

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
G5E870	TRIPC_MOUSE	Mus musculus	E3 ubiquitin-protein ligase TRIP12	26.222628	NaN	S12;S77;S85;S100;S310;S312;S975;S1024;S1030;S1049;S1063;S1350;S1355;S1362;S1409;T1410;S1460	24788674	MSNRPNPNPGGSLRRSQRTAGAQ PQDDSIGGRSCSSSSAVIVPQPEDPD RANTSERQKTKQVPKKDNRSRVKRS ASPDYNRTNSPSSAKKPRAFQHIESF SETNKPHSKSKKRHLDDQEQQLKSA QLPSTSKAHTRKSVAAGSSRNQKRK RTESSCVKSGSGSESTGAEERSAKPI KLASKSATSAGAGCSTITDSSSAAST SSSSSAIASASTVPAGARVKQKQDQ NKARRRSASSPSPRRSSREKEQSK TGGSSKFDWAARFSPKVSLPKTKLS LPGSSKSETSKPGPSGLQAKLASLRK STKKRSESPPAELPSLRRSTROKTTG SCASTSRRGSGLGKRGAAEARRQEK MADPESNQETVNSSAARTDEAPQG AAASSVAGAVGMMTTSGESESDDE MGRQLALLEARGLPPHLFGPLGPRM SQLFHRTIGSGASSKAQQLLQGLQA SDESQQLQAVIEMCQLLVMGNEETL GGFPVKSVVPALITLLQMEHNFDM NHACRALTYMMEALPRSSAVVDAI PVFLEKLQVIQCIDVAEQALTALEML SRRHSKAILQAGGLADCLLYLEFFSI NAQRNALAIAANCCSITPDEFHFV ADSLPLLTQRLTHQDKKSVESTCLC FARLVDFNFHEENLLQVASKDLLT NVQQLLVTPPILSSGMFIMVVRMF SLMCSNCP TLAVQLMKQNIATLHF LLCGASNGSCQEIDLVPRSPQELY ELTSLICELMPCLPKEGIFAVDTMLK KGNAQNTDGAIWQWRDRDGLWHP YNRIDSRHIEAAHQVGEDEISLTLGR VYTIDFNSMQQINEDGTARAIQRKP NPLANSNTSGYSELKDDARAOLM KEDPELAKSFKITLFGVLYEYVSSSA GPAVRHKCLRAILRIYFADAELLKDV LKNHAVSSHASMLSSQDLKIVVGA LQMAEILMQKLPDIFSVYFRREGVM HQVKHLAESESLTSPKACTNGSG SLGSTTPASSGTATAATNASADLGSP SLQHSRDDSLDLSPOGRLSDVLKRR RLPKRGPRRPKYSPPRDDDKVDNQA KSPTTTQSPKSSFLASLNPKTWGRLS AQNSNNIEPARTAGVSGLARAASK DTISNNREKIKGWIKEQAHKVERY FSSSENMDGNSPALNVLQRLCAATE QLNLQVDGGAELVEIRSVSESDVS SFEIQHSGFVKQLLLYLSKNEKDAV GREIRLKRFLHVFFSSPLPGEFPVGR VEPVGHAPLLALVHKMNNCLSQME QFPVKVHDFPSGNGAGGSFSLNRGS QALKFFNTHQLKCCQLQRHPDCANV KQWKGGPVKIDPLALVQAIERYLVVR GYGRVREDDSDDDGSDDEIDESL AAQFLNSGNVRHRLQFYIGEHLHPY NMTVYQAVRQFSVQAEDEDERSTDD ESNPLGRAGIWTHTHTIWKPVRED EESTKDCVGGKRGRAQTAPTSTSPR NAKKHDELWHDGVCPSVANPLEVY LIPTPENITFEDPSLDVILLRVLHAI SRYWYYLDNAMCKEIIPTSEFINSK LTAKANRQLQDPLVIMTGNIPTWLT ELGKTCPPFFPFDTRQMLFVYVAFD RDRAMQRLLDTNPEINQSDSQDSRV APRLDRKKRTVNREELLQAESVMQ DLGSSRAMLEIQYENEVGTGLGPTL EFYALVSQELQRADLCLWRGEEVTL SNPKGSQEGTKYIQNLQGLFALPFG RTAKPAHIAKVMMKFRFLGKLMKA IMDFRLVDLPLGLPFYKWMRLRQETS LTSIDLFDIDPVVARSVYHLEDIVRQ KKRLEQDKSQTKESLQYALETLTMN GCSVEDLGLDFTLPGFPNIELKGG KDIPVTIHNLEEYLRVIFWALNEGV CRQFDSFRDGFESVFPLCHLQYFYP EELDQLCGSKADTWDAKTLMCECC RPDHGYTHDSRAVKFLFEILSSFDN EQQRLFLQFVTGSPRLPVGGRSLN PPLTIVRKT FESTE NPDDFLPSVMTC VNYLKL PDYSSIDIMRDKLLIAAREG	True	False	2.638	4.56	1.533	1.244	0.677	1.425	0.864

