

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracel region
P11442	CLH1_RAT	Rattus norvegicus	Clathrin heavy chain 1	26.1995	NaN	S67;T105;T184;T394;T634;T899;S1167;T1206;S1229;T1477;T1487;S1494	38843836;34502162	MAQILPIRFQEHLLQLNLGINPANIG FSTLTMESDKFICIREKVGEOAQVVII DMNDPSPNPIRRPISADSAIMNPASK VIALKAGKTLQIFNIEMKSKMKAHT MTDDVTFWKWISLNTVALVTDNAVY HWSMEGESQPVKMFDRHSSLAGC QHNYRTDAKQKWLTLTGISAQQNRV VGAMQLYSVDRKVSQPIEGHAASFA QFKMEGNAEESTLFCFAVRGQAGG KLHIEVGTPTGNQPPFKKAVDVFF PPEAQNDFPVAMQISEKHDVFLIT KYGYIHLVDLETGTCIYMNRRISGETIF VTAPHEATAGIIGVNRKGVLSVCVE EENIIPYITNVLQNPDLALRMVRRNN LAGAEELFARKFNALFAQGNYSAAA KVAANAPKGLRTPDTIRRFQSVPAQ PGQTSPLLQYFILLDQQLNKYESL ELCRPVLQGRKQLLEKWLKEDKLE CSEELGDLVKSVDPTLALSVMYLRANV PNKVIQCFEAETGOVQKIVLYAKKVG TPDWIFLLRNVMRISPDQGOQFAQ MLVQDEEPLADITQIVDFMEYNLIQ QCTAFLLDALKNNRPSEGPLQTRLL EMNLMHAPQVADAILGNQMFTHYD RAHIAQLCEKAGLLQRALEHFTDLY DIKRAVVHHTLLNPEWLNVNYFGSLS VEDSLECLRAMLSANIRQNLQIWWQ VASKYHEQLSTQSLIELFESFKSFEG LFYFLGSIVNFSQDPDVHFQYIQAAC KTGQIKEVERICRESNCDPERVKNF LKEAKLTDQLPLIIVCDFDFVHDLV LYLYRNSLQKYIEIYVQKVNPSRLPV VIGLLDVCSEDEVKLNLLVVRGQF STDELVAEVEKRNRLKLLPWLEARI HEGCEEPATHNALAKIYIDSNNNPE RFLRENPHYDSRVVGKYCEKRDPHL ACVAYERGQCDLELINVCNENSLFK SLSRYLVRKDPPELVGWSVLESNPY RRPLIDQVVQTALSETQDPEEVSVTV KAFMTADLPNELIELLEKIVLDNSVF SEHRNLQNLILLTAIKADRTRVMEYI NRLDNYDAPDIANIAISNELFEEAFA IFRKFDVNTSAVQVLIHIGNLDRAV EFAERCNEPAVVWSQLAKAQLQKGM VKEAIDSYIKADDPSSYMEVVQAANT SGNWEELVKYLQMARKKARESYVE TELIKALAKTNRLAELEEFINGPNNA HIQOVGDRCYDEKMYDAAKLLYNN VSNFGRLASTLVHLGEYQAAVDGAR KANSTRTWKEVCFACVDGKEFRLAQ MCGLHIVVHADELEELINYYQDRGY FEELITMLEAALGLERAHMGMTTEL AILYSKFKPQKMRHELELFWSRVNI PKVLRAAEQAHLWAEVFLYDYKYE YDNIHTMMNHPTDAWKEGQFKDII TKVANVELYYKAIQFYLEFKPLLLND LLMVLSPRLAHTRAVNYFSKVKQLP LVKPYLRSVQNHNNKSVNESLNNL FITEEDYQALRTSIDAYDNFDNISLA QRLEKHELIEFRRIAAYLFGNNRW KQSVELCKKDSLYKQDAMQYASESKD TELAEELLQWFLQEEKRECFGACLF TCYDLLRPDVVLETAWRHNMDF MPYFIQVMKEYLTKVDKLDASESLR KEEEEQATETQPIVYGQPLMLTAGP SVAVPPQAPFGYGYTAPPYGPQPGF GYSM	True	True	4.077	4.429	1.574	1.69	3.319	5.0	1.908