

P04083	ANXA1	DITSDTSGDFR	6.761	0.011	0.7745	0.698	0.484	0.592	1.122	0.958	0.507
P09211	GSTP1	TLGLYGK	2.910	0.011	0.7745	1.277	0.269	0.650	1.372	0.048	0.725
P30041	PRDX6	LSILYPATTGR	3.283	0.014	0.7647	1.326	0.269	0.647	1.434	0.077	0.696
P14174	MIF	VYINYYDMNAANVGWNNSTFA	8.416	0.008	0.7598	1.339	0.210	0.681	1.524	0.053	0.719
O43852	CALU	TFDQLTPEESK	4.042	0.016	0.7582	2.083	0.128	0.725	1.578	0.082	0.691
P07237	P4HB	ALAPEYAK	2.741	0.016	0.7582	0.780	0.777	0.536	1.117	0.573	0.562
Q13938	CAPS	SGDGVVTVDLRL	3.670	0.018	0.7549	2.351	0.210	0.681	1.409	0.437	0.583
P22626	HNRNPA2B1	TLETVPLER	2.214	0.020	0.7500	1.412	0.269	0.657	1.536	0.059	0.712
P10451	SPP1	AIPVAQDLNAPSDWDSR	3.958	0.021	0.7484	0.851	0.226	0.675	0.580	0.766	0.533
Q13938	CAPS	EAVIAAAFAK	3.323	0.024	0.7418	2.136	0.248	0.667	1.631	0.299	0.614
P50454	SERPINH1	GVVEVTHDLQK	2.413	0.026	0.7386	5.886	0.062	0.828	3.977	0.038	0.735
Q01995	TAGLN	TLMALGSLAVTK	2.046	0.040	0.7222	3.938	0.269	0.652	6.348	0.016	0.840
P30086	PEBP1	VLTPQVK	1.967	0.040	0.7222	0.766	0.844	0.523	1.392	0.071	0.703
P80188	LCN2	VPLQQNFQDNQFQ GK	2.535	0.044	0.7157	0.661	0.270	0.644	0.648	0.190	0.647
P30086	PEBP1	LYEQLSGK	1.997	0.045	0.7157	0.944	0.720	0.549	1.410	0.077	0.696
P50454	SERPINH1	DTQSGSLLFGR	2.674	0.042	0.7157	5.425	0.210	0.662	4.222	0.046	0.717
P05787	KRT8	LSELEAALQR	12.502	0.047	0.7124	5.547	0.114	0.761	2.612	0.036	0.742
P17931	LGALS3	GNDVAFHFNPR	2.540	0.047	0.7124	1.239	0.300	0.627	1.322	0.018	0.797
P22626	HNRNPA2B1	GGNFGFGDSR	2.706	0.047	0.7108	1.343	0.278	0.637	1.989	0.021	0.775
P17931	LGALS3	IALDFQR	2.606	0.057	0.7026	1.274	0.278	0.641	1.283	0.018	0.794
P09466	PAEP	VLVEDDEIMQGFIR	0.038	0.047	0.6993	0.007	0.248	0.660	0.003	0.054	0.712
P07339	CTSD	VGFAEAAAR	1.575	0.069	0.6928	1.485	0.270	0.644	1.166	0.100	0.680
P07339	CTSD	VSTLPAITLK	1.598	0.069	0.6928	1.217	0.637	0.569	1.104	0.233	0.634
P80188	LCN2	ELTSELK	2.045	0.074	0.6895	0.631	0.278	0.637	0.671	0.233	0.634
Q16658	FSCN1	YLAPSGPSGTLK	1.800	0.084	0.6830	1.463	0.300	0.631	2.187	0.034	0.745
P07355	ANXA2	QDIAFAYQR	8.887	0.066	0.6797	0.719	0.827	0.526	1.114	0.097	0.681
Q01995	TAGLN	EFTESQLQEGK	1.881	0.111	0.6699	5.254	0.269	0.641	5.804	0.021	0.773
Q16658	FSCN1	FLIVAHDDGR	1.960	0.122	0.6634	1.865	0.154	0.709	2.124	0.048	0.724
P05787	KRT8	WSLLQQQK	13.174	0.122	0.6634	6.437	0.114	0.742	2.400	0.048	0.725
P08253	MMP2	VDAAFNWSK	0.727	0.121	0.6634	1.664	0.398	0.608	0.716	0.088	0.688
P15941	MUC1	EGTINVHDTVETQFNQYK	1.751	0.131	0.6585	0.899	0.918	0.511	1.682	0.082	0.693
P15941	MUC1	QGGFLGLSNIK	1.785	0.181	0.6405	1.015	0.656	0.565	1.413	0.190	0.647
P09382	LGALS1	LPDGYEFK	1.368	0.181	0.6405	2.074	0.114	0.745	2.030	0.044	0.732
P14618	PKM	APIIAVTR	1.926	0.181	0.6405	4.230	0.269	0.654	1.492	0.212	0.641
P00441	SOD1	AVCVLK	1.631	0.181	0.6405	0.936	0.827	0.526	1.384	0.091	0.686
P00441	SOD1	TLVVHEK	1.620	0.190	0.6373	0.888	0.702	0.552	1.382	0.114	0.673
P09382	LGALS1	SFVLNLGK	1.249	0.365	0.5980	2.018	0.131	0.729	2.099	0.026	0.761
P01833	PIGR	GGCITLISSEGYVSSK	1.127	0.468	0.5801	0.265	0.210	0.683	0.661	0.290	0.618
Q14508	WFDC2	VSCVTPNF	0.900	0.611	0.5588	0.514	0.656	0.562	0.519	0.096	0.683
P15328	FOLR1	FNWNHCGEMAPACK	0.362	0.628	0.5556	0.557	0.765	0.539	0.530	0.282	0.621
P09603	CSF1	TFYETPLQLLEK	0.917	0.678	0.5458	1.302	0.777	0.533	1.330	0.290	0.614
P01833	PIGR	VYTVDLGR	1.152	0.739	0.5392	0.547	0.475	0.595	0.673	0.311	0.611
P08670	VIM	ILLAELEQLK	0.994	0.757	0.5359	1.189	0.269	0.647	1.485	0.075	0.699
P15328	FOLR1	TELLNVCMNAK	0.399	0.759	0.5343	0.591	0.974	0.503	0.605	0.347	0.601
P16035	TIMP2	EVDSGNDIYGNIPIK	0.876	0.805	0.5278	0.563	0.278	0.637	0.660	0.077	0.696
P08670	VIM	ISLPLPNFSSNLRL	0.965	0.861	0.5196	2.646	0.095	0.804	2.722	0.019	0.784
Q75556	SCGB2A1	TINSDISIPEYK	2.476	0.930	0.5098	0.188	0.827	0.526	0.134	0.835	0.523
Q14508	WFDC2	EGSCPQVNINFPQLGLCR	1.118	0.961	0.5049	0.517	0.765	0.539	0.529	0.299	0.614