

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma
Q9W1X4	NU214_DROME	Drosophila melanogaster	Nuclear pore complex protein Nup214	30.60235	S442;S443;S446;T453;T455;T457;T965;T967;T969;T971;T972;S1116;T1121;T1123;T1124;T1153;T1155;T1254	NaN	33925313;40245499	MAQNAPDCEDTQDFQFKLHHKIVA FKKCGEPRSNVLLAVSSSRGLLFA GSPTQPELKVIVKDLVNAKSTAQQP QARLVPLPSIPNYIACSSDGNLLAVN HTQNGTSLLSIYAVLSFMTPDVRPVY NIRLAAEDHVHGVQLLWNPVLPNSL AVVLSNGALAMYALKEGGNFEMHS LDKNQOVKCGCWSPKKGQIVLGF GGTVKQFKPDLTLAKTLLCPPNIHDA PFDITAIQWLSTFQFAVIFLQHGEDC SPSLYILNAPKAGAPSYINYDICYSM NGPRNHQFVFSHVLPQWNLVVLSVA NGVEVGIMRSTEAGDTPAWQQLTLL DEARIEEMPLSEDKDETFFLGFADFDS TTHQLTINEKKLQTMMPMVHVLSSDG ELLSFNFLNVLPTAVSVCSPPPVAD TSGQFKPLNMLLASEEEEEQPAAWAAS PSKAPAATPAASSDISFAFTPTNTVST PAPSKDKQPSLFSGFGAAAAKAPAP QLSFGTAPTSSPVSFGAPTTNAAKPT TPFGGFGTQATTTAMGSMFASGA NAFGGMALNKPAIASVTPRTAAPGS TVPATPASAPANKPLYTVPLTFTPVD TKPATSAPOIADESLKDDTEPIIKD MIALQIEAFSKDIQKQKEQTKELLKG IAAPSAALRAYAKRLDDLQELNEQAK DVEFELDVQGLRQGLNEAYAIVAEC RGKLEIYRKPETIRLMNSSSCDPSGR RMLARLQSYVAANEALRLAQOHV DLQWEQFQDVVRRNSKSRMHMPC LEGIYQLTRLQNLTSNQRIVQNNIK SKLKERGLLQAAALDQEKSRTRTNE AVDTLTDILTMSLSQVVDSSNAAKLT RERLQKIRNIVQLQKINVICPORPDR VGLKSEVILETKRRAEQIKRAAAKPA TANKYTQAAVAPPSPDPVAPTAVAP MPQATVTVAPPLPKPMPSIPSVVEKP GVPTHTPTVPVATPFSFSQSIPIVKTST VPTTNTVTPGEAAKPLSIFGGSTIS SFSFGGGAAKSALSFGTSPVAVAAPT PKPNPLSAVEKPTPEPTKPKQKAAE SKEFKAVQPETEESKVPQKPKAETE NKSFGGFGFTGTGGTVGNTSSSPFS FGGLGSSLGFGGTAAPVKSEPSSTA TTSVATSASTAPFGIFSAALAKPSNS EPITVTSNTTITTSKPTNVIASSVT DAPSVTTTNAVTSSTDPIGGLFSSVTI CKPNTADTTKPNIFGGGLSAGSFS FGGTIDASKGLFGSTKPVATAPTSVT EANNKTDPISTTPSAISTTTATTVSS PAVVPAAVTAAVPATSTTTSSTAV PGSAFSSNAFSTLSAGGAAAPTTS SAPLAAKSPATATSTGNSSNSVFGG GFAVATSTAAPVASPFQSAAKSPVSS ANIFGSIPKAETSVFGGATTAPSNTT AAATPDAPPAGLFASAAISNPSFPGS PTTRAPASGGNIFGQAVKPSVFGQPA QAGDSGGGIFGGGSASTPFGSSSIFG GGNTQGAAGVAPAGSTISFGQKVF QSSAAAPAAAGGNIFSNVPGSPQASPF GGGNSIFGSPATAPPAGGSGIFGGG SSGGFGSFTOTTPAQGGFGGFGQ GGGGSVAQTGFGSPQAPQQTTPG GFGAKPVFGGSPAFGASPTFGGGAT FGSPKGFGGFGGASPVASPPFGAA AKPAQGNIFETLGGQESGLSFGNLA QTGNSNAQKPAFGGSSFMNYR	True	False	1.5	5.0	False	False	False	0.35