

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q5T5U3	RHG21_HUMAN	Homo sapiens	Rho GTPase-activating protein 21	21.100943	S475;S477;T482;S483;S485;S487;S489	S36;S57;S459;S612;S616;S625;S717;T747;S857;S862;S881;T882;S924;S926;S954;S1099;S1115;S1418;S1432;S1433;S1504;T1516;S1527;S1669;T1682;S1742;S1917	35254053;30059200;29237092;37340703;31492838;30379171	MMATRRTGLSEGDGDKLKACEVSK NKDGKEQSETVSLSEDETFVSWPGPK TVTLKRTSQGFVGLTRHFIVYPPESAI QFSYKDEENGNRGGKQRNRLEPMD TIFVKQVKEGGPAFEAGLCTGDRIK VNGESVIGKTYSQVIALIQNSDITTE LSVMPKDEEDILQVLQFTKDVLTALAYS QDAYLKGNEAYSGNARNIPEPPICYP PWLPSAPSAMAQPVEISPPDSLSKQ QTSTPVLTPQGRAYRMEIQVPPSPTD VAKSNTAVCVCNCSVRTVIVPSEKVV DLLSNRNNHTGPSHRTEEVRYGVSE QTSLKTVSRITSPPLSIPTTHLIHQPA GSRSLPSGILLKSGNYSGHSDGISS SRSQAVEAPSVSVNHYSNHSQHDID WKNYKTYKEYIDNRRLHIGCRTIQR LDSLRAASQSTTDYDYNQVVPNRITLQ GRRRSTSHDRVPSVQIRQRSVSQE RLEDSVLMKYCPRSASQGALTSPSV SFSNHRTRSWDYIEGQDETLNVNS GTPIPDSNGEKKQTYKWSGFTEQDD RRGICERPRQEIHKFRGNSFTVAP SVVNSDNRMRSGRGGVSVSQFKKIP PDLKTLQSNRNFQTTCCGMSLPRGIS QDRSPLVKVRSNSLKPSTHVTKPS FSQKSFVSIKQRPVNHHLHQNLLN QQTWVRTDSAPDQOVETGKSPSLSG ASAKPAPQSSENAGTSDLELPVSQR NQDLSLQEAETEQSDTLDNKEAVIL REKPPSGRQTPQPLRHQSYILAVND QETGSDTTCWLPNDARREVHIKRM EERKASSTSPPGDSLASIPFIDEPTSP SIDHDIAHIPASAVISASTSQVPSIATV PPCLTTSAPLIRRQLSHDHESVGPSP LDAQPNSKTERSKSYDEGLDDYRED AKLSFKHVSSLKGIKIADSQKSEDS GSRKDSSEVFSDAAKEGWLHFRPL VTDKGRVGGVIRPWKQMYVVLRG HSLYLYKDKREQTTPSEEEQPISVNA CLIDISYSETKRKNVFRLLTSDCECL FQAEDRDDMLAWIKTIQESSNLNEE DTGVTNRDLISRRIKEYNNLMSKAE QLPKTPRQSLRQTLGAKSEPKTQ SPHSPKEESERKLLSKDDTSPPKDK GTWRKGIPSIMRKTFEKKPTATGTFG VRLDDCPPAHTNRYIPLIVDICCKLV EERGLEYTGIYRVPGNNAISSMQE ELNKGMAIDIDIQDDKWRDLNVISSL LKSFFRKLPEPLFTNDKYADFIEANR KEDPLDRLKTLKRLIHDLPHEHHYETL KFLSAHLKRTVAENSEKNKMEPRNLA IVFGPTLVRTSEDNMTHMVTMMPD QYKIVETLIQHHDWFFTEEGAEPLT TVQEESTVDSQVVPNIDHLLTNIGRT GVSPGDVSDSATS DSTKSKGSWGSG KDQYSRELLVSSIFAAASRKRKKPKE KAQSSSEDELNVFFKKNVEQCH NDTKEESKKESETLGRKQKIIIAKEN STRKDPSTTKDEKISLGKESTPSEEP SPPHNSKHNSPTLSCRFAILKESPR SLLAQKSSHLEETGSDSGTLLSTSSQ ASLARFSMKKSTSPETKHSEFLANV STITSDYSTTSSATYLTSLDSSRLSPE

VQSVAESKGDDEADDERSELISEGRP
VETDSESEFPVFPALTSERLFRGKL
QEVTKSSRRNSEGSELSCTEGLTS
SLDSRRQLFSSHKLIECDTLRKKSA
RFKSDSGSLGDAKNEKEAPSLTKVF
DVMKKGKSTGSLLPTRGESEKQEP
TWTKIADRLKLRPRAPADDMFGVG
NHKVNAETAKRKSIRRRHTLGHRD
ATEISVLNFWKVHEQSGERESELSA
VNRLKPKCSAQDLSISDWLARELR
TSTDLSRGEIGDPQTENPSTREIAT
TDTPLSLHCNTGSSSSTLASTNRPLL
SIPPQSPDQINGESFQNVSKNASSAA
NAQPHKLETPGSKAEFHPCL