

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasm meml
O75962	TRIO_HUMAN	Homo sapiens	Triple functional domain protein	12.324105	S2291	S1627;S1632;S1633;T1824;S2282;S2455;S2459;S2631	37217939;38253038;38665916	MSGSSGGAAPAASSGPAAAAASAAG SGCGGGAGEGAEFAAKDLADIAAFF RSGFRKNDKAMDVLPILKEKVVAY LSGGRDKRGGPILTFPARSNHDRIR QEDLRRLLISYLACIPSEEVCKRGFTVI VDMRGSKWDSIKPLLKILQESFPCCI HVALIHKPDNFWQKQRTNFGSSKFE FETNMVSLGLELTKVVDPSQLTPEFD GCLEYNHEEWIEIRVAFEDYISNATH MLSRLEELQDILAKKELPDLEGAR NMIEEHSQKKKVIKAPIEDLDLEGQ KLLQRIQSSSEFPKKNSSGSGNADLQ NLLPKVSTMLDRLHSTROHLHQMW HVRKLLDQCFQLRLEQDAEKMF DWITHNKGLFLNSYTEIGTSHPHAM ELQTOHNNHFAMNCMNVYVNNRIM SVANRLVESGHYASQQIRQIASQLEQ EWKAFAAAALDERSTLLDMSSIFHQK AEKYSNVSDSWCKACGEVDLPSEL QDLEDAIHQQGIYEHITLAYSEVSQ DGKSLLDKLRPLTPGSSDSLTAASA NYSKAVHHVLDVIHEVLHHQROLE NIWQHRKVRHLHQRLLQCVFQDDVQ QVLDWIENHGEAFLSKHTGVGKSL HRARALQKRHEDFEVAQNTYINA DKLLEAAEQLAQTGECDPEEIQAA HQLEDRIQDFVRRVEQRKILLDMSV SFHTHVKELWTLLEELQKELDDV YAESVEAVQDLIKRFGQQQTTLQV TVNVKEGEDLIQQLRDSAISSNKTP HNSSINHIETVLQQLDEAQSOMEEL FQERKIKLELFLQLRIFERDAIDIISD LESWNDELSQQMNDFTEDLTIAE QRLQHHADKALTMNNLTFDVIHQG QDLLQYVNEVQASGVLLCDDRVD MATRVQDLLEFLHEKQELDLAAE QHRKHLEQCVQLRHLQAEVKQVLG WIRNGESMLNAGLITASSLQEAEL QREHEQFQHAIEKTHQSALQVQK AEAMLQANHYDMDMIRDCAEKVAS HWQQLMLKMEDRLKLVNASVAFYK TSEQVCSVLESLEQEQYKREEDWCGG ADKLGPNSETDHVTPMISKHLEQKE AFLKACTLARRNADVFLKYLHRNSV NMPGMVTHIKAPEQQVKNILNELFQ RENRLVHYWTMRKRRLDQCQYVV FERSAKQALEWIHDNGEFLYLSHTS TGSSIQHTQELLKEHEEFQITAKQTK ERVKLLIQLADGFCEKGAHAHAIEIKK CVTAVDKRYRDFSLRMEKYRSTLEK ALGSSDSNKKSSSLQDIIIPASIPGS EVKLRDAAHELNEEKRSARRKEFI MAELIQTEKAYVRDLRECMDTYLWE MTSGVEEIPPGIVNKELIIFGNMQUEI YEFHNNIFLKELEKYEQLPEDVGH FVTWADKFMQYVYCKNKPSTQLI LEHAGSYFDEIQQRHGLANSISSYLI KPVQRITKYQLLLEKLLTCEEGKGE IKDGLVMLSVPKRANAMHLMSL EGFDENIESQGELLQESFQVWDPK TLIRKGRERHLFLFEMSLVFSKEVK DSSGRSKYLYKSKLFTSELGVTEHVE GDPCKFALWVGRTPSDNKIVLKAS SIENKQDWIKHIREVIQERTIHLKGA LKEPIHIPKTAPATROKGRRDGEDLD SQGDSSQPDTSIASRTSQNTLSDS KLSGGCELTVVHDFACNSNELTIR RGQTVVFLRPHDKPDWCLVRTTDR SPAAGLVPCGSLCIAHSRSMEME GIFNHKDSLVSNDASPPASVASL QPHMIGAQSSPGKRPNGNLRKWL SPVRRLSGKADGHVKLAHKHKKS REVRKSADAGSQKSDSAAATPQDE TVEERGRNEGLSSGTLKSSSSGMQ SCGEEEGEAGAVPLPPMAIQQH SLLQPDSDDKASSRLLVRPTSSETP SAAELVSAIEELVSKMALEDPRPSSL LVDQGDSSPSFNPSDNLSLSSSPI DEMEERKSSSLKRRHYVLQELVETE RDYVRDLGYVVEGYMALMKEDGVP	True	False	4.684	2.585	1.193	1.151	1.113	1.523

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EVMCIVPRRCNDMMNVGRLQGFDFG
KIVAQKLLQDTFLVTDQDAGLLPR
CRERRIFLFEQIVIFSEPLDKKKGFS
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AEADKMSGTSTPGPSLPPGAAPPEA
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SASSASLRVLGPGMDGIMVTWKD
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