

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q811P8	RHG32_MOUSE	Mus musculus	Rho GTPase-activating protein 32	26.662457	S1027	S706;S709;S732;S738;S852;S856;S892;S952;S1206;S1588	34678516;33300544;22517741;22645316	METESETSSLGDDSVFWLDCEGVT QLTDGDEEEREESFRMKSSIHSEE DDFVPELHRNVHPRERPDWEETLS AMARGADVPEIPGDLTLKSCGSTAST KVXHVKKLPFTKGFHPKMAECAHF HYENVEFGSIQLSLSEEQNEVMKNG CESKELVYLQIACQGKSWIVKRSYE DFRVLDKHLHLICIYDRRFSQLTELPR SDVLKDSPESVTQMLTAYLSRLSTIA GNKINCGPALTWMEIDNKGHLLV HEESSINTPAVGAAHVIKRYTARAPD ELTLEVGDIVSVIDMPPKVLSTWWR GKHGFQVGLFPGHCVELINQKVPQS VTNSVPKPVSKKHGKLTIFLRTFMKS RPTKQKLKQRGILKERVFGCDLGEH LLNSGFVQPVLQSCTAFIERYGIVD GIYRLSGVASNIQRLRHEFDSEHVPD LTKEPVYQDIHSVGSCLKLYFRELPN PLLYQLYEKFSDAVSAATDEERLIKI HDVIQQLPPPHYRTLFLMRHLSLL ADYCSITNMHAKNLAIVWAPNLLRS KQIESACFSGTAAFMEVRIQSVVVEF ILNHVDVLFSGKISAVMQEGAASLS RPKSLLVSSPSTKLLTLEEAQARTQA QVSSPIVTENKYIEVGEGPAALQGKF HTVIEFPLERKRPNKMKKSPVGSW RSFFNLGKSSSVSKRKLQRNESEPS EMKAMALKGGRAEGTLRSKSEESL TSLHAVDGDGSKLFRPRRPRSSDAL SASFNGDVLGNRCNSYDNLPHDNE SEEEVGLLHIPALVSPHSAEDVDLSP PDIGVASLDFDPMSFQCSPKAASE CLESGASFLDSLGYTRDKLSPSKDA EAGGSQSQTPGSTASSEPVSPVQEK LSPFFTLDSLPTDDKSSKPSFTEKV VYAFSPKIGRKLKSPSPMNISEPISVT LPPRVSEVIGTVSNTVAQNASPTSW DKSVEERDVINRSPTQLQLGKMKAG EREAQETCEPEAQPLEQGAAEVEL PGTEERPVLSSQSKAVPSGQSQTGA VTHDPPQDPVPVSSVSLIPPPPPKN VARMLALALAESAQQASSQTLKRP ASQAGCTSYGDTAVVPSEEKLPSSYS SLTLDKTCFQTDRAEQFHPQINGL GNCNQPLPEAAAAMGGPTQSNTTDS GEQLHQVDLIGNSLHRNHISGDPEK ARSTSAPLTDSEKSDDHGSFPEDHA GKSSVSTVSFLEQDQSPLHFSCGDQ PLSYLGTSDVKPHHSELTDKSPMP STLPRDKAHHPLSGSPEENSSTATM AYMMATPARAEPSNSEASRVLAEQP SAADFVAATLQRTHRTNRPLPPPPS QRPAEQPPVVGQVQEAQSIGLNNSH KVQGTAPAPERPPESRAMGDPAPIFL

SDGTAAAQCPMGASAPQGLPEKVR
ESSRAPPLHLRAESFPGHSCGFAAP
VPPTRTMESKMAAALHSSAADATSS
SNYHSFVPSSASVDDVMPVPLPVSQ
PKHASQKIAYSSFARPDVTAEPFGPE
NCLHFNMTPNQCQFRPQSVPPHHNK
LEPHQVYGARSEPPASMGPRYNTYV
APGRNMSGHHSKPCSRVEYVSSLGS
SVRNPCCPEDILPYPTIRRVQSLHAP
PPSMIRSVPIRTEVPPDDEPAYCPR
PVYQYKPYQSSQARSDYHVTQLQPY
FENGRVHYRSPYSSSSSSSYSPEGA
LCDVDAYGTVQLRPLHRLSSRDFAF
YNPRLQGKNVYNYAGLPPRPRANAT
GYFSGNDHNVVTMPPTADGKHTYT
SWDLEDMEKYRMQSIRRESRARQK
VKGPIMSQYDNMTPAVQEDLGGIYV
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SRDCYKEEEHFSQSMVPPPKPERSH
SLKLHHTQNLERDPSVLYQYQTHSK
RQSSMTVVSQYDNLEDYHSLPQHQ
RGGFGGAGMGAYVPSGFVHPQSRT
YATALGQGAFLPTELSLPHPDTQIHA
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