

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q8NFC6	BD1L1_HUMAN	Homo sapiens	Biorientation of chromosomes in cell division protein 1-like 1	22.981145	T1540	S266;S482;S484;S635;S659;T660;T733;S1077;S1145;S1318;T1354;S1531;S1701;S1710;S2013;S2025;S2128;S2203;S2475;S2501;S2618;S2905;S2907;S2954;T2956;S2958;S2964;S2973;S2986;S3019	30379171;28411811;23301498;30620550;35254053;30059200	MATNPQPQPPPPAPPPPPQPPQP PPPPPGGAGPGAGGAGGAGAGD POLVAMIVNHLKSQLFDQFRDCL ADVDTKPAYQNLQRVDNFVANHL ATHHTWSPHLNKNQLRNNIRQVQLK SGMLESgidriHSQVVDPKINHTRFRP QVEKAVHEFLATLNHKEEGSGNTAP DDEKPDTSLITQGVPTPGPSANVAN DAMSILETTITSLNQEASAAARASTETS NAKTSERASKLPSQPTTDTSTDKE RTSEDMADKEKSTADSGGEGLETAP KSEEFSDLPCPVEEIKNYTKEHNNLI LLNKDVQQESSEQKNKSTDKGEKKP DSNEKGERKKEKKEKTEKKFDHSKK SEDTQKVKDEKQAKEKEVESLKLPS EKNSNKAKTVEGTEKDFSLIDSDVD GLTDITVSSVHTSDLSSFEEDTEEEV VTSDSMEEGEITSDDEEKNKQNKTK TQTSDSSEGTKSVRHHVYVHKPYLY SKYYSDSDDELTVQRQSIKAKEKEE RLLRROINREKLEEKRKQKAEKTKS SKTKGGRSSVDLEESSTKSLEPKA ARIKEVLKERVLEKVALSKRRKCD SRNVEENSKKQYEEEDSKETLKTS EHCEKEKISSKELKHVHAKSEPSK PARRLSESLHVVDENKNESKLEREH KRRTSTPVIMEGVQEEETDRDVKRQ VERSEICTEFPQKQKSTLNKNEHLK KDDSETPHLKSLKKEVKSSEKPE REKTPSEDKLSVKHKYKGDGMHKT GDETELHSSSEKGLKVEENIQKQSQQ TKLSSDDKTERKSKHRNERKLSVLG KDGKPVSEYIITDENVRKNNKKE RRLSAEKTAEHKSRRSSDSKIQKD SLGSKOHGITLQRRSESYSEDKCDM DSTNMDSNLKPVEEVHKEKRRTKS LLEEKLVLSKSKTQKQVQVQVETEL QEGATKQATTPKPDKEKNTTEENDSE KQRKSKVEDKPFEEETGVEPVLETAS SSAHSTQKDSHRAKLPLAKEKYKS DKDSTSTRLERKLSDGHKSRSLKHS SKDIKKDENKSDDKDGKEVDSSHE KARGNSSLMEKKLSRRLCENRRGSL SQEMAKGEEKLAANTLSTPSGSSLQ RPKKSQDMTLIPEQEPMEIDSEPGV ENVFEVSKTQDNRNNNSQDDIDSE NMKQKTSATVQKDELRTCTADSKAT APAYKGRGTGVNSNSEKHADHRST LTKKMHQSAVSKMNPGEKEPIHRG TTEVNIDSETVHRMLLSAPSENDRV QKNLKNATAAEHVAQGDATLEHST NLDSSPSLSSVTVPLRESYDPPVIP LFDKRTVLEGSTASTSPADHSALPN QSLTVRESEVLKTSDSKEGGEGFTV DTPAKASITSKRHIPEAHQATLLDGK QGVVIMPLGSKLTGVIVENENITKEG GLVDMAKKENDLNAEPNLKQTIKAT VENGGKDGIAVDHVGLNTEKYAET VKLKHKRSKPGKVKDISIDVERRNEN SEVDTSAAGSGSAPSVLHQRNGQTED VATGPRRAEKTSVATSTEGKDKDVT LSPVKAGPATTSSSETROSEVALPCT SIEADEGLIIGTHSRNNPLHVGAEAS ECTVFAAAEEGGAVVTEGFAESETFL TSTKEGESGECVAESEDRAADLLA VHAVKIEANVNSVVTTEKDDAVTSA GSEKCDGSLSRDSEIVEGTITFISEV ESDGAVTSAGTEIRAGSISSEEVDSG QGNMRRMGPKKETEGETVTCTGAEG RSDNFVICSVTGAGPREERMVTGAG VVLGDNDAPPGTSASQEGDGSVND GTEGESAVTSTGITEDGEGPASCSTGS EDSSEGFAISSESEENGESAMDSTV AKEGTNVPLVAAGPCDDEGIVTSTG AKEEDEEGEDVVTSTGRGNEIGHAS TCTGLGEESEGLICESAEGDSQIGT VVEHVAEAGAAMNANENNVDMS SGTEKSKDITDICSASAKGIVESSVTS AVSGKDEVTPVPGGCEGPMNTSAASD QSDSQLEKVEDTITSTGLVGGSYDVL	None	None	None	None	None	None	None

VSGEVPECEVAHTSPSEKEDEDIITS
VENECDGLMATTASGDITNQNLSLA
GGKNQGLVLIISTTTNDYTPQVSAI
TDVEGGLSDALRTEENMEGTRVTTE
EFEAPMPSAVSGDDSQLTASRSEEK
DECAMISTSIGEEFELPISSATTIKCA
ESLQPVAAAVEERATGPVLISTADFE
GPMPSAPPEAESPLASTSKEEKDEC
ALISTSIAEECEASVSGVVVESENER
AGTVMEEKDGGSIHSTSSVEDCEGPV
SSAVPQEEGDPSTVPAEEMGDTAMI
STSTSEGCEAVMIGAVLQDEDRLITIT
RVEDLSDAAIISTSTAECMPISASIDR
HEENQLTADNPEGNGDLSATEVSK
HKVPMPSLIAENNCRCPGVRGGKE
PGPVLAVSTEEGHNGPSVHKPSAGQ
GHPSAVCAEKEEKHGKECPEIGPFA
GRGQESTLHLINAEKVNLLNSLQ
KEDKSPETGTAGGSSTASYSAGRGL
EGNANSPAHLRGPETSGQTAKDPS
VSIRYLAAVNTGAIKADDMPVQGTV
AEHSFLPAEQGSEDNLKTTTKCIT
GQESKIAPSHTMIPPATYSVALLAPK
CEODLTIKNDYSGKWTDQASAEKGT
DDNSTRKSFPEEGDIMVTVSSEENV
CDIGNEESPLNVLGGLKLANLKME
AYVPSEEEKNGEILAPPESLCGGKPS
GIAELQREPLLVNESLNVENSGFRT
NEEIHSESYNKGEISSGRKDNAAEIS
GHSVEADPKVEEEEEHRMPKRKRK
QHLYSSEDEPDDNPDVLSRIETAQ
RQCPETEPHDTKEENSRDLEELPKT
SSETNSTTSRVMEEKDEYSSSETTG
EKPEQNDDDTIKSQEEDQPIIKRKR
GRPRKYPVETTLKMKDSDKTDGIV
TVEQSPSSSKLVMTDESNETAN
LQERSISNDDGEEKIVTSVRRRGRKP
KRSLTVSDDAESSEPERKRQKSVSD
PVEDKKEQESDEEEEEDEPSGA
TTRSTTRSEAQRSKTQLSPSIKRRKRE
VSPPGARTRGQQRVEEAPVKKAKR