

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q14676	MDC1_HUMAN	Homo sapiens	Mediator of DNA damage checkpoint protein 1	29.836689	S72;S108;S112;T1116;S1132;T1133;T1138;S1337;S1417;S1419;T1582;S1583	T4;S108;T146;S168;S176;S299;T301;S329;T331;S372;S376;T378;S394;S397;S402;T404;S411;T449;S453;T455;S485;S495;S498;S504;S505;S513;T523;S590;S780;S793;S955;S998;S1033;S1068;S1086;T1157;T1198;S1235;T1239;T1280;T1302;S1399;S1400;T1403;T1425;T1466;T1548;S1564;T1567;T1589;S1604;T1608;T1630;T1664;T1671;S1681;T1697;S1702;S1711;S1775;T1800;S1820;T1858	31492838;34019948;29237092;16408927;30620550;33214551;35254053;35132862;23301498;27458206;35289036;32119511;32574038	MEDTQAIWDVVEEEETEQSSESRLR CNVEPVGRLHFSGAHGPEKDFPLH LGKNVVGMRMPDCSVALPFPKSQKH AEIEILAWDKAPILRDCGSLNGTQIL RPPKVLSPGVSHRLRDQELILFADLL CQYHRLDVSLPFVSRGPLTVEETPRV QGETQPQRLLLAEDSSEEVDFLSEER RMVKKSRRTSSSVIVPESDEEGHSP VLGGLGPPFAFNLSDTDVEEGQQP ATEEASSAARRGATVEAKQSEAEV TEIQLEKDQPLVKERDNDTKVKGGA GNGVVPAGVILERSQPPGEDSDTDV DDDSRPPGRPAEVHLERAQPFQFID SDTDAEEERIPATPVVPMKRRKIFH GVGTRGPGAPGLAHLQESQAGSDTD VEEGKAPQAVPLEKSQASMVNSDT DDEEVSAALTLAHLKESQPAIWNR DAEEDMPQRVVLLQRSQTTTERDSD TDVEEELPVENREAVLKDHTKIRAL VRAHSEKDQPPFGSDSDSVEADKSS PGIHLERSQASTTVDINTQVEKEVPP GSIIHIKKHQVSVEGTNQTDVKAVG GPAKLLVVSLEEAWPLHGCETDAE EGTSLTASVVDVRKSQLPAEGDAG AEWAAAALVKQERAHEVGAQGGPPV AQVEQDLPISENLTDLVVDTDTLG ESTQPQREGAQVPTGREEREQHVGGT KDESDNYGDESDLDLQATQCFLN QGLEAVQSMDEPTQAFMLTPPQEL GPSHCSFQTTGTLDEPWEVLATQPF CLRESEDSQPFDTHEAYGPCLS PPRAIPGDQHPESPVHTEPMGIQGR GRQTVDKVMGIPKETAERVGPERGP LERTEKLLPERQTDVTEEELTKG KQDREQKQLLARDTQRQESDKNGE SASPERDRESLKVEIETSEEIQEKQV KQKTLPSKAFEREVERPVANRECDP AELEEKVPKVILERDTQRGEPEGGS QDQKQASSTPEPGVAGDLPDGP SAPVPSGSQSGGRGSPVSPRRHQKG LLNCKMPPAEKASRIRAAEKVSRGD QESPDACLPTVPEAPAPPQKPLNSQ SQKHLAPPLLSPLLSIKPTVRKTR QDGSQEAPEAPLSSELEPFHFKPKIR TRKSSRMTFPFATSAAPEPHSTSTA QPVTPKPTSQATRSRTNRSSVKTPEP VVPTAPELQPSTSTDQPVTSEPTSQV TRGRKSRSSVKTPEVVPTALELQPS TSTDVPVTSEPTSQATRGRKNRSSV KTPEPVVPTAPELQPSTSTDQPVTSE PTYQATRGRKNRSSVKTPEVVPTAP ELRPSTSTDVPVTPEPTSRRTSRRTN MSSVKTPEVVPTAPELQISTSTDQP VTPKPTSRRTSRRTNMSVKNPEST VPIAPELPPSTSTEQVPTPEPTSRATR GRKNRSSGKTPETLVPTAPKLEPSTS TDQPVTPEPTSQATRGRTRNRSSVKT PETVVPTAPELQPSTSTDQPVTPEPT SQATRGRTRDRSSVKTPEVVPTAPEL QASASTDQPVTSEPTSRTTRGRKNR SSVKTPEVVPTAPELQPSTSTDQP TPEPTSRATRGRTRNRSSVKTPEVPI APELQPSTSRNQLVPTPEPTSRATR

TNRSSVKTPEPVVPTAPEPHPTTSTD
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VEPAASDLEPFTPTDQSVTPEAIAQG
GQSKTLRSSTVRAMPVPTTPEFQSP
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VLALGGSLAGSAAEASHLVTDRIRRT
VKFLCALGRGIPILSLDWLHQSRKAG
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