	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	Q8NI35	INADL_HUMAN	Homo sapiens	InaD-like protein	18.379595	S522	S455;S459;S522;S645;T1209;S1212;T1508	30379171	MPENPATDKLQVLQVLDRLKMKLQ EKGDTSQNEKLSMFYETLKSPLFNQ ILTLQQSIKQLKGQLNHIPSDCSANF DFSRKGLLVFTDGSITNGNVHRPSN NSTVSGLFPWTPKLGNEDFNSVIQQ MAQGRQIEYIDIERPSTGGLGFSVVA LRSQNLGKVDIFVKDVQPGSVADRD QRLKENDQILAINHTPLDQNISHQQ AIALLQQTTGSLRLIVAREPVHTKSST SSSLNDTTLPETVCWGHVEEVELIN DGSGLGFGIVGGKTSGVVVRTIVPGG LADRDGRLQTGDHILKIGGTNVQGM TSEQVAQVLRNCGNSVRMLVARDP AGDISVTPPAPAALPVALPTVASKGP GSDSSLFETYNVELVRKDGQSLGIRI VGYVGTSHTGEASGIYVKSIIPGSAAY HNGHIQVNDKIVAVDGVNIQGFANH DVVEVLRNAGQVVHLTLVRRKTSSS TSPLEPPSDRGTVVEPLKPPALFLTG AVETETNVDGEDEEIKERIDTLKND NIQALEKLEKVPDSPENELKSRWEN LLGPDYEVMVATLDTQIADDAELQK YSKLLPIHTLRLGVEVDSFDGHHYIS SIVSGGPVDTLGLLQPEDELLEVNG MQLYGKSRREAVSFLKEVPPPFTLV CCRRLFDDEASVDEPRRTETSLPET EVDHNMDVNTEEDDDGELALWSPE VKIVELVKDCKGLGFSILDYQDPLDP TRSVIVIRSLVADGVAERSGGLLPGD RLVSVNEYCLDNTSLAEAVEILKAVP PGLVHLGICKPLVEDNEEESCYILHS SSNEDKTEFSGTIHDINSSLILEAPK GFRDEPYFKEELVDEPFLDLGKSFH SQQKEIEQSKEAWEMHEFLTPRLQE MDEEREILVDEEYELYQDPSPSMEL YPLSHIQEATPVPSVNELHFGTQWL HDNEPSESQEARTGRTVYSQEAQPY GYCPENVMKENFVMESLPSVPSTEG NSQQGRFDDLENLNSLAKTSLDLG MIPNDVQGPSLLIDLPVVAQRREQE DLPLYQHQATRVISKASAYTGMLSSR YATDTCELPEREEGEGEETPNFSHW GPPRIVEIFREPNVSLGISIVGGQTVI KRLKNGEELKGIFIKQVLEDSPAGKT NALKTGDKILEVSGVDLQNASHSEA VEAIKNAGNPVVFIVQSLSSTPRVIP NVHNKANKITGNQNQDTQEKKEKR QGTAPPPMKLPPPYKALTDDSDENE EEDAFTDQKIRQRYADLPGELHIIEL EKDKNGLGLSLAGNKDRSRMSIFVV GINPEGPAAADGRMRIGDELLEINN QILYGRSHQNASAIIKTAPSKVKLVFI RNEDAVNQMAVTPFPVPSSSPSSIE DQSGTEPISSEEDGSVEVGIKQLPES ESFKLAVSQMKQQKYPTKVSFSSQE IPLAPASSYHSTDADFTGYGGFQAPL SVDPATCPIVPGQEMIIEISKGRSGLG LSIVGGKDTPLNAIVIHEVYEEGAAA RDGRLWAGDQILEVNGVDLRNSSH EEAITALRQTPQKVRLVVYRDEAHYR DEENLEIFPVDLQKKAGRGLGLSIVG KRNGSGVFISDIVKGGAADLDGRLIQ GDQILSVNGEDMRNASQETVATILK CAQGLVQLEIGRLRAGSWTSARTTS QNSQGSQQSAHSSCHPSFAPVITGL QNLVGTKRVSDPSQKNSGTDMEPR TVEINRELSDALGISIAGGRGSPLGDI PVFIAMIQASGVAARTQKLKVGDRIV SINGQPLDGLSHADVVNLLKNAYGR IILQVVADTNISAIAAQLENMSTGYH LGSPTAEHHPEDTEEQLQMTAD	None	None	None	None	None	None	None	None	None