

Hit	Acc.	#Peptide	i/w	StDev	hi/w	StDev	Mass	Description							
Query	Sequence	Score	i/w	StDev	hi/w	StDev	Ret.Time	charge	#R	wild	iso	high	#Spectrum	from	to
*	1 gi 61743954 ref NP_0016	3	11.22	1.2400	7.37	0.7014	628699	AHNAK nucleoprotein isoform 1 [Homo sapiens]							
-	421 IEGEMQVPDVIDR	85	11.93	0.1809	8.35	0.3819	54.004	2	1	628	7486	5230	2	2110	2111
-	484 LPSGSGAASPTGSAVDIR	39	12.25	1.7936	6.73	1.7765	23.167	2	1	117	1446	797	4	1006	1009
-	660 ELLLPNWQGSGSHGLTIAQR	36	9.47	1.0900	7.05	0.7720	59.466	3	1	418	3945	2936	2	2147	2148
*	2 gi 21614499 ref NP_0033	4	12.58	4.0036	5.87	1.7942	69370	villin 2 [Homo sapiens]							
-	95 EKEELMLR	44	5.98	0.9514	2.85	0.3964	22.849	2	1	547	3313	1562	4	1004	1007
-	130 IGFPWSEIR	48	16.59	1.7960	7.15	0.4462	65.56	2	1	282	4633	2004	2	2191	2192
-	136 IGFPWSEIR	37	14.61	2.9748	7.30	1.4285	65.966	2	1	480	7284	3647	5	2191	2195
-	393 QLLTLSSSELSQAR	53	13.14	1.6779	6.17	0.8158	56.396	2	1	503	6537	3069	2	2126	2127