

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma
Q8C3J5	DOCK2_MOUSE	Mus musculus	Dedicator of cytokinesis protein 2	31.872804	S583	S588;S593;S1683;S1704;S1729;S1782	29187734;34418053;39627609	MAPWRKTDKERHGVAIYNFQGSEA QHLLTLQIGDVRRIQETCCGDWYRGLI KHKLSQGFIPSTFIHLKEVTEKRRN IENIIPAEIPLAQEVTTTLWEWGSWIK QLYVASKKERFLQVQSMYDLMEW RSQLLSGTLPKDELKELKQKVTSKID YGNKILELDLIVRDEDGNLDPDKTS VISLFHAHEEATYKITERIKEEMSKD QPDYGVYSRISSSPHSLYVVRNFV CRIGEDAELFMSLYDPHKQTVISENY LVRWGSKGFPEIEMLNKLVVFTD LGNKDLNRDKIFLICQVIRIGKMDLK DINAKKCTOGLRRPFGVAVMDITDII KGKAESDEEKQHFIPFHPVSAENDF LHSLLGKVIASKGDSGGQGLWVTMK MLVGDIIQIRKDYPHLVDRTTVVARK LGFPEIIMPGDVRNDIYITLLQGFDF KYTKTTQRNVEVIMCVCTEDGKVLV NAICVAGADKAMNEYHSVVYVQVK QPRWMETVKVAVPIEDMORIHLLRF MFRHRSSLESKDKGKFNFAMSIVK LMKEDGTTLHDGYHELVLKGDGSK KMEDASAYLTLPSYRHPVENKGATL SRSSSSVGGLSVSRDVFISITLVCS TKLTQNVGLLGLLKWRMKPQLLQE NLEKLVKIVDGEVVKFLQDTLDALF NIMMEHSQSNEYDILVFDALYIIGLI ADRKFQHFNTVLEAYIQHFSAATLA YKKLMTVLKTYLDTSSRGEQCEPILR TLKALEYVFKFIVRSRTLFSQLYEGK EQMEFEESMRRLFESINNLKMSQY KTILLQVAALKYIPSVLHDVETVFDA KLLSQLLYEFYTCIPPVKLQKQVQS MNEIVQSNLFFKKQECRDILLPVITKE LKELLEQRDDGQHQAEEKKHCVELL NSILEVLSQDAAFYDHIQEI MVQL LRTVNRVTITMGRDHALISHFVACM TAILDQMGDQHYSFYIETFTSSDLV DFLMETFIMFKDLIGKNVYPGDWM AMSMVQNRVFLRAINKFAETMNOK FLEHTSFEFQLWNNYFHLAVAFITQ DSLQLEQFTHAKYNKILNKYGDMMR LIGFSIRD MWYKLGONKICFIPGMV GPILEMTLIPAEALRKAIPFFDMM LCEYQRTGAFKKFENEIILKLDHEVE GGRGDEQYMQLLESILMECTAEHPT IAKSVENFVSLVGLLEKLLDYRGV MTDESKDNRMSCVTNLLNFYKDNN REEMYIRYLYKLRDLHLDCENYTEA AYTLLHTWLLKWSDEQCASQVMQ TGQQHPQTHRQLKETLYETHIGYFDK GKMWEEAISLCKELAEQYEMEIFDY ELLSQNL TQAKFYENIMKILRTKPD YFAVGYGQGFPSFLRNKVFYIRGKE YERREDFQMQLLSQFPNAEKMNTT SAPGDDVRNAPGQYIQCFVQPVLD EHPRFKNKVPDQIINFYKSNYVQKF HYSRPVRRGKVDPENEFASMWIERT SFLTAYKLPGLRWFEVVHMSQTTIS PLENAIETMSTVNEKILMMINQYQS DESLPINPLSMLLNGIVPAVMGGF AKYEKAFFTEYSREHPEDQDKLSH LKDLIAWQIPFLGAGIKIHEKRVSDN LRPFFDRMECFKNLKMKEKEYG VREMPDFEDRRVGRPRSMRLRSYRQ MSVISLASMHSDCSTSPKVPAESFD LESAPPKTPKVEEPISPGSTLPEVKL RRSKKRTKRSSVVFADKAAATESDL KRLSRKQEFMSDTNLSHAAPARV SILSQMSFASQSMPTIPALTSVAGV PGLDEANTSPRLSQTFFQVSDGDKK TLKKKKVNQFFKTM LASKSSEESKQ IPDFLSTNM	False	False	3.184	2.091	1.465	1.351	1.038	3.6