

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi appa
Q00610	CLH1_HUMAN	Homo sapiens	Clathrin heavy chain 1	18.813423	S97;S944;T1180	S67;T105;T184;T394;T634;T899;S1167;T1206;S1229;T1477;T1487;S1494	34725712;35083852;38665916;30379171;30397120;39302247;23301498;33214551;35138101;33465208;32119511;34019948;27655845;26853435;36240223;37217939;16408927;18369606;30444036	MAQILPIRFOEHLQLQNLGINPANIGFSTLTMESDKFCIREKVGGEQAQVVIIDMNDPSNPPIRRPISADSAIMNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSMEGESQPVKMFDRHSSLAGCQIINRTDAKQKWLTLTGISAQONRVVGAMQLYSVDRKVSQPIEGHAASFAQFKMEGNAEESTLFCFAVRGQAGGKLHIIIEVGTPTGNQPFKKAVDVFFPPEAQNDFPVAMQISEKHVVFLITKYGYIHLVDLETGTCIYMNRISGETIFVTAPHEATAGIHGVRNRKQVLSVCVEEENIIPYITNVLQNPDLALRMAVRNNLAGAEELFARKFNALFAOQNYSEAAKVAANAPKGIIRTPDTIRRFQSVPAQPGQTSPLLYQYFGILLDQGLNKYESLELCRPVLQQGRKQLEKWLKEDKLECSEELGDLVKSVDPTLALSYYLRANVPNKVIQCFQVQVOKIVLYAKKVGYPDPWIFLLRNVMRISPDQGGQFAQMLVQDEEPLADITQIVDVFMEYNLIQOCTAFLLDALKNNRPSEGPLQTRLL EMNLMHAPQVADAILGNQMFTHYDRAHIAQLCEKAGLLQRALEHFTDLYDIKRAVVHTHLLNPEWLNVYFGSLVEDSLECLRAMLSANIRONLQICVQVASKYHEQLSTQSLIELFESFKSFEGLFYFLGSIWNFSQDPDVHFKYIQAACKTGQIKEVERICRESNCYDPERVKNF LKEAKLTDQLPIIVCDRDFVVDHLVLYLYRNNLQKYIEYVQKVNPSRLPVVIGGLLDVDCSEDIKNNLILVVRGQFSTDELVAEVEKRNRLKLLPWLEARIHEGCEEPATHNALAKIYIDSNNNPE RFLRENPHYDSRVVGVKCEKRDPHLACVAYERGQCDELEINVCNENSLFKSLSRYLVRKDPPELWGSVLLSESNPYRRPLIDQVVQTALSETQDPPEEVSVTVKAFMTADLPNELIELLEKIVLDNSVSEHRNLQNLILLITAIKADRTRVMEYINRLDNYDAPDIANIAISNELFEEFAIFRKFVNTSAVQVLEHIGNLDRAYEFAERCNEPAVWSQLAKAQLQKGMVKEAIDSYKADDPSSYMEVVQAANTSGNWEELVKYLQMARKKARESYYVELIFALAKTNRLAELEEFINGPNNAHIQQVGDRCYDEKMYDAKLLYNNVSNFGRLASTLVHLGEYQAQVDFGAR KANSTRTWKEVCFACVDGKEFRLAQMCGLHIVVHADELEELINYYQDRGYFEELITMLEAALGLERAHMGMTFELAILYSKFKPKMREHLELFWSRVNI PKVLRAAEQAHLWAEVFLYDKYEEYDNIITMMNHPTDAWKEGQFKDII TKVANVELYYRAIQFYLEFKPLLLNDLLMVLSPRLDHTRAVNYFSKVQQLPLVKPYLRSVQNHNNKSVNESLNNL FITEEDYQALRTSIDAYDNFDNISLQRLEKHELIEFRRIAAYLFGNNRWKQSVELCKKDSLYKDAMQYASESKDTELAELLQWFLQEKRECFGACLFTCYDLLRPDVVLETAWRHNIMDFAMPYFIQVMKEYLTKVDKLDASESLRKEEQATETQPIVYQGPQLMLTAGPSVAVPPQAPFGYGTAPPYQGPQPGFGYSM	True	True	4.823	2.461	1.878	2.06	4.507