

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q5SWU9	ACACA_MOUSE	Mus musculus	Acetyl-CoA carboxylase 1	22.479274	S966;S2091;S2285	S5;S23;S25;S29;S34;S47;S49;S52;T57;S77;S79;S79;T609;S834;S1200;S1215;S1217;T1226;S1258;S1262;S1272;T2152	22645316;31010828	MDEPSPLAKTLELNQHSRFIGSVSE DNSEDEISNLVKLDLEEKEGSLSPAS VSSDTLSDLGISGLQDGLAFHMRSS MSGHLHLVKQGRDRKKIDSQRDFTVA SPAEFVTRFGGNKVIEKVLIANNGIA AVKCMRSIRRWSYEMFRNERAIRFV VMVTPEDLKANAHEYIKMADHYVPVP GGPNNNNYANVELILDIAKRIPVQAV WAGWGHASENPKLPELLLKNGIAF MGPPSQAMWALGDKIASSIVAQTAG IPTLPWSGSGLRVDWQENDFSKRIL NVPQDLYEKGYVKDVEDDGLKAAEEV GYPVMIKASEGGGGKIRKVNADD FPNLFROVQAEVPGSPIFVMRLAKQ SRHLEVQILADQYGNAILFGRDCSV QRRHQKIIIEEAPAAIATPAVFEHMEQ CAVKLAKMVGYSAGTVEYLYSQDG SFYFLELNPRLQVEHPCTEMVADV LPAAQLQIAMGIPLFRIKDIRMMYGV SPWGDAPIDFENSAHVPCPRGHVIA ARITSENPDGFKPSSGTVQELNFRS NKNVWGYFSVAAAGLHEFADSQF GHCFSWGENREEAISNMVVALKEL SIRGDFRRTTVEYLIKLETESFQLNRI DTGWLDRLIAEKVQAERPDTMLGVV CGALHVADVSLRNSISNFLHSLERG QVLPAAHTLLNTVDVELIYEGIKYVLK VTRQSPNSYVIMNGSCVEVDVHRL SDGGLLLSYDGSSYTYMKEEVDRY RITIGNKTCVFEKENDPVMRSPSA GKLIQYIVEDGGHVFAGQCYAEIEVM KMVMTLTAVESGCIHYVKRPGAALD PGCVIAKMQLDNPSKVQQAELHTGS LPQIQSTALRGEKLRVVFHYVLDNL VNVVMNGYCLPDFFFSSRVKDWVER LMKTLRDPSPLELQDIMTSVSGRI PLNVEKSIKEMAQYASNITSVLCQF PSQQIANILDSHAATLNRKSEREVFF MNTQSIVQLVQRYRSGIRGHMKAVV MDLLRQYLRVETQFQNGHYDKCVF ALREENKSDMNTVNLNYIFSHAQVTK KNLLVTMLIDQLCGRDPTLTDELLNI LTELTLQSKTTNAKVALRARQVLIA HLPSYELRHNQVESIFLSAIDMYGH QFCIENLQKLILSETSIFDVLNFFYH SNQVVRMAALEVYVRRAYIAYELNS VQHRQLKDNTCVVEFQFMLPTSHP NRGNIPTLNRMSFASNLNHYGMTH VASVSDVLLDNAFTPPCQRMGGMV SFRTFEDFVRIFDEIMGCFCDSPQS PTFPESGHTSLYDEDKVPRDEPIHIL NVAIKTDGDIEDDRLAAMFREFTQQ NKATLVEHGIRRLTFLVAQKDFRKQ

VNCEVDQRFHREFPKFFTFRARDKF
EEDRIYRHLEPALAFQLELNRMRNF
DLTAIPCANHKMHLYLGAAKVEVGT
EVTDYRFFVRAIRHSDLVTKEASFE
YLQNEGERLLLEAMDELEVAFNNT
NVRTDCNHIFLNFVPTVIMDPSKIEE
SVRSMVMRYGSRLWKLRLVLAELKI
NIRLTTTGKAIPIRLFLTNESGYYLDI
SLYKEVTDSTRQAQIMFQAYGDKQGP
LHGMLINTPYVTKDLLQSKRFQAQS
LGTYYIDIPEMFRQSLIKLWESMST
QAFLPSPPLPSDILTYTELVLDDQGG
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DLLFLRASELARAEGIPRIYVAANS
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RSGSMIAGESSLAYDEVITISLVTCR
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PANLDSEAKIIQQAGQVWFPDSAFK
TYQAIKDFNREGLPLMVANWRGFS
GGMKDMYDQVLKFGAYIVDGLREC
SQPVMVYIPPQAE LRGGSWVVIDPTI
NPRHMEMYADRESRGSVLEPEGTV
EIKFRKKDLVKTMRVDPVYIRLAER
LGTPELSPTERKELESKLEREEFLI
PIYHQVAVQFADLHDT PGRMQEKG
INDILDWKT SRFFYWRLLRLLLEDL
VKKKIHNANPELTDGQIQAMLRRWF
VEVEGTVKAYVWDNNKDLVEWLEK
QLTEEDGVRVIEENIKYISRDYVLK
QIRSLVQANPEVAMDSIVHMTQHIS
PTQRAEVVRLSTMDSPST