

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracell region					
O95359	TACC2_HUMAN	Homo sapiens	Transforming acidic coiled-coil-containing protein 2	22.903221	S979	S197;S201;S269;S493;S561;S571;S575;S758;S962;S1025;S1267;S1313;S1562;S2072;S2161;S2226;T2246;S2256;S2317;S2321;S2359;S2389;S2392;S2394;S2403;T2430;T2451;T2455;T2458;S2512;S2534;T2553;S2557;S2569;T325;T2625	38253038	MGNENSTSDNORTLSAQTPRSAQP PGNSQNIKRRKQDTPGSPDHRDASS IGSVGLGGFCTASESSASLDPLVSP EVTEPRKDPQGARGPEGSLLPSPSPS QEREHPSSSMPPFAECPPEGLCLASPA AAPEDGPTQSPRREPAPNAPGDIA AAFAERDSSTPYQEIIVPSAGRER QPKEEGQKSSFSFSSGIDQSPGMSP VPLREPMKAPLCGEGDQPGGFESQE KEAAGGFPPAESRQGVASVQVTEPA PAAAQQTTESSAVLEKSPLKPMAPIP QDPAPRASDRERGQGEAPPQYLTD LEFLRACHLPRNSGAAPEAEVNAA SQESCQQPVGAYLPHAEPLWGLPSP ALVPEAGSGKEALDIDVQGHQPT GMRGTKPNQVVCVAAAGGQPEGGLP VSPEPSLLTPTTEAHPASSLASFPAA QPIAVVEEPGSSSRESVSKAGMPVSA DAAKEVVDAGLVGLERQVSDLGSKG EHPEGDPEVPPAPSPQERGEHLNTE QSHEVQPGVPPPLPKEQSHEVQPG APPPPLPKAPSESARGPPGPTDGAKV HEDSTSPAVAKEGSRSPGDSPGGKE EAPEPPDGGDPGNLQGEDSQAFSSK RDPEVKGDELKPSDDAESRDHPSS HSAQPPRKGAGHTDGHPSQTAEA DASGLPHKLGEEDPVLPPVDPGAGE PTVPEGAIWEGSGLQPKCPDITLQSR EGLGRMESFLTLESEKSDFPPTPVA EVAPKAQEGESTLEIRKMGSCDGE LLTSPDQPRGPACDASRQEFHAGVP HPPQGENLAADLGLTALILDQDQGG IPSCPGEGWIRGAASEWPLLSSEKH LQPSQAQPETSIFDVLKEQAOPPEN GKETSPSHPGFKDQADSSQIHVPV EPQEDNNLPTHGGQEALGSELQS QLPKGTLSDTPTSSPTDMVWESSLT EESELSAPTRQKLPALGKRPPEGAC GDGQSSRVSPAADVLKDFSLAGNF SRKETCCTGQGNPKSQALADALEE GSQHEEACQRHPGASEAADGCSPL WGLSKREMASGNTGEAPPCQFDSV ALLDAVPCLPALAPASPGVPTQDAP ETEACDETEGGRQPPVAPQKME CWATSDAESPKLLASFPQSAGEQGG AGAAETGGSAGAGDPGKQQAPEKPG EATLSCGLLQTEHCLTSGEEASTSAL RESCQAEHPMASCODALLPARELG GIPRSTMDFSTHQAVDPKELLSGP PEVAAPDTPYLHVDSAAQRGAEDSG VKAVSSADPRAPGESPCVGEPLAL ENAAASKLKFAGSLAPLLQPGAAGGEI PAVQASSGSPKARTTEGPDVSMPC DRMPLLAKGKQATGEEKAATAPGAG AKASGEGMAGDAAGETEGSMERMG EPSQDPKQCTSGGVDTSSEQIATLTG FPDFREHIKIFKPVLGALATPGEK AGAGRSVAVKDLTRPLGPEKLLDGP PGVDVTLPPAPPARLQVEKKQQLAG EAEISHLALQDPASDKLLGPAGLTW ERNLPGAGVGMAGVPTTLREDER PEGPAAWPGLEGCQAYSOLERSRQE LASGLPSAATQELPVERAAAFQVAP HSHGEEAVAQDRIPSGKQHQETSAC DSPHGEDGPGDFAHTGVPGHVPRS TCAPSPQREVLTVPPEANSEPWTLDT LGGERRPGVGTAGILEMRNALGNQST PAPPTGEVADTLEPGKVAGAAGEA EGDITLSTAETQACASGDLPEAGTTR TFSVVAGDLVLPGSCQDPACSDKAP GMEGTAALHGDSPARPQQAKEQPG PERPIAGDGKVCVSSPPEPEDETHDP KLQHLAPEELHTDRESRPPGSPMLP SVPKADAPRVMKVTSDETRGAEGT ESSPVADDIIQPAAPADLESPTLAASS YHGDVVGVSTDLIAQISIPAAAHAG LPPSAAEHIVSPSAPAGDRVEASTPS CPDPAKDLRSRSDSEAFETPESTTP VKAPPAPPPPEVIPEPEVSTQPPPE EPGCGETVPPVDPGRSDSVEGSPF	None	None	None	None	None	None	None	None	None	None	None	None	None	None

RPPSHSFSAVFDEKPIASSGTYNLD
FDNIELVDTFQTLPRASDAKNQEG
KVNTRRKSTDSVPISKSTLSRSLSLQ
ASDFDGAASSGNPEAVALAPDAYST
GSSSASSTLKRKPRPPSLKKKQTT
KKPTETPPVKETQEQEPDEESLVPSGE
NLASETKTESAKTEGSPALLEETPL
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EVTPSDSGGQEDSPAAGLSVRLEFD
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DPDTCDESVDPFKTSSTKTPSSPSKSP
ASFEIPASAMEANGVDGDLNKPAP
KKKTPLKTDTRVKKSPKRSPLSDPP
SQDPTPAATPETPPVISAVVHATDEE
KLAVTNQKWTCMTVDLEADKODYP
QPSDLSTFVNETKFSSPTEELDYRNS
YEIEYMEKIGSSLPQDDAPKKQALY
LMFDTSQESPVKSSPVRMSSEPTPC
SGSSFEETEALVNTAAKNQHPVPRG
LAPNQESHQVPEKSSQKELEAMGL
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RIGTAEVEKPAGLLFQQPDLDSALQI
ARAEIITKEREVSEWKDYEESSRREV
MEMRKIVAEYEKTI AQMIEDEQREK
SVSHQTVQQLVLEKEQALADLNSVE
KSLADLFRRYEKMKEVLEGFRKNEE
VLKRCAQEYLSRVKKEEQRYQALKV
HAEKLDRAEIAQVRGKAQQEQEA
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