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.

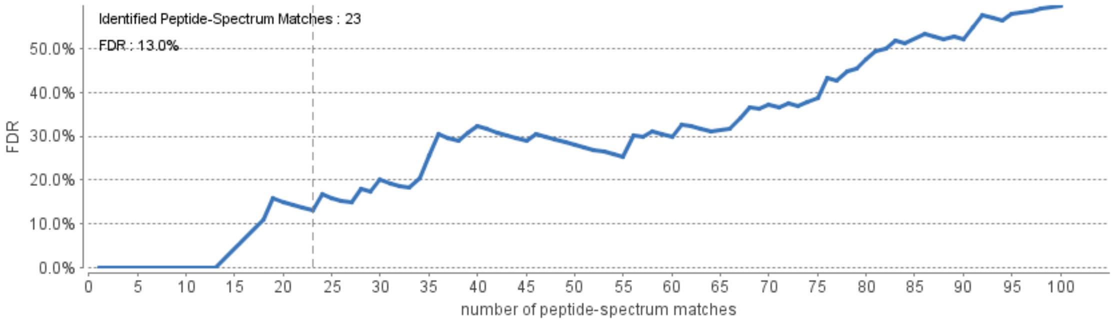
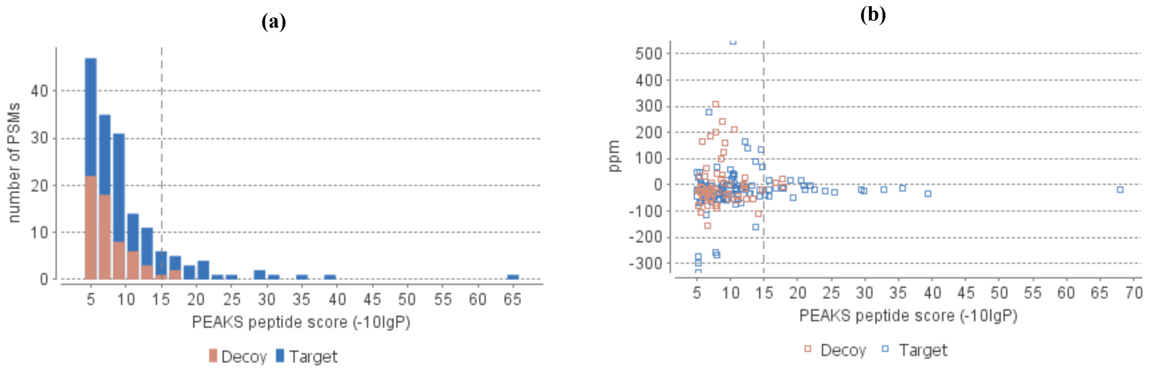
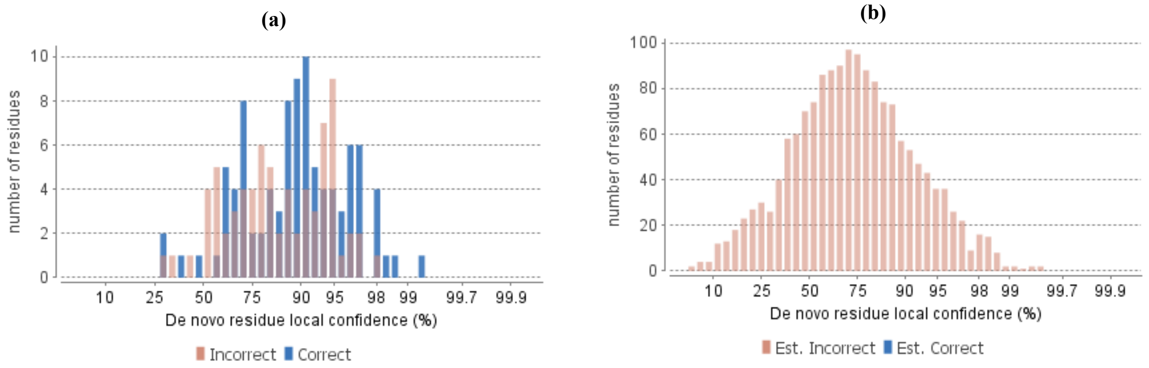


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(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	1181
# of MS/MS Scans	1096

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	23
Peptide Sequences	18

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Carbamidomethyl	57.02	3	C

Protein Groups	10
Proteins	68
Proteins (#Unique Peptides)	0 (>2); 1 (=2); 67 (=1);
FDR (Peptide-Spectrum Matches)	13.0%
FDR (Peptide Sequences)	16.7%
FDR (Protein)	5.9%
De Novo Only Spectra	122

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.

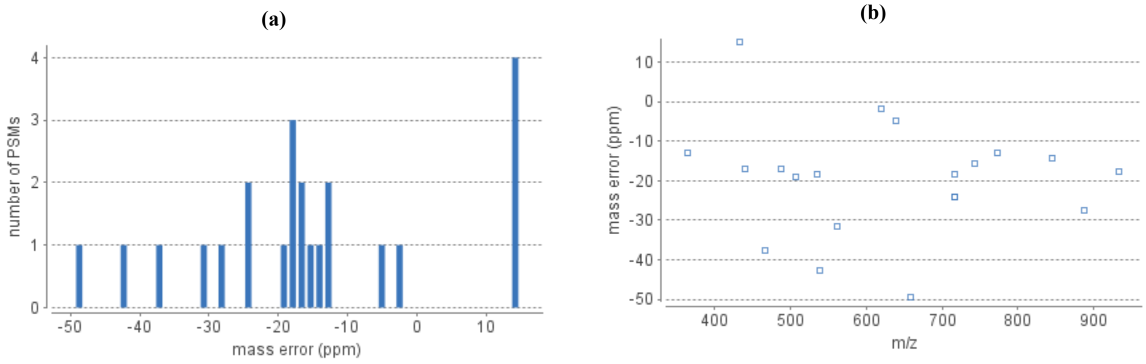


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
Q-TOF	16	1	1	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: 61
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_3_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
5	8131	Q589G4|VKT19_ANOSM	67.94	21	1	1	Y	8494	Kunitz-type serine protease inhibitor As-fr-19 OS=Anoplius samariensis PE=1 SV=1
3	8130	tr|A0A0N0BEI9|A0A0N0BEI9_9HYME	48.38	4	2	2	Y	75503	Angiotensin-converting enzyme (Fragment) OS=Melipona quadrifasciata GN=WN51_03245 PE=3 SV=1
6	8132	tr|E2BSK5|E2BSK5_HARSA	39.35	3	1	1	Y	63832	Glucose dehydrogenase [acceptor] OS=Harpegnathos saltator GN=EAI_14138 PE=4 SV=1
6	8133	tr|E9IBI7|E9IBI7_SOLIN	39.35	1	1	1	Y	130874	Uncharacterized protein (Fragment) OS=Solenopsis invicta GN=SINV_06971 PE=4 SV=1
7	8136	tr|A0A1Y1M757|A0A1Y1M757_PHOPY	32.78	3	1	1	N	32568	Angiotensin-converting enzyme (Fragment) OS=Photinus pyralis PE=3 SV=1
7	8137	tr|A0A1Y1M7A7|A0A1Y1M7A7_PHOPY	32.78	3	1	1	N	32697	Angiotensin-converting enzyme (Fragment) OS=Photinus pyralis PE=3 SV=1
7	8139	tr|A0A1Y1NMS5|A0A1Y1NMS5_PHOPY	32.78	2	1	1	N	41420	Angiotensin-converting enzyme OS=Photinus pyralis PE=3 SV=1
7	8140	tr|D6X4L0|D6X4L0_TRICA	32.78	1	1	1	N	71598	Angiotensin-converting enzyme OS=Tribolium castaneum GN=TcasGA2_TC011052 PE=3 SV=2
7	8141	tr|A0A1Y1NHL6|A0A1Y1NHL6_PHOPY	32.78	1	1	1	N	72105	Angiotensin-converting enzyme OS=Photinus pyralis PE=3 SV=1
7	8142	tr|A0A0U3KDL0|A0A0U3KDL0_MELSA	32.78	1	1	1	N	74790	Angiotensin-converting enzyme OS=Melanoplus sanguinipes P
total 68 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
									E=2 SV=1
7	8143	tr|A0A067RH69|A0A067RH69_ZOONE	32.78	1	1	1	N	124537	Angiotensin-converting enzyme (Fragment) OS=Zootermopsis nevadensis GN=L798_15445 PE=3 SV=1
1	8138	tr|A0A212FPD9|A0A212FPD9_DANPL	29.77	9	1	1	N	14784	Uncharacterized protein OS=Danaus plexippus plexippus GN=KGM_205424 PE=4 SV=1
8	8144	tr|A0A182IYK8|A0A182IYK8_9DIPT	22.48	1	1	1	N	57790	Uncharacterized protein OS=Anopheles atroparvus PE=4 SV=1
8	8145	tr|A0A195FYM1|A0A195FYM1_9HYME	22.48	1	1	1	N	67187	Angiotensin-converting enzyme OS=Trachymyrmex septentrionalis GN=ALC56_00581 PE=3 SV=1
8	8146	tr|A0A158NXU3|A0A158NXU3_ATTCE	22.48	1	1	1	N	73571	Angiotensin-converting enzyme OS=Atta cephalotes GN=105625639 PE=3 SV=1
8	8147	tr|A0A026X3N5|A0A026X3N5_OOCBI	22.48	1	1	1	N	73905	Angiotensin-converting enzyme OS=Ooceraea biroi GN=X777_04634 PE=3 SV=1
8	8148	tr|E2C0X3|E2C0X3_HARSA	22.48	1	1	1	N	75953	Angiotensin-converting enzyme OS=Harpegnathos saltator GN=EAI_13678 PE=3 SV=1
8	8151	tr|A0A151I463|A0A151I463_9HYME	22.48	0	1	1	N	219532	DNA-directed RNA polymerase subunit OS=Atta colombica GN=ALC53_05125 PE=3 SV=1
8	8152	tr|A0A151JMC2|A0A151JMC2_9HYME	22.48	0	1	1	N	221379	DNA-directed RNA polymerase subunit OS=Trachymyrmex cornetzi GN=ALC57_03170 PE=3 SV=1
8	8153	tr|F4WLV0|F4WLV0_ACREC	22.48	0	1	1	N	226184	DNA-directed RNA polymerase subunit (Fragment) OS=Acromyrmex echinatior GN=G5I_06731 PE=3 SV=1
4	8154	tr|A0A0P5A3B7|A0A0P5A3B7_9CRUS	21.89	2	1	1	N	34916	Pentatricopeptide repeat-containing protein 2, mitochondrial OS=Daphnia magna PE=4 SV=1
4	8155	tr|A0A0P5LBI4|A0A0P5LBI4_9CRUS	21.89	2	1	1	N	34738	Putative Mothers against decapentaplegic (Fragment) OS=Daphnia magna PE=4 SV=1
4	8156	tr|A0A0N7ZFR9|A0A0N7ZFR9_9CRUS	21.89	2	1	1	N	36128	Putative Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8157	tr|A0A1I8NYE8|A0A1I8NYE8_STOCA	21.89	2	1	1	N	37579	Uncharacterized protein OS=Stomoxys calcitrans GN=106091417 PE=4 SV=1
4	8158	tr|A0A0N8BB32|A0A0N8BB32_9CRUS	21.89	2	1	1	N	42192	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8159	tr|A0A0P5JFD9|A0A0P5JFD9_9CRUS	21.89	1	1	1	N	46466	Pentatricopeptide repeat-containing protein 2, mitochondrial OS=Daphnia magna GN=APZ42_016913 PE=4 SV=1
4	8160	tr|Q7Q083|Q7Q083_ANOGA	21.89	1	1	1	N	46213	AGAP012308-PA OS=Anopheles gambiae GN=1280386 PE=3 SV=4
4	8162	tr|W5JB06|W5JB06_ANODA	21.89	1	1	1	N	47538	Zinc carboxypeptidase OS=Anopheles darlingi GN=AND_006695 PE=3 SV=1
4	8161	tr|A0A0P5RA30|A0A0P5RA30_9CRUS	21.89	1	1	1	N	47848	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8163	tr|A0A0P5DXU8|A0A0P5DXU8_9CRUS	21.89	1	1	1	N	47655	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8164	tr|Q702G3|Q702G3_ANOGA	21.89	1	1	1	N	48176	Carboxypeptidase B OS=Anopheles gambiae GN=cpbag1 PE=2 SV=1
4	8165	tr|A0A0P5B3S6|A0A0P5B3S6_9CRUS	21.89	1	1	1	N	48417	Mothers against decapentaplegic (Fragment) OS=Daphnia magna PE=4 SV=1
4	8166	tr|Q7PID6|Q7PID6_ANOGA	21.89	1	1	1	N	48569	AGAP006209-PA OS=Anopheles gambiae GN=1276871 PE=3 SV=4
4	8167	tr|A0A0P5M2I6|A0A0P5M2I6_9CRUS	21.89	1	1	1	N	50290	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8168	tr|A0A0P5C2M5|A0A0P5C2M5_9CRUS	21.89	1	1	1	N	50841	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8169	tr|A0A0P5HDA5|A0A0P5HDA5_9CRUS	21.89	1	1	1	N	50939	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8170	tr|A0A0P6EQJ0|A0A0P6EQJ0_9CRUS	21.89	1	1	1	N	51101	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8171	tr|A0A0P5DIN0|A0A0P5DIN0_9CRUS	21.89	1	1	1	N	51516	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8172	tr|A0A0P5M5J7|A0A0P5M5J7_9CRUS	21.89	1	1	1	N	52559	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8173	tr|A0A0N8E8V7|A0A0N8E8V7_9CRUS	21.89	1	1	1	N	52574	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8174	tr|A0A0P5PZQ6|A0A0P5PZQ6_9CRUS	21.89	1	1	1	N	52523	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8175	tr|A0A0P6ET66|A0A0P6ET66_9CRUS	21.89	1	1	1	N	53371	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8176	tr|A0A0P5BMN3|A0A0P5BMN3_9CRUS	21.89	1	1	1	N	52807	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8177	tr|A0A0P6FYK6|A0A0P6FYK6_9CRUS	21.89	1	1	1	N	53057	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8178	tr|A0A0P5TJM7|A0A0P5TJM7_9CRUS	21.89	1	1	1	N	53928	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8179	tr|A0A0P5KXS1|A0A0P5KXS1_9CRUS	21.89	1	1	1	N	54007	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8180	tr|A0A0P5KPE8|A0A0P5KPE8_9CRUS	21.89	1	1	1	N	54686	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8181	tr|A0A0P5SIJ1|A0A0P5SIJ1_9CRUS	21.89	1	1	1	N	54343	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8182	tr|A0A0N8D6J9|A0A0N8D6J9_9CRUS	21.89	1	1	1	N	55033	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8183	tr|A0A0P4XFP1|A0A0P4XFP1_9CRUS	21.89	1	1	1	N	55293	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8184	tr|A0A1B6HBZ2|A0A1B6HBZ2_9HEMI	21.89	1	1	1	N	52982	Uncharacterized protein OS=Homalodisca liturata GN=g.8948 PE=3 SV=1
4	8185	tr|A0A0P5QKL6|A0A0P5QKL6_9CRUS	21.89	1	1	1	N	57441	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8186	tr|A0A0P5S908|A0A0P5S908_9CRUS	21.89	1	1	1	N	57250	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8187	tr|A0A0P5KS39|A0A0P5KS39_9CRUS	21.89	1	1	1	N	58535	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8188	tr|A0A0P5BTW7|A0A0P5BTW7_9CRUS	21.89	1	1	1	N	59853	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
total 68 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
4	8189	tr|A0A0P5QM79|A0A0P5QM79_9CRUS	21.89	1	1	1	N	61539	Sodium/nucleoside cotransporter OS=Daphnia magna PE=3 SV=1
4	8190	tr|A0A0P6HR38|A0A0P6HR38_9CRUS	21.89	1	1	1	N	67749	Mothers against decapentaplegic OS=Daphnia magna PE=4 SV=1
4	8191	tr|A0A1Y1MIY0|A0A1Y1MIY0_PHOPY	21.89	1	1	1	N	70512	Uncharacterized protein OS=Photinus pyralis PE=4 SV=1
10	8150	tr|A0A0J7NMH8|A0A0J7NMH8_LASNI	21.04	2	1	1	N	64285	Glucose dehydrogenase OS=Lasius niger GN=RF55_6207 PE=4 SV=1
9	8149	tr|B3MFH2|B3MFH2_DROAN	21.02	4	1	1	N	33672	Uncharacterized protein OS=Drosophila ananassae GN=Dana\GF11836 PE=4 SV=1
2	8309	tr|B0XJD4|B0XJD4_CULQU	20.50	1	1	1	N	59735	Av71 muscle cell intermediate filament OS=Culex quinquefasciatus GN=6053719 PE=4 SV=1
2	8327	tr|A0A1W4VCE8|A0A1W4VCE8_DROFC	20.50	1	1	1	N	97389	AF4/FMR2 family member 4 isoform X3 OS=Drosophila ficusphila GN=LOC108093614 PE=4 SV=1
2	8397	tr|A0A1B0B969|A0A1B0B969_9MUSC	20.50	0	1	1	N	163380	Uncharacterized protein OS=Glossina palpalis gambiensis PE=4 SV=1
2	8431	tr|A0A0R1EA16|A0A0R1EA16_DROYA	20.50	0	1	1	N	171438	Uncharacterized protein, isoform B OS=Drosophila yakuba GN=Dyak\GE16333 PE=4 SV=1
2	8434	tr|A0A0R1E9C4|A0A0R1E9C4_DROYA	20.50	0	1	1	N	177024	Uncharacterized protein, isoform C OS=Drosophila yakuba GN=Dyak\GE16333 PE=4 SV=1
2	8470	tr|A0A182R4W9|A0A182R4W9_ANOFN	20.50	0	1	1	N	370426	Histone-lysine N-methyltransferase OS=Anopheles funestus PE=4 SV=1
2	8466	tr|A0A226EGW7|A0A226EGW7_FOLCA	20.50	0	1	1	N	344514	Nucleosome-remodeling factor subunit BPTF OS=Folsomia candida GN=Fcan01_09031 PE=4 SV=1
2	8450	tr|B4Q082|B4Q082_DROYA	20.50	0	1	1	N	196414	Uncharacterized protein, isoform A OS=Drosophila yakuba GN=Dyak\GE16333 PE=4 SV=1
total 68 proteins									

Q589G4|VKT19_ANOSM

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMLLVLSISA ILQVSHSVSF CLLPIVPGPC TQYVIRYAFQ PSISACRR**FT FGGCEGNDNN FMTR**RDCEHY CEELL

C Carba

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FTFGGC(+57.02)EGNDNNFMTR.R	Y	67.94	1865.7461	-17.7	933.8638	2	21.42	798	1	49	64	Carbamidomethylation
total 1 peptides												

tr|A0A0N0BEI9|A0A0N0BEI9_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VTKLQRKFHR LLVAVLVTVA WGIPTPEDTS NAAADSEQDL QRAKQFLEQL NEEYGEWNNK YTLANWEYAA NLTEENLAKK

C Carba

81 LNVSAETARY FKSAWEKVNV YPWKDIKDSG IRRQFKKFSV LGRSALPEDR YQEYEK**IISD MENIYSTAK**I CDYKNRSK**CD**

161 **LALEPELTEL LMK**SRDPEEL KYIWIEWRKA TGEKVKSLYP KYVELSNLAA TLNNFSDNAA YWLKDYEADD FPEQIETLWQ

241 QLKPLYLQLH AYVRRELRKK YGENVVSKDG PIPAHLLGNM WAQTWTNIAD FAIPYPGKQM PDVTHAMIKQ GYNATTIFRV

321 AEDFFTSINL TAMPDLFWQR SILEKPKDRE LICHASAWDF YDGKDFRIKQ CTRVNMEDLL TAHHEMGHVE YYLQYKDQPN

401 IFKEGANPGF HEAVGDVISL SASTPSHLKA IKLLDDDSTD TEANINHLFL KGLEKIVFLP FAYMMDKWRW NVFQGQVTSD

481 NYNCNWWDLA EEFQGIEPPV DRSEDDFDPG AKYHIIADVE YMRYFVSFVV QFQFHKALCI EAKQYDPQNP NSKLLHECDI

561 YNNKAAGNLL KNMLELGSSK PWQDAMEKIT GQKSMESAGL LEYFKPLTDW LTAENKKTNE YIGWKPKARQ CVQTRSELAS

641 FEETEAEE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IISDMENIYSTAK.I	Y	35.63	1483.7228	-15.8	742.8569	2	19.26	723	1	137	149	
K.C(+57.02)DLALEPELTELLMK.S	Y	25.49	1773.8893	-27.5	887.9275	2	32.84	1166	1	159	173	Carbamidomethylation
total 2 peptides												

tr|E2BSK5|E2BSK5_HARSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAVHPVVNE PCNHVKPISR PSGTYDFIVV GAGAAGPVVA ARLSEVDKWS VLIVEAGPDE APGMQIPSNL QLYLNTDMDW

C Carba

81 NYKTKNEKYA CLEDGGRCSW PRGK**NLGGCT AHHGMAYHR**G HKEDYTRWVK MGAEGWSWEE VLPHFIKSEN NKDIDKFVNK

161 RYHGYGGPMT VERFPWQPQF AGDVLKAAEQ LDFGITNDMV GEKITGFTIA QTISKGGVRL SSSRAFLWPN RDRKNLQVLV

241 NATATKIHTK MVGKQVKASG ITVVMKNGQS YRVNARKEVI LTAGAINSPH LLLLSGIGPK RHLDTMGINT VVDLPGVGEN

321 LHNHASFGLD FVLDEPNADE LSLDNVKTYF HDQTGPLAST GLAQLTAILA SSYSSNDDPD IQIFSAGYQA ICDTGDRIPD

401 LQTYSENRVV RFTSVNLQTR SRGRITLDSK DPTQPPNIWS NELSKRRDRD IIYEGLQKIL KLPEAEALKK YSMKLIDNTA

481 SKCKKLGEPT ESNAGYWDCQ IRYKTRPENH QAGTCKMGAY NDVMAVVDPQ LRVYGISNLR VADAAVMPQV ISGNPVATIN

561 MIGERAADFI KKDYGMF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLGGC(+57.02)TAHHGMAYHR.G	Y	39.35	1680.7362	-31.4	561.2351	3	7.36	349	1	105	119	Carbamidomethylation
total 1 peptides												

tr|E9IBI7|E9IBI7_SOLIN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTFVVLKLGG SAGAVVASRL SDIHEWKVLL LEAGPDEPPG AEVPSMVAMF LGTDIDWQYQ TTNEMNACLS TGGTCSWPRG C Carba
81 KNLGGTSVHN GMMYNRGHAK DFDNWAARGN PGWSWRDVLP YFMCSENNTE IHRVGRKYHS TGGLLTVERF PWKPPIADDI
161 LAAAAERGYP ISEDLNGDQF TGFSVAQTTS KNGVRVSSAA AYLRPVRHRR NLHVSLNATV TKILIENSKA VGVQFYQDGE
241 LRVARATKEV IASGGAVNSP QLLLLSGIGP KEHLRAMNVT VVKDLPGVGE NLHNHVSYTL SWTINQPNLY DLTWASAAEY
321 IAFQKGPMAS TGLSQLTGML PSIYTTPDHP DIQLFFGGYQ AACATTGEVG AIMNNNGRSI SMSPTMTHPR SKGKLRLASN
401 NPLEAPIIWA NYLSDPMDVT ILVEGIEIAL SLANTNAMAK YNMTLNHRPL PVCSQYPYLS KEYWACAVRQ DTGPENHQAG
481 SCKMGPHNDP MAVVDHRLRV YGIRNLRVAD ASIMPQKKKY KRDHAIVFQG NVQQHGSPGH DDRRKGGRVH QVRLGRCRYT
561 MNVSGISEAT CLSPFVGGLS LTDVCVSNST TLFLSLVNMI AACNPKINGE QRITPIKRPR FVYDFIVVGG GAAGSVVASR
641 LSENEKWNVL LVEAGPDETV GMQIPSNLQL FLNTDMDWKY KTTNESYACL KNNGSCSWPR GK**NLGGCTAH HGMAYHR**GHA

721 KDYSRWVEMG NQGWSWEDVM PYFLKSENNR EIGRVRAEDH ATGGPMTVER YVVLNKKKKS SMSFSKFPWQ PQFAWDIMTA
801 AEETGLGVSE DLVGQNITGF TVAQTISKSG VRLSAARAYL WPYANRPNLD VALNAIVTKI NTKKICSKVK TEGITFIMNG
881 RQHHVRARKE VILTAGTINS PQLLLLSGIG PKSHLKSVGI HTVVDLPGVG ENLHNHMSYG IDFTLKEKNT VELNMPTADL
961 YLYNQTGPMS STGLAQLTGI LASNYTTADD PDIQIFFAGY QAVCNTGGRI EDLKTYDNKP TVRFTAVNLQ ARSRGRITLE
1041 SKNPLQHPII WSNDMSNPQD RSIIYQGIQH ILKLSKANTM KKYHLHMIDE TNSECKQYKK HKNYEYWDCQ FRYNTRPENH
1121 QAGTCKMGPS SDPMSVVDPS LKVHGIEGLR VADASIMPKM VSGNPVAAIN MIGERVADFI KKDYK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NLGGC(+57.02)TAHHGMAYHR.G	Y	39.35	1680.7362	-31.4	561.2351	3	7.36	349	1	703	717	Carbamidomethylation
total 1 peptides												

tr|A0A1Y1M757|A0A1Y1M757_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNARLFLYLV SFITLSVAAD PPLEDEETRG KAYIKLLNEK TATRFNRETL ASWKYDSNIT EQNLEEQLKV STESAKEAKE
81 DWLKTIKFDW GSFSDYDLRR QFKKFSILGR SALPEEKFLK LEKSISDMET IYSTAKICDY NNKTNCDLSL EPEITDILAT
161 SRDPEELK**HV WVEWR**RKNAP ARELFKEYVK YVNEVAVLNN FTSNTAYWLH NYESSTFVQV DTIWEQLKPL YQQLHAYIRF

241 KLRQRYGSIV SKRGPIPAHL LGNMWAQSWV NVADFTI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HVWVEWR.R	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	169	175	
total 1 peptides												

tr|A0A1Y1M7A7|A0A1Y1M7A7_PHOPY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNARLFLYLV SFITLSVAAD PPLEDEETRG KAYIKLLNEK TATRFNRETL ASWKYDSNIT EQNLEEQLKV STESAKEAKE
81 DWLKTIKFDW GSFSDYDLRR QFKKFSILGR SALPEEKFLK LEKSISDMET IYSTAKICDY NNKTNCDLSL EPEITDILAT
161 SRDPEELK**HV WVEWR**RKNAP ARELFKEYVK YVNEVAVLNN FTSNTAYWLH NYESSTFVQE VDTIWEQLKP LYQQLHAYIR

241 FKLRQRYGSI VSKRGPIPAH LLGNMWAQSW VNVADFTI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HVWVEWR.R	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	169	175	
total 1 peptides												

tr|A0A1Y1NMS5|A0A1Y1NMS5_PHOPY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRAHVFVCLV SFIFAAVAKD PSLEDEEIRA RAYVKLLNDK IALRNNRETL AAWKYASNIT EENLKEQLDV SKESAKETKE
81 DWLETIKFNW RSFGDYDLRR QFEKLSILGK SALPEEKFLK LEKIISDMQT IYSTAKICDH KNKTKCDLVL DPEITDILAN
161 SRDPEELK**HV WVEWR**HKNAP AKELFRDYVK YANEAAVLNN FTSNTGFWLY DYESPTFVQD VESIWEQLKP IYTQLHAYIR

241 TKLRQRYGDI VSEKGPIPAH LLGNMWAQSW SNIADFTLPH PSAKRADITS ELLNQGYDAL KMFKTAEEFF VSLNLKKMTP
321 EFWERSILVK PNDGRELVCH ASAWDFFDKK RFPD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HVWVEWR.H	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	169	175	
total 1 peptides												

tr|D6X4L0|D6X4L0_TRICA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDLVLVLVLG LLVHAGGATD PEIEDEELRA RDFLQFLNKK NEESSNRLVL AEWAYASNIT EQNLQNKLAV SAEVAKEHKK
81 DWEEVTKFNW NTFSDPDLKR QFKKYSKLGS DALPEAKLNR YQKIISEMEK IYSTAKICDF HNSSKCDLSL EPHLTQILAT
161 SRNEEELR**HV WVEWR**NAVGP HCKVLFEEYV DLANEAARLN NFTNNAENWL DNYEDAQFRG QIEGLWEQLK PLYLQIHAYV

241 RFKLREKYGE VVSEKGPIPA HLLGNMWAQK WRTVSEFTLP YPDKKDEDIT SELKKQNYTA VKIFQTAEDF FKSINLTEMP
321 ETFWERSILT KPNDREIVCH ASAWDFYDRK DFRIKQCTQI TLEHFITAHH EMGHVEYFIQ YKNQPIPFRE GANSGFHEAV
401 GDLIALSSEK DDPENVLNNL FQIGLDKIVF LPFGYLMDLW RWDVFEGKIT PDEYNCKWWE LREKYQGVEP PLNRSEGDFD
481 PAAKYHIVAS VPYIRYFVSF VVQFQFHKAL CEKAGQYDPN DPSKPLHECD IYQSTEAGNA LKKMLQLGSS KPWHEAMELL
561 TGHKTMDASA ILEYFKPLQK WLENENQKNG AFIGWEKSTK VCVNSQKGEK PKSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.HVWVEWR.N	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	169	175	
total 1 peptides												

tr|A0A1Y1NHL6|A0A1Y1NHL6_PHOPY

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRAHVFVCLV SFIFAAVAKD PSLEDEEIRA RAYVKLLNDK IALRNNRETL AAWKYASNIT EENLKEQLDV SKESAKETKE
81 DWLETIKFNW RSFGDYDLRR QFEKLSILGK SALPEEKFLK LEKIISDMQT IYSTAKICDH KNKTKCDLVL DPEITDILAN
161 SRDPEELK**HV WVEWR**HKNAP AKELFRDYVK YANEAAVLNN FTSNTGFWLY DYESPTFVQD VESIWEQLKP IYTQLHAYIR

241 TKLRQRYGDI VSEKGPIPAH LLGNMWAQSW SNIADFTLPH PSAKRADITS ELLNQGYDAL KMFKTAEEFF VSLNLKKMTP
321 EFWERSILVK PNDGRELVCH ASAWDFFDKK DFRIKQCTSV NFEDFTTAHH EMGHIQYYLQ YSDQPVVYRQ GANDGFHEAV
401 GDVMSLSVSS TKHLKRIGLI DANTPDNDAV DLNALFMIGL DKIAFLPFGY LMDKWRWGIF DGNITAEDYN CKWWEYRTSI
481 QGVEPPVDRS EDDFDAAAKY HIVADVPYLR YFVSFVIQFQ FHRAACELAG EYDPEDPTKP LHKCDIYHST KAGESIAKML
561 QMGSSRPWPD AMEVLTGQRK MDASGLLEYF RPLHKWLEAE NKKNGAYIGW ESTQKKCTKR Q

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HVWVEWR.H	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	169	175	
total 1 peptides												

tr|A0A0U3KDL0|A0A0U3KDL0_MELSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLWRWVWAAV AAAALAAAAG GLDPEQEVRV VDPEQQARHY LQLLDREYGR RANAETLAEW AYAANITDQT LQRKLNISAE
81 HAKFQKQQWL ETIKYPWQTY RDPDIRRQFQ KYSVLGTAAL SEEKFDKLEK LVSEMESIYS TAKVCDYNDA TQCDLSLEPE
161 LTERLAESRD PKELS**HVWVE WR**HASGEKVR SQFEHYVALS NEAAVLNNFT DASAYWLKDY EADDFQDQVK ALWDQVKPLY

241 QQLHAYVRRR LHDKYGDDVV NRRGPIPAHL LGNMWAQTWN NIFDFTIPFP GKQSIDVTEE MVKQGYTPLR MFKLSEEFFV
321 SLNLSAMPEL FWKNSILEKP AGRELICHAS AWDFYDSKDF RIKMCTTVTM KQLFVVHHEM GHIQYYLQYK HQPTVYKGGA
401 NPGFHEAVGD VMALSVSTPK HLRKVGLLDS SSTDDPEATI NYLYLQGLQK VAFLPFAYVV DLWRWAVFQG EITSDAYNCN
481 WWKLRGQYQG IEPPVDRTEE DFDPGAKYHV IASVPYIRYF VSFIIQFQFH RALCIEAGEY DPKDETKPLH ECDIYQSTKA
561 GNLLSKMLQM GSSKPWPDAM EVVTGQRLMD ASGLLEYFRP LHKWLEAENA KTGEYIGWDP TDKHCVQTRV ELEKLKAQPG
641 EAEMAE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.HVWVEWR.H	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	176	182	
total 1 peptides												

tr|A0A067RH69|A0A067RH69_ZOONE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DLVEILRTSR DPEELK**HVWV EWR**KASGEKC RGMFEHYVAL SNEAATLNNF TDTAEYWLKD YESPDFRDQV SRLWDQVQPL
81 YLQIHAYVRR KLRETYGEKL VTRRGPIPAH LLGNIWTQLW GNIQSISAPY PDKSTIDVTS TMVKQGYTPL KMFKLAEEFF
161 ISLNLSAMPE TFWERSILEK PMDRDLICHA SAWDFHDGKD FRIKQCTRIV TDDLFTAHHE MGHVQYFIQY KDQPVAYKDG
241 ANPGFHEAVG DVIALSVLTP KHLREIGLLE GDASTGEDYE ATINYLYLQG LQKIVFIPFA YLMDLWRWDV FKGHITSKNY
321 NCEWWKLRHK YQGIDPPVDR TEEDFDPGAK FHIIANVPYI RYFVSFVIQF QFHRSLCKKA GQFDPNNPKK PLHECDIYRS
401 TEAGNLLREM LQMGSSKPWP DAMEVLSGQR EMDASGMLEY FKPLTEWLEK NNKQFGEHIG WEPNRANPYL LRFRNGVCLK
481 FCQRLAKTAT ENYEMLKQAF GESAMGRAQT FVWHSRFKNG RTSVDDDEQA AKFSKQQWQE TIKYPWTTYT DPDIRRQFKK
561 HSVLGNAALD PDKYEKYEQL VSDMSSIYSK AKICDYKNPN KCDLSLEPGI MHNSYFKDVG GLRENNFRIG IHVLRSYPEL
641 FEAIEEGKSV LDFTDTAEYW LKDYESPDFR DQVSRLWDQV QPLYLQIHAY VRRKLRETYG EKLVTRRGPI PAHLLGNIWS
721 QTWNNIMDIS APYPEKEAID VTPQMKKQGY TPLKMFKLAE EFFISLNLSA MPETFWERSI LEKPDDRELI CHASAWDFYD
801 GKDFRIKQCT RIDLDDLFTA HHEMGHVQYF IQYKDQPLAY KEGANPGFHE AVGDVMSLSV STPKHLREIG LLEGDESTGK
881 DYEATINYLF LQGLQKIVFL PYAYQTDLWR WDVFKGEITS DDYNCKWWKL REKFQGIEPP VDRTEEDFDP GSKYHVIASV
961 PYIRYFVSYV IQFQFHRALC EKAGQFDPKD PKLPLHECDI YRSTEAGNLL GKMLQLGSSK PWPDAMEVLT GQREMDASGL
1041 LDYFRPLADW LEKDNKQTGE YIGW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.HVWVEWR.K	Y	32.78	1010.5086	-19.1	506.2520	2	17.06	652	1	17	23	
total 1 peptides												

tr|A0A212FPD9|A0A212FPD9_DANPL

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDSLMTIIER **YPSETEIVTY TK**HTITTSEK HEDKQEDFDF SREGSAVREL SPSSGRSVAH STVSGKHFTD PASGSWSGQD
81 EELSSSGSFS RARADLMLGS TDSLEATSSN ATRATYNYEV DTPMTGSLTS GGKFHN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.YPSETEIVTYTK.H	Y	29.77	1429.6976	-24.2	715.8388	2	20.31	770	3	11	22	
total 1 peptides												

tr|A0A182IYK8|A0A182IYK8_9DIPT

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPDKRVIPSV PPKGRKAQLE NS**WNVFQGK**A CHPIEPGIQI DSQQSASSFT KKHSPGHIKR PMNPFMVWSQ IERRKICEVT
81 PDMHNAVISK NLGQRWKQLT AAERQPFIDE AERLRQLHSR EYPNYKYRPK KKQVKGTTHK TVAAGSGSPS PASSSSSTGS
161 PESVSSRDSC GSSSSSSSSS SSAPSAAATP TGKPSTGASS KRSRASGKVS KGSYASTNGG LKSKKQVIIH ELGQQTMAAV
241 ATAATVTTLA AQPDCYSLAT PKLLPNSPES ATLYDESSMI SPEPPFGAFS DGTPIFSTDL NMFDVDESKD FDHDGKAFLF
321 ANGANGLGDS ATTNSTNTSI TSSSPNDSIG HGHPNATCNS PLPQHQNHHP QSNLNNNNNN SLQINNNHLQ QQQQQQQQHQ
401 HQLTSEDKLF ECQQQQQHQL SPQQSICYSD TDGDCVKSEK YYDDDDCQSD RFGGILDGDS CLDAVSGINR IDESLDLGPD
481 DLPILDGMFS TARMDGLGFE TMETASSSSG SHLEFITNDN SIFLTEQNLI EYNV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
S.WNVFQGK.A	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	23	29	
total 1 peptides												

tr|A0A195FYM1|A0A195FYM1_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLLAYVGNPR RLAALLKIST HGQIRNYNEF EMTVSKMENI YSTAKICDYH NKSKCDLALE PEIIEISKNS HDSEELKHIW
81 VEWRKVSGEK VKSLYSKYVE LANTVATLNN FSDYAAFWMK DYEADDFPEQ IETQWQQLKP LYLQLHAYVR RELRKKYGED
161 IVSKDGPIPA HLLGNPWAQT WNIANFTVPF SGKQLPDVSA ALVEQGKFMF ESFNTIKELI YYNATSMFRL AENFFISINL
241 TAMPDTFWKK SILTKKHGVD MICHASAWDF YDGEDFRIKQ CTRVNMEDLL TAHHEMGHIE YYLQYKNQPV VFKEGANPGF
321 HEAVGDVISL SVSTPSHLKK IGLLTDDSTD REAFLNHLYM KSLDKIVFLP FAYMMDRWR**W NVFQGK**VTPD NYNCNWWTLA
401 EEYQGIEPPV DRSEEDFDPG SKYHIIAGVE YIRYFVSFVI QFQFHKALCI EAKQYDPSNP NAKPLSQCDI YDNKDAGNLL
481 KSMLELGSSK PWQDAMEKIS GQRQMDAAGL LEYFKPLTDW LIEENKKTNE YIGWKPSKKR THHKYIKYFI KFYFHILCIF
561 YISYFYSNWD IPF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	380	386	
total 1 peptides												

tr|A0A158NXU3|A0A158NXU3_ATTCE

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLRLILVAVV ITLVAAKPTT EDADIKSETS DDLLKSAHEL LKRIDAEYAK WNNIQSITAW NYASNLTNEN LAEKLKCSAE

81 GANVTKHIIQ IVNDFPWRDL KNESMKRQFK KLSILGVAAL PEQSYNEFEM TVSKMENIYS TAKICDYHNK SKCDLALEPE

161 IIEISKSSHD PEELKHIWVE WRKVSGEKVK SLYSKYVELA NTVATLNNFS DYAAFWMKDY EADNFPEQIE TQWQQLKPLY

241 LQLHAYVRRE LRKKYGENIV SKDGPIPAHL LGNPWAQTWN IANFTVPFSG KQLPDVSAAL IEQDYNATSM FRLAENFFIS

321 INLTAMPDTF WKKSILTKKD GVDMICHASA WDFYNAEDFR IKQCTRINME DLLTAHHEMG HIEYYLQYKN QPVVFKEGAN

401 PGFHEAVGDV ISLSVSTPSH LKKIGLLMDD STDREAFLNH LYMKSLDKIV FLPFAYMMDR WR**WNVFQGK**V TPDNYNCNWW

481 TLAEEYQGIE PPVDRSEEDF DPGSKYHIIA GVEYIRYFVS FVIQFQFHKA LCIEAKQYDP SNPNAKPLSQ CDIYDNKDAG

561 NLLKSMLELG SSKPWQDAME KISGQRQMDA AGLLEYFKPL TDWLTEENKK TNEYIGWKHS KKQCVQTRGE LVNYSY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	463	469	
total 1 peptides												

tr|A0A026X3N5|A0A026X3N5_OOCBI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLRLLLVAAV VALTAATPTG EDSASATENP QVAEDVLKNA KDMLKRLDAQ YAEWNNKQSL AGWDYASNLT DENLAKKLNV

81 SAEAARVSKE IAQEVNAFPW RDLKDENIRR QFNKLGILGI SALPEDMYKE FEMTVNKMEK IYSTAKICDY KNKTKCDLAL

161 EPEITEILMR SRDPKELKHI WVEWRKASGE KVKSLFPRYV ELANVAAKLN NFSDYAAYWM KDYEADDFPE QIENLWQQLK

241 PLYLQLHAYV RRELRKKYGE DIVSKDGPIP AHLLGNTWAQ TWSNIADFTT PFPGKQLPDV SAALVEQGYN ATSIFRLAES

321 FFKSINLSAM PDTFWERSIL TKQKDVDMIC HASAWDFYDG KDFRIKQCTR INMEDLLTAH HEMGHVEYYL QYKNQPTVFK

401 EGANPGFHEA VGDVISLSAS TPSHLKKIGL LQDESTDPEA LLNHLYVKSL DKIAFLPFAY MMDRWR**WNVF QGK**VTPDNYN

481 CDWWSLAEEY QGIEPPVDRS EEDFDPGSKY HIIADVEYIR YYVSFVIQFQ FHKALCTKAK QYDPKNPDAN LLSQCDIYDN

561 KDAGNLLKSM LELGSSKPWP DAMEKIAGQR QMDSAGLLEY FKPLIDWLTE ENKKTNEYIG WKPSTKQCVQ TRGELGVTDE

641 PSQ

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	467	473	
total 1 peptides												

tr|E2C0X3|E2C0X3_HARSA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKIEEGREMT IEILLTVAVV ALVITATPTS KEPTEASPVA TNPTEDSQST DVLKNAKSVL KRLDAELGKW YNKQSIAEWN

81 YASNLTKENL AEKLNMSVMV TTALKHISQE ANNFPWEDLK DEDIKRQFKK LSVVGNAMLS EEVQKEFDET ISTMQNIFST

161 AKICDYVNRT KCDIALEPEI TEIFMRSRDP KELEYIWVEW RKASGEKVKS LYIKYVEMAN NIARLYNYPD YAAYWMRDYE

241 TDNFPEQIET LWQQLKPLYL QLHAYVRREL REKYGEDLVS KDGPIPAHLL GNVWAQSWSN IADFTIPFPG KQLPDVSSSL

321 VKQGYNATSI FRLAEDFFKS INLTAMPDSF WEKSILTKIE DVDMICHASA WDFYDGKDFR IKQCTRINME DMFTAHHEMG

401 HVEYFLQYKD QPTIYKQGAN PGFHEAVGDV IALSVSTPSH LKNIGLLQDD STDPEAMLNN LYVKSLEKIV FLPFSYMLDR

481 WR**WNVFQGK**V TSDNYNCNWW SLAEEYQGIE PPVDRSEEDF DPGAKYHVVA DVEYIRYFVS FVIQFQFHKA LCTEAKQYDP

561 KNPEAHLLHQ CDIYNNKDAG NLLKSMLEMG SSKPWPDAME KITKQRDMDS AGLLEYFKPL INWLTEENKK TNEYIGWKPS

641 NRKCVQTRGE LRVIS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	483	489	
total 1 peptides												

tr|A0A151I463|A0A151I463_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKRQFKKLSI LGVAALPEQS YNEFEMTVSK MENIYSTAKI CDYHNKSKCD LALEPEIIEI SKSSHDPEEL KHIWVEWRKV
81 SGEKVKSLYS KYVELANTVA TLNNFSDYAA FWMKDYEADN FPEQIETQWQ QLKPLYLQLH AYVRRELRKK YGENIVSKDG
161 PIPAHLLGNP WAQTWNIANF TVPFLGKQLP DVSAALIEQG RFIFESFKIF TIKESIYYNA TSMFRLAENF FISINLTAMP
241 DTFWKKSILT KKDGVDMICH ASAWDFYNAE DFRIKQCTRI NMEDLLTAHH EMGHIEYYLQ YKNQPVVFKE GANPGFHEAV
321 GDVISLSVST PSHLKKIGLL MDDSTDREAF LNHLYMKSLD KIVFLPFAYM MDRWR**WNVFQ GK**VTPDNYNC NWWTLAEEYQ

401 GIEPPVDRSE EDFDPGSKYH IIAGVEYIRY FVSFVIQFQF HKALCIEAKQ YDPSNPNAKP LSQCDIYDNK DAGNLLKSML
481 ELGSSKPWQD AMEKISGQRQ MDAAGLLEYF KPLTDWLTEE NKKTNEYIGW KHSKKLVFKS RPSMVKEQFR ETNVASEVSH
561 ISFGVNSMLD INMQASVEMI SKNLYNEDTK HTPALQGALD RRMGVSSTGV ECETCNKKLN DCVGHFGYLN LELPVFHVGY
641 FKSIIQILQT ICKSCAHVLL THEERKFFSR SIQNPKSGYL MRKALRKKIL EVARKKTVCP NCKSNNGPVK KAGFLKIVHE
721 KYKNLKKIDP IIQEKLAELA PKMERDIEFK NIVEQNYRLF FKVQELFNRI PTGDIFFLLM NPECAAPVDL VLRRIPVPPI
801 CIRPSILSDL KAGTNEDYLT MKLSEIALIN DVIRRQKGVN INTYMEHWDF LQLHCGLYIN SEMSGIPLHM QPKKSGRGIV
881 QRLKGKQGRF RGNLSGKRVD FTSRTVISPD PNLRIEQVGV PIHVAKTLTY PERVIPSNME LMRKLVRNGP DTHPGANYIQ
961 YKNSQNRRYL GYGDRNKAAQ DLQYGDIVER HLKDDDLVLF NRQPSLHKLS IMTHRTKVLE HRTFRFNECV CAPYNADFDG
1041 DEMNLHLPQT EEARAEALVL LANKSNLVTP RNGDLLIAAT QDFITGAYLL TQKDTFLQLE QVRLALCLLA GSDASTKVTL
1121 PPPAIIKPAR LWTGKQIFSL IIRPNKECPV KANLKAKGKT YTNGKEFCIN DSYIIIRNSE LLAGTMDKSV LGSGSKQNIF
1201 YILLRDWGED VATAAMWRLT RITNHFNFER GISLGIGDLI PSQGLLRAKE KILNTHYSTC NEYIQLMEQG HLVCQPGCSE
1281 EETLETRILN ELSVIRDDVG KACLRELHPT NIPLTMALCG SKGSFINISQ MIACVGQQAI NGCRVPDGFE NRALPHVLTR
1361 SKKPDAKGFV ENSFYSGLVS KEFYFHAMGG REGLTDTAVK TAETGYMQRR LIKSLEDLCI HYDMTVRNSM RDMIQTTYGG
1441 DGLDPTYMEG KDCPVDYERV YEHVRAKMPY ITEEPLDYAS VINATKEMLR SEEYECLSEE FKDELTAVLN KLIVVFCSSF
1521 LKLKVARKIA FYRQNVISNS SVTSQLERFT VSQLVEFIHT CKEKYMRAKI EPGTAVGALA AQSIGEPGTQ MTLKTFHFAG
1601 VAAMNITQGV PRIKEIINAS PKISTPIITA TLINDTSSEF AEQVKARIEK TTLGDVSEYI EEIYLSDDHF LIIKLDIDRI
1681 KMLKLEVDVN SVCYKLCTSK LKLTSKNVEK VTDSVIIIRP NRSKDKDSNF PFRQLTEAIP NVIIKGLPSI NRVVVHNENL
1761 GNKSKFTLFV EGDNFREVMA TRGILGEKTK SNNTIEVFKT LGIEAARTTI MSEIKSVMEN HGISIDCRHL MLLADLMTSR
1841 GEVLGITRQG LAKMKESVLN LASFEKTADH LFDAAYYGQK DVISGVSESI IMGIPVPLGT GIFKLLHKYP FHYFIYETLT
1921 VIFVIKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	376	382	
total 1 peptides												

tr|A0A151JMC2|A0A151JMC2_9HYME

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRRQFKKLSI LGVAALPEQS YNEFEMTVSK MENIYSTAKI CDYHNKSKYL ALEPEIIEIS KSSHDPEELK HIWVEWRKAS
81 GEKVKSLYPK YVELANTVAT LNNFSDYAAF WMKDYEADDF PEQIEIQWQQ LKPLYLQLHA YVRRELRKKY GEDIVSKDGP
161 IPAHLLGNPW AQTWNIANFT VPFSGKQLPD VSVALVEQGT DYNATSMFRL AENFFISINL TAMPDTFWEK SILTKKDGVD
241 MICHASAWDF YDGEDFRIKQ CTRVNMEDLL TAYHEMGHIE YYLQYKNQPV VFKEGANPGF HEAVGDVISL SVSTPSHLKK
321 IGLLTDDSTD REAFLNHLYM KSLDKIVFLP FAYMMDRWR**W NVFQGK**VTPD NYNCNWWTLA EEYQGIEPPV DRSEEDFDPG

401 SKYHIIAGVE YIRYFVSFVI QFQFHKALCI EAKQYDPSNP DAKPLSQCDI YNNKDAGNLL KSMLELGSSK PWQDAMEKIS
481 GQRQMDAAGL LEYFKPLTDW LTEENKKTNE YIGWKPSKKL VFKSRSSMVK EQFRETNVAS EVSHISFGVD SMHDISMQAN
561 VEMISKNLYN EDVKHTPALQ GALDRRMGVS STGVECETCN KKLNDCVGHF GYLNLELPVF HVGYFKSIIQ ILQTICKRCA
641 HVLLTHGERK FFSRSIQNPK SGYLMRKALR RKILEVARKK TVCPNCKSNN GPVKKAGFLK IVHEKYKNLK KIDPIIQEKL
721 AELAPRMERD IDIRTFFKVQ ELFNRIPTGD ICFLLMNPGC ATPVDLILRR IPVPPICIRP SILSDLKAGT NEDHLTMKLS
801 EIAFINDVIR KQKGVTINMH IEQWDFLQLH CGLYINSEMS GIPVHMQPQK FGRGIVQRLK GKQGRFRGNL SGKRVDFTSR
881 TVISPDPNLR IEQVGVPIHV AKTLTYPERV IPSNIELMRQ LVRNGPDTHP GANYIQYKNS QNRRYLGYGD RNKAAQDLQY
961 GDIVERHLKD DDLVLFNRQP SLHKLSIMTH RTKVLEHRTF RFNECVCAPY NADFDGDEMN LHLPQTEEAR AEALVLLANK
1041 SNLVTPRNGD LLIAATQDFI TGAYLLTQKD TFLQLEQARL ALCLLAGSDA SMNVTLPPPA IVKPARLWTG KQIFSLIIRP
1121 NRECPVKANL KARGKTYTNG KEFCINDSYV IIRNSELLAG TMDKSVLGSG SKQNIFYILL RDWGEDVATA AMWRLTRITN
1201 HFNFERGISL GIGDLIPSQG LLRAKERILN THYSTCNEYI QLMEQGRLVC QPGCSEEETL ETRILNELSV IRDDVGKACL
1281 RELHPTNTPL IMALCGSKGS FINISQMIAC VGQQAINGCR VPDGFENRAL PHVLTRSKKP DAKGFVENSF YSGLMSKEFY
1361 FHAMGGREGL TDTAVKTAET GYMQRRLIKS LEDLCIHYDM TVRNSMCDMI QTTYGGDGLD PTYMEGKDCP VDYERVYEHV
1441 RAKMPYITEK PLDYVTVINA TKEMLSAKEY ECLSEEFKDE LTFEQIKRCF CSSFLKLKVA RKIAFYRQNV ISNSPVTSQL
1521 ERFTLSQLVE FIHTCKEKYM RAKIEPGTAV GALAAQSIGE PGTQMTLKTF HFAGVAAMNI TQGVPRIKEI INASPKISTP
1601 IITATLINDT NSEFAEQVKA RIEKTTLGDV SEYIEEIYLP DDHFLIIKLD IDRIRTLKLE VDVNSVCYKL CTSKLKLTSK
1681 NVEKMTDSVI IIRPNRSKDK DSNFPFRQLT EAIPNVIIKG LPSINRVVVH NKNLGSKSKF TLFVEGDNFR EVMATRGILG
1761 EKTKSNNTIE VFKTLGIEAA RTTIMSEIKS VMENHGISID CRHLMLLADL MTSRGEVLGI TRQGLAKMKE SVLNLASFEK
1841 TADHLFDAAY YGQKDVISGV SESIIMGIPV PLGTGIFKLL HRYPFHYFIY ETLTVIFVIK NRLHTTEYTH LHLHVCTYST
1921 DLFSLIIKYG RQRRTMQKGT FI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	360	366	
total 1 peptides												

tr|F4WLV0|F4WLV0_ACREC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ISTNHETTDD LLKSAHELLN RIDAEYAKWN NKQSVTAWNY ASNLTNENLA EKLKWSAEGA NVTKHIIQIV NDFPWRDLKN
81 ESMKRQFKKL SILGVAALPE QSYNEFEMTV SKMENIYSTA KICDYYNKSK CDLALEPEII EISKNSHDPE ELKHIWVEWR
161 KVSGEKVKSL YSTYVELANT VATLNNFSDY AAFWMKDYEA DDFPEQIETQ WQQLKPLYLQ LHAYVRRELR KKYGEDIVSK
241 DGPIPAHLLG NPWAQTWNIA NFTVPFSGKQ LPDVSAALVE QGNYNATSMF RLAENFFISI NLTAMPDTFW EKSILTKKDG
321 VDMICHASAW DFYDGEDFRI KQCTRVNMED LLTAHHEMGH IEYYLQYKNQ PVVFKEGANP GFHEAVGDVI SLSVSTPSHL
401 KKIGLLTDDS TDREAFLNHL YMKSLDKIVF LPFAYMMDRW R**WNVFQGK**VT PDNYNCNWWT LAEEYQGIEP PVDRSEEDFD

481 PGSKYHIIAG VEYIRYFVSF VIQFQFHKAL CIEAKQYDPS NPNAKPLSQC DIYDNKDAGN LLKSMLELGS SKPWQDAMEK
561 ISGQRQMDAA GLLEYFKPLT DWLTEENKKT NEYIGWKPSK KLVFKSRPSM VKEQFRETNV ASEVSHISFG VDSMHDINMQ
641 ASVEMISKNL YNEDTKHTPA LQGALDRRMG VSSTGVECET CNKKLNDCVG HFGYLNLELP VFHVGYFKSI IQILQTICKS
721 CAHVLLTHGE RKFFSRSIQN PKSGYLMRKA LRKKILEVAR KKTVCPNCKS NNGPVKKAGF LKIVHEKYKN LKKTDPIIQE
801 KLTELTPKIE RDTEFKNIVE QNYRCVFDKY LYPNVVQELF NRIPTGDICF LLMNPGCATP VDLVLRRIPV PPICIRPSIL
881 SDLKAGTNED YLTMKLSEIA LINDVIRKQK GVNINTYMEQ WDFLQLHCGL YINSEMSGIP LHMQPKKSGR GIVQRLKGKQ
961 GRFRGNLSGK RVDFTSRTVI SPDPNLRIEQ VGVPIHVAKT LTYPERVIPS NMELMRKLVR NGPDTHPGAN YIQYKNSQNR
1041 RYLGYGDRNK AAQDLQYGDI VERHLKDDDL VLFNRQPSLH KLSIMTHRTK VLEHRTFRFN ECVCAPYNAD FDGDEMNLHL
1121 PQTEEARAEA LVLLANKSNL VTPRNGDLLI AATQDFITGA YLLTQKDTFL QIEQARLALC LLAGSDASMK VTLPPPAIIK
1201 PARLWTGKQI FSLIIRPNKE CSVKANLKAK GKTYTNGKEF CINDSYVIIR NSELLAGTMD KSILGSGSKQ NIFYILLRDW
1281 GEDVATAAMW RLTRITNHFN FERGISLGIG DLIPSQGLLR AKERILNTHY STCNEYIQLM EQGHLVCQPG CSEEETLETR
1361 ILNELSVIRD DVGKACLKEL HPTNTPLTMA LCGSKGSFIN ISQMIACVGQ QAINGCRVPD GFENRALPHV LTRSKKPDAK
1441 GFVENSFYSG LVSKEFYFHA MGGREGLTDT AVKTAETGYM QRRLIKSLED LCIHYDMTVR NSMRDMIQTT YGGDGLDPTY
1521 MEGKDCPVDY ERVYEHVRAK MPYITEEPLD YASVINATKE MLRSEEYECL SEEFKDELTS FLKLKVARKI AFYRQNIISN
1601 SSVTSQLERF TVSQLVEFIH TCKEKYMRAK IEPGTAVGAL AAQSIGEPGT QMTLKTFHFA GVAAMNITQG VPRIKEIINA
1681 SPKISTPIIT ATLINDANSE IAEQVKARIE KTTLGDVSEY IEEIYLPDDH FLIIKLDINR IKMLKLEIDV NSVCYKLCTS
1761 KLKLTSKNVE KVTDSVIIIR PNRSKDKDSN FPFRQLTEAI PNVIIKGLPS INRVVVHNEN LGSKSKFTLF VEGDNFREVM
1841 ATRGILGEKT KSNNTIEVFK TLGIEAARTT IMSEIKSVME NHGISIDCRH LMLLADLMTS RGEVLGITRQ GLAKMKESVL
1921 NLASFEKTAD HLFDAAYYGQ KDVISGVSES IIMGIPVPLG TGIFKLLHKY PFYYFIYETL TVIFVIKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.WNVFQGK.V	Y	22.48	877.4446	-17.1	439.7221	2	17.67	671	1	442	448	
total 1 peptides												

tr|A0A0P5A3B7|A0A0P5A3B7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVTVLGFLNI ASIAFGSFVF GPVIMRFFHS INEPNAMLAM LRNPKTVTMF DQFMSYQIAM DLLLRNKMYN EVMEVFAISQ
81 ERSIQDNKFP KNCFILAMAA LYRMNTPESY EKMKTLANAA SDAGHVPMRR SLTYAAALAL NQNDPQLCLN LLAPSKQQNY
161 VTIRNLK**ALA FAK**VGRLDDT MAILRASLEY DMPAEGGRKR SFNKNIIDSI GELVKESGNK DVQLEFARIL KNMSDRQMIE

241 EQTLEALLDT PIEKLEPRDR DSWNNNRNFV DRGMVKTNFN KQDRYDRNTR PLYPPRRPGL NEME

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.ALAFAK.V	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	168	173	
total 1 peptides												

tr|A0A0P5LBI4|A0A0P5LBI4_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRDNRTEEAK RQIGEGAKVR MDEKGNIHIK RVSKSNIYIK NTSDENGIGN DILKLPQGAL EFGKGYLLFD MKKFQQNVSR
81 ELKRAYPDRR KLEMQCIT**AI AFAK**NDMELL NCPCWVMIVN IVAMDMLKSK MPPVSKRSDI RNRPRIPIPD EDPYSVAGSG

161 SSGSSSHNGN INNGNGSAPA NSNGVVGTKR GDKPPKLPPR DNGIYGSNIP KPDYDEIDEN GYKAFASTRP SKEKLLSTDK
241 KYDDPYYCGL RARVSNFVKN KNTNEKPVKE LGTEIKMKMT PHVGTYQAAL FTATPCRVIK CGIREASTVE W

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	99	104	
total 1 peptides												

tr|A0A0N7ZFR9|A0A0N7ZFR9_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRDNRTVETK RQIGEGAKVR MDEICNIHIK RVSKSNIYIK NTSDENGIGN DILKLPQGAL EFGKGYLLFD MKKFQQNVSR

81 ELKRAYPDRR KLEMQCIT**AI AFAK**NDMELL NCPCWVMIVN IVAMDMLKSK MPPVSKRSDI RNRPRIPIPD EDPYSVAGSG

161 SSGSSSHNGN INNGNGSAPA NSNGVVGTKR GDKPPKLPPR DNGIYGSNIP KPDYDEIDEN GYKAFASTRP SKEKLLSTDK

241 KYADPYSCGL RPRVSNFVKN KNNNEKPVKE LGTEIKMKMT PHVGTYQAAL SHGHPMQSHQ MWHSRSFDSG MDAAEWECYW

321 DA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	99	104	
total 1 peptides												

tr|A0A1I8NYE8|A0A1I8NYE8_STOCA back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIHKANLQIH KVSVNSTSVD GTRHVALLNK PHQVKHLQQS QTLQLDAMHR PVLYHQHNAI QKSIAEKVIR KYAKWMQWRN

81 DGLDSLIDVG TGTGNVLMEI AKPHISKAYR RVVGIDMASD **AIAFAK**TYYK SQRKVEFKIL DIGTENELPA DLIGQFDHVT

161 SFNCLHWVNN QIQALKNIYQ LIRPEGGDFL LCFQPYLPFF DIYEVLQNTS TWSPYIGHID YFGGPLQRIE EDELSNLLDE

241 IGFDNVEIEY SFGVHTYQSE KEFKEHMAAS CMFLKHIPPQ LHSTIMKDFV DIAQRLGCRA SSPSGNKCKY SLNFTNAVVY

321 AKKLPQCH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
D.AIAFAK.T	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	121	126	
total 1 peptides												

tr|A0A0N8BB32|A0A0N8BB32_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MERNRRVAKA YARAIPIQIN GSDDGFDGFR IGLNGFDNPM RDNRTEEAKR QIGEGAKVRM DEKGNIHIKR VSKSNIYIKN

81 TSDENGIGND ILKLPQGALE FGKGYLLFDM KKFQQNVSRE LKRAYPDRRK LEMQCIT**AIA FAK**NDMELLN CPCWVMIVNI

161 VAMDMLKSKM PPVSKRSDIR NRPRIPIPDE DPYSVAGSGS SGSSSHNGNI NNGNGSAPAN SNGVVGTKRG DKPPKLPPRD

241 NGIYGSNIPK PDYDEIDENG YKAFASTRPS KEKLLSTDKK YDDPYYCGLR ARVSNFVKNK NTNEKPVKEL GTEIKMKMTP

321 HVGTYQAALS HGHPMQSHQM WHSRSFDSGM VIKLAERPQR IFLYLGDTFY GLTVSH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	138	143	
total 1 peptides												

tr|A0A0P5JFD9|A0A0P5JFD9_9CRUS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MMRNIPRCLV RLCSQPSVTQ MQYQGFRSLY TAESLGLDGF AASRSKTAVN FHGSQMKEKF RSRMQEFVTP DSTSLIFTDD

81 LKTMINLAEK NPEDIKLLEQ MIEKFHNQST GLRFGSFVFG PVIMRFFHSI NEPNAMLAML RNPKTVTMFD QFMSYQIAMD

161 LLLRNKMYNE VMEVFAISQE RSIQDNKFPK NCFILAMAAL YRMNTPESYE KMKTLANAAS DAGHVPMRRS LTYAAALALN

241 QNDPQLCLNL LAPSKQQNYV TIRNLK**ALAF AK**VGRLDDTM AILRASLEYD MPAEGGRKRS FNKNIIDSIG ELVKESGNKD

321 VQLEFARILK NMSDRQMIEE QTLEALLDTP IEKLEPRDRD SWNNNRNFVD RGMVKTNFNK QDRYDRNTRP LYPPRRPGLN

401 EME

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.ALAFAK.V	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	267	272	
total 1 peptides												

tr|Q7Q083|Q7Q083_ANOGA back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDTRQDTHLA KLNNVTIRPA SAGSLEEEIS RIIEDEPREH PLHLLDLDDL VGKHLVWLRS MPRVTPFYAV KCNDDPAILA

81 TLAALGTGFD CASEAEMRTI LALGVTPDRI IFAHPIKSVQ **ALAFAK**AHGI RRMTFDNECE LEKVAREYPE AELVLRIRHD

161 SDRVLIALGK KFGCDARGDG RVLLARAQAL GVAVIGVSFH VGCGSLDADC FYHAIASARS VFDYAKDELG MRLWLLDVGG

241 GFPGDNDKPI DQYAEAVSRA LQEFFPPEQD EEVYVLGEPG RFYVGSAATL LTTVQGKKIV RDDAGQIQQM MYYINDGVFG

321 TLFDWLSLRE IKDLKRAVPL VRREREHEPA FPTTIWGPTC DSTDIVCEDV PYPEHHIGDY IVFENLGAYG MTFATNFNGF

401 PKPTVQVYVK EHTW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Q.ALAFAK.A	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	121	126	
total 1 peptides												

tr|W5JB06|W5JB06_ANODA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKSLAVVCCC LV**ALAFAK**AG SYHGFELYTV RPETQEQLTE LLRWPVQADV DFWDAPKLNR ESRMMTARTD RKAVVNFLER

81 HDIDYELVVE DVQELLTKEK RRNAEHLRRV RRDSNSRATI DFDHFWPLEE IYDYLDELAA AYTGLVRVSE VGTTHEGRPI

161 KAITISTNGV IDQSRPIVFI DGGIHAREWA GVMSVMYMIH EFVEHSDQYA AQLTNADYVI IPVLNPDGYS YTHRENRLWR

241 KNRSQVSILC YGVDLNRNFA YQWEWTSSEC TNNYAGKAAE SEKETQTMVA LMDQYKSAIR VYLAVHTYGE LILWPWGYDF

321 IHSDNAADLQ RLGEQARDAL VAAGGPTYEV GNSADILYTA SGATDDYAHS LGVPFAYTLE LTGGGLEGFD LPASELPKVT

401 ADTFELFKVF GQHAGTLTVP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.ALAFAK.A	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	13	18	
total 1 peptides												

tr|A0A0P5RA30|A0A0P5RA30_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING

81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF

161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY

321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW

401 HSRSFDSGMD AAEWECYWDA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5DXU8|A0A0P5DXU8_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING

81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF

161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY

321 KAFASTRPSK EKLLSTDKKX XXXXXXXXXX XXXXXXRVST IKYNQSSVCT LVLMNKRSNN RVEVLRLCSL SIGVIGYSVA

401 VAISRVATCC VDVQSGRRHF H

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|Q702G3|Q702G3_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKRLTFVTGC LL**ALAFAK**AG SYHEFELYNV RPETAEQLSV LLKWRNGQEI EVDFWDAPKV GRSARLMVTR EDHKRVEEFL

81 EQHDIEYDLV AEDVQELLNR EQRRNVEHGR RLRRDSNSRA TVNFEHFWTL DEIYEYLDEL AVAYNGLVRV SEIGRTHEDR
161 PIKAITISTR GAVDQTRPIV FMDGGIHARE WAGVMSVMYM IHEFVEHSDQ YAEQLSNTDY VIVPVANPDG YVYTHEQNRL
241 WRKNRSPGNV LCYGVDLNRN FPFQWDRTTS ECTNNFAGHA ASSENETKAL IGLMDQYKAA IRMYLAVHTY GEMILWPWGY
321 DFLHAPNEDD LQRLGERARD ALVAAGGPEY EVGNSADILY TASGATDDYA YSLGVPYSYT LELTGGGSQG FDLPAAELAR
401 VTSQTFELLK VFGQHAGTLS VTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALAFAK.A	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	13	18	
total 1 peptides												

tr|A0A0P5B3S6|A0A0P5B3S6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFASGME TELTDSAYSR IYGRLP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|Q7PID6|Q7PID6_ANOGA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSEAMKRLTF VTGCLL**ALAF AK**AGSYHEFE LYNVRPETAE QLSVLLKWRN GQEIEVDFWD APKVGRSARI MVTREDHKRV

81 EEFLEQHDIE YDLVAEDVQE LLNREQRRNV EHGRRLRRDS NSRATVNFEH FWTLDEIYEY LDELAVAYNG LVRVSEIGRT
161 HEDRPIKAIT ISTMGAVDQT RPIVFMDGGI HAREWAGVMS VMYMIHEFVE HSDQYAEQLS NTDYVIVPVA NPDGYVYTHE
241 QNRLWRKNRS PGNVLCYGVD LNRNFPFQWD RTTSECTNNF AGHAASSENE TKALIGLMDQ YKAAIRMYLA VHTYGEMILW
321 PWGYDFLHAP NEDDLQRLGE RARDALVAAG GPEYEVGNSA DILYTASGAT DDYAYSLGVP YSYTLELTGG GSQGFDLPAA
401 ELARVTSQTF ELLKVFGQHA GTLSVTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
L.ALAFAK.A	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	17	22	
total 1 peptides												

tr|A0A0P5M2I6|A0A0P5M2I6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX P

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5C2M5|A0A0P5C2M5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGME TELTDSAYSR IYGRLPIPRS YVPIAAPSRA SYYGEWN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5HDA5|A0A0P5HDA5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LNLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGRN RAHRLGLLPH LRPLADSAQL CAHCSAFASI VLRGVELMSI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P6EQJ0|A0A0P6EQJ0_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFLEAQGKC VCGPTIGQDM VSRRRILSRS RDDLHLDNFP EEEDDVWHIK EKLYKDHIQE VLDKWHQIDD EIWAKLIVME
81 RNRRVAKAYA RAIPIQINGS DDGFDGFRIG LNGFDNPMRD NRTEEAKRQI GEGAKVRMDE KGNIHIKRVS KSNIYIENTS
161 DENGIGNDIL KLPQGALEFG KGYLLFDMKK FQQNVSRELK RAYPDRRKLE MQCIT**AIAFA K**NDMELLNCP CWVMIVNIVA

241 MDMLKSKMPP VSKRSDIRNR PRIPIPDEDP YSVAGSGSSG SSSHNGNINN GNGSAPANSN GVVGTKRGDK PPKLPPRDNG
321 IYGSNIPKPD YDEIDENGYK AFASTRPSKE KLLSTDKKYD DPYYCGLRAR VSNFVKNKNT NEKPVKELGT EIKMKMTPHV
401 GTYQAALSHG HPMQSHQMWH SRSFDSGMDT ATTIKTYKKA VANIRTLSTP YS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	216	221	
total 1 peptides												

tr|A0A0P5DIN0|A0A0P5DIN0_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMA SLPSSVTPDI QRLWKAYPFE RXXXXXXXXX XXXXVQLKIP CH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5M5J7|A0A0P5M5J7_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XLHKTVYKTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0N8E8V7|A0A0N8E8V7_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMG VAALFPQHWR DWILSGGSNF ACGNMLCRCP IWTEALSLMH LCVCVCVCVT NGLVS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5PZQ6|A0A0P5PZQ6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMK QSSQTRLTPA STAACRFRAA MCPLQRLREH RTTGSGIDVN LSVFGDGAVI SLSRL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P6ET66|A0A0P6ET66_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXS IFFFFFLLHK TVYKTS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5BMN3|A0A0P5BMN3_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSFLEAQGKC VCGPTIGQDM VSRRRILSRS RDDLHLDNFP EEEDDVWHIK EKLYKDHIQE VLDKWHQIDD EIWAKLIVME
 81  RNRRVAKAYA RAIPIQINGS DDGFDGFRIG LNGFDNPMRD NRTEEAKRQI GEGAKVRMDE KGNIHIKRVS KSNIYIKNTS
161  DENGIGNDIL KLPQGALEFG KGYLLFDMKK FQQNVSRELK RAYPDRRKLE MQCITAIAFA KNDMELLNCP CWVMIVNIVA

241  MDMLKSKMPP VSKRSDIRNR PRIPIPDEDP YSVAGSGSSG SSSHNGNINN GNGSAPANSN GVVGTKRGDK PPKLPPRDNG
321  IYGSNIPKPD YDEIDENGYK AFASTRPSKE KLLSTDKKYD DPYYCGLRAR VSNFVKNKNT NEKPVKELGT EIKMKMTPHV
401  GTYQAALSHG HPMQSHQMWH SRSFDSGMET ELTDSAYSRI YGRLPIPRSY VPIAAPSRAS YYGEWN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	216	221	
total 1 peptides												

tr|A0A0P6FYK6|A0A0P6FYK6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MWTLQRSATS NTQTAAKESL ATKSFTLQRL SNVQRDNNRC GPTIGQDMVS RRRILSRSRD DLHLDNFPEE EDDVWHIKEK
 81  LYKDHIQEVL DKWHQIDDEI WAKLIVMERN RRVAKAYARA IPIQINGSDD GFDGFRIGLN GFDNPMRDNR TEEAKRQIGE
161  GAKVRMDEKG NIHIKRVSKS NIYIKNTSDE NGIGNDILKL PQGALEFGKG YLLFDMKKFQ QNVSRELKRA YPDRRKLEMQ
241  CITAIAFAKN DMELLNCPCW VMIVNIVAMD MLKSKMPPVS KRSDIRNRPR IPIPDEDPYS VAGSGSSGSS SHNGNINNGN

321  GSAPANSNGV VGTKRGDKPP KLPPRDNGIY GSNIPKPDYD EIDENGYKAF ASTRPSKEKL LSTDKKYDDP YYCGLRARVS
401  NFVKNKNTNE KPVKELGTEI KMKMTPHVGT YQAALSHGHP MQSHQMWHSR SFDSGMDAAE WECYWDA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	244	249	
total 1 peptides												

tr|A0A0P5TJM7|A0A0P5TJM7_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
 81  SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161  GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCITAIAF AKNDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241  RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321  KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401  HSRSFDSGMX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXYFFFFF LLHKTVYKTS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5KXS1|A0A0P5KXS1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSFLEAQGKC VCGPTIGQDM VSRRRILSRS RDDLHLDNFP EEEDDVWHIK EKLYKDHIQE VLDKWHQIDD EIWAKLIVME
 81  RNRRVAKAYA RAIPIQINGS DDGFDGFRIG LNGFDNPMRD NRTEEAKRQI GEGAKVRMDE KGNIHIKRVS KSNIYIKNTS
161  DENGIGNDIL KLPQGALEFG KGYLLFDMKK FQQNVSRELK RAYPDRRKLE MQCITAIAFA KNDMELLNCP CWVMIVNIVA

241  MDMLKSKMPP VSKRSDIRNR PRIPIPDEDP YSVAGSGSSG SSSHNGNINN GNGSAPANSN GVVGTKRGDK PPKLPPRDNG
321  IYGSNIPKPD YDEIDENGYK AFASTRPSKE KLLSTDKKYD DPYYCGLRAR VSNFVKNKNT NEKPVKELGT EIKMKMTPHV
401  GTYQAALSHG HPMQSHQMWH SRSFDSGMAS LPSSVTPDIQ RLWKAYPFER NPTSWVPSHT HGYSPDAAEW ECYWDA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	216	221	
total 1 peptides												

tr|A0A0P5KPE8|A0A0P5KPE8_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN
241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGME LNVPNASFYT WVTRFMVLRC RTESRHFFIL FLHSLLYSHS KPNVERTFPF LWLASTYSLA ISIRTVAI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5SIJ1|A0A0P5SIJ1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWTLQRSATS NTQTAAKESL ATKSFTLQRL SNVQRDNNRC GPTIGQDMVS RRRILSRSRD DLHLDNFPEE EDDVWHIKEK
81 LYKDHIQEVL DKWHQIDDEI WAKLIVMERN RRVAKAYARA IPIQINGSDD GFDGFRIGLN GFDNPMRDNR TEEAKRQIGE
161 GAKVRMDEKG NIHIKRVSKS NIYIKNTSDE NGIGNDILKL PQGALEFGKG YLLFDMKKFQ QNVSRELKRA YPDRRKLEMQ
241 CIT**AIAFAK**N DMELLNCPCW VMIVNIVAMD MLKSKMPPVS KRSDIRNRPR IPIPDEDPYS VAGSGSSGSS SHNGNINNGN
321 GSAPANSNGV VGTKRGDKPP KLPPRDNGIY GSNIPKPDYD EIDENGYKAF ASTRPSKEKL LSTDKKYDDP YYCGLRARVS
401 NFVKNKNTNE KPVKELGTEI KMKMTPHVGT YQAALSHGHP MQSHQMWHSR SFDSGMDTAT TIKTYKKAVA NIRTLSTPYS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	244	249	
total 1 peptides												

tr|A0A0N8D6J9|A0A0N8D6J9_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN
241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMA SLPSSVTPDI QRLWKAYPFE RNPTSWVPSH THGYSPETEL TDSAYSRIYG RLPIPRSYVP IAAPSRASYY
481 GEWN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P4XFP1|A0A0P4XFP1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFLEAQGKC VCGPTIGQDM VSRRRILSRS RDDLHLDNFP EEEDDVWHIK EKLYKDHIQE VLDKWHQIDD EIWAKLIVME
81 RNRRVAKAYA RAIPIQINGS DDGFDGFRIG LNGFDNPMRD NRTEEAKRQI GEGAKVRMDE KGNIHIKRVS KSNIYIKNTS
161 DENGIGNDIL KLPQGALEFG KGYLLFDMKK FQQNVSRELK RAYPDRRKLE MQCIT**AIAFA K**NDMELLNCP CWVMIVNIVA
241 MDMLKSKMPP VSKRSDIRNR PRIPIPDEDP YSVAGSGSSG SSSHNGNINN GNGSAPANSN GVVGTKRGDK PPKLPPRDNG
321 IYGSNIPKPD YDEIDENGYK AFASTRPSKE KLLSTDKKYD DPYYCGLRAR VSNFVKNKNT NEKPVKELGT EIKMKMTPHV
401 GTYQAALSHG HPMQSHQMWH SRSFDSGMAS LPSSVTPDIQ RLWKAYPFER NPTSWVPSHT HGYSPDTATT IKTYKKAVAN
481 IRTLSTPYS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	216	221	
total 1 peptides												

tr|A0A1B6HBZ2|A0A1B6HBZ2_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPNRTPKIKY TKHFINNEFV DSLDKKTFAV LNPCTAEKIC DVAEGFKADV DIAVKAAKAA FQQNSAWRTL DPSAREVLMN
81 KLADLIERDA DELASILTLE NGKPFKAALW EIHNAAKTMR YYGGWCDKIY GKTIPVDGPF FTITLKEPVG VTGQILPWNF
161 PVALLAAKWG PALATGCTTV LKPAEQTPIT ILQIAALTKE AGFPPGVINV VNGFGPTAGA AITNHPDISK IAFVGSTEVG
241 RIIMESAAKS NLKRVGLELG GKSPIAIFDD VDVDKAVEIA YEAVFINGGQ ACCAGTRTFV QDTIYDAFVK KAAERAAKRK
321 VGDPFSDETE QGPQVDEEMF TKALRMIESG KKEGAKLETG GSRIGDKGYF IQPTVFSNVT DNMTIAREEI FGPVQQILKF
401 SSVEELVERA NNTTYGLAAG IVTNDLNK**AI AFAK**AAQAGS VWVNCFNIVS YQAPFGGYKE SGFGKDMGEE AIHEYLNIKT

481 VTIALPTPSK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AIAFAK.A	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	429	434	
total 1 peptides												

tr|A0A0P5QKL6|A0A0P5QKL6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSXXX XXXXXXXXXX XXXXXXRSDI RNRPRIPIPD EDPYSVAGSG SSGSSSHNGN INNGNGSAPA
321 NSNGVVGTKR GDKPPKLPPR DNGIYGSNIP KPDYDEIDEN GYKAFASTRP SKEKLLSTDK KYDDPYYCGL RARVSNFVKN
401 KNTNEKPVKE LGTEIKMKMT PHVGTYQAAL SHGHPMQSHQ MWHSRSFDSG MASLPSSVTP DIQRLWKAYP FERNPTSWVP
481 SHTHGYSPGE SFPVPIPYLW IYPE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A0P5S908|A0A0P5S908_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWTLQRSATS NTQTAAKESL ATKSFTLQRL SNVQRDNNRC GPTIGQDMVS RRRILSRSRD DLHLDNFPEE EDDVWHIKEK
81 LYKDHIQEVL DKWHQIDDEI WAKLIVMERN RRVAKAYARA IPIQINGSDD GFDGFRIGLN GFDNPMRDNR TEEAKRQIGE
161 GAKVRMDEKG NIHIKRVSKS NIYIKNTSDE NGIGNDILKL PQGALEFGKG YLLFDMKKFQ QNVSRELKRA YPDRRKLEMQ
241 CIT**AIAFAK**N DMELLNCPCW VMIVNIVAMD MLKSKMPPVS KRSDIRNRPR IPIPDEDPYS VAGSGSSGSS SHNGNINNGN

321 GSAPANSNGV VGTKRGDKPP KLPPRDNGIY GSNIPKPDYD EIDENGYKAF ASTRPSKEKL LSTDKKYDDP YYCGLRARVS
401 NFVKNKNTNE KPVKELGTEI KMKMTPHVGT YQAALSHGHP MQSHQMWHSR SFDSGMASLP SSVTPDIQRL WKAYPFERNP
481 TSWVPSHTHG YSPDAAEWEC YWDA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	244	249	
total 1 peptides												

tr|A0A0P5KS39|A0A0P5KS39_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWTLQRSATS NTQTAAKESL ATKSFTLQRL SNVQRDNNRC GPTIGQDMVS RRRILSRSRD DLHLDNFPEE EDDVWHIKEK
81 LYKDHIQEVL DKWHQIDDEI WAKLIVMERN RRVAKAYARA IPIQINGSDD GFDGFRIGLN GFDNPMRDNR TEEAKRQIGE
161 GAKVRMDEKG NIHIKRVSKS NIYIKNTSDE NGIGNDILKL PQGALEFGKG YLLFDMKKFQ QNVSRELKRA YPDRRKLEMQ
241 CIT**AIAFAK**N DMELLNCPCW VMIVNIVAMD MLKSKMPPVS KRSDIRNRPR IPIPDEDPYS VAGSGSSGSS SHNGNINNGN

321 GSAPANSNGV VGTKRGDKPP KLPPRDNGIY GSNIPKPDYD EIDENGYKAF ASTRPSKEKL LSTDKKYDDP YYCGLRARVS
401 NFVKNKNTNE KPVKELGTEI KMKMTPHVGT YQAALSHGHP MQSHQMWHSR SFDSGMASLP SSVTPDIQRL WKAYPFERNP
481 TSWVPSHTHG YSPDTATTIK TYKKAVANIR TLSTPYS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	244	249	
total 1 peptides												

tr|A0A0P5BTW7|A0A0P5BTW7_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFLEAQGKC VCGPTIGQDM VSRRRILSRS RDDLHLDNFP EEEDDVWHIK EKLYKDHIQE VLDKWHQIDD EIWAKLIVME
81 RNRRVAKAYA RAIPIQINGS DDGFDGFRIG LNGFDNPMRD NRTEEAKRQI GEGAKVRMDE KGNIHIKRVS KSNIYIKNTS
161 DENGIGNDIL KLPQGALEFG KGYLLFDMKK FQQNVSRELK RAYPDRRKLE MQCIT**AIAFA K**NDMELLNCP CWVMIVNIVA

241 MDMLKSKMPP VSKRSDIRNR PRIPIPDEDP YSVAGSGSSG SSSHNGNINN GNGSAPANSN GVVGTKRGDK PPKLPPRDNG
321 IYGSNIPKPD YDEIDENGYK AFASTRPSKE KLLSTDKKYD DPYYCGLRAR VSNFVKNKNT NEKPVKELGT EIKMKMTPHV
401 GTYQAALSHG HPMQSHQMWH SRSFDSGMAS LPSSVTPDIQ RLWKAYPFER NPTSWVPSHT HGYSPDTATT IKTYKKAVAN
481 IRTLSTPYSX XXPYVRYLHI QMTTTDDRDR DGNISNDAAE WECYWDA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	216	221	
total 1 peptides												

tr|A0A0P5QM79|A0A0P5QM79_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDLESRTPQG EGKSDGCLVE RVWNAVQNIS KRHQFKFILL LRIFLAISYN CYFVAAVYHA RTERLDIDWC DGVGMLIILT
81 VIVYCGLFYY KIFKPLWGDC AYTRVILPLT IFLERCWSYR YVRVLLILGG AIGFIVGIIF DTEGDRDRLY SLIGLAIFLL
161 FGWIFSKHKA KIKWTQVIWG TVLQFLFGLT VLRWDTGQKV FACMGDRVSI FLKYTDAGSG LVYGHLVTDQ NESGIPLGTI
241 FAFKALSVIF LFSFMVSILY YYGVMQFIVQ KVGWLLQVSL GTTATESINC AANIFLGQTE APLAIKPLLP LLTKSELHAV
321 MTSGFATISG SVLSAYISFG INASHLLSAS VMSAPA**ALAF AK**LFYPESEE SQTKAEDIKV PKGKEANVLD AASQGASNAV

401 FMVINICANL IAFLAFIAFL NGIISWMGGL LGAPYITFEY LVGKCFIPLA WVMGVPAKEC DQIGHVVALK TIVNEFVAYR
481 KLSEYMAQGL VSKRSETIAT YALCGFSNPG SIGIQIAALG SMAPSRQTDL AQVAFRAFIS GSIACFMTAC VAGALIPSSS
561 L

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.ALAFAK.L	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	357	362	
total 1 peptides												

tr|A0A0P6HR38|A0A0P6HR38_9CRUS

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVSRRRILSR SRDDLHLDNF PEEEDDVWHI KEKLYKDHIQ EVLDKWHQID DEIWAKLIVM ERNRRVAKAY ARAIPIQING
81 SDDGFDGFRI GLNGFDNPMR DNRTEEAKRQ IGEGAKVRMD EKGNIHIKRV SKSNIYIKNT SDENGIGNDI LKLPQGALEF
161 GKGYLLFDMK KFQQNVSREL KRAYPDRRKL EMQCIT**AIAF AK**NDMELLNC PCWVMIVNIV AMDMLKSKMP PVSKRSDIRN

241 RPRIPIPDED PYSVAGSGSS GSSSHNGNIN NGNGSAPANS NGVVGTKRGD KPPKLPPRDN GIYGSNIPKP DYDEIDENGY
321 KAFASTRPSK EKLLSTDKKY DDPYYCGLRA RVSNFVKNKN TNEKPVKELG TEIKMKMTPH VGTYQAALSH GHPMQSHQMW
401 HSRSFDSGMA SLPSSVTPDI QRLWKAYPFE RNPTSWVPSH THGYSPDTAT TIKTYKKAVA NIRTLSTPYS XXXXXXXXXX
481 XXXXXXXXLR SLPTYPNDDN RRPRPRWQHF QRRSRMGVLL GCMTRLLGYF LSAVFLCYLL KQSSQTRLTP ASTAACRFRA
561 AMCPLQRLRE HRTTGSGIDV NLSVFGDGAV ISLSRL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
T.AIAFAK.N	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	197	202	
total 1 peptides												

tr|A0A1Y1MIY0|A0A1Y1MIY0_PHOPY

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MWLLAAVIAI ITAFIAKNKR YRWLYIILKT YKRDFRV**AIA FAK**LRIKLWW WGKMQTSVPE RWATIVKRHP NKVAFQFEGS

81 SLTFLQVDEF SNQIANYFKS EGFTKGDNIA LLLENSHEYP CIWLGLTKIG VVTALINTNL VNDPLNHSIN VSNCKAIIFG
161 SNHSNAIKQI QSKLVSVKKY QFHENVGKEE DIVKDCVDLR KALSTVTTKS PGTVQVSVKD PFLYIYTSGT TGLPKAAVIS
241 HVRFMFMATA FNYMSKMRSE DTIYNPLPLY HSAGGMIGMG QTVLHGLSVA IRKKFSASNY WSDCAKYNCT VAQYVGEMCR
321 YILATPRKEP VKHSVRAIFG NGLKAQIWTE FVNTFEIKEV FEFYGATEGI SNIINVDNTP GCVGFVPRYA GPIYPMTLLK
401 CDQETGEPLR NSDGFCMECG INEPGLVISK INQRDPCQEF KGYADKKATN KKILQNVFKK GDAYFNSGDI LERDELGNYF
481 FKDRTGDTFR WKGENVSTSE VEGIISNILQ LNDAVVYGVE IPNTEGRAGM AAVVDTNDSL NLEVLSNGLR NNLPTYSIPI
561 FLRVLKEVPL TGTYKLKKID LQRDGYDIKK ISDQIYFYNA KLRKYEELTK DLMDKIRDGR VSV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.AIAFAK.L	Y	21.89	619.3693	-1.9	620.3754	1	17.45	664	1	38	43	
total 1 peptides												

tr|A0A0J7NMH8|A0A0J7NMH8_LASNI

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MCFTGIIEYV NSFERYLSDT FATRLSSTDS TMFVALRGAA GPVVAARLSE IDNWNVLLVE AGPDEPAGTQ VPSNLLLYLG
81 TDLDWNYTTT NELHACLNNN GSCRWPRGKN LGGCTSHHGM AYHRGHAMDY TRWVEMGNAG WSWQEVLPYF FKSEDNKEIG
161 RVRAQDHGTG GPMTVERFPW QPQFAWDVMS GAQEVGLGVT EDLVGPKITG FTVAQTISRN GVRLSAPRAF LWPHRNRPNL
241 HVALNATVTK INTAKFGSNV VAKGITFVMN GYKYTVNAKK EVILSAGTIN SPQLLLLSGI GPKSQLNNMK ISTVVDLPGV
321 GENLHNHQSY GIDFTLKQPK KDELNMNSAD LYIYNQTGPM SSTGLAQLTG ILVSNYTTAD DPDIQVFFSG FQAVCNTGNR
401 IADLIPYNNK ETVR**FTSVNL HPR**SRGRITL ASNNPLSPPN IWGNDLAEPI DRAIVYQGIQ KILKLSKAKA LKKYGLKRVN
481 QDVPECAQYK KGSTEHWDCQ IQYNTRPENH QAGTCKMGPT VDPMAVVSPD LKVYGVNGLR VADASIMPQM VSGNPVATVN
561 MIGERVADFI KRDYKVINTH VII

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.FTSVNLHPR.S	Y	21.04	1069.5669	-18.4	535.7809	2	12.10	496	1	415	423	
total 1 peptides												

tr|B3MFH2|B3MFH2_DROAN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTANATIELA LDRVDWRDLA AHPENLPRVY TPGEVLMPEA GFMRG**HGTFV EDETIK**ASVA GVIEKVNKLI SVRPLKSRYV
81 GEIGDVVVAR VIEVQQKRWR VDTNSRLDSI LLLSSVNLPG GELRRRSAED EQMMRRYLDE GDLISAEVQN IFEEGTLSLY
161 TRSLKYGKLS QGLLVKVFPA LVKRRKMHFH NLPCGASVIL GNNGYIWIAP TKAQEQDGGE GGFAQNLNEH VPRNDREVIA
241 RLRNCVLALA KCKLMIYDTS IQYAYEESLK YEAHELLQQN AIYDIGEQTQ SRLRDSDE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.HGTFVEDETIK.A	Y	21.02	1274.6143	-4.7	638.3114	2	18.45	698	1	46	56	
total 1 peptides												

tr|B0XJD4|B0XJD4_CULQU

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLQRCKSEAR FLANKIMLEG KIKVEGFTLN RAAVHRRRRR GKFDVVYTIK NLILINILGR DAEWVFKESV RTAPNHGCQT
81 ERVGKKNEQE TRNKKQETRN KKQETRNKKQ ETRNKKQETR NKKQETRNKK QETRNKKQET RNKKQETRNK KQETRNKKQE
161 TRNKKQETRN KKQETRNKKQ ETRNKKQETR NKKQETRNKK QETRNKKQEL LMKPAKVDVP VLFQQKAHKL ISTSFGLSQS
241 SPHLTQPQTR SSELIHWPKG TRYNLSSLLS DKKNEQVKPF GSGNSMLLAN NKSHFPEKMG QSECLWAGKT KFSGDQLEGP
321 LDFTASAQQC EGFRTLEWML AVGGGCPGRQ KCKREDNAQM TGGYPLNLYN LQGAFGLNLP **SAAGK**TWPHD TCARCDEMTY
401 IFFTAAAASL PLEQKVFFAG FSTPFFRDGV NICVEVEEAE QVLCSSVDDA YFNVTVSTQA LETSKHIALA AACGRTSIEW
481 WRNLKPARHH NTPSSKPRVE APAESVSVAA LTLAPVVGAH SLG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SAAGK.T	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	381	385	
total 1 peptides												

tr|A0A1W4VCE8|A0A1W4VCE8_DROFC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MANVVNMNSL LNGKDSRWLQ LEVCREFQRN KCSRQDTECK FAHPPANVEV QNGKVTACYD SIKGRCNRDK PPCKYFHPPQ
  81 HLKDQLLING RNHLALKNAL MQQMGMAPGQ PVISGQVPTV ATSPYLTGIP ANSYSPYYTT GHLVPTLLGP DPTAVASQLG
 161 PVVPQTVQVA QQKIPRSDRL ETSPLTAHHH QQQLQHQLNN INNNNNHSTA GAAAATSTTA TTTTNNAAAA AAAAAAAAAA
 241 AVMGHHTLEV GKKRAADTTD MFPLQFSGMV PFKRPAAEKS GIPVYQPGAT AYQQLMQPYV PVSCEYPQQQ QQQQPPPQQQ
 321 QQLHQQQQQQ QNVLLQQLQL SSAITTTTTT ATASNNMINN INNNKQSIMN AVIATTTNIP SSAVETTTAT SSSTSSASVS
 401 ATIAATAKAI TNPNDSDPDS DRNPDNDKDR ESAADGETDN ADRSDAADQA SNQDNSDQTK LNLNLNLNHN PNSNQNQNPS
 481 PTNDCNTTRT ISPNPDTVAT ETAAVTVAAA AAADTLDTAN AAATPPNGAS PPPPCPSSPQ GESLLPLPNG LGDNNNYLSY
 561 INNNLNNGQL KSANPEELNG DLEGISAAAA SASASRSFAK QNGEGYSRYS VNGHSTGILP TPTTSAPPVS YQSINQAQAQ
 641 AQAQAQGLQR INYAIPSYSY GNLYSPYGGA TSTMVSLPSS TPSYAQAQMQ QQQQQQQQQA QVQAQVQAQA QAQAAYAQQA
 721 YAAYAAAAGL APQAATAGGY YTDPAALAKE VAQKNYALKV ASAAGKPGAS SAAAAYTGLT LNKSYVAAAP APQTIQAAQP

 801 QAVSMATLLQ MQAQAQAQAQ AQAQMRQLSS LPSSGLATPV PGTPVRAAPA GSVGATQYQS AALLRAPSPM PYAQAQGYFY
 881 PGMMPTAAYA MPQTQAAAAQ QYAAAAAAAA AAAQGATPGS AMVLNPYKKM KTS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
A.SAAGK.P	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	762	766	
total 1 peptides												

tr|A0A1B0B969|A0A1B0B969_9MUSC

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MKIMEEKKYN KRKAKAVAEG NREQIAVSCN HLADFYNQQG RYQDAVKEYQ MEAEIYAKMG KDLETGKAQR MIGEMCMLLG
  81 EFDKAKDHIT NYLKQRLLFQ FSNHSILFTF ICIIHIAHDE EIVKKLQNTV EEQRAYTTLG RAHLLHGQSL NDVSASDAMS
 161 QLKQAEKSFL KALLLIKGLA GKISKLEQLD MQARCYLNIG VVKEHMDDFE ASIAYIEKAI KISTSNDIFE LTHLCYVSMS
 241 LLYHVKKADA IMSLRYCNLA LDVAKRLPQK VKKICETLII KGEVLIKEGD FASAKQILTK AYKKNTPDEN DRKNIEKTLK
 321 IGEMNLAKIC QLLDDLITTS IVDYSKRKNL FEKLGDGCCH LGNYTKALEY YHKMLECAEL NNESGKSLIP IYVSLYQTYK
 401 DNKQYEQALE YLRKEYELNK DEPIEAFSTL CAIADIYEMQ LQSFWAIQDI LQQAKQYVPR CGDEKTKLEK IIYSRLRKLQ
 481 IKHDMHSLAD ELLQEANSKG VDLQSTSDDT DTESEFGSSE NNTPELGDDI CLEDLTDSDT SDLDETDKPR PHRVTRGVRS
 561 LTIKRNNKGE TQLHQACISG NIELARRLID QGHVVNVRDH AGWLPLHEAC NHGYRDIAEL LLVRGAAAAI NDKGGTSCDG
 641 ITPLYDACSN GYLDVVELLL DRGADATVKT DFGETCVDGL DKWRLSATLV QGEQAQYEMI RNRLLNYLSK VGINATQKDK
 721 PLTNACSAKQ SFSASAEMSD ESDLPGDEPE VRPSTSLQKH FENRKSRQSL TKNNKYGTEY KHIIEQLKHP NHRPPVEEDA
 801 TLFDERSAAG KRKSAYLGEN EVNEESWLID DMRPDKKKRR FQITRTRSTS TSPTNDIQVS TGWSDFSPPV HDMFEDSLDE

 881 QQHQKKSKKL TLTRSLSISS NASSKGSHRN KSKQQASLLD SGFCRFRSES PLLRDIDSND NVHIIEPDST TTSLNVLKSS
 961 LETSIPNTQA SSLLSTSVSF KVKVEDEFLL VPIDRKKLND VNIRWLAEEA SRRYYNLVGL KPLLRLKTLD GFIYAENDAV
1041 TVALEQNILL GTVLEWEICP LAQRYEEMCD HMKQAVDSRI KDELLNDQMS NTINLTNFWL NSTQCKPVFK SLMHHSNLRV
1121 IVLSNNFIRN EGCRYLAKSL PTLKQLKTLN LEGNFITADG LEILLTSLDN VIDVRLEQLI LNHNPLGNNA IRVLDKFCTS
1201 SQGTEMQKLH LAHCQLSELF DYDLNYQQLS DFDISFNQLN NESFRKLTKK LNSSRLQSVN LSYCCFIRSS GDNCSLENYD
1281 TEYAEKISEF FENGTCEHFK RVYLANCQLN DIIMYRIIQC LSKANDLEVI DITDNVKLST TSFRFILDKF PNLKKLIAIN
1361 CIRFMSIECI EQIKNIPMYM SLSFITNNTD DNHKESLHKI WRSIWGVKAK IKFLQNNVIL YTNDNDFIQY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.SAAGK.R	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	807	811	
total 1 peptides												

tr|A0A0R1EA16|A0A0R1EA16_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MLKKAEYDEE ISYRAIKSCI TLNPSALTPS AATGSSGGSS SSAGHNSSYN STNHRSTDPG QRHKQGGSLQ DLVEAAHRSE
  81 LATTSAAAAA ATTAATQRFN CDYQLSGRPN RRQQQHNQNA TSSASKKIKN SNVSGRQREG GSLPSSVNFD PSAAMEAKQH
 161 KQQAQPSSEA AGGSFSGSVG NKHHHRSSTG SCSSLPSHLG ERDPEASTQF DLDVDDATGV GASAAVGVSG VQDDFMLEQL
 241 DPQNPSVKLL LDALNDKPLE TRYSAAGKKF LIDDRLHFSV LELSARRKLQ QQAQYLAALT GQFGLGLEEE KRKVEAGYVS

 321 LNDNYTACSS VYGGGAGSPA AVEGSKPSTS SSSSTGSNC GASSDTLSSD LRPAKIGRMV PAAASVAATP MGGKTTTRQL
 401 DENGNALGDG FGSSASSGAS AVASSSNGNG NQFTALITTT VGSSAATSSV AHRQNSVSTL LSTGTNTTTT AMAAAAVAAS
 481 YSQLQQTPGG GTAGAGSGIG IGLQQPTKQK AKKKSQQERN TTTVDVESVA GYRGNDPVEQ LVKYIENDVN GGGNSAAGQR
 561 KKERKKQNKL KKSNSLEELR TCSKMEVDDL KRQSATTEMM RQKKGTNNAS SGGSSSTASG SSNSGKHNSA SVADINKNCN
 641 KEQQSTPTVQ VRNSTNPGSQ QRKGERRSWG TEELQYLGDH QEMAAAWSEP ETVRQKQLPL ALPALARMSE LDALNTVLSE
 721 TAEFHVVTKK KKPKKQRAVT MDDAAVAAAA GTGGNLQRMQ QITKSASSNI MSQRMHYYTP YNSNNGGGNA NYKQQHQQGQ
 801 QYQEHYQAQQ GQHHHHHHHH HHHHHHHSGS AVSNQVDSSR RKSTSSMPPS EKSDSSDLDS VHSLPIQTGK KKSLGGGNNK
 881 QRAAQAASQR QAKQNNNSAA PISYADIARN KKEALNNATA SDTELELGDK IQSKCGGKSK SRPDFPELPG AVTTGAASGG
 961 AVNQAAVVSN QTSPPSSSSS ISYSQSLNAT PPSSSSDAES TNSPELLAQV QIPNYSMATP TLTSSTISSV SSSAASTSFT
1041 SCSLPALQKS KSVEHDTSYS CNSSNLDQQY PALERTVKRH STNNVSVAVA ASTSTSASSS LYNFAAAAKQ QLAENAYAAI
1121 SPPAAVTTTS TAVAVSAPVP ASAPAPAAVT VPCYSSSSTQ GSTQSLSSTA SSAIVLSSDK AKVKPKELSP SSSFSKKPTK
1201 PSQDTPSISL SISTTPKATT STSTTTTQKT TAATQTEGAK KLISGIHKLP SNNCIAKGAG AVLEASAGRR AVIILNDDRE
1281 AGRSNNEFIF GDFNEDELKL FDDNLDDDEE DQHKQSSNKK QQTEAESDVG QDDTEDVDQE LDKELECLGR RPEKKQERQQ
1361 DVSASSDQHL NDSGAASDAV NSSASLDMLS ISAEAAQSSP NAGPTASSSS AASLINSSTP SGASSASAST STSSSSVSIS
1441 SSSGGNGAAC LASVSGMLGG VANQSGDSGI YAAANTSIKE HVNTFLSKAS SSEETLPSPH SISMQQLETC NDIEAAIIAA
1521 ARAAAAARST SCSRSNSQEQ ETAHSQVKTK ATPNPEAKVV LPVFMTYNDD DEEDDESLQE LSFMADLKAD AVPEDISVLP
1601 PPPSRPAMMT NTELIVDYIA KTWNAIANSK YVTYYNELEQ ET
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.SAAGK.K	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	264	268	
total 1 peptides												

tr|A0A0R1E9C4|A0A0R1E9C4_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MCTKYDTWED SDFNDLDDAS LKKLLEEAYW YRNPGDRKNK SPRFLQMLKK AEYDEEISYR AIKSCITLNP SALTPSAATG
  81 SSGGSSSSAG HNSSYNSTNH RSTDPGQRHK QGGSLQDLVE AAHRSELATT SAAAAAATTA ATQRFNCDYQ LSGRPNRRQQ
 161 QHNQNATSSA SKKIKNSNVS GRQREGGSLP SSVNFDPSAA MEAKQHKQQA QPSSEAAGGS FSGSVGNKHH HRSSTGSCSS
 241 LPSHLGERDP EASTQFDLDV DDATGVGASA AVGVSGVQDD FMLEQLDPQN PSVKLLLDAL NDKPLETRYS AAGKKFLIDD

 321 RLHFSVLELS ARRKLQQQAQ YLAALTGQFG LGLEEEKRKV EAGYVSLNDN YTACSSVYGG GAGSPAAVEG SKPSTSSSSS
 401 STGSNCGASS DTLSSDLRPA KIGRMVPAAA SVAATPMGGK TTTRQLDENG NALGDGFGSS ASSGASAVAS SSNGNGNQFT
 481 ALITTTVGSS AATSSVAHRQ NSVSTLLSTG TNTTTTAMAA AAVAASYSQL QQTPGGGTAG AGSGIGIGLQ QPTKQKAKKK
 561 SQQERNTTTV DVESVAGYRG NDPVEQLVKY IENDVNGGGN SAAGQRKKER KKQNKLKKSN SLEELRTCSK MEVDDLKRQS
 641 ATTEMMRQKK GTNNASSGGS SSTASGSSNS GKHNSASVAD INKNCNKEQQ STPTVQVRNS TNPGSQQRKG ERRSWGTEEL
 721 QYLGDHQEMA AAWSEPETVR QKQLPLALPA LARMSELDAL NTVLSETAEF HVVTKKKKPK KQRAVTMDDA AVAAAAGTGG
 801 NLQRMQQITK SASSNIMSQR MHYYTPYNSN NGGGNANYKQ QHQQGQQYQE HYQAQQGQHH HHHHHHHHHH HHHSGSAVSN
 881 QVDSSRRKST SSMPPSEKSD SSDLDSVHSL PIQTGKKKSL GGGNNKQRAA QAASQRQAKQ NNNSAAPISY ADIARNKKEA
 961 LNNATASDTE LELGDKIQSK CGGKSKSRPD FPELPGAVTT GAASGGAVNQ AAVVSNQTSP PSSSSSISYS QSLNATPPSS
1041 SSDAESTNSP ELLAQVQIPN YSMATPTLTS STISSVSSSA ASTSFTSCSL PALQKSKSVE HDTSYSCNSS NLDQQYPALE
1121 RTVKRHSTNN VSVAVAASTS TSASSSLYNF AAAAKQQLAE NAYAAISPPA AVTTTSTAVA VSAPVPASAP APAAVTVPCY
1201 SSSSTQGSTQ SLSSTASSAI VLSSDKAKVK PKELSPSSSF SKKPTKPSQD TPSISLSIST TPKATTSTST TTTQKTTAAT
1281 QTEGAKKLIS GIHKLPSNNC IAKGAGAVLE ASAGRRAVII LNDDREAGRS NNEFIFGDFN EDELKLFDDN LDDDEEDQHK
1361 QSSNKKQQTE AESDVGQDDT EDVDQELDKE LECLGRRPEK KQERQQDVSA SSDQHLNDSG AASDAVNSSA SLDMLSISAE
1441 AAQSSPNAGP TASSSSAASL INSSTPSGAS SASASTSTSS SSVSISSSSG GNGAACLASV SGMLGGVANQ SGDSGIYAAA
1521 NTSIKEHVNT FLSKASSSEE TLPSPHSISM QQLETCNDIE AAIIAAARAA AAARSTSCSR SNSQEQETAH SQVKTKATPN
1601 PEAKVVLPVF MTYNDDDEED DESLQELSFM ADLKADAVPE DISVLPPPPS RPAMMTNTEL IVDYIAKTWN AIANSKYVTY
1681 YNELEQET
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.SAAGK.K	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	310	314	
total 1 peptides												

tr|A0A182R4W9|A0A182R4W9_ANOFN

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MTIVKSNTTD ATNPAENAKS PLSSSSSSSS SSDSDDGSDS SSDSDSSSAS TSKTSSKQSS GGGVPPEKPQ QFSVMSSDSA
  81 GLRMKIAIPR SQSNATPTPS PTSLGSNQQQ QQLLMQQDLP SPSGAADRRQ KNAENTLSEA SSALSAQTPL TGSTGSKCDS
 161 FKEHGSVKKG SNANGKSAMV EGSSRGRTST TQQVSTEGGK TLMTAAAHKQ GRTSDKRVHE RGRTAHSKSN KRSASGNGSS
 241 VGRTKKSVSE SDSSSPSSSF SSCTSNSDSD SSSTAGDNSN HNPSDKSKPT AGRTATNART PALTSTTAGN TIAAGKKQKI
 321 LKRKKANRTV TSSSSDEEDE DELPSGRSGS KSGAASRTNE FTSSDSSSSD EVGKGLSAIR AKGKNSQTKL PGVTSSAKAN
 401 ALSSSKDGGL LTMTTAGEGS GLLLNRPPLS TSTPAKQHGA FPPSLGGGGA SSVGDGGLTA EGGSCSSDNE LPALVNAAIR
 481 RVESGSDAES IRGLSAPTQQ YTSSLLRDFV VKTQMLGSVG GNGALANVGG SAANSAVSGS GIGGGNGGGG SPSSSSSSSS
 561 SSGSTSSSSS SSVEEGADPV IGSAGPGPGG GPGPFELDVR KIKTESPVIS SGPAASAGRN TPIVNGLTSG MKGDPLAPAA
 641 PIVKRRGRPP KSSLATAAAA VGARPSASSR SVSIPTVIES PDSGILSTHS STGSPKTDKA RPNLHMRSSI GAGSSSSTRR
 721 SKSEVRGDST ALSAILPASG SPYGGNTLSA SATVGSSGRT STTAYSLSSC LDRNTYATER VLYPPRGPKK RGVGRPPKKD
 801 TAQQQQSSSG RGSQNGPQVR TAATQQSEDR LDPHWQKIDI SKKFHEPRLS GYKSDGGHST ICCSKRLASQ SGYISDYGGV
 881 GASGGRSRLS GYKSDYSSRS RRSCSRGAGY RSDYGRAKSC GYRSDCSTRH RKQVRRKRRK KIGHQQEQHE QHHNNNLNDR
 961 KNYNASSDGG GGGSTKSASV GELEIMFMAG LTLGSTSDED SSSTSSSTSS SSAESRESLF SDNSGIDRPA PSSVDKAKRV
1041 TPEKGRRGST KQLDKPAAKI QRTPRKPTPP KTIAKGRVVK ASERSVVRGS KNISTPTIDR RRKSNHVKDS KEDEQSDEDV
1121 VARRFGDRSR TKSLQATVKE PPPPPPPKPS IAATASVALK QKSSAMIKKP GTRGRPPSVK KQPAVSAGAG SNTASTSKSL
1201 GSLNALLAPK NRATLVLPTN NFDRVFASMS NKQQTAGSPN ESKSAIYTFS SSTVGSKNAF ATFLQRGAAE GASKDDNDDN
1281 GKLMAVKKLP LSKANVIKNS EECNRRFQKS SSSFALTVGG GVGGIAGSVD LLARIADGTI PKASPTKSVC SKRSRRKSCT
1361 SDRLEVMSVK SYGVIGSCGK IRQRRLSTMS RCSSRSAGSR HAAARMKRRK KRLRSMSVAP GATSDMLNAG GTASSSGLDL
1441 KLNAEIDRLS ESFNGMCRIV GGSTDAGTST GGRSVNSPEE TTSANVPSVA TPSGKAHQTK RSVKKRKASE HVTDSPSATG
1521 GGNAAGSGGA GGATGNGGGG GGGTGKRRNK KSVPTQSPDD HKLPLKKRHY LLTPGEKGNN SDNNSGVDEV KSTGGASGGS
1601 SGTGTGTAGS GGGSTNSSFA GSHTVLNPCA FTSGRLSANA AAAGSSMSGA ATKAVTPKKR HLLKSPEPGP VPTDTELQLQ
1681 QIKSSNSPLT IVNGGIAGTV GDVGSSPPEG LTAGRKGLTD FVTGGSPSSG IGHSTTGASG SKKKHNRQQE ASAASAHTGT
1761 SENHNSAGAH HHHHHRSTPP ARPSVIQSSA SVLPSGSGGF SSSSSGPPPG VFEPTVDLEL VIPPPTSIPS LIAKVEMLDS
1841 PRLGKDSAGA IGGSGNITTK LESDELQVLT AAQRKGLAAG SGLLATVTPT SASSEKVLEK LLTKTGAHHL LLKKKRKKPN
1921 RTGFPTVKKK KKKAPESDPL DVGLSVIDLK PEVGPDLFDS SNLTRHVPSE AERTRMKEKH LHQTSTGKNA SCDRVPKEGE
2001 PTDCFIERHS GVGRPRLSVV SLEKLQGKLP IATGTRDVAT TPPATGGRGR KSVINPLAPE HQLVHRSQER NRKDDLSSVS
2081 TGRKGKRKHE VSKTPPDSGS KRKGAAVEVD NRSTKERNRS KSVSASTEQQ QLPNIVRLSE TLSKGTAKEN KENSKLPSGR
2161 SPSAAGKKSS KEPVVSPGTS PEGDSTGVIR RTRSSSVALD PSEVKKIHQD AEDSVGKGTS QSSTPVRLHS WAVSGIHNED

2241 STSLDSMPLL KRIHSRSISR LQSVSTPTVL LEPLATSPKT PGRPRGRPRT TSPITATETP HSPTTGRGRP RTALAITGNT
2321 SIVSTDRVLS SPLRSPTASP IVGGVSGGAV VGRKKQKRDG RKSVPPAIAE PIESAHLATR ISASKSVTPT PPVGTVIPAR
2401 MKRGKSDEIV RSQQLEKPAK KPRKDIASAE PSPEATTVPV PRRNPITSPI VEPVEPEETA HILKPASSTD ELEHDPLPPD
2481 EGPSDFLRLA DTPSPTSSGE TRDLPTGSGG RVTSKKLPRK KYITAGLFSD CYKDDGTGGE GRSGPKTPPE TLLPPPAYCE
2561 RFLRRTVRDF QLPYDLWWLQ ENGKLPGRNS VPSWNYRKIR TNVYYDVKPN PSTDNPQCNC KPDSGCQDDC LNRMVYTECV
2641 PEHCPCGDRC RNTSIQRHEY APGLERFMTE EKGWGIRSRE PIIKGTFIME YLGEVVTERE FKERMRTLYL NDTHHYCLNL
2721 DGGLVIDGHR MGSDCRFVNH SCAPNCEMQK WSVNGLFRMA LFALRDIPPN EELSYDYNFS LFNPSEGQPC RCGSEQCRGV
2801 IGGKSQRIKP IPLGSSNGST GHRNPSEAGP DTDPSKSGGS DGAAGANGPG SGGALVVELS PRSAARSRKR QAKKNQPIVH
2881 LNGTPLPTFH PPTVKERALI AEHHCFLLRN LNKIRRQKER AATMVSAGGA GGGAGTSATD GGPGAASGAD QTTSGKPSLA
2961 SQISALRCPR NIRTRGLAFV EDDPELEKTA RIAVALKDIC TEIATLKDDK GLPYINKLQL PSKKKIPLYY ERIPKPIDLA
3041 QIETNIEQGI YRMPKVFEDD LLIMLSNAIK YYGINSPEGI ASEALKSHYY TCKQQQVPKL QAYIGEENEL LRGFVPKKEP
3121 EEDTGVPKPK RGRRQEQTED IIRCICGLFK DEGLMIQCSK CLVWQHIECT KADPAVENYL CEKCDPRDVN YEIPLNEFTE
3201 EGYQYYISLM RGKLQIRQTD TVYVLRDIPM SPDPDNPSAP VRKHTYETIG KIEYSECDIF RVESLWKDKE GRRFVYGHHY
3281 LRPHETYHEP TRRFYPNEVM RVPLYEVIPI ELVVDRCWVL DPITFCKGRP VDSSEPHVYI CELRVDKSAR LFSKISRHSH
3361 PVCMKSYAFH KFEQKLKIAK TFAPHDLGSL AHLLSIRDRQ KKGSKKDDTN GGQSSTGSVS GTSSFSGTGG SHSSGSKKMT
3441 PIIQLLPPPP KTLAEKRNRL EQVLCRLMLK LTLNPNALPV VDISYLLTGR GARLRRTNNS TPVPVI
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
P.SAAGK.K	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	2163	2167	
total 1 peptides												

tr|A0A226EGW7|A0A226EGW7_FOLCA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MDRPRRSTRN SLYNSTPTTT TTPSTSSTSN QNNNNSNPYK KPTYLAGRSS EAGSTPTSRS GRGRGRGRSS AGGRHSNHDN
  81 GSTPLSGNGG SKSGKSSRPE CVATRVESRR STGGSSGGGG GGASSNKKKR GAYNSQDYHY GSDFSDQNDS ELDEAGSGSE
 161 STSELGNDEA DSDSDYSIKF SKGTSSSDTA VATTPPSRVP SPPVPLWMEA DAVIEELDLP KSSDDLLLAR DLVMKAVAIY
 241 EPLRRFHQLV RLSPFRFEDF CAALGNEETS PLLTEIHIQL LKTILREEEA NATMFGPAEV KDSIQAVLYF IDNLTWPECL
 321 RAYIESDPNW GEVLAEMGSG SGGEYPFGGA EIRIKILSWM VDQFLATSLV RDVLVSENIR HDDYCRSCNK MGEVVMCETC
 401 PAVYHLYCMT PPYKGDDSIP DDWQCPVCKK NNMSGISDCA SELEKAGLLI RHEKLGNDRH GRKYWFLVRR ILAESEDGSS
 481 VWYYSTPLQV EELLYRLDEE GYEAELVENI RNCKDEIVRQ MEVTEQITEQ SNSLLHRKTY IEAENAFLKK IHEDRELAHI
 561 RELENQAKEA ERALEAAKQE EEAAAAEEEE VKQKEELEKK RIREERLLRR NQNKFVDYNP AEWNEDGTPK GGSSGSGDDS
 641 SGETGKMNHC NEDKNDLDDT MTKPDLLSAS QIANAETQLI DSSEDVTIPK LEPEVQTDEK MDTTENGPDD LFIPKMTDTT
 721 TKSVEVKKEE VAAPVSRRKS KALLLDWDTE ERMTRLKATG LYKLGQEGNY RNYVNIYNTD NLALSKFQHG EESIKKRHMS
 801 HKFSLTAASE VKWNSFSSSV GLRTNMVSTL RATLVHLESA VPITLMHTNW GIMRKSWVSA VAGCTGAKDF AKATITLAAC
 881 LRSCIYNPVW TESLAHHKLI RTSALEREER KKAEKRDKKD RDDEEDRLRL LPQWVKYSIP AKHQVYKQKG EEYRIHGRWG
 961 WIWMSTGRRC KPQDCRKLGL LSGPYKHVIQ VKNDSGKVKT ILIDPTTFDK LMAKRTLSQK STPATTPSKV VPPPAQTEAP
1041 PPPPLAITAG GEESKEEKVE KMEVDESPVK EEEEVKPEVK EEEKEEATTE SQEIKDPQPD KESESTPEEK KCDEVVVASP
1121 PPPPQSDDVT PPATETGMEI DPKIEDKPHD QDECGTLIPK DEPVDAPTAA PAETNLSSEM EPLSAVEKVE IKEEKEDEVP
1201 PAPRLTSTTP SSPSTSASSD ALAASNRKFR TDLINVSLGM VVANRILYPK LAHKSAILDS LLARRISLQK LEEDYLLETY
1281 GKEKLEKVQQ IVDAGGQIVD EPNKVEEPTV DEKGDEILDD SFPLAGIYRF KCYSHMCQTA AAAFATQTEN KVRDYEFKCY
1361 SPMCRLKFFV QDSNRRKEER ARINEKAKLV ALVEEVKGKK MFTQTDSSCK ILLKKLPNEL NRRRNQITYP TTSKFCSVST
1441 PLDPSIFVLP WHELRKLSRT AGRTFTPSGF APAPKTGSWA WPYPCGRPLF KTGWQFKAVH SNTLAAAALQ LRILWASVKW
1521 DDIQMKAPNY DGKNQTTTDM EIITSEILSH RVKGRFSERV QYLRKKTVEP IDAPKTIRAK SRDSSEITPS RSGLRKRKLA
1601 ESLQGSDPVV TESWVDEDQL ELWEIKVYHD KLDRKSDPAS SSSKPGTPLG STRSKSGVSI KQPEKFDPSP SSDGTKGDKT
1681 ISPAKTAELM REKLETEEKM QRAVHLSKRD NHPKNNNTAV NKQPTPTASQ QLQQQQAAAG LPANPRSYGG AAPSSAKKVT
1761 IVAPKVLNVS GPGAGDVATT PGAGSTAAAV AILNRSKIAG VVGSTVAIPK VVQQAAQSPT TTVPTPQKIT VFRTSDGKLQ
1841 VRGLLPGQAV YQTADGKIGL TSTPVNKTVQ QAGQQTPQQH VISPQPQGQT ILIQSQGVGT QLQQVAAAGN QLAIQQSTVS
1921 SSQTTPLINI SSPTMRTVLS SSPSAVKFIS QQQNPSATST QSPLALTASG QLVQTYSAAG KGNVRKVNPK FPTAIAPTPA

2001 PVSSASQQVT GTLNAQGQIV LTRGGQVINQ QIVIQPGPAV VVSSSSPNVV GGGNVVAIKS SPISVAQAPA TATTPTSASP
2081 SQMLVSSSSN SPLPPSQQIT TPQGTTALMT YQAGGKIVIQ DGNKTIVVTG GANLTTQQLQ QILQMQMKKP SGTVMTTQVV
2161 PTQPGQQGLK PQQPQQQQQQ QQVIVGGGQQ QQQQIVQGQG GQQQIQIISG GGAAGTIAGQ SLQQIAASGQ GQLVLQGVQN
2241 LASGHQIATL GGQNVIVKKV MKSPIKSGTP LTIQTVPGQP IPTAAQIQQL LAANKNLIRV DPNTGTVNIS SATIQQLQLQ
2321 QQQQQQNQQS PMLGSTSSVG LGVAGSTTVT KTPGLPISIV SPSKNPKIVP TLFPQGNAAA VKTISSVTTP LVTPSTRYIA
2401 PAIVQQQQRL AAPQQMVTSP VLSTNSPPTA VKTTPTTPSS TMQTPPSTPQ TPAASQQPKI AAQFIETEEG PRVIVSGFKP
2481 GDLTQSQLAS LNAQIVKQMQ EHPALREKFL GMTDPATELK IILQPHPPNI AGTPQKIVKV PPSLPAKAAS GLVKGAGASS
2561 PVRGASPVKT SPVKSPVTSA SPMKGLPSSP SALIKSPPNS ANIEAAIAAV ASNADAPVIL PAKSSPMKKT QSVMVASSSS
2641 PPTSLPTPSK EDMLKNILHK VETENHHDHV ISSSPVKPAA SPPRRKASPK KPVPPPEVAH IPTEEEQGIP QPIEGDVVID
2721 DGVVNEIEVS ENNDAEVPRF VLSQDLMGSG QAGHKQLESS SASSMTFFSS PPHVQEHEIA STTNTPTSPN NKPKSGSSRR
2801 KSPVKTKSIM QNSESTMIMS PPKKRINMSP MASPKQINLM HKQTDLLKKD ISKKRVLLER DLAMDVRKEI SQDDKGLLSD
2881 DVDTNPEQNA RPGQGKKRKA SGSKSHGGGA KRKKRNSSPG KNSVVKQRPK SGGNKVHCIC KTPYDKTRFY ICCDICSSWY
2961 HGDCIGIPEE EGKNVPEFIC VACKPSSSSG SDNKSMCLCR QPYVETQFCI ACEKCDEWFH GRCVGILPTE GDSIPAYYCP
3041 TCQPGMKINA INAKSLSNEH YVEISKTLRQ IQSHKSSYPF MNPVNAADVP NYYKVIKEPM DLKTIALRVE EKMYTKLLDF
3121 VADLAKIVDN YRFFNPPESQ IYKAGHVLEK FCSQKMGNLR SVLDKQ
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.SAAGK.G	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	1977	1981	
total 1 peptides												

tr|B4Q082|B4Q082_DROYA

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MNNEQTPSSS DTPADRVGSG GAAAKLPTII PDTPIVSIAA GTMSESTTTT TATKTTPTPF PQEQLMTMMS DHVAKVDAQL
  81 DEAKDDASQG AAAVPANHVA TSGSSSRGSD PKKSSSPSNS HSTGNHVVTT AAKGSPAAED SSFSQVFAML KDSPNAELSR
 161 PNRRVLQYGA TAKGKTQDDQ NVGKRQKKKK TKYDTWEDSD FNDLDDASLK KLLEEAYWYR NPGDRKNKSP RFLQMLKKAE
 241 YDEEISYRAI KSCITLNPSA LTPSAATGSS GGSSSSAGHN SSYNSTNHRS TDPGQRHKQG GSLQDLVEAA HRSELATTSA
 321 AAAAATTAAT QRFNCDYQLS GRPNRRQQQH NQNATSSASK KIKNSNVSGR QREGGSLPSS VNFDPSAAME AKQHKQQAQP
 401 SSEAAGGSFS GSVGNKHHHR SSTGSCSSLP SHLGERDPEA STQFDLDVDD ATGVGASAAV GVSGVQDDFM LEQLDPQNPS
 481 VKLLLDALND KPLETRYSAA GKKFLIDDRL HFSVLELSAR RKLQQQAQYL AALTGQFGLG LEEEKRKVEA GYVSLNDNYT

 561 ACSSVYGGGA GSPAAVEGSK PSTSSSSSST GSNCGASSDT LSSDLRPAKI GRMVPAAASV AATPMGGKTT TRQLDENGNA
 641 LGDGFGSSAS SGASAVASSS NGNGNQFTAL ITTTVGSSAA TSSVAHRQNS VSTLLSTGTN TTTTAMAAAA VAASYSQLQQ
 721 TPGGGTAGAG SGIGIGLQQP TKQKAKKKSQ QERNTTTVDV ESVAGYRGND PVEQLVKYIE NDVNGGGNSA AGQRKKERKK
 801 QNKLKKSNSL EELRTCSKME VDDLKRQSAT TEMMRQKKGT NNASSGGSSS TASGSSNSGK HNSASVADIN KNCNKEQQST
 881 PTVQVRNSTN PGSQQRKGER RSWGTEELQY LGDHQEMAAA WSEPETVRQK QLPLALPALA RMSELDALNT VLSETAEFHV
 961 VTKKKKPKKQ RAVTMDDAAV AAAAGTGGNL QRMQQITKSA SSNIMSQRMH YYTPYNSNNG GGNANYKQQH QQGQQYQEHY
1041 QAQQGQHHHH HHHHHHHHHH HSGSAVSNQV DSSRRKSTSS MPPSEKSDSS DLDSVHSLPI QTGKKKSLGG GNNKQRAAQA
1121 ASQRQAKQNN NSAAPISYAD IARNKKEALN NATASDTELE LGDKIQSKCG GKSKSRPDFP ELPGAVTTGA ASGGAVNQAA
1201 VVSNQTSPPS SSSSISYSQS LNATPPSSSS DAESTNSPEL LAQVQIPNYS MATPTLTSST ISSVSSSAAS TSFTSCSLPA
1281 LQKSKSVEHD TSYSCNSSNL DQQYPALERT VKRHSTNNVS VAVAASTSTS ASSSLYNFAA AAKQQLAENA YAAISPPAAV
1361 TTTSTAVAVS APVPASAPAP AAVTVPCYSS SSTQGSTQSL SSTASSAIVL SSDKAKVKPK ELSPSSSFSK KPTKPSQDTP
1441 SISLSISTTP KATTSTSTTT TQKTTAATQT EGAKKLISGI HKLPSNNCIA KGAGAVLEAS AGRRAVIILN DDREAGRSNN
1521 EFIFGDFNED ELKLFDDNLD DDEEDQHKQS SNKKQQTEAE SDVGQDDTED VDQELDKELE CLGRRPEKKQ ERQQDVSASS
1601 DQHLNDSGAA SDAVNSSASL DMLSISAEAA QSSPNAGPTA SSSSAASLIN SSTPSGASSA SASTSTSSSS VSISSSSGGN
1681 GAACLASVSG MLGGVANQSG DSGIYAAANT SIKEHVNTFL SKASSSEETL PSPHSISMQQ LETCNDIEAA IIAAARAAAA
1761 ARSTSCSRSN SQEQETAHSQ VKTKATPNPE AKVVLPVFMT YNDDDEEDDE SLQELSFMAD LKADAVPEDI SVLPPPPSRP
1841 AMMTNTELIV DYIAKTWNAI ANSKYVTYYN ELEQET
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
Y.SAAGK.K	Y	20.50	432.2332	14.9	433.2469	1	8.71	392	4	498	502	
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)