

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	ext							
Q9H2D6	TARA_HUMAN	Homo sapiens	TRIO and F-actin-binding protein	18.740164	S464;S1925	S1796;S1949;S1955;T457	30379171;37217939;34846842	MEEVPGDALCEHFEANILTONRCQ NCFHPEEAHGARYQELRSPSGAEV YCDLPRCPAPEDPLSASTSGCQSV DPGLRPGPKRGSPSAGLPEEGPTAA PRSRRELEAVPYLEGLTSLCGSCN EDPGSDPTSSPDSATPDDTNSSSV DWDTVEROEEAPSWDELAVMIPR RPREGPRADSSQRAPSLLTRSPVGG DAAGQKKEDTGGGGRSAGQHWARL RGESGLSLERHRSTLTQASSMTPHS GPRSTTSQASPAQRDTAQAASTREIP RASSPHRITQRDTSRASSTQQEISRA SSTQQETSRRASSTQEDTPRASSTQE DTPRASSTQWNTPRASSPSRSTOLD NPRTSSTQQDNPQTSFPTCTPQREN PRTPCVQDDPRASSPNRITQRENS RTSCAQRDNPKASRTSSPNRATRDN PRTSCAQRDNPRASSPSRATRDNP TSCAQRDNPRASRTSSPNRATRDNP RTSCAQRDNPRASSPSRATRDNP TSCAQRDNPRASRTSSPNRATRDNP TSCAQRDNPRASSPNRAARDNP CAQRDNPRASRTSSPNRATRDNP RTSCAQRDNPRASSPNRATRDNP TSCAQRDNPRASRTSSPNRATRDNP TSCAQRDNPRASSPNRATRDNP CAQRDNPRASRTSSPNRATRDNP AQRDNPRASRTSSPNRATRDNP CAQRDNPRASSPNRTTQDQSPRTSC ARRDDPRASSPNRTIQQENPRTSCA LRDNPRASSPNRTIQQENPRTSCA RDDPRASSPNRTIQQENPRTSCARR DNPRASSPNRTIQQENPRTSCARR NPRASSPNRTIQQENLRTSCTRQDN PRTSSPNRATRDNPRTSCAQRDNLR ASSPIRATQQDNPRTCIQQENPRSS TQQDNPKTSCTKRDNLRPTCTQRDR TQSFQFQDNPGTSSQCCTQKENL RPSSPHRSTQWNNPRNSSPHRTNK DIPWASFPLRPTQSDGPRTSSPSRSK QEVWASIALRPTQGRDPTSSPSR PAQHDPQSSFGPTQYNLPSRATSS SHNPGHQSTRTSSPVYPAAYGAPL TSPEPSQPPCAVCIGHRDAPRASSPP RYLQHDFFPFPPEPRAPSEPPHHE PPYIPPAVCIGHRDAPRASSPPRHTQ FDPPFPLPDTSDAEHQCSQSPQHEPL QLPAPVCIGYRDAPRASSPPRAPEP SLLFQDLPRASTESLVPSMDSLHEC PHIPTPVCIGHRDAPFSPPRAPE PSLFFQDPPGTSMESLAPSTDSLHG SPVLIPQVCIGHRDAPRASSPPRHPP SDLAFAPSPSPGSSGGRSAPPGE TRHNLEREYTVLADLPPPRRLAQR QPGPQAQCSSGGRTHSPGRAEVERL FGQERRKSEAAGAFQAQDEGRSQ PSQGSQQLRRQSSPAPSROVTMLP AKQAELTRRSQAEPPHPWSPEKRPE GDRQLQGSPLPRTSARTPERELRT QRPLESGQAGPRQPLGVWQSQEFP GSQGPHRHLERSWSSQEGGLGPGG WWGCCGPESLGAAKAPEGAWGTSR EYKESWGOPEAWEEKPTHELPREL GKRSPLTSPPEWGGPAESSQSWH SGTPTAVGWGAEGACYPYRGSERRP ELDWRDLGLLRAPGEGVWARVP DWEGLLELLQARLPRKDPAGHRDD LARALGPELGPPTNDVPEQESHQ PEGWAEATPVNGHSPALQSQSPVQL PSPACTSTOWPKIKVTRGPATATLAG LEQTGPLGSRSTAKGPSLPELQFQPE EPEESEPSRGDPLTDQKQADSADK RPAEGKAGSPLKGRVTSWRMPGD RPTLFPNPFLLSLGLVLRWRPDLN KKGWMSILDEPGEPPSPSLTTTSTQ WKKHWVFLTDSLSKYRSDTAEEAD ELDGEIDLRSCTDVTEYAVQRNYGF QIHTKDAVYTLAMTSGIRRNWIEAL RKTVRPTAPDVTKLSDSNKENALH SYSTQKGLKAGEQRAGSEVISRGGP RKADGQRQALDYVELSPLTQASQPR ARTPARTPDRDLAKQEELERDLAQRS EERRKWFATDSRTPEVPAGEPRR	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None	No

GLGAPLTDQQNRLSEEIEKKWQEL
EKLPLRENKRVPLTALLNQRGERR
GPPSDGHEALEKEVQALRAQLEAWR
LQGEAPOSALRSQEDGHIPPGYISOE
ACERSLAEMESSHQVMEELQRHH
ERELQRLQOEKEWLLAEETAATASA
IEAMKKAYQEELSRELSKTRSLQQG
PDGLRKQHQSDEALKRELQVLSEQ
YSQKCLEIGALMRQAEEREHTLRRC
QQEGQELLRHNQELHGRLESEIDQL
RGFIASQGMGNCGGRSNERSSCEL
EVLRLVKENELQYLKKEVQCLRDEL
QMMQKDKRFTSGKYQDVYVELSHI
KTRSERIEQLKEHLRLAMAALQEK
ESMRNSLAE