

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
E9Q7G0	NUMA1_MOUSE	Mus musculus	Nuclear mitotic apparatus protein 1	27.281412	S1826;T2074	S160;T161;S167;S201;T209;S269;S386;S398;S1183;S1221;S1583;S1703;S1706;S1710;S1739;S1742;S1751;S1754;T1756;T1758;S1771;S1774;S1782;T1786;S1812;S1815;S1816;T1818;S1822;S1826;S1844;S1869;S1951;S1973;S1974;T1982;S1985;T1997;S2029;T2037;S2044;S2059;S2069;T2085	22645316;28528544;36852467	MTLHATRAATLLSWVNSLHVADPVE TVLQLQDCSIFIKIINTIHDTKEGQQI LQQPLPERLDFVCSFLQKNRKHPS TQCLVSVQKVIEGSEMELAKMIMLF LYQSTMSSRNLRDWEQFEYGVQAE LAVILKFMLDHEESNLNLTEDLESFLE KVPYTHASTLSEELSPPSHQTKRKIR FLEIQRIASSSENFLSGSPSPMG DILQTPQFQMRRLKQLADERSNRD DLELESESLKLLTEKDAQIAMMQQ RIDHLALLNEKQAASSQEPSELEELR GKNESLTVRLHETLTKQCQNLKTEKS QMDRKISQLSEENGDLSEFKVREFAN HLQQLQGAFNDLIEEHSKASQEWA EKQARLENELSTALQDKKCLEEKNE ILQGKLSQLEDQATRLQESPAPKGE VLGDALQLDTLKQEAAKLATDNTQL QTRVETLECEGKQEAQLLAERSRF EDEKQQLASLIADLQSSVSNLSQAK EELEQASQAQGAQLTAQLTSMTGLN ATLQQRDQELASLKEQAKKEQAQM LQTMQEQEAAQGLRQOVELSSS LKLKEQQLEEAQEQEATRQDHAQ QLAIVAEAREASLRERDTARQQLETV EKEKDAKLESLQQQLQAANDARDN AQTSVTQAQQEKAELSQKIGELHACI EASHQEQRQVQARVTELEAQLKAEQ QKTTEREKVVQEKALQEQQLRALEE SLKITKGSLEEEKRRAADALKEQQC RATEMEAESRSLMEQREEREQKELE QEKAGRKGLEARIQQLEEAHQAE ALRHELAEATASQHRAESECEERLIRE VESRQKRFEARQEQEARYGAMFQE QLMALKGEKTGQEVQEEAVEIHSEG QPGQQQSQAQLHASLAKAIQQVQE KEVRAQKLVDDLALQEKMAATNKE VACLKTLVLKAGEQQETASLELLKEP PRAANRASDQLGEQQGRPFSTHAA VKAMEREAEQMGGELERLRAALIKS QGQQQEERGQQEREVARLTQERGQ AQADLAQEKAAKAELEMRLQNTLN EQRVEFAALQEALAHALTEKEGTDQ ELAKLRGQEAARTELKELQQTLEQ LKIQLVKKEKEHPAGGASGEDASGP GTQSETAGKTDAPGPELQALRAEISK LEQQCQQQQQVEGLTHSLKSERA CRAEQDKALETLOGQLEEKARELGH NQAASASAQRELQALRAKAQDHSKA EEEWKAQVARGQQAERKSSLISSL EEEVSILNRQVLEKEGESKELKRLVV AESEKSQKLEERLRLQVETASNSA RAAERSALREEVQSLREEVEKQRV VSENSRQELASQAERAELGQELKA WQEKFFQKEQALSALQLEHTSTQAL

VSELLPAKHLCQQLQAEQAAAQKRF
REELEQSKQAAGGLQAEMLRAQRE
LGELGSLRQKIVEQERAAQQLRAEK
ASYAEQLSMLKKAHGLLAEENRGLG
ERANLGRQFLEVELDQAREKYVQEL
AAVRTDAETHLAEMRQEAQSTSREL
EVMTAKYEGAKVKVLEERQRFQEEER
QKLTAQVEELSKKLTEHDQASKVQQ
QKLKAFQAQRGESQQEVQRLQTL
NELQAQLSQKEQAAEHYKLQMEKA
KTHYDAKKQONQKLQEQLQDLEEL
QKENKELRSEAERLGRELQQAGLKT
KEAEQTCRHLTAQVRSLEAQAHAHAD
QQLRDLGKGFQVATDALKSREPQVKP
QLDLSIDSLDLSLEEGTPCSVASKLP
RTQPDGTSVPGEPASPISQRLPPKVE
SLESLYFTPTPARGQAPLETSLDSL
DAFPDSGRKTRSARRRTTQIINITMT
KKLELEEPDSANSSFYSTQSAPASQA
NLRATSSTQSLARLGPDDGNSALL
SLPGYRPTTRSSARRSQARMSSGAP
QGRNSFYMGTCQDEPEQLDDWNRI
AELQQRNRVCPHLLKTCYPLESRPT
LSLATITDEEMKTGDPRETLRRASM
QPAQIAEGVITTRQQRKRVSETHQ
GPGTPESKKATSCFPRPMTPRDRHE
GRKQSSTADTQKKAAPVLKQADRRQ
SMAFSILNTPKKLGNLRRGASKK
TPAKVSPNPRSGTRRSRIATTTTGT
ATVATTTPRAKGKVKH