

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q6PFD9	NUP98_MOUSE	Mus musculus	Nuclear pore complex protein Nup98-Nup96	51.121228	S262;T263;T264;T268;T281;S1033;T1092	S524;S608;S612;S618;S623;S625;S653;T670;S673;S680;S681;S839;S888;S934;S1027;S1042;S1059;S1063;T1069;S1328;T1771	22645316;34887587;21606357;36852467;29187734;39627609;40997131	MFNKSFGTFFGGSTGGFGTTSTFGQNTGFGTTSGGAFGTSAFGSSNNTGG LFGNSQTKPGGLFGTSSFSQPATSTS TGFGFGTSTGTSNSLFGTASTGTSLF SSQNNFAAQNKPTGFGNFGTSTSSG GLFGTTNTTNSNPFGSTSGSLFGPSSF TAAPTGTTIKFNPTGTDTMVKAGVS TNISTKHQCITAMKEYESKSLLEELRL EDYQANRKGPNQVGGGTTAGLFG SSPATSSATGLFSSSTNSAFSYGQN KTAFTSTTTGFGTNPGGFLGQQNQ TTSLFSKPFQATTPNTGFSFGNTS TLGQPSTNTMGLFGVTQASQPGGLF GTATNTSTGTAFTGTGLFGQPNTG FGAVGSTLFGNNKLTTFGTSTTSAPS FGTTSGGLFGNKPTLTLGTNTNTSN FGFNTNNSGSSIFGSKPAAGTLGTGL GTGFGTALGAGQASLFGNNQPKIGG PLGTGAFGAPGNTSTAILGFGAPQA PVALTDPNAAAQAVLQOHLNSLT YSPFGDSPFRNPMSPDKKKEERLK PTNPAQKALTPPTHYKLTTPRPATRV RPKALQTTGTAKSHLFDGLDDDEPS LANGAFMPKKSIKKLVKLNNSNL FSPVNHSEDLASPSEYPENGERFS FLSPKPVDENNQQDGEDDSLVSRYT NPIAKPIQTPESVGNKNNSSNVE DTIVALNMRALRNGLEGSSETSF HDESLQDDREEIENAYHHIPAGIV LTKVGYTIPSMDDLAKITNEKGECI VSDFTIGRKGYSIYFEGDVNLTNLN LDDIVHRRKEVIVYVDDNQKPPVGE GLNRKAEVTLDGWVPTDKTSRCLIK SPDRLADINYEGRLEAVSRKQGAQF KEYRPTGSWVFKVSHFSKYGLQDS DEEEEEHPPKTTSKKLTAPLPPAGQ ATTFQMTLNGKPAPPQSQSPEVEQ LGRVVELDSDMVDITQEPVPDSVLE ESVPEDEQEPVSASTHIASSLGINPHV LQIMKASLLVDEEDVDAMDQRFGHI PSKGETVQEI CSPRLPISASHSSKSR SIVGGLLQSKFASGTFLSPASVQEC RTPRTSSRMNIPSTSPWSVPLPLATV FTVPSPAPEVQLKTVGIRROPGLVPL EKSITYGKGLLMDMALFMGRSFRV GWGPNWTLANSGEQLHGSHLEN HQVADSMEYGF LNPVAVKSLSESP FKVHLEKGLRQRKLDLQLYQTP LELKHKHSTVHVDELCLVNPVGS VIHADWVKDSPGDFLELPIVKHW SLTWTLCEALWGHKELDQQLDEPS EYIQLERRRAFSRWLSHTAAPQIEE EVSLTRRDSPEAVFSYLTGSRISGA CCLAQQSGDHRLLALLS QLVGSQSV RELLTMQLADWHQLQADSFIHDER LRIFALLAGKPVWQLSEQKQINVC S QLDWKRTLAIHLWYLLPPTASISRAL SMYEEAFQNTPEGDKYACSPSYL EGCGCMVEEEKDSRRPLQDVCFHL LKLYSDRHYELNOLLEPRITADPLD YRLSWHLWEVLRALNYTHLSEQCE GVLQASYAGOLESEGLWEWAIFVFL HIDNSGMREKAVRELLTRHCQLSET PESWAKEAFLTKLCPAEWIHEAK AVRAHMESNKHLEALYLFKAGHWN RCHKLVIRHLASDAIINENYDYLKGF LEDLAPPERSSLIQDWETSGLVYLDY IRVIEMLHRIQVDCSGYELEHLHTK VTSLCNRIEQIPCNAKDRLAQSDM AKRVANLLRVVLSLQHPDATSNST PDPQRVPLRLLAPHIGRLPMPEDYAL EELRGLTQSYLRELTVGSQ	True	False	2.445	5.0	2.368