

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasm reticulum
Q8TEM1	PO210_HUMAN	Homo sapiens	Nuclear pore membrane glycoprotein 210	24.571928	S383;S699;S700;T927	T1844;S1874;S1877;S1881;S1886	34725712;34019948;33214551;30379171;35289036;40307207;32119511;35138101;35083852;40596516;22121020;39534244;37340703	MAARGRGLLLLLLSVLLAAGPSAAA AKLNIPKVLPPFTRATRNVNFTLE GCYRWLSTRPEVASIEPLGLDEQCC SQKAVVQARLTQPARLTSIIFAEDITT GOVLRCDAINVDLIHQIVSTTREL EDSPLLEKIQALDSEGNTFFSTLAGLV FEWTIVKDSEADRFSDSHNALRLTF LESTYIPPSYISEMEKAQKQGD GMKTGSSKLLKARIQEA VYKKNVRPAE VRLILENILLNPAYDVYLMVGT SIH YKVQKIRQOGKITELSMPSDQYEL LQLQ NSIPGPEGDPARPVAVLAQDTS MVT ALQLGQSSLVLGHR SIRMQGASRLP NSTIYVVEPGYLGFTVHPGDR WVLE TCRLYEITIEVFDKFSNKVYVSD NIRI ETVLPAEFFFEVLSSQNGSYHR IRAL KRGQTAIDAALTSVVDQGGVHIL Q VPVWNQQEVEIHIPITLYPSILT FPW QPKTGAYQYTI RAHGGSGNFSWSS SHLVATVTVKGVMTTGS DIGFSVIQA HDVQNP LHFGEMKVYVIEPHSMEF APCQVEARVGOALELPLRISGL MPC GASEVTLSDCSHFDLAVEVENQGV FOPLPGRLLPGSEHCSGIRV KAEAQ GSTLLVSYRHHGHVHLSAKITIA AYL PLKAVDPSSVALVTLGSSKEM LFEG GPRPWILEPSKFFQNVTAEDT DSIGL ALFAPHSSRNYQQHWILVTCO ALGE QVIALSVGNKPSLTNPFP AVEP AVVK FVCAPPSRLTLAPVYTS PQLDMSCPL LQONKQVVPVSSH RNPRLDLAAYDQ EGRRFDNFSSLSIQWEST RPVLASIE PELPMQLVSDDESGQK LHGLQAI LVHEASGTTA TATATGYQESH LSSA RTKQPHDPLVPLS ASIELLIVEDVRV SPEEVTIYNHPGIAEL RIREGSGYF FLNTSTADVVKVAYQ EARGVAMVHP LLPGSS TIMIHDCLCLVFP APAKAVVY VSDIQELYIRVVDK VEIGKTVKAYVRV LDLHKKPF LAKYFPFMDL KLRAASPI ITLVALDEALD NYTITFLIRG VAIGQT SLTASVTNKAGOR INSAPQQIEV FPP FRLMPRKVTL LIGATMQVT SEGGPQ POSNILFSISNE SVALVSAAGL VQGL AIGNGTVSGLV QAVDAETGK VVIISQ DLVQVEVLLLR AVRIRAPIMR MRTGT QMPIYVTGIT NHQNPFSFG NAVPG LTFHWSVTKR DVLDRGRH HEASIRL PSOYNFAMN VLRVKGRT GLRVV KAVDPTSGQ LYGLARELS DEIQVQVF EKQLLNPEIE AEQILMSP NSYIKLQ TNRDGAASLS YRVL DGP EKVPV VHV DEKGF LASGSMIGT STIEVIAQ EPFG ANQTIIVAVK VSPVSLRV SMSPV LH TONKEALVAV PLGMTVTF TVHFHD NSGDV FHAHSSV LNFATNRD DFVQI GKGPTNNTC VVRTVSV GLTLLRV VD AEHPGLSDF MPLPVLQ AISPEL SGA MVVGDV LCLATVLT SLEGLS GTWSS SANSILHID PKTGVAV ARAVGS VTVY YEVAGH LRTYKEV VSV PQRIMARH LHPIQTSFQ EATASKV VIVAGDR SSN LRGECTPTQ REVIQAL HPETLISC QSQ QFKPAVDF PQDVF TVEPQ FDAL GQYFCSIT MHRLTDK QRKHL SMKKT ALVVSASL SSHFST EQVGA EVPFSP GLFADQAE ILLSN HYTSSE IRVFGAP EVLENLE VKSGS PAVLA FAKEK SFG WPSFITYT VGVLD PAAGS QGPLST TL TFSSPVTN QAI AIPVT VAFV DRRGP GPYGASL FQHF LDSYQV MFFTL FAL LAGTAVM IIAYHT VCTPRD LAVPAAL TPRASPGH SPHYFA ASSPT SPNALPP ARKASPPS GLWSPAYASH	False	False	False	4.0	False	3.112