	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitoch
0	Q9HCK8	CHD8_HUMAN	Homo sapiens	Chromodomain-helicase-DNA-binding protein 8	14.730353	S101;S113;S117;S123;T171;T184;S256;T1338;T1340;T1342;S1345;S2518;S2519;T2522;T2523;T2528	S432;S553;S562;S1420;S1424;S1976;S1978;T1993;S1995;S2008;S2046;T2051;S2069;S2071;S2182;S2200;S2202;T2204;S2211;T2215;S2223;S2519	38665916;34019948;33214551;39302247;30379171;39531497;40307207;32119511;35138101;35132862;40136647;29351928;39534244;35254053;37340703	MADPIMDLFDDPNLFGLDSLTDDSF NQVTQDPIEEALGLPSSLDSLDQMN QDGGGGDVGNSSASELVPPPEETAP TELSKESTAPAPESITLHDYTTQPAS QEQPAQPVLQTSTPTSGLLQVSKSQ EILSQGNPFMGVSATAVSSSSAGGQ PPQSAPKIVILKAPPSSSVTGAHVAQI QAQGITSTAQPLVAGTANGGKVTFT KVLTGTPLRPGVSIVSGNTVLAAKVP GNQAAVQRIVQPSRPVKQLVLQPVK GSAPAGNPGATGPPLKPAVTLTSTPT QGESKRITLVLQQPQSGGPQGHRHV VLGSLPGKIVLQGNQLAALTQAKNA QGQPAKVVTIQLQVQQPQQKIQIVPQ PPSSQPQPQQPPSTQPVTLSSVQQA QIMGPGQSPGQRLSVPVKVVLQPQA GSSQGASSGLSVVKVLSASEVAALSS PASSAPHSGGKTGMEENRRLEHQK KQEKANRIVAEAIARARARGEQNIPR VLNEDELPSVRPEEEGEKKRRKKSA GERLKEEKPKKSKTSGASKTKGKSK LNTITPVVGKKRKRNTSSDNSDVEV MPAQSPREDEESSIQKRRSNRQVKR KKYTEDLDIKITDDEEEEEVDVTGPI KPEPILPEPVQEPDGETLPSMQFFVE NPSEEDAAIVDKVLSMRIVKKELPSG QYTEAEEFFVKYKNYSYLHCEWATIS QLEKDKRIHQKLKRFKTKMAQMRH FFHEDEEPFNPDYVEVDRILDESHSI DKDNGEPVIYYLVKWCSLPYEDSTW ELKEDVDEGKIREFKRIQSRHPELKR VNRPQASAWKKLELSHEYKNRNQL REYQLEGVNWLLFNWYNRQNCILA DEMGLGKTIQSIAFLQEVYNVGIHGP FLVIAPLSTITNWEREFNTWTEMNTI VYHGSLASRQMIQQYEMYCKDSRG RLIPGAYKFDALITTFEMILSDCPELR EIEWRCVIIDEAHRLKNRNCKLLDSL KHMDLEHKVLLTGTPLQNTVEELFS LLHFLEPSQFPSESEFLKDFGDLKTE EQVQKLQAILKPMMLRRLKEDVEK NLAPKQETIIEVELTNIQKKYYRAILE KNFSFLSKGAGHTNMPNLLNTMME LRKCCNHPYLINGAEEKILTEFREAC HIIPHDFHLQAMVRSAGKLVLIDKLL PKLKAGGHKVLIFSQMVRCLDILEDY LIQRRYLYERIDGRVRGNLRQAAIDR FSKPDSDRFVFLLCTRAGGLGINLTA ADTCIIFDSDWNPQNDLQAQARCHR IGQSKAVKVYRLITRNSYEREMFDKA SLKLGLDKAVLQSMSGRDGNITGIQ QFSKKEIEDLLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTTITIESEGK GSTFAKASFVASENRTDISLDDPNF WQKWAKKADLDMDLLNSKNNLVID TPRVRKQTRHFSTLKDDDLVEFSDL ESEDDERPRSRRHDRHHAYGRTDC FRVEKHLLVYGWGRWRDILSHGRF KRRMTERDVETICRAILVYCLLHYRG DENIKGFIWDLISPAENGKTKELQN HSGLSIPVPRGRKGKKVKSQSTFDIH KADWIRKYNPDTLFQDESYKKHLKH QCNKVLLRVRMLYYLRQEVIGDQAE KVLGGAIASEIDIWFPVVDQLEVPTT WWDSEADKSLLIGVFKHGYEKYNT MRADPALCFLEKAGRPDDKAIAAEH RVLDNFSDIVEGVDFDKDCEDPEYK PLQGPPKDQDDEGDPLMMMDEEIS VIDGDEAQVTQQPGHLFWPPGSALT ARLRRLVTAYQRSYKREQMKIEAAE RGDRRRRRCEAAFKLKEIARREKQQ RWTRREQTDFYRVVSTFGVEYDPDT MQFHWDRFRTFARLDKKTDESLTK YFHGFVAMCRQVCRLPPAAGDEPPD PNLFIEPITEERASRTLYRIELLRRLR EQVLCHPLLEDRLALCQPPGPELPK WWEPVRHDGELLRGAARHGVSQTD CNIMQDPDFSFLAARMNYMQNHQ AGAPAPSLSRCSTPLLHQQYTSRTAS PLPLRPDAPVEKSPEETATQVPSLES	True	False	1.312	5.0	0.375

									LTLKLEHEVVARSRPTPQDYEMRVS PSDTTPLVSRSVPPVKLEDEDDSDSE LDLSKLSPSSSSSSSSSSSSSTDES EDEKEEKLTDQSRSKLYDEESLLSLT MSQDGFPNEDGEQMTPELLLLQER QRASEWPKDRVLINRIDLVCQAVLS GKWPSSRRSQEMVTGGILGPGNHL LDSPSLTPGEYGDSPVPTPRSSSAAS MAEEEASAVSTAAAQFTKLRRGMDE KEFTVQIKDEEGLKLTFQKHKLMAN GVMGDGHPLFHKKKGNRKKLVELE VECMEEPNHLDVDLETRIPVINKVD GTLLVGEDAPRRAELEMWLQGHPE FAVDPRFLAYMEDRRKQKWQRCKK NNKAELNCLGMEPVQTANSRNGKK GHHTETVFNRVLPGPIAPESSKKRA RRMRPDLSKMMALMQGGSTGSLSL HNTFQHSSSGLQSVSSLGHSSATSA SLPFMPFVMGGAPSSPHVDSSTML HHHHHHPHPHHHHHHHPGLRAPG YPSSPVTTASGTTLRLPPLQPEEDDD EDEEDDDDLSQGYDSSERDFSLIDD PMMPANSDSSEDADD					