

UniprotKB ID	Entry name	organism	full name	oglcncscore	oglcnc sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9VXE6	NU153_DROME	Drosophila melanogaster	Nuclear pore complex protein Nup153	30.404062	NaN	NaN	33925313;28604694	MEDAQEORESSQAELAKKHPLTPLK ELPEEEEEEEEEDESSAGALRES SNNSIMGKMKMRVSSILPASLSGW SPSSKDGNDALSSPANLRQSQPRQ NGRLTTRKRGRRRRIMLAEDVADA DDLDDGSDAKGLNYEEVALADNIAE HDLAAEDEQTRRSEYNVFLLRKRAG AVAAAGGDEDEAEDELEEDDEDG DEEDDDEEQENLQQAQSAVQTKRRR LELETPVNLPMRRLPLLSSTPAAPL AAATSSSSSQMYKGVSHIAPHRRNH LNLYGSQRQREPAYNFFTGNAAEG STGDLPHSIRRSLNIPFGSSTATSY NNSLSSLPNHKRPSLIGKQTHRRDL TMDGTGTPAMSSEHLNHLRISR TNNNTSNNNNNNNNNNNNVIEKTK RRSELSAAAGGCCGDSQSESDMNEY HDNNEGHDGLRPSHYNSNSNLEFY GNLQSSKSIFNRSNTAAQQSHRNST WSLNSLTQRRRFNASIYGSTALS SRLLSGSASNSGSASASSPFYQGR TFGGNSGNRFLFRSRLSSSAASSM LGLNSAGSSPAHQHASMTGGIGYG MKAVIDMRPSDSGSLAETSVMGGGS KKPGTGLSNTTMRILNLESYSTPLI DAKRMGSSIKEHQSSRQQRGTPAT PYLRSTSASRNVSPNHINELAE NKLTVPTMQQLERRRHRVTQNS RDVVHSQNVVRAAGENNQEKPKPTA PYVAPIDQSANHTQHTNKMRSLSH QTRNKETRTAEEEEAPPPLDLPQIS DMASAPKFDLIIKPTVPVSKPSTTD PIQSSKSNLSTNSKQMPNFLA NPQPAAPVNFANAGNVSAISKPSKR TTFSEPTPLSNFQENCIPKPKINRK YFSAAPLDDLITNKQSQPTINGT PSSKEWECDTMVRNKPINKCVA CETAKPVASAAPVQAPLPPSTA QSFVGFGRFKKSTTAWECDACML SNKAEASKCIACETPRKTVPKVN FSPLITNAKSNWEVSVCLVRNVE VSKCVACESAKPGATMALPATSNIA ATPSIITDGFGRFKKATAWECDAC MLSNKAEASKCIACETPRKSSSTPI SSYPSINNNLPAGSGFDISFTRKAN MWEQCTCLVMNKSSDEECIACQTP NSQARNNSNESALISSISSASFSG SLSRPSSRSSGSTSTCGSVCSGSIV SISSTTESAKALSAKKVPKPDAGFQ QLVAAQKTSTWECEACLAKNDMSR KTCICCEQMMPEAFNPAATTANSAA SSVPKFRFGFSHVKEVVKPSVETTT PAPTSAQFSGFGQSNQKDVADSK KTEAPKTFMFGVSKVEPKTVSFGT GIKETTATSSTEATPTAAAAAPV QFVFKAPTATTASSLTTTISTTSNAP ALGGFSGAPSSSTVSSSTTSAN PAAVKPMFWSWAGSASVSTSSSQ PVAKAPTLGFGVSSSTVTTTTSTKV FAFTPASGLDPAATSAPAAGAGFSF GSQSKPATTQNTGTFFGQPTAVAP ATPTNPSVSSIFGAPATSTTASTVSA TTSTSTANAIASSFAPSTPQLFGNW GEKKTDLTTFGASSGSTTTTSPFG WSSNGDAAKSNSAAVGSAAVPS STMATPIFGSSSMFGPSSSNNTTST STTSLPFGSAATTAATPAGGNAALT GLFGNVGNSLAGVGPVATTPAATA AAPLTNIFGNPTVAAAAPVFGSGST IPSAGFGAPAAAAPALPGAFNF GGATAATPAASSAPFVFGSSTNEPLA KPSFNFTGSAASSTAPAFNFTANT AATNPSGGDSTPNANALFQFSATS TAPANIFAFNPPAAGNSAQSSQ RKIRAPVRRLLPPR	None	None	None	None	None	None	None		