

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q13428	TCOF_HUMAN	Homo sapiens	Treacle protein	29.906279	T147;T287;S510;T533;S807;T814;S1085;T1270;S1274;S1469;S1471	S83;T84;S85;S87;S88;T102;S107;S153;S156;S171;T173;S233;T249;T310;T316;S381;S413;S414;S446;S484;S503;T533;T581;S583;S620;S679;S762;S764;S765;S769;S771;S777;S868;S870;S871;S875;S877;S906;T914;S967;T974;T983;S998;S1111;T1175;S1190;T1222;S1228;T1234;S1257;S1350;T1358;S1376;S1378;S1407;S1410;S1469;S1471	3626323;33214551;27655845;32119511;33465208;29351928;31373491;32522876;34019948;23301498;28510447	MAEARKRRELLPLIYHHLLRAGYVR AAREVKEQSGQKCFLAQPVTLLDIYT HWQQTSELGRKRKAEEAALQAKK TRVSDPISTSESSEEEEEAEATAKA TPRLASTNSSVLGADLPSSMKEKAK AETEKAGKTGNSMPHPATGKTVANL LSGKSPRKSAEPSANTTLVSETEEEG SVPAFGAALKPGMVSAGQVSSSEED TSSSSDET DVEGKPSVKPAQVKASSV STKESPAKKAAPAPGKVGVDVTPQVK GGALPPAKRAKKPEEESESESEEGSE SEEEAPAGTRSQVKASEKILQVRAAS APAKGTPGKGATPAPPKGAGAVASQ TKAGKPEEDSESSEESSDSEETPA AKALLQAKASGKTSQVGAASAPAKE SPRKGAAAPPPGKTGPAVAKAQAGK REEDSQSSSEESDSEEEAPAQAKPS GKAPQVRAASAPAKESPRKGAAPAP PRKTGPAAAQVQVQKQEEEDSRSSSE ESDSDREALAAMNAAQVKPLGKSPQ VKPASTMGMGPLGKGAGPVPPGKV GPATPSAQVGKWEEDSESSEESSD SSDGEVPTAVAPAEKSLGNILQAKP TSSPAKPPQKAGPVAVQVKAQKPM DNSESSEESSDADSEEEAPAAMTAA QAKPALKIPQTKACPKKNTTASAKV APVRVGTQAPRKAGTATSPAGSSPAV AGGTQRPAEDSSSSEESDSEEEKTG LAVTVGQAKSVGKGLQVKAASVPVK GSLGQGTAPVLPGKTGPTVTQVKAE KQEDSESSEESDSEEEAASPAQVK TSVKKTQAKANPAAARAPSAGTISA PGKVVTAAAQAKQSPSKVPPVRN PQNSTVLARGPASVPSVGKAVATAA QAQTGPEEDSGSSEESDSEEEAET LAQVKPSGKTHQIRAALAPAKESPRK GAAPTPPGKTGPSAAQAGKQDDSGS SSEESDSDGEAPAAVTSQVIKPLIF VDPNRSAPGPAATPAQAQAASTPRK ARASESTARSSSESEDEDVIPATQC LTPGIRTNVVTMPTAHPRIAPKASMA GASSKESRISDGKKQEGPATQVSK KNPASLPLTQAALKVLAQKASEAQPP VARTQPSSGVDSAVGTLPATSPQSTS VQAKGTNKLKPKLPEVQQATKAPE SSDSEDSSDSSGSEEDGEGPQGA KSAHTLGPTPSRTETLVEETAESSE DDVVAPSQLLSGYMTPLTPANSQ ASKATPKLDSPPSVSSTLAAKDDPDG KQEAQPQAAGMLSPKTGGKEAAS GTPPQKSRKPKKGAGNPQASTLALQ SNITQCLLQGPWPLNEAQVQASVVK VLTELLEQERKKVVDITKESRRKGW ESRKRKLSGDQPAARTPRSKKKKLL GAGEGGEASVSPEKTSTTSKGGAKR DKASGDVKEKKGKGLGSQAKDEP EELQKGMGTVEGGDQSNPKSKKE KKKSDKRKKDKKKEKKKAKKAST KDESSEPSQKKKKKKKTAEQTV