| | 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 | extracellular region |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | P97433 | ARG28_MOUSE | Mus musculus | Rho guanine nucleotide exchange factor 28 | 36.83566 | T532 | S312;S314;S478;S623;S1535;S1604 | 40885482 | MELSCSEVPLYGQKTVYAKFGKNVY<br>LPEDAEFYFVYGGSHQRHVVIADRV<br>QDNVLQSSIPGHWLQETVTVSVCLC<br>SEGYSPVTMGSGSVTYVDNMACRLA<br>RLLVTQADRLTACSHQTLLTPFALTV<br>EALPALDEELVLALTQLELPLGWTVL<br>GNSSLEVSLHRESLLHLAVRWALPK<br>LFHFLLCLPGGVKALKLPNEEATTPL<br>DLALQGGHSTLVEDITNFQGSHSPG<br>FSRLRLNEEATLQFVHSSETLTLTVN<br>HTAEHLLEADIKLFRKYFWDRAFLV<br>KALEQEAKTEKATMPSGAAETEEEV<br>RNLESGRSPSEEEEDAKSIKSQVDG<br>PSEHEDQDRLPLDRSFDGLKKSKHV<br>PASLAAGQLSDVLNGGDEVYANCM<br>VIDQVGDLDINYINLEGLSTHTSPES<br>GRSMLGPQACMHTLPPDTSPCGRP<br>LIENSEGTLDAAASQSFVTPSSSRTS<br>NLNLSFGLHGFEKEQSHLKKRSSSL<br>DALVADSEGEGGSEPPICYAVGSQSS<br>PRTGLPSGDELDSFETNTEPDCNISR<br>TESLSLSSTLHSKESLLSGIRSRSYSC<br>SSPKISSGKSRLVRDFTVCSTSEEQR<br>SYSFQEPPGEKRIQEEEWDEYVIPAK<br>SESEKYKVSRTFSFLMNRMTSPRNK<br>SKMKNKDTKEKEKMNRHQFVPGTF<br>SGVLQCSGCDKTLLGKESLQCANCK<br>ANTHKGCKDAVPPCTKKFQEKYNK<br>NKPQSILGSSSVRDVPAPGLSLHPSS<br>SMPIGLPAGRKEFAAQVHPLSRSVP<br>GTTLESFRRAVTSLESEGDSWRSRS<br>HSDELFQSMGSSPSTESFMMEDVV<br>DSSLWIDLSSDAQEFEAESWSLVVD<br>PSFCSRQEKDVIKRQDVIFELMQTE<br>VHHIQTLLIMSEVFRKGMKEELQLD<br>HSTVDKIFPCLDELLETHRHFFFSM<br>KERRQESCAGSDRNFVINQIGDILVQ<br>QFSEENASKMKRIYGEFCSHHKEA<br>MSLFKELQQNKKFQNFIKIRNSNLL<br>ARRRGIPECILLVTQRITKYPVLVERI<br>LQYTKERTEEHRDLCKALGLIKDMIA<br>AVDLKVSEYEKNQKWLEILNKIENK<br>TYTKLKNGHVFRKQALLSQERALLH<br>DGLVYWKTATGRFKDILALLLTDVLL<br>FLQEKDQKYIFAAVDQKPSVISLQKLI<br>AREVANEERGMFLISASSAGPEMYE<br>IHTNSKEERNNWMRRIQQAVESCP<br>EEEGGRTSESDEERRKAEARVAKIQ<br>QCQEILSNQDQQICTYLEEKLHIYAE<br>LGELSGFEDVHLEPHLLIKPDPGEPP<br>QAASLLAAALREAESLQVAVKASKM<br>GDVSQSSEESPGGTVLMDTPSTQDV<br>PASPTASLVTEGTEGRGCWDVDPGL<br>QGVVTDLAVSDAGEKVEYRSFSGSS<br>QSEIIQAIQNLTRLLYSLQAALTIQDS<br>HIEIHKLVLQQRESLAPSHSFRGGPL<br>QDQEKSRYLEKQREELANIHKLQHQ<br>FQQEQRRWHRTCDQQQREQEAQES<br>WLQARERECQSQEELLLRHRSELD<br>HQLQEYQQSLERLREGQRMVERER<br>QKMRVQQGLLGHCKHSRQRSLPAV<br>FSPGSKEVTELNRAESLCHENSFFI<br>NEAFGHMSLNTSNKPNPSGVPWDA<br>HPLEGSHFDLARTSESPTELKIDISQ<br>PPDVNSELWTTGPGHQRPALQENS<br>KESYKNVADLDSFQSESSSPQDSNQ<br>RGPQPQTLTTEAKLSLPMAAGHGGD<br>AGDGAEENILYL | False | True | 3.601 | 2.905 | 1.477 | 1.577 | 1.52 | 5.0 | 1.797 |