

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
E9Q4Z2	ACACB_MOUSE	Mus musculus	Acetyl-CoA carboxylase 2	24.036206	T2027	S35;S47;S81;S85;S159;S165;S170;S182;S185;S190;T197;S210;S212;S459;T743;S1330;S1332;S1350;S1395	37507081;34418053	MVLLFLFTCLVFSCLTFSWLKIWGK MTDSKPLTNSKVEANLLSSEELSA SELSGEQLQEHGDHSCLSYRGRPDA SQQRNSLPSSCQRPPRNPSSNDTW PSPLEQTNWTAAAPGPEVPDANGLSF PARPPSQRTVSPSREDRKQAHIKRQ LMTSFLGSLDDNSSDEDPSAGSFQ NSSRKSRSRSLGTLSQEAAINTSDP ESHAPTMRPSMSGLHLVKRGREHK KLDLHRDFTVASPAEFVTRFGGNRV IEKVLIANNGIAAVKCMRSIRRWAYE MFRNERAIRFVVMVTPEDLKANAIEY IKMADQYVVPVGGPNNNNYANVELI IDIAKRIPVQAVWAGWGHASENPKL PELLCKHEIAFLGPPSEAMWALGDK IASTIVAQTLQIPTLPWSGSGLTVEW TEDSRHQGKCISVPEVDVYEQGCVKD VDEGLQAAEKIGFPLMIKASEGGGG KGIRKAESAEDFPMLFRQVQSEIPGS PIFLMKLAQNARHLEVOVLADQYGN AVSLFGRDCSIQRRHQKIIIEAPATIA APAVFEFMEQCAVLLAKMVGYSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAALQIAMGVPLH RLKDIRLLYGESPWGVTPIPFETPLSP PIARGHVIAARITSENPDGFKPSSG TVQELNFRSNKNVWGYFSVAAAGG LHEFADSQFGHCFSWGRENREEAIS NMVVALKELSIRGDFRTTVEYLVNL LETESFQNNIDITGWLHDLIAQRVQ AEKPDIMLGVCVGCALNVADAMFRTC MTEFLHSLERGVLPADSLNIVDV ELIYGGIKYALKVARQSLTMFVLMN GCHIEIDAHRLNDGGLLSYNGSSYT TYMKEEVDSYRITIGNKTCVFEKEN DPTVLRSPSAGKLMQYTVEDGDHVE AGSSYAEMVMKMIMTLNVQESGR VKYIKRPGVILEAGCVVARLELDDPS KVHAAQPFTGELPAQQTLPIGKELH QVFHGVLENLNTVMMSGYCLPEPFFS MKLKDWWQKLMMLTRHPSLPLEL QEIMTSVAGRIPAPVEKAVRRVMAQ YASNITSVLCQFPSPQIATILDCHAAT LQRKADREVFMMNTQSIVQLVQRYS SGTRGYMKAVVLDLLRKYLNVEHHF QQAHYDKCVINLREQFKPDMTQVL DCIFSHSQVAKKNQLVTMLIDELCG PDFTLSDELTSILCELTLRSRSEHCK VALRARQVLIASHLPSYELRHNQVES IFLSAIDMYGHQFCPENLKKLILSET TIFDVLPTFFYHENKVVCMASLEVVV RRGYIAYELNSLQHRELPGDTCVVE FQFMLPSSHPNRMAVPISVSNPDL RHSTELFMDSGFSPLCQRMGAMVA FRRFEEFTRNFDEVISCFANVQDIT LLFSKACTSLYSEEDSKSLREPIHIL NVAIQCADHMEDEALVPVFRAFVQS KKHILDYGLRRITFLVAQEREFPKF FTFRARDEFAEDRIYRHLEPALAFQL ELSRMRNFDLTAVPCANHKMHLYL GAAVKKEGLEVTDRHFFIRAIRHSD LITKEASFEYLQNEGERLLLEAMDEL EVAFNNTSVRTDCNHIFLNFVPTVI MDPLKIEESVRDMVMRYGSRLWKL RVLQAEVKINIRQTTSDSAIPRLFIT NESGYLDISLYREVTDSRSGNIMFH SFGNKQGSLSHGMLINTPYVTKDLLQ AKRFQAQSLGTTYVYDFPEMFRQAL FKLWGSPEKYPKDILTYTELVLDSQ QLVEMNRLPGCNEVGMVAFKMRFK TPEYPEGRAVVIGNDITFQISFGIG EDFLYLRASEMARTEGIPQIYLAANS GARMGLAEIKQIFQVAVVDPEDPH KGFRLYLTPQDYTQISSQNSVHCK HIEDEGESRYVIVDVGKNDANLGVEN LRGSGMIAGEASLAYEKTVTISMVTC RALGIGAYLVRGQRVIQVENSIIILT GAGALNKVLGREVYTSNNQLGGVQI MHTNGVSHVTVPDDFEGVCTILEW LSFIPKDNRSVPITTPSDPIDREIEF	None	None	None	None	None	None	None	

TPTKAPYDPRWMLAGRPHPTLKGT
WQSGFFDHGSFKEIMAPWAQTVVT
GRARLGGIPVGVIAVETRTVEVAVPA
DPANLDSEAKIIQQAGQVWFPSAY
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SGGMKDMYEQMLKFGAYIVDGLRL
YEQPILYIPCAELRGGSWVLDSTI
NPLCIEMYADKESRGGVLEPEGTVEI
KFRKKDLVKTIRRIDPVCKKLVGQLG
KAQLPDKDRKELEGQLKAREELLPI
YHQVAVQFADLHDTPGHMLEKGIIS
DVLEWKTARTFFYWRLRRLLEAQV
KQEILRASPELNHEHTQSMRRWFV
ETEGAVKAYLWDSNQVVVQWLEQH
WSAKDGLRSTIRENINYLKRDVSLKT
IQSLVQEHPEVIMDCVAYLSQHLTPA
ERIQVAQLLSTTESPASS