

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrio
P49454	CENPF_HUMAN	Homo sapiens	Centromere protein F	27.360861	T63;S401;T653;S658;S882;S1799	S106;T144;T151;T154;T158;S242;S276;S773;S783;S821;S834;S838;S876;S1248;S1255;S1259;S1651;S1652;S1654;S1726;T1862;S1868;S1892;S2416;S2417;S2900;S2911;S2922;S2936;T2949;S2952;S2998;S3023;S3026;S3054;S3079;S3083	30379171;31492838;23301498;37340703;35289036;29351928	MSWALEEWKEGLPTRLALQKIQIELEGQLDKLKKKEKQRFQFQDLSLEAALQKQKQKVENEKTEGTNLKRENQRLMEICESLEKTKQKISHELQVKESQVNFQEGQLNSGGKQKIEKLEQELKRCCKSELERSQAAQASADVSLNPNCTPQKIFITPLTPSQYYSGSKYEDLKEKYNKEVEERKRLAEVKALQAKKASQTLPOATMNHRRDIARHQASSVFSWQEQETPSHLSSNSQRTPIRRDFASVYFSGEQEVTPSRSTLQIGKRDANSSFFDNSSSPHLLDQLKAQNQELRNKINLELRLQGHEKEMKGVNKFQELQLQLEKAKVELIEKEKVLNKCRCDELVRTTAQYDQASTKYTALEQKLLKLTEDLSCQRONAESARCSLEQKIKEKEKEFEELSROQRSFQTLQECIQMKARLTQELQAKNMHNVLQAEQDCLTSVKQQLNLEEFKQKLCRAEQAFQASQIKENELRRSMEEEMKKNLLKSHSEQAREVCHLEAELKNKQCLNQSQNFEMKAKNTSQETMLRDLQEKINQFENSLTLEKLLAVADLEKQRDCSQDLKKKREHHIEQLNDKLSKTEKESKALLSALELKKKEYEELKEEKLFSQWSENKLLTQMESEKENLQSKINHLETCLKTQQIKSHEYNERVRTLEMDRENLSVEIRNLHNVLDKSKSVEVETQKLAAYMELQQAQAEFSDQKHQKEIENMCLKTSQTLTGQVEDLEHKLQLLSNEIMDKDRCYQDLHAEYSLRDLLKSKDASLVTNEDHQRSLLAFDQQPAMHHSFANIIGEQQSMPSESRSECRLEADQSPKNSAILQNRVDSLEFLESQKQMNSDLQKQCEELVQIKGEIENLMKAEQMHQSFAVETSQRISKLEQEDTSAHQNVVAETLSALENKEKELQLLNDKVEAQAEIQELKKNHLLLEDLKLQQLSETLSLEKEMSSHSILNKREIEELTQENGLTKEINASLNQEKMNLIQKSESFANYIDEREKSISELSDQYKQEKLLILQRCEETGNAYEDLSQYKAAQEKNSKLECLLNECTSLCENRNKNELEQLKEAFAKEHQEFLTKLAFABERNQNLMLELTVQQAARSEMTDNQNNKSEAAGGLKQEIIMTLKKEEQNKMQKEVNDLLQENEQLMKVMKTKHECQNLSEPIRNSVKERESERNQCNFKPQMDLEVKEISLDSYNAQLVQLEAMLRNKELKLQESEKEKECLQHELQTRGDLETSNLQDMQSQEISGLKDCEIDAEEKYISGPHELSTSQNDNAHLQCSLQTTMNKLNELEKICEILQAEKYELVTELNDSRSECITATRKMAEEVQKLLNEVKILNDDSGLLHGELVEDIPGGFGEQPN EQHPVSLAPLDESNSYEHLLTSDKEVQMHFAELQEKFLSLQSEHKILHDQHCQMSSKMSELQTYVDSLKAENLV LSTNLRNFQGDVLEKEMQLGLEEGLVPSLSSCVPSLSSSLGDSFYRALLEQTGDMSLLSNLEGAVSANQCSVDEVFCSSLQEEENLTKETPSAPAKGVEELESCEVYRQSLKLEKEMESQGIMKNKEIQELEQLSSERQELDCLRKQYLSENEQWQKLTSTVLEMESKLAEEKQTEQLSLEVARLQLQGLDLSRSRLLGIDTDAIQGRNESCDISKEHTSETTERTPKHDVHQICDKDAQDNLNDIEKITETGAVKPTGECSGEQSPDTNYEPPGEDKTQGSSECISELSFSGPNALVPMDFLGNQEDIHNLQLRVKETSNNLRLHVIDRDRKVESLLNEMKELDSKLLHQEVQLMTKIEACIELEKIVGELKKENSDDLSEKLEYFSCDHQELLQRVETSEGLNSDLEMHADKSSREDIGDNVAVNDSWKERFLDVENELSRIRSEKASIEHEALYLEADLEVVTQEKLCLEKDNENKQKVIVCLEEELSVVTSERNQLRGELDTMSKKTALDQLSEKMKKKTQELSHQSECL	True	False	4.512	5.0	1.919

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KCELENQIAQLNKEKELLVKESESL
QARLSESDYEKLNVS KALEAALVEK
GEFALRLSSTQEEVHQLRRGIEKLRV
RIEADEKKQLHIAEKLKERERENDSL
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SKTAVEMLQNLKELNEAVAALCG
DQEIWKATEQSLDPPIEEHQLRNSI
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HHADLLKGRVENLERELEIARTNQE
HAALAEANSKGEVETLKAKIEGMTQ
SLRGLLEDVVTIRSEKENLTNELOKE
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DSGTILREPTTKSVVNNLPERSPD
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SENCKVQ