

SRF File: C:\Xcalibur\data\100730RS\100730RS-P09.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
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapi			1e-012	8.5	100.2	0.0	0
19.93	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	6e-012	0.97	4.068	0.777	1246.7 1 21/30
20.04	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	1e-006	0.90	2.264	0.893	613.9 1 15/30
20.68	K.IVLEDGTLHVTEGSGR.Y	1682.8708	3	3e-005	0.68	1.827	-	127.2 1 15/60
21.15	R.GSPLVVISQGK.I	1084.6361	2	7e-011	0.94	2.837	0.762	770.8 1 15/20
21.38	R.GSPLVVISQGK.I	1084.6361	2	3e-006	0.84	2.024	0.706	542.4 1 12/20
21.47	R.GLYDGPVCEVSVTPK.T	1620.7938	2	2e-009	0.94	2.242	0.918	1069.1 1 17/28
21.79	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	2	2e-012	0.90	4.043	-	1191.6 1 22/36
21.86	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	3	0.0002	0.64	2.297	0.864	123.0 1 11/72
21.90	R.KPFPDFVYK.R	1140.6088	2	0.001	0.55	1.583	0.587	305.8 1 8/16
21.96	K.VFNLYPR.K	908.4989	2	8e-005	0.94	2.339	0.738	684.0 1 11/12
22.02	R.AITIANQTNCPLYITK.V	1820.9575	2	1e-012	0.95	3.134	0.805	1202.0 1 17/30
22.06	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	2	0.0004	0.45	1.662	0.863	107.0 1 7/36
22.13	K.QIGENLIVPGGVK.T	1323.7631	2	0.0004	0.87	2.164	0.766	397.2 1 15/24
22.19	K.VFNLYPR.K	908.4989	2	4e-005	0.89	1.892	0.813	455.9 1 9/12
22.28	K.QIGENLIVPGGVK.T	1323.7631	2	0.0007	0.46	1.495	0.754	151.0 1 9/24
25.31	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	3e-005	0.83	2.303	0.897	422.2 1 12/38

16 of 18 peptide matches reported, 2 removed due to filtering

DPYL1_HUMAN	Dihydropyrimidinase-related protein 1 OS=Homo sapi			6e-012	7.9	90.2	0.0	0
19.93	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	6e-012	0.97	4.068	0.777	1246.7 1 21/30
20.04	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	1e-006	0.90	2.264	0.893	613.9 1 15/30
20.61	R.GM*YDGPVYEVPAATPK.Y	1639.7672	2	2e-009	0.96	3.489	0.888	828.1 1 17/28
20.72	R.GM*YDGPVYEVPAATPK.Y	1639.7672	2	2e-008	0.88	2.501	0.924	464.2 1 12/28
21.33	K.IVFEDGNINVNK.G	1361.7060	2	2e-007	0.96	2.457	0.804	1430.7 1 18/22
21.56	K.IVFEDGNINVNK.G	1361.7060	2	0.0001	0.20	0.604	0.545	319.6 1 9/22
21.69	R.EELEVLVQDK.G	1201.6311	2	0.001	0.67	1.507	0.680	282.1 1 10/18
21.70	K.VFGLQVSR.G	962.5418	2	0.0009	0.90	2.301	0.792	493.0 1 11/16
22.13	K.QIGENLIVPGGVK.T	1323.7631	2	0.0004	0.87	2.164	0.766	397.2 1 15/24
22.28	K.QIGENLIVPGGVK.T	1323.7631	2	0.0007	0.46	1.495	0.754	151.0 1 9/24
22.76	K.SAADIIALAR.K	1000.5786	2	2e-006	0.97	3.474	0.656	1477.2 1 16/18
22.82	K.IFNLYPR.K	922.5145	2	0.0005	0.79	1.771	0.476	480.1 1 9/12
22.92	K.SAADIIALAR.K	1000.5786	2	4e-006	0.96	3.155	0.631	1274.9 1 15/18
27.66	- 27.7K.DVYQM*SDSOLYEAFITFLK.G	2201.0107	2	2e-010	0.82	1.881	0.872	524.0 1 13/34

14 of 15 peptide matches reported, 1 removed due to filtering

DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapi			6e-012	2.6	30.2	0.0	0
19.93	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	6e-012	0.97	4.068	0.777	1246.7 1 21/30
20.04	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	1e-006	0.90	2.264	0.893	613.9 1 15/30
22.82	K.IFNLYPR.K	922.5145	2	0.0005	0.79	1.771	0.476	480.1 1 9/12
25.31	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	3e-005	0.83	2.303	0.897	422.2 1 12/38

4 of 5 peptide matches reported, 1 removed due to filtering

2553.3770 3 1e-009 0.73 2.545 0.574 499.2 1 21/96