

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q3L8U1	CHD9_HUMAN	Homo sapiens	Chromodomain-helicase-DNA-binding protein 9	3.245925	T1493	S550;S611;S1468;S1472;S2026;S2058;S2059;S2075;S2079	30379171;34019948	MTDPMMDFFDDANLFGETLEGLSD DAFVQPGPVSLVDELNLGAEFEPLHI DSLNVHQGTPTHQKMTDFEQLNQF DSIKFHVNQSFSGSPAEHVLSPHSQ FNCSPHQPQNPNGLFPDVS DGSPM WGHQTATTISNQNGSPFHQQGHS SMHQNKSFVAHDFALFQANEQQT QCTSLRSQQNRN LNPGQNSLSQS KNFMNVSGPHRVNVNHPQMTNA SNSQQSISMQQFSQTSNPSAHFHK CSSHQEGNFNGPSPNMTSCSVSNS QQFSSHYSFSSNHISPNLLQSSAVL ASNHTNQTLSDFTGSNSFSPHRGIK QUESTQHILNPNTSLNSN NFQILHSS HPQGNYSNSKLSPVHMFDPVDS GTQMGHFNDHVTNGFSSLEENLL HQVESQTEPFTGLDPEDLLQEGLLP HFDESTFGQDNSSHILDHDLDRQFT SHLVTRPSDMAQTQLQSQARSWHS SFSNHQHLHDRNHLCLQRQPPSSK KSDGSGTYTKLQNTQVRVMSEKKQ RKKVESESKQEKANRIISEAIAKAKE RGERNIPRVMSPENFPTASVEGKEE KKGRRMKS KPKDKDSKKTCTCSK EKTGIGKLIITLGKKQKRKNESSEIS DAEQMPQHTLKDQDSQKRRSNRQI KRKKAEDIEGKQSEEEVKGSMKIK KNSAPLPGEQPLQLFVENPSEEDAAI VDKILSSRTVKKEISPGVMIDTEEFF VKYKNYSYLHCEWATEEQLLKDKRI QQKIKRFLRQAQRAHFFADMEEEP FNPDYVEVDRVLEVSFCEDKDTGEP VIYYLVKWCSLPYEDSTWELKEDVD LAKIEEFEQLQASRPDTRRLDRPPSN IWKKIDQSRDYKNGNQLREYQLEGL NWLLFNWYNRRNCILADEMGLGKT IQSITFLYEILLTGIRGPFLIAPLSTIA NWEREFRTWTDINVVVYHGLISRQ MIQQYEMYFRDSQGRIIRGAYRFQAI ITTFEMILGGCGELNAIEWRCVIIDE AHRLKNKNCKLLEGLKLMNLEHKV LLTGTPLQNTVEELFSLHFLEPLRF PSESTFMQEFGDLKTEEQVQKLQAI LKPMMLRRLKEDVEKKLAPKEETIE VELTNIQKKYYRAILEKNFSFLSKGA GQTNVPNLVNTMMELRKCCNHPYL IKGAEEKILGEFRDTYNPAASDFHLQ AMIQSAGKLVLIDKLLPKMKAGGHK VLIFSQMVRCLDILEDYLIHKRYLYE RIDGRVRGNLRQAADRFSKPDSDR FVFLLECTRAGGLGINLTAADTCIIFDS

DWNPQNDLQAQARCHRIGQNKAVK  
VYRLVTRNSYEREMFDRASLKLGLD  
KAVLQSMGRESNVGGIQLSKKEI  
EDLLRRGAYGAIMEEEDEGSKFCEE  
DIDQILLRRTKTTITIESEGRSTFAKA  
SFVASGNRTDISLDDPNFWQKWAK  
KAEIDIEAISGRNSLVIDTPRIRKQTR  
PFSATKDELAELSEAESEGDEKPKLR  
RPCDRSNGYGRTECFRVEKNLLVYG  
WGRWREILSHGRFKRQLNEHDVEII  
CRALLAYCLVHYRGDEKIKGFIWDLI  
TPTEDGQTRELQNHGLSAPVPRGR  
KGKKVKTQTSSFDIQKAEWLRKYNP  
EQLLQDEGYKKHIKHHCNKVLRLVR  
MLYYLKQEVIGNECQKVFDDGVDASD  
IDVWVPEPDHSEVPAEWDFDADK  
LLIGVFKHGYEKYNTIRADPALCFL  
ERVGKPDKAVAAEQRANDYMDGD  
VEDPEYKPAPAIKDDIEDDVSSPGD  
LVIADGDGQLMEGDKVYWPTQSALT  
TRLRRLITAYQRTNKNRQIQIQPTF  
SVPTSVMQPIYEEATLNPKMAAKIER  
QQRWTRREEADFYRVVSTFGVVFD  
DRGQFDWTKFRAMARLHKKTDDSL  
EKYLYAFMSMCRRVCRLPSKEELVD  
PNIFIQPIEERASRTLYRIELLRKVR  
EQALRHPQLFERLKLCHPNPDLPVW  
WECGPHDRDLLIGAAKHGVSRTDY  
HILRDPELSFMAAQRNYSQSKMAHS  
RTSTPLLQYQVALSASPLTSLPRL  
DAKGIILEEMKVKSENKKEEPSSEE  
ESMSSVETRTRLIKSEPVSPKNGVLPQ  
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TPNPASKKPRVHKGSESSSDSDSD  
SERSSCSSRSSSSSSSSSSSHSRSGS  
SSSSSSSCSSASSSSSSSTSSSSSSS  
SSSEESDSDEEEAQKRESTTHMKAY  
DEESVASLSTTQDETQDSFQMNG  
TPESAYILQGGYMLAASYWPKDRVM  
INRLDSICQTVLKGKWPARRSYDA  
NTVASFYTTKLLDSPAATEYSDPSV  
PTPPGAGVKEEHDQSTQMSKVKKH  
VREKEFTVKIKDEGGLKLTQKQGL  
AQKRPFDDGEDGALGQQOYLRLREL  
QSASETSLVNFPSIPVSGTISIPTLG  
ANGVILDNQPIVKKRRGRKNVEGV  
DIFFFNRNKPPNHVSLGTSSQISTG  
INPALSYPQGPDPTEPVPVINLKD  
GTRLAGDDAPKRKDLKWLKEHPG  
YVEDLGAFIPRMQLHEGRPKQKRHR  
CRNPNKLDVNSLTGEERVQLINRRN  
ARKVGGAFAPPLKDLRFLKENSEY  
GVAPEWGDVVKQSGFLPESMYERIL  
TGPVVREEVSRRRRPPKSGIAKATAA

								AAAASATSVSGNPLLANGLLPGVDL TTLQALQQNLQNLQSLQVTAGLMG MPTGLPSGGEAKNMAAMFPMLLSG MAGLPNLLGMGGLLTKPTESGTEK KGSDSKESEGKTERTESQSSENGGE NSVSSSPSTSSTAALNTAAAANPLAL NPLLLSNILYPGMLLTPGLNLHIPTL SQSNTFDVQNKNSDLGSSKSVEVKE EDSRIKDQEDKGGTEPSPLNENSTD EGSEKADASSGSDSTSSSESDSDSS NED
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