

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracell region |
|--------------|-------------|--------------|---|--------------|---------------|-----------------------|-------------------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|------------------|
| Q6YHU6 | THADA_HUMAN | Homo sapiens | tRNA (32'-2'-O)-methyltransferase regulator THADA | 28.621158 | S169 | S1015;S1024;S1161 | 35254053;39894887 | MGVKKKKEMQVAALTICHQDLETLK SFADVEGKNLASLLHCVQLTDGVS QIHYIKQIVP LLEKADKNGMCDPTIQ SCLDILAGIYLSLSLKNPLKVLASSL NSLPDFFLPEAMHRFTSRLQEELNT TDLYSYRKVTDNISSCMENFNLGRA SVNNLLKNVLFHFLQKSLIELEENRK CAGNHIIQTOLMNDLLVGRVSMML VQKVQDFQGNLWKTSDSPIWQNM GLLSIFTKVLSDDDLLQTVQSTGLA IILFIKTMFHPSEKIPHLISSVLLRSV DCTSVPEWFMSSCRSLCCGDISQSA VFLFCQGT LAMLDWQNGSMGRSGE ALLLDTAHVLF T LSSQIKEPTLEMF SRILASWTNSAIQVLESSSPSLTDSL NGNSSIVGRLEVVYTHWEHPLDAL RHQTKIMFKNLLQMHRLTVEGADF VPDPFFVELTESLLRLEWHIKGKYTC LGCLVEGVEHIL AIDKTIPSQILEV MGDQSLVPYASDLLETMFRNHKSH LKSQTAESSWIDQWETWVSPLLFI LCEGNLDQKSYVIDYLPKLLSYSPE SLQYMKILQTSIDAKTGQEQSFP GSCNSRGALGALMACLRIARAHGHL QSATDTWENLVSDARIKQGLIHQHC QVRIDLGLLCESNRSTEIVSMEEM QWIQFFITYNLNSQSPGVRQICSL KFLFCRIQESSQVLYKLEQSKSKREP ENELTKQHPSVSLQYKNFMSSICN SLFEALFPGSSYSTRFSALTILGSIAE VFHVPEGRITYVYQLSHDIDVGRFQT LMECFTSTFEDVKILAFD LLMKLSKT AVHFQDSGKLOGLFQAALELSTSTK PYDCVTASYLLNFIWQDALPSSLSA YLTQQVACDNGDRPAAVVERNTLM VIKCLMENLEEVVSAENSLQAAA AFPMYGRVHCITGALQKLSLNSLQ VSEWRPVVEKLLMSYRLSTVVPVI QSSSPEGLIPMDTSESASRLQML NEIQPRDNDYFNQAKILKEHDSFD MKDLNASVVNIDTSTEIKGKEVKT DVT AQMVLVCCWRSMKEVALLGM LCQLLPMQVPESDGLLTVQVKEI GDYFKQHLLQSRHRGAFELAYTGFV KLTEVLNRCPNVSLQKLPQEWLWS VLEEIKCSDPSSKLCATRRSAGIPFYI QALLASEPKKGRMDLLKITMKELISL AGPTDDIQSTVPQVHALNLRALFRD TRLGENIIPYVADGAKAAILGFTSPV WAVRNSSTLFSALITRIFGVKRAKD EHSKTNRMTGREFFSRFPPELYPFL KQLETVANTVSDMGEPNRHPMSF LLLLVLERLYASPMGTSSALSMGP FVPFIMRCGHSPVYHSREMAARALV PFVMIDHIPNTIRLLSTLPSCTDQC FRQNHIGTLLQVFHLLQAYSDSKH GTNSDFQH ELDITVCTKAKLWLAK RQNPCLVTRAVYIDILFLTCLNRS AKDNQPVLESLGFWEVVRGIISSGSEL ITGFPWAFKVPGLPQYLQSLRLAIA AVWAAAASGERETNPVIFSFQLE SAFPEVRSLTLEALLEKFLAAASGLG EKGVPPLLCNMGEKFLLAMKENH PECFCKILKILHCMDPGEWLPQTEH CVHLTPKEFLIWTMDIASNERSEIQS VALRLASKVISHHMOTCVENRELIA AELKQWVQLVILSCEDHLPTE SRLA VVEVLTSTTFLFTNPHPILELQDTL ALWKCVLTLQSEEQAVRDAATETV TTAMSQENTCQSTEFQVQVDASIA LALALAVLCDLLQQWDQLAPGLPILL GWLLGESDDL VACVESMHQVEEDY LFEKAEVNFWAETLIFVKYLCXHLF CLLSKSGWRPPSPPEMLCHLQRMVS EQCHLLSQFFRELPPAAEFVKTEFT RLRIQEERTLACLRLLAFLLEGKEGED TLVLSVWDSYAESRQLTLPRTEAAC | False | False | 1.181 | False | False | 4.0 | False | 2.906 | False |