

SRF File: C:\Xcalibur\data\100730RS\100730RS-P22.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-030	15.0	170.3	0.0	0
17.82	K.SSAEVIQAAR.K	1031.5480	2	2e-005	0.93	2.667	0.438	1274.3 1 14/18
17.91	K.SSAEVIQAAR.K	1031.5480	2	8e-006	0.94	2.968	0.446	1250.6 1 14/18
19.86	K.GIQEEM*EALVK.D	1262.6297	2	7e-007	0.95	2.820	0.721	1007.0 1 16/20
20.01	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	9e-015	0.98	4.664	0.751	1429.3 1 22/30
20.03	K.GIQEEM*EALVK.D	1262.6297	2	1e-006	0.95	2.641	0.698	979.3 1 16/20
20.78	K.IVLEDGTLHVTGSGR.Y	1682.8708	3	5e-005	0.77	2.484	0.769	248.5 1 20/60
20.96	K.IVLEDGTLHVTGSGR.Y	1682.8708	3	7e-005	0.67	2.374	0.760	147.6 1 16/60
21.11	R.GSPLVVISQGK.I	1084.6361	2	6e-007	0.96	3.461	0.774	860.1 1 15/20
21.27	R.GSPLVVISQGK.I	1084.6361	2	8e-008	0.95	3.067	0.751	785.1 1 15/20
21.60	R.GLYDGPVCEVSVTPK.T	1620.7938	2	3e-010	0.98	3.464	0.907	2028.2 1 22/28
21.71	R.DIGAIAQVHAENGDI IAEQQR.I	2377.1742	3	4e-010	0.91	3.360	0.830	672.8 1 24/84
21.91	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	2	5e-017	0.94	4.821	-	1330.5 1 23/36
21.92	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	3	1e-008	0.98	5.111	0.933	1444.7 1 30/72
22.01	R.KPFPDFVYK.R	1140.6088	2	5e-006	0.92	2.520	0.675	728.0 1 12/16
22.07	K.VFNLYPR.K	908.4989	2	1e-005	0.94	2.492	0.726	718.1 1 11/12
22.08	R.AITIANQTNCLPLYITK.V	1820.9575	2	1e-013	0.97	3.835	0.839	1670.1 1 19/30
22.10	R.KPFPDFVYK.R	1140.6088	2	2e-006	0.91	2.359	0.645	725.3 1 12/16
22.12	R.FQM*PDQGM*TSADDFQGTK.A	2182.9056	2	2e-009	0.75	3.282	-	835.1 1 18/36
22.23	K.QIGENLIVPGGVK.T	1323.7631	2	4e-006	0.91	2.769	0.866	437.6 1 14/24
22.24	K.VFNLYPR.K	908.4989	2	9e-005	0.92	2.135	0.773	567.5 1 10/12
22.29	R.NLHQSGFSLSGAQIDDNIPR.R	2169.0683	3	0.0004	0.72	2.465	0.765	200.5 1 18/76
22.32	R.AITIANQTNCLPLYITK.V	1820.9575	2	2e-011	0.92	2.382	0.900	881.4 1 15/30
22.38	K.QIGENLIVPGGVK.T	1323.7631	2	0.0002	0.82	2.170	0.776	298.4 1 13/24
22.79	K.DNFTLIPGTTNGTEER.M	1792.8348	2	0.0001	0.24	1.326	0.670	95.9 1 8/30
25.29	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	1e-013	0.98	4.615	0.929	1280.6 1 21/38
25.38	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	5e-012	0.97	3.956	0.907	1041.5 1 19/38
25.55	R.IAVGSDADLVIWDPDSVK.T	1899.9698	2	3e-010	0.95	3.366	0.893	810.7 1 18/34
28.57	R.FQLTDCQIYEVLVSVIR.D	1984.0208	2	2e-012	0.95	3.266	0.896	955.2 1 16/30
28.59	R.FQLTDCQIYEVLVSVIR.D	1984.0208	3	2e-005	0.67	2.016	0.803	313.4 1 14/60
28.66	R.FQLTDCQIYEVLVSVIR.D	1984.0208	2	4e-007	0.65	1.758	0.860	268.6 1 9/30

30 of 33 peptide matches reported, 3 removed due to filtering

DPYL1_HUMAN	Dihydropyrimidinase-related protein 1 OS=Homo sapi			9e-015	4.1	50.2	0.0	0
20.01	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	9e-015	0.98	4.664	0.751	1429.3 1 22/30
20.69	R.GM*YDGPVYEVDPATPK.Y	1639.7672	2	3e-006	0.89	2.613	0.906	456.4 1 13/28
21.53	K.IVFEDGNINVNK.G	1361.7060	2	1e-006	0.43	0.774	0.844	230.3 1 9/22
22.23	K.QIGENLIVPGGVK.T	1323.7631	2	4e-006	0.91	2.769	0.866	437.6 1 14/24
22.38	K.QIGENLIVPGGVK.T	1323.7631	2	0.0002	0.82	2.170	0.776	298.4 1 13/24
22.91	K.IFNLYPR.K	922.5145	2	0.0001	0.86	2.167	0.574	470.3 1 9/12

6 of 9 peptide matches reported, 3 removed due to filtering

DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapi			9e-015	2.8	30.2	0.0	0
20.01	K.M*DENQFVAVTSTNAAK.I	1741.8061	2	9e-015	0.98	4.664	0.751	1429.3 1 22/30
22.91	K.IFNLYPR.K	922.5145	2	0.0001	0.86	2.167	0.574	470.3 1 9/12
25.29	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	1e-013	0.98	4.615	0.929	1280.6 1 21/38
25.38	K.IVNDDQSFYADIYM*EDGLIK.Q	2365.0904	2	5e-012	0.97	3.956	0.907	1041.5 1 19/38

4 of 9 peptide matches reported, 5 removed due to filtering

PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH OS=Ho			4e-012	6.5	80.2	0.0	0
22.26	K.SLFSNVVTK.N	994.5568	2	0.0001	0.90	2.411	0.552	540.9 1 13/16
22.75	K.EALGIPAAASF.K	1174.6467	2	0.0003	0.46	1.856	0.443	199.3 1 11/22
23.86	R.DVSELTFPEM*LGGR.V	1623.7683	2	7e-009	0.93	2.808	0.793	623.7 1 17/28
24.13	R.LDFNLIR.V	890.5094	2	0.002	0.75	1.825	0.234	276.8 1 11/12
24.90	R.NLTALGLNLVASGGTAK.A	1599.9064	2	4e-012	0.98	4.806	0.826	2104.7 1 23/32
26.91	R.EVSDGI IAPGYEEEEALTI LSK.K	2234.1438	2	6e-011	0.90	3.118	0.915	283.4 1 16/40
27.23	K.ALFEVPELLTEAEK.K	1717.8895	2	8e-012	0.95	2.948	0.780	929.2 1 20/28
27.45	K.ALFEVPELLTEAEK.K	1717.8895	2	0.0002	0.58	1.799	0.729	207.7 1 10/28
29.01	K.TVASPGVTVEEAVEQIDIGGVTL L R.A	2553.3770	3	0.0001	0.89	3.884	0.593	635.3 1 23/96
29.09	K.TVASPGVTVEEAVEQIDIGGVTL L R.A	2553.3770	3	2e-006	0.64	2.595	0.606	256.0 1 16/96

10 of 12 peptide matches reported, 2 removed due to filtering