| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | enc ret |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | Q811P8 | RHG32_MOUSE | Mus musculus | Rho GTPase-activating protein 32 | 51.867032 | S920;T925;S927;S1007;S1027 | S706;S709;S732;S738;S852;S856;S892;S952;S1206;S1588 | 22517741;22645316;33300544;40885482;36852467;40021952;34678516 | METESETSSLGDDSVFWLDCEGVTQLTDGDEEEREESFRKMKSSIHSEEDDFVPELHRNVHPRERPDWEETLSAMARGADVPEIPGDLTLKSCGSTASTKVKHVKKLPFTKGHFPKMAECAHFHYENVEFGSIQLSLSEEQNEVMKNGCESKELVYLVQIACQGKSWIVKRSYEDFRVLDKHLHLCIYDRRFSQLTELPRSDVLKDSPESVTQMLTAYLSRLSTIAGNKINCGPALTWMEIDNKGNHLLVHEESSINTPAVGAAHVIKRYTARAPDELTLEVGDIVSVIDMPPKVLSTWWRGKHGFQVGLFPGHCVELINQKVPQSVTNSVPKPVSKKHGKLITFLRTFMKSRPTKQKLKQRGILKERVFGCDLGEHLLNSGFEVPQVLQSCTAFIERYGIVDGIYRLSGVASNIQRLRHEFDSEHVPDLTKEPYVQDIHSVGSLCKLYFRELPNPLLTYQLYEKFSDAVSAATDEERLIKIHDVIQQLPPPHYRTLEFLMRHLSLLADYCSITNMHAKNLAIVWAPNLLRSKQIESACFSGTAAFMEVRIQSVVVEFILNHVDVLFSGKISAVMQEGAASLSRPKSLLVSSPSTKLLTLEEAQARTQAQVSSPIVTENKYIEVGEGPAALQGKFHTVIEFPLERKRPQNKMKKSPVGSWRSFFNLGKSSSVSKRKLQRNESEPSEMKAMALKGGRAEGTLRSAKSEESLTSLHAVDGDSKLFRPRRPRSSSDALSASFNGDVLGNRCNSYDNLPHDNESEEEVGLLHIPALVSPHSAEDVDLSPPDIGVASLDFDPMSFQCSPPKAESECLESGASFLDSLGYTRDKLSPSKKDAEAGGSQSQTPGSTASSEPVSPVQEKLSPFFTLDLSPTDDKSSKPSSFTEKVVYAFSPKIGRKLSKSPSMNISEPISVTLPPRVSEVIGTVSNTVAQNASPTSWDKSVEERDVINRSPTQLQLGKMKAGEREAQETCEPEAQPLEQGAAEEVELPGTEERPVLSSQSKAVPSGQSQTGAVTHDPPQDPVPSSVSLIPPPPPPKNVARMLALALAESAQQASSQTLKRPGASQAGCTSYGDTAVVPSEEKLPSSYSSLTLDKTCFQTDRPAEQFHPQINGLGNCNQPLPEAAAMGGPTQSNTTDSGEQLHQVDLIGNSLHRNHISGDPEKARSTSAPLTDSEKSDDHGSFPEDHAGKSSVSTVSFLEQDQSPLHFSCGDQPLSYLGTSVDKPHHSSELTDKSPMPSTLPRDKAHHPLSGSPEENSSTATMAYMMATPARAEPSNSEASRVLAEQPSAADFVAATLQRTHRTNRPLPPPPSQRPAEQPPVVGQVQEAPSIGLNNSHKVQGTAPAPERPPESRAMGDPAPIFLSDGTAAAQCPMGASAPQPGLPEKVRESSRAPPLHLRAESFPGHSCGFAAPVPPTRTMESKMAAALHSSAADATSSSNYHSFVPSSASVDDVMPVPLPVSQPKHASQKIAYSSFARPDVTAEPFGPENCLHFNMTPNCQFRPQSVPPHHNKLEPHQVYGARSEPPASMGPRYNTYVAPGRNMSGHHSKPCSRVEYVSSLGSSVRNPCCPEDILPYPTIRRVQSLHAPPPSMIRSVPISRTEVPPDDEPAYCPRPVYQYKPYQSSQARSDYHVTQLQPYFENGRVHYRYSPYSSSSSSYYSPEGALCDVDAYGTVQLRPLHRLSSRDFAFYNPRLQGKNVYNYAGLPPRPRANATGYFSGNDHNVVTMPPTADGKHTYTSWDLEDMEKYRMQSIRRESRARQKVKGPIMSQYDNMTPAVQEDLGGIYVIHLRSKSDPGKTGLLSVAEGKEGRHPAKAVSPEGDERFYRKHPESEFDRAHHGGYGSTQAEKPSLPQKQSSLRNRKLHDMGCSLPEHRAHQEASHRQLCESKNGPPYPQGAGQLDYGSKGMPDTSEPSNYHNSGKYMTSGQGSLTLNHKEVRLPKDLDRPRARQPPGPEKHSRDCYKEEEHFSQSMVPPPKPERSHSLKLHHTQNLERDPSVLYQYQTHSK | False | False | 2.997 | 2.888 | 0.947 | 3.4 |

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | RQSSMTVVSQYDNLEDYHSLPQHQ<br>RGGFGGAGMGAYVPSGFVHPQSRT<br>YATALGQGAFLPTELSLPHPDTQIHA<br>E | | | | | | | | |