

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golg appa |
|--------------|-------------|--------------|------------------------------------|--------------|---------------|---|--|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------|
| P59764 | DOCK4_MOUSE | Mus musculus | Dedicator of cytokinesis protein 4 | 42.530519 | S1796;T1806 | T167;T193;S1608;S1616;S1623;S1627;S1629;S1640;S1778 | 36852467;22645316;22517741;33300544;34678516 | MWIPTEHEKEYGVVIASFRGTVPYGLS LEIGDVTVOIQLEKCDGWYRCFALKNP NIKGIFFSSVYHLKNCVKNKGQFE MVIPTEDSVITEMTSLRDRWGTMW KQLYVRNEGDLFHRLWHIMNEILD RRQVLVGHLLTHDRMKDVKRHITARL DWGNEQLGLDLVPRKEYAMVDPED ISITELYRLMEHRHRKKDTPVQASS HHLFVQMKSLMCSNLGEELEVIFSL FDSKENRPISEFFLRLNRNGLPKA PDKPERHCSLFVDLGSSELKDIYIT VHIIRIGRMGAGEKKNACSVQYRRP FGCAVLSIADLLTGETKDDLVLKVYM CNTSEWYQIHENIHKLNARYNLT GSNAGLAVSLQLLHGDIQIRREYSS VFSHGVSITRKLGFSDIIMPGEGRN DLYITVERGEFEKGGKSVARNVEVT MFIVDSNGQPLKDFISFGSGEPPASE YHSFVLYHNNSPRWSELLKLPIVD KFRGSHIRFEFRHCSTKEKGEKLF GFSFVPLMQEDGRITPDGTHELIVH KCEENTNLQDTRRYLKLFPKVIPLG NNNQTMKATKESFWITSFLCSTKLT QNGDMLDLLKWRTHPDKITGCLSK LKEIDGSEIVKFLQDTLDTLFGILDE NSQKYGSKVFDLSVHIINLLQDSKF HHFKPVMMDTYIESHFAGALAYRDLI KVLKVVYDRITEAERQEHIEQVKA QEYIFKYIVQSRRLFLSATGGQNEEE FRCCIQELLSVRFSLQESKGTGA LSQSQAVFLSSFPVAVSELLKLFVDR EVANLVQDTLGSPLTIMHVDDSLQA IKLQCIGKTVESQLYTNPDSRYILLPV VLHHLHIHLQEQKDLIMCARILSNV FCLIKNSSEKSVLEIDVIVASLLDI LLRTILEITSRPQASSAMRLOFQDV TGEFVACLLSLLRQMTDRHYQQLLN SFSTKEELRDLFLQIFTVFRILRPEM FPKDWTVMRLVANNVIITVLYLSDA LRKNFLNENFDYKIWDSYFYLAIFI NQLCLQLEMFTPSKKKKVLEKYGD MRVTMGCEIFSMWQNLGEHKLHFI PALIGPFLEVTLPQPDLRNVMIPIFH DMMDWEQRRSGNFQVEAKLIDKL DSLMSSEKGDETYRELNFNSIPLFGP YPSLLKKIERTWRESGVSLIATVTR LMERLLDYRDCMKIGEVGKKGCT VSLNIFYKTELNKEEMYIRYIHKLYD LHLKAQNFTEAAYTLLYDELELWS DRPLREFLYTPMQTEWQRKEHLHL THQNFDRGKCWENGILCRKIAEQY ESYYDYRNLKMRMMEASLYDKIM DQORLEPEFFRVGFYKGFPPFLRN KEFVCRGHDYERLEAFQORMLNEF PHAIAMQHANOQDETIFQAEAQYLO IYAVTPIPESQEVLRQREGVDPNKSFY KVNHIWKFRYDRPFHKGAKDKENE FKSLWVERTSLYLVSQSLPGISRWFV EKREVVEMSPLENAIEVLENKNQQL KTLISQCQTRQMQNINPLTMCLNGV IDAAVNGGVSRYQEAFFVKDYILSHP EDGEKIARLRELMLEQAQILEFGLAV HEKFVPQDMRPLHKKLVDQFFVMK SSFQIQEFPACIQASPVHFPNGSPRV CRNSAPASMSPDGTRVPRRSPLSYP AVNRYSSSSLSQASAEVSNITGQSE SSDEVFNMQPSPSTSSLSSTHSASP NVTSSAPSSARASPLLSKHKHSRE NSCLSPDRPCSAIYTPVPEPSQRLM FNHIGDGLPRSDPNLSAPEKAVNP TPSSWSLDSGKEAKNMSDSGKLISP PVPPRPTQASPARHTTSVSPSPAGR SPLKGSVQSFTPSPEVNSPGLSSNS PVLGSGYSSGSSLSRCSTSETSGFE NQANEQSVPPVPPVPPVPPVPSFG SEEPVRKESKTPPPYSVYERTLRRPV PLPHLSIPVTSPEPALPPKPLAARSS HLENGTRRETPGPRRPLPRKVSQ | True | False | 4.572 | 3.19 | 1.835 | 1.299 | 2.49 |