| | 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 | extracellul region |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q8C147 | DOCK8_MOUSE | Mus musculus | Dedicator of cytokinesis protein 8 | 25.685855 | NaN | S20;S139;S452;S905;S937;S1146;S1244;S2088 | 39627609 | MATLPSAERRAFALKINRYSSSEIRK<br>QFTLPPNLGQYHRHSISTSGFPSLQL<br>PQLYEPVEPVDFEGLVMTHLNSLDA<br>ELAQELGDLTDDDLHVAFTPKECRT<br>LQHSLPEEGVELDPHVRDCVQTYIR<br>EWLIVNRKNQGSSEFCSFKKTGSRR<br>DFQKTLQKQTFESETLECSEPDTQT<br>GPRHPLNVLCDVSGKGPLTSCDFDL<br>RSLQPDERLENLLQLVSAEDFEKEK<br>EEARKTNRPAELFALYPPVDEEDAV<br>EIRPVPECPKEHLGNRILVKVLTLKF<br>EIEIEPLFASIALYDVKERKKISENFH<br>CDLNSDQFKGFLRAHTPSIDPSSQA<br>RSAVFSVTYPSSDIYLVVKIEKVLQQ<br>GEIADCAEPYMIIKESDGGKSKEKVE<br>KLKLQAESFCQRLGKYRMPFAWAPI<br>SLASFFNISTLEREST DVEPGVGRNS<br>VGEKRSLSQSRRPSERTLSLEENGV<br>GSNFKATTLATNIFFKQEGDRLSDE<br>DLFKFLADYKRSSSLQRRVKSIPGSL<br>RLEISPAPDVMNCCLTPEMLPVKPF<br>PENRTRPHKEILEFPIREVYVPHTVY<br>RNLLYVYPQRLNFASKLASARNITIKI<br>QFMCGEDPSNAMPVIFGKSSGPEFL<br>QEVYTAITYHNKSPDFYEEVKIKLPA<br>KLTVNHHLLFTFYHISCQQKQGASG<br>ESLLGYSWLPILLNERLQTGSYCLPV<br>ALEKLPPNYSIHSAEKVPLQNPPIKW<br>AEGHKGVFNIEVQAVSSVHTQDNHL<br>EKFFTLCHSLESQVSFPIRVLDQKIT<br>ESTLEHELKLSIICLNSSRLEPLVLFL<br>HLVLDKLFQLSVQPMVIAGQTANFS<br>QFAFESVVAIANSLHNSKDLRKDQH<br>GRNCLLASYVHYVFRLPELHRDTSK<br>SGGPTTVVPDPRYHTYGRTSAAAVSS<br>KLMQARVMSSSNPDLTGSHCAADE<br>EVKNIMSSKIADRNCSRMSYYCSGN<br>SDAPGSTAAPRPVSKKHFHEELALQ<br>MVVSTGVVRETVFKYAWFFFELLVK<br>SMAQYVHNLDKRDSFRRTRFSDRF<br>KDDITTIVNVVTSEIAALLVKPQKESE<br>QAEKINISLAFFLYDLLSIMDRGFVF<br>NLIKHYCSQLSAKLNILPTLISMRLE<br>FLRILCSHEHYLNLNLLFMNTDTAP<br>ASPCPSISSQNSSSCSSFQDQKIASM<br>FDLTPEYRQQHFLTGLLFTELAVALD<br>AEGDGISRVQRKAVSAIHSLLCSHDL<br>DPRCRKPEVKVKIAALYLPLVGIILDA<br>LPQLYDFTDARSGRSRASGSYEEQD<br>VANGINQNVALAIAGNHFNLKTSGA<br>MLSSLPYKQYNMLNADTTRHLMICF<br>LWIMKNADQSLIRKWIADLPSMQLN<br>RILDLLFICVSCFEYKGKQSSDKVSN<br>QVLQKSRDVKAKLEEALLRGEGARG<br>EMMRRRIPGTDRFPGINENLRWRK<br>EQTQWRQANEKLDKTKAELDQEALI<br>SGNLATEANLIILDMQENIIQASSAL<br>DCKDSLLGGVLRVLVNSLSCDQSTT<br>YLTHCFATLRALIAKFGDLLFEEEME<br>QCADLCQRVLHHCSSSMDVTRSQA<br>CATLYLLMRFSFGATSNFARVKMQV<br>TMALASLVGKAPDFNEEHLRRSLRT<br>ILAYSEEDTAMQTTPFPMQVEELLC<br>NLNSILYDTVKMREFQEDPEMLMD<br>LMYRIAKSYQASPDLRLTWLQNMAE<br>KHTKKKCFTEAAMCLVHAAALVAEY<br>LSMLEDHSYLPVGSVSFQNISSNVL<br>EESAVSDDTLSPDEDGVCSGRYFTE<br>SGLVGLLEQAAELFSTGGLYETVNE<br>VYKLVIPILEAHRDFRKLTSTHDKLQ<br>KAFDNIINKDHKRMFGTYFRVGFYG<br>SRFGDLDEQEFVYKEPAITKLPEISH<br>RLEGFYGQCFGAEFVEVIKDSTPVDK<br>TKLDPNKAYIQITFVEPYFDEYEMKD<br>RVTYFEKNFNLRRFMYTTPFTLEGR<br>PRGELHEQHRRNTVLTTMHAFPYIK<br>TRIRVSQKEEFVLTPIEVAIEDMKKK<br>TLQLAVATHQEPPDAKMLQMVLQG<br>SVGATVNQGPLEVAQVFLAEIPADPK<br>LYRHHNKLRLCFKEFIMRCGEAVEK | False | True | 3.128 | 1.909 | 1.387 | 1.142 | 0.979 | 4.457 | 1.865 |

| | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | NRRLITAEQREYQQELKKNYNKLRD<br>SLRPMIERKIPELYKPIFRVDSQKRD<br>SFHRSSFRKCETQLSQGS | | | | | | | | | | |