

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q6DFV3	RHG21_MOUSE	Mus musculus	Rho GTPase-activating protein 21	27.850091	NaN	S42;S63;S454;S610;S619;T741;S851;S856;S875;T876;S918;S920;S948;S1093;S1109;S1412;S1426;S1427;T1504;S1656;T1669;S1729;T1902;S1906	22517741;30059200;36852467	MMATHWTGLPEEDGDKLKACGAAS ACEVSKNKDGKDQGEVPSPEDEPF SWPGPKTVMLKRTSQGFGLRHF VYPPESAIQFSYKDEENGNRGGKQR NRLEPMDTIFVKQVKEGGPAFEAGL CTGDRIKVNNGESVIGKYSQVIALIQ NSDTTLELSVMPKDEDILQVAYSQD AYLKGNEAYSGNARNIPEPPPVCYP WLPSTPSATAQPVETCPPDSLPNKQ QTSAPVLTQPGRAYRMEIQVPPSPTD VAKSNTAVCVCNCSVRTVIVPSEKVV DLLANRNNPSGSPSHRTEEVRYGVN EQASTKAASRTTSPASVPTAHLIHQT TGSRSLEPSGILLKSGNYSGHSEGIS SSRSQAVDSPVSVNHYSANSHQHI DWKNYKTYKEYIDNRRHLHIGCRTIQ ERLDSLRAASQSAADYNQVVPTRTT LQVRRRSTSHDRVPSVQIRQRSVS QERLEDSVLMKYCPRSASQGALTSP PVSFNNHRTRSWDYIEGQTEATATV NSESQIPDSNGERKQTYKWSGFTEQ DDRRGIHERPRQEMHKPFRGSNL TVAPVVNSDNRRLVGRGVGPVSQFK KIPPDLRPPHSNRNFPPTTGVS LQRG IAQDRSPLVKVRSNSLKVPPPVSKP SFSQHSLASMKDQRPVNHHLHQHSV LSQQTQFRSESTFEHQLETEVSSCL PGTSAKTSPQLSENLTSDLELPAIP RNGDINLQEAIEIQPDVLDNKESVIL REKQSGRQTPQPLRHQSYILAVND QETGSDTTCWLPNDARREVHIKRM EERKASSTSPPGDSLASIPFIDEPTSP SIDHEIAHIPASAVISASTAHVPSIATV PPSLTTSAPLIRRQLSHDQESVGPPS LDGQHSSKTERS KSYDEGLDDYRED AKLSFKHVSSLKGIKITDSQKSSSDS GSRKGSSEVFSDAAREGWLQFRPL VTDKGRVGG SIRPWKQMYVVLRG HSLYLYKDRREQTPSEEEQPISVNA CLIDISYSETKRRNVFRLTSDCECL FQAEDRDDMLSWIKTIQESSNLNEE DTGVTNRDLISRRIKEYNSLLSKTEQ LPKTPRQSL SIRQTLGAKSEPKTQS PHSPKEESERKLLSKDDTSPPKDKG TWRRGIPSIVRKT FEKKPAATGTFGV RLDDCPPAHTNRYIPLIVDICCKLVE ERGLEYTGIYRVPGNNAAISSMQEEL NKGMAIDIQDDKWRDLNVISSLLK SFFRKLPEPLFTNDKYADFIEANRKE DPLDRLRTLKRLIHDLPEHHFETLKF LSAHLKTV AENSEKNKMEPRNLAIV FGPTLVRTSEDNMTHMVTMHPDQY

								KIVETLIQHHDWFFTEEGAEPLTAV QEENTVDSQPVPNIDHLLTNIGRTG VLPGDVSDSATSDSAASKGSWGS GK DQYSRELLVSSIFAAASRKRKPKKEK AQPSSSEDELDSVFFKKENTEQSHS EIKEESKRESETSGSKQRVVAKESN TKKDSGTTKEEKIPWEEPPPHSSK RNRSP T LSCRLAMLKEGPRSLTQK PHCEETGSDSGTLLSTSSQASLLRSS TKKSTSPETKHSEFLSIAGTTTSDYS TTSSTTYLTSLDSSRLSPEVQSVAES KGDEADDERSELVSEGRPVETDSES EFPVFPTTLTSDRLF RGKFQEVARVS RRNSEGSEASCTEGLT PSLDSRRQ QFSSHRLIECDTL SRKKSARFKSDSG SPGDTRTEKETPALAKMFDVMKKGK STGSLTPSRSESEKQEATWKTKIAD RLKLRPRAPADD MFGVGNQKPTAET AKRKNIKRRHTLGGHRDATEISVLSF WKAHEQSADKESEL SAVNRLKPKCS AQDLSISDWLARERVRTSASDL SRG EGLEPQAESP SVLGTPISTHSPPSQ PEARVAATSTLASTSQSPLFTPPQSP DQINRESFQNM SQNASSTANIHPH KQSESPDTKAETPP
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