

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|---|--------------|---------------|--|-------------------|--|
| Q5PSV9 | MDC1_MOUSE | Mus musculus | Mediator of DNA damage checkpoint protein 1 | 16.020267 | NaN | T4;T146;S168;S176;S298;T300;S313;T315;S360;T362;S385;T387;S398;S415;S425;S438;S442;T444;S461;T470;S492;S493;S591;S593;S595;S735;S750;S885;S929;S962;S991;T1056;S1104;S1126;S1128;T1132;T1173;T1234;T1297;T1298;S1327;T1352;S1359;T1375;S1435;S1436;S1439;S1443;T1480 | 28135057;25153642 | MESTQVIDWDAEEEEETEELSSGSLGYSVEPIGQLRFLFSGTHGPERDFPLYLGNVVGRRSPDCSVALPFPISKQHAVIEISAWNKAPILQDCGSLNGTQIVKPPRVLPPGVSHRLRDQELILFADFPCQYHRLDVPPPLVPRSLLTIEKTPIRIRIESQNSRVLLAADSEEEGDFPSGRCVANGQRNTASPSATVVPESDEEVSSPAPSVPGPSSPFGLGSDTDEEQGQP GVEESSLADSSGAAGEAEQPEANGT TAGIQAQPTTEHKLKDTKVKEAGRA GVS DGSV LERSPTLGEDSDTEVDED HKPGFADSETDVEEERIPVTPPVAPV KKNQVLLAVGIGDPEAPGVAHLQDC LAGSGTDVEDKTALDVPLERNHTPM VINS DTDEEEEEEEVSAALTLAHLK ERGIGLWSRDPGAEVKSQPQVLVE QSQSASGRDSDTDVEEESGRKREII PDS PMDVDEALTVTQPESQPPRRPN DAD EYMDMSSPGSHLVVNQASFAV VGKTRAQVEEEVPGPSVILGEKHQV PLEGAQPPEEAWETAVQEGSSSPEA AASVRPSQQPVAEDAGTECATAVSE QESTLEVR SQSGSPAAPVEQVVIHTD TSGDPTLPQREGAQTPTGREAREAHV GRTKSAKECCDAEPEDLCLPATQCF VEGESQHPEAVQSLNEPTQLFPCT LPQEPGSHLSLQTPGADTLDPWE VLATQPFCLREQSETSELHEAHGSQ PSLPREPPGHQHLVHTSPVHTELLRI EGREIQTVEKAMGIPKEMADRMTPE REPLEREIRGR TENSERDVIGEELIQ GTKDREPKKVLARDSQRKEADKDLE GNRESLEVEIEMSKDSQKRERKVEK PEPKREWEPADLEVTPDRGVTEEGS HDQKGQIASLTLKPGVGVKDLGLELA SAPIITGSQADGGKGDPLSPGRQQRG RLSCQTTAGKASRGDPEPPDHCLF SSVPEASTQSLLSQSQKQSTPQPLF STSSSEIPLPESLHTKPNVRPRSSR MTPSPHSSAALKPNTTCPTNQPAAS RPTSRPTRGRANRSSTRTPELIVPVD PELQPSTSTEQPVIPKLT SQVTEGRV QMPEPLLTGPEIQSPTSTEQSVTPDR KPRATRGRPSKSPNKTPEPLISTGPE LQPPTSIEQPVIPKPTRSVTRGRPRKS SVRTPESVVSTGPELQPLTSIEQPVIP EPRATRGRPSKSSIKTPESVVPTGPE LQPLTSAKQPVTNLT SRASRGRSSK |

| | | | | | | | | |
|--|--|--|--|--|--|--|--|--|
| | | | | | | | | SIRTPEPVVQTGPEFHPSTSTEQPDT REPSSQARTRRSAVKTPEASVPTTPE LQPFTSKKQPAPKPTALVTQGRYKP STEDCESVGPVAPDFEPSTSTDHLVT PKVTDQSLTLQSSPLSASPVSSTPDL KPPVPIAQVTPPEPIPQANHQRKRA AGKQGSRTVPLGHKSYSALSEPEPQ SSASQSSGASEADSPRQKRPRRQAS QKTVVIKEEPVETEVKEEPQETAIPTP EKRRDHAEVVTQGKPTRSRRTKPN QETAPKVLFTGVMDSRGERAVLALG GSLASSVNEASHLVTDRIRRTVKFLC ALGKGIPILSLNWLYQSRKAGCFLPP DDYLVTDPEQEKNFSFLRDSL CRA RERRLLEDYEIHVTPGVQPPPPQMG EIIISCCGGTFLPSMPHSYKLRVITC TEDLPRCAIP SRLGLPLLSPEFLLTGV LKQEATPEAFVLSNLEMSST |
|--|--|--|--|--|--|--|--|--|