

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q6P4T2	U520_MOUSE	Mus musculus	U5 small nuclear ribonucleoprotein 200 kDa helicase	36.53089	S8	S17;S26;S225;T389;T709;T1428;T1765;S2002;T2131;S2133;S2135	33300544;36084651;29187734;39627609;37507081	MADV TARSLQY EYKANSNLVLQADR SLIDRTRRDEPTGEVLSLVGKLEGR MGDKAQRTPKPMQEEERRAKRRKR EDRHD MNKMGYTLSE GIDEMVG IYKPKTKETRETYEVLLSFIQAALGD QPRDILCGAADEVLA VLKNEKLRDK ERRREIDLLLQOTDDTRYHVLVNLG KKITDYGGDK EIQNMDDNIDETYG NVQFESDEEEGEDVYGEVREEASD DDMEGDEAVRCTL SANLVASGEL MSSKKKDLHPRDIDAFWLQRLSRF YDDAIVSQKKADEVLEILKTASDDRE CENQLVLLGFNTDFIKVLRQHRM MILYCTLLASAQSEPEKERIVGKMEA DPELSKFLYQLHETEKEDLIREERSR RERVQRSMDDLETMDLDQGGEA LAPRQVLDLEDLVFTQGS HFMANKR CQLPDGSFRRQRKGYEEVHPALKP KPFGESEQLLPVEKLPKYAQAGFEG FKTLNRIQSKLYRAALETDENLLCA PTGAGKT NVALMCMLEIGKHINM DGTINVDDFKIYIAPMRSLVQEMVG SFGKRLATYGITVAELTGDHQLCKEE ISATQIIVCTPEKWDIITRKGGERITY QLVRLIVLDEIHLHDDRGPVLEALV ARAIRNIEMTQEDVRLIGLSATLPNY EDVATFLRVDPKGLFYFDNSFRPV PLEQTYVGT EKKAIKRFQIMNEIYVE KIMEHAGKNQVLFVHSRKTGTGKTA RAIRDMCLEKDTLGLFLREGSASTE VLRTAEAEQCKNLEKDLLPYGFAIH HAGMTRVDRTLVEDL FADKHIQVLV STATLAWGVNLAHTVIKGTQVYSP EKGRWTELGALDILQMLGRAGRPOY DTKGE GILITSHGELQYLLSLLNOQL PIESQMVS KLPDMLNAEIVLGNVQN AKDAVNWLG YAYLYIRMLRSPTLYGI SHDDLKGDPLLDQRRLLDVHTAAL MLDKNNLVKYDKKTGNFQVTELGR I ASHYYITNDTVQTYNQLLKPTLSEIE LFRVFSLSSEFKNITVREEEKLELQK LLERVPIPVKESIEEPSAKINVLQAF ISQLKLEGFALMADMVVYVTSAGRL MRAIFEIVLNRGWAQLTDKTLNLCK MIDKRMWQSMCPLRQFRKLPPEVV KKIEKKNFPPERLYDLNHNEIGELIR MPKMGKTIHKYVHLFPKLELSVHLQ PITRSTLKVETITPDFQWDEKVVHGS SEAFWILVEDVSEVILHHEYFLLKA KYAQDEHLITFFVPVFEPLPPQYFIRV VSDRWLSCETQLPV SFRHLILPEKYP PPTELLDLQPLPV SALRNSAFESLYQ DKFPFFNPIQTQVFN TVYNSDDNVF VGAPTGS GKTICAEFAILRMLLQNSE GRCVYITPMEALAEQVYMDWYEFQ DRLNKKVLLTGETSTDLKLLGKGN I IISTPEKWDILSRRWKQRKNVQINIL FVVDEVHLIGGENGPVLEVICSRMR YISSQIERPIRIVALSSSL SNAKDVAH WLGCSATSTFN FHPNVRPVPLELHI QGFNISHTQTRLLSMAKPVYHAITK HSPKKPVIVFVPSRKQTRLT AIDILTT CAADIQRQRFLHCTEKDLIPYLEKLS DSTLKETLLNGVGYLHEGLSPMERR LVEQLFSSGAIQVVVASRSLCWGMN VA AHLVIIMDTQYYNGKIHAYVDYPI YDVLQMVGHANRPLQDDEGRCVIM CQGSKKDFFKFFLYEPLPVE SHLDH CMHDFNAEIVTKTIENKQDAVDYL TWTFLYRRMTQNP NYNLQGISHR HLSDHLSSELVEQTLSDLEQSKCISIE DEMDVAPLNLGMIAAYYIN YTTIEL FSMSLNAKTKVRGLIEIISNAAEYENI PIRHHEDNLLRQLAQKVPKLNPNK FNDPHVKTNLLLQAHL SRMQLSAEL QSDTEEILSKAIRLIQACVDVLSNG WLSPALAAMELAQMVTQAMWSKD SYLKQLPHFTSEHIKRCRDKGVESVF DIMEMEDEERNALLQLTDSQIADVA RFCNRYPNIELSYEVVDKDSIRSGGP	True	False	2.251	4.681	1.328	0.762	False

								VVVLVQLEREEVTPVIAPLFPQKR								
								EEGWVVVIGDAKSNSLISIKRLTLQQ								
								KAKVKLDFVAPATGGHNYTLYFMSD								
								AYMGCDQEKFSVDVKEAETDSDS								