

SRF File: C:\Xcalibur\data\100730RS\100730RS-P27.srf

Database... 100211 uniprot\_sprot\_human.fasta

Filter(s)... peptide probability&lt;=5e-003 ; # distinct peptides&gt;=2 ; protein probability&lt;=1e-003

Mods: (M\* +15.99492) C=160.03064

Reference	Sequence	MH+	z	P	Sf	Score	Coverage	Accession
Time (s)				P	Sf	XC	DeltaCn	Sp RSp Ions
MP2K1_HUMAN	Dual specificity mitogen-activated protein kinase			5e-014	4.5	60.2	0.0	0
19.04	R.YPIPPDAK.E	997.5353	2	0.002	0.52	1.762	0.567	228.3 1 8/16
20.31	R.IPEQILGK.V	897.5404	2	5e-005	0.89	2.179	0.530	369.5 1 13/14
20.52	K.KLEELELDEQQR.K	1529.7806	2	8e-008	0.95	2.600	0.869	1144.1 1 15/22
20.87	K.LEELELDEQQR.K	1401.6856	2	5e-006	0.79	1.411	0.651	505.1 1 13/20
22.22	K.RLEAFLTQK.Q	1105.6364	2	0.003	0.37	1.547	0.573	171.1 1 7/16
27.29	K.LPSGVFSLEFQDFVVK.C	1826.9323	2	5e-014	0.98	4.402	0.861	1945.2 1 22/30

6 of 11 peptide matches reported, 5 removed due to filtering

KCRB_HUMAN	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1			1e-009	7.6	80.3	0.0	0
19.54	K.LLIEM*EQR.L	1047.5503	2	2e-005	0.93	2.073	0.660	744.1 1 13/14
19.78	K.LLIEM*EQR.L	1047.5503	2	0.0002	0.87	1.775	0.645	521.0 1 11/14
20.00	R.LEQGQAIDDL*PAQK.-	1672.8211	2	1e-010	0.97	3.324	0.726	1463.4 1 20/28
20.18	R.LEQGQAIDDL*PAQK.-	1672.8211	2	2e-007	0.94	2.304	0.663	1304.1 1 20/28
22.91	R.GTGGVDTAAVGGVFDVSNADR.L	1964.9308	2	1e-012	0.98	5.275	0.832	1180.0 1 24/40
23.44	K.TDLNPDNLQGGDDLDPNYVLSR.V	2518.1692	2	1e-013	0.96	3.751	0.965	630.3 1 21/44
23.84	K.VLTPELYAELR.A	1303.7256	2	2e-005	0.91	2.693	0.701	456.9 1 14/20
23.99	K.VLTPELYAELR.A	1303.7256	2	4e-006	0.81	1.786	0.638	450.5 1 13/20
24.66	K.LAVEALSSLDGDLAGR.Y	1586.8384	2	2e-010	0.98	4.602	0.809	2261.3 1 23/30
24.75	K.LAVEALSSLDGDLAGR.Y	1586.8384	2	2e-011	0.98	4.496	0.782	2244.3 1 23/30
25.40	K.DLFDPIIEDR.H	1232.6157	2	7e-005	0.95	2.491	0.721	1063.1 1 15/18
25.57	K.DLFDPIIEDR.H	1232.6157	2	0.0002	0.93	2.375	0.731	791.5 1 13/18

12 of 17 peptide matches reported, 5 removed due to filtering

ACTY_HUMAN	Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1			1e-008	2.8	30.2	0.0	0
19.57	K.AGFAGDQIPK.Y	1003.5207	2	0.003	0.91	1.834	0.689	895.6 1 14/18
24.01	K.VQYTLPDGSLDVGPAR.F	1788.9127	2	1e-011	0.96	3.931	0.808	707.9 1 22/32
24.20	K.DQLQTFSEEHPVLLTEAPLNPSK.N	2593.3144	3	3e-005	0.88	2.926	0.918	439.7 1 20/88

3 of 6 peptide matches reported, 3 removed due to filtering