

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndr
P78527	PRKDC_HUMAN	Homo sapiens	DNA-dependent protein kinase catalytic subunit	11.095259	S318;T1240;S1300;S1658;S1677;S2624;S3313;T3869;S3870	S511;S687;S841;S893;S1065;S2056;T2535;T2609;S2612;T2638;T2647;S2789;S3205;S3731;S3821;S4026	30379171;38665916;35083852;35132862;29351928;33214551;23301498;32870666;32805318;34019948;27655845;26853435;30397120;32119511;34725712;37217939;28510447	MAGSSGAGVRCSSLRLQETLSAADRC GAALAGHQIRLIRGLQECVLSSSPAVL ALQTSLVFSDRFGLLVFVRKLSNIE FRECREEILKFLCIFLEKMGQKIAPY SVEIKNTCTSVYTKDRAACKKIPALD LLIKLLQTFRRSSRLMDEFKIGELFSK FYGELALKKKIPDVTLEKVEYELGLL GEVHPSEMINNAENLFRNFLGELKT QMTSAVREPKLPLVLAGCLKGLSLL CNFTKSMEEEDPQTSREIFNFVLRKAI PQIDLKRYAVPSAGLRLFALHASQFS TCLLDNYVSLFEVLLKWCAHTNVEL KKAALSALLESFLKQVSNMVAKNAE MHKNKLQYFMEQFYGIIRNVDSNN KELSIAIRGYGLFAGPCKVINAKDVD FMYVELIQRCKQMFLTQTDGDDRV YQMPFSLQSVASVLLYLDIVPEVYTP VLEHLVVMQIDSFPQYSPKMLVCC RAIVKVLALAAAGPVLRLNCISTVVH OGLIRICSKPVVLPKGPESSEHRA SGEVRTGKWKVPTYKYVDLFRHLL SSDQMMSILADEAFFSVNSSES NHLLYDEFVKSVLKIVEKLDLTLEIQ TVGEQENGDEAPGVWMIPTSDPAA NLHPAKPKDFSAFINLVEFCREILPE KQAEFFEPWVYSFSEYELILQSTRPLI SGFYKLLSITVRNAKKIKYFEGVSPK SLKHSPEDPEKYSFCALFVKFGKEV AVKMKQYKDELLASCLTFLSLPHNI IELDVRAYVPALQMAFKGLSYTPLA EVGLNALEEWSIYDRHVMQPYKDI LPCLDGYLKTALSDETKNNWEVSA LSRAAQKGFNKVVLKHLKTKNLS NEAISLEIRIRVVQMLGSLGGQINK NLLTVTSSDEMMKSYVAVDREKRL SFAVPFREMKPVIFLDVFLPRVTELA LTASDRQTKVAACELLHSMVMFML GKATQMPGEGQGAPPYQYKRTF PVLRLACDQVTRQLYEPLVMQLI HWFTNKKFESQDTVALLEAILDGI VDPVDSTLRDFCGRCIREFLKWSIKQ ITPQQQEKSPVNTKSLFKRLYSALH PNAFKRLGASLAFNNIYREFREEESL VEQFVFEALVIYMESLALAHADEKSL GTIQCCDAIDHLCRIIEKHHVSLNK AKKRRRLPRGFPPSASLCLLDLVKWL LAHCGRPQTECRHKSIELFYKFPVLL PGRNSPNLWLDVLEKEGVFLINT FEGGCGGQPSGILAQPTLLYLRGPF LQATLCWLDLLAALCEYNTFIGERT VGALQVLGTEAQSSLLKAVAFFLESI AMHDIIAAEKCFGTGAAGNRTSPQE GERYNYSKCTVVVRIMEFTITLLNTS PEGWKLLKDLNTHLMRVLVQTL CEPASIGFNIGDVQVMAHLDPVCVN LMKALKMSPYKDILETHLREKITAQS IEELCAVNLYGPDQVDRSRLAAVVS ACKQLHRAGLLHNLPSQSDLHHS VGTCELLSVYKGIAPGDEROCLPSLD LSCKQLASGLLELAFAGGLCERLVS LLLNPVAVLSTASLGSSQGSVIHFHSHG EYFYSLSFSETINTELLKNLDLAVLEL MQSSVDNTKMVSAVLNGMLDQSFR ERANQKHQGLKLATLILQHWKCD SWWAKDSPLETKMAVLALLAKILQI DSSVFNSTSHGSPFVFTYISLLAD TKLDLHLKGQAVTLLPFFTSLTGSSL EELRRVLEQLIVAFPMQSRFFPPG TPRFNNYVDCMKKFLDALELSQSP MELLEMTVLCREQQHVMELFQS SFRRIARRGSCVTQVGLLESVYEMF RKDDPRLSFTRSFVDRSLLTLLWH CSLDALREFFTIVDAIDVLKSRFT KLNSTFDQTITKMGYKILDVMYS RLPKDDVHAKESKINQVHFGSCITE GNELTKTLIKCYDAFTENMAGENQ LLERRRLYHCAAYNCAISVICCVFNE LKFYQGFLEKPEKNLLIFENLIDL KRRYNFPVEVEVPMERKKKYIEIRKE AREAANGDSDGPSYSSLSYLADST	True	False	4.515	5.0	2.588

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