

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9VCH5	NUP98_DROME	Drosophila melanogaster	Nuclear pore complex protein Nup98-Nup96	28.06426	S17;S434;T603	NaN	40245499	MFGGAKPSFGATPAATSFGGFSGTT TTTTPFQGSFAFGKPAAPAFGNTSTFAA QPAQQSLFGAAATPAQPAGGLFGAN TSTGFGSTATAOPTAFGAFSQPQOTS NIFGSTQTAASLFLGGQSTLPAFGAA KPTMTAFGQTAAAQPTGSLFGQPAA ATSTTGFGGFGTSAPTTTINVFGSGTA SAFAQPQATAVGASGVNTGTAVAKY QPTIGTDTLMKSGQANSVNTKQHCI TAMKEFEKGSLEELRLEDYMCGRK GPQAGNAPGAFGGAQVTQPAQPAS GGLFGSTAQPSTGLFGQVTENKSM FGTTAFGQQPATNNAFGAATQQNN FLQKPFGATTTTFFAAPAADASNPF AKPAFGQGGSLFGQAPATSAAAPAFG QTNTGFGGFGTTAGATQOSTLFGAT PAADPNKSAFGLGTAASAATTGFGF GAPATSTAGGGLFGNKPATSFAPTF GATSTASTPFSNFGGLNTSTAATGGG LFNSGLNKPATSGFGGFGATSAAPL NFNAGNTGGSFLGNTAKPGGGLFG GGTTTLGGTGAAPTGGFLGGGTTSF GGVGGSLGGGFGMGTNNSLTGGI MGAQPTLGIMTPSHQPIHQILARV TSPYGDSPFKDLKLSSEADATRATN PAAQQAVLDTLSNQYKISTSNNPAP MKVKALGSTLNRKSLFDGLEEFDA VEGFNLKPSAKRLVIKPKVKSVEGG NPSSSIGSAPNTPQSRPKGATPNKER ESFSGAIPSEPLPAGNSPGATNGRE SQDNGRRRESWLHPNMLEKVRQHNI QTGMDQGSPhNSTLNELVPRKPLD TYRPSSTVRLSVSTIPENPFEDQSTI ARRETFTSQANESVLSNRSNEAED SAANQSRLAIEAAAAEAADESHT GIVLRRVGYTIPSLDDLRSYLAEDG SCVVPNFTVREGYGNVFFGKEMD VAGLNLDEIVHFRNKEIHYDDENK PPIGQLNRDAQVTLQVWPLDKTK HEAIKDPQRLLEMDWEGKLRVCD KNDTRFIEYRPETGSWVFRVKHFSK YGLGDSDEDELPTDPKKAKIATLEA QQRANAEMTLNLSLRQAQKISEDA RNLDPKALVAGVASGFRPMDDTAEF LLMDKTQFFQAGGNSDFSMFDP QRPTTTSPTAVLAQEMVGNIAHKMQ LMKSSFFVEDNAPEDPEMETTGRLL RHRKFFNVEPLVWKDGASESSQYD FEHPSALPISSVSEASLMCDAHYE ETSSMATGSIVAAVKETFEMPVTK AFKFVCKPKVAPIKLRATTVPLPR SIA YEMRDNIADLGFYKGRSFKLSFGP QNSLVLPTSTYNNMQLKFTGPSLP VSMVFAPRSATDLSPSVMQLVEFN MVKGNEGFRESIIPHLEVQLNDCLS VNVEGSECPCHPDSGKLVSKHFS ESLKORNAGLKEDYSVSVWLLFAL WGDHDELVDLEKNSHYMVMCRRN LSEWLENTLLGKDLLSKKVSTHSY LEHMLDLSCHRVNEACELAFSYDD ANLALVLSQLSSGAVFRLMEEQLF AWQQSKSDKYIDLERLKMMLAAG APMMQSSHGAINLLENKNWLTALA LQLWYFTAPTSSITDALNAYNDAFQ AEECYAEPPKPSYRDAPDTKPKVYD LRYHLLQLHSKRMHSLEETLNPITH TADAMDFRLSWLLQTLRALGRYHC SPLTEARLSVDFASQLENEGLWQW GIFVLLHIKQOTQREAVQMLQRN VSVSAKVALYAEERFIVEELGIPMSW VDYAKAVKAGASGKHHLQAKYLLKA KHFATAHDVIFQHIAPDAIINGKMKY LHSLLIQFEDTEGSSIRVNPWANQG QIFLDFIDISAKFKQIRSVTNIADINA RWENLKPQLSELCSRISLLPCPTSKH RLCQSEISQSLSCLVHGMCIVCPEM ESSTVLKVALERLPLQEFASKELRI WLEELLDKIQNEPPFSERQOPTMM	True	False	2.728	5.0	1.45	1.628	1.119	1.595	1.268

