

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	exti regi
O75417	DPOLQ_HUMAN	Homo sapiens	DNA polymerase theta	19.516373	T1089;S1660	NaN	30379171;29208956;37217939	MNLLRRSGKRRRESGSDSFSGSGG DSSASPOFLSGSVLSPPPGLGRCLKA AAAGECKPTVPDYERDKLLLANWGL PKAVLEKYHSFGVKKMFQWQAECL LLGQVLEGNLVYSAPTSAGKTLVAE LLILKRVLEMRKKALFILPFVSVAKE KKYYLQSLFQEVGKVDGYMGSTSPS RHFSSLDIAVCTIERANGLINRLIEE NKMDLLGMVVDELHMLGDSHRG YLLELLTKICYTRKSASCQADLASS LSNAVQIVGMSATLPNLELVASWLN AELYHTDFRPVPLESVKVGNSIYDS SMKLVREFEPMQVKGDEHDHVSL CYETICDNHVSLLFCPSKKWCEKLA DIIAREFYNLHHQAEGLVKPSECPPV ILEQKELLEVMQRLRRPGLDLSVL QKTPVWGVAFHHAGLTFEERDIEG AFRQGLIRVLAATSTLSSGVNLPARR VIIRTPIFGGRPLDILTYQMVGGRGR KGVDTVGESILICKNSEKSGIALLO GSLKPVRSCLQRREGEEVTSGMIRAI LEIIVGGVASTSQDMHTYAACTFLAA SMKEGKQGIQRNQESVOLGAIEACV MWLLENEFIQSTEASDGTGKVVHP THLGSATLSSSLSPADTLDFADLQR AMKGFVLENDLHILYLVPMFEDWT TIDWYRFFCLWEKLPMSMKRVAELV GVEEFLARCVKGVVARTERQHRQ MAIHKRFFTSLVLLDLISEVPLREIN QKYGCRGQIQSLQSAAVYAGMIT VFSNRLGWHNMELLSQFQKRLTF GIQRELCDLVRVSLNAQRARVLYAS GFHTVADLARANIVEVEVILKNAVPF KSARKAVDEEEAVEERRNMRTIWV TGRKGLTEREAAALIVVEARMILQD LVMGVQWNPCALLHSSTCSLTHS ESEVKEHTFISQTKSSYKLTSKNKS NTIFSDSYIKHSPNIVQDLNKSREHT SSFNCNFQNGNQEHQTCIFRARK RASLDINKEKPGASQNEGKTSDDKKV VQTFSQTKKAPLNFNSEKMSRSFR SWKRRKHLKRSRDSPLKDSGACRI HLOGQTLNPNLCEDEPFTLDEKTE FRNSGPFKAVNSLGGKEKDNKTSFP LQIKQNCSWNITLNDNFVEHVITG SQSKNVTQATSVVSEKGRGVAVEA EKINEVLIQNGSKNQNVYMKHHDIH PINOYLRKQSHEQTSTITKQKNIER QMPCEAVSSYINRDSNVTINCERIKL NTEENKPSHFQALGDDISRTVIPSEV LPSAGAFKSEGOHENFLNISRLQE KTGTYTNTKTKNNHVSDDLGLVLCDF EDSFYLDTQSEKIIQQMATENAKLG AKDTNLAAGIMQKSLVQQNSMNSF QKECHIPFAEQHPLGATKIDHLDLK TVGTMKQSSDSHGVDILTPESPIFHS PILLEENGLFLKKNVSVTDSQLNSF LQGYQTQETVKPVILLIPQKRTPTGV EGECLPVPETSLNMSDLSLFDSPSD DYLVEQLPDMQMKEPLPSEVTSN HFSDSLCLQEDLIKSNVNEQDTH QOLTCSNDESIIFSEMDSVQMEAL DNVDIFPVQEKNTVWSPRALELSD PVLDEHHQGDQDGGDQDERAEKSK LTGTRQNHSPFIWSGASFDLSPGLQR ILDKVSSPLENEKLSMTINFSSLNR KNTLNDEEVEVSNLETKVQVQISFVS SNNEVSKIEMLENNANHDETSLL PRKESNIVDDNGLIPPTPIPTSASKLT FPGILETPVNPWKTNNVLQPGESYL FGSPSDIKNHDLSGSRNGFKDNP ISDTSFSLQSLQDGLQLTPASSSES LSIIDVASDQNLFTQFIKEWRCKKRF SISLACEKIRSLTSSKTATIGSRFKQA SSPOEIPRDDGFPIKGCDDTLVVG AVCWGGRDAYYFSLQKEQKHSEISA SLVPPSLDPSLTKDRMWYLOQSLR KESDKCEVVIYDFIQSYKILLSCGI SLEQSYEDPKVACWLLDPDSQEPTL HSIVTSFLPHELPLLEGMETSQGIQS	True	False	4.658	4.798	1.817	0.647	4.316	0.729	0.65

LGLNAGSEHSGRYRASVESILIFNSM  
NQLNSLLQKENLQDVFRKVMPSQ  
YCLALLELNGIGFSTAECESQKHIMQ  
AKLDAIETQAYQLAGHSFSFTSSDDI  
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VFPLOREKCLNPFLGMEIRIYVPSQ  
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YIDFSKRYTGINQFMETETVKNCKR  
DGFVQITLGRRRYLPGKDNPNYRKA  
HAERQAINIVQGSAAADIVKIATVNIQ  
KQLETFHSTFKSHGHREGMLQSDQ  
TGLSRKRKLQGMFCPIRGGFFILQL  
HDELLYEVAEEDVVQVAQIVKNEME  
SAVKLSVKLVKVKIGASWGELKDF  
DV