

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
P32874	HFA1_YEAST	Saccharomyces cerevisiae	Acetyl-CoA carboxylase, mitochondrial	9.365641	NaN	NaN	33229814	KGKTITHGQSWGARRIHSFYITIFTI TCIRIGQYKLALYLDPYRFYNITGSQI VRLKGORPEYRKRIFAHSYRHSSRIG LNFPSRRRYSNYVDRGNIHKHTRLR PQFIGLNTVESQAQPSILRDFVDLRGG HTVISKILIANNGIAAVKEMRSIRKW AYETFNDEKIIQFVVMATPDDLHAN SEYIRMADQYVQVPGGTNNNNYANI DLILDVAEQTDVDAVWAGWGHASE NPCLPELLASSQRKILFIGPPGRAMR SLGDKISSTIVAQSAKIPCIPWSGSHI DTIHIDNKTNFVSVDDVYVRGCCSS PEDALEKAKLIGFPMIKASEGGGGK GIRRVNEDDFIALYRQAVNETPGSP MFVMKVVTDARHLEVQLLADQYGT NITLFRDCSIQRRHQKIIEEAPVTIT KPETFQRMERAAIRLGELVGYVSAG TVEYLYSPKDDKFYFLELNPRLQVE HPTTEMISGVNLPATQLQIAMGIPM HMISDIRKLYGLDPTGTSYIDFKNLK RSPKGGHCISCRITSEDPNEGFKPST GKIHELNFRSSSNVWGYFSVGNNG AIHSFSDSQFGHIFAVGNDRQDAKQ NMVLALKDFSIRGEFKTPIEYLIELLE TRDFESNNISTGWLDDLILKNLSSD SKLDPTLAIICGAAMKAYVFTEKVRN KYLELLRRGQVPPKDFLKT KFPVDFI FDNNRYLFNVAQSSEEQFILSINKS QCEVNVQKLSSDCLLISVDGKCHTV YWKDDIRGTRLSIDSNTIFLEAELNP TQVISPTPGKLVKYLVRSGDHVFAGQ QYAEIEIMKMQMPLVAKSDGVIELL RQPGSII EAGDVI AKLTL DSPSKANE SSLYRGELPVLGPPLIEGSRPNHKL VLINRLENILNGYHENS GIETTLKELI KILRDGRLPYSEWDSQISTVRNRLPR QLNEGLGNLVKKSVSFPAKELHKLM KRYLEENTNDHVYVALQPLLKISER YSEGLANHECEIFLKLIKKYYAVEKIF ENHDIHEERNLLNLRKDLTNLKKI LCISLSHANVVAKNKLVTAILHEYEP LCQDSSKMSLKFRAVIHDLASLESK WAKEVAVKARSVLLRGIFPPIKRRKE HIKTLLQLHIKDTGAENIHSRNIYSC MRDFGNLIHSNLIQLQDLFFFFGHQ DTALSSIASEIYARYAYGNYQLKSIKI HKGAPDLLMSWQFSSLRNLYVNSD GESDEFTKLSKPPSTSGKSSANSFGL LVNMRALLESLEKTLDEVYEQIHIPEE

RLSSGENSLIVNILSPIRYRSENDLIK
TLKIKLHENERGLSKLKVNRITFAFI
AANAPAVKFYSFDGTTYDEISQIRNM
DPSYEAPLELGKMSNYKIRSLPTYDS
SIRIFEGISKFTPLDKRFFVRKIINSF
MYNDQKTTEENLKAEINAQVVYML
EHLGAVDISNSDLNHIFLSFNTVLNI
PVHRLEEIVSTILKTHETRLFQERITD
VEICISVECLETKKPAPLRLLISNKSG
YVVKIETYEKIGKNGNLILEPCSEQS
HYSQKSLSLPYSVKDWLQPKRYKAQ
FMGTTYVYDFPGLFHQAAIQWKRY
FPKHKLNSFFSWVELIEQNGNLIK
VNREPGLNIGMVAFEIMVOTPEYP
EGRNMIVISNDITYNIGSFGPREDLF
FDRVNTYARERGIPIRYLAANSKAKL
GIAEELIPLFRVAWNPSPDPTKGFQY
LYLAPKDMQLLKDSGKGNVVEH
KMVYGEERYIIKAIVGFEEGLGVECL
QSGGLIAGATSKAYRDIFTITAVTCRS
VGIGSYLVRLGQRTIQVEDKPIILTGA
SAINKVLGTDIYTSNLQIGGTQIMYK
NGIAHLTASNDMKAIEKIMTWLSYV
PAKRDMSPPLETMDRWDRDVFDFK
PAKQVPYEARWLEIEGWDSNNNFQ
SGLFDKDSFFETLSGWAKGVIVGRA
RLGGIPVGVIAVETKTIEEIPADPANL
DSSEFSVKEAGQVWYPNSAFKTAQT
INDFNYGEQLPLILANWRGFSGGQ
RDMYNEVLKYGSFIVDALVDYKQPIL
IYIPPFGELRGGSWVIDPTINPEQM
EMYADVSRGGVLEPDGVVSIKYRK
EKMIETMIRLDSTYGHLRRTLTEKKL
SLEKQNDLTKRLKIRERQLIPIYNQIS
IQFADLHDRSTRMLVKGVIRNELEW
KKSRRFLYWRLRRRLNEGQVIKRLQ
KKTCDNKTMMKYDDLKIVQSWYN
DLDVNDDRAVVEFIERNSSKIDKNIE
EFEISLLIDELKKKFEDRRGNIVLEEL
TRLVDSKRKR