

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
E9Q6J5	BD1L1_MOUSE	Mus musculus	Biorientation of chromosomes in cell division protein 1-like 1	27.339469	T1406	S264;S480;S482;S632;S656;T657;S1071;S1138;S1315;S1364;S1676;S1685;S1989;S2001;S2092;S2166;S2417;S2443;S2554;S2681;S2840;S2841;S2888;T2890;S2892;S2898;S2907;S2920;S3000	28528544;30059200	MATNPQPQPPPPAPPPPPQPPPPPPPPGAGPGASGPGSAGAGADPQLVAMIVNHLKSQGLFDQFRRDCLADVDTKPAYQNLRQRVDNFVANHLATHTWSPHLNKNQLRNNIRQQVLKSGMLESGLDRIISQVVDPKINHTRFPQVEKAVHEFLATLNHKEEAAGSTAPDDEKPESSVITQGAPAPGPGSANVASDAMSILETITSLNQEANAARASTEMSNKV SERTSRKLSQPSTDVSTDKERGSE DATEEREKATSDSGDGLAALKSEE PSDLPCPVEETKNHMKENSLLLLS KDAQQUESTDPKIKSMDKGEKPKDG NEKGERKKEKKEKTEKKIDHSKRNE DTQKVKDERQAKDKEVESTKLPSEK SNRARAEEGTEKDCSLLSDVDGL TDITVSSVHTSDLSSFEEDETEEVVV SESMEEGEITSEDEEKQKQKAKVQ PGDSSDGKARGVRHAYVHKPYLYSK YYSDDDELTVQRRQSIKEKEERL LRRRINREKLEEKRRQKAEKTKSSK VKSQKSTVDLEDSSAKTLEPKAPRI KEVLKERKVLKVALSKRRRKDSR NVDENSKKKPQAEESKEALKTTEY CEKEKASSKDLRHTHGKGEPSRPAR RLSESLHSADENKTESKVEREYKRR TSTPVILEGAQEETDTRDGKQPERS ETNVEETQKQSTLKNKYQKDDP ETHGKGLPKKEAKSAKERPEKEKAQ SEDKPSSKHKHKGDSVHKMSDETE LHSSEKGETEESVRKQGGQTKLSSD DRTERKSKHKSEERRLSVLGRDGKPV SEYTIKTDEHARKDNKKEKHLSSSEK SKAEHKSRRSSDKLQKDALSSQKH SVTSOKRSESCSEDKCETDSTNADS SFKPEELPHKERRRDKSLEDKVVS KSKSKGQSKQTKAAETEAEQEGVTRQ VTTPKPDKEKNTEDNTERQRKFKL EDRTSEETVTDPALENTVSSAHSQ KDSGHRAKLASIKEKHKTDKDSTSS KLERKVS DGHRSRSLKHSNKMCK KEENKPD KNGKEVDS SHEKGRGN GPVTEKLSRRLCENRRGSTSQEMA KEDKLVANMSGTTSSSSLQRPKST ETTSIPEQEPMEIDSEAAENVSELS KTEDISSNSSQQDTDFENVTKHKAT AGVLKDEFRTSMVDSKPAAAVTCKS GRGLAVTSISERHADHKSTLTKKVH SQGNPSKAAPREREPIORGAQEVSV DSEVSRKALSRAPESENEKGQKNLKG MSKTTEECGTHRNASLEYSTDSDL SSSGVTVPQKESHNSNTIPVIDRE AISEGGRASTSLANHSVDPNQYSTV KKSEVHTNGSKEGNDGFTVDMPT KANGGSKRHLSQATLLYSKESKI SIPLADKSM SVTGDKNKNKQ RSLM GTAKRESDLKVNPDIKQD SAAGEHV VDLSTRKEAETVRRKHKEIPTDVE RKTENSEVDTSAARRDSAPVPQQRHG KMERGAAGSGRRDKAFIATSTEGTD KGIMLNTVKTGDATTSSEVGEKGT ALPCTSIEADEGFMGACPKKHPLQ VGAEASECTVFAAAEEGKGVVTEGF AESEILLTSSKEGESGECAVAE SEDR VAGPLAAHTVQAEANVNSITTEEKD DAVTSAGSEKCGGSACTVEGTATFI GEVESDGAVTSAGTEIRAGLSSEDEV DGSQENRIQVGPKKEETEGVTCTET KGRNDNFICLVTRVETQEQRVVTGA DVVQVNAAKPQEANANQDGS GTD GAEGESAVTSTGITEEDGEASANT GSEDNREGCAISSETEE SAESAMDS TEAKDITNAPLVAAGPCDDEGIVTST GAKEEDEDEGVVSTGRGNEPGH ASACTGIEESEGMVCESGEGGAI GPTIDHVNAEAGAA TVNTNDSNVDS MSGAEKEIKDTNICSSAKGIVESSVT SALAGNSDRPPVLCGSEGPMASS HHSDSQLTRKETVEDTTISTGLVKGS DDVLVSGEVPECEVGHMSPRKNEE	None	None	None	None	None	None	None	

CDGLMASTASCDVSNKDSLGSKSQ
GNGLMISTSTNACTPQISAVIDVRGG
HLSTLSTEEIRDGVRVHREGFEAPM
PSAVSGENSQLTASRSEKDECAMI
STSIGEEFELPISSAVTVCAERQQPV
AAVEESTTGPALVSTEDFEVPMPSAP
TEAESPLASTSKEEKDECALISTSIAE
ECEASVFGVSRNAPSVTDGNAVISTS
SVEDCEGSVSSAVPQESVCPVIPVE
ETGDTAMISTSTSEGREAVMVGTIPT
DDDQATTVRGEDLSDAIIISTSTAEC
VLTCTSLSRHEENQATHNPEGNG
GHLATKQSKCELPMPSLVAERNCKC
PGPFRMGKGVGPLMAVGTRGEHDR
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GMDCPGQDLNAKERNTLLSSVQRE
SKSAEAEAAGDSSTARTRVRKDSER
NANSLSETNCLREPEQKPAEDTSGS
THCLTAVNPGA EADGMLPITHAALE
YPDHQEPESNLKTTTKCITGQESQM
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ARQSFHREGNLDVTLPPEDNGCGV
GNEESPFGIGGLELSTGLTTEISVS
SEEDTSHGVVAAPENPCVGRRRGAA
ELQMEALLMRESLNVEKSESRINEE
IHFESQNKEIICCGRKGSSTEALSGCS
VEADPEEVEEEEKQISQRNRKPDYS
SSEELDDSPDVLDSRIETAQRQYSE
TEPHDTKEENSGDVEEFSSVTSKTN
SSTGLEDRDEFSSSEGTGKTEPNE
DDGSIKSQEDDHPIIKRRRGRPRKY
PAETAFKSKEDSKTETDITVEQSSP
SGKLKVSQADESNKEIANLEEKSTS
NDDSEKTASMLRGRKPKRSLTSS
DDAESSEPERKRQKSVSETSEDKKD
EESDEEEEEEEEEPLGATTRSATRS
EAQRKNHSPSTRATSKLGIPETISP
RNRQKLAKEKLTSEKVSXSPPLGR
SKAQLSPSVKRRREVSPPGARTRGQ
QKVDENPLKAKR