

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q13428	TCOF_HUMAN	Homo sapiens	Treacle protein	17.778473	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	29351928;34019948;23301498;33214551;31373491;28510447;33465208;27655845;32119511;32522876;34725712	MAEARKRRELLPLIYHLLRAGYVR AAREVKEQSGQKCFLAQPVTLLDIYT HWQQTSELGRKRKAEEAALQAKK TRVSDPISTSESSEEEEEAEATAKA TPRLASTNSSVLGADLPSSMKEKAK AETEKAGKTGNSMPHPATGKTVANL LSGKSPRKSAEPSANTTLVSETEEEG SVPAFGAAGKPGMVSAGQADSSSED TSSSSDET DVEGKPSVKPAQVKASSV STKESPAKKAAPAGKVGVDVTPQVK GGALPPAKRAKKPEEESSESSEEGSE SEEEAPAGTRSQVKASEKILQVRAAS APAKGTPGKGATPAPPKAGAVASQ TKAGKPEEDSESSESSEESSDSEETPA AKALLQAKASGKTSQVGAASAPAKE SPRKGAAAPPKGKTPAVAKAQAGK REEDSQSSSEESDSEEEAPAQAKPS GKAPQVRAASAPAKESPRKGAAPAP PRKTGPAAAQVQVQKQEEEDSRSSSE ESDSDREALAAMNAAQVKPLGKSPQ VKPASTMGMGPLGKGAGPVPPGKV GPATPSAQVGKWEEDSESSESSEESSD SSDGEVPTAVAPAEKSLGNILQAKP TSSPAKPPQKAGPVAVQVKA EKPM DNSESSEESSDADSEEEAPAAMTAA QAKPALKIPQTKACPKKTNNTASAKV APVRVGTQAPRKAGTATSPAGSSPAV AGGTQRPAEDSSSSEESDSEEEKTG LAVTVGQAKSVGKGLQVKAASVPVK GSLGQGTAPVLPKGTGPTVTQVKAE KQEDSESSEESDSEEEAASPAQVK TSVKKTQAKANPAAARAPSAGKTISA PGKVVTAAAQAKQSPSKVPPVRN PQNSTVLARGPASVPSVGKAVATAA QAQTGPEEDSGSSEESDSEEEAET LAQVKPSGKTHQIRAALAPAKESPRK GAAPTPPGKTPSAAQAGKQDDSGS SSEESDSDGEAPAAVTSQVIKPLIF VDPNRSAPGPAATPAQAQAASTPRK ARASESTARSSSESEDEDVIPATQC LTPGIRTNVVTMPTAHPRIAPKASMA GASSKESRISDGKKQEGPATQVSK KNPASLPLTQAALKVLAQKASEAQPP VARTQPSSGVDSAVGTLPATSPQSTS VQAKGTNKLKPKLPEVQQATKAPE SSDSEDSSDSSGSEEDGEGPQGA KSAHTLGTPSRTETLVEETAESSE DDVVAPSQLLSGYMTPLTPANSQ ASKATPKLDSPPSVSSTLAAKDDPDG KQEAQPQAAGMLSPKTGGKEAAS GTPPQKSRKPKKGAGNPQASTLALQ SNITQCLLQGPWPLNEAQVQASVVK VLELLEQERKKVVDITTKESSRKGW ESRKRKLSGDQPAARTPRSKKKKKL GAGEGGEASVSPEKTSTTSK GKAKR DKASGDVKEKKGKGLGSQAKDEP EELQKGMGTVEGGDQSNPKSKKE KKKSDKRKKDKKKEKKKKAKKAST KDESPPSQKKKKKKKTAEQTV