

SRF File: C:\Xcalibur\data\100730RS\100730RS-P08.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
GDIB_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens				1e-030	16.8	200.3	0.0	0		
18.53	K.LYSESLAR.Y	938.4942	2	0.0002	0.88	1.693	0.545	527.7	1	13/14
18.64	K.LYSESLAR.Y	938.4942	2	0.0001	0.90	1.819	0.597	507.3	1	13/14
19.41	R.TFEGIDPK.K	906.4567	2	0.0004	0.95	2.986	0.734	735.1	1	12/14
19.43	K.VTEGSEFVYK.G	1029.5251	2	2e-006	0.90	1.776	0.610	626.8	1	14/16
19.58	K.VTEGSEFVYK.G	1029.5251	2	4e-006	0.58	1.453	0.485	300.5	1	10/16
20.10	K.NTNDANSCQIIPQNQVNR.K	2199.0571	3	9e-005	0.37	1.894	0.565	156.9	1	13/72
20.18	K.QLICDPSYVK.D	1222.6136	2	4e-005	0.78	1.889	0.450	392.9	1	13/18
20.37	K.QLICDPSYVK.D	1222.6136	2	0.002	0.26	1.398	0.341	164.1	1	9/18
20.70	R.M*TGSEPDFEEM*K.R	1482.5763	2	4e-006	0.23	1.869	-	439.3	1	11/22
20.95	K.M*LLYTEVTR.Y	1141.5922	2	1e-005	0.90	1.993	0.343	1119.9	1	14/16
20.97	R.TDDYLDQPCYETINR.I	1902.8174	2	8e-011	0.97	3.781	0.923	858.7	1	20/28
21.16	K.M*LLYTEVTR.Y	1141.5922	2	0.0008	0.90	2.231	0.326	948.3	1	14/16
21.29	R.VICILSHPIK.N	1179.6918	3	0.0002	0.43	1.651	0.670	146.5	1	12/36
21.32	R.VICILSHPIK.N	1179.6918	2	5e-005	0.91	2.562	0.817	611.4	1	11/18
21.44	K.YIAIVSTTVETK.E	1324.7359	2	2e-009	0.98	3.291	0.812	1775.1	1	20/22
21.65	K.YIAIVSTTVETK.E	1324.7359	2	1e-007	0.96	2.607	0.795	1278.9	1	17/22
22.79	K.DLGTESQIFISR.T	1365.7009	2	5e-008	0.98	4.144	0.797	1898.4	1	19/22
23.14	K.FLVVYVANFDEK DPR.T	1712.8642	3	2e-005	0.71	2.451	0.604	377.6	1	17/52
24.44	K.FLVVYVANFDEK.D	1344.6834	2	2e-005	0.96	3.089	0.805	1131.8	1	15/20
24.53	R.PALELLEPIEQK.F	1379.7781	2	1e-009	0.98	4.125	0.744	1818.4	1	19/22
24.54	K.EIRPALELLEPIEQK.F	1778.0058	3	1e-006	0.93	3.863	0.695	690.7	1	22/56
24.56	R.NPYYGGESASITPLEDLYK.R	2117.0073	2	5e-021	0.98	5.042	0.904	1279.1	1	24/36
24.74	K.EIRPALELLEPIEQK.F	1778.0058	3	3e-005	0.93	3.467	0.786	691.7	1	23/56
24.79	R.NPYYGGESASITPLEDLYK.R	2117.0073	2	1e-012	0.89	2.332	0.948	542.6	1	15/36
24.81	R.PALELLEPIEQK.F	1379.7781	2	2e-007	0.96	3.484	0.768	1102.6	1	16/22
26.64	K.FVSISDLLVPK.D	1217.7140	2	6e-009	0.97	3.230	0.927	1051.9	1	17/20
26.73	K.FVSISDLLVPK.D	1217.7140	2	3e-010	0.97	3.366	0.855	1131.6	1	17/20
27.53	K.SPYLYPLYGLGELPQGFAR.L	2141.1066	2	4e-010	0.96	4.065	0.921	814.8	1	19/36
27.64	K.SPYLYPLYGLGELPQGFAR.L	2141.1066	2	9e-010	0.95	3.549	0.906	703.3	1	18/36
28.27	K.VPSTAEALASSLM*GLFEK.R	1995.9943	2	4e-016	0.98	6.176	0.900	1538.9	1	23/36
28.29	K.VPSTAEALASSLM*GLFEK.R	1995.9943	3	0.0004	0.96	4.595	0.885	885.7	1	23/72
28.36	K.VPSTAEALASSLM*GLFEK.R	1995.9943	2	3e-012	0.98	6.278	0.874	1206.3	1	20/36
28.37	K.VPSTAEALASSLM*GLFEK.R	1995.9943	3	4e-008	0.97	5.590	0.806	1247.4	1	26/72
28.88	K.FDLGQDVIDFTGHALALYR.T	2151.0869	3	0.001	0.43	1.763	0.809	107.6	1	9/72