	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	pl m
0	Q6DFV5	HELZ_MOUSE	Mus musculus	Probable helicase with zinc finger domain	29.804174	S1260;S1668	S248;T1163;S1636;S1760;S1763;S1788	30059200;36852467;35822049	MEDRRAERSCEQACASLQRQDYDM ALQHCTDALLSLGQYSMADFTGPCP VEVERIKIESLLYRIASFLQLKNYGQA DEDCRHVLGEGLAKGERAFRAVLCC MQLKGKLQLVSSILAKSLSGESLNG MVTKDLTRLKTLLTETETATSNVLSG CHVEDLDEGSCNGWHFRPPPRGITS SEEYTLCKRFLEQGICRYGAQCTSAH SQEELAEWQKRYASRLIKLKQQSEN KQLSGSYMETLIEKWMSSLSPEKVL SECIEGVQVEHSPDLSVTVNTKKSH QTWTFALTCKPARMLYRVALLYDAH RPHFSIIAISAGDSTTQVSQEVPENC QEWIGGKMAQNGLDHYVYKVGIAF NTEIFGTFRQTIVFDFGLEPVLMQRV MIDAASTEDLEYLMHAKRQLVTTAK RWDSSSKTIVDFEPNETTDLEKSLLI RYQIPLSADQLFTQSVLDKSLTKTNY QARLHDLLYIEEIAQYKEVSRFNLKV QLQILASFMLTGVSGGAKYAQNGQL FGRFKLTETLSEDTLAGRLVMTRVN AVYLLPVPKEKLVQSQGTKEKVYEAT IEEKTKDYVFLRISRECCEELSLRPD CDIQVELQFQLNRLPLCEMHYALDR IKDNAVLFPDISMTPTIPWSPNRQW DEQLDPRLNAKQKEAVLAITTPLSIQ LPPVLIIGPYGTGKTFTLAQAAKHILQ QQETRILICTHSNSAADLYIKDYLHP YVEAGNPQARPLRVYFRNRWVKTV HPVVHQYCLISSTQSTFQMPQKEDIL KHRVVVVTLSTSQYLCQLDLEPGFFT HVLLDEAAQAMECETIMPLALATKN TRIVLAGDHMQLSPFVYSEFARERN LHVSLLDRLYEHYPAEFPCRILLCEN YRSHEAIINYTSELFYEGKLMASGKQ PAHKDFYPLTFFTARGEDVQEKNST AFYNNAEVFEVVERVEELRRKWPVA WGKLDDGSIGVVTPYADQVFRIRAEL RKKRLSDVNVERVLNVQGKQFRVLF LSTVRTRHTCKHKQTPIKKKEQLLE DSTEDLDYGFLSNYKLLNTAITRAQS LVAVVGDPVALCSIGRCRKFWERFIA LCHENHSLHGITFEQIKAQLEALELK KTYVLNPLAPEFIPRALRLQHSGNSS RQQQSPPKVKSLYHPQSDHFQSDGI VQPNPSVLIGNPIRAYTPPPPLGPHP NLGKSPSPVQRIDPHTGTSILYVPAV YGGNVVMSVPLPVPWTGYQGRFAV DPRIITHQAAMAYNMNLLHTHGRG SPIPYGLGHHPPVSLGQPQSQHAEK DQQEQNRNGKTDTNNPGPEINKIRT PEKKPTEPKQVDLESNPQNRSPESR PGVVYSNTKFPRKDHLNPRHINNLP LPAPHAQYAIPSRHFHPLPQLPRPPF PASQPHTLLNQQQNNLPEQPNQMA PQPNQVAPQPNQMTPQPNQVAPQP NQVVQQQSQAPPQAPQPAPQLSPAF QAGPTNAFFNNAVAHRPQSPAAEAV GPEQPPPPGLPDGHSPLRAITQPGPI LASPLNNFVDESSPGLPIEEALDGVH GSVALETLRQQQARLQQWSEHHAY LSQGGIPYSHHHHPHLPHLPHTPIG LHQPPVRAEWKVAGRADDETETTFS RFQDLLRELSHRDQGDTGELAEMP PPQSRLLQYRQVQPRSPPAVPSPPSS TDHSSQFANFNDSSRDIEVANSPAF PQRLPPQLFGSPFSLPSEHLAPPPLK YLAPEGAWNFANLQQNHLIGPGFPY GLPPLPPRPPQNPFIHIQNHQHAAG QEPFHPLSSRTVSASSLPSLEEYEPR GPGRPLYQRRISSSSAQPCVEEASAP QDSLAQGKESQGHSNPPAFNFPAPE SWANTTSSAPYQNIPCNGSSRTSQP RELIAPPKTVKPPEDQLKPESGEVSS SFNYSMLQHLGQFPPLMPNKQIAES ANCSSQQSPAGSKPAMSYASALRAP PKPRPPPEQAKKGSDPLSLLQELSLG SSPGSNGFYSYFK	None	None	None	None	None	None	None	No