

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	p
Q9JHU4	DYHC1_MOUSE	Mus musculus	Cytoplasmic dynein 1 heavy chain 1	27.903887	NaN	S68;S1228;S4160;T4364;S4366	39627609;39927985;37507081;33300544	MSEPGGGEDGSAGLEVSAVQNVAD VAVLQKHRLRKLVPLLLEDGGDAPAA LEAALEEKSALEQMRKFLSDPQVHT VLVERSTLKEVDGDEGEEKEFISYN INIDIHYGVKSNLAFIKRAPVIDADK PVSSQLRVLTLSEDSPYETLHFSFN AVAPFFKSYIRESGKADRRDGDKMAP SVEKIAELEMGLLHLQONIEIPEISL PIHPITNVAKQCYERGEKPKVTDG DKVEDPTFLNQLQSGVNRWIREIQ VTKLDRDPASGTALQEISFWLNLER ALYRIQEKRESPEVLLTDLKHKGR FHATVDFDITGLKQALETVNDYNP LMKDFPLNDLLSATELTKIRQALVAI FTHLRKIRNTKYPQIRALRLVEAISRD LSSQLLKVGLTRKLMHVAYEEFEKV MVACFEVFTWDDYEKLVLLRDI VKRKREENLKMVWRINPAHRKLQA RLDQMRKFRROHEQLRAVIVRVLRLP QVTAVAQQNOGEAPEPQDMKVAEV LFDAADANAIEEVNLAYENVKEVDG LDVSKEGTEAWAAMKRYDERIDRV ETRITARLDRDQLGTAKNANEMFRIF SRFNALFVRPHIRGAIREYQTQLIQ VKDDIESLHDKFKVQYQSQACKMS HVRDLPPVSGSIIWAKQIDRQLTAYM KRVEDVLGKGWENHVEGQKLDG DSFRMKNLTOEIFDDWARKVQORN LGVSGRIFTIESARVRGRTGNVLLK VNFLPEIITLSKEVRNLKWLGFVRVPL AIVNKAHQANQLYPPFAISLIESVRTY ERTCEKVEERNITISLLVAGLKKEVQA LIAEGIALVWESYKLDPYVQRLAETV FNFQEKVDDLIIIEEKIDLEVRSL CMYDHTKTFSEILNRVQKAVDDLNLH SYSNLPWVWVKLMEIERILGVRLQA GLRAWTQVLLGQAEDKAEDMDTD APQVSHKPGGEPKIKNVHELRLITN QVIYLNPIIEECRYKLYQEMFAWKM VVLSPRIQSORYOVGVHYELTEEEK FYRNALTRMPDGPVALEESYSAVMG IVTEVEQYVWVWVQVCLWDMQAE NIYNRLGEDLNKQVALLVQIRKARG TFDNAETKKEFGPVVIDYGKVQSKV NLKYDSWHKEVLSKFGQMLGNSNMT EFHSQISKSRQEQLEQHSVDTASTSD AVTFITYVQSLKRRKIKQFEKQVELYR NGORLLEKQRFQPPSWLYIDNIEG EWGAFNDIMRRKDSAIQOQVANLQ MKVQEDRAVESRTTDLTDWEKTK PVTGNLRPEEALQALTIYEGKFGRLK DDREKCAKAKEALELTDGLLSGSE ERVQVALEELQDLKGVWSELSKVW EQIDOMKEQPWVSVQPRKLRQNL GLLNQKNFPARLRQYASYEFVQRL LKGMYKINMLVIELKSEALKDRHWK QLMKRLHVNVVSELTLGQIWDVD LQKNEAVVKDVLVAQGEMALEEF KQIREVWNVYELDLVNYQNKCRLLR GWDLDFNKVKEHINSVSAMKLSPPY KVFEEDALSWEDKLNRMALFDVWI DVORRWVYLEGIFTGSADIKHLLPVE TQRFQISISTEFLALMKKVSXSPLVM DVLNIQGVQVRSLELADLLGKIQKAL GEYLERERSSFRFYFVGEDLLEII GNSKNVAKLQKHFKKMFAGVSSIIL NEDNSVVLGSSREGEVFMFKTPVSI TEHPKINEWTLVEKEMRVTLAKLL AESVTEVEIFGKATSIDPNTYITWIDK YQAQLVLSAQIAWSENVENALS GGGGDVGPLQSVLSNVEVTLNVLAD SVLMEQPPLRRRKLHLITELVHQR DVTRSLIKSKIDNAKSFELWLSQMR YFDPKQTDVLLQQLSIQMANAKFNYG FEYLVQVQDKLVQPLTDRCYLTMTQ ALEARLGGSPFGPAGTGKTESVKAL GHQLGRFVLVFNCDFTDFQAMGRI FVGLCQVQVQCFDFNRLRLEERML SAVSQQVQCIQEQALREHSNPNYDKT SAPITCELLNKQVKSVPDMAILFITMN	False	False	1.781	1.453	False	False	False	

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 DRQLIAQVMLYSQGFRTAEVLANKI
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