	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	Q8CIQ7	DOCK3_MOUSE	Mus musculus	Dedicator of cytokinesis protein 3	37.975063	S1733	S1655	33300544;40885482	MWTPTEEEKYGVVICSFRGSVPQGL VLEIGETVQILEKCEGWYRGVSTKKP NVKGLFPANYIHLKKAIVSNRGQYET VVPLEDSIVTEVTTTLQEWASLWKQ LYVKHKVDLFYKLRHVMNELIDLRR QLLSGHLTQDQVREVKRHITVRLDW GNEHLGLDLVPRKDFEVVDSDQISV SDLYKMHLSSRQSVQQSTSQVDTM RPRHGETCRMPVPYHFFFSLKSFTY NTIGEDSDVFFSLYDMREGKQISER FLVRLNKNGGPRNPEKIERMCALFT DLSSKDMKRDLYIVAHVIRIGRMLL NDSKKGPAHLHYRRPYGCAVLSILD VLQSLTELKEEKDFVLKVYTCNNES EWTQIHENIIRKSSTKYSAPSASHGLI ISLQLFRGDMEQIRRENPMIFNRGL AITRKLGFPDVIMPGDIRNDLYLTLE KGDFERGGKSVQKNIEVTMYVLYAD GEILKDCISLGSGEPNRSSYHSFVLY HSNSPRWGEIIKLPIPIDRFRGSHLR FEFRHCSTKDKGEKKLFGFAFSPLM RDDGTTLSDDIHELYVYKCDENSTF NNHALYLGLPCCKEDYNGCPNIPSS LIFQRSKESFFISTQLSSTKLTQNVD LLALLKWKAFPDRIMDILGRLRHVS GEEIVKFLQDILDTLFVILDDNTEKY GLLVFQSLVFIINLLRDIKYFHFRPV MDTYIQKHFAGALAYKELIRCLKWY MDCSAELIRQDHIQEAMRALEYLFK FIVQSRILYSRATCGMEEEQFRSSIQ ELFQSIRFVLSLDSRNSETLLFTQAA LLNSFPTIFDELLQMFTVQEVAEFVR GTLGSMPSTVHIGQSMDVVKLQSIA RTVDSRLFSFSESRRILLPVVLHHIH LHLRQQKELLICSGILGSIFSIVKTSS LEADVMEEVEMMVESLLDVLLQTLL TIMSKSHAQEAVRGHCPVTAEITGEY VSCLLSLLRQMCDTHFQHLLDNFQ SKDELKEFLLKIFCVFRNLMKMSVF PRDWMVMRLLTSNIIVTTVQYLSSA LHKNFTETDFDFKVWNSYFSLAVLF INQPSLQLEIITSAKRKKILDKYGDM RVMMAYELFSMWQNLGEHKIHFIP GMIGPFLGVTLVPQPEVRNIMIPIFH DMMDWEQRKNGNFKQVEAELIDKL DSMVSEGKGDESYRELFGLLTQLFG PYPSLLEKVEQETWRETGISFVTSVT RLMERLLDYRDCMKGEETENKKVG CTVNLMNFYKSEINKEEMYIRYIHKL CDMHLQAENYTEAAFTLLLYCELLQ WEDRPLREFLHYPSQTEWQRKEGL CRKIIHYFNKGKSWEFGIPLCRELAC QYESLYDYQSLSWIRKMEASYYDNII EQQRLEPEFFRVGFYGRKFPFFLRN KEYVCRGHDYERLEAFQQRMLSEFP QAVAMQHPNHPDDAILQCDAQYLQI YAVTPIPDYVDVLQMDRVPDRVKSFY RVNNVRKFRYDRPFHKGPKDKDNE FKSLWIERTTLTLTHSLPGISRWFEV ERRELVEVSPLENAIQVVENKNQEL RALISQYQHKQVHGNINLLSMCLNG VIDAAVNGGIARYQEAFFDKDYITKH PGDAEKISQLKELMQEQVHVLGVGL AVHEKFVHPEMRPLHKKLIDQFQM MRASLYHEFPGLDKLSPACSGTSTP RGNVLASHSPMSPENIKMTHRHSP MNLMGTGRHSSSSLSSHASSEAGN MMMMGDNSMGEAPEDLYHHMQL AYHNPRYQGSVTNVSVLSSSQASPS SSSLSSTHSAPSQMITSAPSSTRGSP SLPDKYRHAREMMLLLPTHRDRPSS AMYPAAILENGQPPNFQRALFQQVV GACKPCSDPNLSMAEKGHYSLHFD AFHHPLGDTPPALPARTLRKSPLHPI PASPTSPQSGLDGSNSTLSGSASSGV SSLSESNFGHSSEAPPRTDTMDSMP SQAWNGDEGLEPPYLPVHYSLSESA VLDAIKSQPCRSHSAPGCVLPQDPM DPPALPPKPYHPRLPALEHDEGMLL	True	False	4.594	1.464	1.036	1.14	0.621	3.27	1.348

								REEAERPRGLHRKASLPPGSVKEEQ ARLAWEHGRGEQ											