	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	extracel region
0	Q5TCS8	KAD9_HUMAN	Homo sapiens	Adenylate kinase 9	20.509114	T541;T1711	NaN	37217939;39894887;30379171	MTSQEKTEEYPFADIFDEDETERNF LLSKPVCFVVFGKPGVGKTTLARYIT QAWKCIRVEALPILEEQIAAETESGV MLQSMLISGQSIPDELVIKLMLEKL NSPEVCHFGYIITEIPSLSQDAMTTL QQIELIKNLNLKPDVIINIKCPDYDLC QRISGQRQHNNTGYIYSRDQWDPEV IENHRKKKKEAQKDGKGEEEEEEEE QEEEEAFIAEMQMVAEILHHLVQRP EDYLENVENIVKLYKETILQTLEEVM AEHNPQYLIELNGNKPAEELFMIVM DRLKYLNLKRAAILTKLQGAEEEIND TMENDELFRTLASYKLIAPRYRWQR SKWGRTCPVNLKDGNIYSGLPDYSV SFLGKIYCLSSEEALKPFLLNPRPYLL PPMPGPPCKVFILGPQYSGKTTLCN MLAENYKGKVVDYAQLVQPRFDKA RETLVENTIAEATAAAIKVVKEKLLR ELQARKQAETALREFQRQYEKMEFG VFPMEATHSSIDEEGYIQGSQRDRG SSLVDTEEAKTKSENVLHDQAAKVD KDDGKETGETFTFKRHSQDASQDVK LYSDTAPTEDLIEEVTADHPEVVTMI EETIKMSQDINFEQPYEKHAEILQEV LGEVMEENKDRFPGAPKYGGWIVD NCPIVKELWMALIKKGIIPDLVIYLSD TENNGKCLFNRIYLQKKSEIDSKILE RLLEELQKKKKEEEEARKATEEELR LEEENRRLLELMKVKAKEAEETDNE DEEEIEGDELEVHEEPEASHDTRGS WLPEEFEASEVPETEPEAVSEPIEET TVETEIPKGSKEGLEIEKLSETVVLPE FPEDSYPDVPEMEPFKEKIGSFIILW KQLEATISEAYIKILNLEIADRTPQEL LQKVVETMEKPFQYTAWELTGEDYE EETEDYQTEAEVDEELEEEEEEEGE DKMKERKRHLGDTKHFCPVVLKEN FILQPGNTEEAAKYREKIYYFSSAEA KEKFLEHPEDYVAHEEPLKAPPLRIC LVGPQGSGKTMCGRQLAEKLNIFHI QFEEVLQEKLLLKTEKKVGPEFEED SENEQAAKQELEELAIQANVKVEEE NTKKQLPEVQLTEEEEVIKSSLMEN EPLPPEILEVILSEWWLKEPIRSTGFI LDGFPRYPEEAQFLGDRGFFPDAAV FIQVDDQDIFDRLLPAQIEKWKLKQK KKLERKKLIKDMKAKIRVDTIAKRRA ELILERDKKRRENVVRDDEEISEEEL EEDNDDIENILEDEFPKDEEEMSGE EDEEQETDAIERLRGELGEKFEADT HNLQIIQDELERYLIPIISINGARRNH IVQYTLNMKLKPLVENRASIFEKCHP IPAPLAQKMLTFTYKYISSFGYWDPV KLSEGETIKPVENAENPIYPVIHRQYI YFLSSKETKEKFMKNPIKYIRQPKPK PTVPIRIIIVGPPKSGKTTVAKKITSEY GLKHLSIGGALRYVLNNHPETELAL MLNWHLHKGMTAPDELAIQALELS LMESVCNTAGVVIDGYPVTKHQMN LLEARSIIPMVIFELSVPSKEIFKRLLL EKENEQRLPYPLHNSAQIVAVNNVK YRKNIGEIRQYYQEQHQNWYVIDGF HSKWWVWNEVIKNVQMVNKYMQT YLERIKAGKAACIDKLCITPQELLSRL GEFEQFCPVSLAESQELFDCSATDS LEFAAEFRGHYYKMSSQEKLNKFLE NPELYVPPLAPHPLPSADMIPKRLTL SELKSRFPKCAELQGYCPVTYKDGN QRYEALVPGSINYALEYHNRIYICEN KEKLQKFLRSPLKYWEQKLPHKLPP LREPILLTSLPLPGYLEQGIATSLIKA MNAAGCLKPKFPFLSIRRSALLYIAL HLKAFNPKGSEYTRKKYKKKMEQF MESCELITYLGAKMTRKYKEPQFRAI DFDHKLKTFLSLRNIDPING	True	False	4.531	5.0	0.797	False	False	0.797	False