

| UniprotKB ID | Entry name  | organism     | full name                        | oglcnacscore | oglcnac sites | phosphorylation sites                               | PMIDS  | sequence   |
|--------------|-------------|--------------|----------------------------------|--------------|---------------|---|--|--|
| Q811P8       | RHG32_MOUSE | Mus musculus | Rho GTPase-activating protein 32 | 32.239119    | S1027         | S706;S709;S732;S738;S852;S856;S892;S952;S1206;S1588 | 22645316;36852467;33300544;34678516;22517741 | METESETSSLGDDSVFWLDCEGVT<br>QLTDGDEEEREESFRMKSSIHSEE<br>DDFVPELHRNVHPRERPDWEETLS<br>AMARGADVPEIPGDLTLKSCGSTAST<br>KVXHVKKLPFTKGFHPKMAECAHF<br>HYENVEFGSIQLSLSEEQNEVMKNG<br>CESKELVYLQIACQGKSWIVKRSYE<br>DFRVLDKHLHLCIYDRRFSQLTELPR<br>SDVLKDSPESVTQMLTAYLSRLSTIA<br>GNKINCGPALTWMEIDNKGHLLV<br>HEESSINTPAVGAAHVIKRYTARAPD<br>ELTLEVGDIVSVIDMPPKVLSTWWR<br>GKHGFQVGLFPGHCVELINQKVPQS<br>VTNSVPKPVSKKHGKLTIFLRTFMKS<br>RPTKQKLKQRGILKERVFGCDLGEH<br>LLNSGFVQPVLQSCTAFIERYGIVD<br>GIYRLSGVASNIQRLRHEFDSEHVPD<br>LTKEPVYQDIHSVGSCLKLYFRELPN<br>PLLYQLYEKFSDAVSAATDEERLIKI<br>HDVIQQLPPPHYRTLFLMRHLSLL<br>ADYCSITNMHAKNLAIWAPNLLRS<br>KQIESACFSGTAAFMEVRIQSVVVEF<br>ILNHVDVLFSGKISAVMQEGAASLS<br>RPKSLLVSSPSTKLLTLEEAQARTQA<br>QVSSPIVTENKYIEVGEGPAALQGKF<br>HTVIEFPLERKRPNKMKKSPVGSW<br>RSFFNLGKSSSVSKRKLQRNESEPS<br>EMKAMALKGRAEGTLRSKSEESL<br>TSLHAVDGDGSKLFRPRRPRSSDAL<br>SASFNGDVLGNRCNSYDNLPHDNE<br>SEEEVGLLHIPALVSPHSAEDVDLSP<br>PDIGVASLDFDPMSFQCSPKAESE<br>CLESGASFLDSLGYTRDKLSPSKDA<br>EAGGSQSQTPGSTASSEPVSPVQEK<br>LSPFFTLDSLPTDDKSSKPSFTEKV<br>VYAFSPKIGRKLKSPSPMNISEPISVT<br>LPPRVSEVIGTVSNTVAQNASPTSW<br>DKSVEERDVINRSPTQLQLGKMKAG<br>EREAQETCEPEAQPLEQGAAEVEL<br>PGTEERPVLSSQSKAVPSGQSQTGA<br>VTHDPPQDPVPVSSVSLIPPPPPKN<br>VARMLALALAESAQQASSQTLKRP<br>ASQAGCTSYGDTAVVPSEEKLPSSYS<br>SLTLDKTCFQTDRAEQFHPQINGL<br>GNCNQPLPEAAAAMGGPTQSNTTDS<br>GEQLHQVDLIGNSLHRNHISGDPEK<br>ARSTSAPLTDSEKSDDHGSFPEDHA<br>GKSSVSTVSFLEQDQSPLHFSCGDQ<br>PLSYLGTSDVKPHHSELTDKSPMP<br>STLPRDKAHHPLSGSPEENSSTATM<br>AYMMATPARAEPSNSEASRVLAEQP<br>SAADFVAATLQRTHRTNRPLPPPS<br>QRPAEQPPVVGQVQEAQSIGLNNSH<br>KVQGTAPAPERPPESRAMGDPAPIFL |

SDGTAAAQCPMGASAPQGLPEKVR  
ESSRAPPLHLRAESFPGHSCGFAAP  
VPPTRTMESKMAAALHSSAADATSS  
SNYHSFVPSSASVDDVMPVPLPVSQ  
PKHASQKIAYSSFARPDVTAEPFGPE  
NCLHFNMTPNQCQFRPQSVPPHHNK  
LEPHQVYGARSEPPASMGPRYNTYV  
APGRNMSGHHSKPCSRVEYVSSLGS  
SVRNPCCPEDILPYPTIRRVQSLHAP  
PPSMIRSVPIRTEVPPDDEPAYCPR  
PVYQYKPYQSSQARSDYHVTQLQPY  
FENGRVHYRSPYSSSSSSSYSPEGA  
LCDVDAYGTVQLRPLHRLSSRDFAF  
YNPRLQGKNVYNYAGLPPRPRANAT  
GYFSGNDHNVVTMPPTADGKHTYT  
SWDLEDMEKYRMQSIRRESRARQK  
VKGPIMSQYDNMTPAVQEDLGGIYV  
IHLRSKSDPGKTGLLSVAEGKEGRH  
PAKAVSPEGDERFYRKHPSEFDRA  
HHHGGYGSTQAEKPSLPQKQSSLR  
NRKLHDMGCSLPEHRAHQEASHRQ  
LCESKNGPPYPQGAGQLDYGSKGM  
PDTSEPSNYHNSGKYMTSGQGSLTL  
NHKEVRLPKDLDRPRARQPPGPEKH  
SRDCYKEEEHFSQSMVPPPKPERSH  
SLKLHHTQNLERDPSVLYQYQTHSK  
RQSSMTVVSQYDNLEDYHSLPQHQ  
RGGFGGAGMGAYVPSGFVHPQSRT  
YATALGQGAFLPTELSLPHPDTQIHA  
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