

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi appa
E9Q7G0	NUMA1_MOUSE	Mus musculus	Nuclear mitotic apparatus protein 1	45.535487	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;40885482;36852467;28528544;39627609	MTLHATRAATLLSWVNSLHVADPVE TVLQLQDQCSIFIKIINTIHTDKEGQOI LQOPLPERLDFVCSFLQKNRKHPPS TQCLVSVQKVIIEGSEMELAKMIMLF LYQSTMSRRNLRDWEQFEYGVQAE LAVILKFMILDHEESLNLTEDLESFLE KVPTYHASTLSEELSPPHSHQTKRKIR FLEIQRIASSSSENNFLSGSPSPMG DILQTPQFQMRRLKKQLADERSNRD DLELESESLKLLTEKDAQIAMMQQ RIDHLALLNEKQAASSQEPSELEELR GKNESLTVRLHETLKQCNLKTTEKS QMDRKISQLSEENGDLKSFVREFAN HLQQLQGFANDLIEEHSKASQEWA EKQARLENELSTALQDKKCLEEKNE ILQGKLSQLEDQATRLQESPAPEKGE VLGDALQLDTLQEAALATDNTQL QTRVETLEECERKQEAQLLAERSRF EDEKQQLASLIADLQSSVNSLSQAK EELEQASQAQGAQLTAQLTSMGLN ATLQQRDQELASLKEQAKKEQAQM LQTMQEQEQAAQGLRQVQEQQLSSS LKLKEQQLLEAAKEQEATRODHAQ QLAIVAEAREASLRERDTARQOLETV EKEKDAKLESLQQQLQAANDARDN AQTSVTAQEQEKAELSQKIGELHACI EASHQEQRQVQARVTELEAQLKAEQ QKTTEREKVQEKALQEQLELRALEE SLKITKGSLEEEKRAADALKEQQC RATEMEAEASRLMEQREREQKELE QEKAGRKGLEARIQLEEAHQAEATE ALRHLEAEATASQHRAESECELRIRE VESROKRFEARQEEARYGAMFQE QLMALKGEKTGQEVQEEAVEIHSEG QPGQQQSOLAQLHASLAKAIQVQVE KEVRAQKLVDDLSALQEKMAATNKE VACLKTLVLKAGEQOETASLELLKEP PRAANRASDQLGEQGRPFSSSTHAA VKAMERAEQMGGELERLRAALIKS QGQQQEEERGQOEREVARLTOERGQ AQADLAQEKAAKAELEMLRQNTLN EQRVFAALQEALAHALTEKEGTDQ ELAKLRGQEAARTELKELQQTLEQ LKIQLVKKEKEHPAGGASGEDASGP GTQSETAGKTDAPGPELQALRAEISK LEQQCQQQQQVEGLTHSLKSERA CRAEQDKALETLLQGLEEKARELGH NQAASASAQRELQALRAKAQDHSKA EEEWKAQVARGQEAERKSSLISSL EEEVSILNRQVLEKEGESKELKRLVV AESEKSQKLEERLRLQVETASNSA RAAERSSALREEVQSLREEVEKQRV VSENSRQELASQAERAELGQELKA WQEKFFQKEQALQLEHTSTQAL VSELLPAKHLCOQLQAEQAAAEKRF REELEQSKQAAGGLQAEMLRAQRE LGELGSLRQKIVEQERAAQQLRAEK ASYAEQLSMLKKAHGLLAEENRGLG ERANLGRQFLEVELDQAREKYVQEL AAVRTDAETHLAEMRQEAQSTSREL EVMTAKYEGAKVKVLEERQRFQEEER QKLTAEVEELSCKLTHEHQASKVQQ QKLKAFQAQRGESQEQEVRLQOTQL NELQAQLSQKEQAAEHYKLOMEKA KTHYDAKKQONQKLQEQLDLEEL QKENKELRSEAEERLGRELQQAAGLKT KEAEQTCRHLLTAQVRSLEAQVAHAD QQLRDLGKFQVATDALKSREPQVKP QLDLSIDSLDLSLEEGTPCSVASKLP RTQPDGTSVPGEPASPISQRLPPKVE SLESYFTPTPARQAPLETSLDLSLG DAFPDGRKTRARRRITQIINITMT KKLELEEPSANSFFYSTQSPASQA NLRATSSTQSLARLGSPPDDGNSALL SLPGYRPTTRSSARRSQARMSSGAP QGRNSFYMGTCDQEPEQLDDWNRI AELQQRNRVCPHLLKTCYPLESRPT LSLATITDEEMKTDGPRETLRRASQ QPAQIAEGVGITRQQRKRVSSETHO GPGTPESKKATSCFRPMTPRDRHE	True	False	3.016	5.0	2.984	1.205	2.821

