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.

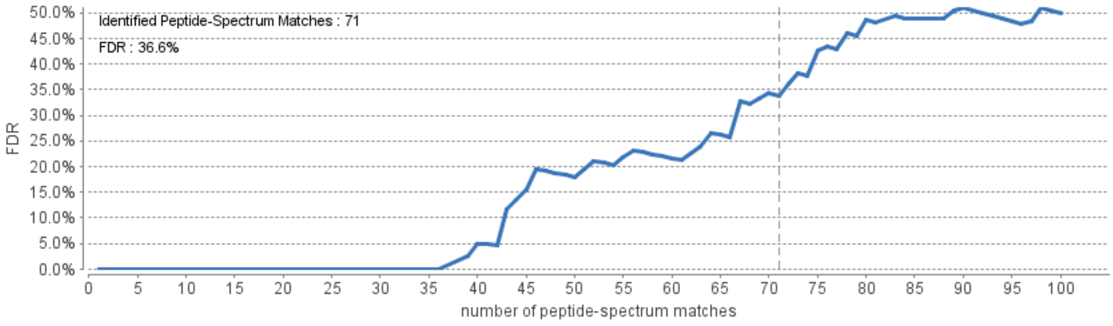
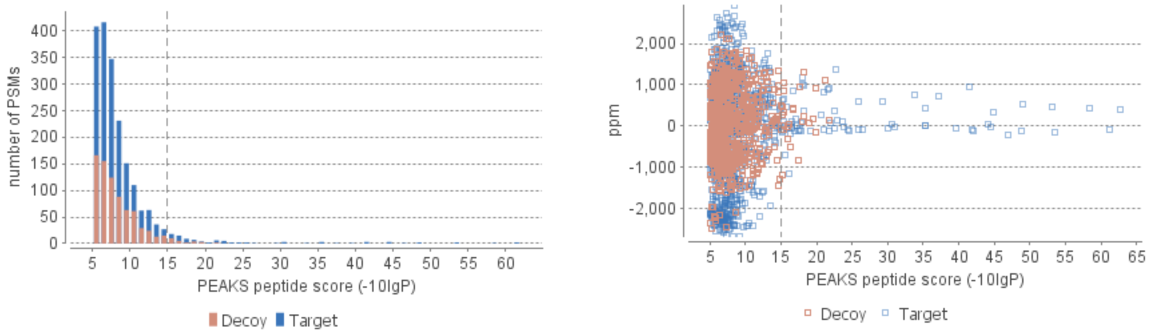
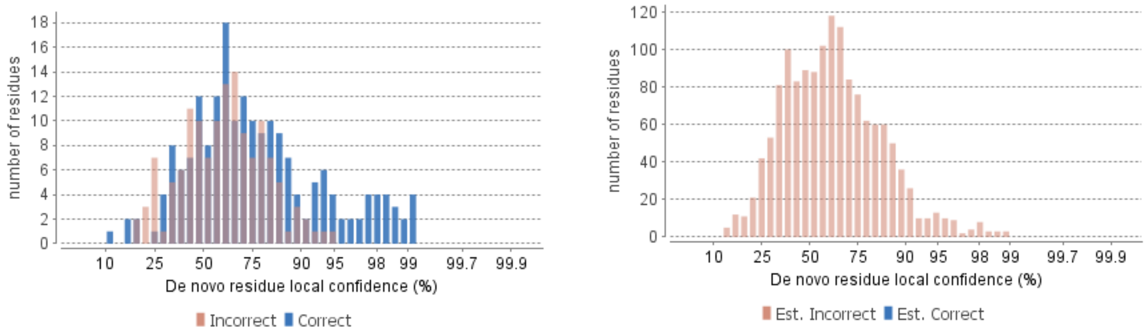


Figure 2. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.


(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	1525
# of MS/MS Scans	4135

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	71
Peptide Sequences	69

Table 4. PTM profile.

Name	ΔMass	#PSM	Position
Oxidation	15.99	7	M
Carbamidomethyl	57.02	4	C
Methyl ester	14.02	1	C-term
Pyro-glu from Q	-17.03	1	N-term
Formylation	27.99	1	N-term
Dihydroxy	31.99	1	Y

Protein Groups	22
Proteins	195
Proteins (#Unique Peptides)	33 (>2); 36 (=2); 126 (=1);
FDR (Peptide-Spectrum Matches)	36.6%
FDR (Peptide Sequences)	37.7%
FDR (Protein)	1.0%
De Novo Only Spectra	153

3. Experiment Control

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

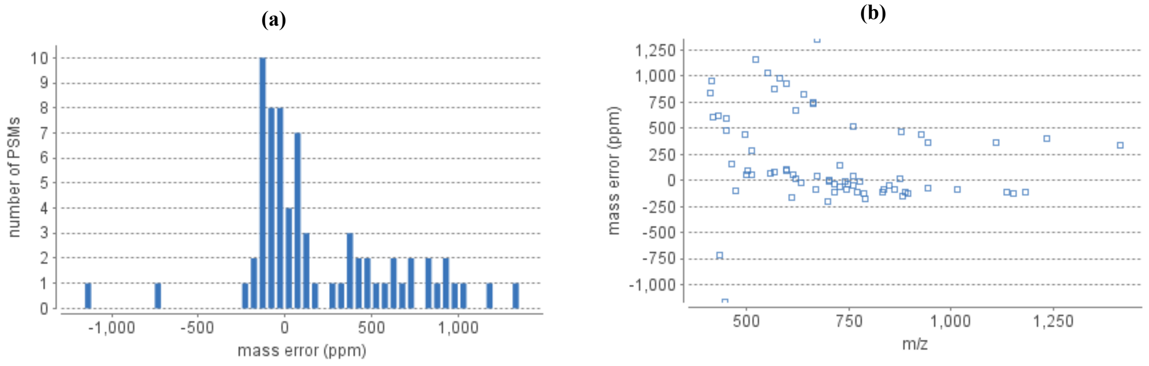


Table 5. Number of identified peptides in each sample by the number of missed cleavages

Missed Cleavages	0	1	2	3	4+
LTQ	0	0	0	0	69

4. Other Information

Table 6. Search parameters.

Query Type: Homology Match
Fixed Modifications:
Carbamidomethylation: 57.02
Variable Modifications:
Oxidation (M): 15.99
Fragment ion tolerance: 0.5
L equals I: true
Q equals K: true
Report number: 1
Maximum # of PTMs: 3
De novo score (ALC%) threshold: 15
Peptide hit threshold (-10logP): 30.0
Peaks run ID: 88
Merge Options: 0.1 min. 0.1 Da
Precursor Options: corrected
Charge Options: no correction
Filter Options: no filter
Process: true

Table 7. Instrument parameters.

Fractions: IT_douglas_2_20170921_02.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID/ECD
MS Scan Mode: Linear Ion Trap
MS/MS Scan Mode: Linear Ion Trap

Protein List

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
4	11607	tr|V9I6A9|V9I6A9_APICE	113.19	7	4	4	Y	112642	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.11 PE=2 SV=1
4	11613	tr|V9I6B1|V9I6B1_APICE	113.19	8	4	4	Y	95944	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.1 PE=2 SV=1
4	11611	tr|V9I733|V9I733_APICE	113.19	8	4	4	Y	90924	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.13 PE=2 SV=1
4	11612	tr|V9I6C2|V9I6C2_APICE	113.19	8	4	4	Y	90968	Sodium/potassium-transporting ATPase subunit alpha OS=Apis cerana GN=ACCB00027.14 PE=2 SV=1
2	22502	tr|A0A0P6A3S1|A0A0P6A3S1_9CRUS	92.88	36	6	6	Y	13057	Histone H2B (Fragment) OS=Daphnia magna PE=3 SV=1
2	22503	tr|A0A0P6CBE1|A0A0P6CBE1_9CRUS	92.88	33	6	6	Y	13952	Histone H2B OS=Daphnia magna PE=3 SV=1
5	11774	tr|V9IK47|V9IK47_APICE	83.52	16	3	3	Y	33013	ADP,ATP carrier protein 2 OS=Apis cerana GN=ACCB10355 PE=2 SV=1
5	11776	tr|M9NYU2|M9NYU2_APICC	83.52	16	3	3	Y	32983	Adenine nucleotide translocase OS=Apis cerana cerana GN=ANT PE=2 SV=1
5	11778	tr|Q6VQ13|Q6VQ13_APIME	83.52	16	3	3	Y	32986	ADP/ATP translocase OS=Apis mellifera GN=Ant PE=2 SV=1
5	22071	tr|E2BR21|E2BR21_HARSA	83.52	16	3	3	Y	33016	ADP,ATP carrier protein 2 OS=Harpegnathos saltator GN=EAI_12316 PE=3 SV=1
1	22001	tr|A0A182FLZ7|A0A182FLZ7_ANOAL	82.60	65	7	7	Y	9050	Histone H4 OS=Anopheles albimanus PE=3 SV=1
total 195 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
1	22002	tr|A0A1D2MA61|A0A1D2MA61_ORCCI	82.60	50	7	7	Y	11381	Histone H4 OS=Orchesella cincta GN=Ocin01_05613 PE=3 SV=1
1	22003	tr|A0A1Z5LH91|A0A1Z5LH91_ORNMO	82.60	50	7	7	Y	11367	Histone H4 (Fragment) OS=Ornithodoros moubata PE=3 SV=1
1	22004	tr|A0A182IZV6|A0A182IZV6_9DIPT	82.60	50	7	7	Y	11381	Histone H4 OS=Anopheles atroparvus PE=3 SV=1
1	22005	tr|B4JH62|B4JH62_DROGR	82.60	50	7	7	Y	11381	Histone H4 OS=Drosophila grimshawi GN=Dgri\GH18656 PE=3 SV=1
1	22006	tr|A0A194Q0V4|A0A194Q0V4_PAPXU	82.60	50	7	7	Y	11381	Histone H4 OS=Papilio xuthus GN=RR46_05365 PE=3 SV=1
1	22007	tr|A0A182FBX3|A0A182FBX3_ANOAL	82.60	50	7	7	Y	11381	Histone H4 OS=Anopheles albimanus PE=3 SV=1
1	22008	tr|A0A151XEG2|A0A151XEG2_9HYME	82.60	50	7	7	Y	11381	Histone H4 OS=Trachymyrmex zeteki GN=ALC60_02422 PE=3 SV=1
1	22009	tr|A0A034WS42|A0A034WS42_BACDO	82.60	50	7	7	Y	11381	Histone H4 OS=Bactrocera dorsalis GN=H4 PE=3 SV=1
1	22010	tr|B4LVM7|B4LVM7_DROVI	82.60	50	7	7	Y	11381	Histone H4 OS=Drosophila virilis GN=Dvir\GJ17459 PE=3 SV=1
1	22011	tr|A0A226DYY4|A0A226DYY4_FOLCA	82.60	50	7	7	Y	11381	Histone H4 OS=Folsomia candida GN=Fcan01_04163 PE=3 SV=1
1	22012	tr|B4ILZ0|B4ILZ0_DROSE	82.60	50	7	7	Y	11397	Histone H4 OS=Drosophila sechellia GN=Dsec\GM19702 PE=3 SV=1
1	22013	tr|Q7PCX0|Q7PCX0_ANOGA	82.60	50	7	7	Y	11381	Histone H4 OS=Anopheles gambiae GN=1267447 PE=3 SV=4
1	22014	tr|A0A023GDJ7|A0A023GDJ7_9ACAR	82.60	50	7	7	Y	11367	Histone H4 OS=Amblyomma triste PE=2 SV=1
1	22015	tr|A0A132ACK5|A0A132ACK5_SARSC	82.60	50	7	7	Y	11367	Histone H4 OS=Sarcoptes scabiei GN=QR98_0039310 PE=3 SV=1
1	22016	tr|A0A1B0D251|A0A1B0D251_PHLPP	82.60	50	7	7	Y	11381	Histone H4 OS=Phlebotomus papatasi PE=3 SV=1
1	22017	tr|A0A0A9WMX0|A0A0A9WMX0_LYGHE	82.60	50	7	7	Y	11353	Histone H4 OS=Lygus hesperus GN=His4 PE=3 SV=1
1	22018	tr|E2A0J1|E2A0J1_CAMFO	82.60	50	7	7	Y	11381	Histone H4 OS=Camponotus floridanus GN=EAG_09814 PE=3 SV=1
1	22019	tr|Q4PM69|Q4PM69_IXOSC	82.60	50	7	7	Y	11367	Histone H4 OS=Ixodes scapularis GN=8030709 PE=2 SV=1
1	22020	tr|A0A1S3DDY8|A0A1S3DDY8_DIACI	82.60	50	7	7	Y	11381	Histone H4 OS=Diaphorina citri GN=LOC103515904 PE=3 SV=1
1	22021	tr|A0A182WXV7|A0A182WXV7_ANOQN	82.60	50	7	7	Y	11381	Histone H4 OS=Anopheles quadriannulatus PE=3 SV=1
1	22022	tr|A0A1V9XAM9|A0A1V9XAM9_9ACAR	82.60	50	7	7	Y	11367	Histone H4 OS=Tropilaelaps mercedesae GN=BIW11_01686 PE=3 SV=1
7	22138	tr|Q7JN37|Q7JN37_ARTSF	70.93	38	2	2	N	8565	Ubiquitin unit I (Fragment) OS=Artemia franciscana PE=4 SV=1
7	22146	tr|A0A034WV44|A0A034WV44_BACDO	70.93	16	2	2	N	20813	Polyubiquitin-B (Fragment) OS=Bactrocera dorsalis GN=UBB PE=4 SV=1
7	22143	tr|A0A0A9Z4T5|A0A0A9Z4T5_LYGHE	70.93	19	2	2	N	17930	Ubiquitin-40S ribosomal protein S27a OS=Lygus hesperus GN=RpS27A_0 PE=4 SV=1
7	22144	tr|Q1W2C4|Q1W2C4_9HEMI	70.93	19	2	2	N	17875	Putative ubiquitin/ribosomal protein S27Ae fusion protein OS=Graphocephala atropunctata GN=g.419 PE=2 SV=1
7	22145	tr|A0A182QI60|A0A182QI60_9DIPT	70.93	19	2	2	N	17983	40S ribosomal protein S27a OS=Anopheles farauti PE=4 SV=1
7	22142	tr|D7RF65|D7RF65_ERISI	70.93	19	2	2	N	17830	Ubiquitin a OS=Eriocheir sinensis PE=2 SV=1
7	22141	tr|E3UKG7|E3UKG7_ERISI	70.93	22	2	2	N	14717	Ubiquitin b OS=Eriocheir sinensis PE=2 SV=1
7	22139	tr|A0A182IKK6|A0A182IKK6_9DIPT	70.93	23	2	2	N	14729	60S ribosomal protein L40 OS=Anopheles atroparvus PE=4 SV=1
7	22140	tr|R4G4B9|R4G4B9_RHOPR	70.93	23	2	2	N	14729	Putative ribosomal protein l40 OS=Rhodnius prolixus PE=2 SV=1
7	22147	tr|E3UKG8|E3UKG8_ERISI	70.93	10	2	2	N	34337	Polyubiquitin OS=Eriocheir sinensis PE=2 SV=1
7	22148	tr|A0A1S3DBX7|A0A1S3DBX7_DIACI	70.93	10	2	2	N	34348	polyubiquitin-B isoform X2 OS=Diaphorina citri GN=LOC103514696 PE=4 SV=1
7	22149	tr|A0A1E1W9H3|A0A1E1W9H3_PECGO	70.93	6	2	2	N	51430	Uncharacterized protein OS=Pectinophora gossypiella GN=g.11061 PE=4 SV=1
7	22150	tr|A0A0Q5U3G2|A0A0Q5U3G2_DROER	70.93	4	2	2	N	77270	Uncharacterized protein, isoform B OS=Drosophila erecta GN=Dere\GG14240 PE=4 SV=1
8	21998	tr|A0A087ZQI5|A0A087ZQI5_APIME	69.91	4	2	1	N	59512	ATP synthase subunit alpha OS=Apis mellifera GN=Atp5a1 PE=3 SV=1
8	21999	tr|A0A0N0BIY2|A0A0N0BIY2_9HYME	69.91	4	2	1	N	59519	ATP synthase subunit alpha OS=Melipona quadrifasciata GN=WN51_07748 PE=3 SV=1
8	22000	tr|V9IFD6|V9IFD6_APICE	69.91	4	2	1	N	59526	ATP synthase subunit alpha OS=Apis cerana GN=ACCB04724 PE=2 SV=1
8	22045	tr|A0A0J7N062|A0A0J7N062_LASNI	69.91	4	2	1	N	59948	ATP synthase subunit alpha OS=Lasius niger GN=RF55_15079 PE=3 SV=1
8	22049	tr|A0A1A9WYG7|A0A1A9WYG7_9MUSC	69.91	4	2	1	N	59478	ATP synthase subunit alpha OS=Glossina brevipalpis PE=3 SV=1
8	22050	tr|A0A1B6KWM9|A0A1B6KWM9_9HEMI	69.91	4	2	1	N	61429	ATP synthase subunit alpha (Fragment) OS=Graphocephala atropunctata GN=g.30172 PE=3 SV=1
8	22026	tr|B4QHN0|B4QHN0_DROSI	69.91	4	2	1	N	51137	GD11704 OS=Drosophila simulans GN=Dsim\GD11704 PE=3 SV=1
8	22027	tr|A0A182TC06|A0A182TC06_9DIPT	69.91	4	2	1	N	53866	Uncharacterized protein OS=Anopheles maculatus PE=3 SV=1
8	22028	tr|A0A182YNR5|A0A182YNR5_ANOST	69.91	4	2	1	N	57574	ATP synthase subunit alpha OS=Anopheles stephensi PE=3 SV=1
8	22029	tr|A0A1B0C955|A0A1B0C955_LUTLO	69.91	4	2	1	N	58520	ATP synthase subunit alpha OS=Lutzomyia longipalpis PE=3 SV=1
8	22030	tr|A0A151J3L9|A0A151J3L9_9HYME	69.91	4	2	1	N	59328	ATP synthase subunit alpha OS=Trachymyrmex cornetzi GN=ALC57_10733 PE=3 SV=1
8	22031	tr|A0A151XGV4|A0A151XGV4_9HYME	69.91	4	2	1	N	59635	ATP synthase subunit alpha OS=Trachymyrmex zeteki GN=ALC60_01388 PE=3 SV=1
8	22032	tr|A0A195CV10|A0A195CV10_9HYME	69.91	4	2	1	N	59555	ATP synthase subunit alpha OS=Cyphomyrmex costatus GN=ALC62_04768 PE=3 SV=1
8	22033	tr|B4LIV0|B4LIV0_DROVI	69.91	4	2	1	N	59176	ATP synthase subunit alpha OS=Drosophila virilis GN=Dvir\GJ22050 PE=3 SV=1
8	22034	tr|A0A0M4EW76|A0A0M4EW76_DROBS	69.91	4	2	1	N	59338	ATP synthase subunit alpha OS=Drosophila busckii GN=Dbus_chr2Rg1866 PE=3 SV=1
8	22035	tr|A0A1L8E154|A0A1L8E154_9DIPT	69.91	4	2	1	N	59331	ATP synthase subunit alpha OS=Nyssomyia neivai PE=3 SV=1
total 195 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
8	22036	tr|A0A182XJA6|A0A182XJA6_ANOQN	69.91	4	2	1	N	59401	ATP synthase subunit alpha OS=Anopheles quadriannulatus PE=3 SV=1
8	22037	tr|A0A182FH95|A0A182FH95_ANOAL	69.91	4	2	1	N	59383	ATP synthase subunit alpha OS=Anopheles albimanus PE=3 SV=1
8	22038	tr|W5J4R5|W5J4R5_ANODA	69.91	4	2	1	N	59383	ATP synthase subunit alpha OS=Anopheles darlingi GN=AND_008921 PE=3 SV=1
8	22039	tr|A0A1J1J483|A0A1J1J483_9DIPT	69.91	4	2	1	N	59428	ATP synthase subunit alpha OS=Clunio marinus GN=CLUMA_CG020197 PE=3 SV=1
8	22040	tr|A0A182N7Z7|A0A182N7Z7_9DIPT	69.91	4	2	1	N	59387	ATP synthase subunit alpha OS=Anopheles dirus PE=3 SV=1
8	22041	tr|Q7PHI8|Q7PHI8_ANOGA	69.91	4	2	1	N	59452	ATP synthase subunit alpha OS=Anopheles gambiae GN=1274812 PE=3 SV=2
8	22042	tr|A0A069DZ92|A0A069DZ92_9HEMI	69.91	4	2	1	N	59539	ATP synthase subunit alpha OS=Panstrongylus megistus PE=2 SV=1
8	22043	tr|A0A067QI29|A0A067QI29_ZOONE	69.91	4	2	1	N	59515	ATP synthase subunit alpha OS=Zootermopsis nevadensis GN=L798_03658 PE=3 SV=1
8	22044	tr|S4VDE6|S4VDE6_LOCMI	69.91	4	2	1	N	59564	ATP synthase subunit alpha OS=Locusta migratoria manilensis GN=atp5a1 PE=2 SV=1
8	22046	tr|A0A182MRL5|A0A182MRL5_9DIPT	69.91	4	2	1	N	59343	ATP synthase subunit alpha OS=Anopheles culicifacies PE=3 SV=1
8	22047	tr|A0A1A9TPM8|A0A1A9TPM8_ANOST	69.91	4	2	1	N	59357	ATP synthase subunit alpha OS=Anopheles stephensi PE=3 SV=1
8	22048	tr|A0A0J9RIM8|A0A0J9RIM8_DROSI	69.91	4	2	1	N	59438	ATP synthase subunit alpha OS=Drosophila simulans GN=Dsim\GD11704 PE=3 SV=1
8	22051	tr|A0A232FBT4|A0A232FBT4_9HYME	69.91	4	2	1	N	61799	ATP synthase subunit alpha OS=Trichomalopsis sarcophagae GN=TSAR_007587 PE=3 SV=1
8	22062	tr|A0A1B0D1L3|A0A1B0D1L3_PHLPP	61.14	5	1	1	N	34054	Uncharacterized protein OS=Phlebotomus papatasi PE=4 SV=1
3	22117	tr|A0A1U9X0H4|A0A1U9X0H4_9HEMI	63.56	23	3	2	N	10789	Histone H2A (Fragment) OS=Iria pilosella GN=H2A PE=3 SV=1
3	22118	tr|A0A1L2C7D6|A0A1L2C7D6_9NEOP	63.56	23	3	2	N	10975	Histone H2A (Fragment) OS=Musoniella margheritae GN=H2A PE=3 SV=1
3	22119	tr|A0A1L2C7C0|A0A1L2C7C0_9NEOP	63.56	23	3	2	N	10975	Histone H2A (Fragment) OS=Musoniola sp. 3 JMR-2016 GN=H2A PE=3 SV=1
3	22120	tr|A0A076G3V3|A0A076G3V3_9HEMI	63.56	22	3	2	N	11072	Histone H2A (Fragment) OS=Hindoloides bipunctata GN=H2A PE=3 SV=1
3	22121	tr|T1IUL1|T1IUL1_STRMM	63.56	19	3	2	N	13299	Histone H2A OS=Strigamia maritima PE=3 SV=1
3	22122	tr|B4JZ46|B4JZ46_DROGR	63.56	19	3	2	N	13363	Histone H2A OS=Drosophila grimshawi GN=Dgri\GH25178 PE=3 SV=1
3	22123	tr|Q7PD33|Q7PD33_ANOGA	63.56	19	3	2	N	13363	Histone H2A OS=Anopheles gambiae GN=1267699 PE=3 SV=1
3	22124	tr|B4LVM8|B4LVM8_DROVI	63.56	19	3	2	N	13363	Histone H2A OS=Drosophila virilis GN=Dvir\GJ22574 PE=3 SV=1
3	22125	tr|Q7Q2C6|Q7Q2C6_ANOGA	63.56	19	3	2	N	13349	Histone H2A OS=Anopheles gambiae GN=1278745 PE=3 SV=4
3	22126	tr|Q7Q2C4|Q7Q2C4_ANOGA	63.56	19	3	2	N	13349	Histone H2A OS=Anopheles gambiae GN=1278737 PE=3 SV=3
3	22127	tr|A0A182XUN7|A0A182XUN7_ANOQN	63.56	19	3	2	N	13363	Histone H2A OS=Anopheles quadriannulatus PE=3 SV=1
3	22128	tr|A0A1S3DA94|A0A1S3DA94_DIACI	63.56	19	3	2	N	13382	Histone H2A OS=Diaphorina citri GN=LOC103514550 PE=3 SV=1
3	22129	tr|A0A132ACK3|A0A132ACK3_SARSC	63.56	19	3	2	N	13307	Histone H2A OS=Sarcoptes scabiei GN=QR98_0072500 PE=3 SV=1
3	22130	tr|E2A0I8|E2A0I8_CAMFO	63.56	19	3	2	N	13335	Histone H2A OS=Camponotus floridanus GN=EAG_11182 PE=3 SV=1
3	22131	tr|B4K329|B4K329_DROGR	63.56	19	3	2	N	13391	Histone H2A OS=Drosophila grimshawi GN=Dgri\GH23503 PE=3 SV=1
3	22132	tr|A0A1B0D249|A0A1B0D249_PHLPP	63.56	19	3	2	N	13407	Histone H2A OS=Phlebotomus papatasi PE=3 SV=1
3	22133	tr|A0A182G0A8|A0A182G0A8_ANOAL	63.56	19	3	2	N	13363	Histone H2A OS=Anopheles albimanus PE=3 SV=1
3	22134	tr|B7PSI5|B7PSI5_IXOSC	63.56	19	3	2	N	13364	Histone H2A OS=Ixodes scapularis GN=8030708 PE=3 SV=1
3	22135	tr|A0A182KSY0|A0A182KSY0_9DIPT	63.56	19	3	2	N	13363	Histone H2A OS=Anopheles coluzzii PE=3 SV=1
3	22136	tr|A0A1S3DIS4|A0A1S3DIS4_DIACI	63.56	19	3	2	N	13352	Histone H2A OS=Diaphorina citri GN=LOC103519432 PE=3 SV=1
3	22137	tr|A0A1S4E9L2|A0A1S4E9L2_DIACI	63.56	17	3	2	N	14272	Histone H2A OS=Diaphorina citri GN=LOC103507294 PE=3 SV=1
6	22101	tr|A0A182JIT9|A0A182JIT9_9DIPT	59.59	16	2	1	N	13191	Histone H2A OS=Anopheles atroparvus PE=3 SV=1
6	22102	tr|A0A182F532|A0A182F532_ANOAL	59.59	16	2	1	N	13243	Histone H2A OS=Anopheles albimanus PE=3 SV=1
6	22103	tr|Q7QF50|Q7QF50_ANOGA	59.59	16	2	1	N	13191	Histone H2A OS=Anopheles gambiae GN=1271957 PE=3 SV=3
6	22104	tr|A0A0A9YW58|A0A0A9YW58_LYGHE	59.59	16	2	1	N	13448	Histone H2A OS=Lygus hesperus GN=H2AFZ PE=3 SV=1
6	22105	tr|J3JTR0|J3JTR0_DENPD	59.59	15	2	1	N	13573	Histone H2A OS=Dendroctonus ponderosae GN=109540730 PE=2 SV=1
6	22106	tr|A0A132A5C4|A0A132A5C4_SARSC	59.59	12	2	1	N	17675	Histone H2A OS=Sarcoptes scabiei GN=QR98_0046350 PE=3 SV=1
13	62637	tr|A0A0M9A898|A0A0M9A898_9HYME	53.03	2	1	1	N	75721	Protein kinase C OS=Melipona quadrifasciata GN=WN51_09077 PE=3 SV=1
13	24933	tr|A0A0P5W4V7|A0A0P5W4V7_9CRUS	53.03	2	1	1	N	91255	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	24863	tr|A0A0N7ZKU6|A0A0N7ZKU6_9CRUS	53.03	2	1	1	N	88252	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	24846	tr|A0A0P5D7F8|A0A0P5D7F8_9CRUS	53.03	2	1	1	N	87265	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	24822	tr|A0A0P6FB91|A0A0P6FB91_9CRUS	53.03	2	1	1	N	86666	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	24817	tr|A0A0P5BRK4|A0A0P5BRK4_9CRUS	53.03	2	1	1	N	86165	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	24802	tr|A0A0P4ZIP3|A0A0P4ZIP3_9CRUS	53.03	2	1	1	N	85758	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	62654	tr|A0A151X2L9|A0A151X2L9_9HYME	53.03	2	1	1	N	81910	Protein kinase C OS=Trachymyrmex zeteki GN=ALC60_06637 PE=3 SV=1
13	62653	tr|A0A0P5DL28|A0A0P5DL28_9CRUS	53.03	2	1	1	N	80253	Protein kinase C OS=Daphnia magna PE=3 SV=1
13	62652	tr|A0A0A9X7J5|A0A0A9X7J5_LYGHE	53.03	2	1	1	N	78243	Protein kinase C (Fragment) OS=Lygus hesperus GN=Pkc53E_2 PE=3 SV=1
total 195 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
13	62651	tr|Q7Q042|Q7Q042_ANOGA	53.03	2	1	1	N	78365	Protein kinase C (Fragment) OS=Anopheles gambiae GN=1280437 PE=3 SV=4
13	39894	tr|V9I8Q4|V9I8Q4_APICE	53.03	2	1	1	N	76716	Protein kinase C OS=Apis cerana GN=ACCB00050.1 PE=2 SV=1
13	62650	tr|A0A146MGA7|A0A146MGA7_LYGHE	53.03	2	1	1	N	76205	Protein kinase C OS=Lygus hesperus GN=Pkc53E_0 PE=3 SV=1
13	62649	tr|A0A023GLQ5|A0A023GLQ5_9ACAR	53.03	2	1	1	N	75587	Protein kinase C (Fragment) OS=Amblyomma triste PE=2 SV=1
13	62648	tr|U5Q0I7|U5Q0I7_ANOST	53.03	2	1	1	N	76204	Protein kinase C OS=Anopheles stephensi GN=cPKC PE=2 SV=1
13	62647	tr|A0A069DWB7|A0A069DWB7_9HEMI	53.03	2	1	1	N	75194	Protein kinase C (Fragment) OS=Panstrongylus megistus PE=2 SV=1
13	62646	tr|W5JP71|W5JP71_ANODA	53.03	3	1	1	N	70984	Protein kinase C OS=Anopheles darlingi GN=AND_002326 PE=3 SV=1
13	62645	tr|A0A0A9WKY4|A0A0A9WKY4_LYGHE	53.03	3	1	1	N	62202	Protein kinase C, brain isozyme OS=Lygus hesperus GN=Pkc53E_3 PE=4 SV=1
13	39892	tr|V9I8A6|V9I8A6_APICE	53.03	3	1	1	N	61413	Protein kinase C alpha type OS=Apis cerana GN=ACCB00050.3 PE=2 SV=1
13	62644	tr|A0A1W4WLP9|A0A1W4WLP9_AGRPL	53.03	3	1	1	N	61209	protein kinase C, brain isozyme OS=Agrilus planipennis GN=LOC108734078 PE=4 SV=1
13	62643	tr|T1HII9|T1HII9_RHOPR	53.03	3	1	1	N	60881	Uncharacterized protein (Fragment) OS=Rhodnius prolixus PE=4 SV=1
13	62642	tr|A0A0J7P1D0|A0A0J7P1D0_LASNI	53.03	3	1	1	N	55074	Protein kinase brain isozyme OS=Lasius niger GN=RF55_1174 PE=3 SV=1
13	62641	tr|A0A1A9W2I3|A0A1A9W2I3_9MUSC	53.03	3	1	1	N	53516	Uncharacterized protein OS=Glossina brevipalpis PE=3 SV=1
13	62640	tr|A0A182Y1W2|A0A182Y1W2_ANOST	53.03	6	1	1	N	28838	Uncharacterized protein OS=Anopheles stephensi PE=4 SV=1
13	62639	tr|A0A1B0CD14|A0A1B0CD14_LUTLO	53.03	6	1	1	N	28518	Uncharacterized protein OS=Lutzomyia longipalpis PE=4 SV=1
13	62638	tr|A0A182SK05|A0A182SK05_9DIPT	53.03	10	1	1	N	18483	Uncharacterized protein OS=Anopheles maculatus PE=4 SV=1
9	62636	tr|F4W666|F4W666_ACREC	48.97	3	1	1	Y	71197	Heat shock 70 kDa protein cognate 4 OS=Acromyrmex echinatior GN=G5I_00959 PE=3 SV=1
10	62657	tr|A0A0P6CG63|A0A0P6CG63_9CRUS	45.04	12	3	3	N	25093	Transmembrane emp24 domain-containing protein OS=Daphnia magna PE=3 SV=1
10	62769	tr|A0A0P5ZY70|A0A0P5ZY70_9CRUS	39.55	12	2	2	N	19820	Transmembrane emp24 domain-containing protein (Fragment) OS=Daphnia magna PE=3 SV=1
17	22509	tr|T1PG74|T1PG74_MUSDO	39.60	9	1	1	Y	16787	Ras family protein OS=Musca domestica PE=2 SV=1
17	22510	tr|T1PDL5|T1PDL5_MUSDO	39.60	9	1	1	Y	16743	Ras family protein OS=Musca domestica PE=2 SV=1
17	22537	tr|W8AQG8|W8AQG8_CERCA	39.60	7	1	1	Y	22239	Ras-related protein Rac1 OS=Ceratitis capitata GN=RAC1 PE=2 SV=1
17	22511	tr|B4ML79|B4ML79_DROWI	39.60	7	1	1	Y	21344	Uncharacterized protein OS=Drosophila willistoni GN=Dwil\GK16805 PE=3 SV=1
17	22512	tr|B4QKE8|B4QKE8_DROSI	39.60	7	1	1	Y	21359	GD13056 OS=Drosophila simulans GN=Dsim\GD13056 PE=3 SV=1
17	22513	tr|B4J295|B4J295_DROGR	39.60	7	1	1	Y	21414	GH16613 OS=Drosophila grimshawi GN=Dgri\GH16613 PE=3 SV=1
17	22514	tr|A0A0K8VMJ4|A0A0K8VMJ4_BACLA	39.60	7	1	1	Y	21496	Ras-related protein Rac2 OS=Bactrocera latifrons GN=Rac2_8 PE=3 SV=1
17	22515	tr|B4LDX8|B4LDX8_DROVI	39.60	7	1	1	Y	21537	Uncharacterized protein OS=Drosophila virilis GN=Dvir\GJ12360 PE=3 SV=1
17	22516	tr|A0A1A9WD10|A0A1A9WD10_9MUSC	39.60	7	1	1	Y	21456	Uncharacterized protein OS=Glossina brevipalpis PE=3 SV=1
17	22517	tr|A0A1I8Q976|A0A1I8Q976_STOCA	39.60	7	1	1	Y	21441	Uncharacterized protein OS=Stomoxys calcitrans GN=106084831 PE=3 SV=1
17	22518	tr|B4HV68|B4HV68_DROSE	39.60	7	1	1	Y	21359	GM13759 OS=Drosophila sechellia GN=Dsec\GM13759 PE=3 SV=1
17	22519	tr|A0A034W5H7|A0A034W5H7_BACDO	39.60	7	1	1	Y	21428	Ras-related protein Rac1 OS=Bactrocera dorsalis GN=RAC1 PE=3 SV=1
17	22520	tr|A0A1W4WMW4|A0A1W4WMW4_AGRPL	39.60	7	1	1	Y	21396	ras-related protein Rac1 OS=Agrilus planipennis GN=LOC108737091 PE=3 SV=1
17	22521	tr|A0A1L8EGW8|A0A1L8EGW8_HAEIR	39.60	7	1	1	Y	21441	Putative ras-related protein rac1 OS=Haematobia irritans PE=3 SV=1
17	22522	tr|B4KYQ8|B4KYQ8_DROMO	39.60	7	1	1	Y	21537	Uncharacterized protein OS=Drosophila mojavensis GN=Dmoj\GI12458 PE=3 SV=1
17	22523	tr|A0A1I8N4Z1|A0A1I8N4Z1_MUSDO	39.60	7	1	1	Y	21440	Uncharacterized protein OS=Musca domestica GN=101900181 PE=3 SV=1
17	22524	tr|A0A0L0CPU9|A0A0L0CPU9_LUCCU	39.60	7	1	1	Y	21544	Ras-related protein Rac2 OS=Lucilia cuprina GN=FF38_05965 PE=3 SV=1
17	22525	tr|A0A1W4U7J3|A0A1W4U7J3_DROFC	39.60	7	1	1	Y	21373	ras-related protein Rac2 OS=Drosophila ficusphila GN=LOC108086981 PE=3 SV=1
17	22526	tr|A0A1I8MG34|A0A1I8MG34_MUSDO	39.60	7	1	1	Y	21396	Uncharacterized protein OS=Musca domestica GN=101893580 PE=3 SV=1
17	22527	tr|A0A0M4EYM2|A0A0M4EYM2_DROBS	39.60	7	1	1	Y	21512	Rac1 OS=Drosophila busckii GN=Dbus_chr3Lg486 PE=3 SV=1
17	22528	tr|D3TPE0|D3TPE0_GLOMM	39.60	7	1	1	Y	21456	Ras-related small GTPase rho type OS=Glossina morsitans morsitans PE=2 SV=1
17	22529	tr|A0A1A9VE20|A0A1A9VE20_GLOAU	39.60	7	1	1	Y	21456	Uncharacterized protein OS=Glossina austeni PE=3 SV=1
17	22530	tr|A0A1A9XE80|A0A1A9XE80_GLOFF	39.60	7	1	1	Y	21456	Uncharacterized protein OS=Glossina fuscipes fuscipes PE=3 SV=1
17	22531	tr|B3NFD1|B3NFD1_DROER	39.60	7	1	1	Y	21359	Uncharacterized protein OS=Drosophila erecta GN=Dere\GG14963 PE=3 SV=1
17	22532	tr|A0A1B0BHT7|A0A1B0BHT7_9MUSC	39.60	7	1	1	Y	21456	Uncharacterized protein OS=Glossina palpalis gambiensis PE=3 SV=1
17	22533	tr|B5DQJ0|B5DQJ0_DROPS	39.60	7	1	1	Y	21451	Uncharacterized protein OS=Drosophila pseudoobscura pseudoobscura GN=Dpse\GA23612 PE=3 SV=1
17	22534	tr|B3M5S1|B3M5S1_DROAN	39.60	7	1	1	Y	21390	Uncharacterized protein OS=Drosophila ananassae GN=Dana\GF23788 PE=3 SV=1
17	22535	tr|A0A1L8EH01|A0A1L8EH01_HAEIR	39.60	7	1	1	Y	21386	Putative ras-related protein rac2 OS=Haematobia irritans PE=3 SV=1
total 195 proteins									

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
17	22536	tr|M9PBU2|M9PBU2_DROME	39.60	7	1	1	Y	21359	Rac2, isoform B OS=Drosophila melanogaster GN=Rac2 PE=3 SV=1
18	22662	tr|A0A0P5VEM3|A0A0P5VEM3_9CRUS	35.37	12	1	1	Y	11058	ATP synthase subunit beta, mitochondrial-like protein OS=Daphnia magna PE=4 SV=1
14	22227	tr|A0A0P6D933|A0A0P6D933_9CRUS	35.26	4	1	1	Y	29096	HNRNPA2B1 protein (Fragment) OS=Daphnia magna PE=4 SV=1
305	22723	tr|K0FA39|K0FA39_9CRUS	27.09	15	2	2	N	10359	Histone 3 (Fragment) OS=Alpioniscus trogirensis GN=H3 PE=3 SV=1
11	22658	tr|D6NTM1|D6NTM1_MARJA	25.86	2	1	1	Y	41784	Actin OS=Marsupenaeus japonicus PE=2 SV=1
20	63073	tr|A0A0P5IP74|A0A0P5IP74_9CRUS	23.82	2	1	1	N	36298	Putative Lymphokine-activated killer T-cell-originated protein kinase (Fragment) OS=Daphnia magna PE=4 SV=1
20	63074	tr|A0A0P5X9B5|A0A0P5X9B5_9CRUS	23.82	2	1	1	N	37342	Putative Lymphokine-activated killer T-cell-originated protein kinase (Fragment) OS=Daphnia magna PE=4 SV=1
20	63076	tr|A0A0P5N7W8|A0A0P5N7W8_9CRUS	23.82	2	1	1	N	39207	Putative Lymphokine-activated killer T-cell-originated protein kinase (Fragment) OS=Daphnia magna PE=4 SV=1
19	22582	tr|A0A182MJI2|A0A182MJI2_9DIPT	23.61	1	1	1	N	124622	Uncharacterized protein OS=Anopheles culicifacies PE=4 SV=1
12	22775	tr|A0A0P5UVM6|A0A0P5UVM6_9CRUS	22.84	1	1	1	N	139088	Leucine-rich repeat-containing protein 16B OS=Daphnia magna PE=4 SV=1
21	22307	tr|W5JLB6|W5JLB6_ANODA	22.03	1	1	1	N	94304	Drop dead OS=Anopheles darlingi GN=AND_003065 PE=4 SV=1
22	63082	tr|A0A1E1X293|A0A1E1X293_9ACAR	21.01	1	1	1	N	115394	Putative polyprotein (Fragment) OS=Amblyomma aureolatum PE=2 SV=1
23	22585	tr|Q17T64|Q17T64_9HYME	20.63	6	1	1	N	18811	Elongation factor-1alpha (Fragment) OS=Bombus caliginosus GN=EF-1a PE=4 SV=1
23	63084	tr|A0A0H3VAG6|A0A0H3VAG6_9ODON	20.63	6	1	1	N	20336	Elongation factor 1 alpha (Fragment) OS=Brachytron pratense GN=Ef1a PE=4 SV=1
23	22586	tr|A0A221J585|A0A221J585_9MUSC	20.63	5	1	1	N	25164	Elongation factor 1-alpha (Fragment) OS=Apodacra plumipes GN=Ef1a PE=4 SV=1
23	22587	tr|D4P281|D4P281_HYPSO	20.63	5	1	1	N	26652	Elongation factor 1 alpha (Fragment) OS=Hyposmocoma saccophora GN=EF1a PE=4 SV=1
23	22589	tr|D4P296|D4P296_9NEOP	20.63	4	1	1	N	28155	Elongation factor 1 alpha (Fragment) OS=Hyposmocoma menehune GN=EF1a PE=4 SV=1
23	22588	tr|A0A0C5DAT0|A0A0C5DAT0_HELNM	20.63	4	1	1	N	28014	Elongation factor 1 alpha (Fragment) OS=Heliconius numata GN=Ef1a PE=4 SV=1
23	22590	tr|D5GRK8|D5GRK8_9NEOP	20.63	4	1	1	N	29242	Elongation factor-1 alpha (Fragment) OS=Oleria padilla padilla GN=ef-1a PE=4 SV=1
23	22591	tr|D7GJQ5|D7GJQ5_9DIPT	20.63	4	1	1	N	30382	Elongation factor 1-alpha (Fragment) OS=Micropsectra seguyi GN=EF-1a PE=4 SV=1
23	22592	tr|A0A1S6JYA4|A0A1S6JYA4_9CUCU	20.63	4	1	1	N	30621	Elongation factor 1-alpha (Fragment) OS=Entiminae gen. 3 aequalis PE=4 SV=1
23	22593	tr|Q9U8J1|Q9U8J1_9HEMI	20.63	4	1	1	N	31678	Elongation factor 1-alpha (Fragment) OS=Uroleucon aeneum PE=4 SV=1
23	22594	tr|A0A0G2T5E8|A0A0G2T5E8_9NEOP	20.63	3	1	1	N	35500	Elongation factor-1 alpha (Fragment) OS=Eumorpha capronnieri GN=EF-1a PE=4 SV=1
23	22595	tr|B3FBI9|B3FBI9_9MUSC	20.63	3	1	1	N	36736	Elongation factor 1-alpha (Fragment) OS=Lasiocnemus lugens GN=EF-1alpha PE=3 SV=1
23	22597	tr|A0A0S1NH65|A0A0S1NH65_9HEMI	20.63	3	1	1	N	38294	Elongation factor 1-alpha (Fragment) OS=Cicadidae sp. 'wingpopper' GN=EF1a PE=3 SV=1
23	63085	tr|E9JV44|E9JV44_9NEOP	20.63	3	1	1	N	38589	Elongation factor 1 alpha (Fragment) OS=Taraka hamada GN=EF1a PE=4 SV=1
23	22598	tr|D5GR67|D5GR67_9NEOP	20.63	3	1	1	N	38718	Elongation factor-1 alpha (Fragment) OS=Hyposcada anchiala mendax GN=ef-1a PE=4 SV=1
23	22600	tr|D1GKQ7|D1GKQ7_9NEOP	20.63	3	1	1	N	39810	Elongation factor 1-alpha (Fragment) OS=Caledopsyche kimminsi GN=ef1a PE=3 SV=1
23	22601	tr|A0A068J3Y4|A0A068J3Y4_9NEOP	20.63	3	1	1	N	43946	Elongation factor 1-alpha (Fragment) OS=Acronicta grisea GN=EF-1alpha PE=3 SV=1
23	63086	tr|Q2VKY2|Q2VKY2_TITHA	20.63	3	1	1	N	43741	Elongation factor 1-alpha (Fragment) OS=Tithorea harmonia GN=EF-1a PE=3 SV=1
23	22602	tr|Q2LB41|Q2LB41_9NEOP	20.63	3	1	1	N	44539	Elongation factor 1-alpha (Fragment) OS=Gnophodes chelys GN=EF1-alpha PE=3 SV=1
23	22604	tr|B5LXT8|B5LXT8_COETU	20.63	3	1	1	N	44632	Elongation factor 1-alpha (Fragment) OS=Coenonympha tullia GN=EF1a PE=3 SV=1
23	22605	tr|A0A0K0MVA6|A0A0K0MVA6_9NEOP	20.63	3	1	1	N	45048	Elongation factor 1-alpha (Fragment) OS=Athyma libnites nieuwenhuisi GN=EF1-alpha PE=3 SV=1
23	22606	tr|A0A0K0MU56|A0A0K0MU56_9NEOP	20.63	3	1	1	N	45083	Elongation factor 1-alpha (Fragment) OS=Parasarpa zayla GN=EF1-alpha PE=3 SV=1
23	22607	tr|Q58GU4|Q58GU4_9NEOP	20.63	3	1	1	N	45091	Elongation factor 1-alpha (Fragment) OS=Ectopatria paurogramma GN=EF-1a PE=3 SV=1
23	22609	tr|B8Y157|B8Y157_9NEOP	20.63	3	1	1	N	45245	Elongation factor 1-alpha (Fragment) OS=Melitaea casta GN=EF-1alpha PE=3 SV=1
total 195 proteins									

tr|V9I6A9|V9I6A9_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MASKGKLATE SRRKNPKRRT DNLEDLKQEL DIDFHKITPE ELYQRFQTHP ENGLSHAKAK ENLERDGPNS LTPPKQTPEW O Oxida
81 VKFCKNLFGG FALLLWIGAI LCFIAYSIQA STSEDPNDDN LYLGIVLAAV VIVTGIFSYY QESKSSKIME SFKNMVPQIA
161 IVIREGEK**LT LKAEELVLGD VVEVK**FGDRI PADIRIIESR GFKVDNSSLT GESEPQSRSP EFTNENPLET KNLAFFSTNA
241 VEGTAKGVVI CCGDQTVMGR IAGLASGLDT GETPIAKEIH HFIHLITGVA VFLGVTFFII AFILGYHWLD AVIFLIGIIV
321 ANVPEGLLAT VTVCLTLTAK RMASKNCLVK NLEAVETLGS TSTICSDKTG TLTQNR**MTVA HMWFDNQIIE ADTTEDQSGL**
401 **QYDR**TSPGFK ALAKIATLCN RAEFKAGQED KPILKREVNG DASEAALLKC MELALGDVMG IRKRNKKVCE IPFNSTNKYQ
481 VSIHESDNPD DPRHLLVMKG APERILDRCS TIFIGGKEKV LDEEMKEAFN NAYLELGGLG ERVLGFCDYI LPSDKFPIGF
561 KFNCDDPNFP VDGLRFVGLM SMIDPPRAAV PDAVAKCRSA GIKVIMVTGD HPITAKAIAK SVGIISEGNE TVEDIAQRLN
641 IPVSEVNPRE AKAAVIHGTE LRELNSDQLD EILRYHTEIV FARTSPQQKL IIVEGCQRMG AIVAVTGDGV NDSPALKKAD
721 IGVAMGIAGS DVSK**QAADMI LLDDNFASIV TGVEEGR**LIF DNLKKSIAYT LTSNIPEISP FLAFILCDIP LPLGTVTILC
801 IDLGTDMVPA ISLAYEEAES DIMKRHPRNP FTDKLVNERL ISMAYGQIGM IQAAAGFFVY FVIMAENGFL PLHLFGIRKQ
881 WDSKAINDLR DSYGQEWTYR DRKTLEFTCH TAFFVSIVIV QWADLIVCKT RRNSIIHQGM RNWALNFGLI FETALAAFLS
961 YTPGMDKGLR MFPLKFVWWL PALPFMFAIF IYDETRRFYL RRNPGGWLEQ ETYY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QAADMILLDDNFASIVTGVEEGR.L	Y	62.72	2463.1951	397.2	1233.0940	2	42.88	3943	1	735	757	
K.LTLKAEELVLGDVVEVK.F	Y	58.42	1854.0713	447.0	928.4573	2	38.12	3404	1	169	185	
K.AEELVLGDVVEVK.F	Y	46.90	1398.7605	-204.1	700.2448	2	36.03	3159	1	173	185	
R.MTVAHM(+15.99)WFDNQIIEADTTEDQSGLQYDR.T	Y	22.50	3329.4604	364.3	1111.2317	3	37.42	3322	1	377	404	Oxidation (M)
total 4 peptides												

tr|V9I6B1|V9I6B1_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MESFKNMVPQ IAIVIREGEK **LTLKAEELVL GDVVEVK**FGD RIPADIRIIE SRGFKVDNSS LTGESEPQSR SPEFTNENPL O Oxida
81 ETKNLAFFST NAVEGTAKGV VICCGDQTVM GRIAGLASGL DTGETPIAKE IHHFIHLITG VAVFLGVTFF IIAFILGYHW
161 LDAVIFLIGI IVANVPEGLL ATVTVCLTLT AKRMASKNCL VKNLEAVETL GSTSTICSDK TGTLTQNR**MT VAHMWFDNQI**
241 **IEADTTEDQS GLQYDR**TSPG FKALAKIATL CNRAEFKAGQ EDKPILKREV NGDASEAALL KCMELALGDV MGIRKRNKKV
321 CEIPFNSTNK YQVSIHESDN PDDPRHLLVM KGAPERILDR CSTIFIGGKE KVLDEEMKEA FNNAYLELGG LGERVLGFCD
401 YILPSDKFPI GFKFNCDDPN FPVDGLRFVG LMSMIDPPRA AVPDAVAKCR SAGIKVIMVT GDHPITAKAI AKSVGIISEG
481 NETVEDIAQR LNIPVSEVNP REAKAAVIHG TELRELNSDQ LDEILRYHTE IVFARTSPQQ KLIIVEGCQR MGAIVAVTGD
561 GVNDSPALKK ADIGVAMGIA GSDVSK**QAAD MILLDDNFAS IVTGVEEGR**L IFDNLKKSIA YTLTSNIPEI SPFLAFILCD
641 IPLPLGTVTI LCIDLGTDMV PAISLAYEAP ESDIMKRQPR DPYRDNLVNR RLISMAYGQI GMIQAAAGFF VYFVIMAENG
721 FLPLHLFGIR KQWDSKAIND LRDSYGQEWT YRDRKTLEFT CHTAFFVSIV IVQWADLIVC KTRRNSIIHQ GMRNWALNFG
801 LIFETALAAF LSYTPGMDKG LRMFPLKFVW WLPALPFMFA IFIYDETRRF YLRRNPGGWL EQETYY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QAADMILLDDNFASIVTGVEEGR.L	Y	62.72	2463.1951	397.2	1233.0940	2	42.88	3943	1	587	609	
K.LTLKAEELVLGDVVEVK.F	Y	58.42	1854.0713	447.0	928.4573	2	38.12	3404	1	21	37	
K.AEELVLGDVVEVK.F	Y	46.90	1398.7605	-204.1	700.2448	2	36.03	3159	1	25	37	
R.MTVAHM(+15.99)WFDNQIIEADTTEDQSGLQYDR.T	Y	22.50	3329.4604	364.3	1111.2317	3	37.42	3322	1	229	256	Oxidation (M)
total 4 peptides												

tr|V9I733|V9I733_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MESFKNMVPQ IAIVIREGEK **LTLKAEELVL GDVVEVK**FGD RIPADIRIIE SRGFKVDNSS LTGESEPQSR SPEFTNENPL O Oxida
81 ETKNLAFFST NAVEGTAKGV VICCGDQTVM GRIAGLASGL DTGETPIAKE IHHFIHLITG VAVFLGVTFF IIAFILGYHW
161 LDAVIFLIGI IVANVPEGLL ATVTVCLTLT AKRMASKNCL VKNLEAVETL GSTSTICSDK TGTLTQNR**MT VAHMWFDNQI**
241 **IEADTTEDQS GLQYDR**TSPG FKALAKIATL CNRAEFKAGQ EDKPILKREV NGDASEAALL KCMELALGDV MGIRKRNKKV
321 CEIPFNSTNK YQVSIHESDN PDDPRHLLVM KGAPERILDR CSTIFIGGKE KVLDEEMKEA FNNAYLELGG LGERVLGFCD
401 YILPSDKFPI GFKFNCDDPN FPVDGLRFVG LMSMIDPPRA AVPDAVAKCR SAGIKVIMVT GDHPITAKAI AKSVGIISEG
481 NETVEDIAQR LNIPVSEVNP REAKAAVIHG TELRELNSDQ LDEILRYHTE IVFARTSPQQ KLIIVEGCQR MGAIVAVTGD
561 GVNDSPALKK ADIGVAMGIA GSDVSK**QAAD MILLDDNFAS IVTGVEEGR**L IFDNLKKSIA YTLTSNIPEI SPFLAFILCD
641 IPLPLGTVTI LCIDLGTDMV PAISLAYEEA ESDIMKRHPR NPFTDKLVNE RLISMAYGQI GMIQAAAGFF VYFVIMAENG
721 FLPLHLFGIR KQWDSKAIND LRDSYGQEWT YRDRKTLEFT CHTAFFVSIV IVQWADLIVC KTRRNSIIHQ GMRNWALNFG
801 LIFETALAAF LSYTPGMDKG LRMFPLK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QAADMILLDDNFASIVTGVEEGR.L	Y	62.72	2463.1951	397.2	1233.0940	2	42.88	3943	1	587	609	
K.LTLKAEELVLGDVVEVK.F	Y	58.42	1854.0713	447.0	928.4573	2	38.12	3404	1	21	37	
K.AEELVLGDVVEVK.F	Y	46.90	1398.7605	-204.1	700.2448	2	36.03	3159	1	25	37	
R.MTVAHM(+15.99)WFDNQIIEADTTEDQSGLQYDR.T	Y	22.50	3329.4604	364.3	1111.2317	3	37.42	3322	1	229	256	Oxidation (M)
total 4 peptides												

tr|V9I6C2|V9I6C2_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MESFKNMVPQ IAIVIREGEK **LTLKAEELVL GDVVEVK**FGD RIPADIRIIE SRGFKVDNSS LTGESEPQSR SPEFTNENPL O Oxida
81 ETKNLAFFST NAVEGTAKGV VICCGDQTVM GRIAGLASGL DTGETPIAKE IHHFIHLITG VAVFLGVTFF IIAFILGYHW
161 LDAVIFLIGI IVANVPEGLL ATVTVCLTLT AKRMASKNCL VKNLEAVETL GSTSTICSDK TGTLTQNR**MT VAHMWFDNQI**
241 **IEADTTEDQS GLQYDR**TSPG FKALAKIATL CNRAEFKAGQ EDKPILKREV NGDASEAALL KCMELALGDV MGIRKRNKKV
321 CEIPFNSTNK YQVSIHESDN PDDPRHLLVM KGAPERILDR CSTIFIGGKE KVLDEEMKEA FNNAYLELGG LGERVLGFCD
401 YILPSDKFPI GFKFNCDDPN FPVDGLRFVG LMSMIDPPRA AVPDAVAKCR SAGIKVIMVT GDHPITAKAI AKSVGIISEG
481 NETVEDIAQR LNIPVSEVNP REAKAAVIHG TELRELNSDQ LDEILRYHTE IVFARTSPQQ KLIIVEGCQR MGAIVAVTGD
561 GVNDSPALKK ADIGVAMGIA GSDVSK**QAAD MILLDDNFAS IVTGVEEGR**L IFDNLKKSIA YTLTSNIPEI SPFLAFILCD
641 IPLPLGTVTI LCIDLGTDMV PAISLAYEAP ESDIMKRQPR DPYRDNLVNR RLISMAYGQI GMIQAAAGFF VYFVIMAENG
721 FLPLHLFGIR KQWDSKAIND LRDSYGQEWT YRDRKTLEFT CHTAFFVSIV IVQWADLIVC KTRRNSIIHQ GMRNWALNFG
801 LIFETALAAF LSYTPGMDKG LRMFPLK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.QAADMILLDDNFASIVTGVEEGR.L	Y	62.72	2463.1951	397.2	1233.0940	2	42.88	3943	1	587	609	
K.LTLKAEELVLGDVVEVK.F	Y	58.42	1854.0713	447.0	928.4573	2	38.12	3404	1	21	37	
K.AEELVLGDVVEVK.F	Y	46.90	1398.7605	-204.1	700.2448	2	36.03	3159	1	25	37	
R.MTVAHM(+15.99)WFDNQIIEADTTEDQSGLQYDR.T	Y	22.50	3329.4604	364.3	1111.2317	3	37.42	3322	1	229	256	Oxidation (M)
total 4 peptides												

tr|A0A0P6A3S1|A0A0P6A3S1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEPSKSAPA PKKGSKKAIS KAQKKDGKKR KRSR**KESYSV YVYK**VLK**QVH PDTGISSK**AM GIMNSFVNDI FERIASEASR f Formy
P Pyro-
81 **LAHYNKRSTI TSR**EIQTAVR LLLPGELAK**H AVSEGTK**A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KESYSVYVYK.V	Y	44.49	1264.6339	-24.7	633.3086	2	29.03	2346	1	35	44	
K.Q(-17.03)VHPDTGISSK.A	Y	41.98	1150.5619	-120.8	1151.4302	1	26.61	2072	1	48	58	Pyro-glu from Q
K.HAVSEGTK.A	Y	41.46	827.4137	950.0	415.1071	2	2.18	159	2	110	117	
R.LAHYNKR.S	Y	25.90	900.4930	592.2	451.5204	2	20.72	1469	1	81	87	
K.Q(+27.99)VHPDTGISSK.A	Y	21.77	1195.5833	929.7	599.3547	2	26.34	2042	1	48	58	Formylation
K.ESYSVYVYK.V	Y	21.62	1136.5389	874.9	569.7739	2	30.98	2571	2	36	44	
K.RSTITSR.E	Y	16.66	819.4562	842.3	411.0805	2	20.69	1466	1	87	93	
total 7 peptides												

tr|A0A0P6CBE1|A0A0P6CBE1_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPEPSKSAPA PKKGSKKAIS KAQKKDGKKR KRSR**KESYSV YVYK**VLK**QVH PDTGISSK**AM GIMNSFVNDI FERIASEASR

81 **LAHYNKRSTI TSR**EIQTAVR LLLPGELAK**H AVSEGTK**AVT KYTSSK

f Formy
p Pyro-

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.KESYSVYVYK.V	Y	44.49	1264.6339	-24.7	633.3086	2	29.03	2346	1	35	44	
K.Q(-17.03)VHPDTGISSK.A	Y	41.98	1150.5619	-120.8	1151.4302	1	26.61	2072	1	48	58	Pyro-glu from Q
K.HAVSEGTK.A	Y	41.46	827.4137	950.0	415.1071	2	2.18	159	2	110	117	
R.LAHYNKR.S	Y	25.90	900.4930	592.2	451.5204	2	20.72	1469	1	81	87	
K.Q(+27.99)VHPDTGISSK.A	Y	21.77	1195.5833	929.7	599.3547	2	26.34	2042	1	48	58	Formylation
K.ESYSVYVYK.V	Y	21.62	1136.5389	874.9	569.7739	2	30.98	2571	2	36	44	
K.RSTITSR.E	Y	16.66	819.4562	842.3	411.0805	2	20.69	1466	1	87	93	
total 7 peptides												

tr|V9IK47|V9IK47_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV

c Carba

131

81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLR**YFVGNLA SGGAAGATSL CFVYPLDFAR** TR**LAADVGK**A GGEREFTGLG

161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM

241 MMQSGRAKSE ILYKNTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	53.51	1218.6608	-165.5	610.2368	2	35.99	3154	2	13	25	
R.YFVGNLASGGAAGATSLC(+57.02)FVYPLDFAR.T	Y	44.88	2823.3689	332.4	1413.1610	2	41.73	3813	2	114	140	Carbamidomethylation
R.LAADVGK.A	Y	22.71	672.3806	1358.1	674.3010	1	24.33	1817	1	143	149	
total 3 peptides												

tr|M9NYU2|M9NYU2_APICC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV

c Carba

131

81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLR**YFVGNLA SGGAAGATSL CFVYPLDFAR** TR**LAADVGK**A GGEREFTGLG

161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKA PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM

241 MMQSGRAKSE ILYKNTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	53.51	1218.6608	-165.5	610.2368	2	35.99	3154	2	13	25	
R.YFVGNLASGGAAGATSLC(+57.02)FVYPLDFAR.T	Y	44.88	2823.3689	332.4	1413.1610	2	41.73	3813	2	114	140	Carbamidomethylation
R.LAADVGK.A	Y	22.71	672.3806	1358.1	674.3010	1	24.33	1817	1	143	149	
total 3 peptides												

tr|Q6VQ13|Q6VQ13_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLADPVAF AK**DFLAGGVA AAISK**TTVAP IERVKLLLQV QHISKQISEE QRYKGMIDCF VRIPKEQGFL SYWRGNLANV

c Carba

131

81 IRYFPTQALN FAFKDKYKQV FLGGVDKNTQ FLR**YFVGNLA SGGAAGATSL CFVYPLDFAR** TR**LAADVGK**A GGEREFTGLG

161 NCLTKIFKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLISWGIAQ VVTTVAGIVS YPFDTVRRRM

241 MMQSGRAKSE ILYKSTLHCW ATIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFLAGGVAAAISK.T	Y	53.51	1218.6608	-165.5	610.2368	2	35.99	3154	2	13	25	
R.YFVGNLASGGAAGATSLC(+57.02)FVYPLDFAR.T	Y	44.88	2823.3689	332.4	1413.1610	2	41.73	3813	2	114	140	Carbamidomethylation
total 3 peptides												

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.LAADVGK.A	Y	22.71	672.3806	1358.1	674.3010	1	24.33	1817	1	143	149	
total 3 peptides												

tr|E2BR21|E2BR21_HARSA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGLTDPVAF AK**DFIAGGVA AAISK**TTVAP IERVKLLLQV QHISKQIAEN QRYKGMIDCF VRIPREQGFL SYWRGNFANV

C Carba

131 C

81 IRYFPTQALN FAFKDKYKQI FLGGVDKNTQ FLR**YFVGNLA SGGAAGATSL CFVYPLDFAR** TR**LAADVGK**G TGEREFTGLA

161 NCLAKISKAD GITGLYRGFG VSVQGIIIYR AAYFGFYDTA RGMLPDPKKT PFLVSWGIAQ AVTTVAGIVS YPFDTVRRRM

241 MMQSGRAKSE ILYKNTLHCW STIYKTEGGN AFFKGAFSNI LRGTGGALVL VLYDEIKNLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.DFIAGGVAAAISK.T	Y	53.51	1218.6608	-165.5	610.2368	2	35.99	3154	2	13	25	
R.YFVGNLASGGAAGATSLC(+57.02)FVYPLDFAR.T	Y	44.88	2823.3689	332.4	1413.1610	2	41.73	3813	2	114	140	Carbamidomethylation
R.LAADVGK.G	Y	22.71	672.3806	1358.1	674.3010	1	24.33	1817	1	143	149	
total 3 peptides												

tr|A0A182FLZ7|A0A182FLZ7_ANOAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

62 O

1 R**DNIQGITKP AIR**RLARRGG VKR**ISGLIYE ETR**GVLKVFL ENVIR**DAVTY TEHAK**RK**TVT AMDVVYALKR** QGR**TLYGFGG**

d Dihyd
m Methy
o Oxida

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	2	13	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	58	69	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	58	70	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	74	80	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	2	13	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	46	55	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	74	80	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	2	9	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	24	33	
total 9 peptides												

tr|A0A1D2MA61|A0A1D2MA61_ORCCI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK VFLENVIR**DA VTYTEHAK**RK

d Dihyd
m Methy
o Oxida

85 O

81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

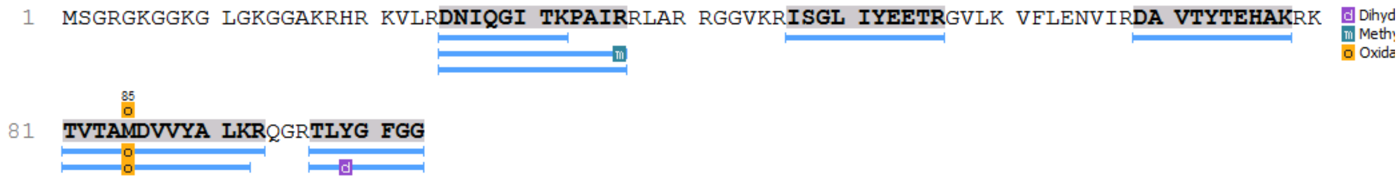
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A1Z5LH91|A0A1Z5LH91_ORNMO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

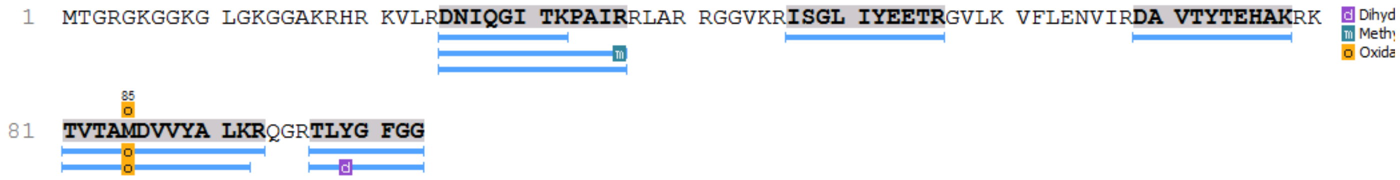
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A182IZV6|A0A182IZV6_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

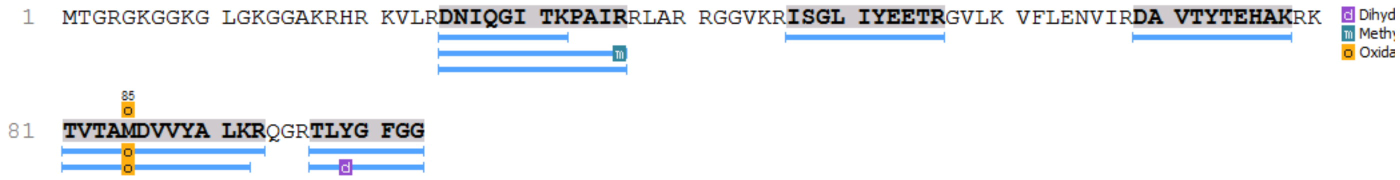
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|B4JH62|B4JH62_DROGR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

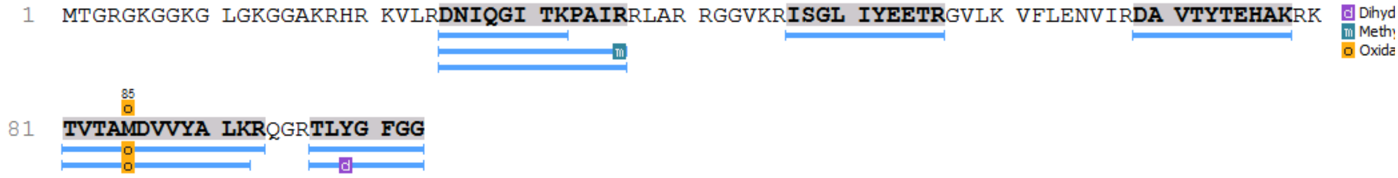
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A194Q0V4|A0A194Q0V4_PAPXU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

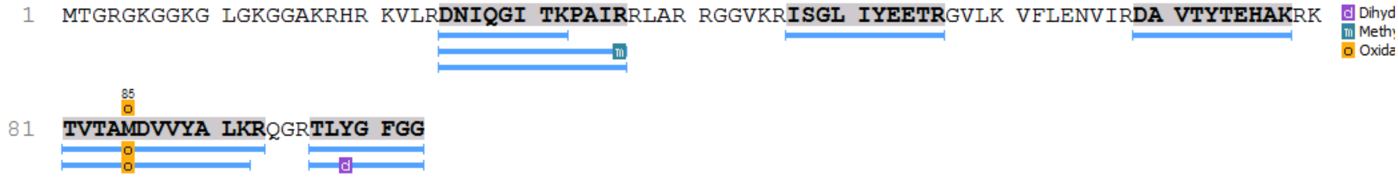
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A182FBX3|A0A182FBX3_ANOAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

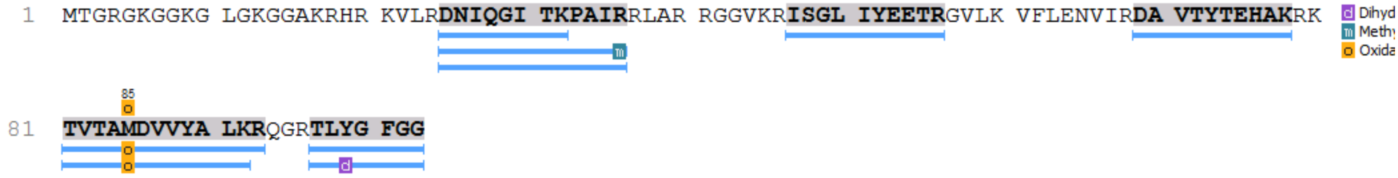
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A151XEG2|A0A151XEG2_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

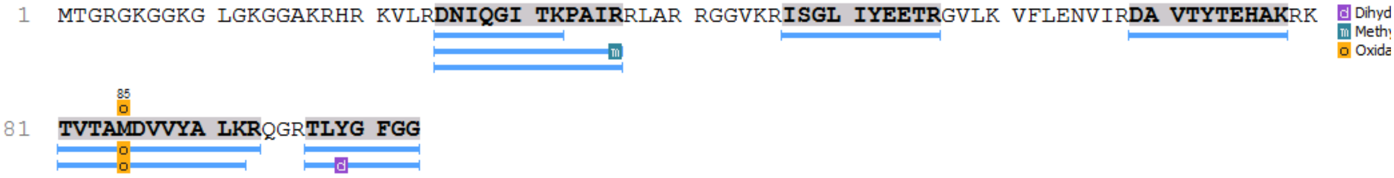
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A034WS42|A0A034WS42_BACDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

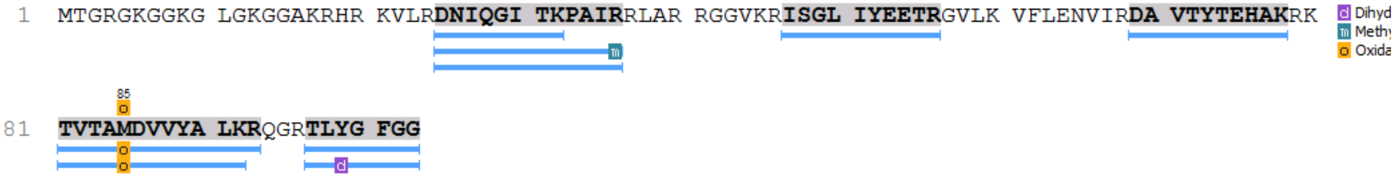
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|B4LVM7|B4LVM7_DROVI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

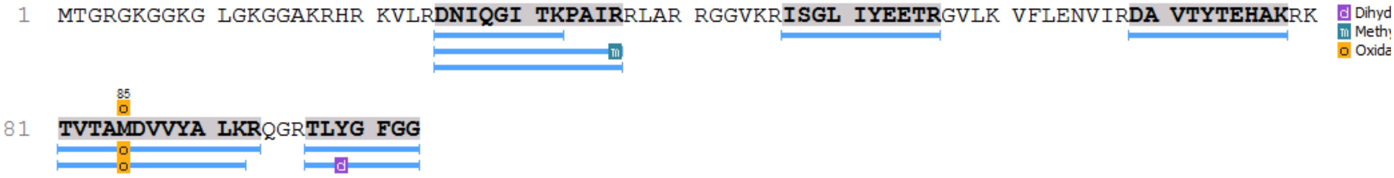
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A226DYY4|A0A226DYY4_FOLCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

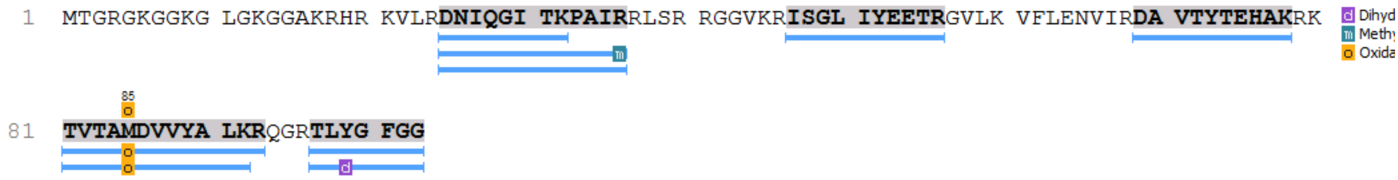
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|B4ILZ0|B4ILZ0_DROSE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

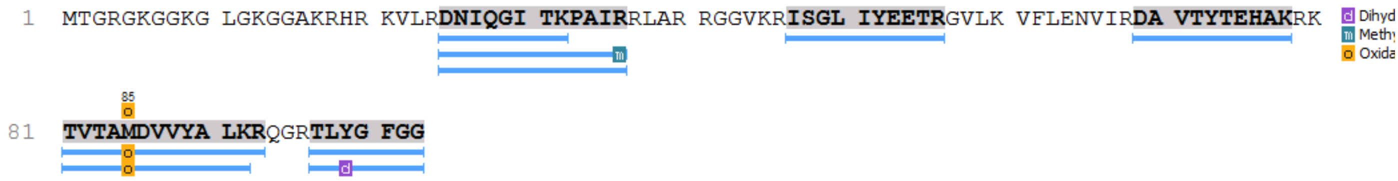
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|Q7PCX0|Q7PCX0_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

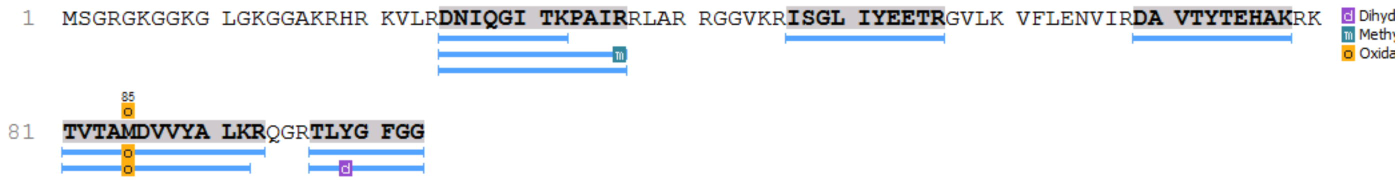
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A023GDJ7|A0A023GDJ7_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A132ACK5|A0A132ACK5_SARSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK VFLENVIR**DA VTYTEHAK**RK

Dihyd
Methy
Oxida

85
81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A1B0D251|A0A1B0D251_PHLPP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK VFLENVIR**DA VTYTEHAK**RK

Dihyd
Methy
Oxida

85
81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A0A9WMX0|A0A0A9WMX0_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MTGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK AFLENVIR**DA VTYTEHAK**RK

Dihyd
Methy
Oxida

85
81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

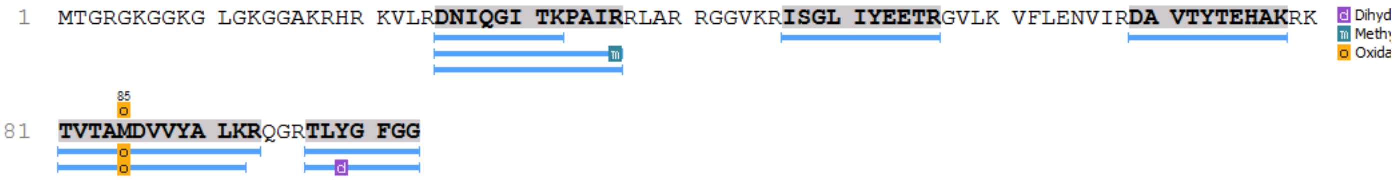
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|E2A0J1|E2A0J1_CAMFO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

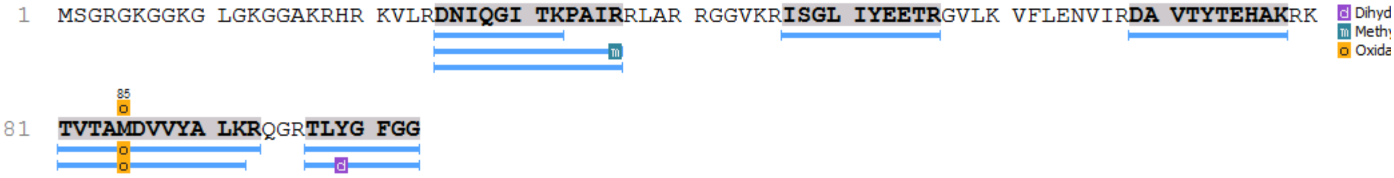
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|Q4PM69|Q4PM69_IXOSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

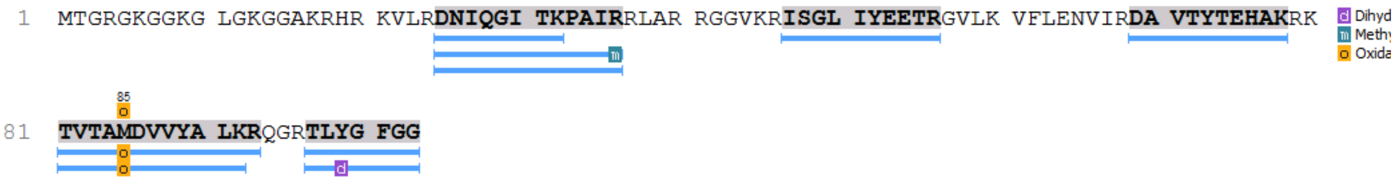
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A1S3DDY8|A0A1S3DDY8_DIACI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

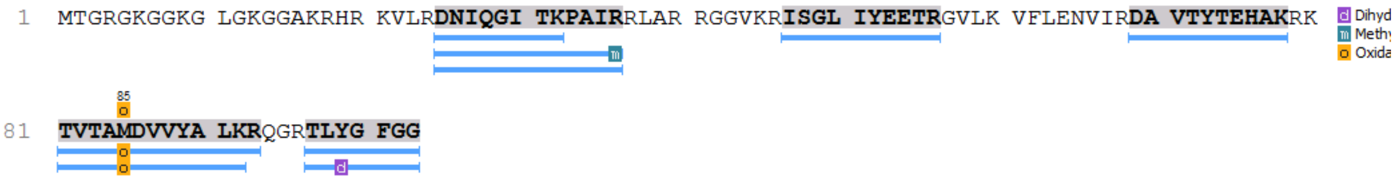
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A182WXV7|A0A182WXV7_ANOQN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MTGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK VFLENVIR**DA VTYTEHAK**RK

81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|A0A1V9XAM9|A0A1V9XAM9_9ACAR

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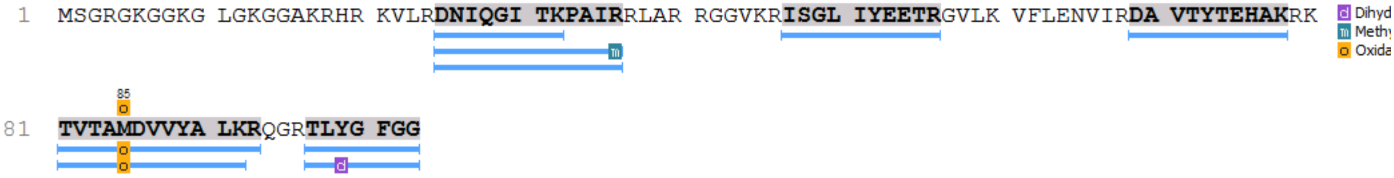
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MSGRGKGGKG LGKGGAKRHR KVLR**DNIQGI TKPAIR**RLAR RGGVKR**ISGL IYEETR**GVLK VFLENVIR**DA VTYTEHAK**RK

81 **TVTAMDVVYA LKR**QGR**TLYG FGG**

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DNIQGITKPAIR.R	Y	37.13	1324.7462	738.5	663.8696	2	29.08	2353	1	25	36	
K.TVTAM(+15.99)DVVYALK.R	Y	33.79	1325.6901	747.8	664.3480	2	35.27	3070	1	81	92	Oxidation (M)
K.TVTAM(+15.99)DVVYALKR.Q	Y	30.97	1481.7911	-6.3	741.8982	2	33.93	2911	1	81	93	Oxidation (M)
R.TLYGFGG	Y	30.03	713.3384	-39.9	714.3173	1	34.27	2953	1	97	103	
R.DNIQGITKPAIR(+14.02).R	Y	26.53	1338.7620	-83.7	670.3322	2	28.97	2339	1	25	36	Methyl ester
R.DAVTYTEHAK.R	Y	24.64	1133.5353	-116.7	1134.4103	1	24.96	1888	1	69	78	
R.TLY(+31.99)GFGG	Y	22.56	745.3282	-37.3	746.3077	1	34.44	2973	1	97	103	Dihydroxy
R.DNIQGITK.P	Y	21.75	887.4713	-116.8	888.3749	1	26.60	2071	1	25	32	
R.ISGLIYEETR.G	Y	15.23	1179.6135	-111.5	1180.4893	1	31.89	2675	1	47	56	
total 9 peptides												

tr|Q7JN37|Q7JN37_ARTSF

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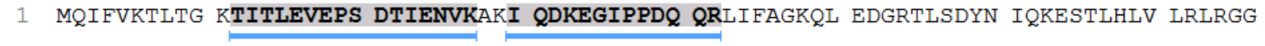
| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGG

Supporting Peptides:

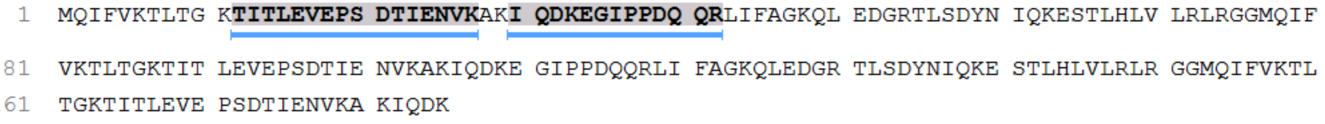
Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A034WV44|A0A034WV44_BACDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF

81 VKTLTGKTIT LEVEPSDTIE NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL

161 TGKTITLEVE PSDTIENVKA KIQDK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A0A9Z4T5|A0A0A9Z4T5_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGAKKR

81 KKKNYSTPKK IKHKKKKIKL AVLKYYKVDE NGKISRLRRE CPSEQCGAGV FMAAMEDRHY CGKCSYTLVF NKPEEK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|Q1W2C4|Q1W2C4_9HEMI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGAKKR

81 KKKNYSTPKK IKHKKKKIKL AVLKYYKVDE NGKISRLRRE CPSEQCGAGV FMAAMDDRHY CGKCSYTLVF SKPEDK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A182QI60|A0A182QI60_9DIPT back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGAKKR

81 KKKNYSTPKK IKHKRKKVKL AVLKYYKVDE NGKIHRLRRE CTSESCGAGV FMAAHEDRHY CGKCHLTLVY SKQEEK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|D7RF65|D7RF65_ERISI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGAKKR

81 KKKNYTTPKK IKHKHKKVKL AMLKFYKVDD NGKITRQRRE CPSDECGAGV FMANMFDRQY CGRCHLTYVF NKPE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|E3UKG7|E3UKG7_ERISI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGVIEP

81 SLKLLAEKYN CNKMICRKCY ARLHPRATNC RKKKCGHTSN IRPKKKIKG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A182IKK6|A0A182IKK6_9DIPT back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGIIEP

81 SLRILAQKYN CDKMICRKCY ARLHPRATNC RKKKCGHTNN LRPKKKLK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|R4G4B9|R4G4B9_RHOPR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGVIEP

81 TLRILAQKYN CDKMICRKCY ARLHPRATNC RKKKCGHTNN IRPKKKIK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|E3UKG8|E3UKG8_ERISI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF

81 VKTLTGKTIT LEVEPSDTIE NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL

161 TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK QLEDGRTLSD YNIQKESTLH LVLRLRGGMQ IFVKTLTGKT

241 ITLEVEPSDT IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRTLSDYNIQ KESTLHLVLR LRGGM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A1S3DBX7|A0A1S3DBX7_DIACI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF

81 VKTLTGKTIT LDVEPSDTIE NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL

161 TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK HLEDGRTLSD YNIQKESTLH LVLRLRGGMQ IFVKTLTGKT

241 ITLEVEPSDT IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRTLSDYNIQ KESTLHLVLR LRGGF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A1E1W9H3|A0A1E1W9H3_PECGO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF

81 VKTLTGKTIT LEVEPSDTIE NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL

161 TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK QLEDGRTLSD YNIQKESTLH LVLRLRGGMQ IFVKTLTGKT

241 ITLEVEPSDT IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRTLSDYNIQ KESTLHLVLR LRGGMQIFVK TLTGKTITLE

321 VEPSDTIENV KAKIQDKEGI PPDQQRLIFA GKQLEDGRTL SDYNIQKEST LHLVLRLRGG MQIFVKTLTG KTITLEVEPS

401 DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGM

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A0Q5U3G2|A0A0Q5U3G2_DROER

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQIFVKTLTG K**TITLEVEPS DTIENVK**AK**I QDKEGIPPDQ QR**LIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF

81 VKTLTGKTIT LEVEPSDTIE NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL
161 TGKTITLEVE PSDTIENVKA KIQDKEGIPP DQQRLIFAGK QLEDGRTLSD YNIQKESTLH LVLRLRGGMQ IFVKTLTGKT
241 ITLEVEPSDT IENVKAKIQD KEGIPPDQQR LIFAGKQLED GRTLSDYNIQ KESTLHLVLR LRGGMQIFVK TLTGKTITLE
321 VEPSDTIENV KAKIQDKEGI PPDQQRLIFA GKQLEDGRTL SDYNIQKEST LHLVLRLRGG MQIFVKTLTG KTITLEVEPS
401 DTIENVKAKI QDKEGIPPDQ QRLIFAGKQL EDGRTLSDYN IQKESTLHLV LRLRGGMQIF VKTLTGKTIT LEVEPSDTIE
481 NVKAKIQDKE GIPPDQQRLI FAGKQLEDGR TLSDYNIQKE STLHLVLRLR GGMQIFVKTL TGKTITLEVE PSDTIENVKA
561 KIQDKEGIPP DQQRLIFAGK QLEDGRTLSD YNIQKESTLH LVLRLRGGMQ IFVKTLTGKT ITLEVEPSDT IENVKAKIQD
641 KEGIPPDQQR LIFAGKQLED GRTLSDYNIQ KESTLHLVLR LRGGMQA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.TITLEVEPSDTIENVK.A	Y	48.84	1786.9200	-126.9	894.3539	2	34.45	2974	1	12	27	
K.IQDKEGIPPDQQR.L	Y	44.17	1522.7739	44.5	762.4281	2	24.94	1885	1	30	42	
total 2 peptides												

tr|A0A087ZQI5|A0A087ZQI5_APIME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLVS SIARQLPNTT IQVKWPLSIS SCKYHVSCSR RSAEISSILE ERILGASPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS

161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG EEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAMDYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR **LTELLK**QGQY VPMAIEEQVA

481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TSQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	83	97	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	461	466	
total 2 peptides												

tr|A0A0N0BIY2|A0A0N0BIY2_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SIARQLPNNS IQIKWPLCIA SCKYHVSCSR RSAEISSILE ERILGSAPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIR EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS

161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG DEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAINYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR **LTELLK**QGQY VPMAIEEQVA

481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TNQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	83	97	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	461	466	
total 2 peptides												

tr|V9IFD6|V9IFD6_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLVS SIARQLPNTT IQVKWPLSIS SCKYHVSCSR RSAEISSILE ERILGATPKA NLEETGRVLS IGDGIARVYG
81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEEL LGRVVDALGN PIDGKGPLNS

161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDAG EEKKKLYCIY
241 VAIGQKRSTV AQIVKRLTDS GAMDYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL
321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ESLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP
401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR **LTELLK**QGQY VPMAIEEQVA

481 VIYCGVRGYL DKMEPTKITA FEKEFLAHIR TSQRDLLNTI AKDNTISEAS DAKLKQVVTD FLASFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	83	97	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	461	466	
total 2 peptides												

tr|A0A0J7N062|A0A0J7N062_LASNI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SLVRHLPNAT AQITWPATAV ASCKYHVSCS RRSVEISSIL EERILGSAPQ TNLEETGRVI SIGDGIARVY
81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEE LLGRVVDALG NPIDGKGPLN
161 NKLRFRIGTK APGIIPRESV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDA GEEKKKLYCI
241 YVAIGQKRST VAQIVKRLTD SGAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGR HALIIYDDLS KQAVAYRQMS
321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NETLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR
401 PAINVGLSVS RVGSAAQTKA MKQVSYVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE
481 EQVAVIYCGV RGYLDKMDPT KITAFEKEFL AHIRSTQQDL LATIAKENII NEASDAKLKK IVTDFLSSFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	84	98	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A1A9WYG7|A0A1A9WYG7_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAT SVARSLPKAA QQVAAKAAYP VATLAARKLH VSSSQRGAEI SSILEERIMG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGSEILGRVV DALGNAIDGK
161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNDGQDETKK
241 LYCIYVAIGQ KRSTVAQIVK RLSDAGAMDY TIIVSATASD AAPLQYLAPY SGCAMGEYFR DKGKHALIIY DDLSKQAVAY
321 RQMSLLLRRP PGREAYPGDV FYLHSRLLER AAKMSPAMGG GSLTALPVIE TQAGDVSAYI PTNVISITDG QIFLETELFY
401 KGIRPAINVG LSVSRVGSAA QTKAMKQVAG SMKLELAQYR EVAAFAQFGS DLDAATQQLL NRGVR**LTELL K**QGQYVPMSI
481 EDQVAVIYCG VRGHLDKMDP AKITKFEKEF LQHIKTSEQS LLSQIAQEGK ISEGADAKLK EVVTKFLSTF QG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	88	102	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	466	471	
total 2 peptides												

tr|A0A1B6KWM9|A0A1B6KWM9_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PIRRLFSCSP SSSRFRAGGK MAQLSVRLAS ALAKQLSVAV PQVVWPTAQV ASRKLHVSCS QRAAEISSIL EDRILGNAPK
81 ADLEETGRVL SIGDGIARVY GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDKLI KEGDIVKRTG AIVDVPVGED
161 LLGRVVDALG NTIDGKGPLK NVTRARVGVK APGIIPRISV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT
241 IINQQRFNNA EDEKKKLYCI YVAIGQKRST VAQIVKRLTD SGSMKYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK
321 HALIIYDDLS KQAVAYRQMS LLLRRPPGRE AYPGDVFYLH SRLLERAAKM SEANGGGSLT ALPVIETQAG DVSAYIPTNV
401 ISITDGQIFL ETELFYKGIR PAINVGLSVS RVGSAAQTRA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV
481 R**LTELLK**QGQ YVPMAIEEQV AVIYCGVRGH LDKLDPAKIT AFEKEFLAHV KASHKDVLAS IAKEGKINEE TDAKMKGIVQ
561 SFLSSFTAS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	104	118	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	482	487	
total 2 peptides												

tr|B4QHN0|B4QHN0_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIFSARLAS SVARNLPKAA NQVACKAAYP AASLAARKLH VASTQRSAEI SNILEERILG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGDELLGRVV DALGNAIDGK
161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNEAQDESKK
241 LYCIYVAIGQ KRSTVAQIVK RLTDSGAMGY SVIVSATASD MSPAMGGGSL TALPVIETQA GDVSAYIPTN VISITDGQIF
321 LETELFYKGI RPAINVGLSV SRVGSAAQTK AMKQVAGSMK LELAQYREVA AFAQFGSDLD AATQQLLNRG VR**LTELLK**QG
401 QYVPMAIEDQ VAVIYCGVRG HLDKMDPAKI TKFEKEFLQH IKTSEQALLD TIAKDGAISE SSDAKLKDIV AKFMSTFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	88	102	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	393	398	
total 2 peptides												

tr|A0A182TC06|A0A182TC06_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VAKIAVPAVS VAARNFHVST ANRGAEISAI LEERILGSAP KADLEETGRV LSIGDGIARV YGLK**NIQADE MVEFSSGLK**G
81 MALNLEPDNV GVVVFGNDKL IKEGDIVKRT GAIVDVPVGD EILGRVVDAL GNAIDGKGEI KTKQRFRVGI KAPGIIPRVS
161 VREPMQTGIK AVDSLVPIGR GQRELIIGDR QTGKTALAID TIINQKRFND GQDESKKLYC IYVAIGQKRS TYLAPYSGCA
241 MGEYFRDNGK HALIIYDDLS KQAVAYRQMS LLLRRPPGRE AYPGDVFYLH SRLLERAAKM SPTLGGGSLT ALPVIETQAG
321 DVSAYIPTNV ISITDGQIFL ETELFYKGIR PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA
401 ATQQLLNRGV R**LTELLK**QGQ YVPMAIEEQV AVIYCGVRGY LDKMDPGKIT KFEKEFLAHV KTNEKALLQQ IASEGKISDE
481 ADAKLKSVVT SFLSTFSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	65	79	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	412	417	
total 2 peptides												

tr|A0A182YNR5|A0A182YNR5_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNWTVAKIAV PAVSVAARNF HVSTANRGAE ISAILEERIL GSAPKADLEE TGRVLSIGDG IARVYGLK**NI QADEMVEFSS**
81 **GLK**GMALNLE PDNVGVVVFG NDKLIKEGDI VKRTGAIVDV PVGDEILGRV VDALGNAIDG KGEIKTKQRF RVGIKAPGII
161 PRVSVREPMQ TGIKAVDSLV PIGRGQRELI IGDRQTGKTA LAIDTIINQK RFNDGQDESK KLYCIYVAIG QKRSTVAQIV
241 KRLTDAGAMN YTIIVSATAS DAAPLQYLAP YSGCAMGEYF RDNGKHALII YDDLSKQAVA YRQMSLLLRR PPGREAYPGD
321 VFYLHSRLLE RAAKMSPTLG GGSLTALPVI ETQAGDVSAY IPTNVISITD GQIFLETELF YKGIRPAINV GLSVSRVGSA
401 AQTKAMKQVA GSMKLELAQY REVAAFAQFG SDLDAATQQL LNRGVR**LTEL LK**QGQYVPMA IEEQVAVIYC GVRGYLDKMD
481 PGKITKFEKE FLAHVKTNEK ALLQQIASEG KISDDADAKL KSVVTSFMST FSA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	69	83	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	447	452	
total 2 peptides												

tr|A0A1B0C955|A0A1B0C955_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSLLSARLAA SVARNLPRTS SQVAKILYPA TSLAARKFHV SSQRNAEISA ILEERILGAA PKADLDETGR VLSIGDGIAR
81 VYGLK**NIQAD EMVEFSSGLK** GMALNLEPDN VGVVVFGNDK LIKEGDIVKR TGAIVDVPVG EELLGRVVDA LGNPIDGKGA
161 ITSKTRFRVG IKAPGIIPRI SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTSLAI DTIINQKRFN DGQDETKKLY
241 CIYVAIGQKR STVAQIVKRL TDTGAMNYSI IVSATASDAA PLQYLAPYSG CAMGEFFRDN GKHALIIYDD LSKQAVAYRQ
321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVR**LTELLK**Q GQLLSSIAVV
481 RGHLDKMDPQ KITKFEKEFT EHVKSNEKAL LQQIATDGKI TEQTDAKLKE IVTKFLATFT G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	86	100	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	464	469	
total 2 peptides												

tr|A0A151J3L9|A0A151J3L9_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MGLLSLRLAS ALIRHLPNAT QINWPATAIA SHKYHVSCSR RSAEISAILE ERILGSAPKA NLEETGRVLS IGDGIARVYG

81 LK**NIQADEMV EFSSGLK**GMA LNLEPDNVGV VVFGNDRHIK EGDIVKRTGA IVDVPVGEQL LGRVVDALGN PIDGKGPLNS

161 KLRFRIGTKA PGIIPRVSVR EPMQTGIKAV DSLVPIGRGQ RELIIGDRQT GKTALAIDTI INQKRFNDGG EEKKKLYCIY

241 VAIGQKRSTV AQIVKRLTDS GAINYTIIVS ATASDAAPLQ YLAPYSGCAM GEFFRDNGKH ALIIYDDLSK QAVAYRQMSL

321 LLRRPPGREA YPGDVFYLHS RLLERAAKMN ENLGGGSLTA LPVIETQAGD VSAYIPTNVI SITDGQIFLE TELFYKGIRP

401 AINVGLSVSR VGSAAQTKAM KQVAGSMKLE LAQYREVAAF AQFGSDLDAA TQQLLNRGVR **LTELLK**QGQY VPMAIEEQVA

481 VIYCGVRGYL DKMDPTKITG FEKEFLAHIR STQQDLLATI AKENVISEAS DAKLKKVVTD FLSSFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	83	97	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	461	466	
total 2 peptides												

tr|A0A151XGV4|A0A151XGV4_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS FLTRHLPNTT AQINWPVTAI ASRKYHVSCS RHSAEISAIL EERILGSAPK ANLEETGRVL SIGDGIARVY

81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEQ LLGRVVDALG NPIDGKGPLN

161 NKLRFRIGTK APGIIPRVSV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDG GEEKKKLYCI

241 YVAIGQKRST VAQIVKRLTD SSAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK HALIIYDDLS KQAVAYRQMS

321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NENLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR

401 PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV R**LTELLK**QGQ YVPMAIEEQV

481 AVIYCGVRGY LDKMDPTKIT GFEKEFLAHI RSTQQDLLAT IAKENVISEA SDTKLKKVVI DFLSSFSG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	84	98	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	462	467	
total 2 peptides												

tr|A0A195CV10|A0A195CV10_9HYME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAS SLARHLPNTT GQINWSVTTI ASRKYHVSCN RRSAEISAIL EERILGSAPK ANLEETGRVL SIGDGIARVY

81 GLK**NIQADEM VEFSSGLK**GM ALNLEPDNVG VVVFGNDRHI KEGDIVKRTG AIVDVPVGEQ LLGRVVDALG NPIDGKGPLN

161 NKLRFRIGTK APGIIPRVSV REPMQTGIKA VDSLVPIGRG QRELIIGDRQ TGKTALAIDT IINQKRFNDG GEEKKKLYCI

241 YVAIGQKRST VAQIVKRLTD SGAINYTIIV SATASDAAPL QYLAPYSGCA MGEFFRDNGK HALIIYDDLS KQAVAYRQMS

321 LLLRRPPGRE AYPGDVFYLH SRLLERAAKM NENLGGGSLT ALPVIETQAG DVSAYIPTNV ISITDGQIFL ETELFYKGIR

401 PAINVGLSVS RVGSAAQTKA MKQVAGSMKL ELAQYREVAA FAQFGSDLDA ATQQLLNRGV R**LTELLK**QGQ YVPMAIEEQV

481 AVIYCGVRGY LDKMDPSKIT SFEKEFLAHI RATQQDLLAT IAKENVISEA SDAKLKKVVT DFLSSFSS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	84	98	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	462	467	
total 2 peptides												

tr|B4LIV0|B4LIV0_DROVI back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MISARLASSV ARNLPKAAAQ VACKAAYPAT SLAARKLHVA STQRSAEISS VLEERILGVA PKADLEETGR VLSIGDGIAR
81 VYGLN**NIQAD EMVEFSSGLK** GMALNLEADN VGVVVFGNDK LIKQGDIVKR TGAIVDVPVG NELLGRVVDA LGNAIDGKGA

161 INTKDRFRVG IKAPGIIPRV SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTALAI DTIINQKRFN DGQDESKKLY
241 CIYVAIGQKR STVAQILKRL TDSGAMGYTI IVSATASDAA PLQYLAPYSG CAMGEFFRDK GKHALIIYDD LSKQAVAYRQ
321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DASTQQLLNR GVR**LTELLK**Q GQYVPMAIED

481 QVAVIYCGVR GHLDKMDPSK ITKFEKEFLQ HIKTSEQGLL DGIAKDGQIS EAADAKLKDI VQKFMSTFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	86	100	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	464	469	
total 2 peptides												

tr|A0A0M4EW76|A0A0M4EW76_DROBS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MISARLASSV ARNLPKAASQ VACKAAYPAA TLAARKFHVA STQRSAEISN ILEERILGVA PKADLEETGR VLSIGDGIAR
81 VYGLN**NIQAD EMVEFSSGLK** GMALNLEPDN VGVVVFGNDK LIKQGDIVKR TGAIVDVPVG DELLGRVVDA LGNAIDGRGA

161 INTKDRFRVG IKAPGIIPRV SVRDPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTALAI DTIINQKRFN DGQDDTKKLY
241 CIYVAIGQKR STVAQIVKRL TDSGAMDYSV IVSATASDAA PLQYLAPYSG CAMGEYFRDK GKHALIIYDD LSKQAVAYRQ
321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVR**LTELLK**Q GQYVPMSIED

481 QVAVIYCGVR GHLDKMDPAK ITKFEKEFLQ HIKTTEQGLL DTIAKEGQIS QASDAKLKDV VTKFMATFQG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	86	100	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	464	469	
total 2 peptides												

tr|A0A1L8E154|A0A1L8E154_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSLLSARLAA SVARNLPRTS SQVAKIIYPA TSLAARKFHL SSQRNAEISA ILEERILGAA PKADLDETGR VLSIGDGIAR
81 VYGLK**NIQAD EMVEFSSGLK** GMALNLEPDN VGVVVFGNDK LIKEGDIVKR TGAIVDVPVG EELLGRVVDA LGNPIDGKGA

161 ITSKTRFRVG IKAPGIIPRI SVREPMQTGI KAVDSLVPIG RGQRELIIGD RQTGKTSLAI DTIINQKRFN DGQDESKKLY
241 CIYVAIGQKR STVAQIVKRL TDSGAMGYSV IVSATASDAA PLQYLAPYSG CAMGEFFRDN GKHALIIYDD LSKQAVAYRQ
321 MSLLLRRPPG REAYPGDVFY LHSRLLERAA KMSPAMGGGS LTALPVIETQ AGDVSAYIPT NVISITDGQI FLETELFYKG
401 IRPAINVGLS VSRVGSAAQT KAMKQVAGSM KLELAQYREV AAFAQFGSDL DAATQQLLNR GVR**LTELLK**Q GQYVPMAIEE

481 QVAVIYCGVR GHLDKMDPQK ITKFEKEFTE HVKSSEKALL SQIAADGQIT EQTDAKLKDV VAKFLATFAG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	86	100	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	464	469	
total 2 peptides												

tr|A0A182XJA6|A0A182XJA6_ANOQN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGA APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A182FH95|A0A182FH95_ANOAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA GQVAKIAVPA VSVAARNFHV ATPNRGAEIS SILEERILGS APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL

241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGAG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|W5J4R5|W5J4R5_ANODA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA GQVAKIAVPA VSVAARNFHV ATPNRGAEIS SILEERILGS APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL

241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGAG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A1J1J483|A0A1J1J483_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMLSARLAA SVARNLPRSA QQVARAVIPA SQIVARKIHL STPAKGAEIS TILEERILGA APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND RLIREGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGRG

161 EIKTGQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL

241 YCIYVAIGQK RSTVAQIVKR LTDAGAMDYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPALGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGHLDKMDPA KITSFEKEFL AHITTNEQGL LKQIATEGKI SDEVDAKLKS IVTNFLSTFT G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A182N7Z7|A0A182N7Z7_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA SQVAKIAVPA VSVAARNFHV STANRGAEIS SILEERILGA APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|Q7PHI8|Q7PHI8_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISVRLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STAHRGAEIS AILEERILGA APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPS KITKFEREFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A069DZ92|A0A069DZ92_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALISARVLS SVARQFTSSV PQVGNLSWAG SQNTFRALHV SCSHRAAEIS SILEERILGS APKTDLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLISEGDIVK RTGAIVDVPV GEDLLGRVVD ALGNPIDGKG

161 PLATKNRMRV GIKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NEGDEEKKKL
241 YCIYVAIGQK RSTVAQIVKR LTDTGSMQYT IIVSATASDA APLQYLAPYS GCAMGEHFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNDANGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLA RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGHLDKLDPS KITAFEKEFL QHIKSSHRDL LASIAKEGKI TDDVDGKLKE IVTSFIAGFQ G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A067QI29|A0A067QI29_ZOONE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSLRLAT SVARHFPSAA PQVANLTWPA AQVASRKLHV SCSQRAAEIS SILEERILGS APKADLEETG RVLSIGDGIA
81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEAD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GADLLGRVVD ALGNPIDGKG

161 PFKSVTRARV GVKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NEGDDEKKKL
241 YCIYVAIGQK RSTVAQIVKR LTDSGAIGYT IIVSATASDA APLQYLAPYS GCAMGEFFRD NGKHALIIYD DLSKQAVAYR
321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNETNGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK
401 GIRPAINVGL SVSRVGSAAQ TRAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGHLDKLDPA KITAFEKEFL QHIKTSHKDL LAIIAKEGKI NEDADAKLKK IVSEFLISFT S

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|S4VDE6|S4VDE6_LOCMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLSFRLAS AVAKHLPAAT PQISGLTWPA AQITNRNIHV SCSQRAAEIS SILEERILGA APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND RLIKEGDIVK RTGAIVDVPV GEELLGRVVD ALGNPIDGKG

161 PLKASKRFRV GIKAPGIIPR ISVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGEDEKKKL

241 YCIYVAIGQK RSTVAQIVKR LTDSGAIGYS IIVSATASDA APLQYLAPYS GCAMGEFFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMNDAHGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TRAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGHLDKLDPS KITAFEKEFL QHIKTSEAAL LANIAKEGKI TDEIDVKLKK IVTDFVANFQ G

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A182MRL5|A0A182MRL5_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGS APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL

241 YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPG KITKFEKEFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS VVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A1A9TPM8|A0A1A9TPM8_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSMISARLAA SVARSLPRTA TQVAKIAVPA VSVAARNFHV STANRGAEIS AILEERILGS APKADLEETG RVLSIGDGIA

81 RVYGLK**NIQA DEMVEFSSGL K**GMALNLEPD NVGVVVFGND KLIKEGDIVK RTGAIVDVPV GDEILGRVVD ALGNAIDGKG

161 EIKTKQRFRV GIKAPGIIPR VSVREPMQTG IKAVDSLVPI GRGQRELIIG DRQTGKTALA IDTIINQKRF NDGQDESKKL

241 YCIYVAIGQK RSTVAQIVKR LTDAGAMNYT IIVSATASDA APLQYLAPYS GCAMGEYFRD NGKHALIIYD DLSKQAVAYR

321 QMSLLLRRPP GREAYPGDVF YLHSRLLERA AKMSPTLGGG SLTALPVIET QAGDVSAYIP TNVISITDGQ IFLETELFYK

401 GIRPAINVGL SVSRVGSAAQ TKAMKQVAGS MKLELAQYRE VAAFAQFGSD LDAATQQLLN RGVR**LTELLK** QGQYVPMAIE

481 EQVAVIYCGV RGYLDKMDPG KITKFEKEFL AHVKTNEKAL LQQIASEGKI SDDADAKLKS IVTSFMSTFS A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	87	101	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	465	470	
total 2 peptides												

tr|A0A0J9RIM8|A0A0J9RIM8_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSIFSARLAS SVARNLPKAA NQVACKAAYP AASLAARKLH VASTQRSAEI SNILEERILG VAPKADLEET GRVLSIGDGI
81 ARVYGLN**NIQ ADEMVEFSSG LK**GMALNLEP DNVGVVVFGN DKLIKQGDIV KRTGAIVDVP VGDELLGRVV DALGNAIDGK

161 GAINTKDRFR VGIKAPGIIP RVSVREPMQT GIKAVDSLVP IGRGQRELII GDRQTGKTAL AIDTIINQKR FNEAQDESKK
241 LYCIYVAIGQ KRSTVAQIVK RLTDSGAMGY SVIVSATASD AAPLQYLAPY SGCAMGEYFR DKGKHALIIY DDLSKQAVAY
321 RQMSLLLRRP PGREAYPGDV FYLHSRLLER AAKMSPAMGG GSLTALPVIE TQAGDVSAYI PTNVISITDG QIFLETELFY
401 KGIRPAINVG LSVSRVGSAA QTKAMKQVAG SMKLELAQYR EVAAFAQFGS DLDAATQQLL NRGVR**LTELL K**QGQYVPMAI

481 EDQVAVIYCG VRGHLDKMDP AKITKFEKEF LQHIKTSEQA LLDTIAKDGA ISESSDAKLK DIVAKFMSTF QG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	88	102	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	466	471	
total 2 peptides												

tr|A0A232FBT4|A0A232FBT4_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MALLTVRLAA SVARQLPSTQ VSWPAAVVAS RKYHVSCSRR SAEISSILEE RILGASSKTN LEETGRVLSI GDGIARVYGL
81 K**NIQADEMVE FSSGLK**GMAL NLEPDNVGIV VFGNDRHIKE GDIVKRTGAI VDVPVGNELL GRVVDALGNP IDGKGPLNNK

161 LRFRIGTKAP GIIPRESVRE PMQTGIKAVD SLVPIGRGQR ELIIGDRQTG KTALAIDTII NQKRFNEAGD ENKKLYCIYV
241 AVGQKRSTVA QIVKRLTDAG AINYSIIVSA TASDAAPLQY LAPYSGCAMG EFFRYDIAEF NDLKSIVDNG KHALIIYDDL
321 SKQAVAYRQM SLLLRRPPGR EAYPGDVFYL HSRLLERAAK MNKSLGGGSL TALPVIETQA GDVSAYIPTN VISITDGQIF
401 LETELFYKGI RPAINVGLSV SRVGSAAQTK AMKQVAGSMK LELAQYREVA AFAQFGSDLD AATQQLLNRG VR**LTELLK**QG

481 QYERSISNGF VLSVPMAIEE QVAVIYCGVR GYLDKMDPAK ITAFEKEFLA HIKATQQDLL ATIAKENIIS EASDAKLKKV
561 VTDFLSSFGA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	82	96	
R.LTELLK.Q	N	17.53	715.4480	-109.0	716.3773	1	29.89	2445	1	473	478	
total 2 peptides												

tr|A0A1B0D1L3|A0A1B0D1L3_PHLPP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAHLARVAAS VARSLPKTSS QVTRILYPAT SLAARKFHVS SQKNAEISAI LEERILGAAP KADLDETGRV LSIGDGIARV
81 YGLK**NIQADE MVEFSSGLK**G MALNLEPDNV GVVVFGNDKL IKEGDIVKRT GAIVDVPVGE ELLGRVVDAL GNPIDGKGAI

161 TSKTRFRVGL KAPGIIPRIS VREPMQTGIK AVDSLVPIGR GQRELIIGDR QTGKTALAID TIINQKRFND GQDESKKLYC
241 IYVAIGQKRS TVAQIVKRLT DTGAMNYSII VSATASDAAP LQYLAPYSGC AMGEYHSHLN TFFPFSYLPI SDSLQFV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.NIQADEMVEFSSGLK.G	Y	61.14	1666.7872	-81.2	834.3333	2	35.84	3137	1	85	99	
total 1 peptides												

tr|A0A1U9X0H4|A0A1U9X0H4_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GKVKGKAKSR SSR**AGLQFPV GR**IHRLLR**KG NYAER**VGAGA PVYLAAVMEY LAAEVLELAG NAARDNKKTR IIPRHLQLAI

81 R**NDEELNK**LL SGVTIAQGGV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	14	22	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	29	35	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	82	88	
total 3 peptides												

tr|A0A1L2C7D6|A0A1L2C7D6_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGKVKGKSKS RSSR**AGLQFP VGR**IHRLLR**K GNYAER**VGAG APVYLAAVME YLAAEVLELA GNAARDNKKT RIIPRHLQLA

81 IR**NDEELNK**L LSGVTIAQGG VL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	15	23	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	30	36	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	83	89	
total 3 peptides												

tr|A0A1L2C7C0|A0A1L2C7C0_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGKVKGKSKS RSSR**AGLQFP VGR**IHRLLR**K GNYAER**VGAG APVYLAAVME YLAAEVLELA GNAARDNKKT RIIPRHLQLA

81 IR**NDEELNK**L LSGVTIAQGG VL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	15	23	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	30	36	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	83	89	
total 3 peptides												

tr|A0A076G3V3|A0A076G3V3_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GGKVKGKSKS RSSR**AGLQFP VGR**IHRLLR**K GNYAER**VGAG APVYLAAVME YLAAEVLELA GNAARDNKKT RIIPRHLQLA

81 IR**NDEELNK**L LSGVTIAQGG VLP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	15	23	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	30	36	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	83	89	
total 3 peptides												

tr|T1IUL1|T1IUL1_STRMM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKT KSKSKSRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLGA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|B4JZ46|B4JZ46_DROGR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|Q7PD33|Q7PD33_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR AGLQFPVGRI HRLLRKGNYA ERVGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIRND EELNKLLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|B4LVM8|B4LVM8_DROVI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR AGLQFPVGRI HRLLRKGNYA ERVGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIRND EELNKLLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|Q7Q2C6|Q7Q2C6_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR AGLQFPVGRI HRLLRKGNYA ERVGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIRND EELNKLLSGV TIAQGGVLPN IQAVLLPKKS EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|Q7Q2C4|Q7Q2C4_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR AGLQFPVGRI HRLLRKGNYA ERVGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIRND EELNKLLSGV TIAQGGVLPN IQAVLLPKKT EKNA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A182XUN7|A0A182XUN7_ANOQN

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR AGLQFPVGRI HRLLRKGNYA ERVGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIRND EELNKLLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A1S3DA94|A0A1S3DA94_DIACI

back to list

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

Protein Coverage:

1 MSGRGKGGKA KTKSKTRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A132ACK3|A0A132ACK3_SARSC

back to list

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

Protein Coverage:

1 MSGRGKGGKV KSKAKSRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVLEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN INAVLLPKKT EKTA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|E2A0I8|E2A0I8_CAMFO

back to list

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

Protein Coverage:

1 MSGRGKGGKA KGKAKSRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|B4K329|B4K329_DROGR

back to list

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

Protein Coverage:

1 MSGRGKGGKV KGKARSRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A1B0D249|A0A1B0D249_PHLPP

back to list

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

Protein Coverage:

1 MSGRGKGGKV KGKAKTRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A182G0A8|A0A182G0A8_ANOAL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|B7PSI5|B7PSI5_IXOSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKSKTRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVLEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A182KSY0|A0A182KSY0_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKV KGKAKSRSNR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A1S3DIS4|A0A1S3DIS4_DIACI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKA KAKSKTRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVMEYLAA EVLELAGNAA RDNKKTRIIP

81 RHLQLAIR**ND EELNK**LLSGV TIAQGGVLPN IQAVLLPKKT EKKA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	
total 3 peptides												

tr|A0A1S4E9L2|A0A1S4E9L2_DIACI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSGRGKGGKA KTKSKTRSSR **AGLQFPVGR**I HRLLR**KGNYA ER**VGAGAPVY LAAVLEYLVA EVLELAGNAA RDNKKTRIIP

81 RHIQLAIR**ND EELNK**LLNGV TIAQGGVLPN IQAVLLPKKS ETAKGKSNSQ EY

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	21	29	
R.KGNYAER.V	Y	29.28	836.4141	609.6	419.4692	2	12.13	864	2	36	42	
R.NDEELNK.L	Y	20.95	860.3876	-79.3	861.3267	1	23.01	1669	1	89	95	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
total 3 peptides												

tr|A0A182JIT9|A0A182JIT9_9DIPT back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAGGKAGKDS GKAKAKAVSR SAR**AGLQFPV GR**IHRHLKNR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

81 RITPRHLQLA IRGDEELDSL IK**ATIAGGGV IPH**IHKSLIG KKGGPE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	24	32	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	103	113	
total 2 peptides												

tr|A0A182F532|A0A182F532_ANOAL back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAAGKAGKDS GKAKAKAVSR SAR**AGLQFPV GR**MHRHLKHR TTNHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

81 RITPRHLQLA IRGDEELDGL IK**ATIAGGGV IPH**IHKSLIG KKGGPE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.M	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	24	32	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	103	113	
total 2 peptides												

tr|Q7QF50|Q7QF50_ANOGA back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAGGKAGKDS GKAKAKAVSR SAR**AGLQFPV GR**IHRHLKNR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

81 RITPRHLQLA IRGDEELDSL IK**ATIAGGGV IPH**IHKSLIG KKGGPE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	24	32	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	103	113	
total 2 peptides												

tr|A0A0A9YW58|A0A0A9YW58_LYGHE back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAGGKAGKDS GKAKAKAVSR SAR**AGLQFPV GR**IHRHLKNR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

81 RITPRHLQLA IRGDEELDSL IK**ATIAGGGV IPH**IHKSLIG KKGSQKPV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	24	32	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	103	113	
total 2 peptides												

tr|J3JTR0|J3JTR0_DENPD back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAGGKAGKDS GKAKAKAVSR SAR**AGLQFPV GR**IHRHLKNR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

81 RITPRHLQLA IRGDEELDSL IK**ATIAGGGV IPH**IHKSLIG KKGAGHSQPS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	24	32	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	103	113	
total 2 peptides												

tr|A0A132A5C4|A0A132A5C4_SARSC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKQSESGRRA KFEKNRSSRT VRQSEIVENE MSTFVAGGKA GKDSGKAKAK AVSRSAR**AGL QFPVGR**IHRH LKNRTTSHGR

81 VGATAAVYSA AILEYLTAEV LELAGNASKD LKVKRITPRH LQLAIRGDEE LDSLIK**ATIA GGGVIPH**IHK YLIGKKGNAP

161 QKPA

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.AGLQFPVGR.I	N	41.93	943.5239	-98.1	472.7230	2	32.83	2784	2	58	66	
K.ATIAGGGVIPH.I	Y	35.32	991.5450	437.5	496.9967	2	30.30	2492	1	137	147	
total 2 peptides												

tr|A0A0M9A898|A0A0M9A898_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADDEANNTC EDSLGPGDAN TAFAKKIRGR KGALKKKNVY VVKNHSFMPR FFKQPTFCSH CKDFIWGFGK QGYQCQVCSF
81 VVHKRCHEYV TFTCPGADKG ADSDDTRTKH QFKQHTYNSP TFCDHCGSLL YGVIHQGMKC QACDMNVHKR CEESVPNLCG
161 CDHTERRGRI NLHISCSGSK LTVEVKQGRN LIPMDPNGLS DPYVKLKLIP DSDNVKKKTK TIKSSLNPEK PEDKDRRLLI
241 EVWDWDRTSR **NDFMGSLSFG ISELIK**APAT GWFKLLTQEE GEFYNVPVPE EGVDLAELKM KVRKTSVTRK TTTTQDKEVP

321 HNMGKSDLIR ASDFHFLMVL GKGSFGKVML AERKGTDELY AIKILKKDII IQDDDVECTM VEKRVLALSS KPPFLVQLHS
401 CFQTMDRLYF VMEYVNGGDL MYQIQQCGKF KEPVAVFYAS EIAIGLFYLH GRGIVYRDLK LDNVLLDQDG HIKIADFGMC
481 KEGITGDKTT KTFCGTPDYI APEIILYQPY GKSVDWWAYG VLLYEMLVGQ PPFDGEDEEE LFAAITEHNV SYPKSLSKEA
561 REICKAFLTK NPVKRLGCGL RGEEDVRSHA FFRRIDWEKI ENREVQPPFK PKIKHRKDVS NFDKQFTSEK TDLTPTDKLF
641 MMNLDQTEFM GFSFLNPEFV QHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	251	266	
total 1 peptides												

tr|A0A0P5W4V7|A0A0P5W4V7_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADEKETNGG GSGHGNHNPD SSEGPGTGDL NTVFGMKQRG RKGALKKKNI YIVKDHKFIP RFFKQPTFCS HCKDFIWGFG
81 KQGYQCHICS FVVHKRCHEY VSFTCPGVTK GVECEDSRTT HKFKPYTYSS PTFCDHCGSL LYGVIHQGMK CEACDMNVHK
161 RCTESVPHLC GCDHTERRGR IEIKISCTRD KLILEVRQGK NLMPMDPNGL SDPFVKARLI PDTDNVKMKT KTIKASLNPE
241 WNETLTFDLK AEDKDRRILV EVWDWDRLSG **NDFMGSLSFG ISEIIK**SPVE GWFKLLSEEE GEFYNVPVSD GIDTEVFRKQ

321 IRQKASIISV AKPKEPSRFE TEIPHNMSRK DIIRATDFNF LMVLGKGSFG KVMLAERKGT DELYAIKILK KDIIIQDDDV
401 ECTLVEKHVL ALASKPPFLV QLHSCFQTMD RLYFVMEYVN GGDLMFQIQQ CGKFKEPVAV FYAAEIAVGL FFLHSRGIIY
481 RDLKLDNILL DQDGHIKIAD FGMCKEGIDG EKVTKTFCGT PDYIAPEIIL YQPYGRSVDW WAYGVLLYEM LVGQPPFDGE
561 DEEELFAAIT DQNVSYPKSL SKEAKEICKG LLTKQPAKRL GCTPKGEEDV RTHPFFRRID WLKIESREVQ PPFKPKIKNP
641 RMAENFDPIF TRAKVELTPP DRNALMILKH LNPGDFAEFD WVNPYYEPII DPPLIEHLFL VSTTSAPQRS GPNSPRSANS
721 AASTTSLPLT KEFKLKIESR EVQPPFKPKI KHRKDVSNFD KQFTSEKLDL TPTDKLFMMN LDQNEFLGFS FLNPEFVQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	271	286	
total 1 peptides												

tr|A0A0N7ZKU6|A0A0N7ZKU6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MERLCTRERR LSADSRWCRV ESAVCQSKMA DEKETNGGGS GHGNHNPDSS EGPGTGDLNT VFGMKQRGRK GALKKKNIYI
81 VKDHKFIPRF FKQPTFCSHC KDFIWGFGKQ GYQCHICSFV VHKRCHEYVS FTCPGVTKGV ECEDSRTTHK FKPYTYSSPT
161 FCDHCGSLLY GVIHQGMKCE ACDMNVHKRC TESVPHLCGC DHTERRGRIE IKISCTRDKL ILEVRQGKNL MPMDPNGLSD
241 PFVKARLIPD TDNVKMKTKT IKASLNPEWN ETLTFDLKAE DKDRRILVEV WDWDRLSG**ND FMGSLSFGIS EIIK**SPVEGW

321 FKLLSEEEGE FYNVPVSDGI DTEVFRKQIR QKASIISVAK PKEPSRFETE IPHNMSRKDI IRATDFNFLM VLGKGSFGKV
401 MLAERKGTDE LYAIKILKKD IIIQDDDVEC TLVEKHVLAL ASKPPFLVQL HSCFQTMDRL YFVMEYVNGG DLMFQIQQCG
481 KFKEPVAVFY AAEIAVGLFF LHSRGIIYRD LKLDNILLDQ DGHIKIADFG MCKEGIDGEK VTKTFCGTPD YIAPEIILYQ
561 PYGRSVDWWA YGVLLYEMLV GQPPFDGEDE EELFAAITDQ NVSYPKSLSK EAKEICKGLL TKQPAKRLGC TPKGEEDVRT
641 HPFFRRIDWL KIESREVQPP FKPKIKNPRM AENFDPIFTR AKVELTPPDR NALMILKHLN PGDFAEFDWV NPYYEPIIDP
721 PLIEHLFLVS TTSAPQRSGP NSPRSANSAA STTSLPLTKE FKSALKVYSF DKNKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	299	314	
total 1 peptides												

tr|A0A0P5D7F8|A0A0P5D7F8_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADEKETNGG GSGHGNHNPD SSEGPGTGDL NTVFGMKQRG RKGALKKKNI YIVKDHKFIP RFFKQPTFCS HCKDFIWGFG
81 KQGYQCHICS FVVHKRCHEY VSFTCPGVTK GVECEDSRTT HKFKPYTYSS PTFCDHCGSL LYGVIHQGMK CEACDMNVHK
161 RCTESVPHLC GCDHTERRGR IEIKISCTRD KLILEVRQGK NLMPMDPNGL SDPFVKARLI PDTDNVKMKT KTIKASLNPE
241 WNETLTFDLK AEDKDRRILV EVWDWDRLSG **NDFMGSLSFG ISEIIK**SPVE GWFKLLSEEE GEFYNVPVSD GIDTEVFRKQ

321 IRQKASIISV AKPKEPSRFE TEIPHNMSRK DIIRATDFNF LMVLGKGSFG KVMLAERKGT DELYAIKILK KDIIIQDDDV
401 ECTLVEKHVL ALASKPPFLV QLHSCFQTMD RLYFVMEYVN GGDLMFQIQQ CGKFKEPVAV FYAAEIAVGL FFLHSRGIIY
481 RDLKLDNILL DQDGHIKIAD FGMCKEGIDG EKVTKTFCGT PDYIAPEIIL YQPYGRSVDW WAYGVLLYEM LVGQPPFDGE
561 DEEELFAAIT DQNVSYPKSL SKEAKEICKG LLTKQPAKRL GCTPKGEEDV RTHPFFRRID WLKIESREVQ PPFKPKIKNP
641 RMAENFDPIF TRAKVELTPP DRNALMILKH LNPGDFAEFD WVNPYYEPII DPPLIEHLFL VSTTSAPQRS GPNSPRSANS
721 AASTTSLPLT KEFKSALXXX XXXXXXXXXX XXXRSTVSIK TRSDVKKT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	271	286	
total 1 peptides												

tr|A0A0P6FB91|A0A0P6FB91_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRWCRVESA VCQSKMADEK ETNGGGSGHG NHNPDSSEGP GTGDLNTVFG MKQRGRKGAL KKKNIYIVKD HKFIPRFFKQ
81 PTFCSHCKDF IWGFGKQGYQ CHICSFVVHK RCHEYVSFTC PGVTKGVECE DSRTTHKFKP YTYSSPTFCD HCGSLLYGVI
161 HQGMKCEACD MNVHKRCTES VPHLCGCDHT ERRGRIEIKI SCTRDKLILE VRQGKNLMPM DPNGLSDPFV KARLIPDTDN
241 VKMKTKTIKA SLNPEWNETL TFDLKAEDKD RRILVEVWDW DRLSG**NDFMG SLSFGISEII K**SPVEGWFKL LSEEEGEFYN

321 VPVSDGIDTE VFRKQIRQKA SIISVAKPKE PSRFETEIPH NMSRKDIIRA TDFNFLMVLG KGSFGKVMLA ERKGTDELYA
401 IKILKKDIII QDDDVECTLV EKHVLALASK PPFLVQLHSC FQTMDRLYFV MEYVNGGDLM FQIQQCGKFK EPVAVFYAAE
481 IAVGLFFLHS RGIIYRDLKL DNILLDQDGH IKIADFGMCK EGIDGEKVTK TFCGTPDYIA PEIILYQPYG RSVDWWAYGV
561 LLYEMLVGQP PFDGEDEEEL FAAITDQNVS YPKSLSKEAK EICKGLLTKQ PAKRLGCTPK GEEDVRTHPF FRRIDWLKIE
641 SREVQPPFKP KIKNPRMAEN FDPIFTRAKV ELTPPDRNAL MILKHLNPGD FAEFDWVNPY YEPIIDPPLI EHLFLVSTTS
721 APQRSGPNSP RSANSAASTT SLPLTKEFKS ALKVYSFDKN KK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	286	301	
total 1 peptides												

tr|A0A0P5BRK4|A0A0P5BRK4_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MPKTVFKSPV PGPSDEKETN GGGSGHGNHN PDSSEGPGTG DLNTVFGMKQ RGRKGALKKK NIYIVKDHKF IPRFFKQPTF
81 CSHCKDFIWG FGKQGYQCHI CSFVVHKRCH EYVSFTCPGV TKGVECEDSR TTHKFKPYTY SSPTFCDHCG SLLYGVIHQG
161 MKCEACDMNV HKRCTESVPH LCGCDHTERR GRIEIKISCT RDKLILEVRQ GKNLMPMDPN GLSDPFVKAR LIPDTDNVKM
241 KTKTIKASLN PEWNETLTFD LKAEDKDRRI LVEVWDWDRL SG**NDFMGSLS FGISEIIK**SP VEGWFKLLSE EEGEFYNVPV

321 SDGIDTEVFR KQIRQKASII SVAKPKEPSR FETEIPHNMS RKDIIRATDF NFLMVLGKGS FGKVMLAERK GTDELYAIKI
401 LKKDIIIQDD DVECTLVEKH VLALASKPPF LVQLHSCFQT MDRLYFVMEY VNGGDLMFQI QQCGKFKEPV AVFYAAEIAV
481 GLFFLHSRGI IYRDLKLDNI LLDQDGHIKI ADFGMCKEGI DGEKVTKTFC GTPDYIAPEI ILYQPYGRSV DWWAYGVLLY
561 EMLVGQPPFD GEDEEELFAA ITDQNVSYPK SLSKEAKEIC KGLLTKQPAK RLGCTPKGEE DVRTHPFFRR IDWLKIESRE
641 VQPPFKPKIK NPRMAENFDP IFTRAKVELT PPDRNALMIL KHLNPGDFAE FDWVNPYYEP IIDPPLIEHL FLVSTTSAPQ
721 RSGPNSPRSA NSAASTTSLP LTKEFKSALK VYSFDKNKK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	283	298	
total 1 peptides												

tr|A0A0P4ZIP3|A0A0P4ZIP3_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADEKETNGG GSGHGNHNPD SSEGPGTGDL NTVFGMKQRG RKGALKKKNI YIVKDHKFIP RFFKQPTFCS HCKDFIWGFG
81 KQGYQCHICS FVVHKRCHEY VSFTCPGVTK GVECEDSRTT HKFKPYTYSS PTFCDHCGSL LYGVIHQGMK CEACDMNVHK
161 RCTESVPHLC GCDHTERRGR IEIKISCTRD KLILEVRQGK NLMPMDPNGL SDPFVKARLI PDTDNVKMKT KTIKASLNPE
241 WNETLTFDLK AEDKDRRILV EVWDWDRLSG **NDFMGSLSFG ISEIIK**SPVE GWFKLLSEEE GEFYNVPVSD GIDTEVFRKQ

321 IRQKASIISV AKPKEPSRFE TEIPHNMSRK DIIRATDFNF LMVLGKGSFG KVMLAERKGT DELYAIKILK KDIIIQDDDV
401 ECTLVEKHVL ALASKPPFLV QLHSCFQTMD RLYFVMEYVN GGDLMFQIQQ CGKFKEPVAV FYAAEIAVGL FFLHSRGIIY
481 RDLKLDNILL DQDGHIKIAD FGMCKEGIDG EKVTKTFCGT PDYIAPEIIL YQPYGRSVDW WAYGVLLYEM LVGQPPFDGE
561 DEEELFAAIT DQNVSYPKSL SKEAKEICKG LLTKQPAKRL GCTPKGEEDV RTHPFFRRID WLKIESREVQ PPFKPKIKNP
641 RMAENFDPIF TRAKVELTPP DRNALMILKH LNPGDFAEFD WVNPYYEPII DPPLIEHLFL VSTTSAPQRS GPNSPRSANS
721 AASTTSLPLT KEFKSALNEE KIFFFFFFSK SFH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	271	286	
total 1 peptides												

tr|A0A151X2L9|A0A151X2L9_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADDQENNTC EDSLGTGDTN TAFAKKLRGR KGALKKKNVY MVKNHSFMPR FFKQPTFCSH CKDFICWKFR SLCSFVVHKR
81 CHEYVTFTCP GADKGADSDR FGRFVPTIDT RTKHQFKQHT YNSPTFCDHC GSLLYGVIHQ GMKCQDISHI NPAPPPLPLI
161 PVIVSQEFDH LGCPNICPGR MIDLTACDMN VHKRCEESVP NLCGCDHTER RGRIHLHISC AGSKLSIQVR EGRNLIPMDP
241 NGLSDPYVKL KLIPDSDNVK KKTKTIKSCL NPEWNETIIF DLKPEDKDRR LLIEVWDWDR TSR**NDFMGSL SFGISELIK**A

321 PSSGWYKLLT QEEGEFYNVP VPEEGVDLAE LKTKMRKTSV TKKTHTTQDK DVPHNMGKSD LIRASDFNFL MVLGKGSFGK
401 VLLAERKGTD ELYAIKILKK DIIIQDDDVE CTMVEKRVLA LSSKPPFLVQ LHSCFQTMDR LYFVMEYVNG GDLMYQIQQC
481 GKFKEPVAVF YSSEIAIGLF FLHSRGIVYR DLKLDNVLLD QDGHIKIADF GMCKEGITGD KTTKTFCGTP DYIAPEIILY
561 QPYGKSVDWW AYGVLLYEML VGQPPFDGED EDELFSAITD HNVSYPKSLS KEAKEVCKAF LTKNPSKRLG CGMRGEDDVR
641 SHAFFRRIDW EKIENREVQP PFKPKIQHRK DVSNFDKQFT SEKTDLTPTD KLFMMNLDQT EFMGFSYLNP EFVQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	304	319	
total 1 peptides												

tr|A0A0P5DL28|A0A0P5DL28_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSRWCRVESA VCQSKMADEK ETNGGGSGHG NHNPDSSEGP GTGDLNTVFG MKQRGRKGAL KKKNIYIVKD HKFIPRFFKQ

81 PTFCSHCKDF IWGFGKQGYQ CHICSFVVHK RCHEYVSFTC PGVTKGVECE DSRTTHKFKP YTYSSPTFCD HCGSLLYGVI

161 HQGMKCEACD MNVHKRCTES VPHLCGCDHT ERRGRIEIKI SCTRDKLILE VRQGKNLMPM DPNGLSDPFV KARLIPDTDN

241 VKMKTKTIKA SLNPEWNETL TFDLKAEDKD RRILVEVWDW DRLSG**NDFMG SLSFGISEII K**SPVEGWFKL LSEEEGEFYN

321 VPVSDGIDTE VFRKQIRQKA SIISVAKPKE PSRFETEIPH NMSRKDIIRA TDFNFLMVLG KGSFGKVMLA ERKGTDELYA

401 IKILKKDIII QDDDVECTLV EKHVLALASK PPFLVQLHSC FQTMDRLYFV MEYVNGGDLM FQIQQCGKFK EPVAVFYAAE

481 IAVGLFFLHS RGIIYRDLKL DNILLDQDGH IKIADFGMCK EGIDGEKVTK TFCGTPDYIA PEIILYQPYG RSVDWWAYGV

561 LLYEMLVGQP PFDGEDEEEL FAAITDQNVS YPKSLSKEAK EICKGLLTKQ PAKRLGCTPK GEEDVRTHPF FRRIDWLKIE

641 SREVQPPFKP KIKHRKDVSN FDKQFTSEKL DLTPTDKLFM MNLDQNEFLG FSFLNPEFVQ HV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.NDFMGSLSFGISEIIK.S	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	286	301	
total 1 peptides												

tr|A0A0A9X7J5|A0A0A9X7J5_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PRGALGSSGL ASVLLSLGLT ADMAEDEAST NDDSTGDKTQ LGGFGARGRK GALKKKNVYN VKGHKFIPRF FKQPTFCSHC

81 KDFIWGFGKQ GFQCQVCSFV VHKRCHEYVS FTCPGADKGP DSDAEFSKHK FEVYTYLAPT FCDHCGSMLH GLTQQGLKCS

161 ACDMNVHKRC KESVPNLCGC DHTERRGRIE LKITCANNHL SADIRQGKNL IPMDPNGLSD PYVKLKLIPD SDNVKKKTKT

241 IKANLNPVWN ETLNFELKAE DKDRRLLIEV WDWDRTSR**ND FMGSLSFGIS ELIK**APVEGW FKLLTQEEGE FYNVPVPEEG

321 ADLAQLKSQM RQTSITKKAP VVTDKDVPHN MNKKDVIRAS DFNFLMVLGK GSFGKVMLAE RKGTDELYAI KILKKDIIIQ

401 DDDVECTMVE KRVLALSHKP PFLVQLHSCF QTMDRLYFVM EYVNGGDLMF QIQQCGKFKE PVAVFYSAEI AIGLFYLHVR

481 GIIYRDLKLD NVLLDQDGHI KIADFGMCKE GISGEKTTKT FCGTPDYIAP EIILYQPYGK SVDWWAYGVL LYEMLVGQPP

561 FDGEDEEELF AAITDHSVSY PKGLSKEAKE ACKGFLTKNP SKRLGCGARG EEDVRGHSFF RRIDWERIEA REVQPPFKPK

641 IKHRKDVSNF DKQFTSEKTD LTPTDKLFMM NLDQTEFMGF SYLNPEFIQH V

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	279	294	
total 1 peptides												

tr|Q7Q042|Q7Q042_ANOGA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GTGRGKMADD DNTLEEIPEA ENKMALRNRG RKGALKKKNV YNVKDHRFIP RFFKQPTFCS HCKDFICGFQ AVFCHLGFGK

81 QGFQCQVCSF VVHKRCHEYV TFKCPGADKG ADSDDTRTKH EFKEWTYSSP TFCDHCGSLL YGLIHQGLKC TACDMNVHKR

161 CEESVPNLCG CDHTERRGRI QLTITYAAGK LNIEVKQGRN LIPMDPNGSS DPYVKIKLIP DADNVKKKTK TIRASLNPVW

241 NETLIFDLKP EDKDRRLLIE VWDWDRTSR**N DFMGSLSFGI SEILK**NPVDG WFKLLTQEEG EYYNVPVPEE GADLVQLKSQ

321 MRKIPMMGDK DVPHNMTKKD VIRATDFNFL MVLGKGSFGK VMLAERKGTD ELYAIKILKK DIIIQDDDVE CTMVEKRVLA

401 LSSKPPFLVQ LHSCFQTMDR LYFVMEYVNG GDLMFQIQQC GKFKEPVAVA IIPIANNAAR TMTQRTRVAR GMLLRKFCPL

481 DNTSERAKER EQTKIADFGM CKEGILGDKT TKTFCGTPDY IAPEIILYQP YGKSVDWWAY GVLLYEMLVG QPPFDGEDEE

561 ELFAAITDHN VSYPKSLSKE AKDVCKGLLT KNPQKRLGCG ARGEEDVRAH AFFRRIDWEK IENREVQPPF KPKIKHRKDV

641 SNFDRQFTSE KTDLTPTDKL FMMNLDQTEF NGFSYLNPEF VQYV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	270	285	
total 1 peptides												

tr|V9I8Q4|V9I8Q4_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MADDQEANNT CEDSLGPGDA NTAFAKKIRG RKGALKKKNV YVVKNHSFMP RFFKQPTFCS HCKDFIWGFG KQGYQCQVCS
 81  FVVHKRCHEY VTFTCPGADK GADSDMSTAH KWEVFTYLTP TFCDHCGSML HGIAHQGLKC SACDMNVHKR CEESVPNLCG
161  CDHTERRGRI NLYISCSGSK LTVEVKQGRN LIPMDPNGLS DPYVKLKLIP DSDTVKKKTK TIKSSLNPEW NETIIFDLKP
241  EDKDRRLLIE VWDWDRTSRN DFMGSLSFGI SELIKAPANG WFKLLTQEEG EYYNVPVPEE GVDLAELKMK MRKTSVTKKT

321  TTTQDKEVPH NMGKSDLIRA SDFNFLMVLG KGSFGKVMLA ERKGTDELYA IKILKKDIII QDDDVECTMV EKRVLALSTK
401  PPFLVQLHSC FQTMDRLYFV MEYVNGGDLM YQIQQCGKFK EPVAVFYASE IAIGLFFLHG RGIVYRDLKL DNVLLDQDGH
481  IKIADFGMCK EGISGDKTTK TFCGTPDYIA PEIILYQPYG KSVDWWAYGV LLYEMLVGQP PFDGEDEEEL FAAITEHNVS
561  YPKSLSKEAR EICKAFLTKN PVKRLGCGLR GEEDVRSHAF FRRIDWEKIE NREVQPPFKP KIKHRKDVSN FDKQFTSEKT
641  DLTPTDKLFM MNLDQTEFMG FSFLNPEFVQ HV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	260	275	
total 1 peptides												

tr|A0A146MGA7|A0A146MGA7_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEDEASTND DSTGDKTQLG GFGARGRKGA LKKKNVYNVK GHKFIPRFFK QPTFCSHCKD FIWGFGKQGF QCQVCSFVVH
 81  KRCHEYVSFT CPGADKGPDS DAEFSKHKFE VYTYLAPTFC DHCGSMLHGL TQQGLKCSAC DMNVHKRCKE SVPNLCGCDH
161  TERRGRIELK ITCANNHLSA DIRQGKNLIP MDPNGLSDPY VKLKLIPDSD NVKKKTKTIK ANLNPVWNET LNFELKAEDK
241  DRRLLIEVWD WDRTSRNDFM GSLSFGISEL IKAPVEGWFK LLTQEEGEFY NVPVPEEGAD LAQLKSQMRQ TSITKKAPVV

321  TDKDVPHNMN KKDVIRASDF NFLMVLGKGS FGKVMLAERK GTDELYAIKI LKKDIIIQDD DVECTMVEKR VLALSHKPPF
401  LVQLHSCFQT MDRLYFVMEY VNGGDLMFQI QQCGKFKEPV AVFYSAEIAI GLFYLHVRGI IYRDLKLDNV LLDQDGHIKI
481  ADFGMCKEGI SGEKTTKTFC GTPDYIAPEI ILYQPYGKSV DWWAYGVLLY EMLVGQPPFD GEDEEELFAA ITDHSVSYPK
561  GLSKEAKEAC KGFLTKNPSK RLGCGARGEE DVRGHSFFRR IDWERIEARE VQPPFKPKIK HRKDVSNFDK QFTSEKTDLT
641  PTDKLFMMNL DQTEFMGFSY LNPEFIQHV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	257	272	
total 1 peptides												

tr|A0A023GLQ5|A0A023GLQ5_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  PIGHGDDGEE LSEQFSSGFR LRARKGALKK KNVFEVKNHK FIPRFFKQPT FCSHCKDFIW GFGKQGYQCQ ICSFVVHKRC
 81  HEFVTFKCPG KDKGVDSDDA RTKHQFQLQT YTSPTFCDHC GSLLYGLIHQ GYKCKACDMN VHKRCQESVP NLCGCDHTER
161  RGRIHLKVSA TPTRLTCEVR QARNLIPMDP NGLSDPYVKL KLIPDIGDSA KRKTKTIKAC LNPEWNETLT FDLKPVDKDR
241  RLLIELWDWD RTSRNDFMGS LSFGISEILK APAEGWFKLL TAEEGEFYNV PVPPEDPALA ATHHPTARVR STPQASSDLI

321  PHNMGKQDVI RASDFNFLLV LGKGSFGKVL LAERRGTDEL YAVKVLKKDV IIQDDDVECA MVEKRVLALA AKPPFLVQLH
401  SCFQTMERLY FVMEYVNGGD LMFQIQQCGK FKEPVAVFYA AEIAVGLFFL HARSIVYRDL KLDNILLDQD GHIKIADFGM
481  CKEGIQGDKT TKTFCGTPDY IAPEIILYQP YGKSVDWWAY GVLLYEMLVG QPPFDGEDEE ELFASITDHN VSYPKALSKE
561  AKEACKGFLT KNPVRRLGCG LSGEEDVRTH PFFRRIDWDK IENREVQPPF KPRIKNPRSG ENFDPVFTQA KMTLSPGDPL
641  VMRNLTGNEF QGFTFVNSQF GGVCSF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	255	270	
total 1 peptides												

tr|U5Q0I7|U5Q0I7_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MADDDNTLEE IPEAENKNAL RNRGRKGALK KKNVYNVKDH RFIPRFFKQP TFCSHCKDFI XXXXXXXXXX GFGKQGFQCQ
81 VCSFVVHKRC HEYVTFKCPG ADKGADSDAQ NPHKWQGYTF ITPTFCDHCG SMLHGIAHQG LKSCDMNVHK RCEESVPNLC
161 GCDHTERRGR IQLTITHSVG KLNIEVKQGR NLIPMDPNGS SDPYVKIKLI PDADNVKKKT KTIRASLNPV WNETLIFDLK
241 AEDKDRRLLI EVWDWDRTSR **NDFMGSLSFG ISEILK**NPVD GWFKLLTQEE GEYYNVPVPE EGADLVQLKS QMRKIPMMGD

321 KDVPHNMTKK DVIRATDFNF LMVLGKGSFG KVMLAERKGT DELYAIKILK KDIIIQDDDV ECTMVEKRVW HCRVSHHFWC
401 NCIPDRLYFV MEYVNGGDLM FQIQQCGKFK EPVAVFYASE IAIGLFYLHA RGIVYRDLKL DNVLLDMDGH IKIADFGMCK
481 EGILGDKTTK TFCGTPDYIA PEIILYQPYG KSVDWWAYGV LLYEMLVGQP PFDGEDEEEL FAAITDHNVS YPKSLSKEAK
561 DVCKGLLTKN PQKRLGCGAR GEEDVRAHAF FRRIDWEKIE NREVQPPFKP KIKHRKDVSN FDRQFTSEKT DLTPTDKLFM
641 MNLDQTEFNG FSYLNPEFVQ YV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	261	276	
total 1 peptides												

tr|A0A069DWB7|A0A069DWB7_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EVGSGDTNTK FGLGVRGRKG ALKKKNVYNV KGHKFIPRFF KQPTFCSHCK DFIWGFGKQG FQCQVCSFVV HKRCHEYVSF
81 TCPGADKGPD SDAEISKHKF EVYTYLTPTF CDHCGSMLHG LTSQGLKCTA CDMNVHKRCK ESVPNLCGCD HTERRGRIEL
161 KISCVSNKLS AEVRQGKNLI PMDPNGSSDP YVKLKLIPDA DNVKKKTKTI KSSLNPVWNE TLSFELKSED KDRRLLIEVW
241 DWDRTSR**NDF MGSLSFGISE IIK**APVEGWF KLLTQEEGEF YNVPVPEEGA DLAQLKSQMR KTSITKKAPV MTDKDVPHNM

321 SKKDVIRASD FNFLMVLGKG SFGKVMLAER KGTDELYAIK ILKKDIIIQD DDVECTMVEK RVLALSQKPP FLVQLHSCFQ
401 TMDRLYFVME YVNGGDLMFQ IQQCGKFKEP VAVFYSAEIA IGLFYLHVRG IIYRDLKLDN VLLDQDGHIK IADFGMCKEG
481 ISGDKTTKTF CGTPDYIAPE IILYQPYGKS VDWWAYGVLL YEMLVGQPPF DGEDEEELFA AITDHSVSYP KGLSKEAKEA
561 CKGFLTKNPS KRLGCGMRGE EDVRGHSFFR RIDWERIEAR EVQPPFKPKI KHRKDVSNFD KQFTSEKTDL TPTDKLFMMN
641 LDQTEFMGFS YLNPEFIQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEIIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	248	263	
total 1 peptides												

tr|W5JP71|W5JP71_ANODA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MHDHSVTEAT ELAKQQQQQ KDGEIEGEFP FRSVPFFVPY ARIRETTLND TRTKHEFKEW TYSSPTFCDH CGSLLYGLIH
81 QGLKCTACDM NVHKRCEESV PNLCGCDHTE RRGRIQLTIT HMGGKLNIEV KQGRNLIPMD PNGSSDPYVK IKLIPDADNV
161 KKKTKTIRAS LNPVWNETLI FDLKAEDKDR RLLIEVWDWD RTSR**NDFMGS LSFGISEILK** NPVDGWFKLL TQEEGEYYNV

241 PVPEEGADLV QLKSQMRKTS ITKKIPMMGD KDVPHNMTKK DVIRATDFNF LMVLGKGSFG KVMLAERKGT DELYAIKILK
321 KDIIIQDDDV ECTMVEKRVL ALSSKPPFLV QLHSCFQTMD RLYFVMEYVN GGDLMFQIQQ CGKFKEPVAV FYSSEIAIGL
401 FYLHARGIVY RDLKLDNVLL DQDGHIKIAD FGMCKEGIMG DKTTKTFCGT PDYIAPEIIL YQPYGKSVDW WAYGVLLYEM
481 LVGQPPFDGE DEEELFAAIT DHNVSYPKSL SKEAKDVCKG LLTKNPQKRL GCGARGEEDV RAHAFYRRID WEKIENREVQ
561 PPFKPKIKHR KDVSNFDRQF TSEKTDLTPT DKLFMMNLDQ TEFNGFSYLN PEFVQYV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	205	220	
total 1 peptides												

tr|A0A0A9WKY4|A0A0A9WKY4_LYGHE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MLHGLTQQGL KCSACDMNVH KRCKESVPNL CGCDHTERRG RIELKITCAN NHLSADIRQG KNLIPMDPNG LSDPYVKLKL
81 IPDSDNVKKK TKTIKANLNP VWNETLNFEL KAEDKDRRLL IEVWDWDRTS R**NDFMGSLSF GISELIK**APV EGWFKLLTQE

161 EGEFYNVPVP EEGADLAQLK SQMRQTSITK KAPVVTDKDV PHNMNKKDVI RASDFNFLMV LGKGSFGKVM LAERKGTDEL
241 YAIKILKKDI IIQDDDVECT MVEKRVLALS HKPPFLVQLH SCFQTMDRLY FVMEYVNGGD LMFQIQQCGK FKEPVAVFYS
321 AEIAIGLFYL HVRGIIYRDL KLDNVLLDQD GHIKIADFGM CKEGISGEKT TKTFCGTPDY IAPEIILYQP YGKSVDWWAY
401 GVLLYEMLVG QPPFDGEDEE ELFAAITDHS VSYPKGLSKE AKEACKGFLT KNPSKRLGCG ARGEEDVRGH SFFRRIDWER
481 IEAREVQPPF KPKIKHRKDV SNFDKQFTSE KTDLTPTDKL FMMNLDQTEF MGFSYLNPEF IQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	132	147	
total 1 peptides												

tr|V9I8A6|V9I8A6_APICE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKCQACDMNV HKRCEESVPN LCGCDHTERR GRINLYISCS GSKLTVEVKQ GRNLIPMDPN GLSDPYVKLK LIPDSDTVKK

81 KTKTIKSSLN PEWNETIIFD LKPEDKDRRL LIEVWDWDRT SR**NDFMGSLS FGISELIK**AP ANGWFKLLTQ EEGEYYNVPV

161 PEEGVDLAEL KMKMRKTSVT KKTTTTQDKE VPHNMGKSDL IRASDFNFLM VLGKGSFGKV MLAERKGTDE LYAIKILKKD

241 IIIQDDDVEC TMVEKRVLAL STKPPFLVQL HSCFQTMDRL YFVMEYVNGG DLMYQIQQCG KFKEPVAVFY ASEIAIGLFF

321 LHGRGIVYRD LKLDNVLLDQ DGHIKIADFG MCKEGISGDK TTKTFCGTPD YIAPEIILYQ PYGKSVDWWA YGVLLYEMLV

401 GQPPFDGEDE EELFAAITEH NVSYPKSLSK EAREICKAFL TKNPVKRLGC GLRGEEDVRS HAFFRRIDWE KIENREVQPP

481 FKPKIKHRKD VSNFDKQFTS EKTDLTPTDK LFMMNLDQTE FMGFSFLNPE FVQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	123	138	
total 1 peptides												

tr|A0A1W4WLP9|A0A1W4WLP9_AGRPL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MKCAACDMNV HKRCEESVPN LCGCDHTERR GRIQLKINCV GNKLTIEVCQ GRNLIPMDPN GSSDPYVKLK LIPDTDAVKK

81 KTKTIRASLN PVWNETITFE LKPEDKDRRL LVEVWDWDRT SR**NDFMGSLS FGISEIIK**AP ADGWFKLLTQ EEGEFYNVPV

161 PEEGVDLAQM KMQMRKTSIT KKPSVAADKD VPHNMGKKDV IRASDFNFLM VLGKGSFGKV MLAERKGTDE LYAIKILKKD

241 IIIQDDDVEC TMVEKRVLAL SSKPPFLVQL HSCFQTMERL YFVMEYVNGG DLMFQIQQCG KFKEPVAVFY AAEIAIGLFF

321 LHHRGIIYRD LKLDNVLLDQ DGHIKIADFG MCKEGIMGDK TTKTFCGTPD YIAPEIILYQ PYGKSVDWWA YGVLLYEMLV

401 GQPPFDGEDE EELFAAITDH NVSYPKGLSK EAKEVCKGLL TKNPNKRLGC GPEGEENIRV HAFFRRIDWE KIENREVQPP

481 FKPKIKHRKD VSNFDKQFTS EKTDLTPTDK LFMMNLDQTE FMGFSFLNPE FVQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEIIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	123	138	
total 1 peptides												

tr|T1HII9|T1HII9_RHOPR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SACDMNVHKR CKESVPNLCG CDHTERRGRI ELKISCLSNK LSAEVRQGKN LIPMDPNGSS DPYVKLKLIP DADNVKKKTK

81 TIKSSLNPVW NETLTFELKP EDKDRRLLIE VWDWDRTSR**N DFMGSLSFGI SEIIK**APVEG WFKLLTQEEG EFYNVPVPEE

161 GADLAQLKSQ MRKTSITKKA PVMTDKDVPH NMSKKDVIRA SDFNFLMVLG KGSFGKVMLA ERKGTDELYA IKILKKDIII

241 QDDDVECTMV EKRVLALSQK PPFLVQLHSC FQTMDRLYFV MEYVNGGDLM FQIQQCGKFK EPVAVFYSAE IAIGLFYLHV

321 RGIIYRDLKL DNVLLDQDGH IKIADFGMCK EGISADKTTK TFCGTPDYIA PEIILYQPYG KSVDWWAYGV LLYEMLVGQP

401 PFDGEDEEEL FAAITDHSVS YPKGLSKEAK EACKGFLTKN PSKRLGCGLR GEEDVRGHSF FRRIDWERIE AREVQPPFKP

481 KIKHRKDVSN FDKQFTSEKT DLTPTDKLFM MNLDQTEFMG FSYLNPEFIQ HV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEIIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	120	135	
total 1 peptides												

tr|A0A0J7P1D0|A0A0J7P1D0_LASNI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDPNGLSDPY VKLKLIPDSD NVKKKTKTIK SCLNPEWNET LSFDLKPEDK DRRLLIEVWD WDRTSR**NDFM GSLSFGISEL**

81 **IK**APASGWFK LLTQEEGEFY NVPVPEEGVD LAELKTKMRK TSVTKKTHAA QDKDVPHNMG KSDLIRASDF NFLMVLGKGS

161 FGKVLLAERK GTDELYAIKI LKKDIIIQDD DVECTMVEKR VLALSHKPPF LVQLHSCFQT MDRLYFVMEY VNGGDLMYQI

241 QQCGKFKEPV AVFYSSEIAI GLFYLHLRGI VYRDLKLDNV LLDQDGHIKI ADFGMCKEGI TGDKTTKTFC GTPDYIAPEI

321 ILYQPYGKSV DWWAYGVLLY EMLVGQPPFD GEDEDELFSA ITDHNVSYPK SLSKEAKEVC KAFLTKNPSK RLGCGMRGED

401 DVRSHAFFRR IDWEKIENRE VQPPFKPKIQ HRKDVSNFDK QFTSEKTDLT PTDKLFMMNL DQTEFMGFSY LNPEFVQHV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISELIK.A	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	67	82	
total 1 peptides												

tr|A0A1A9W2I3|A0A1A9W2I3_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNVHARCKEN VPSLCGCDHT ERRGRINLEL IVKENTLTAQ SNELKPEDKD RRVLIEVWDW DRTSR**NDFMG SLSFGISEII**

81 **K**NPANGWFKL LTQDEGEYYN VPCADATQDL LKLKSQMRKS SQKKPLVMRT ETNAQAQSRK DMLRTSDFNF IKVLGKGSFG

161 KVLLAERKGS EELYAIKILK KDVIIQDDDV ECTMIEKRVL ALSDKPPFLD RLFFVMEFVN GGDLMFQIQQ FGKFKEPVAV

241 FYAAEIASGL FFLHTKGILY RDLKLDNVLL DADGHVKIAD FGMCKENVVG DKTTKTFCGT PDYIAPEIIL YQPYGKSVDW

321 WAYGVLLYEM LVGQPPFDGE DEEELFAAIT DHNVSYPKSL SKEAKEACKG FLTKQPSKRL GCGATGEEDV RLHPFFRRID

401 WEKIENREVQ PPFKPKIKHR KDVSNFDKQF TSEKTDLTPT DKVFMMNLDQ TEFVGFSYVN PDYTVSL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEIIK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	66	81	
total 1 peptides												

tr|A0A182Y1W2|A0A182Y1W2_ANOST

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNVHKRCEES VPNLCGCDHT ERRGRIQLTI THSVGKLNIE VKQGRNLIPM DPNGSSDPYV KIKLIPDADN VKKKTKTIRA

81 SLNPVWNETL IFDLKAEDKD RRLLIEVWDW DRTSR**NDFMG SLSFGISEIL K**NPVDGWFKL LTQEEGEYYN VPVPEEGADL

161 VQLKSQMRDR LYFVMEYVNG GDLMFQIQQC GKFKEPVAKH RKDVSNFDRQ FTSEKTDLTP TDKLFMMNLD QTEFNGFSYL

241 NPEFVQYV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	116	131	
total 1 peptides												

tr|A0A1B0CD14|A0A1B0CD14_LUTLO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNVHKRCEES VPNLCGCDHT ERRGRIQLAI SCTANKLTAI VKQGRNLIPM DPNGLSDPYV KLKLIPDTDN VKKKTKTIRS

81 TLNPEWNETL AFDLKAEDKD RRLLIEVWDW DRTSR**NDFMG SLSFGISEII K**NPADGWYKL LTQEEGEFYN VPVPDEAADL

161 AQIKSQMRDR LYFVMEFVNG GDLMFQIQQC GKFKEPVAVL KEKINKFKFH KDRLYFVMEF VNGGDLMFQI QQCGKFKEPV

241 AVIIVKC

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEIIK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	116	131	
total 1 peptides												

tr|A0A182SK05|A0A182SK05_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MDPNGSSDPY VKIKLIPDAD NVKKKTKTIR ASLNPVWNET LIFDLKAEDK DRRLLIEVWD WDRTSR**NDFM GSLSFGISEI**

81 **LK**NPVDGWFK LLTQEEGEYY NVPVPEEGAD LVQLKSQMRK TSITKKIPMM GDKDVPHNMT KKDVIRATDF NFLMVLGKGS

161 F

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.NDFMGSLSFGISEILK.N	Y	53.03	1756.8705	468.2	879.8538	2	42.78	3931	1	67	82	
total 1 peptides												

tr|F4W666|F4W666_ACREC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MAK**APAVGID LGTTYSCVGV FQHGK**VEIIA NDQGNRTTPS YVAFTETERL IGDAAKNQVA MNPNNTIFDA KRLIGRRFED C Carba
81 PTILADMKHW PFTVINDSGK PKIQVQYKGE TKTFFPEEVS SMVLVKMKET AEAYLGKTVT NAVITVPAYF NDSQRQATKD
161 AGTISGLNVL RIINEPTAAA IAYGLDKKAT GERNVLIFDL GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH
241 FVQEFKRKYK KDLTSNKRAL RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA RFEELCADLF RGTLEPVEKS
321 LRDAKMDKAQ IHDIVLVGGS TRIPKIQKLL QDFFNGKELN KSINPDEAVA YGAAVQAAIL HGDKSEEVQD LLLLDVTPLS
401 LGIETAGGVM TALIKRNTTI PTKQTQTFTT YADNQPGVLI QVYEGERAMT KDNNLLGKFE LSGIPPAPRG VPQIEVTFDI
481 DANGILNVSA VDKSTGKENK ITITNDKGRL SKEDIERMVN EAEKYRSEDE KQKETISAKN GLESYCFNMK STVEDEKLKD
561 KISASDKQTI LDKCNDIIKW LDANQLADKE EYEHKQKELE AICNPIVTKL YQGAGGMPGG MPGGFPGAGG ATPGGAPSSG
641 GASGPTIEEV D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.APAVGIDLGTTYSC(+57.02)VGVFQHGK.V	Y	48.97	2276.1260	516.0	760.1074	3	35.85	3139	1	4	25	Carbamidomethylation
total 1 peptides												

tr|A0A0P6CG63|A0A0P6CG63_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRAFLLLLWL AARGSALYFH IGETEKKCFI EEIPDETMVI GNYRTQLYDK QREEYQPATP GLGMFVEVKD PEDKVILARQ
81 YGSEGRFTFT SHTPGEHQIC LHSNSTKFSL FAGGMLRVHL DIQVGEHAND YAEIAAK**DKL SELQLR**VR**QL VEQVEQIQK**E
161 QNYQRWREER FRQTSESTNQ RVLWWSILQT LILVAIGVWQ MRHLK**SFFEA K**KLV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.QLVEQVEQIQK.E	Y	30.54	1340.7300	49.1	671.4052	2	30.76	2545	1	149	159	
K.DKLSELQLR.V	Y	18.02	1100.6189	1026.6	551.8817	2	30.67	2534	1	138	146	
K.SFFEAK.K	Y	16.47	727.3541	-55.1	728.3213	1	29.79	2433	1	206	211	
total 3 peptides												

tr|A0A0P5ZY70|A0A0P5ZY70_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MRAFLLLLWL AARGSALYFH IGETEKKCFI EEIPDETMVI GNYRTQLYDK QREEYQPATP GLGMFVEVKD PEDKVILARQ
81 YGSEGRFTFT SHTPGEHQIC LHSNSTKFSL FAGGMLRVHL DIQVGEHAND YAEIAAK**DKL SELQLR**VR**QL VEQVEQIQK**E
161 QNYQRWREER

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.QLVEQVEQIQK.E	Y	30.54	1340.7300	49.1	671.4052	2	30.76	2545	1	149	159	
K.DKLSELQLR.V	Y	18.02	1100.6189	1026.6	551.8817	2	30.67	2534	1	138	146	
total 2 peptides												

tr|T1PG74|T1PG74_MUSDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVDAKPINLG LWDTAGQEDY DRLRPLSYPQ TDVFLICFSL VNPASFENVR AKWYPEVRHH CPNTPIILVG TKLDLRDDKI O Oxida
81 TIEKLRDKK**L TPITYPQGLA MAK**EIGAVKY LECSALTQKG LKTVFDEAIR SVLCPVLQPK SKRKCTLL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	90	103	Oxidation (M)
total 1 peptides												

tr|T1PDL5|T1PDL5_MUSDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVDAKPINLG LWDTAGQEDY DRLRPLSYPQ TDVFLICFSL VNPASFENVR AKWYPEVRHH CPNVPIILVG TKLDLRDDKA O Oxida
81 TIEKLKDKK**L TPITYPQGLA MAK**EIGAVKY LECSALTQKG LKTVFDEAIR SVLCPVMRAP KKRRCAIL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	90	103	Oxidation (M)
total 1 peptides												

Prepared with PEAKS ™ (bioinfor.com)

tr|W8AQG8|W8AQG8_CERCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MARSLRPLKI TIVGDGMVGK TCLLITYTQN EFPEEYIPTV FDNHACNITV DGNEYNLTLW DTAGQEDYDR LRPLSYPQTD o Oxida
81 VFLICFSLVN PASFENVRAK WYPEVRHHCP NVPIILVGTK LDLRDDKATI EKLKEKK**LTP ITYPQGLAMA K**EIGAVKYLE
161 CSALTQKGLK TVFDEAIRSV LCPVMRVKRS RKCALL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	138	151	Oxidation (M)
total 1 peptides												

tr|B4ML79|B4ML79_DROWI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPNVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV MRGNVSKKCS LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B4QKE8|B4QKE8_DROSI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV VRGPKRHKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B4J295|B4J295_DROGR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCNNVPI ILVGTKLDLR DDKPTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPP SRRPHKRGCV LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A0K8VMJ4|A0A0K8VMJ4_BACLA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK EKK**LTPITYP QGLAMAK**EIV AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV TRIRRTRKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B4LDX8|B4LDX8_DROVI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWFPE VRHHCNNVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPP IRNTRKRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1A9WD10|A0A1A9WD10_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1I8Q976|A0A1I8Q976_STOCA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWYPE VRHHCPNTPI ILVGTKLDLR DDKNTIEKLR DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV LQPKSKRKCT LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B4HV68|B4HV68_DROSE

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV VRGPKRHKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A034W5H7|A0A034W5H7_BACDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK EKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1W4WMW4|A0A1W4WMW4_AGRPL

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDGKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida

81 CFSLVNPASF ENVRAKWYPE VRHHCPSTPI ILVGTKLDLR DDRATIEKLK DKK**LTPITYP QGLAMAK**EIS AVKYLECSAL

161 TQKGLKTVFD EAIRAVLCPV MPVRPKRKCV IL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1L8EGW8|A0A1L8EGW8_HAEIR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNTPI ILVGTKLDLR DDKNTIEKLR DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV LQPKSKRKCT LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B4KYQ8|B4KYQ8_DROMO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCNNVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPP IRNTRKRKCL IL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1I8N4Z1|A0A1I8N4Z1_MUSDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNTPI ILVGTKLDLR DDKITIEKLR DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV LQPKSKRKCT LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A0L0CPU9|A0A0L0CPU9_LUCCU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPQVPI ILVGTKLDLR DDKATIEKLK EKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV MRMPKRRKCM IL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1W4U7J3|A0A1W4U7J3_DROFC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKQTIEKLK EKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
161 TQKGLKTVFD EAIRSVLCPV VRGPKRHKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1I8MG34|A0A1I8MG34_MUSDO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
o

161 TQKGLKTVFD EAIRSVLCPV MRAPKKRRCA IL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A0M4EYM2|A0A0M4EYM2_DROBS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCNNVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL
o

161 TQKGLKTVFD EAIRSVLCPP IRHGHKRKCQ LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|D3TPE0|D3TPE0_GLOMM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
o

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1A9VE20|A0A1A9VE20_GLOAU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
o

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1A9XE80|A0A1A9XE80_GLOFF

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL
o

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B3NFD1|B3NFD1_DROER

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV VRGPKRHKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1B0BHT7|A0A1B0BHT7_9MUSC back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV MRVKRSRKCI LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B5DQJ0|B5DQJ0_DROPS back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPSVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV VRRPPRRMCK LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|B3M5S1|B3M5S1_DROAN back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV VRSPRRHKCT LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A1L8EH01|A0A1L8EH01_HAEIR back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWYPE VRHHCPNVPI ILVGTKLDLR DDKATIEKLK DKK**LTPITYP QGLAMAK**EIG AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV MRVSKKRKCA IL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|M9PBU2|M9PBU2_DROME back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MQAIKCVVVG DGAVGKTCLL ISYTTNAFPG EYIPTVFDNY SANVMVDAKP INLGLWDTAG QEDYDRLRPL SYPQTDVFLI o Oxida
81 CFSLVNPASF ENVRAKWFPE VRHHCPSVPI ILVGTKLDLR DDKQTIEKLK DKK**LTPITYP QGLAMAK**EIA AVKYLECSAL

161 TQKGLKTVFD EAIRSVLCPV VRGPKRHKCA LL

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.LTPITYPQGLAM(+15.99)AK.E	Y	39.60	1518.8115	-46.6	760.3776	2	33.41	2851	1	134	147	Oxidation (M)
total 1 peptides												

tr|A0A0P5VEM3|A0A0P5VEM3_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MIKLILGQPV LDPGSPIKIP VGPETLGR**IM NVIGEPIDER** GPIVTDKFAA IHAEDPEFVE MNDAQEILIT GIRSSTCSHP o Oxida

81 TPREAKLGLF GGAGVGKTVL IMET

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.IM(+15.99)NVIGEPIDER.G	Y	35.37	1400.6969	9.0	701.3621	2	31.59	2639	1	29	40	Oxidation (M)
total 1 peptides												

tr|A0A0P6D933|A0A0P6D933_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AAVAAAPVPC AGAPLRPSFL AIACSPHSAR TSPVRVRPRR SFSSRSAAGN RAEATESAME REKEQFRKLF IGGLSFETTE o Oxida

81 ESLRNYYEQW GKLTDCVVMR DPASKRSRGF GFVTFSSMAE VDAAMAARPH SIDGRVVEPK RAVAREESGK PGAHVTVKKL

239

161 FVGGIKEDTE EHHLRDYFEE YGKIDTIEII TDRQSGKKRG FGFVTFDDHD PVDKIVLQKY HTINGHNAEV RKALSR**QEMQ**

241 **EVQSSR**SGRG GNFGLGILVV AVAI

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.QEM(+15.99)QEVQSSR.S	Y	35.26	1236.5404	12.3	619.2851	2	22.98	1666	1	237	246	Oxidation (M)
total 1 peptides												

tr|K0FA39|K0FA39_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 SAPATGGVKK PHRYRPGTVA LREIRRYQK**S TELLIR**KLPF QRLVR**EIAQD FK**TDLRFQSS AVMALQEASE AYLVGLFEDT

81 NLCAIHAKRV T

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.STELLIR.K	Y	19.16	830.4861	-111.2	831.4011	1	30.72	2540	1	30	36	
R.EIAQDFK.T	Y	15.85	849.4232	-40.5	850.3961	1	27.56	2179	1	46	52	
total 2 peptides												

tr|D6NTM1|D6NTM1_MARJA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MCDDEVAALV VDNGSGMCKA GFAGDDAPRA VFPSIVGRPR HQGVMVGMGQ KDSYVGDEAQ SKRGILTLKY PIEHGIVTNW o Oxida

81 DDMEKIWHHT FYNELRVAPE EHPVLLTEAP LNPKANREKM TQIMFGTFNT PAMYVAIQAV LSLYASGRTT GIVLDSGDGV

161 SHTVPIYEGY ALPHAILRLD LAGR**DLTDYL MK**ILTERGYT FTTTAEREIV RDIKEKLCYV ALDFEQEMTT AASSSSLEKS

241 YELPDGQVIT IGNERFRCPE ALFQPSFLGM ESCGIHETTY NSIMKCDVDI RKDLYANTVL SGGTTMYPGI ADRMQKEITA

321 LAPSTMKIKI TAPPERKYSV WIGGSILASL STFQQMWISK QEYDESGPSI VHRKCF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
R.DLTDYLM(+15.99)K.I	Y	25.86	1013.4739	-85.0	1014.3950	1	33.54	2866	2	185	192	Oxidation (M)
total 1 peptides												

tr|A0A0P5IP74|A0A0P5IP74_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 AEHLPNGQTW RKATAYFTGN **DGFVVLK**ASV HVDYFWSRPR LSSDIKLIWF GLAIGFLECH SNAKITQFGH FKIPKNXXXX

81 XXXXXXXXXX XXXXXXKAVD GTWCLAMEKA ENCLMDLIEQ RLDSRAGPFP PHQIKCVGID IARALEYLHT EKLLMHGDMK

161 SGNILIFGDF KVAKLCDFGV AMALKEANGQ AKPDQFYIGT QAWSAPEVID MDGSFENDEA VITCKADIFS YGLTIWEMLS

241 LCVPHADLLQ DEEEDEEDDE KSYGSDCPDL AYQEALGTRP PLPDLPEVPD YSTAIAVFIA TTEYDPEKRP LASEVMNIWN

321 LSN

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.DGFVVLK.A	Y	23.82	776.4432	-8.3	777.4441	1	33.81	2896	1	21	27	
total 1 peptides												

tr|A0A0P5X9B5|A0A0P5X9B5_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFDNFRTPM KNRLHSLVLG QNGGFEASPG RKITVPASPS LERLGYGTGV SVYLMERAPI SGGGYRSPWA VKKVAKRFAN

81 QEHQDFSKRL LEEADILKKL EHPNIIGFRT LTKAVDGTWC LAMEKAENCL MDLIEQRLDS RAGPFPPHQI KCVGIDIARA

161 LEYLHTEKLL MHGDMKSGNI LIFGDFKVAK LCDFGVAMAL KEANGQAKPD QFYIGTQAWS APEVIDMDGS FENDEAVITX

241 XXXXXXXXXX XXXXXXXXXX XXXXXXXXVI GHFWNVWQWR SSSQSFLQIG VRHTKAEHLP NGQTWRKATA YFTGN**DGFVV**

321 **LK**ASVHVDYF W

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.DGFVVLK.A	Y	23.82	776.4432	-8.3	777.4441	1	33.81	2896	1	316	322	
total 1 peptides												

tr|A0A0P5N7W8|A0A0P5N7W8_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MNFDNFRTPM KNRLHSLVLG QNGGFEASPG RKITVPASPS LERLGYGTGV SVYLMERAPI SGGGYRSPWA VKKVAKRFAN

81 QEHQDFSKRL LEEADILKKL EHPNIIGFRT LTKAVDGTWC LAMEKAENCL MDLIEQRLDS RAGPFPPHQI KCVGIDIARA

161 LEYLHTEKLL MHGDMKSGNI LIFGDFKVAK LCDFGVAMAL KEANGQAKPD QFYIGTQAWS APEVIDMDGS FENDEAVITX

241 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXWK VWQWRSSSQS FLQIGVRHTK AEHLPNGQTW

321 RKATAYFTGN **DGFVVLK**ASV HVDYFW

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
N.DGFVVLK.A	Y	23.82	776.4432	-8.3	777.4441	1	33.81	2896	1	331	337	
total 1 peptides												

tr|A0A182MJI2|A0A182MJI2_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MVNIEPASKT TMADILTEPE LLEILCKQFY ESRDALRRVE AEKVLYHFQD DPEALSKCQT LLDRANSSFS QLFATTVLTK

81 LVTKNIQVLR MQQRVDIRNY VLNYLATRPN LQPF**VIQALI SLLVK**ITKLC WIDMYEHEYV FQNILQDVKE FLGGSVEHCV

161 IGVQILSQLT VEMNQQSEAA CNLTFPKHLR ITSLYRDKML YDIFILACTL LSQAKDSVCK NQNCLDEAQQ GLFTHLLELA

241 RNCLSYDFVG ATADESSDDI ATVQIPTNWR PAFLDSESDS LKLFFDLYHM LPTHLSSLAL SCLAQITSIR RSIFSNVERI

321 KFLTKLVKGA TDILKTSHGL SDPDNYHEFC RLLARLKSNY QLSELVIVEN YPEAIQLIAK FTVQSLQMWQ SAPNSIHYLL

401 SLWQRLIASL PYVKSPEPHY LETYTPEVTK AFITSKLDAV PVIVREGLED PVDDTDMVQQ QLEQFATIGR CEYDKTCALL

481 VQLFDQTANR YQEILSSPSA ANHIDLQICE GQLTWLVYII GASIGGRIAT PSLDDHDVLE CDIIIRVLQL MTLTDSRLPQ

561 CGCEKLELAF MYFLAHVRKI YITEHMQKLK MFPRLSEILG VSDDDMTMLT VTSRKIITNL KYLGNSEPVL RKTLALLNDL

641 TLICSSVRKL IKLDEIQFML NNRTREHFSF LGSGTVAATR CRSMFYTCLG RLLMMDLGED VERFNTFMLP LTKTIENIIM

721 MNFPSEEAKK ELIGLSRDLR GLALAFNAKM PYMMLFDWIY PDYSPILIRA VQMWAHDPTV TTPVLKLFTE LVYNRSQRLV

801 FDVSSPNGIL LFRETSKLIC CYGESMLSLN VPNEQMYPMK LKGISVCFQM LKQILSGNYV NFGVFKLYGD NALDNVLNMT

881 AKLILTIPHE DILVYPKLSL SYYTLIQCLA QDHISYLSTL EPPLFLYILE SISQGLNALV STFPNKKHRQ AVPPENNMFL

961 KVMELHPEIL QGLLSTMMNI VMFEDCKHHW SMSRPLLVLI LLYEDCFRRI RETFIQSQPV AKQQNIARLF DLLMDGIERN

1041 LLIQNRDKFT QNLLQFRRDV NASLKITPQP NSTANEMVVY CARNDH

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
F.VIQALISLLVK.I	Y	23.61	1195.7904	112.9	598.9700	2	33.71	2885	1	115	125	
total 1 peptides												

tr|A0A0P5UVM6|A0A0P5UVM6_9CRUS

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSFWYTMTHS IQVHLIYALP DSRFTGATHL SSSLSKAHRG LVKLSLSHCG LTGKGVVQIG HALVLNKCMA SSLQHLDLSN
81 NVAKDDINTI CSFLAQPNVL TFLNLSSTDI ALEPIFGALL RGGTTYLRHL DLSKNYFSTK KGKELPPSFK QYFTSALALR
161 TIILSHCKIT PEALKNLLLG LACNESIDNV TLDLSNNILG NGGCHVLESC IHGVRCVSTL DISDNGIDVE MAGVLLSISR
241 NKSMKKLILN KNFQNMKSKH ATTVIDAFVH LLQEEDCVIE ALSLVDCKLK SELYSLINAV GSNQSLQHLD LNGNYMGDPG
321 ARLLSKALQI NTSLKALSID RNSITVHGYS DIAYALESNR TLRCLSYPLH DIMVAAKTGT DKVDILWKQI QEALQRNMSL
401 IGPSPNGTSA SVRSHQKGET THNTSQNQLL DRLIIQVNEA IRTLQRQGSE GRAGDIEIAR NLLVDAHSAK E**LLGKLVSSV**
481 **EVAQD**NISLS SATKPMVEEL QALLTSHLQS IGDNLWHCAL QHCNTVMSNS CVSDQLRKSI ESQSFFPVSV IRKAVMENAT
561 LQLTEKFDEL STALCRTVSE NVMDEVVQSL TNIFKTLAGD SNVTLDCKKR SSTPDVLKSR TRINSEMNTQ RGEDESEDTI
641 DQQSDRSPVA TPVASKRRNL LSRKLRPKST VGMGQGASAD DIPDLVPPLN EQLSGIHHQG EDPDANEEEP GVNVDESQAD
721 VSRKSAPLKH LGLSRPKKPK TRLPTRSAAA LRVGNSETAS QESLDVEGDL SQGLDTFFHT TTMATTTGGS SVSLGSSRMR
801 GSLGSVSSAE LGSPSLESMS AESSPMHRSV AGDKLGEEVG SSSREELTLD EDAVKSKEKR KSEDDLSSVT KEKRKDSGRG
881 MGVRLLSSIF GKNPSPSPTG DGSPSPAPSK SPVAKTKLAS VTKEPESESK PVEDEAEPAV PKRSAVPSKL GIGVGGNVLA
961 EMKARQERRI SGILHKQNSE ESDFSERGME KPEANKANNL SPNPLGGIRL RPTPHTPEEQ EPPKLPERNN VRFIRPIGLE
1041 EVESDRNKPA NPLTGFRLRH RGGADEPETA KLEDKSNALN QIRLRATSTV VDDSPSPDPS GDAKANPLSG VRLRSTGINV
1121 TDPLKSPNNG DSNAENKSDS RNSLTKLKPP PLAPKPRPWS IVGSDKKTDD IDAADAAKEN DAKEAVKPSK VRAMAAAVNF
1201 NNSGSDVVRR SNKHSHEEQD GLPVEFLESK DGEVEQAYGQ DSLSSIAFLT NQQATLPQQQ QPLISQQSPA SLILNNFSLE
1281 DAVDV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
E.LLGKLVSSVEVAQD.N	Y	22.84	1456.8137	145.7	729.5203	2	41.19	3752	1	472	485	
total 1 peptides												

tr|W5JLB6|W5JLB6_ANODA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MATTVWMMTV VAVATTATFS NVCQTDDYAR EQLAGILSSI YLSESRSSTV PAPDWGTSSN TTSSSRTSSR QPAVNGSDVG
81 GASGNDTPSM VQLAELDAYL LELGNRDEQT EQIEQQHQQP TSYGSAEAVH QQIIHRIPEY VNVARNDTNG YMKRFIAALN
161 AKVFSRNAPF NPAYSDRVSA ECKRQSAHFL RSYRSSQLWA FRMHDASAKL SHGILNGNIN QYGDFDQCVR LQEEQQQQH
241 GGSGTPAIVG RYCMAEVQPT VKPNTVMLQY LFDLVQAHRM LKSNLHDPGH RVPRFSTVHW ALCVPAGCTA ADVQASLADF
321 LAEYIAGTGI ETEVKVNPAL CQTRHQLWQD YFTDRTLLVW AGFALYGLLV LGATVYDYRM ATGKAEWLTA FSLIKNTRSI
401 VCLKEERNDI SCVHGIRFLN AMLLLIAHKS MALFFNPYVN RTEMSEILGQ PWTVIGRAAA IFTDPFIMFS GFLTTFSFVE
481 RLQRGQRVRL HQEYVGRLLR IMPPLGALIL FCTFVLPFLG TGPLWNLVVT NHGTICKRYW WRNMLFIHNY FGFQNMCLTH
561 THHVGIDTEL FLIAPLFIYL VWRWPRPG**IA ALAAIASLTT** VHRFYTTYHL RLANYVYFGT SVKQLFDTAD HMYTLPYYRV
641 TVYLMGVILG YVCSKYKTIK LSVRQIKIGW YLSSLSIAVA FFGPAPMGSI HYVYDPMHAA SYAAFSPIAW CLFFAWTVFT
721 AHLGYRNMVI DFFSWRGFRV TTRISYAVYL TQFPIFFYNV GRTRAPQYFE FIPAVIFNTN EYLVVFLASF LLTVLFETPF
801 INLKKLLFPS KSRTALQAET IRPLISGACS VR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
G.IAALAAIASLTT.V	Y	22.03	1114.6598	66.9	558.3745	2	28.85	2325	1	589	600	
total 1 peptides												

tr|A0A1E1X293|A0A1E1X293_9ACAR

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 PLSVEPPLPV VPRLCTLEFV RLPPKAASYV PFSSVPPVPD GPYVVTPALD ISLTRNIALA HTVVTMTANR AYLPVLNFAS
81 FVEPLPQGIS LATLSPAVDC VISAVTSSVP TFTGSLCAAV RPLDEYAKMI APNLPPPQAN DLRLLLSSFR DIFDFDERPL
161 ARTSVVKHRI NTGDAAPLHR RPYRVSSSER NIIQREVDKM LDRDIIEPSS SPWASPVVLV KKKDGSWRFC VDYRHLNRIT
241 KKDVYPLPRI DDALDCLHGA KYFSSIDLRS GYWQIAVDEQ DREKTAFVTP DGLYQFKVMP FGLCNAPATF ERMMDSLLRG
321 FKWSTCLCYL DDVVVFSPTF ATHLERLTSI LEVFRTAGLQ LNSSKCTFGS RQLTILGHLV DASGVRPDPT KIQAVRDFPP
401 PRTSKDVRSF IGLCSYFRRF IQDFAGIARP LTDLLKNDAP FTWGPAQENA FSTLIHSLTC PPILAHFDPS APTEVRTDAS
481 GYGIGAVLAQ RHQGHDRVIA YASRLLSAAE KNYSITEREC LALVWAVAKF RPYLFGRTFS VITDHHALCW LSSLKDPIGR
561 LGRWALRV**QE YSYTVVYK**SG RLHQDADCLS RYPVDPPDLG EADTVPCLLA ISALVNIADE QRQDPALRSL IDGLISGNTN

641 PSLKLFVLQD GILYRRNLHP DGPPLLLVVP QRLRSSVLEE LHDLPTAGHL GVSRTYDRVR RRFFWPGLYR SVKRYVTGCD
721 LCQRRKTPTT LPAGLLQPID VPLEPFYRIC LDLLGPFPTS QSGNKWIAVA TDYATQYAIT RAIPTSCATD VADFILQDII
801 LHHGAPRQLL TDRGRYFLSR VVDDILRSCS TQHKIATAYH PQTNGLTERL NRTLTDMLAM YVSPDHRDWD IALPYVTFAY
881 NSSRHDTTGY SPYYLLFGRH PTLPLDTLLP PSAVPTTSYA SDAIAHATQA RQIARSRLHA SQTYQKSAYD RRHRPVYYEP
961 GSVVLLWSPA RRVGLSEKLL CKYSGPFRVV RQVTDVTYEI APLAPSPSFP RTATDIVHVA RLKPYVSPAS ST

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
V.QEYSYTVVYK.S	Y	21.01	1278.6132	832.0	640.8458	2	30.34	2497	1	569	578	
total 1 peptides												

tr|Q17T64|Q17T64_9HYME

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ADCAVLIVAA GTGEFEAGIS KNGQTREHAL LAFTLGVKQL IVGVNKMDST EPPYSETRFE EIKKEVSSYI KKIGYNPVAV
81 AFVPISGWHG DNMLEVSGKM PWFKGWTVER KEGKVEGKCL IEALDAILPP TRPTDKALRL PLQDVYK**IGG IGTVPVGR**VE

161 TGVLKPGMVV TFAP

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	148	158	
total 1 peptides												

tr|A0A0H3VAG6|A0A0H3VAG6_9ODON

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 EAGISKNGQT REHALLAFTL GVKQLIVGVN KMDSTEPPYS EARFEEIKKE VGNYIKKIGY NPAAVAFVPI SGWHGDNMLE
81 ASDKMPLFKG WKVERKEGNA DGKCLIEALD AILPPSRPTE KPLRLPLQDV YK**IGGIGTVP VGR**VETGVMK PGMLVTFAPA

161 NLTTEVKSVE MHHEALQEAL PGDNVGF

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	133	143	
total 1 peptides												

tr|A0A221J585|A0A221J585_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DNMLEASTNM PWFKGWTIER KEGNAEGKTL IDALDAILPP THPTEKRLRL RLQDVYK**IGG IGTVPVGR**VA TGILKPDTVV

81 VFAPANITTE VKSVEMHHET LAEAVPGDNV GFKVKNVSVK ELRRGYVAGD SKASPPRGAA DFTAQVIVLN HPGQISNGYT
161 PVLDCHTAHI ACKFAEIKEK VDRRSGKTTE ENPKFIKSGD AAIVNLVPSK PLCVEAFQEF PPLGRFAVRD M

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	58	68	
total 1 peptides												

tr|D4P281|D4P281_HYPSO

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 ERERGITIDI ALWKFETAKY YVTIIDAPGH RDFIKNMITG TSQADCAVLI VAAGTGEFEA GISKNGQTRE HALLAFTLGV
81 KQLIVGVNKM DSTEPPYSEP RFEEIKKEVS SYIKKIGYNP AAVAFVPISG WHGDNMLEPS TKMPWFKGWQ VERKEGKAEG
161 KCLIEALDAI LPPARPTDKP LRLPLQDVYK **IGGIGTVPVG R**VETGILKPG TIVVFAPANI TTEVKSVEMH HEALQEAVPG

241 DNVG

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	191	201	
total 1 peptides												

tr|D4P296|D4P296_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 LDKLKSERER GITIDIALWK FETAKYYVTI IDAPGHRDFI KNMITGTSQA DCAVLIVTAG TGEFEAGISK NGQTREHALL
81 AFTLGVKQLI VGVNKMDSTE PPYSEPRFEE IKKEVSSYIK KIGYNPAAVA FVPISGWHGD NMLEPSTKMP WFKGWQVERK
161 EGKAEGKCLI EALDAILPPA RPTDKPLRLP LQDVYK**IGGI GTVPVGR**VET GILKPGTIVV FAPANITTEV KSVEMHHEAL
241 QEAVPGDNVG FNVKNVS

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	197	207	
total 1 peptides												

tr|A0A0C5DAT0|A0A0C5DAT0_HELNM

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RERGITIDIA LWKFETAKYY VTIIDAPGHR DFIKNMITGT SQADCAVLIV AAGTGEFEAG ISKNGQTREH ALLAFTLGVK
81 QLIVGVNKMD STEPPYNEAR FEEIKKEVSS YIKKIGYNPA AVAFVPISGW HGDNMLEAST KMPWFKGWQV ERKEGKADGK
161 CLIEALDAIL PPARPTDKAL RLPLQDVYK**I GGIGTVPVGR** VETGVLKPGT IVVFAPANIT TEVKSVEMHH EALQEAVPGD
241 NVGFNVKNVS VKELRR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	190	200	
total 1 peptides												

tr|D5GRK8|D5GRK8_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GTGEFEAGIS KNGQTREHAL LAFTLGVKQL IVGVNKMDST EPPYSEPRFE EIKKEVSSYI KKIGYNPAAV AFVPISGWHG
81 DNMLEASTKM PWFKGWQVER KEGKAEGKCL IEALDAILPP ARPTDKALRL PLQDVYK**IGG IGTVPVGR**VE TGVLKPGTIV
161 VFAPANITTE VKSVEMHHEA LQEAVPGDNV GFNVKNVSVK ELRRGYVAGD SKNSPPKGAA DFTAQVIVLN HPGQISNGYT
241 PVLDCHSAHI ACKFAEIKEK VDRRSGKSTE

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	138	148	
total 1 peptides												

tr|D7GJQ5|D7GJQ5_9DIPT

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QYAWVLDKLK AERERGITID IALWKFETGR YYVTIIDAPG HRDFIKNMIT GTSQADCAVL IVAAGTGEFE AGISKNGQTR
81 EHALLAFTLG VKQLIVGVNK MDSTDPPFSE PRFEEIKKEV SSYIKKIGYN PLAVAFVPIS GWHGDNMLEP SEKMPWFKGW
161 AVERKDGNGS GKCLIEALDA ILPPSRPTDK ALRLPLQDVY K**IGGIGTVPV GR**VETGVLKP GMVVVFAPVM LTTEVKSVEM
241 HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDTKT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	202	212	
total 1 peptides												

tr|A0A1S6JYA4|A0A1S6JYA4_9CUCU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 VLDKLKAERE RGITIDIALW KFETAKYYVT IIDAPGHRDF IKNMITGTSQ ADCAVLIVAA GTGEFEAGIS KNGQTREHAL

81 LAFTLGVKQL IVGVNKMDST EPPYSEPRFE EIKKEVSSYI KKIGYNPAAV AFVPISGWHG DNMLEPSAKM PWFKGWNVER

161 KEGKAEGKCL IEALDAILPP SRPTDKPLRL PLQDVYK**IGG IGTVPVGR**VE TGVLKPGTVV VFAPANITTE VKSVEMHHEA

241 LQEAVPGDNV GFNVKNVSVK ELRRGYVAGD SKNNPPRGAS D

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	198	208	
total 1 peptides												

tr|Q9U8J1|Q9U8J1_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 DIALWKFETA KYYVTIIDAP GHRDFIKNMI TGTSQADCAV LIVAAGTGEF EAGISKNGQT REHALLAFTL GVKQLIVGVN

81 KMDSTEPPYS ESRFEEIKKE VSSYIKKIGY NPAAVAFVPI SGWNGDNMLE VSEKMSWFKG WAVERKEGKA DGKCLIEALX

161 AILPPSRPTD KALRLPLQDV YK**IGGIGTVP VGR**VETGLLK PGMVVVFAPA NITTEVKSVE MHHEALTEAY PGDNVGFNVK

241 NVSVKELRRG FVAGDTKNNP PKGAADFTAQ VIVLNHPGQI SNGYTPVLDC HT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	183	193	
total 1 peptides												

tr|A0A0G2T5E8|A0A0G2T5E8_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 YVTIIDAPGH RDFIKNMITG TSQADCAVLI VAAGTGEFEA GISKNGQTRE HALLAFTLGV KQLIVGVNKM DSTEPPYSEP

81 RFEEIKKEVS SYIKKIGYNP AAVAFVPISG WHGDNMLEPS TKMPWFKGWL VERKEGKAEG KCLIEALDAI LPPARPTDKP

161 LRLPLQDVYK **IGGIGTVPVG R**VETGILKPG TIVVFAPANI TTEVKSVEMH HEALQEAVPG DNVGFNVKNV SVKELRRGYV

241 AGDSKNNPPK GAADFTAQVI VLNHPGQISN GYTPVLDCHT AHIACKFAEI KEKVDRRTGK STEDNPKSIK SGDAAIVNLV

321 PSKPLCVES

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	171	181	
total 1 peptides												

tr|B3FBI9|B3FBI9_9MUSC

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KCGGIDKRTI EKFEKEAQEM GKGSFKYAWV LDKLKAERER GITIDIALWK FETAKYYVTI IDAPGHRDFI KNMITGTSQA

81 DCAVLIVAAG TGEFEAGISK NGQTREHALL AFTLGVKQLI VGVNKMDSSE PPYSESRYEE IKKEVSSYIK KIGYNPAAVA

161 FVPISGWHGD NMLEPSTNMP WFKGWKVERK EGNAEGKTLI DALDAILPPS RPTEKPLRLP LQDVYK**IGGI GTVPVGR**VET

241 GILKPGMVVV FAPANITTEV KSVEMHHEAL PEAVPGDNVG FNVKNVSVKE LRRGFVAGDS KSNPPRGAAD FTAQVIVLNH

321 PGQISNGYTP VLDCHT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	227	237	
total 1 peptides												

tr|A0A0S1NH65|A0A0S1NH65_9HEMI

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 RTIEKFEKEA QEMGKGSFKY AWVLDKLKAE RERGITIDIA LWKFETAKYY VTIIDAPGHR DFIKNMITGT SQADCAVLIV

81 AAGTGEFEAG ISKNGQTREH ALLAFTLGVK QLIVGVNKMD NTEPQYSEPR FEEIKKEVSN YIKKIGYNPA AVAFVPISGW

161 NGDNMLEPSD KMPWFKGWNI ERKEGKAEGK TLIEALDAIL PPSRPTEKPL RLPLQDVYK**I GGIGTVPVGR** VETGVLKPGM

241 VVTFAPANIT TEVKSVEMHH EALQEAVPGD NVGFNVKNVS VKELRRGFVA GDSKNNPPKA AADFTAQVIV LNHPGQISNG

321 YTPVLDCHTA HIACKFAEIK EKCDRRT

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	220	230	

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
total 1 peptides												

tr|E9JV44|E9JV44_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IDIALWKFET AKYYVTIIDA PGHRDFIKNM ITGTSQADCA VLIVAAGTGE FEAGISKNGQ TREHALLAFT LGVKQLIVGV
81 NKMDSTEPPY NEGRFEEIKK EVSSYIKKIG YNPAAVAFVP ISGWHGDNML EASTKMPWFK GWQVERKEGK AEGKCLIEAL
161 DAILPPARPT DKALRLPLQD VYK**IGGIGTV PVGR**VETGVL KPGTIVVFAP AQITTEVKSV EMHHEALQEA VPGDNVGFNV

241 KNVSVKELRR GYVAGDSKNN PPKGAADFTA QVIVLNHPGQ ISNGYTPVLD CHTAHIACKF AEIKEKVDRR SGKSTEENPK
321 SIKSGDAAIV NLVPSKPLCV ESFQEFPPLG RFAIR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	184	194	
total 1 peptides												

tr|D5GR67|D5GR67_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 TIDIALWKFE TAKFYVTIID APGHRDFIKN MITGTSQADC AVLIVAAGTG EFEAGISKNG QTREHALLAF TLGVKQLIVG
81 VNKMDSTEPP YSEPRFEEIK KEVSSYIKKI GYNPAAVAFV PISGWHGDNM LEASTKMPWF KGWQVERKEG KAEGKCLIEA
161 LDAILPPARP TDKALRLPLQ DVYK**IGGIGT VPVGR**VETGV LKPGTIVVFA PANITTEVKS VEMHHEALQE AVPGDNVGFN

241 VKNVSVKELR RGYVAGDSKN SPPKGAADFT AQVIVLNHPG QISNGYTPVL DCHTAHIACK FAEIKEKVDR RSGKSTEDNP
321 KSIKSGDAAI VNLVPSKPLC VEAFQEFPPL GRFAVRD

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	185	195	
total 1 peptides												

tr|D1GKQ7|D1GKQ7_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 QEMGKGSFKY AWVLDKLKAE RERGITIDIA LWKFETAKYY VTIIDAPGHR DFIKNMITGT SQADCAVLIV AAGTGEFEAG
81 ISKNGQTREH ALLAFTLGVK QLIVGVNKMD STEPAYSEPR FEEIKKEVSS YIKKIGYNPA AVAFVPISGW HGDNMLEPSS
161 KMPWFKGWNV ERKEGKAEGK CLIEALDAIL PPARPTDKAL RLPLQDVYK**I GGIGTVPVGR** VETGILKPGT IVVFAPANLT

241 TEVKSVEMHH EALQEAVPGD NVGFNVKNVS VKELRRGYVA GDTKANPPKG ASDFTAQVIV LNHPGQIANG YTPVLDCHTA
321 HIACKFAEIQ QKVDRRTGKS TEDNPKSIKS GDAAIVNLVP SKPMCV

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	210	220	
total 1 peptides												

tr|A0A068J3Y4|A0A068J3Y4_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 IYKCGGIDKR TIEKFEKEAQ EMGKGSFKYA WVLDKLKAER ERGITIDIAL WKFETAKYYV TIIDAPGHRD FIKNMITGTS
81 QADCAVLIVA AGTGEFEAGI SKNGQTREHA LLAFTLGVKQ LIVGVNKMDS TEPPYSESRF EEIKKEVSSY IKKIGXXPAA
161 VXFVXITGWH GDNMLEPSTK MPWFKGWQVE RKEGKAEGKC LIEALDAILP PARPTDKALR LPLQDVYK**IG GIGTVPVGR**V

241 XTGVLKPGTI VXFAPANITT EVKSVEMHHE ALQEAVPGDN VGFNVKNVSV KELRRGYXXG DSKNNPPKGA ADFTAQVIVL
321 NHPGQISNGY TPVLDCHTAH IACKFAEIKE KVDRRTGKST EDNPKSIKSG DAAIVNLVPS KPLCVESFQE FPPLGRFAVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	229	239	
total 1 peptides												

tr|Q2VKY2|Q2VKY2_TITHA

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 GHLIYKCGGI DKRTIEKFEK EAQEMGKGSF KYAWVLDKLK AERERGITID IALWKFETSK FYVTIIDAPG HRDFIKNMIT

81 GTSQADCAVL IVAAGTGEFE AGISKNGQTR EHALLAFTLG VKQLIVGVNK MDSTEPPYSE SRFEEIKKEV PSYIKKIGYN

161 PAAVAFVPIS GWHGATMLEP SPKMPWFKGW PVERKEGKAD GKCLIEALDA ILPPARPTDK ALRLPLQDVY K**IGGIGTVPV**

241 **GR**VETGVLKP GTIVVFAPAN ITTEVKSVEM HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDSKNSPP KGAADFXAQV

321 IVLNHPGQIS NGYTPVLDCH TAHIACKFAE IKEKVDRRSG KSTEDNPKSI KSGDAAIVNL VPSKPLCVEA FQEFPPLGRF

401 A

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	232	242	
total 1 peptides												

tr|Q2LB41|Q2LB41_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KSTTTGHLIY KCGGIDKRTI EKFEKEAQEM GKGSFKYAWV LDKLKAERER GITIDIALWK FETAKYYVTI IDAPGHRDFI

81 KNMITGTSQA DCAVLIVAAG TGEFEAGISK NGQTREHALL AFTLGVKQLI VGVNKMDSTE PPYSEPRFEE IKKEVSSYIK

161 KIGYNPAAVA FVPISGWHGD NMLEASTKMP WFKGWQVERK EGKAEGKCLI EALDAILPPA RSTDKALRLP LQDVYK**IGGI**

241 **GTVPVGR**VET GVLKPGTVVV FAPANITTEV KSVEMHHEAL SEAVPGDNVG FNVKNVSVKE LRRGYVAGDS KNNPPKGAAD

321 FTAQVIVLNH PGQISNGYTP VLDCHTAHIA CKFAEIKEKV DRRSGKSTED NPKSIKSGDA AIVNLVPSKP LCVEAFQEFP

401 PLGRFAVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	237	247	
total 1 peptides												

tr|B5LXT8|B5LXT8_COETU

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 KSTTTGHLIY KCGGIDKRTI EKFEKEAQEM GKGSFKYAWV LDKLKAERER GITIDIALWK FETAKYYVTI IDAPGHRDII

81 KNMITGTSQA DCAVLIVAAG TGEFEAGISK NGQTREHALL AFTLGVKQLI VGVNKMDSTE PXYSDLRFEE ITKEVSSYIK

161 KIGYNPAAVA FVPISGWHGD NMLEPSTKMP WFKGWQVERK EGKAERKCLI EALDAILPPA RPTDKPLRLP LQDVYK**IGGI**

241 **GTVPVGR**VET GVLKPGTIVV FAPANITTEV KSVEMHHEAL SEAVPGDNVG FNVKNVSVKE LRRGYVAGDS KNNPPKGAAD

321 FTAQVIVLNH PGQISNGYTP VLDCHTAHIA CKFAEIKEKV DRRSGKSTEE NPKSIKSGDA AIVNLVPSKP LCVEAFQEFP

401 PLGPFAVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	237	247	
total 1 peptides												

tr|A0A0K0MVA6|A0A0K0MVA6_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HVDSGKSTTT GHLIYKCGGI DKRTIEKFEK EAQEMGKGSF KYAWVLDKLK AERERGITID IALWKFETAK YYVTIIDAPG

81 HRDFIKNMIT GTSQADCAVL IVAAGTGEFE AGISKNGQTR EHALLAFTLG VKQLIVGVNK MDSTEPPYSE SRFEEIKKEV

161 SSYIKKIGYN PAAVAFVPIS GWHGDNMLEA STKMPWFKGW AVERKEGKAD GKCLIEALDA ILPPARPTDK ALRLPLQDVY

241 K**IGGIGTVPV GR**VETGVLKP GTVVVFAPAN ITTEVKSVEM HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDSKNNPP

321 KGAADFTAQV IVLNHPGQIS NGYTPVLDCH TAHIACKFAE IKEKVDRRSG KSTEENPKSI KSGDAAIVNL QPSKPLCVEA

401 FQEFPPLGRF AVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	242	252	
total 1 peptides												

tr|A0A0K0MU56|A0A0K0MU56_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HVDSGKSTTT GHLIYKCGGI DKRTIEKFEK EAQEMGKGSF KYAWVLDKLK AERERGITID IALWKFETAK YYVTIIDAPG
81 HRDFIKNMIT GTSQADCAVL IVAAGTGEFE AGISKNGQTR EHALLAFTLG VKQLIVGVNK MDSTEPPYSE PRFEEIKKEV
161 SSYIKKIGYN PAAVAFVPIS GWHGDNMLEP STKMPWFKGW AVERKEGKAD GKCLIEALDA ILPPARPTDK ALRLPLQDVY
241 K**IGGIGTVPV GR**VETGVLKP GTVVVFAPAN ITTEVKSVEM HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDSKNNPP
321 KGAADFTAQV IVLNHPGQIS NGYTPVLDCH TAHIACKFAE IKEKVDRRSG KSTEENPKSI KSGDAAIVIL QPSKPLCVEA
401 FQEFPPLGRF AVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	242	252	
total 1 peptides												

tr|Q58GU4|Q58GU4_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HVDSGKSTTT GHLIYKCGGI DKRTIEKFEK EAQEMGKGSF KYAWVLDKLK AERERGITID IALWKFETAK YYVTIIDAPG
81 HRDFIKNMIT GTSQADCAVL IVAAGTGEFE AGISKNGQTR EHALLAFTLG VKQLIVGVNK MDSTEPPYSE SRFEEIKKEV
161 SSYIKKIGYN PAAVAFVPIS GWHGDNMLEV STKMPWFKGW NVERKEGKAD GKCLIEALDA ILPPARPTDK ALRLPLQDVY
241 K**IGGIGTVPV GR**VETGILKP GTIVVFAPAN ITTEVKSVEM HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDSKNNPP
321 KGAADFTAQV IVLNHPGAIS NGYTPVLDCH TAHIACKFAE IKEKVDRRTG KSTEENPKSI KSGDAAIVNL VPSKPLCVES
401 FQEFPPLGRF AVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	242	252	
total 1 peptides												

tr|B8Y157|B8Y157_9NEOP

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 HVDSGKSATT GHLIYKCRGI DKRTIEKFEK EAQEMGKGSF KYAWVLDKLK AERERGITID IALWKFETSK YYVTIIDAPG
81 HRDFIKNMIT GTSQADCAVL IVAAGTGEFE AGISKNGQTR EHALLAFTLG VKQLIVGVNK MDSTEPPYSE SRFEEIKKEV
161 SSYIKKIGYN PAAVAFVPIS GWHGDNMLEP STKMPWFKGW QVERKEGKAE GKCLIEALDA ILPPARPTDK ALRLPLQDVY
241 K**IGGIGTVPV GR**VETGVLKP GTIVVFAPAN ITTEVKSVEM HHEALQEAVP GDNVGFNVKN VSVKELRRGY VAGDSKNNPP
321 KGAADFTAQV IVLNHPGQIS NGYTPVLDCH TAHIACKFAE IKEKVDRRTG KSTEENPKSI KSGDAAIVNL VPSKPLCVES
401 FQEFPPLGRF AVR

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.IGGIGTVPVGR.V	Y	20.63	1024.6029	282.5	513.4534	2	30.78	2547	1	242	252	
total 1 peptides												