	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ex re
0	Q5PSV9	MDC1_MOUSE	Mus musculus	Mediator of DNA damage checkpoint protein 1	29.384333	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	25153642;28135057	MESTQVIDWDAEEEEETELSSGSLG YSVEPIGQLRLFSGTHGPERDFPLYL GKNVVGRSPDCSVALPFPSISKQHA VIEISAWNKAPILQDCGSLNGTQIVK PPRVLPPGVSHRLRDQELILFADFPC QYHRLDVPPPLVPRSLLTIEKTPRIRI ESQNSRVLLAADSEEEGDFPSGRCV ANGQRNTASPSATVVPESDEEVSSP APSVPGPSSPFGLGSDTDEEQGQQP GVEESSLADSSGAAGEAEQPEANGT TAGIQAQPTEHKLKDTKVKKEAGRA GVSDGSVLERSPTLGEDSDTEVDED HKPGFADSETDVEEERIPVTPPVAPV KKNQVLLAVGIGDPEAPGVAHLQDC LAGSGTDVEDKTALDVPLERNHTPM VINSDTDEEEEEEEEVSAALTLAHLK ERGIGLWSRDPGAEEVKSQPQVLVE QSQSASGRDSDTDVEEESSGRKREII PDSPMDVDEALTVTQPESQPPRRPN DADEYMDMSSPGSHLVVNQASFAV VGKTRAQVEEEVPGPSVILGEKHQV PLEGAQPPEEAWETAVQEGSSSPEA AASVRPSQQPVAEDAGTECATAVSE QESTLEVRSQSGSPAAPVEQVVIHTD TSGDPTLPQREGAQTPTGREREAHV GRTKSAKECCDAEPEDLCLPATQCF VEGESQHPEAVQSLENEPTQLFPCT LPQEPGPSHLSLQTPGADTLDVPWE VLATQPFCLREQSETSELHEAHGSQ PSLPREPPGHQHLVHTSPVHTELLRI EGREIQTVEKAMGIPKEMADRMTPE REPLEREIRGRTENSERDVIGEELIQ GTKDREPKKVLARDSQRKEADKDLE GNRESLEVEIEMSKDSQKRERKVEK PEPKREWEPADLEVTPDRGVTEEGS HDQKGQIASLTLKPGVGVKDLEGLA SAPIITGSQADGGKGDPLSPGRQQRG RLSCQTTPAGKASRGDPEPPDHCLF SSVPEASTQSLLTSQSQKQSTPQPLF STSSSEIPLPESLHTKPNVRPRRSSR MTPSPHSSAALKPNTTCPTNQPAAS RPTSRPTRGRANRSSTRTPELIVPVD PELQPSTSTEQPVIPKLTSQVTEGRV QMPEPLLTGPEIQSPTSTEQSVTPDR KPRATRGRPSKSPNKTPEPLISTGPE LQPPTSIEQPVIPKPTSRVTRGRPRKS SVRTPESVVSTGPELQPLTSIEQPVIP EPRATRGRPSKSSIKTPESVVPTGPE LQPLTSAKQPVTPNLTSRASRGRSSK SIRTPEPVVQTGPEFHPSTSTEQPDT REPSSQARTRRSAVKTPEASVPTTPE LQPFTSKKQPAPKPTALVTQGRTYKP STEDCESVGPVAPDFEPSTSTDHLVT PKVTDQSLTLQSSPLSASPVSSTPDL KPPVPIAQPVTPEPIPQANHQRKRRA AGKQGSRTVPLGHKSYSALSEPEPQ SSASQSSGASEADSPRQKRPRRQAS QKTVVIKEEPVETEVKEEPQETAIPTP EKRKRDHAEEVTQGKPTRSRRTKPN QETAPKVLFTGVMDSRGERAVLALG GSLASSVNEASHLVTDRIRRTVKFLC ALGKGIPILSLNWLYQSRKAGCFLPP DDYLVTDPEQEKNFSFSLRDSLCRA RERRLLEDYEIHVTPGVQPPPPQMG EIISCCGGTFLPSMPHSYKLHRVIITC TEDLPRCAIPSRLGLPLLSPEFLLTGV LKQEATPEAFVLSNLEMSST	None	None	None	None	None	None	None	None	No