

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracell region
Q8N4C6	NIN_HUMAN	Homo sapiens	Ninein	17.680565	T1398	S152;S269;S1550;S1837	30379171;36240223;37217939	MDEVEQDQHEARLKELFDSFDTTG TGSLGQEEITDLCHMLSLSEEVAPVL QQTLLQDNLLGRVHFDQFKEALILIL SRTLSEEHFQEPDCSLEAQPKYVR GGKRYGRRSLPEFQESVEEFPVTVI EPLDEEARPSHIPAGDCSEHWKTQR SEEEYAEQQLRFWNPDLLNASQSG SSPPQDWIEEKLQEVCEDLGITRDG HLNRKLVSIQEQYGLQNVGDGEMLE EVFHNLDPDGTMVSEDFYGLFKN GKSLTPSASTPYRQLKRHLSMQSFD ESGRRTTSSAMTSTIGFRVFSCLDD GMGHASVERILDWQEEGIENSQEI LKALDFSLDGNINLTELTLALENELL VTKNSIHQAAALASFKAIRHLLERVD QVVREKEKLRSDLDKAEKLSMAS EVDDHHAIERRNEYNLRLKDEEYK ERIAALKNELRKEREQILQQAGKQRL ELEQEIEKAKTEENYIRDRLALSKE NSRLENELLENAEKLAEYENLTNKL QRNLENVLAEKFGDLDPSAEFFLQ EERLTQMRNEYERQCRVLDQDQVE LQSELEEYRAQGRVLRPLKNPSE EVEANSGGIEPEHGLGSEECNPLNM SIEAELVIEQMKEQHHRDICCLRLEL EDKVRHYEKQLDET VVSCCKAQEN MKORHENETHHTLEKQISDLKNEIAE LQQAALVKEAHHEATCRHEEEK QLQVKLEEEKTHLQEKLRLOHEME LKARLTQAQASFEREREGLQSSAWT EEKVRGLTQELEQFHQEQLTSLVEK HTLEKEELRKELLEKHQRELQEGRE KMETECNRRTSQIEAQFQSDCKVT ERCESALQSLEGRYRQELKDLQEQQ REEKSQWEFEKDELTOECAEAQELL KETLKREKTTSLVLTQEREMLEKTY KEHLNSMVVERQQLQDLEDLRNV SETQQSLSDQILELKSCHKRELRE EEVLCQAGASEQLASQRLELEMEH DOERQEMMSKLLAMENIHKATCET ADREAEAMSTEISRLQSKIKEMQQA TSPLSMLQSGCQVIGEEVEGDGAL SLLQOGEQLLENGDVLLSLQRAHE QAVKENVKMATEISRLQRLQKLEP GLVMSSCLDEPATEFFGNATAEQTEQ FLQQNRKQVEGVTRRHVLSLDEDD EVRDLGSTGTSSVQRQEVKIESEAS VEGFSELENSEETRTESWELKNQIS QLQEQMLMLCADCDRASEKQDILL FDVSVLKKKLMLERIPEASPKYKLL YEDVSRENDCLQEELRMMETRYDE ALENNKELTAEVFRLQDELKMMEEV TETFLSLEKSYDEVKIENEGLNVVL RLQKIEKLQESVVQRCDCLWEAS LENLEIEPDGNILQLNQTLEECVPRV RSVHHVIEECKQENQYLEGNTQLLE KVKAHEIAWLHGTHQERPRVQN QVILEENTLLGFQDKHFQHQATIA ELELEKTKLQELTRKLVKERTVILVQ KDVLSHGEKEEELKAMMHDQITC SEMQQVELLRYESEKQEQENSILR NEITTLNEEDSISNLKGLTNGSQEE MWQKTETVKQENAAVQKRVENLK KQISELKIKNQDLENTLSQKNS QNQEKLQELNQRLTEMLCQKEKEP GNSALEEREQEFNLKEELERCKVQ SSTLVSSLEAELSEVKIQTHIVQOEN HLLKDELEKMKQLHRCPLSDFFQ KISSVLSYNEKLLKEKEALSEELNSC VDKLAKSSLEHRIATMKQEKSWE HQASLKSQLVASQEKVQNLEDTVQ NVNLQMSRMKSDLRVTQKEKALK QEVMSLHKQLQNAAGGKSWAPEIAT HPSGLHNQKRLSWDKLDHLMNE EQQLLWQENERLQTMVQNTKALTE HSREKVRQLESNLLPKHQKHLNPS GTMNPTEQEKLKSLKRECDQFQKEQ SPANRQVSMNSLEQELETIHLENE GLKKKQVKLDEQLMEMQHLRSTAT PSPSPHAWDLQLLQQACPMVPRE	None	None	None	None	None	None	None	None	

