

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	15.07034	NaN	S729;S786;S2276	34019948;23301498;33214551;28510447;16408927;34725712;26853435	MAADTQVSETLKRKFAGKVTTASVKE RREILSELGKCVAGKDLPEGAVKGL CKLFCCLTLHRYRDAASRRALQAAIQ QLAEAQPEATAKNLLHSLQSSGIGS KAGVPSKSSGSAALLALTWTCLLVRI VFPSRAKRQGDIWNKLVEVQCLLLL EVLGGSHKHAVDGAVKKLTKLWKE NPGLVEQYLSAILSLEPNQNYAGML GLLVQFCTSHKEMDVVSQHKSALL DFYMKNILMSKVKPPKYLLDSCAPL LRYLSHSEFKDLILPTIQKSLLRSPEN VIETISSLLASVTLDLSQYAMDIVKGL AGHLKSNPRLMDEAVLALRNLAR QCSDDSAMESLTKHLFAILGGSEGK LTVVAQKMSVLSGIGSVSHHVSGP SSQVLNGIVAELFIPFLQQEVHEGTL VHAVSVLALWCNRFTMEVPKCLTE WFKKAFSLKTSTSAVRHAYLQCMLA SYRGDTLLQALDPLLIIQTVEKAAS QSTQVPTITTEGVAAALLLKLVSADS QAEAKLSSFWQLIVDEKKQVFTSEK FLVMASEDALCTVLHLTERLFLDHP HRLTGNKVQYHRALVAVLLSRTW HVRRAQQTVRKLLSSLGGFKLAHG LLEELKTVLSSHKVLPLEALVTDAGE VTEAGKAYVPPRVLQEALCVISGVPG LKGDVTDTEQLAQEMLIISHHPSLVA VQSGLWPALLARMKIDPEAFITRHL DQIIPRMTTQSPLNQSSMNAMGSLS VLSPDRVLPQLISTITASVQNPALRLV TREEFAIMQTPAGELYDKSIIQSAQQ DSIKKANMKRENKAYSFKEQIIELEL KEEIKKKKGIKEEVQLTSKQKEMLQ AQLDREAQVRRRLQELDGELEAALG LLDIILAKNPSGLTQYIPVLVDSFLPL LKSPLAAPRIKNPFLSLAACVMPSRL KALGTLVSHVTLRLLKPECVLDKSW CQEELSVAVKRAVMLLHTHTITSRV GKGEPGAAPLSAPAFSLVFPFLKMV LTEMPHHSEEEEEWMAQILQILTVO AQLRASPNTPPGRVDENGPPELLPRV AMLRLLTWVIGTGSPLRQLVLSDTL TTLCASSGDDGCAFAEQEEVDVLL CALQSPCASVRETVLRGLMELHMVL PAPDTDEKNGLNLLRRLWVVKFDKE EEIRKLAERLWSMMGLDLQPDLCSL LIDDVIYHEAAVRQAGAEALSQAVAR YQRQAAEVMGRLMEIYQEKLYRPPP VLDALGRVISESPPDQWEARCGLAL

ALNKLSQYLDSSQVKPLFQFFVPPDA
LNDRHPDVRKCMLEAALATLNTHG
KENVNSLLPVFEEFLKNAPNDASYD
AVRQSVVVLMSGSLAKHLDKSDPKVK
PIVAKLIAALSTPSQQVQESVASCLPP
LVPAIKEDAGGMIQRLMQQLLESDK
YAERKGAAYGLAGLVKGLGILSLKQQ
EMMAALTDAIQDKKNFRRREGALFA
FEMLCTMLGKLFEPYVVHVLPHLLL
CFGDGNQYVREAADDCAKAVMSNL
SAHGVKLVLPSELLAALEEEESWRTKA
GSVELLGAMAYCAPKQLSSCLPNIVP
KLTEVLTDSHVQKQKAGQQALRQIG
SVIRNPEILAIAPVLLDALTDPSRKTQ
KCLQTLDDTKFVHFIDAPSLALIMPIV
QRAFQDRSTDTRKMAAQIIGNMYSL
TDQKDLAPYLPVTPGLKASLLDPVP
EVRTVSAKALGAMVKGMGESCFCED
LLPWLMETLTYEQSSVDRSGAAQGL
AEVMAGLGVEKLEKLMPEIVATASK
VDIAPHVRDGYIMMFNYLPITFGDKF
TPYVGPPIPCILKALADENEFVRDTAL
RAGQRVISMAYAETAIALLLPQLEQGL
FDDLWRIRFSSVQLLGDLLFHISGVT
GKMTTETASEDDNFGTAQSNKAIT
ALGVERRNRVLAGLYMGRSDTQLVV
RQASLHVWKIVVSNTPRTLREILPTL
FGLLGFLASTCADKRTIAARTLGDL
VRKLGKILPEIPILEEGLRSQKSDE
RQGVICIGLSEIMKSTSRDAVLYFSES
LVPTARKALCDPLEEVREAAAKTFEQ
LHSTIGHQALEDILPFLKQLDDEEV
SEFALDGLKQVMAIKSRVLPYLVPK
LTTTPVNTRVLAFLSSVAGDALTRHL
GVILPAVMLALKEKLGTPDEQLEMA
NCQAVILSVEDDTGHRHIEYLLEATR
SPEVGMRQAAAILNIYCSRSKADYT
SHLRSLVSGLIRLFNDSSPVVLEESW
DALNAITKKLDAGNQLALIEELHKEI
RLIGNESKGEHVPGFCLPKKGVTSL
PVLREGVLTGSPEQKEEAAKALGLVI
RLTSADALRPSVVSITGPLIRILGDRF
SWNVKAALLETLSELLAKVGIKLPF
LPQLQTTFTKALQDSNRGVRLKAAD
ALGKLISIHIVDPLFTELLNGIRAME
DPGVRDTMLQALRFVIOGAGAKVDA
VIRKNIVSLLSMLGHDEDNTRISSA
GCLGELCAFLTEEELSAVLQOCLLA
DVSGIDWMVRHGRSLALSVAVNVAP
GRLCAGRYSSDVQEMILSSATADRIP
IAVSGVRGMGFLMRHHIETGGGQLP
AKLSSLFVKCLQNPSDIRLVAEKMI

								WWANKDPLPPLDPQAIKPILKALLD NTKDKNTVVRAYSQAIVNLLKMRQ GEEVFQSLSKILDVASLEVLNEVNRR SLKKLASQADSTEQVDDTILT
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