

sp P16070 CD44_HUMAN	TEAADLCK	458.220217	2
sp P15328 FOLR1_HUMAN	TELLNVCMNAK	646.820498	2
sp P15328 FOLR1_HUMAN	TELLNVCMNAK	650.827597	2
sp P15328 FOLR1_HUMAN	FNWNHCGEMAPACK	574.570893	3
sp P15328 FOLR1_HUMAN	FNWNHCGEMAPACK	577.242293	3
sp O43852 CALU_HUMAN	TFDQLTPESK	647.811707	2
sp O43852 CALU_HUMAN	TFDQLTPESK	651.818806	2
sp P09603 CSF1_HUMAN	AFLLVQDIMEDTMR	841.418033	2
sp P09603 CSF1_HUMAN	AFLLVQDIMEDTMR	846.422168	2
sp P09603 CSF1_HUMAN	TFYETPLQLEK	741.39795	2
sp P09603 CSF1_HUMAN	TFYETPLQLEK	745.405049	2
sp Q06830 PRDX1_HUMAN	ADEGISFR	447.719424	2
sp Q06830 PRDX1_HUMAN	ADEGISFR	452.723558	2
sp Q06830 PRDX1_HUMAN	LVQAFQFTDK	598.819138	2
sp Q06830 PRDX1_HUMAN	LVQAFQFTDK	602.826238	2
sp O75556 SG2A1_HUMAN	TINSDISIPEYK	690.356282	2
sp O75556 SG2A1_HUMAN	TINSDISIPEYK	694.363381	2
sp O75556 SG2A1_HUMAN	ELLQEFIDSDAAAEAMGK	646.643546	3
sp O75556 SG2A1_HUMAN	ELLQEFIDSDAAAEAMGK	649.314945	3
sp P22626 ROA2_HUMAN	TLETVPLER	529.298038	2
sp P22626 ROA2_HUMAN	TLETVPLER	534.302173	2
sp P22626 ROA2_HUMAN	GGNFGFGDSR	507.225405	2
sp P22626 ROA2_HUMAN	GGNFGFGDSR	512.229539	2
sp P09211 GSTP1_HUMAN	ASCLYGQLPK	568.792066	2
sp P09211 GSTP1_HUMAN	ASCLYGQLPK	572.799166	2
sp P09211 GSTP1_HUMAN	TLGLYGK	376.221071	2
sp P09211 GSTP1_HUMAN	TLGLYGK	380.228171	2
sp Q01995 TAGL_HUMAN	TLMALGSLAVTK	602.852124	2
sp Q01995 TAGL_HUMAN	TLMALGSLAVTK	606.859223	2
sp Q01995 TAGL_HUMAN	EFTESQLQEGK	648.309331	2
sp Q01995 TAGL_HUMAN	EFTESQLQEGK	652.316431	2
sp P00441 SODC_HUMAN	AVCVLK	345.204367	2
sp P00441 SODC_HUMAN	AVCVLK	349.211466	2
sp P00441 SODC_HUMAN	TLVVHEK	413.245078	2
sp P00441 SODC_HUMAN	TLVVHEK	417.252177	2
sp P04083 ANXA1_HUMAN	GGPGSAVSPYPTFNPSSDVAALHK	786.057118	3
sp P04083 ANXA1_HUMAN	GGPGSAVSPYPTFNPSSDVAALHK	788.728517	3
sp P04083 ANXA1_HUMAN	DITSDTSGDFR	607.270206	2
sp P04083 ANXA1_HUMAN	DITSDTSGDFR	612.274341	2
sp Q01469 FABP5_HUMAN	ELGVGIALR	464.284734	2
sp Q01469 FABP5_HUMAN	ELGVGIALR	469.288869	2
sp Q01469 FABP5_HUMAN	LVVECMNNVTCTR	847.904767	2
sp Q01469 FABP5_HUMAN	LVVECMNNVTCTR	852.908902	2
sp P08253 MMP2_HUMAN	IDAVYEAPQEEK	696.338089	2
sp P08253 MMP2_HUMAN	IDAVYEAPQEEK	700.345188	2
sp P08253 MMP2_HUMAN	VDAAFNWSK	519.256174	2
sp P08253 MMP2_HUMAN	VDAAFNWSK	523.263273	2
sp P07237 PDIA1_HUMAN	ALAPEYAK	431.737085	2
sp P07237 PDIA1_HUMAN	ALAPEYAK	435.744185	2
sp P07237 PDIA1_HUMAN	ILEFFGLK	483.786578	2
sp P07237 PDIA1_HUMAN	ILEFFGLK	487.793678	2
sp P12830 CADH1_HUMAN	NLVQIK	357.729063	2
sp P12830 CADH1_HUMAN	NLVQIK	361.736163	2
sp P12830 CADH1_HUMAN	VFYSITGQGADTPPVGVFIIR	789.417875	3
sp P12830 CADH1_HUMAN	VFYSITGQGADTPPVGVFIIR	792.753965	3
sp P61604 CH10_HUMAN	FLPLFDR	454.255445	2
sp P61604 CH10_HUMAN	FLPLFDR	459.25958	2
sp P61604 CH10_HUMAN	VLLPEYGGTK	538.802957	2
sp P61604 CH10_HUMAN	VLLPEYGGTK	542.810056	2
sp P30086 PEBP1_HUMAN	VLTPQVK	443.273835	2
sp P30086 PEBP1_HUMAN	VLTPQVK	447.280935	2
sp P30086 PEBP1_HUMAN	LYEQLSGK	469.2531	2
sp P30086 PEBP1_HUMAN	LYEQLSGK	473.260199	2
sp P09466 PAEP_HUMAN	VLVEDDEIMQGFIR	832.42163	2
sp P09466 PAEP_HUMAN	VLVEDDEIMQGFIR	837.425764	2
sp P80188 NGAL_HUMAN	VPLQQNFQDNQFQGGK	597.632192	3