| | UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochndrion | endoplasmic reticulum | golgi apparatus | plasma membrane | ex re |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q9JKF1 | IQGA1_MOUSE | Mus musculus | Ras GTPase-activating-like protein IQGAP1 | 40.088201 | NaN | S2;T172;S330;S1441 | 22645316;34887587;29125738;25153642;39627609;37507081 | MSAAEEVDGLGVVRPHYGSVLDNE<br>RLTAEEMDERRRQNVAYEYLCHLEE<br>AKRWMEACLGEDLPPTTELEEGLR<br>NGVYLAKLGNFFSPKVVSLKKIYDRE<br>QTRYKATGLHFRHTDNVIQWLNAM<br>DEIGLPKIFYPETTDIYDRKNMPRCIY<br>CIHALSLYLFKLGLAPQIQDLYGKVD<br>FTEEEINNMKIELEKYGIQMPAFSKI<br>GGILANELSVDEAALHAAVIAINEAI<br>DRRVAADTFTALKNPNAMLVNLEE<br>GLAPTYQDVLYQAKQDKMTNAKNR<br>TENSDRERDVYEELLTQAEIQGNVN<br>KVNTSSALANISLALEQGCAVTLLKA<br>LQSLALGLRGLQTQNSDWYMKQLQ<br>SDLQQKRQSGQTDPLQKEEVQAGV<br>DAANSAAQQYQRRLAAVAAINAAIQ<br>KGIAEKTVLELMNPEAQLPQVYPFA<br>ADLYQKELATLQQQSPEHSLTHPEL<br>TVAVEMLSSVALINRALESGDMTTV<br>WKQLSSSVTGLTNIEEENCQRYLDE<br>LMKLKAQAHAENNAFITWNDIQAC<br>VDHVNLVVHEEHERILAIGLINEALD<br>EGDAQKTLQALQIPAAKLEGVLAEVA<br>QHYQDTLIRAKREKAQETQDESAVL<br>WLDEIQGGIWQSNKDTQEAQRFAL<br>GISAINEAVDSGDVGRTLSALRSPDV<br>GLYGVIPECGETYQSDLAEAKKKRLA<br>AGDNNSKWVKHWVKGGYHYYHNL<br>ETQAGGWAEPPDFVQNSVQLSREEI<br>QSSISGVTAAYNREQLWLANEGLITK<br>LQACCRGYLVRQEFRSRMNFLKKQI<br>PAITCIQSQWRGYKQKKAYQDRLAYL<br>HSHKDEVVKIQSLARMHQARKRYR<br>DRLQYFRDHINDIIKIQAFIRANKAR<br>DDYKTLINAEDPPMIVVRKFVHLLD<br>QSDQDFQEELDLMKMREEVITLIRS<br>NQQLENDLNLMDIKIGLLVKNKITL<br>QDVVSHSKKLTKKNKEQLSDMMMI<br>NKQKGGLKALSKEKREKLEAYQHLF<br>YLLQTNPTYLAKLIFQMPQNKSTKF<br>MDSVIFTLYNYASNQREEYLLLRLFQ<br>TALQEEIKSKVDQIQEIVTGNPTVIK<br>MVVSFNRGARGQNALRQILAPVVKE<br>IMDDKSLNIKTDPVDIYKSWVNQME<br>SQTGEASKLPYDVTPEQALSHEEVK<br>TRLDNSIRNMRAVTDKFLSAIVSSVD<br>KIPYGMRFIAKVLKDSLHEKFPDAGE<br>DELLKIIGNLLYYRYMNPAIVAPDAF<br>DIIDLSAGGQLTTDQRRNLGSIAKML<br>QHAASNKMFLGDNAHLSIINEYLSQ<br>SYQKFRRFFQVACDVPELQDKFNVD<br>EYSDLVTLTKPVIYISIGEIINTHTLLL<br>DHQDAIAPEHNDPIHELLDDLGEVP<br>TIESLIGESCGNSNDPNKEALAKTEV<br>SLTLTNKFDVPGDENAEMDARTILL<br>NTKRLIVDVIRFQPGETLTEILETPAT<br>NEQEAEHQRAMQRRAIRDAKTPDK<br>MKKSKPMKEDNNLSLQEKKEKIQT<br>GLKKLTELGTVDPKNRYQELINDIAK<br>DIRNQRRYRQRRKAELVKLQQTYSA<br>LNSKATFYGEQVDYYKSYIKTCLDNL<br>ASKGKVSKKPREMKGKKSKKISLKY<br>TAARLHEKGVLLEIEDLQANQFKNVI<br>FEIGPTEEVGDFEVKAKFMGVQMET<br>FMLHYQDLLQLQYEGVAVMKLFDR<br>AKVNVNLLIFLLNKKFYGK | True | True | 2.775 | 5.0 | 1.792 | 1.722 | 1.581 | 5.0 | 1.9 |