

SRF File: C:\Xcalibur\data\100730RS\100730RS-P19.srf

Database... 100211 uniprot_sprot_human.fasta

Filter(s)... peptide probability<=5e-003 ; # distinct peptides>=2 ; protein probability<=1e-003

Mods: (M* +15.99492) C=160.03064

Reference	Sequence	MH+	z	P	Sf	Score	Coverage	Accession
Time (s)				P	Sf	XC	DeltaCn	RSp Ions
IMMT_HUMAN	Mitochondrial inner membrane protein OS=Homo sapien			1e-011	7.9	100.2	0.0	0
18.66 - 18.7K	K.SEFEQNLSEK.L	1210.5586	2	8e-006	0.95	2.699	0.763	889.7 1 14/18
18.74 - 18.7R	R.GVYSEETLR.A	1053.5211	2	4e-005	0.86	1.614	0.518	687.2 1 13/16
19.47	R.GIEQAVQSHAVAEVEEAR.K	1823.8882	3	1e-011	0.95	3.273	0.853	1138.5 1 26/64
19.50	K.TDHPEIGEGKPTPALSEEASSSSIR.E	2595.2533	4	0.001	0.31	1.975	0.412	123.8 1 12/144
19.77	K.VVSQYHELIVVQAR.D	1527.8278	3	0.0002	0.31	1.320	0.860	63.3 1 9/48
20.61	R.KAVDEAADALLK.A	1243.6892	2	3e-007	0.94	2.842	0.706	1050.9 1 14/22
20.68	R.KAVDEAADALLK.A	1243.6892	2	4e-007	0.84	2.202	0.746	654.6 1 11/22
20.96	K.LSEQELQFR.R	1149.5899	2	1e-006	0.94	3.047	0.318	1314.7 1 14/16
21.12	K.LSEQELQFR.R	1149.5899	2	6e-006	0.90	2.322	0.294	1136.2 1 13/16
21.36	K.AVDEAADALLK.A	1115.5943	2	6e-005	0.94	3.535	0.489	783.4 1 15/20
21.44	K.AVDEAADALLK.A	1115.5943	2	0.0002	0.93	3.574	0.466	780.1 1 15/20
23.92	K.TSSAETPTIPLGSAVEAIK.A	1871.9960	2	1e-007	0.77	1.884	0.752	389.7 1 16/36
25.62	K.LFEM*VLGPAAYNVPLPK.K	1875.0085	2	5e-009	0.95	3.066	0.955	761.9 1 17/32
25.71	K.LFEM*VLGPAAYNVPLPK.K	1875.0085	2	6e-006	0.87	2.258	0.910	476.8 1 14/32

14 of 21 peptide matches reported, 7 removed due to filtering

TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B P			4e-007	1.6	20.1	0.0	0
20.83	K.DVNAAIATIK.T	1015.5782	2	0.0005	0.74	1.862	0.649	462.5 1 10/18
28.34	R.LISQIVSSITASLR.F	1487.8792	2	1e-006	0.94	2.201	0.929	919.7 1 16/26
28.42	R.LISQIVSSITASLR.F	1487.8792	2	4e-007	0.88	1.893	0.945	633.3 1 13/26

3 of 5 peptide matches reported, 2 removed due to filtering

TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C P			4e-007	1.6	20.1	0.0	0
20.83	K.DVNAAIATIK.T	1015.5782	2	0.0005	0.74	1.862	0.649	462.5 1 10/18
28.34	R.LISQIVSSITASLR.F	1487.8792	2	1e-006	0.94	2.201	0.929	919.7 1 16/26
28.42	R.LISQIVSSITASLR.F	1487.8792	2	4e-007	0.88	1.893	0.945	633.3 1 13/26

3 of 5 peptide matches reported, 2 removed due to filtering

ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2			4e-006	2.5	30.2	0.0	0
20.85	K.YLYEIAR.R	927.4934	2	0.0002	0.89	2.087	0.509	453.5 1 11/12
20.94	K.KVPQVSTPTLVEVSR.N	1639.9377	3	6e-006	0.97	4.378	0.911	1092.4 1 26/56
20.97	K.YLYEIAR.R	927.4934	2	0.004	0.83	1.511	0.579	373.6 1 10/12
21.77	K.VPQVSTPTLVEVSR.N	1511.8428	2	4e-006	0.61	2.512	0.425	356.1 1 11/26
21.92	K.VPQVSTPTLVEVSR.N	1511.8428	2	0.004	0.03	1.224	0.279	118.5 1 6/26

5 of 8 peptide matches reported, 3 removed due to filtering