

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q14980	NUMA1_HUMAN	Homo sapiens	Nuclear mitotic apparatus protein 1	35.208039	S158;T159;S745;S962;T963;S1317;T1489;S1800;S1837;S1840;S1844;S1847;T2092;T2093;T2094;S2096;T2099;T2106	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	32119511;34725712;35132862;23301498;34229054;32574038;28510447;30059200;20068230;35289036;33214551;35083852;34019948;16408927;35254053;26853435;37340703;27655845;28657654;35138101;33465208;34846842;31492838;29351928	MTLHATRGAALLSWVNSLHVADPV EAVLQLQDCSIFIKIDRIHGTTEEGQQ ILKQPVSERLDFVCSFLQNRKHPSS PECLVSAQKVLEGSLELAKMTMLL LYHSTMSKSPRDWEQFEYKIQAEL AVILKFVLDHEDGLNLNEDLENFLQ KAPVSTCSSTFPEELSPPSHQAKRE IRFLELQKVASSSSGNNFLSGSPASP MGDILQTPQFQMRRLKQLADERS NRDELELELAENRKLLETKDAQIAM MQQRIDRLALLNEKQAASPLEPKEL EELRDKNESLTMRLHETLKQCQDL KTEKQMDRINQLSENGDLSFKL REFASHLQQLQDALNELTEHHSKAT QEWLEKQAQLEKELSAALQDKKCLE EKNEILQGGKLSQLEEHLSQLQDNPP QEKGEVLGDVQLLETTLKQEAATLAA NNTQLQARVEMLETERGQQEAKLL AERGFHEEKQQLSSLITDLQSSISN LSQAKEELEQASQAHGARLTAQVAS LTSELTTLNATIQQQDQELAGLKQO AKEKQAQLAQLTQQQEASQGLRH QVEQLSSSLKQKEQQLKEVAEKQEA TRQDHAQQLATAAEEREASLRERDA ALKQLEALEKEKAAKLEILQQQLQVA NEARDSAQTSVTQAQREKAELSRKV EELQACVETARQEQHEAQVAEAELE LQLRSEQQKATEKERVAQEKDQLQE QLQALKESLKVTKGSLSEEEKRRAAD ALEEQRCISELKAETRSLVEQHKR ERKELEERAGRKGLEARLQQLGEA HQAETEVLRRLEAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEAAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELAE LHANLARALQQVQKEVRAQKLD DLSTLQEKMAATSKEVARLETIVRK AGEQQETASRELVKEPARAGDRQPE WLEEQQGRQFCSTQAALQAMEREA EQMGNELERLRAALMESQGGQQEE RGQQEREVARLTQERGRAQADLAE KAARAELEMRLQNALNEQRFVAFATL QEALAHALTEKEGKDQELAKLRGLE AAQIKELEELRQTVKQLKEQLAKKE KEHASGGAQSEAAGRTEPTGPKLE ALRAEVSKLEQQCQKQEQADSLER SLEAERASRAERDSALETLQGQLEE KAQELGHSQSALASAQRELAAFRTK VQDHSKAEDEWKAQVARGRQEAER KNSLISSLEEEVSILNRQVLEKEGES KELKRLVMAESEKSKLEERLRLLO AETASNSARAAERSALREEVQSLR EEAEKQRVASENLRQELTSQAERAE ELGQELKAWQEKFFQKEQALSTLQL EHTSTQALVSELLPAKHLCQQLQAE QAAAEKRHRELEQSKQAAGGLRAE LLRAQRELGELIPLRQKVAEQERTAQ QLRAEKASYAEQLSMLKKAHGLLAE ENRGLGERANLGRQFLEVELDQAR EKYVQELAAVRADAETRLAEVQREA QSTARELEVMTAKYEGAKVKVLEER QRFOEERQKLTAQVEQLEVFQREQT KQVEELSKKLADSDQASKVQQQKLK

