	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	P50748	KNTC1_HUMAN	Homo sapiens	Kinetochore-associated protein 1	19.994096	NaN	T1035;S1045	37217939	MWNDIELLTNDDTGSGYLSVGSRKE HGTALYQVDLLVKISSEKASLNPKIQ ACSLSDGFIIVADQSVILLDSICRSLQ LHLVFDTEVDVVGLCQEGKFLLVGE RSGNLHLIHVTSKQTLLTNAFVQKA NDENRRTYQNLVIEKDGSNEGTYY MLLLTYSGFFCITNLQLLKIQQAIEN VDFSTAKKLQGQIKSSFISTENYHTL GCLSLVAGDLASEVPVIIGGTGNCAF SKWEPDSSKKGMTVKNLIDAEIIKGA KKFQLIDNLLFVLDTDNVLSLWDIYT LTPVWNWPSLHVEEFLLTTEADSPS SVTWQGITNLKLIALTASANKKMKN LMVYSLPTMEILYSLEVSSVSSLVQT GISTDTIYLLEGVCKNDPKLSEDSVS VLVLRCLTEALPENRLSRLLHKHRF AEAESFAIQFGLDVELVYKVKSNHIL EKLALSSVDASEQTEWQQLVDDAKE NLHKIQDDEFVVNYCLKAQWITYET TQEMLNYAKTRLLKKEDKTALIYSD GLKEVLRAHAKLTTFYGAFGPEKFS GSSWIEFLNNEDDLKDIFLQLKEGN LVCAQYLWLRHRANFESRFDVKML ESLLNSMSASVSLQKLCPWFKNDVI PFVRRTVPEGQIILAKWLEQAARNLE LTDKANWPENGLQLAEIFFTAEKTD ELGLASSWHWISLKDYQNTEEVCQL RTLVNNLRELITLHRKYNCKLALSDF EKENTTTIVFRMFDKVLAPELIPSILE KFIRVYMREHDLQEEELLLLYIEDLL NRCSSKSTSLFETAWEAKAMAVIAC LSDTDLIFDAVLKIMYAAVVPWSAAV EQLVKQHLEMDHPKVKLLQESYKL MEMKKLLRGYGIREVNLLNKEIMRV VRYILKQDVPSSLEDALKVAQAFMLS DDEIYSLRIIDLIDREQGEDCLLLLKS LPPAEAEKTAERVIIWARLALQEEPD HSKEGKAWRMSVAKTSVDILKILCDI QKDNLQKKDECEEMLKLFKEVASL QENFEVFLSFEDYSNSSLVADLREQ HIKAHEVAQAKHKPGSTPEPIAAEVR SPSMESKLHRQALALQMSKQELEA ELTLRALKDGNIKTALKKCSDLFKYH CNADTGKLLFLTCQKLCQMLADNV PVTVPVGLNLPSMIHDLASQAATICS PDFLLDALELCKHTLMAVELSRQCQ MDDCGILMKASFGTHKDPYEEWSY SDFFSEDGIVLESQMVLPVIYELISSL VPLAESKRYPLESTSLPYCSLNEGDG LVLPVINSISALLQNLQESSQWELAL RFVVGSFGTCLQHSVSNFMNATLSE KLFGETTLVKSRHVVMELKEKAVIFI RENATTLLHKVFNCRLVDLDLALGY CTLLPQKDVFENLWKLIDKAWQNY DKILAISLVGSELASLYQEIEMGLKF RELSTDAQWGIRLGKLGISFQPVFRQ HFLTKKDLIKALVENIDMDTSLILEY CSTFQLDCDAVLQLFIETLLHNTNA GQGQGDASMDSAKRRHPKLLAKAL EMVPLLTSTKDLVISLSGILHKLDPY DYEMIEVVLKVIERADEKITNININQ ALSILKHLKSYRRISPPVDLEYQYML EHVITLPSAAQTRLPFHLIFFGTAQN FWKILSTELSEESFPTLLLISKLMKF SLDTLYVSTAKHVFEKKLKPKLLKLT QAKSSTLINKEITKITQTIESCLLSIVN PEWAVAIAISLAQDIPEGSFKISALKF CLYLAERWLQNIPSQDEKREKAEAL LKKLHIQYRRSGTEAVLIAHKLNTEE YLRVIGKPAHLIVSLYEHPSINQRIQN SSGTDYPDIHAAAKEIAEVNEINLEK VWDMLLEKWLCPSTKPGEKPSELFE LQEDEALRRVQYLLLSRPIDYSSRML FVFATSTTTTLGMHQLTFAHRTRAL QCLFYLADKETIESLFKKPIEEVKSYL RCITFLASFETLNIPITYELFCSSPKE	None	None	None	None	None	None	None	None	None

								GMIKGLWKNHSHESMAVRLVTELC LEYKIYDLQLWNGLLQKLLGFNMIP YLRKVLKAISSIHSLWQVPYFSKAWQ RVIQIPLLSASCPLSPDQLSDCSESLI AVLECPVSGDLDLIGVARQYIQLELP AFALACLMLMPHSEKRHQQIKNFL GSCDPQVILKQLEEHMNTGQLAGFS HQIRSLILNNIINKKEFGILAKTKYFQ MLKMHAMNTNNITELVNYLANDLS LDEASVLITEYSKHCGKPVPPDTAPC EILKMFLSGLS									