

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8TEM1	PO210_HUMAN	Homo sapiens	Nuclear pore membrane glycoprotein 210	12.402749	S383	T1844;S1874;S1877;S1881;S1886	32119511;34725712;34019948;22121020;35083852;35138101;35289036;30379171;33214551	MAARGRGLLLLTLSVLLAAGPSAAA AKLNIPKVLLPFTRATRVNFTLEASE GCYRWLSTRPEVASIEPLGLDEQQC SQKAVVQARLTQPARLTSIIFAEDITT GQVLRCDIAIVDLIHDIQIVSTTRELYL EDSPLELKIQALDSEGNFSTLAGLV FEWTIVKDSEADRFSDSHNALRILTF LESTYIPPSYISEMEKAAKQGDTILVS GMKTGSSKLKARIQEAVYKNVRPAE VRLILENILLNPAYDVYLMVGTSTH YKVQKIRQGGKITELSMPSDQYELQLQ NSIPGPEGDPARPVAVLAQDTSMTV ALQLGQSSLVLGHRMIRMQGASRLP NSTIYVVEPGYLGFTVHPGDRWVLE TGRLYEITIEVFDKFSNKVYVSDNIRI ETVLPAEFFEVLSSSQNGSYHRIRAL KRGQTAIDAALTSVVDQDGGVHILQ VPVWNQQEVEIHIPITLYPSILTFPW QPKTGAYQYTIRAHGGSGNFSWSSS SHLVATVTVKGVMTTGSDIGFSVIQA HDVQNPLHFGEMKVYVIEPHSMEF APCQVEARVQALELPLRISGLMPG GASEVVTLSDCSHFDLAVEVENQGV FQPLPGRLLPPGSEHC GIRVKAEAQ GSTLLVSYRHGHVHLSAKITIAAYL PLKAVDPSSVALVTLGSSKEMLFEG GPRPWILEPSKFFQNVTAEDTDSIGL ALFAPHSSRNYQQHWILVTCQALGE QVIALSVGNKPSLTNPFPAVEPAVK FVCAPPSRLTLAPVYTSPQLDMSCPL LQONKQVVPVSSHNRNPRDLAAYDQ EGRRFDNFSSLSIQWESTRPVLASIE PELPMQLVSQDDESGQKKLHGLQAI LVHEASGTTAITATATGYQESHLSSA RTKQPHDPLVPLSASIELILVEDVRV SPEEVTIYNHPGIQAE LRIREGSGYF FLNTSTADVVKVAYQEARGVAMVHP LLPGSSTIMIHDLCVFPAPAKAVVY VSDIQELYIRVVDKVEIGKTVKAYVRV LDLHKKPFLAKYFPFMDLKLRAASPI ITLVALDEALDNYTITFLIRGVAIGQT SLTASVTNKAGQRINSAPQQIEVFPP FRLMPRKVTLLIGATMQVTSEGGPQ PQSNILFISISNESVALVSAAGLVQGL AIGNGTVSGLVQAVDAETGKVVISQ DLVQVEVLLLRAVRIRAPIMRMRTGT QMPIYVTGITNHQNPFSFGNAVPG TFHWSVTKRDVLDLRGRHHEASIRL PSQYNFAMNVLGRVKGRGTGLRVVV KAVDPTSGQLYGLARELSDEIQVQVF EKLQLLNPEIEAEQILMSPNSYIKLQ TNRDGAASLSYRVLDGPEKVPVVHV DEKGFASGSMIGTSTIEVIAQEPFG ANQTIIVAVKVSPVSYLRVSMSPVLH

TQNKEALVAVPLGMTVFTVHFHD
NSGDVFH AHSSVLNFATNRDDFVQI
GKGPTNNTCVVRTVSVGLTLLRVWD
AEHPGLSDFMPLPVLQAISPELSGA
MVVGDVLC LATVLTSLLEGLSGTWSS
SANSILHIDPKTGVAVARAVGSVTVY
YEVAGHLR TYKEVVVSVPQRIMARH
LHPIQTSFQEATASKVIVAVGDRSSN
LRGECTPTQREVIQALHPETLISCQS
QFKPAVDFPSQDVFTVEPQFD TAL
GQYFCSITMHRLTDKQRKHL SMKKT
ALVVSASLSSSHFSTEQVGA EVPFSP
GLFADQAEILLSNHYTSSEIRVFGAP
EVLNLEVKSGSPAVLAF AKEK SFG
WPSFITYTVGVLDPAAGS QGPLSTTL
TFSSPVTNQAIAIPVTVA FVVDRRGP
GPYGASLFQHFLDSYQVMFFTLFAL
LAGTAVMIIAYHTVCTPRDLAVPAAL
TPRASPGHSPHYFAASSPTSPNALPP
ARKASPPSGLWSPAYASH