

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q13085	ACACA_HUMAN	Homo sapiens	Acetyl-CoA carboxylase 1	8.309827	NaN	S5;S23;S25;S29;S34;S48;S50;S53;T58;S78;S80;S488;T610;S835;S1201;S1216;S1218;T1227;S1259;S1263;S1273;T2153	34019948;33214551;35008409;28510447;34725712;32119511;35138101;35083852	MDEPSPLAQPLELNQHSRFIIGSVSE DNSEDEISNLVKLDLLEEKEGSLSPA SVGSDTLDLGISSLQDGLALHIRSS MSGHLHLVKQGRDRKKIDSQRDFTVA SPAEFVTRFGGNKVIEKVLIANNGIA AVKCMRSIRRWSYEMFRNERAIRFV VMVTPEDLKANA EYIKMADHYVPVP GGPNNNNYANVELILDI AKRIPVQAV WAGWGHASENPKLPELLLKNGIAF MGPPSQAMWALGDKIASSIVAQTAG IPTLPWSGSGLRVDWQENDFSKRIL NVPQELYEKGYVKD VDDGLQAAEEV GYPVMIKASEGGGK GIRKVN NADD FPNLF RQVQAEVPGSPIFVMRLAKQ SRHLEVQILADQYGN AISLFG RDCSV QRRHQKIIEEAPATIATPAVFEHMEQ CAVKLAKMVGYSAGTVEYLYSQDG SFYFLELNPRLQVEHPCTEMVADVN LPAAQLQIAMGIPLYRIKDIRMMYGV SPWGDSPIDFEDSAHVPCPRGHVIA ARITSENPDEGFKPSSGTVQELNFRS NKNVWGYFSVAAAGGLHEFADSQF GHCFSWGENREEAISNMVVALKEL SIRGDFRTTVEYLK LLETESFQMNR IDTGWLDRLIAEKVQAERPDTMLGV VCGALHVADVSLRNSVSNFLHSLER GOVLP AHTLLNTVDVELIYEGVKYVL KVTRQSPNSYVIMNGSCVEVDVHR LSDGGLLSYDGSSYTTYMKEEVDR YRITIGNKTCVFEKENDPSVMRSPSA GKLIQYIVEDGGHV FAGQCYAEIEVM KMVMTLTAVESGCIHYVKRPGAALD PGCVLAKMQLDNPSKVQQAELHTG SLPRIQSTALRGEKLHRV FHYVLDNL VNV MNGYCLPDPFFSSKVKDWVER LMKTLRDP SLPLLELQDIMTSVSGRI PPNVEKSIKEMAQYASNITSVLCQF 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
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LHGMLINTPYVTKDLLQSKRFQAQS
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QAFLPSPPLPSDMLTYTELVLDDQG
QLVHMNRLPGGNEIGMVAWKMTF
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QEDLLFLRASELARAEGIPRIYVSAN
SGARIGLAEIRHMFHVAWVDPEDP
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NLRGSGMIAGESSLAYNEIITISLVTC
RAIGIGAYLVRLGQRTIQVENSHLILT
GAGALNKVLGREVYTSNNQLGGIQI
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WLSYMPKSVHSSVPLLNSKDPIDRII
EFVPTKTPYDPRWMLAGRPHPTQKG
QWLSGFFDYGSFSEIMQPWAQTVVV
GRARLGGIPVGVVAVETRVELSIPA
DPANLDSEAKIIQQAGQVWFPSAF
KTYQAIKDFNREGLPLMVFANWRGF
SGGMKDMYDQVLKFGAYIVDGLRE
CCQPVLVYIPPQAE LRGGSWVIDSS
INPRHMEMYADRESRGSVLEPEGTV
EIKFRRKDLVKTMRVDPVYIHLAER
LGTPELSTAERKELENKLKEREFLI
PIYHQVAVQFADLHDTFGRMQEKGV
ISDILDWKTSRTFFYWRLRRLLEDL
VKKKIHNANPELTDGQIQAMLRRWF
VEVEGTVKAYVVDNNDLAEWLEK
QLTEEDGVHVSIEENIKCISRDYVLK
QIRSLVQANPEVAMDSIIHMTQHISP
TQRAEVIRILSTMDSPST