

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extra regio
Q9QXL2	KI21A_MOUSE	Mus musculus	Kinesin-like protein KIF21A	26.986372	T287	S258;S524;S1227;S1231;S1241;S1660;T1662;S1671;S1101;S1102;S1207	33300544;30059200	MLGAADESSVRVAVRIRPQLAKEKIE GCHICTSVTPGEPQVFLGKDKAFTF DYVFDIDSQQEQIYTQCIKLEIGCFE GYNATVFAYGQTGAGKTYTMTGTGF VNIMEEQGIISRAVRHLFKSIDEKK TSAIKNGLPPPEFKVNAQFLELYNEE VLDLFDITRDIKAKKSNIRIHEDS TGGIYTVGVTRTRVNTPEPMMQCLK LGALSRTTASTQMNVOSSRSHAIFTI HVCQTRVCPQTDNAENATDNKLISES SPMNEFETLTAKFFHVDLAGSERLK RTGATGERAKEGINSINCGLLALGNVI SALGDKSKRATHVPYRDSKLRLLQ DSLGGNSQTIMIACVSPSDDRFMET LNTLKYANRARNIKNKVMVNDRA SQINALRSEITRLOMELMEYKTGK RIIDEEGVESINDMFHENAMLOTEN NNLRVRIKAMQETVDALARARITQLV SEQANQVLARAGEGNEEISNMIHSY IKEIEDLRAKLLSEAVNENLRKNLT RATARSFYFSSASSAFPTLSSDKETI EIIDLAKKDLEKLRKKEKKKKRLOK LEESGREERSVAGKDDNADTDQEK KEEKGVSEKENNELDVEENQEVSD HEDEEEEEDEEEEEDDIEGEESSE SDSESDKANYQADLANITCEIAIKQ KLIDELENSQKRLQTLKKQYEEKLM MLQHKIRDQLERDQVQLNGSVES YSEKAKKVKCEYEKHLHAMNKELO RLQTAQKEHARLLKNQSQYEQKLLK LQDDVMEMKKTVKVRLMKQMKKEEQ EKARLTERRRNREIAQLKDKQRKRD HQLRLEAQKRNOEVLRRKTEEVT ALRRQVRPMSDKVAGKVTRKLSSE SPAPDTGSSAASGEADTSRPQTQK MRIPVARVQALPTPTTNGTRKKYOR KGFTGRVFTSKTARMKWQLLERRVT DIIMQKMTISNMEADMNRLLRQRE ELTKRREKLSKRREKIVKESGEGDKS VANIIIEEMESLTANIDYINDSIADCO ANIMQMEEAKEEGETLDVTAVINAC TLTEARYLLDHFLSMGINKGLQAAQ KEAQIKVLEGRKQTEITSATQNQLL FHMLKEKALNPELDALLGHALQDL DGAPPENEESSSEEDGPLHSPGSEG STLSSDLMKLCGEVKPKNKARRRTT TOMELLYADSSEVASDTSAGDASLS GPLAPVAEGQEIGMNTTETSATSARD KELLAPSGLPSKIGSISRQSSSSEKVV PEPSPVTRRKAYEKADKPKAKEHKKH SDSGAETSLSPPSSPPSRPRNELNV FNRLTVPQGTSPVQKDSDESDESSL SEVHRGIINFPACKGVRASPLQCVH IAEGHTKAVLCVDSTDDLFTGSKD RTCKVWNLVTGQEIMSLGVHPNNV VSVKVCNYTSLVFTVSTSYIKVWDIR ESAKCIRLTSSGQVTLGEACASASTS RTVAIPSGEQINQIALNPTGTFLYAA SGNAVRMWDLKRFOSTGKLTGHLG PVMCLTVQISNGQDLIITGSKDHYI KMFVDTEGALGTVSPHNFEPHYD GIEALAIQGDNLFSGSRDNGIKKWD LAQKGLLQQVPAHAKDWVCALGLV PGHPVLLSGCRGGILKLVNVDTFVP VGEMRGHDSFINAICVNSTHVFTAA DDRTVRIWKAHNLQDGLSDTGDGL GEDIASN	False	False	3.961	2.579	1.166	0.693	0.759	2.761	0.846