| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | endoplasmic reticulum | golgi apparatus | pla me |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q9QUH6 | SYGP1_RAT | Rattus norvegicus | Ras/Rap GTPase-activating protein SynGAP | 47.957484 | NaN | T34;T39;S117;S371;S379;S385;S449;S466;S752;S766;S780;S823;S825;T828;S836;S840;S842;S876;S892;S895;S898;S985;S1114;S1118;S1121;S1165;S1204 | 35637289;22645316;17496889;19322778 | MSRSRASIHRGSIPAMSYAPFRDVR<br>GPPMHRTQYVHSPYDRPGWNPRFC<br>IISGNQLLMLDEDEIHPLLIRDRRSE<br>SSRNKLLRRTVSVPVEGRPHGEHEY<br>HLGRSRRKSVPGGKQYSMEAAPAAP<br>FRPSQGFLSRRLKSSIKRTKSQPKLD<br>RTSSFRQILPRFRSADHDRARLMQS<br>FKESHSHESLLSPSSAAEALELNLD<br>EDSIIKPVHSSILGQEFCFEVTTSSGT<br>KCFACRSAAERDKWIENLQRAVKPN<br>KDNSRRVDNVLKLWIIEARELPPKK<br>RYYCELCLDDMLYARTTSKPRSASG<br>DTVFWGEHFEFNNLPAVRALRLHLY<br>RDSDKKRKKDKAGYVGLVTVPVATL<br>AGRHFTEQWYPVTLPTGSGGSGGM<br>GSGGGGGSGGGSGGKGKGGCPAVR<br>LKARYQTMSILPMELYKEFAEYVTN<br>HYRMLCAVLEPALNVKGKEEVASAL<br>VHILQSTGKAKDFLSDMAMSEVDRF<br>MEREHLIFRENTLATKAIEEYMRLIG<br>QKYLKDAIGEFIRALYESEENCEVDP<br>IKCTASSLAEHQANLRMCCELALCK<br>VVNSHCVFPRELKEVFASWRLRCAE<br>RGREDIADRLISASLFLRFLCPAIMSP<br>SLFGLMQEYPDEQTSRTLTLIAKVIQ<br>NLANFSKFTSKEDFLGFMNEFLELE<br>WGSMQQFLYEISNLDTLTNSSSFEG<br>YIDLGRELSTLHALLWEVLPQLSKEA<br>LLKLGPLPRLLSDISTALRNPNIQRQ<br>PSRQSERARSQPMVLRGPSAEMQG<br>YMMRDLNSSIDLQSFMARGLNSSM<br>DMARLPSPTKEKPPPPPPGGGKDLF<br>YVSRPPLARSSPAYCTSSSDITEPEQ<br>KMLSVNKSVSMLDLQGDGPGGRLN<br>SSSVSNLAAVGDLLHSSQASLTAAL<br>GLRPAPAGRLSQGSGSSITAAGMRL<br>SQMGVTTDGVPAQQLRIPLSFQNPL<br>FHMAADGPGPPAGHGGSSGHGPPS<br>SHHHHHHHHHHRGGEPPGDTFAP<br>FHGYSKSEDLSTGVPKPPAASILHSH<br>SYSDEFGPSGTDFTRRQLSLQDNLQ<br>HMLSPPQITIGPQRPAPSGPGGGSG<br>GGSGGGGGGQPPPLQRGKSQQLTV<br>SAAQKPRPSSGNLLQSPEPSYGPARP<br>RQQSLSKEGSIGGSGGSGGGGGGGL<br>KPSITKQHSQTPSTLNPTMPASERTV<br>AWVSNMPHLSADIESAHIEREEYKL<br>KEYSKSMDESRLDRVKEYEEEIHSL<br>KERLHMSNRKLEEYERRLLSQEEQT<br>SKILMQYQARLEQSEKRLRQQQVEK<br>DSQIKSIIGRLMLVEEELRRDHPAMA<br>EPLPEPKKRLLDAQRGSFPPWVQQT<br>RV | None | None | None | None | None | None | None | No |