

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellul region
Q9JIX5	CHD8_RAT	Rattus norvegicus	Chromodomain-helicase-DNA-binding protein 8	23.439218	NaN	S432;S553;S562;S1420;S1424;S1976;S1978;T1993;S1995;S1997;S2008;S2068;S2070;S2182;S2200;S2202;T2204;S2211;T2215;S2223;S2519	38843836	MADPIMDLFDDPNLFGDLSLTDSSFNQVTDPIEEALGLPSSLDLSDQMNQDGGSGDVGNSASDLVPPPEETAS TELPKESTAPAPESLTLHDYTTQPTS QEQAQPVLTSTPTSGLLQVSKSQ EILSQGNPFMGVSATAVSPSNTGGQ PSQSAPKIVLKAPPNSSVTGAHVAQI QAQGITSTAQPLVAGTANGGKVTFT KVLGTGTPLRPGVSIVSGNTVLATKVP GNQAAVQRIVQPSRPVKQLVLQPVK GSAPAGNPGATGPPLKPAVTLTSTPA QGSEKRITLVLQQPQSGGPGQHRHV VLGSLPGKIVLQGNQLAALTOAKSA QGQPAKVVTIQLQVQPPQKQIIVPQ PPSSQPQPFPSSAQPLTSSVQQAQ IMGPGQNPQRLSVPLKMLVLPQA GSSQGASSGLSVVKVLSASEVAALSS PASCAPHTAGKTGMEENRRLEHQK KQEKANRIVAEIARARARGEQNIPR VLNEDELPSVRPEEEGKRRRKKSS GERLKEEKPKKSKTAAASKTKGKSK LNTITPVVGKRRKRTSSDNDVDEV MPAQSPREDEESSIQRRSNRQVKR KKYTEDLDIKITDDEEEEVDTVGP KPEPILPEPVPEPDGETLPSMQFFVE NPSEEDAIVDKVLSMRVVKKELPS GOYTEAEFFVKYKNYSYLHCEWAT ISQLEKDKRIHQKLRFKTKMAQMR HFFHEDEEFPNPDYVEVDRILDESH SVDKDNGEFVYIYLVKWCCLPYEDS TWELKEDVDEGKIREFKRIQSRHPE LKRVRNPQANAWKKLELSHEYKNR NQLREYQLEGVNWLFFNWNQRON CILADEMGLGKTIQSIQAFLEQVYVNG IHGPFVIAPLSTITNWEREFNTWTE MNTIVYHGSLASRQMIQYEMYCK DSRGRILPGAYKFDALITTFEMILSD CPELREIEWRCVHIDEAHLKRNRC KLLDSLKHMDLEHKVLLTGTPLQNT VEELFLLHFLFLEPSQFSEFLKDF GDLKTEEQVQKLQAILKPMMLRRLK EDVEKNLAPKQETIIEVELTNIQKKY YRAILEKNFSFLSKGAGHTNMPNLL NTMMELRKCENHPYLINGAEKIL MEFREACHIIIPQDFHLQAMVRSAGK LVLIDKLLPKLKAGGHKVLIFSQMVR CLDILEDYLIQRRYLYERIDGRVRGN LRQAADRFSKPDSDRFVLLCTRAG GLGINLTAADTCIIFSDWNPQNDL QAQARCHRIGQSKAVKVYRLITRNSY EREMFDKASLKLGLDKAVLQSMMSG RDGNITGIQQFSKKEIEDLLRKGAYA AIMEEDDEGSKFCEEDIDQILLRRTT TITIESEGGKSTFAKASFVAENRTDI SLDDPNFWQKWAKKADLMDLLNS KNNLVIDTPVRKQTRHFSTLKDDD LVEFSDLESEDDERPRRRHRHHT YGRDTCFRVEKHLVYGWGRWRDIL SHGRFKRRMTERDVETICRAILVYCL LHYRGDENIKSFIWDLISPAENGKTK ELQNHSGLSIPVPRGRKGKVKVKSQS TFDIHKADWIRKYNPDTLFDQESYK KHLKHQCNKVLRLVRMLYLRQEV GDQAEKVLGGAIASEIDIWFPVVDQL EVPTTWWDSEADKSLIGVFKHGYE KYNTMRADPALCFLEKAGRPDDKAI AAEHRVLDNFSDLVEGIDFDKDCED PEYKPLQGPPKDPDDEGDPLMMMD EISVIDGDEAPVTQPGHLFWPPG SALTARLRLVTAYQRSYKREQMKIE AAERGDRRRRRCEAAFKLKEIARRE KQQRWTRREQTDYFRVSTFGVEYD PDNMQFHWDRFRIFARLDKKTDES LTKYFHGFVAMCRQVCRLPPAAGDE PPDPNLFIEPTEERASRTLYRIELLR RLREQVLCHPLLEDRLALCOPPGLE LPKWWEPVRHDGELLRGAARHGVS QTDCNIMQDPDFSFLAARMNMQN HQAGASAAASLRCSTPLHQQCTSR TASPSLRLPDPVPAEKSPENAVQVPS	True	False	2.364	5.0	1.217	False	False	1.344	1.202

