropoda laboriosa GN=WH47_06326 PE=3 SV=1
2	10742	Q9U6V9|HUGA_POLAN	26.73	2	1	1	N	43020	Hyaluronidase (Fragment) OS=Polistes annularis PE=1 SV=1
2	10743	tr|A0A1L8DQ89|A0A1L8DQ89_9DIPT	26.73	2	1	1	N	43342	Hyaluronidase OS=Nyssomyia neivai PE=3 SV=1
2	10744	tr|A0A1L8DQI1|A0A1L8DQI1_9DIPT	26.73	2	1	1	N	43282	Hyaluronidase OS=Nyssomyia neivai PE=3 SV=1
2	10745	tr|D1MEJ6|D1MEJ6_9HYME	26.73	2	1	1	N	43784	Hyaluronidase OS=Eumenes pomiformis GN=Hya1 PE=2 SV=1
2	10746	tr|I1VC83|I1VC83_APICA	26.73	2	1	1	N	44131	Hyaluronidase OS=Apis mellifera carnica PE=2 SV=1
2	10747	Q08169|HUGA_APIME	26.73	2	1	1	N	44260	Hyaluronidase OS=Apis mellifera PE=1 SV=1
2	10748	tr|A0A088AMF4|A0A088AMF4_APIME	26.73	2	1	1	N	44232	Hyaluronidase OS=Apis mellifera GN=LOC406146 PE=3 SV=1
2	10749	tr|Q95PD7|Q95PD7_APICC	26.73	2	1	1	N	44657	Hyaluronidase OS=Apis cerana cerana PE=2 SV=2
2	10750	tr|A0A2A3EHG0|A0A2A3EHG0_APICC	26.73	2	1	1	N	44671	Hyaluronidase OS=Apis cerana cerana GN=APICC_10171 PE=4 SV=1
2	10751	tr|A0A067QPK9|A0A067QPK9_ZOONE	26.73	1	1	1	N	62542	Hyaluronidase (Fragment) OS=Zootermopsis nevadensis GN=L798_07575 PE=3 SV=1
2	10752	tr|E2C0S4|E2C0S4_HARSA	26.73	1	1	1	N	87849	Hyaluronidase OS=Harpegnathos saltator GN=EAI_13340 PE=3 SV=1
4	10753	tr|Q2Q0U9|Q2Q0U9_9DIPT	26.58	4	1	1	Y	15690	Glutathione S-transferase (Fragment) OS=Anopheles sacharovi GN=GSTe2 PE=4 SV=1
6	10755	tr|A0A132AL00|A0A132AL00_SARSC	21.93	6	1	1	N	12685	Rad51-like protein OS=Sarcoptes scabiei GN=QR98_0102550 PE=3 SV=1
6	10756	tr|W8C706|W8C706_CERCA	21.93	3	1	1	N	24003	Laminin subunit alpha-1 (Fragment) OS=Ceratitis capitata GN=LAMA1 PE=2 SV=1
6	10757	tr|T1J4F5|T1J4F5_STRMM	21.93	2	1	1	N	46081	Uncharacterized protein OS=Strigamia maritima PE=4 SV=1
6	10758	tr|A0A1U9X1T2|A0A1U9X1T2_CNAME	21.93	1	1	1	N	60034	Carboxylic ester hydrolase OS=Cnaphalocrocis medinalis PE=2 SV=1
7	10759	tr|A0A131Y3Z3|A0A131Y3Z3_IXORI	20.89	2	1	1	N	51941	Putative ankyrin OS=Ixodes ricinus PE=2 SV=1
7	10760	tr|A0A147BG19|A0A147BG19_IXORI	20.89	2	1	1	N	51953	Putative ankyrin OS=Ixodes ricinus PE=4 SV=1
total 34 proteins									

tr|A0A1V9X4S6|A0A1V9X4S6_9ACAR

back to list

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

Protein Coverage:

68

1 IALFTYYSLT VGPAGLSTPI PAQSIFIFNP RHKFEIWRYF SYFLVHNGWL HLGFNIVIQL **FVGLPLEM**LH GSWRIGFVYI Oxida

81 AAVIAGVVGL PELAPLSESA SQGRPDWLLA YAGKKKTEEQ QQQVSVKQPN SSLLAYESRV RQAPPSNQGR GSVFCSVVDP

161 TAFLVGASCP VYALLSAHLA NILLNHDALA EFGLSKFFLR ITLVFLLSSI DFGFALFDRV SEPDGLTLAF LGPFVGVAFG

241 VSVGCVVVKS YEQKLREQLA CWLVMVFYVA TIAGAIVYNV LNFDALRQAS AALF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.FVGLPLEM(+15.99).L	Y	31.12	920.4677	21.4	921.4947	1	33.17	1205	1	61	68	Oxidation (M)
total 1 peptides												

tr|A0A0J7K0B6|A0A0J7K0B6_LASNI

back to list

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

Protein Coverage:

1 MTSNPGRTMT IYDIPGIVAK ALPL**AVTHQN IVSGF**EYTRI SSFNPDIFQE YEFLPSSVTD RENPFTSADP EEANLNAADP

81 DTVEPDAADQ NGNEFDPTAS AMSRRGTRNL SATL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVTHQNIVSGF.E	Y	26.74	1171.5985	-35.0	586.7860	2	17.38	685	2	25	35	
total 1 peptides												

tr|A0A0J7KCY6|A0A0J7KCY6_LASNI

back to list

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

Protein Coverage:

1 MTSNPGRTVM IYDIPGIVAK ALPL**AVTHQN IVSGF**ECTGI SPFNPDIFQE YKYLPSNVTD RENPSTSTDP EEANLNAAEL

81 DAADSDTVEF DAADQNGNEF DFTAFSMSRR GDTRNLSATL KSIRVFPKAA SRQQTCKGRK QEREPFLMTR LK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.AVTHQNIVSGF.E	Y	26.74	1171.5985	-35.0	586.7860	2	17.38	685	2	25	35	
total 1 peptides												

tr|A0A0M9A8V0|A0A0M9A8V0_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 FLVSLAPTTP RNNETDEFNI Y**WNVPTFM**CH KYGLHFEEVS EKYGILQNTM DNFRGEEMAI LYDPGTFPAL LKDSNVMRNG
81 GVPQEGNLTK HLEVFREHLI HQIPDKSFHG VGVIDFESWR PIFRQNWASL QPYKKLSIEI VRREHPFWDN QSVEQEARRQ
161 FEKYGRLFVE ETLKAAKQIR PYAKWGYYAY PYCYNLTPSQ PSXXXXXXXX XMTE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	22	28	
total 1 peptides												

tr|E3PQY2|E3PQY2_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAEAKKFKIY **WNVPTFM**CHT HGMKFEEVSQ VYNITQNSND TFNGNEIAIL YHAGDFPTYI KFENDTEITM NGKVPQRGDL
81 QKHLNQLEID LNGNVTDPNF SGIGVLDYER WRPVFRQNFN DVNRIYKEYS INLESSSFKI LTYKQARTLA EKAYDYSARV
161 FYEETIKLVR KHRPK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	11	17	
total 1 peptides												

tr|E3PQY4|E3PQY4_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFFIRMICF FNYSVFIIHI ILISLVMIET RKYKIY**WNVP TFM**CHRHGMK FEEVSKVYDM VQNINDTFNG NEIAILYHAG
81 YFPTYEVHNN DSPLMINNIV PQKGNIQKHL NQLEIDLNGN VTDPNFSGIG ILDYERWRAV FRQNFNKNNR VYREYSIALE
161 RNEFNILTYD QARTLAALAF NYSAQIFFEE TIKLIKRKRP YAAWGYYDYP KCFYLTSKDS ATPCGEVHEE NDKMK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	37	43	
total 1 peptides												

P49370|HUGAA_VESVU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SERPKRVFNI Y**WNVPTFM**CH QYDLYFDEVT NFNIKRNSKD DFQGDKIAIF YDPGEFPALL SLKDGKYKKR NGGVPQEGNI
81 TIHLQKFIEN LDKIYPNRNF SGIGVIDFER WRPIFRQNWG NMKIHKNFSI DLVRNEHPTW NKKMIELEAS KRFEKYARFF
161 MEETLKLAKK TRKQADWGYY GYPYCFNMSP NNLVPECDVT AMHENDKMSW LFNNQNVLLP SVYVRQELTP DQRIGLVQGR
241 VKEAVRISNN LKHSPKVLSY WWYVYQDETN TFLTETDVKK TFQEIVINGG DGIIIWGSSS DVNSLSKCKR LQDYLLTVLG
321 PIAINVTEAV N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	12	18	
total 1 peptides												

tr|Q05FZ2|Q05FZ2_VESGE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SERPKRVFNI Y**WNVPTFM**CH QYDLYFDEVT NFNIKRNSKD DFQGDKIAIF YDPGEFPALL SLKDGKYKKR NGGVPQEGNI
81 TIHLQKFIEN LDKTYPNRNF SGIGVIDFER WRPIFRQNWG NMKIHKNFSI DLVRNEHPTW NKKMIELEAS KRFEKYARFF
161 MEETLKLAKK TRKQADWGYY GYPYCFNMSP NNLVPECDVT AMHENDKMSW LFNNQNVLLP SVYVRQELTP DQRIGLVQGR
241 VKEAVRISNN LKHSPKVLSY WWYVYQDETN TYLTETDVKK TFQEIVINGG DGIIIWGSSS DVNSLSKCKR LQDYLLTVLG
321 PIAVNVTEAV N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	12	18	
total 1 peptides												

P49371|HUGA_DOLMA

back to list

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

Protein Coverage:

1 SERPKRVFNI Y**WNVPTFM**CH QYGLYFDEVT NFNIKHNSKD DFQGDKISIF YDPGEFPALL PLKEGNYKIR NGGVPQEGNI
81 TIHLQRFIEN LDKTYPNRNF NGIGVIDFER WRPIFRQNWG NMMIHKKFSI DLVRNEHPFW DKKMIELEAS KRFEKYARLF
161 MEETLKLAKK TRKQADWGYY GYPYCFNMSP NNLVPDCDAT AMLENDKMSW LFNNQNVLLP SVYIRHELTP DQRVGLVQGR
241 VKEAVRISNN LKHSPKVLSY WWYVYQDDTN TFLTETDVKK TFQEIAINGG DGIIIWGSSS DVNSLSKCKR LREYLLTVLG
321 PITVNVTETV N

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	12	18	
total 1 peptides												

tr|S6CWF7|S6CWF7_COTCN

back to list

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

Protein Coverage:

1 MNKSVGGKFN RLRKKARDYK VY**WNVPTFM**C HKYGMYFNDL DKFGIIQNTN DQFRGEKIAI LYDPGMFPAL IKNPDGTITR
81 RNGGVPQEGN LQSHLNLFKI HLEEQIQENF SGLGVIDFES WRPIFRQNSA SLAPYRDLSI ELEAARHRNW SKNAIKQHAV
161 QLFETAGRVF MEETIKLAKQ LRPNASWSYY AYPYCFNLTP NQPSASCDPR VLQENDQMSW LWKLEDTFLP SVYLRKSLSN
241 DERLGLIVGR LHVAVRLSRK FPNRPVIPYF WFKFLDQRDI YLNKEDILSS FKVMIKNGAD GHIIWGSSQD FNSQQKCEKF
321 KSYLNDILGP AAKEITSLGS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	23	29	
total 1 peptides												

tr|E0AD89|E0AD89_POLPI

back to list

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

Protein Coverage:

1 SWVEFALSER PKRVFNIY**WN VPTFM**CHQYG INFDEVTDFN IKHNSKDNFR GETLAIYYDP GNFPALIPVN NGKYKERNGG
81 VPQRGNITIH LQQFNEDLDK MTPDKSFGGI GVIDFERWRP VFRQNWGNTE IHKEYSIELV RKEHPKWSKS MIEAEATKKF
161 EKYARYFMEE TLKLAKKTRK RAKWGYYGFP YCYNASPNNP GPSCDAKAII ENDRMSWMYN NQEILLPSVY VRHKQDPEER
241 IYLVQGRVKE AVRVSNNLEH SPSVLPYWWY VYQDEMEIFL SETDVKKTFQ EIVTNGGDGI IIWGSSSDVN SLSKCKRLRE
321 YLLNTLGPIA VNVTETVNRR SSLNF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	19	25	
total 1 peptides												

P86875|HUGA_VESMG

back to list

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

Protein Coverage:

1 MLLVTLFLFF LQALVNGDSC GSNCEKSERP KRVFNIY**WNV PTFM**CHQYGL YFDEVTNFNI KHNSKDNFQG DKIAIFYDPG
81 EFPALLPLNY GKYKIRNGGV PQEGNITIHL QRFIEYLDKT YPNRNFSGIG VIDFERWRPI FRQNWGNMKI YKNFSIDLVR
161 KEHPFWNKKM IELEASKRFE KYARLFMEET LKLAKKTRKQ ADWGYYGYPY CFNMSPTNFV PDCDVTARDE NNEMSWLFNN
241 QNVLLPSVYI RRELTPDQRI GLVQGRVKEA VRISNKLKHS PKVFSYWWYV YQDETNTFLT ETDVKKTFQE IVINGGDGII
321 IWGSSSDVNS LSKCTRLREY LLTVLGPIAV NVTEAVN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	38	44	
total 1 peptides												

tr|A0JCZ2|A0JCZ2_GLYIN

back to list

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

Protein Coverage:

1 MLSLPIFLLS IGQLEDTNYK TRDYKVY**WNV PTFM**CHKYGM YFDDLEKFGI IQNTNDHFRG EKITILYDPG MFPALIKNPN
81 GTITRRNGGV PQEGNLQSHL DLFKTHLEEQ VQENFSGLGV IDFESWRPIF RQNWASLAPY RDLSIELETA SHKNWSKNAI
161 KQHAVKLFES AGRLFMEETI KLAKQLRPYA SWSYYAFPYC FNLTPNQPNA SCDPRVFKEN DQLSWLWKIE DSILPSVYLR
241 KSLTSHQRSD FIAKELQESV RLSKKFSNRP ILPYVWYKFQ DQPDVYLSEN DLLNSFKAIL DNGASGFVVW GSYKDVNTRK
321 KCFNFKTYLK RMLGPAVVTI KAIALTYTPA DDINSDEL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	28	34	
total 1 peptides												

tr|A0A158NRG0|A0A158NRG0_ATTCE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLRYSLILA FASVAAATFL GWGTTTLQSN NSRKFDVY**WN VPTFM**CNQYN VIFDDLKDFG IHQNTMDEFR GEEIAILYDP
81 GMFPALLTDK TGTITNVRNG GVPQEGDLKK HLEMFQKNLI KQIPDGSFSG IGVIDFESWR PIFRQNWASL EPYKTLSIKL
161 EHKRHPFWNE SAVKKEAKRR FEKYARIFME ETLNMAKKLR PKAKWGYYGY PHCFNQTPGQ PTAHCNRQTM AENNEMSWLF
241 TLEDVYLSSV YLRQEIKGED RVGFVKGRVS EALRMAGKIL RKQQVLPYYW FKYQDNRDNF LSEKDTENTF NTIVNLGADG
321 LIIWGSSEDT NTEQKCKDLL QYVRTVLGPA IKRIKYNSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	39	45	
total 1 peptides												

tr|A0A151I2G6|A0A151I2G6_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLRYSLILA FASVAAATFL GWGTTTLQSN NSREFDVY**WN VPTFM**CNQYN VIFDDLKDFG IHQNTMDEFR GEEIAILYDP
81 GMFPALLTDK TGTVTNVRNG GVPQEGDLKK HLEIFQKNLI KQIPNGSFSG IGVIDFESWR PIFRQNWASL EPYKTLSIKL
161 EHKRHPFWNE SAVKKEAKRR FEKYARIFME ETLNMAKKLR PKAKWGYYGY PHCFNQTPGQ PTAHCNRQTM AENNEMSWLF
241 TLEDVYLSSV YLRQEIKGED RVGFVKGRVS EALRMAGKIL RKQQVLPYYW FKYQDNRDNF LSEKDTENTF NTIVNLGADG
321 LIIWGSSEDT NTEQKCKDLL QYVRTVLGPA IKRIKYNSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	39	45	
total 1 peptides												

tr|A0A0L7RCK4|A0A0L7RCK4_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LVSFVPTTPN VIEDHRSREF NVY**WNVPTFM** CHKYGLHFEE VSDRYGILQN KMDKFRGDEI AILYDPGMFP ALLKSANGDV
81 VMRNGGVPQE GNLTKHLEVF REHLINQIPD KSFHGVGVID FESWRPIFRQ NWASLQPYKK LSVDLVRREH PFWDSKSVEQ
161 EAKRRFEKYG KLFMEETLKA AKQMRPEAIW GYYAYPYCYN LTPNQPSSQC DSTTIQENDK LSWLFELEDV LLPSVYLRRS
241 LTSGQRVGLV GGRVKEALRI AKQMTSRKKV LPYYWYKYQD QRDSYLTKVD LEATLRKISD LGADGLIIWG SSNDINTKQK
321 CLQFREYLNN DLGPIVDRIR RTALGLSQRS GNSLDNRVGV SVDQV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	24	30	
total 1 peptides												

Q9U6V9|HUGA_POLAN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 YVSLSPDSVF NIITDDISHQ ILSRSNCERS KRPKRVFSIY **WNVPTFM**CHQ YGMNFDEVTD FNIKHNSKDN FRGETISIYY
81 DPGKFPALMP LKNGNYEERN GGVPQRGNIT IHLQQFNEDL DKMTPDKNFG GIGVIDFERW KPIFRQNWGN TEIHKKYSIE
161 LVRKEHPKWS ESMIEAEATK KFEKYARYFM EETLKLAKKT RKRAKWGYYG FPYCYNVTPN NPGPDCDAKA TIENDRLSWM
241 YNNQEILFPS VYVRHEQKPE ERVYLVQGRI KEAVRISNNL EHSPSVLAYW WYVYQDKMDI YLSETDVEKT FQEIVTNGGD
321 GIIIWGSSSD VNSLSKCKRL REYLLNTLGP FAVNVTETVN GRSSLNF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	41	47	
total 1 peptides												

tr|A0A1L8DQ89|A0A1L8DQ89_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFASNFYAFS PKICTNFLLI LTFYLTELPH ATAYIRVY**WN VPTFM**CTKYG INFMDVEREY GVIQNVNDTF RGNEISILYD
81 PGNFPALLEN SSSGRLVKRN GGVPQEGNLP EHLKIFTKHV DELIPNKDYE GLAVIDFESW RPVFRQNFGT LQPYRNLSIR
161 IEREKHRHWS HREIVREASK VFESTGRKFM EQTLKMAKEA RPRALWGYYA FPYCFNGNSR DPLSCSNEVQ QENNRIMWLF
241 ENSDVILPSV YLTEAWAPNM RKSIIKGRVG EANRVARATH KRPRPQVLTY IRYAYTDTLN FLSQGDLYDA FSVMDQKKSD
321 GILWGSSFDL NSETKCKNFR KYLEDQLGPM LRLFTRPKYS VQGILQQQWN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	39	45	
total 1 peptides												

tr|A0A1L8DQI1|A0A1L8DQI1_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MFASNFCAFS PKICTNFLLI LTFYLTELPH ATAYIRVY**WN VPTFM**CTKYG INFMDVEREY GVIQNVNDTF RGNEISILYD
81 PGNFPALLEN SSSGRLVKRN GGVPQEGNLP EHLKIFTKHV DELIPNKDYE GLAVIDFESW RPVFRQNFGT LQPYRNLSIR
161 IEREKHRHWS HREIVREASK VFESTGRKFM EQTLKMAKEA RPRALWGYYA FPYCFNGNSR DPLSCSNEVQ QENNRIMWLF
241 ENSDVILPSV YLTEAWAPNM RKSIIKGRVG EANRVARATH KRPRPQVLTY IRYAYTDTLN FLSQGDLYDA FSVMDQKKSD
321 GILWGSSFDL NSETKCKNFR KYLEDQLGPM LRLFTRPKYS VQGILQQQWN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	39	45	
total 1 peptides												

tr|D1MEJ6|D1MEJ6_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MILAVQLVLL LLYPIVRAGI TDICGFYCTP EYRVKRHFYI Y**WNVPTFM**CH KYGLDFSEVK DFNIMQNKDD LFHGDVVTIM
81 YDPGSFPAML PLNKTTKKDK YKKRNGGVPQ MGNYQKHRTA FIEDLDKYVP DVDYDGIGVI DFEHWKPIFR QNWGTQKLYK
161 DLSYDLVKQM HPLWSRPTIE SEAIKKFEKN GRYFMEETLK TAKKYRFKGD WGYYGYPYCY NLSPGHPGID CNQKAMSDND
241 KMSWLFNNQD LLMPSVYVKY FMQAFERAAL VQGRVKEAVR ISNNHKNLPR VIPYWWYKYT DQMDVFLSEK DVKNTFREIL
321 YNGGDGIIIW GSSADVNSES KCKRLRKYLI EMLGPLAAKL IHSANEGTFL DY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	42	48	
total 1 peptides												

tr|I1VC83|I1VC83_APICA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRPLVITEG MMIGVLLMLA PINALLLGFV QSTPDNNKTV REFNVY**WNVP TFM**CHKYGLR FEEVSEKYGI LQNWMDKFRG
81 EEIAILYDPG MFPALLKDPN GNVVARNGGV PQLGNLTKHL QVFRDHLINQ IPDKSFPGVG VIDFESWRPI FRQNWASLQP
161 YKKLSVEVVR REHPFWDDQR VEQEAKRRFE KYGQLFMETL KAAKRMRPAA NWGYYAYPYC YNLTPNQPSA QCEATTMQEN
241 DKMSWLFESE DVLLPSVYLR WNLTSGERVG LVGGRVKEAL RIARQMTTSR KKVLPYYWYK YQDRRDTDLS RADLEATLRK
321 ITDLGADGFI IWGSSDDINT KAKCLQFREY LNNELGPAVK RIALNNNAND RLTVDVSVDQ V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	47	53	
total 1 peptides												

Q08169|HUGA_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRPLVITEG MMIGVLLMLA PINALLLGFV QSTPDNNKTV REFNVY**WNVP TFM**CHKYGLR FEEVSEKYGI LQNWMDKFRG

81 EEIAILYDPG MFPALLKDPN GNVVARNGGV PQLGNLTKHL QVFRDHLINQ IPDKSFPGVG VIDFESWRPI FRQNWASLQP

161 YKKLSVEVVR REHPFWDDQR VEQEAKRRFE KYGQLFMEET LKAAKRMRPA ANWGYYAYPY CYNLTPNQPS AQCEATTMQE

241 NDKMSWLFES EDVLLPSVYL RWNLTSGERV GLVGGRVKEA LRIARQMTTS RKKVLPYYWY KYQDRRDTDL SRADLEATLR

321 KITDLGADGF IIWGSSDDIN TKAKCLQFRE YLNNELGPAV KRIALNNNAN DRLTVDVSVD QV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	47	53	
total 1 peptides												

tr|A0A088AMF4|A0A088AMF4_APIME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRPLVITEG MMIGVLLMLA PINALLLGFV QSTPDNNKTV REFNVY**WNVP TFM**CHKYGLR FEEVSEKYGI LQNWMDKFRG

81 EEIAILYDPG MFPALLKDPN GNVVARNGGV PQLGNLTKHL QVFRDHLINQ IPDKSFPGVG VIDFESWRPI FRQNWASLQP

161 YKKLSVEVVR REHPFWDDQR VEQEAKRRFE KYGQLFMEET LKAAKRMRPA ANWGYYAYPY CYNLTPNQPS AQCEATTMQE

241 NDKMSWLFES EDVLLPSVYL RWNLTSGERV GLVGGRVKEA LRIARQMTTS RKKVLPYYWY KYQDRRDTDL SRADLEATLR

321 KITDLGADGF IIWGSSDDIN TKAKCLQFRE YLNNELGPAV KRIALNNNAN SRLTVDVSVD QV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	47	53	
total 1 peptides												

tr|Q95PD7|Q95PD7_APICC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRPLVIAEE MMVGVLLMLA PVLRINALLL GFVPSTPNDN NKTKREFNVY **WNVPTFM**CHK YGLRFEEVSE KYGILQNWMD

81 KFWGEEIAIL YDPGMFPALL KDSNGNVVAR NGGVPQLGNL TKHLQVFRDH LINQIPDKSF PGVGVIDFES WRPIFRQNWA

161 SLQPYKKLSI DVVRREHPSW GDQRVEQEAK RRFEKYGKLF MEETLKAAKR MRPAANWGHY AYPYCYNLTP NQPSSQCEAT

241 TMQENDKMSW LFESEDVLLP SVYLRWNLTS GERVGLVGGR VKEALRIARQ MTTSRKKVLP YYWYKYQDRR DTDLSRADLE

321 ATLRKITDLG ADGFIIWGSS NDINTKAKCV QFREYLNNDL GPVVKRIALN SNAPAAKSRL DVSVDQV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	51	57	
total 1 peptides												

tr|A0A2A3EHG0|A0A2A3EHG0_APICC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRPLVTTEE MMVGVLLMLA PVLRINALLL GFVPSTPNDN NKTKREFNVY **WNVPTFM**CHK YGLRFEEVSE KYGILQNWMD

81 KFRGEEIAIL YDPGMFPALL KDSNGNVVAR NGGVPQLGNL TKHLQVFRDH LINQIPDKSF PGVGVIDFES WRPIFRQNWA

161 SLQPYKKLSI DVVRREHPSW GDQRVEQEAK RRFEKYGKLF MEETLKAAKR MRPAANWGYY AYPYCYNLTP NQPSSQCEAT

241 TMQENDKMSW LFESEDVLLP SVYLRWNLTS GERVGLVGGR VKEALRIARQ MTTSRKKVLP YYWYKYQDRR DTDLSRADLE

321 ATLRKITDLG ADGFIIWGSS NDINTKAKCV QFREYLNNDL GPVVKRIALN SNAPAAKSRL DVSVDQV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	51	57	
total 1 peptides												

tr|A0A067QPK9|A0A067QPK9_ZOONE back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EFRVF**WNVPT FM**CHRYGMDF SDVSSRWSIV QNSGDIFRGE RMVILYDPGE FPALLHDKHG NLLYRNGGVP QEGDLGRHLS

81 KLRTQVDELV PDHNFQGLGV IDFEAWRPIW RQNWASLLPY RDVSRKIEKQ RHPFWWTPQK IEAEATRRFE KAARDFMLST

161 LELLKQMRPS GQWGYYAFPY CFNYTPKNMQ PSCPVQVQRE NNGIQWLFDS SAVVFPSLYL SKLHMSPEQH AQFAIGRMNE

241 AVRIAQNVPR LVKPTVNAYI RYRYHDADEF LSREDLRNSL AIVHRFHAGG VVLWGSANDT NSRERCSALE NYLNSVLGPT

321 IKELSTMHDE ALFVYVPLLV LTNFNSHKIM KMILIVVPLV EKPVTDLTAL KKARIKSRSE SGPLEHQDED EDGDSGGNES

401 HDENDTAVSN QSVLERAVGW NIIASLRRLL AVMCCCLVAR SVTAHREHKV HNIVLYPDKH SWCNTTPIKQ VVAFPGCNSV

481 EIDNNVCVGA CFSYSIPRTA PSAPGELIKP YCDSCQPSTV TWHHVTLNCT GEDPESLQKR VQIIRNC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	6	12	
total 1 peptides												

tr|E2C0S4|E2C0S4_HARSA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTSFDKRKEK EMNSTRATTL REGNPHKFDV Y**WNVPTFM**CH KYGMKFENLN DYGIQQNAMD KFRGDKIVIL YDPGMFPALL

81 VSKNGTVTKR NGGVPQEGDL KEHLEKFRED LVTQIPHESF SGVAVIDFES WRPIFRQNWA SLEPYKTLSI KLERERHPFW

161 SDAAVKKEAK RRFEKFGRMF MEESLKMAKK LRPWAMWGYY GYPHCFNKSP GQQSMHCDRS TMTENDEMSW LFMLEDVHAP

241 SVYLRLEIKE GDRPGFVKGR VSEAQRLAVK SLRKQQILPY YWFKYQDNRD KLLSEKDTMN TIEMIANHGA DGAIIWGSSN

321 DVNTQRKCED LLQYMKDVLG PTKEELKGNP LLLVLMLVVV VVVVVVVVMV MVVVVVMLAV VMLVSVVEEK EVEEEEEEEE

401 EEEEEKEVVK EEATDGREDE EEEDGTREIG STVSCSTQLG IMGPMWRLFA TVLLLMMHSA SLDAHREHKV HNIVLYPDKH

481 SWCKTTPIKQ VVTWPQCSSQ ELDNNVCVGA CFSYMVPHSE PSAPGDLIRP YCDSCQPLDS VWHTVTLDCK DEQNNPMTMQ

561 KKVQIITNCS CSSCMETSKI KPDYNTLLQS LTEENLDKNV NVAHETPDIL LDPNLNASKN NTSKDGAQTN ERFLQLFKKF

641 NAQKLDEADV KELFSQEKEV DQEKLRELLK KYSQEEQESR HEHHHQHQHQ HQHQHQHQHQ QQQQQHLHRG PHHSLVLDSD

721 VKEKIDVEPH YLQPAVAGQE ISYHDNILVD KEKKKEF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.WNVPTFM.C	Y	26.73	893.4106	-12.4	894.4068	1	29.09	1066	1	32	38	
total 1 peptides												

tr|Q2Q0U9|Q2Q0U9_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ITESHAIMIY LVTKYAKDDA LYPKDPVKQA RVNAALHFES GVLFARMRFV FERILFYGKS DIPEDRAEYV QKAYRLLEDT o Oxida

91 o

81 LTDNY**VAGPV M**TVADFSCIS TVSSIMGVVP LDESEHPKIY AWIGRLKQLP YYEEANGG

o

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.VAGPVM(+15.99).T	Y	26.58	588.2941	45.8	589.3284	1	22.46	851	2	86	91	Oxidation (M)
total 1 peptides												

tr|A0A132AL00|A0A132AL00_SARSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALFRVDYSG RGELNERQIK LGQFMSKLQK LSEEYNVAIF ITNQMTADPG ATMSFQADPK KPIGGHVLAH ASTVRLQLKK

81 GRGENRIVKV YDSPDLPENE ATF**SITDGGI** ADAKD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.SITDGGI.A	Y	21.93	661.3282	16.2	662.3463	1	19.90	769	1	104	110	
total 1 peptides												

tr|W8C706|W8C706_CERCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QQQQQRAHKR KKHLQQQQQR RRQEDLQPHK SRKHEKSHKQ REREHQQQQQ HGMQSSHHAA HRKTKSGLPI ESNINSNEFV

81 ADNIALADAT NAATKAAAAT SALAVNTNKR ATTTAMEQQQ QQKKKNGRNG ASGGGGSGGG GGSGRSGHGI RDVGRQKLHR

161 NVLRMLNSQS E**SLTDGGL**FP PLFNVAPRAH ITVNATCGQS GREEYCKLVD AYPHKKW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.SLTDGGL.F	Y	21.93	661.3282	16.2	662.3463	1	19.90	769	1	172	178	
total 1 peptides												

tr|T1J4F5|T1J4F5_STRMM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWPHNTQFTM DRNSERIPSL TGSSAHISCL YPEILALIFR FLDLRDKGRV AQVCVAWRDA AYHRSVWWGV EAKLHLRRTN
81 PCLFQSLVQR GIRHVQVLSL RRSLREVIHG IPDLESLSLS GCYNVLDESL AQAINRPLSS LVKLNLSLCK QITDETLLNL
161 AQYCPNLEVL DLAGCDRITN SGLLFVSKRL CRLVNLNLRS CRHVSDSGIA ALGGLSSEAG KGTLQLEQLS LQDCQKLTDD
241 ALRNVSTGLV SLKYINLSFC A**SITDGGL**KF MAKMPMLSEL NLRSCDNITD LGIAYLAEGG SKITSLDVSF CDKISDQALT
321 HVSQGLFTLR SLSMSACHIS DEGLLRIART VPELNTLNVG QCHRITDRSL IAISENLTGL QSIDLYGCTK ITTVGLERIM
401 QLPQLNSLNL GLWIKR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.SITDGGL.K	Y	21.93	661.3282	16.2	662.3463	1	19.90	769	1	262	268	
total 1 peptides												

tr|A0A1U9X1T2|A0A1U9X1T2_CNAME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDIMAFVEVS QGPLRGAR**SI TDGGL**EYNQF LGIPYAKPPV GNLRFQSPQS PEPWENVRDA TQFDQNNISC QLNILTGGTT
81 GSEDCLYLNV YTPEVTPEIT LRPVMVFIHG GGFIGGNGTL KSENGPDYLL ENGMVVVTIN YRLGILGFLS LDIPEAAGNM
161 GLKDQVKALE WIRDNISGFG GDKNNVTIMG LSAGSASVDY LMLSPLAKGL FHKAILQSGS TLNHWAINLK TEDFTQQFVT
241 ELGYKGSFDD KHAIYELLLK TPADKLVSLS YLVTEKYTSD RLSFGFVPTV EKDFGNGDAF LTTSPFKLLK EGRFNKVPAI
321 RGFCNKEGAL TCWMKAHILN KLKEKKDFAN VWPCQLNSES KNKYNLKFST IYFDCEKVDE VWEDFFGDID FAAGISIAGK
401 ISSRYAPVYM YKFSYVGDIN YCRNMAAIIP NLTPIPINGA MHGDDNTYVW KIDADAYKNP NEQDILVRKR MVKMFSDFAK
481 TGEPVRSTTN LIQTTWEPYK ESSPVYLGID KELSILEDYE PKKIAIFEEL YENHFP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SITDGGL.E	Y	21.93	661.3282	16.2	662.3463	1	19.90	769	1	19	25	
total 1 peptides												

tr|A0A131Y3Z3|A0A131Y3Z3_IXORI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MENTKHALLE LLSTLSCAQC KQLLSEPHVV GLCGHTVCRK CIASAEACGI CGTPTTHREV KPDHQIKNLI TCTAQLKDLL
81 FTQTPGPAVT SRTTSHNPEV EERSNNAKDE RPPKQAPSED PPPVAPSRAG SLDRRASKGT TNPVSKALEK RNKLGETMLQ
161 VAAIKGNADR VRQLLEEGAD PNVRDHAGWT PLHEACNHGF REVARLLLSH GACVDVAGPG GVTPLHDATV NGHPDVVLLL
241 VRSGATLDAK TSDGLTAQDL AQGEVMRAAL CTAVPPKVVA LRSEGVAS**GP PPVLLASGL**D EAQCRDLARC AELLGGSCRS
321 SFSEEVSHLV VSCDERGNCR QRTLKVLSAL VAGTWILSFS WVEACLRQGR RVDELEHEAK GTRQHPDNGA PARARLRRAS
401 HVDRLFSGLS AVLQGPFARG PSKDDLAALL ALGGASLLSR PPPADAAGVV LLVTEREGRP AQQSGRPGVF GVGAPWLLDC
481 ISKFEVDLPA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GPPPVLLASGL.D	Y	20.89	1019.6015	-56.6	1020.5511	1	25.73	964	1	289	299	
total 1 peptides												

tr|A0A147BG19|A0A147BG19_IXORI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MENTKHALLE LLSTLSCAQC KQLLSEPHVV GLCGHTVCRK CIASAEACGI CGTPTTHREV KPDHQIKNLI TCTAQLKDLL
81 FTQTPGPAVT SRTTSHNPEV EERSNNAKDE RPPKQAPSED PPPVAPSRAG SLDRRASKGT TNPVSKALEK RNKLGETMLQ
161 VAAIKGNADR VRQLLEEGAD PNVRDHAGWT PLHEACNHGF REVARLLLSH GACVDVAGPG GVTPLHDATV NGHPDIVLLL
241 VRSGATLDAK TSDGLTAQDL AQGEVMRAAL CTAVPPKVVA LRSEGVAS**GP PPVLLASGL**D EAQCRDLARC AELLGGSCRS
321 SFSEEVSHLV VSCDERGNCR QRTLKVLSAL VAGTWILSFS WVEACLRQGR RVDELEHEAK GTRQHPDNGA PARARLRRAS
401 HVDRLFSGLS AVLQGPFARG PSKDDLAALL VLGGASLLSR PPPADAAGVV LLVTEREGRP AQQGGRPGVF GVGAPWLLDC
481 ISKFEVDLPA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.GPPPVLLASGL.D	Y	20.89	1019.6015	-56.6	1020.5511	1	25.73	964	1	289	299	
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)