	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	extracell region
0	Q76NI1	KNDC1_HUMAN	Homo sapiens	Kinase non-catalytic C-lobe domain-containing protein 1	27.461863	S982;T1145;S1389 (Q76NI1-4)	S964	30620550;38253038	MQAMDPAAADLYEEDGKDLDFYDF EPLPTLPEDEENVSLADILSLRDRGL SEQEAWAVCLECSLSMRSVAHAAIF QSLCITPDTLAFNTSGNVCFMEQLS DDPEGAFVPPEFDVTGNTFEAHIYSL GATLKAALEYVAEPTLEPRLSQDLEA LLSRMQAEDPGDRPDLESIIALCEEK LQLTSSCRVCRSLSAVGRRVLSIESF GALQDVSESSWRERPAPGNAGPRRP PGDPSTDPEVLPTPEGPESETSRGPR ASPTKALLSTPVRNGESHSREGLAG LVLDAERTLGELDRDALRRSRLRKV QTFPRLLSDSPEATLCLPLTRGKSQL PISELFSPDPRKAFLDRKNGLSSFQA QPKCRLWPEQEPEHQLGRVPCAGR STDRGPGVPGSPGQPETSHPSQGPA EAPADPRDASGEAQTPRDDERIPEG ARQLESAAAEQWVSLQDLLSQLGRP FREYELWALCLACLRALQTRPEHPA YLCLDSVLVAEDGAVLFQPPPANGS YDSFFLAPELAEERLVTEKASVYCVA AVLWTAAKFSVPRNHKLALPRRLKT LLLDMARRSAPERPSAAEAIKVCGSY LLQRGMDSRKILAHLRASICQVYQE EETISLQNAFSVVELKPSVAPAPEPS PGFLPVNSDTGLVAVPGPVPGQHPC GEEATQLPAAFTSEATHFKPIVLAQN ASVARDQPALAQEESEERGGQREGE GEEKLSLEAHAGSPSLKTPDGPVPG PGPQGAAPEPLGASVQRDSAQGRPC PPPQAPANQPEGASSAAPGSPVPAPP TKASALPVEQGPAEPIPPGVASGGLR PDALGPTTAHHGPRHPPKPPRSKAT ERPGQEPEGPGATPAGERDDQSPDS VPERPRPADRRLCLPCVDASPLPGRT ACPSLQEATRLIQEEFAFDGYLDNGL EALIMGEYIFALKDLTFATFCGAISEK FCDLYWDEKLLQNLFKVVNGQASPS PSTAEEAGSQLEGSQSPRSPSSKRPS LHRLGKEKPAMARTSSRAPCSPTSV SDVDSDALSRGNFEVGFRPQRSVKA ERAQQPEAGEDRRPAGGASDVEAVT RLARSKGVGPALSPGPAGFQSCSPG WCSAFYEADCFGADVHNYVKDLGR QQADGALPDAQSPELEQQLMMEKR NYRKTLKFYQKLLQKEKRNKGSDVK TMLSKLKGQLEEMKSRVQFLSLVKK YLQVMYAERWGLEPCTLPVIVNIAAA PCDTLDFSPLDESSSLIFYNVNKHPG GRQKARILQAGTPLGLMAYLYSSDA FLEGYVQQFLYTFRYFCTPHDFLHF LLDRINSTLTRAHQDPTSTFTKIYRR SLCVLQAWVEDCYAVDFPRNSGLLG KLEDFISSKILPLDGSAKHLLGLLEV GMDRRAEGNPRGTDLENPREAEED ARPFNALCKRLSEDGISRKSFPWRL PRGNGLVLPPHKERPYTIAAALPKPC FLEDFYGPCAKTSEKGPYFLTEYSTH QLFSQLTLLQQELFQKCHPVHFLNS RALGVMDKSTAIPKASSSESLSAKTC SLFLPNYVQDKYLLQLLRNADDVST WVAAEIVTSHTSKLQVNLLSKFLLIA KSCYEQRNFATAMQILSGLEHLAVR QSPAWRILPAKIAEVMEELKAVEVFL KSDSLCLMEGRRFRAQPTLPSAHLL AMHIQQLETGGFTMTNGAHRWSKL RNIAKVVSQVHAFQENPYTFSPDPK LQSYLKQRIARFSGADISTLAADSRA NFHQVSSEKHSRKIQDKLRRMKATF Q	None	None	None	None	None	None	None	None	None