

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q14204	DYHC1_HUMAN	Homo sapiens	Cytoplasmic dynein 1 heavy chain 1	11.709756	T260;S1828;S1835;S2384;T3531;S3533;T3928	S70;S1230;S4162;T4366;S4368	34229054;29237092;23301498;29351928;37217939;30379171;33214551;16408927;40596516;38665916;26374642;34725712;32119511;40914422;34019948;35138101;38253038	MSEPGGGGGEDGSAGLEVSAVQNV ADVSVLQKHLRRLKLVPLLEDGGEAP AALEAALEEKSALEQMRKFLSDPQV HTVLVERSTLKEDVGEDEGEEKEFIS YNINIDHYGVKSNLSLAFIKRTPVIDA DKPVSSQLRVLTLSSESPYETLHSFI SNAVAPFFKSYIRESGKADRDGDKM APSVKKAIAELEMGLLHLQQNIEIPE ISLPIHPMITNVAKQCYERGEKPKVT DFGDKVEDPTFLNQLQSGVNRWIRE IQKVTKLDLDRDPASGTALQEISFWLNL ERALYRIQEKRESPEVLLTLDILKHG KRFHATVSFDTDTGLKQALETVNDY NPLMKDFPLNDLLSATELTKIRQAL VAIFTHLRKIRNTKYPQIRALRLVEAI SRDLSSQLLKVGLTRKLMHVAYEEF EKVMVACFEVFTWDDYEYKLVL LRDIVKRKREENLKMVWRINPAHRK LQARLDQMRKFRQHEQLRAVIVRV LRPQVTAVAQQNOGEVPEPODMKV AEVLFDAADANAIEEVNLAYENVKE VDGLDVSKEGTEAWEAAMKRYDERI DRVETRITARLRDQLGTAKNANEMF RIFSRFNALFVRPHIRGAIREYQTLI QRVKDDIESLHDKFKVQYPQSQACK MSHVRDLPPVSGSIWAKQIDRQLTA YMKRVEDVLGKGWENHVEGQKQKQ DGDSEFRMMLNTQEIFDDWARKVQQ RNLGVSGRIFTIESTRVRGRTGNVLK LKVNFLPEIITLSKEVRNLKWLGRV PLAIVNKAHQANQLYPPAISLIESVRT YERTCEKVEERTISLLVAGLKKEVQ ALIAEGIALVWESYKLDPYVQRLAET VFNFAQEKVDDLLIIEEKIDLEVRSL CMYDHTFTSEILNRVQKAVDDLNLH SYSNLPWVWVKLMEIERILGVRLQA GLRAWTQVLLGQAEDKAEDMDMTD APQVSHKPGGEPKIKNVVHELRLITN QVIYLNPPIEECRYKLYQEMFAWKM VVLSLPRIQSQRYQVGVHYELTEEEK FYRNALTRMPDGFVALEESYSAVMG IVSEVEQYVWVWVQVCLWDMQAE NIYNRLGEDLNKQVALLVQIRKARG TFDNAETKKEFGPVVIDYGKVQSKV NLKYDSWHKEVLSKFGQMLGNSNMT EFHSQISKSRQELEQHSVDTASTSD AVTFITYVQSLKRRKIKQFEKQVELYR NGORLLEKQRFQFPPSWLYIDNIEG EWGAFNDIMRRKDSAIQOQVANLQ MKIVQEDRAVESRTDLDLTDWEKTK PVTGNLRPEEALQALTIYEGKFGRLK DDREKCAKAKEALELTDGLLSSGSE ERVQVALEELQDLKGVWSELKVVW EQIDQMKQPWVSVQPRKLRQNL ALLNQLKSFPARLROYASYEFVQRL KGYMKINMLVIELKSEALKDRHWK QLMKRLHVNVVSELTLGQIWDVD LQKNEAIVKDVLLVAQGEALEEFL KQIREVWNTYELDLVNYQNKCRLLR GWDLDFNKVKEHINSVSAMKLSPPY KVFEEDALSWEDKLNRMALFDVWI DVQRRWVYLEGIFTGSADIKHLLPVE TQRFQISISTEFLALMKKVKSPVLM DVLNIQGVQVRSLERLADLLGKIQKAL GEYLERERSSFRPFYVFGEDLLEII GNSKNVAKLQKHFKKMFAGVSSIIL NEDNSVVLGSSREGVEVMFKTPVSI TEHPKINEWLTLVEKEMRVTLAKLL AESVTEVEIFGKATSIDPNTYITWIDK YQAQLVLSAQIAWSENVTALSSM GGGGDAAPLHVSLSNVVETLNLVAD SVLMEQPPRRRRLKLEHLITELVHQR DVTRSLIKSKIDNAKSFEWLSQMRF YFDPKQTDVLOQLSIQMANAKFNYG FEYLVQDKLVQPLTDRCYLTMTO ALEARLGGSPFGPAGTGKTESVKAL GHQLGRFVLVFNCDFTDFQAMGRI FVGLCQVGAWGCFDEFNRLEERML SAVSQQVQCIQALREHSNPNYDKT SAPITCELLNKQVKVSPDMAIFITMN	True	False	4.683	2.834	1.775

PGYAGRSNLPDNLKKLFRSLAMTKP
 DRQLIAQVMLYSQGFRTAEVLANKI
 VPPFKLCDEQLSSQSHYDFGLRALK
 SVLVSAGNVKRERIQKIKREKEERGE
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 PKLVAEDIPLLFSLSDVFPVQYHR
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 EEVGGMWVEKVLQLYQITQINHGL
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 DDNKLTLTPNGERLSLPPNVRIMFE
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 HEALRLFQDRLVEDEERRWTDENID
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 MSVKEDLDKVEPAVIEAQNVAKSJK
 KQHLVEVRSMANPPAAVKLALESIC
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 ADMMLKRVEPLRNLQKLEDDAKDN
 QQKANEVEQMIRDLEASIARYKEYE
 AVLISEAQAIKADLAAVEAKVNRSTA
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 LFTTWSHHLQQANIQFRTDIARTEY
 LSNADERLRWQASSLPADDLCTENA
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 RDPTVEFPDLCRVTFVNFVTRSS
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 SSPEQTVPYLWSEETPATPIGQAIHR
 LLLIQAFRPDRLLAMAHMFVSTNLG
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