

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
O15050	TRNK1_HUMAN	Homo sapiens	TPR and ankyrin repeat-containing protein 1	33.754801	S1439	NaN	41018975;30379171;39531497	MWDPRAAARVPPRDLAVLLCNKSNA FFSLGKWNFAVAAKECLQWDP VKGYRAGYLLRLHQPYEAARMFF EGLRLVQRSQDQAPVADFLVGVFT MSSDSIVLQSFPCFDHIFTTGFTE VWQSVIEKLAKKGLWHSFLLS DRLPRNIHVPELSLKLFEKYVFIGL YEKMEQVPKLVQWLISIGASVETIGP YPLHALMRLCIQARENHLFRWLMD HKPEWKGRINQKDGDCVTLHVVA AHS PGYLVKRQTEDVQMLLRFGADP TLDRQSRVVDVLRKNKNFAIEKI NSHLEKLATCSKDLGFSNGDGPTS ENDIFRQVLEQLVKYMNSGNRLH NFKQEVVQRFRLRLSTLQEI CDINQDCATTVFKFLEKQRWPEVL LLLTRKVS GEPPLGDCLIKDCN DICTIIPHLSTWDQRKKQLLGL GALPDGLQESQERPVVTCCLKH LAFLLLTGADPRAISLTEGDTPL ALHIFLEIKADIGFSFLSHLLD NPTEFDYLNPNVQDSNGNTLM QKGM LKRVKLLDLLVKFDINFN NKEGDARHRIKND SLLAWNKA LMENRRRSRQDSAHLGKLSKST GHTSQLKSQGSF KSVPCGATART EGSAVPDSWETLPGTQVTRKEPG RPCSLRDCLMQDITVLIQVVEP PEDCLOSSEPLEAGAGKEGKDDK TLGAGAPDCSEVGEHQAQVGLG LVPDDNRGKEGNDQDDWSTQEI ACLQDFDNMTWEIECTSEMLKLS SKVMTKVIKKIILAIQQLNGE GLQKRLKHLKGSIQLEAKLDKGA MLWELAIDFSPRCSENPEKIIATE TCAMEKSGRIYTEIIRIWDIVLH ADSIKAI CNAYNRGLSCVLRK NKGQV SANMKIQKRIPRCYVEDTE EKGREHVNPEYFPPASAVETEYNI KFHSFSTNMAFNILNDTTATVEY RVGELEYAVIDLNPRLPEPIILIG TGKTTCCLYRLWKKFHVYWEKAE AGSPLLAQVWLKRRLEVEPGKESP GGEEEEEEDEEEDSIEVETVESID EQEYACAGGAGVEPAGDQAAEVC APEHPHQLEHLHQIFVTKNHVLCQ VORNFIELSKSTKATSHYKPLDPN KLQDLRDEFPLFVTSKQLLLLDAS LPKPFRLRNEDGSLKRTIIGWSAQ STIPSWQEDDEEAEVDGDYSEEDKA VEMRTGSDPRVYVTFEVFKNEIWP KMTKGR TAYNPALIWKEIKSFLKGS EALSCPHGRLTEEVYKKGGRKRCPN FKEDRSEIYSLFSLYQIORSQKGYF EEDVLYNISRRLSKLRVLPWSIHEL GDEIQDFTQAE LALLMKINDPN FLTGDTAQSIMKGVAFRFDLRS HYASRNTIDKQCAVRKPKKIHQLY NYRSHSGILNLAGVVDLLQFYFPE FDRLPRDSGLFDGPKPTVLESCSV DLAILLRGNKRKTQPIEFGAHQVIL ANETAKEKIP ELGLALVLTIEAKGL EFDDVLLNFFTDSEAYKEWKHSSF TPTSDSRENRLVEVPLDKPGSSQ GRSLMVNPEMYKLLNGELKQLYTAI TRARVNLWIFDENREKRAPAFKYFIR RDFVQVKT DENKDFDSSMFVKTS TPAEWIAQGDYAKHCWKVAAKCY QKGAFAKEKLAHDTALSMKSKK VSPKEKQLEYLELAKTYLECKEPTLS LKCLSYAKEFQLSAQLCERLKGIRDA AYFYKRSQCYKDAFRCFEQIQEFDLA LKMYCQEELFEEAAIIVEKYEMLK TKTLPISKLSYSASQFYLEAAAKYLSA NKMKE MMAVLSKLDIEDQLVFLKS RKRLAEADLLNREGREEAALLMK QHGCLEAARLTADKDFQASCLLGA ARLNVARDSIEHTKDILREALDICY QTGQLSGIAEAHFLQGVILRDFQKLR DAFFKFDTLNHSAGVVEALYEAASQ	False	False	2.102	3.931	1.157	False	0.386	1.257	1.199

CEAEPEKILGLAPGGLEILLSLVRALK  
RVTNNAEKEMVKSCFEFFGISQVDA  
KYCQIAQNPDGPIRHHFDLNLREK  
KTKDHFLLIMTDQVKLALNKHLLGRL  
CQITRSLGKTYRGVCMRFIVGLKCE  
DENCEHFHRRPLRRCEAKCLVQSKM  
NLVAINGLLEAKKVFPKILAEELKEI  
DYILSTDMYGLCKSILDVLFPKHFHQ  
RVLSENPMACKEILKPNYKSFYR  
FALKEYIHFLFENESARNRRESTDJ  
WLSAMQAFLLSSNYPEEFKLLHQE  
EDNYNRELKALESEKDERGRGRGSR  
IKGIEGKFGMLAPNRDDENMDKTH  
LCFIRLLENCIDQFYVYRNPEDYKRL  
FFRFMNVLIKRCKEPLIPSGNTVAL  
LEFQFIHCGVVLARLWKNVILCLPKS  
YIALLHYWEFLFSKDKELGDVFSII  
QEYKPKDVTRAIQDFRHLVSYLAKVL  
CGYENVNFNVLDAFSEIDYVVSGE  
AERTLVLCVMLVNAEEILOPYCKPL  
LYRHFREIESRLQLMSMDCPGQVPE  
RLLKVVKRVLVAVNVKSVAEALQDL  
LFRDEEYLMDCDWRWDPVHTKGS  
IVRGLYEEVRLNRLCLDPVDYFAE  
PECEFGQDEMDELALEDRDHVLATI  
LSQKORKASIQKLRRAACLVVSLCIS  
WRRRVGTQMEREVREEAREPRAGNF  
KKADVDRTOCDLGVKFTRGPENYF  
SPSKAFEGAASEVAVLSRAELERECC  
QERNSESYEQHHLEHHQRQQVAY  
QKSEFFHEKVDPAIDEGKLVQDIE  
QSVWIHSHVGSKEHSHMLQKVQEH  
IKRVSDMVEDLYRRKAWAGAEEM  
TRLVNILISVRDARDWLMKTETRLK  
KEGIVQEDDYENEVEDFGELRPRRR  
SRKCGQRKY