

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q92616	GCN1_HUMAN	Homo sapiens	eIF-2-alpha kinase activator GCN1	16.793083	NaN	S729;S786;S2276	23301498;16408927;34019948;26853435;33214551;28510447;34725712;35138101;35083852	MAADTQVSETLKRKFAGKVTTASVKE RREILSELGKCVAGKDLPEGAVKGL CKLFCLTLHRYRDAASRRALQAAIQ QLAEAQPEATAKNLLHSLQSSGIGS KAGVPSKSSGSAALLALTWTCLLVRI VFPSRAKRQGDIWNKLVEVQCLLLL EVLGGSHKHAVDGAVKKLTKLWKE NPGLVEQYLSAILSLEPNQNYAGML GLLVQFCTSHKEMDVVSQHKSALL DFYMKNILMSKVKPPKYLLDSCAPL LRYLSHSEFKDLILPTIQKSLLRSPEN VIETISSLLASVTLDLSQYAMDIVKGL AGHLKSNSPRLMDEAVLALRNLAR QCSDDSAMESLTKHLFAILGGSEGK LTVVAQKMSVLSGIGSVSHHVSGP SSQVLNGIVAELFIPFLQQEVHEGTL VHAVSVLALWCNRFTMEVPKCLTE WFKKAFSLKTSTSAVRHAYLQCMLA SYRGDTLLQALDPLLIIQTVEKAAS QSTQVPTITTEGVAAAALLLKLVSADS QAEAKLSSFQWLIVDEKKQVFTSEK FLVMASEDALCTVLHLTERLFLDHP HRLTGNKVQYHRALVAVLLSRTW HVRROAQQTVRKLSSLGGFKLAHG LLEELKTVLSSHKVLPLEALVTDAGE VTEAGKAYVPPRVLQEALCVISGVPG LKGDVTDTEQLAQEMLIISHHPSLVA VQSGLWPALLARMKIDPEAFITRHL DQIIPRMTTQSPLNQSSMNAMGSLS VLSPDRVLPQLISTITASVQNPALRLV TREEFAIMQTPAGELYDKSIIQSAQQ DSIKKANMKRENKAYSFKEQIELEL KEEIKKKKGIKEEVQLTSKQKEMLQ AQLDREAQVRRRLQELDGELEAALG LLDIILAKNPSGLTQYIPVLVDSFLPL LKSPLAAPRIKNPFLSLAACVMPSRL KALGTLVSHVTLRLLKPECVLDKSW CQEELSVAVKRAVMLLHTHTITSRV GKGEPGAAPLSAPAFSLVFPFLKMV LTEMPHHSEEEEEWMAQILQILTVQ AQLRASPNTPPGRVDENGPELLPRV AMLRLLTWVIGTGPSRLQVLASDTL TTLCASSGDDGCAFAEQEEVDVLL CALQSPCASVRETVLRGLMELHMVL PAPDTDEKNGLNLLRRLWVVKFDKE EEIRKLAERLWSMMGLDLQPDLCSL LIDDVIYHEAAVRQAGAEALSQAVAR YQRQAAEVMGRLMEIYQEKLYRPPP VLDALGRVISESPPDQWEARCGLAL

ALNKLSQYLDSSQVKPLFQFFVDPDA
LNDRHPDVRKCMLEAALATLNTHG
KENVNSLLPVFEEFLKNAPNDASYD
AVRQSVVVLMSGSLAKHLDKSDPKVK
PIVAKLIAALSTPSQQVQESVASCLPP
LVPAIKEDAGGMIQRLMQQLLESDK
YAERKGAAYGLAGLVKGLGILSLKQQ
EMMAALTDAIQDKKNFRRREGALFA
FEMLCTMLGKLFEPYVVHVLPHLLL
CFGDGNQYVREAADDCAKAVMSNL
SAHGVKLVLPSELLAALEEEESWRTKA
GSVELLGAMAYCAPKQLSSCLPNIVP
KLTEVLTDSHVQKAGQQALRQIG
SVIRNPEILAIAPVLLDALTDPSRKTQ
KCLQTLDDTKFVHFIDAPSLALIMPIV
QRAFQDRSTDTRKMAAQIIGNMYSL
TDQKDLAPYLPVTPGLKASLLDPVP
EVRTVSAKALGAMVKMGESCFCED
LLPWLMETLTYEQSSVDRSGAAQGL
AEVMAGLGVEKLEKLMPEIVATASK
VDIAPHVRDGYIMMFNYLPITFGDKF
TPYVGPPIPCILKALADENEFVRDTAL
RAGQRVISMAYAETAIALLLPQLEQGL
FDDLWRIRFSSVQLLGDLLFHISGVT
GKMTTETASEDDNFGTAQSNKAIT
ALGVERRNRVLAGLYMGRSDTQLVV
RQASLHVWKIVVSNTPRTLREILPTL
FGLLGFLASTCADKRTIAARTLGDL
VRKLGKILPEIPILEEGLRSQKSDE
RQGVCIGLSEIMKSTSRDAVLYFSES
LVPTARKALCDPLEEVREAAAKTFEQ
LHSTIGHQALEDILPFLKQLDDEEV
SEFALDGLKQVMAIKSRVLPYLVPK
LTTTPVNTRVLAFLSSVAGDALTRHL
GVILPAVMLALKEKLGTPDEQLEMA
NCQAVILSVEDDTGHRHIEDLLEATR
SPEVGMRQAAAILNIYCSRSKADYT
SHLRSLSGLIRLFNDSSPVVLEESW
DALNAITKKLDAGNQLALIEELHKEI
RLIGNESKGEHVPGFCLPKKGVTSL
PVLREGVLTGSPEQKEEAAKALGLVI
RLTSADALRPSVVSITGPLIRILGDRF
SWNVKAALLETLSELLAKVGIKLPF
LPQLQTTFTKALQDSNRGVRLKAAD
ALGKLISIHIVDPLFTELLNGIRAME
DPGVRDTMLQALRFVIQAGAKVDA
VIRKNIVSLLSMLGHDEDNTRISSA
GCLGELCAFLTEEELSAVLQOCLLA
DVSGIDWMVRHGRSLALSVAVNVAP
GRLCAGRYSSDVQEMILSSATADRIP
IAVSGVRGMGFLMRHHIETGGGQLP
AKLSSLFVKCLQNPSSDIRLVAEKMI

