

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
000763	ACACB_HUMAN	Homo sapiens	Acetyl-CoA carboxylase 2	22.903221	S1752	S35;T70;S91;S95;S169;S175;S192;S195;S200;T207;S220;S222;S469;T753;S1340;T1342;S1360;S1405	38253038	MVLLLLCLSLIFSCLTFSWLKIWKG MTDSKPIKSKSEANLPSQEPFPAS DNSGETPQRNGEGHTLPKTPSQAEP ASHKGPKDAGRNRNSLPPSHQKPPR NPLSSDAAPSPELQANGTGTQGLE ATDTNGLSSARPQGGQAGSPSKED KKQANIKRQLMTNFILGSFDDYSSD EDSVAGSSRESTRKGSRASLGALSLE AYLTTGEAETRVPTMRPMSGLHLV KRGREHKKLDLHRDFTVASPAEFVT RFGGDRVIEKVLIANNGIAAVKCMR SIRRWAYEMFRNERAIRFVVMVTPE DLKANAHEYKMDHYVPVPGGPNN NNYANVELIVDIKRIPVQAVWAGW GHASENPKLPELLCKNGVAFLGPPS EAMWALGDKIASTVVAQTLQVPTLP WSGSGLTVEWTEDDLQQKGRISVPE DVYDKGCVKDVDEGLEAAERIGFPL MIKASEGGGKGIKKAESAEDFPILF RQVQSEIPGSPFLMKLAQHARHLE VQILADQYGNVSLFGRDCSIQRHH QKIVEEAPATIAPLAIFEFMEQCAIRL AKTVGYVSAGTVEYLYSQDGSFHF ELNPRLQVEHPCTEMIADVNLPAAQ LQIAMGVPLHRLKDIRLLYGESPWG VTPISFETPSNPPLARGHVIAARITSE NPDEGFKPSSGTVOELNFRSSKNV WGYFVAATGGLHEFADSQFGHCF SWGENSEEAINMVAALKELSRGD FRITVEYLINLLETESFQNNNDITGW LDYLAIEKVQAEKPDIMLVGVCALN VADAMFRCTMTDFLHSLERGVLP ADSLNLVDVELYGGVKYILKVARQ SLTMFVLMNGCHIEIDAHRLNDGG LLSYNGNSYTTYMKEEVDYRITIG NKTCTFEKENDPTVLRSPSAGKLTQ YTVEDGGHVEAGSSYAEMEVMKMI MTLNVQERGRVYIKRPGAVLEAGC VVARLEDDPSKVHPAEPFTGELPA QQTLPILGKELHQVFHSLVLENLTNV MSGFCLPEPVFSIKLKEVWQKLM TLRHPSLPLELQEIIMTSVAGRIPAP VEKSVRRVMAQYASNITSVLCQFPS QIATILDCHAATLQRKADREVFFIN TQSIQVLVQRYRSGIRGYMKTVVLDL LRRYLREHHFQQAHYDKCVINLRE QFKPDMSQVLDICIFSHAQVAKKNQL VIMLIDELCGPDPSSLDELISILNELT QLSKSEHCKVALRARQILIASHLPSY ELRHNQVESIFLSAIDMYGHQFCPE NLKLLILSETTIFDVLPTFFYHANKV VCMASLEVYVRRGYIAYELNSLQHR QLPDGTCVVEFQFMLPSSHPNRMT VPISITNPDLRHSSTELFMDSGFSPL CORMGAMVAFRRFEDFTRNFDEVI SCFANVPKDTPLFSEARTSLYSEDDC KSLREPIHILNVSICADHLEDEAL VPILRTFVQSKKNILVDYGLRRITFLI AQEKEFPKFFTFRARDEFAEDRIYRH LEPALAFQLELNRMRNFDLTAVPCA NHKMHLYLGAAKVKEGVEVTDHRF FIRAIIRHSDLITKEASFEYLQNEGER LLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRLVQAEVKINIRQTTGS AVPIRLFITNESGYLDISLYKEVTD RSGNIMFHSFGNKGQPGHGMINT PYVTKDLLQAKRFQAQTLGTYIYDF PEMFRQALFKLWGSPPDKYPKDILTY TELVLDSQGLVEMNRLPGGNEVG MVAFKMRFTQEQYEPGRDVIVIGND ITFRIGSFGPEDLLYLRASEMARAE GIPKIYVAANSGARIGMAEIKHMFH VAWVDPEDPHKGFKYLYLTPQDYTR ISSLSVHCKHIEEGGESRYMITDIG KDDGLGVENLRGSGMIAGESSLAYE EIVTISLVTICRAIGAYLVRGQRVI QVENSHILTASALNKVLRGVEVYTS NNQLGGVQIMHYNGVSHITVPDDF EGVYTTLEWLSYMPKDNHSPVPIITP	True	False	4.653	5.0	5.0	2.421	1.205	3.286	2.182

TDPIDREIEFLPSRAPYDPRWMLAGR
PHPTLKGTWQSGFFDHGSFKEIMAP
WAQTVVTGRARLGGIPVGVIAVETRT
VEVAVPADPANLDSEAKIIQAGQV
WFPDSAYKTAQAVKDFNREKLPLMI
FANWRGFSGGMKDMYDQVLKFGAY
IVDGLRQYKQPILYIPPYAELRGGSW
VVIDATINPLCIEMYADKESRGGVLE
PEGTVEIKFRKKDLIKSMRRIDPAYK
KLMEQLGEPDLSKDRKDLEGRKA
REDLLPIYHQVAVQFADFHDTPGR
MLEKGVISDILEWKTARTFLYWRLR
RLLEDQVKQEILQASGELSHVHIQS
MLRRWFVETEGAVKAYLWDNNQVV
VQWLEQHWQAGDGPRSTIRENITYL
KHDSVLKTIRGLVEENPEVAVDCVIY
LSQHISPAERAQVVHLLSTMDSPAS
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