

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q13085	ACACA_HUMAN	Homo sapiens	Acetyl-CoA carboxylase 1	21.19731	NaN	S5;S23;S25;S29;S34;S48;S50;S53;T58;S78;S80;S488;T610;S835;S1201;S1216;S1218;T1227;S1259;S1263;S1273;T2153	3626323;33214551;32119511;34019948;28510447	MDEPSPLAQPLELNQHSRFIIGSVSE DNSEDEISNLVKLDLLEEKEGSLSPA SVGSDTLDLGISSLQDGLALHIRSS MSGHLHLVKQGRDRKKIDSQRDFTVA SPAEFVTRFGGNKVIEKVLIANNGIA AVKCMRSIRRWSYEMFRNERAIRFV VMVTPEDLKANA EYIKMADHYVPVP GGPNNNNYANVELILDI AKRIPVQAV WAGWGHASENPKLPELLLKNGIAF MGPPSQAMWALGDKIASSIVAQTAG IPTLPWSGSGLRVDWQENDFSKRIL NVPQELYEKGYVKD VDDGLQAAEEV GYPVMIKASEGGGGK GIRKVN NADD FPNLF RQVQAEVPGSPIFVMRLAKQ SRHLEVQILADQYGN AISLFG RDCSV QRRHQKIIEEAPATIATPAVFEHMEQ CAVKLAKMVGYSAGTVEYLYSQDG SFYFLELNPRLQVEHPCTEMVADVN LPAAQLQIAMGIPLYRIKDIRMMYGV SPWGDSPIDFEDSAHVPCPRGHVIA ARITSENPDEGFKPSSGTVQELNFRS NKNVWGYFSVAAAGGLHEFADSQF GHCFSWGENREEAISNMVVALKEL SIRGDFRTTVEYLK LLETESFQMNR IDTGWLDRLIAEKVQAERPDTMLGV VCGALHVADVSLRNSVSNFLHSLER GOVLP AHTLLNTVDVELIYEGVKYVL KVTRQSPNSYVIMNGSCVEVDVHR LSDGGLLSYDGSSYTTYMKEEVDR YRITIGNKTCVFEKENDP SVMRSPSA GKLIQYIVEDGGHVFAGQCYAEIEVM KMVMTLTAVESGCIHYVKRPGAALD PGCVLAKMQLDNPSKVQQAELHTG SLPRIQSTALRGEKLHRVFHYVLDNL VNVMN GYCLPDPFFSSKVKDWVER LMKTLRDP SLPLLELQDIMTSVSGRI PPNVEKSIKKEMAQYASNITSVLCQF PSQQIANILDSHAATLNRKSEREVFF MNTQSIVQLVQRYRSGIRGHMKAVV MDLLRQYLRVETQFQNGHYDKCVF ALREENKSDMNTVLNYIFSHAQVTK KNLLVTMLIDQLCGRDPTLTDELLNI LTELTQLSKTTNAKVALRARQVLIAS HLPSYELRHNQVESIFLSAIDMYGH QFCIENLQKLILSETSIFDVLPNFFYH SNQVVRMAALEVYVRRAYIAYELNS VQHRQLKDNTCVVEFQFMLPTSHP NRGNIPTLNRMSFSSNLNHYGMTH VASVSDVLLDNSFTPPCQRMGGMV SFRTFEDFVRIFDEVMGCFSDSPPQ SPTFPEAGHTSLYDEDK VPRDEPIHI LNVAIKTDCDIEDDRLAAMFREFTQ QNKATLVDHGIRRLTFLVAQKDFRK QVNYEVDRRFHREFPKFFTFRARDK FEEDRIYRHLEPALAFQLELNRMRN

FDLTAIPCANHMKHLYLGAACKVEVG  
TEVTDYRFFVRAIIRHSDLVTKEASF  
EYLQNEGERLLEAMDELEVAFNNT  
NVRTDCNHIFLNFVPTVIMDPSKIEE  
SVRSMVMRYGSRLWKLRLVQAEKI  
NIRLTPTGKAIPIRLFLTNEGGYLDI  
SLYKEVTDSTRQAQIMFQAYGDKQGP  
LHGMLINTPYVTKDLLQSKRFQAQS  
LGTYYIDIPEMFRQSLIKLWESMST  
QAFLPSPPLPSDMLTYTELVLDDQG  
QLVHMNRLPGGNEIGMVAWKMTF  
KSPEYPEGRDIIVIGNDITYRIGSFGP  
QEDLLFLRASELARAEGIPRIYVSAN  
SGARIGLAEIRHMFHVAWVDPEDP  
YKGYRYLYLTPQDYKRVSALNSVHC  
EHVEDEGESRYKITDIIGKEEGIGPE  
NLRGSGMIAGESSLAYNEIITISLVTC  
RAIGIGAYLVRLGQRTIQVENSHLILT  
GAGALNKVLGREVYTSNNQLGGIQI  
MHNNGVTHCTVCDDFEGVFTVLH  
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EFVPTKTPYDPRWMLAGRPHPTQKG  
QWLSGFFDYGSFSEIMQPWAQTVVV  
GRARLGGIPVGVVAVETRVELSIPA  
DPANLDSEAKIIQQAGQVWFPSAF  
KTYQAIKDFNREGLPLMVFANWRGF  
SGGMKDMYDQVLKFGAYIVDGLRE  
CCQPVLVYIPPAELRGGSWVIDSS  
INPRHMEMYADRESRGSVLEPEGTV  
EIKFRRKDLVKTMRVDPVYIHLAER  
LGTPELSTAERKELENKLKEREFLI  
PIYHQVAVQFADLHDTFGRMQEKGV  
ISDILDWKTSRTFFYWRLRRLLEDL  
VKKKIHNANPELTDGQIQAMLRRWF  
VEVEGTVKAYVVDNNDLAEWLEK  
QLTEEDGVHVSIEENIKCISRDYVLK  
QIRSLVQANPEVAMDSIIHMTQHISP  
TQRAEVIRILSTMDSPST