

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q64511	TOP2B_MOUSE	Mus musculus	DNA topoisomerase 2-beta	25.470095	NaN	S1224;T1280;S1324;S1328;S1330;S1332;S1346;T1358;S1363;S1376;S1387;T1390;S1400;T1408;S1411;S1428;S1439;S1441;S1448;S1453;S1460;S1509;S1511;S1513;S1537;S1539;T1562;S1563;S1568;T1596;S1600	39627609;37507081;34887587	MAKSSLAGSDGALTWVNNATKKEE LETANKNDSTKKLSEVRVYQKKTQL EHILLRPDITYIGSVEPLTQLMWVYDE DVGMNCREVTVPGLYKIFDEILVN AADNKQRDKNMTCKIVSIDPESNHS IWNNGKGIPIVVEHKVEKVVYPALIFG QLLTSSNYDDDEKKVTGGRNGYGAK LCNIFSTKFTVETACKEYKHSFKQT WMNMMKTSEAKIKHFDGEDYTCI TFQPDLSKFKMEKLDKDIVALMTRR AYDLAGSCKGVKVMFNGKLPVNG FRSYVDLYVKDKLDETVGALKVIHEL ANERWDVCLTLSEKGFQOISFVNSI ATTGGGRHVYVVDQVVSCLIEVVK KKNKAGVSVKPFQVKNHIWVFINCL IENPTFDSQTKENMTLQPKSFGSKC QLSEKFFKAASNCGIVESILNWKFK AQTQLNKKCSSVKYSKIKGIPKDDA NDAGGKHSLECTLILTEGDSAKSLA VSLGLVIGRDRYGVFPLRGKILNVRE ASHKQIMENAEINNIKIVGLQYKKS YDDAESLKTLYGKIMIMTDQDQDG SHIKGLLINFIIHNNWPSLLKHGFLEE FITPIVKASKNKQELSFYSIPEFDEW KKHIENQKAWKIKYKGLGTSTAKE AKEYFADMERHRLFRYAGPEDDAAI TLAFSKKIDDRKEWLTNFMEDRRQ RRLHGLPEQFLYGTATKHLTYNDFI NKEILIFSNSDNERISIPSLVDGFKPG QRKVLFTCFKRNDKREVKVAQLAGS VAEMSAYHHGEQALMMTIVNLAQN FVGSNNINLLQPIGQFGRHLHGKGD AASPRYIFTMLSSLARLLFPVADDNL LKFLYDDNQRVPEPEWYIPIIPMLIN GAEGIGTGWACKLPNYDAREIVNNV RRMLEGLDPHPMLPNYKNEFKGTIQ ELGQNYAVSGEIFVVDNRNTVEITEL PVRTWTQVYKEQVLEPMLNGTDKTP ALISDYKEYHTDITVKFVVKMTEEKL AQAEAAAGLHKVFKLQTLTNCNSMVL FDHMGCLKKYETVQDILKEFFDLRL SYYGLRKEWLVGMLGAESTKLNNO ARFILEKIQKITIENRSKDLIQMLV QRGYESDPVKAWKEAQEKAAEEEDS QNQHDDSSSDSGTSPGDFNYILN MSLWSLTKEKVEELIKQRDTKGREV NDLKRKSPDLWKEDLAAFVEELDK VEAQEREDILAGMSGKAIKGVGKP KVKKQLEETMPSPYGRRIVPEITAM KADASRLLKKKKGDPTTVVKVEF DEEFGTPEAGTGEETLTPSAPVNK GPKPKREKKEPGTRVRKTPSTGKT NAKKVKKRNPWSDDSKSESLEE AEPVVIPRDSLLRRAAERPKYTFDF SEEDDDAAAADDSDNDEELKVKAS PITNDGEDEFVPSDGLDKDEYAFSS GSKATPEKSSNDKKSQDFGNLFSF PSYSQKSEDDSAKFDSEEDTASVF APSFGLQTDKLPKVTAAKGGKPPS DTAPKAKRAPKQKKIVETINSDDSE FGIPKTTTPKGGKRAKKAASGSE NEGDYNPGRKPSKTAASKPKKTSFD QSDVDIFPSDFTSEPPALPRTGRAR KEVKYFAESDEEDVDVFAMFN	True	False	3.644	5.0	2.251	1.515	0.84