

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	gol app
Q14669	TRIPC_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase TRIP12	26.325226	T387;T758;T764 (Q14669-2)	S12;S77;S85;S100;S310;S312;S942;S991;S997;S1016;S1030;S1317;S1322;S1329;S1376;T1377;S1427	40596516;36240223;34725712;40914422;28510447;38253038	MSNRPNPNPGGSLRRSRNTAGAQ PQDDSIGGRSCSSSAVIVPQPEDPD RANTSERQKTQVPPKDNISRGVKRS ASPDYNRITNSPSSAKKPKALQHTES PSETNKPHSKSKRRHLDQEQQLKSA QSPSTSKAHTRKSAGTGGRSQKRK RTESSCVKSGSGESTGAEERSAKPT KLASKSATSAGAGCSTITDSSAAST SSSSAVASASSTVPPGARVKQKGD QNKARRRSASSTVPPRRSREKEQS KTGGSSKFDWAARFSPKVSLPKTKL SLPGSSKSETSKPGPSGLQAKLASLR KSTKKRSESPPAELPSLRRTROKTT GSCASTSRRGSGLGKRGAAEARQEQ KMADPESNQEAVNNSAARTDEAPQ GAAGAVGTTTSGESESDDSEMGRLL QALLEARGLPPHLFGPLGPRMSQLF HRTIGSGASSKAQQLLQGLQASDES QQLQAVIEMCQLLVMGNEETLGGF PVKSVPALITLLQMEHNFDMNHA CRALTYMMEALPRSSAVVVDIAPVFL EKLQVQCIDVAEQALTALEMLSRR HSKAILQAGGLADCLLYLEFFSINAQ RNALAIANCCQSITPDEFHFVADSL PLLTQRLTHQDKKSVETCLCFARL VDNFQHEENLLQQVASKDLLTNVQ QLLVVTPPILSSGMFIMVVRMFSLM CSNCPFLAVQLMKQNIETLHFLLC GASNGSCQEQIDLVRSPQELYELTS LICEMLPCLPKEGIFAVDTMLKKG AQNTDGAIWQWRDRGLWHPYNYRI DSRIIEQINEDGTARAIQRKPNPLA NSNTSGYSESKDDARAQLMKEDP ELAKSFIKTLFGVLYEVYSSAGPAV RHKCLRAILRIYFADAELLKDVLN HAVSSHASMLSSQDLKIVGALQM AEILMQKLPDIFSVYFRREGVMHQV KHLAESESLTSPPKACTNGSGSMG STTSVSSGTATAATHAAADLGSPSLQ HSRDDSLDLSPOGRSLSDVLRKRLP KRGPRRPKYSPPRDDDKVDNQAKSP TTTQSPKSSFLASLNPKTWGRLSTQ SNSNNIEPARTAGGSGLARAASKDTI SNNREKIKGWIKEQAHKFVERYFSS ENMDGSNPALNVLQRLCAATEQLN LQVDGGAECLEIERSIVSESDVSSFEI QHSGFVKQLLLYLSKSEKDAVSREI RLKRFLHVFFSSPLGEEPIGRVEPV GNAPLLALVHKMNNCLSQMEQFPV KVHDFPSSNGTGGFSLNRGSQALK FFNTHQLKCQLQRHPDCANVKQWK GGPVKIDPLALVQAIERYLVVRGYGR VREDDSDDDGSDDEIDESLAAQF LNSGNVRHRLQFYIGEHLPPYNMTV YQAVRQFSIQAEERESTDDENPL GRAGIWTKTHTIWYKPVREDEESNK DCVGGKRGRAQTAPTKTSPRNAKKH DELWHDGVCPSVSNPLEVYLIPPE NITFEDPSLDVILLRVLHAISRYWYY LYDNAMCKEIIPTSEFINSKLTAKAN RQLQDPLVIMTGNIPTWLTELKTC PFFFPDTRQMLFYVTAFFDRDRAMQ RLDTPNPEINQSDSQDSRVAPRLDR KKRTVNREELLKQAESVMQDLGSSR AMLEIQYENEVGTGLGPTLEFYALVS QELQRADLGLWRGEEVTLNPNKGS QEGTKYIQNLQGLFALPFGRTAKPA HIAKVKMKFRFLGKLMKAIMDFRL VDLPLGLPFYKWMLROETSLTSHDL FDIDPVVARSVYHLEDIVRQKKRLEQ DKSQTKESLQYALETLTMNGCSVED LGLDFTLPGFPNIELKGGKDIPTI HNLEEYLRVIFWALNEGVSROFDS FRDGFESVFLSHLQYFYPEELDQLL CGSKADTWDAKTLMCCRPHDGYT HDSRAVKFLFEILSSFDNEQQLFL QFVTGSPRLPVGGFRSLNPLTIVRK TFESTENPDDFLPSVMTVCVNYLKL DYSSIEIMREKLLIAAREGQQSFHLS	True	False	4.531	5.0	1.594	1.369	0.9