Summary

1. Notes

2. Result Statistics

Protein List

Protein Accession Contains:

Protein Description Contains:

Protein Sample Area >=

Protein PTM Contains:

Figure S8. False discovery rate (FDR) curve. X axis is the number of peptide-spectrum matches (PSM) being kept. Y axis is the corre sponding FDR.

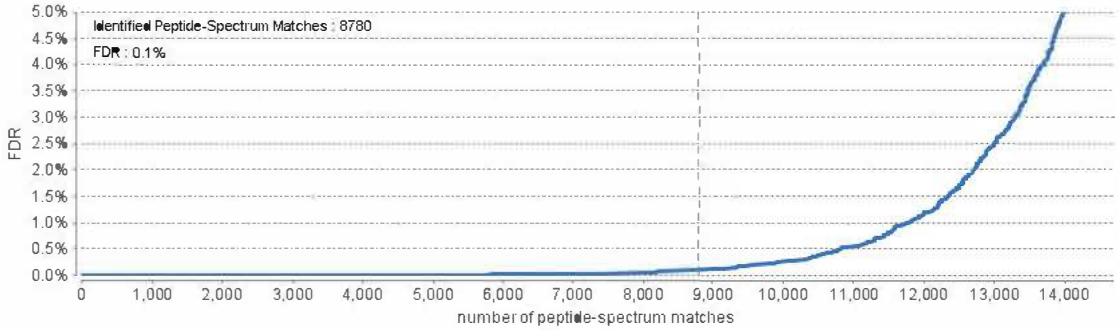
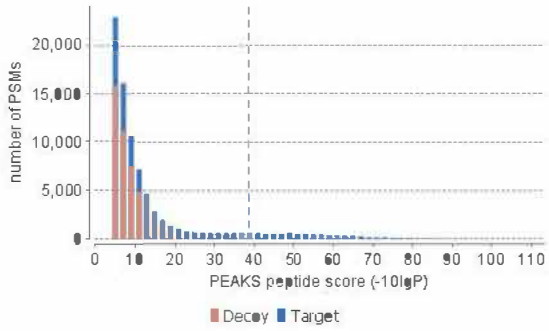


Figure S9. PSM score distribution. **(a)** Distribution of PEAKS peptide score; **(b)** Scatterplot of PEAKS peptide score versus precursor mass error.

(a)



(b)

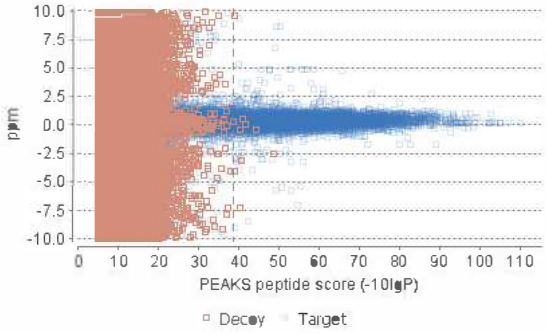


Table S5. Statistics of data.

	#Scans		#Features	Identified			#Peptides	#Sequences	#Proteins*		
	MS1	MS2		#PSMs	#Scans	#Features			Groups	All	Top
Total	61192	194255	216084	8780	8613	17484	1139	1016	164	1225	501
F1	7283	29947	27286	1302	1268	2226	443	403	82	583	228
F2	8579	27501	25645	1296	1262	1693	414	362	84	586	213
F3	7215	29271	40734	1484	1472	2985	422	374	84	578	237
F4	7830	28612	34895	1302	1292	2937	485	432	101	693	343
F5	10472	25367	27892	1009	976	2239	278	251	82	519	263
F6	10484	26040	26892	832	814	2188	293	269	74	467	280
F7	9329	27517	32740	1555	1529	3216	344	313	91	466	246

* proteins with significant peptides are used in counts.

Figure S10. Sample overlap for Proteins and Peptides (up to 8 samples). **(a)** All Proteins; **(b)** Top Proteins; **(c)** Peptides;

(a)

	1	2	3	4	5	6	7	Unique
1	583	421	408	420	290	264	162	94
2	421	586	435	446	318	269	170	69
3	408	435	578	461	345	294	227	39
4	420	446	461	693	404	414	263	38
5	290	318	345	404	519	376	279	16
6	264	269	294	414	376	467	247	19
7	162	170	227	263	279	247	466	138

(b)

	1	2	3	4	5	6	7	Unique
1	228	168	152	192	128	148	93	27
2	168	213	165	190	128	132	90	13
3	152	165	237	220	168	169	133	8
4	192	190	220	343	226	253	159	14
5	128	128	168	226	263	228	168	4
6	148	132	169	253	228	280	159	4
7	93	90	133	159	168	159	246	54

(c)

	1	2	3	4	5	6	7	Unique
1	443	255	220	239	158	143	122	122
2	255	414	259	254	154	130	115	71
3	220	259	422	274	162	141	115	82
4	239	254	274	485	205	199	151	85
5	158	154	162	205	278	177	146	27
6	143	130	141	199	177	293	139	50
7	122	115	115	151	146	139	344	154

Figure S11. Distribution of peptide feature detection. **(a)** Feature m/z distribution; **(b)** Feature RT distribution.

(a) **(b)**

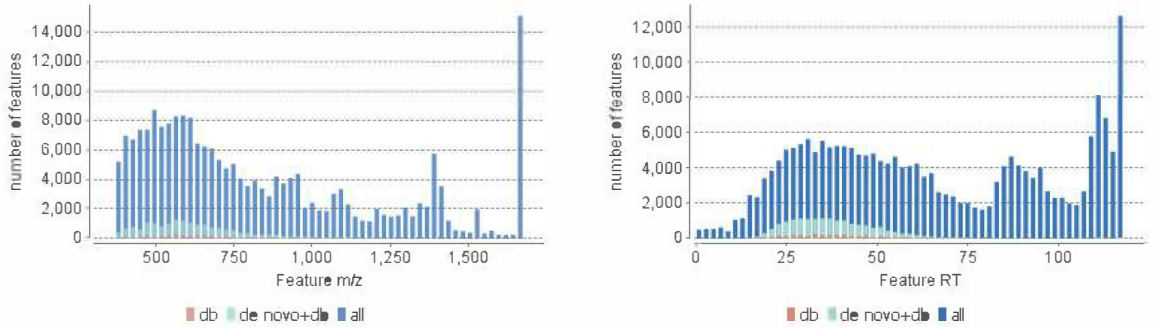


Figure S12. Distribution of identified peptide features. **(a)** Feature abundance distribution; **(b)** *De novo* sequencing validation.

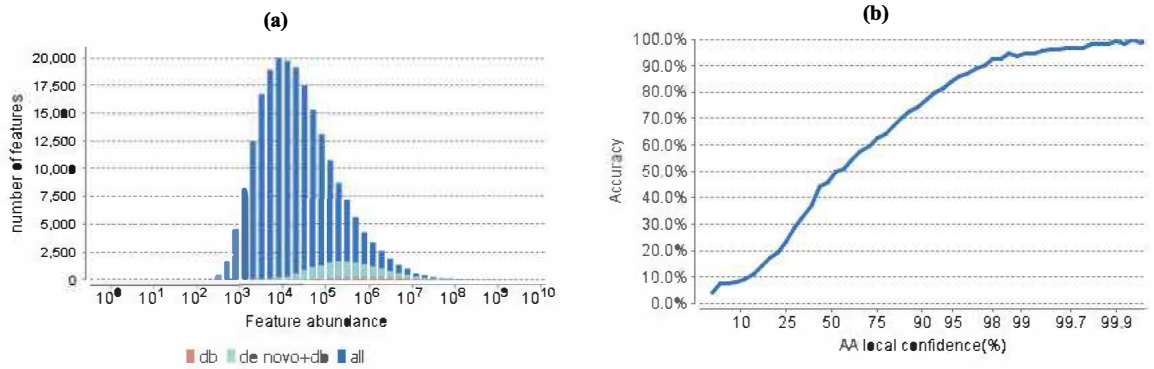


Table S6. Result filtration parameters.

Peptide -10lgP	≥38.7
PTM Ascore	≥0
Protein -10lgP	≥20
Proteins unique peptides	≥1
De novo score(%)	≥50%

Table S7. Statistics of filtered result.

FDR (Peptide-Spectrum Matches)	0.1%
FDR (Peptide Sequences)	0.8%
FDR (Protein Group)	6.0%
De Novo Only Spectra	25886

Table S8. PTM profile.

Name	ΔMass	Position	#PSM	-10lgP	Abundance	AScore
Oxidation	15.99	M	1758	89.44	5.86E6	1000.00
Carbamidomethyl	57.02	C	28	60.69	1.42E6	1000.00

3. Experiment Control

Figure S13. 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.

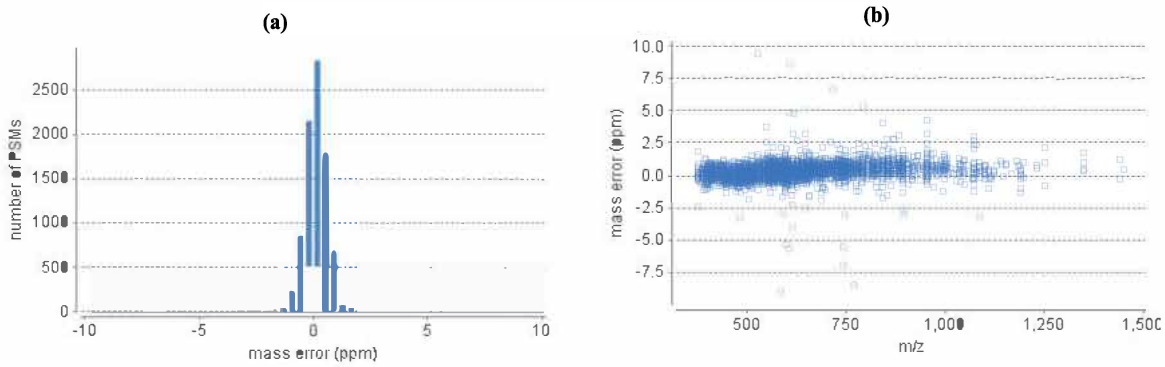


Table S9. Number of identified peptides in each sample by the number of missed cleavages.

Missed Cleavages	0	1	2	3	4+
F1	313	113	15	2	0
F2	325	78	11	0	0
F3	308	96	18	0	0
F4	381	94	9	1	0
F5	235	39	4	0	0
F6	239	49	5	0	0
F7	276	60	8	0	0

4. Other Information

Table S10. Search parameters.

Search Engine Name: PEAKS
Parent Mass Error Tolerance: 10.0 ppm
Fragment Mass Error Tolerance: 0.6 Da
Precursor Mass Search Type: monoisotopic
Enzyme: Trypsin
Max Missed Cleavages: 3
Digest Mode: Semispecific
Fixed Modifications:
Carbamidomethylation: 57.02
Variable Modifications:
Oxidation (M): 15.99
Max Variable PTM Per Peptide: 3
Database: Dpal_Serpent_NR
Taxon: All
Contaminant Database: cRAP_contaminants
Searched Entry: 572962
FDR Estimation: Enabled
Merge Options: no merge
Precursor Options: corrected
Charge Options: no correction
Filter m/z: 200.0 - 1800.0
Filter Charge: 1 - 8
Process: true
Associate chimera: yes

Table S11. Instrument parameters.

Fractions: 12112021_RID_2349_DP1.raw, 12112021_RID_2349_DP2.raw, 17112021_RID_2349_DP3.raw, 17112021_RID_2349_DP4.raw, 17112021_RID_2349_DP5.raw, 17112021_RID_2349_DP6.raw, 17112021_RID_2349_DP7.raw
Ion Source: ESI(nano-spray)
Fragmentation Mode: CID, CAD(y and b ions)
MS Scan Mode: FT-ICR/Orbitrap
MS/MS Scan Mode: FT-ICR/Orbitrap

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
1	69771	TRINITY_DN9	397.42	65	42	40	48	38	21	15	7	6.0902E8	1.4832E8	2.8298E8	1.4
21	69773	TRINITY_DN233	359.11	51	42	45	24	26	5	4	3	1.5641E8	4.5667E7	1.4274E7	4.2
27	7	AHJ80886.1	337.24	49	38	34	36	40	16	3	9	6.4491E7	1.3431E7	2.4346E7	1.3
12	5	G8XQX1.1	332.80	56	28	25	27	23	13	9	17				
12	6	ACF70483.1	332.80	56	28	25	27	23	13	9	17				
18	69775	TRINITY_DN0	307.80	38	16	31	27	23	11	6	4	9.7514E5	9.7519E7	3.3637E7	1.3
50	69777	TRINITY_DN132	293.50	30	24	11	13	7	0	0	0	8.2659E7	8.1798E6	8.9798E6	3.8
17	69809	TRINITY_DN441	270.06	71	29	29	29	71	37	38	0	1.7543E6	2.3578E6	5.09E8	1.3
101	69780	TRINITY_DN1507	257.03	24	24	5	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
101	69780	TRINITY_DN1507	257.03	24	24	5	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
101	69782	TRINITY_DN1507	257.03	22	22	5	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
101	69783	TRINITY_DN1507	257.03	21	21	4	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
101	69784	TRINITY_DN1507	257.03	22	22	5	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
101	69785	TRINITY_DN1507	257.03	20	20	4	1	1	0	0	0	2.7944E7	1.0493E5	4.3717E4	1.4
61	69796	TRINITY_DN30	254.87	13	10	10	13	10	6	1	0	2.1784E5	1.6365E6	7.4177E6	3.3
61	239	TRINITY_DN30	254.87	13	10	10	13	10	6	1	0	2.1784E5	1.6365E6	7.4177E6	3.3
39	70	BAN82155.1	251.91	22	6	17	12	11	5	2	0		3.5059E4		

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
79	69799	TRINITY_DN266	248.99	36	22	25	16	30	18	0	4	4.5074E6	4.1083E6	2.5052E6	4.8
5	69839	TRINITY_DN240	245.05	44	13	13	44	28	20	8	6	2.2296E6	1.724E7	8.9727E9	2.7
68	69803	TRINITY_DN59	243.26	37	6	0	0	0	16	37	9	2.9622E6			
68	69804	TRINITY_DN59	243.26	37	6	0	0	0	16	37	9	2.9622E6			
68	69803	TRINITY_DN59	243.26	37	6	0	0	0	16	37	9	2.9622E6			
43	69825	TRINITY_DN1385	231.26	40	37	32	33	31	31	0	0	2.7681E7	2.4791E7	1.6852E8	2.7
90	304	QHR82712.1	229.92	32	17	25	16	24	13	0	0		6.057E5	4.6515E6	
86	129	AFE84762.1	229.84	35	0	35	9	10	3	0	0		3.0729E6		
14	69867	TRINITY_DN554	226.40	16	0	0	0	0	16	11	11				
144	69793	TRINITY_DN1031	219.72	19	0	6	12	6	0	0	0		1.7546E6	7.494E7	1.6
144	69793	TRINITY_DN1031	219.72	19	0	6	12	6	0	0	0		1.7546E6	7.494E7	1.6
144	69793	TRINITY_DN1031	219.72	19	0	6	12	6	0	0	0		1.7546E6	7.494E7	1.6
32	382	Q9PT40.1	215.17	26	8	17	23	18	11	3	0	3.788E5	1.6386E8	5.3429E8	5.4
32	383	CAB62591.1	215.17	26	8	17	23	18	11	3	0	3.788E5	1.6386E8	5.3429E8	5.4
46	505	P0DL42.1	206.88	39	0	0	0	7	0	0	39				
75	285	Q4VM07.1	205.78	12	9	6	9	4	2	4	1	2.3772E6	4.2446E5	8.333E6	2.5
75	286	AAX38182.1	205.78	12	9	6	9	4	2	4	1	2.3772E6	4.2446E5	8.333E6	2.5
25	70177	TRINITY_DN459	199.41	11	11	11	11	11	11	11	11	1.2856E8	3.7626E6	6.1058E7	4.1
25	70311	TRINITY_DN1910	199.41	23	23	23	23	23	23	23	23	1.2856E8	3.7626E6	6.1058E7	4.1
180	69790	TRINITY_DN509	198.91	18	0	6	0	12	3	0	0		1.3078E5		5.3
180	69791	TRINITY_DN509	198.91	17	0	6	0	11	2	0	0		1.3078E5		5.3
41	465	ADK22823.1	197.97	31	0	0	0	0	5	14	21				
41	466	ABA86561.1	197.97	31	0	0	0	0	5	14	21				
41	467	Q38L02.1	197.97	31	0	0	0	0	5	14	21				

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
41	476	ADK22821.1	197.97	31	0	0	0	0	5	14	21				
22	442	AAZ53176.1	195.25	40	9	9	9	9	9	9	40	5.8348E5	5.2464E4	1.2575E6	2.1
22	443	A8CG78.1	195.25	40	9	9	9	9	9	9	40	5.8348E5	5.2464E4	1.2575E6	2.1
22	444	AAZ53181.1	195.25	40	9	9	9	9	9	9	40	5.8348E5	5.2464E4	1.2575E6	2.1
22	445	A8CG87.1	195.25	40	9	9	9	9	9	9	40	5.8348E5	5.2464E4	1.2575E6	2.1
91	69842	TRINITY_DN64	193.05	37	8	8	19	19	37	8	8			5.8246E5	1.5
91	525	B4XSY9.1	193.05	30	6	6	15	15	30	6	6			5.8246E5	1.5
91	526	ABW82661.1	193.05	30	6	6	15	15	30	6	6			5.8246E5	1.5
91	527	B4XSZ0.1	193.05	30	6	6	15	15	30	6	6			5.8246E5	1.5
91	528	ABW82662.1	193.05	30	6	6	15	15	30	6	6			5.8246E5	1.5
195	223	TRINITY_DN91	192.10	8	8	0	0	0	0	0	0	5.1733E5			
195	223	TRINITY_DN91	192.10	8	8	0	0	0	0	0	0	5.1733E5			
195	223	TRINITY_DN91	192.10	8	8	0	0	0	0	0	0	5.1733E5			
195	223	TRINITY_DN91	192.10	8	8	0	0	0	0	0	0	5.1733E5			
195	223	TRINITY_DN91	192.10	8	8	0	0	0	0	0	0	5.1733E5			
146	165	ETE57948.1	190.95	30	6	30	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	166	JAC96363.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	167	JAA97900.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	168	LAA21099.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	169	JAI10342.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	170	JAG68843.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	171	XP_013921350.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	172	JAB54771.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	173	JAA97901.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	174	JAG68844.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	175	LAA21098.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	176	JAV51374.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	177	JAG47580.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	178	AFJ49303.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	179	JAI14496.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	180	JAI10341.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	181	JAI14495.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	182	JAC96364.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
146	183	JAG47579.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	184	JAV51372.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	185	AFJ49302.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	186	BAQ22177.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	187	JAG45996.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	188	JAG45999.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	189	JAB54395.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
146	190	ETE74025.1	190.95	29	6	29	6	13	3	9	0	3.5744E5	4.2136E6	1.2599E5	5.4
78	529	ADK22827.1	188.30	28	6	6	6	13	28	13	13				1.4
78	530	ADK22825.1	188.30	28	6	6	6	13	28	13	13				1.4
60	540	ADN04916.1	186.74	21	4	21	13	12	3	0	0	5.4582E5	1.8664E8	4.7221E7	2.0
60	541	E0Y418.1	186.74	21	4	21	13	12	3	0	0	5.4582E5	1.8664E8	4.7221E7	2.0
11	394	ADK22824.1	186.62	35	0	0	0	0	5	0	35				
11	395	AAY63876.1	186.62	35	0	0	0	0	5	0	35				
11	396	ADK22822.1	186.62	35	0	0	0	0	5	0	35				
11	397	Q4PRC6.1	186.62	35	0	0	0	0	5	0	35				
94	70178	TRINITY_DN459	183.64	13	13	13	13	13	13	10	6	1.125E6	1.1654E6	6.0058E5	1.5
155	69806	TRINITY_DN157	183.50	36	4	4	4	4	4	4	36				
107	430	P18964.1	181.11	18	0	0	18	18	0	0	18			2.9668E7	1.3
107	439	ADP88558.1	181.11	17	0	0	17	17	0	0	17			2.9668E7	1.3
107	441	P18965.2	181.11	17	0	0	17	17	0	0	17			2.9668E7	1.3
178	295	TRINITY_DN2646	180.73	28	0	19	28	0	0	0	0		3.8106E5	7.4529E6	
178	295	TRINITY_DN2646	180.73	28	0	19	28	0	0	0	0		3.8106E5	7.4529E6	
196	69797	TRINITY_DN300	179.20	13	13	0	0	0	0	0	0	1.7343E6			
196	69797	TRINITY_DN300	179.20	13	13	0	0	0	0	0	0	1.7343E6			
147	308	B8K1W0.1	178.02	10	10	3	4	2	0	0	1	1.2744E7	1.1059E5		2.1
147	309	AAZ39880.1	178.02	10	10	3	4	2	0	0	1	1.2744E7	1.1059E5		2.1
129	410	ACE73567.1	175.01	15	4	0	0	14	10	0	15				8.1

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
189	69815	TRINITY_DN324	174.06	15	0	13	6	0	0	0	0		1.5152E6	1.8195E6	
13	69822	TRINITY_DN441	172.25	35	11	18	26	22	16	22	0		1.2908E7	7.0313E9	2.2
113	348	AUF41660.1	170.03	10	6	3	7	5	4	3	4				
28	512	CAR40186.1	169.60	28	9	9	9	9	9	8	28	8.1854E6	6.5995E6	3.4681E7	2.1
28	513	B5U6Z2.1	169.60	28	9	9	9	9	9	8	28	8.1854E6	6.5995E6	3.4681E7	2.1
125	69855	TRINITY_DN59	169.25	23	0	0	0	7	6	23	14				9.8
157	69824	TRINITY_DN278	169.22	33	0	0	0	11	0	0	33				1.4
157	403	AJO70723.1	169.22	27	0	0	0	9	0	0	27				1.4
64	440	XP_034272439.1	168.51	5	3	3	2	4	4	4	5	5.1514E5	3.8767E5	3.8979E5	2.4
93	769	QBF53416.1	167.52	9	4	4	5	9	5	5	5				4.3
44	69826	TRINITY_DN59	166.98	37	0	0	0	0	6	34	15				
44	69826	TRINITY_DN59	166.98	37	0	0	0	0	6	34	15				
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
179	236	TRINITY_DN283	165.03	10	1	10	0	0	0	0	0	4.1868E4	2.2513E6		
134	69816	TRINITY_DN714	161.86	15	4	4	4	5	8	7	0				2.3
183	69817	TRINITY_DN249	161.22	28	0	0	28	0	0	0	0			4.6706E6	
183	69817	TRINITY_DN249	161.22	28	0	0	28	0	0	0	0			4.6706E6	
183	69817	TRINITY_DN249	161.22	28	0	0	28	0	0	0	0			4.6706E6	
173	69821	TRINITY_DN77	157.32	24	0	0	0	24	0	0	2				1.6

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
173	69823	TRINITY_DN77	157.32	31	0	0	0	31	0	0	3				1.(
152	69807	TRINITY_DN3925	157.17	14	10	5	10	3	0	0	0	1.8455E6	3.6002E5	4.3445E6	2.4
152	69808	TRINITY_DN3925	157.17	11	8	4	8	2	0	0	0	1.8455E6	3.6002E5	4.3445E6	2.4
36	419	APB93444.1	156.68	34	7	7	0	7	28	7	34				
226	69853	TRINITY_DN195	156.40	23	0	0	0	0	0	0	23				
137	69852	TRINITY_DN1793	155.08	21	4	0	0	21	10	0	10				1.5
114	69914	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
114	69914	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
114	69914	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
114	69914	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
114	69914	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
114	69919	TRINITY_DN240	153.29	22	8	22	22	21	0	8	8		8.1563E6	4.8348E7	7.9
133	468	ETE70217.1	151.88	1	0	0	0	1	1	1	1				
246	565	XP_034291429.1	148.76	5	5	0	0	0	0	0	0	6.0941E4			
246	566	XP_034291427.1	148.76	5	5	0	0	0	0	0	0	6.0941E4			
246	567	XP_034291428.1	148.76	5	5	0	0	0	0	0	0	6.0941E4			
194	69934	TRINITY_DN743	148.55	15	0	0	0	0	0	15	15				
194	69961	TRINITY_DN743	148.55	23	0	0	0	0	0	22	23				
26	69833	TRINITY_DN0	148.09	19	18	18	14	19	9	14	9	6.4332E6	1.8506E6	1.3941E8	5.3
26	69834	TRINITY_DN0	148.09	18	17	17	13	18	8	13	8	6.4332E6	1.8506E6	1.3941E8	5.3
89	918	CBM40646.1	146.67	12	0	5	9	7	0	3	0			0	
89	943	CBM40645.1	146.67	12	0	5	9	7	0	3	0			0	
89	944	AAR24534.1	146.67	12	0	5	9	7	0	3	0			0	
89	945	Q6T6S7.1	146.67	12	0	5	9	7	0	3	0			0	
224	69820	TRINITY_DN94	144.95	12	0	12	0	0	0	0	0		8.0435E5		
95	690	E5AJX2.1	137.19	13	0	4	9	8	0	0	0			5.4903E6	
95	691	CBW30778.1	137.19	13	0	4	9	8	0	0	0			5.4903E6	
185	69894	TRINITY_DN4675	137.11	13	0	0	0	0	13	0	0				

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
149	890	TRINITY_DN59	137.06	22	0	0	0	0	22	0	0				
149	890	TRINITY_DN59	137.06	22	0	0	0	0	22	0	0				
149	891	AJO70724.1	137.06	18	0	0	0	0	18	0	0				
49	69863	TRINITY_DN588	135.41	20	12	6	6	11	6	6	14				
49	69863	TRINITY_DN588	135.41	20	12	6	6	11	6	6	14				
218	514	TRINITY_DN6726	131.08	30	0	0	0	0	6	0	30				
201	341	TRINITY_DN3927	130.90	5	4	0	0	2	0	0	0	9.7972E5			1.1
167	69841	TRINITY_DN2452	130.54	24	14	12	19	0	4	0	0	5.2396E5	1.7998E6	2.7782E6	
48	759	P82475.2	130.50	26	17	8	8	8	8	8	17				
166	69828	TRINITY_DN30	128.97	8	6	6	2	0	0	0	0		0		
119	844	JAS04521.1	128.01	12	0	0	5	8	12	12	3				
119	845	AAG12169.1	128.01	12	0	0	5	8	12	12	3				
119	998	JAG46131.1	128.01	12	0	0	5	8	12	12	3				
119	999	BAN82015.1	128.01	12	0	0	5	8	12	12	3				
119	1000	JAS04781.1	128.01	12	0	0	5	8	12	12	3				
119	1001	JAI10407.1	128.01	12	0	0	5	8	12	12	3				
119	1002	JAS05454.1	128.01	12	0	0	5	8	12	12	3				
119	1003	JAS04703.1	128.01	12	0	0	5	8	12	12	3				
119	1004	JAG46130.1	128.01	12	0	0	5	8	12	12	3				
119	1005	JAA98018.1	128.01	12	0	0	5	8	12	12	3				
119	1006	AAG30924.1	128.01	12	0	0	5	8	12	12	3				
119	1007	JAS05315.1	128.01	12	0	0	5	8	12	12	3				
119	1008	JAV01886.1	128.01	12	0	0	5	8	12	12	3				
119	1009	JAS04865.1	128.01	12	0	0	5	8	12	12	3				
119	1010	JAA98019.1	128.01	12	0	0	5	8	12	12	3				
119	1011	JAA94888.1	128.01	12	0	0	5	8	12	12	3				
119	1012	JAS04864.1	128.01	12	0	0	5	8	12	12	3				
119	1013	AFJ49196.1	128.01	12	0	0	5	8	12	12	3				
119	1014	JAS04866.1	128.01	12	0	0	5	8	12	12	3				

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
119	1015	JAG43651.1	128.01	12	0	0	5	8	12	12	3				
119	1016	JAV48424.1	128.01	12	0	0	5	8	12	12	3				
119	1017	JAG46132.1	128.01	12	0	0	5	8	12	12	3				
119	1018	JAA97946.1	128.01	12	0	0	5	8	12	12	3				
119	982	BAP39981.1	128.01	10	0	0	4	6	10	10	2				
119	983	BAN82142.1	128.01	10	0	0	4	6	10	10	2				
151	638	CAP74088.1	127.36	14	0	0	0	14	6	0	9				3.1
241	518	ADJ67475.1	127.31	5	2	3	0	0	0	0	2				
221	69843	XP_034278116.1	126.21	5	0	0	5	2	0	0	0			2.9581E6	1.2
138	69858	TRINITY_DN12452	126.04	19	0	0	9	9	9	19	9			3.0778E5	5.5
153	515	AUS82489.1	125.09	11	0	0	7	8	4	3	0				1.(
153	557	JAA98031.1	125.09	11	0	0	7	8	4	3	0				1.(
164	1055	TRINITY_DN471	123.14	19	19	19	12	12	0	12	0	1.3286E6	4.833E6	1.0924E7	2.3
117	1178	ADN04917.1	122.90	8	8	8	8	4	0	4	0	6.4186E7	1.0631E7	3.0723E5	
117	1179	E0Y419.1	122.90	8	8	8	8	4	0	4	0	6.4186E7	1.0631E7	3.0723E5	
123	877	AEH59582.1	120.92	12	0	0	5	8	12	8	3				
123	866	QBF53420.1	120.92	13	0	0	5	8	13	8	3				
123	878	QHR82782.1	120.92	12	0	0	5	8	12	8	3				
123	882	TRINITY_DN1356	120.92	10	0	0	4	6	10	6	2				
123	882	TRINITY_DN1356	120.92	10	0	0	4	6	10	6	2				
123	882	TRINITY_DN1356	120.92	10	0	0	4	6	10	6	2				
123	882	TRINITY_DN1356	120.92	10	0	0	4	6	10	6	2				
205	69831	TRINITY_DN180	120.88	2	0	0	0	0	0	2	0		1.0785E4		1.2
205	69832	TRINITY_DN180	120.88	2	0	0	0	0	0	2	0		1.0785E4		1.2
205	454	XP_034285002.1	120.88	2	0	0	0	0	0	2	0		1.0785E4		1.2
205	456	XP_034285001.1	120.88	2	0	0	0	0	0	2	0		1.0785E4		1.2
205	453	XP_034285000.1	120.88	2	0	0	0	0	0	2	0		1.0785E4		1.2
228	988	JAG67762.1	120.52	20	0	0	0	0	0	0	20				
228	989	JAG67761.1	120.52	20	0	0	0	0	0	0	20				
212	928	XP_015679695.1	120.08	11	5	0	0	6	6	6	0	2.0856E5			1.(
128	722	ADP88559.1	117.89	11	3	3	3	8	0	3	8				1.(

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
128	723	E5L0E3.1	117.89	11	3	3	3	8	0	3	8				1.(
193	914	P0DJL5.1	116.25	22	0	0	7	0	7	6	22			1.1179E5	
193	921	AMB36341.1	116.25	18	0	0	6	0	6	5	18			1.1179E5	
92	69869	TRINITY_DN554	114.68	20	0	7	7	12	12	20	20		9.8869E4	8.6025E5	1.4
92	69870	TRINITY_DN554	114.68	24	0	9	9	15	15	24	24		9.8869E4	8.6025E5	1.4
210	621	XP_015666085.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	622	XP_015666086.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	615	XP_034258446.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	616	XP_034258445.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	617	XP_034258444.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	610	XP_032092626.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	611	XP_032092625.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	612	XP_032092628.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	613	XP_013922774.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	614	XP_032092627.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	623	JAV50864.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	624	JAI13760.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	625	AFJ49766.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	604	JAG47096.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	626	TRINITY_DN8397	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	609	ETE69371.1	114.12	9	6	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	710	XP_026529384.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
210	725	XP_026563995.1	114.12	8	5	3	3	3	0	0	0	3.4283E5	1.3335E5	8.9043E4	1.(
88	2092	P86497.1	114.04	15	0	15	15	15	0	0	0		1.4585E7	4.8687E7	1.4
269	949	JAG46182.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	950	XP_015674504.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	951	JAG43702.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	952	JAA96331.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	953	XP_015674505.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	954	JAV49839.1	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	69874	TRINITY_DN3815	109.91	6	0	6	0	0	0	0	0		1.1978E5		

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
269	69874	TRINITY_DN3815	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	69874	TRINITY_DN3815	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	69874	TRINITY_DN3815	109.91	6	0	6	0	0	0	0	0		1.1978E5		
269	69874	TRINITY_DN3815	109.91	6	0	6	0	0	0	0	0		1.1978E5		
256	684	TRINITY_DN28984	109.74	2	0	0	0	0	0	0	2				
256	69854	TRINITY_DN28984	109.74	2	0	0	0	0	0	0	2				
280	832	JAV50910.1	109.42	12	0	0	0	12	0	0	0				5.3
280	833	JAI10138.1	109.42	12	0	0	0	12	0	0	0				5.3
280	834	JAB54484.1	109.42	12	0	0	0	12	0	0	0				5.3
280	835	XP_026541233.1	109.42	12	0	0	0	12	0	0	0				5.3
280	836	XP_026576189.1	109.42	12	0	0	0	12	0	0	0				5.3
280	837	LAB45561.1	109.42	11	0	0	0	11	0	0	0				5.3
280	69868	TRINITY_DN178	109.42	9	0	0	0	9	0	0	0				5.3
280	1039	LAB63521.1	109.42	12	0	0	0	12	0	0	0				5.3
280	1040	JAG68347.1	109.42	12	0	0	0	12	0	0	0				5.3
280	1041	ETE58466.1	109.42	10	0	0	0	10	0	0	0				5.3
258	69851	TRINITY_DN7999	108.70	7	0	0	0	0	0	0	7				
240	498	JAV50725.1	105.94	6	0	0	2	0	0	0	4			9.5286E4	
127	1155	ADP88560.1	105.88	10	10	10	4	4	6	4	6	3.9743E5	3.772E5		
127	1156	E5L0E4.1	105.88	10	10	10	4	4	6	4	6	3.9743E5	3.772E5		
262	695	XP_026535564.1	105.27	3	0	0	0	0	0	0	3				
262	696	XP_026535563.1	105.27	3	0	0	0	0	0	0	3				
262	655	XP_013918193.1	105.27	3	0	0	0	0	0	0	3				
262	598	XP_034271810.1	105.27	3	0	0	0	0	0	0	3				
262	705	XP_013918195.1	105.27	3	0	0	0	0	0	0	3				
262	678	XP_013918194.1	105.27	3	0	0	0	0	0	0	3				
262	637	XP_034271811.1	105.27	3	0	0	0	0	0	0	3				
262	706	XP_029143180.1	105.27	3	0	0	0	0	0	0	3				
242	452	JAC95757.1	104.83	9	0	0	3	2	0	0	4			1.1168E5	8.8
202	1548	ADI47590.1	104.60	5	5	3	5	0	0	0	0	1.4223E6	4.9549E5	1.8109E6	

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
110	1500	E0Y421.1	103.68	8	4	4	4	4	0	0	0	1.8692E7			
110	1501	ADN04919.1	103.68	8	4	4	4	4	0	0	0	1.8692E7			
110	1707	QBF53413.1	103.68	8	4	4	4	4	0	0	0	1.8692E7			
191	1327	XP_007435739.1	103.31	4	2	2	2	4	2	2	2	6.6638E5	2.0438E5	3.7003E5	1.4
191	1555	XP_015672252.1	103.31	4	2	2	2	4	2	2	2	6.6638E5	2.0438E5	3.7003E5	1.4
191	1528	JAG44290.1	103.31	4	2	2	2	4	2	2	2	6.6638E5	2.0438E5	3.7003E5	1.4
191	69929	TRINITY_DN6008	103.31	4	2	2	2	4	2	2	2	6.6638E5	2.0438E5	3.7003E5	1.4
191	1538	AFJ50411.1	103.31	4	2	2	2	4	2	2	2	6.6638E5	2.0438E5	3.7003E5	1.4
192	70234	TRINITY_DN2736	103.13	14	14	14	14	14	0	0	0	1.8674E5	1.5622E6	7.1135E5	5.8
177	69888	TRINITY_DN471	102.97	11	11	11	11	11	11	0	0	4.0439E6	6.1514E6	1.3556E7	4.8
264	69847	TRINITY_DN1497	102.43	2	2	0	0	0	0	0	0	1.3496E5			
264	69848	TRINITY_DN1497	102.43	3	3	0	0	0	0	0	0	1.3496E5			
238	639	ETE68218.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	651	XP_025022318.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	656	JAG67632.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	664	JAG44306.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	665	JAA96758.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	666	JAG46538.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	676	LAB43566.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	654	JAV50234.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	657	XP_026576301.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	658	XP_026525656.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	659	XP_026576299.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	660	XP_026525655.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	661	XP_026525654.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	662	XP_026576298.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	663	XP_013919280.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	667	TRINITY_DN206	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	667	TRINITY_DN206	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	668	XP_032091066.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	669	XP_032091065.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	670	XP_034271617.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
238	671	XP_034271615.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	672	XP_034271618.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	673	XP_034271616.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	674	XP_025022317.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
238	675	XP_007428111.1	95.05	4	1	0	0	1	0	4	0	5.5682E4			1.1
148	70063	TRINITY_DN459	94.14	11	11	11	11	11	11	0	0	3.6789E6	3.4934E5	9.2485E5	6.1
148	70205	TRINITY_DN459	94.14	9	9	9	9	9	9	0	0	3.6789E6	3.4934E5	9.2485E5	6.1
148	2962	TRINITY_DN3041	94.14	31	31	31	31	31	31	0	0	3.6789E6	3.4934E5	9.2485E5	6.1
274	1102	TRINITY_DN2	93.78	5	0	0	2	3	0	0	0			7.0205E4	3.8
257	69921	TRINITY_DN7999	93.52	3	0	0	0	0	0	0	3				
257	69922	TRINITY_DN7999	93.52	3	0	0	0	0	0	0	3				
265	1267	TRINITY_DN13494	92.73	7	0	7	0	0	0	0	0		7.3443E5		
254	2971	A8Y7P1.1	92.20	12	0	0	0	0	0	0	12				
254	2972	CAL69604.1	92.20	12	0	0	0	0	0	0	12				
254	2973	A8Y7N6.1	92.20	12	0	0	0	0	0	0	12				
254	2974	CAL69609.1	92.20	12	0	0	0	0	0	0	12				
254	2975	A8Y7P5.1	92.20	11	0	0	0	0	0	0	11				
254	2976	AFD04724.1	92.20	11	0	0	0	0	0	0	11				
254	2977	CAL69613.1	92.20	11	0	0	0	0	0	0	11				
254	2978	A8Y7N7.1	92.20	11	0	0	0	0	0	0	11				
254	2979	CAL69605.1	92.20	11	0	0	0	0	0	0	11				
233	69924	TRINITY_DN960	90.47	8	0	0	0	0	8	4	0				
233	69925	TRINITY_DN960	90.47	7	0	0	0	0	7	3	0				
233	69926	TRINITY_DN960	90.47	6	0	0	0	0	6	3	0				

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
233	69927	TRINITY_DN960	90.47	5	0	0	0	0	5	3	0				
233	69956	TRINITY_DN960	90.47	7	0	0	0	0	7	3	0				
233	69957	TRINITY_DN960	90.47	6	0	0	0	0	6	3	0				
233	69958	TRINITY_DN960	90.47	6	0	0	0	0	6	3	0				
244	69895	TRINITY_DN672	89.92	5	0	0	0	0	0	0	5				
275	1984	1OQS	89.80	14	0	0	0	0	0	0	14				
275	1984	1OQS	89.80	14	0	0	0	0	0	0	14				
275	1984	1OQS	89.80	14	0	0	0	0	0	0	14				
275	1984	1OQS	89.80	14	0	0	0	0	0	0	14				
275	1986	CAA48456.1	89.80	12	0	0	0	0	0	0	12				
275	1987	AAZ53185.1	89.80	12	0	0	0	0	0	0	12				
275	1988	Q02471.1	89.80	12	0	0	0	0	0	0	12				
275	1989	S29298	89.80	12	0	0	0	0	0	0	12				
275	1990	ACD43467.1	89.80	12	0	0	0	0	0	0	12				
275	1991	ACD43465.1	89.80	12	0	0	0	0	0	0	12				
203	1737	AFD04723.1	87.78	11	0	0	0	10	10	10	11				8.1
203	1738	AFB74191.1	87.78	11	0	0	0	10	10	10	11				8.1
203	1739	A8Y7N4.1	87.78	11	0	0	0	10	10	10	11				8.1
203	1740	H6VC05.1	87.78	11	0	0	0	10	10	10	11				8.1
203	1741	CAL69602.1	87.78	11	0	0	0	10	10	10	11				8.1
207	1970	ABD24041.1	86.71	26	26	13	0	0	0	0	11	3.3819E5	1.6087E5		
207	1971	Q2ES49.1	86.71	26	26	13	0	0	0	0	11	3.3819E5	1.6087E5		
255	842	TRINITY_DN157	86.44	13	0	0	0	0	0	0	13				
213	1995	AAB36402.1	85.29	13	0	0	0	0	0	0	13				

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
213	1996	Q9PSM8.1	85.29	13	0	0	0	0	0	0	13				
284	1099	XP_029141923.1	81.62	7	0	0	0	0	0	0	7				
267	69887	TRINITY_DN1424	81.20	5	0	0	0	0	5	0	5				
215	997	ART88739.1	79.86	7	0	4	3	0	0	0	0		1.254E5		
296	69884	TRINITY_DN1526	79.05	7	0	0	0	0	0	0	7				
296	69885	TRINITY_DN1526	79.05	6	0	0	0	0	0	0	6				
296	69886	TRINITY_DN1526	79.05	5	0	0	0	0	0	0	5				
236	70327	TRINITY_DN2452	77.88	9	0	8	0	8	9	8	0		3.2643E4		4.1
187	3019	P00990.1	76.97	17	0	0	15	15	15	15	17			4.065E5	8.(
187	3020	TIVRV2	76.97	17	0	0	15	15	15	15	17			4.065E5	8.(
187	3028	CAL69611.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3029	A8Y7P3.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	2948	CAL69610.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	2949	A8Y7P2.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3030	CAL69615.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3031	AFE83617.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3032	A8Y7P4.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3033	AFE83616.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3034	AFB74192.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3035	CAL69614.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3036	A8Y7P6.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3037	A8Y7N5.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3038	CAL69608.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3039	ABD24040.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3040	CAL69612.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
187	3041	A8Y7P0.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3042	AFE83615.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3043	Q2ES50.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3044	CAL69603.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
187	3045	H6VC06.1	76.97	12	0	0	11	11	11	11	12			4.065E5	8.(
307	70026	TRINITY_DN5102	76.41	3	0	3	0	0	0	0	0		8.6583E4		
229	1035	CAE47141.1	75.31	12	0	0	0	0	0	0	12				
252	955	ABB76279.1	73.14	9	0	0	0	9	0	0	0				7.1
230	1518	ADI47595.1	73.04	6	6	0	0	0	0	0	0	4.3022E6			
230	1676	ADI47604.1	73.04	6	6	0	0	0	0	0	0	4.3022E6			
297	69935	TRINITY_DN722	72.61	3	0	3	0	0	0	0	0		3.0191E5		
297	70165	TRINITY_DN722	72.61	11	0	11	0	0	0	0	0		3.0191E5		
297	70166	TRINITY_DN722	72.61	9	0	9	0	0	0	0	0		3.0191E5		
261	1482	TRINITY_DN86540	70.73	11	0	0	0	0	4	0	11				
261	1972	P0C0U6.1	70.73	16	0	0	0	0	6	0	16				
261	1973	XP_026532450.1	70.73	15	0	0	0	0	6	0	15				
261	1974	XP_026570824.1	70.73	15	0	0	0	0	6	0	15				
261	1975	XP_034284997.1	70.73	15	0	0	0	0	6	0	15				
261	1976	XP_032079120.1	70.73	15	0	0	0	0	6	0	15				
261	1977	JAC95434.1	70.73	15	0	0	0	0	6	0	15				
261	1978	LAA66838.1	70.73	14	0	0	0	0	6	0	14				
290	1384	XP_029140879.1	70.10	0	0	0	0	0	0	0	0				
248	1817	AJO70722.1	68.21	6	0	0	0	0	0	0	6				
343	2091	XP_029142225.1	64.45	1	0	0	1	0	0	0	0			9.5811E4	
343	2123	XP_015677107.1	64.45	3	0	0	3	0	0	0	0			9.5811E4	
343	70209	TRINITY_DN1914	64.45	3	0	0	3	0	0	0	0			9.5811E4	
403	2994	TRINITY_DN1889	63.54	8	0	0	0	0	0	0	8				
200	3016	CCH15044.1	63.13	9	9	9	9	9	9	9	9	8.2206E5	5.5535E5	2.9889E6	2.:

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
200	3017	I2G9B4.1	63.13	9	9	9	9	9	9	9	9	8.2206E5	5.5535E5	2.9889E6	2.3
200	3010	AMH40736.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	3011	AMH40741.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	3012	P00991.2	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	3013	AAP04484.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	2915	AAP04485.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	2916	P00992.2	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	2917	AMH40733.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	2918	AMH40738.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	2919	AMH40740.1	63.13	10	10	10	10	10	10	10	10	8.2206E5	5.5535E5	2.9889E6	2.3
200	3014	E5AJX3.1	63.13	9	9	9	9	9	9	9	9	8.2206E5	5.5535E5	2.9889E6	2.3
200	3015	CBW30779.1	63.13	9	9	9	9	9	9	9	9	8.2206E5	5.5535E5	2.9889E6	2.3
200	70321	TRINITY_DN151	63.13	8	8	8	8	8	8	8	8	8.2206E5	5.5535E5	2.9889E6	2.3
200	3047	Q6T269.1	63.13	6	6	6	6	6	6	6	6	8.2206E5	5.5535E5	2.9889E6	2.3
200	3048	AAR19275.1	63.13	6	6	6	6	6	6	6	6	8.2206E5	5.5535E5	2.9889E6	2.3
245	1804	LAA93895.1	61.86	5	5	0	0	5	5	5	5	2.8419E4			7.8
285	2986	CAJ34939.1	61.72	19	0	0	0	0	0	19	19				
285	2987	Q3BK14.1	61.72	19	0	0	0	0	0	19	19				
285	70319	TRINITY_DN160	61.72	15	0	0	0	0	0	15	15				
223	1689	JAS05406.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1667	JAS05289.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1668	JAS05287.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1669	ABG26980.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1670	JAS05286.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1671	JAS05288.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1672	JAS05285.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1734	JAS05407.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	1735	JAS05408.1	60.18	2	0	2	0	2	0	0	0		2.6453E5		1.0
223	2063	QIV64953.1	60.18	4	0	4	0	4	0	0	0		2.6453E5		1.0

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Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
303	1894	ETE57622.1	55.32	3	0	0	0	0	0	0	3				
376	70075	XP_015672332.1	52.38	2	2	0	0	0	0	0	0	7.951E4			
374	2170	TRINITY_DN27458	51.48	2	0	0	0	2	0	0	0				1.3
374	3082	XP_015683432.1	51.48	2	0	0	0	2	0	0	0				1.3
378	2213	XP_007421015.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	70211	TRINITY_DN13676	50.81	2	2	0	0	0	0	0	0	1.4791E5			
378	70212	TRINITY_DN13676	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	70212	TRINITY_DN13676	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	70214	TRINITY_DN13676	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	70215	TRINITY_DN13676	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2289	JAV50100.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	3080	LAB58574.1	50.81	9	9	0	0	0	0	0	0	1.4791E5			
378	2671	XP_007421016.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2545	XP_026552070.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2254	JAA96625.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2546	XP_026537394.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2255	JAG44103.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2547	XP_026537257.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2596	LAB27223.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	1935	XP_032065032.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	2302	XP_034262785.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
378	1936	XP_013919874.1	50.81	1	1	0	0	0	0	0	0	1.4791E5			
295	1454	JAV49704.1	50.02	2	0	0	0	0	0	0	2				
295	1473	JAA96208.1	50.02	2	0	0	0	0	0	0	2				
295	69903	TRINITY_DN159	50.02	2	0	0	0	0	0	0	2				
295	69904	TRINITY_DN159	50.02	2	0	0	0	0	0	0	2				
295	69905	TRINITY_DN159	50.02	2	0	0	0	0	0	0	2				
295	1488	AFJ50884.1	50.02	2	0	0	0	0	0	0	2				
295	1489	JAI12151.1	50.02	2	0	0	0	0	0	0	2				
270	2182	JAG67907.1	49.83	2	0	0	0	2	0	2	0				1.3
270	3150	TRINITY_DN3991	49.83	2	0	0	0	2	0	2	0				1.3
298	2284	CAJ01683.1	48.76	3	0	0	3	0	0	0	0			2.178E5	
298	2041	ADW54336.1	48.76	3	0	0	3	0	0	0	0			2.178E5	

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
298	2225	ADW54337.1	48.76	4	0	0	4	0	0	0	0			2.178E5	
298	2593	ADW54335.1	48.76	4	0	0	4	0	0	0	0			2.178E5	
169	70050	P86541.2	47.76	13	13	13	0	13	13	13	13	1.9149E5	2.2353E4		3.2
169	2070	P01440.1	47.76	13	13	13	0	13	13	13	13	1.9149E5	2.2353E4		3.2
169	2071	AAC61315.1	47.76	13	13	13	0	13	13	13	13	1.9149E5	2.2353E4		3.2
169	2073	BAU24665.1	47.76	11	11	11	0	11	11	11	11	1.9149E5	2.2353E4		3.2
169	2075	O93472.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2076	Q9PST3.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2077	AAK49439.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2078	AAC27686.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2079	Q9PST4.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2080	AAC27687.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
169	2081	AAC27685.1	47.76	10	10	10	0	10	10	10	10	1.9149E5	2.2353E4		3.2
283	2262	ETE69494.1	47.54	2	0	0	0	2	2	2	0				4.7
283	3123	ETE65060.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3124	XP_013915314.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3102	XP_013919189.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3103	XP_013919188.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3104	ETE65301.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3105	JAG46644.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3106	JAI09932.1	47.54	7	0	0	0	7	7	7	0				4.7
283	70333	XP_007430054.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3107	JAI13025.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3108	AFJ50305.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3109	JAG44453.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3110	JAI09933.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3111	JAG46643.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3112	AFJ50304.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3113	JAG67733.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3114	JAB54108.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3115	JAC95409.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3116	JAI13026.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3117	JAA96854.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3118	JAG44452.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3119	JAA96855.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3120	XP_013930707.1	47.54	7	0	0	0	7	7	7	0				4.7

total 523 p

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	Coverage (%) F1	Coverage (%) F2	Coverage (%) F3	Coverage (%) F4	Coverage (%) F5	Coverage (%) F6	Coverage (%) F7	Area F1	Area F2	Area F3	A
283	3122	XP_013931116.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3125	XP_013908942.1	47.54	7	0	0	0	7	7	7	0				4.7
283	3100	XP_013911300.1	47.54	6	0	0	0	6	6	6	0				4.7
283	3127	ETE60792.1	47.54	6	0	0	0	6	6	6	0				4.7
283	3129	XP_013924759.1	47.54	6	0	0	0	6	6	6	0				4.7
283	70335	XP_026542761.1	47.54	6	0	0	0	6	6	6	0				4.7
283	3130	ETE59971.1	47.54	5	0	0	0	5	5	5	0				4.7
283	2863	XP_013921022.1	47.54	5	0	0	0	5	5	5	0				4.7
283	3131	LAB40587.1	47.54	5	0	0	0	5	5	5	0				4.7
404	70338	TRINITY_DN1911	46.25	25	0	0	0	0	25	0	0				
404	70338	TRINITY_DN1911	46.25	25	0	0	0	0	25	0	0				
305	70262	XP_026548138.1	45.78	1	0	0	0	0	0	0	1				
375	2015	XP_032092456.1	42.06	5	0	0	0	0	0	0	5				
304	2452	XP_007437884.2	40.82	1	0	0	0	0	0	1	0				
304	2453	XP_007437883.2	40.82	1	0	0	0	0	0	1	0				
304	2910	XP_007437886.2	40.82	1	0	0	0	0	0	1	0				
304	2911	XP_007437885.2	40.82	1	0	0	0	0	0	1	0				
165	2674	XP_007421854.1	39.14	2	0	0	0	2	2	0	0				4.3
														total 523 p	

TRINITY_DN9
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
K.YPVKPSEEGKSAGELYEESLRK.A	Y	103.19	2495.2544	22	0.3	624.8210	4	41.37	1	F1:12431	12112021_RID_2349_DP1.raw
K.YAMGAITTFTPYQFQHFSEALTAPVGR.I	N	93.35	3003.4587	27	0.8	1002.1609	3	68.16	3	F3:20530	17112021_RID_2349_DP3.raw
R.FDEIVGGMDKLPTSMHQDIK.E	Y	92.44	2260.0867	20	0.3	754.3698	3	47.85	3	F3:13952	17112021_RID_2349_DP3.raw
K.DPGLLKYPVKPSEEGK.S	N	90.01	1755.9407	16	1.1	586.3215	3	37.86	1	F1:11209	12112021_RID_2349_DP1.raw
R.NVKEGWYANLGPMR.L	N	89.97	1633.8035	14	1.1	817.9099	2	46.58	1	F1:14171	12112021_RID_2349_DP1.raw
K.SGLTAARDVNRASEL	N	81.95	1558.8063	15	-0.1	520.6093	3	35.16	1	F1:10323	12112021_RID_2349_DP1.raw
K.RFDEIVGGMDK.L	N	81.31	1265.6074	11	0.1	633.8110	2	38.73	1	F1:11503	12112021_RID_2349_DP1.raw
K.YDTYSTKEYLIK.E	N	80.80	1522.7555	12	0.9	762.3857	2	38.58	2	F2:10545	12112021_RID_2349_DP2.raw
K.HIVVVGAGMSGLSAAYVLAGAGHK.V	Y	80.72	2264.2100	24	-0.3	755.7437	3	58.30	3	F3:17243	17112021_RID_2349_DP3.raw
K.KDPGLLKYPVKPSEEGK.S	N	80.37	1884.0355	17	-0.1	472.0161	4	43.31	1	F1:13296	12112021_RID_2349_DP1.raw
K.YAM(+15.99)GAITTFTPYQFQHFSEALTAPVGR.I	N	80.23	3019.4539	27	0.9	1007.4928	3	64.54	3	F3:19257	17112021_RID_2349_DP3.raw
K.KFWEDDGIHGGK.S	N	78.30	1387.6520	12	0.2	694.8334	2	31.47	3	F3:8478	17112021_RID_2349_DP3.raw
K.SAGELYEESLRK.A	Y	76.14	1380.6885	12	0.1	691.3516	2	32.27	1	F1:9527	12112021_RID_2349_DP1.raw
K.RFDEIVGGMDKLPTSMHQDIK.E	Y	75.67	2416.1877	21	0.3	605.0544	4	49.40	3	F3:14259	17112021_RID_2349_DP3.raw
K.FWEDDGIHGGK.S	N	74.52	1259.5570	11	0.6	630.7861	2	33.77	2	F2:8859	12112021_RID_2349_DP2.raw
K.EGWYANLGPMR.L	N	74.35	1292.5972	11	0.2	647.3060	2	50.70	1	F1:15490	12112021_RID_2349_DP1.raw
R.EDDYEEFLEIAK.N	N	74.11	1499.6667	12	0.7	750.8412	2	59.88	5	F5:17908	17112021_RID_2349_DP5.raw
K.LPTSMHQDIK.E	Y	73.02	1168.5911	10	0.7	585.3032	2	26.70	2	F2:6395	12112021_RID_2349_DP2.raw

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
R.NVKEGWYANLGPM(+15.99)R.L	N	71.22	1649.7983	14	0.4	825.9067	2	41.24	1	F1:12368	12112021_RID_2349_DP1.raw
D.PGLLKYPVKPSEEGK.S	N	71.12	1640.9137	15	0.7	547.9789	3	36.73	1	F1:10817	12112021_RID_2349_DP1.raw
K.EGWYANLGPM(+15.99)R.L	N	70.55	1308.5920	11	0.5	655.3036	2	44.48	3	F3:12782	17112021_RID_2349_DP3.raw
K.HDDIFAYEK.R	N	70.19	1136.5138	9	0.4	569.2644	2	36.68	2	F2:9942	12112021_RID_2349_DP2.raw
K.YPVKPSEEGKSAGELYEESLR.K	Y	70.02	2367.1594	21	0.8	790.0610	3	41.55	1	F1:12377	12112021_RID_2349_DP1.raw
L.ELNEFVQETENGWYFIK.N	Y	68.81	2145.0054	17	0.3	1073.5103	2	67.16	2	F2:19907	12112021_RID_2349_DP2.raw
K.SAGELYEESLR.K	Y	68.45	1252.5935	11	-0.9	627.3035	2	38.10	1	F1:11394	12112021_RID_2349_DP1.raw
K.RFDEIVGGM(+15.99)DK.L	N	67.11	1281.6023	11	0.5	641.8087	2	36.31	2	F2:10416	12112021_RID_2349_DP2.raw
K.YPVKPSEEGK.S	N	66.22	1132.5764	10	0.6	567.2958	2	19.01	5	F5:4120	17112021_RID_2349_DP5.raw
K.ESVHFNAR.V	Y	64.04	958.4620	8	-0.8	480.2379	2	23.05	1	F1:6037	12112021_RID_2349_DP1.raw
R.VGEVKKDPGLLK.Y	N	63.88	1281.7656	12	-0.3	428.2624	3	28.13	1	F1:8041	12112021_RID_2349_DP1.raw
L.NEFVQETENGWYFIK.N	N	63.17	1902.8788	15	0.5	952.4471	2	60.53	2	F2:17717	12112021_RID_2349_DP2.raw
D.DYEEFLEIAK.N	N	63.01	1255.5972	10	0.6	628.8062	2	58.64	1	F1:18007	12112021_RID_2349_DP1.raw
R.IKFEPPLPPK.K	N	62.32	1164.6907	10	0.5	583.3529	2	42.88	1	F1:12794	12112021_RID_2349_DP1.raw
D.SGYYVSFIESLK.H	N	61.77	1391.6973	12	0.1	696.8560	2	60.36	3	F3:17967	17112021_RID_2349_DP3.raw
K.EGNLSPGAVDMIGDLLNED.S	N	61.67	1957.8938	19	0.0	979.9542	2	76.89	4	F4:23445	17112021_RID_2349_DP4.raw
R.DVNRASEL	N	60.54	902.4457	8	-0.6	452.2299	2	26.74	1	F1:7420	12112021_RID_2349_DP1.raw
K.VTVLEASERPGGR.V	N	60.35	1369.7313	13	-0.1	457.5843	3	29.25	1	F1:8170	12112021_RID_2349_DP1.raw
K.HDDIFAYEKR.F	N	60.12	1292.6149	10	0.0	431.8789	3	32.95	3	F3:8849	17112021_RID_2349_DP3.raw
R.NVKEGWYANL.G	N	59.21	1192.5876	10	-0.3	597.3009	2	47.98	1	F1:14543	12112021_RID_2349_DP1.raw
K.VTVLEASER.P	N	58.47	1002.5345	9	-0.5	502.2743	2	30.13	5	F5:7870	17112021_RID_2349_DP5.raw
R.IKFEPPLPPKK.E	N	58.07	1292.7855	11	0.1	647.4001	2	39.85	2	F2:10760	12112021_RID_2349_DP2.raw
K.SGLTAARDVNR.A	N	57.18	1158.6105	11	-0.1	387.2107	3	21.39	1	F1:5502	12112021_RID_2349_DP1.raw
Y.QFQHFSEALTAPVGR.I	N	56.85	1686.8478	15	0.7	844.4318	2	42.64	4	F4:12109	17112021_RID_2349_DP4.raw
R.FDEIVGGMDK.L	N	56.21	1109.5062	10	0.9	555.7609	2	39.99	2	F2:11060	12112021_RID_2349_DP2.raw
N.AHGWIDSTIK.S	N	55.64	1126.5771	10	1.1	564.2964	2	35.13	3	F3:9624	17112021_RID_2349_DP3.raw
K.WSLDKYAMGA.I	N	55.33	1140.5273	10	0.5	571.2712	2	50.51	1	F1:15333	12112021_RID_2349_DP1.raw
K.STTDLPSR.F	N	55.31	875.4348	8	0.5	438.7249	2	22.15	1	F1:5769	12112021_RID_2349_DP1.raw
D.YEEFLEIAK.N	N	55.22	1140.5702	9	-0.1	571.2923	2	49.00	1	F1:14874	12112021_RID_2349_DP1.raw
H.FSEALTAPVGR.I	N	55.11	1146.6033	11	0.5	574.3092	2	39.16	5	F5:11001	17112021_RID_2349_DP5.raw
R.IFFAGEYTAN.A	N	54.27	1131.5237	10	0.8	1132.5319	1	55.58	1	F1:16980	12112021_RID_2349_DP1.raw
R.FDEIVGGM(+15.99)DK.L	N	53.88	1125.5012	10	-0.3	563.7577	2	37.17	1	F1:10962	12112021_RID_2349_DP1.raw
K.LPTSM(+15.99)HQDIK.E	Y	53.34	1184.5859	10	0.8	395.8696	3	26.70	2	F2:6476	12112021_RID_2349_DP2.raw
K.EGWYANLGPMRLPEK.H	N	52.68	1759.8716	15	0.9	587.6317	3	52.96	2	F2:15393	12112021_RID_2349_DP2.raw
K.RFDEIVGGMDKLPTSMHQD.I	Y	52.19	2175.0088	19	1.0	726.0109	3	48.28	3	F3:14082	17112021_RID_2349_DP3.raw
N.DLSSIHQLPK.E	N	51.71	1136.6189	10	0.9	569.3173	2	34.51	1	F1:10039	12112021_RID_2349_DP1.raw
K.FEPPLPPKK.E	N	51.31	1051.6066	9	0.2	526.8107	2	31.13	3	F3:8589	17112021_RID_2349_DP3.raw

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
K.EGNLSPGAVDM(+15.99)IGDLLNED.S	N	51.30	1973.8888	19	0.5	987.9521	2	67.55	4	F4:20200	17112021_RID_2349_DP4.raw
S.AAYVLAGAGHK.V	N	50.59	1056.5715	11	1.1	529.2936	2	24.54	3	F3:6001	17112021_RID_2349_DP3.raw
D.LLNEDSGYYVSFIESLK.H	N	49.92	1975.9778	17	0.7	988.9969	2	68.81	3	F3:20708	17112021_RID_2349_DP3.raw
K.RFDEIVGGMDKLPTSM(+15.99)HQDIK.E	Y	49.70	2432.1829	21	0.4	609.0532	4	45.01	3	F3:12950	17112021_RID_2349_DP3.raw
K.RFDEIVGGM(+15.99)D.K	N	49.15	1153.5073	10	0.1	577.7610	2	38.54	3	F3:10739	17112021_RID_2349_DP3.raw
R.RIKFEPPLPPK.K	N	49.13	1320.7917	11	0.5	441.2714	3	45.59	2	F2:12721	12112021_RID_2349_DP2.raw
D.DIFAYEKR.F	N	48.19	1040.5291	8	0.1	521.2719	2	35.16	3	F3:9617	17112021_RID_2349_DP3.raw
K.HIVVVGAGM(+15.99)SGLSAAYVLAGAGHK.V	Y	47.83	2280.2048	24	-0.2	761.0754	3	51.51	3	F3:14961	17112021_RID_2349_DP3.raw
K.YAMGAITTFTPY.Q	N	46.88	1334.6217	12	0.9	668.3187	2	64.07	4	F4:19119	17112021_RID_2349_DP4.raw
R.FDEIVGGMDKLPTSM(+15.99)HQDIK.E	Y	46.36	2276.0818	20	0.4	759.7015	3	43.40	4	F4:12371	17112021_RID_2349_DP4.raw
K.EGNLSPGAVDM(+15.99)IGD.L	N	46.09	1389.6082	14	0.2	695.8115	2	46.47	4	F4:13379	17112021_RID_2349_DP4.raw
Y.PVKPSEEGK.S	N	45.74	969.5131	9	-0.5	485.7636	2	19.27	2	F2:3861	12112021_RID_2349_DP2.raw
K.IQQNANEVTVTY.Q	Y	45.71	1378.6729	12	0.8	690.3442	2	41.87	4	F4:11834	17112021_RID_2349_DP4.raw
K.RFDEIVGGMD.K	N	45.54	1137.5125	10	-0.5	569.7632	2	45.56	3	F3:13157	17112021_RID_2349_DP3.raw
K.VTVLEASERPGGRVR.T	N	45.40	1624.9009	15	0.3	542.6411	3	30.01	1	F1:8563	12112021_RID_2349_DP1.raw
Q.HFSEALTAPVGR.I	N	42.43	1283.6622	12	0.5	642.8387	2	34.80	4	F4:9467	17112021_RID_2349_DP4.raw
R.IVREYIK.K	N	41.49	919.5491	7	0.1	460.7819	2	25.34	1	F1:6965	12112021_RID_2349_DP1.raw
K.YAMGAITTFTPYQF.Q	N	41.39	1609.7487	14	-0.2	805.8814	2	71.88	3	F3:21650	17112021_RID_2349_DP3.raw
K.RFDEIVGGMDKLPTSMH.Q	Y	41.32	1931.9233	17	0.7	644.9822	3	48.99	3	F3:14232	17112021_RID_2349_DP3.raw
K.EGWYANLGPM(+15.99)RLPEK.H	N	40.61	1775.8665	15	0.9	592.9633	3	45.16	3	F3:12960	17112021_RID_2349_DP3.raw
L.SAAYVLAGAGHK.V	N	40.21	1143.6036	12	0.7	572.8095	2	26.75	5	F5:6718	17112021_RID_2349_DP5.raw
K.RFDEIVGGM(+15.99)DKLPTSMHQDIK.E	Y	40.16	2432.1829	21	1.5	811.7361	3	42.94	3	F3:12300	17112021_RID_2349_DP3.raw
F.SEALTAPVGR.I	N	40.05	999.5349	10	-0.1	500.7746	2	30.20	3	F3:7936	17112021_RID_2349_DP3.raw
D.DIFAYEK.R	N	39.75	884.4279	7	0.8	885.4359	1	41.87	4	F4:11928	17112021_RID_2349_DP4.raw
K.RVGEVKKDPGLLK.Y	N	39.62	1437.8667	13	1.0	480.2967	3	39.89	1	F1:11650	12112021_RID_2349_DP1.raw
R.FDEIVGGM(+15.99)DKLPTSMHQDIK.E	Y	38.92	2276.0818	20	0.9	759.7019	3	41.79	3	F3:11943	17112021_RID_2349_DP3.raw
K.WSLDKYAMGAITTF.T	N	38.72	1602.7751	14	1.3	802.3959	2	67.34	3	F3:20215	17112021_RID_2349_DP3.raw

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MAPVSYLLQA WILLSLHGCI TSYPKQARSA SEDIRNCTTN PQYLPPTVVV TGERLKTLRE HMKTHRLSAY IVPNTDAHLS
 81 EYVAERDMRL SWMTGFSGSE GTGVITLQKA ALFTDSRYWI QAERQMDCNW ELQKSAWINF IGQWILNEVP AGGTIGLDPF
                                                   213
161 LFSVDTWYNY HQVLEGANRT LDLLEVNLVD LVWGSERLPP PTNTIYRLAD DFMGGTWQEK VANARGQMEE HSKKPTAILL

241 SGLEETAWLF NLRGDDIPYT PVFYAYTLLT KTDISLFTNR SRLSKEALQM LTAGCPESPC VKVEDYDQIG ASLRKYAHQD
                                          367
321 GVIVWIGTEY TTLGLYKEIP QENLLEDDFS PVMLSKAVKN SKEQKMMEAA HIRDAVALIR YLVWLEKNVP KNSVDELSGA

401 NYLDTLRSEE LHCKGPSFQT ISASGLNAAL AHYSPSSLTS RKLSLNEMYL LDSGGQYFDG TTDITRTIHW GEPTAFQKEA
        486
481 YTRVLMGNID LSKLVFPPRM SGRLVESFAR RPLWEAGLNY GHGTGHGIGN FLSVHEWPVG FQSNNVPLDK GMFTSIEPGY

561 YHDGEFGIRI EDVALVVPAK TKYPVQEDPY LTFKVVSLVP YARNLINESL LSQDQIQYIN RYYETIRQVI GPELQRRQLE

641 EEYRWLEKNT EPFSHGSVLA ASLGTLAVST LASGLLPAAQ H
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F
R.NLINESLLSQDQIQYINR.Y	Y	102.57	2160.1174	18	0.2	1081.0662	2	57.94	2	F2:16943	12112021_RID_2349_DP2.raw	1.6872E
R.LADDFMGGTWQEKVANAR.G	Y	97.16	2007.9473	18	0.4	1004.9813	2	49.13	1	F1:14896	12112021_RID_2349_DP1.raw	1.1424E
K.NSVDELSGANYLDTLR.S	Y	96.75	1765.8483	16	0.7	883.9320	2	53.81	2	F2:15577	12112021_RID_2349_DP2.raw	1.6193E
K.EIPQENLLEDDFSPVMLSK.A	N	94.92	2203.0718	19	0.2	1102.5433	2	65.59	1	F1:20182	12112021_RID_2349_DP1.raw	4.4307E
K.TKYPVQEDPYLTFK.V	Y	84.98	1727.8770	14	0.9	576.9668	3	46.95	1	F1:14170	12112021_RID_2349_DP1.raw	2.0786E
K.VEDYDQIGASLR.K	Y	81.88	1364.6572	12	0.7	683.3364	2	42.99	2	F2:12000	12112021_RID_2349_DP2.raw	2.0691E
R.TIHWGEPTAFQK.E	N	81.74	1413.7041	12	0.9	707.8600	2	42.18	1	F1:12610	12112021_RID_2349_DP1.raw	4.9198E
R.LADDFM(+15.99)GGTWQEKVANAR.G	Y	80.31	2023.9421	18	0.5	675.6550	3	43.18	1	F1:12956	12112021_RID_2349_DP1.raw	6.9069E
R.IEDVALVVPAK.T	Y	80.13	1152.6754	11	-0.4	577.3447	2	45.25	1	F1:13594	12112021_RID_2349_DP1.raw	2.7331E
R.LADDFM(+15.99)GGTWQEK.V	Y	79.06	1512.6555	13	0.1	757.3351	2	41.88	1	F1:12596	12112021_RID_2349_DP1.raw	9.9489E
R.LADDFMGGTWQEK.V	Y	75.54	1496.6605	13	1.0	749.3383	2	49.98	1	F1:15195	12112021_RID_2349_DP1.raw	1.722E7
R.VLMGNIDLSK.L	N	74.32	1088.5900	10	0.9	545.3027	2	44.91	1	F1:13547	12112021_RID_2349_DP1.raw	7.3687E
R.YLVWLEKNVPK.N	N	74.01	1387.7864	11	0.1	694.9005	2	48.76	1	F1:14779	12112021_RID_2349_DP1.raw	3.2724E
K.EIPQENLLEDDFSPVM(+15.99)LSK.A	N	72.70	2219.0667	19	-0.3	1110.5403	2	61.58	2	F2:18110	12112021_RID_2349_DP2.raw	1.502E6
K.VEDYDQIGASLRK.Y	Y	72.65	1492.7521	13	1.0	747.3841	2	37.40	1	F1:11075	12112021_RID_2349_DP1.raw	2.5025E
K.YPVQEDPYLTFK.V	Y	72.14	1498.7344	12	0.1	750.3745	2	49.80	4	F4:14509	17112021_RID_2349_DP4.raw	1.1678E
K.AALFTDSR.Y	Y	69.22	879.4450	8	-0.4	440.7296	2	32.38	2	F2:8405	12112021_RID_2349_DP2.raw	3.6699E
R.VLM(+15.99)GNIDLSK.L	N	68.66	1104.5848	10	0.1	553.2997	2	44.91	1	F1:13558	12112021_RID_2349_DP1.raw	5.0787E
K.VVSLVPYAR.N	N	63.21	1002.5862	9	0.4	502.3006	2	43.57	1	F1:13098	12112021_RID_2349_DP1.raw	3.175E7
K.MMEAAHIR.D	N	61.26	957.4525	8	0.5	479.7338	2	24.46	2	F2:5605	12112021_RID_2349_DP2.raw	2.5335E
R.LPPPTNTIYR.L	N	61.17	1170.6396	10	0.3	586.3273	2	35.87	1	F1:10436	12112021_RID_2349_DP1.raw	2.508E7
K.NTEPFSHGSVLA.A	Y	60.30	1257.5989	12	0.5	629.8070	2	40.01	1	F1:11896	12112021_RID_2349_DP1.raw	8.7833E

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F
R.LSAYIVPNTDAHLSEYVAER.D	Y	60.08	2247.1172	20	0.6	750.0468	3	50.55	2	F2:14530	12112021_RID_2349_DP2.raw	1.5595E
D.ELSGANYLDTLR.S	Y	59.09	1350.6779	12	0.5	676.3466	2	48.45	4	F4:14024	17112021_RID_2349_DP4.raw	
R.RQLEEEYR.W	Y	56.64	1121.5465	8	0.2	561.7806	2	21.08	3	F3:4733	17112021_RID_2349_DP3.raw	
K.MM(+15.99)EAAHIR.D	N	56.35	973.4473	8	-0.3	487.7308	2	24.42	2	F2:5548	12112021_RID_2349_DP2.raw	
K.M(+15.99)MEAAHIR.D	N	55.53	973.4473	8	-0.6	487.7307	2	22.62	2	F2:5124	12112021_RID_2349_DP2.raw	
R.MSGRLVESFAR.R	Y	55.47	1251.6394	11	0.0	418.2204	3	38.02	1	F1:11242	12112021_RID_2349_DP1.raw	1.6579E
D.SGGQYFDGTTDITR.T	N	55.24	1516.6793	14	0.9	759.3477	2	39.61	4	F4:11084	17112021_RID_2349_DP4.raw	
R.QVIGPELQR.R	Y	54.67	1038.5822	9	-0.4	520.2982	2	34.14	1	F1:10002	12112021_RID_2349_DP1.raw	2.1413E
R.LSWMTGFSGSEGTGVITLQK.A	Y	53.91	2098.0405	20	0.2	1050.0277	2	62.94	2	F2:18422	12112021_RID_2349_DP2.raw	2.1277E
R.YWIQAER.Q	N	52.15	964.4766	7	-0.4	483.2454	2	36.97	2	F2:9988	12112021_RID_2349_DP2.raw	1.3881E
R.GDDIPYTPVFYAYTLLTK.T	N	51.60	2076.0454	18	0.2	1039.0302	2	78.46	1	F1:24532	12112021_RID_2349_DP1.raw	3.0975E
K.GPSFQTISASGLNAALAHYSPSSLTSR.K	Y	50.90	2719.3564	27	0.3	907.4597	3	60.52	2	F2:17711	12112021_RID_2349_DP2.raw	
K.NVPKNSVDELSGANYLDTLR.S	Y	50.02	2204.1072	20	0.7	1103.0616	2	50.58	1	F1:15379	12112021_RID_2349_DP1.raw	2.6389E
K.GMFTSIEPGYYHDGEFGIR.I	N	48.84	2174.9731	19	0.7	725.9988	3	56.28	2	F2:16416	12112021_RID_2349_DP2.raw	
K.GM(+15.99)FTSIEPGYYHDGEFGIR.I	N	46.73	2190.9680	19	0.3	731.3302	3	51.35	2	F2:14719	12112021_RID_2349_DP2.raw	
R.TIHWGEPTAFQKEAYTR.V	N	46.04	2033.9958	17	0.9	679.0065	3	45.28	1	F1:13603	12112021_RID_2349_DP1.raw	2.9881E
R.QVIGPELQRR.Q	Y	45.98	1194.6832	10	0.8	598.3494	2	28.93	1	F1:8159	12112021_RID_2349_DP1.raw	4.0244E
R.LVESFAR.R	Y	45.21	820.4443	7	-0.1	411.2294	2	31.00	4	F4:8159	17112021_RID_2349_DP4.raw	2.2969E
R.YLVWLEK.N	N	43.98	949.5273	7	-0.5	475.7707	2	51.37	1	F1:15594	12112021_RID_2349_DP1.raw	3.0018E
K.NSVDELSGANYLDTLRSEE.L	Y	41.99	2110.9653	19	0.7	1056.4907	2	55.67	1	F1:17087	12112021_RID_2349_DP1.raw	7.1446E
K.TKYPVQED.P	Y	39.43	978.4658	8	0.6	490.2405	2	23.69	1	F1:6389	12112021_RID_2349_DP1.raw	1.8089E
R.QLEEEYR.W	Y	39.22	965.4454	7	-0.3	483.7298	2	24.68	2	F2:5729	12112021_RID_2349_DP2.raw	

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  AREKVGIIGY TTKETPVLSN PGPYLEFRDE VEELQIHANK LTTLGVNKII ALGHSGFFED QRIARKVKGV DVVVGGHTNT
 81  FLYTGSPPST EVPAGNYPFM VQSDDGRQVP VVQAYAFGKY LGYLNVVFND KGNVIKASGN PILLNKDIPE DQVVKAQVNK
161  MKIQLQNYYS QEIGKTIVYL NGTTQACRFH ECNLGNLICD AVIYNNLRHP DDNEWNHVSM CIVNGGGIRS PIDERANNGI
241  ITLEELTSVL PFGGTFDLLQ IKGSALKQAF EHSVHRHGQG TGELLQVSGI KVVYDLSQKP GSRVVSLNVL CTKCRVPTYV
                                345                                 370
321  PLEMEKTYKV LLPSFLATGG DGYHMLKGDS SNHNSGDLDI SIVGDYIKRM EKVFPAVEGR VTFLDGTLFQ AQLFLTWGLC
401  ISLLFFIL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1
R.HGQGTGELLQVSGIK.V	N	95.91	1522.8103	15	0.4	762.4127	2	39.99	3	F3:11299	17112021_RID_2349_DP3.raw	2.7833E6
K.IQLQNYYSQEIGK.T	Y	93.83	1582.7991	13	0.7	792.4073	2	45.41	1	F1:13679	12112021_RID_2349_DP1.raw	8.8534E6
K.IIALGHSGFFEDQR.I	N	93.42	1588.7997	14	0.8	795.4078	2	47.13	2	F2:13392	12112021_RID_2349_DP2.raw	1.2282E6
K.VLLPSFLATGGDGYHMLK.G	Y	87.27	1918.0022	18	0.7	960.0090	2	60.01	3	F3:17866	17112021_RID_2349_DP3.raw	
R.VPTYVPLEMEKTYK.V	N	87.11	1696.8745	14	0.4	566.6323	3	45.65	1	F1:13767	12112021_RID_2349_DP1.raw	5.018E6
K.ASGNPILLNKDIPEDQVVKAQVNK.M	Y	87.11	2589.4126	24	1.2	864.1459	3	45.05	1	F1:13591	12112021_RID_2349_DP1.raw	9.398E6
K.ASGNPILLNKDIPEDQVVK.A	Y	83.55	2049.1106	19	0.8	684.0447	3	45.02	1	F1:13569	12112021_RID_2349_DP1.raw	3.5624E7
R.QVPVVQAYAFGK.Y	N	78.42	1305.7081	12	0.2	653.8615	2	46.67	2	F2:13272	12112021_RID_2349_DP2.raw	4.2275E6
K.DIPEDQVVKAQVNK.M	Y	77.75	1581.8362	14	1.0	791.9261	2	34.51	1	F1:10105	12112021_RID_2349_DP1.raw	1.479E6
K.QAFEHSVHR.H	N	75.67	1109.5366	9	0.7	555.7760	2	21.01	1	F1:5462	12112021_RID_2349_DP1.raw	1.4117E6
R.VPTYVPLEMEK.T	N	71.68	1304.6686	11	0.5	653.3419	2	47.31	2	F2:13493	12112021_RID_2349_DP2.raw	8.3497E6
R.MEKVFPAVEGR.V	N	70.69	1261.6488	11	0.2	421.5570	3	35.91	1	F1:10572	12112021_RID_2349_DP1.raw	6.3631E6
R.DEVEELQIHANK.L	N	70.10	1423.6943	12	0.6	712.8549	2	34.19	4	F4:9279	17112021_RID_2349_DP4.raw	
K.ASGNPILLNK.D	N	67.11	1025.5869	10	-0.1	513.8007	2	34.04	1	F1:9894	12112021_RID_2349_DP1.raw	2.3772E7
R.VTFLDGTLFQA.Q	Y	67.07	1210.6234	11	0.9	606.3195	2	72.56	1	F1:22584	12112021_RID_2349_DP1.raw	1.349E5
R.VPTYVPLEM(+15.99)EK.T	N	64.43	1320.6635	11	0.7	661.3395	2	41.27	1	F1:12376	12112021_RID_2349_DP1.raw	5.2823E6
K.ETPVLSNPGPYLEFR.D	N	63.99	1717.8674	15	0.3	859.9412	2	55.85	4	F4:16529	17112021_RID_2349_DP4.raw	
K.VGIIGYTTK.E	N	60.94	950.5436	9	-0.2	476.2790	2	37.93	1	F1:11149	12112021_RID_2349_DP1.raw	9.0552E6
K.RMEKVFPAVEGR.V	N	60.62	1417.7500	12	-0.5	473.5904	3	38.18	1	F1:11332	12112021_RID_2349_DP1.raw	1.0596E6
R.M(+15.99)EKVFPAVEGR.V	N	56.35	1277.6438	11	-0.1	426.8885	3	34.90	1	F1:10583	12112021_RID_2349_DP1.raw	4.4201E6
K.VFPAVEGR.V	N	54.60	873.4708	8	0.2	437.7428	2	33.73	1	F1:9818	12112021_RID_2349_DP1.raw	2.3327E7
R.VPTYVPLEM(+15.99)EKTYK.V	N	53.59	1712.8695	14	-0.2	571.9637	3	45.68	1	F1:13801	12112021_RID_2349_DP1.raw	1.6172E6
K.VVYDLSQKPGSR.V	N	53.26	1347.7146	12	0.8	674.8651	2	28.72	7	F7:7430	17112021_RID_2349_DP7.raw	
K.ASGNPILLNKD.I	N	52.23	1140.6139	11	0.6	571.3146	2	34.93	4	F4:9472	17112021_RID_2349_DP4.raw	
R.VTFLDGTLFQ.A	Y	52.01	1139.5863	10	0.1	570.8005	2	71.52	1	F1:22214	12112021_RID_2349_DP1.raw	1.731E6
K.VFPAVEGRVTFLD.G	Y	50.74	1448.7664	13	0.1	725.3905	2	58.64	1	F1:18050	12112021_RID_2349_DP1.raw	2.5813E5
K.VFPAVEGRVTFLDGTLF.Q	Y	49.96	1866.9879	17	1.5	934.5026	2	72.35	1	F1:22539	12112021_RID_2349_DP1.raw	6.8832E5
K.LTTLGVNK.I	N	48.37	844.5018	8	-0.2	423.2581	2	28.18	2	F2:6923	12112021_RID_2349_DP2.raw	1.9323E6
R.VTFLDGTLFQAQ.L	Y	48.28	1338.6819	12	1.0	670.3489	2	70.39	1	F1:21836	12112021_RID_2349_DP1.raw	2.3504E5
K.DIPEDQVVK.A	Y	47.98	1041.5342	9	0.0	521.7744	2	33.23	1	F1:9696	12112021_RID_2349_DP1.raw	6.0307E6
K.VLLPSFLATGGDGYHM(+15.99)LK.G	Y	47.16	1933.9971	18	1.6	968.0073	2	55.51	4	F4:16340	17112021_RID_2349_DP4.raw	
L.NKDIPEDQVVK.A	Y	45.22	1283.6721	11	0.5	642.8436	2	26.35	1	F1:7247	12112021_RID_2349_DP1.raw	5.8334E4
K.VLLPSFLATGGD.G	N	44.90	1188.6390	12	0.8	1189.6472	1	70.35	1	F1:21823	12112021_RID_2349_DP1.raw	1.8966E5
R.MEKVFPAVE.G	N	39.13	1048.5262	9	-0.6	525.2701	2	42.65	1	F1:12815	12112021_RID_2349_DP1.raw	2.9669E5

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MNVFFMFSLL FLATLGSCAD DKNPLEECFR EDDYEEFLEI AKNGLKKTSN PKHIVIVGAG MSGLSAAYVL AGAGHKVTVL
 81 EASERPGGRV RTHRNVKEGW YANLGPMRVP EKHRIIREYI RKFGLKLNEF VQETENGWYF IKNIRKRVGE VKKDPGLLKY
161 PVKPSEAGKS AGQLYQESLG KAVEELKRTN CSYILNKYDT YSTKEYLIKE GNLSPGAVDM IGDLLNEDSG YYVSFIESLK
241 HDDIFAYEKR FDEIVGGMDQ LPTSMYRAIE ESVHFKARVI KIQQNAEKVT VTYQTTQKNL LLETADYVIV CTTSRAARRI
321 TFKPPLPPKK AHALRSVHYR SGTKIFLTCT KKFWEDDGIQ GGKSTTDLPS RFIYYPNHNF TTGVGVIIAY GIGDDANFFQ
                                                   445
401 ALNLNECADI VFNDLSSIHQ LPKKDLQTFC YPSIIQKWSL DKYAMGAITT FTPYQFQHFS EALTAPVGRI FFAGEYTANA
481 HGWIDSTIKS GLTAARDVNR ASEL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
K.YAMGAITTFTPYQFQHFSEALTAPVGR.I	N	93.35	3003.4587	27	0.8	1002.1609	3	68.16	3	F3:20530	17112021_RID_2349_DP3.raw
R.NVKEGWYANLGPMR.V	N	89.97	1633.8035	14	1.1	817.9099	2	46.58	1	F1:14171	12112021_RID_2349_DP1.raw
K.SGLTAARDVNRASEL	N	81.95	1558.8063	15	-0.1	520.6093	3	35.16	1	F1:10323	12112021_RID_2349_DP1.raw
K.YDTYSTKEYLIK.E	N	80.80	1522.7555	12	0.9	762.3857	2	38.58	2	F2:10545	12112021_RID_2349_DP2.raw
K.YAM(+15.99)GAITTFTPYQFQHFSEALTAPVGR.I	N	80.23	3019.4539	27	0.9	1007.4928	3	64.54	3	F3:19257	17112021_RID_2349_DP3.raw
K.SAGQLYQESLGK.A	N	80.13	1279.6407	12	0.1	640.8277	2	34.93	1	F1:10235	12112021_RID_2349_DP1.raw
K.EGWYANLGPMR.V	N	74.35	1292.5972	11	0.2	647.3060	2	50.70	1	F1:15490	12112021_RID_2349_DP1.raw
R.EDDYEEFLEIAK.N	N	74.11	1499.6667	12	0.7	750.8412	2	59.88	5	F5:17908	17112021_RID_2349_DP5.raw
R.NVKEGWYANLGPM(+15.99)R.V	N	71.22	1649.7983	14	0.4	825.9067	2	41.24	1	F1:12368	12112021_RID_2349_DP1.raw
K.EGWYANLGPM(+15.99)R.V	N	70.55	1308.5920	11	0.5	655.3036	2	44.48	3	F3:12782	17112021_RID_2349_DP3.raw
K.HDDIFAYEK.R	N	70.19	1136.5138	9	0.4	569.2644	2	36.68	2	F2:9942	12112021_RID_2349_DP2.raw
R.VGEVKKDPGLLK.Y	N	63.88	1281.7656	12	-0.3	428.2624	3	28.13	1	F1:8041	12112021_RID_2349_DP1.raw
L.NEFVQETENGWYFIK.N	N	63.17	1902.8788	15	0.5	952.4471	2	60.53	2	F2:17717	12112021_RID_2349_DP2.raw
D.DYEEFLEIAK.N	N	63.01	1255.5972	10	0.6	628.8062	2	58.64	1	F1:18007	12112021_RID_2349_DP1.raw
D.SGYYVSFIESLK.H	N	61.77	1391.6973	12	0.1	696.8560	2	60.36	3	F3:17967	17112021_RID_2349_DP3.raw
K.EGNLSPGAVDMIGDLLNED.S	N	61.67	1957.8938	19	0.0	979.9542	2	76.89	4	F4:23445	17112021_RID_2349_DP4.raw
R.DVNRASEL	N	60.54	902.4457	8	-0.6	452.2299	2	26.74	1	F1:7420	12112021_RID_2349_DP1.raw
K.VTVLEASERPGGR.V	N	60.35	1369.7313	13	-0.1	457.5843	3	29.25	1	F1:8170	12112021_RID_2349_DP1.raw
K.HDDIFAYEKR.F	N	60.12	1292.6149	10	0.0	431.8789	3	32.95	3	F3:8849	17112021_RID_2349_DP3.raw
R.NVKEGWYANL.G	N	59.21	1192.5876	10	-0.3	597.3009	2	47.98	1	F1:14543	12112021_RID_2349_DP1.raw
K.VTVLEASER.P	N	58.47	1002.5345	9	-0.5	502.2743	2	30.13	5	F5:7870	17112021_RID_2349_DP5.raw
R.AIEESVHFK.A	Y	58.30	1058.5397	9	-0.1	530.2770	2	29.87	7	F7:7843	17112021_RID_2349_DP7.raw
K.VTVTYQTTQK.N	N	57.89	1167.6135	10	0.3	584.8142	2	25.60	7	F7:6331	17112021_RID_2349_DP7.raw
K.SGLTAARDVNR.A	N	57.18	1158.6105	11	-0.1	387.2107	3	21.39	1	F1:5502	12112021_RID_2349_DP1.raw

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
Y.QFQHFSEALTAPVGR.I	N	56.85	1686.8478	15	0.7	844.4318	2	42.64	4	F4:12109	17112021_RID_2349_DP4.raw
N.AHGWIDSTIK.S	N	55.64	1126.5771	10	1.1	564.2964	2	35.13	3	F3:9624	17112021_RID_2349_DP3.raw
K.WSLDKYAMGA.I	N	55.33	1140.5273	10	0.5	571.2712	2	50.51	1	F1:15333	12112021_RID_2349_DP1.raw
K.STTDLPSR.F	N	55.31	875.4348	8	0.5	438.7249	2	22.15	1	F1:5769	12112021_RID_2349_DP1.raw
D.YEEFLEIAK.N	N	55.22	1140.5702	9	-0.1	571.2923	2	49.00	1	F1:14874	12112021_RID_2349_DP1.raw
H.FSEALTAPVGR.I	N	55.11	1146.6033	11	0.5	574.3092	2	39.16	5	F5:11001	17112021_RID_2349_DP5.raw
R.IFFAGEYTAN.A	N	54.27	1131.5237	10	0.8	1132.5319	1	55.58	1	F1:16980	12112021_RID_2349_DP1.raw
R.ITFKPPLPPK.K	N	54.10	1136.6957	10	0.3	379.9059	3	40.53	7	F7:11518	17112021_RID_2349_DP7.raw
N.DLSSIHQLPK.K	N	51.71	1136.6189	10	0.9	569.3173	2	34.51	1	F1:10039	12112021_RID_2349_DP1.raw
K.EGNLSPGAVDM(+15.99)IGDLLNED.S	N	51.30	1973.8888	19	0.5	987.9521	2	67.55	4	F4:20200	17112021_RID_2349_DP4.raw
S.AAYVLAGAGHK.V	N	50.59	1056.5715	11	1.1	529.2936	2	24.54	3	F3:6001	17112021_RID_2349_DP3.raw
D.LLNEDSGYYVSFIESLK.H	N	49.92	1975.9778	17	0.7	988.9969	2	68.81	3	F3:20708	17112021_RID_2349_DP3.raw
K.RFDEIVGGM(+15.99)D.Q	N	49.15	1153.5073	10	0.1	577.7610	2	38.54	3	F3:10739	17112021_RID_2349_DP3.raw
D.DIFAYEKR.F	N	48.19	1040.5291	8	0.1	521.2719	2	35.16	3	F3:9617	17112021_RID_2349_DP3.raw
K.YAMGAITTFTPY.Q	N	46.88	1334.6217	12	0.9	668.3187	2	64.07	4	F4:19119	17112021_RID_2349_DP4.raw
K.EGNLSPGAVDM(+15.99)IGD.L	N	46.09	1389.6082	14	0.2	695.8115	2	46.47	4	F4:13379	17112021_RID_2349_DP4.raw
K.RFDEIVGGMD.Q	N	45.54	1137.5125	10	-0.5	569.7632	2	45.56	3	F3:13157	17112021_RID_2349_DP3.raw
K.VTVLEASERPGGRVR.T	N	45.40	1624.9009	15	0.3	542.6411	3	30.01	1	F1:8563	12112021_RID_2349_DP1.raw
K.KFWEDDGIQGGK.S	N	44.74	1378.6517	12	-2.0	690.3318	2	35.62	7	F7:9823	17112021_RID_2349_DP7.raw
Q.HFSEALTAPVGR.I	N	42.43	1283.6622	12	0.5	642.8387	2	34.80	4	F4:9467	17112021_RID_2349_DP4.raw
K.YAMGAITTFTPYQF.Q	N	41.39	1609.7487	14	-0.2	805.8814	2	71.88	3	F3:21650	17112021_RID_2349_DP3.raw
L.SAAYVLAGAGHK.V	N	40.21	1143.6036	12	0.7	572.8095	2	26.75	5	F5:6718	17112021_RID_2349_DP5.raw
F.SEALTAPVGR.I	N	40.05	999.5349	10	-0.1	500.7746	2	30.20	3	F3:7936	17112021_RID_2349_DP3.raw
D.DIFAYEK.R	N	39.75	884.4279	7	0.8	885.4359	1	41.87	4	F4:11928	17112021_RID_2349_DP4.raw
K.RVGEVKKDPGLLK.Y	N	39.62	1437.8667	13	1.0	480.2967	3	39.89	1	F1:11650	12112021_RID_2349_DP1.raw
K.WSLDKYAMGAITTF.T	N	38.72	1602.7751	14	1.3	802.3959	2	67.34	3	F3:20215	17112021_RID_2349_DP3.raw

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MNVFFMFSLL FLATLGSCAD DKNPLEECFR EDDYEEFLEI AKNGLKKTSN PKHIVIVGAG MSGLSAAYVL AGAGHKVTVL
 81 EASERPGGRV RTHRNVKEGW YANLGPMRVP EKHRIIREYI RKFGLKLNEF VQETENGWYF IKNIRKRVGE VKKDPGLLKY
161 PVKPSEAGKS AGQLYQESLG KAVEELKRTN CSYILNKYDT YSTKEYLIKE GNLSPGAVDM IGDLLNEDSG YYVSFIESLK
241 HDDIFAYEKR FDEIVGGMDQ LPTSMYRAIE ESVHFKARVI KIQQNAEKVT VTYQTTQKNL LLETADYVIV CTTSRAARRI
321 TFKPPLPPKK AHALRSVHYR SGTKIFLTCT KKFWEDDGIQ GGKSTTDLPS RFIYYPNHNF TTGVGVIIAY GIGDDANFFQ
                                                445
401 ALNLNECADI VFNDLSSIHQ LPKKDLQTFC YPSIIQKWSL DKYAMGAITT FTPYQFQHFS EALTAPVGRI FFAGEYTANA
481 HGWIDSTIKS GLTAARDVNR ASEL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
K.YAMGAITTFTPYQFQHFSEALTAPVGR.I	N	93.35	3003.4587	27	0.8	1002.1609	3	68.16	3	F3:20530	17112021_RID_2349_DP3.raw
R.NVKEGWYANLGPMR.V	N	89.97	1633.8035	14	1.1	817.9099	2	46.58	1	F1:14171	12112021_RID_2349_DP1.raw
K.SGLTAARDVNRASEL	N	81.95	1558.8063	15	-0.1	520.6093	3	35.16	1	F1:10323	12112021_RID_2349_DP1.raw
K.YDTYSTKEYLIK.E	N	80.80	1522.7555	12	0.9	762.3857	2	38.58	2	F2:10545	12112021_RID_2349_DP2.raw
K.YAM(+15.99)GAITTFTPYQFQHFSEALTAPVGR.I	N	80.23	3019.4539	27	0.9	1007.4928	3	64.54	3	F3:19257	17112021_RID_2349_DP3.raw
K.SAGQLYQESLGK.A	N	80.13	1279.6407	12	0.1	640.8277	2	34.93	1	F1:10235	12112021_RID_2349_DP1.raw
K.EGWYANLGPMR.V	N	74.35	1292.5972	11	0.2	647.3060	2	50.70	1	F1:15490	12112021_RID_2349_DP1.raw
R.EDDYEEFLEIAK.N	N	74.11	1499.6667	12	0.7	750.8412	2	59.88	5	F5:17908	17112021_RID_2349_DP5.raw
R.NVKEGWYANLGPM(+15.99)R.V	N	71.22	1649.7983	14	0.4	825.9067	2	41.24	1	F1:12368	12112021_RID_2349_DP1.raw
K.EGWYANLGPM(+15.99)R.V	N	70.55	1308.5920	11	0.5	655.3036	2	44.48	3	F3:12782	17112021_RID_2349_DP3.raw
K.HDDIFAYEK.R	N	70.19	1136.5138	9	0.4	569.2644	2	36.68	2	F2:9942	12112021_RID_2349_DP2.raw
R.VGEVKKDPGLLK.Y	N	63.88	1281.7656	12	-0.3	428.2624	3	28.13	1	F1:8041	12112021_RID_2349_DP1.raw
L.NEFVQETENGWYFIK.N	N	63.17	1902.8788	15	0.5	952.4471	2	60.53	2	F2:17717	12112021_RID_2349_DP2.raw
D.DYEEFLEIAK.N	N	63.01	1255.5972	10	0.6	628.8062	2	58.64	1	F1:18007	12112021_RID_2349_DP1.raw
D.SGYYVSFIESLK.H	N	61.77	1391.6973	12	0.1	696.8560	2	60.36	3	F3:17967	17112021_RID_2349_DP3.raw
K.EGNLSPGAVDMIGDLLNED.S	N	61.67	1957.8938	19	0.0	979.9542	2	76.89	4	F4:23445	17112021_RID_2349_DP4.raw
R.DVNRASEL	N	60.54	902.4457	8	-0.6	452.2299	2	26.74	1	F1:7420	12112021_RID_2349_DP1.raw
K.VTVLEASERPGGR.V	N	60.35	1369.7313	13	-0.1	457.5843	3	29.25	1	F1:8170	12112021_RID_2349_DP1.raw
K.HDDIFAYEKR.F	N	60.12	1292.6149	10	0.0	431.8789	3	32.95	3	F3:8849	17112021_RID_2349_DP3.raw
R.NVKEGWYANL.G	N	59.21	1192.5876	10	-0.3	597.3009	2	47.98	1	F1:14543	12112021_RID_2349_DP1.raw
K.VTVLEASER.P	N	58.47	1002.5345	9	-0.5	502.2743	2	30.13	5	F5:7870	17112021_RID_2349_DP5.raw
R.AIEESVHFK.A	Y	58.30	1058.5397	9	-0.1	530.2770	2	29.87	7	F7:7843	17112021_RID_2349_DP7.raw
K.VTVTYQTTQK.N	N	57.89	1167.6135	10	0.3	584.8142	2	25.60	7	F7:6331	17112021_RID_2349_DP7.raw
K.SGLTAARDVNR.A	N	57.18	1158.6105	11	-0.1	387.2107	3	21.39	1	F1:5502	12112021_RID_2349_DP1.raw

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File
Y.QFQHFSEALTAPVGR.I	N	56.85	1686.8478	15	0.7	844.4318	2	42.64	4	F4:12109	17112021_RID_2349_DP4.raw
N.AHGWIDSTIK.S	N	55.64	1126.5771	10	1.1	564.2964	2	35.13	3	F3:9624	17112021_RID_2349_DP3.raw
K.WSLDKYAMGA.I	N	55.33	1140.5273	10	0.5	571.2712	2	50.51	1	F1:15333	12112021_RID_2349_DP1.raw
K.STTDLPSR.F	N	55.31	875.4348	8	0.5	438.7249	2	22.15	1	F1:5769	12112021_RID_2349_DP1.raw
D.YEEFLEIAK.N	N	55.22	1140.5702	9	-0.1	571.2923	2	49.00	1	F1:14874	12112021_RID_2349_DP1.raw
H.FSEALTAPVGR.I	N	55.11	1146.6033	11	0.5	574.3092	2	39.16	5	F5:11001	17112021_RID_2349_DP5.raw
R.IFFAGEYTAN.A	N	54.27	1131.5237	10	0.8	1132.5319	1	55.58	1	F1:16980	12112021_RID_2349_DP1.raw
R.ITFKPPLPPK.K	N	54.10	1136.6957	10	0.3	379.9059	3	40.53	7	F7:11518	17112021_RID_2349_DP7.raw
N.DLSSIHQLPK.K	N	51.71	1136.6189	10	0.9	569.3173	2	34.51	1	F1:10039	12112021_RID_2349_DP1.raw
K.EGNLSPGAVDM(+15.99)IGDLLNED.S	N	51.30	1973.8888	19	0.5	987.9521	2	67.55	4	F4:20200	17112021_RID_2349_DP4.raw
S.AAYVLAGAGHK.V	N	50.59	1056.5715	11	1.1	529.2936	2	24.54	3	F3:6001	17112021_RID_2349_DP3.raw
D.LLNEDSGYYVSFIESLK.H	N	49.92	1975.9778	17	0.7	988.9969	2	68.81	3	F3:20708	17112021_RID_2349_DP3.raw
K.RFDEIVGGM(+15.99)D.Q	N	49.15	1153.5073	10	0.1	577.7610	2	38.54	3	F3:10739	17112021_RID_2349_DP3.raw
D.DIFAYEKR.F	N	48.19	1040.5291	8	0.1	521.2719	2	35.16	3	F3:9617	17112021_RID_2349_DP3.raw
K.YAMGAITTFTPY.Q	N	46.88	1334.6217	12	0.9	668.3187	2	64.07	4	F4:19119	17112021_RID_2349_DP4.raw
K.EGNLSPGAVDM(+15.99)IGD.L	N	46.09	1389.6082	14	0.2	695.8115	2	46.47	4	F4:13379	17112021_RID_2349_DP4.raw
K.RFDEIVGGMD.Q	N	45.54	1137.5125	10	-0.5	569.7632	2	45.56	3	F3:13157	17112021_RID_2349_DP3.raw
K.VTVLEASERPGGRVR.T	N	45.40	1624.9009	15	0.3	542.6411	3	30.01	1	F1:8563	12112021_RID_2349_DP1.raw
K.KFWEDDGIQGGK.S	N	44.74	1378.6517	12	-2.0	690.3318	2	35.62	7	F7:9823	17112021_RID_2349_DP7.raw
Q.HFSEALTAPVGR.I	N	42.43	1283.6622	12	0.5	642.8387	2	34.80	4	F4:9467	17112021_RID_2349_DP4.raw
K.YAMGAITTFTPYQF.Q	N	41.39	1609.7487	14	-0.2	805.8814	2	71.88	3	F3:21650	17112021_RID_2349_DP3.raw
L.SAAYVLAGAGHK.V	N	40.21	1143.6036	12	0.7	572.8095	2	26.75	5	F5:6718	17112021_RID_2349_DP5.raw
F.SEALTAPVGR.I	N	40.05	999.5349	10	-0.1	500.7746	2	30.20	3	F3:7936	17112021_RID_2349_DP3.raw
D.DIFAYEK.R	N	39.75	884.4279	7	0.8	885.4359	1	41.87	4	F4:11928	17112021_RID_2349_DP4.raw
K.RVGEVKKDPGLLK.Y	N	39.62	1437.8667	13	1.0	480.2967	3	39.89	1	F1:11650	12112021_RID_2349_DP1.raw
K.WSLDKYAMGAITTF.T	N	38.72	1602.7751	14	1.3	802.3959	2	67.34	3	F3:20215	17112021_RID_2349_DP3.raw

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MIRFGNPSSS DKRRQRCWSW YWGGLLLLWA VAETRADIRY ATVYWLEAEK SFQIKDVLDK NGDAYGYYND TIQSTGWGIL
 81 EIKAGYGNQR ISNEILMYAA GFLEGYLTAS HMSDNFANLF PVMIKNVIIE QKVKDFIQKQ DEWTRQQIKN NKDDPFWRNA
161 GYVIAQLDGL YMGNVEWAKR QKRTPLTDFE ISFLNAVGDL LDLIPALNSQ LRKSDFRSMP DVSRIYQWDM GHCSALIKVL
241 PGYENIYFAH SSWFTYAATL RIYKHWDFKI TDPQTKTGRA SFSSYPGLLV SLDDFYILGS GLIMLQTTNS VFNFFLLKQV
                     336 337                                361
321 VPESLFAWER VRIANMMADS GKTWAQTFEK ENSGTYNNQY MILDTKKIKL QRSLEDGTLY IIEQIPKLVK YSDQTKVLRN
                                                435                     452
401 GYWPSYNIPF HKVIYNMSGY TEYVQRYGLE FSYEMAPRAK IFRRDQGKVT DMESMKHIMR YNNYKEDPYT KHNPCNTICC
                                                                                549
481 RQDLSHKSPV PAGCYDSKVA DISMAAKFTA YAISGPPVEK DLPVFSWVHF NQTKHQGLPE SYNFDFVTMK PVL
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1
R.SLEDGTLYIIEQIPK.L	N	90.40	1717.9138	15	0.5	859.9646	2	67.04	2	F2:19818	12112021_RID_2349_DP2.raw	1.408E6
K.ENSGTYNNQYMILDTK.K	N	89.12	1889.8466	16	0.8	945.9313	2	45.52	2	F2:12882	12112021_RID_2349_DP2.raw	
K.FTAYAISGPPVEK.D	Y	88.93	1378.7133	13	0.3	690.3641	2	43.87	2	F2:12308	12112021_RID_2349_DP2.raw	1.5569E5
R.YGLEFSYEMAPR.A	Y	88.54	1461.6598	12	0.5	731.8375	2	55.35	2	F2:16085	12112021_RID_2349_DP2.raw	2.0566E5
R.YGLEFSYEM(+15.99)APR.A	Y	85.59	1477.6547	12	0.8	739.8352	2	48.84	2	F2:14018	12112021_RID_2349_DP2.raw	
K.QVVPESLFAWER.V	Y	81.73	1459.7460	12	0.3	730.8805	2	59.87	2	F2:17521	12112021_RID_2349_DP2.raw	8.9291E4
R.IANMM(+15.99)ADSGK.T	N	76.74	1052.4630	10	-0.3	527.2386	2	24.17	2	F2:6829	12112021_RID_2349_DP2.raw	9.0092E4
K.TWAQTFEKENSGTYNNQYMILDTK.K	Y	75.94	2881.3228	24	0.0	961.4482	3	54.25	2	F2:15686	12112021_RID_2349_DP2.raw	
R.YNNYKEDPYTK.H	Y	75.77	1433.6462	11	1.1	717.8312	2	23.44	3	F3:5597	17112021_RID_2349_DP3.raw	2.3721E5
R.IANM(+15.99)MADSGK.T	N	75.38	1052.4630	10	-0.3	527.2386	2	24.17	2	F2:6725	12112021_RID_2349_DP2.raw	
R.DQGKVTDMESMK.H	N	72.75	1367.6061	12	0.5	684.8107	2	27.78	2	F2:6747	12112021_RID_2349_DP2.raw	
R.YATVYWLEAEK.S	N	72.57	1371.6710	11	0.7	686.8433	2	51.85	5	F5:15257	17112021_RID_2349_DP5.raw	
K.HQGLPESYNFDFVTM(+15.99)KPVL	N	71.29	2237.0828	19	0.8	746.7021	3	59.87	2	F2:17492	12112021_RID_2349_DP2.raw	
K.HQGLPESYNFDFVTMKPVL	N	70.10	2221.0876	19	0.3	1111.5514	2	65.61	2	F2:19349	12112021_RID_2349_DP2.raw	
K.ENSGTYNNQYM(+15.99)ILDTK.K	N	68.81	1905.8414	16	0.6	953.9286	2	41.00	2	F2:11307	12112021_RID_2349_DP2.raw	
K.FTAYAISGPPVEKD.L	Y	67.71	1493.7401	14	0.6	747.8778	2	44.70	3	F3:12805	17112021_RID_2349_DP3.raw	
R.NGYWPSYNIPFHK.V	Y	67.54	1621.7677	13	1.2	811.8921	2	51.95	2	F2:14850	12112021_RID_2349_DP2.raw	
R.DQGKVTDMESM(+15.99)K.H	N	66.01	1383.6010	12	0.7	692.8082	2	27.71	2	F2:6798	12112021_RID_2349_DP2.raw	
K.VADISMAAK.F	Y	62.72	904.4688	9	0.4	453.2418	2	29.56	2	F2:7416	12112021_RID_2349_DP2.raw	2.873E5
K.YSDQTKVLR.N	N	60.88	1108.5876	9	-0.4	555.3009	2	23.23	1	F1:6160	12112021_RID_2349_DP1.raw	4.0413E5
R.DQGKVTDM(+15.99)ESM(+15.99)K.H	N	60.55	1399.5959	12	-0.3	700.8051	2	27.86	2	F2:6821	12112021_RID_2349_DP2.raw	
K.TWAQTFEK.E	Y	59.18	1009.4869	8	0.9	505.7512	2	37.49	2	F2:10261	12112021_RID_2349_DP2.raw	
R.DQGKVTDM(+15.99)ESMK.H	N	55.19	1383.6010	12	0.0	692.8077	2	19.49	2	F2:3974	12112021_RID_2349_DP2.raw	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1
K.ENSGTYNNQYMILDTKK.I	N	48.36	2017.9415	17	0.5	673.6548	3	39.15	2	F2:10720	12112021_RID_2349_DP2.raw	
D.GTLYIIEQIPK.L	N	47.53	1273.7281	11	0.8	637.8719	2	53.61	4	F4:15815	17112021_RID_2349_DP4.raw	
K.TWAQTFEKENSGTYNNQYMILDTKK.I	Y	47.17	3009.4177	25	0.8	1004.1473	3	51.07	2	F2:14750	12112021_RID_2349_DP2.raw	
K.ENSGTYNNQYM(+15.99)ILDTKK.I	N	47.15	2033.9364	17	0.0	678.9861	3	39.23	2	F2:10730	12112021_RID_2349_DP2.raw	
K.SFQIKDVLDK.N	Y	46.69	1191.6499	10	0.9	596.8328	2	44.01	5	F5:12690	17112021_RID_2349_DP5.raw	
K.VLPGYENIYFAH.S	N	46.58	1421.6979	12	0.6	711.8566	2	53.52	2	F2:15534	12112021_RID_2349_DP2.raw	
K.VTDM(+15.99)ESMK.H	N	45.53	955.3990	8	-0.3	478.7067	2	24.77	2	F2:5754	12112021_RID_2349_DP2.raw	
K.HQGLPESYNFD.F	N	44.27	1305.5625	11	-0.5	653.7882	2	42.77	2	F2:11932	12112021_RID_2349_DP2.raw	
K.VTDMESM(+15.99)K.H	N	43.61	955.3990	8	-0.3	478.7067	2	24.77	2	F2:5660	12112021_RID_2349_DP2.raw	
K.VTDM(+15.99)ESM(+15.99)K.H	N	42.57	971.3940	8	-0.2	486.7042	2	24.80	2	F2:5663	12112021_RID_2349_DP2.raw	
R.IYKHWDFK.I	Y	42.43	1135.5814	8	0.2	379.5345	3	39.94	2	F2:10734	12112021_RID_2349_DP2.raw	
K.NNKDDPFWR.N	N	41.45	1190.5469	9	0.5	596.2810	2	35.13	5	F5:9629	17112021_RID_2349_DP5.raw	
K.VTDMESMK.H	N	39.74	939.4042	8	0.0	470.7094	2	24.77	2	F2:5674	12112021_RID_2349_DP2.raw	

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MQGMGIEDKS SKMHCMKGKH VAIICGVVIV VGLILGLGLG LGLDTEACNP PEVNEQVSTK SPISNTPDVT NPSGSSVFCS

                                                                      146
 81 AKNDENGPWT DFRLPNYVHP VHYDLHLTPE MEAEVYTGMV NISIRLEEQT TKHLWLHLRE TKITEMPQLR TSSGQVIEIK

161 RCFGYEPQEY VVIEAEEDLR PSNYFLSMKF KGYLNGSLVG FYSTTYGENG KIKYIAATDH EPTDARKSFP CFDEPNIKAT

241 YTISITHEHD YEAISNMPVE KTISIDNKWT KTIFKKSVPM STYLVAWAVH QFKYEERISS RGIPLRIYAQ PQQINTAIYA
321 ANVTKVVFDY FENYFNMNYS LPKLDKIAIP DFGTGAMENW GLITYRETNL LYDSQESAAS NKQRVATVIA HELVHQWFGN

401 IVTMDWWDDL WLNEGFASFF EYMGVNAKEE KWQMLDQILI ADVLPVLKDD SLVSSHAITV NVSSPDEITS VFDGISYSKG
481 ASILRMLEDW ISPDHFRAGC QKYLKTHYFK NAKTDDFWKA MEEVSGKPVR DVMDTWTRQM GYPVLKVDLS STVTQQRFLL

561 DPKADPSKPS SEFSYKWNIP VKWKEGNTSN IIFYNKSELA GITITRPSDL PPNSFLKVNK DHVGFYRVNY EPQVWRALTD

                                                                  704
641 IMMKDHQNFN LADRAGFIDD AFALARAGLL KYADALNLTR YLQNEIEYIP WQRAVVAVSY IRHMLEDDKA LYPKFQRYFG

721 NLVKPIASEL KWENDEDHIK SLLRTTVLEF ACNMDDPEAL GNASLLFKSW TSGISLDVNL RLLVYRFGMQ NSGDEQAWNY

801 MFQKYRIATL AQEKEKLLYG LASVKNITLL NRFLNCIKNT SLIRSQDVFT VLRYISFNSY GKTMAWDWVR LNWEYLVKRY

881 TLNDRNLGRL ISSISGTFNT ELQLWQMENF FERYPDAGAG EASRKQALET TKSNIEWLKQ YRDDVATWLE NSEHPKFA
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
R.AGFIDDAFALAR.A	Y	82.36	1265.6404	12	0.1	633.8275	2	61.37	1	F1:18887	12112021_RID_2349_DP1.raw	5.6662E6	2.7487E
R.YLQNEIEYIPWQR.A	Y	81.85	1750.8678	13	0.8	876.4419	2	57.41	1	F1:17599	12112021_RID_2349_DP1.raw	4.2599E6	1.9498E
R.ETNLLYDSQESAASNK.Q	Y	79.61	1768.8115	16	1.0	885.4139	2	37.10	2	F2:10076	12112021_RID_2349_DP2.raw	2.2867E5	2.6048E
K.YIAATDHEPTDAR.K	Y	77.36	1458.6738	13	0.8	730.3448	2	24.63	1	F1:6617	12112021_RID_2349_DP1.raw	5.1544E5	
R.HMLEDDKALYPK.F	Y	74.41	1458.7177	12	0.1	487.2466	3	38.63	1	F1:11459	12112021_RID_2349_DP1.raw	1.8307E6	
K.NDENGPWTDFR.L	Y	73.51	1349.5636	11	0.3	675.7893	2	46.11	1	F1:13951	12112021_RID_2349_DP1.raw	3.5973E5	5.0695E

total 32

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
K.YIAATDHEPTDARK.S	Y	69.82	1586.7688	14	0.7	794.3922	2	21.59	1	F1:5582	12112021_RID_2349_DP1.raw	3.4793E6	
R.MLEDWISPDHFR.A	Y	67.50	1544.7081	12	1.1	773.3622	2	54.12	1	F1:16564	12112021_RID_2349_DP1.raw	1.5051E5	
R.FGMQNSGDEQAWNYMFQK.Y	Y	66.58	2179.9092	18	-0.2	1090.9617	2	58.16	3	F3:17233	17112021_RID_2349_DP3.raw		3.2503E
R.SQDVFTVLR.Y	Y	66.02	1063.5662	9	-0.4	532.7902	2	47.74	1	F1:14400	12112021_RID_2349_DP1.raw	1.7467E6	2.2202E
K.VDLSSTVTQQR.F	Y	65.72	1232.6361	11	4.7	617.3282	2	32.63	2	F2:8691	12112021_RID_2349_DP2.raw	4.1055E7	6.9159E
R.VNYEPQVWR.A	Y	64.09	1189.5880	9	-0.2	595.8011	2	41.81	1	F1:12508	12112021_RID_2349_DP1.raw	5.2545E6	
R.DVMDTWTR.Q	Y	63.49	1022.4492	8	0.2	512.2319	2	43.94	1	F1:13265	12112021_RID_2349_DP1.raw	3.9974E5	
R.YPDAGAGEASR.K	Y	63.05	1092.4835	11	0.3	547.2492	2	22.63	1	F1:5917	12112021_RID_2349_DP1.raw	3.2708E5	3.7776E
R.AVVAVSYIR.H	Y	61.55	976.5706	9	-0.4	489.2924	2	40.15	1	F1:11950	12112021_RID_2349_DP1.raw	5.7775E6	1.9065E
K.VNKDHVGFYR.V	Y	60.88	1233.6254	10	0.0	617.8199	2	29.25	1	F1:8313	12112021_RID_2349_DP1.raw	2.0841E6	
R.TSSGQVIEIKR.C	Y	59.17	1216.6775	11	0.0	609.3460	2	27.07	1	F1:7509	12112021_RID_2349_DP1.raw	2.1937E6	
K.AMEEVSGKPVR.D	Y	59.15	1201.6124	11	0.6	601.8138	2	21.99	1	F1:5707	12112021_RID_2349_DP1.raw	2.2834E5	
K.ITEMPQLR.T	Y	58.29	986.5219	8	-0.1	494.2682	2	37.37	1	F1:11034	12112021_RID_2349_DP1.raw	1.9443E6	
K.TMAWDWVR.L	Y	54.89	1063.4910	8	0.1	532.7528	2	53.75	3	F3:15730	17112021_RID_2349_DP3.raw		
R.TSSGQVIEIK.R	Y	54.73	1060.5764	10	-0.3	531.2953	2	31.42	4	F4:8292	17112021_RID_2349_DP4.raw	2.0041E5	
R.QMGYPVLK.V	Y	54.53	934.4946	8	-0.5	468.2543	2	38.30	1	F1:11404	12112021_RID_2349_DP1.raw	2.02E6	
K.QYRDDVATWLENSEHPK.F	Y	53.56	2086.9707	17	0.5	696.6646	3	46.31	3	F3:13434	17112021_RID_2349_DP3.raw		
R.YISFNSYGK.T	Y	51.64	1077.5131	9	-0.5	539.7635	2	39.29	1	F1:11645	12112021_RID_2349_DP1.raw	8.8725E5	
K.ITEM(+15.99)PQLR.T	Y	49.55	1002.5168	8	0.8	502.2661	2	37.31	1	F1:10990	12112021_RID_2349_DP1.raw	8.909E5	
R.M(+15.99)LEDWISPDHFR.A	Y	47.01	1560.7031	12	1.0	781.3596	2	51.01	1	F1:15476	12112021_RID_2349_DP1.raw	6.1745E4	
R.ALTDIM(+15.99)MK.D	Y	47.00	937.4613	8	0.1	469.7380	2	44.85	1	F1:13477	12112021_RID_2349_DP1.raw	6.7217E4	
R.LNWEYLVK.R	Y	44.24	1063.5702	8	0.0	532.7924	2	53.65	3	F3:15847	17112021_RID_2349_DP3.raw		
K.ADPSKPSSEFSYK.W	Y	42.02	1441.6725	13	0.0	721.8435	2	29.31	1	F1:8282	12112021_RID_2349_DP1.raw	1.8949E5	
K.VDLSSTVTQQRFLLD.P	Y	41.88	1720.8995	15	0.1	861.4572	2	57.49	1	F1:17638	12112021_RID_2349_DP1.raw	6.4276E4	
K.LLYGLASVK.N	Y	41.79	962.5800	9	0.3	482.2974	2	45.33	3	F3:13034	17112021_RID_2349_DP3.raw		
R.HM(+15.99)LEDDKALYPK.F	Y	40.30	1474.7125	12	0.3	492.5783	3	35.26	1	F1:10364	12112021_RID_2349_DP1.raw	7.7591E5	

total 32

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2

total

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
K.KVLNEDEQTREPTEK.F	Y	86.02	1814.9010	15	0.9	908.4586	2	20.05	3	F3:4488	17112021_RID_2349_DP3.raw	1.2849E6	1.492E6
K.VLNEDEQTREPTEK.F	Y	84.29	1686.8060	14	0.1	844.4104	2	21.98	3	F3:5114	17112021_RID_2349_DP3.raw	4.6932E5	8.6582E5
R.IMGWGTITTTK.V	N	78.23	1207.6271	11	-0.4	604.8206	2	47.11	3	F3:13741	17112021_RID_2349_DP3.raw	1.7839E6	2.7374E7
R.IM(+15.99)GWGTITTTK.V	N	67.99	1223.6221	11	0.3	612.8185	2	40.75	2	F2:11290	12112021_RID_2349_DP2.raw	7.1945E5	1.2257E7
K.TSTHIAPLSLPSSAPSVG.S	Y	64.26	1720.8995	18	0.0	861.4570	2	49.46	4	F4:14366	17112021_RID_2349_DP4.raw		
K.VLNEDEQTR.E	N	63.83	1102.5254	9	0.5	552.2703	2	19.87	4	F4:4313	17112021_RID_2349_DP4.raw		
A.GYQNNDWDKDIMLIK.L	Y	60.88	1851.8826	15	0.1	926.9486	2	52.32	4	F4:15363	17112021_RID_2349_DP4.raw		
K.TSTHIAPLSLPSS.A	N	60.21	1309.6877	13	-0.1	655.8511	2	44.76	4	F4:12858	17112021_RID_2349_DP4.raw		
K.TSTHIAPLSLPSSAPSVGSV.C	Y	59.73	1907.0000	20	-0.1	954.5072	2	53.14	4	F4:15583	17112021_RID_2349_DP4.raw		
D.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6
N.DWDKDIMLIK.L	Y	56.94	1275.6533	10	0.0	638.8339	2	53.04	4	F4:15596	17112021_RID_2349_DP4.raw		
K.KVLNEDEQTR.E	N	55.31	1230.6204	10	0.8	616.3179	2	16.73	4	F4:3273	17112021_RID_2349_DP4.raw		
N.SDNFQMQFGVHSK.K	N	55.26	1523.6827	13	0.6	762.8491	2	41.31	4	F4:11754	17112021_RID_2349_DP4.raw		
N.NDWDKDIMLIK.L	Y	53.12	1389.6962	11	-0.9	695.8547	2	51.77	4	F4:15198	17112021_RID_2349_DP4.raw		
D.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6
C.AGYQNNDWDKDIMLIK.L	Y	50.85	1922.9197	16	0.5	641.9808	3	52.44	4	F4:15407	17112021_RID_2349_DP4.raw		
K.TSTHIAPLSLPSSAPS.V	Y	49.77	1564.8097	16	0.1	783.4122	2	45.91	5	F5:13244	17112021_RID_2349_DP5.raw		
N.NDWDKDIM(+15.99)LIK.L	Y	48.22	1405.6912	11	0.8	703.8534	2	47.57	4	F4:13818	17112021_RID_2349_DP4.raw		
K.VLNEDEQTREPT.E	Y	47.20	1429.6685	12	0.5	715.8419	2	25.27	4	F4:6180	17112021_RID_2349_DP4.raw		
Y.QNNDWDKDIMLIK.L	Y	44.19	1631.7977	13	0.5	544.9401	3	50.35	4	F4:14806	17112021_RID_2349_DP4.raw		
K.KVLNEDEQTRE.P	N	43.42	1359.6630	11	0.2	680.8389	2	18.27	4	F4:3798	17112021_RID_2349_DP4.raw		
A.GYQNNDWDK.D	Y	42.46	1138.4679	9	-0.2	570.2411	2	26.69	4	F4:6675	17112021_RID_2349_DP4.raw		
K.VLNEDEQTREPTEKFY.C	Y	42.44	1996.9377	16	0.0	999.4762	2	36.81	4	F4:10173	17112021_RID_2349_DP4.raw		
N.SDNFQM(+15.99)QFGVHSK.K	N	42.19	1539.6776	13	1.2	770.8470	2	32.62	4	F4:8609	17112021_RID_2349_DP4.raw		
F.QMQFGVHSK.K	N	40.86	1060.5125	9	0.7	531.2639	2	24.46	4	F4:5894	17112021_RID_2349_DP4.raw		
K.KVLNEDEQTREPTEKFY.C	Y	40.79	2125.0327	17	0.6	709.3519	3	34.27	4	F4:9275	17112021_RID_2349_DP4.raw		
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw		
K.TSTHIAPLSLPSSAPSVGS.V	Y	39.31	1807.9315	19	0.9	904.9738	2	49.11	4	F4:14246	17112021_RID_2349_DP4.raw		

total

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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                                                                                                  74
  1  MANVLCSCSE DCLEKKDCCT DYKSICKGET SWLKDQCASS SAAQCPAGFE QSPLILFSMD GFRAGYLETW DSLMPNINKL
 81  KTCGTHAKYM RAVYPTKTFV NHYTIVTGLY PESHGIIDNN IYDVTLNLNF SLSAPTMTNP AWWGGQPIWH TVTYQGLKAA
161  TYFWPGSEVK INGSYPTIYK VYNKSIPFEA RVTEVLKWLD LPKAERPDFV TLYIEEPDTT GHKFGPVSGE IIMALQMADR
241  TLGMLMEGLK QRNLHNCVNL ILLADHGMEQ ISCNRLEYMT DYFDKVDFFM YEGPAPRIRS KNVPKDFYTF DSEGIVRNLT
321  CQKPKQYFKA YLAKDLPKRL HYVNNIRIDK VNLMVDQQWM AVRNKNYNRC NGGTHGYDNE FKSMQAIFLA HGPGFKGKNE
401  VTSFENIEVY NLMCDLLKLK PAPNNGTHGS LNHLLKNPFY NPSPAKEQSS PLLCPFGPVP SPDVSGCKCS SITDLGKVNE
481  RLNLNNQAKT ESEAHNLPYG RPQVLQNHSK YCLLHQAKYI SAYSQDILMP LWSSYTINKS PPTSVPPSAS DCLRLDVRIP
561  AAQSQTCSNY QPDLTITPGF LYPPNFGSSN FEQYDALITS NLVPMFKGFT RLWNYFHGTL LPKYARERNG LNVISGPIFD
641  YNYDGHFDSY DTIKEHVNDT KIPIPTHFFV VLTSCENQIN TPLNCPGSLK VLSFILPHRP DNSESCADTS PDNLWVEERI
721  QTHTARVRDV ELLTGLNFYS GLKQSLPETL QLKTFLPIFV NPVN
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
												total	1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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                                                                                                  74
  1  MANVLCSCSE DCLEKKDCCT DYKSICKGET SWLKDQCASS SAAQCPAGFE QSPLILFSMD GFRAGYLETW DSLMPNINKL
 81  KTCGTHAKYM RAVYPTKTFV NHYTIVTGLY PESHGIIDNN IYDVTLNLNF SLSAPTMTNP AWWGGQPIWH TVTYQGLKAA
161  TYFWPGSEVK INGSYPTIYK VYNKSIPFEA RVTEVLKWLD LPKAERPDFV TLYIEEPDTT GHKFGPVSGE IIMALQMADR
241  TLGMLMEGLK QRNLHNCVNL ILLADHGMEQ ISCNRLEYMT DYFDKVDFFM YEGPAPRIRS KNVPKDFYTF DSEGIVRNLT
321  CQKPKQYFKA YLAKDLPKRL HYVNNIRIDK VNLMVDQQWM AVRNKNYNRC NGGTHGYDNE FKSMQAIFLA HGPGFKGKNE
401  VTSFENIEVY NLMCDLLKLK PAPNNGTHGS LNHLLKNPFY NPSPAKEQSS PLLCPFGPVP SPDVSGCKCS SITDLGKVNE
481  RLNLNNQAKT ESEAHNLPYG RPQVLQNHSK YCLLHQAKYI SAYSQDILMP LWSSYTINKS PPTSVPPSAS DCLRLDVRIP
561  AAQSQTCSNY QPDLTITPGF LYPPNFGSSN FEQYDALITS NLVPMFKGFT RLWNYFHGTL LPKYARERNG LNVISGPIFD
641  YNYDGHFDSY DTIKEHVNDT KIPIPTHFFV VLTSCENQIN TPLNCPGSLK VLSFILPHRP DNSESCADTS PDNLWVEERI
721  QTHTARVRDV ELLTGLNFYS GLKQSLPETL QLKTFLPIFV NPVN
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
												total	1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MASGCSCDDK CTERQACCQD YEDTCVLPTQ SWSCSKLRCS EKRMANVLCS CSEDCLEKKD CCTDYKSICK GETSWLKDQC
                                        117
 81 ASSSAAQCPA GFEQSPLILF SMDGFRAGYL ETWDSLMPNI NKLKTCGTHA KYMRAVYPTK TFVNHYTIVT GLYPESHGII
161 DNNIYDVTLN LNFSLSAPTM TNPAWWGGQP IWHTVTYQGL KAATYFWPGS EVKINGSYPT IYKVYNKSIP FEARVTEVLK
241 WLDLPKAERP DFVTLYIEEP DTTGHKFGPV SGEIIMALQM ADRTLGMLME GLKQRNLHNC VNLILLADHG MEQISCNRLE
321 YMTDYFDKVD FFMYEGPAPR IRSKNVPKDF YTFDSEGIVR NLTCQKPKQY FKAYLAKDLP KRLHYVNNIR IDKVNLMVDQ
401 QWMAVRNKNY NRCNGGTHGY DNEFKSMQAI FLAHGPGFKG KNEVTSFENI EVYNLMCDLL KLKPAPNNGT HGSLNHLLKN
481 PFYNPSPAKE QSSPLLCPFG PVPSPDVSGC KCSSITDLGK VNERLNLNNQ AKTESEAHNL PYGRPQVLQN HSKYCLLHQA
561 KYISAYSQDI LMPLWSSYTI NKSPPTSVPP SASDCLRLDV RIPAAQSQTC SNYQPDLTIT PGFLYPPNFG SSNFEQYDAL
641 ITSNLVPMFK GFTRLWNYFH GTLLPKYARE RNGLNVISGP IFDYNYDGHF DSYDTIKEHV NDTKIPIPTH FFVVLTSCEN
721 QINTPLNCPG SLKVLSFILP HRPDNSESCA DTSPDNLWVE ERIQTHTARV RDVELLTGLN FYSGLKQSLP ETLQLKTFLP
801 IFVNPVN
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
												total	1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MIQQKVLFIS LVAVALGLGL GLGLKESVEP QVSCRYRCNE TFSKMASGCS CDDKCTERQA CCQDYEDTCV LPTQSWSCSK
 81 LRCSEKRMAN VLCSCSEDCL EKKDCCTDYK SICKGETSWL KDQCASSSAA QCPAGFEQSP LILFSMDGFR AGYLETWDSL

161 MPNINKLKTC GTHAKYMRAV YPTKTFVNHY TIVTGLYPES HGIIDNNIYD VTLNLNFSLS APTMTNPAWW GGQPIWHTVT

241 YQGLKAATYF WPGSEVKING SYPTIYKVYN KSIPFEARVT EVLKWLDLPK AERPDFVTLY IEEPDTTGHK FGPVSGEIIM

321 ALQMADRTLG MLMEGLKQRN LHNCVNLILL ADHGMEQISC NRLEYMTDYF DKVDFFMYEG PAPRIRSKNV PKDFYTFDSE

401 GIVRNLTCQK PKQYFKAYLA KDLPKRLHYV NNIRIDKVNL MVDQQWMAVR NKNYNRCNGG THGYDNEFKS MQAIFLAHGP

481 GFKGKNEVTS FENIEVYNLM CDLLKLKPAP NNGTHGSLNH LLKNPFYNPS PAKEQSSPLL CPFGPVPSPD VSGCKCSSIT

561 DLGKVNERLN LNNQAKTESE AHNLPYGRPQ VLQNHSKYCL LHQAKYISAY SQDILMPLWS SYTINKSPPT SVPPSASDCL

641 RLDVRIPAAQ SQTCSNYQPD LTITPGFLYP PNFGSSNFEQ YDALITSNLV PMFKGFTRLW NYFHGTLLPK YARERNGLNV
721 ISGPIFDYNY DGHFDSYDTI KEHVNDTKIP IPTHFFVVLT SCENQINTPL NCPGSLKVLS FILPHRPDNS ESCADTSPDN
801 LWVEERIQTH TARVRDVELL TGLNFYSGLK QSLPETLQLK TFLPIFVNPV N
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
													total 1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MIQQKVLFIS LVAVALGLGL GLGLKESVEP QAQSWSCSKL RCSEKRMANV LCSCSEDCLE KKDCCTDYKS ICKGETSWLK
                                                 120
 81  DQCASSSAAQ CPAGFEQSPL ILFSMDGFRA GYLETWDSLM PNINKLKTCG THAKYMRAVY PTKTFVNHYT IVTGLYPESH
161  GIIDNNIYDV TLNLNFSLSA PTMTNPAWWG GQPIWHTVTY QGLKAATYFW PGSEVKINGS YPTIYKVYNK SIPFEARVTE
241  VLKWLDLPKA ERPDFVTLYI EEPDTTGHKF GPVSGEIIMA LQMADRTLGM LMEGLKQRNL HNCVNLILLA DHGMEQISCN
321  RLEYMTDYFD KVDFFMYEGP APRIRSKNVP KDFYTFDSEG IVRNLTCQKP KQYFKAYLAK DLPKRLHYVN NIRIDKVNLM
401  VDQQWMAVRN KNYNRCNGGT HGYDNEFKSM QAIFLAHGPG FKGKNEVTSF ENIEVYNLMC DLLKLKPAPN NGTHGSLNHL
481  LKNPFYNPSP AKEQSSPLLC PFGPVPSPDV SGCKCSSITD LGKVNERLNL NNQAKTESEA HNLPYGRPQV LQNHSKYCLL
561  HQAKYISAYS QDILMPLWSS YTINKSPPTS VPPSASDCLR LDVRIPAAQS QTCSNYQPDL TITPGFLYPP NFGSSNFEQY
641  DALITSNLVP MFKGFTRLWN YFHGTLLPKY ARERNGLNVI SGPIFDYNYD GHFDSYDTIK EHVNDTKIPI PTHFFVVLTS
721  CENQINTPLN CPGSLKVLSF ILPHRPDNSE SCADTSPDNL WVEERIQTHT ARVRDVELLT GLNFYSGLKQ SLPETLQLKT
801  FLPIFVNPVN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
												total	1

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Protein Coverage:

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  1 MEMFPEDETE RGKKRTLDLI DFQTETIIKR STLRKYKILC VVLFISLVAV ALGLGLGLGL KESVEPQVSC RYRCNETFSK
 81 MASGCSCDDK CTERQACCQD YEDTCVLPTQ SWSCSKLRCS EKRMANVLCS CSEDCLEKKD CCTDYKSICK GETSWLKDQC
                                        197
161 ASSSAAQCPA GFEQSPLILF SMDGFRAGYL ETWDSLMPNI NKLKTCGTHA KYMRAVYPTK TFVNHYTIVT GLYPESHGII
241 DNNIYDVTLN LNFSLSAPTM TNPAWWGGQP IWHTVTYQGL KAATYFWPGS EVKINGSYPT IYKVYNKSIP FEARVTEVLK
321 WLDLPKAERP DFVTLYIEEP DTTGHKFGPV SGEIIMALQM ADRTLGMLME GLKQRNLHNC VNLILLADHG MEQISCNRLE
401 YMTDYFDKVD FFMYEGPAPR IRSKNVPKDF YTFDSEGIVR NLTCQKPKQY FKAYLAKDLP KRLHYVNNIR IDKVNLMVDQ
481 QWMAVRNKNY NRCNGGTHGY DNEFKSMQAI FLAHGPGFKG KNEVTSFENI EVYNLMCDLL KLKPAPNNGT HGSLNHLLKN
561 PFYNPSPAKE QSSPLLCPFG PVPSPDVSGC KCSSITDLGK VNERLNLNNQ AKTESEAHNL PYGRPQVLQN HSKYCLLHQA
641 KYISAYSQDI LMPLWSSYTI NKSPPTSVPP SASDCLRLDV RIPAAQSQTC SNYQPDLTIT PGFLYPPNFG SSNFEQYDAL
721 ITSNLVPMFK GFTRLWNYFH GTLLPKYARE RNGLNVISGP IFDYNYDGHF DSYDTIKEHV NDTKIPIPTH FFVVLTSCEN
801 QINTPLNCPG SLKVLSFILP HRPDNSESCA DTSPDNLWVE ERIQTHTARV RDVELLTGLN FYSGLKQSLP ETLQLKTFLP
881 IFVNPVN
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.DFYTFDSEGIVR.N	Y	89.31	1447.6619	12	0.7	724.8387	2	56.67	1	F1:17397	12112021_RID_2349_DP1.raw	1.3223E6	
K.NPFYNPSPAK.E	N	84.62	1133.5505	10	0.0	567.7825	2	34.93	1	F1:10324	12112021_RID_2349_DP1.raw	1.138E7	1.617
K.SMQAIFLAHGPGFK.G	Y	77.40	1502.7704	14	1.0	752.3932	2	50.76	1	F1:15524	12112021_RID_2349_DP1.raw	2.4779E5	
K.AATYFWPGSEVK.I	N	74.08	1354.6558	12	0.4	678.3354	2	50.11	1	F1:15322	12112021_RID_2349_DP1.raw	1.6628E6	1.581
K.TFLPIFVNPVN	Y	72.44	1259.6914	11	0.6	630.8533	2	74.54	1	F1:23258	12112021_RID_2349_DP1.raw	1.257E7	
R.AGYLETWDSLMPNINK.L	Y	71.20	1850.8872	16	0.6	926.4514	2	65.24	1	F1:20092	12112021_RID_2349_DP1.raw	7.1448E5	1.049
R.TLGMLMEGLK.Q	N	65.62	1091.5719	10	-0.1	546.7932	2	53.13	1	F1:16226	12112021_RID_2349_DP1.raw	2.9888E5	
K.VNERLNLNNQAK.T	Y	65.11	1411.7532	12	-0.6	471.5914	3	25.48	1	F1:6986	12112021_RID_2349_DP1.raw	2.9466E6	
K.VNLMVDQQWMAVR.N	N	63.98	1588.7854	13	0.2	795.4001	2	56.99	1	F1:17428	12112021_RID_2349_DP1.raw	1.178E5	
R.TLGMLM(+15.99)EGLK.Q	N	62.95	1107.5668	10	0.0	554.7906	2	53.06	1	F1:16245	12112021_RID_2349_DP1.raw	1.4377E5	
K.NVPKDFYTFDSEGIVR.N	Y	60.51	1885.9210	16	0.3	629.6478	3	51.20	1	F1:15596	12112021_RID_2349_DP1.raw	9.4201E5	
K.QSLPETLQLK.T	Y	58.68	1155.6499	10	0.3	578.8324	2	43.37	1	F1:13055	12112021_RID_2349_DP1.raw	7.7551E6	
R.AGYLETWDSLM(+15.99)PNINK.L	Y	57.35	1866.8822	16	0.6	934.4489	2	65.26	1	F1:20129	12112021_RID_2349_DP1.raw	2.6064E5	
K.AYLAKDLPK.R	N	54.37	1017.5858	9	-0.3	509.8000	2	31.16	1	F1:8942	12112021_RID_2349_DP1.raw	1.0616E6	
K.VDFFMYEGPAPR.I	N	48.08	1427.6543	12	0.8	714.8350	2	56.53	1	F1:17314	12112021_RID_2349_DP1.raw	2.1345E4	
K.AERPDFVTLYIEEPDTTGHK.F	Y	47.01	2317.1226	20	0.9	773.3821	3	51.14	1	F1:15544	12112021_RID_2349_DP1.raw	1.1012E6	
K.SIPFEAR.V	N	41.70	818.4286	7	-0.3	410.2214	2	34.74	1	F1:10150	12112021_RID_2349_DP1.raw	2.9409E6	
K.RLHYVNNIR.I	Y	41.43	1183.6573	9	0.5	395.5599	3	35.06	1	F1:10272	12112021_RID_2349_DP1.raw	8.4331E4	
												total	1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MIQPLLVVTC LVVFPYQGSS IILESGNVND YEVVYPQKVT ALPKGAIQQL EQKYEDAIQY QFKVKGEPVV LHLEKNKDFF
 81  PENYSETHYS PDDREITTNP PVEDHCYYHG HIQNEADSTA SISACNGLKG HFKLQGETYL IEPLKIPDSE AHAVYKYENI
161  EKEDEAPKMC GVTQTNWESD EPIKKASQLV ATSEQQSYYD RFRYIKLVIV VDHSMVTKYN GDLTAIRTKI YQRVNILNEI

241  YGPFSIRVPL VGVEIWVNRD FISVTSASNV TLKSFGEWRK RDLLSRKRHD YAQLLTAINF DEQIVGRAYI STMCQPLRSV

321  AIVEDYSPID HAVAATMAHE MGHNLGMHHD GKQCNCGANS CIMAPEISDP PPTYFSDCSR NYYQTFLTNY RPDCTLIRPS

401  RTDIVSPPVC GNELLEVGEE CDCGSPANCR NPCCDAASCR LHSWVQCESG ECCQQCRFKR AGTECRPAMD ECDMAEQCTG
481  KSADCPVDGF HANGRPCLHN LGYCYNGKCP ITLYQCRALL GKNVTGVQDS CFQHNRLGYS YGYCRKENGR KIPCAPEDEK
561  CGRLYCSYNL LGNHIPCYPY YRRNREDKGM VDHGTKCGDG KVCSNRHCVD VTTAY
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.LVIVVDHSMVTK.Y	N	86.31	1339.7533	12	0.8	670.8845	2	40.72	2	F2:11182	12112021_RID_2349_DP2.raw		6.7627E5	6.
A.SQLVATSEQQSYYDR.F	N	85.45	1773.8169	15	0.1	887.9158	2	35.26	3	F3:9651	17112021_RID_2349_DP3.raw			3.
R.VNILNEIYGPFSIR.V	Y	80.46	1633.8827	14	0.4	817.9489	2	68.10	3	F3:20508	17112021_RID_2349_DP3.raw	2.1784E5	1.6365E6	7.
K.LVIVVDHSM(+15.99)VTK.Y	N	80.36	1355.7483	12	0.3	678.8816	2	40.62	2	F2:11272	12112021_RID_2349_DP2.raw		3.9309E5	1.
K.YNGDLTAIR.T	N	72.64	1021.5192	9	-0.1	511.7668	2	35.19	1	F1:10334	12112021_RID_2349_DP1.raw	2.7287E6	6.3775E6	1.
V.ATSEQQSYYDR.F	N	70.49	1346.5739	11	0.3	674.2944	2	23.13	2	F2:5110	12112021_RID_2349_DP2.raw	1.2012E5	4.4545E5	7.
R.NYYQTFLTNYRPD.C	N	66.53	1693.7736	13	0.4	847.8944	2	54.36	2	F2:15683	12112021_RID_2349_DP2.raw	2.3745E5	9.7382E5	7.
S.QLVATSEQQSYYDR.F	N	63.01	1686.7849	14	1.1	844.4006	2	47.86	5	F5:13912	17112021_RID_2349_DP5.raw		1.5966E5	2.
T.SEQQSYYDR.F	N	62.38	1174.4890	9	0.7	588.2522	2	21.94	2	F2:4785	12112021_RID_2349_DP2.raw	3.2418E4	2.9845E5	2.
A.TSEQQSYYDR.F	N	58.61	1275.5367	10	0.4	638.7759	2	22.62	5	F5:5328	17112021_RID_2349_DP5.raw	1.2834E5	4.8542E5	8.
R.VNILNEIYGPF.S	Y	48.96	1277.6655	11	0.3	639.8402	2	74.71	3	F3:22527	17112021_RID_2349_DP3.raw			2.
A.TSEQQSYYDRFR.Y	N	45.69	1578.7063	12	-0.5	527.2424	3	33.88	1	F1:9791	12112021_RID_2349_DP1.raw	5.1666E6		1.
R.NYYQTFLTNY.R	N	45.63	1325.5928	10	0.5	663.8040	2	61.33	4	F4:18230	17112021_RID_2349_DP4.raw			
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.
T.SEQQSYYDRFR.Y	N	42.54	1477.6586	11	0.6	739.8370	2	32.22	3	F3:8513	17112021_RID_2349_DP3.raw		1.2544E6	3.
V.ATSEQQSYYDRFR.Y	N	41.91	1649.7434	13	0.5	550.9220	3	32.84	3	F3:8815	17112021_RID_2349_DP3.raw	1.9978E6		5.
R.NYYQTFLTN.Y	N	40.03	1162.5295	9	0.5	582.2723	2	54.02	4	F4:15903	17112021_RID_2349_DP4.raw			
														total

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MMQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPQKVT ALPKGAIQQL EQKYEDAIQY QFKVKGEPVV LHLEKNKDFF
 81  PENYSETHYS PDDREITTNP PVEDHCYYHG HIQNEADSTA SISACNGLKG HFKLQGETYL IEPLKIPDSE AHAVYKYENI
161  EKEDEAPKMC GVTQTNWESD EPIKKASQLV ATSEQQSYYD RFRYIKLVIV VDHSMVTKYN GDLTAIRTKI YQRVNILNEI

241  YGPFSIRVPL VGVEIWVNRD FISVTSASNV TLKSFGEWRK RDLLSRKRHD YAQLLTAINF DEQIVGRAYI STMCQPLRSV

321  AIVEDYSPID HAVAATMAHE MGHNLGMHHD GKQCNCGANS CIMAPEISDP PPTYFSDCSR NYYQTFLTNY RPDCTLIRPS

401  RTDIVSPPVC GNELLEVGEE CDCGSPANCR NPCCDAASCR LHSWVQCESG ECCQQCRFKR AGTECRPAMD ECDMAEQCTG
481  KSADCPVDGF HANGRPCLHN LGYCYNGKCP ITLYQCRALL GKNVTGVQDS CFQHNRLGYS YGYCRKENGR KIPCAPEDEK
561  CGRLYCSYNL LGNHIPCYPY YRRNREDKGM VDHGTKCGDG KVCSNRHCVD VTTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.LVIVVDHSMVTK.Y	N	86.31	1339.7533	12	0.8	670.8845	2	40.72	2	F2:11182	12112021_RID_2349_DP2.raw		6.7627E5	6.
A.SQLVATSEQQSYYDR.F	N	85.45	1773.8169	15	0.1	887.9158	2	35.26	3	F3:9651	17112021_RID_2349_DP3.raw			3.
R.VNILNEIYGPFSIR.V	Y	80.46	1633.8827	14	0.4	817.9489	2	68.10	3	F3:20508	17112021_RID_2349_DP3.raw	2.1784E5	1.6365E6	7.
K.LVIVVDHSM(+15.99)VTK.Y	N	80.36	1355.7483	12	0.3	678.8816	2	40.62	2	F2:11272	12112021_RID_2349_DP2.raw		3.9309E5	1.
K.YNGDLTAIR.T	N	72.64	1021.5192	9	-0.1	511.7668	2	35.19	1	F1:10334	12112021_RID_2349_DP1.raw	2.7287E6	6.3775E6	1.
V.ATSEQQSYYDR.F	N	70.49	1346.5739	11	0.3	674.2944	2	23.13	2	F2:5110	12112021_RID_2349_DP2.raw	1.2012E5	4.4545E5	7.
R.NYYQTFLTNYRPD.C	N	66.53	1693.7736	13	0.4	847.8944	2	54.36	2	F2:15683	12112021_RID_2349_DP2.raw	2.3745E5	9.7382E5	7.
S.QLVATSEQQSYYDR.F	N	63.01	1686.7849	14	1.1	844.4006	2	47.86	5	F5:13912	17112021_RID_2349_DP5.raw		1.5966E5	2.
T.SEQQSYYDR.F	N	62.38	1174.4890	9	0.7	588.2522	2	21.94	2	F2:4785	12112021_RID_2349_DP2.raw	3.2418E4	2.9845E5	2.
A.TSEQQSYYDR.F	N	58.61	1275.5367	10	0.4	638.7759	2	22.62	5	F5:5328	17112021_RID_2349_DP5.raw	1.2834E5	4.8542E5	8.
R.VNILNEIYGPF.S	Y	48.96	1277.6655	11	0.3	639.8402	2	74.71	3	F3:22527	17112021_RID_2349_DP3.raw			2.
A.TSEQQSYYDRFR.Y	N	45.69	1578.7063	12	-0.5	527.2424	3	33.88	1	F1:9791	12112021_RID_2349_DP1.raw	5.1666E6		1.
R.NYYQTFLTNY.R	N	45.63	1325.5928	10	0.5	663.8040	2	61.33	4	F4:18230	17112021_RID_2349_DP4.raw			
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.
T.SEQQSYYDRFR.Y	N	42.54	1477.6586	11	0.6	739.8370	2	32.22	3	F3:8513	17112021_RID_2349_DP3.raw		1.2544E6	3.
V.ATSEQQSYYDRFR.Y	N	41.91	1649.7434	13	0.5	550.9220	3	32.84	3	F3:8815	17112021_RID_2349_DP3.raw	1.9978E6		5.
R.NYYQTFLTN.Y	N	40.03	1162.5295	9	0.5	582.2723	2	54.02	4	F4:15903	17112021_RID_2349_DP4.raw			
														total

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MIRFGNPSSS VKRRQRCRSW YWGGLLLLWA VAETRADIHY ATVYWLEAEK SFQIKAVLDK NGDAYGYYND TIQSTGWGIL
 81 EIKAGYGNQP ISNEILMYAA GFLEGYLTAS HMSDHFANLF PLMIKNVIIE QKVKDFIQKQ DEWTRQQIKN NKDDPFWRNA
161 GYVIVQLDGL YMGNVEWAKQ QKRTPLTNFE ISFLNVIGDL LDLIPALYSE LRKSDFRSMP DVSRIYQWDM GHCSALIKVL
241 PGYENIYFAH SSWFTYAATL RIYKHLDFKI TDPQTKTGRA SFSSYPGFLS SLDDFYILGS GLIMLQTTNS VFNLSLLKKV
                    336 37                                361
321 VPESLFAWER VRIANMMADS GKTWAETFEK ENSGTYNNQY MILDTKKIKL QRSLEDGTLY IIEQIPKLVK YSDQTKVLRN
                                                                    452
401 GYWPSYNIPF DKVIYNMSGY REYVQRHGLE FSYEMAPRAK IFRRDQGKVT DMESMKSIMR YNNYKEDPYA KRNPCNTICC
                                                                                549
481 RQDLDRRTPV PAGCYDSKVA DISMASKFTA YAINGPPVEK GLPVFSWVHF NKTKHQGLPE SYNFDFVTMK PVL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
R.SLEDGTLYIIEQIPK.L	N	90.40	1717.9138	15	0.5	859.9646	2	67.04	2	F2:19818	12112021_RID_2349_DP2.raw	1.408E6	2.
K.ENSGTYNNQYMILDTK.K	N	89.12	1889.8466	16	0.8	945.9313	2	45.52	2	F2:12882	12112021_RID_2349_DP2.raw		1.
R.IANMM(+15.99)ADSGK.T	N	76.74	1052.4630	10	-0.3	527.2386	2	24.17	2	F2:6829	12112021_RID_2349_DP2.raw	9.0092E4	1.
R.IANM(+15.99)MADSGK.T	N	75.38	1052.4630	10	-0.3	527.2386	2	24.17	2	F2:6725	12112021_RID_2349_DP2.raw		1.
R.DQGKVTDMESMK.S	N	72.75	1367.6061	12	0.5	684.8107	2	27.78	2	F2:6747	12112021_RID_2349_DP2.raw		2.
H.YATVYWLEAEK.S	N	72.57	1371.6710	11	0.7	686.8433	2	51.85	5	F5:15257	17112021_RID_2349_DP5.raw		
K.HQGLPESYNFDFVTM(+15.99)KPVL	N	71.29	2237.0828	19	0.8	746.7021	3	59.87	2	F2:17492	12112021_RID_2349_DP2.raw		1.
K.HQGLPESYNFDFVTMKPVL	N	70.10	2221.0876	19	0.3	1111.5514	2	65.61	2	F2:19349	12112021_RID_2349_DP2.raw		1.
K.ENSGTYNNQYM(+15.99)ILDTK.K	N	68.81	1905.8414	16	0.6	953.9286	2	41.00	2	F2:11307	12112021_RID_2349_DP2.raw		9.
R.DQGKVTDMESM(+15.99)K.S	N	66.01	1383.6010	12	0.7	692.8082	2	27.71	2	F2:6798	12112021_RID_2349_DP2.raw		1.
K.YSDQTKVLR.N	N	60.88	1108.5876	9	-0.4	555.3009	2	23.23	1	F1:6160	12112021_RID_2349_DP1.raw	4.0413E5	
R.DQGKVTDM(+15.99)ESM(+15.99)K.S	N	60.55	1399.5959	12	-0.3	700.8051	2	27.86	2	F2:6821	12112021_RID_2349_DP2.raw		7.
R.DQGKVTDM(+15.99)ESMK.S	N	55.19	1383.6010	12	0.0	692.8077	2	19.49	2	F2:3974	12112021_RID_2349_DP2.raw		2.
K.ENSGTYNNQYMILDTKK.I	N	48.36	2017.9415	17	0.5	673.6548	3	39.15	2	F2:10720	12112021_RID_2349_DP2.raw		2.
D.GTLYIIEQIPK.L	N	47.53	1273.7281	11	0.8	637.8719	2	53.61	4	F4:15815	17112021_RID_2349_DP4.raw		
K.ENSGTYNNQYM(+15.99)ILDTKK.I	N	47.15	2033.9364	17	0.0	678.9861	3	39.23	2	F2:10730	12112021_RID_2349_DP2.raw		1.
K.VLPGYENIYFAH.S	N	46.58	1421.6979	12	0.6	711.8566	2	53.52	2	F2:15534	12112021_RID_2349_DP2.raw		1.
K.VTDM(+15.99)ESMK.S	N	45.53	955.3990	8	-0.3	478.7067	2	24.77	2	F2:5754	12112021_RID_2349_DP2.raw		1.
K.HQGLPESYNFD.F	N	44.27	1305.5625	11	-0.5	653.7882	2	42.77	2	F2:11932	12112021_RID_2349_DP2.raw		1.
K.VADISM(+15.99)ASK.F	Y	43.92	936.4586	9	-0.6	469.2363	2	29.56	2	F2:7390	12112021_RID_2349_DP2.raw		3.
K.VTDMESM(+15.99)K.S	N	43.61	955.3990	8	-0.3	478.7067	2	24.77	2	F2:5660	12112021_RID_2349_DP2.raw		1.
K.VTDM(+15.99)ESM(+15.99)K.S	N	42.57	971.3940	8	-0.2	486.7042	2	24.80	2	F2:5663	12112021_RID_2349_DP2.raw		8.
K.NNKDDPFWR.N	N	41.45	1190.5469	9	0.5	596.2810	2	35.13	5	F5:9629	17112021_RID_2349_DP5.raw		
K.VTDMESMK.S	N	39.74	939.4042	8	0.0	470.7094	2	24.77	2	F2:5674	12112021_RID_2349_DP2.raw		7.

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MQTPKRRRGA QGCPRSSLSP PPPLLLLVGA VWFGAALSVA AGSFELTILH TNDVHARVEQ TSRDSGKCTG QDCYGGVARR
 81 ATKIRELRAK HRHVLLLDAG DQYQGTVWFS FFKGREVLKF MKSLRYDAMA LGNHEFDNGL AGLLDPLLKN ANFPILSANI
161 RPKGPIASTI SGYILPYKII KVGSEKVGII GYTTKETPVL SNPGPYLEFR DEVEELQIHA NKLTTLGVNK IIALGHSGFF
241 EDQRIAQKVK GVDVVVGGHT NTFLYTGMLF LHKIGFLYNL AIRVPSILPT T
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area I
K.IIALGHSGFFEDQR.I	N	93.42	1588.7997	14	0.8	795.4078	2	47.13	2	F2:13392	12112021_RID_2349_DP2.raw	1.2282E6	4.8241E6	2.973E
K.NANFPILSANIRPK.G	N	87.65	1553.8678	14	0.6	777.9417	2	47.24	1	F1:14300	12112021_RID_2349_DP1.raw	2.5082E7	3.0757E6	
K.GPIASTISGYILPYK.I	Y	85.78	1578.8657	15	0.7	790.4407	2	58.67	2	F2:17142	12112021_RID_2349_DP2.raw	4.5074E6	4.1083E6	2.5052
K.VGSEKVGIIGYTTK.E	N	74.20	1450.8031	14	0.9	726.4095	2	36.48	1	F1:10777	12112021_RID_2349_DP1.raw	2.8559E6		
R.DEVEELQIHANK.L	N	70.10	1423.6943	12	0.6	712.8549	2	34.19	4	F4:9279	17112021_RID_2349_DP4.raw		2.6545E4	
K.ETPVLSNPGPYLEFR.D	N	63.99	1717.8674	15	0.3	859.9412	2	55.85	4	F4:16529	17112021_RID_2349_DP4.raw			
K.VGIIGYTTK.E	N	60.94	950.5436	9	-0.2	476.2790	2	37.93	1	F1:11149	12112021_RID_2349_DP1.raw	9.0552E6	3.6938E6	2.4626
R.YDAMALGNHEFD.N	N	53.56	1381.5608	12	1.0	691.7883	2	46.21	7	F7:13460	17112021_RID_2349_DP7.raw			
K.LTTLGVNK.I	N	48.37	844.5018	8	-0.2	423.2581	2	28.18	2	F2:6923	12112021_RID_2349_DP2.raw	1.9323E6	3.4738E6	2.4241

total 9 pepti

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                          31
  1 RLDRPVTNST HIAPLSLPSS PPIVGSVCRI MGWGTISTTK VILSDVPRCA NIEILKYSKC QEVHPELPAK GRVVCAGVWQ
                                                                                142
 81 GGKDTCKGDS GGPLICNGQF QGLLSWGGDP CAQPLQPGLY TDIFDYSDWI KSIIAGNTAV TCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
R.IMGWGTISTTKVILSDVPR.C	Y	96.96	2073.1292	19	0.2	692.0505	3	59.98	3	F3:17898	17112021_RID_2349_DP3.raw		
R.IMGWGTISTTK.V	N	74.23	1193.6115	11	0.6	597.8134	2	46.31	2	F2:13130	12112021_RID_2349_DP2.raw	1.0272E6	8
G.LYTDIFDYSDWIK.S	N	70.95	1677.7926	13	1.1	839.9045	2	72.40	3	F3:21807	17112021_RID_2349_DP3.raw		
P.GLYTDIFDYSDWIK.S	N	70.77	1734.8141	14	0.1	868.4144	2	74.37	3	F3:22479	17112021_RID_2349_DP3.raw		
L.YTDIFDYSDWIK.S	N	69.44	1564.7085	12	0.3	783.3618	2	68.09	3	F3:20399	17112021_RID_2349_DP3.raw		
Y.TDIFDYSDWIK.S	N	66.08	1401.6453	11	0.8	701.8304	2	66.55	4	F4:19959	17112021_RID_2349_DP4.raw		
R.IM(+15.99)GWGTISTTKVILSDVPR.C	Y	65.54	2089.1240	19	0.7	697.3824	3	56.07	3	F3:16589	17112021_RID_2349_DP3.raw		
R.IM(+15.99)GWGTISTTK.V	N	65.43	1209.6063	11	0.2	605.8105	2	41.63	3	F3:12035	17112021_RID_2349_DP3.raw		4
K.SIIAGNTAVTC(+57.02)PP	N	58.39	1299.6493	13	0.5	650.8323	2	45.43	3	F3:13053	17112021_RID_2349_DP3.raw		
K.VILSDVPR.C	Y	53.60	897.5283	8	0.4	449.7716	2	36.96	1	F1:10936	12112021_RID_2349_DP1.raw	2.2296E6	1
L.QPGLYTDIFDYSDWIK.S	N	51.31	1959.9254	16	0.7	980.9707	2	73.83	3	F3:22207	17112021_RID_2349_DP3.raw		

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
K.SIIAGNTAVT.C	N	48.53	945.5131	10	0.0	473.7639	2	39.62	3	F3:11085	17112021_RID_2349_DP3.raw		
K.C(+57.02)QEVHPELPAK.G	Y	46.74	1306.6339	11	0.6	654.3246	2	27.17	3	F3:6836	17112021_RID_2349_DP3.raw		
M.GWGTISTTK.V	N	46.73	949.4869	9	-0.6	475.7504	2	32.18	3	F3:8600	17112021_RID_2349_DP3.raw		
T.KVILSDVPR.C	Y	42.92	1025.6233	9	0.3	513.8191	2	30.86	3	F3:8089	17112021_RID_2349_DP3.raw		
C.AQPLQPGLYTDIFDYSDWIK.S	N	41.95	2369.1580	20	0.7	1185.5870	2	75.98	3	F3:23000	17112021_RID_2349_DP3.raw		
C.QEVHPELPAK.G	Y	38.96	1146.6033	10	0.2	574.3090	2	26.03	3	F3:6524	17112021_RID_2349_DP3.raw		

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFG WLVVFLSPSG TRADCPSDWS SHEGNCYKVF NLRKTWEEAE KFCTKQANGV HLVSIDSKKE ANFVAKLVSQ

 81  NIKESRGIEF VWIGLRDQSE RQHCSSEWSD GSSINYQNWI EAESRKCLGL EKETGYRKWV NIYCGLRNPF TCEI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.QANGVHLVSIDSK.K	Y	81.82	1366.7205	13	0.6	456.5811	3	32.64	5	F5:8755	17112021_RID_2349_DP5.raw				
K.QANGVHLVSIDSKK.E	Y	77.07	1494.8154	14	0.1	499.2791	3	28.38	5	F5:7341	17112021_RID_2349_DP5.raw				
D.GSSINYQNWIEAESR.K	Y	62.77	1752.8066	15	0.2	877.4108	2	50.91	6	F6:14917	17112021_RID_2349_DP6.raw				
S.SINYQNWIEAESR.K	Y	61.57	1608.7532	13	0.1	805.3839	2	51.12	6	F6:14982	17112021_RID_2349_DP6.raw				
K.LVSQNIKESR.G	Y	59.45	1172.6514	10	0.9	587.3335	2	20.11	1	F1:5091	12112021_RID_2349_DP1.raw	2.9622E6			
N.GVHLVSIDSK.K	Y	56.37	1053.5818	10	-0.5	527.7979	2	31.63	6	F6:8277	17112021_RID_2349_DP6.raw				
N.YQNWIEAESR.K	Y	55.48	1294.5942	10	0.8	648.3049	2	40.44	6	F6:11179	17112021_RID_2349_DP6.raw				
W.SDGSSINYQNWIEAESR.K	Y	51.52	1954.8657	17	0.3	978.4404	2	52.50	6	F6:15474	17112021_RID_2349_DP6.raw				
G.SSINYQNWIEAESR.K	Y	51.20	1695.7853	14	0.8	848.9006	2	50.80	6	F6:14944	17112021_RID_2349_DP6.raw				
Y.QNWIEAESR.K	Y	48.46	1131.5309	9	-0.5	566.7725	2	35.70	6	F6:9679	17112021_RID_2349_DP6.raw				
K.TWEEAEKF.C	N	47.94	1038.4658	8	0.3	520.2404	2	39.87	6	F6:11136	17112021_RID_2349_DP6.raw				
N.GVHLVSIDSKK.E	Y	47.32	1181.6768	11	-0.8	394.8992	3	27.85	6	F6:6922	17112021_RID_2349_DP6.raw				
A.NGVHLVSIDSK.K	Y	47.22	1167.6248	11	-0.5	584.8193	2	32.17	6	F6:8523	17112021_RID_2349_DP6.raw				
K.EANFVAKLVSQN.I	Y	45.69	1318.6881	12	0.1	660.3514	2	48.74	6	F6:14195	17112021_RID_2349_DP6.raw				
R.KTWEEAEK.F	N	45.16	1019.4923	8	0.3	510.7536	2	17.57	6	F6:3741	17112021_RID_2349_DP6.raw				
K.QANGVHLVSID.S	Y	43.90	1151.5935	11	0.4	576.8043	2	40.57	6	F6:11384	17112021_RID_2349_DP6.raw				
K.KEANFVAK.L	Y	42.38	905.4970	8	-0.4	453.7556	2	16.96	6	F6:3318	17112021_RID_2349_DP6.raw				
S.DGSSINYQNWIEAESR.K	Y	42.17	1867.8336	16	0.4	934.9245	2	54.93	6	F6:16268	17112021_RID_2349_DP6.raw				
K.EANFVAK.L	Y	41.77	777.4021	7	0.2	389.7084	2	22.39	6	F6:5158	17112021_RID_2349_DP6.raw				
V.HLVSIDSK.K	N	41.41	897.4919	8	-0.6	449.7530	2	23.13	6	F6:5416	17112021_RID_2349_DP6.raw				
S.INYQNWIEAESR.K	Y	39.32	1521.7212	12	0.5	761.8683	2	49.89	6	F6:14631	17112021_RID_2349_DP6.raw				

total 21 peptide

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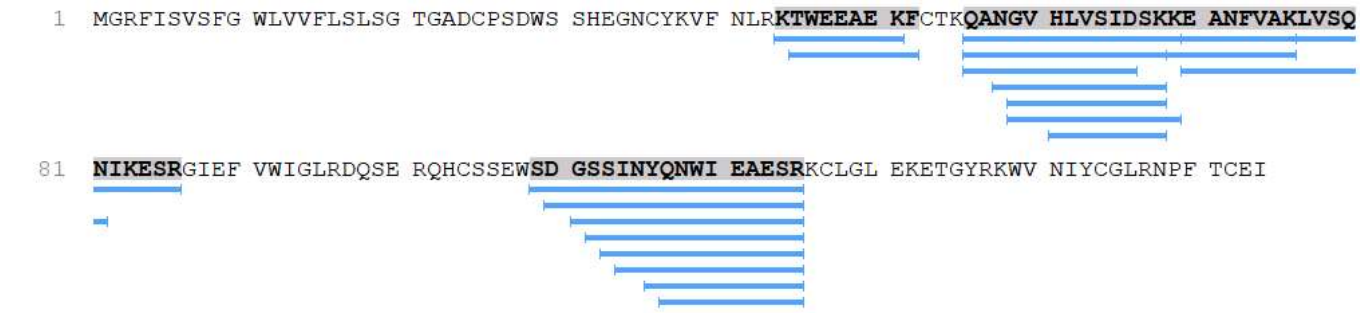
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area A 1
K.QANGVHLVSIDSK.K	Y	81.82	1366.7205	13	0.6	456.5811	3	32.64	5	F5:8755	17112021_RID_2349_DP5.raw				
K.QANGVHLVSIDSKK.E	Y	77.07	1494.8154	14	0.1	499.2791	3	28.38	5	F5:7341	17112021_RID_2349_DP5.raw				
D.GSSINYQNWIEAESR.K	Y	62.77	1752.8066	15	0.2	877.4108	2	50.91	6	F6:14917	17112021_RID_2349_DP6.raw				
S.SINYQNWIEAESR.K	Y	61.57	1608.7532	13	0.1	805.3839	2	51.12	6	F6:14982	17112021_RID_2349_DP6.raw				
K.LVSQNIKESR.G	Y	59.45	1172.6514	10	0.9	587.3335	2	20.11	1	F1:5091	12112021_RID_2349_DP1.raw	2.9622E6			
N.GVHLVSIDSK.K	Y	56.37	1053.5818	10	-0.5	527.7979	2	31.63	6	F6:8277	17112021_RID_2349_DP6.raw				
N.YQNWIEAESR.K	Y	55.48	1294.5942	10	0.8	648.3049	2	40.44	6	F6:11179	17112021_RID_2349_DP6.raw				
W.SDGSSINYQNWIEAESR.K	Y	51.52	1954.8657	17	0.3	978.4404	2	52.50	6	F6:15474	17112021_RID_2349_DP6.raw				
G.SSINYQNWIEAESR.K	Y	51.20	1695.7853	14	0.8	848.9006	2	50.80	6	F6:14944	17112021_RID_2349_DP6.raw				
Y.QNWIEAESR.K	Y	48.46	1131.5309	9	-0.5	566.7725	2	35.70	6	F6:9679	17112021_RID_2349_DP6.raw				
K.TWEEAEKF.C	N	47.94	1038.4658	8	0.3	520.2404	2	39.87	6	F6:11136	17112021_RID_2349_DP6.raw				
N.GVHLVSIDSKK.E	Y	47.32	1181.6768	11	-0.8	394.8992	3	27.85	6	F6:6922	17112021_RID_2349_DP6.raw				
A.NGVHLVSIDSK.K	Y	47.22	1167.6248	11	-0.5	584.8193	2	32.17	6	F6:8523	17112021_RID_2349_DP6.raw				
K.EANFVAKLVSQN.I	Y	45.69	1318.6881	12	0.1	660.3514	2	48.74	6	F6:14195	17112021_RID_2349_DP6.raw				
R.KTWEEAEK.F	N	45.16	1019.4923	8	0.3	510.7536	2	17.57	6	F6:3741	17112021_RID_2349_DP6.raw				
K.QANGVHLVSID.S	Y	43.90	1151.5935	11	0.4	576.8043	2	40.57	6	F6:11384	17112021_RID_2349_DP6.raw				
K.KEANFVAK.L	Y	42.38	905.4970	8	-0.4	453.7556	2	16.96	6	F6:3318	17112021_RID_2349_DP6.raw				
S.DGSSINYQNWIEAESR.K	Y	42.17	1867.8336	16	0.4	934.9245	2	54.93	6	F6:16268	17112021_RID_2349_DP6.raw				
K.EANFVAK.L	Y	41.77	777.4021	7	0.2	389.7084	2	22.39	6	F6:5158	17112021_RID_2349_DP6.raw				
V.HLVSIDSK.K	N	41.41	897.4919	8	-0.6	449.7530	2	23.13	6	F6:5416	17112021_RID_2349_DP6.raw				
S.INYQNWIEAESR.K	Y	39.32	1521.7212	12	0.5	761.8683	2	49.89	6	F6:14631	17112021_RID_2349_DP6.raw				

total 21 peptide

TRINITY_DN59
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
1   MGRFISVSFG WLVVFLSPSG TRADCPSDWS SHEGNCYKVF NLRKTWEEAE KFCTKQANGV HLVSIDSKKE ANFVAKLVSQ

81  NIKESRGIEF VWIGLRDQSE RQHCSSEWSD GSSINYQNWI EAESRKCLGL EKETGYRKWV NIYCGLRNPF TCEI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.QANGVHLVSIDSK.K	Y	81.82	1366.7205	13	0.6	456.5811	3	32.64	5	F5:8755	17112021_RID_2349_DP5.raw				
K.QANGVHLVSIDSKK.E	Y	77.07	1494.8154	14	0.1	499.2791	3	28.38	5	F5:7341	17112021_RID_2349_DP5.raw				
D.GSSINYQNWIEAESR.K	Y	62.77	1752.8066	15	0.2	877.4108	2	50.91	6	F6:14917	17112021_RID_2349_DP6.raw				
S.SINYQNWIEAESR.K	Y	61.57	1608.7532	13	0.1	805.3839	2	51.12	6	F6:14982	17112021_RID_2349_DP6.raw				
K.LVSQNIKESR.G	Y	59.45	1172.6514	10	0.9	587.3335	2	20.11	1	F1:5091	12112021_RID_2349_DP1.raw	2.9622E6			
N.GVHLVSIDSK.K	Y	56.37	1053.5818	10	-0.5	527.7979	2	31.63	6	F6:8277	17112021_RID_2349_DP6.raw				
N.YQNWIEAESR.K	Y	55.48	1294.5942	10	0.8	648.3049	2	40.44	6	F6:11179	17112021_RID_2349_DP6.raw				
W.SDGSSINYQNWIEAESR.K	Y	51.52	1954.8657	17	0.3	978.4404	2	52.50	6	F6:15474	17112021_RID_2349_DP6.raw				
G.SSINYQNWIEAESR.K	Y	51.20	1695.7853	14	0.8	848.9006	2	50.80	6	F6:14944	17112021_RID_2349_DP6.raw				
Y.QNWIEAESR.K	Y	48.46	1131.5309	9	-0.5	566.7725	2	35.70	6	F6:9679	17112021_RID_2349_DP6.raw				
K.TWEEAEKF.C	N	47.94	1038.4658	8	0.3	520.2404	2	39.87	6	F6:11136	17112021_RID_2349_DP6.raw				
N.GVHLVSIDSKK.E	Y	47.32	1181.6768	11	-0.8	394.8992	3	27.85	6	F6:6922	17112021_RID_2349_DP6.raw				
A.NGVHLVSIDSK.K	Y	47.22	1167.6248	11	-0.5	584.8193	2	32.17	6	F6:8523	17112021_RID_2349_DP6.raw				
K.EANFVAKLVSQN.I	Y	45.69	1318.6881	12	0.1	660.3514	2	48.74	6	F6:14195	17112021_RID_2349_DP6.raw				
R.KTWEEAEK.F	N	45.16	1019.4923	8	0.3	510.7536	2	17.57	6	F6:3741	17112021_RID_2349_DP6.raw				
K.QANGVHLVSID.S	Y	43.90	1151.5935	11	0.4	576.8043	2	40.57	6	F6:11384	17112021_RID_2349_DP6.raw				
K.KEANFVAK.L	Y	42.38	905.4970	8	-0.4	453.7556	2	16.96	6	F6:3318	17112021_RID_2349_DP6.raw				
S.DGSSINYQNWIEAESR.K	Y	42.17	1867.8336	16	0.4	934.9245	2	54.93	6	F6:16268	17112021_RID_2349_DP6.raw				
K.EANFVAK.L	Y	41.77	777.4021	7	0.2	389.7084	2	22.39	6	F6:5158	17112021_RID_2349_DP6.raw				
V.HLVSIDSK.K	N	41.41	897.4919	8	-0.6	449.7530	2	23.13	6	F6:5416	17112021_RID_2349_DP6.raw				
S.INYQNWIEAESR.K	Y	39.32	1521.7212	12	0.5	761.8683	2	49.89	6	F6:14631	17112021_RID_2349_DP6.raw				

total 21 peptide

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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1   SQLVATSEQQ SYYDRFRYIK LAIVADHSMV EKYKGNLKKL RKRIYRTVNT VNEMYLPLNI RVPLVHVEIW DDRDLINVTS
                          29                                  54
81  SGGATLKSFG KWRGSDLLSR KRHDNAQLLT GIDLNGQTLG IAPNSGMCHP NRSV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
K.LAIVADHSMVEK.Y	Y	88.02	1311.6857	12	0.2	656.8502	2	34.96	2	F2:9288	12112021_RID_2349_DP2.raw	4.5317E6	5.8499E

total

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
SQLVATSEQQSYYDR.F	N	85.45	1773.8169	15	0.1	887.9158	2	35.26	3	F3:9651	17112021_RID_2349_DP3.raw		
K.LAIVADHSM(+15.99)VEK.Y	Y	78.52	1327.6805	12	0.4	664.8478	2	35.33	1	F1:10345	12112021_RID_2349_DP1.raw	2.4019E6	2.9689E
R.TVNTVNEM(+15.99)YLPLNIR.V	Y	72.02	1791.9189	15	0.5	896.9672	2	56.15	2	F2:16974	12112021_RID_2349_DP2.raw	7.951E6	6.1112E
V.ATSEQQSYYDR.F	N	70.49	1346.5739	11	0.3	674.2944	2	23.13	2	F2:5110	12112021_RID_2349_DP2.raw	1.2012E5	4.4545E
R.TVNTVNEMYLPLNIR.V	Y	66.01	1775.9240	15	0.2	888.9694	2	57.79	4	F4:17087	17112021_RID_2349_DP4.raw	8.7541E6	9.8614E
S.QLVATSEQQSYYDR.F	N	63.01	1686.7849	14	1.1	844.4006	2	47.86	5	F5:13912	17112021_RID_2349_DP5.raw		1.5966E
T.SEQQSYYDR.F	N	62.38	1174.4890	9	0.7	588.2522	2	21.94	2	F2:4785	12112021_RID_2349_DP2.raw	3.2418E4	2.9845E
A.TSEQQSYYDR.F	N	58.61	1275.5367	10	0.4	638.7759	2	22.62	5	F5:5328	17112021_RID_2349_DP5.raw	1.2834E5	4.8542E
K.WRGSDLLSR.K	Y	50.67	1088.5726	9	-0.1	545.2935	2	37.47	1	F1:11043	12112021_RID_2349_DP1.raw	4.0422E6	
A.TSEQQSYYDRFR.Y	N	45.69	1578.7063	12	-0.5	527.2424	3	33.88	1	F1:9791	12112021_RID_2349_DP1.raw	5.1666E6	
T.SEQQSYYDRFR.Y	N	42.54	1477.6586	11	0.6	739.8370	2	32.22	3	F3:8513	17112021_RID_2349_DP3.raw		1.2544E
V.ATSEQQSYYDRFR.Y	N	41.91	1649.7434	13	0.5	550.9220	3	32.84	3	F3:8815	17112021_RID_2349_DP3.raw	1.9978E6	
													total

QHR82712.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  ALGNHEFDNG LDGLLDPLLK NANFPILSAN IRPKGPIASN ISGYILPYKI INVGSEKVGI IGYTTKETPV LSNPGPYLEF

 81  RDEVEELQIH ANKLTTLGIN KIIALGHSGF LEDQRIAQKV KGVDVVVGGH TNTFLYSGSP PSTEVPAGNY PFMVQSDDGR

161  QVPVVQAYAF GKYLGYLNVV FDDKGNVIKA SGNPILLNKD IPEDQDLKAE VNKMKIQLQS YSSQEIGKTI VYLNGTTQAC

241  RFQECNLGNL ICDAVIYNNL RHPDDNEWNH VSMCIVNGGG IRSPIDERAN NGNKEGPF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.NANFPILSANIRPK.G	N	87.65	1553.8678	14	0.6	777.9417	2	47.24	1	F1:14300	12112021_RID_2349_DP1.raw	2.5082E7	3.0757E6	
R.QVPVVQAYAFGK.Y	N	78.42	1305.7081	12	0.2	653.8615	2	46.67	2	F2:13272	12112021_RID_2349_DP2.raw	4.2275E6	4.4501E6	1.
N.VGSEKVGIIGYTTK.E	N	74.20	1450.8031	14	0.9	726.4095	2	36.48	1	F1:10777	12112021_RID_2349_DP1.raw	2.8559E6		
K.YLGYLNVVFDDKGNVIK.A	Y	73.37	1956.0356	17	0.4	979.0255	2	58.81	3	F3:17436	17112021_RID_2349_DP3.raw		6.057E5	4.
R.DEVEELQIHANK.L	N	70.10	1423.6943	12	0.6	712.8549	2	34.19	4	F4:9279	17112021_RID_2349_DP4.raw		2.6545E4	
K.ASGNPILLNK.D	N	67.11	1025.5869	10	-0.1	513.8007	2	34.04	1	F1:9894	12112021_RID_2349_DP1.raw	2.3772E7	7.6734E6	2.
K.ETPVLSNPGPYLEFR.D	N	63.99	1717.8674	15	0.3	859.9412	2	55.85	4	F4:16529	17112021_RID_2349_DP4.raw			
K.VGIIGYTTK.E	N	60.94	950.5436	9	-0.2	476.2790	2	37.93	1	F1:11149	12112021_RID_2349_DP1.raw	9.0552E6	3.6938E6	2.
K.ASGNPILLNKD.I	N	52.23	1140.6139	11	0.6	571.3146	2	34.93	4	F4:9472	17112021_RID_2349_DP4.raw			
														total 9 pepti

AFE84762.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MARERRDSKA AAFFCLAWAL GLPLLGFPQH VGGREDRADW TQEKYSHRPT ILNATSILQV TSQTNVSRMW QNDLHPIMIE
 81 RYPGSPGSYA VRQHIKHRLQ GLQAGWLVEE DTFQSHTPYG YRTFSNIIST LNPLAKRHLV IACHYDSKYF PPQLDGKVFV
161 GATDSAVPCA MMLELARSLD RQLSFLKQSS LPTKADLSLK LIFFDGEEAF VRWSPSDSLY GSRSLAQKMS STPHPPGARN
241 TYQTQGIDLF VLLDLIGARN PVFPVYFLNT ARWFGRLEAI EQNLHDLGLL NNYSSERQYF RSNLRQHPVE DDHIPFLRRG
321 VPILHLIPSP FPRVWHVMED NEENLDKPTI DNLSKILQIF VLEYLNLG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.MWQNDLHPIMIER.Y	N	92.13	1681.8069	13	0.1	841.9108	2	49.27	2	F2:14104	12112021_RID_2349_DP2.raw		1.384
R.NPVFPVYFLNTAR.W	N	83.53	1536.8088	13	0.7	769.4122	2	63.32	2	F2:18598	12112021_RID_2349_DP2.raw		7.791
K.LIFFDGEEAFVR.W	N	83.44	1441.7241	12	0.9	721.8700	2	63.41	2	F2:18652	12112021_RID_2349_DP2.raw		4.154
R.WSPSDSLYGSR.S	N	76.49	1253.5676	11	-0.1	627.7910	2	42.62	2	F2:11930	12112021_RID_2349_DP2.raw		4.928
R.YPGSPGSYAVR.Q	N	69.52	1152.5563	11	0.6	577.2858	2	32.51	2	F2:8432	12112021_RID_2349_DP2.raw		8.721
K.M(+15.99)SSTPHPPGAR.N	Y	65.00	1152.5345	11	0.0	577.2745	2	18.26	2	F2:4172	12112021_RID_2349_DP2.raw		9.335
K.MSSTPHPPGAR.N	Y	61.11	1136.5397	11	-0.9	569.2766	2	19.88	5	F5:4334	17112021_RID_2349_DP5.raw		2.139
R.GVPILHLIPSPFPR.V	N	55.94	1541.9082	14	0.5	771.9617	2	63.34	2	F2:18577	12112021_RID_2349_DP2.raw		4.547
Q.HPVEDDHIPFLR.R	N	53.57	1473.7365	12	-0.1	492.2527	3	46.37	2	F2:13060	12112021_RID_2349_DP2.raw		7.548
K.YFPPQLDGK.V	N	51.22	1063.5338	9	0.4	532.7744	2	39.95	2	F2:11061	12112021_RID_2349_DP2.raw		3.278
R.M(+15.99)WQNDLHPIMIER.Y	N	44.14	1697.8018	13	2.2	849.9100	2	47.25	2	F2:13379	12112021_RID_2349_DP2.raw		1.065
R.LQGLQAGWLVEEDTFQSHTPYGYR.T	N	38.86	2794.3350	24	0.8	932.4530	3	60.00	2	F2:17677	12112021_RID_2349_DP2.raw		1.957
													total 1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 LSAGKEGRKT MGRFISVSFS LLVVFLSLSG TEAGFCCPNG WSSFGQHCYK VIEPLKNWTD AEKFCTEQHK GSHLASIHSS
 81 EEEAFVSKVA SKVLKFGSVW IGLNDPWNNC HWEWSDNAKF DYKAMTRRPY CTVMVLKPDK IFWFNRGCEK SVSFVCKFLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.GSHLASIHSSEEEAFVSK.V	Y	110.07	1913.9119	18	0.2	957.9634	2	35.00	5	F5:9814	17112021_RID_2349_DP5.raw				2
H.LASIHSSEEEAFVSK.V	Y	75.78	1632.7994	15	0.6	545.2741	3	35.12	5	F5:9694	17112021_RID_2349_DP5.raw				2
A.SIHSSEEEAFVSK.V	Y	74.21	1448.6783	13	0.6	725.3469	2	28.87	5	F5:7463	17112021_RID_2349_DP5.raw				3
S.IHSSEEEAFVSK.V	Y	64.59	1361.6462	12	0.3	681.8306	2	27.01	5	F5:6866	17112021_RID_2349_DP5.raw				1
H.SSEEEAFVSK.V	Y	58.46	1111.5033	10	0.4	556.7592	2	28.18	5	F5:7267	17112021_RID_2349_DP5.raw				7
L.ASIHSSEEEAFVSK.V	Y	54.72	1519.7155	14	0.6	507.5794	3	30.04	5	F5:7917	17112021_RID_2349_DP5.raw				1
S.SEEEAFVSK.V	Y	47.15	1024.4713	9	1.0	513.2435	2	27.17	5	F5:6857	17112021_RID_2349_DP5.raw				2
K.FDYKAMTR.R	Y	46.61	1030.4906	8	0.0	516.2526	2	31.54	5	F5:8441	17112021_RID_2349_DP5.raw				1
															total 8 peptides

TRINITY_DN1031
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEKLILLTWA TGFLVVNCVQ LHQQLQTLPM LGDVYHVTGI LKLPYAEIEE PFEAWFNKTG GKSRIQYYDG QVITYQLGYI

 81 KPFGASFKVT PETTETEVNI KECFQFNGTS ENPVRPQSLF PNLTNFQPVR HEHYNGQHCT VLESVSYWGK KKNTYKFWVA

161 DGSRGPLPVH YEMKGYNTLL GSHYDKYEID YISYSHSFSP SIFNLPPGIK CAHWPKGGPE HRILANPMQE FVGGTGEVSQ

241 HHEHLFHHYK KKFRKTYKNK KEIEHRQHNF IHNMRYIHSK NRANLSFKLA ANHLADRTPE ELAVLRGRLQ TDEPRKAGAF

321 PSDSYRGLTL PDSLDWRLYG AVTRVKDQAV CGSCWSFATT GALEGAIFLK TGVLTPLSQQ VLIDCSWGFG NRACDGGQEP

401 QAFEWIMKHG GIASAEAYGP YMGQNGYCHY NQSELIAPIA GYIVITSQNI TDLKAALYKH GPIAVNVDAS HKSFAFYSSG

481 IYYEPNCGNT TMELDHAVLA VGYGDLQGEP YWLIKNSWST YWGNDGYILM SMKENNCGVA SSATYPILA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.IQYYDGQVITYQLGYIKPFGASFK.V	Y	89.84	2798.4319	24	0.6	933.8185	3	64.33	3	F3:19267	17112021_RID_2349_DP3.raw		
K.VTPETTETEVNIK.E	Y	80.09	1459.7406	13	-0.1	730.8775	2	33.29	3	F3:8992	17112021_RID_2349_DP3.raw		
K.HGPIAVNVDASHK.S	Y	76.92	1343.6946	13	0.3	672.8547	2	28.24	2	F2:6976	12112021_RID_2349_DP2.raw		1.321
R.GPLPVHYEMK.G	Y	72.68	1169.5903	10	0.8	585.8029	2	35.42	3	F3:9693	17112021_RID_2349_DP3.raw		
R.IQYYDGQVITYQLGYIKPF.G	Y	66.66	2308.1780	19	0.9	1155.0973	2	67.58	3	F3:20288	17112021_RID_2349_DP3.raw		
R.GLTLPDSLDWR.L	Y	63.18	1271.6510	11	0.0	636.8328	2	58.34	2	F2:17069	12112021_RID_2349_DP2.raw		1.203
R.GPLPVHYEM(+15.99)K.G	Y	57.86	1185.5852	10	-0.2	396.2023	3	29.39	3	F3:7623	17112021_RID_2349_DP3.raw		
R.KAGAFPSDSYR.G	Y	51.41	1197.5778	11	0.2	599.7963	2	27.19	2	F2:6677	12112021_RID_2349_DP2.raw		4.193
K.FWVADGSR.G	Y	49.35	936.4453	8	0.1	469.2300	2	37.70	3	F3:10542	17112021_RID_2349_DP3.raw		
F.SPSIFNLPPGIK.C	Y	45.13	1268.7128	12	0.8	635.3642	2	55.02	3	F3:16255	17112021_RID_2349_DP3.raw		
													total 1

TRINITY_DN1031

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEKLILLTWA TGFLVVNCVQ LHQQLQTLPM LGDVYHVTGI LKLPYAEIEE PFEAWFNKTG GKSRIQYYDG QVITYQLGYI

 81 KPFGASFKVT PETTETEVNI KECFQFNGTS ENPVRPQSLF PNLTNFQPVR HEHYNGQHCT VLESVSYWGK KKNTYKFWVA

161 DGSRGPLPVH YEMKGYNTLL GSHYDKYEID YISYSHSFSP SIFNLPPGIK CAHWPKGGPE HRILANPMQE FVGGTGEVSQ

241 HHEHLFHHYK KKFRKTYKNK KEIEHRQHNF IHNMRYIHSK NRANLSFKLA ANHLADRTPE ELAVLRGRLQ TDEPRKAGAF

321 PSDSYRGLTL PDSLDWRLYG AVTRVKDQAV CGSCWSFATT GALEGAIFLK TGVLTPLSQQ VLIDCSWGFG NRACDGGQEP

401 QAFEWIMKHG GIASAEAYGP YMGQNGYCHY NQSELIAPIA GYIVITSQNI TDLKAALYKH GPIAVNVDAS HKSFAFYSSG

481 IYYEPNCGNT TMELDHAVLA VGYGDLQGEP YWLIKNSWST YWGNDGYILM SMKENNCGVA SSATYPILA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.IQYYDGQVITYQLGYIKPFGASFK.V	Y	89.84	2798.4319	24	0.6	933.8185	3	64.33	3	F3:19267	17112021_RID_2349_DP3.raw		
K.VTPETTETEVNIK.E	Y	80.09	1459.7406	13	-0.1	730.8775	2	33.29	3	F3:8992	17112021_RID_2349_DP3.raw		
K.HGPIAVNVDASHK.S	Y	76.92	1343.6946	13	0.3	672.8547	2	28.24	2	F2:6976	12112021_RID_2349_DP2.raw		1.321
R.GPLPVHYEMK.G	Y	72.68	1169.5903	10	0.8	585.8029	2	35.42	3	F3:9693	17112021_RID_2349_DP3.raw		
R.IQYYDGQVITYQLGYIKPF.G	Y	66.66	2308.1780	19	0.9	1155.0973	2	67.58	3	F3:20288	17112021_RID_2349_DP3.raw		
R.GLTLPDSLDWR.L	Y	63.18	1271.6510	11	0.0	636.8328	2	58.34	2	F2:17069	12112021_RID_2349_DP2.raw		1.203
													total 1

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.GPLPVHYEM(+15.99)K.G	Y	57.86	1185.5852	10	-0.2	396.2023	3	29.39	3	F3:7623	17112021_RID_2349_DP3.raw		
R.KAGAFPSDSYR.G	Y	51.41	1197.5778	11	0.2	599.7963	2	27.19	2	F2:6677	12112021_RID_2349_DP2.raw		4.193
K.FWVADGSR.G	Y	49.35	936.4453	8	0.1	469.2300	2	37.70	3	F3:10542	17112021_RID_2349_DP3.raw		
F.SPSIFNLPPGIK.C	Y	45.13	1268.7128	12	0.8	635.3642	2	55.02	3	F3:16255	17112021_RID_2349_DP3.raw		
													total 1

TRINITY_DN1031
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MEKLILLTWA TGFLVVNCVQ LHQQLQTLPM LGDVYHVTGI LKLPYAEIEE PFEAWFNKTG GKSRIQYYDG QVITYQLGYI
 81 KPFGASFKVT PETTETEVNI KECFQFNGTS ENPVRPQSLF PNLTNFQPVR HEHYNGQHCT VLESVSYWGK KKNTYKFWVA
161 DGSRGPLPVH YEMKGYNTLL GSHYDKYEID YISYSHSFSP SIFNLPPGIK CAHWPKGGPE HRILANPMQE FVGGTGEVSQ
241 HHEHLFHHYK KKFRKTYKNK KEIEHRQHNF IHNMRYIHSK NRANLSFKLA ANHLADRTPE ELAVLRGRLQ TDEPRKAGAF
321 PSDSYRGLTL PDSLDWRLYG AVTRVKDQAV CGSCWSFATT GALEGAIFLK TGVLTPLSQQ VLIDCSWGFG NRACDGGQEP
401 QAFEWIMKHG GIASAEAYGP YMGQNGYCHY NQSELIAPIA GYIVITSQNI TDLKAALYKH GPIAVNVDAS HKSFAFYSSG
481 IYYEPNCGNT TMELDHAVLA VGYGDLQGEP YWLIKNSWST YWGNDGYILM SMKENNCGVA SSATYPILA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.IQYYDGQVITYQLGYIKPFGASFK.V	Y	89.84	2798.4319	24	0.6	933.8185	3	64.33	3	F3:19267	17112021_RID_2349_DP3.raw		
K.VTPETTETEVNIK.E	Y	80.09	1459.7406	13	-0.1	730.8775	2	33.29	3	F3:8992	17112021_RID_2349_DP3.raw		
K.HGPIAVNVDASHK.S	Y	76.92	1343.6946	13	0.3	672.8547	2	28.24	2	F2:6976	12112021_RID_2349_DP2.raw		1.321
R.GPLPVHYEMK.G	Y	72.68	1169.5903	10	0.8	585.8029	2	35.42	3	F3:9693	17112021_RID_2349_DP3.raw		
R.IQYYDGQVITYQLGYIKPF.G	Y	66.66	2308.1780	19	0.9	1155.0973	2	67.58	3	F3:20288	17112021_RID_2349_DP3.raw		
R.GLTLPDSLDWR.L	Y	63.18	1271.6510	11	0.0	636.8328	2	58.34	2	F2:17069	12112021_RID_2349_DP2.raw		1.203
R.GPLPVHYEM(+15.99)K.G	Y	57.86	1185.5852	10	-0.2	396.2023	3	29.39	3	F3:7623	17112021_RID_2349_DP3.raw		
R.KAGAFPSDSYR.G	Y	51.41	1197.5778	11	0.2	599.7963	2	27.19	2	F2:6677	12112021_RID_2349_DP2.raw		4.193
K.FWVADGSR.G	Y	49.35	936.4453	8	0.1	469.2300	2	37.70	3	F3:10542	17112021_RID_2349_DP3.raw		
F.SPSIFNLPPGIK.C	Y	45.13	1268.7128	12	0.8	635.3642	2	55.02	3	F3:16255	17112021_RID_2349_DP3.raw		
													total 1

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVLIRVLANL LVLQLSYAQK SSELVIGGDE CNINEHPFPV ALHTARSKRF YCAGTLINQE WVLTAARCDR KNIRIILGVH
                                   114                                     147
 81 SKNVPNEDQQ IRVPKEKFFC LSSKTYTRWD KDIMLIRLKK PVNDSTHIVP LSLPSSPPSV GSVCRIMGWG TITTTKVTYP
161 DVPHCANINM FDYSVCRKVY RKLPEKSRTL CAGILQGGID SCKVDNGGPL ICNGQIQGIV SWGGHPCAQP HKPALYTNVF
241 DYTDWIQSII AGNITATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.73
R.IMGWGTITTTK.V	N	78.23	1207.6271	11	-0.4	604.8206	2	47.11	3	F3:13741	17112021_RID_2349_DP3.raw	1.7839E6	2.7374E7	1.67
														total 1

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.NVPNEDQQIRVPK.E	Y	74.15	1535.8055	13	0.1	768.9101	2	30.88	2	F2:7842	12112021_RID_2349_DP2.raw		1.5351E7	1.45
K.NVPNEDQQIR.V	Y	72.95	1211.5895	10	0.4	606.8022	2	24.54	2	F2:5672	12112021_RID_2349_DP2.raw	3.788E5	1.1029E8	3.95
R.IM(+15.99)GWGTITTTK.V	N	67.99	1223.6221	11	0.3	612.8185	2	40.75	2	F2:11290	12112021_RID_2349_DP2.raw	7.1945E5	1.2257E7	3.31
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.37
N.VPNEDQQIR.V	Y	58.49	1097.5465	9	1.3	549.7812	2	22.54	3	F3:5342	17112021_RID_2349_DP3.raw		1.7116E5	6.42
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.00
A.GTLINQEWVLTAAR.C	N	48.88	1570.8467	14	0.5	786.4310	2	56.07	3	F3:16574	17112021_RID_2349_DP3.raw			2.60
V.PNEDQQIRVPK.E	Y	48.77	1322.6942	11	0.1	662.3544	2	30.86	2	F2:7883	12112021_RID_2349_DP2.raw		2.0109E5	
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.86
R.IILGVHSK.N	Y	43.01	865.5385	8	0.7	433.7769	2	26.46	2	F2:6227	12112021_RID_2349_DP2.raw		3.7847E7	1.23
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.70
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			
														total 1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVLIRVLANL LVLQLSYAQK SSELVIGGDE CNINEHPFPV ALHTARSKRF YCAGTLINQE WVLTAARCDR KNIRIILGVH
                                                                                          C
                                      114                                     147
 81 SKNVPNEDQQ IRVPKEKFFC LSSKTYTRWD KDIMLIRLKK PVNDSTHIVP LSLPSSPPSV GSVCRIMGWG TITTTKVTYP

161 DVPHCANINM FDYSVCRKVY RKLPEKSRTL CAGILQGGID SCKVDNGGPL ICNGQIQGIV SWGGHPCAQP HKPALYTNVF

241 DYTDWIQSII AGNITATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.73
R.IMGWGTITTTK.V	N	78.23	1207.6271	11	-0.4	604.8206	2	47.11	3	F3:13741	17112021_RID_2349_DP3.raw	1.7839E6	2.7374E7	1.67
K.NVPNEDQQIRVPK.E	Y	74.15	1535.8055	13	0.1	768.9101	2	30.88	2	F2:7842	12112021_RID_2349_DP2.raw		1.5351E7	1.45
K.NVPNEDQQIR.V	Y	72.95	1211.5895	10	0.4	606.8022	2	24.54	2	F2:5672	12112021_RID_2349_DP2.raw	3.788E5	1.1029E8	3.95
R.IM(+15.99)GWGTITTTK.V	N	67.99	1223.6221	11	0.3	612.8185	2	40.75	2	F2:11290	12112021_RID_2349_DP2.raw	7.1945E5	1.2257E7	3.31
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.37
N.VPNEDQQIR.V	Y	58.49	1097.5465	9	1.3	549.7812	2	22.54	3	F3:5342	17112021_RID_2349_DP3.raw		1.7116E5	6.42
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.00
A.GTLINQEWVLTAAR.C	N	48.88	1570.8467	14	0.5	786.4310	2	56.07	3	F3:16574	17112021_RID_2349_DP3.raw			2.60
V.PNEDQQIRVPK.E	Y	48.77	1322.6942	11	0.1	662.3544	2	30.86	2	F2:7883	12112021_RID_2349_DP2.raw		2.0109E5	
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.86
R.IILGVHSK.N	Y	43.01	865.5385	8	0.7	433.7769	2	26.46	2	F2:6227	12112021_RID_2349_DP2.raw		3.7847E7	1.23
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.70
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			
														total 1

P0DL42.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  EVRPFLDVYQ RSACQTRETL VSILQEHPDE ISDIFRPSCV AVLRCSGCCT DESMKCTPVG KHTADIQIMR MNPRTHSSKM
 81  EVMKFMEHTA CECRPRWKQG EPEGPKEPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
R.WKQGEPEGPKEPR	Y	78.94	1536.7684	13	-0.2	769.3914	2	21.61	7	F7:5034	17112021_RID_2349_DP7.raw					
K.HTADIQIMR.M	Y	70.22	1083.5496	9	0.5	542.7823	2	29.75	7	F7:8013	17112021_RID_2349_DP7.raw					
K.QGEPEGPKEPR	Y	69.86	1222.5941	11	-0.4	612.3041	2	17.34	7	F7:3495	17112021_RID_2349_DP7.raw					
K.HTADIQIM(+15.99)R.M	Y	62.06	1099.5444	9	0.2	550.7796	2	27.83	7	F7:7145	17112021_RID_2349_DP7.raw					
R.WKQGEPEGPK.E	Y	53.45	1154.5720	10	0.0	578.2933	2	19.26	7	F7:4324	17112021_RID_2349_DP7.raw					
R.PFLDVYQR.S	N	49.73	1036.5342	8	-0.1	519.2743	2	44.38	7	F7:12800	17112021_RID_2349_DP7.raw				0	
H.TADIQIMR.M	Y	49.17	946.4906	8	-0.5	474.2523	2	35.36	7	F7:9694	17112021_RID_2349_DP7.raw					
R.ETLVSILQEHPD.E	Y	48.06	1379.6932	12	0.5	690.8542	2	54.14	7	F7:16136	17112021_RID_2349_DP7.raw					
R.ETLVSILQEHP.D	Y	47.00	1264.6663	11	0.4	633.3406	2	55.20	7	F7:16471	17112021_RID_2349_DP7.raw					
V.RPFLDVYQR.S	N	45.90	1192.6353	9	1.7	597.3259	2	38.63	7	F7:10909	17112021_RID_2349_DP7.raw					
K.QGEPEGPKEP.R	Y	45.10	1066.4930	10	-0.3	534.2537	2	21.94	7	F7:5155	17112021_RID_2349_DP7.raw					
R.WKQGEPEGP.K	Y	44.23	1026.4771	9	0.6	514.2461	2	25.35	7	F7:6256	17112021_RID_2349_DP7.raw					
K.QGEPEGPK.E	Y	43.80	840.3977	8	0.3	421.2063	2	14.33	7	F7:2604	17112021_RID_2349_DP7.raw					
R.WKQGEPEGPKE.P	Y	42.99	1283.6145	11	0.6	642.8149	2	21.26	7	F7:4833	17112021_RID_2349_DP7.raw					
H.TADIQIM(+15.99)R.M	Y	40.76	962.4855	8	-0.7	482.2497	2	28.10	7	F7:7206	17112021_RID_2349_DP7.raw					

total 15 peptides

Q4VM07.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MMQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPQKIT ALPKGAIQQP EQKYEDAIKY EFKVNGKPVV LHLEKNKGLF
 81  SEDYSETHYT PDGREITINP PVEDHCYYHG RIQNDADSTA SISACNGLKG HFKLQGEMYL IEPLRIPDSE AHAIYKYENI
161  EKEDEAPKMC GVTQTNWESD EPIKASQLNL TPEQRTYLKS KKYVELVIVA DYIMFWKYDR SLSTIRTRIY EIVNTLNVIY
241  RFLNIYIALV AVEIWSKGDL INVTSSAYDT LDSFGEWRER DLLNRKRHDN AQLLTGINFN GPSAGRGFVG RMCQPKYSVG
321  IVQDHSKIYL LVASAMAHEM GHNLGMDHDR IDCTCGAKSC IMSGILRCET SYLFSDCSRE EHRKYLINKM PQCILNKPLK
401  TDIVSPAVCG NYFVEVGEEC DCGSPANCQD RCCDAATCKL RPGAQCGDGV CCYQCKFRRA GTVCRPANGE CDVSDLCTGQ
481  SAECPTDQFQ RNGQPCQNNK GYCYNGTCPI MEKQCISLFG ASATVAQDSC FQFNRRGNHY GYCRKENNTK IACAPEDVKC
561  GRLYCLDNSS GHKNPCQIYY IPSDENKGMV DPGTKCGDGM VCSNGKCVDV TIAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
R.IYEIVNTLNVIYR.F	N	74.30	1608.8875	13	0.4	805.4514	2	61.67	3	F3:18319	17112021_RID_2349_DP3.raw		
R.HDNAQLLTGINFNGPSAGR.G	Y	73.01	1980.9766	19	0.3	991.4958	2	49.32	1	F1:15000	12112021_RID_2349_DP1.raw	2.0256E6	
K.YSVGIVQDHSK.I	Y	72.55	1231.6196	11	0.5	616.8174	2	28.91	3	F3:7512	17112021_RID_2349_DP3.raw	3.3389E5	4.2446E5
I.KASQLNLTPEQR.T	N	68.58	1383.7469	12	0.5	692.8811	2	28.68	1	F1:8063	12112021_RID_2349_DP1.raw	1.981E6	1.3728E5

total 12

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
A.SQLNLTPEQR.T	N	61.22	1184.6150	10	0.3	593.3149	2	32.62	1	F1:9376	12112021_RID_2349_DP1.raw	1.0663E7	3.1363E6
K.ASQLNLTPEQR.T	N	61.13	1255.6521	11	0.9	628.8339	2	32.86	2	F2:8565	12112021_RID_2349_DP2.raw	5.7571E7	1.162E7
D.SFGEWRER.D	N	55.07	1065.4991	8	0.1	533.7569	2	31.26	2	F2:7954	12112021_RID_2349_DP2.raw	6.0265E6	2.4122E6
D.TLDSFGEWR.E	N	52.86	1109.5142	9	0.7	555.7648	2	47.54	2	F2:13529	12112021_RID_2349_DP2.raw		8.0796E4
R.HDNAQLLTGINFN.G	N	48.53	1455.7106	13	1.2	728.8634	2	53.68	3	F3:15808	17112021_RID_2349_DP3.raw		
R.ERDLLNR.K	N	42.02	914.4933	7	-0.1	458.2539	2	23.23	1	F1:6203	12112021_RID_2349_DP1.raw	1.8049E7	3.2804E6
Q.LNLTPEQR.T	N	41.26	969.5243	8	0.0	485.7694	2	30.89	7	F7:8269	17112021_RID_2349_DP7.raw	4.4645E5	
D.NAQLLTGINFNGPSAGR.G	Y	40.64	1728.8907	17	0.3	865.4529	2	51.82	1	F1:15761	12112021_RID_2349_DP1.raw	1.7741E4	

total 12

AAX38182.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MMQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPQKIT ALPKGAIQQP EQKYEDAIKY EFKVNGKPVV LHLEKNKGLF
 81 SEDYSETHYT PDGREITINP PVEDHCYYHG RIQNDADSTA SISACNGLKG HFKLQGEMYL IEPLRIPDSE AHAIYKYENI
161 EKEDEAPKMC GVTQTNWESD EPIKASQLNL TPEQRTYLKS KKYVELVIVA DYIMFWKYDR SLSTIRTRIY EIVNTLNVIY

241 RFLNIYIALV AVEIWSKGDL INVTSSAYDT LDSFGEWRER DLLNRKRHDN AQLLTGINFN GPSAGRGFVG RMCQPKYSVG

321 IVQDHSKIYL LVASAMAHEM GHNLGMDHDR IDCTCGAKSC IMSGILRCET SYLFSDCSRE EHRKYLINKM PQCILNKPLK

401 TDIVSPAVCG NYFVEVGEEC DCGSPANCQD RCCDAATCKL RPGAQCGDGV CCYQCKFRRA GTVCRPANGE CDVSDLCTGQ
481 SAECPTDQFQ RNGQPCQNNK GYCYNGTCPI MEKQCISLFG ASATVAQDSC FQFNRRGNHY GYCRKENNTK IACAPEDVKC
561 GRLYCLDNSS GHKNPCQIYY IPSDENKGMV DPGTKCGDGM VCSNGKCVDV TIAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
R.IYEIVNTLNVIYR.F	N	74.30	1608.8875	13	0.4	805.4514	2	61.67	3	F3:18319	17112021_RID_2349_DP3.raw		
R.HDNAQLLTGINFNGPSAGR.G	Y	73.01	1980.9766	19	0.3	991.4958	2	49.32	1	F1:15000	12112021_RID_2349_DP1.raw	2.0256E6	
K.YSVGIVQDHSK.I	Y	72.55	1231.6196	11	0.5	616.8174	2	28.91	3	F3:7512	17112021_RID_2349_DP3.raw	3.3389E5	4.2446E5
I.KASQLNLTPEQR.T	N	68.58	1383.7469	12	0.5	692.8811	2	28.68	1	F1:8063	12112021_RID_2349_DP1.raw	1.981E6	1.3728E5
A.SQLNLTPEQR.T	N	61.22	1184.6150	10	0.3	593.3149	2	32.62	1	F1:9376	12112021_RID_2349_DP1.raw	1.0663E7	3.1363E6
K.ASQLNLTPEQR.T	N	61.13	1255.6521	11	0.9	628.8339	2	32.86	2	F2:8565	12112021_RID_2349_DP2.raw	5.7571E7	1.162E7
D.SFGEWRER.D	N	55.07	1065.4991	8	0.1	533.7569	2	31.26	2	F2:7954	12112021_RID_2349_DP2.raw	6.0265E6	2.4122E6
D.TLDSFGEWR.E	N	52.86	1109.5142	9	0.7	555.7648	2	47.54	2	F2:13529	12112021_RID_2349_DP2.raw		8.0796E4
R.HDNAQLLTGINFN.G	N	48.53	1455.7106	13	1.2	728.8634	2	53.68	3	F3:15808	17112021_RID_2349_DP3.raw		
R.ERDLLNR.K	N	42.02	914.4933	7	-0.1	458.2539	2	23.23	1	F1:6203	12112021_RID_2349_DP1.raw	1.8049E7	3.2804E6
Q.LNLTPEQR.T	N	41.26	969.5243	8	0.0	485.7694	2	30.89	7	F7:8269	17112021_RID_2349_DP7.raw	4.4645E5	
D.NAQLLTGINFNGPSAGR.G	Y	40.64	1728.8907	17	0.3	865.4529	2	51.82	1	F1:15761	12112021_RID_2349_DP1.raw	1.7741E4	

total 12

TRINITY_DN459
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
1   GQSAECPTDV FQRNGQPCQN NKGYCYNGDC PILTNQCISL FGSSVTVAPD VCFDYNLQGT EDYHCRRENG RYIKCEPQDK
                                     111
81  KCGRLFCVKP PTGNTISCKF SRSKDDPDYG MVDLGTKCAD GKVCNSNRQC VDVNTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.SKDDPDYGM(+15.99)VDLGTK.C	Y	89.44	1655.7349	15	0.4	552.9191	3	38.10	1	F1:11983	12112021_RID_2349_DP1.raw	4.6116E7	1.206E
R.SKDDPDYGMVDLGTK.C	Y	87.92	1639.7399	15	-0.1	820.8771	2	39.20	3	F3:10983	17112021_RID_2349_DP3.raw	8.1952E7	2.5565
K.DDPDYGMVDLGTK.C	N	86.80	1424.6129	13	0.9	713.3144	2	48.02	1	F1:14542	12112021_RID_2349_DP1.raw	3.1015E5	
D.PDYGMVDLGTK.C	N	73.86	1194.5591	11	-0.1	598.2867	2	43.94	1	F1:13219	12112021_RID_2349_DP1.raw	7.4048E6	4.1966
D.PDYGM(+15.99)VDLGTK.C	N	71.86	1210.5540	11	0.4	606.2845	2	40.64	1	F1:13230	12112021_RID_2349_DP1.raw	6.7718E6	3.5085
K.DDPDYGM(+15.99)VDLGTK.C	N	69.19	1440.6078	13	0.3	721.3114	2	40.35	6	F6:11298	17112021_RID_2349_DP6.raw	7.0367E4	
D.DPDYGMVDLGTK.C	N	68.28	1309.5859	12	1.2	655.8010	2	47.41	1	F1:14315	12112021_RID_2349_DP1.raw	7.5385E5	
D.DPDYGM(+15.99)VDLGTK.C	N	61.75	1325.5809	12	0.8	663.7983	2	39.96	1	F1:11872	12112021_RID_2349_DP1.raw	2.7576E5	
D.YGM(+15.99)VDLGTK.C	N	54.16	998.4742	9	0.8	500.2448	2	39.32	1	F1:11674	12112021_RID_2349_DP1.raw	1.0157E5	
R.SKDDPDYGMVD.L	Y	46.37	1240.4917	11	0.7	621.2535	2	34.22	1	F1:10024	12112021_RID_2349_DP1.raw	4.9296E5	
D.YGMVDLGTK.C	N	45.13	982.4794	9	-0.5	492.2467	2	39.32	1	F1:11699	12112021_RID_2349_DP1.raw	1.3963E5	
Y.GMVDLGTK.C	N	44.20	819.4160	8	0.0	410.7153	2	30.74	7	F7:8124	17112021_RID_2349_DP7.raw		

TRINITY_DN1910
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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                                17
1   TISCKFSRSK DDPDYGMVDL GTKCADGKNS ANQCFDPIMC ERREETCAS GPCCRRCKVR LAHF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
R.SKDDPDYGM(+15.99)VDLGTK.C	Y	89.44	1655.7349	15	0.4	552.9191	3	38.10	1	F1:11983	12112021_RID_2349_DP1.raw	4.6116E7	1.206E
R.SKDDPDYGMVDLGTK.C	Y	87.92	1639.7399	15	-0.1	820.8771	2	39.20	3	F3:10983	17112021_RID_2349_DP3.raw	8.1952E7	2.5565
K.DDPDYGMVDLGTK.C	N	86.80	1424.6129	13	0.9	713.3144	2	48.02	1	F1:14542	12112021_RID_2349_DP1.raw	3.1015E5	
D.PDYGMVDLGTK.C	N	73.86	1194.5591	11	-0.1	598.2867	2	43.94	1	F1:13219	12112021_RID_2349_DP1.raw	7.4048E6	4.1966
D.PDYGM(+15.99)VDLGTK.C	N	71.86	1210.5540	11	0.4	606.2845	2	40.64	1	F1:13230	12112021_RID_2349_DP1.raw	6.7718E6	3.5085
K.DDPDYGM(+15.99)VDLGTK.C	N	69.19	1440.6078	13	0.3	721.3114	2	40.35	6	F6:11298	17112021_RID_2349_DP6.raw	7.0367E4	
D.DPDYGMVDLGTK.C	N	68.28	1309.5859	12	1.2	655.8010	2	47.41	1	F1:14315	12112021_RID_2349_DP1.raw	7.5385E5	
D.DPDYGM(+15.99)VDLGTK.C	N	61.75	1325.5809	12	0.8	663.7983	2	39.96	1	F1:11872	12112021_RID_2349_DP1.raw	2.7576E5	
D.YGM(+15.99)VDLGTK.C	N	54.16	998.4742	9	0.8	500.2448	2	39.32	1	F1:11674	12112021_RID_2349_DP1.raw	1.0157E5	
R.SKDDPDYGMVD.L	Y	46.37	1240.4917	11	0.7	621.2535	2	34.22	1	F1:10024	12112021_RID_2349_DP1.raw	4.9296E5	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
D.YGMVDLGTK.C	N	45.13	982.4794	9	-0.5	492.2467	2	39.32	1	F1:11699	12112021_RID_2349_DP1.raw	1.3963E5	
Y.GMVDLGTK.C	N	44.20	819.4160	8	0.0	410.7153	2	30.74	7	F7:8124	17112021_RID_2349_DP7.raw		

TRINITY_DN509
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKYAIVCLLL VGSVFAAEDD DKKEDVGTVV GIDLGTTYSC VGVFKNGRVE IIANDQGNRI TPSYVAFTPE GERLIGDAAK
 81 NQLTSNPENT VFDAKRLIGR TWNDPSVQQD IKYLPFKVIE KKTKPYIQVD VGGGQTKTFA PEEISAMVLT KMKETAEAYL
161 GKKVTHAVVT VPAYFNDAQR QATKDAGTIA GLNVMRIINE PTAAAIAYGL DKREGEKNIL VFDLGGGTFD VSLLTIDNGV
241 FEVVATNGDT HLGGEDFDQR VMEHFIKLYK KKTGKDVRKD NRAVQKLRRE VEKAKRALSS QHQARIEIES FFEGEDFSET
321 LTRAKFEELN MDLFRSTMKP VQKVLEDADL KKPDIDEIVL VGGSTRIPKI QQLVKEFFNG KEPSRGINPD EAVAYGAAVQ
401 AGVLSGDQDT GDLVLLDVCP LTLGIETVGG VMTKLIPRNT VVPTKKSQIF STASDNQPTV TIKVYEGERP LTKDNHLLGT
481 FDLTGIPPAP RGVPQIEVTF EIDVNGILRV TAEDKGTGNK NKITITNDQN RLTPEEIERM VNDAEKFAEE DKKLKERIDA
561 RNELESYAYS LKNQIGDKEK LGGKLSTEDK ETIEKAVEEK IEWLESHQEA DIEDFKAQKK ELEEVVQPIV GKLYGGAGPP
641 PGGEEPGEKD EL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are: F3
K.SQIFSTASDNQPTVTIK.V	Y	78.43	1835.9265	17	0.7	918.9712	2	43.86	4	F4:12557	17112021_RID_2349_DP4.raw			
K.ELEEVVQPIVGK.L	Y	68.74	1338.7394	12	0.1	670.3770	2	46.15	4	F4:13270	17112021_RID_2349_DP4.raw			
R.NELESYAYSLK.N	Y	67.75	1315.6295	11	0.6	658.8224	2	45.74	4	F4:13114	17112021_RID_2349_DP4.raw			
R.ITPSYVAFTPEGER.L	Y	63.57	1565.7725	14	0.5	783.8939	2	46.47	2	F2:13149	12112021_RID_2349_DP2.raw		8.8984E4	
K.VYEGERPLTK.D	Y	55.73	1190.6295	10	0.6	596.3224	2	22.63	4	F4:5257	17112021_RID_2349_DP4.raw			
R.LTPEEIER.M	Y	49.69	985.5080	8	-0.1	493.7612	2	31.13	4	F4:8215	17112021_RID_2349_DP4.raw			
K.NQLTSNPENTVFDAK.R	Y	48.37	1676.8005	15	1.1	839.4084	2	40.91	2	F2:11316	12112021_RID_2349_DP2.raw		1.9104E4	
K.LYGGAGPPPGGEEPGEKDEL	Y	45.98	1967.9111	20	0.8	984.9636	2	40.85	4	F4:11534	17112021_RID_2349_DP4.raw			
R.TWNDPSVQQDIK.Y	Y	45.02	1429.6837	12	0.3	715.8494	2	37.71	2	F2:10252	12112021_RID_2349_DP2.raw		2.2693E4	
K.LYGGAGPPPGGEEPGEKDE.L	Y	42.79	1854.8271	19	1.1	928.4219	2	33.35	4	F4:8886	17112021_RID_2349_DP4.raw			
K.LYGGAGPPPGGEEPGEK.D	Y	38.90	1610.7576	17	0.9	806.3868	2	31.58	4	F4:8348	17112021_RID_2349_DP4.raw			

total 11 peptide

TRINITY_DN509
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 PREAAGGYIS ADGRPGLNTR SGETSAWEGS ERRSAAAGSP SRRDRVLLLV WCVREHPPSK SNMKYAIVCL LLVGSVFAAE
 81 DDDKKEDVGT VVGIDLGTTY SCVGVFKNGR VEIIANDQGN RITPSYVAFT PEGERLIGDA AKNQLTSNPE NTVFDAKRLI
161 GRTWNDPSVQ QDIKYLPFKV IEKKTKPYIQ VDVGGGQTKT FAPEEISAMV LTKMKETAEA YLGKKVTHAV VTVPAYFNDA
241 QRQATKDAGT IAGLNVMRII NEPTAAAIAY GLDKREGEKN ILVFDLGGGT FDVSLLTIDN GVFEVVATNG DTHLGGEDFD
321 QRVMEHFIKL YKKKTGKDVR KDNRAVQKLR REVEKAKRAL SSQHQARIEI ESFFEGEDFS ETLTRAKFEE LNMDLFRSTM
401 KPVQKVLEDA DLKKPDIDEI VLVGGSTRIP KIQQLVKEFF NGKEPSRGIN PDEAVAYGAA VQAGVLSGDQ DTGDLVLLDV
481 CPLTLGIETV GGVMTKLIPR NTVVPTKKSQ IFSTASDNQP TVTIKVYEGE RPLTKDNHLL GTFDLTGIPP APRGVPQIEV
561 TFEIDVNGIL RVTAEDKGTG NKNKITITND QNRLTPEEIE RMVNDAEKFA EEDKKLKERI DARNELESYA YSLKNQIGDK
641 EKLGGKLSTE DKETIEKAVE EKIEWLESHQ EADIEDFKAQ KKELEEVVQP IVGKLYGGAG PPPGGEEPGE KDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.SQIFSTASDNQPTVTIK.V	Y	78.43	1835.9265	17	0.7	918.9712	2	43.86	4	F4:12557	17112021_RID_2349_DP4.raw			
K.ELEEVVQPIVGK.L	Y	68.74	1338.7394	12	0.1	670.3770	2	46.15	4	F4:13270	17112021_RID_2349_DP4.raw			
R.NELESYAYSLK.N	Y	67.75	1315.6295	11	0.6	658.8224	2	45.74	4	F4:13114	17112021_RID_2349_DP4.raw			
R.ITPSYVAFTPEGER.L	Y	63.57	1565.7725	14	0.5	783.8939	2	46.47	2	F2:13149	12112021_RID_2349_DP2.raw		8.8984E4	
K.VYEGERPLTK.D	Y	55.73	1190.6295	10	0.6	596.3224	2	22.63	4	F4:5257	17112021_RID_2349_DP4.raw			
R.LTPEEIER.M	Y	49.69	985.5080	8	-0.1	493.7612	2	31.13	4	F4:8215	17112021_RID_2349_DP4.raw			
K.NQLTSNPENTVFDAK.R	Y	48.37	1676.8005	15	1.1	839.4084	2	40.91	2	F2:11316	12112021_RID_2349_DP2.raw		1.9104E4	
K.LYGGAGPPPGGEEPGEKDEL	Y	45.98	1967.9111	20	0.8	984.9636	2	40.85	4	F4:11534	17112021_RID_2349_DP4.raw			
R.TWNDPSVQQDIK.Y	Y	45.02	1429.6837	12	0.3	715.8494	2	37.71	2	F2:10252	12112021_RID_2349_DP2.raw		2.2693E4	
K.LYGGAGPPPGGEEPGEKDE.L	Y	42.79	1854.8271	19	1.1	928.4219	2	33.35	4	F4:8886	17112021_RID_2349_DP4.raw			
K.LYGGAGPPPGGEEPGEK.D	Y	38.90	1610.7576	17	0.9	806.3868	2	31.58	4	F4:8348	17112021_RID_2349_DP4.raw			

total 11 peptide

ADK22823.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFG LLVVFLSLSG TGADCPSEWS SHEGHCYKVF KLLKTWEDAE KFCTQQANGW HLASIESVEE ANFVAQLASE

 81  TLTKSKYHAW IGLRDQSKRQ QCSSHWTDGS AVSYETVTKY TKCFGLNKET KYHEWITLPC GDKNPFICKS WVLH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.LLKTWEDAEK.F	N	73.82	1231.6448	10	0.3	616.8298	2	32.46	7	F7:8767	17112021_RID_2349_DP7.raw					
F.VAQLASETLTK.S	Y	64.28	1159.6448	11	0.4	580.8299	2	32.58	7	F7:8832	17112021_RID_2349_DP7.raw					
N.FVAQLASETLTK.S	Y	63.48	1306.7133	12	0.5	654.3643	2	44.09	7	F7:12823	17112021_RID_2349_DP7.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
V.AQLASETLTK.S	Y	56.80	1060.5764	10	0.2	531.2956	2	28.42	7	F7:7389	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
A.QLASETLTK.S	Y	44.28	989.5393	9	-0.3	495.7768	2	26.35	7	F7:6702	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptides

ABA86561.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MGRFISVSFG LLVVFLSLSG TGADCPSEWS SHEGHCYKVF KLLKTWEDAE KFCTQQANGW HLASIESVEE ANFVAQLASE

 81  TLTKSKYHAW IGLRDQSKRQ QCSSHWTDGS AVSYETVTKY TKCFGLNKET KYHEWITLPC GDKNPFICKS WVLH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.LLKTWEDAEK.F	N	73.82	1231.6448	10	0.3	616.8298	2	32.46	7	F7:8767	17112021_RID_2349_DP7.raw					
F.VAQLASETLTK.S	Y	64.28	1159.6448	11	0.4	580.8299	2	32.58	7	F7:8832	17112021_RID_2349_DP7.raw					
N.FVAQLASETLTK.S	Y	63.48	1306.7133	12	0.5	654.3643	2	44.09	7	F7:12823	17112021_RID_2349_DP7.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
V.AQLASETLTK.S	Y	56.80	1060.5764	10	0.2	531.2956	2	28.42	7	F7:7389	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
A.QLASETLTK.S	Y	44.28	989.5393	9	-0.3	495.7768	2	26.35	7	F7:6702	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptides

Q38L02.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFG LLVVFLSLSG TGADCPSEWS SHEGHCYKVF KLLKTWEDAE KFCTQQANGW HLASIESVEE ANFVAQLASE

 81  TLTKSKYHAW IGLRDQSKRQ QCSSHWTDGS AVSYETVTKY TKCFGLNKET KYHEWITLPC GDKNPFICKS WVLH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.LLKTWEDAEK.F	N	73.82	1231.6448	10	0.3	616.8298	2	32.46	7	F7:8767	17112021_RID_2349_DP7.raw					
F.VAQLASETLTK.S	Y	64.28	1159.6448	11	0.4	580.8299	2	32.58	7	F7:8832	17112021_RID_2349_DP7.raw					
N.FVAQLASETLTK.S	Y	63.48	1306.7133	12	0.5	654.3643	2	44.09	7	F7:12823	17112021_RID_2349_DP7.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
V.AQLASETLTK.S	Y	56.80	1060.5764	10	0.2	531.2956	2	28.42	7	F7:7389	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
A.QLASETLTK.S	Y	44.28	989.5393	9	-0.3	495.7768	2	26.35	7	F7:6702	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptides

ADK22821.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFG LLVVFLSLSG TGADCPSDWS SHEGHCYKVF KLLKTWEDAE KFCTQQANGW HLASIESVEE ANFVAQLASE

 81  TLTKSKYHAW IGLRDQSQRQ QCSSHWTDGS AVSYETVTKY TKCFGLNKET KYHEWITLPC GDKNPFICKS WVLH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.LLKTWEDAEK.F	N	73.82	1231.6448	10	0.3	616.8298	2	32.46	7	F7:8767	17112021_RID_2349_DP7.raw					
F.VAQLASETLTK.S	Y	64.28	1159.6448	11	0.4	580.8299	2	32.58	7	F7:8832	17112021_RID_2349_DP7.raw					
N.FVAQLASETLTK.S	Y	63.48	1306.7133	12	0.5	654.3643	2	44.09	7	F7:12823	17112021_RID_2349_DP7.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
V.AQLASETLTK.S	Y	56.80	1060.5764	10	0.2	531.2956	2	28.42	7	F7:7389	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
A.QLASETLTK.S	Y	44.28	989.5393	9	-0.3	495.7768	2	26.35	7	F7:6702	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptides

AAZ53176.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                   24
                                   o
  1  MRTLWIVAVC LIGVEGNLYQ FGEMINQKTG NFGLLSYVYY GCYCGWGGKG KPQDATDRCC FVHDCCYGRV KGCDPKTATY  o C
                                   o
                                   o

 81  SYSFENGDIV CGGDDPCLRA VCECDRVAAI CFRENMNTYD KKYMLYSIFD CKEESDQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.NLYQFGEM(+15.99)INQK.T	Y	70.27	1499.7079	12	-0.1	750.8611	2	48.50	7	F7:14280	17112021_RID_2349_DP7.raw	1.5509E5	5.2464E4	2.
G.NLYQFGEMINQK.T	Y	69.45	1483.7129	12	0.2	742.8639	2	50.67	7	F7:15227	17112021_RID_2349_DP7.raw	4.284E5		1.
N.LYQFGEM(+15.99)INQK.T	Y	66.62	1385.6649	11	0.4	693.8400	2	39.94	7	F7:11327	17112021_RID_2349_DP7.raw			
N.LYQFGEMINQK.T	Y	66.11	1369.6700	11	0.2	685.8424	2	47.17	7	F7:13715	17112021_RID_2349_DP7.raw			
E.GNLYQFGEMINQK.T	Y	61.39	1540.7344	13	0.5	771.3749	2	54.08	7	F7:16198	17112021_RID_2349_DP7.raw			
L.YQFGEMINQK.T	Y	61.03	1256.5859	10	0.0	629.3002	2	42.06	7	F7:12071	17112021_RID_2349_DP7.raw			
K.TATYSYSFENGDIV.C	Y	54.07	1565.6885	14	0.6	783.8520	2	57.78	7	F7:17385	17112021_RID_2349_DP7.raw			
R.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
C.FRENMNTYDKK.Y	Y	45.46	1444.6769	11	-0.4	482.5660	3	21.59	7	F7:4995	17112021_RID_2349_DP7.raw			
R.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			

tota

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.KYMLYSIFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			
R.ENMNTYDKKY.M	Y	42.65	1304.5707	10	-0.7	653.2922	2	23.23	7	F7:5555	17112021_RID_2349_DP7.raw			
Q.FGEMINQK.T	Y	39.53	965.4641	8	-0.3	483.7391	2	31.06	7	F7:8248	17112021_RID_2349_DP7.raw			
C.FRENMNTYDK.K	Y	39.33	1316.5819	10	0.4	659.2985	2	24.51	7	F7:6037	17112021_RID_2349_DP7.raw			

tota

A8CG78.1
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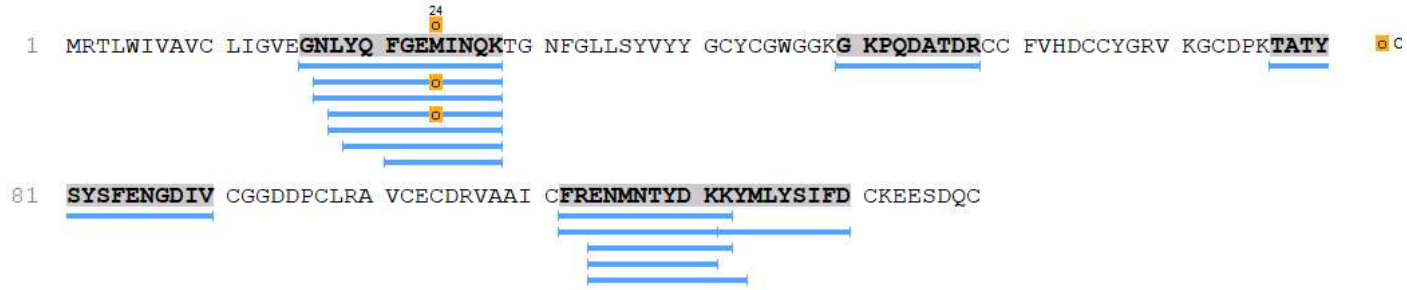
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.NLYQFGEM(+15.99)INQK.T	Y	70.27	1499.7079	12	-0.1	750.8611	2	48.50	7	F7:14280	17112021_RID_2349_DP7.raw	1.5509E5	5.2464E4	2.
G.NLYQFGEMINQK.T	Y	69.45	1483.7129	12	0.2	742.8639	2	50.67	7	F7:15227	17112021_RID_2349_DP7.raw	4.284E5		1.
N.LYQFGEM(+15.99)INQK.T	Y	66.62	1385.6649	11	0.4	693.8400	2	39.94	7	F7:11327	17112021_RID_2349_DP7.raw			
N.LYQFGEMINQK.T	Y	66.11	1369.6700	11	0.2	685.8424	2	47.17	7	F7:13715	17112021_RID_2349_DP7.raw			
E.GNLYQFGEMINQK.T	Y	61.39	1540.7344	13	0.5	771.3749	2	54.08	7	F7:16198	17112021_RID_2349_DP7.raw			
L.YQFGEMINQK.T	Y	61.03	1256.5859	10	0.0	629.3002	2	42.06	7	F7:12071	17112021_RID_2349_DP7.raw			
K.TATYSYSFENGDIV.C	Y	54.07	1565.6885	14	0.6	783.8520	2	57.78	7	F7:17385	17112021_RID_2349_DP7.raw			
R.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
C.FRENMNTYDKK.Y	Y	45.46	1444.6769	11	-0.4	482.5660	3	21.59	7	F7:4995	17112021_RID_2349_DP7.raw			
R.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			
K.KYMLYSIFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			
R.ENMNTYDKKY.M	Y	42.65	1304.5707	10	-0.7	653.2922	2	23.23	7	F7:5555	17112021_RID_2349_DP7.raw			
Q.FGEMINQK.T	Y	39.53	965.4641	8	-0.3	483.7391	2	31.06	7	F7:8248	17112021_RID_2349_DP7.raw			
C.FRENMNTYDK.K	Y	39.33	1316.5819	10	0.4	659.2985	2	24.51	7	F7:6037	17112021_RID_2349_DP7.raw			

tota

AAZ53181.1
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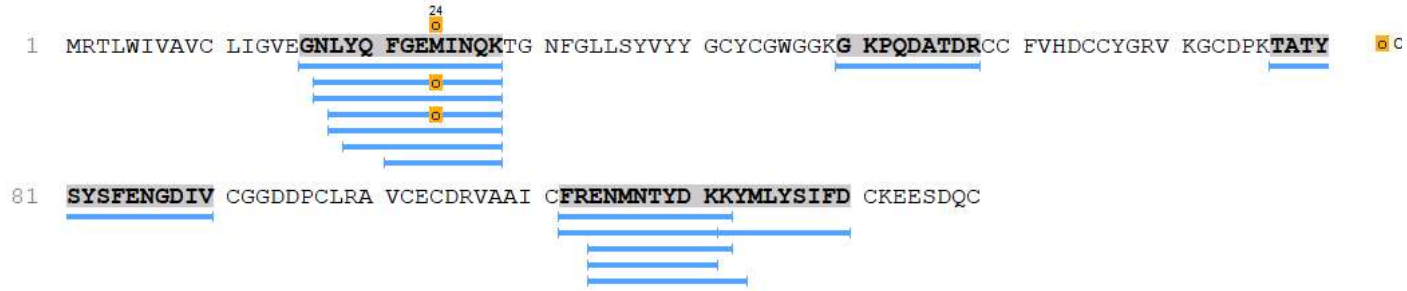
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.NLYQFGEM(+15.99)INQK.T	Y	70.27	1499.7079	12	-0.1	750.8611	2	48.50	7	F7:14280	17112021_RID_2349_DP7.raw	1.5509E5	5.2464E4	2.
G.NLYQFGEMINQK.T	Y	69.45	1483.7129	12	0.2	742.8639	2	50.67	7	F7:15227	17112021_RID_2349_DP7.raw	4.284E5		1.(
N.LYQFGEM(+15.99)INQK.T	Y	66.62	1385.6649	11	0.4	693.8400	2	39.94	7	F7:11327	17112021_RID_2349_DP7.raw			
N.LYQFGEMINQK.T	Y	66.11	1369.6700	11	0.2	685.8424	2	47.17	7	F7:13715	17112021_RID_2349_DP7.raw			
E.GNLYQFGEMINQK.T	Y	61.39	1540.7344	13	0.5	771.3749	2	54.08	7	F7:16198	17112021_RID_2349_DP7.raw			
L.YQFGEMINQK.T	Y	61.03	1256.5859	10	0.0	629.3002	2	42.06	7	F7:12071	17112021_RID_2349_DP7.raw			
K.TATYSYSFENGDIV.C	Y	54.07	1565.6885	14	0.6	783.8520	2	57.78	7	F7:17385	17112021_RID_2349_DP7.raw			
R.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
C.FRENMNTYDKK.Y	Y	45.46	1444.6769	11	-0.4	482.5660	3	21.59	7	F7:4995	17112021_RID_2349_DP7.raw			
R.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			
K.KYMLYSIFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			
R.ENMNTYDKKY.M	Y	42.65	1304.5707	10	-0.7	653.2922	2	23.23	7	F7:5555	17112021_RID_2349_DP7.raw			
Q.FGEMINQK.T	Y	39.53	965.4641	8	-0.3	483.7391	2	31.06	7	F7:8248	17112021_RID_2349_DP7.raw			
C.FRENMNTYDK.K	Y	39.33	1316.5819	10	0.4	659.2985	2	24.51	7	F7:6037	17112021_RID_2349_DP7.raw			

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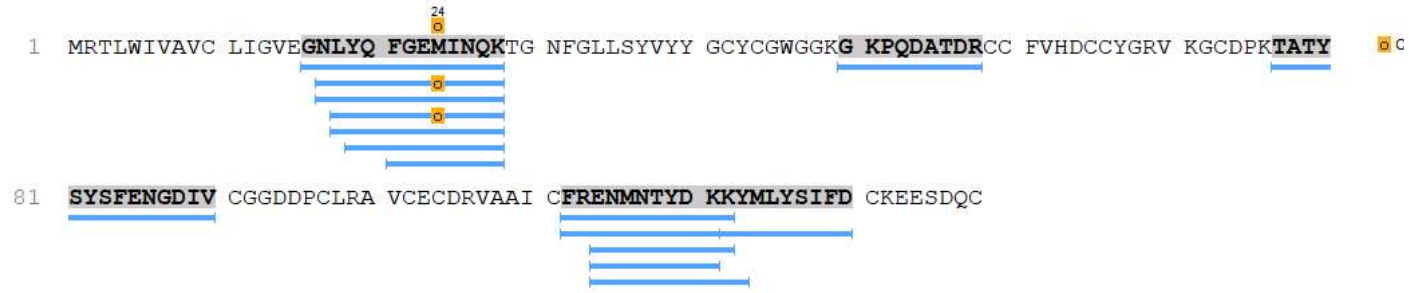
A8CG87.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.NLYQFGEM(+15.99)INQK.T	Y	70.27	1499.7079	12	-0.1	750.8611	2	48.50	7	F7:14280	17112021_RID_2349_DP7.raw	1.5509E5	5.2464E4	2.
G.NLYQFGEMINQK.T	Y	69.45	1483.7129	12	0.2	742.8639	2	50.67	7	F7:15227	17112021_RID_2349_DP7.raw	4.284E5		1.(
N.LYQFGEM(+15.99)INQK.T	Y	66.62	1385.6649	11	0.4	693.8400	2	39.94	7	F7:11327	17112021_RID_2349_DP7.raw			
N.LYQFGEMINQK.T	Y	66.11	1369.6700	11	0.2	685.8424	2	47.17	7	F7:13715	17112021_RID_2349_DP7.raw			
E.GNLYQFGEMINQK.T	Y	61.39	1540.7344	13	0.5	771.3749	2	54.08	7	F7:16198	17112021_RID_2349_DP7.raw			
L.YQFGEMINQK.T	Y	61.03	1256.5859	10	0.0	629.3002	2	42.06	7	F7:12071	17112021_RID_2349_DP7.raw			
K.TATYSYSFENGDIV.C	Y	54.07	1565.6885	14	0.6	783.8520	2	57.78	7	F7:17385	17112021_RID_2349_DP7.raw			
R.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
C.FRENMNTYDKK.Y	Y	45.46	1444.6769	11	-0.4	482.5660	3	21.59	7	F7:4995	17112021_RID_2349_DP7.raw			
R.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			
K.KYMLYSIFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			

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Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
R.ENMNTYDKKY.M	Y	42.65	1304.5707	10	-0.7	653.2922	2	23.23	7	F7:5555	17112021_RID_2349_DP7.raw			
Q.FGEMINQK.T	Y	39.53	965.4641	8	-0.3	483.7391	2	31.06	7	F7:8248	17112021_RID_2349_DP7.raw			
C.FRENMNTYDK.K	Y	39.33	1316.5819	10	0.4	659.2985	2	24.51	7	F7:6037	17112021_RID_2349_DP7.raw			

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TRINITY_DN64
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  WSAYDQHCYK AFDEPKRSGD AEKFCTEQAN GGHLVSIESV EEAEFVAQLI SENIKTSADY VWIGLWNQRK AQYCISKWTD

 81  GSSVIYKNVI ERFIKNCFGL EKQTNYRTWF NLSCGDDYPF VCKFPPRC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSADYVWIGLWNQR.K	Y	81.64	1707.8369	14	0.9	854.9265	2	65.28	5	F5:19507	17112021_RID_2349_DP5.raw			5.8246
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

B4XSY9.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFIFVRVG LLVVFLSLSG TGADFDCPPD WSAYDQHCYK AFDEPKRSGD AEKFCTQQAN GGHLVSIESV EEAEFVAQLI

 81  SENIKTSADY VWIGLWNQRK APYCVSKWTD GSSVIYKNVI ERFIKNCFGL EKETNYRTWF NLSCGDDYPF VCKSPA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSADYVWIGLWNQR.K	Y	81.64	1707.8369	14	0.9	854.9265	2	65.28	5	F5:19507	17112021_RID_2349_DP5.raw			5.8246
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

ABW82661.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFIFVRVG LLVVFLSLSG TGADFDCPPD WSAYDQHCYK AFDEPKRSGD AEKFCTQQAN GGHLVSIESV EEAEFVAQLI

 81  SENIKTSADY VWIGLWNQRK APYCVSKWTD GSSVIYKNVI ERFIKNCFGL EKETNYRTWF NLSCGDDYPF VCKSPA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSADYVWIGLWNQR.K	Y	81.64	1707.8369	14	0.9	854.9265	2	65.28	5	F5:19507	17112021_RID_2349_DP5.raw			5.8246
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

B4XSZ0.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFIFVRFG LLVVFLSLSG TGADFDCPPD WSAYDQHCYK AFDEPKRSGD AEKFCTQQAN GGHLVSIESV EEAEFVAQLI

 81  SENIKTSADY VWIGLWNQRK APYCVSKWTD GSSVIYKNVI ERFIKNCFGL EKETNYRTWF NLSCGDDYPF VCKSPA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSADYVWIGLWNQR.K	Y	81.64	1707.8369	14	0.9	854.9265	2	65.28	5	F5:19507	17112021_RID_2349_DP5.raw			5.8246
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

ABW82662.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFIFVRFG LLVVFLSLSG TGADFDCPPD WSAYDQHCYK AFDEPKRSGD AEKFCTQQAN GGHLVSIESV EEAEFVAQLI

 81  SENIKTSADY VWIGLWNQRK APYCVSKWTD GSSVIYKNVI ERFIKNCFGL EKETNYRTWF NLSCGDDYPF VCKSPA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSADYVWIGLWNQR.K	Y	81.64	1707.8369	14	0.9	854.9265	2	65.28	5	F5:19507	17112021_RID_2349_DP5.raw			5.8246
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			

total 8 pe

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

TRINITY_DN91
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MAKGFFISKS LGVVGIVLGL GAVATIIALS VVYSQEKQRA DELANQAPSS TSVAGTPSAT IAGTAQATTT NGTIQATTVK
 81 PLEPWDHMRL PKTLMPTFYT ISLQPFLIPD LYIFKGNSTV EFQCKQPTDL ILIHSKKLNY TIQGPFLVSL TGTKVVAPAI
161 DSTWLEDKTE YLVVKLKENL QQNENYQLHA SFTGELADDL AGFYRSEYTE GVARKVLATT QMQAADARKA FPCFDEPAMK
241 ANFSITLIHL PTYKALSNMP IKKAEEVKMP DGSTWVQTEF HPTLKMSTYL LGFIVSEFEN VSTIENNTLI QIWGRPTAIR
321 EGQGNYALNA TWPILSFFEQ QYSVPYPLTR LDQVALPDFN AGAMENWGLI TYRESALLFD EKYSSIGNKE RIVTVIAHEV
401 AHQWFGNLVT LEWWNELWLN EGFASYVEYL GAHEAESTWN IRDLIVPNDV YRVMAIDALA SSHPLSSPAE EINTPAQISE
481 VFDAISYSKG AAVIRMLAEF LTDAVFREGL QTYFETYQYG NTVCDDLWEQ LQKAVSKKNV YLPSTVKTIM DRWTLQMGFP
561 VLTVDTSKGI ITQKHFLLDP ESPVERPSQF NYVWIVPVSW LSKGKEAEMY WLTDILAENA NFSTSTDPAQ WLLLNVNVTG
641 YFRVNYDLGN WQRLMNQLNE DLQTIPVLNR AQIIDDAFNL ARAKHVGTDL ALNTTRYLAQ ERDYLPWDAA LDNLDYFRLM
721 FDRSEVYGPM QKYIRKQVTP LFDHFRNLTH NWTQIPDGLM NQYNQILAIR TACSHGVPGC NELASSWFEA WKNNPNVNDI
801 SPNLRSAVYC SAIRTGSLED WDFAWKMFRQ APVISEADKL RSALTCSQTP WILQRYLQYT LDPSMIRRQD AMSTINSIAS
881 NVVGQSLAWD FVRMNWKTLF QQFGRSSFSF SSLIQSVTQR FASPFELQQL EQFKADNADV GFGSATRALE QALERTKANI
961 KWVAENKALV LKWFQDNS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
R.VNYDLGNWQR.L	Y	60.42	1263.5996	10	1.0	632.8077	2	44.31	1	F1:13320	12112021_RID_2349_DP1.raw	6.6887E4			
R.YLQYTLDPSMIR.R	Y	59.84	1498.7490	12	0.1	750.3818	2	54.59	1	F1:16715	12112021_RID_2349_DP1.raw	2.8801E5			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.TLFQQFGR.S	Y	50.21	995.5189	8	0.2	498.7668	2	44.91	1	F1:13507	12112021_RID_2349_DP1.raw	1.1534E5			
K.NNPNVNDISPNLR.S	Y	47.74	1465.7273	13	1.2	733.8718	2	37.43	1	F1:11020	12112021_RID_2349_DP1.raw	4.7098E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 7 peptides

TRINITY_DN91
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MAKGFFISKS LGVVGIVLGL GAVATIIALS VVYSQEKQRA DELANQAPSS TSVAGTPSAT IAGTAQATTT NGTIQATTVK
 81 PLEPWDHMRL PKTLMPTFYT ISLQPFLIPD LYIFKGNSTV EFQCKQPTDL ILIHSKKLNY TIQGPFLVSL TGTKVVAPAI
161 DSTWLEDKTE YLVVKLKENL QQNENYQLHA SFTGELADDL AGFYRSEYTE GVARKVLATT QMQAADARKA FPCFDEPAMK
241 ANFSITLIHL PTYKALSNMP IKKAEEVKMP DGSTWVQTEF HPTLKMSTYL LGFIVSEFEN VSTIENNTLI QIWGRPTAIR
321 EGQGNYALNA TWPILSFFEQ QYSVPYPLTR LDQVALPDFN AGAMENWGLI TYRESALLFD EKYSSIGNKE RIVTVIAHEV
401 AHQWFGNLVT LEWWNELWLN EGFASYVEYL GAHEAESTWN IRDLIVPNDV YRVMAIDALA SSHPLSSPAE EINTPAQISE
481 VFDAISYSKG AAVIRMLAEF LTDAVFREGL QTYFETYQYG NTVCDDLWEQ LQKAVSKKNV YLPSTVKTIM DRWTLQMGFP
561 VLTVDTSKGI ITQKHFLLDP ESPVERPSQF NYVWIVPVSW LSKGKEAEMY WLTDILAENA NFSTSTDPAQ WLLLNVNVTG
641 YFRVNYDLGN WQRLMNQLNE DLQTIPVLNR AQIIDDAFNL ARAKHVGTDL ALNTTRYLAQ ERDYLPWDAA LDNLDYFRLM
721 FDRSEVYGPM QKYIRKQVTP LFDHFRNLTH NWTQIPDGLM NQYNQILAIR TACSHGVPGC NELASSWFEA WKNNPNVNDI
801 SPNLRSAVYC SAIRTGSLED WDFAWKMFRQ APVISEADKL RSALTCSQTP WILQRYLQYT LDPSMIRRQD AMSTINSIAS
881 NVVGQSLAWD FVRMNWKTLF QQFGRSSFSF SSLIQSVTQR FASPFELQQL EQFKADNADV GFGSATRALE QALERTKANI
961 KWVAENKALV LKWFQDNS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
R.VNYDLGNWQR.L	Y	60.42	1263.5996	10	1.0	632.8077	2	44.31	1	F1:13320	12112021_RID_2349_DP1.raw	6.6887E4			
R.YLQYTLDPSMIR.R	Y	59.84	1498.7490	12	0.1	750.3818	2	54.59	1	F1:16715	12112021_RID_2349_DP1.raw	2.8801E5			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.TLFQQFGR.S	Y	50.21	995.5189	8	0.2	498.7668	2	44.91	1	F1:13507	12112021_RID_2349_DP1.raw	1.1534E5			
K.NNPNVNDISPNLR.S	Y	47.74	1465.7273	13	1.2	733.8718	2	37.43	1	F1:11020	12112021_RID_2349_DP1.raw	4.7098E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 7 peptides

TRINITY_DN91
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAKGFFISKS LGVVGIVLGL GAVATIIALS VVYSQEKQRA DELANQAPSS TSVAGTPSAT IAGTAQATTT NGTIQATTVK
 81 PLEPWDHMRL PKTLMPTFYT ISLQPFLIPD LYIFKGNSTV EFQCKQPTDL ILIHSKKLNY TIQGPFLVSL TGTKVVAPAI
161 DSTWLEDKTE YLVVKLKENL QQNENYQLHA SFTGELADDL AGFYRSEYTE GVARKVLATT QMQAADARKA FPCFDEPAMK
241 ANFSITLIHL PTYKALSNMP IKKAEEVKMP DGSTWVQTEF HPTLKMSTYL LGFIVSEFEN VSTIENNTLI QIWGRPTAIR
321 EGQGNYALNA TWPILSFFEQ QYSVPYPLTR LDQVALPDFN AGAMENWGLI TYRESALLFD EKYSSIGNKE RIVTVIAHEV
401 AHQWFGNLVT LEWWNELWLN EGFASYVEYL GAHEAESTWN IRDLIVPNDV YRVMAIDALA SSHPLSSPAE EINTPAQISE
481 VFDAISYSKG AAVIRMLAEF LTDAVFREGL QTYFETYQYG NTVCDDLWEQ LQKAVSKKNV YLPSTVKTIM DRWTLQMGFP
561 VLTVDTSKGI ITQKHFLLDP ESPVERPSQF NYVWIVPVSW LSKGKEAEMY WLTDILAENA NFSTSTDPAQ WLLLNVNVTG
641 YFRVNYDLGN WQRLMNQLNE DLQTIPVLNR AQIIDDAFNL ARAKHVGTDL ALNTTRYLAQ ERDYLPWDAA LDNLDYFRLM
721 FDRSEVYGPM QKYIRKQVTP LFDHFRNLTH NWTQIPDGLM NQYNQILAIR TACSHGVPGC NELASSWFEA WKNNPNVNDI
801 SPNLRSAVYC SAIRTGSLED WDFAWKMFRQ APVISEADKL RSALTCSQTP WILQRYLQYT LDPSMIRRQD AMSTINSIAS
881 NVVGQSLAWD FVRMNWKTLF QQFGRSSFSF SSLIQSVTQR FASPFELQQL EQFKADNADV GFGSATRALE QALERTKANI
961 KWVAENKALV LKWFQDNS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
R.VNYDLGNWQR.L	Y	60.42	1263.5996	10	1.0	632.8077	2	44.31	1	F1:13320	12112021_RID_2349_DP1.raw	6.6887E4			
R.YLQYTLDPSMIR.R	Y	59.84	1498.7490	12	0.1	750.3818	2	54.59	1	F1:16715	12112021_RID_2349_DP1.raw	2.8801E5			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.TLFQQFGR.S	Y	50.21	995.5189	8	0.2	498.7668	2	44.91	1	F1:13507	12112021_RID_2349_DP1.raw	1.1534E5			

total 7 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.NNPNVNDISPNLR.S	Y	47.74	1465.7273	13	1.2	733.8718	2	37.43	1	F1:11020	12112021_RID_2349_DP1.raw	4.7098E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			
												total 7 peptides			

TRINITY_DN91
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAKGFFISKS LGVVGIVLGL GAVATIIALS VVYSQEKQRA DELANQAPSS TSVAGTPSAT IAGTAQATTT NGTIQATTVK
 81 PLEPWDHMRL PKTLMPTFYT ISLQPFLIPD LYIFKGNSTV EFQCKQPTDL ILIHSKKLNY TIQGPFLVSL TGTKVVAPAI
161 DSTWLEDKTE YLVVKLKENL QQNENYQLHA SFTGELADDL AGFYRSEYTE GVARKVLATT QMQAADARKA FPCFDEPAMK
241 ANFSITLIHL PTYKALSNMP IKKAEEVKMP DGSTWVQTEF HPTLKMSTYL LGFIVSEFEN VSTIENNTLI QIWGRPTAIR
321 EGQGNYALNA TWPILSFFEQ QYSVPYPLTR LDQVALPDFN AGAMENWGLI TYRESALLFD EKYSSIGNKE RIVTVIAHEV
401 AHQWFGNLVT LEWWNELWLN EGFASYVEYL GAHEAESTWN IRDLIVPNDV YRVMAIDALA SSHPLSSPAE EINTPAQISE
481 VFDAISYSKG AAVIRMLAEF LTDAVFREGL QTYFETYQYG NTVCDDLWEQ LQKAVSKKNV YLPSTVKTIM DRWTLQMGFP
561 VLTVDTSKGI ITQKHFLLDP ESPVERPSQF NYVWIVPVSW LSKGKEAEMY WLTDILAENA NFSTSTDPAQ WLLLNVNVTG
641 YFRVNYDLGN WQRLMNQLNE DLQTIPVLNR AQIIDDAFNL ARAKHVGTDL ALNTTRYLAQ ERDYLPWDAA LDNLDYFRLM
721 FDRSEVYGPM QKYIRKQVTP LFDHFRNLTH NWTQIPDGLM NQYNQILAIR TACSHGVPGC NELASSWFEA WKNNPNVNDI
801 SPNLRSAVYC SAIRTGSLED WDFAWKMFRQ APVISEADKL RSALTCSQTP WILQRYLQYT LDPSMIRRQD AMSTINSIAS
881 NVVGQSLAWD FVRMNWKTLF QQFGRSSFSF SSLIQSVTQR FASPFELQQL EQFKADNADV GFGSATRALE QALERTKANI
961 KWVAENKALV LKWFQDNS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
R.VNYDLGNWQR.L	Y	60.42	1263.5996	10	1.0	632.8077	2	44.31	1	F1:13320	12112021_RID_2349_DP1.raw	6.6887E4			
R.YLQYTLDPSMIR.R	Y	59.84	1498.7490	12	0.1	750.3818	2	54.59	1	F1:16715	12112021_RID_2349_DP1.raw	2.8801E5			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.TLFQQFGR.S	Y	50.21	995.5189	8	0.2	498.7668	2	44.91	1	F1:13507	12112021_RID_2349_DP1.raw	1.1534E5			
K.NNPNVNDISPNLR.S	Y	47.74	1465.7273	13	1.2	733.8718	2	37.43	1	F1:11020	12112021_RID_2349_DP1.raw	4.7098E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			
												total 7 peptides			

TRINITY_DN91
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAKGFFISKS LGVVGIVLGL GAVATIIALS VVYSQEKQRA DELANQAPSS TSVAGTPSAT IAGTAQATTT NGTIQATTVK
 81 PLEPWDHMRL PKTLMPTFYT ISLQPFLIPD LYIFKGNSTV EFQCKQPTDL ILIHSKKLNY TIQGPFLVSL TGTKVVAPAI
161 DSTWLEDKTE YLVVKLKENL QQNENYQLHA SFTGELADDL AGFYRSEYTE GVARKVLATT QMQAADARKA FPCFDEPAMK
241 ANFSITLIHL PTYKALSNMP IKKAEEVKMP DGSTWVQTEF HPTLKMSTYL LGFIVSEFEN VSTIENNTLI QIWGRPTAIR
321 EGQGNYALNA TWPILSFFEQ QYSVPYPLTR LDQVALPDFN AGAMENWGLI TYRESALLFD EKYSSIGNKE RIVTVIAHEV
401 AHQWFGNLVT LEWWNELWLN EGFASYVEYL GAHEAESTWN IRDLIVPNDV YRVMAIDALA SSHPLSSPAE EINTPAQISE
481 VFDAISYSKG AAVIRMLAEF LTDAVFREGL QTYFETYQYG NTVCDDLWEQ LQKAVSKKNV YLPSTVKTIM DRWTLQMGFP
561 VLTVDTSKGI ITQKHFLLDP ESPVERPSQF NYVWIVPVSW LSKGKEAEMY WLTDILAENA NFSTSTDPAQ WLLLNVNVTG
641 YFRVNYDLGN WQRLMNQLNE DLQTIPVLNR AQIIDDAFNL ARAKHVGTDL ALNTTRYLAQ ERDYLPWDAA LDNLDYFRLM
721 FDRSEVYGPM QKYIRKQVTP LFDHFRNLTH NWTQIPDGLM NQYNQILAIR TACSHGVPGC NELASSWFEA WKNNPNVNDI
801 SPNLRSAVYC SAIRTGSLED WDFAWKMFRQ APVISEADKL RSALTCSQTP WILQRYLQYT LDPSMIRRQD AMSTINSIAS
881 NVVGQSLAWD FVRMNWKTLF QQFGRSSFSF SSLIQSVTQR FASPFELQQL EQFKADNADV GFGSATRALE QALERTKANI
961 KWVAENKALV LKWFQDNS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
R.VNYDLGNWQR.L	Y	60.42	1263.5996	10	1.0	632.8077	2	44.31	1	F1:13320	12112021_RID_2349_DP1.raw	6.6887E4			
R.YLQYTLDPSMIR.R	Y	59.84	1498.7490	12	0.1	750.3818	2	54.59	1	F1:16715	12112021_RID_2349_DP1.raw	2.8801E5			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.TLFQQFGR.S	Y	50.21	995.5189	8	0.2	498.7668	2	44.91	1	F1:13507	12112021_RID_2349_DP1.raw	1.1534E5			
K.NNPNVNDISPNLR.S	Y	47.74	1465.7273	13	1.2	733.8718	2	37.43	1	F1:11020	12112021_RID_2349_DP1.raw	4.7098E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 7 peptides

ETE57948.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MCKAGFAGDD APRAVFPSIV GRPRHQGVMV GMGQKDSYVG DEAQSKRGIL TLKYPIEHGI VTNWDDMEKI WHHTFYNELR

 81  VAPEEHPVLL TEAPLNPKAN REKMTQIMFE TFNTPAMYVA IQAVLSLYAS GRTTGIVMDS GDGVTHTVPI YEGYALPHAI

161  LRLDLAGRDL TDYLMKILTE RGYSFTTTAE REIVRDIKEK LCYVALDFEQ EMATAASSSS LEKSYELPDG QVITIGNERF

241  RCPEALFQPS FLGMESCGIH ETTFNSIMKC DVDIRKDLYA NTVLSGGTTM YPGIADRMQK EITALAPSTM KIKIIAPPER

321  KYSVWIGGSI LASLSTFQQM WISKQEYDES GPSIVHRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAC96363.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAA97900.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

LAA21099.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAI10342.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG68843.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

XP_013921350.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAB54771.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAA97901.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG68844.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

LAA21098.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAV51374.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG47580.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

AFJ49303.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAI14496.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAI10341.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAI14495.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAC96364.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG47579.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAV51372.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

AFJ49302.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

BAQ22177.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG45996.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAG45999.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDDDIAALVV DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

JAB54395.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD

 81 DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT

161 HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY

241 ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL

321 APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

ETE74025.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MEEEIAALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK DSYVGDEAQS KRGILTLKYP IEHGIVTNWD
 81  DMEKIWHHTF YNELRVAPEE HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRTTG IVMDSGDGVT
161  HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY
241  ELPDGQVITI GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS GGTTMYPGIA DRMQKEITAL
321  APSTMKIKII APPERKYSVW IGGSILASLS TFQQMWISKQ EYDESGPSIV HRKCF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area
R.GYSFTTTAER.E	Y	72.34	1131.5197	10	1.1	566.7677	2	33.52	2	F2:8772	12112021_RID_2349_DP2.raw	
K.SYELPDGQVITIGNER.F	Y	71.69	1789.8846	16	0.3	895.9499	2	53.88	2	F2:15567	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSK.R	Y	67.44	1197.5149	11	1.1	599.7654	2	23.86	2	F2:5370	12112021_RID_2349_DP2.raw	2.1509
R.VAPEEHPVLLTEAPLNPK.A	Y	63.91	1953.0570	18	0.6	977.5364	2	45.29	2	F2:12822	12112021_RID_2349_DP2.raw	
K.AGFAGDDAPR.A	Y	60.62	975.4410	10	0.5	488.7280	2	26.11	1	F1:7167	12112021_RID_2349_DP1.raw	3.3593
K.EITALAPSTMK.I	Y	52.44	1160.6111	11	0.0	581.3128	2	38.85	2	F2:10632	12112021_RID_2349_DP2.raw	
K.DSYVGDEAQSKR.G	Y	50.46	1353.6160	12	0.4	677.8156	2	20.64	2	F2:4244	12112021_RID_2349_DP2.raw	
K.EITALAPSTM(+15.99)K.I	Y	47.42	1176.6060	11	0.9	589.3108	2	32.91	2	F2:8537	12112021_RID_2349_DP2.raw	
R.AVFPSIVGRPR.H	Y	44.25	1197.6981	11	1.0	599.8569	2	40.62	2	F2:11273	12112021_RID_2349_DP2.raw	
K.DLYANTVLSGGTTM(+15.99)YPGIADR.M	Y	41.30	2230.0576	21	-0.2	1116.0359	2	56.05	2	F2:16292	12112021_RID_2349_DP2.raw	

ADK22827.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFR LLVVFLSLSG TRADFDCPSG WSAHDQHCYK AFDEPKRSGD AETFCTEQAN SGHLVSIESV EEAEFVAQLI
 81  SENIKTPADY VWIGLRNQRK AQYCISKWTD GSSVIYKNVI ERFIKNCFGL EKQTDYRTWF NLSCGDDYPF VCKFPPRC
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.TPADYVWIGLR.N	Y	76.52	1289.6768	11	0.6	645.8461	2	57.87	7	F7:17384	17112021_RID_2349_DP7.raw			
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pe

ADK22825.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1  MGRFISVSFG LLVVFLSLSG TRADFDCPSG WSAHDQHCYK AFDEPKRSGD AETFCTEQAN SGHLVSIESV EEAEFVAQLI
 81  SENIKTPADY VWIGLRNQRK AQYCISKWTD GSSVIYKNVI ERFIKNCFGL EKESDYRTWF NLSCGDDYPF VCKFPPRC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.WTDGSSVIYK.N	N	77.27	1154.5608	10	0.0	578.2877	2	37.40	5	F5:10403	17112021_RID_2349_DP5.raw	2.1576E5	2.5151E5	1.7167
K.TPADYVWIGLR.N	Y	76.52	1289.6768	11	0.6	645.8461	2	57.87	7	F7:17384	17112021_RID_2349_DP7.raw			
K.WTDGSSVIYKNVIER.F	N	71.65	1765.8999	15	0.3	883.9575	2	44.92	5	F5:12969	17112021_RID_2349_DP5.raw			
F.VAQLISENIK.T	N	48.99	1113.6394	10	-0.4	557.8268	2	37.53	5	F5:10425	17112021_RID_2349_DP5.raw			
W.TDGSSVIYK.N	N	44.54	968.4814	9	0.1	485.2480	2	26.37	5	F5:6664	17112021_RID_2349_DP5.raw			
E.FVAQLISENIK.T	N	44.08	1260.7078	11	0.3	631.3613	2	49.39	5	F5:14370	17112021_RID_2349_DP5.raw			
K.AFDEPKR.S	N	40.54	861.4344	7	-0.5	431.7243	2	18.04	5	F5:3641	17112021_RID_2349_DP5.raw			
V.AQLISENIK.T	N	39.19	1014.5709	9	0.0	508.2927	2	33.55	5	F5:9140	17112021_RID_2349_DP5.raw			

total 8 pep

ADN04916.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MVLIRVLANL LVLHLSYAQK SSELVIGGDE CNINEHPFLA LMYNSTSMKF HCSGTLLNEE WVLTAAHCDM ENMQIYLGVH
                                        114
 81  DKKNPNKDQQ TRVPKEMFFC LSNKSYTPWD KDIMLIRLNS PVTYSTHIAP FSLPSSPPTV GSVCRIMGWG AITSPNETYP

161  DVPHCANIEI YDYSVCRKAY GGLPEKSRTL CAGVLQGGID TCLADSGGPL ICNGQFQGIV AWGRHPCAQP QLPAFYTKVF

241  DYSDWIQSII AGNTAATCPS
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Are
R.KAYGGLPEKSR.T	Y	66.51	1204.6564	11	-0.1	603.3354	2	21.80	2	F2:4728	12112021_RID_2349_DP2.raw	5.4582E5	2.00
K.AYGGLPEKSR.T	N	64.80	1076.5614	10	0.4	539.2882	2	22.20	2	F2:4846	12112021_RID_2349_DP2.raw		5.68
P.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.01
R.LNSPVTYSTH.I	Y	58.68	1117.5404	10	0.6	559.7778	2	32.48	2	F2:8433	12112021_RID_2349_DP2.raw		5.06
R.KAYGGLPEK.S	Y	58.02	961.5233	9	0.5	481.7692	2	22.09	2	F2:4938	12112021_RID_2349_DP2.raw		1.43
K.AYGGLPEK.S	N	56.12	833.4283	8	0.6	417.7217	2	26.79	2	F2:6388	12112021_RID_2349_DP2.raw	3.9735E5	1.69
R.LNSPVTYSTHIAPF.S	Y	54.49	1545.7827	14	0.3	773.8989	2	53.38	2	F2:15391	12112021_RID_2349_DP2.raw		3.47
P.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.42
R.LNSPVTYSTHIAPFSLPSSPPTVG.S	Y	49.67	2468.2588	24	0.8	1235.1377	2	61.33	2	F2:18069	12112021_RID_2349_DP2.raw		1.89
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw		
C.AQPQLPAFYTK.V	Y	42.49	1262.6659	11	0.8	632.3407	2	45.16	2	F2:12753	12112021_RID_2349_DP2.raw		8.03
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw		

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E0Y418.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1  MVLIRVLANL LVLHLSYAQK SSELVIGGDE CNINEHPFLA LMYNSTSMKF HCSGTLLNEE WVLTAAHCDM ENMQIYLGVH
                                      114
 81  DKKNPNKDQQ TRVPKEMFFC LSNKSYTPWD KDIMLIRLNS PVTYSTHIAP FSLPSSPPTV GSVCRIMGWG AITSPNETYP

161  DVPHCANIEI YDYSVCRKAY GGLPEKSRTL CAGVLQGGID TCLADSGGPL ICNGQFQGIV AWGRHPCAQP QLPAFYTKVF

241  DYSDWIQSII AGNTAATCPS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Are
R.KAYGGLPEKSR.T	Y	66.51	1204.6564	11	-0.1	603.3354	2	21.80	2	F2:4728	12112021_RID_2349_DP2.raw	5.4582E5	2.00
K.AYGGLPEKSR.T	N	64.80	1076.5614	10	0.4	539.2882	2	22.20	2	F2:4846	12112021_RID_2349_DP2.raw		5.68
P.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.01
R.LNSPVTYSTH.I	Y	58.68	1117.5404	10	0.6	559.7778	2	32.48	2	F2:8433	12112021_RID_2349_DP2.raw		5.06
R.KAYGGLPEK.S	Y	58.02	961.5233	9	0.5	481.7692	2	22.09	2	F2:4938	12112021_RID_2349_DP2.raw		1.43
K.AYGGLPEK.S	N	56.12	833.4283	8	0.6	417.7217	2	26.79	2	F2:6388	12112021_RID_2349_DP2.raw	3.9735E5	1.69
R.LNSPVTYSTHIAPF.S	Y	54.49	1545.7827	14	0.3	773.8989	2	53.38	2	F2:15391	12112021_RID_2349_DP2.raw		3.47
P.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.42
R.LNSPVTYSTHIAPFSLPSSPPTVG.S	Y	49.67	2468.2588	24	0.8	1235.1377	2	61.33	2	F2:18069	12112021_RID_2349_DP2.raw		1.89
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw		
C.AQPQLPAFYTK.V	Y	42.49	1262.6659	11	0.8	632.3407	2	45.16	2	F2:12753	12112021_RID_2349_DP2.raw		8.03
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw		

tota

ADK22824.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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                                                                                  73
  1  MGRFISISFG LLVVFLSLSG TGAKQDCLSD WSFYEGYCYK VFNEKKTWED AEKFCNEQVN GGYLVSFRSS EEMDFVIRMT

 81  FPIFRFDFFW IGLRDFWRDC YWRWSDGVNL DYKAWSREPN CFVSKTTDNQ WLRWNCNDPR YFVCKSRVSC
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
R.WSDGVNLDYK.A	Y	76.23	1195.5509	10	-0.2	598.7826	2	42.63	7	F7:12181	17112021_RID_2349_DP7.raw					
R.SSEEMDFVIR.M	Y	63.84	1211.5492	10	-0.1	606.7818	2	46.89	7	F7:13707	17112021_RID_2349_DP7.raw					
K.TTDNQWLR.W	N	59.51	1032.4989	8	0.4	517.2570	2	33.81	7	F7:9330	17112021_RID_2349_DP7.raw					8.7
R.FDFFWIGLR.D	Y	57.64	1199.6127	9	-0.2	600.8135	2	74.61	7	F7:23057	17112021_RID_2349_DP7.raw					
R.SSEEM(+15.99)DFVIR.M	Y	57.28	1227.5441	10	0.3	614.7795	2	44.29	7	F7:12932	17112021_RID_2349_DP7.raw					
W.SDGVNLDYK.A	Y	51.62	1009.4716	9	-0.2	505.7430	2	32.58	7	F7:8732	17112021_RID_2349_DP7.raw					
R.MTFPIFR.F	Y	47.81	910.4734	7	0.7	456.2443	2	54.20	7	F7:16176	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
S.SEEM(+15.99)DFVIR.M	Y	42.14	1140.5121	9	0.0	571.2633	2	38.69	7	F7:10887	17112021_RID_2349_DP7.raw					
K.KTWEDAEKF.C	N	40.81	1152.5450	9	0.6	577.2802	2	34.65	7	F7:9456	17112021_RID_2349_DP7.raw					
R.M(+15.99)TFPIFR.F	Y	40.76	926.4684	7	-0.1	464.2414	2	47.07	7	F7:13700	17112021_RID_2349_DP7.raw					

total 12 peptide

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptide

AAY63876.1
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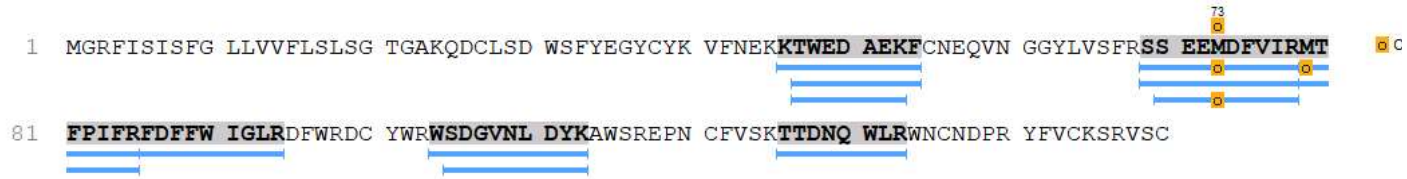
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
R.WSDGVNLDYK.A	Y	76.23	1195.5509	10	-0.2	598.7826	2	42.63	7	F7:12181	17112021_RID_2349_DP7.raw					
R.SSEEMDFVIR.M	Y	63.84	1211.5492	10	-0.1	606.7818	2	46.89	7	F7:13707	17112021_RID_2349_DP7.raw					
K.TTDNQWLR.W	N	59.51	1032.4989	8	0.4	517.2570	2	33.81	7	F7:9330	17112021_RID_2349_DP7.raw					8.7
R.FDFFWIGLR.D	Y	57.64	1199.6127	9	-0.2	600.8135	2	74.61	7	F7:23057	17112021_RID_2349_DP7.raw					
R.SSEEM(+15.99)DFVIR.M	Y	57.28	1227.5441	10	0.3	614.7795	2	44.29	7	F7:12932	17112021_RID_2349_DP7.raw					
W.SDGVNLDYK.A	Y	51.62	1009.4716	9	-0.2	505.7430	2	32.58	7	F7:8732	17112021_RID_2349_DP7.raw					
R.MTFPIFR.F	Y	47.81	910.4734	7	0.7	456.2443	2	54.20	7	F7:16176	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
S.SEEM(+15.99)DFVIR.M	Y	42.14	1140.5121	9	0.0	571.2633	2	38.69	7	F7:10887	17112021_RID_2349_DP7.raw					
K.KTWEDAEKF.C	N	40.81	1152.5450	9	0.6	577.2802	2	34.65	7	F7:9456	17112021_RID_2349_DP7.raw					
R.M(+15.99)TFPIFR.F	Y	40.76	926.4684	7	-0.1	464.2414	2	47.07	7	F7:13700	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptide

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| Protein Coverage | Supporting Peptides |
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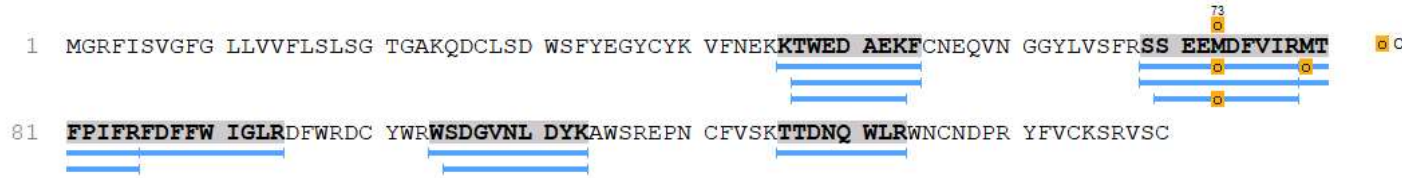

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
R.WSDGVNLDYK.A	Y	76.23	1195.5509	10	-0.2	598.7826	2	42.63	7	F7:12181	17112021_RID_2349_DP7.raw					
R.SSEEMDFVIR.M	Y	63.84	1211.5492	10	-0.1	606.7818	2	46.89	7	F7:13707	17112021_RID_2349_DP7.raw					
K.TTDNQWLR.W	N	59.51	1032.4989	8	0.4	517.2570	2	33.81	7	F7:9330	17112021_RID_2349_DP7.raw					8.7
R.FDFFWIGLR.D	Y	57.64	1199.6127	9	-0.2	600.8135	2	74.61	7	F7:23057	17112021_RID_2349_DP7.raw					
R.SSEEM(+15.99)DFVIR.M	Y	57.28	1227.5441	10	0.3	614.7795	2	44.29	7	F7:12932	17112021_RID_2349_DP7.raw					
W.SDGVNLDYK.A	Y	51.62	1009.4716	9	-0.2	505.7430	2	32.58	7	F7:8732	17112021_RID_2349_DP7.raw					
R.MTFPIFR.F	Y	47.81	910.4734	7	0.7	456.2443	2	54.20	7	F7:16176	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
S.SEEM(+15.99)DFVIR.M	Y	42.14	1140.5121	9	0.0	571.2633	2	38.69	7	F7:10887	17112021_RID_2349_DP7.raw					

total 12 peptide

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
K.KTWEDAEKF.C	N	40.81	1152.5450	9	0.6	577.2802	2	34.65	7	F7:9456	17112021_RID_2349_DP7.raw					
R.M(+15.99)TFPIFR.F	Y	40.76	926.4684	7	-0.1	464.2414	2	47.07	7	F7:13700	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptide

Q4PRC6.1
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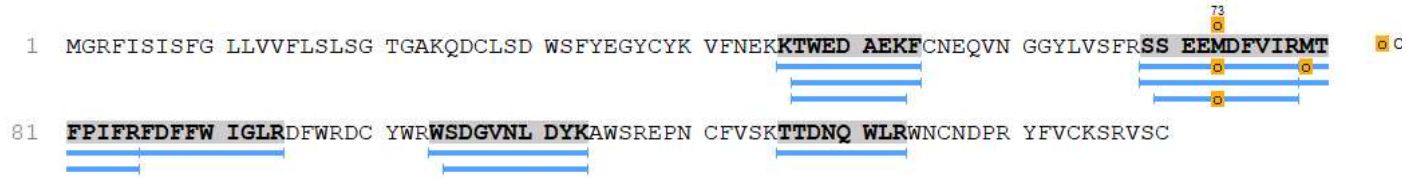
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar
R.WSDGVNLDYK.A	Y	76.23	1195.5509	10	-0.2	598.7826	2	42.63	7	F7:12181	17112021_RID_2349_DP7.raw					
R.SSEEMDFVIR.M	Y	63.84	1211.5492	10	-0.1	606.7818	2	46.89	7	F7:13707	17112021_RID_2349_DP7.raw					
K.TTDNQWLR.W	N	59.51	1032.4989	8	0.4	517.2570	2	33.81	7	F7:9330	17112021_RID_2349_DP7.raw					8.7
R.FDFFWIGLR.D	Y	57.64	1199.6127	9	-0.2	600.8135	2	74.61	7	F7:23057	17112021_RID_2349_DP7.raw					
R.SSEEM(+15.99)DFVIR.M	Y	57.28	1227.5441	10	0.3	614.7795	2	44.29	7	F7:12932	17112021_RID_2349_DP7.raw					
W.SDGVNLDYK.A	Y	51.62	1009.4716	9	-0.2	505.7430	2	32.58	7	F7:8732	17112021_RID_2349_DP7.raw					
R.MTFPIFR.F	Y	47.81	910.4734	7	0.7	456.2443	2	54.20	7	F7:16176	17112021_RID_2349_DP7.raw					
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw					
S.SEEM(+15.99)DFVIR.M	Y	42.14	1140.5121	9	0.0	571.2633	2	38.69	7	F7:10887	17112021_RID_2349_DP7.raw					
K.KTWEDAEKF.C	N	40.81	1152.5450	9	0.6	577.2802	2	34.65	7	F7:9456	17112021_RID_2349_DP7.raw					
R.M(+15.99)TFPIFR.F	Y	40.76	926.4684	7	-0.1	464.2414	2	47.07	7	F7:13700	17112021_RID_2349_DP7.raw					
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw					

total 12 peptide

TRINITY_DN459
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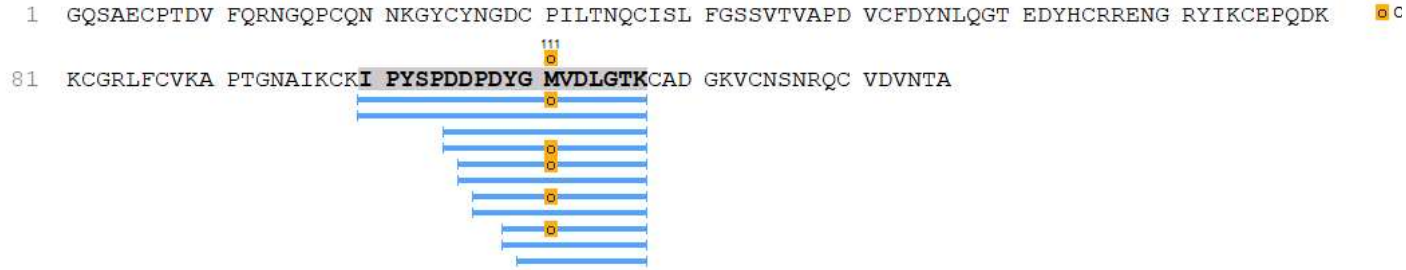
| Protein Coverage | Supporting Peptides |
Protein Coverage:



Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Ar
P.DDPDYGMVDLGTK.C	N	86.80	1424.6129	13	0.9	713.3144	2	48.02	1	F1:14542	12112021_RID_2349_DP1.raw	3.1015E5	
K.IPYSPDDPDYGMVDLGTK.C	Y	73.90	1981.8978	18	1.1	991.9573	2	53.28	3	F3:15640	17112021_RID_2349_DP3.raw	9.0784E5	1.1
D.PDYGMVDLGTK.C	N	73.86	1194.5591	11	-0.1	598.2867	2	43.94	1	F1:13219	12112021_RID_2349_DP1.raw	7.4048E6	4.1
D.PDYGM(+15.99)VDLGTK.C	N	71.86	1210.5540	11	0.4	606.2845	2	40.64	1	F1:13230	12112021_RID_2349_DP1.raw	6.7718E6	3.5
P.DDPDYGM(+15.99)VDLGTK.C	N	69.19	1440.6078	13	0.3	721.3114	2	40.35	6	F6:11298	17112021_RID_2349_DP6.raw	7.0367E4	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
D.DPDYGMVDLGTK.C	N	68.28	1309.5859	12	1.2	655.8010	2	47.41	1	F1:14315	12112021_RID_2349_DP1.raw	7.5385E5	
D.DPDYGM(+15.99)VDLGTK.C	N	61.75	1325.5809	12	0.8	663.7983	2	39.96	1	F1:11872	12112021_RID_2349_DP1.raw	2.7576E5	
K.IPYSPDDPDYGM(+15.99)VDLGTK.C	Y	56.68	1997.8928	18	0.4	999.9541	2	47.71	4	F4:13784	17112021_RID_2349_DP4.raw	2.172E5	
D.YGM(+15.99)VDLGTK.C	N	54.16	998.4742	9	0.8	500.2448	2	39.32	1	F1:11674	12112021_RID_2349_DP1.raw	1.0157E5	
D.YGMVDLGTK.C	N	45.13	982.4794	9	-0.5	492.2467	2	39.32	1	F1:11699	12112021_RID_2349_DP1.raw	1.3963E5	
Y.GMVDLGTK.C	N	44.20	819.4160	8	0.0	410.7153	2	30.74	7	F7:8124	17112021_RID_2349_DP7.raw		

TRINITY_DN157
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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 81  PTASRALRPP SASMVHWSAE EKQLITSLWS KVDVPEVGGA TLGKLLVVYP WTQRFFAHFG NLSGPSAICG NPLVKAHGKK
161  VLTSFGEAIK HLDNIKETFA KLSELHCDKL HVDPENFKLL GNILIIVLAG HHGKEFTPST HAAFQKLTHV VAHSLALRYH
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.VDVPEVGGATLGK.L	Y	80.51	1240.6663	13	0.6	621.3408	2	42.05	7	F7:11994	17112021_RID_2349_DP7.raw			
K.LLVVYPWTQR.F	N	62.42	1273.7183	10	0.7	637.8668	2	56.17	4	F4:16617	17112021_RID_2349_DP4.raw	5.7141E5	2.1702E5	1.0063E6
K.HLDNIKETFAK.L	Y	61.67	1314.6931	11	0.6	439.2386	3	30.74	7	F7:8165	17112021_RID_2349_DP7.raw			
K.VLTSFGEAIK.H	N	61.56	1063.5913	10	-0.1	532.8029	2	41.86	7	F7:11920	17112021_RID_2349_DP7.raw			
M.VHWSAEEK.Q	N	52.31	984.4665	8	0.7	493.2408	2	21.02	7	F7:4832	17112021_RID_2349_DP7.raw			
K.EFTPSTHAAFQK.L	N	50.12	1362.6567	12	0.3	682.3358	2	30.43	7	F7:8112	17112021_RID_2349_DP7.raw			
K.KVLTSFGEAIK.H	N	48.51	1191.6863	11	1.5	596.8513	2	36.27	7	F7:10106	17112021_RID_2349_DP7.raw			
K.QLITSLWSK.V	Y	42.95	1074.6073	9	-0.1	538.3109	2	50.81	7	F7:15061	17112021_RID_2349_DP7.raw			
K.LTHVVAHSLALR.Y	Y	42.42	1315.7725	12	0.2	439.5982	3	32.34	7	F7:8705	17112021_RID_2349_DP7.raw			

total 9 pept

P18964.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  VVGGDECNIN EHPFLVALYT STSSTIHCGG ALINREWVLT AAHCDRRNIR IKLGMHSKNI RNEDEQIRVP RGKYFCLNTK
                                                                                          C
                                                                                          o
                                                                                          o
                                                                                          o
```

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.FPNGLDKDIM(+15.99)LIR.L	Y	47.93	1546.8177	13	0.2	516.6133	3	50.38	3	F3:14752	17112021_RID_2349_DP3.raw			2.1323E5
L.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6
K.FPNGLDK.D	Y	41.98	789.4021	7	1.3	395.7088	2	29.86	7	F7:7802	17112021_RID_2349_DP7.raw			
L.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6
														total 10 pe

ADP88558.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIKVLANL LVLQLSYAQK SSELVVGGDE CNINEHPFLV ALYTSASSTI HCAGALINRE WVLTAAHCDR RNIRIKLGMH
                                                 114
 81  SKNIRNEDEQ IRVPRGKYFC LNTKFPNGLD KDIMLIRLRR PVTYSTHIAP VSLPSRSRGV GSRCRIMGWG KISTTEDTYP

161  DVPHCTNIFI VKHKWCEPLY PWVPADSRTL CAGILKGGRD TCKGDSGGPL ICNGEMHGIV AGGSEPCGQH LKPAVYTKVF
241  DYNNWIQSII AGNRTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.FPNGLDKDIMLIR.L	Y	66.83	1530.8228	13	0.2	511.2816	3	54.26	3	F3:15907	17112021_RID_2349_DP3.raw			2.7289E6
Y.STHIAPVSLPSR.S	Y	63.76	1263.6935	12	0.2	632.8541	2	34.00	7	F7:9308	17112021_RID_2349_DP7.raw			
R.NEDEQIRVPR.G	Y	62.99	1254.6316	10	0.2	628.3232	2	27.46	7	F7:7050	17112021_RID_2349_DP7.raw			7.022E6
K.NIRNEDEQIRVPR.G	Y	61.00	1637.8597	13	0.5	546.9608	3	29.37	7	F7:7736	17112021_RID_2349_DP7.raw			2.8569E6
R.RPVTYSTHIAPVSLPSR.S	Y	57.58	1880.0267	17	0.6	627.6832	3	39.74	4	F4:11137	17112021_RID_2349_DP4.raw			1.6115E7
K.NIRNEDEQIR.V	Y	56.31	1285.6375	10	0.5	643.8263	2	20.61	7	F7:4677	17112021_RID_2349_DP7.raw			7.3183E5
K.FPNGLDKDIM(+15.99)LIR.L	Y	47.93	1546.8177	13	0.2	516.6133	3	50.38	3	F3:14752	17112021_RID_2349_DP3.raw			2.1323E5
L.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6
K.FPNGLDK.D	Y	41.98	789.4021	7	1.3	395.7088	2	29.86	7	F7:7802	17112021_RID_2349_DP7.raw			
L.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6
														total 10 pe

P18965.2
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIKVLANL LVLQLSYAQK SSELVVGGDE CNINEHPFLV ALYTSASSTI HCAGALINRE WVLTAAHCDR RNIRIKLGMH
                                                 114
 81  SKNIRNEDEQ IRVPRGKYFC LNTKFPNGLD KDIMLIRLRR PVTYSTHIAP VSLPSRSRGV GSRCRIMGWG KISTTEDTYP

161  DVPHCTNIFI VKHKWCEPLY PWVPADSRTL CAGILKGGRD TCHGDSGGPL ICNGEMHGIV AGGSEPCGQH LKPAVYTKVF
241  DYNNWIQSII AGNRTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.FPNGLDKDIMLIR.L	Y	66.83	1530.8228	13	0.2	511.2816	3	54.26	3	F3:15907	17112021_RID_2349_DP3.raw			2.7289E6
Y.STHIAPVSLPSR.S	Y	63.76	1263.6935	12	0.2	632.8541	2	34.00	7	F7:9308	17112021_RID_2349_DP7.raw			
R.NEDEQIRVPR.G	Y	62.99	1254.6316	10	0.2	628.3232	2	27.46	7	F7:7050	17112021_RID_2349_DP7.raw			7.022E6
K.NIRNEDEQIRVPR.G	Y	61.00	1637.8597	13	0.5	546.9608	3	29.37	7	F7:7736	17112021_RID_2349_DP7.raw			2.8569E6
R.RPVTYSTHIAPVSLPSR.S	Y	57.58	1880.0267	17	0.6	627.6832	3	39.74	4	F4:11137	17112021_RID_2349_DP4.raw			1.6115E7
														total 10 pe

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NIRNEDEQIR.V	Y	56.31	1285.6375	10	0.5	643.8263	2	20.61	7	F7:4677	17112021_RID_2349_DP7.raw			7.3183E5
K.FPNGLDKDIM(+15.99)LIR.L	Y	47.93	1546.8177	13	0.2	516.6133	3	50.38	3	F3:14752	17112021_RID_2349_DP3.raw			2.1323E5
L.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6
K.FPNGLDK.D	Y	41.98	789.4021	7	1.3	395.7088	2	29.86	7	F7:7802	17112021_RID_2349_DP7.raw			
L.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6

total 10 pe

TRINITY_DN2646
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAPGGWMLLA GLLLLLGGLD RPSSGSAAGP VPLVIWHGMG DSCCNPLSMG YIKKIVEEKI PGIYVLSLKI GNTLIDDMEN
                                   110
 81  SFFMDVNNQV KKVCDQLSKD PKLQGGYNAM GFSQGGQFLR AVVQRCPSPP MFNLISIGGQ HQGVFGFPHC PGESSHLCDW

161  LRKVLNIAYT DKIQKHLVQA QYWHDPVNEQ QYRRSSLFLA DINQERVINE TYKKNLMTLK KFVMVRFLND TMVDPPASEW

241  FGYYRSGQTK ETIPLQETTL YTEDRLGLKE MDQAGKLVFL GAEGDHLRFS KEWFFKNIVP FLSDAAGDDS QAVLS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.LQGGYNAMGFSQGGQFLR.A	Y	84.07	1929.9155	18	0.4	965.9654	2	52.55	3	F3:15482	17112021_RID_2349_DP3.raw		1.037
K.ETIPLQETTLYTEDR.L	Y	70.72	1807.8839	15	0.1	904.9493	2	48.94	2	F2:13963	12112021_RID_2349_DP2.raw		9.553
R.SSLFLADINQER.V	Y	67.59	1391.7045	12	0.3	696.8597	2	50.21	3	F3:14633	17112021_RID_2349_DP3.raw		1.288
K.IPGIYVLSLK.I	Y	62.71	1101.6797	10	0.6	551.8475	2	57.36	3	F3:16947	17112021_RID_2349_DP3.raw		
K.NIVPFLSDAAGDDSQA.V	Y	54.50	1618.7474	16	0.8	810.3817	2	64.67	3	F3:19306	17112021_RID_2349_DP3.raw		5.298
K.HLVQAQYWHDPVNEQQYR.R	Y	46.16	2310.0930	18	0.6	771.0388	3	40.68	3	F3:11579	17112021_RID_2349_DP3.raw		
K.LQGGYNAM(+15.99)GFSQGGQFLR.A	Y	39.61	1945.9104	18	0.7	973.9631	2	47.17	3	F3:13705	17112021_RID_2349_DP3.raw		

total 7 p

TRINITY_DN2646
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAPGGWMLLA GLLLLLGGLD RPSSGSAAGP VPLVIWHGMG DSCCNPLSMG YIKKIVEEKI PGIYVLSLKI GNTLIDDMEN
                                   110
 81  SFFMDVNNQV KKVCDQLSKD PKLQGGYNAM GFSQGGQFLR AVVQRCPSPP MFNLISIGGQ HQGVFGFPHC PGESSHLCDW

161  LRKVLNIAYT DKIQKHLVQA QYWHDPVNEQ QYRRSSLFLA DINQERVINE TYKKNLMTLK KFVMVRFLND TMVDPPASEW

241  FGYYRSGQTK ETIPLQETTL YTEDRLGLKE MDQAGKLVFL GAEGDHLRFS KEWFFKNIVP FLSDAAGDDS QAVLS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
K.LQGGYNAMGFSQGGQFLR.A	Y	84.07	1929.9155	18	0.4	965.9654	2	52.55	3	F3:15482	17112021_RID_2349_DP3.raw		1.037
K.ETIPLQETTLYTEDR.L	Y	70.72	1807.8839	15	0.1	904.9493	2	48.94	2	F2:13963	12112021_RID_2349_DP2.raw		9.553
R.SSLFLADINQER.V	Y	67.59	1391.7045	12	0.3	696.8597	2	50.21	3	F3:14633	17112021_RID_2349_DP3.raw		1.288
K.IPGIYVLSLK.I	Y	62.71	1101.6797	10	0.6	551.8475	2	57.36	3	F3:16947	17112021_RID_2349_DP3.raw		
K.NIVPFLSDAAGDDSQA.V	Y	54.50	1618.7474	16	0.8	810.3817	2	64.67	3	F3:19306	17112021_RID_2349_DP3.raw		5.298
K.HLVQAQYWHDPVNEQQYR.R	Y	46.16	2310.0930	18	0.6	771.0388	3	40.68	3	F3:11579	17112021_RID_2349_DP3.raw		
K.LQGGYNAM(+15.99)GFSQGGQFLR.A	Y	39.61	1945.9104	18	0.7	973.9631	2	47.17	3	F3:13705	17112021_RID_2349_DP3.raw		

total 7 p

TRINITY_DN300
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAKSESQMDI TEMNSPKPKR KLRWSPLEIG LAAVVLLLAI VAITMIILYA TYDDGICKTS DCIKSAARII ENMDTTAEPC
 81  SNFYQYACGG WLKKHIIPET SSRYSNFDIL RDELEVVLKD VLEKKDSNDI DAVAKAKTLY RSCINETAIN SKKGKPLINL
161  MTNISEWPIA AESWDGSTWS AEKSIAELNF QFGRKVIINM FVGTDDKNSS QHVLHVDQPR LGLPSRDYYE CTGLYKEACS
241  AYESFMTSVA KLIRQERNLP INDTEISIEA ERIMALEKEI ANVTTKDEDR NDPLLLYHKM KLSDLQKNFS MEINNKTFDW
321  IKFVNNIMTT VAIEVKNTED IIVYAPEYLI KLKSVISKYS AREIQNYISW RYIMDMVSSL SREYKDTRNN FRKVLYGTTS
401  DAAIWRRCAN YVNSIMGNAV GRLYVQEAFA GESKHVVQEM ITQIREVFIK TLEELSWMDA KTKKKAEEKA VAIKERIGYP
481  DEILTNPVKL NQEYKGLNYK EEEYFENLIE NLKFGQKERL KKLREKVDKD EWITGAAVVN AFYSPNRNQI VFPAGILQPP
561  FFSASQPKSL NFGGIGMVIG HEITHGFDDN GRNFNAQGDL VDWWSQESAN NFKSQSRCMI YQYGNFTWDL AGGQNLSGIN
641  TLGENIADNG GIRQAYRAYE SYVQKNGEEK RLPGLDLNHK QLFFLNFAQI WCGTYRPEYA VNSIKTDVHS PGKFRVLGSL
721  QNNLEFSEAF KCTDKDYMDP VKKCRVW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Ar F
K.SIAELNFQFGR.K	Y	73.70	1280.6512	11	0.1	641.3329	2	55.39	1	F1:16912	12112021_RID_2349_DP1.raw	5.654E4		
R.IGYPDEILTNPVK.L	Y	70.66	1457.7766	13	0.2	729.8957	2	50.37	1	F1:15355	12112021_RID_2349_DP1.raw	5.763E5		
R.YIMDMVSSLSR.E	Y	62.87	1300.6155	11	0.5	651.3153	2	54.99	1	F1:16794	12112021_RID_2349_DP1.raw	6.491E4		
R.AYESYVQK.N	Y	61.21	986.4709	8	-0.6	494.2424	2	26.11	1	F1:7228	12112021_RID_2349_DP1.raw	5.2803E5		
R.EIQNYISWR.Y	Y	55.38	1207.5985	9	0.2	604.8066	2	48.42	1	F1:14642	12112021_RID_2349_DP1.raw	5.0876E4		
R.NQIVFPAGILQPPFFSASQPK.S	Y	53.84	2285.2207	21	1.1	1143.6189	2	71.77	1	F1:22334	12112021_RID_2349_DP1.raw	1.8483E5		
R.LYVQEAFAGESK.H	Y	53.64	1340.6611	12	0.4	671.3381	2	42.18	1	F1:12626	12112021_RID_2349_DP1.raw	1.0438E5		
K.TDVHSPGKFR.V	Y	49.57	1142.5833	10	-0.4	381.8682	3	22.83	1	F1:6017	12112021_RID_2349_DP1.raw	1.6839E5		

total 8 peptides

TRINITY_DN300
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAKSESQMDI TEMNSPKPKR KLRWSPLEIG LAAVVLLLAI VAITMIILYA TYDDGICKTS DCIKSAARII ENMDTTAEPC
 81  SNFYQYACGG WLKKHIIPET SSRYSNFDIL RDELEVVLKD VLEKKDSNDI DAVAKAKTLY RSCINETAIN SKKGKPLINL
161  MTNISEWPIA AESWDGSTWS AEKSIAELNF QFGRKVIINM FVGTDDKNSS QHVLHVDQPR LGLPSRDYYE CTGLYKEACS
241  AYESFMTSVA KLIRQERNLP INDTEISIEA ERIMALEKEI ANVTTKDEDR NDPLLLYHKM KLSDLQKNFS MEINNKTFDW
321  IKFVNNIMTT VAIEVKNTED IIVYAPEYLI KLKSVISKYS AREIQNYISW RYIMDMVSSL SREYKDTRNN FRKVLYGTTS
401  DAAIWRRCAN YVNSIMGNAV GRLYVQEAFA GESKHVVQEM ITQIREVFIK TLEELSWMDA KTKKKAEEKA VAIKERIGYP
481  DEILTNPVKL NQEYKGLNYK EEEYFENLIE NLKFGQKERL KKLREKVDKD EWITGAAVVN AFYSPNRNQI VFPAGILQPP
561  FFSASQPKSL NFGGIGMVIG HEITHGFDDN GRNFNAQGDL VDWWSQESAN NFKSQSRCMI YQYGNFTWDL AGGQNLSGIN
641  TLGENIADNG GIRQAYRAYE SYVQKNGEEK RLPGLDLNHK QLFFLNFAQI WCGTYRPEYA VNSIKTDVHS PGKFRVLGSL
721  QNNLEFSEAF KCTDKDYMDP VKKCRVW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Ar F
K.SIAELNFQFGR.K	Y	73.70	1280.6512	11	0.1	641.3329	2	55.39	1	F1:16912	12112021_RID_2349_DP1.raw	5.654E4		
R.IGYPDEILTNPVK.L	Y	70.66	1457.7766	13	0.2	729.8957	2	50.37	1	F1:15355	12112021_RID_2349_DP1.raw	5.763E5		
R.YIMDMVSSLSR.E	Y	62.87	1300.6155	11	0.5	651.3153	2	54.99	1	F1:16794	12112021_RID_2349_DP1.raw	6.491E4		
R.AYESYVQK.N	Y	61.21	986.4709	8	-0.6	494.2424	2	26.11	1	F1:7228	12112021_RID_2349_DP1.raw	5.2803E5		
R.EIQNYISWR.Y	Y	55.38	1207.5985	9	0.2	604.8066	2	48.42	1	F1:14642	12112021_RID_2349_DP1.raw	5.0876E4		

total 8 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Ar F
R.NQIVFPAGILQPPFFSASQPK.S	Y	53.84	2285.2207	21	1.1	1143.6189	2	71.77	1	F1:22334	12112021_RID_2349_DP1.raw	1.8483E5		
R.LYVQEAFAGESK.H	Y	53.64	1340.6611	12	0.4	671.3381	2	42.18	1	F1:12626	12112021_RID_2349_DP1.raw	1.0438E5		
K.TDVHSPGKFR.V	Y	49.57	1142.5833	10	-0.4	381.8682	3	22.83	1	F1:6017	12112021_RID_2349_DP1.raw	1.6839E5		

total 8 peptides

B8K1W0.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MMQVLLVTIC LAVFPYHGSS IILESGNVND YEVVYPQKVT AMPKEAVKQP EQKYEDAMQY KFEVNGEPVL LHLEKNKDLF
 81  SEDYSETHYS PDGREITTKP LVQDHCYYHG HIQNDAHSSA SISACNGLKG HFKLRGEMYL IEPLKLSDSE AHAVYKYENV
161  EKEDEALKMC GVTQTNWESD EPIKKASLLV ATSERNRYFN PYSYVELIIT VDHSMVTKYK NDLTAIRTWV FELVNTINEI

241  FKYLYIRVPL VGLEIWKNRD LINVTSAANV TLDLFGEWRK SYLLPRKIHD NSQLLTAIDL NGLTIGMAYV STMCQSKYSV

321  GVVQDHSKIN LRVAVTMAHE IGHNLGLTHD GVYCTCGGYS CIMSAVLGDQ PSKYFSNCSY NQYRRFLTEH NPECIINPPL

401  RTDIVSPPAC GNELLERGEE CDCGSPENCR DPCCDAASCK LHSWVECESG KCCNQCRFKR AGTECRPARD ECDKAEQCTG
481  RSANCPVDEF HENGRPCLHN FGYCYNGKCP IMYHQCHALF GQNVTGVQDS CFQYNRLGVY YAYCRKENGR KIPCAPKDEK
561  CGRLYCSYKS PGNQIPCLPY YIPSDENKGM VDHGTKCGDG KVCSNGQCVD LNIAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.YKNDLTAIR.T	N	69.36	1092.5928	9	0.5	547.3040	2	30.48	1	F1:8695	12112021_RID_2349_DP1.raw	1.0161E6	3.056E5	9.9469E5
K.ASLLVATSER.N	Y	65.12	1045.5768	10	-0.4	523.7955	2	35.52	1	F1:10437	12112021_RID_2349_DP1.raw	8.3446E5		
R.VPLVGLEIWK.N	Y	64.06	1152.6907	10	-0.3	577.3524	2	61.59	1	F1:19008	12112021_RID_2349_DP1.raw	1.8214E6		
R.KSYLLPR.K	Y	52.02	875.5228	7	0.7	438.7690	2	31.78	1	F1:9234	12112021_RID_2349_DP1.raw	7.7747E6		
A.SLLVATSER.N	Y	50.58	974.5396	9	-0.5	488.2769	2	33.39	1	F1:9720	12112021_RID_2349_DP1.raw	6.4327E5		
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.2185E4
K.NDLTAIR.T	N	44.81	801.4344	7	0.3	401.7246	2	29.16	7	F7:7605	17112021_RID_2349_DP7.raw	1.0951E5	4.7012E4	
Q.SKYSVGVVQDHSK.I	Y	43.60	1432.7310	13	-0.6	478.5840	3	27.74	1	F1:7696	12112021_RID_2349_DP1.raw	1.9427E5		
K.SYLLPRK.I	Y	42.55	875.5228	7	0.2	438.7688	2	28.14	1	F1:7822	12112021_RID_2349_DP1.raw	1.2424E6		
K.YSVGVVQDHSK.I	Y	42.32	1217.6040	11	0.5	406.8755	3	26.34	1	F1:7230	12112021_RID_2349_DP1.raw	2.3403E5	1.1059E5	

total 10 peptides

AAZ39880.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MMQVLLVTIC LAVFPYHGSS IILESGNVND YEVVYPQKVT AMPKEAVKQP EQKYEDAMQY KFEVNGEPVL LHLEKNKDLF
 81  SEDYSETHYS PDGREITTKP LVQDHCYYHG HIQNDAHSSA SISACNGLKG HFKLRGEMYL IEPLKLSDSE AHAVYKYENV
161  EKEDEALKMC GVTQTNWESD EPIKKASLLV ATSERNRYFN PYSYVELIIT VDHSMVTKYK NDLTAIRTWV FELVNTINEI

241  FKYLYIRVPL VGLEIWKNRD LINVTSAANV TLDLFGEWRK SYLLPRKIHD NSQLLTAIDL NGLTIGMAYV STMCQSKYSV

321  GVVQDHSKIN LRVAVTMAHE IGHNLGLTHD GVYCTCGGYS CIMSAVLGDQ PSKYFSNCSY NQYRRFLTEH NPECIINPPL

401  RTDIVSPPAC GNELLERGEE CDCGSPENCR DPCCDAASCK LHSWVECESG KCCNQCRFKR AGTECRPARD ECDKAEQCTG
481  RSANCPVDEF HENGRPCLHN FGYCYNGKCP IMYHQCHALF GQNVTGVQDS CFQYNRLGVY YAYCRKENGR KIPCAPKDEK
561  CGRLYCSYKS PGNQIPCLPY YIPSDENKGM VDHGTKCGDG KVCSNGQCVD LNIAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.YKNDLTAIR.T	N	69.36	1092.5928	9	0.5	547.3040	2	30.48	1	F1:8695	12112021_RID_2349_DP1.raw	1.0161E6	3.056E5	9.9469E5

total 10 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ASLLVATSER.N	Y	65.12	1045.5768	10	-0.4	523.7955	2	35.52	1	F1:10437	12112021_RID_2349_DP1.raw	8.3446E5		
R.VPLVGLEIWK.N	Y	64.06	1152.6907	10	-0.3	577.3524	2	61.59	1	F1:19008	12112021_RID_2349_DP1.raw	1.8214E6		
R.KSYLLPR.K	Y	52.02	875.5228	7	0.7	438.7690	2	31.78	1	F1:9234	12112021_RID_2349_DP1.raw	7.7747E6		
A.SLLVATSER.N	Y	50.58	974.5396	9	-0.5	488.2769	2	33.39	1	F1:9720	12112021_RID_2349_DP1.raw	6.4327E5		
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.2185E4
K.NDLTAIR.T	N	44.81	801.4344	7	0.3	401.7246	2	29.16	7	F7:7605	17112021_RID_2349_DP7.raw	1.0951E5	4.7012E4	
Q.SKYSVGVVQDHSK.I	Y	43.60	1432.7310	13	-0.6	478.5840	3	27.74	1	F1:7696	12112021_RID_2349_DP1.raw	1.9427E5		
K.SYLLPRK.I	Y	42.55	875.5228	7	0.2	438.7688	2	28.14	1	F1:7822	12112021_RID_2349_DP1.raw	1.2424E6		
K.YSVGVVQDHSK.I	Y	42.32	1217.6040	11	0.5	406.8755	3	26.34	1	F1:7230	12112021_RID_2349_DP1.raw	2.3403E5	1.1059E5	

total 10 peptides

ACE73567.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MIAFIVLPIL AAVLQQSSGS VDFDSESPRR PEIQNEIVDL HNSLRRSVTP TASNMLKMEW YPEAAANAER WAFRCILNHS
 81 PYNSRVIGGI KCGENIYMSP YPMKWTAIIH EWHKEKKDFV YGQGASPANA VVGHYTQIVW YKSYRSGCAA AYCPSSEYNY
161 FYVCQYCPAG NIIGKIATPY TSGPPCGDCP SACDNGLCTN PCSHHDEFTN CKDLVKQGCH SNYLKTKCPA SCFCHNEII
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Ar F.
K.MEWYPEAAANAER.W	N	85.56	1536.6667	13	0.5	769.3411	2	45.12	7	F7:13118	17112021_RID_2349_DP7.raw			
K.M(+15.99)EWYPEAAANAER.W	N	83.36	1552.6616	13	0.4	777.3384	2	40.79	7	F7:11501	17112021_RID_2349_DP7.raw			
G.SVDFDSESPR.R	N	67.58	1137.4938	10	-0.1	569.7541	2	30.74	7	F7:8132	17112021_RID_2349_DP7.raw	4.0226E4		
R.SVTPTASNMLK.M	Y	66.97	1147.5907	11	0.0	574.8026	2	33.55	7	F7:9166	17112021_RID_2349_DP7.raw			
R.RSVTPTASNMLK.M	Y	56.72	1303.6918	12	0.4	652.8535	2	28.75	7	F7:7373	17112021_RID_2349_DP7.raw			
R.SVTPTASNM(+15.99)LK.M	Y	41.99	1163.5856	11	0.4	582.8003	2	24.98	4	F4:6074	17112021_RID_2349_DP4.raw			

total 6

TRINITY_DN324
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAEAAAAETA ALFGLLLVLL LAPAALAAPG WAVPVDVRGD SVREAARFAL AEAFPEGHPR GLWALCGART QVVNGIKHYL
 81 EVVLLQSPCR RGEMADCDSP SGSLPLGKPE HVSCHFEVWS QPWASSKNLL KQDCHPTEPL TEIQAASLGP WETFPLNSPF
161 VDVAEASLRQ EESLQNVSAH LVSLFKDFLI TYRKSYLDDR ETQRRFQIFA ENLERARLYQ ELDQGTAEYG VTKFSDLTEE
241 EFHSTYLNPL LAKLPGRPMK EASIPNGSFP EEWDWRDHGA VTEVKNQGEC GSCWAFSVTG NIEGQWFLHK GTLLSLSEQE
321 LVDCDVIDKA CGGGLPSNAY EAIEKLGGLE TERDYSYQGF EQNCGFSREK VAVYINSSVG VSRDESEIAA WLAKNGPISI
401 ALNAFAMQFY RKGVSHPFFM LCNPWMIDHA VLLVGYGTRG QIPFWAIKNS WGEDWGEKGY YYLYRGKHAC GMNTMCSSAV
481 IN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
R.LYQELDQGTAEYGVTK.F	Y	91.90	1813.8734	16	0.9	907.9448	2	42.13	2	F2:11774	12112021_RID_2349_DP2.raw	6.0013E5		
R.DESEIAAWLAK.N	Y	64.98	1231.6084	11	0.0	616.8115	2	58.67	2	F2:17147	12112021_RID_2349_DP2.raw	5.887E4	3.37	
R.GQIPFWAIK.N	Y	50.17	1058.5913	9	0.3	530.3031	2	54.72	3	F3:16090	17112021_RID_2349_DP3.raw		8.69	
K.LGGLETER.D	Y	50.13	873.4556	8	-0.2	437.7350	2	26.62	2	F2:6331	12112021_RID_2349_DP2.raw	2.0992E5	6.12	
R.FQIFAENLER.A	Y	44.23	1265.6404	10	0.2	633.8276	2	51.63	2	F2:14817	12112021_RID_2349_DP2.raw	2.5367E5		

total 6 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.FSDLTEEEFHSTYLNPLLAK.L	Y	41.38	2353.1477	20	0.6	785.3903	3	58.68	2	F2:17169	12112021_RID_2349_DP2.raw		3.9261E5	
														total 6 peptides

TRINITY_DN441
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  TGILQGNILP RRVEAMVLIR VLANLLVLQL SYAQKSSELV VGGHRCNINE HRFLALVNSD KKQCGGTLIN QEWVLTAAHC
                                                                                          C

                                                                  126
 81  DGKIMKIQLG VHSKKVPNKD KQTRVPKQKF FCLSSKNYTM WDKDIMLIKL NGPVKTSTHI APLSLPSS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.TSTHIAPLSLPSS	N	60.21	1309.6877	13	-0.1	655.8511	2	44.76	4	F4:12858	17112021_RID_2349_DP4.raw			
R.FLALVNSDKK.Q	Y	57.18	1133.6444	10	0.1	567.8295	2	34.21	2	F2:9023	12112021_RID_2349_DP2.raw		8.9311E6	4.923E
M.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
K.SSELVVGGHR.C	Y	56.70	1039.5410	10	-0.1	520.7777	2	21.39	3	F3:4900	17112021_RID_2349_DP3.raw			2.3028
R.FLALVNSDK.K	Y	53.75	1005.5494	9	-0.6	503.7817	2	41.29	5	F5:11774	17112021_RID_2349_DP5.raw		3.9766E6	2.0733
M.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157
K.IQLGVHSKK.V	N	42.78	1008.6080	9	0.2	505.3113	2	18.69	3	F3:4026	17112021_RID_2349_DP3.raw			5.2609
K.IQLGVHSK.K	N	40.36	880.5131	8	-0.5	441.2636	2	23.29	1	F1:6181	12112021_RID_2349_DP1.raw	3.6053E6	1.5875E7	1.7023
R.FLALVNSDKKQ.C	Y	39.83	1261.7030	11	-0.2	631.8586	2	33.21	3	F3:8944	17112021_RID_2349_DP3.raw			7.979E
F.LALVNSDKK.Q	Y	38.72	986.5760	9	-0.8	494.2949	2	33.30	3	F3:8929	17112021_RID_2349_DP3.raw			2.4679
														total 10

AUF41660.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MMQVLLVTIS LAVFPYQGSS IILESGNVND YEVVYPQKVT ALPKGAVQQP EQKYEDTMQY EFEVNGEPVV LHLEKNKILF
 81  SEDYSETHYS PDGREITTNP PVEDHCYYHG RIQNDAHSSA SISACNGLKG HFKLRGEMYF IEPLKLSNNE AHAVYKYENI
161  EKEDETPKMC GVTQTNWESD EPIKKASLLN LTPEQRTYLK SKKYIEVIII ADYIIYLKYG RNLFTIRTRI YEIVNILNVI

241  YRVLNIYIAL LGLEIWNNGD KINVLPEAKV TLDLFGKWKA SDLLNHRNHD NAYLLTGINF NGPTAGLGYL GGMCHPEYSA

321  GIVQDHNKLN YLVALAMAHE MGHNLGMEHD KIHCTCGAKS CIMSGTLSCE ASNRFSDCSR EEHQKYLIDK MPQCILNKPL
401  KTDIVSPAVC GNYLVELGED CDCGSPSVCQ NPCCNAATCK LTQGSQCADE ECCDQCKFRR AGTVCRAANG ECDVSDLCTG
481  QSAECPTDQF QRNGHPCQNN NGYCYNGKCP IMGKQCISLF GSRATVAEDA CFNFNSLGNA YGYCRKENGR KIPCAPQDVK
561  CGRLYCFDNL PEHKNPCQIY YTPSDENKGM VDLGTKCGDG KACSSNRQCV DVNTAYQST
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.IYEIVNILNVIYR.V	N	76.22	1620.9238	13	0.7	811.4697	2	75.23	4	F4:22905	17112021_RID_2349_DP4.raw			1.5149E6
K.VTLDLFGK.W	N	54.13	891.5065	8	-0.2	446.7604	2	51.79	1	F1:15754	12112021_RID_2349_DP1.raw	8.9865E6	9.162E6	4.6551E7
K.ASLLNLTPEQR.T	Y	49.74	1240.6775	11	-0.1	621.3459	2	44.70	7	F7:12940	17112021_RID_2349_DP7.raw			
K.INVLPEAK.V	N	47.44	882.5175	8	0.8	442.2664	2	35.58	1	F1:10479	12112021_RID_2349_DP1.raw	8.9247E6	1.1229E7	4.4088E7
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.2185E4
K.GMVDLGTK.C	N	44.20	819.4160	8	0.0	410.7153	2	30.74	7	F7:8124	17112021_RID_2349_DP7.raw			
L.LNLTPEQR.T	N	41.26	969.5243	8	0.0	485.7694	2	30.89	7	F7:8269	17112021_RID_2349_DP7.raw	4.4645E5		
														total 7 pept

CAR40186.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
                                        24
  1  MRTLWIVAVC LMGVEGHLTQ FGDMINKKTG TFGLLSYVYY GCYCGLGGKG KPQDATDRCC FVHDCCYGTV NGCDPKLSTY
                        o
                        o
                        o

 81  SYSFQNGDIV CGDDDPCLRA VCECDRVAAI CFGENMNTYD KKYMLYSLFD CMEESEKC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.HLTQFGDMINKK.T	Y	78.52	1430.7340	12	0.0	477.9186	3	34.29	7	F7:9506	17112021_RID_2349_DP7.raw	2.9174E6	3.5177E6	2.(
G.HLTQFGDMINK.K	Y	74.36	1302.6390	11	-0.1	652.3267	2	37.85	7	F7:10612	17112021_RID_2349_DP7.raw	1.8546E6	6.6203E5	4.:
G.HLTQFGDM(+15.99)INK.K	Y	69.44	1318.6339	11	-0.1	660.3242	2	37.85	7	F7:10613	17112021_RID_2349_DP7.raw	4.5507E5	3.4443E5	1.(
G.HLTQFGDM(+15.99)INKK.T	Y	68.29	1446.7289	12	-0.4	483.2501	3	26.61	7	F7:6724	17112021_RID_2349_DP7.raw	2.9583E6	2.0754E6	8.:
G.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
G.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			
K.KYMLYSLFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			

tot

B5U6Z2.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
                                        24
  1  MRTLWIVAVC LMGVEGHLTQ FGDMINKKTG TFGLLSYVYY GCYCGLGGKG KPQDATDRCC FVHDCCYGTV NGCDPKLSTY
                        o
                        o
                        o

 81  SYSFQNGDIV CGDDDPCLRA VCECDRVAAI CFGENMNTYD KKYMLYSLFD CMEESEKC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
G.HLTQFGDMINKK.T	Y	78.52	1430.7340	12	0.0	477.9186	3	34.29	7	F7:9506	17112021_RID_2349_DP7.raw	2.9174E6	3.5177E6	2.(
G.HLTQFGDMINK.K	Y	74.36	1302.6390	11	-0.1	652.3267	2	37.85	7	F7:10612	17112021_RID_2349_DP7.raw	1.8546E6	6.6203E5	4.:
G.HLTQFGDM(+15.99)INK.K	Y	69.44	1318.6339	11	-0.1	660.3242	2	37.85	7	F7:10613	17112021_RID_2349_DP7.raw	4.5507E5	3.4443E5	1.(
G.HLTQFGDM(+15.99)INKK.T	Y	68.29	1446.7289	12	-0.4	483.2501	3	26.61	7	F7:6724	17112021_RID_2349_DP7.raw	2.9583E6	2.0754E6	8.:
G.ENMNTYDK.K	N	52.21	1013.4124	8	0.7	507.7138	2	19.60	7	F7:4282	17112021_RID_2349_DP7.raw			
K.GKPQDATDR.C	N	48.61	986.4781	9	-0.5	494.2461	2	11.50	7	F7:1839	17112021_RID_2349_DP7.raw			
G.ENMNTYDKK.Y	N	43.49	1141.5073	9	-0.1	571.7609	2	15.11	7	F7:2868	17112021_RID_2349_DP7.raw			
K.KYMLYSLFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw			

tot

TRINITY_DN59

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MGRFISVSFG WLVVFLSLSG TGADQDCLPG WSFYEGNCYK AFDEPKSWVD AEKFCQKQSN GKHLATIEWL GKANFVAELV

 81  TLREPETHVW IGLRVEDKRQ QCSSHWTDGS AVSYETVTKY TKCFGLNKDK GYLEWVTLPC EDNIPFICKS WVPH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4

total 5 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.HLATIEWLGK.A	N	75.80	1166.6448	10	0.6	584.3300	2	45.31	7	F7:13096	17112021_RID_2349_DP7.raw				
K.ANFVAELVTLR.E	Y	67.48	1231.6924	11	0.3	616.8536	2	60.68	6	F6:18179	17112021_RID_2349_DP6.raw				9.8423E4
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw				
H.LATIEWLGK.A	N	49.74	1029.5858	9	-0.3	515.8000	2	50.89	7	F7:15056	17112021_RID_2349_DP7.raw				
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw				

total 5 peptides

TRINITY_DN278
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                  18
  1  SGWSAYDQNC YKVFKEEMNW ADAEKFCTEQ HKGSHLVSLH NIAEADFVVK KTLAMLKDGV IWMGLNDVWN ECNWGWTDGA
                                                                                            C

 81  KLDYKAWNEG TNCFVFKIAK NHWSHMDCSR THNFVCKFRV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.VFKEEMNWADAEK.F	Y	78.10	1595.7290	13	0.4	798.8721	2	40.09	7	F7:11338	17112021_RID_2349_DP7.raw				1.4
K.EEMNWADAEK.F	N	64.38	1221.4972	10	0.6	611.7562	2	36.04	7	F7:10022	17112021_RID_2349_DP7.raw				
K.VFKEEM(+15.99)NWADAEK.F	Y	62.41	1611.7239	13	0.5	806.8696	2	33.88	7	F7:9194	17112021_RID_2349_DP7.raw				
K.LDYKAWNEGTN.C	N	59.40	1309.5939	11	-0.2	655.8041	2	39.53	7	F7:11171	17112021_RID_2349_DP7.raw				
K.KTLAMLK.D	N	50.24	803.4939	7	0.4	402.7544	2	24.60	7	F7:5931	17112021_RID_2349_DP7.raw				
K.EEM(+15.99)NWADAEK.F	N	48.33	1237.4921	10	0.6	619.7537	2	28.66	7	F7:7336	17112021_RID_2349_DP7.raw				
K.GSHLVSLHN.I	N	46.52	962.4933	9	-0.1	482.2539	2	23.67	7	F7:5711	17112021_RID_2349_DP7.raw				
K.GSHLVSLH.N	N	45.55	848.4504	8	0.0	425.2325	2	23.74	7	F7:5731	17112021_RID_2349_DP7.raw				

total 8 pepti

AJO70723.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                  46
  1  MGRFISVSFG WLVVFLSLSG TEAAFCCPSG WSAYDQNCYK VFKEEMNWAD AEKFCTEQHK GSHLVSLHNI AEADFVVKKT
                                                                                            C

 81  LAMLKDGVIW MGLNDVWNEC NWGWTDGAKL DYKAWNEGTN CFVFKIAKNH WSRMDCSKTH NFVCKFRV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.VFKEEMNWADAEK.F	Y	78.10	1595.7290	13	0.4	798.8721	2	40.09	7	F7:11338	17112021_RID_2349_DP7.raw				1.4
K.EEMNWADAEK.F	N	64.38	1221.4972	10	0.6	611.7562	2	36.04	7	F7:10022	17112021_RID_2349_DP7.raw				
K.VFKEEM(+15.99)NWADAEK.F	Y	62.41	1611.7239	13	0.5	806.8696	2	33.88	7	F7:9194	17112021_RID_2349_DP7.raw				
K.LDYKAWNEGTN.C	N	59.40	1309.5939	11	-0.2	655.8041	2	39.53	7	F7:11171	17112021_RID_2349_DP7.raw				
K.KTLAMLK.D	N	50.24	803.4939	7	0.4	402.7544	2	24.60	7	F7:5931	17112021_RID_2349_DP7.raw				
K.EEM(+15.99)NWADAEK.F	N	48.33	1237.4921	10	0.6	619.7537	2	28.66	7	F7:7336	17112021_RID_2349_DP7.raw				
K.GSHLVSLHN.I	N	46.52	962.4933	9	-0.1	482.2539	2	23.67	7	F7:5711	17112021_RID_2349_DP7.raw				
K.GSHLVSLH.N	N	45.55	848.4504	8	0.0	425.2325	2	23.74	7	F7:5731	17112021_RID_2349_DP7.raw				

total 8 pepti

XP_034272439.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MNTYSFRQSS SNIGGGGFGG SSSFRTPSIH GGSGGYGISV SSARLASSGF GGSLGGGYGG GYGGGSFNFG SGCFGGAGGA
                                99
 81 GGNINASDGL LSGNEKVTMQ NLNDRLANYL DKVRALEEAN TELEVKIREW YQKQGPTATR DYSPYYKTIE DLRDKILVAT

161 IENNKMILQI DNARLAADDF KTKFETEQAL RMSVEADING LRRVLDELTL ARTDLELQIE SLKEELAYLK KNHEEEMSAL

241 SGQLGGQVSV EVDSAPGIDL TKILADMRDQ YELLADKNRR DAEAWFTSKT EELTKEVAIN TEQLQTSKTE ITDLRRTLQG
321 LEIELQSQLS MKSALEGTLG DTEARYGAQL CQIQSLISNL EAQLVDVRSD MERQNNDYKM LMDIKSRLEQ EIETYRQLLD
401 GQDFNFSGNA SGMYGKTKQL LATSLEDYPL RYAQIFNTQI SMAGIIEWTQ LELDNLDQKT RKLMTMHCAL HPKSDIDQLY
481 LPRSQDGKGL LQVKQTVEEE KHSLNDYIQK EKEPLLKETK PSNSLASELS FTMSHYYQSS SSSYGGGGGG GSGRVASVRH
561 GPSSIHGGAG GRVSASSARF VSSGSGYGGG YGYGSGLGGG CAIGYGSVGG LGYGNYFGSS GGYGGGVGGG YGCGVGGGYG
641 GGVGGGYGGG LDFVVGGGGG GDGGLLTGNE KITMQNLNDR LANYLDKVRA LEEANTELEI KIRDWHQKQA PSSPAKDYSH
721 YYKIISDLRD KIHDATIDNS RTILEIDNAR LAADDFRLKY ENELHLRQGV ESDINGLRRV LDELTLFKSD MEMQIEEKKE

801 DLAYLKKNHE ELMKEFSTQL TGKVSVEMDA APGVDLTKIL ADMREQYEQM AERNRKDAEA WFFTKTEELN REVATHTEQL
881 QTSKTEISEL RRTIQSLEIE LQSQLSMKAG LETSLAETEG RYCAQLAQIQ NLITNVEEQL AELRNDMERQ NHEYRMLMDI
961 KTRLEQEIAT YRNLLEGQDS KLPGWSPKDA TYGGSSTINY SSGGSGSGGG GAISGSGYSS GGSSVTTSKV RSGNF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
K.VTMQNLNDR.L	N	68.95	1089.5237	9	0.0	545.7691	2	27.78	6	F6:7010	17112021_RID_2349_DP6.raw	1.3099E6	6.7229E5	5.3516
R.ALEEANTELEVK.I	N	67.86	1344.6772	12	0.3	673.3461	2	36.35	6	F6:9844	17112021_RID_2349_DP6.raw			
K.VTM(+15.99)QNLNDR.L	N	67.75	1105.5186	9	-0.5	553.7663	2	28.09	1	F1:7841	12112021_RID_2349_DP1.raw	7.8553E5	3.4355E5	1.125
R.VLDELTLAR.T	Y	63.40	1028.5865	9	1.0	515.3011	2	44.76	7	F7:12937	17112021_RID_2349_DP7.raw	5.1514E5	3.8767E5	3.897
K.TRLEQEIATYR.N	N	60.70	1378.7205	11	-0.1	690.3674	2	36.59	4	F4:9988	17112021_RID_2349_DP4.raw		4.6159E4	
R.LEQEIATYR.N	N	59.72	1121.5717	9	-0.1	561.7930	2	32.42	6	F6:8521	17112021_RID_2349_DP6.raw	2.3192E4		
R.LAADDFRLK.Y	N	56.97	1047.5713	9	0.6	524.7932	2	38.21	1	F1:11342	12112021_RID_2349_DP1.raw	4.5823E5		
R.LAADDFR.L	N	55.06	806.3922	7	0.0	404.2034	2	31.43	2	F2:8068	12112021_RID_2349_DP2.raw	2.1578E6	1.4275E6	3.776
														total

QBF53416.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MIQVLLVIIC LAVFPYQVSS IILESGNINN YEVVYPQKVT ALPKGAIQQL EQKYEDAMQY QFKVKGEPVV LHLEKNKDFF
 81 PEDYSETHYS PDDREITTNP PVEDHCYYYG HIQNDADSTA SISACNGLKG YFTLRGVTYL IEPLKIPESE AHAIYKYENV

161 EKEDEDPKKC EFRRAGTECR PARSECDVAE YCTGQSAECP TDVFHSNGKP CLNNFGYCYN GNCPIMYHQC YALFGPNATV
                                                                299
241 GQDGCFEWNK KGESYFYCRK ENDVPIPCAP EDIKCGRLFC ELIKNTCKYD YSEDPDYGMV DHGTKCGDGK VCINRHCVDV

321 TTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
K.YDYSEDPDYGMVDHGTK.C	N	86.45	1990.7891	17	0.5	996.4023	2	37.41	4	F4:10370	17112021_RID_2349_DP4.raw		
E.DPDYGM(+15.99)VDHGTK.C	N	72.65	1349.5558	12	0.3	675.7854	2	22.45	4	F4:5264	17112021_RID_2349_DP4.raw		1.1
E.DPDYGMVDHGTK.C	N	64.82	1333.5608	12	0.6	667.7881	2	28.50	3	F3:7288	17112021_RID_2349_DP3.raw	1.1371E6	
K.YDYSEDPDYGM(+15.99)VDHGTK.C	N	61.79	2006.7839	17	0.2	669.9354	3	32.76	4	F4:8703	17112021_RID_2349_DP4.raw		
D.PDYGMVDHGTK.C	N	55.63	1218.5339	11	0.9	407.1856	3	24.91	5	F5:6050	17112021_RID_2349_DP5.raw		

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	A
K.YENVEKEDEDPKK.C	Y	51.92	1621.7471	13	-0.1	541.5896	3	17.62	4	F4:3552	17112021_RID_2349_DP4.raw		

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  ADCPSDWCSH EGHCYKVFRL FKTWEEAEKF CMQQVNGWHL ASIESVEEAN FVAELVSKTL IKSKYHAWIG LRDQSERQQC

 81  SSHWTDGSAV SYETVTKYTK CFGLNKDKGY LEWVTLPCED NIPFICKSWV PH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A F
E.SVEEANFVAELVSK.T	Y	64.69	1520.7722	14	0.7	761.3939	2	57.97	6	F6:17304	17112021_RID_2349_DP6.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
R.LFKTWEEAEK.F	N	55.19	1279.6448	10	0.9	640.8303	2	35.62	7	F7:9816	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
K.TWEEAEKF.C	N	47.94	1038.4658	8	0.3	520.2404	2	39.87	6	F6:11136	17112021_RID_2349_DP6.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
F.KTWEEAEK.F	N	45.16	1019.4923	8	0.3	510.7536	2	17.57	6	F6:3741	17112021_RID_2349_DP6.raw					

total 9 peptides

TRINITY_DN59
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  ADCPSDWCSH EGHCYKVFRL FKTWEEAEKF CMQQVNGWHL ASIESVEEAN FVAELVSKTL IKSKYHAWIG LRDQSERQQC

 81  SSHWTDGSAV SYETVTKYTK CFGLNKDKGY LEWVTLPCED NIPFICKSWV PH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A F
E.SVEEANFVAELVSK.T	Y	64.69	1520.7722	14	0.7	761.3939	2	57.97	6	F6:17304	17112021_RID_2349_DP6.raw					
K.YHAWIGLR.D	N	61.14	1014.5399	8	-0.1	508.2772	2	40.32	7	F7:11939	17112021_RID_2349_DP7.raw					3.38
D.GSAVSYETVTK.Y	N	57.05	1140.5663	11	0.1	571.2905	2	28.66	6	F6:7260	17112021_RID_2349_DP6.raw					
R.LFKTWEEAEK.F	N	55.19	1279.6448	10	0.9	640.8303	2	35.62	7	F7:9816	17112021_RID_2349_DP7.raw					
K.SKYHAWIGLR.D	N	51.39	1229.6669	10	0.3	615.8409	2	41.34	7	F7:11753	17112021_RID_2349_DP7.raw					
K.TWEEAEKF.C	N	47.94	1038.4658	8	0.3	520.2404	2	39.87	6	F6:11136	17112021_RID_2349_DP6.raw					
Y.HAWIGLR.D	N	46.00	851.4766	7	0.5	426.7458	2	35.11	7	F7:9748	17112021_RID_2349_DP7.raw					
H.WTDGSAVSYETVTK.Y	N	45.93	1542.7202	14	0.5	772.3678	2	39.78	6	F6:11115	17112021_RID_2349_DP6.raw					
F.KTWEEAEK.F	N	45.16	1019.4923	8	0.3	510.7536	2	17.57	6	F6:3741	17112021_RID_2349_DP6.raw					

total 9 peptides

TRINITY_DN283
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	

total 8 peptide

TRINITY_DN283
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| Protein Coverage | Supporting Peptides |

Protein Coverage:


```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	

total 8 peptide

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	
														total 8 peptide

TRINITY_DN283
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	
														total 8 peptide

TRINITY_DN283
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	
														total 8 peptide

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	
														total 8 peptide

TRINITY_DN283
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLKKSKMFLL LSILSFLCAT SCSFARDESN LFPWDKIRLP KYVVPVHYDL LIHPNLTTLS FTGLSKIEIL ITEQTSSIIL
 81 HSKYLQITKA TIHNTKDSAD TAKGMMVLEH PPFEQIALVS TEPLQDGQSY IISIEYSANL SESFHGFYKS TYRTLEGETR
161 VLASTQFEAT AARMAFPCFD EPALKATFSI KIRRSPKHLA LSNMPLVKSV NINEWLIEDQ FDISVKMSTY LVAFIISDFK
241 SVTKRTLRGI KVSVYTVPHK IKQAEYALDA AVKLLDFFEG YFGIAYPLPK QDLAAIPDFQ SGAMENWGLT TYRESALLYD
321 SEKSSVSKKL VITMTVAHEL AHQWFGNLVT MEWWNDLWLN EGFAKFMEFV SVRKTHPELK VEDHFLNKYF NAMEVDALNS
401 SHPISTPVED PAQILEMFDE VSYDKGACIL NMLQDYLSPE VFQAGLAKYL LRFSYQNTKN KDLWDSLSDV CPYADGSHIQ
481 NGVCIRNKKK VLNSHWTKAV LQDVQAVMNT WTLQKGFPLV TVTIKGKNIH LQQEHYSKKA TLSSAGSLWH IPLTYITNKC
561 NDVRRFLLTT KTNNIVLPEE VEWIKFNVGM NGYYIVHYGD HGWDSLIRLL KDNHETISSN DRASLINNAF QLVSAGKLSI
641 EKALDLTLYL KHESEIAPVY QGLNELIPLY KLLEKTNISD TEQQLKAYIV NLFKNMIDKQ SWDDEGTVSE QMLRNSLLTF
721 ACVRKYKPCV DKAQEYFMKW KNSDGTLKLP NNIKMAVYAV GIQTDENWDF LFSKYQLPEF DTEKNQIEVV LCLSQNKEKL
801 QWLMDQALQG DIIKTQELPS ILVSVGRNPY GYQLAWKFLK QNWQKLVKKF DFGSHSLAQM ITGITNQYST KEQLAEVKNY
881 FSSMDKKTSE LRAVQQAIET IEENIQWMDK NLEKLKAWLQ INSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ASLINNAFQLVSAGK.L	Y	67.88	1531.8358	15	-0.2	766.9250	2	59.92	2	F2:17595	12112021_RID_2349_DP2.raw		2.8511E5	
K.TQELPSILVSVGR.N	Y	67.46	1397.7878	13	0.4	699.9015	2	55.31	2	F2:16054	12112021_RID_2349_DP2.raw	4.1868E4	3.6255E5	
K.AYIVNLFK.N	Y	58.66	966.5538	8	0.5	484.2844	2	53.23	2	F2:15426	12112021_RID_2349_DP2.raw		2.4274E5	
K.LQWLMDQALQGDIIK.T	Y	56.30	1770.9338	15	-0.1	886.4741	2	65.16	2	F2:19201	12112021_RID_2349_DP2.raw		7.7937E4	
K.NYFSSM(+15.99)DKK.T	Y	40.82	1134.5016	9	-0.6	568.2578	2	29.43	2	F2:7291	12112021_RID_2349_DP2.raw		3.9503E4	
R.NPYGYQLAWK.F	Y	40.39	1238.6084	10	-0.4	620.3112	2	47.34	2	F2:13416	12112021_RID_2349_DP2.raw		1.0503E6	
K.AQEYFMK.W	Y	39.57	915.4160	7	0.6	458.7155	2	32.48	2	F2:8440	12112021_RID_2349_DP2.raw		3.5139E4	
R.LLKDNHETISSNDR.A	Y	39.52	1640.8118	14	0.6	547.9449	3	22.93	2	F2:5192	12112021_RID_2349_DP2.raw		1.5804E5	
														total 8 peptide

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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 VVDVTLNSFG EWRERDLLNR KKHDNAQLLT GINFNGDTVG FGFVGSICMP KESVGIVQDH SKTHLLVATT MAHELGHNLG
 81 INHDEKQCNC GANSCIMAAM VSDPPPLYFS DCSRDQYQKF LTNFKPDCTL IRPSRTDIVS PPACGNELLE KGEECDCGSL
161 WYCRNPCCDA ATCKLKPGAQ CGDGMCCYQC RFVTAGTVCR PARDECDIPE YCSGQSVECP MDHFQKNGKP CLMNYGYCYN
241 GRCPIMIHQC IALWGPGTTV SPDVCFQKNK SGQDYYYCRR ENNKNIPCAP QDVKCGRLYC KLHNVDTFSC NIRYSDVALD
321 YGMVDHGTKC GDGKVCNSNR QCVDVNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Are
R.YSDVALDYGMVDHGTK.C	Y	87.37	1769.7930	16	0.7	885.9044	2	41.97	4	F4:11928	17112021_RID_2349_DP4.raw		
R.YSDVALDYGM(+15.99)VDHGTK.C	Y	69.95	1785.7880	16	0.5	893.9017	2	37.05	5	F5:10247	17112021_RID_2349_DP5.raw		
K.ESVGIVQDHSK.T	N	58.55	1197.5989	11	0.9	599.8073	2	22.46	5	F5:5229	17112021_RID_2349_DP5.raw		
N.SFGEWRER.D	N	55.07	1065.4991	8	0.1	533.7569	2	31.26	2	F2:7954	12112021_RID_2349_DP2.raw	6.0265E6	2.41
K.HDNAQLLTGINFN.G	N	48.53	1455.7106	13	1.2	728.8634	2	53.68	3	F3:15808	17112021_RID_2349_DP3.raw		
R.ERDLLNR.K	N	42.02	914.4933	7	-0.1	458.2539	2	23.23	1	F1:6203	12112021_RID_2349_DP1.raw	1.8049E7	3.28

TRINITY_DN249
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLLLLFLLSA SWSNVPTNGE VVDSFEANCP QFFLRETPPV IRHPPRSVRI CQRYQNLYRF ATLYNEDNCI PVYSAYIYNP
 81 GKAKRPKKWM IEPQLINSSF QPEMETEGEF LNKKGSKEAL QESQAILQDY KNLTDCNRGH LNPNGHQPDY SAKSSTFTLT
161 NIVPQFIKLN GGAWNNYEQS TMVQMTKGCQ ETFAVVGAVP GDTSVSGGRV NRPSHLWSAA CCVIDNNHLR SWAILARNDQ
241 NVVETFTLGQ LEYQLARLYN VNRVSLFHSD CPRQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Ar F
R.NDQNVVETFTLGQLEYQLAR.L	Y	78.63	2337.1602	20	0.1	1169.5875	2	68.98	3	F3:20748	17112021_RID_2349_DP3.raw		
R.GHLNPNGHQPDYSAK.S	Y	73.72	1633.7596	15	1.0	545.5944	3	20.98	3	F3:4807	17112021_RID_2349_DP3.raw		
K.KWMIEPQLINSSFQPEMETEGEFLNK.K	Y	56.53	3124.4885	26	-0.5	1042.5029	3	65.30	3	F3:19500	17112021_RID_2349_DP3.raw		
K.SSTFTLTNIVPQFIK.L	Y	54.61	1694.9243	15	1.1	848.4703	2	67.54	3	F3:20255	17112021_RID_2349_DP3.raw		

total 4 peptid

TRINITY_DN249
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLLLLFLLSA SWSNVPTNGE VVDSFEANCP QFFLRETPPV IRHPPRSVRI CQRYQNLYRF ATLYNEDNCI PVYSAYIYNP
 81 GKAKRPKKWM IEPQLINSSF QPEMETEGEF LNKKGSKEAL QESQAILQDY KNLTDCNRGH LNPNGHQPDY SAKSSTFTLT
161 NIVPQFIKLN GGAWNNYEQS TMVQMTKGCQ ETFAVVGAVP GDTSVSGGRV NRPSHLWSAA CCVIDNNHLR SWAILARNDQ
241 NVVETFTLGQ LEYQLARLYN VNRVSLFHSD CPRQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Ar F
R.NDQNVVETFTLGQLEYQLAR.L	Y	78.63	2337.1602	20	0.1	1169.5875	2	68.98	3	F3:20748	17112021_RID_2349_DP3.raw		
R.GHLNPNGHQPDYSAK.S	Y	73.72	1633.7596	15	1.0	545.5944	3	20.98	3	F3:4807	17112021_RID_2349_DP3.raw		
K.KWMIEPQLINSSFQPEMETEGEFLNK.K	Y	56.53	3124.4885	26	-0.5	1042.5029	3	65.30	3	F3:19500	17112021_RID_2349_DP3.raw		
K.SSTFTLTNIVPQFIK.L	Y	54.61	1694.9243	15	1.1	848.4703	2	67.54	3	F3:20255	17112021_RID_2349_DP3.raw		

total 4 peptid

TRINITY_DN249
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLLLLFLLSA SWSNVPTNGE VVDSFEANCP QFFLRETPPV IRHPPRSVRI CQRYQNLYRF ATLYNEDNCI PVYSAYIYNP
 81 GKAKRPKKWM IEPQLINSSF QPEMETEGEF LNKKGSKEAL QESQAILQDY KNLTDCNRGH LNPNGHQPDY SAKSSTFTLT
161 NIVPQFIKLN GGAWNNYEQS TMVQMTKGCQ ETFAVVGAVP GDTSVSGGRV NRPSHLWSAA CCVIDNNHLR SWAILARNDQ
241 NVVETFTLGQ LEYQLARLYN VNRVSLFHSD CPRQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Ar F
R.NDQNVVETFTLGQLEYQLAR.L	Y	78.63	2337.1602	20	0.1	1169.5875	2	68.98	3	F3:20748	17112021_RID_2349_DP3.raw		
R.GHLNPNGHQPDYSAK.S	Y	73.72	1633.7596	15	1.0	545.5944	3	20.98	3	F3:4807	17112021_RID_2349_DP3.raw		
K.KWMIEPQLINSSFQPEMETEGEFLNK.K	Y	56.53	3124.4885	26	-0.5	1042.5029	3	65.30	3	F3:19500	17112021_RID_2349_DP3.raw		
K.SSTFTLTNIVPQFIK.L	Y	54.61	1694.9243	15	1.1	848.4703	2	67.54	3	F3:20255	17112021_RID_2349_DP3.raw		

total 4 peptid

TRINITY_DN77
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAAHGWLWGC LLFAVWGSLV LGQEKIEVLE NKAVSLPCKA IRSQPNPTRQ EWKFQKDGTT LLFYHDNKFT DNYKDRATFT
 81 PYEIHLASVT RKDSGLYTCE VLGESFSQSQ VQLVVQVPAA KPTAHVPSVV TIGNKVVLRC EETEANPRPT FKWFKNDIQM
161 PLDPKTSTIF KNSSYTIDAD TGVLAFEPAT ALDTGDYSCE AENKVGPPQR SEVIHMETSE LNVGGIVAAV VVLLIILGLV
241 IFGIWFAYNR GYFSKRTTSG SKKVIYSQPS NRSDGDFKQT SSFLV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.ATFTPYEIHLASVTR.K	Y	73.13	1704.8835	15	0.6	853.4496	2	49.18	4	F4:14269	17112021_RID_2349_DP4.raw				3.0429E6
K.NDIQMPLDPK.T	Y	67.48	1169.5751	10	0.6	585.7952	2	41.29	4	F4:11774	17112021_RID_2349_DP4.raw				7.7188E6
R.SEVIHMETS.E	Y	61.05	1031.4594	9	0.4	516.7372	2	31.03	4	F4:8170	17112021_RID_2349_DP4.raw				1.6121E6
K.DGTTLLFYHDNK.F	Y	55.18	1422.6780	12	0.9	712.3469	2	45.59	4	F4:13096	17112021_RID_2349_DP4.raw				1.0471E6
K.PTAHVPSVVTIGNK.V	Y	48.30	1418.7881	14	0.6	473.9369	3	35.53	4	F4:9662	17112021_RID_2349_DP4.raw				9.978E5
R.SEVIHM(+15.99)ETS.E	Y	43.01	1047.4542	9	-0.1	524.7343	2	31.06	4	F4:8181	17112021_RID_2349_DP4.raw				4.2082E5
K.IEVLENK.A	Y	39.82	843.4702	7	0.1	422.7424	2	28.48	4	F4:7332	17112021_RID_2349_DP4.raw				1.5645E6

total 7 peptides

TRINITY_DN77
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MAAHGWLWGC LLFAVWGSLV LGQEKIEVLE NKAVSLPCKA IRSQPNPTRQ EWKFQKDGTT LLFYHDNKFT DNYKDRATFT
 81 PYEIHLASVT RKDSGLYTCE VLGESFSQSQ VQLVVQVPAA KPTAHVPSVV TIGNKVVLRC EETEANPRPT FKWFKNDIQM
161 PLDPKTSTIF KNSSYTIDAD TGVLAFEPAT ALDTGDYSCE AENKVGPPQR SEVIHMETS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.ATFTPYEIHLASVTR.K	Y	73.13	1704.8835	15	0.6	853.4496	2	49.18	4	F4:14269	17112021_RID_2349_DP4.raw				3.0429E6
K.NDIQMPLDPK.T	Y	67.48	1169.5751	10	0.6	585.7952	2	41.29	4	F4:11774	17112021_RID_2349_DP4.raw				7.7188E6
R.SEVIHMETS	Y	61.05	1031.4594	9	0.4	516.7372	2	31.03	4	F4:8170	17112021_RID_2349_DP4.raw				1.6121E6
K.DGTTLLFYHDNK.F	Y	55.18	1422.6780	12	0.9	712.3469	2	45.59	4	F4:13096	17112021_RID_2349_DP4.raw				1.0471E6
K.PTAHVPSVVTIGNK.V	Y	48.30	1418.7881	14	0.6	473.9369	3	35.53	4	F4:9662	17112021_RID_2349_DP4.raw				9.978E5
R.SEVIHM(+15.99)ETS	Y	43.01	1047.4542	9	-0.1	524.7343	2	31.06	4	F4:8181	17112021_RID_2349_DP4.raw				4.2082E5
K.IEVLENK.A	Y	39.82	843.4702	7	0.1	422.7424	2	28.48	4	F4:7332	17112021_RID_2349_DP4.raw				1.5645E6

total 7 peptides

TRINITY_DN3925
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MYQLWIKCLA AWIFLKRFNG VHVMQAKAPM YPNEPFLVFW NAPTTQCRLR YKVDLDLKTF HIVTNANDSL SGSAVTIFYS
 81 NHLGVYPHID DRGHFFHGII PQNESLTKHL DKSKSDINRM IPLKTFHGLG VIDWENWRPQ WDRNWGSKNV YRNRSVQFAK
161 DLHPELSEDK IRRLAKKQYE KAAKSFMRDT LLLAEEMRPD GYWGYYLYPD CQNYDYKTKG DQYTGKCPEI EMSRNDQLLW
241 LWRDSTALFP NVYLEIILRS SENALKFVHH RLKESMRIAS MAREDYALPV FAYARPFYAY TFEPLTQEDL VTTVGESAAM
321 GAAGIVFWGS MQYASTVDSC QKVKKYMNGP LGRYIVNVTT AAKICSRVLC RKNGRCVRKH SDSKAFLHLF PESFRIMVHA
401 NATEKKVIVK GKLELENLIY LRENFMCHCY QGWKGLYCEE DSINDIRKI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.DLHPELSEDKIR.R	Y	69.19	1450.7416	12	0.1	484.5879	3	33.81	1	F1:9852	12112021_RID_2349_DP1.raw	1.1766E6	1.5248E5	1.0234E6	2.

total 6 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
R.EDYALPVFAYAR.P	Y	58.82	1413.6927	12	0.2	707.8538	2	59.74	3	F3:17800	17112021_RID_2349_DP3.raw	3.0486E5	2.0754E5	1.9353E6	
R.NDQLLWLWR.D	Y	55.03	1242.6509	9	0.4	622.3329	2	65.33	3	F3:19554	17112021_RID_2349_DP3.raw			6.8841E5	
K.AFLHLFPESFR.I	Y	54.74	1362.7084	11	-0.4	455.2432	3	56.66	3	F3:16716	17112021_RID_2349_DP3.raw			6.974E5	
K.HLDKSKSDINR.M	Y	48.25	1311.6895	11	0.3	438.2372	3	26.05	1	F1:7151	12112021_RID_2349_DP1.raw	0			
K.YMNGPLGR.Y	Y	45.34	906.4382	8	0.1	454.2264	2	31.12	1	F1:8845	12112021_RID_2349_DP1.raw	3.6398E5			

total 6 peptides

TRINITY_DN3925
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MGSQSLPGTI ICFGLYSPGC YSWLLLFALP HLEGRSPHFV LDLILLWRST FGLCFTEALE RLLFWDLFRL PLSCAWTLPG
 81 GLDLEPWNLP CERTPTLGAF LELTVPEKLH IMYQLWIKCL AAWIFLKRFN GVHVMQAKAP MYPNEPFLVF WNAPTTQCRL
161 RYKVDLDLKT FHIVTNANDS LSGSAVTIFY SNHLGVYPHI DDRGHFFHGI IPQNESLTKH LDKSKSDINR MIPLKTFHGL
241 GVIDWENWRP QWDRNWGSKN VYRNRSVQFA KDLHPELSED KIRRLAKKQY EKAAKSFMRD TLLLAEEMRP DGYWGYYLYP
321 DCQNYDYKTK GDQYTGKCPE IEMSRNDQLL WLWRDSTALF PNVYLEIILR SSENALKFVH HRLKESMRIA SMAREDYALP
401 VFAYARPFYA YTFEPLTQED LVTTVGESAA MGAAGIVFWG SMQYASTVDS CQKVKKYMNG PLGRYIVNVT TAAKICSRVL
481 CRKNGRCVRK HSDSKAFLHL FPESFRIMVH ANATEKKVIV KGKLELENLI YLRENFMCHC YQGWKGLYCE EDSINDIRKI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.DLHPELSEDKIR.R	Y	69.19	1450.7416	12	0.1	484.5879	3	33.81	1	F1:9852	12112021_RID_2349_DP1.raw	1.1766E6	1.5248E5	1.0234E6	2.
R.EDYALPVFAYAR.P	Y	58.82	1413.6927	12	0.2	707.8538	2	59.74	3	F3:17800	17112021_RID_2349_DP3.raw	3.0486E5	2.0754E5	1.9353E6	
R.NDQLLWLWR.D	Y	55.03	1242.6509	9	0.4	622.3329	2	65.33	3	F3:19554	17112021_RID_2349_DP3.raw			6.8841E5	
K.AFLHLFPESFR.I	Y	54.74	1362.7084	11	-0.4	455.2432	3	56.66	3	F3:16716	17112021_RID_2349_DP3.raw			6.974E5	
K.HLDKSKSDINR.M	Y	48.25	1311.6895	11	0.3	438.2372	3	26.05	1	F1:7151	12112021_RID_2349_DP1.raw	0			
K.YMNGPLGR.Y	Y	45.34	906.4382	8	0.1	454.2264	2	31.12	1	F1:8845	12112021_RID_2349_DP1.raw	3.6398E5			

total 6 peptides

APB93444.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                   74
  1 MGRFISVSFS FLVVFLSLSG TGADCPSDWS SHEGHCYKVF KERKTWEDAE KFCTEQARGG HLISLKSTEE VDFMIKLAYP
                                                                                   o
                                                                                   o
 81 ILKADLVWIG LRDFWRDCHM GWRDHAQLLY KAWSDEPNCF AAKTTDNQWL RRKCNSSQYF VCQSRVPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.STEEVDFMIK.L	N	71.04	1197.5587	10	0.3	599.7868	2	46.71	5	F5:13738	17112021_RID_2349_DP5.raw		4.9086E5	
K.STEEVDFM(+15.99)IK.L	N	68.50	1213.5536	10	1.2	607.7848	2	41.28	7	F7:11785	17112021_RID_2349_DP7.raw	2.9758E5	1.0635E5	
K.TTDNQWLR.R	N	59.51	1032.4989	8	0.4	517.2570	2	33.81	7	F7:9330	17112021_RID_2349_DP7.raw			
K.ADLVWIGLR.D	Y	57.52	1041.5970	9	0.0	521.8058	2	58.17	5	F5:17416	17112021_RID_2349_DP5.raw			
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw			
R.GGHLISLK.S	N	41.82	823.4916	8	0.0	412.7531	2	27.22	7	F7:6877	17112021_RID_2349_DP7.raw			
R.KTWEDAEKF.C	N	40.81	1152.5450	9	0.6	577.2802	2	34.65	7	F7:9456	17112021_RID_2349_DP7.raw			
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw			

total 9

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.LAYPILK.A	N	40.30	816.5109	7	0.3	409.2628	2	42.38	5	F5:12212	17112021_RID_2349_DP5.raw			

total 9

TRINITY_DN195
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  LNSHAEAEQP AGAGLLGSGR GLGQVGGALR LRTWGICVKS APERRLALLA LLTCLPACLP AGPIMHSRLP VAAPLCLLLL
 81  LLLPWALPAI MPGGLSPRDV TDPEVQEAAV FAVEKYNARS ANDNYFKALR VVEAQSQVVS GVKYYLKMEL VKTTCRKTVG

161  KPKLYQEIQN CNLPPENQQE ELTCQFEVWS RPWLQSTLLT KMSCN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.DVTDPEVQEAAVFAVEK.Y	Y	82.05	1845.8995	17	0.6	923.9576	2	55.65	7	F7:16625	17112021_RID_2349_DP7.raw				
R.VVEAQSQVVSGVK.Y	Y	75.55	1328.7300	13	0.3	665.3724	2	29.88	7	F7:7845	17112021_RID_2349_DP7.raw				
R.SANDNYFK.A	Y	48.33	957.4192	8	0.0	479.7169	2	26.12	7	F7:6538	17112021_RID_2349_DP7.raw				
P.AIMPGGLSPR.D	Y	46.28	997.5378	10	0.8	499.7766	2	38.34	7	F7:10743	17112021_RID_2349_DP7.raw				
I.MPGGLSPR.D	Y	44.41	813.4167	8	-0.3	407.7155	2	28.28	7	F7:7342	17112021_RID_2349_DP7.raw				

total 5 peptides

TRINITY_DN1793
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MIAFIVLPIL AAVLQQSSGS VDFDSESPRK PEIQNEIVDL HNTLRRSVNP TASNMLKMEW YPEAAANAER WAFRCIYDHS

 81  PRDSRVIGGI KCGENIYMSP YPMKWTAIIH EWHDEKKNFV YGQGASPANA VVGHYTQVVW YKSYRSGCAA AYCPSSKYNY

161  FYVCQYCPAG NIIGKTATPY TSGPPCGDCP SACDNGLCTN PCRREDEFTN CKDLVKQGCH SNYLKTNCPA SCFCHNEII
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Ar F
K.MEWYPEAAANAER.W	N	85.56	1536.6667	13	0.5	769.3411	2	45.12	7	F7:13118	17112021_RID_2349_DP7.raw			
K.M(+15.99)EWYPEAAANAER.W	N	83.36	1552.6616	13	0.4	777.3384	2	40.79	7	F7:11501	17112021_RID_2349_DP7.raw			
G.SVDFDSESPR.K	N	67.58	1137.4938	10	-0.1	569.7541	2	30.74	7	F7:8132	17112021_RID_2349_DP7.raw	4.0226E4		
R.KPEIQNEIVDLHNTLR.R	Y	67.27	1918.0272	16	0.5	640.3500	3	44.88	4	F4:12951	17112021_RID_2349_DP4.raw			
R.SVNPTASNMLK.M	N	53.18	1160.5859	11	0.3	581.3004	2	32.34	4	F4:8661	17112021_RID_2349_DP4.raw			
R.SVNPTASNM(+15.99)LK.M	N	48.77	1176.5808	11	0.8	589.2982	2	24.27	4	F4:5833	17112021_RID_2349_DP4.raw			

total 6

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP

 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDH CLYSQTQLLM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Arc
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00

total 5

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP
 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDH CLYSQTQLLM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP
 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDH CLYSQTQLLM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP
 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDH CLYSQTQLLM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11

total 5

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP
                                                                                  o
                                                                                  o
 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDH CLYSQTQLLM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

TRINITY_DN240
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  64
  1  ICGGTLINQQ WVLSAAHCDM ENMQIYLGLH NFRLPNKDQK RRVAEEKFFC LSNKSYTKWD KDIMLIKLNR RVKTSTHITP
                                                                                  o
                                                                                  o
 81  LSLPSNPPRL RSVCRIMGWG SITSPNGRDL CLYSQTQFFM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.TSTHITPLSLPSNPPR.L	Y	84.36	1716.9159	16	0.1	859.4653	2	41.01	3	F3:11600	17112021_RID_2349_DP3.raw		7.6443E6	4.73
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.VKTSTHITPLSLPSNPPR.L	Y	50.77	1944.0792	18	0.2	649.0338	3	40.72	2	F2:11199	12112021_RID_2349_DP2.raw		5.1195E5	1.00
P.LSLPSNPPR.L	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

ETE70217.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MPMFFFPEGS HISRLDGQLP QQYRIKETGR GENCSYCLQS TWLPRAGLRY PFIMNTYSFR QSSSTISGGG FGGSSSFRTP
  81 SIHGGSGGYG ISVSSARLGS SPGFGGGLGS GLGGGSFSYG SGCFGGAGGA GGVFGGNLNV SDSLLSGNEK ITMQNLNDRL
 161 ANYLDKVRAL EEANTELEVK IREWYQKQGP TATRDYSPYY KTIEELRDKI LVETIENNKM ILQIDNARLA ADDFKTKFET
 241 EQALRMSVEA DINGLRRVLD ELTLSRADLE MQIESLKEEL AYLKKNHEEE MSALSGQLGG QVSVEVDSAP GIDLTKILAD
 321 MRDQYELLAE KNRRDAEAWF SSKTEELNKE VAINTEQLQT SKTEITDLRR TLQGLEIELQ SQLSMKTALE GTLADTEGRY
 401 GSQLCQIQSL ISNIEAQLVE VRSDMERQNN DYKMLMDIKT RLEQEIGTYR QLLDGQDFNL ASELSFTMSY YYQSSSSSYG
 481 GGGGGGSGRV ASVRLGPSSI HGGAGGRVSA SSARFVSSGS GYGGGYGYGS GLGGGCGIGY GSGGGVGYGS CFGGGVGGGY
 561 GGGLDFAVCS GGGGDGGLLT GNEKITMQNL NDRLANYLDK VRALEEANTE LEIKIRDWHQ RQAPSSPTKD YSHYYKTISE
 641 LRDKIHDTTI DNSRIILEID NARLAADDFR LKYENELHLR QGVESDINGL RRVLDELTLF KSDMEMQIEE KKEDLAYLKK
 721 NHEELMKEYG SQLTGKVSVE MDAAPGVDLT KILADMREQY EQMAERNRRD AEAWFFTKTE ELNREVATHT EQLQTSKTEI
 801 SELRRTIQSL EIELQSQLSM KAGLETSLAE TEGRYCAQLA QIQTLITGVE EQLADLRNDM ERQNHEYRML MDIKTRLEQE
 881 IATYRNLLEG QDSKGSKQLK LVKMKNQTKL KSADYFAGLG SPCVPSPSNC SFPHHEEESF SCNVKEMIEF SNSHFSNYLK
 961 GVHTLECENA GLECKIREWF EMNSSHGFYH LSSGYLGGPS GCLLQPIGDC YRTSNFHGVS SSLPMPLSFG SPIWLASDAE
1041 TSWGTFSGSQ GNLFMGGNEK RTMQELNDRL ASYLEKVRSL EEANTQLEGC IREWHQKRSH GTQRDFKDYE HNISDMHERI
1121 ETGRVTNAGL VLQIDNAKMA TEDFRLKYEA EKALRQNVQN DVENIRKELD NMTIIITDLE MEIEALREDH ILKKKEHETN
1201 MQAHGSPKDF KVNVKVNKTP QEDLSKILAG IRADYEAIIE KNRRSLDSWF QQQIGNESSE GQHNQEELQN SQKEICELNR
1281 TLQTLEIDFQ TELNKKFALE NNMGETKARY AFQLQSIQNL IKKCEEELSK FRHDIKYQNN QYKVLFGIKT RLEREISTYR
1361 QLLDGNVDGK TSTSFREHRS SNQNLKKIVQ ETVDGEEEEE EDSKDSVNSE THIYTLPMAR SGSVNLKNVF FESGGPSAAG
1441 SIYRMSSIKK PRTPSVHGGA GGFGTRISFG SNYSNTFGSN LLRSTSINEL LLTSNEKTTM QNLNDRLAAY LEKVHSLETS
1521 NSVLEKQIRE WYEKSSPIVK QDYNAFFKVI EELQDKITKA RIDNTRIILQ IDNSKLAADD FRVKYETELS LRLNVENDIT
1601 GLQGLIDELT LVRTDLEHQI ESLKEELAYL KKQHEEETAG LRRQLSGNVS VEVDAAPGID LAQAMENMRQ QYEILAEKNR
1681 QEAKDRFDKL IEQLNVEVTT TTHQLETHRS EITDRRNTLQ SLEIELQSQL SWKTERENAV AEIEAHYRTI LTQIQMAIGN
1761 IEAQLMQLRS DMEQQSIEYS ILLDIKVKLE VEIATYRRLL EGENWRMITS DLETSKEAEK GGEGGRLSGD EKQTMQNLND
1841 RLATYLGNVQ ALEEANSELE SKIAEWYEMF AAGNQAGQQQ DYSEYYAIID DLRNQIVATS IDNGTMILQI DNARLAGADF
1921 KLKYDNELAL HQSVEMDTNG LRKALEEIEI TSSDLKVQIN SFTEELEYMK KNHEEDMGSM NGSTAAGGIN VEMNVTPGVD
2001 LTTLLNEMRG EYEVLAEQNR EDIETWFNEQ SQELNKQINT SVEETSTNKS EITELKRALQ SLEIELQSQQ SLKQSLEATL
2081 VETESQYCGQ LSQIQEVIGS VEGQVQQIRD DMECQNREYE QLLDVKIRLE NEIDTYRSLL DGSERESSSG IQSRSGESAE
2161 QRFKIQEYAT SQSQSKGSGS GDSKQTDKLG SGNNPRDPQK TRVIRTIVED RIGDQVVSTR RGSSTGSFSS GVVWGFRSGW
2241 GKTGGGGGGA TGSCFHIYNS SPAGGDVGLL AGGDKETMQN LNDRLASYLA KVHALEEANG DLEQKIRNWY QKSATHINEG
2321 LHNDSKYNSS IDDLRNKIIA ASIRNASMIL QIDNARLAAD DFRMKYENEL FLHQNVEADI NGLKKVLDEL SMSKSDLEIQ
2401 IESLIEELAF LKKNHEEEMK NWQGTVAGDI NVEINAAPGV DLTAILNKMR TEYEALAEQN RKDAETWFVE KSKELNMTIN
2481 MSAKETTTNK KEITDLRHTL QSLEIDLKTQ LSLRQSLEST LAETEGQYCA QLLQIQGTIS NVENQVQQIR EDMECQNADY
2561 RCLLDIKIRL ENEIETYRHL IDGEALGKGM KELSGKRGES VQRSSKDLGS QNLRSEKGSG LRASGSDSRS TKTGTETSTR
2641 KSEARNVEAT TKDKEIKKTR VIKTIIEELD EYGRVTSSKV QSLACWHSTG LPSCSNTMAL SVLTSGSSRQ ISSYSMGGGG
2721 SVRLSSGVGF SGGSKFTGGY SGGGFGGGSL AGGYGTGMGG GFASGSFAGG FGGGFGVGGG DGGLLTGDEK QTMQNLNDRL
2801 ANYLGKVHAL EEANAELEVK IKEWYAKFST PDTDRDYSKY FNIIEDLRNQ ICRHTIENAG IVLQVDNARL AADDFKLKVL
2881 DDLTMNKSDL ELQIESLNEE LLYLKKNHEE ELMSFRGVTS GDVTVEMDAA PGVDLTKLLN DMRAQYEELA DKNRREAEEQ
2961 FNKQARTIYL NVGALRQEIS ANVDQLSSSK SEVTELRRTM QGLELELQAQ IAMKQSLEGT LAETERNYCD QLGQIQIQIS
3041 SLEEQLLQIR SDMENQNAEY QQLLGIKTRL EKEIETYHRL LEGEGGSALN EASQTGVPQP FPPPRHSPWV DDGIEAREQL
3121 AAESANSGDS KVEDRISEKQ IILFMSKSFK KISSYEGGAK MSGIGGGSLY GFGGGSMGGL GSSYGGAICS GYGGSGFGGG
3201 VGFGSASVAG GSYGANYRSS SSVSMSGAYG AGDSVFLAGA EKETMQNLNS RLANYLEKVR SLEEANAELE RKIRHWYEKN
3281 GPGAPGVTRD YSKYHHMIDE LRNQIVNVTI ENANVVLQID NARLAADDFR MKFENELFLR QSVEGDINGL RRVLDDLTMN
3361 RSDLEAQLES LTEELAYLKK NHEEEMTLLR SSSTGDVTVE MNAAPGIDLT KLLNDMRAQY EDLAEQNRRE AEEQFIKMSQ
3441 PLQQQIHDDA GAASTARNEL IELKRSFQSL EIELQSLLAK KASLEGTLAE TEGNYSTQLS QLQLQVSSLE EQLQQIRAET
3521 ECQNSEYQQL LGIKTRLEME IETYRRLLDG ESIRTAYETK VQIREPTKTR VVKTIVEELV DGKVISSQVK SAGNVLQQSS
3601 HPINKVQLAK VEDGSSMELS QLLNEIRANY ETLFSRSQIE TILSAGTQVI YSLLQLQEQT TLQKEQMNDN LFQKVGGSLT
3681 QVKFKFSLFL TMLTWHCKYS LQLEKVITAR MNKDEEILKA ARAELNEARR QWHHMQTEID SLHAMERGLE NSLQATELRY
3761 QTQLKHLETE IEDLEKELQE VRQDIEKQLQ QHEILLNSKM RLEQEIATYR SLLEKEEKRY LCLNRLRLTE KVDEVIKEWE
3841 GSFFKDNPHL RKKSVSLRFD LHLAATDEDC LHMKQKSRPD IEVRLVMRRS CSIPSIKT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
R.ALEEANTELEVK.I	N	67.86	1344.6772	12	0.3	673.3461	2	36.35	6	F6:9844	17112021_RID_2349_DP6.raw				

total 6 pepti

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.TRLEQEIATYR.N	N	60.70	1378.7205	11	-0.1	690.3674	2	36.59	4	F4:9988	17112021_RID_2349_DP4.raw		4.6159E4		9.
R.LEQEIATYR.N	N	59.72	1121.5717	9	-0.1	561.7930	2	32.42	6	F6:8521	17112021_RID_2349_DP6.raw	2.3192E4			
R.LAADDFRLK.Y	N	56.97	1047.5713	9	0.6	524.7932	2	38.21	1	F1:11342	12112021_RID_2349_DP1.raw	4.5823E5			8.
R.LAADDFR.L	N	55.06	806.3922	7	0.0	404.2034	2	31.43	2	F2:8068	12112021_RID_2349_DP2.raw	2.1578E6	1.4275E6	3.7768E6	7.
R.LENEIETYR.H	Y	50.96	1165.5615	9	-0.2	583.7879	2	33.11	6	F6:8783	17112021_RID_2349_DP6.raw				

total 6 pepti

XP_034291429.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAKGFFISKS LGIVGIVLGL GAVATIIALS VVYTQEKQRA DNALANQGPS STITAGATIA GTVQATTAGA TRATTASTTR
 81 ATTASTTRAT TAGANSTITT KPLEPWDHMR LPKTLMPTFY TISLQPFLKE VSPDFYIFKG NSTVEFQCKQ PTDLILIHSK
161 KLNYTLQETF LASLTGINVV APAIERTWLV EKTEYLVVKL KEKLQQDKAY RLHAEFTGEL ADDLAGFYRS AYMEEGKSKL
241 VATTQMQAAD ARKAFPCFDE PAMKANFSIT LIHLPAYKAL SNMPINKTEE VAMSDGSIWT RTEFEPTLKM STYLLAFIVS
321 EFENVSAIQH NTLIQIWGRP KSIKEGQGDY ALNVSWPILS FFEQQYNVPY PLKRLDQVAL PDFNAGAMEN WGLITYRESA
401 LLFDPEFSSI GNKERIVTVI AHEVAHQWFG NLVTLEWWNE LWLNEGFASY VEYLGANEAE PTWNIKDLIV PNDVYRVMAI
481 DALASSHPLS SPAEEINTPA QISEVFDSIS YSKGASVIRM LSEFLTEPVF REGLQSYFET YQYENTVCDD LWKQLQLVVN
561 KKNMSLPDTV KTIMDRWTLQ MGFPVLTVNT TTGIITQKHF LLDPESPVER PSQFNYTWIV PVSWLSKGKE AEMYWLTDTS
641 AENANFSTSA NPAQWLLLNI NVVGYFRVNY DLENWERLMN QLNDDLQKIP VLNRAQIIDD AFNLARAKHV GSDLALNTTR
721 YLAKEREYLP WDTALDNLDY FRLMFDRSEV YGPMQKYIQK QVTPLFDHFK KITLNWTQIP DGLMDQYNQI LAIRTACSYG
801 IPECNELASS WFKAWKANPS INRIPPNLRS AIYCSAIRTG GVEAWDFAWQ MFQQAQVISE ADKLRGALTC SQTPWILQRY
881 LQYTLDSTLI RRQDATSTIN SIASNVVGQP LAWDFVRMNW RTLFQQFGGS SFSFSSLIQS VTQRFASPFE LQQLEQFKAD
961 NADVGFGSAT RALEQALERT KANIKWVAEN QPLVLQWFKE NS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.LVATTQMQAADAR.K	Y	51.71	1374.6925	13	0.4	688.3538	2	31.31	1	F1:8938	12112021_RID_2349_DP1.raw	6.0941E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 4 peptides

XP_034291427.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAKGFFISKS LGIVGIVLGL GAVATIIALS VVYTQEKQRA DNALANQGPS STITAGATIA GTVQATTAGA TRATTASTTR
 81 ATTASTTRAT TAGANSTITT KPLEPWDHMR LPKTLMPTFY TISLQPFLKE VSPDFYIFKG NSTVEFQCKQ PTDLILIHSK
161 KLNYTLQETF LASLTGINVV APAIERTWLV EKTEYLVVKL KEKLQQDKAY RLHAEFTGEL ADDLAGFYRS AYMEEGKSKL
241 VATTQMQAAD ARKAFPCFDE PAMKANFSIT LIHLPAYKAL SNMPINKTEE VAMSDGSIWT RTEFEPTLKM STYLLAFIVS
321 EFENVSAIQH NTLIQIWGRP KSIKEGQGDY ALNVSWPILS FFEQQYNVPY PLKRLDQVAL PDFNAGAMEN WGLITYRESA
401 LLFDPEFSSI GNKERIVTVI AHEVAHQWFG NLVTLEWWNE LWLNEGFASY VEYLGANEAE PTWNIKDLIV PNDVYRVMAI
481 DALASSHPLS SPAEEINTPA QISEVFDSIS YSKGASVIRM LSEFLTEPVF REGLQSYFET YQYENTVCDD LWKQLQLVVN
561 KKNMSLPDTV KTIMDRWTLQ MGFPVLTVNT TTGIITQKHF LLDPESPVER PSQFNYTWIV PVSWLSKGKE AEMYWLTDTS
641 AENANFSTSA NPAQWLLLNI NVVGYFRVNY DLENWERLMN QLNDDLQKIP VLNRAQIIDD AFNLARAKHV GSDLALNTTR
721 YLAKEREYLP WDTALDNLDY FRLMFDRSEV YGPMQKYIQK QVTPLFDHFK KITLNWTQIP DGLMDQYNQI LAIRTACSYG
801 IPECNELASS WFKAWKANPS INRIPPNLRS AIYCSAIRTG GVEAWDFAWQ MFQQAQVISE ADKLRGALTC SQTPWILQRY
881 LQYTLDSTLI RRQDATSTIN SIASNVVGQP LAWDFVRMNW RTLFQQFGGS SFSFSSLIQS VTQRFASPFE LQQLEQFKAD
961 NADVGFGSAT RALEQALERT KANIKWVAEN QPLVLQWFKE NS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.LVATTQMQAADAR.K	Y	51.71	1374.6925	13	0.4	688.3538	2	31.31	1	F1:8938	12112021_RID_2349_DP1.raw	6.0941E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 4 peptides

XP_034291428.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAKGFFISKS LGIVGIVLGL GAVATIIALS VVYTQEKQRA DNALANQGPS STITAGATIA GTVQATTAGA TRATTASTTR
 81 ATTASTTRAT TAGANSTITT KPLEPWDHMR LPKTLMPTFY TISLQPFLKE VSPDFYIFKG NSTVEFQCKQ PTDLILIHSK
161 KLNYTLQETF LASLTGINVV APAIERTWLV EKTEYLVVKL KEKLQQDKAY RLHAEFTGEL ADDLAGFYRS AYMEEGKSKL
241 VATTQMQAAD ARKAFPCFDE PAMKANFSIT LIHLPAYKAL SNMPINKTEE VAMSDGSIWT RTEFEPTLKM STYLLAFIVS
321 EFENVSAIQH NTLIQIWGRP KSIKEGQGDY ALNVSWPILS FFEQQYNVPY PLKRLDQVAL PDFNAGAMEN WGLITYRESA
401 LLFDPEFSSI GNKERIVTVI AHEVAHQWFG NLVTLEWWNE LWLNEGFASY VEYLGANEAE PTWNIKDLIV PNDVYRVMAI
481 DALASSHPLS SPAEEINTPA QISEVFDSIS YSKGASVIRM LSEFLTEPVF REGLQSYFET YQYENTVCDD LWKQLQLVVN
561 KKNMSLPDTV KTIMDRWTLQ MGFPVLTVNT TTGIITQKHF LLDPESPVER PSQFNYTWIV PVSWLSKGKE AEMYWLTDTS
641 AENANFSTSA NPAQWLLLNI NVVGYFRVNY DLENWERLMN QLNDDLQKIP VLNRAQIIDD AFNLARAKHV GSDLALNTTR
721 YLAKEREYLP WDTALDNLDY FRLMFDRSEV YGPMQKYIQK QVTPLFDHFK KITLNWTQIP DGLMDQYNQI LAIRTACSYG
801 IPECNELASS WFKAWKANPS INRIPPNLRS AIYCSAIRTG GVEAWDFAWQ MFQQAQVISE ADKLRGALTC SQTPWILQRY
881 LQYTLDSTLI RRQDATSTIN SIASNVVGQP LAWDFVRMNW RTLFQQFGGS SFSFSSLIQS VTQRFASPFE LQQLEQFKAD
961 NADVGFGSAT RALEQALERT KANIKWVAEN QPLVLQWFKE NS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.AQIIDDAFNLAR.A	N	93.46	1345.6990	12	0.6	673.8572	2	54.45	1	F1:16660	12112021_RID_2349_DP1.raw	1.3295E6			
K.ADNADVGFGSATR.A	N	56.38	1279.5792	13	0.7	640.7974	2	31.66	1	F1:9065	12112021_RID_2349_DP1.raw	7.2844E4			
K.LVATTQMQAADAR.K	Y	51.71	1374.6925	13	0.4	688.3538	2	31.31	1	F1:8938	12112021_RID_2349_DP1.raw	6.0941E4			
R.LMFDRSEVYGPMQK.Y	N	39.50	1699.8062	14	0.1	567.6094	3	44.88	1	F1:13512	12112021_RID_2349_DP1.raw	8.2001E4			

total 4 peptides

TRINITY_DN743
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 VASEQSCYLW RLKDSSLCRE GRKTMGRSIS VSFGLLVVFL SPSGAKGSTC PFNWLPMYGL CYKVFNEPKT WDDAEMFCRK
 81 YKPGCHLASL HSKGDSTEFA EYIADYRKGW GNIWIGLWGK KKGFSWEWTD GSSTKYLPWK KNQPNHYLNK EFCAEIVYFT
161 GYRLWNDQDC KVKNAFLCQC RF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.GDSTEFAEYIADYRK.G	Y	82.76	1763.8002	15	0.8	882.9081	2	48.40	7	F7:14317	17112021_RID_2349_DP7.raw					
K.GFSWEWTDGSSTK.Y	Y	80.18	1486.6365	13	0.1	744.3256	2	52.71	7	F7:15715	17112021_RID_2349_DP7.raw					
K.GDSTEFAEYIADYR.K	Y	77.07	1635.7052	14	0.6	818.8604	2	55.01	7	F7:16481	17112021_RID_2349_DP7.raw					

total 3 peptides

TRINITY_DN743
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 THTHTHTRFF SAGQMPFFVT AVSQMFCRKY KPGCHLASLH SKGDSTEFAE YIADYRKGWG NIWIGLWGKK KGFSWEWTDG
 81 SSTKYLPWKK NQPNHYLNKE FCAEIVYFTA TSNFGEEMVG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.GDSTEFAEYIADYRK.G	Y	82.76	1763.8002	15	0.8	882.9081	2	48.40	7	F7:14317	17112021_RID_2349_DP7.raw					
K.GFSWEWTDGSSTK.Y	Y	80.18	1486.6365	13	0.1	744.3256	2	52.71	7	F7:15715	17112021_RID_2349_DP7.raw					
K.GDSTEFAEYIADYR.K	Y	77.07	1635.7052	14	0.6	818.8604	2	55.01	7	F7:16481	17112021_RID_2349_DP7.raw					
																total 3 peptides

TRINITY_DN0
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                    29
  1  NKDKQTRVPK QKFFCLSSKN YTMWDKDIML IKLNRPVTYS THIAPLSLPS SPPTVGSVCR IMGWGAITSP NETYPDVPHC
                                    o
                                                                                          146
 81  ANINVLDHTA CQKAYPWLLA KSRTLCAGIL QGGIDTCHAD SGGPLICNGQ LQGIVSWGYP CGQPRMPGVY TKVFDYTDWI
                                                                                          o
161  QSIIAGNTAA TCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
M.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
K.AYPWLLAKSR.T	Y	56.89	1203.6764	10	-0.7	602.8450	2	44.38	4	F4:12697	17112021_RID_2349_DP4.raw			
R.MPGVYTK.V	N	56.65	794.3997	7	0.2	398.2072	2	26.42	4	F4:6530	17112021_RID_2349_DP4.raw	1.5867E7	1.6435E6	9.2719
K.AYPWLLAK.S	Y	56.25	960.5433	8	-0.5	481.2787	2	51.66	4	F4:15033	17112021_RID_2349_DP4.raw	6.4332E6	1.8506E6	1.3941
M.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157
K.LNRPVTY.S	N	50.91	861.4708	7	0.0	431.7427	2	27.71	2	F2:6756	12112021_RID_2349_DP2.raw	1.1931E5	4.6213E5	
R.M(+15.99)PGVYTK.V	N	49.06	810.3946	7	1.2	811.4028	1	23.10	3	F3:5226	17112021_RID_2349_DP3.raw	6.2476E6	4.4572E5	2.9093
														total

TRINITY_DN0
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                    37
  1  GVHSKKVPNK DKQTRVPKQK FFCLSSKNYT MWDKDIMLIK LNRPVTYSTH IAPLSLPSSP PTVGSVCRIM GWGAITSPNE
                                    o
                                                                                          154
 81  TYPDVPHCAN INVLDHTACQ KAYPWLLAKS RTLCAGILQG GIDTCHADSG GPLICNGQLQ GIVSWGYPCG QPRMPGVYTK
                                                                                          o
161  VFDYTDWIQS IIAGNTAATC PP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
M.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
K.AYPWLLAKSR.T	Y	56.89	1203.6764	10	-0.7	602.8450	2	44.38	4	F4:12697	17112021_RID_2349_DP4.raw			
R.MPGVYTK.V	N	56.65	794.3997	7	0.2	398.2072	2	26.42	4	F4:6530	17112021_RID_2349_DP4.raw	1.5867E7	1.6435E6	9.2719
K.AYPWLLAK.S	Y	56.25	960.5433	8	-0.5	481.2787	2	51.66	4	F4:15033	17112021_RID_2349_DP4.raw	6.4332E6	1.8506E6	1.3941
M.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157
K.LNRPVTY.S	N	50.91	861.4708	7	0.0	431.7427	2	27.71	2	F2:6756	12112021_RID_2349_DP2.raw	1.1931E5	4.6213E5	
R.M(+15.99)PGVYTK.V	N	49.06	810.3946	7	1.2	811.4028	1	23.10	3	F3:5226	17112021_RID_2349_DP3.raw	6.2476E6	4.4572E5	2.9093
														total

CBM40646.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  VLIRVLANLL LLQLSYAQES SELVIGGDEC DINEHPFLVA LHTARSKRFH CAGTLLNKEW VLTAARCDME NMQIYLGLHN
                                     113                                     146
 81  ISRPNQDQKR RVPKEKHFCV SSKTYTRWDK DIMLIRLKRP VNDGTHIAPL SLPSNPPSVG SVCRIMGWGS ITTTKVTYPD

161  VPHCANIKLF DYSVCRDAYK GLPEKSRTLC AGILEGGIDS CKVDNGGPLI CNGQFQGIGS WEGHPCAQPL KPALYTNVFE

241  YTDWIEGIIA RNTTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.7394E
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706E
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085E
R.IM(+15.99)GWGSITTTK.V	Y	46.02	1209.6063	11	-0.6	605.8101	2	67.06	3	F3:20099	17112021_RID_2349_DP3.raw			0
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			

total 7 pe

CBM40645.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  VLIRVLANLL LLQLSYAQES SELVIGGDEC DINEHPFLVA LHTARSKRFH CAGTLLNKEW VLTAARCDRK NIRIKFGVHN
                                     113                                     146
 81  KNVQNEDEEM RVPKEKHFCV SSKTYTRWDK DIMLIRLKRP VNDGTHIAPL SLPSNPPSVG SVCRIMGWGS ITTTKVTYPD

161  VPHCANIKLF DYSVCRDAYK GLPEKSRTLC AGILEGGIDS CKVDNGGPLI CNGQFQGIGS WEGHPCAQPL KPALYTNVFE

241  YTDWIEGIIA RNTTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.7394E
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706E
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085E
R.IM(+15.99)GWGSITTTK.V	Y	46.02	1209.6063	11	-0.6	605.8101	2	67.06	3	F3:20099	17112021_RID_2349_DP3.raw			0
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			

total 7 pe

AAR24534.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIRVLANL LLLQLSYAQE SSELVIGGDE CDINEHPFLV ALHTARSKRF HCAGTLLNKE WVLTAARCDR KNIRIKFGVH
                                     114                                     147
 81  NKNVQNEDEE MRVPKEKHFC VSSKTYTRWD KDIMLIRLKR PVNDGTHIAP LSLPSNPPSV GSVCRIMGWG SITTTKVTYP

161  DVPHCANIKL FDYSVCRDAY KGLPEKSRTL CAGILEGGID SCKVDNGGPL ICNGQFQGIG SWEGHPCAQP LKPALYTNVF

241  EYTDWIEGII ARNTTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.7394E7
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706E8
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085E7
R.IM(+15.99)GWGSITTTK.V	Y	46.02	1209.6063	11	-0.6	605.8101	2	67.06	3	F3:20099	17112021_RID_2349_DP3.raw			0
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			

total 7 pep

Q6T6S7.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIRVLANL LLLQLSYAQE SSELVIGGDE CDINEHPFLV ALHTARSKRF HCAGTLLNKE WVLTAARCDR KNIRIKFGVH
                                                 114                                147
 81  NKNVQNEDEE MRVPKEKHFC VSSKTYTRWD KDIMLIRLKR PVNDGTHIAP LSLPSNPPSV GSVCRIMGWG SITTTKVTYP

161  DVPHCANIKL FDYSVCRDAY KGLPEKSRTL CAGILEGGID SCKVDNGGPL ICNGQFQGIG SWEGHPCAQP LKPALYTNVF

241  EYTDWIEGII ARNTTVTCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.TYTRWDKDIMLIR.L	N	82.41	1709.8923	13	0.4	570.9716	3	49.33	3	F3:14370	17112021_RID_2349_DP3.raw		1.4395E6	1.7394E7
R.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706E8
R.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085E7
R.IM(+15.99)GWGSITTTK.V	Y	46.02	1209.6063	11	-0.6	605.8101	2	67.06	3	F3:20099	17112021_RID_2349_DP3.raw			0
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6
K.VTYPDVPH.C	N	39.33	926.4498	8	-0.6	464.2319	2	35.54	6	F6:9635	17112021_RID_2349_DP6.raw			

total 7 pep

TRINITY_DN94
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MMRLRDLILL ACLVAACSAL IRIPLKKFPS MRSIYNEYGT NIQDLTELGQ MLKYKFGGPG AEIPTPEALK NYMDAQYYGE
 81  IGIGTPPQKF TVVFDTGSSN LWVPSVHCSL LDIACLLHHK YDSSKSSTYV KNGTDFAIHY GTGSLSGYLS QDTVTIGDIS
161  VKNQLFGEAT KQPGITFIAA KFDGILGMAY PKISVDKVAP FFDNVMEQGL LEKNIFSFYL NRDPKGETGG ELLFGGTDSQ

241  YYTGDFHWNN VTRQAYWQVH MDKIDVANGL TVCKDGCEAI IDTGTSLITG PTKEIKELQK AIGAKPIIKG QYILQCDKLS
321  TLPTVSLVLG GKSYVLTPDQ YALKVTVQGE TLCLSGFSGL DVPPPGGPLW ILGDVLIGAY YTVFDRDNDS VGFAKCTSKV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Ar F
K.SYVLTPDQYALK.V	Y	68.30	1396.7238	12	0.7	699.3696	2	47.84	2	F2:13587	12112021_RID_2349_DP2.raw		3.5687E5		
K.VAPFFDNVMEQGLLEK.N	Y	60.45	1835.9127	16	0.0	918.9636	2	64.86	2	F2:19175	12112021_RID_2349_DP2.raw		3.9332E5		
K.FDGILGM(+15.99)AYPK.I	Y	49.32	1226.6005	11	0.6	614.3079	2	55.72	2	F2:16218	12112021_RID_2349_DP2.raw		5.4166E4		
K.NIFSFYLNR.D	Y	46.37	1172.5978	9	2.2	587.3074	2	59.79	2	F2:17511	12112021_RID_2349_DP2.raw		0		

total 4 peptides

E5AJX2.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIRVLANL LLLQLSYAQK SSELVIGGDE CNINEHPFLA FVTSDRRRCA GTLINQEWVL TAAHCNGKYM KIELGVHDKM
                                     111
 81  VRNEDKQTRV PKQKFFCLSS KEYTMWDKDI MLIRLNTPVN NSTHIAPVSL ASRPPVVGSV CRIMGWGTIS SPKVILPDVP

161  HCANIEIIKY SKCQGVHPEL PAKGRVVCAG IWQGGKDSCH GDSGAPLICN GQLQGLLSWG GDPCAQPLQP GLYTDIFDYS

241  DWIQSIIAGN TTATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
M.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706
M.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085
Y.TMWDKDIMLIR.L	N	50.40	1420.7207	11	0.6	711.3680	2	53.82	3	F3:15851	17112021_RID_2349_DP3.raw			1.1002
R.IMGWGTISSPK.V	Y	46.07	1175.6008	11	0.7	588.8081	2	66.82	3	F3:20035	17112021_RID_2349_DP3.raw			5.4903
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097
R.VVC(+57.02)AGIWQGGK.D	N	39.18	1173.5964	11	0.7	587.8059	2	34.83	4	F4:9494	17112021_RID_2349_DP4.raw			

CBW30778.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIRVLANL LLLQLSYAQK SSELVIGGDE CNINEHPFLA FVTSDRRRCA GTLINQEWVL TAAHCNGKYM KIELGVHDKM
                                     111
 81  VRNEDKQTRV PKQKFFCLSS KEYTMWDKDI MLIRLNTPVN NSTHIAPVSL ASRPPVVGSV CRIMGWGTIS SPKVILPDVP

161  HCANIEIIKY SKCQGVHPEL PAKGRVVCAG IWQGGKDSCH GDSGAPLICN GQLQGLLSWG GDPCAQPLQP GLYTDIFDYS

241  DWIQSIIAGN TTATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
M.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706
M.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085
Y.TMWDKDIMLIR.L	N	50.40	1420.7207	11	0.6	711.3680	2	53.82	3	F3:15851	17112021_RID_2349_DP3.raw			1.1002
R.IMGWGTISSPK.V	Y	46.07	1175.6008	11	0.7	588.8081	2	66.82	3	F3:20035	17112021_RID_2349_DP3.raw			5.4903
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097
R.VVC(+57.02)AGIWQGGK.D	N	39.18	1173.5964	11	0.7	587.8059	2	34.83	4	F4:9494	17112021_RID_2349_DP4.raw			

TRINITY_DN4675

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  VASEQSCYLW RPRDSSLCRE GRKTMGRSIS VSFGCLVVFL SLSGTGAGLK CPPDSSPYRY FCYRVFKEQK TWEDAERFCV

 81  EHPNDGHLVS IESMEEAEFV AQLISNITGK FITHFWIGLR IEDKKQQCRS EWSDGSSVSY DNLLKREFRK CFGLEKGTGY

161  RMWFNLNCEE TYPFICKVPP YC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.SEWSDGSSVSYDNLLK.R	Y	83.22	1785.8057	16	0.7	893.9108	2	51.99	5	F5:15311	17112021_RID_2349_DP5.raw				
												total 3 peptides			

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.SEWSDGSSVSYDNLLKR.E	Y	79.37	1941.9067	17	0.4	971.9610	2	46.71	5	F5:13597	17112021_RID_2349_DP5.raw				
K.TWEDAER.F	N	42.62	905.3879	7	0.3	453.7014	2	24.88	5	F5:6121	17112021_RID_2349_DP5.raw				
															total 3 peptides

TRINITY_DN59
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  GWSAYDQHCY QAVDEPKTWA DAEKFCTEQA NGGHLVSIEN VGEANFVAQL ASGFIQKPGI YVWIGLRDRR KEQQCRSEWN

 81  DGSKIIYVNW KEGESKMCQG LAKWTDFHKW DYVNCAERYR FVCKFPPQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
K.IIYVNWKEGESK.M	Y	79.43	1464.7612	12	0.4	733.3882	2	38.97	5	F5:10919	17112021_RID_2349_DP5.raw					2.829E7
C.YQAVDEPK.T	N	56.88	948.4552	8	0.4	475.2351	2	22.42	5	F5:5214	17112021_RID_2349_DP5.raw					4.8543E
K.TWADAEKF.C	N	39.07	966.4446	8	0.5	484.2298	2	41.22	5	F5:11753	17112021_RID_2349_DP5.raw					2.1565E
																total 3 peptides

TRINITY_DN59
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  GWSAYDQHCY QAVDEPKTWA DAEKFCTEQA NGGHLVSIEN VGEANFVAQL ASGFIQKPGI YVWIGLRDRR KEQQCRSEWN

 81  DGSKIIYVNW KEGESKMCQG LAKWTDFHKW DYVNCAERYR FVCKFPPQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
K.IIYVNWKEGESK.M	Y	79.43	1464.7612	12	0.4	733.3882	2	38.97	5	F5:10919	17112021_RID_2349_DP5.raw					2.829E7
C.YQAVDEPK.T	N	56.88	948.4552	8	0.4	475.2351	2	22.42	5	F5:5214	17112021_RID_2349_DP5.raw					4.8543E
K.TWADAEKF.C	N	39.07	966.4446	8	0.5	484.2298	2	41.22	5	F5:11753	17112021_RID_2349_DP5.raw					2.1565E
																total 3 peptides

AJO70724.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MGRFISVSFG LLVVFLSLSG TGADFDCPSG WSAYDQHCYQ AVDEPKTWAD AEKFCTEQAN GGHLVSIENV GEANFVAQLA

 81  SGFIQKPGIY VWIGLRDRRK EQQCRSEWND GSKIIYVNWK EGESKMCQGL AKWTDFHKWD YVNCAERYRF VCKFPPQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
K.IIYVNWKEGESK.M	Y	79.43	1464.7612	12	0.4	733.3882	2	38.97	5	F5:10919	17112021_RID_2349_DP5.raw					2.829E7
C.YQAVDEPK.T	N	56.88	948.4552	8	0.4	475.2351	2	22.42	5	F5:5214	17112021_RID_2349_DP5.raw					4.8543E
K.TWADAEKF.C	N	39.07	966.4446	8	0.5	484.2298	2	41.22	5	F5:11753	17112021_RID_2349_DP5.raw					2.1565E
																total 3 peptides

TRINITY_DN588
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAAYLLAVAI LFCIQGWPSG TVQGQVRPFL DVYQRSACQA RETLVSILQE YPDEISDIFR PSCVAVLRCS GCCTDESLKC

 81  TPVGKHTVDM QIMRVNPRTQ SSKMEVMKFT EHTACECRPR RKQGEPDGPK EKPRRGGVRA KFPFDQLLTP GAL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
K.HTVDMQIMR.V	N	70.60	1129.5372	9	-0.2	565.7758	2	32.19	7	F7:8643	17112021_RID_2349_DP7.raw	1.1569E6	7.4694E
K.HTVDMQIM(+15.99)R.V	N	68.64	1145.5321	9	1.0	573.7739	2	24.76	7	F7:6460	17112021_RID_2349_DP7.raw	5.9884E5	4.6869E
K.HTVDM(+15.99)QIM(+15.99)R.V	N	62.07	1161.5271	9	0.3	581.7710	2	18.23	7	F7:3828	17112021_RID_2349_DP7.raw	7.9377E4	3.9021E
K.HTVDM(+15.99)QIMR.V	N	58.98	1145.5321	9	0.3	573.7735	2	23.27	7	F7:5513	17112021_RID_2349_DP7.raw	7.1174E5	
Q.GQVRPFLDVYQR.S	Y	55.17	1476.7837	12	-0.3	493.2684	3	42.18	7	F7:12014	17112021_RID_2349_DP7.raw		
R.PFLDVYQR.S	N	49.73	1036.5342	8	-0.1	519.2743	2	44.38	7	F7:12800	17112021_RID_2349_DP7.raw		
V.RPFLDVYQR.S	N	45.90	1192.6353	9	1.7	597.3259	2	38.63	7	F7:10909	17112021_RID_2349_DP7.raw		
R.TQSSKMEVMK.F	N	45.83	1167.5627	10	-0.2	584.7885	2	20.39	1	F1:5202	12112021_RID_2349_DP1.raw	1.9831E5	

TRINITY_DN588
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAAYLLAVAI LFCIQGWPSG TVQGQVRPFL DVYQRSACQA RETLVSILQE YPDEISDIFR PSCVAVLRCS GCCTDESLKC
 81  TPVGKHTVDM QIMRVNPRTQ SSKMEVMKFT EHTACECRPR RKQGEPDGPK EKPRRGGVRA KFPFDQLLTP GAL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
K.HTVDMQIMR.V	N	70.60	1129.5372	9	-0.2	565.7758	2	32.19	7	F7:8643	17112021_RID_2349_DP7.raw	1.1569E6	7.4694E
K.HTVDMQIM(+15.99)R.V	N	68.64	1145.5321	9	1.0	573.7739	2	24.76	7	F7:6460	17112021_RID_2349_DP7.raw	5.9884E5	4.6869E
K.HTVDM(+15.99)QIM(+15.99)R.V	N	62.07	1161.5271	9	0.3	581.7710	2	18.23	7	F7:3828	17112021_RID_2349_DP7.raw	7.9377E4	3.9021E
K.HTVDM(+15.99)QIMR.V	N	58.98	1145.5321	9	0.3	573.7735	2	23.27	7	F7:5513	17112021_RID_2349_DP7.raw	7.1174E5	
Q.GQVRPFLDVYQR.S	Y	55.17	1476.7837	12	-0.3	493.2684	3	42.18	7	F7:12014	17112021_RID_2349_DP7.raw		
R.PFLDVYQR.S	N	49.73	1036.5342	8	-0.1	519.2743	2	44.38	7	F7:12800	17112021_RID_2349_DP7.raw		
V.RPFLDVYQR.S	N	45.90	1192.6353	9	1.7	597.3259	2	38.63	7	F7:10909	17112021_RID_2349_DP7.raw		
R.TQSSKMEVMK.F	N	45.83	1167.5627	10	-0.2	584.7885	2	20.39	1	F1:5202	12112021_RID_2349_DP1.raw	1.9831E5	

TRINITY_DN6726
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLTAEDRRL LQASVAKLGC RLEDIGADAL NRLLIVYPSS KTYFSHYNLS PGSKDIIHQG EKVGKALDSA LKHLDDIRGT
 81  LSQLSDLHAY NLRVDPVNFK LLSKCFHVSL ATHLRNEYNA CCCLAWDKFL EQVSDMLCEK YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.LEDIGADALNR.L	Y	73.37	1185.5989	11	0.8	593.8072	2	39.17	7	F7:11029	17112021_RID_2349_DP7.raw					
K.TYFSHYNLSPGSK.D	Y	66.43	1499.7045	13	1.3	750.8605	2	36.62	7	F7:10149	17112021_RID_2349_DP7.raw					
N.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.6379
R.LLIVYPSSK.T	Y	41.76	1018.6063	9	-0.6	510.3101	2	43.65	7	F7:12634	17112021_RID_2349_DP7.raw					
																total 4 peptides

TRINITY_DN3927
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MTPVAGFFLS LSVGVALALD ASLMPPNYNM TEEGARLFAN DYNTTGEIVF FESISASWNY NTNLTNHNAQ KQIAAFLKEQ
  81  EFTELWGGKA KENYGKIWQN FTDPQLKKII SSIQTLGPSN LPVQKREEYN TILSEMDSIY STATVCLPNQ NSHCWALEPD

 161  ITDIMATSHS YRKLLYAWEG WHNSAGNPLR SKYEKFVSLS NEAYKMDGFQ DTGAYWRSWY DSPTFKEDLE QLYQQLEPLY
 241  LNLHAYVRRK LYNQYGSKYI NLKGPIPAHL LGNMWAQQWN NIYDIMVPFA NKSHLDVTNT MKQKNWNTTH MFRVSEEFFT
 321  SLGMFGMPPE FWEKSMLEKP TDGRDVVCHA SAWDFFNRKD FRIKQCTTVT MEQLFTVHHE MGHVQYYLQY KNQPISFRSG
 401  ANPGFHEAIG DVMSLSVSTP IHLKKIELLT HVTEDKESDI NYLLKMALEK IAFLPFGYLI DQWRWDVFSG RTPPSRYNFD
 481  WWYLRTKYQG ICPPIARNET NFDPGAKYHI PGNTPYIRYF VSFILQFQFH KALCQAANHT GDLHTCDIYN SKDAGQKLSE
 561  AMKAGSSQPW QDILQQLTGT NKMDASALLE YFKPVMEWLE KENGKNNETL GWPEFDWRPP VPEGYPEGLD KITDEAEAKA
 641  FLEKYNSTAE VVWNAYTEAS WTYNVNITEH NKQIMLEKNF AMSNHTLQNG LKARQFDSTD FKDPKIKRIL KKLSDIERSA
 721  LPEAELKEYN QLLSEMETIY SVAKICGKDT DCKALDPDLT DTMAKSRDYD ELLNTWKGWR DASGKKIRRH YERYVQLSNK

 801  AAKLNGHADN GAYWRSLYET PTFETDLENI WYQLQPLYFN LHAYVRRALY KKYGEKRINL KGPIPAHLLG NMWAQSWANI
 881  FDLVMPFPDA TKVDATPAMI QQGWTPTKMF EQSDSFFKSL GLIPMPPEFW EKSMLEKPSD GREVVCHASA WDFYNRKDFR

 961  IKQCTVVNMD DLITVHHEMG HVQYFLQYKD QPISFREGAN PGFHEAIGDV MALSVSTPKH LKNIKLLEHL EDNIESDINY
1041  LMSIALDKIA FLPFGYLIDQ WRWKVFDGRI PKKEYNQQWW NLRLKYQGLC PPTPRSEEDF DPGAKFHIPA NVPYVRYFVS

1121  FIIQFQFHQA LCKAAGHTGP LYKCDIYQSK EAGKILGDAL KLGFSRPWPE VMQNITGQPN MSAEGLLTYF EPLTKWLIEK
1201  NRQNNETLGW PEYTWQAYAG GSEVNFLGMS LSSSQIETGQ WILLAIGLML LITTIALSVI YFRRRRKGFK SSSEMELK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.MFEQSDSFFK.S	Y	55.53	1264.5433	10	0.0	633.2789	2	49.45	1	F1:15052	12112021_RID_2349_DP1.raw	2.2329E5			7.
K.VDATPAMIQQGWTPTK.M	Y	54.44	1742.8661	16	1.2	872.4414	2	48.04	1	F1:14537	12112021_RID_2349_DP1.raw	9.7075E4			
K.IISSIQTLGPSNLPVQK.R	Y	50.12	1794.0250	17	1.2	898.0209	2	50.02	1	F1:15184	12112021_RID_2349_DP1.raw	4.8193E5			
R.SEEDFDPGAK.F	Y	47.52	1093.4563	10	0.2	547.7355	2	27.98	1	F1:7775	12112021_RID_2349_DP1.raw	1.7742E5			
K.ALDPDLTDTMAK.S	Y	45.71	1289.6173	12	1.4	645.8168	2	42.38	4	F4:12047	17112021_RID_2349_DP4.raw				4.

total 5 peptides

TRINITY_DN2452
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  SETHYSPDGR EITTNPPVED HCYYYGRIQN DADSTASISA CNGLKGHFQL QGKTYLIEPL KIPESEAHAI YKYENIEKED
  81  EGPKKCGVTQ TNWESDEPIK KASQLVATSE QRRFPKRYIK LVVVADHRMF TKYNNDSTAI RTWIYEMINT VNEVFLPLNI

 161  HVPLVGVEIW CKEDLISVVS SSGDTLDSFG EWRKRDLLNR KRHDNAYLLT AIDFHG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area
A.SQLVATSEQR.R	N	61.23	1117.5728	10	0.3	559.7938	2	23.26	1	F1:6173	12112021_RID_2349_DP1.raw	8.3452E4	1.575
D.TLDSFGEWR.K	N	52.86	1109.5142	9	0.7	555.7648	2	47.54	2	F2:13529	12112021_RID_2349_DP2.raw		8.079
K.EDLISVVSSSGDTLDSFGEWR.K	Y	47.78	2298.0652	21	-0.1	1150.0398	2	71.06	3	F3:21425	17112021_RID_2349_DP3.raw		
K.LVVVADHR.M	Y	47.56	907.5239	8	-0.4	454.7690	2	23.50	2	F2:5404	12112021_RID_2349_DP2.raw	5.2396E5	1.799
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5	

total 5 pept

P82475.2
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
                                                                                  66
   1  QVRPFPDVYQ RSACQARETL VSILQEYPDE ISDIFRPSCV AVLRCSGCCT DESLKCTPVG KHTVDMQIMR VNPRTQSSKM  C

  81  EVMKFTEHTA CECRPRRKQG EPDGPKEKPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F
K.HTVDMQIMR.V	N	70.60	1129.5372	9	-0.2	565.7758	2	32.19	7	F7:8643	17112021_RID_2349_DP7.raw	1.1569E6	7.4694E
K.HTVDMQIM(+15.99)R.V	N	68.64	1145.5321	9	1.0	573.7739	2	24.76	7	F7:6460	17112021_RID_2349_DP7.raw	5.9884E5	4.6869E
K.HTVDM(+15.99)QIM(+15.99)R.V	N	62.07	1161.5271	9	0.3	581.7710	2	18.23	7	F7:3828	17112021_RID_2349_DP7.raw	7.9377E4	3.9021E
K.HTVDM(+15.99)QIMR.V	N	58.98	1145.5321	9	0.3	573.7735	2	23.27	7	F7:5513	17112021_RID_2349_DP7.raw	7.1174E5	
R.PFPDVYQR.S	Y	50.92	1020.5028	8	0.4	511.2589	2	39.38	7	F7:11284	17112021_RID_2349_DP7.raw		
R.TQSSKMEVMK.F	N	45.83	1167.5627	10	-0.2	584.7885	2	20.39	1	F1:5202	12112021_RID_2349_DP1.raw	1.9831E5	
V.RPFPDVYQR.S	Y	42.95	1176.6040	9	0.6	589.3096	2	33.46	7	F7:9070	17112021_RID_2349_DP7.raw		
Q.VRPFPDVYQR.S	Y	42.10	1275.6724	10	0.8	638.8440	2	37.19	7	F7:10314	17112021_RID_2349_DP7.raw		

TRINITY_DN30
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MMQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPQKVT ALPKGAIQQL EQKYEDAIQY QFKVKGEPVV LHLEKNKDFF
 81 PENYSETHYS PDDREITTNP PVEDHCYYHG HIQNEADSTA SISACNGLKG HFKLQGETYL IEPLKIPDSE AHAVYKYENI
161 EKEDEAPKMC GVTQTNWESD EPIKKASQLV ATSEQRRNFQ KYIELVIVVD NVMFRKYTGN STAIRTRIYE IVNTLNLIYT
241 ILNIHIALVY LEIWSKGDLI NVQSVVDVTL NSFGEWRERD LLNRKRHDNA QLLTGMTFDL STLGITFFAG MCQAYRSVGV
321 IQYYSTTNLR IAVTMAHEIG HNVGMKHDTY YCTCGGNSCI MSAVLSNQPS KPFSNCSNHD YQRYLTRYKP KCIFNPPLRT
401 DIVSRAVCGN EIWEEGEECD CGSPGNCQNP CCNAATCKLT PGSQCADGEC CDQCRIQTAG TVCRRARDEC DVPEHCTGQS
481 AECPVDGFHA NGQPCQNNNG YCYNGNCPIL TDQCISLFGS RATVAEDSCF QENQKGSYYG YCRKENGRKI PCAPEDEKCG
561 RLYCSYNLLG NHIPCYPYYR RNREDKGMVD HGTKCGDGKV CSNRHCVDVT TAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
A.SQLVATSEQR.R	N	61.23	1117.5728	10	0.3	559.7938	2	23.26	1	F1:6173	12112021_RID_2349_DP1.raw	8.3452E4	1.5759E4	
N.SFGEWRER.D	N	55.07	1065.4991	8	0.1	533.7569	2	31.26	2	F2:7954	12112021_RID_2349_DP2.raw	6.0265E6	2.4122E6	
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5		7.2185E4
R.SVGVIQYYSTTNLR.I	Y	42.94	1599.8257	14	1.7	800.9214	2	48.04	2	F2:13703	12112021_RID_2349_DP2.raw		0	
R.ERDLLNR.K	N	42.02	914.4933	7	-0.1	458.2539	2	23.23	1	F1:6203	12112021_RID_2349_DP1.raw	1.8049E7	3.2804E6	
												total 5 peptides		

JAS04521.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81 LFQKRRFQSP RVLFSTQPPP LSRDEQNVDN ANSLNRNIRA KREDHPVHNR GEYSVCDSVN VWVANKTTAT DIRGNVVTVM
                                                          213
161 VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF
241 G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

AAG12169.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMLCYTLII TLLIGIWAAP KSEDNVPLGS PATSDLSVTS CTKTHEALKT SRNTDQHYPA PKKEEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDD ANSLNRNIRA KREDHPVHNR GEYSVCDSVN VWVANKTTAT DIRGNVVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDTACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAG46131.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

BAN82015.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRS KREDHPVHNR GEYSVCDSVS VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNLNNNVY KQYFFETKCR NPNPVPTGCR GIDSRHWNSY CTTTHTFVRA LTMEGNQASW RFIRIDTACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS04781.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAI10407.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS05454.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHNQ GEYSVCDSVD VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTETFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS04703.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAG46130.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAA98018.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS YAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVD VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

AAG30924.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNIDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                  213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS05315.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFV SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHNR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                  213
161  VNVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTETFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAV01886.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII TFLTGIWAAP KSEDNVPLGS PATSDLSVTS CTKTHEALKT SRNTDQHYPA PKKEEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHNR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                  213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDTACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS04865.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAA98019.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS YAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAA94888.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS04864.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

AFJ49196.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAS04866.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAG43651.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAV48424.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAG46132.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSFNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

JAA97946.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVPLGS PATSDLSDTS YAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSVDN ANSLNRNIRA KREDHPVHKR GEYSVCDSVN VWVANKTTAT DIRGNLVTVM
                                                                   213
161  VDVNINNNVY KQYFFETKCR NPNPVPTGCR GIDARHWNSY CTTTNTFVKA LTMEGNQASW RFIRIDSACV CVISRKNENF

241  G
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

BAP39981.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  NQYRGGAVLQ ATSTDCQLPV VQQFDPDWLQ VDSAFHPSEN LALLENIKVH SVMSMLCYTL IIAFLIGIWA APKSEDNVPL
 81  GSPATSDLSD TSCAKTHEAL KTSRNTDQHY PAPKKAEDQE FGSAANIIVD PKLFQKRRFQ SPRVLFSTQP PPLSRDEQSV
161  DNANSLNRNI RSKREDHPVH NRGEYSVCDS VSVWVANKTT ATDIRGNLVT VMVDVNLNNN VYKQYFFETK CRNPNPVPTG
                                   265
241  CRGIDSRHWN SYCTTTHTFV RALTMEGNQA SWRFIRIDTA CVCVISRKNE NFG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

BAN82142.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MGNQYRGGAV LQATSTDCQL PVVQQFDPDW LQVDSAFHPS ENLALLENIK VHSVMSMLCY TLIIAFLIGI WAAPKSEDNV
 81  PLGSPATSDL SDTSCAKTYE ALKTSRNTDQ HYPAPKKAED QEFGSAANII VDPKLFQKRR FQSPRVLFST QPPPLSRDEQ
161  SVDNANSLNR NIRAKREDHP VHNRGEYSVC DSVNVWVANK TTATDIRGNL VTVMVDVNLN NNVYKQYFFE TKCRNPNPVP
                                   267
241  TGCRGIDSRH WNSYCTTTHT FVKALTMEGN QASWRFIRID AACVCVISRK NENFG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
K.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.NPNPVPTGC(+57.02)R.G	Y	58.52	1110.5240	10	0.3	556.2695	2	23.20	5	F5:5451	17112021_RID_2349_DP5.raw			
K.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			

CAP74088.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  GNVDFDSESP RKPEIQNEII DLHNSLRRSV NPTASNMLKM EWYPEAAANA ERWAFRCILS HSPRDSRVIG GIKCGENIYM
 81  STSPMKWTAI IHKWHGEEKD FVYGQGASPA NAVVGHYTQI VWYKSYRSGC AAAYCPSSEY KYFYVCQYCP AGNMQGKTAT
161  PYTSGPPCGD CPSACDNGLC TNPCTHEDKF TNCKDLVKQG CNNNYLKTNC PASCSCHNEI I
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
K.MEWYPEAAANAER.W	N	85.56	1536.6667	13	0.5	769.3411	2	45.12	7	F7:13118	17112021_RID_2349_DP7.raw				4
K.M(+15.99)EWYPEAAANAER.W	N	83.36	1552.6616	13	0.4	777.3384	2	40.79	7	F7:11501	17112021_RID_2349_DP7.raw				1
R.SVNPTASNMLK.M	N	53.18	1160.5859	11	0.3	581.3004	2	32.34	4	F4:8661	17112021_RID_2349_DP4.raw				1
R.SVNPTASNM(+15.99)LK.M	N	48.77	1176.5808	11	0.8	589.2982	2	24.27	4	F4:5833	17112021_RID_2349_DP4.raw				9
K.WTAIIHK.W	Y	45.59	867.4966	7	-0.1	434.7556	2	29.95	7	F7:7835	17112021_RID_2349_DP7.raw				3

total 5 pe

ADJ67475.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MMQVLLVTIS LAVFPYQGSS IILESGNVND YEVVYPQKVT AMPKGAVKQP EQKYEDTMQY EFEVNGEPVV LHLEKNKILF
 81  SEDYSETHYY PDGREITTNP PVEDHCYYHG HIQNDGHSSA SISACNGLKG HFKLRGEMYF IEPLKLSNNE AHAVYKYENI
161  EKEDETPKMC GVTQTNWESD KPIKKASQLV STSAQFNKAF IELIIIVDHS MAKKCNSTAT NTKIYEIVNS ANEIFNPLNI
241  HVTLIGVEFW CDRDLINVTS SADETLDSFG EWRASDLMTR KSHDNALLFT DMRFDLNTLG ITFLAGMCQA YRSVGIVQVQ
321  GNRNFKTAVI MAHELSHNLG MYHDGKNCIC NDSSCVMSPV LSDQPSKLFS NCSIHDYQRY LTRYKPKCIL YPPLRKDIVS
401  PPVCGNEIWE EGEECDCGSP ADCQNPCCDA ATCKLKPGAE CGNGLCCYQC KIKTAGTVCR RARNECDVPE HCTGQSAECP
481  RDQLQQNGQP CQNNRGYCYN GDCPIMRNQC ISLFGSRATV AKDSCFQENL KGSYYGYCRK ENGRKIPCAP QDVKCGRLFC
561  LNNSPRNKNP CNMHYSCMDQ HKGMVDPGTK CEDGKVCNNK RQCVDVNTAY QSTTGFSQI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.SVGIVQVQGNR.N	N	67.43	1155.6360	11	0.4	578.8255	2	32.21	1	F1:9249	12112021_RID_2349_DP1.raw	4.3558E5	7.7637E4		
A.SQLVSTSAQFNK.A	Y	53.22	1308.6674	12	1.0	655.3416	2	32.83	7	F7:8869	17112021_RID_2349_DP7.raw				
E.TLDSFGEWR.A	N	52.86	1109.5142	9	0.7	555.7648	2	47.54	2	F2:13529	12112021_RID_2349_DP2.raw		8.0796E4		

total 3 peptides

XP_034278116.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MCPRLVTSLL GLVLGINVCA GFTAHRVRRS GEFGEEGPDS VLSDSPWIST YGSCKNRCFE LDEAEPPVCR CDNLCKSYSS
 81  CCVDFDELCL KTAGGWECTK ERCGETRNED HACHCSEDCL ARGDCCSNYQ VVCKGDTPWV MDDCEDIRTP VCPAGFLHPP
161  LIIFSVDGFR ASYMKKGEKV MRNIEKLRSC GTHAPYMRPV YPTKTFPNLY TLATGLYPES HGIIGNSMYD PVFDAIFNLR
241  GREKFNHRWW GGQPIWITAA KQGVKAGTFF WSNVIPYERR ILTILQWLTL ADNERVYTRP YAYAFYSDQP DMAGHRYGPF
321  SSEMLGPLRD IDKILGQLMD GLKQLNLHRC ANIIFVGDHG MEDVTCERTE YLSNYLSNVD DITLIPGTLG RIRAKANSNV
401  KFDPKAIVAN LTCKKPDQHF KPYLKQHLPK RLHYANNRRI EDIHLLVERR WHVAKRPGDV FKKITGKCYF HGDHGYDNKI
481  NSMQTVFLGY GPSFKYKTKV PPFENIELYN LMCDLLGLKP APNNGTHGSL NHLLRSSTYR PTMPEEVARP LHPVATTPSS
561  DYDLGCSCDD KNRLDELSRR PYSKGTEART YTGGEGFYTN DPENVLPEDG CVPPPEKHLL YGRPAVLFRI KYSLLHHHDF
641  ESGYSETFQM PLWTSYTISK QAETSGVPDQ VISCVRPDLR ISPSNSQSCT AYRVDRQMSY GFLFPPQLSS SVETKYDAFL
721  ITNVIPMYPA FKKVWNYFQR ILVKRYAIER NGVNVISGPI FDYDFDGLHD TPDKIKLYVE GSSIPVPTHY YSIITSCLDF
801  TQPADKCDGP LSVLAYIFPH RPDNDESCNN SSEDESRWVE ELLKMHTARV RDIEQITGLD FYRKTSRSYS EILSLKTYLH
881  TFESEI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
R.DIEQITGLDFYR.K	Y	62.33	1468.7197	12	1.2	735.3680	2	63.03	3	F3:18811	17112021_RID_2349_DP3.raw			1.9643E5	5

total 5 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
R.VRDIEQITGLDFYR.K	Y	47.90	1723.8893	14	-0.3	575.6368	3	54.41	3	F3:16066	17112021_RID_2349_DP3.raw			2.9338E5	
K.VWNYFQR.I	Y	44.68	1011.4926	7	0.6	506.7539	2	44.05	4	F4:12592	17112021_RID_2349_DP4.raw			5.0789E5	7
K.TYLHTFESEI	Y	43.72	1238.5819	10	0.0	620.2982	2	49.94	3	F3:14629	17112021_RID_2349_DP3.raw			1.7866E6	
K.YDAFLITNVIPMYPAFK.K	Y	43.12	2002.0273	17	1.4	1002.0223	2	75.89	3	F3:22897	17112021_RID_2349_DP3.raw			1.7377E5	

total 5 peptides

TRINITY_DN12452
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 CLPGWSFYEG NCYKAFDEPK SWVDAEKFCQ KQSNGKHLAS IEGLGKANFV AKLVSETLRE PQIHVWIGLR DQSERQQCSS

 81 HWTDGSAVSY EKVVRFTKCF GLNKKTDYRT WVGLRCG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
K.HLASIEGLGK.A	Y	68.91	1023.5713	10	-0.9	512.7925	2	32.04	7	F7:8674	17112021_RID_2349_DP7.raw			3.0778E5	5.5199E5	2.
K.LVSETLREPQIH.V	Y	46.38	1420.7673	12	1.1	711.3917	2	35.06	6	F6:9422	17112021_RID_2349_DP6.raw					

total 2 peptides

AUS82489.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVLIRVLANL LILQLSYAQK SSELVVGGDE CNINEHRSLV VLFNSSSFLC AGTLINEEWV LTAAHCDSKN FQMQLGVHSK
                                   112
 81 KVLNEDEQTR DPKEKFICPN KKKDDENDKD IMLIRLDSPV SNSEHIAPLS LPSSPPSVGS VCRIMGWGTI TPTKETYPDV

161 PRCANINILD HAVCRAAYPW NPVASTTLCA GTQQGGKDTC RGDSGGPLIC NGQFQGIVSW GGHPCGQAHE PGVYTKVFDY
241 TDWIQSIIAG NTDATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.VLNEDEQTR.D	N	63.83	1102.5254	9	0.5	552.2703	2	19.87	4	F4:4313	17112021_RID_2349_DP4.raw			2.2851E5	9.6629E
K.KVLNEDEQTR.D	N	55.31	1230.6204	10	0.8	616.3179	2	16.73	4	F4:3273	17112021_RID_2349_DP4.raw			2.4946E4	2.7539E
R.IMGWGTITPTK.E	Y	45.91	1203.6322	11	1.2	602.8241	2	49.08	4	F4:14280	17112021_RID_2349_DP4.raw				1.0911E
N.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6	
N.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6	

total 5 pepti

JAA98031.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVLIRVLAHL LILQLSYAQK SSELVVGGHP CNINEHRSLV VLFNSSGFLC AGTLINEEWV LTAAHCDSKN FQMQLGVHSK
                                   112
 81 KVLNEDEQTR DPKEKFICPN KKKDDEKDKD IMLIRLDSPV SNSEHIAPLS LPSSPPSVGS VCRIMGWGTI TPTKETYPDV

161 PHCANINILD HAVCRAAYPW NPVASTTLCA GTQQGGKDTC RADSGGPLIC NGEIQGIVSW GGHPCGQARE PGVYTKVFDY
241 TDWIQSIIAG KKTVNCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.VLNEDEQTR.D	N	63.83	1102.5254	9	0.5	552.2703	2	19.87	4	F4:4313	17112021_RID_2349_DP4.raw			2.2851E5	9.6629E
K.KVLNEDEQTR.D	N	55.31	1230.6204	10	0.8	616.3179	2	16.73	4	F4:3273	17112021_RID_2349_DP4.raw			2.4946E4	2.7539E
R.IMGWGTITPTK.E	Y	45.91	1203.6322	11	1.2	602.8241	2	49.08	4	F4:14280	17112021_RID_2349_DP4.raw				1.0911E
K.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6	

total 5 pepti

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6	

total 5 pepti

TRINITY_DN471
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  INVTSAANVT LKSFGEWRER DLLSRKRHDN AQLLTDIDFD GPTIGMAHMF SMCHSERSVG IIQDYSPIDR VVATIMAHEM

 81  GHNLGLNHDE KQCNCGANSC IMSAVLSDP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	A
R.SVGIIQDYSPIDR.V	Y	83.80	1461.7463	13	0.4	731.8807	2	48.90	2	F2:13984	12112021_RID_2349_DP2.raw	1.3286E6	4.833E6	1.0924E7	2
K.SFGEWRER.D	N	55.07	1065.4991	8	0.1	533.7569	2	31.26	2	F2:7954	12112021_RID_2349_DP2.raw	6.0265E6	2.4122E6		

total 2 peptides

ADN04917.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LLLQLSHAQK SSELVVGGDE CNINEHRSLV FLYNSSFGCG GTLINQEWVL SAAHCDMENM RIYLGWHNFS

 81  LPNMNQKRRV AKEKFFCLSS KNYTEWDKDI MLIKMNRPVT YSTHVAPLSL PSSPPSVGSV CRIMGWGAIT SPNETYPDVP

161  HCANINILNY TVCRAAHPWL PAQSRTLCAG ILQGGIDTCK GDSGGPLICN GQIQGIVSWG DNPCAQPLKP GHYTNVFDYT

241  DWIQSIIAGN TTATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
R.AAHPWLPAQSR.T	Y	82.07	1232.6414	11	-1.1	617.3273	2	33.26	1	F1:9553	12112021_RID_2349_DP1.raw	6.4186E7	1.0631E7	3.0723
E.WDKDIMLIK.M	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
E.WDKDIM(+15.99)LIK.M	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157

total 3 pe

E0Y419.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LLLQLSHAQK SSELVVGGDE CNINEHRSLV FLYNSSFGCG GTLINQEWVL SAAHCDMENM RIYLGWHNFS

 81  LPNMNQKRRV AKEKFFCLSS KNYTEWDKDI MLIKMNRPVT YSTHVAPLSL PSSPPSVGSV CRIMGWGAIT SPNETYPDVP

161  HCANINILNY TVCRAAHPWL PAQSRTLCAG ILQGGIDTCK GDSGGPLICN GQIQGIVSWG DNPCAQPLKP GHYTNVFDYT

241  DWIQSIIAGN TTATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area
R.AAHPWLPAQSR.T	Y	82.07	1232.6414	11	-1.1	617.3273	2	33.26	1	F1:9553	12112021_RID_2349_DP1.raw	6.4186E7	1.0631E7	3.0723
E.WDKDIMLIK.M	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
E.WDKDIM(+15.99)LIK.M	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157

total 3 pe

AEH59582.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVSLGS LATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSMEF LDNADSLNRN IRAKRGTHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV
                                                                   216
161  TVMVDVNLNN NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKN

241  DNL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

QBF53420.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVHSVMSMLC YTLIIAFLIG IWAAPKSEDN VSLGSPATPD LSDTSCAKTH EALKTSRNTD QHYPAPKKAE DQEFGSAANI
 81  IVDPKLFQKR RFQSPRVLFS TQPPPLSRDE QSVEFLDSAD SLNRNIRTKR GTHPVHNRGE FSVCDSVSVW VANKTTATDI
                                                                  221
161  RGNVVTVMVD VNLNNNVYRQ YFFETKCKNP NPVPSGCRGI DAKHWNSYCT TTDTFVRALT MEGNQASWRF IRIDTACV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

QHR82782.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSMLCYTLII AFLIGIWAAP KSEDNVSLGS PATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK
 81  LFQKRRFQSP RVLFSTQPPP LSRDEQSMEF LDNADSLNRN IRAKRGTHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV
                                                                   216
161  TVMVDVNLNN NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKN

241  DNLG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

TRINITY_DN1356
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLIRWAGGWG QLGKAYVKRW EAIAPCANFV CCQFAVSVTE RLPERSFIKA SHLSTLLLVS CWSQGMVHSV MSMLCYTLII
 81 AFLIGIWAAP KSEDNVSLGS PATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK LFQKRRFQSP
161 RVLFSTQPPP LSRDEQSLEF LDNADSLNRN IRAKRETHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV TVMVDVNLNN
                                                                                 286
241 NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

TRINITY_DN1356
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:


```
  1 MLIRWAGGWG QLGKAYVKRW EAIAPCANFV CCQFAVSVTE RLPERSFIKA SHLSTLLLVS CWSQGMVHSV MSMLCYTLII
 81 AFLIGIWAAP KSEDNVSLGS PATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK LFQKRRFQSP
161 RVLFSTQPPP LSRDEQSLEF LDNADSLNRN IRAKRETHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV TVMVDVNLNN
                                                                                 286
241 NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

TRINITY_DN1356
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLIRWAGGWG QLGKAYVKRW EAIAPCANFV CCQFAVSVTE RLPERSFIKA SHLSTLLLVS CWSQGMVHSV MSMLCYTLII
 81 AFLIGIWAAP KSEDNVSLGS PATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK LFQKRRFQSP
161 RVLFSTQPPP LSRDEQSLEF LDNADSLNRN IRAKRETHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV TVMVDVNLNN
                                                                                 286
241 NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			
														total 4

TRINITY_DN1356
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1  MLIRWAGGWG QLGKAYVKRW EAIAPCANFV CCQFAVSVTE RLPERSFIKA SHLSTLLLVS CWSQGMVHSV MSMLCYTLII
  81  AFLIGIWAAP KSEDNVSLGS PATPDLSDTS CAKTHEALKT SRNTDQHYPA PKKAEDQEFG SAANIIVDPK LFQKRRFQSP
 161  RVLFSTQPPP LSRDEQSLEF LDNADSLNRN IRAKRETHPV HNRGEFSVCD SVSVWVANKT TATDIRGNVV TVMVDVNLNN

                                                                   288
 241  NVYRQYFFET KCKNPNPVPS GCRGIDAKHW NSYCTTTDTF VRALTMEGNQ ASWRFIRIDT ACVCVISRKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.ALTMEGNQASWR.F	N	80.22	1362.6350	12	0.4	682.3251	2	38.77	5	F5:10781	17112021_RID_2349_DP5.raw			4.2979E5
R.ALTM(+15.99)EGNQASWR.F	N	77.11	1378.6299	12	0.1	690.3223	2	36.09	5	F5:10910	17112021_RID_2349_DP5.raw			
R.QYFFETK.C	N	55.57	961.4545	7	0.5	481.7347	2	40.77	5	F5:11527	17112021_RID_2349_DP5.raw			
M.VDVNLNNNVYR.Q	Y	38.71	1318.6630	11	1.1	660.3395	2	37.96	5	F5:10607	17112021_RID_2349_DP5.raw			

total 4

TRINITY_DN180
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1  MSMNGSHPRL NTLGRMVRAE SGPDMRYDMN SHMMMGGGGG GGGGSGHTHK MYYVQKSYVG DVNSEGYTQN GTATVSRRQN
  81  TIQDLLQVCS DCLMRAELIV QPELKYGDGI QISRNRELEE CFTQATEHME MLEALIREMR QMGQPCELYQ KRLLQLQEQM

 161  RALYKAISVP RVRRASSKGG GYSSQSASGW DEYTRRVTSE CLNWMRQQKT EMELIKWGFD AAAIEQQIAE HRRFHNSIGD
 241  YRWHLDKVKT DLREKAAVHQ LEEEYEYLLR FSFERMDQLR QLQNIIQATS REIMWINDCE EEELLYDWSD RNTDIARKQE

 321  AFSKRMSQLE VKEKELNKLK QECDQLVLSQ HPASDKIEAY MDTLQTQWSW ILQITKCIDV HLKENAAYFQ FFEEAQSTEN
 401  YLKNLQDVIR KRFICDKNMS LQVLLEQIKE LEAEREKILE YKRQVQNLVN KSKKIVQLKP RNPEYKSNKP IILRALCDYK

 481  QDLKTMRKGD ECILKDNSER SKWHVTGPGG LDMLVPSVSL IIPPPNPLAV DLATKIEQYY DAIMALWNQL YINMKSLVSW
 561  HYCLIDIEKI KVMTIAKLKT MRREDYQRII SDLEIHYQEF IRNSQGSEMF GDEDKRTMQT RITDAQKHYQ TLVIQLPDLQ
 641  TQPLPPQPTI VTEVINIEKQ EAWLLMELQK LRRQIENCEL RMVQRTPFQL DQGATHNLCV RISELESIQN ESQSLAEILN
 721  RQNDYLPNFR GSEKYHYLQS EISALFQKLE NINGISACYL DSLNALRSLL QAILQTDDMI RVFEIRLTEE DTLSLDPDKV
 801  EAYRACLKKM KADLSMKKSL LGTLEAELQK ALQVHSQSSQ TYPHYELDLG KFADRVSQLT DRWQRLEKQL DDRSWDLEKQ
 881  VKQLRIYRDL YQALNKWICD ARRRQETIEA MKLGDVSTVM RYLQEQKNLH SEVTSKRDRV EEVIKHAEVC SLAIKDYELQ
 961  AAAYSSGLET LLNIPVKRSM VQSPSGLILQ EAGEIQSRYI ELLTRSGDYY KFLSEMLKSL EDIKMKSTRI ELLEEELRLA
1041  KDANSDSNNK HKFLEQNLQK YQVECSQLKA KFISLEEMKR QVEMDSSTSK QNLDKCYAQI KDLNDRITRL TYEIEDEKRK
1121  RKLLEDRYEQ QKADFDQLQK TRQNEKETLG WQKIESEKII KEKEYELERL RVLLQDEGTR KRECENELAK VRNQFNEEMS
1201  NIKNKYETEI NIKKTTIHQI AAQKEDDAKN LRTQIDRLQR ENRDLKDEIV RLNEAILDTT EQRRRAEENI LQQKACGSEV
1281  LQQKQQIELE LKQIIQLRND DNTRYKQALE DATSTIHEKV KEIERLKIQL KEEAKSRWEL ENELAKTSHR IQESKNQCNH
1361  VMQERETLLI KIKTLEQDKA RLLRLEEDLN RTKGMLESES RLKVRLENEK QQILNDLNQW KSQYSRKEET IRKTESERDK
1441  SEREKSALLI EIERLQAEIK RIEERYRCRL EETSRKSQAE METERLRLQR EIEKLKQRPK GAPRGTQTEE DLMIDPSKLL
1521  FSGLRKKITA VQLYECQLID KCTLDKLLRG QKSVEEVAAE LEPYLRGAGA IAGASLNTKV KFSLVEAKRK QLLTPENTVL
1601  LLEAQAATGG VIDPHRNELL SVDSAVARDL IDFDDREQIY MAEKAITGFK DPFSGKMMPV AEAMKKNLVD RETGLRLLEA
1681  QLASGGIVDP INSIFLPKDI ALSRGLIDRD LYRALNNPSK PLIDPLSKVA ISYMKLREKC RVEQHTGLLL LPVQKRNTSF
1761  QGIRKQISVS ELVESGIIRE STANELETGA ITVEEVTDRI KDFLQGSSCI AGIYNEATGE KLGVYQAMKI GLVRPGTALE
1841  LLEAQAATGF IVDPVNNLRL PVEEAYKRGL VGIEFKEKLL SAERAVTGYK DPETGNIISL FQAMNKELIE KGHGIRLLEA

1921  QIATGGIIDP KESHRLPVHT AYQRGYFNEE LNDILSDPSD DTKGFFDPNT EENLTYLQLK GRCKIDESTR LCLLPLREKK

2001  KVVQTSQKNT LRKRRVVIVD PDTNKEMSVQ EAYNKGLIDY STYMELSDQE CEWEEITTTG SDGSTRVVLV DRKTGHQYDI
2081  EDALDKGLVD RKFFDQYRSG SLSLTQFADM IASRNGGDEV FRQESIIRSP TVVSVKSSSI LLKSSSGSFS DSPEETTPIA
2161  AIFDTENLEK ISISEAVQRG IVDTITAQRL LEAQTCTGGI LCPTTGQRLS LQDAVAQGII DHEMATRLKP AQKAFLGFEG
2241  IKGRKRMSAA EAVKEKWLPY EAGQRFLEFQ FITGGLIDPE VHGRISTEEA IRKGLIDGRT SQRLQDISNY AKILTCPKTK
2321  LKISYREAMN RSMVEDQTGL KLLEASSVSS KGISSPYNVS SAPGSRSGSR SGSRSGSRSG SRRGSFDAGT SSSYSYSYTA
2401  VSSNSSLGR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.LLEAQIATGGIIDPK.E	Y	62.51	1537.8715	15	0.8	769.9436	2	51.54	6	F6:15197	17112021_RID_2349_DP6.raw				
R.QLQNIIQATSR.E	Y	51.48	1270.6993	11	0.2	636.3571	2	38.60	2	F2:10594	12112021_RID_2349_DP2.raw		1.0785E4		1.2228

total 4 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
K.SNKPIILR.A	Y	44.33	939.5865	8	-0.1	470.8005	2	24.97	6	F6:6034	17112021_RID_2349_DP6.raw				
R.AELIVQPELK.Y	Y	42.71	1138.6597	10	-0.2	570.3370	2	43.74	6	F6:12471	17112021_RID_2349_DP6.raw				

total 4 peptides

TRINITY_DN180
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MSMNGSHPRL NTLGRMVRAE SGPDMRYDMN SHMMMGGGGG GGGGSGHTHK MYYVQKSYVG DVNSEGYTQN GTATVSRRQN
  81 TIQDLLQVCS DCLMRAELIV QPELKYGDGI QISRNRELEE CFTQATEHME MLEALIREMR QMGQPCELYQ KRLLQLQEQM
 161 RALYKAISVP RVRRASSKGG GYSSQSASGW DEYTRRVTSE CLNWMRQQKT EMELIKWGFD AAAIEQQIAE HRRFHNSIGD
 241 YRWHLDKVKT DLREKAAVHQ LEEEYEYLLR FSFERMDQLR QLQNIIQATS REIMWINDCE EEELLYDWSD RNTDIARKQE
 321 AFSKRMSQLE VKEKELNKLK QECDQLVLSQ HPASDKIEAY MDTLQTQWSW ILQITKCIDV HLKENAAYFQ FFEEAQSTEN
 401 YLKNLQDVIR KRFICDKNMS LQVLLEQIKE LEAEREKILE YKRQVQNLVN KSKKIVQLKP RNPEYKSNKP IILRALCDYK
 481 QDLKTMRKGD ECILKDNSER SKWHVTGPGG LDMLVPSVSL IIPPPNPLAV DLATKIEQYY DAIMALWNQL YINMKSLVSW
 561 HYCLIDIEKI KVMTIAKLKT MRREDYQRII SDLEIHYQEF IRNSQGSEMF GDEDKRTMQT RITDAQKHYQ TLVIQLPDLQ
 641 TQPLPPQPTI VTEVINIEKQ EAWLLMELQK LRRQIENCEL RMVQRTPFQL DQGATHNLCV RISELESIQN ESQSLAEILN
 721 RQNDYLPNFR GSEKYHYLQS EISALFQKLE NINGISACYL DSLNALRSLL QAILQTDDMI RVFEIRLTEE DTLSLDPDKV
 801 EAYRACLKKM KADLSMKKSL LGTLEAELQK ALQVHSQSSQ TYPHYELDLG KFADRVSQLT DRWQRLEKQL DDRSWDLEKQ
 881 VKQLRIYRDL YQALNKWICD ARRRQETIEA MKLGDVSTVM RYLQEQKNLH SEVTSKRDRV EEVIKHAEVC SLAIKDYELQ
 961 AAAYSSGLET LLNIPVKRSM VQSPSGLILQ EAGEIQSRYI ELLTRSGDYY KFLSEMLKSL EDIKMKSTRI ELLEEELRLA
1041 KDANSDSNNK HKFLEQNLQK YQVECSQLKA KFISLEEMKR QVEMDSSTSK QNLDKCYAQI KDLNDRITRL TYEIEDEKRK
1121 RKLLEDRYEQ QKADFDQLQK TRQNEKETLG WQKIESEKII KEKEYELERL RVLLQDEGTR KRECENELAK VRNQFNEEMS
1201 NIKNKYETEI NIKKTTIHQI AAQKEDDAKN LRTQIDRLQR ENRDLKDEIV RLNEAILDTT EQRRRAEENI LQQKACGSEV
1281 LQQKQQIELE LKQIIQLRND DNTRYKQALE DATSTIHEKV KEIERLKIQL KEEAKSRWEL ENELAKVRNS YDEEIISLKN
1361 KYETEINITK TTINQVTVKK EEEASNYRAQ LDNAVRENRS LCEELRRLKN TLSQTTENLR KVEESVHQQK SIGSEISQKK
1441 QQLEKELKQT VQKFTEEIAH YKQSLDEAGR TIKEKNKEIE KNRKLLDAEI SQRKSMEEEN IHLQRIQYDL EKANINAKET
1521 ISRLKVQEQE LGRLKSEYER LAQDKKGKDQ ESTRLQSTVK ELQHQKHMLE EELNRQSRIV ADETSKRKNA EEELEAMRRT
1601 LRDQAVKITN LTQQIEEISI VKKRSEDDLR HQREVLDNHM REKQRYMEEI RKYTSEVESL RRQMVQEQEN LKQAHIRNEH
1681 LQKAIEDKSK SLNECKIEIE RLQCLTENLT KEHLMLEEEL RNLRLEYDDL RRGRSEVDEE KNAAILDLKN QLQTSNKHAL
1761 ELQGVINGLQ KERENLRQEI EKFQKQALET SHRIQESKNQ CNHVMQERET LLIKIKTLEQ DKARLLRLEE DLNRTKGMLE
1841 SESRLKVRLE NEKQQILNDL NQWKSQYSRK EETIRKTESE RDKSEREKSA LLIEIERLQA EIKRIEERYR CRLEETSRKS
1921 QAEMETERLR LQREIEKLKQ RPKGAPRGTQ TEEDLMIDPS KLLFSGLRKK ITAVQLYECQ LIDKCTLDKL LRGQKSVEEV
2001 AAELEPYLRG AGAIAGASLN TKVKFSLVEA KRKQLLTPEN TVLLLEAQAA TGGVIDPHRN ELLSVDSAVA RDLIDFDDRE
2081 QIYMAEKAIT GFKDPFSGKM MPVAEAMKKN LVDRETGLRL LEAQLASGGI VDPINSIFLP KDIALSRGLI DRDLYRALNN
2161 PSKPLIDPLS KVAISYMKLR EKCRVEQHTG LLLLPVQKRN TSFQGIRKQI SVSELVESGI IRESTANELE TGAITVEEVT
2241 DRIKDFLQGS SCIAGIYNEA TGEKLGVYQA MKIGLVRPGT ALELLEAQAA TGFIVDPVNN LRLPVEEAYK RGLVGIEFKE
2321 KLLSAERAVT GYKDPETGNI ISLFQAMNKE LIEKGHGIRL LEAQIATGGI IDPKESHRLP VHTAYQRGYF NEELNDILSD
2401 PSDDTKGFFD PNTEENLTYL QLKGRCKIDE STRLCLLPLR EKKKVVQTSQ KNTLRKRRVV IVDPDTNKEM SVQEAYNKGL
2481 IDYSTYMELS DQECEWEEIT TTGSDGSTRV VLVDRKTGHQ YDIEDALDKG LVDRKFFDQY RSGSLSLTQF ADMIASRNGG
2561 DEVFRQESII RSPTVVSVKS SSILLKSSSG SFSDSPEETT PIAAIFDTEN LEKISISEAV QRGIVDTITA QRLLEAQTCT
2641 GGILCPTTGQ RLSLQDAVAQ GIIDHEMATR LKPAQKAFLG FEGIKGRKRM SAAEAVKEKW LPYEAGQRFL EFQFITGGLI
2721 DPEVHGRIST EEAIRKGLID GRTSQRLQDI SNYAKILTCP KTKLKISYRE AMNRSMVEDQ TGLKLLEASS VSSKGISSPY
2801 NVSSAPGSRS GSRSGSRSGS RSGSRRGSFD AGTSSSYSYS YTAVSSNSSL GR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.LLEAQIATGGIIDPK.E	Y	62.51	1537.8715	15	0.8	769.9436	2	51.54	6	F6:15197	17112021_RID_2349_DP6.raw				
R.QLQNIIQATSR.E	Y	51.48	1270.6993	11	0.2	636.3571	2	38.60	2	F2:10594	12112021_RID_2349_DP2.raw		1.0785E4		1.2228
K.SNKPIILR.A	Y	44.33	939.5865	8	-0.1	470.8005	2	24.97	6	F6:6034	17112021_RID_2349_DP6.raw				
R.AELIVQPELK.Y	Y	42.71	1138.6597	10	-0.2	570.3370	2	43.74	6	F6:12471	17112021_RID_2349_DP6.raw				

total 4 peptides

XP_034285002.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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   1 MSINGSHPRL NTLGRMVRSE SGPDMRYDMN SHMMMGGGGG GGGGGGSSHA HKMYYVQKCY VGDINSEGYT QNGTATVSRR
  81 QNTIQDLLQA CSDCLMRAEL IVQPELKYGD GIQISRNREL EDCFGQANEH MDILDGLIRE MRQMGQPCDL YQKRLLQLQE

 161 QMRALYKAIS VPRVRRASSK GGGYSSQSAS GWDEYTRRVT SECLNWMRQQ KTEMELVKWG FDAAAIEQQI AEHRRFHNSI
 241 GDYRWHLDKV KTDLREKAAV HQLEEEYEYL LRFSFERMDQ LRQLQNIIQA TSREIMWIND CEEEELLYDW SDRNTDIARK

 321 QEVFSKRMSQ LEVKEKELNK LKQECDQLVL SQHPASDKIE AYMDTLQTQW SWILQITKCI DVHLKENAAY FQFFEEAHST
 401 ENYLKNLQDA IRKRFICDKN MSLQVLLEQI KELEAEREKI LEYKRQVQNL VNKSKKIVQL KPRNPEYKSN KPIILRALCD

 481 YKQDLKTMRK GDECILKDNS ERSKWHVTGP GGLDMLVPSV SLIIPPPNPL AVDLATKIEQ YYDAIMALWN QLYINMKSLV
 561 SWHYCMIDVE KIRAMTIAKL KTMRREDYQR IIADLEIHYQ EFIRNSQGSE MFGDDDKRNM QTQITDAQKH YQTLVMTLPR
 641 QTQTGPPIVT EVITIEKEKQ EAWLLMELQK LRRQIENCEF RMVQRTPFQL DQGASHNLSV RISELESIQI ESQSMAEALN
 721 RQKDYLPNFR GSEKYHYLQS EISALFQKLE NINGVSACYL DSLNALRSLL QAILQTDDVI RVFEIRLTEE DTLSLDPDKV
 801 EGYRVCLKKM KADLTMKKSL LGTLEAELQK ALQVHSQSSQ TYPHYDLDLG KFADRVSQLR DRWQRLEKQL DDRSWDLEKQ
 881 VKQLRIYREL YQALNKWICD ARRRQDTIEA MKLGDVSTVM RYLQEQKNLH SEITSKRDRV EDVVKNAEVC SLAIKDYELQ
 961 AAAYSSGLET LLNIPVKRSM VQSPSGLILQ EAGEIQSRYI ELLTRSGDYY KFLSEMLKSL EDIKMKSTRI ELLEEELRLA
1041 KDANSDSNNK HKFLEQNLQK YQVECSQLKA KFISLEEMKR QVEMDGSTAK QNLDKCYAQI KDLNERITRL TYEIEDEKRK
1121 RKLLEDRYDQ QKSDFDQLQK TRHNEKETLG WQKIESEKII KEKEYEIERL RVLLQDEGTR KRECENELAK TSHRIQESKS
1201 QCNHIMQERE TLLVKIKTLE QDKARLLRLE EDLNRTKGML ESESRLKARL ENEKQQILND LNQWKSQYSR KEETIRKTEC
1281 ERDKSEREKS SLLIEIERLQ AEIKRIEERY RCRLEETSRK SQAEMETERS RWQKEIDKLK KRPYGAHRST QTEEDLMIDP
1361 SKLLFNGLRK KITAVQLYEC QLIDKCTLDK LLRGQKSVEE VAAELEPYLK GAGAIAGASL NTKEKYSLVE AKRKQLLTPE
1441 NTILLLEAQA ATGGVIDPHR NELLSVDSAV ARDLVDFDDR EQIYMAEKAI TGFKDPFSGK TMSVAEAIKK NLVDRETGMR
1521 LLEAQLASGG IVDPINSIFL PKDIALSRGL IDRDLYRALN NPSKPLIDPL SKNAISYMKL RERCRIEPHT GLLLLPVQKR
1601 SMSFQGIRKL ITVSELVDSG IIRESTANEL ETGAITVEEV TDRIKDFLQG SSCIAGIYNE ATGEKLGVYQ AMKIGLVRPG
1681 TALELLEAQA ATGFIVDPVN NLRLPVEEGY KRGLVGIEFK EKLLSAERAV TGYRDPETGN IISLFQAMNK ELIEKGHGVR
1761 LLEAQIATGG IIDPKESHRL PVHTAYQRGY FNEELNDILS DPSDDTKGFF DPNTEENLTY LQLKGRCKID ELTGLCLLPL

1841 REKKKVVQTS QKNTLRKRRV VIVDPDTSKE MSVQEAYNKG LIDYSTYMEL SDQECEWEEI TTTGSDGSTR VVLVDRKTGH
1921 QYDIEDAIEK GLVDRKFFEQ YRSGSLSLTQ FADMIASRNG GDEVFKHESI IRSPTVLSVK SSSILLKSSS GSFSDSPEEA
2001 TPIAAIFDTE NLEKISIPEA VQRGIVDTIT AQRLLEAQSC TGGIICPTTG QRLSLQDAVA QGIIDHEMAT RLKPAQKAFL
2081 GFEGIKGRKR MSAAEAVKEK WLPYEAGQRF LEFQFITGGL VDPEVHGRIS TEEAIRKGLI DGRTSQRLQD IGNYAKILTC
2161 PKTKLKISYR EAMNRSMVED QTGLRLLEAS SVSSKGISSP YNVSSAPGSR SGSRSGSRSG SRSGSRRGSF DAGTSSSYSY
2241 SYTTVSSGSL GR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.LLEAQIATGGIIDPK.E	Y	62.51	1537.8715	15	0.8	769.9436	2	51.54	6	F6:15197	17112021_RID_2349_DP6.raw				
R.QLQNIIQATSR.E	Y	51.48	1270.6993	11	0.2	636.3571	2	38.60	2	F2:10594	12112021_RID_2349_DP2.raw		1.0785E4		1.2228
K.SNKPIILR.A	Y	44.33	939.5865	8	-0.1	470.8005	2	24.97	6	F6:6034	17112021_RID_2349_DP6.raw				
R.AELIVQPELK.Y	Y	42.71	1138.6597	10	-0.2	570.3370	2	43.74	6	F6:12471	17112021_RID_2349_DP6.raw				

total 4 peptides

XP_034285001.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MSINGSHPRL NTLGRMVRSE SGPDMRYDMN SHMMMGGGGG GGGGGGSSHA HKMYYVQKCY VGDINSEGYT QNGTATVSRR
  81 QNTIQDLLQA CSDCLMRAEL IVQPELKYGD GIQISRNREL EDCFGQANEH MDILDGLIRE MRQMGQPCDL YQKRLLQLQE
 161 QMRALYKAIS VPRVRRASSK GGGYSSQSAS GWDEYTRRVT SECLNWMRQQ KTEMELVKWG FDAAAIEQQI AEHRRFHNSI
 241 GDYRWHLDKV KTDLREKAAV HQLEEEYEYL LRFSFERMDQ LRQLQNIIQA TSREIMWIND CEEEELLYDW SDRNTDIARK
 321 QEVFSKRMSQ LEVKEKELNK LKQECDQLVL SQHPASDKIE AYMDTLQTQW SWILQITKCI DVHLKENAAY FQFFEEAHST
 401 ENYLKNLQDA IRKRFICDKN MSLQVLLEQI KELEAEREKI LEYKRQVQNL VNKSKKIVQL KPRNPEYKSN KPIILRALCD
 481 YKQDLKTMRK GDECILKDNS ERSKWHVTGP GGLDMLVPSV SLIIPPPNPL AVDLATKIEQ YYDAIMALWN QLYINMKSLV
 561 SWHYCMIDVE KIRAMTIAKL KTMRREDYQR IIADLEIHYQ EFIRNSQGSE MFGDDDKRNM QTQITDAQKH YQTLVMTLPR
 641 QTQTGPPIVT EVITIEKEKQ EAWLLMELQK LRRQIENCEF RMVQRTPFQL DQGASHNLSV RISELESIQI ESQSMAEALN
 721 RQKDYLPNFR GSEKYHYLQS EISALFQKLE NINGVSACYL DSLNALRSLL QAILQTDDVI RVFEIRLTEE DTLSLDPDKV
 801 EGYRVCLKKM KADLTMKKSL LGTLEAELQK ALQVHSQSSQ TYPHYDLDLG KFADRVSQLR DRWQRLEKQL DDRSWDLEKQ
 881 VKQLRIYREL YQALNKWICD ARRRQDTIEA MKLGDVSTVM RYLQEQKNLH SEITSKRDRV EDVVKNAEVC SLAIKDYELQ
 961 AAAYSSGLET LLNIPVKRSM VQSPSGLILQ EAGEIQSRYI ELLTRSGDYY KFLSEMLKSL EDIKMKSTRI ELLEEELRLA
1041 KDANSDSNNK HKFLEQNLQK YQVECSQLKA KFISLEEMKR QVEMDGSTAK QNLDKCYAQI KDLNERITRL TYEIEDEKRK
1121 RKLLEDRYDQ QKSDFDQLQK TRHNEKETLG WQKIESEKII KEKEYEIERL RVLLQDEGTR KRECENELAK VRNQFNEEMS
1201 NIKNKYETEI NIKKTTIHQI AAQKEDDAKN LRTQIERLQR ENRDLKDEIV RLNEAILDTT EQRRRAEENV LQQKACGSEV
1281 IQQKQQIELE LKQIIQLRND DNTRYKQALE DATSTIHEKV KELERLKIQL QEEAKSRWEL ENELAKTSHR IQESKSQCNH
1361 IMQERETLLV KIKTLEQDKA RLLRLEEDLN RTKGMLESES RLKARLENEK QQILNDLNQW KSQYSRKEET IRKTECERDK
1441 SEREKSSLLI EIERLQAEIK RIEERYRCRL EETSRKSQAE METERSRWQK EIDKLKKRPY GAHRSTQTEE DLMIDPSKLL
1521 FNGLRKKITA VQLYECQLID KCTLDKLLRG QKSVEEVAAE LEPYLKGAGA IAGASLNTKE KYSLVEAKRK QLLTPENTIL
1601 LLEAQAATGG VIDPHRNELL SVDSAVARDL VDFDDREQIY MAEKAITGFK DPFSGKTMSV AEAIKKNLVD RETGMRLLEA
1681 QLASGGIVDP INSIFLPKDI ALSRGLIDRD LYRALNNPSK PLIDPLSKNA ISYMKLRERC RIEPHTGLLL LPVQKRSMSF
1761 QGIRKLITVS ELVDSGIIRE STANELETGA ITVEEVTDRI KDFLQGSSCI AGIYNEATGE KLGVYQAMKI GLVRPGTALE
1841 LLEAQAATGF IVDPVNNLRL PVEEGYKRGL VGIEFKEKLL SAERAVTGYR DPETGNIISL FQAMNKELIE KGHGVRLLEA
1921 QIATGGIIDP KESHRLPVHT AYQRGYFNEE LNDILSDPSD DTKGFFDPNT EENLTYLQLK GRCKIDELTG LCLLPLREKK
2001 KVVQTSQKNT LRKRRVVIVD PDTSKEMSVQ EAYNKGLIDY STYMELSDQE CEWEEITTTG SDGSTRVVLV DRKTGHQYDI
2081 EDAIEKGLVD RKFFEQYRSG SLSLTQFADM IASRNGGDEV FKHESIIRSP TVLSVKSSSI LLKSSSGSFS DSPEEATPIA
2161 AIFDTENLEK ISIPEAVQRG IVDTITAQRL LEAQSCTGGI ICPTTGQRLS LQDAVAQGII DHEMATRLKP AQKAFLGFEG
2241 IKGRKRMSAA EAVKEKWLPY EAGQRFLEFQ FITGGLVDPE VHGRISTEEA IRKGLIDGRT SQRLQDIGNY AKILTCPKTK
2321 LKISYREAMN RSMVEDQTGL RLLEASSVSS KGISSPYNVS SAPGSRSGSR SGSRSGSRSG SRRGSFDAGT SSSYSYSYTT
2401 VSSGSLGR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.LLEAQIATGGIIDPK.E	Y	62.51	1537.8715	15	0.8	769.9436	2	51.54	6	F6:15197	17112021_RID_2349_DP6.raw				
R.QLQNIIQATSR.E	Y	51.48	1270.6993	11	0.2	636.3571	2	38.60	2	F2:10594	12112021_RID_2349_DP2.raw		1.0785E4		1.2228
K.SNKPIILR.A	Y	44.33	939.5865	8	-0.1	470.8005	2	24.97	6	F6:6034	17112021_RID_2349_DP6.raw				
R.AELIVQPELK.Y	Y	42.71	1138.6597	10	-0.2	570.3370	2	43.74	6	F6:12471	17112021_RID_2349_DP6.raw				

total 4 peptides

XP_034285000.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MSINGSHPRL NTLGRMVRSE SGPDMRYDMN SHMMMGGGGG GGGGGGSSHA HKMYYVQKCY VGDINSEGYT QNGTATVSRR
  81 QNTIQDLLQA CSDCLMRAEL IVQPELKYGD GIQISRNREL EDCFGQANEH MDILDGLIRE MRQMGQPCDL YQKRLLQLQE
 161 QMRALYKAIS VPRVRRASSK GGGYSSQSAS GWDEYTRRVT SECLNWMRQQ KTEMELVKWG FDAAAIEQQI AEHRRFHNSI
 241 GDYRWHLDKV KTDLREKAAV HQLEEEYEYL LRFSFERMDQ LRQLQNIIQA TSREIMWIND CEEEELLYDW SDRNTDIARK
 321 QEVFSKRMSQ LEVKEKELNK LKQECDQLVL SQHPASDKIE AYMDTLQTQW SWILQITKCI DVHLKENAAY FQFFEEAHST
 401 ENYLKNLQDA IRKRFICDKN MSLQVLLEQI KELEAEREKI LEYKRQVQNL VNKSKKIVQL KPRNPEYKSN KPIILRALCD
 481 YKQDLKTMRK GDECILKDNS ERSKWHVTGP GGLDMLVPSV SLIIPPPNPL AVDLATKIEQ YYDAIMALWN QLYINMKSLV
 561 SWHYCMIDVE KIRAMTIAKL KTMRREDYQR IIADLEIHYQ EFIRNSQGSE MFGDDDKRNM QTQITDAQKH YQTLVMTLPR
 641 QTQTGPPIVT EVITIEKEKQ EAWLLMELQK LRRQIENCEF RMVQRTPFQL DQGASHNLSV RISELESIQI ESQSMAEALN
 721 RQKDYLPNFR GSEKYHYLQS EISALFQKLE NINGVSACYL DSLNALRSLL QAILQTDDVI RVFEIRLTEE DTLSLDPDKV
 801 EGYRVCLKKM KADLTMKKSL LGTLEAELQK ALQVHSQSSQ TYPHYDLDLG KFADRVSQLR DRWQRLEKQL DDRSWDLEKQ
 881 VKQLRIYREL YQALNKWICD ARRRQDTIEA MKLGDVSTVM RYLQEQKNLH SEITSKRDRV EDVVKNAEVC SLAIKDYELQ
 961 AAAYSSGLET LLNIPVKRSM VQSPSGLILQ EAGEIQSRYI ELLTRSGDYY KFLSEMLKSL EDIKMKSTRI ELLEEELRLA
1041 KDANSDSNNK HKFLEQNLQK YQVECSQLKA KFISLEEMKR QVEMDGSTAK QNLDKCYAQI KDLNERITRL TYEIEDEKRK
1121 RKLLEDRYDQ QKSDFDQLQK TRHNEKETLG WQKIESEKII KEKEYEIERL RVLLQDEGTR KRECENELAK VRNQFNEEMS
1201 NIKNKYETEI NIKKTTIHQI AAQKEDDAKN LRTQIERLQR ENRDLKDEIV RLNEAILDTT EQRRRAEENV LQQKACGSEV
1281 IQQKQQIELE LKQIIQLRND DNTRYKQALE DATSTIHEKV KELERLKIQL QEEAKSRWEL ENELAKVRNS YDEEIISLKN
1361 KYETEINITK TTINQVTVKK EEEASNYRAQ LDNAVRENRS LCEEIRRLKN TLSQTTENLR KVEENAHQQK AIGSEISQKK
1441 QHLEKELKQT VQKFTEEIAH YKQSLDEAGR TLKEKNKEIE KNRKLLDAEI CQRKSLEEEN IRLQRIQYDL EKANINATET
1521 ISRLKVQEQD LGRLKSEYER LAQDKKGKDQ ESTRLQSTIK EMQHQKHMLE EELNRQSRIA ADETSKRKNA EEELEAMRRT
1601 LREQAVKITN LTQQIEEISI VKKRSEDDLR HQREVLDSQM RDKQRYMEEI RKYTSEVEAL RRQMVQEQEN LKQAHIRNEH
1681 LQKAIEDKSK SLNECKIEIE RLQCLTENLT KEHLMLEEEL RNLRLEYDDL RRGRSEVDEE KNATILDLKN QLQTSNKHAL
1761 ELQGVINGLQ KERENLRQEI EKFQKQALET SHRIQESKSQ CNHIMQERET LLVKIKTLEQ DKARLLRLEE DLNRTKGMLE
1841 SESRLKARLE NEKQQILNDL NQWKSQYSRK EETIRKTECE RDKSEREKSS LLIEIERLQA EIKRIEERYR CRLEETSRKS
1921 QAEMETERSR WQKEIDKLKK RPYGAHRSTQ TEEDLMIDPS KLLFNGLRKK ITAVQLYECQ LIDKCTLDKL LRGQKSVEEV
2001 AAELEPYLKG AGAIAGASLN TKEKYSLVEA KRKQLLTPEN TILLLEAQAA TGGVIDPHRN ELLSVDSAVA RDLVDFDDRE
2081 QIYMAEKAIT GFKDPFSGKT MSVAEAIKKN LVDRETGMRL LEAQLASGGI VDPINSIFLP KDIALSRGLI DRDLYRALNN
2161 PSKPLIDPLS KNAISYMKLR ERCRIEPHTG LLLLPVQKRS MSFQGIRKLI TVSELVDSGI IRESTANELE TGAITVEEVT
2241 DRIKDFLQGS SCIAGIYNEA TGEKLGVYQA MKIGLVRPGT ALELLEAQAA TGFIVDPVNN LRLPVEEGYK RGLVGIEFKE
2321 KLLSAERAVT GYRDPETGNI ISLFQAMNKE LIEKGHGVRL LEAQIATGGI IDPKESHRLP VHTAYQRGYF NEELNDILSD
2401 PSDDTKGFFD PNTEENLTYL QLKGRCKIDE LTGLCLLPLR EKKKVVQTSQ KNTLRKRRVV IVDPDTSKEM SVQEAYNKGL
2481 IDYSTYMELS DQECEWEEIT TTGSDGSTRV VLVDRKTGHQ YDIEDAIEKG LVDRKFFEQY RSGSLSLTQF ADMIASRNGG
2561 DEVFKHESII RSPTVLSVKS SSILLKSSSG SFSDSPEEAT PIAAIFDTEN LEKISIPEAV QRGIVDTITA QRLLEAQSCT
2641 GGIICPTTGQ RLSLQDAVAQ GIIDHEMATR LKPAQKAFLG FEGIKGRKRM SAAEAVKEKW LPYEAGQRFL EFQFITGGLV
2721 DPEVHGRIST EEAIRKGLID GRTSQRLQDI GNYAKILTCP KTKLKISYRE AMNRSMVEDQ TGLRLLEASS VSSKGISSPY
2801 NVSSAPGSRS GSRSGSRSGS RSGSRRGSFD AGTSSSYSYS YTTVSSGSLG R
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F
R.LLEAQIATGGIIDPK.E	Y	62.51	1537.8715	15	0.8	769.9436	2	51.54	6	F6:15197	17112021_RID_2349_DP6.raw				
R.QLQNIIQATSR.E	Y	51.48	1270.6993	11	0.2	636.3571	2	38.60	2	F2:10594	12112021_RID_2349_DP2.raw		1.0785E4		1.2228
K.SNKPIILR.A	Y	44.33	939.5865	8	-0.1	470.8005	2	24.97	6	F6:6034	17112021_RID_2349_DP6.raw				
R.AELIVQPELK.Y	Y	42.71	1138.6597	10	-0.2	570.3370	2	43.74	6	F6:12471	17112021_RID_2349_DP6.raw				

total 4 peptides

JAG67762.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MVHWSAEEKH MITSLWSKVD VAEVGGATLG KLMVVYPWTQ RFFAHFGNLS GPSAICGNPQ VKAHGKKVLT SFGEAIKHLD
  81 NVKETFAKLS ELHCDKLHVD PENFKLLGNI LIIVLAGHHG KEFTPCVHAT FQKLTNVVAH SLARRYH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area A
K.VLTSFGEAIK.H	N	61.56	1063.5913	10	-0.1	532.8029	2	41.86	7	F7:11920	17112021_RID_2349_DP7.raw					

total 5 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
K.LMVVYPWTQR.F	Y	58.78	1291.6747	10	0.4	646.8448	2	54.62	7	F7:16340	17112021_RID_2349_DP7.raw					
M.VHWSAEEK.H	N	52.31	984.4665	8	0.7	493.2408	2	21.02	7	F7:4832	17112021_RID_2349_DP7.raw					
K.LM(+15.99)VVYPWTQR.F	Y	50.62	1307.6697	10	0.1	654.8422	2	51.02	7	F7:15084	17112021_RID_2349_DP7.raw					
K.KVLTSFGEAIK.H	N	48.51	1191.6863	11	1.5	596.8513	2	36.27	7	F7:10106	17112021_RID_2349_DP7.raw					

total 5 peptides

JAG67761.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVHWSAEEKH MITSLWSKVD VAEVGGATLG KLMVVYPWTQ RFFAHFGNLS GPSAICGNPQ VKAHGKKVLT SFGEAIKHLD
 81  NVKETFAKLS ELHCDKLHVD PENFKLLGNI LIIVLAGHHG KEFTPCVHAT FQKLTNVVAH SLARRYH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
K.VLTSFGEAIK.H	N	61.56	1063.5913	10	-0.1	532.8029	2	41.86	7	F7:11920	17112021_RID_2349_DP7.raw					
K.LMVVYPWTQR.F	Y	58.78	1291.6747	10	0.4	646.8448	2	54.62	7	F7:16340	17112021_RID_2349_DP7.raw					
M.VHWSAEEK.H	N	52.31	984.4665	8	0.7	493.2408	2	21.02	7	F7:4832	17112021_RID_2349_DP7.raw					
K.LM(+15.99)VVYPWTQR.F	Y	50.62	1307.6697	10	0.1	654.8422	2	51.02	7	F7:15084	17112021_RID_2349_DP7.raw					
K.KVLTSFGEAIK.H	N	48.51	1191.6863	11	1.5	596.8513	2	36.27	7	F7:10106	17112021_RID_2349_DP7.raw					

total 5 peptides

XP_015679695.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MKGRLKGAWI LSLLLAGLFQ PNLGQEQQEI LTGLQLSHQH DEARSCLHAQ PIPDRAKVDC YDSVQGSAHD YGALSLSGEY
 81  IPFRNYAGKY ILFVNVATYU GLTGQYLELN ALQTSLGIDR LVILGFPCNQ FGKQEPGQNS EILQGIKHVR PGGGFVPNFQ
161  LFQKGDVNGE NEQRIYTFLK NSCPPVVENF GDPAKLFWSP LKTHDIKWNF EKFLVNPQGK PVMRWFQRTN VSSVKNDIIR
241  YMRKNG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F
K.QEPGQNSEILQGIK.H	Y	85.68	1539.7893	14	0.2	770.9021	2	41.31	5	F5:11775	17112021_RID_2349_DP5.raw				1.0455E
R.TNVSSVKNDIIR.Y	Y	68.80	1344.7361	12	0.4	673.3756	2	32.75	1	F1:9508	12112021_RID_2349_DP1.raw	2.0856E5			

total 2 peptides

ADP88559.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LVLQLSYAQK SSELVVGGHP CNIYEHHFLA FMYNSSGFMC SGTLINQQWV LSAAHCDMEN MHIYLGLHSF
                                     112
 81  KLPNKDQKKR VAKEKFFCLS SKSYTKWDKD IMLIKLNKPV TYSTHIASLS LPSNPPRVGS VCRIMGWGSI TSPKKILPFV
161  PHCANINIVP YTVCRVIYRP LPEQSRTLCA GVSGRRIGSC LGDSGGPLIC NGQIQGIVSW GSDPCVNRGA PSIYTKVFDY
241  TDWIHSIIAG NTAATCPS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.IM(+15.99)GWGSITSPK.K	Y	51.75	1191.5958	11	1.1	596.8058	2	41.44	7	F7:11830	17112021_RID_2349_DP7.raw			
S.LSLPSNPPR.V	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			

total 5

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
R.IMGWGSITSPK.K	Y	40.20	1175.6008	11	-0.1	588.8076	2	47.84	4	F4:13831	17112021_RID_2349_DP4.raw			

total 5

E5L0E3.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LVLQLSYAQK SSELVVGGHP CNIYEHHFLA FMYNSSGFMC SGTLINQQWV LSAAHCDMEN MHIYLGLHSF
                                        112
 81  KLPNKDQKKR VAKEKFFCLS SKSYTKWDKD IMLIKLNKPV TYSTHIASLS LPSNPPRVGS VCRIMGWGSI TSPKKILPFV
161  PHCANINIVP YTVCRVIYRP LPEQSRTLCA GVSGRRIGSC LGDSGGPLIC NGQIQGIVSW GSDPCVNRGA PSIYTKVFDY
241  TDWIHSIIAG NTAATCPS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.51
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.11
R.IM(+15.99)GWGSITSPK.K	Y	51.75	1191.5958	11	1.1	596.8058	2	41.44	7	F7:11830	17112021_RID_2349_DP7.raw			
S.LSLPSNPPR.V	N	41.33	979.5450	9	-0.2	490.7797	2	34.94	7	F7:9564	17112021_RID_2349_DP7.raw			
R.IMGWGSITSPK.K	Y	40.20	1175.6008	11	-0.1	588.8076	2	47.84	4	F4:13831	17112021_RID_2349_DP4.raw			

total 5

P0DJL5.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  68
  1  DQDCLPGWSY FEKYCYKVFQ VKKNWEDAEK FCTEEVKDGH LISLHSNEEV EFMTSLAFPI LKYDIVWMGL RNFWRDCPWK
 81  WSDDAKLDYK AWSDEPNCYG AMTTDYQWLR WNCNDPRYFV CKSPA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are F4
K.YDIVWMGLR.N	Y	67.55	1151.5797	9	0.6	576.7975	2	60.05	7	F7:18181	17112021_RID_2349_DP7.raw			1.1179E5	
K.YDIVWM(+15.99)GLR.N	Y	64.95	1167.5747	9	0.9	584.7952	2	53.11	7	F7:15854	17112021_RID_2349_DP7.raw				
K.WSDDAKLDYK.A	Y	58.85	1239.5771	10	0.7	620.7963	2	32.61	7	F7:8789	17112021_RID_2349_DP7.raw				
M.TTDYQWLR.W	Y	57.81	1081.5193	8	0.1	541.7670	2	42.38	7	F7:12141	17112021_RID_2349_DP7.raw				

total 4 pep

AMB36341.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                                  91
  1  MGRLISISFG LLVVFLSLSG TGADQDCLPG WSYFEKYCYK VFKVKKNWEE AEKFCTEEVK DGHLISLHSN EEVEFMTSLA
 81  FPILKYDIVW MGLRNFWRDC PWKWSDDAKL DYKAWSDEPN CYGAKTTDYQ WLRWNCNDPR YFVCKSLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are F4
K.YDIVWMGLR.N	Y	67.55	1151.5797	9	0.6	576.7975	2	60.05	7	F7:18181	17112021_RID_2349_DP7.raw			1.1179E5	
K.YDIVWM(+15.99)GLR.N	Y	64.95	1167.5747	9	0.9	584.7952	2	53.11	7	F7:15854	17112021_RID_2349_DP7.raw				
K.WSDDAKLDYK.A	Y	58.85	1239.5771	10	0.7	620.7963	2	32.61	7	F7:8789	17112021_RID_2349_DP7.raw				
K.TTDYQWLR.W	Y	57.81	1081.5193	8	0.1	541.7670	2	42.38	7	F7:12141	17112021_RID_2349_DP7.raw				

total 4 pep

TRINITY_DN554
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LSAGKEGRKT MGRFISVSFS LLVVFLSLSG TEAGFCCPNG WSSFGQHCYK VIEPLKNWTD AEKFCTEQHK GSHLASIHSS
                                    101
 81  EEEAFVVKLA FQTLKSEILW MGLSKVWNEC NWGWSNGAKL KYEAWAEESY CVYFSS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.SEILWMGLSK.V	Y	72.18	1162.6056	10	0.3	582.3102	2	55.68	7	F7:16745	17112021_RID_2349_DP7.raw		9.069E4	8.6025E5
K.SEILWM(+15.99)GLSK.V	Y	64.35	1178.6006	10	-0.5	590.3073	2	48.60	7	F7:14258	17112021_RID_2349_DP7.raw		8.1789E3	
H.SSEEEAFVVK.L	N	41.08	1123.5397	10	-0.5	562.7769	2	34.73	6	F6:9332	17112021_RID_2349_DP6.raw			
K.LAFQTLK.S	N	39.89	819.4854	7	0.6	410.7502	2	37.72	7	F7:10543	17112021_RID_2349_DP7.raw			

total 4

TRINITY_DN554
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LSAGKEGRKT MGRFISVSFS LLVVFLSLSG TEAGFCCPNG WSSFGQHCYK VIEPLKNWTD AEKFCTEQHK GSHLASIHSS
                                    101
 81  EEEAFVVKLA FQTLKSEILW MGLSKVWNVG CL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.SEILWMGLSK.V	Y	72.18	1162.6056	10	0.3	582.3102	2	55.68	7	F7:16745	17112021_RID_2349_DP7.raw		9.069E4	8.6025E5
K.SEILWM(+15.99)GLSK.V	Y	64.35	1178.6006	10	-0.5	590.3073	2	48.60	7	F7:14258	17112021_RID_2349_DP7.raw		8.1789E3	
H.SSEEEAFVVK.L	N	41.08	1123.5397	10	-0.5	562.7769	2	34.73	6	F6:9332	17112021_RID_2349_DP6.raw			
K.LAFQTLK.S	N	39.89	819.4854	7	0.6	410.7502	2	37.72	7	F7:10543	17112021_RID_2349_DP7.raw			

total 4

XP_015666085.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MCKITTALLG LLSLSFFLEL SSCHVRRNAM GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81  SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161  NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241  VAIGDGLCDP EVMLGGYAEF LYQIGLVDEN QKIYVQNQSN LGQQYIQQKK WKEAFEVFDI LLNSDKTGTP SYIQTVSGCS
321  NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SVVEEYLLED VMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401  APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_015666086.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MCKITTALLG LLSLSFFLEL SSCHVRRNAM GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYAEF LYQIGLVDEN QKIYVQNQSN LGQQYIQQKK WKEAFEVFDI LLNSDKTGTP SYIQTVSGCS
321 NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SVVEEYLLED VMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_034258446.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTVLLA LLSLSFSLEL SSCHVRWSAM GNIFRRLKYA LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHLPGPNVK
 81 SYSGYLTVNK TYNNNLFFWF FPAQVQPEKA PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE VDVGRDLYSA IVQFFQLFPD YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYAEF LYQIGLVDEK QRIYVQNQTN LGQKYIQQKK WKEAFEVFDT LLNGDKTGSS PYIQTVTGCS
321 NYFNFLQCEE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SIVEEHLIED VMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKEWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_034258445.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTVLLA LLSLSFSLEL SSCHVRWSAM GNIFRRLKYA LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHLPGPNVK
 81 SYSGYLTVNK TYNNNLFFWF FPAQVQPEKA PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE VDVGRDLYSA IVQFFQLFPD YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYAEF LYQIGLVDEK QRIYVQNQTN LGQKYIQQKK WKEAFEVFDT LLNGDKTGSS PYIQTVTGCS
321 NYFNFLQCEE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SIVEEHLIED VMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKEWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_034258444.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTVLLA LLSLSFSLEL SSCHVRWSAM GNIFRRLKYA LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHLPGPNVK
 81 SYSGYLTVNK TYNNNLFFWF FPAQVQPEKA PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE VDVGRDLYSA IVQFFQLFPD YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYAEF LYQIGLVDEK QRIYVQNQTN LGQKYIQQKK WKEAFEVFDT LLNGDKTGSS PYIQTVTGCS
321 NYFNFLQCEE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SIVEEHLIED VMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKEWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_032092626.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MCKITALLAL LSLIFSLELS SCHVRWSAMG SIFRRLKYAL PSQGDPGQPL FLTPYIESGE TEEGRQLSLV EHLPGPNVKS
 81 YSGYLTVNKT YNSNLFFWFF PAQFQPEKAP VLLWLQGGPG GTSMFGLFVE HGPYVVQKNL SLTERKFPWT SKFSMLYIDN
161 PVGTGFSFTD DPKGYAKNED DVGRDLYSAI VQFFQLFPDY QKNDFYATGE SYAGKYVPAI GYYIHSNNPT AKIKINFKGV
241 AIGDGLCDPE VMLGGYAEFL YQIGLLDEKQ KIYVQNQTNL GQQYIQQKKW KEAFEVFDTL LNGDKTGSPP YVDTVTGCSN
321 YFNFLKCEEP EDQKYFGKLL SLPNIRKSIH VGNLTFHDGS MVEEHLVEDI MKTIKPWLAV LMDHYKVLLY NGQLDIIVAA
401 PLTERFLPTV PWGKVKEYKN AERIIWRIHD KDPEVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKEWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_032092625.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MCKITALLAL LSLIFSLELS SCHVRWSAMG SIFRRLKYAL PSQGDPGQPL FLTPYIESGE TEEGRQLSLV EHLPGPNVKS
 81 YSGYLTVNKT YNSNLFFWFF PAQFQPEKAP VLLWLQGGPG GTSMFGLFVE HGPYVVQKNL SLTERKFPWT SKFSMLYIDN
161 PVGTGFSFTD DPKGYAKNED DVGRDLYSAI VQFFQLFPDY QKNDFYATGE SYAGKYVPAI GYYIHSNNPT AKIKINFKGV
241 AIGDGLCDPE VMLGGYAEFL YQIGLLDEKQ KIYVQNQTNL GQQYIQQKKW KEAFEVFDTL LNGDKTGSPP YVDTVTGCSN
321 YFNFLKCEEP EDQKYFGKLL SLPNIRKSIH VGNLTFHDGS MVEEHLVEDI MKTIKPWLAV LMDHYKVLLY NGQLDIIVAA
401 PLTERFLPTV PWGKVKEYKN AERIIWRIHD KDPEVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKEWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_032092628.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MCKITALLAL LSLIFSLELS SCHVRWSAMG SIFRRLKYAL PSQGDPGQPL FLTPYIESGE TEEGRQLSLV EHLPGPNVKS
 81 YSGYLTVNKT YNSNLFFWFF PAQFQPEKAP VLLWLQGGPG GTSMFGLFVE HGPYVVQKNL SLTERKFPWT SKFSMLYIDN
161 PVGTGFSFTD DPKGYAKNED DVGRDLYSAI VQFFQLFPDY QKNDFYATGE SYAGKYVPAI GYYIHSNNPT AKIKINFKGV
241 AIGDGLCDPE VMLGGYAEFL YQIGLLDEKQ KIYVQNQTNL GQQYIQQKKW KEAFEVFDTL LNGDKTGSPP YVDTVTGCSN
321 YFNFLKCEEP EDQKYFGKLL SLPNIRKSIH VGNLTFHDGS MVEEHLVEDI MKTIKPWLAV LMDHYKVLLY NGQLDIIVAA
401 PLTERFLPTV PWGKVKEYKN AERIIWRIHD KDPEVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKEWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_013922774.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITALLAL LSLIFSLELS SCHVRWSAMG SIFRRLKYAL PSQGDPGQPL FLTPYIESGE TEEGRQLSLV EHLPGPNVKS
 81 YSGYLTVNKT YNSNLFFWFF PAQFQPEKAP VLLWLQGGPG GTSMFGLFVE HGPYVVQKNL SLTERKFPWT SKFSMLYIDN
161 PVGTGFSFTD DPKGYAKNED DVGRDLYSAI VQFFQLFPDY QKNDFYATGE SYAGKYVPAI GYYIHSNNPT AKIKINFKGV
241 AIGDGLCDPE VMLGGYAEFL YQIGLLDEKQ KIYVQNQTNL GQQYIQQKKW KEAFEVFDTL LNGDKTGSPP YVHTVTGCSN
321 YFNFLKCEEP EDQEYFGNLL SLPNIRKSIH VGNLTFHDGS MVEEHLVEDI MKTIKPWLAV LMDHYRVLLY NGQLDIIVAA
401 PLTERFLPTV PWGKVKEYKD AERIIWRIHD KDPEVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKEWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

XP_032092627.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITALLAL LSLIFSLELS SCHVRWSAMG SIFRRLKYAL PSQGDPGQPL FLTPYIESGE TEEGRQLSLV EHLPGPNVKS
 81 YSGYLTVNKT YNSNLFFWFF PAQFQPEKAP VLLWLQGGPG GTSMFGLFVE HGPYVVQKNL SLTERKFPWT SKFSMLYIDN
161 PVGTGFSFTD DPKGYAKNED DVGRDLYSAI VQFFQLFPDY QKNDFYATGE SYAGKYVPAI GYYIHSNNPT AKIKINFKGV
241 AIGDGLCDPE VMLGGYAEFL YQIGLLDEKQ KIYVQNQTNL GQQYIQQKKW KEAFEVFDTL LNGDKTGSPP YVDTVTGCSN
321 YFNFLKCEEP EDQKYFGKLL SLPNIRKSIH VGNLTFHDGS MVEEHLVEDI MKTIKPWLAV LMDHYKVLLY NGQLDIIVAA
401 PLTERFLPTV PWGKVKEYKN AERIIWRIHD KDPEVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKEWK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

JAV50864.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLG LLSLSFFLEL SSCHVRWNAI GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYAEF LYQIGLVDEN QRIYVQNQSN LGQQYIQQKK WKEAFEVFDI LLNGDKTGTP SYIQTVSGCS
321 NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SMVEEYLLED IMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

JAI13760.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLC LLSLSFFLEL SSCHVRRNAI GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYADF LYQIGLVDEN QRIYVQNQSN LGQQYIQQKK WKEAFEVFDI LLNDDKTGTP SYIQTISGCS
321 NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SMVEEYLLED IMKTIKPWLA VLMDHYRVLI YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

AFJ49766.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLC LLSLSFFLEL SSCHVRRNAI GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYADF LYQIGLVDEN QRIYVQNQSN LGQQYIQQKK WKEAFEVFDI LLNDDKTGTP SYIQTISGCS
321 NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SMVEEYLLED IMKTIKPWLA VLMDHYRVLI YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4

total 3 peptides

JAG47096.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLG LLSLSFFLEL SSCHVRRNAI GSIFRRLKHA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYVD
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IIQFFQLFPH YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYADF LYQIGLVDEN QRIYVQNQSN LGQQYIQQKK WKEAVEVFDI LLNDDKTGTP SYIQTISGCS
321 NYFNFMQCQE PEDQEYFGKL LSLPNIRKSI HVGNLTFHDG SMVEEYLLED IMKTIKPWLA VLMDHYRVLI YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
481 QSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4
														total 3 peptides

TRINITY_DN8397
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLG LLSLSFFLEL SSCHVRRGAM GSIFRRLKYA LPSQGDPGQP LFLTPYIESG KIEEGRQLSL VEHLPGPHVK
 81 SYSGYLTVNK THNSNLFFWF FPAQVQPEKT PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161 NPVGTGFSFT DDPKGYAKNE DDVGRDLYSA IVQFFQLFPQ YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241 VAIGDGLCDP EVMLGGYADF LYQIGLVDEK QRIYVQNQSD LGQQYIQQKK WKEAFEVFDI LLNGDKTGSP PYIETVSGCS
321 NYFNFLQCQD PEDQKYFGKL LSLPNIRKSI HVGNLTFHDG SMVEEYLIED IMKTIKPWLA VLMDHYRVLL YNGQLDIIVA
401 APLTERFLPT VPWGKVKEYK NAERIVWRIH DKDPEVAGYV RQVGEFYQVI VRGGGHILPY DQPERALDMM DRFIMGKGWK
481 QSGYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4
														total 3 peptides

ETE69371.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MCKITTALLA LLSLSFFLEL SSYHVRWSAM GSIFRRRKYT LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHFPGPNVK
 81 SYSGYLTVNM TYNSNLFFWF FPAQVGTGFS FTDDLKGYAK NEDDVGRDLY SAIVQFFQLF PDYQKNDFYA TGESYAGKYV
161 PAIGYYIHSN NPTAKIKINF KGVAIGDGLC DPEVMLGGYA EFLYQIGLVD EKQRLYVQNQ TNLGQQYIQQ KKWKEAFEVF
241 DILLNGDKTG SPYIQNVTGC SNYFNFLQCN EPEDQEYFGK LLSLPNIRKS IHVGNLTFHD GSMVEEHLIE DIMKTIKPWL
321 AVLMDNYRVL LYNGQLDIIV AASLTERFLP TVPWGKAKEY KNAERIVWRI HDKDPEVAGY VRQVGEFYQV IVRGGGHILP
401 YDQPERALDM MDRFTMGKGW KQSRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4
														total 3 peptides

XP_026529384.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MCKITTALLA LLSLSFFLEL SSYHVQWSAM GSIFRRLKYT LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHFPGPNVK
 81  SYSGYLTVNM TYNSNLFFWF FPAQDQPEKA PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161  NPVGTGFSFT DDLKGYAKNE DDVGRDLYSA IVQFFQLFPD YQKNDFYATG ESYAGKYVPA IGYYIHSNNP TAKIKINFKG
241  VAIGDGLCDP EVMLGGYAEF LYQIGLVDEK QRIYVQNQTN LGQQYIQQKK WKEAFEVFDI LLNGDKTGNP YIQNVTGCSN
321  YFNFLQCNEP EDQEYFGKLL SLPNIRKSIH VGNLTFHDGS MVEEHLIEDI MKTIKPWLAV LMDNYRVLLY NGQLDIIVAA
401  SLTERFLPTV PWSKAKEYKN AERIVWRIHD KDPEVAGYVH QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKGWKQ
481  SRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
H.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4
														total 3 peptides

XP_026563995.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MCKITTTLLA LLSLSFFLEL SSYHVRWSAM GSIFRRLKYT LPSQGDPGQP LFLTPYIESG KTEEGRQLSL VEHFPGPNVK
 81  SYSDYLTVNM TYNSNLFFWF FPAQDQPEKA PVLLWLQGGP GGTSMFGLFV EHGPYVVQKN LSLTERKFPW TSKFSMLYID
161  NPVGTGFSFT DELKGYAKNE DDVGRDLYSA IVQFFQLFPD YQKNDFYATG ESYAGKYVPA VGYYIHSNNP TAKIKINFKG
241  VAIGDGLCDP EVMLGGYAEF LYQIGLVDEK QRIYVQNQTN LGQQYIQQKK WKKAFEVFDI LLNGDKTGNP YIQNVTGCSN
321  YFNFLQCNEP EDQEYFGKLL SLPNIRKSIH VGNLTFHDGS IVEEHLIEDI MKTIKPWLAV LMDNYRVLLY NGQLDIIVAA
401  SLTERFLPTV PWSKAKEYKN AERIVWRIHD KDPDVAGYVR QVGEFYQVIV RGGGHILPYD QPERALDMMD RFIMGKGWKQ
481  SRYGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.NDFYATGESYAGK.Y	Y	72.10	1421.6099	13	-0.1	711.8121	2	37.11	2	F2:10004	12112021_RID_2349_DP2.raw	1.9882E5	1.3335E5	
R.QVGEFYQVIVR.G	Y	42.38	1336.7139	11	0.4	669.3645	2	51.49	1	F1:15706	12112021_RID_2349_DP1.raw	1.4401E5		
R.GGGHILPYDQPER.A	Y	40.27	1437.7001	13	1.0	719.8580	2	31.99	3	F3:8551	17112021_RID_2349_DP3.raw			8.9043E4
														total 3 peptides

P86497.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
                                                   47
  1  VIGGAECDIN EHPSLALIYS TSMRFHCAGT LLNQEWVSFT MWDKDIMLIR TLCAGVLEGG KDTCLAHPCA QPLLPAFYTK
                                                 ooo
                                                 oo
                                                 o
                                                   o
                                                   o
                                                    o
                                                    o
 81  VFDYIPWIK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area I
M.WDKDIMLIR.T	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105
M.WDKDIM(+15.99)LIR.T	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264
V.SFTM(+15.99)WDKDIMLIR.T	Y	52.39	1670.8160	13	0.4	836.4156	2	57.93	2	F2:16952	12112021_RID_2349_DP2.raw		1.0184
F.TMWDKDIMLIR.T	N	50.40	1420.7207	11	0.6	711.3680	2	53.82	3	F3:15851	17112021_RID_2349_DP3.raw		
W.DKDIMLIR.T	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw		
V.SFTM(+15.99)WDKDIM(+15.99)LIR.T	Y	42.80	1686.8109	13	0.4	844.4131	2	54.20	2	F2:15770	12112021_RID_2349_DP2.raw		4.4011
W.DKDIM(+15.99)LIR.T	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw		

JAG46182.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYLCFP QNHLSLEELG SDIGIQVFNQ LVKTRAGENV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEASFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

XP_015674504.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYACFP QNHLSLEELG SDIGIQVFNQ LVKTRAGDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP GDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

JAG43702.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYLCFP QNHLSLEELG SDIGIQVFNQ LVKTRAGENV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEASFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

JAA96331.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYLCFP QNHLSLEELG SDIGIQVFNQ LVKTRAGENV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEASFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

XP_015674505.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYACFP QNHLSLEELG SDIGIQVFNQ LVKTRAGDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP GDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

JAV49839.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYFCFP QNHLSLEELG SDIGIQVFNQ LVKTRAGDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  EGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNEGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAES STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

TRINITY_DN3815
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYVCFP QNHLSLEELG SDIGIQVFNQ LVKTRADDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  QGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNGGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAQI STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

TRINITY_DN3815
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MYWHFPLLFA ALISTYVCFP QNHLSLEELG SDIGIQVFNQ LVKTRADDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  QGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNGGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAQI STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

TRINITY_DN3815
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:


```
  1  MYWHFPLLFA ALISTYVCFP QNHLSLEELG SDIGIQVFNQ LVKTRADDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  QGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNGGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAQI STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

TRINITY_DN3815
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MYWHFPLLFA ALISTYVCFP QNHLSLEELG SDIGIQVFNQ LVKTRADDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  QGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNGGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAQI STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
													total 2 peptides			

TRINITY_DN3815
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MYWHFPLLFA ALISTYVCFP QNHLSLEELG SDIGIQVFNQ LVKTRADDNV VVSPHGIASV LGMLQLGADS KTKKQLTTVM
 81  RYSVNGAGKV LKKINKAIVS RKNKDIVKIA NVVFANSGLK MEAPFISRNS EVFQCPVKNI NFKDPNAASD TMNQWVKNKT
161  QGMIDSVLTP DDIDSALTRL VVINAVYFKG LWRSRFQPEN TKKRTFNGGD GKTYQVPMLA QLSVFRCGTT STPNDLWYNT
241  IELPYHGESI SMLIALPAQI STPLSAIIPH ISTKTIQSWM TTMVQKRVQV ILPKFTAEAE TDLKEPLKEL GIRDMFDQSR
321  ANFAKITRSE NIYVSQLLQK AKIEVSEDGT KASAATTAIV TARSSPPWFV VDRPFLFFIR HNPTGAVLFM GQITKP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.IANVVFANSGLK.M	Y	77.60	1231.6924	12	0.3	616.8536	2	44.26	2	F2:12431	12112021_RID_2349_DP2.raw		7.2043E4			
													total 2 peptides			

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
R.SENIYVSQLLQK.A	Y	41.15	1420.7561	12	0.3	711.3856	2	49.58	2	F2:14262	12112021_RID_2349_DP2.raw		4.7741E4			
													total 2 peptides			

TRINITY_DN28984
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1  ETKPRELYGR RLPLREYLVL VPVVVPTETS RKICVQLNHL NESVTLSITL EYGLQNRSLL REEVSKKDLF QCTEFQIPKW
  81  ERSFNSHIAL FTVEVTGATL RYLDRKRVYI ENQESLTFVQ TDKPIYKPGH KVLFRAVSLT KEFIPVTEKV PLIYIEDPKR
 161  NRLFHWKDVE LKGGLVQLEF PLSSEPALGT YKVVVQKDSG RKVEHPYTVD EYELPKFEVT VKSTPVITIL DNKLDVTVCG
 241  KYTFGKPVPG LVNIRVCRKF SFFGSTCYGE ESKAICEEFH GKADIHGCFS QEVDLKIFQL KRNGFQMQIQ TEGTITEEGT
 321  EIVLTGSGTT QITSTLSVVS FENVDAYYKP GLPLSGEIKL VDGRTKPIAN QVVELQVSGV KNSTYHNTDD QGRARFSIDT
 401  SDFTNDAVQL TATYKQLDYC YDSNWISPQH QTAFTSLSRF YSPSQSYLKI ERHLGSLTCG EHAVIPVHYI LKPELIKDKE
 481  VVFYYLVVAR GDIVKTGTHP LKGKESKGTF NLNLLVDIKS APLARVLLYT ILDNGELVVH SADFPVEPCF ANKVNLRFAE
 561  PEGLPGSSIN LQLSAAQNSL CAIHAVDQSV FLLKPEAELS PRTVYDLLPV KDLRGYYYKS ENLEDPDTNP CVPPRKIIVD
 641  GIRYQTDTYS YGEGDAYTIL KDIGFKTFTS TQIHKPNICS SPDVYYSRAY DVAGGMAAPL AAELKRESAE AVETTIRSFF
 721  PETWLWSIKS LSSETEVTLP VTIPDTITEW RAGAFCLSPV VGFGLAKTTF LKAMQPFFVE VTQPYSVVRG EAFNLKATVF
 801  SYQKRPIQVS LSLLLSPDYD ASPVEKEQDS YCLPVDGRKT VSWKVTPKTL GKVNFTITAE ALKSAQLCGN EIVEVPTKGQ
 881  RDIVIKSLLV EPEGIEKEVV INNLLCGDKG TPSATISLKV PEKVVEKSAR AFFSVLGDIL SSAIQNVHQL IRLPTGCGEQ
 961  NMALLAPNIY ILDYLNATGQ LNEDMKSKAI GFLVAGYQRQ LNYKHADGSY STFGERNNEP GNVWLTAFVL KCLSQMKRYI
1041  PVEERHLIDA QHFLALKQKP NGCFQITGTL LNNALKGGVD DEVTLSTYIA IALLEMSLPV THSVLRNALF CLETASQQKD
1121  IPVYNLALLG YAFALAHKQD KVAEILHTLQ GKAVKGEDGS IHWERPAKPE AKKPLYYESR ASSAEVELNS YMLLTYLKRN
1201  PSPTQDDLAM ASKIVTWLTK QQNPSGGFSS TQDTVVALQA LSLYAAATFS NSAEGIRVTL KSGENNLKEF QVDNSNRILL
1281  QTQDLPTVPG EYSAVVTGKG CTYVQTTLRY NVLPHPEDDP FAVTVDTIPE TCVGVKAHKE FEIVMNVSYT GKRPASNMAI
1361  INVKMVSGFV PNAPSLKKLK KQAPIQQVEV TATNVMLYLE KVTNVTIPIS FTVERSFDIQ NQRPAFVHMY DYYEDESTVV
1441  PYSAPCSKAK FGNA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.NPSPTQDDLAMASK.I	Y	58.60	1473.6769	14	1.1	737.8466	2	32.86	7	F7:8878	17112021_RID_2349_DP7.raw					
S.AEAVETTIR.S	Y	52.94	988.5189	9	-0.1	495.2667	2	26.18	7	F7:6550	17112021_RID_2349_DP7.raw					
K.ATVFSYQK.R	Y	50.25	942.4811	8	-0.2	472.2477	2	31.69	7	F7:8446	17112021_RID_2349_DP7.raw					
													total 3 peptides			

TRINITY_DN28984
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MGKNRLLAGP CLFLLGLFLL PGGTSASTPK PEYLVLVPVV VPTETSRKIC VQLNHLNESV TLSITLEYGL QNRSLLREEV
  81 SKKDLFQCTE FQIPKWERSF NSHIALFTVE VTGATLRYLD RKRVYIENQE SLTFVQTDKP IYKPGHKVLF RAVSLTKEFI
 161 PVTEKVPLIY IEDPKRNRLF HWKDVELKGG LVQLEFPLSS EPALGTYKVV VQKDSGRKVE HPYTVDEYEL PKFEVTVKST
 241 PVITILDNKL DVTVCGKYTF GKPVPGLVNI RVCRKFSFFG STCYGEESKA ICEEFHGKAD IHGCFSQEVD LKIFQLKRNG
 321 FQMQIQTEGT ITEEGTEIVL TGSGTTQITS TLSVVSFENV DAYYKPGLPL SGEIKLVDGR TKPIANQVVE LQVSGVKNST
 401 YHNTDDQGRA RFSIDTSDFT NDAVQLTATY KQLDYCYDSN WISPQHQTAF TSLSRFYSPS QSYLKIERHL GSLTCGEHAV
 481 IPVHYILKPE LIKDKEVVFY YLVVARGDIV KTGTHPLKGK ESKGTFNLNL LVDIKSAPLA RVLLYTILDN GELVVHSADF
 561 PVEPCFANKV NLRFAEPEGL PGSSINLQLS AAQNSLCAIH AVDQSVFLLK PEAELSPRTV YDLLPVKDLR GYYYKSENLE
 641 DPDTNPCVPP RKIIVDGIRY QTDTYSYGEG DAYTILKDIG FKTFTSTQIH KPNICSSPDV YYSRAYDVAG GMAAPLAAEL
 721 KRESAEAVET TIRSFFPETW LWSIKSLSSE TEVTLPVTIP DTITEWRAGA FCLSPVVGFG LAKTTFLKAM QPFFVEVTQP
 801 YSVVRGEAFN LKATVFSYQK RPIQVSLSLL LSPDYDASPV EKEQDSYCLP VDGRKTVSWK VTPKTLGKVN FTITAEALKS
 881 AQLCGNEIVE VPTKGQRDIV IKSLLVEPEG IEKEVVINNL LCGDKGTPSA TISLKVPEKV VEKSARAFFS VLGDILSSAI
 961 QNVHQLIRLP TGCGEQNMAL LAPNIYILDY LNATGQLNED MKSKAIGFLV AGYQRQLNYK HADGSYSTFG ERNNEPGNVW
1041 LTAFVLKCLS QMKRYIPVEE RHLIDAQHFL ALKQKPNGCF QITGTLLNNA LKGGVDDEVT LSTYIAIALL EMSLPVTHSV
1121 LRNALFCLET ASQQKDIPVY NLALLGYAFA LAHKQDKVAE ILHTLQGKAV KGEDGSIHWE RPAKPEAKKP LYYESRASSA
1201 EVELNSYMLL TYLKRNPSPT QDDLAMASKI VTWLTKQQNP SGGFSSTQDT VVALQALSLY AAATFSNSAE GIRVTLKSGE
1281 NNLKEFQVDN SNRILLQTQD LPTVPGEYSA VVTGKGCTYV QTTLRYNVLP HPEDDPFAVT VDTIPETCVG VKAHKEFEIV
1361 MNVSYTGKRP ASNMAIINVK MVSGFVPNAP SLKKLKKQAP IQQVEVTATN VMLYLEKVTN VTIPISFTVE RSFDIQNQRP
1441 AFVHMYDYYE DESTVVPYSA PCSKAKFGNA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.NPSPTQDDLAMASK.I	Y	58.60	1473.6769	14	1.1	737.8466	2	32.86	7	F7:8878	17112021_RID_2349_DP7.raw					
S.AEAVETTIR.S	Y	52.94	988.5189	9	-0.1	495.2667	2	26.18	7	F7:6550	17112021_RID_2349_DP7.raw					
K.ATVFSYQK.R	Y	50.25	942.4811	8	-0.2	472.2477	2	31.69	7	F7:8446	17112021_RID_2349_DP7.raw					

total 3 peptides

JAV50910.1
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKI
  81 EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DVYLMTPQPE EVDENSAEDE
 161 GQSNRKFLDG DELTLADCNL LPKLHIVKVV CKKYRNFTIP EEFCGIHRYL KNAYAREEFA STCPDDEEIE LAYELVAKAL
 241 K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49

total 2 peptides

JAI10138.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
   1 MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKV
  81 EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DVYLMTPQPE EVDENSAEDE
 161 GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
 241 K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49

total 2 peptides

JAB54484.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKV
 81  EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DVYLMTPQPE EVDENSAEDE
161  GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
241  K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

XP_026541233.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKV
 81  EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DVYLMTPQPE EVDENSAEDE
161  GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
241  KA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

XP_026576189.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKI
 81  EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DVYLMTPQPE EVDENSAEDE
161  GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
241  KA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

LAB45561.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  TWGPPAARLS FAAPWVHASL PRLNHAPSVE SSSSSSAMAE EKPQVELFVK AGSDGAKIGN CPFSQRLFMV LWLKGVTFNV
 81  TTVDTKRRTE AVQKLCPGGQ LPFLMYGTEV HTDTNKVEEF LEEVLCPPKY PKLAANNPES NTAGLDVFAK FSAYIKNSNP
161  SLNANLEKGL LKALKVLDVY LMTPQPEEVD ENSAEDEGQS NRKFLDGNEL TLADCNLLPK LHIVKVVCKK YRDFTIPEEF
241  RGIHRYLKNA YAREEFSSTC PDDEEIELAY ELVAKALK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

TRINITY_DN178

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  SSTGGSRVEA SRPEPRGGRL FPRGPSQQGP LAGWLGSVPG RGRSSGGKLR RSCESRLLGA APGSPPALPR RPLGPREPPL
 81  PSQSVQASSS SSSSSAMAEE KPQVELFVKA GSDGAKIGNC PFSQRLFMVL WLKGVTFNVT TVDTKRRTEA VQKLCPGGQL
161  PFLMYGTEVH TDTNKIEEFL EEVLCPPRYP KLAANNPESN TAGLDVFAKF SAYIKNSNPS LNANLEKGLL KALKVLDVYL
241  MTPQPEEVDE NSAEDEGQSN RKFLDGNELT LADCNLLPKL HIVKVVCKKY RNFTIPEEFC GIHRYLKNAY AREEFASTCP
321  DDEEIELAYE LVAKALK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

LAB63521.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKV
 81  EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL DLYLMTPQPE EVDENSAEDE
161  GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
241  K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

JAG68347.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAEEKPQVEL FVKAGSDGAK IGNCPFSQRL FMVLWLKGVT FNVTTVDTKR RTEAVQKLCP GGQLPFLMYG TEVHTDTNKV
 81  EEFLEEVLCP PKYPKLAANN PESNTAGLDV FAKFSAYIKN SNPSLNANLE KGLLKALKVL BVYLMTPQPE EVDENSAEDE
161  GQSNRKFLDG NELTLADCNL LPKLHIVKVV CKKYRDFTIP EEFRGIHRYL KNAYAREEFS STCPDDEEIE LAYELVAKAL
241  K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

ETE58466.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVELVEILGI LEEARRGEVK VKRKGVRKAL CERGKGGGER EGRKKEGKRK RKKEGKERRK EGEKERREKR EKRERKKKKK
 81  ERPFPIAKKE RKKERQAIWL FLAGSDGAKI GNCPFSQRLF MVLWLKGVTF NVTTVDTKRY PKLAANNPES NTAGLDVFAK
161  FSAYIKNSNP SLNANLEKGL LKALKVLDIY LMTPQPEEVD ENSAEDEGQS NRKFLDGNEL TLADCNLLPK LHIVKVVCKK
241  YRDFTIPEEF RGIHRYLKNA YAREEFSSTC PDDEEIELAY ELVAKALK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.LAANNPESNTAGLDVFAK.F	Y	72.78	1830.9111	18	1.0	916.4637	2	47.50	4	F4:13719	17112021_RID_2349_DP4.raw				4.70
K.GVTFNVTTVDTK.R	Y	48.38	1280.6613	12	1.0	641.3386	2	41.97	4	F4:11922	17112021_RID_2349_DP4.raw				6.49
														total 2 peptides	

TRINITY_DN7999

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MTPHFLILIM LFAFSKGGLS QIVLTQSDPV LKKPGEAHKL TCAVTGFNVN SYWMGWIRQK PGQGLEWLVR YYDTSNTIYY
                                                                                          C
                                   101
 81  SPTIQGRFTP SKDSSNFYLQ MNNLKAEDTA VYYCARDRQV RDFYYWGKGT TVTVTSAGKT APTVFPLSPC NQDIATASLV

161  SIGCFIKGYF PEPATVQWNS GAITSGIQNF PPVLLASNHY SHTSLLTIPA SQWQSESFQC NVEHAATNTR INKIIERSAI
241  RSPVGPEITV FHSCDSRDSD GTVQLWCHIS GFYPKQLDID WKVGSRSGQL HPYNYPPWQN PGTYTFSTAS VVNITQDDWL
321  EGNSYYCEAT HAASQTKVKG KAKKCKDGSS CPSGDIKVDI LPPRPKALYI DRNSKISCVV SNLQNEQGLK FTWFREKSGH
401  LTPDAIETTE GSNGGYIVLS RLGIFSEDWD SGETFTCVVE HPTFVSPVTK KISKSRGKHS APKVYVFPPH QEELNPGRSV
481  SLTCLVTGFS PEAADVQWLE DHNPLSEDNS VTTPPMKNKH DDSYFLYSKL LVPKTDWNTK SFTCMVVHED LPMKFTQRNI
561  SRTQGKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Ar F
K.DSSNFYLQMNNLK.A	Y	63.76	1572.7242	13	0.8	787.3700	2	52.45	7	F7:15573	17112021_RID_2349_DP7.raw				
K.DSSNFYLQM(+15.99)NNLK.A	Y	48.08	1588.7191	13	1.4	795.3679	2	43.09	7	F7:12421	17112021_RID_2349_DP7.raw				
S.NTIYYSPTIQGR.F	Y	42.97	1411.7096	12	1.2	706.8629	2	39.01	7	F7:11021	17112021_RID_2349_DP7.raw				
S.QIVLTQSDPVLK.K	Y	42.47	1339.7711	12	0.7	670.8933	2	59.10	7	F7:17836	17112021_RID_2349_DP7.raw				

total 4 peptide

JAV50725.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVSPRTCINK LGSTLPLLLV LWDLHYEGVQ CGINAEVEKQ LELGKKLLAA GQLADALSHF HAAIEGDADN YLAYYRRATV
 81  YLAMGKSKAA IRDLSRVVEL KQDFTSARLQ RGHLLLKQGK LNEAVEDFEG VLLSNPNDKE EGEARAQLLK SDEARNLRSQ
161  AQSAFLESDY YTAITLLDKI LEVCVWDVDM RELRAESYIK EGEPGKAISD LKAAAKLKSD NTEAFYKIST IYYELGDHEM

241  SLSEVRECLK LDQDHKECFS HYKRIKKLNK QIVSAEDLIQ ERRYQEATEK YEAVMKMETN VPVYTTRAKE RICHCLSKNQ

321  QSTEAIKVCT EVLQLEPENV NALKDRAEAY LLEEMYEEAI QDYETAKKHS DNDQQILESL EKAQRMLKQS QKRDYYKILG
401  VKRNARKQEI IKAYRKLAMQ WHPDNFQDEE EKKKAEKKFI DIAAAKEVLT DPEMRKKFDA GEDPLDAESQ QGGGHPFHRS

481  WNSWQGFDPF SSGGPFQFKF HFN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
K.QIVSAEDLIQER.R	Y	58.67	1399.7307	12	0.2	700.8728	2	46.91	3	F3:13615	17112021_RID_2349_DP3.raw			9.5286E4		
K.LKSDNTEAFYK.I	N	47.39	1314.6455	11	1.2	658.3308	2	27.25	7	F7:6950	17112021_RID_2349_DP7.raw					
K.EVLTDPEMR.K	N	42.20	1088.5172	9	0.9	545.2664	2	34.55	7	F7:9479	17112021_RID_2349_DP7.raw					

total 3 peptides

ADP88560.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIKVLANL LVLQLSYAQK SSELVVGGDE CNINEHRSLV FLYNNSFGCS GTLINQQWVL SAVHCDMENV RIYLGVHNLT
                                                                                          C
                                   110
 81  LRNNAEIRLP EERFFCLSNK NYTKWDKDIM LIKLDRPVKT STYIAPLSLP SSPPRVGSVC RIMGWGAITS PNETFPGVTH

161  CANINILPYS VCRAAYKGLP AQSRTLCGGI LEGGIGSCMG DSGGPLICNG EMHGIVAWGD DTCAQPHKPV HYTKVYDYTD
241  WIQSIIAGNT AATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
K.TSTYIAPLSLPSSPPR.V	Y	65.05	1685.8988	16	0.6	843.9572	2	51.64	7	F7:15270	17112021_RID_2349_DP7.raw	3.9743E5	3.772E5	
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157

total

E5L0E4.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIKVLANL LVLQLSYAQK SSELVVGGDE CNINEHRSLV FLYNNSFGCS GTLINQQWVL SAVHCDMENV RIYLGVHNLT
                                     110
 81  LRNNAEIRLP EERFFCLSNK NYTKWDKDIM LIKLDRPVKT STYIAPLSLP SSPPRVGSVC RIMGWGAITS PNETFPGVTH

161  CANINILPYS VCRAAYKGLP AQSRTLCGGI LEGGIGSCMG DSGGPLICNG EMHGIVAWGD DTCAQPHKPV HYTKVYDYTD
241  WIQSIIAGNT AATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
K.TSTYIAPLSLPSSPPR.V	Y	65.05	1685.8988	16	0.6	843.9572	2	51.64	7	F7:15270	17112021_RID_2349_DP7.raw	3.9743E5	3.772E5	
K.WDKDIMLIK.L	N	57.12	1160.6263	9	-0.1	581.3204	2	46.64	2	F2:13338	12112021_RID_2349_DP2.raw	2.1169E5	9.915E6	1.5104
K.WDKDIM(+15.99)LIK.L	N	52.20	1176.6212	9	-0.2	589.3177	2	41.27	2	F2:11445	12112021_RID_2349_DP2.raw		6.6323E6	2.1157
														total

XP_026535564.1

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSLASGDSSS SSPGEEPRGT EPVKSLISHK ASHNSYVELH ELVMDKNNEF RWMEASRWIK LEEDFEEMGQ WGRPHLSYLT
 81  FQSLLEVRKA FSKGTVLLDL QERSLAGIAN QVLSQMIYEG KLKPDDQEVL LRTLLLQHSQ PSESTSLNTL LPARVQRTDA

161  KDTTEPLLQE QHQIEMKTFF NGSEQGESSH SGFRKQLLEK IPPDAEATLG LVGCATFLDR PILAFVRLKE AVELDSVLEV
241  PVPVRFLFVV LGPDSPHISY HEIGRAISTM MSERVFRNDS YLAEGRQDLI KSLDEFLDCC IVLPPSEIQS ERLLKMLLPV

321  QKDFLRKRYL PVEKKLEEPL KDLGHKLKDI TAEDSGDSLR RTGNIFGGLV KDIKRRYPKY LSDIKDALNP QCLAAVIFIY
401  FAALSPAITF GGLLAEKTDR LIGVSELLLS TAVQSGLFCL LGAQPLLVVG FSGPLLVFEE AFYAFCTANG IEYIVGRVWI
481  GFWLILIVIL VVAFEGSFLV RFISRYTQEI FSILISLIFI LETFFKLIKI FKEHPLKEAY KNVTFSRDED PREPVPNTAL
561  LSLVLMGGTF FIAFFLRKFK NSSFFPGRLR RVIGDFGVPI AILIMTLADN LIKDTYTQKL KVPKGLQVSN PEKRDWFIHP
641  LGNEFPKWMM FASLVPALLV FILIFLETQI TTLIVSKPER KMVKGSGFHL DLLLIVGMGG IAPLLGMPWL SATTVRTVTH
721  ANALTVMSKT TLPGEKACIQ EVKEQRVTGF LVAILVGLSI LMEPILKLIP LAVLFGIFLY MGVTSLNGIQ LYDRILLMLK
801  PPKYHPDVPY VTKVKTWHMH IFTLTQILCL GLLWGVKTSP ASLALPFILI LTVPLRYFLL PVIFTDIELK CLDAEDTELT
881  FDETEGQDVY DEVQMPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						
																	total 3 peptides

XP_026535563.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAFQEDYESG IKEKLDLEAY GDSSLKQSNM SLASGDSSSS SPGEEPRGTE PVKSLISHKA SHNSYVELHE LVMDKNNEFR
 81  WMEASRWIKL EEDFEEMGQW GRPHLSYLTF QSLLEVRKAF SKGTVLLDLQ ERSLAGIANQ VLSQMIYEGK LKPDDQEVLL

161  RTLLLQHSQP SESTSLNTLL PARVQRTDAK DTTEPLLQEQ HQIEMKTFFN GSEQGESSHS GFRKQLLEKI PPDAEATLGL
241  VGCATFLDRP ILAFVRLKEA VELDSVLEVP VPVRFLFVVL GPDSPHISYH EIGRAISTMM SERVFRNDSY LAEGRQDLIK

321  SLDEFLDCCI VLPPSEIQSE RLLKMLLPVQ KDFLRKRYLP VEKKLEEPLK DLGHKLKDIT AEDSGDSLRR TGNIFGGLVK
401  DIKRRYPKYL SDIKDALNPQ CLAAVIFIYF AALSPAITFG GLLAEKTDRL IGVSELLLST AVQSGLFCLL GAQPLLVVGF
481  SGPLLVFEEA FYAFCTANGI EYIVGRVWIG FWLILIVILV VAFEGSFLVR FISRYTQEIF SILISLIFIL ETFFKLIKIF
561  KEHPLKEAYK NVTFSRDEDP REPVPNTALL SLVLMGGTFF IAFFLRKFKN SSFFPGRLRR VIGDFGVPIA ILIMTLADNL
641  IKDTYTQKLK VPKGLQVSNP EKRDWFIHPL GNEFPKWMMF ASLVPALLVF ILIFLETQIT TLIVSKPERK MVKGSGFHLD
721  LLLIVGMGGI APLLGMPWLS ATTVRTVTHA NALTVMSKTT LPGEKACIQE VKEQRVTGFL VAILVGLSIL MEPILKLIPL
801  AVLFGIFLYM GVTSLNGIQL YDRILLMLKP PKYHPDVPYV TKVKTWHMHI FTLTQILCLG LLWGVKTSPA SLALPFILIL
881  TVPLRYFLLP VIFTDIELKC LDAEDTELTF DETEGQDVYD EVQMPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_013918193.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MERVSMGKAG SYQRHMDTSS SSSSEEEPRG TEPAKPLISH KASHNSYVEL HELVMDKNNE FRWMEASHWI KLEEDFEEMG
 81 HWGRPHLSYL TFQSLLEVRK AFSKGTVLLD LQERSLAGIA NQVLSQMIYE GKLKPDDQEV LLRTLLLQHS HPSESASLNT
161 LLPALVQRTD TKDSTQPLLQ EHQQIEMKTF SNGSEQGESS HSDFKKQLLD KIPPDAEATL GLVGCATFLD RPTVAFVRLK
241 EAVELDSVLE VPVPVRFLFV VLGPDSPHIS YHEIGRAIST MMSERVFRND SYLAEGRQDL IKSLDEFLDC CIVLPPSEIQ
321 NERLLKMLLP VQKDFLRKRY LPVEKKLEEP LKDLGHKLKD HDITAEDSDD SLRRTGKIFG GMVKDIKRRY PKYLSDIKDA
401 LNPQCLAAVI FIYFAALSPA ITFGGLLAEK TERLIGVSEL LLSTAVQSGL FCLLGAQPLL VVGFSGPLLV FEEAFYAFCV
481 NKNYEYLVGR VWIGFWLILI VVVVVAFEGS FLVRFISRYT QEIFSILISL IFILETFFKL IKIFKEHPLK EVYKNITYPP
561 DEEPRYPVPN TALLSLVLMG GTFFIAFFLR KFKNSSFFPG KLRRVIGDFG VPIAIFIMTL ADYLIKDTYT QKLKVPKGLQ
641 VSNPEQRNWF IHPLGSSLGN PFPIWMMFAT ALPALLVFIL IFLETQITTL IVSKPERKML KGSGFHLDLL LIVGMGGIAP
721 LLGMPWLSAT TVRTVTHANA LTVMSKTTLP GEKACIQEVK EQRVTGFLVA ILVGLSILME PILKLIPLAV LFGIFLYMGV
801 TSLNGIQLYD RILLLLKPPK YHPDVSYVTK VKTWRMHIFT FTQMLCLGLL WGVKSSPASL ALPFILILTV PLRLFLLPFI
881 FTDVELKCLD ADDAEVTFDE TEGQDVYDEV QMPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_034271810.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSICQHICIS FSQYSCPGHQ GIYHLSKRRR MERVSMGKAG SYQRHVDTSS SSSSEEEPRG TEPAKPLISH KASHNSYVEL
 81 HELVMDKNNE FRWMEASHWI KLEEDFEEMG HWGRPHLSYL TFQSLLEVRK AFSKGTVLLD LQERSLAGIA NQVLSQMIYE
161 GKLKPDDQEV LLRTLLLQHS HPSESASLNT LLPARVQRTD AKDSTQPLLQ EHHQIEMKTF SNGSEQGESS HSGFKKQLLD
241 KIPPDAEATL GLVGCATFLD RPTLAFVRLK EAVELDSVLE VPVPVRFLFV VLGPDSPHIN YHEIGRAIST MMSERVFRND
321 SYLAEGRQDL IKSLDEFLDC CIVLPPSEIQ NERLLKMLLP VQKDFLRKRY LPVEKKLEEP LKDLAHKLKD HDITAEDSDD
401 PLRRTGRIFG GLVKDIKRRY PKYLSDIKDA LNPQCLAAVI FIYFAALSPA ITFGGLLAEE TERLIGVSEL LLSTAVQSGL
481 FCLLGAQPLL VVGFSGPLLV FEKAFYAFCT NYNIEYLVGR VWIGFWLILI VILVVAFEGS FLVRYISRYT QEIFSILISL
561 IFIQETFSNL IKIFKAHPLK GVYKNITFSG EEEPREPVPN TALLSLVLMG GTFFIAFFLR KFKNSSFFPG RLRRVIGDFG
641 VPIAIFIMTL ADNLIKDTYT QKLKVPKGLQ VSNTDKRDWF IHPLKEPIPK WFLFAAALPA LLVFILIFLE TQITTLIVSK
721 PERKLLKGSG FHLDLLLIVG MGGIAPLLGM PWLSATTVRT VTHANALTIM SKTTLPGEKA CIQEVKEQRI TGFLVALLVG
801 LSILMEPILK LIPLAVLFGI FLYMGVTSLS GIQLYDRILL MLKPPKYHPD VSYVTKVKSW RMHIFTFSQI LCLGLLWGVK
881 SSPASLALPF ILILTVPLRR FLLPVIFTDI ELKCLDADDA EVTFDETEGQ DVYDEVQMPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_013918195.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MQKKSYVELH ELVMDKNNEF RWMEASHWIK LEEDFEEMGH WGRPHLSYLT FQSLLEVRKA FSKGTVLLDL QERSLAGIAN

 81 QVLSQMIYEG KLKPDDQEVL LRTLLLQHSH PSESASLNTL LPALVQRTDT KDSTQPLLQE HQQIEMKTFS NGSEQGESSH
161 SDFKKQLLDK IPPDAEATLG LVGCATFLDR PTVAFVRLKE AVELDSVLEV PVPVRFLFVV LGPDSPHISY HEIGRAISTM

241 MSERVFRNDS YLAEGRQDLI KSLDEFLDCC IVLPPSEIQN ERLLKMLLPV QKDFLRKRYL PVEKKLEEPL KDLGHKLKDH

321 DITAEDSDDS LRRTGKIFGG MVKDIKRRYP KYLSDIKDAL NPQCLAAVIF IYFAALSPAI TFGGLLAEKT ERLIGVSELL
401 LSTAVQSGLF CLLGAQPLLV VGFSGPLLVF EEAFYAFCVN KNYEYLVGRV WIGFWLILIV VVVVAFEGSF LVRFISRYTQ
481 EIFSILISLI FILETFFKLI KIFKEHPLKE VYKNITYPPD EEPRYPVPNT ALLSLVLMGG TFFIAFFLRK FKNSSFFPGK
561 LRRVIGDFGV PIAIFIMTLA DYLIKDTYTQ KLKVPKGLQV SNPEQRNWFI HPLGSSLGNP FPIWMMFATA LPALLVFILI
641 FLETQITTLI VSKPERKMLK GSGFHLDLLL IVGMGGIAPL LGMPWLSATT VRTVTHANAL TVMSKTTLPG EKACIQEVKE
721 QRVTGFLVAI LVGLSILMEP ILKLIPLAVL FGIFLYMGVT SLNGIQLYDR ILLLLKPPKY HPDVSYVTKV KTWRMHIFTF
801 TQMLCLGLLW GVKSSPASLA LPFILILTVP LRLFLLPFIF TDVELKCLDA DDAEVTFDET EGQDVYDEVQ MPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_013918194.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MASQEDYESG IKAKLDVEAY GDSSLKQSNM SLASGNSSSS SSEEEPRGTE PAKPLISHKA SHNSYVELHE LVMDKNNEFR
 81 WMEASHWIKL EEDFEEMGHW GRPHLSYLTF QSLLEVRKAF SKGTVLLDLQ ERSLAGIANQ VLSQMIYEGK LKPDDQEVLL

161 RTLLLQHSHP SESASLNTLL PALVQRTDTK DSTQPLLQEH QQIEMKTFSN GSEQGESSHS DFKKQLLDKI PPDAEATLGL
241 VGCATFLDRP TVAFVRLKEA VELDSVLEVP VPVRFLFVVL GPDSPHISYH EIGRAISTMM SERVFRNDSY LAEGRQDLIK

321 SLDEFLDCCI VLPPSEIQNE RLLKMLLPVQ KDFLRKRYLP VEKKLEEPLK DLGHKLKDHD ITAEDSDDSL RRTGKIFGGM
401 VKDIKRRYPK YLSDIKDALN PQCLAAVIFI YFAALSPAIT FGGLLAEKTE RLIGVSELLL STAVQSGLFC LLGAQPLLVV
481 GFSGPLLVFE EAFYAFCVNK NYEYLVGRVW IGFWLILIVV VVVAFEGSFL VRFISRYTQE IFSILISLIF ILETFFKLIK
561 IFKEHPLKEV YKNITYPPDE EPRYPVPNTA LLSLVLMGGT FFIAFFLRKF KNSSFFPGKL RRVIGDFGVP IAIFIMTLAD
641 YLIKDTYTQK LKVPKGLQVS NPEQRNWFIH PLGSSLGNPF PIWMMFATAL PALLVFILIF LETQITTLIV SKPERKMLKG
721 SGFHLDLLLI VGMGGIAPLL GMPWLSATTV RTVTHANALT VMSKTTLPGE KACIQEVKEQ RVTGFLVAIL VGLSILMEPI
801 LKLIPLAVLF GIFLYMGVTS LNGIQLYDRI LLLLKPPKYH PDVSYVTKVK TWRMHIFTFT QMLCLGLLWG VKSSPASLAL
881 PFILILTVPL RLFLLPFIFT DVELKCLDAD DAEVTFDETE GQDVYDEVQM PV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_034271811.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MASQEDYESG IKAKLDLEAY GDSSLKQSNM SLASGDSSSS SSEEEPRGTE PAKPLISHKA SHNSYVELHE LVMDKNNEFR
 81 WMEASHWIKL EEDFEEMGHW GRPHLSYLTF QSLLEVRKAF SKGTVLLDLQ ERSLAGIANQ VLSQMIYEGK LKPDDQEVLL
161 RTLLLQHSHP SESASLNTLL PARVQRTDAK DSTQPLLQEH HQIEMKTFSN GSEQGESSHS GFKKQLLDKI PPDAEATLGL
241 VGCATFLDRP TLAFVRLKEA VELDSVLEVP VPVRFLFVVL GPDSPHINYH EIGRAISTMM SERVFRNDSY LAEGRQDLIK
321 SLDEFLDCCI VLPPSEIQNE RLLKMLLPVQ KDFLRKRYLP VEKKLEEPLK DLAHKLKDHD ITAEDSDDPL RRTGRIFGGL
401 VKDIKRRYPK YLSDIKDALN PQCLAAVIFI YFAALSPAIT FGGLLAEETE RLIGVSELLL STAVQSGLFC LLGAQPLLVV
481 GFSGPLLVFE KAFYAFCTNY NIEYLVGRVW IGFWLILIVI LVVAFEGSFL VRYISRYTQE IFSILISLIF IQETFSNLIK
561 IFKAHPLKGV YKNITFSGEE EPREPVPNTA LLSLVLMGGT FFIAFFLRKF KNSSFFPGRL RRVIGDFGVP IAIFIMTLAD
641 NLIKDTYTQK LKVPKGLQVS NTDKRDWFIH PLKEPIPKWF LFAAALPALL VFILIFLETQ ITTLIVSKPE RKLLKGSGFH
721 LDLLLIVGMG GIAPLLGMPW LSATTVRTVT HANALTIMSK TTLPGEKACI QEVKEQRITG FLVALLVGLS ILMEPILKLI
801 PLAVLFGIFL YMGVTSLSGI QLYDRILLML KPPKYHPDVS YVTKVKSWRM HIFTFSQILC LGLLWGVKSS PASLALPFIL
881 ILTVPLRRFL LPVIFTDIEL KCLDADDAEV TFDETEGQDV YDEVQMPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

XP_029143180.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSLASGDSSS SSPEEEPRGT EPVKPLISHK ASHNSYVELH ELVMDKNNEF RWMEASHWIK LEEDFEEMGH WGRPHLSYLT
 81 FQSLLEVRKA FNKGTVLLDL QERSLAGIAN QVLSQMTNEG KLKPDDQEVL LRTLLLQHSH PNESTSLNTL LPARVQQTDA
161 KDSTQPLLQE HHQIEMKTFF NGSEQGESSH SDFKKQLLDK IPSDAEATLG LVGCATFLDR PTLAFVRLKE AVELDSVLEV
241 PVPVRFLFVV LGPDSPHISY HEIGRAISTM MSERVFRNDS YLAEGRQDLI KSLDEFLDCC IVLPPSEIQN ERLLKMLLPV
321 QKDFLRKRYL PVEKKLEESL KDLGHKLKDH EVKAEDSDDS LRRTGRIFGG VVKDIKRRYP KYLSDIKDAL NPQCLAAVIF
401 IYFAALSPAI TFGGLLAEKT ERLIGVSELL LSTAVQSGLF CLLGAQPLLV VGFSGPLLVF EEAFYTFCTK NNIEYIVGRV
481 WIGFWLILIV IVVVAFEGSF LVRYISRYTQ EIFSILISLI FILETFFKLI KIFKEHPLKE VYTNITFSRD EEPRGPAPNT
561 ALLSLVLMGG TFFIAFFLRK FKNSSFFPGR LRRVIGDFGV PIAIFIMTLA DNLIKDTYTQ KLKVPKGLQV SNPEKRGWFI
641 YPTGIAFPIW MMFAAALPAL LVFILIFLET QITTLIVSKP ERKMLKGSGF HLDLLLIVGM GGIAPLLGMP WLSATTVRTV
721 THANALTVMS KTTLPGEKAC IQEVKEQRVT GFLVAILVGL SILMEPILKL IPLAVLFGIF LYMGVTSLNG IQLYDRILLM
801 LKPPKYHPDI SYVTKVKTWR MHIFTLTQIL CLGLLWGVKS SPASLALPFI LILTVPLRRF LLPVIFRDIE LKCLDSDDAE
881 VTFDETEGQD VYDEVQMPI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.AISTMMSER.V	Y	54.88	1024.4681	9	0.2	513.2415	2	31.14	7	F7:8285	17112021_RID_2349_DP7.raw						
K.GTVLLDLQER.S	Y	50.80	1142.6295	10	0.8	572.3225	2	45.59	7	F7:13262	17112021_RID_2349_DP7.raw						
R.NDSYLAEGR.Q	Y	47.45	1023.4621	9	0.6	512.7386	2	26.44	7	F7:6652	17112021_RID_2349_DP7.raw						

total 3 peptides

JAC95757.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVSPRTCVHK LGSTLPLLLV LWDLHYEGVQ CGINAEVEKQ LELGKKLLAA GQLADALSHF HAAIEGDXDN YLAYYRRATV
 81 YLAMGKSKAA IRDLSRVVEL KQDFTSARLQ RGHLLLKQGK LDEAVEDFEG VLLSNPSDKE EGEARAQLLK SDEARRLCSQ
161 AQSAFLEKDY YTAITLLDKI LEVCVWDADM RELRAESYIK EGEPGKAISD LKAAAKLKSD NTEAFYKIST IYYELGDHEM
241 SLSEVRECLK LDQDHKECFS HYKRVKKLNK HIVSAEELIQ EGRYQEATEK YEAVMKMETN VPVYTTRAKE RICHCFSKNQ
321 QTTEAIKVCT EVLQLEPENV NALKDRAEAY LLEEMYEEAI QDYETAKKYS DNDQQIQESL EKAQRMLKQS QKRDYYKILG
401 VKRNARKQEI IKAYRKLAMQ WHPDNFQDEE EKKKAEKKFI DIAAAKEVLT DPEMRRKFDA GEDPLDAESQ QGGGHPFHRT
481 WNSWQGFDPF SSGGPFQFKF HFN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F
K.YSDNDQQIQESLEK.A	Y	49.17	1695.7588	14	0.5	848.8871	2	35.45	3	F3:9753	17112021_RID_2349_DP3.raw			1.1168E5	
K.LKSDNTEAFYK.I	N	47.39	1314.6455	11	1.2	658.3308	2	27.25	7	F7:6950	17112021_RID_2349_DP7.raw				
K.EVLTDPEMR.R	N	42.20	1088.5172	9	0.9	545.2664	2	34.55	7	F7:9479	17112021_RID_2349_DP7.raw				
C.SQAQSAFLEK.D	Y	41.16	1107.5560	10	0.3	554.7855	2	29.85	4	F4:7720	17112021_RID_2349_DP4.raw				8.8606E
															total 4 peptides

ADI47590.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MMQVLLATIC LAVFPYQGSS IILESGNVND YEVVYPQKVT ALPQGAIQQP EQKYEDTMQY EIEVNGEPVV LHLEKNKDLF
 81 SEDYSETHYS PDGRKITTNP PVQDHCYYHG RIQNDAHSTA SMSACNGLKG YFKLRGETYF IEPLKIPDSE AHAVYKYENL
161 EKEDETPKIC GVTQTNWESD EPIKKASQLV ATSEQQRYYD RFRYVXXIVV VDHRMCKKYN GNLRRIRRRL YQLINFLNEM
241 YLPWNLRVPL VGMEFWNQRD LINVTSSPKV TLDLFGEWRE SDLLNRKEHD YAQLLTAIDF DGPTIGMAHI ATMCHSKLSV
321 GIVEDYRPAE SVVAAIMAHE MGHNLGLIHD ENQCNCDADS CIMYHQINNP PPMYFSNCSW NYYQNFLTNY KPDCTLIRPS
401 RTDIVSPPVC GNALLEKGEE CDCGSPANCQ DPCCDAASCK LHSWVECEIG ECCDQCRFKP AGTECRAIRS ECDLPEYCTG
481 QSVDCPIDRF HRNGKPCQSN NGYCYNGACP IMQNQCYALF GPDATVGQDA CFEENKKGKS YFYCRKENDV KIPCAPEDVK
561 CGRLLCEIVK NTCKYDYSED PNYGMVDEGT KCADGKVCRN RHCVDVTTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area I
R.TDIVSPPVC(+57.02)GNALLEK.G	Y	60.69	1711.8815	16	0.8	856.9487	2	49.01	1	F1:14875	12112021_RID_2349_DP1.raw	1.4223E6	4.9549
V.TQTNWESDEPIKK.A	N	44.98	1574.7576	13	0.5	788.3865	2	30.75	1	F1:8710	12112021_RID_2349_DP1.raw	3.3503E5	

E0Y421.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVLIRVLANL LLLQLSYAQK SSELVVGGDE CNINEHRSLV FLYNSSFGCG GTLINQQWVL SAAHCDMENV QIYLGLHNLR
                                    111
 81 LRNQDEQIRV AEEKFFCLSN KSYTKWDKDI MLIRLNSSVT YNTHIAPLSL PSSPPRVGSV CRIMGWGAIT SPNETFPNVP
161 HCANINILRY SVCRAAYRGL PAQSRTLCAG ILQGGIGSCM GDSGGPLICN GEIQGIVSWG DDICAQPHKP VHYTKVFDYS
241 DWIQSIIAGN TTATCPL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
K.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706I
R.AAYRGLPAQSR.T	Y	57.92	1188.6364	11	0.5	397.2196	3	24.28	1	F1:6637	12112021_RID_2349_DP1.raw	1.8692E7		
K.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085I
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616I
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097I
														total 5 pept

ADN04919.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVLIRVLANL LLLQLSYAQK SSELVVGGDE CNINEHRSLV FLYNSSFGCG GTLINQQWVL SAAHCDMENV QIYLGLHNLR
                                    111
 81 LRNQDEQIRV AEEKFFCLSN KSYTKWDKDI MLIRLNSSVT YNTHIAPLSL PSSPPRVGSV CRIMGWGAIT SPNETFPNVP
161 HCANINILRY SVCRAAYRGL PAQSRTLCAG ILQGGIGSCM GDSGGPLICN GEIQGIVSWG DDICAQPHKP VHYTKVFDYS
241 DWIQSIIAGN TTATCPL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
K.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706
R.AAYRGLPAQSR.T	Y	57.92	1188.6364	11	0.5	397.2196	3	24.28	1	F1:6637	12112021_RID_2349_DP1.raw	1.8692E7		
K.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097

total 5 pept

QBF53413.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LVLQLSYAQK SSELVVGGDE CNINEHRSLV FLYNSSFGCG GILINQEWVL SAAHCNMENV QIYLGMHNLR
                                      111
 81  PRNKDEQIRV AEEKFFCLSS KNYTKWDKDI MLIRLNSSVT YNTHIAPLSL PSSPPRVGSV CRIMGWGAIT SPNETFPNVP

161  HCANINILHY SVCRAAYRGL PAQSRTLCAG ILQGGIGSCM GDSGGPLICN GEIQGIVSWG DDICAQPHKP VHYTKVFDYS

241  DWIQSIIAGN TTATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
K.WDKDIMLIR.L	N	59.98	1188.6324	9	0.8	595.3240	2	47.61	2	F2:13483	12112021_RID_2349_DP2.raw		2.0105E7	1.3706
R.AAYRGLPAQSR.T	Y	57.92	1188.6364	11	0.5	397.2196	3	24.28	1	F1:6637	12112021_RID_2349_DP1.raw	1.8692E7		
K.WDKDIM(+15.99)LIR.L	N	54.14	1204.6274	9	0.6	603.3214	2	42.22	2	F2:11819	12112021_RID_2349_DP2.raw		1.4264E7	3.0085
W.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616
W.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097

total 5 pept

XP_007435739.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MIKSQRNASS TVRSFSSRSY TPGPVSSSRI STSYVSSGFG GSRYGGGGSF RGASAGSLGG ITAVSVNKSL LAPLNLEIDP
 81  TIHQVKTKEK EEIKTLNNKF ANLIDKVRFL EQQNKMLETK WSLLQNQKTT RSNMDSMFEA YISNLRRQLE NLGQERARLD
161  AELANMQGLV EDFKNRYEDE INRRTEKENE FVLLKKDVDE AYMNKVELES RLECLTDEIN FLRQLYDEEL RVLQSQISDT
241  SVILSMDNNR SLDLDGIIAE VRAQYEEIAN RSRSEAEKMY QIKYEELQTV AGKHGDDLRN TKNEINELNR MITRIQSEID

321  GLKGQRASLE AAITEAEERG ELAVKDANNK LAELEAALQR AKQDMARQLR EYQELMNVKL ALDIEIATYR KLLEGEESRL

401  ESGMQNLSIQ TKTTGYSGGL SSGFSSYGGG YSSSYSSGGY SINALPLESS AISKTKAIVI KKIETRDGKL VSESSDVLSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
R.AQYEEIANR.S	Y	73.65	1092.5199	9	0.5	547.2675	2	27.32	1	F1:7637	12112021_RID_2349_DP1.raw	6.6638E5	2.0438E5	3.7003E5	1.43
K.LALDIEIATYR.K	N	59.31	1276.7026	11	1.2	639.3594	2	57.61	4	F4:17049	17112021_RID_2349_DP4.raw				0

total 2 peptide

XP_015672252.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MMRKNYRNTS STVRSFSSRS SGPVASSRIS TSYSSAGSGF GGSRYGGGAS FRGTSAGSLG GITAVSVNKS LLAPLNLEID
 81 PAIQQVRIKE KEEIKTLNNK FANLIDKVRF LEQQNKMLET KWSLLQNQKT TRSNMDSMFE AYINNLRRQL ENLGQERARL
161 DAELGNMQGL VEEFKNKYED EINHRTEKEN EFVLLKKDVD EAYMNKVELE SRMECLTDEI NFLRQFYDEE LRVLQSQISD
241 TSVILSMDNN RSLDLDGIIT DVKAQYEEIA NRSRAEAERM YQIKYEELQT VAGKHGDDLR STKNEINELS RMINRIQSEI
321 DGLKGQRASL EAAITEAEER GELAVKDANN KLAELESAMQ RAKQDMARQL REYQELLNTK LALDIEIATY RKLLEGEEIR
401 LESGMQNLSI QTKTTGYSGG LSSGFSGYGG GYNSSYSSGG YSMNMLPMES SAISKTKAIV IKKIETRDGK LVSESSDVLS
481 K
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.AQYEEIANR.S	Y	73.65	1092.5199	9	0.5	547.2675	2	27.32	1	F1:7637	12112021_RID_2349_DP1.raw	6.6638E5	2.0438E5	3.7003E5	1.43
K.LALDIEIATYR.K	N	59.31	1276.7026	11	1.2	639.3594	2	57.61	4	F4:17049	17112021_RID_2349_DP4.raw				0

total 2 peptide

JAG44290.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MMRKNYRNTS NTVRTFSSRS SGPIASSRIS TSYSCSGFGG GRYGSGASFR GPSAGSLGGI TAVSVNKSLL APLNLEIDPA
 81 IQQVRTKEKE EIKILNNKFA NLIDKVRFLE QQNKMLETKW SLLQNQKTTR SNMDSMFEAY INTLRRQLEN LGQERARLGA
161 ELGNMQGLVE EFKNKYEDEI NHRTEKENEF VLLKKDVDEA YMNKVELESR MECLTDEINF LRQFYDEELR VLQSQISDTS
241 VILSMDNNRS LDLDGIITDV KAQYEEIANR SRAEAERMYQ IKYEELQTVA GKHGDDLRCT KNEINELSRM ITRIQSEIDG
321 LKGQRASLEA AITEAEERGE LAVKDANTKL AELECAMQRA KQDMARQLRE YQELLNTKLA LDIEIATYRK LLEGEEIRLE
401 SGMQNLSIQT KTTGYSGGLS CGFSGYGGGY NPSYSSGGYS MNMLPMESSA VSKTKAIVIK KIETRDGKLV SESSDVLSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.AQYEEIANR.S	Y	73.65	1092.5199	9	0.5	547.2675	2	27.32	1	F1:7637	12112021_RID_2349_DP1.raw	6.6638E5	2.0438E5	3.7003E5	1.43
K.LALDIEIATYR.K	N	59.31	1276.7026	11	1.2	639.3594	2	57.61	4	F4:17049	17112021_RID_2349_DP4.raw				0

total 2 peptide

TRINITY_DN6008
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKNYRNTSST VRSFSSRSYT PGPVASSRIS SSYSSSGFGG GSRYGGGASF RGASAGSLGG ITAVSVNKSL LAPLNLEIDP
 81 AMQQVRTKEK EEIKTLNNKF ANLIDKVRFL EQQNKMLETK WSLMQNQKTT RSNMDSMFEA YINTLRRQLD NLGQERARLD
161 AELANMQGLV EEFKNKYEDE INHRTEKENE FVLLKKDVDE AYMNKVELES RMECMTDEVN FLRQLYDEEL RVLQSQISDT
241 SVILSMDNNR SLNLEGIIAD VKAQYEEIAN RSRAEAERMY QIKYEELQNV AGKHGDDLRS TKNEINELNR MISRIQSEID
321 GLKGQRASLE AAITEAEERG ELAVKDANAK LAELESAMQR AKQDMARQLR EYQELLNTKL ALDIEIATYR KLLEGEEIRL
401 ESGMQNLSIQ TKTTGYSGGL SSGFSGYGGG YSSSYSGGGY SINMLPMESS AIGKTKAIVI KKIETRDGKL VSESSDVLSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.AQYEEIANR.S	Y	73.65	1092.5199	9	0.5	547.2675	2	27.32	1	F1:7637	12112021_RID_2349_DP1.raw	6.6638E5	2.0438E5	3.7003E5	1.43
K.LALDIEIATYR.K	N	59.31	1276.7026	11	1.2	639.3594	2	57.61	4	F4:17049	17112021_RID_2349_DP4.raw				0

total 2 peptide

AFJ50411.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MMRKNYRNTS NTVRTFSSRS SGPIASSRIS TSYSCSGFGG GRYGSGASFR GPSAGSLGGI TAVSVNKSLL APLNLEIDPA
 81 IQQVRTKEKE EIKILNNKFA NLIDKVRFLE QQNKMLETKW SLLQNQKTTR SNMDSMFEAY INTLRRQLEN LGQERARLGA
161 ELGNMQGLVE EFKNKYEDEI NHRTEKENEF VLLKKDVDEA YMNKVELESR MECLTDEINF LRQFYDEELR VLQSQISDTS
241 VILSMDNNRS LDLDGIITDV KAQYEEIANR SRAEAERMYQ IKYEELQTVA GKHGDDLRCT KNEINELSRM ITRIQSEIDG
321 LKGQRASLEA AITEAEERGE LAVKDANTKL AELECAMQRA KQDMARQLRE YQELLNTKLA LDIEIATYRK LLEGEEIRLE
401 SGMQNLSIQT KTTGYSGGLS CGFSGYGGGY NSSYSSGGYS MNMLPMESSA VSKTKAIVIK KIETRDGKLV SESSDVLSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Are
K.AQYEEIANR.S	Y	73.65	1092.5199	9	0.5	547.2675	2	27.32	1	F1:7637	12112021_RID_2349_DP1.raw	6.6638E5	2.0438E5	3.7003E5	1.43
K.LALDIEIATYR.K	N	59.31	1276.7026	11	1.2	639.3594	2	57.61	4	F4:17049	17112021_RID_2349_DP4.raw				0

total 2 peptide

TRINITY_DN2736
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  AASVTLDLFG DWRDKNLLRR KRHDNAQLLT GIDLNRQTLG IAHVEGMCNG KLSVGVIQDY CKSYLLVAIT MAHEMGHNLG

 81  MKHDNANCNC PDTSCIMS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F
R.HDNAQLLTGIDLNR.Q	Y	77.18	1578.8114	14	0.9	790.4137	2	46.31	2	F2:13153	12112021_RID_2349_DP2.raw	1.8674E5	1.5439E6	7.1135E
D.NAQLLTGIDLNR.Q	Y	51.88	1326.7256	12	1.0	664.3707	2	48.90	2	F2:13982	12112021_RID_2349_DP2.raw		1.8287E4	

total 2 peptides

TRINITY_DN471
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MCQPLRSVAI VEDYSPIDRV VAAIMAHEMG HNLGITHDEN PCSCGANSCI MAPQISDPPP MKFSDCSWDQ YQNFLTNDKA

 81  NCTLIRPSRT DIVSPPACGN ELLEVGEECD CGSP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.SVAIVEDYSPIDR.V	Y	83.77	1462.7303	13	0.2	732.3726	2	47.47	2	F2:13537	12112021_RID_2349_DP2.raw	4.0439E6	6.1514E6	1.3556E7 4

total 1 peptides

TRINITY_DN1497
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MTDLEREMGL PPIEQKLGLQ IWTINNMKMD PIPAKAYGSF FEGDCYIVLN NSKRQHSFAT DLHYWIGRTA TQDEQGAAAF
 81  YVTQMDDSLG GRAIQHREVQ GHESAAFKSY FKKGIIYKKG GLASGFKHVE TNMYNIKRLL HVKGKKHVTA TEVDLSWDSF
161  NKGDVFLMDL GKVLIQWNGP FCNVAEKSKG MILARSIRDG ERGGRAQIAI IDNEKDCPEL MQIMKATLGE RTQEIREPLT
241  DEKADEHQKA NVRLYHVYEN GKDLVVQEIA TRPLTQDLLS HEDCHIIDQG GLKIYVWRGK ESSKEERKAA FTRAVGFIQA
321  KGYPPSTNVE VVNDGAESAM FKQLFQKWTE KYTTQGLGKA YTLGKIAKVD QAKFDITQLY VTPEVAAEER MPDDASGKVE
401  VWRIENREMV PVNPKTYGQF YSGDCYLVLY TYTKSGRPHY IIYMWQGRHA SVDEITACAF NAVELDKKYG DEPVQVRVTM

481  GKEPRHFLAI FKGNLIIYEG GISHGQKMGP EPAIQLFQVR GTDEFNTKTV EVPARASSLN SNDVFILKTN QVCYLWCGKG
561  CSGDEREMAK TVADVISKWD KQTILEGQEP AEFWVALGGK APYASDKRFQ ERVPHYQSRL FECSNQTGRF IMTEIVDFGQ
641  DDLDEEDVML LDTWEEVFLW VGKAANSYEK TESISAAKEY LKNHPAGRDA ATPIIMVKQG HEPLNFTGWF TAWDPYKWSD

721  EKSYEQMKSS LGDVSAVSEI TMDLKNANFN HRSTSNKPVT ANADISEARS SMQDDQTFTN SSNCYNANTP CQEPNETGTF
801  PRDLLINKTV DELPDGVDPT KKEYYLSDAE FCDIFGKTKD AFYQMPAWKQ QNEKKQYGLF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area A
K.YGDEPVQVR.V	Y	57.76	1061.5142	9	0.2	531.7645	2	29.19	1	F1:8248	12112021_RID_2349_DP1.raw	4.705E4					
R.DAATPIIMVK.Q	Y	48.71	1057.5841	10	0.8	529.7997	2	45.65	1	F1:13790	12112021_RID_2349_DP1.raw	8.7907E4					

total 2 peptides

TRINITY_DN1497
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MYNIKRLLHV KGKKHVTATE VDLSWDSFNK GDVFLMDLGK VLIQWNGPFC NVAEKSKGMI LARSIRDGER GGRAQIAIID
 81 NEKDCPELMQ IMKATLGERT QEIREPLTDE KADEHQKANV RLYHVYENGK DLVVQEIATR PLTQDLLSHE DCHIIDQGGL
161 KIYVWRGKES SKEERKAAFT RAVGFIQAKG YPPSTNVEVV NDGAESAMFK QLFQKWTEKY TTQGLGKAYT LGKIAKVDQA
241 KFDITQLYVT PEVAAEERMP DDASGKVEVW RIENREMVPV NPKTYGQFYS GDCYLVLYTY TKSGRPHYII YMWQGRHASV
321 DEITACAFNA VELDKKYGDE PVQVRVTMGK EPRHFLAIFK GNLIIYEGGI SHGQKMGPEP AIQLFQVRGT DEFNTKTVEV
401 PARASSLNSN DVFILKTNQV CYLWCGKGCS GDEREMAKTV ADVISKWDKQ TILEGQEPAE FWVALGGKAP YASDKRFQER
481 VPHYQSRLFE CSNQTGRFIM TEIVDFGQDD LDEEDVMLLD TWEEVFLWVG KAANSYEKTE SISAAKEYLK NHPAGRDAAT
561 PIIMVKQGHE PLNFTGWFTA WDPYKWSDEK SYEQMKSSLG DVSAVSEITM DLKNANFNHR STSNKPVTAN ADISEARSSM
641 QDDQTFTNSS NCYNANTPCQ EPNETGTFPR DLLINKTVDE LPDGVDPTKK EYYLSDAEFC DIFGKTKDAF YQMPAWKQQN
721 EKKQYGLF
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
K.YGDEPVQVR.V	Y	57.76	1061.5142	9	0.2	531.7645	2	29.19	1	F1:8248	12112021_RID_2349_DP1.raw	4.705E4					
R.DAATPIIMVK.Q	Y	48.71	1057.5841	10	0.8	529.7997	2	45.65	1	F1:13790	12112021_RID_2349_DP1.raw	8.7907E4					

total 2 peptides

ETE68218.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTFKKTTY SQPGSGQTQT QAELESQLAM
 81 TRAQRIRAAM YPETAEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL INYQDDAELA TRAIPELTKL LNDEDPVVVS
161 KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH NLSHHREGLL SIFKSGGIPA LVRMLSSPVE
241 SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD CLQLLAYGNQ ESKLIILANG GPQALVQIMR
321 SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ NCLWTLRNLS DVATKQEGLD GVLKILVNQL
401 SSDDIHVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED ITEPAVCALR HLTSRHPEAE MAQNSVRLNY
481 GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHAPLQE AAVIPRLVQL LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV
561 EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QVRISEWMEV LLYSPVENIQ RVAAGVLCEL AQDKEAADAI DAEGASAPLM
641 ELLHSRNEGT ATYAAAVLFR ISEDKNPDYR KRVSVELTNS LFKHDPAAWE AAQSMIPIHE PYADELDGGY RGMYSGEIPM
721 DPMDMHMDMD GDYPMDTYSD GVRAPYPDHM LA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_025022318.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDVMNLIEQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQAGPGQAQ AQAQELESQL
 81 AMTRAQRIRA AMYPETVEDH SLLVTTQVEG QQTNVQRLAE PSQMLKSAIV HLINYQDDAE LATRAIPELT KLLNDEDPVV
161 VSKAAMIVNQ LSKKEASRRA LMQSAQIVAA VVRTMQNTSD LDTARCTTSI LHNLSHHREG LLSIFKSGGI PALVRMLSSP
241 VESVLFYAIT TLHNLLLYQE GAKMAVRLAD GLQKMVPLLT KNNPKFLAIT TDCLQLLAYG NQESKLIILA NGGPQALVQI
321 MRSYTYEKLL WTTSRVLKVL SVCPSNKPAI VEAGGMQALG KHLTSSSPRL VQNCLWTLRN LSDVATKQEG LDGVLKILVN
401 QLSSDDINVL TCATGTLSNL TCNNSKNKTL VTQSNGVEAL IHTILRAGDK EDITEPAVCA LRHLTSRHPE AEMAQNSVRL
481 NYGIPAIVKL LNQPNQWPLI KATIGLIRNL ALCPANHAPL QEAAVIPRLV QLLVKAHQDA QRHAAAGTQQ PYTDGVKMEE
561 IVEGCTGALH ILARDPMNRM EIFRLNTIPL FVQLLYSPVE NIQRVAAGVL CELAQDKEAA DAIDAEGASA PLMELLHSRN
641 EGTATYAAAV LFRISEDKNP DYRKRVSVEL TNSLFKHDPA AWEAAQSMIP IHEPYADELD GGYRGMYPGE IPMDPMDMHM
721 DMDGDYPMDT YSDGVRAPYP DHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

JAG67632.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQGQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PIDPMDLHMD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

JAG44306.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDA GYRGMYSAEI PMDPMDMHLD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

JAA96758.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDA GYRGMYSAEI PMDPMDMHLD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

JAG46538.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDA GYRGMYSAEI PMDPMDMHLD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

LAB43566.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 STWGERGGVE RGNQGGGDGA GRIAMEVVNI IDQPIKVTEW QQTYTYDSGI HSGMNTQVPS VSSKGLMDED DLYGNQYTIK
 81 KTTTYSQPGS GKAQTQAELE SQLAMTRAQR IRAAMYPETT EDHSLLVTTQ VEGQQTNVQR LAEPSQMLKS AIVHLINYQD
161 DAELATRAIP ELTKLLNDED PVVVSKAAMI VNQLSKKEAS RRALMQSAQI VAAVVRTMQN TSDLDTARCT TSILHNLSHH
241 REGLLSIFKS GGIPALVRML SSPVESVLFY AITTLHNLLL YQEGAKMAVR LADGLQKMVP LLTKNNPKFL AITTDCLQLL
321 AYGNQESKLI ILANGGPQAL VQIMRSYTYE KLLWTTSRVL KVLSVCPSNK PAIVEAGGMQ ALGKHLTSSS PRLVQNCLWT
401 LRNLSDVATK QEGLDGVLKI LVNQLSSDDI HVLTCATGTL SNLTCNNSKN KTLVTQSNGV EALIHTILRA GDKEDITEPA
481 VCALRHLTSR HPEAEMAQNS VRLNYGIPAI VKLLNQPNQW PLIKATIGLI RNLALCPANH APLQEAAVIP RLVQLLVKAH
561 AAAGTQQPYT DGVKMEEIVE GCTGALHILA RDPMNRMEIF RLNTIPLFVQ LLYSPVENIQ RVAAGVLCEL AQDKEAADAI
641 DAEGASAPLM ELLHSRNEGT ATYAAAVLFR ISEDKNPDYR KRVSVELTNS LFKHDPAAWE AAQSMIPIHE PYADELDGGY
721 RGMYSGEIPM DPMDMHMDMD GDYPMDTYSD GVRAPYPDHM LA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

JAV50234.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRLE IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDA GYRAMYSAEI PMDALDMDGD
721 YPMDTYSDGV RAPYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026576301.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQELESQLAM
 81 TRAQRIRAAM YPETAEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL INYQDDAELA TRAIPELTKL LNDEDPVVVS
161 KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH NLSHHREGLL SIFKSGGIPA LVRMLSSPVE
241 SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD CLQLLAYGNQ ESKLIILANG GPQALVQIMR
321 SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ NCLWTLRNLS DVATKQEGLD GVLKILVNQL
401 SSDDIHVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED ITEPAVCALR HLTSRHPEAE MAQNSVRLNY
481 GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHAPLQE AAVIPRLVQL LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV
561 EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSPVENI QRVAAGVLCE LAQDKEAADA IDAEGASAPL MELLHSRNEG
641 TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIH EPYADELDGG YRGMYSGEIP MDAMDMDGDY
721 PMDTYSDGVR APYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026525656.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQELESQLAM
 81 TRAQRIRAAM YPETAEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL INYQDDAELA TRAIPELTKL LNDEDPVVVS
161 KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH NLSHHREGLL SIFKSGGIPA LVRMLSSPVE
241 SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD CLQLLAYGNQ ESKLIILANG GPQALVQIMR
321 SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ NCLWTLRNLS DVATKQEGLD GVLKILVNQL
401 SSDDIHVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED ITEPAVCALR HLTSRHPEAE MAQNSVRLNY
481 GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHAPLQE AAVIPRLVQL LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV
561 EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSPVENI QRVAAGVLCE LAQDKEAADA IDAEGASAPL MELLHSRNEG
641 TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIH EPYADELDGG YRGMYSGEIP MDAMDMDGDY
721 PMDTYSDGVR APYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026576299.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDIHVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDAMDMDGD
721 YPMDTYSDGV RAPYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026525655.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDIHVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDAMDMDGD
721 YPMDTYSDGV RAPYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026525654.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDIHVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDAMDMDGD
721 YPMDTYSDGV RAPYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_026576298.1
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MEVMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDIHVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDAMDMDGD
721 YPMDTYSDGV RAPYPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

XP_013919280.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQIA
 81 MTRAQRIRAA MYPETAEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRAMYSGEI PMDHMDMHMD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

TRINITY_DN206
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 PLFAGTSHLE RGGVERGKQG GGDGAGRIAM DMMNIIDQPI KVTEWQQTYT YDSGIHSGMN TQVPSVSSKG LMDEDDLYGK
 81 QYTIKKTTTY SQPGSGQAQS QAELESQLAM TRAQRIRAAM YPETAEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL
161 INYQDDAELA TRAIPELTKL LNDEDPVVVS KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH
241 NLSHHREGLL SIFKSGGIPA LVRMLSSPVE SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD
321 CLQLLAYGNQ ESKLIILANG GPQALVQIMR SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ
401 NCLWTLRNLS DVATKQEGLD GVLKILVNQL SSDDINVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED
481 ITEPAVCALR HLTSRHPEAE MAQNSVRLNY GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHVPLQE AAVIPRLVQL
561 LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSPVENI QRVAAGVLCE
641 LAQDKEAADA IDAEGASAPL MELLHSRNEG TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIH
721 EPYADDVDAG YRGMYSGEIP MDPMDMHLDM DGDYPMDTYS DGVRAPYPGH MLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

TRINITY_DN206
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 PLFAGTSHLE RGGVERGKQG GGDGAGRIAM DMMNIIDQPI KVTEWQQTYT YDSGIHSGMN TQVPSVSSKG LMDEDDLYGK
 81 QYTIKKTTTY SQPGSGQAQS QAELESQLAM TRAQRIRAAM YPETAEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL
161 INYQDDAELA TRAIPELTKL LNDEDPVVVS KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH
241 NLSHHREGLL SIFKSGGIPA LVRMLSSPVE SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD
321 CLQLLAYGNQ ESKLIILANG GPQALVQIMR SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ
401 NCLWTLRNLS DVATKQEGLD GVLKILVNQL SSDDINVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED
481 ITEPAVCALR HLTSRHPEAE MAQNSVRLNY GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHVPLQE AAVIPRLVQL
561 LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSPVENI QRVAAGVLCE
641 LAQDKEAADA IDAEGASAPL MELLHSRNEG TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIH
721 EPYADDVDAG YRGMYSGEIP MDPMDMHLDM DGDYPMDTYS DGVRAPYPGH MLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

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back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MGTRDGLCQA RCSPPLFAES SHLERGGVER SNQGGGDGAS RIAMDMMNII DQPIKVTEWQ QTYTYDSGIH SGMNTQVPSV
 81 SSKGLMDEDD LYGKQYTIKK TTTYSQPGSG QAQTQAELES QLAMTRAQRI RAAMYPETAE DHTLLLTTQV EGQQTNVQRL
161 AEPSQMLKSA IVHLINYQDD AELATRAIPE LTKLLNDEDP VVVSKAAMIV NQLSKKDASR RALMQSAQIV AAVVRTMQNT
241 SDLDTARCTT SILHNLSHHR EGLLSIFKSG GIPALVRMLS SPVESVLFYA ITTLHNLLLY QEGAKMAVRL ADGLQKMVPL
321 LTKNNPKFLA ITTDCLQLLA YGNQESKLII LANGGPQALV QIMRSYTYEK LLWTTSRVLK VLSVCPSNKP AIVEAGGMQA
401 LGKHLTSSSP RLVQNCLWTL RNLSDVATKQ EGLDGVLKIL VNQLSSDDIN VLTCATGTLS NLTCNNSKNK TLVTQSNGVE
481 ALIHTILRAG DKEDITEPAV CALRHLTSRH PEAEMAQNSV RLNYGIPAIV KLLNQPNQWP LIKATIGLIR NLALCPANHA
561 PLQEAAVIPR LVQLLVKAHQ DAQRHAAAGT QQPYTDGVKM EEIVEGCTGA LHILARDPMN RMEIFRLNTI PLFVQLLYSP
641 VENIQRVAAG VLCELAQDKE AADAIDAEGA SAPLMELLHS RNEGTATYAA AVLFRISEDK NPDYRKRVSV ELTNSLFKHD
721 PAAWEAAQSM IPIHEPYADE LDGGYRAMYS GEIPMDHMDM HMDMDGDYPM DTYSDGVRAP YPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_032091065.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MGTRDGLCQA RCSPPLFAES SHLERGGVER SNQGGGDGAS RIAMDMMNII DQPIKVTEWQ QTYTYDSGIH SGMNTQVPSV
 81 SSKGLMDEDD LYGKQYTIKK TTTYSQPGSG QAQTQAELES QLAMTRAQRI RAAMYPETAE DHTLLLTTQV EGQQTNVQRL
161 AEPSQMLKSA IVHLINYQDD AELATRAIPE LTKLLNDEDP VVVSKAAMIV NQLSKKDASR RALMQSAQIV AAVVRTMQNT
241 SDLDTARCTT SILHNLSHHR EGLLSIFKSG GIPALVRMLS SPVESVLFYA ITTLHNLLLY QEGAKMAVRL ADGLQKMVPL
321 LTKNNPKFLA ITTDCLQLLA YGNQESKLII LANGGPQALV QIMRSYTYEK LLWTTSRVLK VLSVCPSNKP AIVEAGGMQA
401 LGKHLTSSSP RLVQNCLWTL RNLSDVATKQ EGLDGVLKIL VNQLSSDDIN VLTCATGTLS NLTCNNSKNK TLVTQSNGVE
481 ALIHTILRAG DKEDITEPAV CALRHLTSRH PEAEMAQNSV RLNYGIPAIV KLLNQPNQWP LIKATIGLIR NLALCPANHA
561 PLQEAAVIPR LVQLLVKAHQ DAQRHAAAGT QQPYTDGVKM EEIVEGCTGA LHILARDPMN RMEIFRLNTI PLFVQLLYSP
641 VENIQRVAAG VLCELAQDKE AADAIDAEGA SAPLMELLHS RNEGTATYAA AVLFRISEDK NPDYRKRVSV ELTNSLFKHD
721 PAAWEAAQSM IPIHEPYADE LDGGYRAMYS GEIPMDHMDM HMDMDGDYPM DTYSDGVRAP YPDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_034271617.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQELESQLAM
 81 TRAQRIRAAM YPETTEDHTL LLTTQVEGQQ TNVQRLAEPS QMLKSAIVHL INYQDDAELA TRAIPELTKL LNDEDPVVVS
161 KAAMIVNQLS KKEASRRALM QSAQIVAAVV RTMQNTSDLD TARCTTSILH NLSHHREGLL SIFKSGGIPA LVRMLSSPVE
241 SVLFYAITTL HNLLLYQEGA KMAVRLADGL QKMVPLLTKN NPKFLAITTD CLQLLAYGNQ ESKLIILANG GPQALVQIMR
321 SYTYEKLLWT TSRVLKVLSV CPSNKPAIVE AGGMQALGKH LTSSSPRLVQ NCLWTLRNLS DVATKQEGLD GVLKILVNQL
401 SSDDINVLTC ATGTLSNLTC NNSKNKTLVT QSNGVEALIH TILRAGDKED ITEPAVCALR HLTSRHPEAE MAQNSVRLNY
481 GIPAIVKLLN QPNQWPLIKA TIGLIRNLAL CPANHAPLQE AAVIPRLVQL LVKAHQDAQR HAAAGTQQPY TDGVKMEEIV
561 EGCTGALHIL ARDPMNRMEI FRLNTIPLFV QLLYSPVENI QRVAAGVLCE LAQDKEAADA IDAEGASAPL MELLHSRNEG
641 TATYAAAVLF RISEDKNPDY RKRVSVELTN SLFKHDPAAW EAAQSMIPIH EPYADELDGG YRGMYSGEIP MDPMDMHMDM
721 DGDYPMDTYS DGVRAPYPDH MLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_034271615.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETTEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDPMDMHMD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_034271618.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETTEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDPMDMHMD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_034271616.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDMMNIIDQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQPGSGQAQ TQAELESQLA
 81 MTRAQRIRAA MYPETTEDHT LLLTTQVEGQ QTNVQRLAEP SQMLKSAIVH LINYQDDAEL ATRAIPELTK LLNDEDPVVV
161 SKAAMIVNQL SKKEASRRAL MQSAQIVAAV VRTMQNTSDL DTARCTTSIL HNLSHHREGL LSIFKSGGIP ALVRMLSSPV
241 ESVLFYAITT LHNLLLYQEG AKMAVRLADG LQKMVPLLTK NNPKFLAITT DCLQLLAYGN QESKLIILAN GGPQALVQIM
321 RSYTYEKLLW TTSRVLKVLS VCPSNKPAIV EAGGMQALGK HLTSSSPRLV QNCLWTLRNL SDVATKQEGL DGVLKILVNQ
401 LSSDDINVLT CATGTLSNLT CNNSKNKTLV TQSNGVEALI HTILRAGDKE DITEPAVCAL RHLTSRHPEA EMAQNSVRLN
481 YGIPAIVKLL NQPNQWPLIK ATIGLIRNLA LCPANHAPLQ EAAVIPRLVQ LLVKAHQDAQ RHAAAGTQQP YTDGVKMEEI
561 VEGCTGALHI LARDPMNRME IFRLNTIPLF VQLLYSPVEN IQRVAAGVLC ELAQDKEAAD AIDAEGASAP LMELLHSRNE
641 GTATYAAAVL FRISEDKNPD YRKRVSVELT NSLFKHDPAA WEAAQSMIPI HEPYADELDG GYRGMYSGEI PMDPMDMHMD
721 MDGDYPMDTY SDGVRAPYPD HMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_025022317.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDVMNLIEQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQAGPGQAQ AQAQAELESQ
 81 LAMTRAQRIR AAMYPETVED HSLLVTTQVE GQQTNVQRLA EPSQMLKSAI VHLINYQDDA ELATRAIPEL TKLLNDEDPV
161 VVSKAAMIVN QLSKKEASRR ALMQSAQIVA AVVRTMQNTS DLDTARCTTS ILHNLSHHRE GLLSIFKSGG IPALVRMLSS
241 PVESVLFYAI TTLHNLLLYQ EGAKMAVRLA DGLQKMVPLL TKNNPKFLAI TTDCLQLLAY GNQESKLIIL ANGGPQALVQ
321 IMRSYTYEKL LWTTSRVLKV LSVCPSNKPA IVEAGGMQAL GKHLTSSSPR LVQNCLWTLR NLSDVATKQE GLDGVLKILV
401 NQLSSDDINV LTCATGTLSN LTCNNSKNKT LVTQSNGVEA LIHTILRAGD KEDITEPAVC ALRHLTSRHP EAEMAQNSVR
481 LNYGIPAIVK LLNQPNQWPL IKATIGLIRN LALCPANHAP LQEAAVIPRL VQLLVKAHQD AQRHAAAGTQ QPYTDGVKME
561 EIVEGCTGAL HILARDPMNR MEIFRLNTIP LFVQLLYSPV ENIQRVAAGV LCELAQDKEA ADAIDAEGAS APLMELLHSR
641 NEGTATYAAA VLFRISEDKN PDYRKRVSVE LTNSLFKHDP AAWEAAQSMI PIHEPYADEL DGGYRGMYPG EIPMDPMDMH
721 MDMDGDYPMD TYSDGVRAPY PDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				

total 3 peptides

XP_007428111.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MDVMNLIEQP IKVTEWQQTY TYDSGIHSGM NTQVPSVSSK GLMDEDDLYG KQYTIKKTTT YSQAGPGQAQ AQAQAELESQ
 81 LAMTRAQRIR AAMYPETVED HSLLVTTQVE GQQTNVQRLA EPSQMLKSAI VHLINYQDDA ELATRAIPEL TKLLNDEDPV
161 VVSKAAMIVN QLSKKEASRR ALMQSAQIVA AVVRTMQNTS DLDTARCTTS ILHNLSHHRE GLLSIFKSGG IPALVRMLSS
241 PVESVLFYAI TTLHNLLLYQ EGAKMAVRLA DGLQKMVPLL TKNNPKFLAI TTDCLQLLAY GNQESKLIIL ANGGPQALVQ
321 IMRSYTYEKL LWTTSRVLKV LSVCPSNKPA IVEAGGMQAL GKHLTSSSPR LVQNCLWTLR NLSDVATKQE GLDGVLKILV
401 NQLSSDDINV LTCATGTLSN LTCNNSKNKT LVTQSNGVEA LIHTILRAGD KEDITEPAVC ALRHLTSRHP EAEMAQNSVR
481 LNYGIPAIVK LLNQPNQWPL IKATIGLIRN LALCPANHAP LQEAAVIPRL VQLLVKAHQD AQRHAAAGTQ QPYTDGVKME
561 EIVEGCTGAL HILARDPMNR MEIFRLNTIP LFVQLLYSPV ENIQRVAAGV LCELAQDKEA ADAIDAEGAS APLMELLHSR
641 NEGTATYAAA VLFRISEDKN PDYRKRVSVE LTNSLFKHDP AAWEAAQSMI PIHEPYADEL DGGYRGMYPG EIPMDPMDMH
721 MDMDGDYPMD TYSDGVRAPY PDHMLA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.LNYGIPAIVK.L	Y	54.39	1086.6437	10	0.2	544.3292	2	49.42	6	F6:14436	17112021_RID_2349_DP6.raw	5.5682E4			1.1942E5
R.TMQNTSDLDTAR.C	Y	50.31	1351.6038	12	0.9	676.8098	2	26.03	6	F6:6391	17112021_RID_2349_DP6.raw				
R.ISEDKNPDYR.K	Y	46.51	1235.5781	10	1.3	618.7971	2	18.97	6	F6:3975	17112021_RID_2349_DP6.raw				
															total 3 peptides

TRINITY_DN459
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 QSADCPIDRY HRNGQPCLQN YGYCYNGKCP IMHHQCYYLF GANSTKGQDG CFDWNKKGTG DFYCRKENDV PIPCAPEDVK
                                102
 81 CGRLFCEILP NTCKHAPEDN GMVDPGTKCE DKKVCMNRKC VDVNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
K.HAPEDNGMVDPGTK.C	Y	76.97	1466.6460	14	-0.6	734.3298	2	23.50	4	F4:5677	17112021_RID_2349_DP4.raw	1.8448E6	3.4934E5
K.HAPEDNGM(+15.99)VDPGTK.C	Y	63.27	1482.6409	14	0.1	742.3278	2	23.52	4	F4:5529	17112021_RID_2349_DP4.raw	1.8341E6	
													total

TRINITY_DN459
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 CEQCRFKRAG TECRRASECD LPEYCTGQSA ECPTDVFHSN GKPCLNNFGY CYNGKCPIMY HQCYALFGAN ATVGQDGCFE
                                                          131
 81 WNKKGESYFY CRKENGVPIP CAPEDGYVKC GRLFCEILPN TCKHAPEDNG MVDPGTKCED KKVCMNRKCV DVNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
K.HAPEDNGMVDPGTK.C	Y	76.97	1466.6460	14	-0.6	734.3298	2	23.50	4	F4:5677	17112021_RID_2349_DP4.raw	1.8448E6	3.4934E5
K.HAPEDNGM(+15.99)VDPGTK.C	Y	63.27	1482.6409	14	0.1	742.3278	2	23.52	4	F4:5529	17112021_RID_2349_DP4.raw	1.8341E6	
													total

TRINITY_DN3041
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                        20
  1 RLFCEILPNT CKHAPEDNGM VDPGTKCEDK KVCMNRKCVD VNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2
K.HAPEDNGMVDPGTK.C	Y	76.97	1466.6460	14	-0.6	734.3298	2	23.50	4	F4:5677	17112021_RID_2349_DP4.raw	1.8448E6	3.4934E5
K.HAPEDNGM(+15.99)VDPGTK.C	Y	63.27	1482.6409	14	0.1	742.3278	2	23.52	4	F4:5529	17112021_RID_2349_DP4.raw	1.8341E6	
													total

TRINITY_DN2

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 RAASHMKERL PRVGITCRRS LFNPRSNWIW SAGRTMRCWV FLAVVAATLL AVRARDPFAE DCRIHEYPPA GPTYKGTIPE
 81 YVINLDLPPS ERWVQVIHDK KNELKAVIKT VRDIVLSFIH EKFVASMESK IGWLCSTLPY PFNEEIKGIA SAIDGPLGDV
161 VLFNIFYEIF TVCTSIIAED KTGKLYHARN LDFGLFLGWD IQNNSWDTTQ KLKPLMVSLD FQKNNKTVFK SANFAGYVGI
241 VSGVKQGLFT LTMNERFSLD GGYIGIFEWL IGKRDGWWMS FLTRAVLENS TSYEDAKDKL VNTKLLAPAY FIVGGNKLDE
321 GCIITRSRTA TLNIKNLDAK NGNWFVIETN YDPWKAPLII DDRRHPAMNC LNQTGQEKIA LPGLYNVLST KPILNKLTVS
401 TTLLEVSEGH IETYLRDCPD PCSPW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.LLAPAYFIVGGNK.L	Y	56.67	1361.7706	13	0.3	681.8928	2	57.51	4	F4:17066	17112021_RID_2349_DP4.raw				3.8785E:
R.DGWWMSFLTR.A	Y	52.96	1297.5913	10	3.2	649.8050	2	74.68	3	F3:22606	17112021_RID_2349_DP3.raw			7.0205E4	
														total 2 peptides	

TRINITY_DN7999

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 KSQMYLQMNH LRSGDTTVYH CSGDGNYYAF DVWGPGTVVT VTNDPPKAPS VFPLTPGHET QVAKALSTAS NVTIGCLIKN
 81 YFPEPATVQW NSGAITSGIQ NFPPVLLASN HYSHTSLLTI PASQWQSESF QCNVEHAATN TRINKIIERS AIRSPVGPEI
161 TVFHSCDSRD SDGTVQLWCH ISGFYPKQLD IDWKVGSRSG QLHPYNYPPW QNPGTYTFST ASVVNITQDD WLEGNSYYCE
241 ATHAASQTKV KGKAKKCKDG SSCPSGDIKV DILPPRPKAL YIDRNSKISC VVSNLQNEQG LKFTWFREKS GHLTPDAIET
321 TEGSNGGYIV LSRLGIFSED WDSGETFTCV VEHPTFVSPV TKKISKSRGK HSAPKVYVFP PHQEELNPGR SVSLTCLVTG
401 FSPEAADVQW LEDHNPLSED NSVTTPPMKN KHDDSYFLYS KLLVPKTDWN TKSFTCMVVH EDLPMKFTQR NISRTQGKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.APSVFPLTPGHETQVA.K	Y	55.91	1649.8413	16	0.2	825.9281	2	48.79	7	F7:14307	17112021_RID_2349_DP7.raw					
K.APSVFPLTPGHETQ.V	Y	50.42	1479.7357	14	0.6	740.8756	2	45.66	7	F7:13339	17112021_RID_2349_DP7.raw					
															total 2 peptides	

TRINITY_DN7999

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 AKSQLYLQMS SLKAEDTAVY YCTRHIYGLG WLYYAFDVWG PGTVVTVTND PPKAPSVFPL TPGHETQVAK ALSTASNVTI
 81 GCLIKNYFPE PATVQWNSGA ITSGIQNFPP VLLASNHYSH TSLLTIPASQ WQSESFQCNV EHAATNTRIN KIIERSAIRS
161 PVGPEITVFH SCDSRDSDGT VQLWCHISGF YPKQLDIDWK VGSRSGQLHP YNYPPWQNPG TYTFSTASVV NITQDDWLEG
241 NSYYCEATHA ASQTKVKGKA KKCKDGSSCP SGDIKVDILP PRPKALYIDR NSKISCVVSN LQNEQGLKFT WFREKSGHLT
321 PDAIETTEGS NGGYIVLSRL GIFSEDWDSG ETFTCVVEHP TFVSPVTKKI SKSRGKHSAP KVYVFPPHQE ELNPGRSVSL
401 TCLVTGFSPE AADVQWLEDH NPLSEDNSVT TPPMKNKHDD SYFLYSKLLV PKTDWNTKSF TCMVVHEDLP MKFTQRNISR
481 TQGKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Ar F
K.APSVFPLTPGHETQVA.K	Y	55.91	1649.8413	16	0.2	825.9281	2	48.79	7	F7:14307	17112021_RID_2349_DP7.raw					
K.APSVFPLTPGHETQ.V	Y	50.42	1479.7357	14	0.6	740.8756	2	45.66	7	F7:13339	17112021_RID_2349_DP7.raw					
															total 2 peptides	

TRINITY_DN13494

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEGLRGGLSL AGLLSLLLVA GVMKEASTEV SCGVPALGRI VGGSDARNGQ WPWQANLNFN GVHACGGTLI TLQWLVTAAH
 81 CFPKANQIDM YEVALGSYQL KNPSPDIQVI LVEEVIKYPD YSEDESSQGD IALVKLKVPA TYTRTVRPIC LPASSVTFPP
161 GMRCTVTGWG NVLADTSLPS PMTLQQLEVP IIGLENCKCL YGRNPDPDGS HTLHNDMMCA GFAEGKKDAC QGDSGGPLSC
241 LVDNAWFLAG VVSWGDNCGE PNRPGVYIRL PVYADWIKQR VPEVQLQQVT VPPGPTPEES FCPNSTSGGG PYDDIQPSPG
321 WSRPLNPDKS TPSGSVSIAC MVGLPLLLLL LQSCLW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
R.LPVYADWIK.Q	Y	65.35	1103.6014	9	0.5	552.8083	2	54.90	2	F2:15975	12112021_RID_2349_DP2.raw		6.1755E5	
K.ANQIDMYEVALGSYQLK.N	Y	54.76	1941.9506	17	1.7	971.9843	2	60.47	2	F2:17731	12112021_RID_2349_DP2.raw		1.1688E5	
													total 2 peptides	

A8Y7P1.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC LAHMRSFYYD SESKKCKEFI YGGCHGNANK FPSRDKCRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw						3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw						4
													total 2 peptides				

CAL69604.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC MAYIRSFYYD SESKKCKEFI YGGCHGNANN FPTRDKCRQT

 81  CRGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw						3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw						4
													total 2 peptides				

A8Y7N6.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC MAYIRSFYYD SESKKCKEFI YGGCHGNANN FPTRDKCRQT

 81  CRGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw						3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw						4
													total 2 peptides				

CAL69609.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC LAHMRSFYYD SESKKCKEFI YGGCHGNANK FPSRDKCRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw						3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw						4
													total 2 peptides				

A8Y7P5.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC LAHMRSFYYD SESKKCKEFI YGGCHGNANK FPSRDKCRQT

 81  CGASAKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw							3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw							4
																	total 2 peptides	

AFD04724.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLALWAELT PISGHDRPKF CYLPADPGEC MAYIRSFYYD SESKKCKEFI YGGCHGNANN FPTRDKCRQT

 81  CRAPRKGRHT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw							3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw							4
																	total 2 peptides	

CAL69613.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC LAHMRSFYYD SESKKCKEFI YGGCHGNANK FPSRDKCRQT

 81  CGASAKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw							3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw							4
																	total 2 peptides	

A8Y7N7.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC MAYIRSFYYD SESKKCKEFI YGGCHGNANN FPTRDKCRQT

 81  CRAPRKGRHT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw							3
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw							4
																	total 2 peptides	

CAL69605.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPKF CYLPADPGEC MAYIRSFYYD SESKKCKEFI YGGCHGNANN FPTRDKCRQT

 81  CRAPRKGRHT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESKK.C	Y	70.58	1252.5612	10	0.4	627.2881	2	25.22	7	F7:6242	17112021_RID_2349_DP7.raw							3
																	total 2 peptides	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
R.SFYYDSESK.K	Y	43.22	1124.4662	9	0.1	563.2404	2	31.78	7	F7:8493	17112021_RID_2349_DP7.raw							4
																	total 2 peptides	

TRINITY_DN960
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 AWDGLPRPWC PAVRGSRARK ARSEEEEEEA PAELRPQSAP SGPVPSPPPR PGEGGPASDG WLDRDGSPLL LPPPPPPAGA
 81 EDAVGASPAG RLYKARTAMP PLRANPARQA NAAPFGSAVR AFEDSLSLSL ARSRPEALPA PAHSGMFVSR LAASGLLLLS
161 LLALSLDGKP LKQKWPMPGP EIPPLEQRWP GPKVPPLEQR WPGPEIPPLE QRWPGPQIPP LQQKWRGPLQ PEAPPLMEPH
241 QLSAGGTTAL REELSPRAEA AQHPGGSGGG WRDENEPPKK LPPSSCFGHK IDRIGSVSGL GCNKFKPGH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
															total 2 peptides	

TRINITY_DN960
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 AWDGLPRPWC PAVRGSRARK ARSEEEEEEA PAELRPQSAP SGPVPSPPPR PGEGGPASDG WLDRDGSPLL LPPPPPPAGA
 81 EDAVGASPAG RLYKARTAMP PLRANPARQA NAAPFGSAVR AFEDSLSLSL ARSRPEALPA PAHSGMFVSR LAASGLLLLS
161 LLALSLDGKP LKQKWPMPGP EIPPLEQRWP GPKVPPLEQR WPGPEIPPLE QRWPGPKVPP LEQRWPGPEI PPLEQRWPGP
241 KVPPLEQRWP GPQIPPLQQK WRGPLQPEAP PLMEPHQLSA GGTTALREEL SPRAEAAQHP GGSGGGWRDE NEPPKKLPPS
321 SCFGHKIDRI GSVSGLGCNK FKPGH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
															total 2 peptides	

TRINITY_DN960
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 KKERKKERKK ERKKERKKER KKERKKEAGW GGRRGFSTPT FCQPSPTQSV CKAWDGLPRP WCPAVRGSRA RKARSEEEEE
 81 EAPAELRPQS APSGPVPSPP PRPGEGGPAS DGWLDRDGSP LLLPPPPPPA GAEDAVGASP AGRLYKARTA MPPLRANPAR
161 QANAAPFGSA VRAFEDSLSL SLARSRPEAL PAPAHSGMFV SRLAASGLLL LSLLALSLDG KPLKQKWPMP GPEIPPLEQR
241 WPGPKVPPLE QRWPGPEIPP LEQRWPGPQI PPLQQKWRGP LQPEAPPLME PHQVSRRRAP PARLAFPRRG SRACFGSVLG
321 GGEETGGPFA ALGGSGDGDV GLGSRGGESR ARSGEGTTHP IGPSSLGHCS RGAPGWSEGA GGWWERTAGP PLAFFPPCTR
401 PV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
															total 2 peptides	

TRINITY_DN960
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 KKERKKERKK ERKKERKKER KKERKKEAGW GGRRGFSTPT FCQPSPTQSV CKAWDGLPRP WCPAVRGSRA RKARSEEEEE
 81 EAPAELRPQS APSGPVPSPP PRPGEGGPAS DGWLDRDGSP LLLPPPPPPA GAEDAVGASP AGRLYKARTA MPPLRANPAR
161 QANAAPFGSA VRAFEDSLSL SLARSRPEAL PAPAHSGMFV SRLAASGLLL LSLLALSLDG KPLKQKWPMP GPEIPPLEQR
241 WPGPKVPPLE QRWPGPEIPP LEQRWPGPKV PPLEQRWPGP EIPPLEQRWP GPKVPPLEQR WPGPQIPPLQ QKWRGPLQPE
321 APPLMEPHQV SRRRAPPARL AFPRRGSRAC FGSVLGGGEE TGGPFAALGG SGDGDVGLGS RGGESRARSG EGTTHPIGPS
401 SLGHCSRGAP GWSEGAGGWW ERTAGPPLAF FPPCTRPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
																total 2 peptides

TRINITY_DN960
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 AWDGLPRPWC PAVRGSRARK ARSEEEEEEA PAELRPQSAP SGPVPSPPPR PGEGGPASDG WLDRDGSPLL LPPPPPPAGA
 81 EDAVGASPAG RLYKARTAMP PLRANPARQA NAAPFGSAVR AFEDSLSLSL ARSRPEALPA PAHSGMFVSR LAASGLLLLS
161 LLALSLDGKP LKQKWPMPGP EIPPLEQRWP GPKVPPLEQR WPGPEIPPLE QRWPGPQIPP LQQKWRGPLQ PEAPPLMEPH
241 QVSRRRAPPA RLAFPRRGSR ACFGSVLGGG EETGGPFAAL GGSGDGDVGL GSRGGGESRA RSGEGTTHPI GPSSLGHCSR
321 GAPGWSEGAG GWWERTAGPP LAFFPPCTRP V
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
																total 2 peptides

TRINITY_DN960
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MGGQKGFLNP NFLPTFPNSK RLQAWDGLPR PWCPAVRGSR ARKARSEEEE EEAPAELRPQ SAPSGPVPSP PPRPGEGGPA
 81 SDGWLDRDGS PLLLPPPPPP AGAEDAVGAS PAGRLYKART AMPPLRANPA RQANAAPFGS AVRAFEDSLS LSLARSRPEA
161 LPAPAHSGMF VSRLAASGLL LLSLLALSLD GKPLKQKWPM PGPEIPPLEQ RWPGPKVPPL EQRWPGPEIP PLEQRWPGPQ
241 IPPLQQKWRG PLQPEAPPLM EPHQVSRRRA PPARLAFPRR GSRACFGSVL GGGEETGGPF AALGGSGDGD VGLGSRGGES
321 RARSGEGTTH PIGPSSLGHC SRGAPGWSEG AGGWWERTAG PPLAFFPPCT RPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E
																total 2 peptides

TRINITY_DN960
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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MGGQKGFLNP NFLPTFPNSK RLQAWDGLPR PWCPAVRGSR ARKARSEEEE EEAPAELRPQ SAPSGPVPSP PPRPGEGGPA
 81 SDGWLDRDGS PLLLPPPPPP AGAEDAVGAS PAGRLYKART AMPPLRANPA RQANAAPFGS AVRAFEDSLS LSLARSRPEA
161 LPAPAHSGMF VSRLAASGLL LLSLLALSLD GKPLKQKWPM PGPEIPPLEQ RWPGPKVPPL EQRWPGPEIP PLEQRWPGPK
241 VPPLEQRWPG PEIPPLEQRW PGPKVPPLEQ RWPGPQIPPL QQKWRGPLQP EAPPLMEPHQ VSRRRAPPAR LAFPRRGSRA
321 CFGSVLGGGE ETGGPFAALG GSGDGDVGLG SRGGESRARS GEGTTHPIGP SSLGHCSRGA PGWSEGAGGW WERTAGPPLA
401 FFPPCTRPV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPQIPPLQQK.W	Y	61.81	1387.7612	12	0.7	694.8884	2	49.77	5	F5:14595	17112021_RID_2349_DP5.raw					3.7975E
																total 2 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F
R.WPGPEIPPLEQR.W	Y	57.32	1417.7354	12	0.2	709.8751	2	53.12	5	F5:15698	17112021_RID_2349_DP5.raw					2.0576E

total 2 peptides

TRINITY_DN672
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| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  QSVAMALNCY GGLTVLLFCF GAFSQAQVTQ NGPVSVDIAG TTVLTCALQG VEFISPTNPS WYQHKEGKSP RLLIYKSRER
 81  ASGTPQRFSA DTYGNTAKLT ISSVEVGDEG DYYCAVWHNN GFVFGGGTRV TVTGQPTVSP SVQVFAPSPE EIRSPNPHTV

161  VCLLSEFYPR SFVLQWKCDD KVMTSGVETT KATKQGDKYL ASSYLKLSAS EYEKYGTFTC EVTHERKTIV KSVSKSGSC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
S.VQVFAPSPEEIR.S	Y	51.69	1370.7194	12	1.2	686.3678	2	44.58	7	F7:12865	17112021_RID_2349_DP7.raw						
F.APSPEEIR.S	Y	39.94	897.4556	8	-0.4	449.7349	2	24.57	7	F7:5992	17112021_RID_2349_DP7.raw						

total 2 peptides

1OQS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  NLFQFARMIN GKLGAFSVWN YISYGCYCGW GGQGTPKDAT DRCCFVHDCC YGGVKGCNPK LAIYSYSFQR GNIVCGRNNG

 81  CLRTICECDR VAANCFHQNK NTYNKEYKFL SSSKCRQRSE QC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

1OQS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  NLFQFARMIN GKLGAFSVWN YISYGCYCGW GGQGTPKDAT DRCCFVHDCC YGGVKGCNPK LAIYSYSFQR GNIVCGRNNG

 81  CLRTICECDR VAANCFHQNK NTYNKEYKFL SSSKCRQRSE QC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

1OQS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  NLFQFARMIN GKLGAFSVWN YISYGCYCGW GGQGTPKDAT DRCCFVHDCC YGGVKGCNPK LAIYSYSFQR GNIVCGRNNG

 81  CLRTICECDR VAANCFHQNK NTYNKEYKFL SSSKCRQRSE QC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

1OQS
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  NLFQFARMIN GKLGAFSVWN YISYGCYCGW GGQGTPKDAT DRCCFVHDCC YGGVKGCNPK LAIYSYSFQR GNIVCGRNNG

 81  CLRTICECDR VAANCFHQNK NTYNKEYKFL SSSKCRQRSE QC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

CAA48456.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWIVAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KEYKFLSSSK CRQRSEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

AAZ53185.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWILAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KRYKFLSSYY CRQTSEKC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

Q02471.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWIVAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KEYKFLSSSK CRQRSEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

S29298
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWIVAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KEYKFLSSSK CRQRSEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

ACD43467.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWIVAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KEYKFLSSSK CRQRSEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

ACD43465.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRTLWIVAVC LIGVEGNLFQ FARMINGKLG AFSVWNYISY GCYCGWGGQG TPKDATDRCC FVHDCCYGGV KGCNPKLAIY

 81  SYSFQRGNIV CGRNNGCLRT ICECDRVAAN CFHQNKNTYN KEYKFLSSSK CRQRSEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.LAIYSYSFQR.G	Y	68.53	1246.6345	10	0.4	624.3248	2	48.21	7	F7:14191	17112021_RID_2349_DP7.raw						
G.NLFQFAR.M	Y	42.54	894.4711	7	0.0	448.2429	2	47.18	7	F7:13859	17112021_RID_2349_DP7.raw						

total 2 peptides

AFD04723.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGQDRPKF CNLAPESGRC RGHLRRIYYN PDSNKCEVFF YGGCGGNDNN FETRKKCRQT

 81  CGAPRKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IYYNPDSNK.C	Y	52.18	1112.5138	9	-0.5	557.2639	2	26.99	7	F7:6866	17112021_RID_2349_DP7.raw				8.1126E5	8.8307E
R.RIYYNPDSNK.C	Y	51.68	1268.6149	10	-0.6	635.3143	2	23.49	7	F7:5623	17112021_RID_2349_DP7.raw					

total 2 peptides

AFB74191.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGQDRPKF CNLAPESGRC RGHLRRIYYN PDSNKCEVFF YGGCGGNDNN FETRKKCRQT

 81  CGAPRKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IYYNPDSNK.C	Y	52.18	1112.5138	9	-0.5	557.2639	2	26.99	7	F7:6866	17112021_RID_2349_DP7.raw				8.1126E5	8.8307E
R.RIYYNPDSNK.C	Y	51.68	1268.6149	10	-0.6	635.3143	2	23.49	7	F7:5623	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7N4.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGQDRPKF CNLAPESGRC RGHLRRIYYN PDSNKCEVFF YGGCGGNDNN FETRKKCRQT

 81  CGAPRKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IYYNPDSNK.C	Y	52.18	1112.5138	9	-0.5	557.2639	2	26.99	7	F7:6866	17112021_RID_2349_DP7.raw				8.1126E5	8.8307E.
R.RIYYNPDSNK.C	Y	51.68	1268.6149	10	-0.6	635.3143	2	23.49	7	F7:5623	17112021_RID_2349_DP7.raw					

total 2 peptides

H6VC05.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGQDRPKF CNLAPESGRC RGHLRRIYYN PDSNKCEVFF YGGCGGNDNN FETRKKCRQT

 81  CGAPRKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IYYNPDSNK.C	Y	52.18	1112.5138	9	-0.5	557.2639	2	26.99	7	F7:6866	17112021_RID_2349_DP7.raw				8.1126E5	8.8307E.
R.RIYYNPDSNK.C	Y	51.68	1268.6149	10	-0.6	635.3143	2	23.49	7	F7:5623	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69602.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGQDRPKF CNLAPESGRC RGHLRRIYYN PDSNKCEVFF YGGCGGNDNN FETRKKCRQT

 81  CGAPRKGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IYYNPDSNK.C	Y	52.18	1112.5138	9	-0.5	557.2639	2	26.99	7	F7:6866	17112021_RID_2349_DP7.raw				8.1126E5	8.8307E.
R.RIYYNPDSNK.C	Y	51.68	1268.6149	10	-0.6	635.3143	2	23.49	7	F7:5623	17112021_RID_2349_DP7.raw					

total 2 peptides

ABD24041.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAEPT PISGQDRPKF CFLRPDFGRY GHPRPRFYYN PATNQCQGFL AQRSRENTNN FDTRDKCRQT

 81  CGRK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.FYYNPATNQ.C	Y	53.01	1116.4875	9	0.4	559.2513	2	42.16	7	F7:12041	17112021_RID_2349_DP7.raw	1.5234E5			
R.SRENTNNFDTRDK.C	Y	41.21	1595.7288	13	0.2	532.9170	3	18.70	1	F1:4666	12112021_RID_2349_DP1.raw	1.8585E5			
R.SRENTNNFDTR.D	Y	39.27	1352.6069	11	-0.4	451.8761	3	17.84	2	F2:3446	12112021_RID_2349_DP2.raw			1.6087E5	

total 3 peptides

Q2ES49.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAEPT PISGQDRPKF CFLRPDFGRY GHPRPRFYYN PATNQCQGFL AQRSRENTNN FDTRDKCRQT

 81  CGRK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.FYYNPATNQ.C	Y	53.01	1116.4875	9	0.4	559.2513	2	42.16	7	F7:12041	17112021_RID_2349_DP7.raw	1.5234E5			
R.SRENTNNFDTRDK.C	Y	41.21	1595.7288	13	0.2	532.9170	3	18.70	1	F1:4666	12112021_RID_2349_DP1.raw	1.8585E5			
R.SRENTNNFDTR.D	Y	39.27	1352.6069	11	-0.4	451.8761	3	17.84	2	F2:3446	12112021_RID_2349_DP2.raw			1.6087E5	

total 3 peptides

TRINITY_DN157

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVHWTAEEKS TITAVWSKVD VPAVGAEALS NLLIVCPWTQ RFFPNFGNLS NAAAIQSNAQ VKAHGKKVFT AFGDAVKNPE

 81  GVKDTFAKLS ELHCDKLHVD PVNFKLLGDS LITVLAAHFG KEFTPHVQAC FQKLVAVVAH ALAHRYH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.STITAVWSK.V	Y	55.57	991.5338	9	0.2	496.7743	2	39.29	7	F7:11035	17112021_RID_2349_DP7.raw						
K.VFTAFGDAVK.N	N	40.99	1053.5494	10	0.9	527.7825	2	44.38	7	F7:12863	17112021_RID_2349_DP7.raw						

total 2 peptides

AAB36402.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  DCSSGWTAYG KHCYKVFDEP KTWEDAEKFC SEQANGGHLV SFRSSKEADF VVTLTAQTKE SEIVWMGLSK IWNQCDWGWT

 81  NGAKLNYEAW AEAESYCVWF SSTNKEWKSR PCSLFGHFVC KSPAW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw							0
N.GGHLVSFR.S	Y	42.19	871.4664	8	0.1	436.7405	2	27.12	7	F7:6878	17112021_RID_2349_DP7.raw							3.9
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw							9.4

total 3 peptides

Q9PSM8.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  DCSSGWTAYG KHCYKVFDEP KTWEDAEKFC SEQANGGHLV SFRSSKEADF VVTLTAQTKE SEIVWMGLSK IWNQCDWGWT

 81  NGAKLNYEAW AEAESYCVWF SSTNKEWKSR PCSLFGHFVC KSPAW
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
K.TWEDAEK.F	N	42.92	877.3817	7	0.0	439.6982	2	23.16	7	F7:5532	17112021_RID_2349_DP7.raw							0
N.GGHLVSFR.S	Y	42.19	871.4664	8	0.1	436.7405	2	27.12	7	F7:6878	17112021_RID_2349_DP7.raw							3.9
K.TWEDAEKF.C	N	40.38	1024.4502	8	-0.9	513.2319	2	40.86	7	F7:11654	17112021_RID_2349_DP7.raw							9.4

total 3 peptides

XP_029141923.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVPWLNLMSL LVVLRGVQSE VQLVESGGEG RRPGESLHLS CQGSGFTFGN YWMVWVRQAP GKGLECVLVF KGYQYGCHMV  C

 81  RMERIRSVST ESTEFYFTNS SFIRAELHIT PYEYLLDLRK QVEIMLSACL NIFPSVRILH TFERAKMALW LNIMFLLVVL

161  GGAQSEVQLV ETGGDVRRPG ESLRLSCQAS GFTFSSSWMS WVRQAPGKGL EWVARIRYDS ATIYYPDKVK GRFTISRDNA

                248
241  KSQLYLQMNS LKAEDTAVYY CVRDTMVYPD VYWFSSQGNT NMRWAIFSMS AMEDEGTLET QSSVYLFYPE GYVNSVTASC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
K.SQLYLQMNSLK.A	N	55.00	1323.6857	11	0.6	662.8505	2	45.98	7	F7:13334	17112021_RID_2349_DP7.raw					
S.EVQLVETGGDVR.R	Y	53.24	1300.6622	12	0.4	651.3386	2	35.98	7	F7:9917	17112021_RID_2349_DP7.raw					
K.SQLYLQM(+15.99)NSLK.A	N	41.82	1339.6805	11	0.6	670.8480	2	37.34	7	F7:10474	17112021_RID_2349_DP7.raw					

total 3 peptides

TRINITY_DN1424

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  GRLARGRGRM LAARRALWPG WRGWSCERRK MKLLAAAALL GLGGGLLMLL LPGTRAEERK KGPKVTVKVQ FDVKIGEEEV
 81  GRIVIGLFGK TVPKTVENFV ALTTGEKGFG FKGSKFHRII KDFMIQGGDF TRGDGTGGKS IYGDRFPDEN FKLKHYGPGW
161  VSMANAGKDT NGSQFFITTV KTSWLDGKHV VFGKVLEGMD VVRKMESTKT DSRDKPLKDV IIADCNVIEV EKPFAIAKE
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
K.TVENFVALTTGEK.G	Y	65.95	1407.7245	13	0.5	704.8699	2	47.57	7	F7:13936	17112021_RID_2349_DP7.raw					6.0446
																total 1 peptides

ART88739.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLIRVLANL LILQLSYAQR SSELVAGGDE CNINEHRSLV VLFNSSGFLC GGTLINQEWV LTAAHCDSKN FQMQLGVHSK
                                     110
 81  KVLNDDEQTR DPKEKFLCLG RKNEKDKDIM LIRLNSPVHE STHIAPVSLP SSSPTVGSVC RIMGWGLTTP TKETYPDVPN
161  CANINILDHA VCQRAYPGLL VKSRTLCAGI LKGGKDTCVG DSGGPLICNG QFQGIVSWGG HPCAEPLRPG VYTTVFDYND
241  WIKSIIAGNT AATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
R.IMGWGLTTPTK.E	Y	45.69	1203.6322	11	0.2	602.8235	2	49.32	2	F2:14064	12112021_RID_2349_DP2.raw		1.254E5		
K.DKDIMLIR.L	N	44.22	1002.5532	8	-0.5	502.2836	2	37.38	3	F3:10341	17112021_RID_2349_DP3.raw			5.8616E6	
K.DKDIM(+15.99)LIR.L	N	39.37	1018.5481	8	0.3	510.2815	2	31.54	3	F3:8358	17112021_RID_2349_DP3.raw			1.7097E6	
															total 3 peptides

TRINITY_DN1526

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LGLSREQLQG GVSAKKGGRG RKGRREKGRG ECTKQTPTPG YLAVRAPVER RQTFSGSPGL HSRVMDPCRR KQIRWRTTLL
 81  QQCVLLLTYV VIILEAVPID VDKTKVQEQE KDSATVDNPE TGLYYDAYLR QVIEVLETDA HFREKLQTTN VEDIKNGKLS
161  KELDLVGHKV RTKLDELKRQ EVARLRMLIK AKMDAYQDSG IDHQALLKQF EHLNHHNPHT FEVKDLDMLI KAATHDLENY
241  DNTRHEEFKK YEMMKEHERR EYLKTLDEDK RRQEEAKYEE MKKKHNDHPK VNHPGSKDQL KEVWEEADGL DPNDFDAKTF
321  FKLHDVNADG FLDEQELEAL FTREVNMCNW IISESYFIWL SA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.MDAYQDSGIDHQALLK.Q	Y	59.48	1803.8461	16	1.3	902.9315	2	39.75	7	F7:11265	17112021_RID_2349_DP7.raw				
K.ELDLVGHK.V	Y	39.13	909.4919	8	0.8	455.7536	2	27.94	7	F7:7151	17112021_RID_2349_DP7.raw				
															total 2 peptides

TRINITY_DN1526

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| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LGLSREQLQG GVSAKKGGRG RKGRREKGRG ECTKQTPTPG YLAVRAPVER RQTFSGSPGL HSRVMDPCRR KQIRWRTTLL
 81  QQCVLLLTYV VIILEAVPID VDKTKVQEQE KDSATVDNPE TGLYYDAYLR QVIEVLETDA HFREKLQTTN VEDIKNGKLS
161  KELDLVGHKV RTKLDELKRQ EVARLRMLIK AKMDAYQDSG IDHQALLKQF EHLNHHNPHT FEVKDLDMLI KAATHDLENY
241  DNTRHEEFKK YEMMKEHERR EYLKTLDEDK RRQEEAKYEE MKKKHNDHPK VNHPGSKDQL KEVWEEADGL DPNDFDAKTF
321  FKLHDVNADG FLDEQELEAL FTRELEKVYD PKNEEDDMIE MEEERLRMRE HVMNEVDINK DRLITLEEFM RITEKREFSE
401  PESWEVQMAL LN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.MDAYQDSGIDHQALLK.Q	Y	59.48	1803.8461	16	1.3	902.9315	2	39.75	7	F7:11265	17112021_RID_2349_DP7.raw				
K.ELDLVGHK.V	Y	39.13	909.4919	8	0.8	455.7536	2	27.94	7	F7:7151	17112021_RID_2349_DP7.raw				
															total 2 peptides

TRINITY_DN1526

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LGLSREQLQG GVSAKKGGRG RKGRREKGRG ECTKQTPTPG YLAVRAPVER RQTFSGSPGL HSRVMDPCRR KQIRWRTTLL
 81  QQCVLLLTYV VIILEAVPID VDKTKVQEQE KDSATVDNPE TGLYYDAYLR QVIEVLETDA HFREKLQTTN VEDIKNGKLS
161  KELDLVGHKV RTKLDELKRQ EVARLRMLIK AKMDAYQDSG IDHQALLKQF EHLNHHNPHT FEVKDLDMLI KAATHDLENY
241  DNTRHEEFKK YEMMKEHERR EYLKTLDEDK RRQEEAKYEE MKKKHNDHPK VNHPGSKDQL KEVWEEADGL DPNDFDAKTF
321  FKLHDVNADG FLDEQELEAL FTRELEKVYD PKNEEDDMIE MEEERLRMRE HVMNEVDINK DRLITLEEFM RITEKREFSE
401  PESWETLDQQ EVFTEEELKQ FESHIFQQED ELQKKALELQ KKREELEQQQ DFLQAQKQEL EMAFKQMQQK KLQQGHPPSG
481  PGGELKFQPS VSQLDGNVQN HPVSSNQPLA PGNIPVQEAA ARSDHAQSHP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
K.MDAYQDSGIDHQALLK.Q	Y	59.48	1803.8461	16	1.3	902.9315	2	39.75	7	F7:11265	17112021_RID_2349_DP7.raw					
K.ELDLVGHK.V	Y	39.13	909.4919	8	0.8	455.7536	2	27.94	7	F7:7151	17112021_RID_2349_DP7.raw					
																total 2 peptides

TRINITY_DN2452
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LPDSEAHAIY KYENIEKEDE GPKKCGVTQT NWESDEPIKA SQFILTPEQR AYMNANKYIK LVIVVDNVMF RKYTGDLIAI

 81  RTRIYEIVNT LNLIYTILNI HIALVY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are
K.YTGDLIAIR.T	Y	54.91	1020.5604	9	0.2	511.2876	2	43.73	5	F5:12611	17112021_RID_2349_DP5.raw		3.2643E4		4.1422E4	3.85
R.KYTGDLIAIR.T	Y	45.94	1148.6553	10	0.5	575.3352	2	37.96	5	F5:10653	17112021_RID_2349_DP5.raw					1.57
																total 2 peptides

P00990.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  HDRPTFCNLA PESGRCRGHL RRIYYNLESN KCKVFFYGGC GGNANNFETR DECRETCGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

TIVRV2
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  HDRPTFCNLA PESGRCRGHL RRIYYNLESN KCKVFFYGGC GGNANNFETR DECRETCGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

CAL69611.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTRDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7P3.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTRDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69610.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCNVFF YGGCGGNDNN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7P2.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCNVFF YGGCGGNDNN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69615.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNANN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

AFE83617.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNDNN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

A8Y7P4.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTWDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

AFE83616.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTWDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

AFB74192.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RAHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTWDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					
																total 2 peptides

CAL69614.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISSHDRPKF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNANN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
																total 2 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7P6.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISSHDRPKF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNANN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7N5.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL ALLTLWAELT PISGHDRPTF CNLAPESGRC RAHLRRIYYN LESNKCEVFF YGGCGGNDNN FSSWDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69608.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNANN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

ABD24040.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLRRIYYN LESNKCKVFF YGGCGGNANN FETRDECRQT

 81  CGGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69612.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

1 MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLR**RIYYN LESNK**CEVFF YGGCGGNDNN FSTWDECRHT

81 CVGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

A8Y7P0.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLR**RIYYN LESNK**CKVFF YGGCGGNANN FETRDECRQT

81 CGGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

AFE83615.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLR**RIYYN LESNK**CKVFF YGGCGGNANN FETRDECRQT

81 CGGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

Q2ES50.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RGHLR**RIYYN LESNK**CKVFF YGGCGGNANN FETRDECRQT

81 CGGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

CAL69603.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

1 MSSGGLLLLL ALLTLWAELT PISGHDRPTF CNLAPESGRC RAHLR**RIYYN LESNK**CEVFF YGGCGGNDNN FSSWDECRHT

81 CVGK

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

H6VC06.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGHDRPTF CNLAPESGRC RAHLRRIYYN LESNKCEVFF YGGCGGNDNN FSTWDECRHT

 81  CVGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
R.IYYNLESNK.C	Y	53.68	1142.5608	9	-0.1	572.2876	2	34.45	7	F7:9462	17112021_RID_2349_DP7.raw			4.065E5	8.0118E5	1.074
R.RIYYNLESNK.C	Y	46.56	1298.6619	10	0.4	650.3384	2	30.29	7	F7:8008	17112021_RID_2349_DP7.raw					

total 2 peptides

TRINITY_DN5102
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAPPALLCFG LGLCLCAAVA GSRRDSATGE QLFKAWASRH RRAYRSEGEF RHRMQIFLDN KQKIDKHNAG NYSFRMGLNQ

 81  FSDMTFAEFK KTYLWQEPQN CSATTGNFPR SAGPCPRAID WRKKGRFVSP VKNQGPCGSC WTFSTTGCLE SAIAIKTGKL
161  LNLAEQQLID CAQNFNNFGC NGGLPSQAFE YILYNKGLMD EEAYPYRAQN GTCKFQPQKA VAFIKDVVNI SLYDEHGLMQ
241  AVGTYNPVSI AFEVKEDFVH YQEGVYTSTD CDKTPDKVNH AVLAVGYGEE DGVPFWIVKN SWGPSWGLDG YFNIERGKNT
321  CGLADCASFP VPLL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.DSATGEQLFK.A	Y	60.36	1094.5244	10	-0.1	548.2694	2	37.40	2	F2:10112	12112021_RID_2349_DP2.raw		8.6583E4				

total 1 peptides

CAE47141.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MRILWIVAVC LIGAEGHLSQ FGDMINKKTG IFGIMSYIYY GCYCGWGGKG KPLDATDRCC FVHDCCYGRV NGCDPKMGTY
 81  SYSFQNGDIV CGGDDPCLRA VCECDRVAAI CFGENMNTYD RKYMLYSLFD CKEESEQC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.KYMLYSLFD.C	N	43.04	1178.5681	9	0.2	590.2914	2	60.72	7	F7:18383	17112021_RID_2349_DP7.raw						
G.ENMNTYDRK.Y	Y	39.03	1169.5135	9	-9.0	585.7588	2	23.22	7	F7:5585	17112021_RID_2349_DP7.raw						

total 2 peptides

ABB76279.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLIRVLANL LILQLSYAQK SSELVIGGDE CNINEHRSLA LVYITSGFLC GGTLINQQWV LTAAHCDRGN MLIFFDVHSL
 81  KGLNKDVQSR VAKEKFICPN RKKDDEKDKD IMLIKLDSPV SNSEHIAPLS LPSNPPSVGS VCRIMGWGAI TSPNVTLPGV
161  PHCANINILD YEVCRKAYTG LPATSRTLCA GILEGGKDSC KGDSGGPLIC NGQFQGIVSW GAHPCGQSLK PGVYTKVFDY
241  TEWIQSILAG NADATCPP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Ar F
K.VFDYTEWIQSILAGNADATC(+57.02)PP	Y	43.47	2467.1365	22	0.5	1234.5762	2	83.71	4	F4:25719	17112021_RID_2349_DP4.raw		

ADI47595.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 DLTAMRTRVY EMINTVNEIY IYMDIRVPLV GIEFWCNGDL ITVTSSAENT LNSFGDWRAS DLLSHKTHDN AQLLTTITLS
 81 GSVVGLAHVS SMCQATRSVG VIEDHSPIVR EVAVTMAHEM GHNLGMSHDG NQCKCGDNSC IMYPYLSEPL PMFFSNCSKD
161 QYQKFLTNFK PDCTLIRPSR TDIVSPPVCG NDLLERGEEC DCGSPENCEN PCCDAASCKL HSWIECEFGE CCETCRLKPA
241 GTECRGIRNE CDLPEYCTGQ SGDCPTDHFH
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
R.TDIVSPPVC(+57.02)GNDLLER.G	Y	54.09	1783.8774	16	0.3	892.9462	2	47.68	1	F1:14421	12112021_RID_2349_DP1.raw	4.3022E6		

ADI47604.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 CIMYPYLSEP LPMFFSNCSK DQYQKFLTNF KPDCTLIRPS RTDIVSPPVC GNDLLERGEE CDCGSPENCE NPCCDAASCK
 81 LHSWIECEFG ECCEQCRLKP AGTECRGIRN ECDLPEYCTG QSGDCPTDHF HRNGKPCLYN NGYCYNGACP IMEYQCYDHF
161 GPDAVVSQDA CFEKNKEGKG DFYCRNENYV KTPCAPEDVK CGRLFCDIGP NRCIFPYGDT GMVNPGTKCG DKKVCXHRKC
241 IDVNTTY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
R.TDIVSPPVC(+57.02)GNDLLER.G	Y	54.09	1783.8774	16	0.3	892.9462	2	47.68	1	F1:14421	12112021_RID_2349_DP1.raw	4.3022E6		

TRINITY_DN722
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLLILALSLA HTYVVYGSIS CYDDSGKPVD WFIVYKLPKS HQSSLAEGMQ YMYQDGRTQG WVQGRSLMNS TEGAVGRTLN
 81 ELYLEAANRQ REKEVAYVLY NDEPPQDSSS GSKGHTKGVI FLDRTQGFWL VHSTPRFPPK LDEKYAWPHT ALTYGQSFLC
161 VTYPYSQFKA IGNQLLFTEP HVYDYQVPVA FARDLPALLN ASEGQHVQEE PWNSRVTLTS KGGKEFVSFA KFRFFHDDLY
241 SGWLAQALAT DLYVEFWLKS HGVLASNCSG KYKVYNVEQL AFQDPATTFF STSDHSKWCV GIESDSEWAC VGDMNRNRAE
321 EHRGGGTICC RDVTIWKSFH SLVQNYRDCD TTGYGL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
R.TLNELYLEAANR.Q	Y	72.61	1405.7201	12	0.9	703.8679	2	46.94	2	F2:13276	12112021_RID_2349_DP2.raw		3.0191E5			
													total 1 peptides			

TRINITY_DN722
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MLLILALSLA HTYVVYGSIS CYDDSGKPVD WFIVYKLPKS HQSSLAEGMQ YMYQDGRTQG WVQGRSLMNS TEGAVGRTLN
 81 ELYLEAANRQ VSLQKEQFQF LLVSKIVVMG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
R.TLNELYLEAANR.Q	Y	72.61	1405.7201	12	0.9	703.8679	2	46.94	2	F2:13276	12112021_RID_2349_DP2.raw		3.0191E5			
													total 1 peptides			

TRINITY_DN722
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 FCKILMLLIL ALSLAHTYVV YGSISCYDDS GKPVDWFIVY KLPKSHQSSL AEGMQYMYQD GRTQGWVQGR SLMNSTEGAV
 81 GRTLNELYLE AANRQREKEV AYVLYNDEPP QDSSSGSKGH TKGSALASNV FKERG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
R.TLNELYLEAANR.Q	Y	72.61	1405.7201	12	0.9	703.8679	2	46.94	2	F2:13276	12112021_RID_2349_DP2.raw		3.0191E5			
													total 1 peptides			

TRINITY_DN86540
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  GGRQSERLGS PPEKARQRLY SPPREEGVCC FGRDGEGVLP SASPGLIKGQ PGCRGHEPAK MVLSEDDKSK VRASWSPVCK
 81  NPELYGSETL TRMFAAHPTT KTYFPHFDLS PGSSDLKAHG KKVIDALTEA VNNLDDVAGA LSKLSDLHAH KLRVDPVNFK
161  LLAHCLEVTI AAHNGGPLKP EVILALDKFL CLVAKVLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

P0C0U6.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  VLTEEDKSRV RAAWGPVSKN AELYGAETLT RLFTAYPATK TYFHHFDLSP GSSNLKTHGK KVIDAITEAV NNLDDVAGAL
 81  SKLSDLHAQK LRVDPVNFKL LGHCLEVTIA AHNGGPLKPE VILSLDKFLC LVAKTLVSRY R
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

XP_026532450.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLTEEDKAR VRACWVPVSK NAELYGAETI TRLFAAHPTT KTYFPHFDVS PGSNDLKAHG KKVIDALTEA VNNLDDVAGA
 81  LSKLSDLHAQ KLRVDPVNFK FLAHCLEVTI AAHNGGPLKP EVILSLDKFM DIVSKVLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.F	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

XP_026570824.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLTEEDKAR VRASWVPVSK NAELYGAETL TRLFSAHPTT KTYFPHFDLS PGSHDLKAHG KKVIDALTEA VNNLDDVAGA
 81  LSKLSDLHAQ KLRVDPVNFK LLGQCLEVTI AAHNGGPLKP EVILSLDKFL DLASKLLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

XP_034284997.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MVLTEEDKAR VRASWGTVSK NAELYGSETL SRLFTVYPAT KTYFHHFDVS PGSSDLKSHG KKVIDAITEA VNNLDDVAGA
 81  LSKLSDLHAQ KLRVDPVNFK LLAHCLEVTI AAHNGGPLKP EVILSVDKFL DKVAKVLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
																total 2 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

XP_032079120.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLTEEDKAR VRACWGPVSK NAELYGSEAL TRLFAAHPAA KTYFHHFDVS PGSSDLKTHG KKVIDAITEA VNNLDDVAGA

 81  LSKLSDLHAQ KLRVDPVNFK LLGHCLEVTI AAHNGGPLKA EVLLSLDKFL CKVAKVLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

JAC95434.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MVLTEEDKAR VRACWGPVCK NAEVYGAESL TRMFAAHPTT KTYFHHLDVS PGSNDLKTHG KKVIDAITEA VNNLDDVAGA

 81  LSKLSDLHAQ KLRVDPVNFK LLAHCLEITI AAHNGGPLKP EVILSLDKFL CLVAKVLVSR YR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

LAA66838.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  VHGEGSPAVG GHQPAKMVLT DEDKARVRAC WGPVSKNAEL YGSEALTRLF AAYPTTKTYF HHFDLSPGSN DLKSHGKKVI

 81  DALTEAVNNL DDVAGALSKL SDLHAQKLRV DPVNFKLLGH SLEVTIAAHN GGPLKAEVLL SLDKFLDRVA KVLVSRYR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area
A.VNNLDDVAGALSK.L	Y	49.66	1314.6779	13	1.5	658.3472	2	43.46	7	F7:12535	17112021_RID_2349_DP7.raw					
K.LRVDPVNFK.L	N	42.14	1086.6185	9	0.0	544.3165	2	36.89	7	F7:10234	17112021_RID_2349_DP7.raw					4.637
																total 2 peptides

XP_029140879.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MGHPQLWPLL LLLLLSNEAL TRDATRFKPF RKYIYHYETE ITSGVTGTAD SHSGSKIKCK AELEVPQLHN FVLKINQCTL
  81 EEVYGIDVQG KALLKKSKNS DEFAAAMSQY ELKVKIQNEK NVELYPVDSE ATHILNIKRG IISALLVPTE REDNIQTLSM
 161 DTVYGKCDSS IEVKNRKTTA NLADIEITRN LKSCENFNPI RDYVSPIAFI KGLNAPLSTL ISSNQHCHYT VDTKKKHISE
 241 AICTEKHLFL PSSYKNQYGM MAKVIQTLKY ESIANSNTRS MDVTGLIKRE LSLENVEAKI LRHGDAVLKS LQELKKLSVS
 321 QQNHKRASLF YRFVTGLRSL HNSTLGPMVP KLMETSSSIT IQALIQCGTP ECFGAILQIL RTSNIDPLVA DAVTFSLGLL
 401 PSPCTKTIRE ILNMAEYHPS RASFYALSHS VNRFYSQKKI ITPELTDVAN FVTSLISNEC SGNEDLTYLT LRVIGNMGNI
 481 LENVNPNVKQ SLKLCIRSNA ASLDIQKAAI QALRKMDLND EDRGMLIRVF QEASSPADKR LAAYLLLMKN PSTSDLSKII
 561 KVSLRDKNEQ VKNFVASHIA NILDTIDFSN EPYLPMLRIK IQEALKGNQM PTVKDFRRFS QNYQVSKTMT VPWSQDPFTA
 641 KLEGNLLFDP SSYIAKEAML KTTLELFGLR PLDVFEIGLD GKNLEPTVEA MFGPEGFFPD AATKALYWID GKVPEQFSQA
 721 LFNYFGYSKD ATQDQDIMKG IMLNFEKLVK EISNKPTPDV KAYFRLFQEE LGYLKFSDIK LLGNVILKSF KTLQSIPQKI
 801 VQTISQGTEN DLMIHYIFMD NEFELPTSAG LQLQVALSGV ATPGAKVGMK ISQRNIHADL IVKPSMAVEF ITHLGVNIPE
 881 FARNGVQMNT NIYHESGIEA NVALKAGHLK FTIPAPKAPI KLFSISNVLH LVTPTRNEVI PPLMENRVTQ NNCSPFFTGL
 961 KFCTIIEYSN ASSTVAAPYY PLTGETRYEI ELQPTGRVKE YIASANYELN KEGKDLVDTL KFIAQAKGVK ESEAKIVFTF
1041 NRGKKIFISD FQAPGFNINF GTNLKITDSS NQEKKAVAFI LDILNEKSPE ITITGRLSSA FGRESSLEAA ISIPRLQTQA

1121 KTDISLRRSS NAMIFQFDSS ATSYGSSVSE RIVLRYDTEK VELQWNSGTS AALKRICANL PGDLEGYSKA LQNKANGLLN
1201 HKVANTDMTL RHIVSHFIVA TNTWLQKTSK DIPYAQNLQD KLSKLQQLDF QIVDVITIPE ELFFKSDGKI KYVWNKESTF
1281 ITIPMPFGGQ SSQVISIPKI IRAPAMVVES LGLNIPSQEY KIPQFTIPND YTLRLPLLGT FEITSNLYNN YYNWSGSYSL
1361 ANTTKDAYGL KTRYFMKADS VLDLLSYNVQ GQAEASYDGN GLTCDYENSL RHSLLNSNFK FSKVNRYGLN PTVKYSMTFD
1441 TSSPVGVMFS LSAHQDSTED DNSHVGVTNL EGQLNVATLF AKTTYLQSIT SKKKSLDLVW DSTLKFDSSL FGATNQMIQK
1521 ITEDAWTINS ITNIQNYILT NKVSLRYQNS QLKLSSEAIG TYTNFETINK FDLTLDKQQA ILHSKLKATY FKNVYYALVS
1601 GSVNNQGVEL IGDLSWENER NKAEHKSALS IKQDGLVSSA TTKLQLLLLI LENEMNARIG TSGASVKIDT NGRAGTHNAR
1681 FSLDGKLALT EIALLSTYQG SILEVDSKNI LNFRVNNGEL RFSNSLTGSH KEMQFEHTHE LNIVGLSLTY VSNLDHTINP
1761 DVSHKHHVDL QLQPSSLTAN LNNDLKYSSA NVNNKARLQL ELLKVNLDGN IKGAYSGNEI KHTYIFTYGD LAAHMKTDTA
1841 ASIQGAAVTH KVNLNVAGLS STINVNTNCD SKFLTFSNEI RSMAAPFTVT FDMHTNGDGQ LGEQSGRLYS KFLLKAEPLA
1921 IVFSHDYQGS TNHNINSGER YNTGLDSKVT VVLTPSEQSS AWKMKSQLNN HVHTQDINMF NNAENIGLEL TGQTLADLSA
2001 LDFPMKIPFT NDRRLNLIDT LDLRENIAEP QEFGLSLSLK YDKNADMHVI NLPFLERLPA YYEQFRRSIL TAMKSIQKNL
2081 KNINIDQLMR KYKIALDKFP QQVNDYVNSF DLERKVNKLK ENLDAFTKDY SITVEDLQNT LENAKANLLK ALTQLQVFLT
2161 ETEKYMKENY DLRPAIMQLI EKIVEKLKVL DDQYEISVTM INTIQQLQSF ISQYDPSEIG SNAAAWVQNV DTTYKIRAQI
2241 QEKLDQLKSQ IQNFDAQHIA ETLKQQIETI DTKILIEKLK IQFPFEKINQ LLEQIKNILL NFMEDYEISE KINAFRVRMH
2321 ELIVKYNIDE QAKVLMDKVI ELYKQQKITE TVLRLTNTLK QIDIKPFFNQ ILKFIDDAIK KLQTVDYKKL VDGINDFLDI
2401 MIKKLKSFDY NKFVDETNNK IRQATQKINE EIKALELPQK IEAAKQYIKE VYTVVSRYIE KLKDSRLAAT VNWLNDLISS
2481 TAIDELKSKI RDFLEDARKR IYEMDIPAEC QRFLHKASQL YRVIVSFLVD KWDIISKKIS VSAEKYNVKN MADHLNQFVK
2561 TGFIVPAIKL GVINIPAFEV SLRALQDATF KTPDFILPLT DLHVPSYQIN FKKLNEIRIP IRFSTPEFTI LNTIKVPSYT
2641 IDFNEIKLKI VRIIDQIMTS DFQLPATDTY FQEIKIKDLY FSDFSLPEIN LPQLQISELL IPKLNLNEFQ FPDIKIPEFQ
2721 LPRIPHTVTI PTFGKLSGTC RITSPFFTLT TNAGFQNVTA HPYSPEFVAS LSAIAVSKID YLAFTLTANT HLLAPELKKL
2801 ILKENLKFTH LYLKADHGSE VVFLTASVQG NAETTASFRS TRNAIELHNK LTVNLNKIIS MDSKTLYTHR LNIPKAQFTS
2881 QAELSNEIKT ALEAGHISVT STGKGDWKWT AHDYSDEGTH ESKVSFTIER SIAAFIAENR INAKYLRVNQ RMVYEYNLPS
2961 SSKLQVESTI ESPQLGQSVL NVQGTGNLVQ LKMELSGTHN AKVIGRTSGT INNDVSFSVQ PFEIKASANN NMNLKVSFPF
3041 KIVGKIESLN NYGLVLSPST QQVSWVAEGR FNQYRYTHNL SAGNNEDSTE AIISMNGEAN LEFLNIPISF PEQFVPYLGI
3121 KTPQVQAYSL WEETGLKGLL KTPKQSFDLN VKLQYKKNKD VHSFPIPLDR VHKTLNSYIV NFNKYFERNR DHTLAFLTES
3201 YNQAKVKFDK YKVDTSVNQS PQIFTIPSYT IPLLNIEVSP FTAELPTFGY VLPKEMRTPD FTVPFVQYSM PSYTVVLPSL
3281 ELPVLHIPQG LRTLKLPNYR VSPLPNQIYI PAFGNVTYDF SFKSSVITLN TNAGFFNQSD IIARLSSSST SVIEALQYQL
3361 TGTTSITRKR GLKLATALSL KNKFVEGNHD STISFTKKNI EALVVTTAKI MAPGLKVNYG QELKGNAKTM PIISSKINLN
3441 YDVDTNYVNA KGAIVHQANL ESIISYISAD TSTSGFINGD FYEGKPFSGK LVHEANTYLN SKGIRSAMKF ETSSNSGDFW
3521 NFDAKENVAI EASTNRLYAL WDHSGENYLN YFPLPRTRGN QICRVTLELA SDIMSAALQI QVAQPNNFLE ETSVNQAFSL
3601 TVNNGNQKIN WKSESQIHNF FLGHDLELAN DNVEARVGLS ASLGGHINFL REFTLPVYER SLWHILKLDL TTRPEEKQFL
3681 NASTNIVYTK NQDGYFFPIS ISQLADRFII KFPAIKAVGI HVQFFTIGLH EFNVLERVNN TSFDINLPLL PKMQLDEITK
3761 YNNLGQNKIP YFELTVPKHP KLVTIPQFTL PKRLFLGNIN IDLDVVANKI ADFDLPTITI PQQQIEIPVF TFTLPAGIYF
3841 PKFGALSSSF KIASPLYSAT WKTDLKNTKE AFEHSIDFTA NSPLQFLEYD LDGVTTYQYE GNRFTLNRQY DLAHPELSGK

3921 YKAVYITEGD RIVRDKASLD ITSPTFTDVQ MRYQGDDSRV STMISSSSAG TLRFLISLDS SILNSKIFYQ TQSNPQNEVE
4001 ILKSEISFKN PELIQIKTNW KEDAVTELLE GLKEKVPKMA DALYYTANKY HREHTGMEIS SAASKLKDTL RSNIDQTYVN
4081 TVNSISELEQ QLHEVTNQVT GKYEQIKTES QKLYHKAADQ ASQIEYDQIR TQFLDAIMDS IVEYHKQIKR LIDSAIEFLK
4161 VTRFQVPGLP GKHTGEELYV IITEKVAKAV DQSIARVQEY FDSLITFVNE AEIKIPASSE IIKGSDILAE IKTFLTHVQK
4241 KVSQIFVGLR EIDFAQHLRD LKERIQQVFQ KIEELIKNLQ AQNYDHLKEQ TKQLFVNFLN ALNSLAGDVK YFSPRIENII
4321 QNTFSEIYNK LEELLHSIRD LRKEYFDPNV VGWSLKYYEV EEKFINWLKT FFNTILEWHI KWINEAADLI TNLTDQAKEA
4401 LENQEKLAEF SKTAHEKIQY WSKVAKQSAA EQNQQVKAKL QETYNHLFNS YEMLISETKR LIDLTIEKYT TFFQYLQKLL
4481 DWLEKVTADA LRPYIAVRQG ELRIDIPKPF NLSAIYQGPL SDEDLQQQQT ILANQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.SPEITITGR.L	Y	49.73	972.5240	9	0.1	487.2693	2	33.18	7	F7:9009	17112021_RID_2349_DP7.raw							1.38
K.FGALSSSFK.I	Y	40.73	942.4810	9	-0.4	472.2476	2	38.95	7	F7:10968	17112021_RID_2349_DP7.raw							5.80

total 2 peptides

AJO70722.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MGRFISVSFG CLVVFLSLSG TGADQDCPSD WSSHEGHCYK VFNLRMNWAD AEKFCTEVVS GGHLISLNSA EEVDFMIKLV
 81 FPILKFDFIW IGLRDFWRDC HWGWSDGVKL DYKAWSDEPN CYVAKTVDYQ WLFRDCNRTS RFICKSRVPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	A
K.FDFIWIGLR.D	Y	51.10	1165.6284	9	0.3	583.8217	2	71.27	7	F7:21945	17112021_RID_2349_DP7.raw							0

total 1 peptides

XP_029142225.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MSEILMGVFG IWTKSSIFML SCLIEGGKNC NGPPRIENGD IITLSEKRYR SGSSVEFRCQ RFYAMEGQKI SFCNNGTWTK
  81 VPICLDPCRI PTAELERQKI EVKDGMDASE NIFVQHGHSI ELICRTGYVL AADSSQSASI IHCDGTTPVI PKCKEIICNS
 161 PRISNGSFRP KRNIYHVGDL IQIQCYSGFT FEPDNRGQVV ECTKNGWSPP SKCVLVNPLI VCEEPDDIAF GEIVTMEKAK
 241 YLENDRVQYR CYPGYVLEGL EWIQCKGQQW TPRPPKCLAP CSITRQQLVT KNLFVFGSQR KSRFIQSNHS LQFQCSEGYV
 321 LVVPSVRKCV DGYMDLPLCI SERGKNCSDP PRIENGDITT LSEKQYRSGS SVEFRCQRYY TIEGQNRSFC DNGTWTKVPI
 401 CLDPCMIPRA ELETQKIEVK GGMDASENIF VPRGHSIELT CRTGYVLAAD SSQLACDGTP PVIPKCKEIT CSSPRILKGS
 481 FRPQRNIYND GDLIRIQCDN GFTLEQDNGG QVAECTRNGW LPSPKCVQVE RTCKVSLLHG SFVPEQQSIQ INDKAKYICQ
 561 DGYTTSKGET EVETQCLTEG WSPEPECIRT CLKPPADNFI FNTTKPVFLP GDVLHYECKE EFEITKNSIS DTVVCTEEGW
 641 EPTPPRCVAF VCQAPFLENG AIDPRENVFQ HKMVVRFNCD TGFTRVGSES AQCYHFGWSP QPPVCKGIAS VCHAPFLENG
 721 AINPREDVFQ HKMVVRFNCD RGFIRVGSES AQCYHFGWSP QPPVCKENVK SCQASPRISH GMVTDERKAV HQHGDLLEVQ
 801 CDISFALRGS KTIECVDGEW APLPSCIEEV KTCGPPRKIT RGIPVDAMSS IYRHGETVAY QCQQPSVSIG TNPAKCLHGQ
 881 WELPSCLETC PPPPQLPNAI NIAEMRIYRS EEEISFKCQG NFLLRGPPKI KCEDGKWQTP PRCLACEEPE DIDFGEIVTT
 961 EKAKYLENER VQYRCNPAYV LEGPEWIQCK GQKWTPHPPK CLAPCSITRQ QLATKNLFVF GSQRKALLIQ SNHSRQFQCN
1041 EGYVLVAPSV RMCVDGYMEL PLCISERGRN CSGPPRIENG DITTLSEKRY RSGSSVEFRC QKDYAMEDQN RSFCDNGTWT
1121 KVPICLDPCV IPRAELESQM IELKDGIDVP ENTFVQRGHS IELTCRTGYV LAVDSSQSAS IIHCDGTTPV IPKCKEITCN
1201 SPRISNGSFL PQRTIYHDGD LIRIRCESGF TFKPDNGEKV VECTKNGWSP PPKCVSRGSQ PPAMAHYHAV ACLKPGHVSG
1281 WPVHTCVRAA QVA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IENGDITTLSEK.Q	Y	64.45	1318.6616	12	0.5	660.3384	2	34.80	3	F3:9504	17112021_RID_2349_DP3.raw			9.5811E4		

total 1 peptides

XP_015677107.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1 MKSWLLLVVV FLLWPGCSSQ NVCEEPDDID FGEIVTTEKA KYLENDRVQY RCYPGYVLEG PEWIQCKGQQ WTPHPPKCLA
  81 PCIITRQQLA TKNLFVFGGQ RKTWIIQNNH SVQFQCNERH VLVVPSVRKC VDGYMDLPLC LSERGGNCSG PPRIENGDIT
 161 TLSEKRYRSG SSVEFKCQKY YAMEGQKRSF CDNGTWTKVP ICLDPCMIPT AELERQKIEV KDGMDASENI FVQRGHSIEL
 241 ICRTGYVLAA DSSQSASIIH CDGTPPVIPK CKEITCNSPR ILNGSFRSQR TIYHDGDLIR IQCDSGFTLE PDNGEKVVEC
 321 TRNGWSPSPK CVEIQCSPPE VRKGRIEPRR SQYMYNDEIE IICHRRIFFT AIQRKYISKC TANGWSPSPL CEEIRCSPPE
 401 VRNGYIRPTQ SQYMHNDEIE ITCFRWPFFK GDRKSRSNCT ANGWDPPPSC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IENGDITTLSEK.R	Y	64.45	1318.6616	12	0.5	660.3384	2	34.80	3	F3:9504	17112021_RID_2349_DP3.raw			9.5811E4		

total 1 peptides

TRINITY_DN1914
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MKNWLLLVAA FLLWPCCSSQ NACEEPEDID FGEIVSIEKA KYLENDRVQY RCNPAYVLEG PEWIQCKGQK WTPHPPKCLA
 81  PCSITRQQLT TKNLFVFGSQ RKARLIQSNH SLQFQCNEGY VLVAPSVRKC VDGYMEFPLC ISERAGNCRG PPRIENGDIT
161  TLSEKQYRSG SSVEFRCQKH YAMEGQNRSF CDNGTWTKVP ICLDPCVIPR VELESQMIEL EDGIDVPENI FVQRGHSIEL
241  TCRTGYVLAV NSSQSASIIH CDGTRPVIPK CKEITCHSPR ISNGSFRPQR TIYHDGDLIR IQCDSGFTFE RDNGEEVVEC
321  TKNGWSPPPK CVTACTTSEE DMREHNIKLK WAIGNKIYST DGNIIEFQCI RGHKLHPSYR TLRINCVNGK FDYPRCIPI
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.IENGDITTLSEK.Q	Y	64.45	1318.6616	12	0.5	660.3384	2	34.80	3	F3:9504	17112021_RID_2349_DP3.raw			9.5811E4		
														total 1 peptides		

TRINITY_DN1889
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MFRCRLLLCL AGLLVLSEAG GRLPALQAAL EQVLEDFHGR SLVQAAFLGE TARELVEVLP MGTYVQLEVD LVQTVCRKHQ
 81  WRSQNCQIKA GGRRQKCLAC FKFDDNNNPG RLLNKSLRCL SEQNPLFQEA RRRQEAECQA IKAANEDRYL PGKFAFSVGL
161  PS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5
R.SLVQAAFLGETAR.E	Y	63.54	1361.7302	13	1.1	681.8732	2	50.30	7	F7:14849	17112021_RID_2349_DP7.raw					
														total 1 peptides		

CCH15044.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSSQDRPKF CYLPADPAEC NAYMPRFYYD SASNKCKEFI YGGCRGNANN FKNRAECRHT
 81  CVASRKGIQP RIASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037
														total 1 peptides	

I2G9B4.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSSQDRPKF CYLPADPAEC NAYMPRFYYD SASNKCKEFI YGGCRGNANN FKNRAECRHT
 81  CVASRKGIQP RIASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037
														total 1 peptides	

AMH40736.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PISGRDRPKF CHLPADPGIC KAHTPRFYYD SASNKCKQFS FGGCPGNANN SKTWDECRHT
 81  CVASGKGIQP
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037
														total 1 peptides	

AMH40741.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSGQDHPKF CYLPADPGRC KAHIPRFYYD SASNKCNKFI YGGCPGNANN FKTWDECRQT

 81  CGASAMGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

P00991.2
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSGQDHPKF CYLPADPGRC KAHIPRFYYD SASNKCNKFI YGGCPGNANN FKTWDECRQT

 81  CGASAMGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AAP04484.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSGQDHPKF CYLPADPGRC KAHIPRFYYD SASNKCNKFI YGGCPGNANN FKTWDECRQT

 81  CGASAMGRPT
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AAP04485.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSTRDRPKF CYLPADPGRC LAYMPSFYYD SASNKCKKFI YGGCRGNANN FKTWDECRHT

 81  CVASGIQPRI ASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

P00992.2
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSTRDRPKF CYLPADPGRC LAYMPSFYYD SASNKCKKFI YGGCRGNANN FKTWDECRHT

 81  CVASGIQPRI ASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AMH40733.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSTRDRPKF CYLPADPGRC LAYIPSFYYD SASNKCKKFI YGGCRGNANN FKTWDECRHT

 81  CVASGIQPRI ASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I

total 1 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AMH40738.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSTRDRPKF CYLPADPGRC LAYIPSFYYD SASNKCKKFI YGGCRGNANN FKTWDECRHT

 81  CVASGIQPRI ASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AMH40740.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSTRDRPKF CYLPADPGRC LAYIPSFYYD SASNKCKKFI YGGCRGNANN FKTWDECRHT

 81  CVASGIQPRI ASN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

E5AJX3.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSSRDRPKF CYLPAEPGEC NAYMPSFYYD SASNKCKKFI YGGCRGNANN FKTRDECHHT

 81  CVASGKGIQP RIGSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

CBW30779.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSSGGLLLLL GLLTLWAELT PVSSRDRPKF CYLPAEPGEC NAYMPSFYYD SASNKCKKFI YGGCRGNANN FKTRDECHHT

 81  CVASGKGIQP RIGSN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
S.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

TRINITY_DN151
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MQQQNPEFKE QDPSFSHLVQ PRKLNKTSQM ALDHVQTEHA RRAPEFCYLP ADPAECNAYM PRFYYDSASN KCKEFIYGGC

 81  RGNANNFKNR AECRHTCVAS RKGIQPRIAS N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

Q6T269.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  PLRPGTEKHT FPFPAEFCNL PADLGPCKNY TGRFYYDSAS NKCEVFIYGG CPGNANNFKT REECRKTCVE ICILPAELGP

 81  CDEYTGRFYY DSASNKCEVF IYGGCQGNAN NFKTRDECRK TCVEICILPA ELGPCDEYTG RLLLRLGIKQ M
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

AAR19275.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  PLRPGTEKHT FPFPAEFCNL PADLGPCKNY TGRFYYDSAS NKCEVFIYGG CPGNANNFKT REECRKTCVE ICILPAELGP

 81  CDEYTGRFYY DSASNKCEVF IYGGCQGNAN NFKTRDECRK TCVEICILPA ELGPCDEYTG RLLLRLGIKQ M
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area I
R.FYYDSASNK.C	Y	63.13	1093.4716	9	0.3	547.7432	2	28.93	5	F5:7517	17112021_RID_2349_DP5.raw	8.2206E5	5.5535E5	2.9889E6	2.3037

total 1 peptides

LAA93895.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  YEELQDTAGR HNDDVRNAKH EISELNRHVQ RLKAEIEGVK KQCGNLKGKI AEAEDRGELA LKDARQKLAE LEEALQKAKQ

 81  EMAKQLKEYQ QLLNVKISLD IEIATYKKLL EGEEYRLAND AGDAVNMSVI SSHISRGSAA GSGLGYGSGL SMGGGSCFAV
161  GGGGGCSNIV DLGNGSCSSM KFIS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
K.LAELEEALQK.A	Y	61.86	1142.6183	10	0.8	572.3169	2	41.52	4	F4:11731	17112021_RID_2349_DP4.raw	2.8419E4			7.8314E5	1.0

total 1 peptides

CAJ34939.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MIQVLLVIIC LAVFPFQGSS KTLKSGNVND YEVVNPGTVT GLPKGAVEEK HEPMKGNTLQ KFPLCTTGPC CRQCKLKPAG

 81  TTCWKTSRTS HYCTGKSCDC PSYPGNG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
K.SGNVNDYEVVNPGTVTGLPK.G	Y	61.72	2059.0222	20	-0.3	1030.5181	2	48.96	7	F7:14386	17112021_RID_2349_DP7.raw			

total 1 peptides

Q3BK14.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MIQVLLVIIC LAVFPFQGSS KTLKSGNVND YEVVNPGTVT GLPKGAVEEK HEPMKGNTLQ KFPLCTTGPC CRQCKLKPAG

 81  TTCWKTSRTS HYCTGKSCDC PSYPGNG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
K.SGNVNDYEVVNPGTVTGLPK.G	Y	61.72	2059.0222	20	-0.3	1030.5181	2	48.96	7	F7:14386	17112021_RID_2349_DP7.raw			

total 1 peptides

TRINITY_DN160

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  LASHSQREKN SGWLESRKRL PVFKPNPASK MIQVLLVIIC LAVFPFQGSS KTLKSGNVND YEVVNPGTVT GLPKGAVEEK

 81  HEPMKGNTLQ KFPLCTTGPC CRQCKLKPAG TTCWKTSRTS HYCTGKSCDC PMYPGNG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3
K.SGNVNDYEVVNPGTVTGLPK.G	Y	61.72	2059.0222	20	-0.3	1030.5181	2	48.96	7	F7:14386	17112021_RID_2349_DP7.raw			

total 1 peptides

JAS05406.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT AFPKGAVQPK YEDAMQYEFK VNGESVVLHL EKNKGLFSKD
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGKIYLIEP LKLSDSEAHA VYKYENVEKE
161 DEAPKMCGVT QNWKSYEPIK KPSQLVVTAE QQRIAKRYVE FVIVVDHGMV TKHNETLRTW VFQIVNTINE IYIPLNIRFA
241 LVGLEIWSNG DKINVQSSAH NTLHLFGNWR RRVLLKRKRH DNAQLLTSID FDGQTVGLAH VSSMCNQKLS TGVIQDHSAI
321 NLLVAVTMAH ELGHNLGMDH DGNQCHCDAP SCVMSARLRE RPSYGFSNCS QNEYQMFIIN YNPQCILNEP LPTDIVSPPV
401 CGNELLEVGE ECDCGSPNNC QDPCCDATTC KQHSWVECES GECCEQCRFK GAGTECRAAS SECDIAESCT GQSADCPTDD
481 LHRNGQPCLN NHGYCYNGMC PIMDHQCIAL YGADATVAED ACFDSNLQGQ GNFYCRRENG RIFPCAPQDV KCGRLFCKFD
561 HYSCQYQYSG DPDFGMVDHG TKCADGKVCN NRRCVDVTTA Y
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

JAS05289.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

JAS05287.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

ABG26980.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

JAS05286.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

JAS05288.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLLTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	

total 1 peptides

JAS05285.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIEVLLLTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPN YEDAMQYEFK VNGESVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGEMYLIEP LELPDSEAHA VFKYENVEKE
161 DEAPKMCGVT QTNWKSYEPI KKPSHLVVTA EQQRLTKRYV ELVIVADHGM FMKHNETLRT WVFQMVNTIN EIYIPLNIRF
241 ALVGLEIWSN GDKITVQSSA HNTLHLFGNW RKRVLLKRKK HDNAQLLTSI DFDGRTVGLA HVSSMCNQKL STGVIQDHSA
321 INLVMAVTMA HELGHNLGMD HDIKYCTCGA PACVMGNTLS EQPSYGFSNC SQNQYQTFII NYNPQCILNE PLPTDIVSPP
401 VCGNELLEVG EECDCGSPNT CRDPCCDATT CKQHSWVECE SGECCEQCKF KGAGTECRAA RSECDIAESC TGQSADCPTD
481 DLHRNGQPCL NNHGYCYNGM CPIMDHQCIA LYGADATVAP DACFDFNLKG QDNFYCRREK ARIFPCAPQD VKCGRLFCEF
561 GHYSCQYQYS GDPDFGMVDH GTKCADGKVC KNRQCVDVTT AY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	
															total 1 peptides	

JAS05407.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MIQVLLVTIC LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPK YEDAMQYEFK VNGEPVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGKIYLIEP LKLSDSEAHA VYKYENVEKE
161 DEAPKMCGVT QNWKSYEPIK KASQLVVTAE QQRIAKRYVE FVIVVDHGMV TKHNETLRTW VFQIVNTINE IYIPLNIRFA
241 LVGLEIWSNG DKINVQSSAH NTLHLFGNWR RRVLLKRKRH DNAQLLTSID FDGQTVGLAH VSSMCNQKLS TGVIQDHSAI
321 NLLVAVTMAH ELGHNLGMDH DGNQCHCDAP SCVMSARLRE RPSYGFSNCS QNEYQMFIIN YNPQCILNEP LPTDIVSPPV
401 CGNELLEVGE ECDCGSPNNC QDPCCDATTC KQHSWVECES GECCEQCRFK GAGTECRAAS SECDIAESCT GQSADCPTDD
481 LHRNGQPCLN NHGYCYNGMC PIMDHQCIAL YGADATVAED ACFDSNLQGQ GNFYCRRENG RIFPCAPQDV KCGRLFCKFD
561 HYSCQYQYSG DPDFGMVDHG TKCADGKVCN NRRCVDVTTA Y
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	
															total 1 peptides	

JAS05408.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MIEVLLVTIF LAVFPYQGSS IILESGNVND YEVVYPRKVT ALPKGAVQPK YEDAMQYEFK VNGEPVVLHL EKNKELFSEN
 81 YSETHYSPDG REITTYPPAE DHCYYHGRIE NDADSTASIS ACNGLKGHFK LQGKIYLIEP LKLSDSEAHA VYKYENVEKE
161 DEAPKMCGVT QNWKSYEPIK KPSQLVVTAE QQRIAKRYVE FVIVVDHGMV TKHNETLRTW VFQIVNTINE IYIPLNIRFA
241 LVGLEIWSNG DKINVQSSAH NTLHLFGNWR RRVLLKRKRH DNAQLLTSID FDGQTVGLAH VSSMCNQKLS TGVIQDHSAI
321 NLLVAVTMAH ELGHNLGMDH DGNQCHCDAP SCVMSARLRE RPSYGFSNCS QNEYQMFIIN YNPQCILNEP LPTDIVSPPV
401 CGNELLEVGE ECDCGSPNNC QDPCCDATTC KQHSWVECES GECCEQCRFK GAGTECRAAS SECDIAESCT GQSADCPTDD
481 LHRNGQPCLN NHGYCYNGMC PIMDHQCIAL YGADATVAED ACFDSNLQGQ GNFYCRRENG RIFPCAPQDV KCGRLFCKFD
561 HYSCQYQYSG DPDFGMVDHG TKCADGKVCN NRRCVDVTTA Y
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	
															total 1 peptides	

QIV64953.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 TIDFDGQTVG LAHISSMCNS KLSTGVIQDH SPINLLMAVT MAHELGHNLG MDHDTKYCTC GAPACIISDT LSHQPSKQFS
 81 NCSKEDYRTY LINRRPQCIL NEPLPTDIIS PPVCGNELLE VGEECDCGSP NTCQDPCCDA TTCKQHSWVE CESGECCEQC
161 KFKGAGTECQ AAKDDCDMAE SCTGRSAYCP TDDLHRNGQP CLNNHGYCYN GMCPIMDHQC IALYGADATV AEDACFDLNL
241 QGQGNFYCRR EKARIVPCAP QDVKCGRLFC KFDHYSCQYQ YSGDPDFGMV DHGTKCADGK VCKNRQCVDV TTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	A
G.DPDFGMVDHGTK.C	Y	60.18	1317.5659	12	1.0	659.7909	2	34.72	4	F4:9473	17112021_RID_2349_DP4.raw		2.6453E5		1.04E6	
															total 1 peptides	

ETE57622.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MSHVSMWRTS SSTLLEKLSS LHNIKSNVVH PNDGSGIFGG SHGITGLHYI FFSLPLCKGI TSQPTLTQPV SQSGSPGGTV
 81 KLSCAISSNP NNVRWVQQKS GEAPRFVHCD ACSSRGDGIP DRFMATRSGN NGYLTITNLQ AEDEADYFCC MWYSSGNMFH
161 IISHSGPLRG TIKLSCAISS DEMAISWLQQ RSGGAPHFVH CDGCNRGPGI PGRFTGTRSG NNGYLTITTL QAEDKANYYC
241 YMWYSSGGRF HRSFAQYVLT QPASVSVPLR QNARITCSAN NIASKNVHWY QQKPGDPPVL IIYNDNQRPT GISDQFSGTN
321 SGNTATLSIS RAQAQDEAVY YCQVFDSNQC TKAQFSIMAW SLLLAFFFLG CTRATAQFTL TQPAAQSFPL GQPAKISCTM
401 SRDSQVGSYD ISWHQQKAGE SPKYLLSNMG SNGRFKGSKD ASANAAYLTI TNLQAEEEAD YYCGGAYGSG NNWWFPQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
Q.FSGTNSGNTATLSISR.A	Y	55.32	1611.7853	16	0.3	806.9001	2	36.24	7	F7:10113	17112021_RID_2349_DP7.raw					

total 1 peptides

XP_015672332.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MPKPVNVRVT TMDAELEFAI QPNTTGKQLF DQVVKTIGLR EVWYFGLQCT DNKGFPTWLK LEKKVSAQEI RKENPLQFKF
 81 RAKFFPEDVF EELIQDITQK LFFLQVKEGI LSDEIYCPPE TAVLLGSYAV QAKFGDYNKE LHKAGYLSSE RLVPQRVMNQ
161 HKLSREQWEE RIQVWHAEHG GMLKENAMLE YLKIAQDLEM YGINYFEIKN KKGTDLWLGV DALGLNIYEK EDKLTPKIGF
241 PWSEIRNISF NDKKFVIKPI DKKSPDFIFY APRLRINKRI LQLCMGNHEL YMRRRKPDTI EVQQMKAQAR EEKNQKELER
321 KMLEKEKKKR ETIEKEKEQM MREKEELMIR LQEYEVKTQK AEKELSDQIE KARQLEDERT RAQEEAERLE NERLMALQAK
401 EELEKQAVDQ MKSQEQLATE LAEYTAKISL LEEARKHKET EVEEWQHRAK EAQDDLVKTK EELHLVMTAP PPPPPPAYEP
481 VNYHVHDPLQ DEGIESSGYS AEFSSEGILN DRNEEKRITE TEKNERVQRQ LKTLTDELAQ ARDDEKKTQN DLIHTENMRQ
561 GRDKYKTLRQ IRQGNTKQRI DEFESM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
K.SPDFIFYAPR.L	Y	52.38	1211.5974	10	0.5	606.8063	2	55.07	1	F1:16773	12112021_RID_2349_DP1.raw	7.951E4					

total 1 peptides

TRINITY_DN27458
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MTQGSVLLFI LYMSHHVFAQ GQNSYLIQEC LNNNYTEKSC EKVFCQPWQT CIEGTCHCKI PYQCPRNGTS VCSTMRRSFQ
 81 TYCQLKSYEC RQRLSKFLSR GVCNREAHFN VLFSHENASS EGIIQVELSN SEKSFLCGKG LTIHEANVIC RHLGFAEGAD
161 GKESVEPDED QNSHECLKAT CRGTETSLAE CGLKKLRLTT CKLAKVICHT EQRDCSPREF RCVNGKCISS AKTCDGLNDC
241 GDLSDELCCK ACKRKHFHCN SDVCIPSSFV CNNELDCLTG EDELNCNKTG GSKKVETEGR RTSNKEESNQ VIQSMDEERK
321 RTKSLFPVLS CGITNHTVTR RKRIIGGFTA KPHEFPWQVA IRGEGQIMNC GGVYIGGCWI LTAAHCVRRS RLHIYKIWTG
401 IVDSMKYSTR VDTFSLKDMI IHEHYNAKTY QNDIALLEMK TKNEGTPCSP RHTVPVCIPW SQYMFGSGHQ CKVSGWGLDE
481 ESTRQYILKW GYVTLMDNCS EIYKNRYFKG MECAGTDDGS VDACKGDSGG PLVCFDHNNV GYVWGVVSWG ENCGEKGHPG
561 VYTKVALYFD WIAQHTGISL ISKYNL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.TYQNDIALLEMK.T	Y	51.48	1437.7173	12	1.1	719.8667	2	52.54	4	F4:15401	17112021_RID_2349_DP4.raw				1.3912E5	

total 1 peptides

XP_015683432.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MTQGSVLLFI LYLSHHVFAQ GQNSYLIEEC LENNYTEQSC EKVFCQPWQT CIEGTCHCKI PYQCPRNGTL VCSTTRRSFQ
 81 TYCQLKSYEC RQRSSKFLSR GLCNREARFN VLFSHKNASS EGIIQVELSN SEKSFLCEKG LTIHEANVIC KHLGFAEGAD
161 GKESVEPDED QNSHECLKAT CRGTETSLAE CGLKKMRLTI GKLAKVICHT EQRDCSPREF RCVNGKCISS TKTCDGLNDC
241 GDLSDELCCK ACKRKTFHCN SDVCIPSSSV CNNELDCLTG EDELNCNKTG RSKKGDSNQV IESVDEERKR TKTLLPVISC
321 GITNHTVTRR KRVIGGFTAK PHDFPWQVAI RGEGQTMNCG GVYIGGCWIL TAAHCVRRSR LHVYKIWTGV VDSIKFNSRV
401 ETFSLKDMII HEHYNSKTYQ NDIALLEMKT KNEGTPCSPP DTVPVCIPWS QYMFGGGHQC KVSGWGLDEG STRQYILKWG
481 YVTLMDNCSE IYKNRYFKGM ECAGTDDGSV DACKGDSGGP LVCFDHNNVG YLWGVVSWGE NCGERGHPGV YTKVANYFDW
561 IAQRTGIALI SKYNL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Are F5
K.TYQNDIALLEMK.T	Y	51.48	1437.7173	12	1.1	719.8667	2	52.54	4	F4:15401	17112021_RID_2349_DP4.raw				1.3912E5	

total 1 peptides

XP_007421015.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MGFPVALVFF LGGAVLRGAA VRCGYQSCPV TEPDMLNIHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVRQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKS HRESLREMEQ LWRASRNLDP PVADLFTGIL PNVYNPPVSL
241 CWDQICSDNP IVDDDSDENN VENIVAYFLG TATAQAKHYR TNHIVMTMGS DFQYENALLW YKNMDKLIHH VNAQQLRGSR
321 INVFYSTPSC YLWELNKANM SWSVKYDDFF PYADGPHQFW TGYFTSRPAL KRYERLSNNF LQICNQLEVL VGPKANLGPY
401 GSANSSVLRQ AMGVAQHHDA VSGTAKQHVT NDYAKQLSVG WDACQIVMSN ALASLVGSKE NFIYCTYLNI SVCPLTEAAP
481 TFTVIIYNPL ARSVDWNVRL PVNGSHYSVV APDGQNVLNE IIPVSSFTRA VRHNQGSAIN ELVFQASLPP LGYSTYSISR
561 LSARDPVRSR LLKRLRPQPA AEYLMLAIEN EHLQVLFDPR TGLMKEIRNL DKNISLPLLQ SFLWYNASVG NEEHSQPSGA
641 YIFRPDTSKP FPIAQEARIY QMKTQVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIWDHRGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RVTWNLSQTE PVAGNYYPVN SRIYIKDRKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVGEPL LEPGDYHNGL VVRGRHLVFL DTVESSAEQH RLRAQQEYMA PQLVLAPGGG PPYQPGQGIV KEFSALHHAL
881 PSNIHLLTLA QWEPDAVLIR LEHQFEHGEA VNGSLPVVIN LLNLFSSFNI VTVQEMNLSA NQKREDVSRL LWQPAEGVAA
961 EQRSGTGLDP AHIELFPMEI RTFLLQIRYQ DKPRQEM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
T.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

TRINITY_DN13676
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAVAQHHDAV SGTAKQHVTN DYAKQLSIGW DACQIVMNNA FANLLGSTEN FIYCTYLNIS ACPLTEATPT FRVIIYNPLA
 81 RSVDWNVRLP VNGSHYSVVA PDGQNILNEI IPVSSFTRAV RHNRGSAINE LVFQASLPPL GYKTYSVSRL SLRDPAHPKL
161 LKRMRPQPAA AHLTPSIENE HLQVLFDPST GLMKEIRNLD KSISLPLLQS FLWYNASDGN GEYSQASGAY IFHPDPSKAF
241 PIAHGAHVYQ IKTQVVQELY QNFSDWCSQV VRLYAGQPYV ELEWTVGPIP IGDQQGKEII SRFETNLQTE GLFYTDSNGR
321 EILERRRDYR FTWNLSQTEP VAGNYYPVNS RIYIKDRKTQ LTVLTDRSQG GSSLTDGSLE LMVHRRLLHD DNRGVQEPLL
401 EPGEYHNGLV VRGRHLIFLD TVESSAEQHR LWAQQEYMAP QVVLTPDSHD VVKEFSALRY ALPLNVHLLT LAQWEPDAVL
481 IRLEHQFEYG EAVNGSLPVV INLLDLFSSF NIIAVQETNL SANQKRENVS RLIWQSTEGI AAERRSGTGL DPAHIELFPM
561 QIRTFLLQIR S
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

TRINITY_DN13676
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNGYDPPMAL
241 CWDQICSDNP IVDDDSDENN VEKIVAYFLG IAAAQAKHYR TNHIVMTMGS DFQYENAMLW YKNLDKLIHH VNTQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYANGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGTKANFGPY
401 GNANSSVLRQ TMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SACPLTEATP
481 TFRVIIYNPL ARSVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGSAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPK LLKRMRPQPA AAHLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NGEYSQASGA
641 YIFHPDPSKA FPIAHGAHVY QIKVGKAQRH LLQIDLFAQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6

total 1 peptides

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

TRINITY_DN13676
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNGYDPPMAL
241 CWDQICSDNP IVDDDSDENN VEKIVAYFLG IAAAQAKHYR TNHIVMTMGS DFQYENAMLW YKNLDKLIHH VNTQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYANGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGTKANFGPY
401 GNANSSVLRQ TMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SACPLTEATP
481 TFRVIIYNPL ARSVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGSAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPK LLKRMRPQPA AAHLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NGEYSQASGA
641 YIFHPDPSKA FPIAHGAHVY QIKVGKAQRH LLQIDLFAQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

TRINITY_DN13676
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNGYDPPMAL
241 CWDQICSDNP IVDDDSDENN VEKIVAYFLG IAAAQAKHYR TNHIVMTMGS DFQYENAMLW YKNLDKLIHH VNTQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYANGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGTKANFGPY
401 GNANSSVLRQ TMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SACPLTEATP
481 TFRVIIYNPL ARSVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGSAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPK LLKRMRPQPA AAHLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NGEYSQASGA
641 YIFHPDPSKA FPIAHGAHVY QIKTQVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIGDQQGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RFTWNLSQTE PVAGNYYPVN SRIYIKVTIS HGSAQTWLFL VSYRTACPHK A
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Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

TRINITY_DN13676
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNGYDPPMAL
241 CWDQICSDNP IVDDDSDENN VEKIVAYFLG IAAAQAKHYR TNHIVMTMGS DFQYENAMLW YKNLDKLIHH VNTQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYANGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGTKANFGPY
401 GNANSSVLRQ TMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SACPLTEATP
481 TFRVIIYNPL ARSVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGSAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPK LLKRMRPQPA AAHLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NGEYSQASGA
641 YIFHPDPSKA FPIAHGAHVY QIKTQVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIGDQQGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RFTWNLSQTE PVAGNYYPVN SRIYIKDRKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DVVKEFSALR YALPLNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV VINLLDLFSS FNIIAVQETN LSANQKRENV SRLIWQSTEG IAAERRSGTG
961 LDPAHIELFP MQIRTFLLQI RS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

JAV50100.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAIRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYSA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNVYNPPMSL
241 CWDQICSDNP IVDDDSDENN VENIVAYFLG IAAFQAKHYR TNHIVMTMGS DFQYENALLW YKNLDKLIHH VNAQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYADGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGTKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFVYCTYLNI SACLLTEADP
481 TFRVIIYNPL ARPVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGSAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPR LLNRMRPQPA AAHLTPSIKN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYKASDG NAEHSQASGA
641 YIFRPDTFKA FPIAYGADVY QIKNRVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIGDQQGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RFTWNLSQTE PVAGNYYPVN SRIYIKDRKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALR HALPLNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV VINLLNLFSS FNIITVQEMN LSANQKRENV SRLIWQSTEG IAAKRRSGTG
961 LDPAHIELFP MQIRTFLVQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.VIIYNPLAR.P	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

LAB58574.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SACSLTEVAP AFRVIIYNPL
 81 ARSVDWNIRL PVNGSHYSVV APDG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_007421016.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MLNIHLIPHT HDDVGWLKTV DQYFFGVRND IQHAGVQYIL DSVIPQLLAD PSKRFIYVEV AFFARWWGLQ TEAMRQAVRQ
 81 LVAEGRLEFV NGGWCMNDEA SVHYNAVIDQ MSLGLHFLKE TFGECGRPRV AWHIDPFGHS REQASLFAQM GYDGFFLGRI
161 DYQDKSHRES LREMEQLWRA SRNLDPPVAD LFTGILPNVY NPPVSLCWDQ ICSDNPIVDD DSDENNVENI VAYFLGTATA
241 QAKHYRTNHI VMTMGSDFQY ENALLWYKNM DKLIHHVNAQ QLRGSRINVF YSTPSCYLWE LNKANMSWSV KYDDFFPYAD
321 GPHQFWTGYF TSRPALKRYE RLSNNFLQIC NQLEVLVGPK ANLGPYGSAN SSVLRQAMGV AQHHDAVSGT AKQHVTNDYA
401 KQLSVGWDAC QIVMSNALAS LVGSKENFIY CTYLNISVCP LTEAAPTFTV IIYNPLARSV DWNVRLPVNG SHYSVVAPDG
481 QNVLNEIIPV SSFTRAVRHN QGSAINELVF QASLPPLGYS TYSISRLSAR DPVRSRLLKR LRPQPAAEYL MLAIENEHLQ
561 VLFDPRTGLM KEIRNLDKNI SLPLLQSFLW YNASVGNEEH SQPSGAYIFR PDTSKPFPIA QEARIYQMKT QVVQELYQNF
641 SDWCSQVVRL YAGQPYVELE WTVGPIPIWD HRGKEIISRF ETNLQTEGLF YTDSNGREIL ERRRDYRVTW NLSQTEPVAG
721 NYYPVNSRIY IKDRKTQLTV LTDRSQGGSS LTDGSLELMV HRRLLHDDNR GVGEPLLEPG DYHNGLVVRG RHLVFLDTVE
801 SSAEQHRLRA QQEYMAPQLV LAPGGGPPYQ PGQGIVKEFS ALHHALPSNI HLLTLAQWEP DAVLIRLEHQ FEHGEAVNGS
881 LPVVINLLNL FSSFNIVTVQ EMNLSANQKR EDVSRLLWQP AEGVAAEQRS GTGLDPAHIE LFPMEIRTFL LQIRYQDKPR
961 QEM
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
T.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_026552070.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MRFPVALVFF LGGAVLRGSA VKCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPNKRFI YVEVVFFARW WELQTEAMRQ AVRQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECS
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PSADLFTGIL PNGYNPPMSL
241 CWDQICSDNP IVDDNSDENN VESIVAYFLG TAAAQAKHYR TNHIVMTMGS DFQYENALLW YKNMDKLIYH VNAQQLRGSR
321 VNVLYSTPSC YLWELNKANM TWSMKYDDFF PYADGPHQFW TGYFTSRPAL KRYERLSNNF LQICNQLEVL VGTKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SVCSLTEFAP
481 TFRVIIYNPL ARSVDWNIRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNQGSATN ELVFQASLPP LGYRTYSVSR
561 LSGKDSTHPR LLKRLRPRPA AARLTPSIEN EHLQVLFDPN TGLMKEIRNL DKNISLPLSQ SFLWYNASDG NAAFSQASGA
641 YIFRPDTSKA FPIAQKVRVY QIKTQVVQEL YQNFSNWCSQ VVRLYAGQPY VELEWTVGPI PIADHYGKEI ISRFETNLQT
721 GGLFYTDSNG REILERRRDY RVTWNLSQTE PVAGNYYPVN TRMYIKDQKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALR HALPSNVHLL
881 TLAQWEPNAV LIRLEHQFEY GEAVNGSLPV AINLLNLFSS FNIITVQEMN LSANQKRENV SRLIWRSTQG IAAERQSGTR
961 LDPAHIELSP MQIRTFLLQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

JAA96625.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYSA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNVYNPPMSL
241 CWDQICSDNP IVDDDSDENN VENIVAYFLG IAAFQAKHYR TNHIVMTMGS DFQYENALLW YKNLDKLIHH VNAQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYADGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGRKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMSN AFANLLGSTE NFVYCTYLNI SACPLTEADP
481 TFRVIIYNPL ARPVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGNAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPR LLNRMRPQPV AAPLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NAEHSQASGA
641 YIFRPDTFKA FPIAYGADVY QIKNQVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIGDQQGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RFTWNLSQTE PVAGNYYPVN SRIYIKDRKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLR
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALQ HALPLNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV VVNLLNLFSS FNIITVQEMN LSANQKRENV SRLIWQSIEG IAAKRRSGTG
961 LDPAHVELFP MQIRTFLLQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.P	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_026537394.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

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  1 MRFPVALVFF LGGAVLRGSA VKCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVVFFARW WELQTEAMRQ AVRQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECS
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PSADLFTGIL PNGYNPPMSL
241 CWDQICSDNP IVDNNSDENN VESIVAYFLG TAAAQAKHYR TNHIVMTMGS DFQYENALLW YKNMDKLIYH VNAQQLRGSR
321 VNVLYSTPSC YLWELNKANM TWSMKYDDFF PYADGPHQFW TGYFTSRPAL KRYERLSNNF LQICNQLEVL VGTKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SVCSLTEVAP
481 TFRVIIYNPL ARSVDWNIRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNQGSATN ELVFQASLPP LGYRTYSVSR
561 LSGKDSTRPR LLKRLRPQPA AARLTPSIEN EHLQVLFDPN TGLMKEIRNL DKNISLPLSQ SFLWYNASVG NAAFPQASGA
641 YIFRPDTSKA FPIAQKVRVY QIKTQVVQEL YQNFSNWCSQ VVRLYAGQPY VELEWTVGPI PIADHYGKEI ISRFETNLQT
721 GGLFYTDANG REILERRRDY RVTWNLSQTE PVAGNYYPVN TRMYIKDQKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALR HALPSNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV AINLLNLFSS FNIITVQEMN LSANQKRENV SRLIWQSTQG IAAERQSGTR
961 LDPAHIELSP MQIRTFLLQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

JAG44103.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

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  1 MRFPVALVFF LGGAVLRGSA VRCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVAFFARW WGLQTEAMRQ AVQQLVAEGR LEFVNGGWCM NDEASVHYSA VIDQMSLGLH FLKETFGECG
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PAADLFTGIL PNVYNPPMSL
241 CWDQICSDNP IVDDDSDENN VENIVAYFLG IAAFQAKHYR TNHIVMTMGS DFQYENALLW YKNLDKLIHH VNAQQLKGSR
321 VNVLYSTPSC YLWELNKANM TWSLKYDDFF PYADGPHQFW TGYYTSRPAL KRYERLSNNF LQICNQLEVI VGRKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMSN AFANLLGSTE NFVYCTYLNI SACPLTEADP
481 TFRVIIYNPL ARPVDWNVRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNRGNAIN ELVFQASLPP LGYKTYSVSR
561 LSLRDPAHPR LLNRMRPQPV AAPLTPSIEN EHLQVLFDPS TGLMKEIRNL DKSISLPLLQ SFLWYNASDG NAEHSQASGA
641 YIFRPDTFKA FPIAYGADVY QIKNQVVQEL YQNFSDWCSQ VVRLYAGQPY VELEWTVGPI PIGDQQGKEI ISRFETNLQT
721 EGLFYTDSNG REILERRRDY RFTWNLSQTE PVAGNYYPVN SRIYIKDRKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLR
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALQ HALPLNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV VVNLLNLFSS FNIITVQEMN LSANQKRENV SRLIWQSIEG IAAKRRSGTG
961 LDPAHVELFP MQIRTFLLQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.P	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_026537257.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MRFPVALVFF LGGAVLRGSA VKCGYQSCPV TKPDMLNVHL IPHTHDDVGW LKTVDQYFFG VRNDIQHAGV QYILDSVIPQ
 81 LLADPSKRFI YVEVVFFARW WELQTEAMRQ AVRQLVAEGR LEFVNGGWCM NDEASVHYNA VIDQMSLGLH FLKETFGECS
161 RPRVAWHIDP FGHSREQASL FAQMGYDGFF LGRIDYQDKF HRESLREMEQ LWRASRNLDP PSADLFTGIL PNGYNPPMSL
241 CWDQICSDNP IVDDNSDENN VESIVAYFLG TAAAQAKHYR TNHIVMTMGS DFQYENALLW YKNMDKLIYH VNAQQLRGSR
321 VNVLYSTPSC YLWELNKANM TWSMKYDDFF PYADGPHQFW TGYFTSRPAL KRYERLSNNF LQICNQLEVL VGTKANFGPY
401 GNANSSVLRQ AMAVAQHHDA VSGTAKQHVT NDYAKQLSIG WDACQIVMNN AFANLLGSTE NFIYCTYLNI SVCSLTEVAP
481 TFRVIIYNPL ARSVDWNIRL PVNGSHYSVV APDGQNILNE IIPVSSFTRA VRHNQGSATN ELVFQASLPP LGYRTYSVSR
561 LSGKDSTRPR LLKRLRPQPA AARLTLSIEN EHLQVLFDPN TGLMKEIRNL DKNISLPLSQ SFLWYNASVG NAAFPQASGA
641 YIFRPDTSKA FPIAQKVRVY QIKTQVVQEL YQNFSNWCSQ VVRLYAGQPY VELEWTVGPI PIADHYGKEI ISRFETNLQT
721 GGLFYTDANG REILERRRDY RVTWNLSQTE PVAGNYYPVN TRMYIKDQKT QLTVLTDRSQ GGSSLTDGSL ELMVHRRLLH
801 DDNRGVQEPL LEPGEYHNGL VVRGRHLIFL DTVESSAEQH RLWAQQEYMA PQVVLTPDSH DIVKEFSALR HALPSNVHLL
881 TLAQWEPDAV LIRLEHQFEY GEAVNGSLPV AINLLNLFSS FNIFTVQEMN LSANQKRENV SRLIWQSTQG IAAERQSGTR
961 LDPAHIELSP MQIRTFLLQI RY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

LAB27223.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 STWGSLSCRN RVGVMGFPVA LVFFLGGAVL RGSAVKCGYQ SCPVTKPDML NVHLIPHTHD DVGWLKTVDQ YFFGVRNDIQ
 81 HAGVQYILDS VIPQLLADPS KRFIYVEVVF FARWWELQTE AMHQAVRQLV AEGRLEFVNG GWCMNDEASV HYNAVIDQMS
161 LGLHFLKETF GECSRPRVAW HIDPFGHSRE QASLFAQMGY DGFFLGRIDY QDKFHRESLR EMEQLWRASR NLDPPSADLF
241 TGILPNGYNP PMSLCWDQIC SDNPIVDDDS DENNVENIVA YFLGTAAAQA KHYRTNHIVM TMGSDFQYEN ALLWYKNMDK
321 LIYHVNAQQV RGSRVNVLYS TPSCYLWELN KANMTWSMKY DDFFPYADGP HQFWTGYFTS RPALKRYERL SNNFLQICNQ
401 LEVLVGTKAN FGPYGNANSS VLRKAMAVAQ HHDAVSGTAK QHVTNDYAKQ LSIGWDACQI VMNNAFANLL GSTENFIYCT
481 YLNISACSLT EVAPAFRVII YNPLARSVDW NIRLPVNGSH YSVVAPDGQN IMNEIIPVSS FTRAVRHNRG SATNELVFQA
561 SLPPLGYRTY SIARLSDKDS AHPRLLKRLR PQPAAAHLTP LIENEHLQVL FDPNTGLMKE IRNLKKNISL PLSQSFLWYN
641 ASVGNAAFSQ ASGAYIFRPD TSKAFPIAQK VGVYQIKTQV VQELYQNFSN WCSQVVRLYA GQPYVELEWT VGPIPIADHY
721 GKEIISRFET NLQTGGLFYT DSNGREILER RRDYRVTWNL NQTEPVAGNY YPVNTRMYIK DQKTQLTVLT DRSQGGSSLT
801 DGSLELMVHR RLLHDDNRGV QEPLLEPGDY HNGLVVRGRH LIFLDTVESS AEQHRLWAQQ EYMAPQVVLT PDSHDIVKEF
881 SALRHALPSN VHLLTLAQWE PDAVLIRLEH QFEYGEAVNG SLPVTINLLN LFSSFNIITV QEMNLSANQK RENVSRLIWQ
961 STQGIAAERQ SGTRLDPAHI ELSPMQIRTF LLQIRY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_032065032.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIIAVRMSCW KGVGTMGFHV ALVFFLGGAV LGGSAVRCGY QSCPVTKPDM LNVHLIPHTH DDVGWLKTVD QYFFGVRNDI
 81 QHAGVQYILD SVIPQLLADP SKRFIYVEVV FFARWWGLQT EAMRQAVRQL VAEGRLEFVN GGWCMNDEAS VHYSAVIDQM
161 SLGLQFLKET FGECARPRVA WHIDPFGHSR EQASLFAQMG YDGFFLGRID YQDKSHRESL REMEQLWRAS RNLDPPAADL
241 FTGILPNGYN PPMSLCWDQI CSDNPIVDDD SDENNVENIV AYFLGTAAVQ AKHYRTNHIV MTMGSDFQYE NALLWYKNMD
321 KLIYHVNAQQ LKGSHVNVFY STPSCYLWEL NKANMTWSIK YDDFFPYADG PHQFWTGYFT SRPAFKRYER LSNNFLQICN
401 QLEVLVGTKA NFGPYGNANS SVLRQAMAVA QHHDAVSGTA KQHVTNDYAK QLSIGWDTCQ IVMNNALANL LGSTENFIYC
481 TYLNISACPL TEATPAFRVI IYNPLARSVD WNVRLPVNGS HYSVVAPDGQ NILNELIPVS SFTRAVRHNR GSAINELVFQ
561 ASLPPLGYRT YSISRLSGRD SARPKLLKRL RPQQAGAHFT PLIENEHLQV LFDPNTGLMK EIRNLDKNIS LPLFQSFLWY
641 NASVGDASYS QASGAYIFRP DTSKAFPIAQ KVGVYQIKTQ VVQELYQNFS NWCSQVVRLY AGQPYVELEW TVGPIPIQDQ
721 YGKEIISRFE TNLQTGGHFY TDSNGREILE RRRDYRATWN LSQTEPVAGN YYPVNTRIYI KDQKTQLTVL TDRSQGGSSL
801 ADGSLELMVH RRLLHDDNRG VQEPLLEFGE YHNGLVVRGR HLVFLDTVES SAEKHRLWAQ QEYMAPQVVL TPDSHDIVKE
881 FSALRHALPL NVHLLTLAQW EPDAVLIRLE HQFEYGEAVN GSLPVAINLL NLFSSFNIIS VQEVNLSANQ KRENVSRLTW
961 QSTQGMAAER RSGTVLDPAH IELFPMQIRT FLVQIRY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_034262785.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MIAAVSLSCW NGVGAMGIPV ALVFLLGGAV LRGSAVRCGY QSCPVTKPDM LNVHLIPHTH DDVGWLKTVD QYFFGVRNDI
 81 QHAGVQYILD SVVPQLLADP SKRFIYVEVV FFARWWGLQT EAMRQAVRQL VAEGRLEFVN GGWCMNDEAS VHYNAVIDQM
161 SLGLHFLKET FGECGRPRVA WHIDPFGHSR EQASLFAQMG YDGFFLGRID YQDKFHRESL REMEQLWRAS SNLDPPAADL
241 FTGILPNGYN PPMSLCWDQI CSDNPIVDDD SDENNVENIV AYFLGVAAAQ AKHYRTNHIV MTMGSDFQYE NALLWYKNMD
321 KLIYHVNAQQ LKGSRVNVFY STPSCYLWEL NKANITWTMK YDDFFPYADG PHQFWTGYFT SRPALKRYER LSNNFLQICN
401 QLEVLVGTKA NFGPYGNANS SVLRQAMAVA QHHDAVSGTA KQHVTNDYAK QLSIGWDACQ IVMNNAFANL LGSTENFIYC
481 TYLNISACPL TEATPAFRVI IYNPLARSVD WNVRLPVNGS HYSVVAPDGQ NILNEIIPVS SFTRAVRHNR GSAINELVFQ
561 ASLPPLGYRT YSISRLSGRD SARPRLQKRL RPRPAAAHLT PSIENEHLQV LFDPKTGLMK EIRNLDKNIS LPLFQSFLWY
641 NASDGNAAYS QASGAYIFRP DTSKAFPIAQ KVRVYQIKTQ VVQELYQNFS DWCSQVVRLY AGQPYVELEW TVGPIPIEDL
721 YGKEIISRFE TNLQTGGLFY TDSNGREILE RRRDYRVTWN LSQTEPVAGN YDPVNTRIYI KDQKTQLTVL TDRSQGGSSL
801 TDGSLELMVH RRLLHDDNRG VQEPLLEPGE YHNGLVVRGR HLVFLDTVES SAEQHRLWAQ QEYMAPQVVL TPDSHDIVKE
881 FSALRHALPL NVHLLTLAQW EPDAVLIRLE HQFEYGEAVN GSLPVAINLL NLFSSFNIIA VQEMNLSANQ KRENVSRLIW
961 QSTQGIAAER RSGTRLDPAH IELSPMQIRT FLVQIRY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

XP_013919874.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MIIAIRMSCW KGVGTMGFHV ALVFFLGGAV LGGSAVRCGY QSCPVTKPDM LNVHLIPHTH DDVGWLKTVD QYFFGVRNDI
 81 QHAGVQYILD SVIPQLLADP SKRFIYVEVV FFARWWGLQT EAMRQAVRQL VAEGRLEFVN GGWCMNDEAS VHYSAVIDQM
161 SLGLQFLKET FGECARPRVA WHIDPFGHSR EQASLFAQMG YDGFFLGRID YQDKSHRESL REMEQLWRAS RNLDPPAADL
241 FTGILPNGYN PPMSLCWDQI CSDNPIVDDD SDENNVENIV AYFLGTAAVQ AKHYRTNHIV MTMGSDFQYE NALLWYKNMD
321 KLIYHVNAQQ LKGSHVNVFY STPSCYLWEL NKANMTWSIK YDDFFPYADG PHQFWTGYFT SRPAFKRYER LSNNFLQICN
401 QLEVLVGTKA NFGPYGNANS SVLRQAMAVA QHHDAVSGTA KQHVTNDYAK QLSIGWDTCQ IVMNNALANL LGSTENFIYC
481 TYLNISACPL TEATPAFRVI IYNPLARSVD WNVRLPVNGN HYSVVAPDGQ NILNELIPVS SFTRAVRHNR GNAINELVFQ
561 ASLPPLGYRT YSISRLSGRD SARPRLLKRL RPQQAGAHFT PLIENEHLQV LFDPNTGLMK EIRNLDKNIS LPLFQSFLWY
641 NASVGDASYS QASGAYIFRP DTSKAFPIAQ KVGVYQIKTQ VVQELYQNFS NWCSQVVRLY AGQPYVELEW TVGPIPIQDQ
721 YGKEIISRFE TNLQTGGHFY TDSNGREILE RRRDYRATWN LSQTEPVAGN YYPVNTRIYI KDQKTQLTVL TDRSQGGSSL
801 ADGSLELMVH RRLLHDDNRG VQEPLLEFGE YHNGLVVRGR HLVFLDTVES SAEKHRLWAQ QEYMAPQVVL TPDSHDIVKE
881 FSALRHALPL NVHLLTLAQW EPDAVLIRLE HQFEYGEAVN GSLPVAINLL NLFSSFNIVS VQEVNLSANQ KRENVSRLTW
961 QSTQGMAAER RSGTGLDPAH IELFPMQIRT FLVQIRY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
R.VIIYNPLAR.S	Y	50.81	1057.6284	9	0.8	529.8219	2	50.08	1	F1:15258	12112021_RID_2349_DP1.raw	1.4791E5					

total 1 peptides

JAV49704.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKVLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKSANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS
 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA VEELVESNEV
161 AVIGFFKDVE SDVAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVVL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KTAAEDFRGK ILFIYIDSDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIRDFCHK FLEGKVKPHL MSQEISDDWD KQPVKVLVGK NFEEVAFDEN KNVFVEFYAP
401 WCGHCKQLAP IWDKLGETYK DHENIIIAKM DSTVNEVEVV KVHSFPTLKY FPAGPDRTVV DYNGERTLEG FKKFLESGGK
481 DGGVDENDLE DLEDAEEEPD VEEEEEETGA KKDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

JAA96208.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKVLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKSANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS

 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA AEELVESNEV

161 AVIGFFKDAE SDVAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVAL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KAAAEDFRGK ILFIYIDSDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIRDFCHK FLEGKVKPHL MSQEISDDWD KQPVKVLVGK NFEEVAFDEN KNVFVEFYAP
401 WCGHCKQLAP IWDKLGETYK DHENIIIAKM DSTVNEVEVV KVHSFPTLKY FPAGPDRTVV DYNGERTLEG FKKFLESGGK
481 DGGVDENDLE DLEDAEEEPD VEEEEEEETG AKKDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

TRINITY_DN159
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKLLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKAANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS

 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA AEELVESNEV

161 AVIGFFKDVE SDMAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVAL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KKAAEDFKGK ILFIYIDGDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIKDFCHK FLEGKVKVIV LFFPNGVFGA GSHVGKS
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

TRINITY_DN159
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKLLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKAANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS

 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA AEELVESNEV

161 AVIGFFKDVE SDMAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVAL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KKAAEDFKGK ILFIYIDGDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIKDFCHK FLEGKVKPHL MSQEISDDWD KHPVKVLVGN NFEEVAFDEN KNVFVEFYAP
401 WCGHCKQLAP IWDKLGETYK DHENIIIAKM DATVNEVEAV KVHSFPTLKY FPAGPDRTVS QLYIET
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

TRINITY_DN159
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MEGIGRKYTI HLMLCLLDVQ FFPPTDAPWC GHCKALAPEY VKAAAKLLSE NSEIRLAKVD ATEESELAQQ FGVRGYPTIK

 81 FFKNGDKSSP KEYTAGREAD DILNWLKKRT GPAATTLADV AAAEELVESN EVAVIGFFKD VESDMAKEFL LAAEAIDDIP
161 FGITSKSDIF AKYQLKKDGV ALFKKFDEGR NNFDGEITKD NLLNFIKSNQ LPLVIEFTEQ TAPKIFGGEI KTHILLFLPK
241 SVEEYQGKLD NFKKAAEDFK GKILFIYIDG DHSDNQRILE FFGLKKEECP AIRLITLEEE MTKYKPESDE LTPENIKDFC
321 HKFLEGKVKP HLMSQEISDD WDKHPVKVLV GNNFEEVAFD ENKNVFVEFY APWCGHCKQL APIWDKLGET YKDHENIIIA
401 KMDATVNEVE AVKVHSFPTL KYFPAGPDRT VVDYNGDRTL EGFKKFLESG GKDGGVDEND LEDLEDAEAE PDVEEEDEET
481 GAKKDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

AFJ50884.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKVLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKSANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS
 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA AEELVESNEV
161 AVIGFFKDVE SDVAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVAL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KTAAEDFRGK ILFIYIDSDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIRDFCHK FLEGKVKPHL MSQEISDDWD KQPVKVLVGK NFEEVAFDEN KNVFVEFYAP
401 WCGHCKQLAP IWDKLGETYK DHENIIIAKM DSTVNEVEVV KVHSFPTLKY FPAGPDRTVV DYNGERTLEG FKKFLESGGK
481 DGGVDENDLE DLEDAEEEPD VEEEEEEEET GAKKDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

JAI12151.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MKVLRFFAPV LCLLWLGQVC LAVDIEEEEG VLVLKSANFD QALEQYPNIL VEFYAPWCGH CKALAPEYVK AAAKLLSENS
 81 EIRLAKVDAT EESELAQQFG VRGYPTIKFF KNGDKSSPKE YTAGREADDI LNWLKKRTGP AATTLADVAA AEELVESNEV
161 AVIGFFKDVE SDVAKEFLLA AEAIDDIPFG ITSKSDIFAK YQLKKDGVAL FKKFDEGRNN FDGEITKDNL LNFIKSNQLP
241 LVIEFTEQTA PKIFGGEIKT HILLFLPKSV EEYQGKLDNF KTAAEDFRGK ILFIYIDSDH SDNQRILEFF GLKKEECPAI
321 RLITLEEEMT KYKPESDELT PENIRDFCHK FLEGKVKPHL MSQEISDDWD KQPVKVLVGK NFEEVAFDEN KNVFVEFYAP
401 WCGHCKQLAP IWDKLGETYK DHENIIIAKM DSTVNEVEVV KVHSFPTLKY FPAGPDRTVV DYNGERTLEG FKKFLESGGK
481 DGGVDENDLE DLEDAEEEPD VEEEEEEEET GAKKDEL
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Are
K.LLSENSEIR.L	Y	50.02	1059.5560	9	0.3	530.7855	2	30.07	7	F7:7892	17112021_RID_2349_DP7.raw							1.33

total 1 peptides

JAG67907.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVKVGVNGFG RIGRLVTRAA FVSGKVEVVA INDPFIDLNY MTYMFKYDST HGRFHGTVHA ENGKLVINGH AITVFQERDP
 81 ANIKWGEAGA DYVVESTGVF TTTEKASAHL KGGAKRVIIS APSADAPMFV MGVNHEKYDK SLKVVSNASC TTNCLAPLAK
161 VIHDNYGIVE GLMTTVHAIT ATQKTVDGPS GKLWRDGRGA AQNIIPASTG AAKAVGKVIP ELNGKLTGMA FRVPTPNVSV
241 VDLTCRLEKP AKYDDIKKVV KAASEGPMKG ILGYTEDQVV SSDFNGDTHS SIFDAAAGIA LNDHFVKLIS WYDNEYGYSN
321 RVVDLMVHMA SKE
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F
K.VGVNGFGR.I	Y	49.83	804.4242	8	0.7	403.2197	2	30.24	4	F4:7860	17112021_RID_2349_DP4.raw				1.365E5		1.3546E

total 1 peptides

TRINITY_DN3991

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MVKVGVNGFG RIGRLVTRAA ILRGNVEVVA INDPFIDLNY MVYMFKYDST HGRWKGDVKA EGGKLVIDGH AITIFQERDP
 81 SNIKWGEAGA TYVVESTGVF TTVEKASTHL KGGAKKVIIS APSADAPMFV VGVNHQKYDP AVNVVSNASC TTNCLAPLAK
161 VINDNFVILE GLMTTVHAYT ATQKTVDGPS GKLWRDGRGA HQNIIPASTG AAKAVGKVIP ELNGKITGMA FRVPTPNVSV
241 VDLTVRLEKP ATYDAIKAKV KEAANGPMKG ILGYTEDQVV STDFNGDTRS SIFDAGAGIA LNDHFVKLVT WYDNEFGYSN
321 RVVDLVLYMV SKDK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F
K.VGVNGFGR.I	Y	49.83	804.4242	8	0.7	403.2197	2	30.24	4	F4:7860	17112021_RID_2349_DP4.raw				1.365E5		1.3546E

total 1 peptides

CAJ01683.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MMQVLLVTIC LAVFPYEGSS IILESGNVND YEIVYPQKVT AMPIEAILQP EQKYEDVMQY EFEVNGEPVV LHLEKNKDLF
 81 SEDYSETYYT PDGREITTNL PVEDHCYYHG RLQNDAHSSA IISACNGLKG HFKLRGETYL IEPLKVPDSE AHAVYKYENI
161 EKEDEAPKMC GVTQTNWESD EPIKEASQLF ATSEQKSYYD RFRHIELVIV VDHRMVEKYN GNLRKIRRRI YQIVNILNQI
241 YIFMNIRVPL VGVEFWTNGD LINVTSEAEA TLNSFGEWRA SYLLSRKNHD HAQLFTAIDL EGLTIGMAPM AGMCQSERSV
321 GIFEDYSPVD HVVAVIIAHE MGHNLGIFHD VHQCNCGANS CIMYAKISNP PPMYFSDCSQ EQYQFFLDNY KPDCTLIRPP
401 RTDIVSPPVC GNDLLEKGEE CDCGSPENCQ NPCCDAASCK LHSWIECEFG ECCEQCRFKP AGTECRGIRN ECDLPEYCTG
481 QSAECPIDRS HRNGKPCLNN YGYCYNGTCP IMYHQCYALF GPKAVVGQDV CFEENKRGES YFYCRKENDV KIPCAPEDIK
561 CGRLFCRHDI YECRYDYSEN PNYGMVEEGT KCGDGKVCSK RHCVDVTTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
R.TDIVSPPVC(+57.02)GNDLLEK.G	Y	48.76	1755.8712	16	0.4	878.9432	2	46.31	3	F3:13400	17112021_RID_2349_DP3.raw			2.178

ADW54336.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MMQVLLVTIC LAVFPYEGSS IILESGNVND YEIVYPQKVT AMPIEAILQP EQKYEDVMQY EFEVNGEPVV LHLEKNKDLF
 81 SEDYSETYYT PDGREITTNL PVEDHCYYHG RLQNDAHSSA IISAXHGLKG HFKLRGETYL IEPLKVPDSX XXXXXXXXXX
161 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
241 XXXXXXXXXX XXXXXXXIRR RIYQIVNILN QIYIFMNIRV PLVGVEFWTN GDLINVTSEA EATLNSFGEW RASYLLSRKN
321 HDHAQLFTAI DLEGLTIGMA PMAGMCQSER SVGIFEDYSP VDHVVAVIIA HEMGHNLGIF HDVHQCNCGA NSCIMYAKIS
401 NPPPMYFSDC SQEQYQFFLD NYKPDCTLIR PPRTDIVSPP VCGNDLLEKG EECDCGSPEN CQNPCCDAAS CKLHSWIECE
481 FGECCEQCRF KPAGTECRGI RSECDLPEYC TGQSLDCPID HFHRNGKPCQ NNNGYCYNGI CPTMQNQCLA HFGPDAVMAQ
561 DGCFEWNKKG EGDFYCRKEN NVTIPCASED IKCGRLFCEI VPNICRRAYG DKGMVDPGTK CEDGKVCINR KCTNVNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
R.TDIVSPPVC(+57.02)GNDLLEK.G	Y	48.76	1755.8712	16	0.4	878.9432	2	46.31	3	F3:13400	17112021_RID_2349_DP3.raw			2.178

ADW54337.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 QLFATSEQKS YYDRFRHIEL VIVVDHRMVE KYNGNLRKIR RRIYQIVNIL NQIYIFMNIR VPLVGVEFWT NGDLINVTSE
 81 AEATLNSFGE WRASYLLSRK NHDHAQLFTA IDLEGLTIGM APMAGMCQSE RSVGIFEDYS PVDHVVAVII AHEMGHNLGI
161 FHDVHQCNCG ANSCIMYAKI SNPPPMYFSD CSQEQYQFFL DNYKPDCTLI RPPRTDIVSP PVCGNDLLEK GEECDCGSPE
241 NCQNPCCDAA SCKLHSWIEC EFGECCEPCR FKPAGTECRG IRSECDLPEY CTGQSLDCPI DHFHRNGKPC QNNNGYCYNG
321 ICPTMQNQCL AHFGPDAVMA QDGCFEWNKK GEGDFYCRKE NNVTIPCASE DIKCGRLFCE IVPNICRRAY GDKGMVDPGT
401 KCEDGKVCIN RKCTNVNTAY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
R.TDIVSPPVC(+57.02)GNDLLEK.G	Y	48.76	1755.8712	16	0.4	878.9432	2	46.31	3	F3:13400	17112021_RID_2349_DP3.raw			2.178

ADW54335.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MVEKYNGNLR KIRRRIYQIV NILNQIYIFM NIRVPLVGVE FWTNGDLINV TSEAEATLNS FGEWRASYLL SRKNHDHAQL
 81 FTAIDLEGLT IGMAPMAGMC QSERSVGIFE DYSPVDHVVA VIIAHEMGHN LGIFHDVHQC NCGANSCIMY AKIREPPPMY
161 FSDCSQEQYQ FFLDNYKPDC TLIRPPRTDI VSPPVCGNDL LEKGEECDCG SPENCQNPCC DAASCKLHSW IECEFGECCE
241 QCRFKPAGTE CRGIRSECDL PEHCTGQSLD CPIDHFHRXG KPCQTNXGYX YNGICPTMXN QCLXHFGPXA VXAQXGXFEW
321 XXKGXGDFXC RKENXVTLPX ASEDIKRGRL XCEIVPNICR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Are F3
R.TDIVSPPVC(+57.02)GNDLLEK.G	Y	48.76	1755.8712	16	0.4	878.9432	2	46.31	3	F3:13400	17112021_RID_2349_DP3.raw			2.178

P86541.2
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                   24 28
1  LKCNKLVPLF YKTCPAGKDL CYKMYMVATP KVPVKRGCID VCPKSSLLVK YVCCNTDRCN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

P01440.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                   24 28
1  LKCNKLVPLF YKTCPAGKNL CYKMYMVATP KVPVKRGCID VCPKSSLVLK YVCCNTDRCN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

AAC61315.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                   26 28
1  YTLKCNKLVP LFYKTCPAGK NLCYKMYMVA TPKVPVKRGC IDVCPKSSLL VKYVCCNTDR CN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

BAU24665.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                   36 38
1  VVTIVCLDLG YTLKCNKLVP LFYKTCPAGK NLCYKMYMVA TPKVPVKRGC IDVCPKSSLL VKYVCCNTDR CN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A l
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

O93472.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
45 47
1   MKTLLLTLVL VTIVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVYPKSSLLV KYVCCNTDRC
81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A l
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

Q9PST3.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
45 47
1   MKTLLLTLVV VTTVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVCPKSSLLV KYVCCNTDRC
81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A l
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

AAK49439.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
45 47
1   MKTLLLTLVV VTIVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVCPKSSLLV KYVCCNTDRC
81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A l
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

AAC27686.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                  45 47
  1  MKTLLLTLVV VTTVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVCPKSSLLV KYVCCNTDRC
                                                                  45 47

 81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

Q9PST4.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                  45 47
  1  MKTLLLTLVV VTIVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVCPKSSLLV KYVCCNTDRC
                                                                  45 47

 81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

AAC27687.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                  45 47
  1  MKTLLLTLVL VTIVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVYPKSSLLV KYVCCNTDRC
                                                                  45 47

 81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

AAC27685.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
                                                                  45 47
  1  MKTLLLTLVV VTIVCLDLGY TLKCNKLVPL FYKTCPAGKN LCYKMYMVAT PKVPVKRGCI DVCPKSSLLV KYVCCNTDRC
                                                                  45 47

 81  N
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYMVATPK.V	Y	47.76	939.4558	8	0.4	470.7354	2	34.94	7	F7:9610	17112021_RID_2349_DP7.raw			
K.M(+15.99)YM(+15.99)VATPK.V	Y	46.26	971.4456	8	0.1	486.7301	2	25.61	6	F6:6222	17112021_RID_2349_DP6.raw	1.4689E5		

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	A
K.MYM(+15.99)VATPK.V	Y	45.65	955.4507	8	0.4	478.7328	2	30.13	2	F2:7655	12112021_RID_2349_DP2.raw	4.4599E4	2.2353E4	

ETE69494.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81 RITPRHLQLA IRGDEELDSL IKATIAGGVL LEAIMKNGSA AGSGTHCRKP ASKNDKSKTN SMKDSSASAA GEIGKTYTKE
161 QIEGVQSIKK CKNYYEVLGV SKDAGEEDLK KAYRKLALKF HPDKNHAPGA TEAFKKIGNA YAVLSNPEKR KQYDLTGSED
241 PCNQPGNGRF NFHRGCEADI TPEDLFNMFF GGAFPTGSVH SFSNGRSGFS HHNQHRHSGH EREEERGDGG FSMFIQLMPI
321 IVLIFVSLLS QLMVSNPPYS LYPRSSSGQT IQMQTENLGV VYYVNKDFKN EYKGPNLQKV EKSVEEDYVS NIRNNCWKER
401 QQKTDLLYAA KVYRDDRLRK KAEAISMDNC KELERLTSIY RGG
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
															total 1 peptides		

ETE65060.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSGRGKQGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII

 81 PRHLQLAVRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK TESHKAKGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
															total 1 peptides		

XP_013915314.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSGRGKQGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII

 81 PRHLQLAVRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK TESHKAKGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
															total 1 peptides		

XP_013919189.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSGRGKSGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLS AEILELAGNA ARDNKKTRII

 81 PRHLQLAIRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK TQSSKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
															total 1 peptides		

XP_013919188.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MSGRGKSGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLS AEILELAGNA ARDNKKTRII

 81 PRHLQLAIRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK TQSSKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
															total 1 peptides		

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

ETE65301.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSGRGKSGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLS AEILELAGNA ARDNKKTRII

 81  PRHLQLAIRN DEELNKLLGG VTIAQGGVLP NIQAVLLPKK TQSSKK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

JAG46644.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAI09932.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

XP_007430054.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAI13025.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

AFJ50305.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAG44453.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAI09933.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAG46643.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

AFJ50304.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAG67733.1

back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAB54108.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAC95409.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAI13026.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAA96854.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAG44452.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

JAA96855.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKAKAKAVSR SQRAGLQFPV GRIHRHLKTR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

XP_013930707.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MAGGKAGKDS GKTKTKTVSR SQRAGLQFPV GRIHRHLKSR TTSHGRVGAT AAVYSAAILE YLTAEVLELA GNASKDLKVK

 81  RITPRHLQLA IRGDEELDSL IKATIAGGGV IPHIHKSLIG KKGQQKTV
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

XP_013931116.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSGRGKQGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII

 81  PRHLQLAIRN DEELNKLLGK VTIAQGGVLP NIQAVLLPKK TESHKAKGK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

XP_013908942.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSGRGKQGGK TRAKAKTRSS RAGLQFPVGR VHRLLRKGNY AERVGAGAPV YLAAVLEYLT AEILELAGNA ARDNKKTRII

 81  PRHLQLAIRN DEELNKLLGR VTIAQGGVLP NIQAVLLPKK TESHKAKAK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

XP_013911300.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSGRGKVGGG KTRSKAKSRS SRAGLQFPVG RVHRLLRRGR YAERVGAGAP VYLAAVLEYL TAEILELAGN AARDNRKTRI

 81  VPRHVQLAVR NDEELSRLLG RVTIAQGGVL PNIPAALLPR KAAAQGGGAA GRKKGALQAS QEY
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

ETE60792.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1  MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERIGGGAPV YLAAVLEYLS AEILELAGNA ARDNKKSRII

 81  PRHLQLAVRN DEELNKLLGG VTIAQGGVLP NIHAVLLPKK TEILHSASSS KPTTSVSKST KVPKVAVKPT TAPVSV
```

Supporting Peptides:

| Peptide | Uniq | -10lgP | Mass | Length | ppm | m/z | z | RT | Fraction | Scan | Source File | Area F1 | Area F2 | Area F3 | Area F4 | Area F5 | A |

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

XP_013924759.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERIGGGAPV YLAAVLEYLS AEILELAGNA ARDNKKSRII

 81  PRHLQLAVRN DEELNKLLGG VTIAQGGVLP NIHAVLLPKK TEILHSASSS KPTTSVSKSA KVPKVAVKPT TAPVAVQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

XP_026542761.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MSGRGKTGGK ARAKAKSRSS RAGLQFPVGR VHRLLRKGNY AERIGGGAPV YLAAVLEYLS AEILELAGNA ARDNKKSRII

 81  PRHLQLAVRN DEELNKLLGG VTIAQGGVLP NIHAVLLPKK TEILHSASSS KPTTSVSKST KVPKVAVKPT TAPVSVQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.
																total 1 peptides	

ETE59971.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  GRGRPGSLLA PRRVIVSRLS QAALARNRDR TSPRSDANMA GGKAGKDSGK AKAKAVSRSQ RAGLQFPVGR IHRHLKTRTT

 81  SHGRVGATAA VYSAAILEYL TAEVLELAGN ASKDLKVKRI TPRHLQLAIR GDEELDSLIK ATIAGGGVIP HIHKSLIGKK

161  GQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

XP_013921022.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MLFHLTILFK KFHISPYFFC PNYSTMTGRN RDRTSPRSDA NMAGGKAGKD SGKAKAKAVS RSQRAGLQFP VGRIHRHLKT

 81  RTTSHGRVGA TAAVYSAAIL EYLTAEVLEL AGNASKDLKV KRITPRHLQL AIRGDEELDS LIKATIAGGG VIPHIHKSLI

161  GKKGQQKTA
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.I	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.1
																total 1 peptides	

LAB40587.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  MPDVSLEERL PSILSTHSGA GGKYKSRSSW QHGLQFQVVS RWLRIRMSGR GKQDSKARAK AKTRSSRAGL QFPVGRVHRL

 81  LRRGHYAERV GAGAPVYLAA VLEYLTAEIL ELAGNAARDN RKTRIVPRHV QLAVRNDEEL SRLLGRVTIA QGGVLPNIPA

161  ALLPRKAAAA GGGTAGRQKG THQASQEN
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
																total 1 peptides	

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	A
R.AGLQFPVGR.V	Y	47.54	943.5239	9	0.3	472.7694	2	42.70	5	F5:12209	17112021_RID_2349_DP5.raw				4.76E4	5.9883E4	9.

total 1 peptides

TRINITY_DN1911
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  VAQLASGFIQ KPGIYVWIGL RDRRKEQVVL NFMTTTESRI SVAK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Ar F
VAQLASGFIQK.P	Y	46.25	1160.6553	11	0.8	581.3354	2	40.26	5	F5:11370	17112021_RID_2349_DP5.raw					2.6109E5	

total 1 peptides

TRINITY_DN1911
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1  VAQLASGFIQ KPGIYVWIGL RDRRKEQVVL NFMTTTESRI SVAK
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Ar F
VAQLASGFIQK.P	Y	46.25	1160.6553	11	0.8	581.3354	2	40.26	5	F5:11370	17112021_RID_2349_DP5.raw					2.6109E5	

total 1 peptides

XP_026548138.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1  MAQLDQLSPY VKKVDRSAQA DPPQQASSTP VEKWPDPIPI ERLQRSLSLN LGEGTSSATE PVAARTRAKT EQASLVAPLR
  81  QVDQLAINPK KPSESVTLSL FQHVPFTSSD LLNWKLHYGP FSEKPMEVAD LVKTIMDAHN PNWLDVQQLM GTLFSPEERE
 161  KIKNAISEIL KPDVTLYHSL TDLMDEKYPS SNPDWDLYTD EGKTRLRDYQ SLVVRAIRLA GKPVINMSKP ALVLQEPTES
 241  PEAFYTRLVE SYRMYTPIDP SAPENARMMT MAFISQSALD IRRKLQRLEG ALGKPMSELM EVARKVFANR DKEEDKKKDH
 321  KMQRKAELLA AAIAWPSRGR VNPLRGMGPG PQRGRGNSLQ RGVSWDLGPN QCAFCKQQGH WKGECPERND RGRSGDRGDS
 401  PRNLTFAVEE EWDXGRPGSE SLPEPMVSLK VGGKPVTFLV DTGATRSVLT QPMAQASRQT INIQGATGNT LQRPFLEPLE
 481  CTVKGQAITH QFVYMPDCPV PLLGRDLLCK LRAQISFAED GSMHLGYGKL GFSIPIEESW RLMVARTTGQ ETEETWRQFE
 561  VPYLWAEDNP PGFAAHHPPI LVEEVPTKPP VRIRQRAYPR HVMQAIQDII DIYLQHHILV PTESPWNTQI LPIPKGDGRF
 641  RPVQDLRPVN LATVTIHPVV PNPYVILGLI PQAAQWFSVI DLKDAFFTIA IHELSQHLFA FEWENPATGR KQQYTWTRLP
 721  QGFKNSPTLF GTALAKDLEN LHIPAPDLVL QYVDDLLVTG LTEDRCWENT KDLLSLLQTL GYKASRNKAQ LVLQKVRYLG
 801  YDIERGKRTL GHERKEAICQ LPRPINKKDL RGFLGAAGFC RIWIPKFSLI AKPLYEATKG ANRDPLHWGP EEEASFCALK
 881  QALLQAPSLG LPDLDKPFQL FVDTKKEVAV GVLTQTIGSW HRPVAYLSKQ LDNVAKGWPA CLKAVAGTAL LTQEANKLTF
 961  GQQLDIFTPH ALKSVLDMKG HLWLTNPRML KYQGLLTHNP MITLTQSTLL NPATLLPEPD MGVHHDCIHT IEETYASRPD
1041  MRDTPLPAPD YSLFTDGTSF LQEGMRKAGY AVVTLDEVWE AKPLPPGTSA QLAELHALTR ALELAKGLAV NIYTDSKYAF
1121  LTVQVHGALY KERGLITAGG KDIKYGPHIL RLLDSVWSPS KVAVMHCRGH QKVVTDIHRG NERADKFARK AAMLEFIPEE
1201  RNLAVWLPDD NPKPHYSSED RDRLDALEAH PDGHWWVLPD NRVAEIKSWI HWSRVKLAAP TSWKVETCPD SLLKVILKRA
1281  KKDISPGGDT PEAVPLPTGD EEDLPSPSGD TPEAVPQPTG GVERQTPAGV TPDADAHRTG LPWRLRSSAK RQ
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6	Area F
K.YGPHILR.L	Y	45.78	854.4763	7	1.0	428.2458	2	29.13	7	F7:7565	17112021_RID_2349_DP7.raw							1.3984E

total 1 peptides

XP_032092456.1
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
   1  MILWLNLVSL LVSLGGVRSD VQLVESGGDV RRPGESLRLS CQASGFTFSS YYMNWVRQAP GKGLEWVASI SESSGTYTYY
  81  SDKVKGRFTI SRDNAKSQLY LQMNNLKEED TAVYYCARGT VRGSLSEEFS LKLLFLGIQS EVQLVESGGG VRRPGESLRL
 161  SCQGSGFTFS CYYMNWVRQA PGKRPEWVVY ISISSSNIYY SDKVKGRFTI SRDDSNNLLY LQMKNLKPED TAVYYCARDA
 241  Q
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Ar F

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Are F6
S.EVQLVESGGGVR.R	Y	42.06	1228.6411	12	-0.8	615.3273	2	33.46	7	F7:9095	17112021_RID_2349_DP7.raw						
																	total 1 peptides

XP_007437884.2
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MFCGKLNMHV NIQTGKWETD PSGTKSCFGR KEEILEYCQE IYPDLRITNV VELNEPVCIK NWCKKGKKQC KGHTHIVVPF
 81 KCLVGEFVSD VLLVPEKCRF FHRERMVVCK SHQYWHIVAK EACLTEGMIL HSYGMLLPCG VDKFHGTEYV CCPQTKIVDE
161 ALSKEKEDED EEEDEDEDDD GIKSELPTEA DTDDFTVGVM EMNEEDEEEQ EENEEEVVVD QDYYYDSYKD YNEELPSEPS
241 NGRSFSQKEI ISDVKAVCSQ EAMTGPCRAM MPRWYFDMYK KKCIRFIYGG CGGNRNNFES EEYCMAVCKK MIPPTPLPTD
321 DVDVYFETPA DDNEHARFQK AKEQLEIRHR NRMDRVKKEW EEAEKQAKNL PKTERQALMQ RFQTMAKSLE KEAASEKQQL
401 VETHLARVEA MLDDRHRIAL ENYLVALQTD PPRPHRILQA LKRYVRAENK DRLHTIHHYQ HVLAVDPEKA AQMKSQVMTH
481 LHVIEERMNQ SLSLLYKVPY VAEEIQNEID ELLQEQRTDM DQFTSSISES QVDVHVSSEE SEESPLFDGK PFRPFQVKTF
561 PASSKSEGSG LADLDGLIGA EEKVINSKNK LDENVKYPVP TMPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.KEWEEAEK.Q	Y	40.82	1047.4873	8	0.1	524.7510	2	26.98	6	F6:6676	17112021_RID_2349_DP6.raw						2.3088E5
																	total 1 peptides

XP_007437883.2
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MFCGKLNMHV NIQTGKWETD PSGTKSCFGR KEEILEYCQE IYPDLRITNV VELNEPVCIK NWCKKGKKQC KGHTHIVVPF
 81 KCLVGEFVSD VLLVPEKCRF FHRERMVVCK SHQYWHIVAK EACLTEGMIL HSYGMLLPCG VDKFHGTEYV CCPQTKIVDE
161 ALSKEKEDED EEEDEDEDDD GIKSELPTEA DTDDFTVGVM EMNEEDEEEQ EENEEEVVVD QDYYYDSYKD YNEELPSEPS
241 NGRSFSQKEI ISDVKAVCSQ EAMTGPCRAM MPRWYFDMYK KKCIRFIYGG CGGNRNNFES EEYCMAVCKK MIPPTPLPTD
321 DVDVYFETPA DDNEHARFQK AKEQLEIRHR NRMDRVKKEW EEAEKQAKNL PKTERQALMQ RFQTMAKSLE KEAASEKQQL
401 VETHLARVEA MLDDRHRIAL ENYLVALQTD PPRPHRILQA LKRYVRAENK DRLHTIHHYQ HVLAVDPEKA AQMKSQVMTH
481 LHVIEERMNQ SLSLLYKVPY VAEEIQNEID ELLQEQRTDM DQFTSSISES QVDVHVSSEE SEESPLFDGK PFRPFQVKTF
561 PASSKSEDSQ PDLYHPEKKG SGLADLDGLI GAEEKVINSK NKLDENVKYP VPTMPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.KEWEEAEK.Q	Y	40.82	1047.4873	8	0.1	524.7510	2	26.98	6	F6:6676	17112021_RID_2349_DP6.raw						2.3088E5
																	total 1 peptides

XP_007437886.2
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MFCGKLNMHV NIQTGKWETD PSGTKSCFGR KEEILEYCQE IYPDLRITNV VELNEPVCIK NWCKKGKKQC KGHTHIVVPF
 81 KCLVGEFVSD VLLVPEKCRF FHRERMVVCK SHQYWHIVAK EACLTEGMIL HSYGMLLPCG VDKFHGTEYV CCPQTKIVDE
161 ALSKEKEDED EEEDEDEDDD GIKSELPTEA DTDDFTVGVM EMNEEDEEEQ EENEEEVVVD QDYYYDSYKD YNEELPSEPS
241 NGRSFSQKEI ISDVKVPPTP LPTDDVDVYF ETPADDNEHA RFQKAKEQLE IRHRNRMDRV KKEWEEAEKQ AKNLPKTERQ
321 ALMQRFQTMA KSLEKEAASE KQQLVETHLA RVEAMLDDRH RIALENYLVA LQTDPPRPHR ILQALKRYVR AENKDRLHTI
401 HHYQHVLAVD PEKAAQMKSQ VMTHLHVIEE RMNQSLSLLY KVPYVAEEIQ NEIDELLQEQ RTDMDQFTSS ISESQVDVHV
481 SSEESEESPL FDGKPFRPFQ VKTFPASSKS EGSGLADLDG LIGAEEKVIN SKNKLDENVK YPVPTMPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.KEWEEAEK.Q	Y	40.82	1047.4873	8	0.1	524.7510	2	26.98	6	F6:6676	17112021_RID_2349_DP6.raw						2.3088E5
																	total 1 peptides

XP_007437885.2
back to list

| Protein Coverage | Supporting Peptides |
Protein Coverage:

```
  1 MFCGKLNMHV NIQTGKWETD PSGTKSCFGR KEEILEYCQE IYPDLRITNV VELNEPVCIK NWCKKGKKQC KGHTHIVVPF
 81 KCLVGEFVSD VLLVPEKCRF FHRERMVVCK SHQYWHIVAK EACLTEGMIL HSYGMLLPCG VDKFHGTEYV CCPQTKIVDE
161 ALSKEKEDED EEEDEDEDDD GIKSELPTEA DTDDFTVGVM EMNEEDEEEQ EENEEEVVVD QDYYYDSYKD YNEELPSEPS
241 NGRSFSQKEI ISDVKVPPTP LPTDDVDVYF ETPADDNEHA RFQKAKEQLE IRHRNRMDRV KKEWEEAEKQ AKNLPKTERQ
321 ALMQRFQTMA KSLEKEAASE KQQLVETHLA RVEAMLDDRH RIALENYLVA LQTDPPRPHR ILQALKRYVR AENKDRLHTI
401 HHYQHVLAVD PEKAAQMKSQ VMTHLHVIEE RMNQSLSLLY KVPYVAEEIQ NEIDELLQEQ RTDMDQFTSS ISESQVDVHV
481 SSEESEESPL FDGKPFRPFQ VKTFPASSKS EDSQPDLYHP EKKGSGLADL DGLIGAEEKV INSKNKLDEN VKYPVPTMPR
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4	Area F5	Area F6
K.KEWEEAEK.Q	Y	40.82	1047.4873	8	0.1	524.7510	2	26.98	6	F6:6676	17112021_RID_2349_DP6.raw						2.3088E5
														total 1 peptides			

XP_007421854.1
back to list

| Protein Coverage | Supporting Peptides |

Protein Coverage:

```
  1 MQRLRDADSS MFKPECIYTS GGGWTEGGGS ADSQSMPYFA KLMLLIFCGV LLGESRKHKR GRWTEEADVQ KTSHTYKKNY
 81 DMTKAWSGNN KQLLRVEDHD FTMRPAFGGP AIPVGVDVQV ESLDSISEVN MDFTMTLYLR HYWKDERLSF PSHANKSMTF
161 DGRLVKKIWV PDIFFVHSKR SFIHDTTTDN IMLRVFPDGH VLYSMRITVT AMCNMDFSRF PLDSQTCSLE LESYAYTDED
241 LMLYWKNGSE SLKTDEKISL SQFLIQKFHT TSRLAFYSST GRYNRLYINF ILRRHIFFFL LQTYFPATLM VMLSWVSFWI
321 DRRAVPARVS LGITTVLTMS TIITGVNASM PGVSYIKAVD IYLWVSFVFV FLSVIEYAAV NYLTTVQERK QRKQQEKFPC
401 VSGISSTKRM TLDGIYNELD ASSLEGDPRS QMVAEEDKQE KMVIHLTMSN ESNSSKKKGL KEHVSLRIIQ NTHAIDKYSR
481 LIFPGTYIFF NIVYWSVFC
```

Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	Length	ppm	m/z	z	RT	Fraction	Scan	Source File	Area F1	Area F2	Area F3	Area F4
K.FPC(+57.02)VSGISSTK.R	Y	39.14	1181.5751	11	-0.4	591.7946	2	42.28	5	F5:12814	17112021_RID_2349_DP5.raw				4.3217E7

Peptide List

Prepared with PEAKS ™ (bioinfor.com)