

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitoch
Q8NDV7	TNR6A_HUMAN	Homo sapiens	Trinucleotide repeat-containing gene 6A protein	25.411336	S264;S273;S1266;S1657;S1659;S1660;S1661;S1662;T1665;T1666;S1669;T1670;S1671;S1674;S1675;S1679;S1686;S1687;T1688;S1691;T1692;S1693;T1702;S1704;S1707;T1711;S1712;S1884;S1890	S739;S878;S991;S1212;S1270;T1470;S1585;S1869;S1890	38665916;23301498;33214551;39302247;39531497;38253038;39534244;35254053;31492838;40307207;32119511;34019948;29237092;35132862;30397120;34846842;40136647;37217939;37340703;30059200;35138101;29351928;36240223	MRELEAKATKDVNRLSRDLVQEEE QLMEEKKKKKDDKKKKEAAQKKAT EQKIKVPEQIKPSVSPQPANSNNG TSTATSTNNNAKRATANNQPPQQ QQQQQQQQPPQQPQPQQPQQQ PQQQPQALPRYPREVPPFRFRHQEHK QLLKRQGHFPVIAANLGSVAVKVLNS QSESSALTNQQFPQNNGEVQNSKNQ SDINHSTSGSHYENSQRGPVSTSD SSTNCKNAVVDLSEKEAWPSAPGS DPELASECMDADSASSSESERNITI MASGNTGGEKDGRLNSTGLGSQNK FVVGSSNNVGHGSSTGPWGFSGH AIISTCQVSDAPEKSESSNNRNM AWGTVSSSSNGGLNPSTLNSASNH GAWPVLENGLALKGPVSGSSGIN IQCSTIGQMPNNQINSKVSQGGSTH GTWGSQETCESEVSGTQKVSFSGQ PQNITTEMTGPNNTTFNMTSSLPNS GSVQNNELPSSNTGAWRVSTMNHP QMQAPSGMNGTSLSHLSNGESKSG GSYGTTWGAYGSNYSGDKCSGPN QANGDTVNATLMQPGVNGPMGTN FQVNTNKGGGVWESGAANSQSTSW GSGNGANSRRRGTGTPAQNTGT NLPVSEWKNLPSNQHSNDSANGNG KFTFTNGWKSTEEEDQGSATSQTNE QSSVWAKTGGTVESDGSTESTGRLE EKGTGESQSRDRRKIDQHTLLQSV NRDLDPRVLSNSGWGQTPIKQNTA WDTETSPRGERKTDNGTEAWGSSA TQTFNSGACIDKTSPNGNDTSSVSG WGDPKPALRWGDSKGSNCQGGWE DDSAATGMVKSNQWGNCKEEKAA WNDSQKNKQGWGDGQKSSQGWV SASDNWGETSRNNHWGEANKKSSS GGSDSDRSVSGWNLGKTSSTWG NNINPNSSSGWDESSKPTPSQGWG DPPKSNQSLGWGDSSKPVSSPDWN KQODIVGSWGPATGKPPGTGWL GPIPAPAKEEPTGWEEPSPEIRRK MEIDDGTSAWGDPKYNKYNM WNKNVPNGNSRSDQQAQVHLLTP ASAINKEASSSGWGEPPWGEPTP ATTVDNGTSAWGKPIDSGPSWGEPI AAASSTTWGSSVGPQALSQSGPK SMQDGCDDMPLPGRNPTGWEE EEDVEIGMWNSSQELNSSLNWP PYTKKMSKGLSGKRRRERGMK GGNKQEEAWINPFVKQFSNISFRD SPEENVQSNKMDLSSGMLQDKRM EIDKHSNLNIGDYNRTVKGKPGSRPOI SKESSMERNPYFDKDGIVADESQN MQFMSSQSMKLPSSNSALPNQALG SIAGLGMQNLNSVRQNGNPSMFGV GNTAAQPRGMQPPAQLSSSQPN LRAQVPPPLSPQVPVSLKYAPNNG GLNPLFGPQQVAMLNQLSGLNQLS QISQLRLLAQQRAQSQRVPSGN RPQQDQQRPLSVQQQMMQSQRO LDPNLLVKQQTPPSQQPLHQPAM KSFLDNVMPHTTPELQKGPSPINAF SNFPIGLNSLNVNMDMNSIKEPQ SRLRKWTVDSISVNTSLDQNSSKH GAISSGFRLEESPFVYPDFMNSSTSP ASPPGSIQDQWPRAKSPNGSSSVNW PPEFRPGEPWKGYPNIDPETDPYVTP GSVINLNTVREVDHLDRNSGS SSSLNTLTPSTSAWSSIRASNYNVP SSTAQSTSARNSDSKLTWSPGSVTN TSLAHELWVKVPLPKNITAPSRPPG LTGQKPLSTWDNSPLRIGGGWGN DARYTPGSSWGESSEGRITNWLVLK NLTPOIDGSTRTLQCMQHGPLITFHL NLPHGALVRYSSKEEVVKAQKSLH MCVLGNTTILAEFASEEEISRFFAQ QSLTPSPGWQLGSSQSRGLSDCS HSFSSRTDLNHWNGAGLSGTNCGD LHGTSLWGTPHYSTSLWGPSSSDP RGISSPINAFLVDHLGGGEGSM	True	False	4.319	4.675	False