

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q14980	NUMA1_HUMAN	Homo sapiens	Nuclear mitotic apparatus protein 1	42.417556	S745;S962;T963;S1317;T1489;S1837;S1840;S1844;S1847;T2093	S162;T163;S169;S203;T211;S271;S388;S395;S820;T1047;S1187;S1225;S1601;S1721;S1724;S1728;S1757;S1760;S1769;S1772;T1774;T1776;S1788;S1789;S1792;S1800;T1804;S1830;S1833;S1834;T1836;S1840;S1844;S1862;S1887;S1969;S1991;T2000;S2003;T2015;S2047;T2055;S2062;S2077;S2087;T2106	3626323;16408927;20068230;33214551;30059200;27655845;31492838;32119511;34229054;33465208;28657654;32574038;29351928;34019948;26853435;23301498;28510447	MTLHATRGAALLSWVNSLHVADPV EAVLQLQDCSIFIKIIDRIHGTTEEGQQ ILKQPVSERLDFVCSFLQKNRKHFPSS PECLVSAQKVLEGSLELAKMTMLL LYHSTMSSKSPRDWEQFEYKIQAEL AVILKFVLDHEDGLNLNEDLENFLQ KAPVPSTCSSTFPEELSPPSHKAKRE IRFLELQKVASSSSGNNFLSGSPASP MGDILQTPQFQMRRLKQLADERS NRDELELELAENRKLLETKDAQIAM MQQRIDRLALLNEKQAASPLEPKEL EELRDKNESLTMRLHETLKQCQDL KTEKQMDRINQLSENGDLSFKL REFASHLQQLQDALNELTEHHSKAT QEWLEKQAQLEKELSAALQDKKCLE EKNEILQGKLSQLEEHLSQLQDNPP QEKGEVLGDVQLLETTLKQEAATLAA NNTQLQARVEMLETERGQQEAKLL AERGFHEEKQQLSSLITDLQSSISN LSQAKEELEQASQAHGARLTAQVAS LTSELTTLNATIQQDQELAGLKQO AKEKQAQLAQTLLQQEQASQGLRH QVEQLSSSLKQKEQQLKEVAEKQEA TRQDHAQQLATAAEEREASLRERDA ALKQLEALEKEKAAKLEILQQQLQVA NEARDAQTSVTAQREKAELSRKV EELQACVETARQEQHEAQAQVAELE LQLRSEQQKATEKERVAQEKDQLQE QLQALKEKSLKVTKGSLEEEKRRAAD ALEEQRCISELKAETRSLVEQHQR ERKELEERAGRKGLEARLQQLGEA HQAETEVLRRLEAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEEAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELAE LHANLARALQQVQKEVRAQKLD DLSTLQEKMAATSKEVARLETLVK AGEQQETASRELVKEPARAGDRQPE WLEEQQGRQFCSTQAALQAMEREA EQMGNELERLRAALMESQGGQQEE RGQQEREVARLTQERGRAQADLAE KAARAELEMRLQNALNEQRFVATL QEALAHALTEKEGKDQELAKLRGLE AAQIKELEELRQTVKQLKEQLAKKE KEHASGSGAQSEAAGRTEPTGPKLE ALRAEVSKLEQQCQKQEQADSLER SLEAERASRAERDSALETLQGQLEE KAQELGHSQSALASAQRELAAFRTK VQDHSKAEDEWKAQVARGRQEAER KNSLISSLEEEVSILNRQVLEKEGES KELKRLVMAESEKSKLEERLRLLO AETASNSARAAERSALREEVQSLR EEAEKQRVASENLRQELTSQAERAE ELGQELKAWQEKFFQKEQALSTLQL EHTSTQALVSELLPAKHLCQQLQAE QAAAEKRHRELEQSKQAAGGLRAE LLRAQRELGELIPLRQKVAEQERTAQ QLRAEKASYAEQLSMLKKAHGLLAE ENRGLGERANLGRQFLEVELDQAR EKYVQELAAVRDAETRLAEVQREA QSTARELEVMTAKYEGAKVKVLEER QRFOEERQKLTAEVQLEVFQREOT KQVEELSKKLADSDQASKVQQQKLK

AVQAQGGESQQAERLQAQLNELQ
AQLSQKEQAAEHYKLQMEKAKTHY
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LNTPKKLGNLRRGASKKALKAS
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