

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma mem
O14647	CHD2_HUMAN	Homo sapiens	Chromodomain-helicase-DNA-binding protein 2	23.995357	S1075;S1076	S207;S208;T240;S242;S1085;S1087;S1365;S1386;S1807	30620550;37217939	MMRNKDKSQEEDSSLHSNASSHSA SEFASGSDSGSQSESEEQSDPGSGH GSESNSSSESESESESESESEAGSKS QPVLPEAKEKPAKKERIAADVKKMW EYYPDVYGVRRSNRSRQEPSRFNIK EEASSGSESGSPKRRGQORQLKKQEK WKQEPSEDEQEQGTSAESEPEQKK VKARRPVPRRTVPKPRVKKQPKTQR GKRKKQDSSDEDDDDDEAPKRQTR RRAAKNVSYKEDDDDFETDSDDLIEM TGEQVDEQQDNSETIEKVLDLRLGK KGATGASTTVYAIEANGDPSGDFDTE KDEGEIQYLKWKGWYIHSWSESE ESLQQQKVKGLKLENFKKKEDEIK QWLGKVSPEDEVYFNCQELASEL NKQYQIVERVIAVKTSTLGTDFP AHSRKPAPSNEPEYLCKWMGLPYSE CSWEDEALIGKKFQNCIDSFHSRNN SKTIPTRECKALKQRPFRVALLKKQPA YLGGENLELRDYQLEGLNWLHLSW CKNNSVILADEMGLGKTIQTSIFLSY LFHQHQLYGPFLIVVPLSTLTSWQR EFEIWAPEINVVVYIGDLMSRNTIRE YEWIHSQTKRLKFNALITTYEILLKD KTVLGSINWAFGLGVDEAHLKNDSDS LLYKTLIDFKSNHRLITGTPLQNSL KELWLLHFIMPEKFEFWEDEED HGKGRENGYQSLHKVLEPFLRRVK KDVEKSLPAKVEQILRVMSALQKQ YYKWILTRNYKALAKGTRGSTSGFL NIVMELKCCNHCYLKIPPEENERE NGQEILLSLIRSSGKLLLDKLLTRLR ERGNRVLFSQMVRLDILAELYTIK HYPFQRLDGSIKGEIRKQALDHFNA DGSDFCFLLSTRAGGLGINLASADT VVIFDSDWNPQNDLQAQARHRIGQ KKQVNIYRLVTGTVVEEIERAKKK MVLDDLVIQRMDTTGRTILENNSGR SNSNPFNKEELTAILKFGAEDLFKEL EGEESQPQEMDIDEILRLAETRENE VSTSATDELLSQFKVANFATMEDEE ELEERPDKDWEIPEEQRKKVEEE ERQKELEIYMLPRISSTKKAQTND SDSDTESKRQAQRSSASESETESSD DDKPKRRGRPRSVRKDLVGEFTDA EIRRFKAYKKFGLPLERLECIARDAE LVDKSVADLKRGLIHNSCVSAMQ EYEEQLKENASEGKGPGRRGPTIKI SGVQVNVKSIQHEEEFEMLHKSIPV DPEEKKKYCLTCRVKAAHFVDEWGV EDDSRLLGIYEHGYGNWELIKTDP ELKLTDKILPVETDKKPGQKQLQTRA DYLLKLLRKGLEKKGAVTGGEAKL KKRKPVRKKNKVPRLKEEHGIELS SPRHSNDNPSEEGEVKDDGLEKSPM KKKQKKKENKENKEKQMSRDKDE GDKERKSKDKKPKSGDAKSSSK SKRSQGPVHITAGSEPVPIGEDEDD LDQETFICKERMVRPKKALKQLDK PDKGLNVQEQLEHTRNCLLKIGDRI AECLKAYSQEHKLRWRRNLWIFVS KFTFEDARKLHKLYKMAHKRSQEE EEQKKDDVTGGKKPFRPEASGSSR DSLISQSHSHNLHPKPHLPASHG PQMHGHPRDNYNHPNKRHFSNAD RGDWQREKFNYYGGGNNPPWGS DRHHQYEQHWYKDDHYGDRRHMD AHRGSRPNMMSRKRYPDYQYSSD RDHRGRDYDRHHHDSKRRRSDE FRPQNYHQDFRRMSDHRPAMGY HGQGPSDDHYRSHFTDKLGEYKQPLP PLHPAVSDPRSPSQKSPHDSKSPL DHRSPLESLQKNNPDYWNVVK T	None	None	None	None	None	None	None	