

| UniprotKB ID | Entry name | organism | full name | oglnacscore | oglnacsites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|---|-------------|-------------|---|---|---|
| Q14839 | CHD4_HUMAN | Homo sapiens | Chromodomain-helicase-DNA-binding protein 4 | 10.055886 | T1725 | S44;S303;S308;S309;S310;S319;T367;S428;S515;T517;T529;S531;T703;S1209;S1308;S1349;S1370;S1531;S1535;S1537;T1542;T1549;T1553;S1570;S1576;S1602;T1653;T1679 | 34229054;34019948;32522876;34725712;28510447;37217939;33214551;37340703;23301498;27231347 | MASGLGSPSPCSAGSEEDMDALL NNSLPPHPENEEDPEEDLSETETP KLKKKKPKKPRDPKIPKSKRQKKE RMLLCRQLGDSSGEGPEFVEEEEEV ALRSDSEGSdyTPGKKKKKLGPKK EKKSkskrkeEEEEEDDDDSKEPK SSAQLLEDWGMEDIDHVFSEEDYRT LTNYKAFSQFVRPLIAAKNPKIAVSK MMMVLGAKWREFSTNNPFKGSSG ASVAAAAAAVAVVESMVTATEVAP PPPPVEVPIRAKTKEGKGNARRKP KGSPrVPDAKKPKKkVAPLKIKLGG FGSKRKRSSSEDDDLVESDFDDAS INSYSVSDGSTSRSSRSRKLRTTK KKKGEEVTAVDGYETHQDYCEVC QQGGEIILCDTCPRAYHVMVCLDPDM EKAPEGKWSCPHEKEGIQWEAKE DNSEGEIIEVGGDLEEDDHHM EFCRVCKDGGELLCDCPSSYHIH CLNPPLPEIPNGEWLCPRCTCPALK GKVQKILIKWGWQPPSPTVPRPPD ADPNTPSPKPLEGRPERQFFVKWQG MSYWHCSWVSELQLELHCQVMFR NYQRKNDMDEPPSGDFGGDEEKS KRKNKDPKFAEMEERFYRYGIKPEW MMIHRILNHSVDKKGHVHYLIKWR DLPYDQASWESEDVEIQDYDLFKQS YWNHRELMRGEEGRPGKLLKVKL RKLERPPETPTVDPTVKYERQPEYLD ATGRTLHPYQMEGLNWLRFSWAQQ TDTILADEMGLGKTVQTAVFLYSLYK EGHSGPFLVSAPLSTIINWEREFE MWAPDMYVVTVYVGDKDSRAIIRENE FSFEDNAIRGGKKASRMKKEASVKF HVLLTSYELITIDMAILGSIDWACLIV DEAHLKNNQSKFFRVLNGYSLQH KLLLTGTPLQNNLEELFHLLNFLT ERFHNLEGFLEEFADIAKEDQIKKL HDMLGPHMLRRLKADVFNMPSKT ELIVRVELSPMQKKYKYILTRNFEA LNARGGGNQVSLNVMMDLKKCCN HPYLPVAAMEAPKMPNGMYDGS LIRASGKLLLQKMLKLNKEGGHRV LIFSQMTKMLDLLEDLEHEGYKYE RIDGGITGNMRQEAIDRFNAPGAQQ FCFLSTRAGGLGINLATADTVIYDS DWNPHNDIQAFSRAHRIGQNKKVM IYRFVTRASVEERITQVAKKMMMLT HLVVRPGLGSKTGSMSKQELDDILK FGTEELFKDEATDGGDNKEGEDSS VIHYDDKAIERLLDRNQDETETEL QGMNEYLSSFKAQYVVEEMGE EEEVEREIIKQEEVDPDYWEKLLRH HYEQQEDLARNLGKGRIRKQVNY NDGSQEDRDWQDDQSDNQSDYSV |

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| | | | | | | | ASEEGDEDFDERSEAPRRPSRKGLR NDKDKPLPPLLARVGGNIEVLGFNA RQRKAFLNAIMRYGMPPQDAFTTQ WLVRDLRGKSEKEFKAYVSLFMRHL CEPGADGAETFADGVPREGLSRQHV LTRIGVMSLIRKKVQEFEHVNGRWS MPELAEVEENKKMSQPGSPSPKTPT PSTPGDTQPNTAPVPPAEDGIKIEE NSLKEEESIEGEKEVKSTAPETAIEC TQAPAPASEDEKVVVEPPEGEEKVE KAEVKERTEEPMETEPKGAADVEKV EEKSAIDLTPIVVEDKEEKKEEEKK EVMLQNGETPKDLNDEKQKKNIKQ RFMFNIADGGFTELHSLWQNEERA ATVTKKTYEIWHRHDYWLLAGIIN HGYARWQDIQNDPRYAILNEPFKGE MNRGNFLEIKNKFLARRFKLLEQAL VIEEQLRRAAYLNMSIEDPSHPSMAL NTRFAEVECLAESHQHSKESMAG NKPANAVLHKVLKQLEELSDMKA DVTRLPATIARIPPAVAVRLQMSERNI LSRLANRAPEPTPQQAQQQ |
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