

SEQUENCES

ABBREVIATIONS

- eco - *Escherichia coli* K-12 MG1655
- sce - *Saccharomyces cerevisiae*
- cel - *Caenorhabditis elegans*
- dme - *Drosophila melanogaster*
- mmu - *Mus musculus*
- hsa - *Homo sapiens*

ACONITATE HYDRATASE

>eco:b0118 K01682 aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99] | (RefSeq) acnB; hypothetical protein (A)

MLEEYRKHVAERAAEGIAPKPLDANQMAALVELLKNPPAGEEEFLDLLTNRVPPGVDEA
AYVKAGFLAAIAKGEAKSPLLTPEKAIELLGTMQGGYNIHPLIDALDDAKLAPIAAKALS
HTLLMFDNFYDVEEKAKAGNEYAKQVMQSWADAEWFLNRPALAEKLTVTVFVKTGETNTD
DLSPAPDAWSRPDIPLHALAMLKNAREGIEPDQPGVVGPIKQIEALQQKGFPPLAYVGDVV
GTGSSRSKATNSVLWFMGDDIPHVPNKRGGGLCLGGKIAPIFFNTMEDAGALPIEVDVSN
LNMGDVIDVYPYKGEVRNHETGELLATFELKTDVLIDEV RAGGRIPLIIGRGLTTKAREA
LGLPHSDVFRQAKDVAESDRGFSLAQKMVGRACGVKGIRPGAYCEPKMTSVGSQDTTGPM
TRDELKDLACLGF SADLVMQSFCHTAAYPKPVDVNTHTLPDFIMNRGGVSLRPGDGVIIH
SWLNRMLLPDVTGTGGDSHTRFPIGISFPAGSGLVAFAAATGV MPLDMPESVLVRFKGKM
QPGITLRDLVHAIPLYAIKQGLLTVEKKKGKKNIFSGRILEIEGLPDLKVEQAFELTDASA
ERSAAGCTIKLNKEPIIEYLNSNIVLLKWMIAEGYGDRRTLERRIQGMEKWLANPELLEA
DADAEYAAVIDIDLADIKEPILCAPNDPDDARPLSAVQGEKIDEVFIGSCMTNIGHFRAA
GKLLDAHKGQLPTRLWWAPPTRMDAAQLTEEGYYSVFGKSGARIEIPGCSLCMGNQARVA
DGATVVSTSTRNFPNRLGTGANVFLASAELA AVALIGKLPTPEEYQTYVAQVDKTAVDT
YRYLNFNQLSQYTEKADGVIFQTAV

>eco:b0771 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) ybhJ; putative hydratase YbhJ (A)

MIKLSEKGVFLASNNEIIAEEHFTGEIKKEEAKKG TIAWSILSSHNTSGNMDKLKIKFDS
LASHDITFVGIVQTAKASGMERFPLPYVLTNCHNSLCAVGGTINGDDHVFGLSAAQRYGG
IFVPPHIAVIHQYMMREMMAGGGKMILGSDSHTRYGALGTMAVGEGGGELVKQLLNDTWDI
DYPGVVAVHLTGKPAPYVGPQDVALAIGAVFKNGYVKNKVMFVGPVGSALSTDFRNSV
DVMTTETTCLSSVWQTDEEVHNWLALHGRGQDYCQLNPQPMAYYDGCISVDLSAIKPMIA

LPFHPSNVYEIDTLNQNLTDILREIEIESERVAHGKAKLSLLDKVENGRCLKVQQGIIAGC
SGGNYENVIAAANALRGQSCGNDTFS LAVYPSSQPVFMDLAKKGVVADLIGAGAIIRTAF
CGPCFGAGDTPINNGLSIRHTTRNFPNREGSKPANGQMSAVALMDARSIAATAANGGYLT
SASELDCWDNVPEYAFDVTPYKNRVYQGFVKGATQQPLIYGPNIKDWPELGALTDNIVLK
VCSKILDEVTTTDELIPSGETSSYRSNPIGLAEFTLSRRDPGYVSRSKATAELENQRLAG
NVSELTEVFARIKQIAGQEHDPLQTEIGSMVYAVKPGDGSAREQAASCQRVIGGLANIA
EEYATKRYRSNVINWGMLPLQMAEVPTFEVGDYIYIPGIKAALDNPGTTFKGYVIHEDAP
VTEITLYMESLTAEEREIHKAGSLINFNKNRQM

>eco:b1276 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) acnA; aconitate hydratase 1 (A)

MSSTLREASKDTLQAKDKTYHYYSPLAAKSLGDITRLPKSLKVLLNLLRWQDGNSVTE
EDIHALAGWLKNAHADREIAYRPARVLMQDFTGVPVVDLAAMREAVKRLGGDTAKVNPL
SPVDLVIDHSVTVD RFGDDEAFEENVRL EMERNHERYVFLKWGKQAFSRFSVPPGTGIC
HQVNLEYLGKAVWSELQDGEWIAYPDTLVGTDSHTTMINGLGLVWGWGGIEAEAAMLGQ
PVSM LIPDVVGFKLTGKLREGITATDLVLTVTQMLRKHG VVGKFVEFYGDGLDSLPLADR
ATIANMSPEYGATCGFFPIDAVTL DYMRLSGRSEDQVELVEKYAKAQGMWRNPGDEPIFT
STLELDMNDVEASLAGPKRPQDRVALPDV PKAFAASNELEVNATHKDRQPV DYVMNGHQY
QLPDGAVVIAAIT SCTNTSNPSVLMAAGLLAKKAVTLGLKRQPWVKASLAPGSKVVS DYL
AKAKLTPYLDELGFNLVGYGCTTCIGNSGPLDP IETAIKKS DLTVGAVLSGNRNFEGRI
HPLVKTNWLAS PPLVVAYALAGNMNINLASEPIGHDRKGD PVYLKDIWPSAQEIARAVEQ
VSTEMFRKEYAEVFEGTAEWKGINVTRSDTYGWQEDSTYIRLSPFFDEM QATPAPVEDIH
GARILAMLGDSVTTDHISPAGSIKPDSPAGRYLQGRGVERKDFNSYGSRRGNHEVMMRGT
FANIRIRNEMVPGVEGGMTRHLPDSDVVSIYDAAMRYKQEQTPLAVIAGKEYGSGSSRDW
AAKGPRLLGIRVVIAESFERIHRSNLIGMGILPLEFPQGVTRKTLGLTGEEKIDIGDLQN
LQPGATVPVTLTRADGSQEVVPCR CRIDTATELTYYQNDGILHYVIRNMLK

>sce:YLR304C K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) ACO1, GLU1; aconitate hydratase ACO1 (A)

MLSARSAIKRPIVRGLATVSNLTRDSKVNQNLL EDHSFINYKQNVETLDIVRKRLNRPFT
YAEKILYGHLD DPHGQDIQRGVSYLLKRPDRVACQDATAQMAILQFMSAGLPQVAKPVTV
HCDHLIQAQVGGEKDLKRAIDLNKEVYDFLASATAKYNMGFWKPGSGIIHQIVLENYAFP
GALIIGTDSHTPNAGGLGQLAIGVGGADAVDVMAGR PWELKAPKILGVKLTGKMNGWTSP
KDIILKLAGITTVKGGTGKIVEYFGDGVDTFSATGMGTICNMGA EIGATTSVFPFNKSMI
EYLEATGRGKIADFAKLYHKDLLSADKDAEYDEVVEIDLNTLEPYINGPFTPDLATPVSK
MKEVAVANNWPLDVRVGLIGSCTNSSYEDMSRSASIVKDAAAHGLKSKTIFTVTPGSEQI
RATIERDGGQLET FKEFGGIVLANACGPCIGQWDRRDIKKGD KNTIVSSYNRNFTSRNDGN
PQTHAFVASPELVTAFAIAGDLRFNPLTDK LKDKDGNEFMLKPPHGDGLPQRGYDAGENT
YQAPPADRSTVEVKVSPTS DRLQLLKPFKPWDGKDAKDMPILIKAVGKTTTDHISMAGPW
LKYRGHLENISNNYMIGAINAENKKANCVKNVYTGEYKGV PDTARDYRDQGIKWVIGDE
NFGEGSSREHAAL EPRFLGGFAITKSFARIHETNLKKQGLLPLNFKNPADYDKINPDDR
IDILGLAELAPGKPV TMRVHPKNGKPWD AVLTHTFNDEQIEWFKYGSALN KIKADEKK

>cel:CELE_F54H12.1 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) aco-2; putative aconitate hydratase, mitochondrial (A)

MNSLLRLSHLAGPAHYRALHSSSSIWSKVAISKFEPKSYLPYEKLSQTVKIVKDRLKRPL
TLSEKILYGHLDPKTQDIERGVSYLRLRPDRVAMQDATAQMAMLQFISSGLPKTAVPST
IHCDHLIEAQKGGGAQDLARAKDLNKEVFNFATAGSKYGVGFWKPGSGIIHQIILENYAF
PGLLLIGTDSHTPNNGGGLGGLCIGVGGADAVDVMADIPWELKCPKVIGIKLTGKLNWTS
AKDVILKVADILTVKGGTGAIVEYFGPGVDSISATGMGTICNMGAIEGATTSVFPYNESM
YKYLEATGRKEIAEEARKYKDLLTADDGANYDQIIEINLDTLTPHVNGPFTPDCLASSIDK
LGENAKKNGWPLDVKVSLIGSCTNSSYEDMTRAASIAKQALDKGLKAKTIFTITPGSEQV
RATIERDGLSKIFADFGGMVLANACGPCIGQWDRQDVKKGEKNTIVTSYNNRFTGRNDAN
PATHGFVTSPDITTAMASGRLDNFNPLTDELTAADGSKFKLQAPTGLDLPPKGYDPGEDT
FQAPSGSGQVDVSPSSDRLQLLSPFDKWDGKDLEDKILIKVTGKCTTDHISAAGPWLYK
RGHLDNISNNLFLTAINADNGEMNKVKNQVTGEYGAVPATARKYKADGVRWVAIGDENYG
EGSSREHAALPRHLGGRAIIVKSFARIHETNLKKQGMLPLTFANPADYDKIDPSDNVSI
VGLSSFAPGKPLTAIFKKTNGSKVEVTLNHTFNEQQIEWFKAGSALNRMKEVFAKSK

>cel:CELE_ZK455.1 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) aco-1; Cytoplasmic aconitate hydratase (A)

MAFNLLIRNLAIGDNVYKYFDLNGLNLDARYNELPISIKYLLEAAVRHCDEFHVLKKDVET
ILDWKN SQRNQAEIPFKPARVILQDFTGVPVVDLAAMRDAVQNMGADPAKINPVCPVDL
VIDHSVQVDHYGNLEALAKNQSIEFERNRERFNFLKWGSKAFDNLLIVPPGSGIVHQVNL
EYLARTVFVGKDGVLYPDSVVGTDSTTMDGSGVLGWGVGGIEAEAVMLGQPISMVPIE
VIGYELVGTLSDTVTSTDVLVTITKNLRDLGVVGKFVEFFGTGVASLSIADRATIANMCP
EYGATIGFFPVDSRTIDYLTQTGRD TDY TQRVEQYLKSVGMFVNFTDDSYRPTYTTTTLKL
DLGSSVPSVSGPKRPHDRVELASLAQDFSKGLTDKISFKAFLKPEDATKSVTITNHGRT
AELTHGSVVIAAITSCTNTSNPSVMLAAGLVAKKAVELGLNVQPYVKTSLSPGSGVVTKY
LEASGLLPYLEKIGFNIAGYGCMTICIGNSGPLDEPVTKAIEENNLVVAGVLSGNRNFEGR
IHPHVRANYLASPPLAVLYSIIGNVNV DINGVLAVTPDGKEIRLADIWPTRKEVAKFEEE
FVKPQFFREVYANIELGSTEWQQLECPAVKLYPWDDASTYIKKVPFFDGMTSELPSQSDI
VNAHVLLNLGDSVTTDHISPAGSISKTSAPARFLAGRGVTPRDFNTYGARRGNDEIMARG
TFANIRLVNKLASKVGPI TLHVPSGEELDIFDAAQKYKDAGIPAILAGKEYGCGSSRDW
AAKGPFLQGVKAVIAESFERIHRSNLIGMGIIPFQYQAGQNADSLGLTGKEQFSIGVPDD
LKPGQLIDVNVSNNGSVFQVICRFDTEVELTYRNGGILQYMIRKLIQ

>dme:Dmel_CG4706 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) mAcon2; mitochondrial aconitase 2 (A)

MAQRTHRYICLAGSMVRNFHTARFPRCDKVAMSNFDTGIPLPYKKLRENLDICIGRLGGP
LTLSEKVLVSHLDQPDQSQEIERGKSYLRLRPDRVALQDATAQMTLLQFISSGLKKVAVPS
TVHCDHLIEAQISGDKDLARAKDLNKEVYDFLSSACAKYNLGFWKPGSGIIHQIILENYA
FPGLLMIGTDSHTPNNGGGLGCLCVGVGGADAVDVMANIPWELKCPTVIGCHLTGKISGWT

SPKDVILKVAEILTVKGGTGAIVEYHGPVGVESISCTGMATITNMGAEIGATTSIFPFNER
MVTYL RATGRGAIAD EATKNKDLLVPDEGCKYDKVIEINLDTLEPLVNGPFTPDLAHPIS
KLGQNSEKNGYPMEIKVSLIGSCTNSSYEDMGR CASIANDALGHGLKSCVPFNVTPGSEQ
VRATIARDGIIDVLEKFGGTVLANACGPCIGQWDRKDV KMGEKNTIVTSYNRNFTGRNDA
NPATHC FVTSP EMATALAIAGRLDFNPMTDELTGTDGKTFKLKEPHGEELPSKGFDPGED
TYQAPPAKADDIKVNVDPKSDRLQLLEPF EKWDGKDYIDL MVLIKIKGKCTTDHISAAGP
WLKYRGHLDNISNNMFIGATNAENNEMNKVKNQKTGSF DAVPAVARDYKANKIKWCAVGE
ENYGE GSSREHAALEPRHLGGVAIVKSFARIHETNLKKQGMLALT FANPGDYDKVQPSS
KISILNLKDLAPGKPVDAEIKNNGSSDKIQLNHTL NELQIQWFQAGSALNLMKELAAKGG
DKK

>dme:Dmel_CG4900 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) Irp-1A; iron regulatory protein 1A (A)

MSGSGANPFAQFQESFTQDGNVYKYFDLPSIDSKYESLPFSIRVLLES AVRNCNDFH VLE
KDVQSILGWTPSLKQETSDVEVSFKPARVILQDFTGVP AVVDFAAMRDAVRELGGNPEKI
NPICPADLVIDHSVQVDFVRSSDALTKNESLEFQRNKERFTFLKWGARAFDNMLIVPPGS
GIVHQVNLEYLARVVFESDSSADGSKILYPDSVVGTD SHTTMINGLGVLGWGVGGIEAEA
VMLGQSISMLLPEVIGYRLEGKLGPLATSTDVLVTITKHLRQLGVVGKFVEFYGPGVAEL
SIADRATISNMCP EYGATVG YFPIDENTLSYMRQTNRSEKKIDIIRKYLKATRQLRDYSL
VDQDPQYTESVTLDLSTVVTSVSGPKRPHDRVSVSSMCEDFKSCLISPVGFKGFAIPPSA
LAASGEFQWDDGKSYKIGHGSVVIAAITSCTNTSNPSVMLGAGLLAKNAVQKGLSILPYI
KTSLSPGSGVVTTYLRESGVIPYLEQLGFDIVGYGCMTCIGNSGPLDENNVNTIEKNGLV
CCGVLSGNRNFEGRIHPNTRANYLASPLLVIAYAIAGRVDIDFEIEPLGVDSNGKEVFLR
DIWPTRSEIQEVEHKHVIPAMFQEVYSKIQLGSRDWQTLEVSDSKLYPWSEISTYIKLPP
FFEGMTRALPKLKGIEKARCLLLLGD SVTTDHISPAGSIARKSPAARYLSERGLTPRDFN
SYGSRRGNDAVMARGTFANIRLVNKLASKTGPSTLHVPSGEEMDIFDAAERYASEGTPLV
LVVGKDYGSGSSRDWAAKGPFLLGKAVIAESYERIHRSNLVGMGIPLQLFLPGQSADTL
KLSGREVYNIVLPEGELKPGQRIQVDADGNVFETTLRFDTEVDITYYKNGGILNYMIRKM
LD

>dme:Dmel_CG6342 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) Irp-1B; iron regulatory protein 1B (A)

MSGANPFAQFEKTF SQAGTTYKYFDLASIDSKYDQLPYSIRVLLES AVRNCNDFHILEKD
VQSILGWSPALKQGSNDVEVSFKPARVILQDFTGVP AVVDFAAMRDAVLDLGGDPEKINP
ICPADLVIDHSVQVDFARAPDALAKNQSL EFERNKERFTFLKWGAKAFNNMLIVPPGSGI
VHQVNLEYLARVVFENDATD GSKILYPDSVVGTD SHTTMINGLGVLGWGVGGIEAEAVML
GQSISMLLPEVIGYKLEGKLSPLVTSTDVLVTITKHLRQLGVVGKFVEFYGPGVAELSIA
DRATISNMCP EYGATVG YFPIDENTLGYMKQTNRSEKKIDIIRQYLKATQQLRNYADAAQ
DPKFTQSITL DLSTVVTSVSGPKRPHDRVSVSDMPEDFKSCLSSPVGFKGFAIAPEAQSA
FGEFQWDDGKTYKLHHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVEKGLSILPYIKTS
LSPGSGVVTTYLKESGVIPYLEKL GFDIVGYGCMTCIGNSGPLEENVNTIEKNGLVCAG
VLSGNRNFEGRIHPNTRANYLASPLLVIAYAIAGRVDIDFEKEPLGVDANGKNVFLQDIW

PTRSEIQEVENKHVIPAMFQEVYSKIELGSQDWQTLQVSEGKLFWSWSADSTYIKRPPFFE
GMTRDLPKLQSIQKARCLLFLGDSVTTDHISPAGSIARTSPAARFLSERNITPRDFNSYG
SRRGNDAIMSRTGFANIRLVNKLVEKTGPRTVHIPSQEELDIFDAAERYREEGTPLVLVV
GKDYGSGSSRDWAAKGPFLLGVKAVIAESYERIHRSNLVGMGIPLQLPGQSAETLNL
GREVYNIALPESGLKPGQKIQVEADGTVFETILRFDTEVDITYYKNGGILNYMIRKMMLS

>dme:Dmel_CG9244 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) mAcon1;
mitochondrial aconitase 1, isoform E (A)

MAARLMNAQAQVCRLGKHVASEATVVRQFHASCYTASKVALSKFSDVYLPYEKLNKRLE
VVRGRLNRPLTLSEKVLVSHLDDPANQDIVRGTSYLRLRPDRVAMQDATAQMALLQFISS
GLKKVAVPSTVHCDHLIEAQIGGPKDLARAKDLNKEVYDFLASTCAKYGLGFWKPGSGII
HQIILENYAFPGLLMIGTDSHTPNGGGLGGLCIGVGGADAVDVMADIPWELKCPKVIGVN
LTGKISGWTSPKDVILKVADILTVKGGTGAIIEYHGKGVDSISCTGMATICNMGAIEIGAT
TSLFPFNQRMADYLYKSTGRAGIASEAQKYQAKILSADKNCEYDELIEINLDTLEPHVNGP
FTPDLGHPISKLGENSEKKNGYPMDIRVGLIGSCTNSSYEDMGRCAKSIKAMSHGLKSKI
PFNVTPGSEQIRATIERDGISEVFDKFGGTVLANACGPCIGQWDRKDVKKGDKNITVTSY
NRNFTGRNDANPATHCFVTSPELVTALSIAGRDFNPLTDELTDGADGKKFKLKAPFGDEL
PAKGFDPGQDITYTAPPPSGENVKVAVDPKSTRLLQLEPFDKWNGQDLTDLTVLIKVKGKC
TTDHISAAGPWLKYRGHLNINNMFIGATNYENNEMNNIKNQNRNGSWGVPDVARDYKA
NGIKWVAVGDENYGESSREHAALPRHLGGRAIVKSFARIHETNLKKQGLLPLTFANP
ADYDKIQPTSKISLLNLKSLAPGKPVDAEIKNGDKVERIKLNHTLNDLQIGWFKAGSALN
RMKELAQ

>mmu:11428 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) Aco1, Aco-1, Irebp, Irp1;
aconitase 1 (A)

MKNPFAHLAEPLDAAQPGKRFFNLNKLEDSRYGRLPFSIRVLLEAAVRNCDEFLVKKNDI
ENILNWNVMQHKNIIEVPFKPARVILQDFTGVPVVDFAAMRDAVKKLGGNPEKINPVCPA
DLVIDHSIQVDFNRRADSLQKNQDLEFERNKERFEFLKWGSQAFCNMRIIPPGSGIIHQV
NLEYLARVVFDDQGCYYPDSLVTGDSHTTMIDGLGVLGWGVGGIEAEAVMLGQPISMVLP
QVIGYKLMGKPHPLVTSTDIVLTITKHLRQVGVGKFEFFGPGVAQLSIADRATIANMC
PEYGATAAFFPVDEVSIAYLLQTGREEDKVKHQKYLQAVGMFRDFNDTSQDPDFTQVVE
LDLKTVPCCSGPKRPQDKVAVSEMKKDFESCLGAKQGFKGFQVAPDRHNDRKTFLYSNS
EFTLAHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVEAGLSVKPYIKTSLSPGSGVVTY
YLRESGVMPYLSQLGFDVVGYGCMTICIGNSGPLPEPVVEAITQGDLVAVGVLSGNRNFE
RVHPNTRANYLASPPLVIAYAIAGTVRIDFEKEPLGVNAQGRQVFLKDIWPTRDEIQAVE
RQHVIPGMFKEVYQKIETVKNKSWNALAAPSEKLYAWNPKSTYIKSPFFESLTLDLQPPK
SIVDAYVLLNLGDSVTTDHISPAGNIARNSPAARYLTNRGLTPREFNSYGSRRGNDAIMA
RGTFANIRLLNKFLNKQAPQTVHLPSGETLDVFDAAERYQQAGLPLIVLAGKEYGSGSSR
DWAAGPFLLGKAVLAESYERIHRSNLVGMGVIPLEYLPGETADSLGLTGRERYTINIP
EDLKPRMTVQIKLDTGKTFQAVMRFDTDVELTYFHNGGILNYMIRKMAQ

>mmu:11429 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) Aco2, Aco-2, Aco3, D10Wsu183e, Irp1; aconitase 2, mitochondrial (A)
MAPYSLLVTRLQKALGVRQYHVASVLCQRAKVAMSHFEPSEYIRYDLLEKNINIVRKRLN
RPLTLSEKIVYGHLDLDPANQEIERGKTYLRLRPDRVAMQDATAQMAMLQFISSGLPKVAV
PSTIHCDHLIEAQVGGEKDLRRAKDINQEVYNFLATAGAKYGVGFWRPGSGIIHQILEN
YAYPGVLLIGTDSHTPNNGGLGGICIGVGGADAVDVMAGIPWELKCPKVIGVKLTGSLSG
WTSPKDVILKVAGILTVKGGTGAIVEYHGPVDSISCTGMATICNMGAIEGATTSVFPYN
HRMKKYLSKTGRTDIANLAEFKDHLVPDPGCQYDQVIEINLNELKPHINGPFTPDLAHP
VADVGTVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGS
EQIRATIERDGYAQILRDVGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYNRNFTGRN
DANPETHAFVTSPEIVTALAIAGTLKFNPETDFLTGKDGGKFKLEAPDADELPRSDFDPG
QDTYQHPPKDSSGQRVDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAA
GPWLKFRGHLDNISNNLLIGAINIENGKANSVRNAVQTQFPGVPDTARYYKKHGIRWVVI
GDENYGESSSREHAALPRHLGGRAITKSFARIHETNLKKQGLLPLTFADPSDYNKIHP
VDKLTIQGLKDFAPGKPLKCVIKHPNGTQETILLNHTFNETQIEWFRAGSALNRMKELQQ

>hsa:48 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) ACO1, ACONS, HEL60, IREB1, IREBP, IREBP1, IRP1; aconitase 1 (A)
MSNPFAHLAEPLDPVQPGKKFFNLNKLEDSRYGRLPFSIRVLLEAAIRNCDEFLVKKQDI
ENILHWNVTQHKNIEVPFKPARVILQDFTGVPVVDFAAMRDAVKKLGGDPEKINPVCPA
DLVIDHSIQVDFNRRADSLQKNQDLEFERNRERFEFLKWGSQAFHNMRIIPPGSGIIHQV
NLEYLARVVFDDQGYYPDSLVTGDSHTTMIDGLGILGWGVGGIEAEAVMLGQPISMVLP
QVIGYRLMGKPHPLVTSTDIVLTITKHLRQVGVVGKFVEFFGPGVAQLSIADRATIANMC
PEYGATAAFFPVDEVSTITYLVQTGRDEEKLKYIKKYLQAVGMFRDFNDPSQDPDFTQVVE
LDLKTVPCCSGPKRPQDKVAVSDMKKDFESCLGAKQGFKGFQVAPEHHNDHKTFIYDNT
EFTLAHGSSVIAAITSCTNTSNPSVMLGAGLLAKKAVDAGLNVMPYIKTSLSPGSGVVTY
YLQESGVMPYLSQLGFDVVGYGCMTCIGNSGPLPEPVVEAITQGDLVAVGVLSGNRNFEF
RVHPNTRANYLASPLVIAYAIAGTIRIDFEKEPLGVNAKGQVFLKDIWPTRDEIQAVE
RQYVIPGMFKEVYQKIETVNESWNALATPSDKLFFWNSKSTYIKSPFFENLTDLQPPK
SIVDAYVLLNLGDSVTTDHISPAGNIARNSPAARYLTNRGLTPREFNSYGSRRGNDAVMA
RGTFANIRLLNRFLNKQAPQTIHLPSGEILDVFDAERYQQAGLPLIVLAGKEYGAGSSR
DWAAGPFPLLGIKAVLAESYERIHRSNLVGMGVIPLEYLPGENADALGLTGQERYTIIP
ENLKPQMKVQVKLDTGKTFQAVMRFDTDVELTYFLNGGILNYMIRKMAK

>hsa:50 K01681 aconitate hydratase [EC:4.2.1.3] | (RefSeq) ACO2, ACONM, HEL-S-284, ICRD, OCA8, OPA9; aconitase 2 (A)
MAPYSLLVTRLQKALGVRQYHVASVLCQRAKVAMSHFEPNEYIHYDLLEKNINIVRKRLN
RPLTLSEKIVYGHLDLDPASQEIERGKSYLRLRPDRVAMQDATAQMAMLQFISSGLSKVAV
PSTIHCDHLIEAQVGGEKDLRRAKDINQEVYNFLATAGAKYGVGFWKPGSGIIHQILEN
YAYPGVLLIGTDSHTPNNGGLGGICIGVGGADAVDVMAGIPWELKCPKVIGVKLTGSLSG
WSSPKDVILKVAGILTVKGGTGAIVEYHGPVDSISCTGMATICNMGAIEGATTSVFPYN
HRMKKYLSKTGREDIANLADEFKDHLVPDPGCHYDQLIEINLSELKPHINGPFTPDLAHP

VAEVGKVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGS
EQIRATIERDGYAQILRDLGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYNRNFTGRN
DANPETHAFVTSPEIVTALAIAGTLKFNPETDYLTGTDGKKFRLEAPDADELPKGEFDPG
QDTYQHPPKDSSGQHVDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAA
GPWLKFRGHLDNISNLLIGAINIENGKANSVRNAVQTQFGPVPDTARYYKKHGIRWVVI
GDENYGEGSSREHAALPRHLGGRAITKSFARIHETNLKKQGLLPLTFADPADYNKIHP
VDKLTIQGLKDFTPGKPLKCIKHPNGTQETILLNHTFNETQIEWFRAGSALNRMKELQQ

CITRATE LYASE

>cel:CELE_B0365.1 K01648 ATP citrate (pro-S)-lyase [EC:2.3.3.8] | (RefSeq) acly-2;
ATP-citrate synthase (A)

MSAKAVSELSGKEVLYKYFESTGIVSAPHAFHVKAGDKFSDVAAKYEWLAQDNKGVIKPD
QLIKRRGKLGVLKIGSPKELEAWFGKTANSYVKVGQTEGRLHTFIVEPFCAHTENEEMYI
AIYSERCRDVIMFYEQGGVDIGDVEEKARSVHVPVQLDDNAMSISERELGVLLGPCSDKD
DIRKFVRSLEYEAYKALHFTYLEINPFVLTNGKIHILDLAAKLDETASFLCSDKWSGRNAS
ARIAPTLEFPAPFGRDLTSEEQYISDMDAKTGASLKLTLNRKGRVWTMVAGGGASVVFT
DTVCDLGGSELANYGEYSGDPSEAQTIEYAKTILSVMTEGAPRPDGKVLIIIGGSIANFT
NVAKTFGGIVRAFETFIDKLKEHNVSIYVRRGGPNYQEGLRRVKDAATKLEIPIYVFGPE
THMTAIVGAALGLKPMPTVPTAPQTTGQFLLSPERN TAGTERPPASPAPNTSTIEHPLAK
RHPLHQSLFENDTKAIIWGQQHKAIQGMLDFDFVCCRHSVSVASTYPFTGDNKQKYYFG
QKEILIPAYKSMAKAFASHPDATVMVTFASMRSVFETVLEALQFTQIKVIAIIAEGVPEN
QTRKLLKIAEDKGVTLIGPATVGGIKPGCFKIGNTGGMMDNILASKLYRPGSVAYVSRSG
GMSNELNNIISQNTNGVYEGIAIGGDRYPGSTYTDHVMRYQHDDRVMIVLLGEVGGIEE
YRIVELLKEKKITKPLIAWCIGTCADHITSEVQFGHAGASANGQGETAACKNTALRTAGA
LVPDSFDDLGNKIRQTYEELLRLIIVPQPEVPPPAVPMDYAWARELGLIRKPASFMSTI
CDERGEELNYAGVPITKVLESMDGIGGVLGLLWFQKRLPPHANKFIEICLMLTADHGPVAV
SGAHTNIVCARAGKDLISSLTSGLLTIGDRFGGALDGAARQFSEAFDQGWSPNQFVGEMR
KRGTHIMGIGHRVKSINNPDKRVEILKRFALNKKEFAQETPLLDYALEVEKITTAKKPNL
ILNVDGAIIIFVDILRNSGMFTTAEAEQEVIEIGALNGMFVLGRSIGFIGHYLDQSRLKQ
GLYRHPWDDISYIMPERNL

>cel:CELE_D1005.1 K01648 ATP citrate (pro-S)-lyase [EC:2.3.3.8] | (RefSeq) acly-1; putative
ATP-citrate synthase (A)

MSAKAVSELSGKEVLYKYFEP SGLLSAPHAFHVKAGENFDEIANKYEWLARDNKGVIKPD
QLIKRRGKLGVLKIGTPQELKAWFEKTGDSYVRVGQTEGRLHTFIVEPFCAHTEKDEMYI
AIYSERFRDVIMFYEQGGVDIGDVEEKARTVSVPVQLNENAMTPSDEELTTLLGPLKDSD
IVRRFVVELYKAYKDLHFTYLEINPFVLLNNQIHVLDLAARLDETANFLCADKWKSRLTP
YGGPNHVEFPAPFGRDLTSEEQYISEMDAKTGASLKLTLNRKGRVWTMVAGGGASVVFT
DTVCDLGGASELANANYGEYSGDPSESQTIEYAKTLLSVMTEGTTPRPDGKVLIIIGGSIANFT
NVAKTFGGIVRAFETFVSKLKEHKVTIFVRRGGPNYQEGLRRIKDAATKLELPIHVFGPE
THMTAIVGAALGVKPMPTVPTAPQTTGQFLLSPERN TGGTERAPPSPAANATPTEHPLTT
AQQNKLSFRGLFEDDTKAIIWGQQAKAIQGMLDFDYVCCRSSPSVSVASTYPFTGDNKQK
YYFGQKEILIPAYKSMAKAFATHPDASIMVTFASMRSVFETVLEALEFPQIKVIAIIAEG
VPENQTRKLLKIAHDRGVTLVGPATVGGIKPGCFKIGNTGGMMDNILASKLYRPGSVAYV
SRSGGMSNELNNIISQNTNGVYEGIAIGGDRYPGSTYTDHVIRYQNDDRVMIVLLGEVG
GVEEYKIVDLLKQKKVTKPLVAWCIGTCADHITSEVQFGHAGASANALGETAACKNAALR
ASGALVPESFDDLGNKIRQTYDELVSQQIIVPQPEVPPPAVPMDYAWARELGLIRKPASF
MTSICDERGEELNYAGVPITKVLESMDGIGGVLGLLWFQKRLPPHANKFIEICLMLTADH
GPAVSGAHTNIVCARAGKDLISSLTSGLLTIGDRFGGALDGAARQFSEAFDQGWSANQFV

SEMRKKKGKHIMGIGHRVKSINNPDKRVEILKRFAMDKKEFAQETPLFEYALEVEKITTA
KPNLILNVDGAIAILFVDILRHSGMFTKQEAETIEIGSLNGLFVLGRSIGFIGHYLDQS
RLKQGLYRHPWDDISYIMPESNLVKF

>dme:Dmel_CG8322 K01648 ATP citrate (pro-S)-lyase [EC:2.3.3.8] | (RefSeq) ATPCL; ATP citrate lyase, isoform E (A)

MSAKAITEASGKDILNRHLNTHGAGAATCRFSTVNSTTDWSKLAVDHPWLLTTPLVCKPD
QLIKRRGKLGLIGVKKNFEQVKQWIGERLNKDQKIGNAVGKLRFIIEPFVPHDAEEMY
VCIYSHRAADTILFYHQGGVDIGDVDAKAVKLDVPVNSSLADVKSKLLKEVKDAGTKE
RIAKFVSALYTTYVDLYFTYLEINPLVVTADNLYILDAAKLDSTADFICRPKWGEIDYP
PPFGRDAYPEEAYIADLDAKSGASLKLTLNRNGRIWTMVAGGGASVIYSDTICDLGGAS
ELANYGEYSGAPSEQQTYEYAKTILNLMTSSPKHPDGKVLITGGGIANFTNVAATFQGII
TALREFQPKLVEHNVSIFVRRAGPNYQEGLRKM RDFGSTLGIPLHVFGPETHMTAICGMA
LGKRPIPQTASVEFSTANFLLPGGQQAQADLKAASDASEALGSGSALSPTAAKPIKLPI
SADEADSAGISGAQRNGSSLNRFKFSNTTKAIVWGMQQRVQSMDFDFICRRDEPSVVA
MVYPFTGDHKQKYYWGHKEILIPVYKKMSDAIHKHKEVDVMVNFASMR SAYESTLEVLEF
PQIRTV AIIAEGIPENMTRKLIIEADKKGV AIGPATVGGVKPGCFKIGNTGGMLDNILH
SKLYRPGSVAYVSRSGGMSNELNNISKATDGVIEGIAIGGDRYPGSTFMDHILRYQADP
ETKLIVLLGEVGGTEEYDVCAALKDGRITKPLVAWCIGTCASMFTSEVQFGHAGSCANS
RETATAKNKGLRDAGAYVPDSFDTLGELIHHVYGELVKTGRVVPKEEVPPTVPM DYSWA
RELGLIRKPASFMTSICDERGQELIYAGMPISEVLSKDVGIGGVISLLWFQRCLPSYVCK
FFEMCLMVTADHGPVSGAHNTIVCARAGKDLVSSVVSGLLTIGDRFGGALDGSARQFSE
AYDTNLHPMEFVNKMRKEGKLILGIGHRVKSINNP DVRVKIIEFVLENFPACPLLKYAL
EVEKITTNKKPNLILNVDGVIATAFVDMLRNSGSFTSEEAQEYINVGAINSLFVLGRSIG
FIGHYMDQKRLKQGLYRHPWDDISYVIPEQYN

>mmu:104112 K01648 ATP citrate (pro-S)-lyase [EC:2.3.3.8] | (RefSeq) Acly, A730098H14Rik; ATP citrate lyase (A)

MSAKAISEQTGKELLYKYICTTSAIQNRFKYARVTPD TDWAHLLQDHPWLLSQSLVVKPD
QLIKRRGKLGLVGVNLSLDGVKSWLK PRLGHEATVGKAKGFLKNFLIEPFVPHSQAE EFY
VCIYATREGDYVLFHHEGGVDVGDVDAKAQKLLVGVDEKLNTEDIKRHLLVHAPEDKKEV
LASFISGLFNFYEDLYFTYLEINPLVVT KDGVYILDAAKV DATADYICKVKWGDIEFPP
PFGREAYPEEAYIADLDAKSGASLKL TLLNPKGRIWTMVAGGGASVVYSDTICDLGGVNE
LANYGEYSGAPSEQQTYDYAKTILSLMTREKHPEGKILIIGGSIANFTNVAATFKGIVRA
IRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFGTETHMTAIVGMALG
HRPIPNQPPTAAHTANFLLNASGSTSTPAPSRTASFSESRADEVAPAKKAKPAMPQGKSA
TLFSRHTKAIVWGMQTRAVQGMLDFDYVCSRDEPSVAAMVYPFTGDHKQKFWGHKEILI
PVFKNMADAMKKHPEVDVLINFASLRSAYDSTMETMNYAQIRTI AIIAEGIPEALTRKLI
KKADQKGV TIIGPATVGGIKPGCFKIGNTGGMLDNILASKLYRPGSVAYVSRSGGMSNEL
NNIISRTTDGVYEGVAIGGDRYPGSTFMDHVLRYQDTPGVKMIVVLGEIGGTEEYKICRG
IKEGRLTKPVVCWIGTCATMFSSEVQFGHAGACANQASETAVAKNQALKEAGVFVPRSF
DELGEIISVYEDLVAKGAIVPAQEVPPPTVPM DYSWARELGLIRKPASFMTSICDERGQ

ELIYAGMPITEVFKEEMGIGGV LGLLWFQRR LPKYSCQFIEMCLMVTADH GPAVSGAHNT
IICARAGKDLVSSLTSGLLTIGDRFGGALDAAAKMFSKAFDSGIIPMEFVNKMKEGKLI
MGIGHRVKSINNPDMRVQILKDFVKQHFPATPLLDYALEVEKITTSKKPNLILNVDGFIG
VAFVDMLRNCGSFTREEADEYVDIGALNGIFVLGRSMGFIGHYLDQKRLKQGLYRHPWDD
ISYVLPEHMSM

>hsa:47 K01648 ATP citrate (pro-S)-lyase [EC:2.3.3.8] | (RefSeq) ACLY, ACL, ATPCL, CLATP;
ATP citrate lyase (A)

MSAKAISEQTGKELLYKFICTTSAIQNRFKYARVTPD TDWARLLQDHPWLLSQNLVVKPD
QLIKRRGKLG LVGVNLTLDGVKSWLKPRLGQEATVGKATGFLKNFLIEPFVPHSQAE EFY
VCIYATREGDYVLFHHEGGVDVGDVDAKAQKLLVGVDEKLN PEDIKKHLLVHAPEDKKEI
LASFISGLFN FYEDLYFTYLEINPLVVT KDGVYVLDLAAKV DATADYICKVKWGDIEFPP
PFGREAYPEEAYIADLDAKSGASLKL TLLNPKGRIWTM VAGGGASVVYS DTICDLGGVNE
LANYGEYSGAPSEQQTYDYAKTILSLMTREKHPDGKILIIGGSIANFTNVAATFKGIVRA
IRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFGTETHMTAIVGMALG
HRPIPNQPPTAAHTANFLLNASGSTSTPAPSRTASFSESRADEVAPAKKAKPAMPQDSVP
SPRSLQGKSTTLFSRHTKAIVWGMQTRAVQGMLDFDYVCSRDEPSVAAMVYPFTGDHKQK
FYWGHKEILIPVFKNMADAMRKHPEVDVLINFASLSAYDSTMETMNYAQIRTIAIIAEG
IPEALTRKLIK KADQKGV TIIGPATVGGIKPGCFKIGNTGGMLDNILASKLYRPGSVAYV
SRSGGMSNELNNIISRTTDGVYEGVAIGGDRYPGSTFMDHVLRYQDTPGVKMIVVLGEIG
GTEEYKICRGIKEGRLTKPIVCWCIGTCATMFSSEVQFGHAGACANQASETAVAKNQALK
EAGVFVPRSFDELGEIIQSVYEDLVANGVIVPAQEVPPPTVPMDY SWARELGLIRKPASF
MTSICDERGQELIYAGMPITEVFKEEMGIGGV LGLLWFQKRLPKYSCQFIEMCLMVTADH
GPAVSGAHNTIICARAGKDLVSSLTSGLLTIGDRFGGALDAAAKMFSKAFDSGIIPMEFV
NKMKEGKLI MGIGHRVKSINNPDMRVQILKDYVRQHFPATPLLDYALEVEKITTSKKPN
LILNVDGLIGVAFVDMLRNCGSFTREEADEYIDIGALNGIFVLGRSMGFIGHYLDQKRLK
QGLYRHPWDDISYVLPEHMSM

CITRATE SYNTHASE

>eco:b0720 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) gltA; citrate synthase (A)
MADTKAKLTLNGDTAVELDVLKGTLGQDVIDIRTLGSKGVFTFDPGFTSTASCESKITFI
DGDEGILLHRGFPIDQLATDSNYLEVVCYILLNGEKPTQEYDEFKTTVTRHTMIHEQITR
LFHAFRRDSHPMAVVMCGITGALAAFYHDSLDVNNPRHREIAAFRLLSKMPTMAAMCYKYS
IGQPFVYPRNDLSYAGNFLNMMFSTPCEPYEVNPILERAMDRILILHADHEQNASTSTVR
TAGSSGANPFACIAAGIASLWGPAHGGANEAAALKMLEEISSVKHIPEFVRRAKDKNDSFR
LMGFGHRVYKNYDPRATVMRETCHVLKELGTKDDLLEVAMELENIALNDPYFIEKKLYP
NVDFYSGIILKAMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMKIARPRQLYTGYEKRD
FKSDIKR

>sce:YCR005C K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT2; citrate (Si)-synthase
CIT2 (A)
MTVPYLNNSNRNVASYLQSNSSQEKTLKERFSEIYPIHAQDVRQFVKEHGKTKISDVLLEQ
VYGGMRGIPGSVWEGSVLDPEDGIRFRGRTIADIQKDLPAKAGSSQPLPEALFWLLTGE
VPTQAQVENLSADLMRSSELP SHVVQLLDNL PKDLHPMAQFSIAVTALESESKFAKAYAQ
GISKQDYWSYTFEDSLDLLGKLPVIAAKIYRNVFKD GKMGEVDPNADYAKNLVNLIGSKD
EDFVDLMRLYLTIHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEV
LEWLFALKEEVNDDYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHF
PDYELFKLVSSYIEVAPGVLTEHGKTKNPWPVNDAHSGVLLQYYGLKESSFYTVLFGVSR
AFGILAQLITDRAIGASIERPKSYSTEKYKELVKNIESKL

>sce:YNR001C K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT1, LYS6; citrate
(Si)-synthase CIT1 (A)
MSAILSTTSKSFLSRGSTRQCQNMQKALFALLNARHYSSASEQTLKERFAEIIPAKAEEI
KKFKKEHGKTVIGEVLEQAYGGMRGIKGLVWEGSVLDPEEGIRFRGRTIPEIQRELPAK
EGSTEPLPEALFWLLTGEIPTDAQVKALSADLAARSEIPEHVIQLLDSL PKDLHPMAQF
SIAVTALESESKFAKAYAQGVSKKEYWSYTFEDSLDLLGKLPVIA SKIYRNVFKDGKITS
TDPNADYGKNLAQLLGYENKDFIDLMRLYLTIHSDHEGGNVSAHTTHLVGSALSSPYLSL
AAGLNGLAGPLHGRANQEVLEWLFKLREEVKG DYSKETIEKYLWDTLNAGRVPVPGYGHAV
LRKTDPRYTAQREFALKHFPDYELFKLVSTIYEVAPGVLT KHGKTKNPWPNVDSHSGVLL
QYYGLTEASFYTVLFGVARAIGVLPQLIIDRAVGAPIERPKSFSTEKYKELVKKIESKN

>sce:YPR001W K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT3; citrate (Si)-synthase
CIT3 (A)
MVQRLLPGAHCRRSFNSSAIKSSALTLKEALENVIPKKRDAVKKLKACYGSTFVGPIT
ISSVLGGMRGNQSMFWQGTSLDPEHGIKFQGLTIEECQNRLPNTGIDGDNFLPESMLWLL
MTGGVPTFQQAASFRKELAIRGRKLPHYTEKVLSSLPKDMHPMTQLAIGLASMNKGSLFA
TNYQKGLIGKMEFWKDTLED SLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNIC

SLLGMTNGTNSSNTCNLTQQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPY
LSYSSGIMGLAGPLHGLAAQEVVRFLIEMNSNISSIAREQEIKDYLWKILNSNRVIPGYG
HAVLRKPDPRFTAMLEFAQKRPIEFENDKNVLLMQKLAEIAPKVLLHKGKSKNPFNPVDS
ASGILFYHYGIRELLFFTIVIFGCSRAMGPLTQLVWDRILGLPIERPCKSLNLEGLEALTKA
SNVNKL

>cel:CELE_T20G5.2 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) cts-1; putative citrate synthase, mitochondrial (A)

MSLSGMAIRRLITKGVIPVCQVAPLSTSAEGSTNLKEVLSKKIPAHNAKVKSFRTEHGST
VVQNVNIDMIYGGMRSMKGMVTETSVLDPEEGIRFRGYSIPECQKLLPKAKGGEEPLPEA
IWWLLCTGDVPSEAQTAAITKEWNARADLPTHVVRMLDNFPDNLHPMAQFIAAIAALNNE
SKFAGAYARGVAKASYWEYAYEDSMDLLAKLPTVAIIYRNLYRDGSAVSVIDPKKDWSA
NFSSMLGYDDPLFAELMRLYLVIHSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAG
PLHGLANQEVLVFLNKIVGEIGFNYTEEQLEKEVWWKHLKSGQVVPGYGHAVLRKTDPRYE
CQREFALKHLPNDLDFKLVTLYKITPGILLEQGKAKNPWPVNVDHSGVLLQYFGMTEMS
FYTVLFGVSRALGCLSQLIWARGMGLPLERPKSHSTDGLIKLALAACK

>dme:Dmel_CG3861 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) kdn; knockdown, isoform A (A)

MSLYRISARKLSEAQKLPNVGAYVRMIAADGKSLRDVLAAKVPQEQERVKNFRKQHGATK
MGETTIDMMYGGMRGKALVTETSVLDADEGIRFRGLSIPECQKVLPAADGGTEPLPEGL
FWLLLTGEVPTKSQVQQLSREWAERAALPQHVVTMLNNMPTTLHPMSQFAAAVTALNHDS
KFAKAYSDGVHKSKEYWEYVYEDSMDLIAKLPVVAATIYCNTYRGGKGSRSIDSSLDWSAN
FVKMLGYDNAPFTELMRLYLTIHSDHEGGNVSAHTVHLVGSALSDPYLSFAAGLNGLAGP
LHGLANQEVLVWLRKLQKEAGNNPSEEQLKEYIWKTLKSGQVVPGYGHAVLRKTDPRYTC
QREFALKHLPEDETFQLVSKIYKVVPILTETGKVKNPWPNVDAHSGVLLQYYGMKEMNY
YTVLFGVSRALGVLASLVWDRALGLPIERPCKSFSTDLLVKMVQK

>dme:Dmel_CG14740 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CG14740; uncharacterized protein (A)

MQKTNNYKSFKIFFKNVPFRSYPDCKNGKGSGLKAKLAKKIPIEREKFLGIKCLHGKKII
GQISVNSVIGGMRGLPLLFCETSSLDKNKGIYYRGKLLKDVCALPRVQEGTQEGTPEGC
FFLLTSGSMPTKKEAQEVTNEWLKRGSVPRYCLRMIDSMDKRVHPMAQLCAASACLN PQS
QFVEAYTKGARRADYWKYSYEDSMNLIAMLPVAAAISNVFRDGEFSREVNYEEDWSGN
FCRMLGLPEKDFVDLMRLYMILHADHESGNVSAHACHLVGTALSDPFLSFSASMCGLAGP
LHGLANQEVLVWLTKLRKAIGDDPSDEELKKFIDDTLKGQVIPGYGHAVLRDTPRFVL
QNEFAMKHCKDDPGVKLVTRLWKIPEVLKKNLVANPYPNVDAHSGVLLQHYCLKELKF
YTVLFGVSRALGVLSQLIWSRALGAPIERPCKSFSSIEICKFINEADKKAGKKNKKKC

>mmu:12974 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) Cs, 2610511A05Rik, 9030605P22Rik, Ahl4, Cis; citrate synthase (A)
MALLTAATRLLGAKNSSCLVLAARHASASSTNLKDVLNLIPEQARIKTFKQQHGKTVV
GQITVDDMMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLF
WLLVTGQMPTEEQVSWLSREWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAITALNSES
FARAYAEGMNRAKYWELIYEDCMDLIAKLPCVAAKIYRNLYREGSSIGAIDSRLDWSHNF
TNMLGYTDPQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL
HGLANQEVLVWLTQLQKEVGKDVSDKLRDYIWNTLNHSGRVVPGYGHAVLRKTDPRYSCQ
REFALKHLPKDPMFKLVAQLYKIVPNILLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYY
TVLFGVSRALGVLAQLIWSRALGFPLERPCKSMSTDGLMKFVDSK

>mmu:71832 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) Csl, 1700007H16Rik; citrate synthase like (A)
MALLTAAAWFLGTKNPPCLVLAARHASASSTNLKDVLRNLIPEQARIKTFRKKHGKTVV
GQITVDDMMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQKLLPKAKGGKEPLPEGLF
WLLVTGQMPTEEQVSWLSQEWVKRAALPSHVVTMLDNFPTKLHPMSQLSAAITVLNNESEN
FARAYAQGMNRTKYWELTYEDCMDLLAKLPCVAAKIYRNLYREDRNEAIDSKLDWSHNF
TNMLGYTDPQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAALNGLAGPL
HGLANQEVLVWLTQLQKEVGEDASDEKLKNYIWNTLNHSGRVVPGYGHAVLRKTDPRYSCQ
REFALKHLPKDPMFKLVGQLYKIVPDILLEQGKAKNPWPNVDAHSGVLLQYYGMREMNY
TVLFGVSRALGVLSQLIWSRALGFPLERPCKSMSTDALMKFVNSESG

>hsa:1431 K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CS; citrate synthase (A)
MALLTAAARLLGTKNASCLVLAARHASASSTNLKDILADLIPEQARIKTFRQQHGKTVV
GQITVDDMMYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQKLLPKAKGGEEPLPEGLF
WLLVTGHIPTTEEQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSES
FARAYAQQISRTKYWELIYEDSMDLIAKLPCVAAKIYRNLYREGSGIGAIDSRLDWSHNF
TNMLGYTDHQFTELRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL
HGLANQEVLVWLTQLQKEVGKDVSDKLRDYIWNTLNHSGRVVPGYGHAVLRKTDPRYTCQ
REFALKHLPNDPMFKLVAQLYKIVPNVLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYY
TVLFGVSRALGVLAQLIWSRALGFPLERPCKSMSTEGLMKFVDSKSG

DIHYDROLIPOAMIDE S- ACETYLTRANSFERASE

>mmu:235339 K00627 pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) Dlat, 6332404G05Rik, DLTA, PDC-E2; dihydrolipoamide S-acetyltransferase (A)

MWRVCARRARSAVPRDGFRRWAALKEGPGAPCGSPRIGPAAVRCGSGIPRYGVRSLCGW
SSGSGTVPRNRLLRQLLGSPSRRSYSLPPHQKVPLPSLSPTMQAGTIARWEKKEGEKISE
GDLIAEVETDKATVGFESLEECYMAKILVPEGTRDVPVGSIIICITVEKPQDIEAFKNYTL
DLAAAAAPQAAPAAAPAPAAAPASAPGSSYPHMQIVLPALSPTMTMGTVQRWEKK
VGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGAPLCIIVEKQEDIA
AFADYRPTTEVTSKLPQAAPPAPPPVAAVPPTPQPVAPTPSAAPAGPKGRVFSPLAKKLA
AEKGIDLTQVKGTGPEGRIKKDIDSFVPSKAAPAAAAAMAPPGPRVAPAPAGVFTDIPI
SNIRRVIAQRLMQSKQTIPHYLSVDVNMGEVLLVRKELNKMLEGKGKISVNDFIKASA
LACLKVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNAHIKGLETIASDVVSLA
SKAREGKLQPHEFQGGTFTISNLGMFGIKNFSAIINPPQACILAIGASEDKLIPADNEKG
FDVASVMSVTLSCDHRVVDGAVGAQWLAEFKKYLEKPITMLL

>hsa:1737 K00627 pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) DLAT, DLTA, E2, PBC, PDC-E2, PDCE2; dihydrolipoamide S-acetyltransferase (A)

MWRVCARRAQNVAPWAGLEARWTALQEVPGTPRVTSRSGPAPARRNSVTTGYGGVRLCG
WTPSSGATPRNRLLLQLLGSPGRRYYSLPPHQKVPLPSLSPTMQAGTIARWEKKEGDKIN
EGDLIAEVETDKATVGFESLEECYMAKILVAEGTRDVPIGAIICITVGKPEDIEAFKNYT
LDSSAAPTQQAAPAPTPAATASPPTPSAQAPGSSYPHMQVLLPALSPMTMGTVQRWEK
KVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGTPLCIIVEKEADI
SAFADYRPTTEVTDLKPQVPPPTPPPVAAPPTPQPLAPTPSAPCPATPAGPKGRVFSPL
AKKLAVEKGIDLTQVKGTGPDGRITKKDIDSFVPSKVAPAPAAVPPTPGPGMAPVPTGVF
TDIPISNIRRVIAQRLMQSKQTIPHYLSIDVNMGEVLLVRKELNKILEGRSKISVNDFI
IKASALACLKVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNAHIKGVETIAND
VVSLATKAREGKLQPHEFQGGTFTISNLGMFGIKNFSAIINPPQACILAIGASEDKLVPA
DNEKGFDVASMMSVTLSCDHRVVDGAVGAQWLAEFRKYLEKPITMLL

DIHYDROLIPOAMIDE S- SUCCINYLTRANSFERASE

>mmu:78920 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) Dlst, 1600017E01Rik, 4632413C10Rik, 4930529O08Rik, DLTS; dihydrolipoamide S-succinyltransferase (A)
MLSRSRCVSRAFSRSLSAFQKGNCP LGRRSLPGVSLCRGPGYPDNRMVINSGSVFRVRF
FQTAVCKNDVITVQTPAFAESVTEGDVRWEKAVGDAVAEDEVVCEIETDKTSVQVPSPA
NGIIEALLVPDGGKVEGGTPLFTLRKTGAAPAKAKPAETPAPAHKAEPAAAPPPPAAP
VLTQMPPVPSPSQPPSSKPVSAIKPTAAPPLAEAGAAKGLRSEHREKMNRMRQRIAQRLK
EAQNTCAMLTTFNEDMSNIQEMRARHKDAFLKKHNLKLGFM SAFVKASAFALQEQPVVN
AVIDDATKEVVYRDYIDISVAVATPRGLVVPVIRNVETMNYADIERTINELGEKARKNEL
AIEDMDGGTFTISNGGVFGSLFGTPIINPPQSAILGMHAIFDRPVAVGGKVEVRPMMYVA
LTYDHRLIDGREAVTFLRKIKAAVEDPRVLLLDL

>hsa:1743 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) DLST, DLTS, KGD2, PGL7, PPGL7; dihydrolipoamide S-succinyltransferase (A)
MLSRSRCVSRAFSRSLSAFQKGNCP LGRRSLPGVSLCQGPGYPNSRKVVINNSVFSVRFF
RTTAVCKDDLVTVKTPAFAESVTEGDVRWEKAVGDTVAEDEVVCEIETDKTSVQVPSPAN
GVIEALLVPDGGKVEGGTPLFTLRKTGAAPAKAKPAEAPAAAAPKAAPTAAAVPPPAAP
PTQMPPVPSPSQPPSGKPVSAVKPTVAPPLAEPGAGKGLRSEHREKMNRMRQRIAQRLKE
AQNTCAMLTTFNEDMSNIQEMRARHKEAFLKKHNLKLGFM SAFVKASAFALQEQPVVNA
VIDDTTKEVVYRDYIDISVAVATPRGLVVPVIRNVEAMNFADIERTITELGEKARKNELA
IEDMDGGTFTISNGGVFGSLFGTPIINPPQSAILGMHGIFDRPVAIGGKVEVRPMMYVAL
TYDHRLIDGREAVTFLRKIKAAVEDPRVLLLDL

DIHYDROLIPOYL DEHYDROGENASE

>eco:b0116 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) lpd; lipoamide dehydrogenase (A)

MSTEIKTQVVVLGAGPAGYSAAFRCADLGLETVIVERYNTLGGVCLNVGCIPSKALLHVA
KVIEEAKALAEHGIVFGPKTDIDKIRTWKEKVINQLTGGLAGMAKGRKVKVNVNGLGKFT
GANTLEVEGENGKTVINFDNAIIAAGSRPIQLPFIPHEDPRIWDSTDALELKEVPERLLV
MGGGIIGLEMGTVYHALGSQIDVVMFDDQVIPAADKDIVKVFTKRISKKNLMLLETKVTA
VEAKEDGIYVTMEGKKAPAEPQRYDAVLVAIGRVPNGKNLDAGKAGVEVDDRGRFIRVDKQ
LRTNVPHIFAIGDIVGQPM LAHKGVHEGHVAAEVIAGKKHYFDPKVIPSIAYTEPEVAWV
GLTEKEAKEKGISYETATFPWAASGRAIASDCADGMTKLIFDKESHVIGGAIVGTNGGE
LLGEIGLAIEMGCDAEDIALTIHAHPTLHESVGLAAEVFEGSITDLNPNKAKKK

>sce:YFL018C K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) LPD1, HPD1; dihydrolipoyl dehydrogenase (A)

MLRIRSLNNKRAFSSTVRTLTINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGK
LGGTCLNVGCIPSKALLNNSHLFHQMHTAQKRGIDVNGDIKINVANFQKAKDDAVKQLT
GGIELLFKKNKVTTYKNGSGFEDET KIRVTPVDGLEGT VKEDHILDVKNIIVATGSEVTP
FPGIEIDEEKIVSSTGALSLKEIPKRLTIIGGGIIGLEMGSVYSRLGSKVTVVEFQPGIG
ASMDGEVAKATQKFLKKQGLDFKLSTKVISAKRNDKNNVVEIVVEDTKTNKQENLEAEVL
LVAVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDTVFGPMLAHKAE
GIAAVEMLKTGHGHVNNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRA
KTNQDTEGFVKILIDSKTERILGAHIIIPNAGEMIAEAGLALEYGASAEDVARVCHAHPT
LSEAFKEANMAAYDKAIHC

>cel:CELE_LL1.3 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) dld-1; Dihydrolipoyl dehydrogenase, mitochondrial (A)

MSLSRTTQLPFAKRQFFQVLARNYSNTQDADLVVIGGGPGGYVAAIKAAQLGMKTVCVEK
NATLGGTCLNVGCIPSKALLNNSHYLHMAQHDFARGIDCTASLNLPKMMEAKSNSVKQL
TGGIKQLFKANKVGHVEGFATIVGPNTVQAKKNDGSGVETINARNILIASGSEVTPFPGIT
IDEKQIVSSTGALSLGQVPKMMVIGAGVIGLELGSVWQRLGAEVTAVEFLGHVGGMGID
GEVSKNFQRLTKQGFKLLNTKVMGASQNGSTITVEVEGAKDGKKQTLECDTLLVSVGR
RPYTEGLGLSNVQIDLDNRGRVPVNERFQTKVPSIFAIGDVIEGPMLAHKAEDEGILC
VEGIAGGPVHIDYNCVPSVVYTHPEVAWVGKAEELKQEGVAYKIGKFPFVANSRAKTNDQ
EGFVKVLADKQTDRLGLVHIIPNAGEMIAEATLAMEYGASAEDVARVCHPHPTLSEAFR
EANLAAYCGKAINNV

>dme:Dmel_CG7430 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) CG7430; uncharacterized protein, isoform B (A)

MQFTLRHVVSAAVAKTPLRTNAAILGALNARCYSSTHEADIVVIGSGPGGYVAAIKAAQMG

MKTVSVEKEATLGGTCLNVGCIPSKALLNNSHYYHMAHSGDLEKRGISCGSVSLDLEKLM
GQKSNVAVKALTGGIAMLFKKNKVTQLTGFGTIVNPNEVEVKKSDGSTETVTKNLIATG
SEVTPFPGIEIDEEVIVSSTGALKLAKVPKHLVVIGAGVIGLELGSVWSRLGAEVTAIEF
MDTIGGVGIDNEVSKTFQKVLTQQLKFKLGTKVTAASRSGDNVTVSVENAKSGEKEEIQ
CDALLVSVGRRPYTEGLGLEAVGIVKDDRGRIPVNATFQTVVPNIYAIGDCIHGPMLAHK
AEDEGLITIEGINGGHVHIDYNCVPSVYTHPEVAWVGKSEEQLKQEGVAYKVGKFPFLA
NSRAKTNNDTDGFKVLADQATDKILGTHIIGPGAGELINEAVLAMEYGAAAEDVARVCH
AHPTCSEALREANVAAAFGKPINF

>mmu:13382 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) Dld;
dihydrolipoamide dehydrogenase (A)

MQSWSRVYRSLAKKGHFNRISHGLQGVSPLRTYADQPIEADVTVIGSGPGGYVAAIKS
AQLGFKTVICIEKNETLGGTCLNVGCIPSKALLNNSHYYHMAHGKDFASRGIEIPEVRLNL
EKMMEQKHSVAVKALTGGIAHLFKQNKVVHVNGFGKITGKNQVTATKADGSTQVIDTKNIL
VATGSEVTPFPGITIDEDTIVSSTGALSLLKVPEKLVVIGAGVIGVELGSVWQRLGADVT
AVEFLGHVGGIGIDMEISKNFQRILQRQGFKFKLNTKVTGATKKSDGKIDVSVEAASGGK
AEVITCDVLLVCIGRRPFTQNLGLEELGIELDPKGRIPVNNRFQTKIPNIYAIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEFKIGK
FPFAANSRAKTNADTDGMVKILGHKSTDRVLGAHILGPGAGEMVNEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAAAFGKPINF

>hsa:1738 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) DLD, DLDD, DLDH,
E3, GCSL, LAD, OGDC-E3, PHE3; dihydrolipoamide dehydrogenase (A)

MQSWSRVYCSLAKRGHFNRISHGLQGLSAVPLRTYADQPIDADVTVIGSGPGGYVAAIKA
AQLGFKTVICIEKNETLGGTCLNVGCIPSKALLNNSHYYHMAHGKDFASRGIEIEMSEVRLNL
DKMMEQKSTAVKALTGGIAHLFKQNKVVHVNGYGKITGKNQVTATKADGGTQVIDTKNIL
IATGSEVTPFPGITIDEDTIVSSTGALSLLKVPEKMMVVIGAGVIGVELGSVWQRLGADVT
AVEFLGHVGGVGIDMEISKNFQRILQKQGFKFKLNTKVTGATKKSDGKIDVSIEAASGGK
AEVITCDVLLVCIGRRPFTKNLGLEELGIELDPRGRIPVNTRFQTKIPNIYAIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEYKVGK
FPFAANSRAKTNADTDGMVKILGQKSTDRVLGAHILGPGAGEMVNEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAASFGKSINF

FUMARATE HYDRATASE

>eco:b1611 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) fumC; fumarase C (A)
MNTVRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPTSLIHALALTKRAAAKVNE
DLGLLSEEKASAIRQAADEVLAGQHDDEFPLAIWQTGSGTQSNMNMNEVLANRASELLGG
VRGMERKVHPNDDVNKSQSSNDVFPTAMHVAALLALRKQLIPQLKTLTQTLNEKSRAFAD
IVKIGRTHLQDATPLTLGQEISGWVAMLEHNLKHIEYSLPHVAELALGGTAVGTGLNTHP
EYARRVADELAVITCAPFVTAPNKFALATCDALVQAHGALKGLAASLMKIANDVRWLAS
GPRCGIGEISIPENEPGSSIMPGKVNPTQCEALTMLCCQVMGNDVAINMGGASGNFELNV
FRPMVIHNFLQSVRLADGMESFNKHCAVGIEPNRERINQLLNESLMLVTALNTHIGYDK
AAEIAKKAHKEGLTLKAAALALGYLSEAEFDSWVRPEQMVGSMKAGR

>eco:b1612 K01676 fumarate hydratase, class I [EC:4.2.1.2] | (RefSeq) fumA; fumarase A (A)
MSNKPFHYQAPFPLKKDDTEYYLLTSEHVSSEFEGQEILKVAPEALTLLARQAFHDASF
MLRPAHQQQVADILRDPEASENDKYVALQFLRNSDIAAKGVLPTCQDTGTAIIVGKKGQR
VWTGGGDEAALARGVYNTYIEDNLRYSQNAPLDMYKEVNTGTNLPAQIDLYAVDGDYEYKF
LCIAKGGGSANKTYLYQETKALLTPGKLKNYLVEKMRTLGTACPPYHIAFVIGGTS AET
NLKTVKLASAKYYDELPTEGNEHGQAFRDVELEKELLIEAQNGLGAQFGGKYFAHDIRV
IRLPRHGASCPVGMGVSCSADRNIKAKINRQGIWIEKLEHNPGKYIPEELRKAGEGEAVR
VDLNRPMKEILAQLSQYPVSTRLSLNGTIIVGRDIAHAKLKERMMDNGEGLPQYIKDHPIY
YAGPAKTPEGYASGSLGPTTAGRMDSYVDQLQAQGGSMIMLAKGNRSQQVTDACKKHGGF
YLSIGGPAAVLAQGSISLECEVEPELGMEAIWKIEVEDFPFILVDDKGNDFQIQIL
TQCTRCVK

>eco:b1675 K01675 fumarate hydratase D [EC:4.2.1.2] | (RefSeq) fumD; fumarase D (A)
MGNRTKEDELYREMCRVVGKVVLEMRDLGQEPKHIVIAGVLRTALANKRIQRSELEKQAM
ETVINALVK

>eco:b2929 K01774 fumarate hydratase E [EC:4.2.1.2] | (RefSeq) fumE; fumarase E (A)
MATLTEDDVLEQLDAQDNLF SFMKTAHTILLQGIRQFLPSLFVDNDEEIVEYAVKPLLAQ
SGPLDDIDVALRLIYALGKMDKWLYADITHFSQFWHYLNEQDET PGFADDMTWDFISNVN
SITRNAMLYDALKAMKFADFSVWSEARFSGMVKTALT LAVTTTLKELTP

>eco:b4122 K01676 fumarate hydratase, class I [EC:4.2.1.2] | (RefSeq) fumB; fumarase B (A)
MSNKPFIIYQAPFPMGKDNTEYYLLTSDYVSVA DFDGETILKVEPEALTLLAQQA FHDASF
MLRPAHQKQVAAILHDPEASENDKYVALQFLRNSEIAAKGVLPTCQDTGTAIIVGKKGQR
VWTGGGDEETLSKGVYNTYIEDNLRYSQNAALDMYKEVNTGTNLPAQIDLYAVDGDYEYKF
LCVAKGGGSANKTYLYQETKALLTPGKLKNFLVEKMRTLGTACPPYHIAFVIGGTS AET
NLKTVKLASAHHYDELPTEGNEHGQAFRDVQLEQELLEEAQKLGLGAQFGGKYFAHDIRV

IRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIEKLEHNPGQYIPQELRQAGEGEAVK
VDLNRPMKEILAQLSQYPVSTRSLTGTIIVGRDIAHAKLKEIDAGKELPQYIKDHPIY
YAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAKGNRSQQVTDACHKHGGF
YLGSI GGPAAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPFILVDDKGNDDFFQQIVN
KQCANCTK

>sce:YPL262W K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) FUM1; fumarase
FUM1 (A)

MLRFTNCSCKTFVKSSYKLNIRRMNSSFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIG
GARERMPLPLVHAFGVLKKSAIVNESLGGLDPKISKAIQQADEVASGKLDDHFPLVVF
QTGSGTQSNMNANEVISNRAIEILGGKIGSKQVHPNNHCNQSQSSNDTFPTVMHIAASLQ
IQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLTLGQEFSGYVQQVENGIQRV
AHSLKTL SFLAQGGTAVGTGLNTPGFDVKIAEQISKETGLKFQTAPNKFEEALAAHDAIV
ECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELMLENPGSSIMPGKVNPTQNEALTQ
VCVQVMGNNAAITFAGSQGFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGIKANE
PRIHELLTKSLMLVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVV
PEHMLGPK

>cel:CELE_H14A12.2 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) fum-1;
putative fumarate hydratase, mitochondrial (A)

MSAVSMLQGEMLARGGAVIARGASLATARNFSRTTVPMKIRKERDTFGELEV PADKYYG
AQTARSQMNFKIGGPEERMPIPIVHAFGILKKAALVNTEFGLDKKLADAISQAADEVVD
GKLDEHFPLVTWQTGSGTQSNMNVNEVISNRAIEILGGELGSKKPVHPNDHVNMSQSSND
TFPTAMHIAVGREVNSRLLPALKKLRTALHNKAEFEKDIKIGRTHHTQDAVPLTLGQEFS
AYVTQLDNSIARVESTLPRLYQLAAGGTAVGTGLNTRKGFAEKVAATVSELTGLPFVTAP
NKFEALAAHDALVEVHGALNTVAVSFMKIGNDIRFLGSGPRCGLGELSLPENEPGSSIMP
GKVNPTQCEAITMVAQVMGNQVAVSVGGSNGHFELNVFKPLIVRNVLQSTRLLADSAVS
FTDHCVDGIVANKDNIKIMRESLMLVTALNPHIGYDNAAKIAKTAHKNGTTLVQEAVKL
GILTEEQFAQWVKPENMLGPK

>dme:Dmel_CG4094 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) Fum1;
fumarase 1, isoform A (A)

MVLPLLQRSTLRGVQQMTKPWAAIGSLRLASQEFRVESDTFGELKVPADKYYGAQTMRSQ
INFPIGGATERMPKPVVQAMGILKKA AEVNKEFGLDSKVSEAIKAADDVISGKLYDDH
FPLVIWQTGSGTQSNMNVNEVISNRAIELLGGKLGSKTPVHPNDHVNKSQSSNDTFPTAI
HISVALELNNNLKPAIKTLHDALRAKSEFEKDIKIGRTHHTMDAVPLTLGQEFSGYAQQ
AYAQERIDACLPRVYELALGGTAVGTGLNTRKGFAEKCAAKIAELTSLPFVTAPNKFEEAL
AARDAMVEVHGV LNTIAVSLMKIANDIRFLGSGPRCGLGELSLPENEPGSSIMPGKVNPT
QCESLTMLSAQVMGNQVAVTIGGSNGHFELNVFKPLIVSNVLR SIRLLSDGSRTFTANCV
NGIQANRENIKIMNESLMLVTALNPHIGYDKAAKIAKTAHKNGTTLKEEAINLGYLTEQ
QFNDWVRPEQMLGPK

>dme:Dmel_CG4095 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) Fum2;
fumarase 2 (A)
MLKQNNGLHLARRNLWVCSGLRAKDCDSGGKGGKKGKENGKFRTEKDTFGELKVPADKLY
GAQTMRSKLNFPIDIGERMPPVIQAMGILKKACAEVNKDYGLDGKVSDAVSCACDDVI
SGKLYKQGHFPLVIWQTGSGTQTNMNTNEVISNAAIKMMGGELGSKKPVHPNDHVNKSQS
SNDTFPTAIHISVGMELNERLVPVTHLRDALKSKSDEFKDIKIGRTHLMDAVPLTLGQ
EFSGYTQQLTNGLERIKGCLPRVYELALGGTAVGTGLNTRKGFAEKVAKRISELTCLPFV
SAPNKFEALAARDAMVEVHGVNLTIAVSLMKIANDIRLLGSGPRCGLGELMLPENEPGSS
IMPGKVNPTQCESMTMLCAQVMGNQVAVTIGGSNGHFELNVFKPLVVS NVLRSIRLLADG
SMTFSKNCVEGLQANKERIDKIMNESLMLVTALNPHIGYDKAALIAKTAHKNTTLKEEA
LKTGITEEQFKEWVNPKEMLGPK

>dme:Dmel_CG6140 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) Fum3;
fumarase 3, isoform B (A)
MSSTKKVETRQESDTLGPM EVPMDRYYG AQTMRCLINFRIGGEEERM PRQIIQAMGILKK
AAETNQEFGLDPKLSTAISNAADDVISGKLYDEGHFPLPIWQTGSGTQSNMNSNEVIGN
RAIELLGGRIGTKDPVHPNDHVNKSQSSNDTFPSAIIHAVATALT KDLRPAVTALRDSLQ
AKSNEWKDIIKIGRTHTQDAVPLTLGQEFSGYAQQLTNGLQRIDAVLPRVYQLALGGTAV
GTGLNTRRGFAEKC VKRIAQLSGLPFV VAPNFFEALACRDAMVEVHGALNVLA VSLMKVT
NDIRFLGSGPRCGLGELFLPENEPGSSIMPGKVNPTQCEAMT MICAQVMGNHVAVSVGGA
NGHFELNVFKPLIAS NVLRSIKLLADGCISFNCNCVKG IKNKEKLAKIVNESLMLVTAL
NPHIGYDKSAQIAKAAHKN GTTLKVEALNAGISEKDFNEWVRPEKMLGPS

>dme:Dmel_CG31874 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) Fum4;
fumarase 4 (A)
MSFDQKEIFSLMYKLARLIVPDTRVEYDSMGAVHIPLDRMFGPQTM RSLMKFP IGGVEER
MPRPLIKALGIVKKSAAETNKIHCLEEHLCDAISKACDDVISGKLYDEEHFPLVIWQDGS
GEHTNMNVNEVICNRAIEILGGQMGSKEPVDPNEHV NMAQSSHDTFSTAVRIAVAMQLQE
TLYPSLRTFIDLLGKKSNDWMDLIKIGRTHLMDAVPLSLGQEFSGYQQQLVNGRTRLDC A
MCRLYQLPMGGTSVGTKVDTKAEYSAQCIKRIAELTFLPFVESPNFFESISACDCLVELH
GELNTIAASVMKIANDIRFLGSGPRCGFGELHLPENEPGSSIMPGKVNPTQCEAMSMICA
QVMGNHVAVSMGGSSGHFQLNTFMPMIAS NVLRSITLLGDGMKSFCTNCLEGIEPNRSKI
GSIVKESLMLVTALSPHIGYERSAAIAKAAHHNGTTLEQEAILDGIQREDFREWVQPSKM
LGPE

>mmu:14194 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) Fh1, Fh, Fh-1;
fumarate hydratase 1 (A)
MYRALRLLARSRLLRVPSAGAAVS GEATTLPRCAPNVARMASQNSFRVEFDTFGELKVP
TDKYYGAQTVRSTMNFKIGGATERMPIPVIQAFGILKRAAAEVNQEYGLDPKIASAIMKA
ADEVAEGKLNDHFPLVWQTGSGTQTNMNVNEVISNRAIEM LGGELGSKKPVHPNDHVNK

SQSSNDTFPTAMHIAAAVEVHKVLLPGLQKLHDALSAKSKEFAQVIKIGRTHQTQDAVPLT
LGQEFSGYVQQVQYAMVRIKAAMPRIYELAAGGTAVGTGLNTRIGFAEKVAAKVAALTGL
PFVTAPNKFEALAAHDALVELSGAMNTAACSLMKIANDIRFLGSGPRSGLGELILPENEP
GSSIMPGKVNPTQCEAMTMVAAQVMGNHVAVTVGGSNGHFELNVFKPMMIKNVLHSARLL
GDASVSFTDNCVVGIQANTERINKLMNESLMLVTALNPHIGYDKAAKIAKTAHKNGSTLK
ETAIELGYLTAEQFDEWVKPKDMLGPK

>hsa:2271 K01679 fumarate hydratase, class II [EC:4.2.1.2] | (RefSeq) FH, FMRD, HLRCC,
HsFH, LRCC, MCL, MCUL1; fumarate hydratase (A)

MYRALRLLARSRPLVRAPAAALASAPGLGGAAPSWPPNAARMASQNSFRIEYDTFGEL
KVPNDKYYGAQTVRSTMNFKIGGVTERMPTPVIAFGILKRAAAEVNQDYGLDPKIANAI
MKAADVAEGKLNDFPLVWQTGSGTQTNMNVNEVISNRAIEMLGELGSKIPVHPNDH
VNKSQSSNDTFPTAMHIAAAIEVHEVLLPGLQKLHDALDAKSKEFAQIIKIGRTHQTQDAV
PLTLGQEFSGYVQQVKYAMTRIKAAMPRIYELAAGGTAVGTGLNTRIGFAEKVAAKVAAL
TGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMKIANDIRFLGSGPRSGLGELILPE
NEPGSSIMPGKVNPTQCEAMTMVAAQVMGNHVAVTVGGSNGHFELNVFKPMMIKNVLHSA
RLLGDASVSFTENCVVGIQANTERINKLMNESLMLVTALNPHIGYDKAAKIAKTAHKNGS
TLKETAIELGYLTAEQFDEWVKPKDMLGPK

ISOCITRATE DEHYDROGENASE

>eco:b1136 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) icd; isocitrate dehydrogenase (A)

MESKVVVPAQGKKITLQNGKLNVPENPIIPYIEGDGIGVDVTPAMLKVVDAAVEKAYKGE
RKISWMEIYTGEKSTQVYGQDVWLPAETLDLIREYRVAIKGPLTTPVGGGIRSLNVALRQ
ELDLYICLRPVYYYQGTPSPVKHPELTDMMVIFRENSEDIYAGIEWKADSADAEEKVIKFLR
EEMGVKKIRFPEHCGIGIKPCSEEGTKRLVRAAIEYAIANDRDSVTLVHKGNIMKFTEGA
FKDWGYQLAREEFGGELIDGGPWLVKKNPNTGKEIVIKDVIADAFLLQILLRPAEYDVIA
CMNLNGDYISDALAAQVGGIGIAPGANIGDECALFEATHGTAPKYAGQDKVNPGSILSA
EMMLRHMGWTEAADLIVKGMEGAINAKTVTYDFERLMDGAKLLKCSEFGDAIENM

>sce:YDL066W K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) IDP1; isocitrate dehydrogenase (NADP(+)) IDP1 (A)

MSMLSRRLFSTSRLLAFSKIKVKQPVELDGDDEMTRIWDKIKKKLILPYLDVDLKYDDL
SVESRDATSDKITQDAAEAIKKYGVGIKCATITPDEARVKEFNLHKMWKSPNGTIRNILG
GTVFREPIVIPRIPLVPRWEKPIIIGRHAHGDQYKATDTLIPGPSLELVYKPSDPTTA
QPQTLKVYDYKSGSVAMAMYNTDESIEGFAHSSFKLAIDKKLNLFLSTKNTILKKYDGRF
KDIFQEVYEAQYKSKFEQLGIHYEHLIDDMVAQMIKSKGGFIMALKNYDGDVQSDIVAQ
GFGSLGLMTSILVTPDGKTFESEAAHGTVTRHYRKYQKGEETSTNSIASIFAWSRGLLKR
GELDNTPALCKFANILESATLNTVQQDGIMTKDLALACGNERSAYVTTEEFDAVEKRL
QKEKSIE

>sce:YLR174W K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) IDP2; isocitrate dehydrogenase (NADP(+)) IDP2 (A)

MTKIKVANPIVEMDGEQTRIIWHLIRDKLVLPYLDVDLKYDLSVEYRDQTNDQVTVDS
ATATLKYGVAVKCATITPDEARVEEFHLKKMWKSPNGTIRNILGGTVFREPIIIPRIPL
VPQWEKPIIIGRHAFGDQYKATDVIVPEEGELRLVYKSKSGTHDVLKVFDPYEHGGVAM
MMYNTTDSIEGFAKASFELAIERKLPLYSTTKNTILKKYDGKFKDVFEAMYARSYKEKFE
SLGIWYEHRLIDDMVAQMLKSKGGYIIAMKNYDGDVESDIVAQQGFGSLGLMTSVLITPDG
KTFESEAAHGTVTRHFRQHQQGKETSTNSIASIFAWTRGIIQRGKLDNTPDVVKFGQILE
SATVNTVQEDGIMTKDLALILGKSERSAYVTTEEFIDAVESRLKKEFEAAAL

>sce:YNL009W K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) IDP3; isocitrate dehydrogenase (NADP(+)) IDP3 (A)

MSKIKVVHPIVEMDGEQTRVIWKLIEKLILPYLDVDLKYDLSIQERDRTNDQVTKDS
SYATLKYGVAVKCATITPDEARMKEFNLKEMWKSPNGTIRNILGGTVFREPIIIPKIPRL
VPHWEKPIIIGRHAFGDQYRATDIKIKKAGKLRLQFSSDDGKENIDLKVYEFPKSGGIAM
AMFNTNDSIKGFAKASFELALKRKLPLFFTTKNTILKNYDNQFKQIFDNLFDKEYKEKFKQ
ALKITYEHRLIDDMVAQMLKSKGGFIAMKNYDGDVQSDIVAQQGFGSLGLMTSILITPDG

KTFESEAAHGTVTRHFRKHQRGEETSTNSIASIFAWTRAIQRGKLDNTDDVIKFGNLL
KATLDTVQVGGMKTKDALMLGKTNRSSYVTTEEFIDEVAKRLQNMMLSSNEDKKGMCKL

>sce:YNL037C K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) IDH1;
isocitrate dehydrogenase (NAD(+)) IDH1 (A)

MLNRTIAKRTLATAAQAERTLPKKYGGRTVTLPDGDVGKEITDSVRTIFEAEENIPIDW
ETINIKQTDHKEGVYEAVESLKRNIKGLKGLWHTPADQTGHGSLNVALRKQLDIYANVAL
FKSLKGVKTRIPDIDLIVIRENTEGEFSGLEHESVPGVVESLKVMTRPKTERIARFAFDF
AKKYNRKSVTAVHKANIMKLGDGLFRNIITEIGQKEYPDIDVSSIIVDNASMQAVAKPHQ
FDVLVTPSMYGTILGNIGAALIGGPGLVAGANFGRDYAVFEPGSRHVGLDIKGQNVANPT
AMILSSTLMLNHLGLNEYATRISKAVHETIAEGKHTTRDIGGSSSTTDFTEIINKLSTM

>sce:YOR136W K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) IDH2;
isocitrate dehydrogenase (NAD(+)) IDH2 (A)

MLRNTFFRNTSRRFLATVKQPSIGRYTGKPNPSTGKYTVSFIEGDGIGPEISKSVKKIFS
AANVPIEWESCDVSPIFVNGLTTPDAVQSITKNLVALKGPLATPIGKGHRSLNLTLRK
TFGLFANVRPAKSIEGFKTTYENVDLVLIRENTEGEYSGLIEHIVCPGVVQSIKLITRDAS
ERVIRYAFEYARAIGRPRVIVVHKSTIQRLADGLFVNVAKELSKYDPDLTLETIDNSV
LKVVTPNSAYTDAVSVCNLYGDILSDLNSGLSAGSLGLTPSANIGHKISIFEAVHGSAP
DIAGQDKANPTALLSSVMMLNHMGLTNHADQIQNAVLSTIASGPENRTGDLAGTATTSS
FTEAVIKRL

>cel:CELE_C30F12.7 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
idhg-2; Isocitrate dehydrogenase [NAD] subunit, mitochondrial (A)

MFSKLPIQAVRGAASAIRTHQIPGHRPLAKYGGRTVCALPGDGIGPEMIAHIRNIFSF
CHAPVNFEEVQVSSSLLDGMDAAMLAIERNGVAIKGNIETKHDDPQFNSRNVELRTKLD
LYANILHCVTIPTVPTRHSGIDIVLIRENTEGEYSGLEHEAVPGIVESIKIVTREKIERI
SRMAFEYAKANGRKKVTAVHKANIQKLGDGLFLKVVRDMSEDYKDIKFEAMIVDNASMQL
VSKPQQFDVMVMPNLYGNIISNIACGLVGGPGLVSGMNLGDKYAVFETGTRNTGTSLAGK
DIANPTAFIRASVDMLRYLGCHYHANIISDALWKALVEQRIHTADIGGNNSASDVINATL
QNIKVLMDENPKH

>cel:CELE_C34F6.8 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) idh-2; Isocitrate
dehydrogenase [NADP] (A)

MLSRLTSRNVLLARNVATAATQERQKIKVDNPVVDLDGDEMTRIHWKEIKNKLILPYLDL
DIKYYDLGLEJRDETNDQVTIDAHAILEHSGIKCATITPDEARIKEFNLKKMWLSPNG
TIRNILGGTVFREPILCKNIPRLVPGWTQPITIGRHAFGDQYKCTDLVIPSGSTLQLLVN
KPDGSKDVHNVYDFKKSGGVGLAMYNTDESIKGAHSCFQYALMKQWPLYLSTKNILKK
YDGRFKDIFQDIYEKKYEADFKNNKIWYEHRLIDDQVAQALKSSGGFVWACKNYDGDVQS
DIVAQGYGSLGLMSSVLMCPDGKTIEAEAAHGTVTRHYREHQKGNSTSTNPIASIFAWTR

GLHHRGVLDNNEALKTFSLTLEKACIDTVEEGKMTKDLSICIHGTTKKGTEKGAYLITEDF
LSAIDTKMAELMRQD

>cel:CELE_C37E2.1 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) idhb-1;
putative isocitrate dehydrogenase [NAD] subunit beta, mitochondrial (A)
MLSRTVSSLSRVAPQTLGAVNAASSRQYSITAPRPPTELNQKLKVTIIPGDGVGPELIYT
VQDIVKQTGIPIEFEEIFLSEVHYTRSSSIENAVESIGRNNNVALKGAIEESAHLHTEGE
LQGLNMRLRRSLDLFANVVHIKTLDGIKTRHGKQLDFVIVREQTEGEYSSLEHELVPGLV
ECLKISTRRTKAERIAKFAFDYATKTGRKKVTAVHKANIMKLGDGLFLRTCEGVAKQYPKI
QFESMIIDNTCMQLVSKPEQFDVMVMPNLYGNIIDNLAAGLVGGAGVVPQGQSVGRDFVIF
EPGSRHSFQEAMGRSIANPTAMILCAANMLNHLHLDAGWNSLRQAVADVKEGKVRTRDL
GGYATTVDFAVIDKFRI

>cel:CELE_F35G12.2 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
idhg-1; Isocitrate dehydrogenase [NAD] subunit, mitochondrial (A)
MSSNVLGHTLRSSKNVVQKAFVATSPNSDMLRFRSPVLQTNNTKLARYGGRHNVTVLPGD
GIGPEMLHHVERILSAVQAPVDFEVNLTSKEDASEDLAEAITAIKRNGVALKGNIETKF
DNPSFVSRNLELRRQLNLYANVLHCSTIPTVPSRHTGIDMVIIRENTEGEYSGNEHEAVN
APHPRVVESLKVVTREKSEQITRFAFQFAKKYGRKKVTAVHKANIKLGDGLFLKVATDI
AKAEYPDIEFNAMIVDNASMLVSRPQQFDVMLMPNLYGNIISNIACGLVGGPGLVSGMN
IGEDYAVFETGTRNTGTTLGKDLANPTAFIRAADMLRFLGLQSHADMISDSLFRTLVD
KRIHTADIGGTSKSELVQSVLDFIEKELEDNRNYRV

>cel:CELE_F43G9.1 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) idha-1;
putative isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (A)
MLGKCIKKASSTVGQSIRYSSGDVRRVTLIPGDGIGPEISASVQKIFEAADAPIAWDPVD
VTPVKGRDGVFRIPSRICELMHANKVGLKGPLETPIGKGHRSLNLAVRKEFSLYANVRPC
RSLEGHKTLYDNVDVVTIRENTEGEYSGIEHEIVPGVVQSIKLITETASRNVASFAFEYA
RQNGRKVVTAHVKANIMRQSDGLFLSICREQAALYPDIKFKEAYLDTVCLNMVQDPSQYD
VLVMPNLYGDILSDLCAGLVGGLGVTPSGNIGKGAAVFESVHGTAPDIAGQDKANPTALL
LSAVMMLRYMNLQPQHAARIEKAVFDAIADGRAKTGDLGGTGTCSSTADVCAVVKDLE

>cel:CELE_F59B8.2 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) idh-1; Isocitrate
dehydrogenase [NADP] (A)
MRPFLACSSLARHVFRGFTTTNMAAAQKIQGGDIVEMQGDDEMTRIWDLIKEKLILPYVD
LNVHFFDLGIEHRDATDDQVTIDAANATLKYNVAVKCATITPDEARVEEFKLKKMWKSPN
GTIRNILGGTVFREPIIVKNVPRLVNTWSKPPIIGRHAHADQYKATDFVVPAGKLEIKF
VSADGTQTIQETVDFDKGPGVSLSMYNTDDSIKDFAHASFYALQRKFPLYLSTKNTILK
KYDGRFKDIFAEIYPEYEAFAAGIWEYHRLIDDMVAQAMKSDGGFWACKNYDGDVQS
DSVAQGYGSLGLMTSVLVCPDGKTVEAEAAHGTVTRHYRMHQKGQETSTNPIASIFAWSR

GLAHRATLDKNSALETFANNLEAVCIETMEAGFLTKDLAICVKGGNASAVTRTDYLNTE
FLDKLAENLAKKQAH

>dme:Dmel_CG3483 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
CG3483; uncharacterized protein (A)
MNTLRKLNSLPPFRSVGGAYRLFAGKDQKKDSAGQKTRQPEKPPQDKQKSKGASGKAKSA
GSTDSAKKTTKVTLINGEGVGRELMDAVQEIVCAVKAPIEWDVHDEFKAKDSDDVSPEVL
KSLRANKVGIKGPVDSRHWQRQIRKQFAQFAYVSLCSHIEGLDSPYGDFFDVIIIRDQMEG
DYSGIEHLVVPVGMQTIKVSTTAGAARIAEFVFNYAVKNKRKRITVAHKANIMRMTDGNF
LEAMRAEADKHVDDVLFEEERYLDTCILKILLKPHKCDVMVSSSMYGDVLRVIAGGMMGV
GICPGYSVSSLGTVFDCRMKACHALAGKDLANPTGPLLSAALMLRHVKMDKQADQVDCAI
RKVYKDTDIRTPDVGGKAKCSEFVKAVCDCL

>dme:Dmel_CG5028 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3g;
isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit gamma, isoform B (A)
MALRLTQRLQTQTPFLTRGYPLLVTKEKTEDVAHTKSALQKKVTGTDIPSAQYGGRHAV
TMLPGGGIGPELMGYVREIFRYCGAPIDFEVIDIDPSTEGNDDLDYAITSIKRNGVALKG
NIETKSQSLTEVSRNVAIRNELDLYVNVVHCKSYPGIPARHHDIDVVLIRQNTDGEYAML
EHESVPGIVESMKVVTVENAERVARYAFEFARQNNRKKVTTIHKANIMKLSDGLFLEVAN
RVHKDYPELEHNNMIIDNTCMQSVSNPHQFDVMNMTNLYGTIVSNVLCGLMGGAGLISGR
NYGDHYAIFEPGTRNTGTAIAGKNIANPVAMISASIDMLNHLGHKEHANVIQEAVYQTIV
NDAIRTPDIGGTNSSTDVVENILKILSAKRVNWPBGNYFSQI

>dme:Dmel_CG6439 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3b;
isocitrate dehydrogenase 3b, isoform B (A)
MSMLARTVGRFTMQAAAARSLHTTSTLRATDNYGANRTTCTLIPGDGVGPELVYSLQEVE
KAASVPVDFECYFLSEINPVLSAKLEDVVASIQKNKVCIKGVLATPDYSNVGDLQTLNMK
LRNDLDLYANVVHVRSLPGVKTRHTNIDTVIIREQTEGEYSALEHESVPGIVECLKIITA
KKSMRIAKFAFDYATKNQRKKVTAVHKANIMKLGDGLFLRSCEEVSRLYPRIQFEKMIVD
NTTMQMVSNNPNQFDVMVTPNLYGAIVDNLASGLVGGAGVVAGASYSSSESVVFEPGARHTF
AEAVGKNVANPTAMLLCGVKLLRHINLPTYGEIIQNAINKVLNDGKVRTKDLGGQSTTQD
FTRAILNMS

>dme:Dmel_CG7176 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) Idh; isocitrate
dehydrogenase, isoform K (A)
MFALRRTAAMMTSVHRQPHLSQAVFRANFAISAADPKTHKISMDNERMSAVSEHSSVCS
PEQMAQKIKAGPVVDVLGDEMTRIWDSEIKSQLILPFLDIELHTYDLGIENRDKTEDQVT
IDCAEAIKKYNVGIKCATITPDEKRVEEFNLKMMWKSPNGTIRNILGGTVFREAICKNV
PRLVTGWQKPIVIGRHAHADQYKAVDYVVPVPGPKLTLTWKGTDGQVIDEVINDFKGPGIA
LGMFNTDDSIVDFAHASFKYALDRKLPLYMSTKNTILKKYDGRFKDIFEDLYNKQYKKEY

EAAGIWYEHRLIDDMVAYAMKSEGGFWACKNYDGDVQSDSVAQGYGSLGLMTSVLLCPD
GKTVEAEAAHGTVTRHFRFYQQGKETSTNPIASIFAWTRGLLHRAKLDNNEPLKQFADTL
EQVCIDTIESGAMTKDLAICIKGNINAVTRRDYQETFEFINTLAKNLEGALAKNAVAAK

>dme:Dmel_CG12233 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
ldh3a; isocitrate dehydrogenase 3a, isoform D (A)

MAARFIQKILNQLGLIAARDAPAVTATPAVSQVNATPAASRSYSSGTTKKVTLIPGDGIGP
EISAAVQKIFTAANVPIEWEAVDVTVPVRGPDGKFGIPQAAIDSVNTNKIGLKGPLMTPVG
KGHRSLNLALRKEFNLYANVRPCRSLEGYKTLYDDVDVVTIRENTEGEYSGIEHEIVDGV
VQSIKLITEEASKRVAEYAFQYAKNNNRKKVTVVHKANIMRMSDGLFLRCVRDMAQKFPE
IQFEEKYLDTVCLNMVQNPVKYDVLVMPNLYGDILSDMCAGLVGGLGLTPSGNMGLNGAL
FESVHGTAPDIAGKDLANPTALLLSAVMMLRHMELENTYADKIERAAFETIKEGKYLTGDL
GGRACSEFTNEICAKL

>dme:Dmel_CG32026 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
CG32026; uncharacterized protein (A)

MSGNWFKWTALHGRPRTVGLNTNGRILRLDDAVVRFRQPFYESWRRRRRLEDIEKREIP
VRQQVPRIRHNRCPGAKENPCRKMPSVLPKGGEVLVPSRIQPPRNSMGFSVIRLFGSSTN
DGGSGEPPENREGKLIKFTVGSRIAKPKTGKIEISKKGPLGFETTKLPVQESLPQSDYLS
GLSKKSPDKDTPDSTTQASDRSGKEGNEEKIKDDIPRSFSEYIIHWDSESKNPSGIQS
QQPERCESAGNPPSGGKPPPTKPPTGPSTPSGPSNPSRPPSRKDNNPFSGMGSEPPKKPPL
GSKPPSKLPPRSTSPKKPPTGSTPPQKPTKSSKPPNKPAPGPGKKSASKPPTASKPPVKS
PAGGQQGQGGAGGKSGKASGEPRVITLMPGDGIGPEISMAVIKILEAAKTPLIFEPVDVT
PVLNSQGMTSVPEQVIESMNRTKVGLKGPLMTPVGTGFRSLNLTNRQLFNLYANIRPCRS
LPGVETVYGDVDIVTIRENTEGEYSGIEHTLVNGVVQSIKLITRNASLRVAEYTFQYALA
MKRKKVTAVAESQVMRMSDGLFLRCVREMAAKYKSKMDQAGIKYEESTMTTVCLNIVQDP
KRYDMLVLPNLYGDIISDTCAGLIGGLGLTPSGNVGTNGAIFESVHGTAPDIAGKDLANP
TALLSSVMMLHYIGLHEHADKIEKAVLKTIRDDNIRTMDLGGKAKCSEYTDALIKNLK

>mmu:15926 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) ldh1, E030024J03Rik,
ld-1, ldh-1, ldpc; isocitrate dehydrogenase 1 (NADP+), soluble (A)

MSRKIQGGSVVEMQGDDEMTRIWEELIKEKLILPYVELDLHSYDLGIENRDATNDQVTKDA
AEAIIKYNVGVKCATITPDEKRVEEFKLKQMWKSPNGTIRNILGGTVFREAIICKNIPRL
VTGWVKPIIIGRHAYGDQYRATDFVVPGPVKVEITYTPKDGTTQKVTYMVHDFEEGGGVAM
GMYNQDKSIEDFAHSSSQMALSKGWPLYLSTKNTILKKYDGRFKDIFQEIYDKKYKSQFE
AQKICYEHRLIDDMVAQAMKSEGGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLICPDG
KTVEAEAAHGTVTRHYRMYQKGQETSTNPIASIFAWSRGLAHRKLDNNTLSFFAKALE
DVCIIETIEAGFMTKDLAACIKGLPNVQRSDYLNTFEFMDKLGENLKAKLAQAKL

>mmu:15929 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3g;
isocitrate dehydrogenase 3 (NAD+), gamma (A)
MALKVAIAAGGAAKAMLKPTLLCRPWEVLAHVAPRRSISQQTIPPSAKYGGRHTVTMI
PGDGIGPELMLHVKS VFRHACVPVDFEEVHVSSNADEEDIRNAIMAIRNRVALKGNIET
NHNLP PSHKSRNNILRTSLDLYANVIHCKSLPGVVTRHKDIDILIVRENT EGEYSSLEHE
SVAGVVESLKIITKAKSLRIA EYAFKLAQESGRKKVTAVHKANIMKLG DGLFLQCCREVA
AHYPQITFDSMIVDNTTMQLVSRPQQFDVMVMPNLYGNIVNNVCAGLVGGPGLVAGANYG
HVYAVFETATRNTGKSIANKNIANPTATLLASCMMLDHLKLHSYATSIRKAVLASMDNEN
MHTPDIGGGQGTTSQAIQDIIRHIRIINGRAVEA

>mmu:67834 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3a,
1110003P10Rik, 1500012E04Rik; isocitrate dehydrogenase 3 (NAD+) alpha (A)
MAGSAWVSKVSRLLGAFHNTKQVTRGFAGGVQTVTLIPGDGIGPEISASVMKIFDAAKAP
IQWEERNVTAIQGPGGKWMIPPEAKESMDKNKMGLKGPLKTPIAAGHPSMNLRLKTFDL
YANVRPCVSIEGYKTPYTDVNIVTIRENT EGEYSGIEHVIVDGVVQSIKLITEEASKRIA
EFAFEYARNNHRSNVTAVHKANIMRMSDGLFLQKCREVAENCKDIKFNEMYLDTVCLNMV
QDPSQFDVLVMPNLYGDILSDLCAGLIGGLGVTPSGNIGANGVAIFESVHGTAPDIAGKD
MANPTALLLSAVMMLRHMGLFDHAAKIEAACFATIKDGKSLTKDLGGNAKCSDFTEEICR
RVKDLD

>mmu:170718 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3b;
isocitrate dehydrogenase 3 (NAD+) beta (A)
MAALSNVRWLTRAVLAARNSGAWRGLGTSTAHAAQSQAQDVRVEGAFFVTMLPGDGVGP
ELMHAVKEVFKA AAVPVEFKEHHLSEVQNMASEEKLEQVLSSMKENKVAIIGKIYTPMEY
KGELASYDMQLRRKLDLFANVVHVKS LPGYKTRHNNLDLVIREQTEGEYSSLEHESAKG
VIECLKIVTRTKSQRIAKFAFDYATKKGRSKVTAVHKANIMKLG DGLFLQCCEEVAELYP
KIKFETMIIDNCCMQLVQNPYQFDVLVMPNLYGNIIDNLAAGLVGGAGVVPGESYSAEYA
VFETGARHPFAQAVGRNIANPTAMLLSATNMLRHLNLEYHSSMIADAVKKVIKAGKVRTS
DMGGYATCHDFTEAVITALS

>mmu:243996 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
4933405O20Rik; RIKEN cDNA 4933405O20 gene (A)
MLAVTSCSMKTVLQYAVFLGHSREVVC ELVTSFRSFCSHCAVPPSPKYGGRHTVAMIPGD
GIGPELMVHVKKIFRSNCVPVDFEEVWVTSTSN EEEINNALMAIRNRNRVALKGNIATNHN
LPARYKSHNTKFRTILDLYASVVHFKTFPGVMTRHKDIDILVVRENT EGEYTNLEHESVK
GVVESLKIVTKTKSVRIADYAFKLAQKMGRKKVTVVHKANIMKLG DGLFLQCKDVAAHY
PQITLESMIIDNTTMQLVSKPQQFDVMVMPNLYGNIINSICTGLVGGSGIVPGANYGDSY
AIFEMGSKEIGKDLAHRNIANPVAMLLTSCIMLDYLDLQPYATHIRSAVMASLQNKAVCT
PDIGGGQGN TASTVEYILHMHMKEQTSGCHPNFFLQFT

>mmu:269951 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) Idh2, E430004F23, IDPm, Idh-2; isocitrate dehydrogenase 2 (NADP+), mitochondrial (A)
MAGYLRVSSLCRASGSARTWAPAALTVPSPWEQPRRHAYAEKRIKVEKPVVEMDGDDEMTR
IIWQFIKEKLILPHVDVQLKYFDLGLPNRDQTNDQVTIDSALATQKYSVAVKCATITPDE
ARVEEFKLKMMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGWTKPITIGRHAHGDQYK
ATDFVVDRAAGTFKLVFTPKDGSSAKEWEVYNFPAGGVGMGMYNNTDESISGFAHSCFQYSI
QKKWPLYLSTKNILKAYDGRFKDIFQEIFDKHYKTDFDKNKIWYEHRLIDDMVAQVLKS
SGGFVWACKNYDGDVQSDILAQQFGSLGLMTSVLPCPDGKTIEAEAAHGTVTRHYREHQB
GRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIRFAQTLEKVCVQTVESGAMTKDLAGCIH
GLSNVKLNEHFLNTTDFLDTIKSNLDRALGKQ

>hsa:3417 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) IDH1, HEL-216, HEL-S-26, IDCD, IDH, IDP, IDPC, PICD; isocitrate dehydrogenase (NADP(+)) 1 (A)
MSKKISGGSVVEMQGDDEMTRIIEWELIKEKLIFPYVELDLHSYDLGIENRDATNDQVTKDA
AEAIKHNHVGKCATITPDEKRVVEEFKLKQMMWKSPNGTIRNILGGTVFREAIICKNIPRL
VSGWVKPIIIGRHAYGDQYRATDFVVPGPVKVEITYTPSDGTQKVTVLVHNFEEGGGVAM
GMYNQDKSIEDFAHSSSQMALSKGWPLYLSTKNILKKYDGRFKDIFQEIDKQYKSQFE
AQKIWYEHRLIDDMVAQAMKSEGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLVPCPDG
KTVEAEAAHGTVTRHYRMYQKGQETSTNPIASIFAWTRGLAHRKLDNNKELAFFANALE
EVSITIEAGFMTKDLAACIKGLPNVQRSDYLNTFEFMDKLGKLNKIKLAQAKL

>hsa:3418 K00031 isocitrate dehydrogenase [EC:1.1.1.42] | (RefSeq) IDH2, D2HGA2, ICD-M, IDH, IDH-2, IDHM, IDP, IDPM, mNADP-IDH; isocitrate dehydrogenase (NADP(+)) 2 (A)
MAGYLRVVRSLCRASGSRPAWAPAALTAPTSQEPRRHAYADKRIKVAKPVVEMDGDDEMTR
IIWQFIKEKLILPHVDIQLKYFDLGLPNRDQTDDQVTIDSALATQKYSVAVKCATITPDE
ARVEEFKLKMMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGWTKPITIGRHAHGDQYK
ATDFVADRAAGTFKMFVFTPKDGSGVKEWEVYNFPAGGVGMGMYNNTDESISGFAHSCFQYAI
QKKWPLYMSTKNILKAYDGRFKDIFQEIFDKHYKTDFDKNKIWYEHRLIDDMVAQVLKS
SGGFVWACKNYDGDVQSDILAQQFGSLGLMTSVLPCPDGKTIEAEAAHGTVTRHYREHQB
GRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIRFAQMLEKVCVETVESGAMTKDLAGCIH
GLSNVKLNEHFLNTTDFLDTIKSNLDRALGRQ

>hsa:3419 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) IDH3A, RP90; isocitrate dehydrogenase (NAD(+)) 3 catalytic subunit alpha (A)
MAGPAWISKVSRLLGAFHNPKQVTRGFTGGVQTVTLIPGDGIGPEISAAVMKIFDAAKAP
IQWEERNVTAIQGPGGKWMIPSEAKESMDKNKMGLKGPLKTPIAAGHPSMNLRLKTFDL
YANVRPCVSIEGYKTPYTDVNIVTIRENTEGEYSIEHVIVDGVVQSIKLITEGASKRIA
EFAFEYARNNHRSNVTAVHKANIMRMSDGLFLQKCREVAESCKDIKFNEMYLDTVCLNMV
QDPSQFQDVLMVPMNLYGDILSDLCAGLIGGLGVTPSGNIGANGVAIFESVHGTAPDIAGKD
MANPTALLLSAVMMLRHMGLFDHAARIEAACFATIKDGKSLTKDLGGNAKCSDFTEEICR
RVKDLD

>hsa:3420 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) IDH3B, RP46;
isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit beta (A)
MAALSGVRWLTRALVSAGNPGAWRGLSTSAAHAASRSQAEDVRVEGSFPVTMLPGDGVG
PELMHAVKEVFKAAPVEFQEHHLSEVQNMASEEKLEQVLSSMKENKVAIIGKIHTPME
YKGELASYDMRLRRKLDLFANVVHVKSPLGYMTRHNNLDLVIIREQTEGEYSSLEHESAR
GVIECLKIVTRAKSQRIAKFAFDYATKKGRGKVTAVHKANIMKLGDGLFLQCCEEVAELY
PKIKFETMIIDNCCMQLVQNPYQFDVLVMPNLYGNIIDNLAAGLVGGAGVVPGESYSAEY
AVFETGARHPFAQAVGRNIANPTAMLLSASNMLRHLNLEYHSSMIADAVKKVIKVGKVRT
RDMGGYSTTTDFIKSVIGHLQTKGS

>hsa:3421 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) IDH3G, H-IDHG;
isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit gamma (A)
MALKVATVAGSAAKAVLGPALLCRPWELGAHEVPSRNIFSEQTIPPSAKYGGRHTVTMI
PGDGIGPELMLHVKS VFRHACVPVDFEEVHVSSNADEEDIRNAIMAIRNRVALKGNIET
NHNLP PSHKSRNNILRTSLDLYANVIHCKSLPGVVTRHKDIDILIVRENTAGEYSSLEHE
SVAGVVESLKIITKAKSLRIA EYAFKLAQESGRKKVTAVHKANIMKLGDGLFLQCCREVA
ARYPQITFENMIVDNTTMQLVSRPQQFDVMVMPNLYGNIVNNVCAGLVGGPGLVAGANYG
HVYAVFETATRNTGKSIANKNIANPTATLLASCMMLDHLKLHSYATSIRKAVLASMDNEN
MHTPDIGGQGTTSEAIQDVIRHIRVINGRAVEA

MALATE DEHYDROGENASE

>eco:b2210 K00116 malate dehydrogenase (quinone) [EC:1.1.5.4] | (RefSeq) mqo;

malate:quinone oxidoreductase (A)

MKKVTAMLFMAVGLNAVSMMAKAKASEEQETDVLLIGGGIMSATLGTYLRELEPEWSMT
MVERLEGVAQESSNGWNNAGTGHSALMELNYTPQNADGSISIEKAVAINAEAFQISRQFWA
HQVERGVLRTPRSFINTVPHMSFVWGEDNVNFLRARYAALQQSSLFRGMRYSEDHAQIKE
WAPLVMGRDPQKQVAATRTEIGTDVNYGEITRQLIASLQKKS NFSLQLSSEVRALKRND
DNTWTVTVADLKNGTAQNIRAKFVFIGAGGAALKLLQESGIPEAKDYAGFPVGGQFLVSE
NPDVVNHHLAKVYGKASVGAPPMSVPHIDTRVLDGKRVLFGPFATFSTKFLKNGSLWDL
MSSTTTSNVMPMMHVGLDNFDLVKYLVSQVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQ
RVQIIKRDAEKGGVLRRLGTEVVSDQQGTIAALLGASPGASTAAPIMLNLEKVFGRVSS
PQWQATLKAIVPSYGRKLNGDVAATERELQYTSEVLGLNYDKPQAADSTPKPQLKPQPVQ
KEVADIAL

>eco:b3236 K00024 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) mdh; malate

dehydrogenase (A)

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSG
EDATPALEGADVVLISAGVARKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNP
VNTTVAIAAEVLKKAGVYDKNKLFVTTLDIIRSNTFVAELKGKQPGEVEVPVIGGHSGV
TILPLLSQVPGVSFTEQEVA DLTKRIQNAGTEVVEAKAGGGSATLSMGQAAARFGLSLVR
ALQGEQGVVECAYVEGDGQYARFFSQPLLLGKNGVEERKSIGTLSAFEQNALEGMLDTLK
KDIALGEEFVNK

>sce:YDL078C K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) MDH3; malate

dehydrogenase MDH3 (A)

MVKVAILGASGGVGQPLSLLLKLSPIYSELALYDIRAAEGIGKDLSHINTNSSCVGYDKD
SIENTLSNAQVVLIPAGVPRKPGLTRDDL FKMNAGIVKSLVTAVGKFAPNARILVISNPV
NSLVPIAVETLKKMGKFKPGNVMGVTNLDLVRAETFLVDYMLKNPKIGQE QDKTTMHRK
VTVIGGHSGETIPIITDKSLVFQLDKQYEHFIHRVQFGGDEIVKAKQGAGSATLSMAFA
GAKFAEEVLR SFHNEKPETESLSAFVYLPGLKNGKKAQQLVGDNSIEYFSLPIVLRNGSV
VSIDTSVLEKLSPREEQLVNTAVKELRKNIEKGKSFILDSSKL

>sce:YKL085W K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) MDH1; malate

dehydrogenase MDH1 (A)

MLSRVAKRAFSSTVANPYKVTVLGAGGGIGQPLSLLLKNHKVTDLRLYDLKGAKGVATD
LSHIPTNSVVKGFTPEEPDGLNNALKD TDMVLIPAGVPRKPGMTRDDLFAINASIVRDLA
AATAESAPNAAILVISNPVNSTVPIVAQVLKNKGVYNPKKLFGVTTLDSIRAARFISEVE
NTDPTQERVNVIGGHSGITIIP LISQTNHKLMSDDKRHELIHRIQFGGDEVVKAKNGAGS
ATLSMAHAGAKFANAVLSGFKGERDVIEPSFVDSPLFKSEGIEFFASPVTLGPDGIEKIH

PIGELSSEEEEMLQCKETLKKNIEKGVNFBASK

>sce:YOL126C K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) MDH2; malate dehydrogenase MDH2 (A)

MPHSVTPSIEQDSLKIAILGAAGGIGQSLSLLLKAQLQYQLKESNRSVTHIHLALYDVNQ
EAINGVTADLSHIDTPISVSSHSPAGGIENCLHNASIVVIPAGVPRKPGMTRDDLFNVNA
GIISQLGDSIAECCDLSKVFLVISNPVNSLVPVMVSNILKNHPQSRNSGIERRIMGVTK
LDIVRASTFLREINIESGLTPRVNSMPDVPVIGGHSGETIIPLFSQSNFLSRLNEDQLKY
LIHRVQYGGDEVVKAKNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQIHGTYVPLKDAN
NFPIAPGADQLLPLVDGADYFAIPLTITTKGVSYVDYDIVNRMNDMERNQMLPICVSQK
KNIDKGLEFVASRSASS

>cel:CELE_F20H11.3 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) mdh-2; Malate dehydrogenase, mitochondrial (A)

MSLPAKTLVQAAANSGLRAVSVRHSSQAPKVALLGAAGGIGQPLGLLLKQDPLVAHLALY
DVVNTPGVAADLSHIDSNKVTHTGPKELYAAVENADVIVIPAGVPRKPGMTRDDLFNT
NAGIVRDLAAVIAKASPKALIAITNPVNSTVPIASEVLKKAGVYDPKRVFGVTTLDVVR
SQAFVSELKGHDAKSTVVPVVGGHAGITIIPLLSQVKPSTKFSEEEISKLTPIQDAGTE
VVNAKAGAGSATLSMALAGARFANALVRGIKGEKNVQCAYVASDAVKGVEYFSTPVELGP
NGVEKILGVGKVSAYEQKLIDASVPELNKNIAKGVAFAVKGN

>cel:CELE_F46E10.10 K00025 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) mdh-1; Malate dehydrogenase, cytoplasmic (A)

MSAPLRVLVTGAAGQIGYSIVIRIADGTVFGKEQPVELVLLDVPQCSNILEGVVFELQDC
ALPTLFSVAVTDEKSAFTGIDYAFVLGAMPRREGMERKDLLAANVKIFKSQGKALAEYA
KPTTKVIVVGNPANTNAFIAAKYAAGKIPAKNFSAMTRLDHNRALAQLALKTGTTIGNVK
NVIIWGNHSGTQFPDVTHATVNKNGTETDAYAAVGDNALQGPFIATVQKRGGVIIKCRK
LSSAMSAAKAACDHIHDWHFGTKAGQFVSMAPSDGSYGIPQGLIFSPVTIEGGEWKIV
QGLSFDDFAKGKIAATTKELEEERDDALKACDDANI

>dme:Dmel_CG5362 K00025 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) Mdh1; malate dehydrogenase 1, isoform B (A)

MAEPIRVVVTGAAGQIAYSLLYMIARGEVFGKDQPIVLHLLDIPPMVGVLEGVVMELADC
ALPLLVEVPTTDPVAGFKDVSAFLVGAMPRKEGMERKDLLSANVKIFRTQGGALDKFA
KKDKVKVLVGNPANTNALVCSSYAPSIPRENFSAMTRLDQNRATSQIAAKLGVPISAVKN
IIIWGNHSSTQYPDAGQAKVTANGTVKSVVDAINDNGYLQGSFVETVQKRGAAVIAARKM
SSAMSAAKAACDHMHDDWNGTAPGQFVSMGVFSDGSYDSPKDVIFSFPVEIKNKQWKIVS
GLTLSDFAKTKLSVTGKELQEEKDEALSVLDSNVSNL

>dme:Dmel_CG7998 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) Mdh2; malate dehydrogenase 2 (A)

MLKQVTKQLALQGVRTFSVGQQNNYKVTVCGAAGGIGQPLSLLLKQNPLVTDLALYDIVH
TPGVAADLSHIDTKSKTAGFIGADQLGDSLKGSDVVVIPAGVPRKPGMTRDDLNFVNAGI
IKDISNSIAKNCPKALVAITNPVNTCVPIAAEILKKAGVYDPKRLFGVSTLDVVRARAF
IGHALGVDPQTVQIPVIGGHSGVTILPVLSQSQPLFKGNQDTIEKLTVRIQEAGTEVVKA
KAGAGSATLSMAYAGARFAGSLLKGLNGEKNVIECSYVQSTVTEATFFSTPLVLGKNGVQ
ENLGLPKLNDYEKKLLEAAIPELKKNIQKGIDFANA

>dme:Dmel_CG10748 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) CG10748; uncharacterized protein (A)

MLLLTSLKSLAKPATWGVVVRTLKVAVVGAGGGIGQPLSLLLRCPGIDELALHDLSEMK
GIATDLSHISQTGKVIQFTGEKELESASVGADVVAAGMPRLPGMQRDHLMAANGNVAV
KVATAISNASPRAHLAFITNPVNMIVPAAAEVLMAHGTFDSRRLFGITTLDVVRSKKFIG
DSMNISPDDVNIPVIGGHAGITILPLISQCQPIYRCDLQEIQNLTHRIQEAGTEVVNAKA
GKGSATLSMAYAGATFVNSLLRGIAGQDGLIECAFVASKLTDAPFFASPLELGKDGKRY
IPLPQMSDYEKEALEKLLPILRQNADEGVNFAKMILSGQSHSPIAALP

>dme:Dmel_CG10749 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) CG10749; uncharacterized protein (A)

MFLASRLLSHVGNLPPKVQQLGYINRGLKVAVVGSVGGIGQPLSLLLKHNPIQISTLSLYD
IKNTTGVGVDLSHINTRASVCPFEGKNGLLKKAMDKADIVVIPAGLPRKPGMKREDLVDVN
ASVACEVAFAASEVCPGAMLAFITNPINVIVPIVATILKAKGTYDPNRLFGVTTLDVVRA
QTFVADILNVDPQKVNIPIVIGGHTGRTILPILSQCDPPFKGTDKEREALIQRIQNAGTEV
VNAKDGLGSATLSMAFAATQFVSSLIKIGKSGKDECIVECAYVESDVTEAQFFATPLILG
PQGVKENTGLPDLDDDEERKALNGMLPILKESIAKGIKLGEGMICSCA

>mmu:17448 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) Mdh2, MDH, Mdh-2, Mor-1, Mor1; malate dehydrogenase 2, NAD (mitochondrial) (A)

MLSALARPAGAALRRSFSTSAQNNAKVAVLGASGGIGQPLSLLLKNSPLVSRLTYDIAH
TPGVAADLSHIETRANVKGYLGPEQLPDCLKGCDVVVIPAGVPRKPGMTRDDLNFNTATI
VATLTAACAQHCPEAMVCIANPVNSTIPITAEVFKKHGVYNPNKIFGVTTLDIVRANTF
VAELKGLDPARVNPVIGGHAGKTIPLISQCTPKVDFPQDQLATLTGRIQEAGTEVVKA
KAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVQSKETECTYFSTPLLLGKKGLE
KNLGIGKITPFEEKMIAEAIPELKASIKKGEDFVKNMK

>mmu:17449 K00025 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) Mdh1, B230377B03Rik, KAR, MDH-s, MDHA, Mor-2, Mor2; malate dehydrogenase 1, NAD (soluble) (A)

MSEPIRVLTGAAGQIAYSLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMEQLDC
ALPLLQDVIAATDKEEIAFKDLDVAVLVGSMPPREGMERKDLLKANVKIFKSQGTALEKYA

KKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCLTRLDHNRKASQIALKLGVTADDVKN
VIIWGNHSSTQYPDVNHAKVKLQGKEVGVEALKDDSWLKGEFITTQQRGAAVIKARKL
SSAMSAAKAIADHIRDIWFGTPEGEFVSMGVISDGNSYGVPPDLLYSFPVVIKNKTKWKFV
EGLPINDFSREKMDLTAKELTEEEKETAFAFEFLSSA

>hsa:4190 K00025 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) MDH1, DEE88, EIEE88,
HEL-S-32, KAR, MDH-s, MDHA, MGC:1375, MOR2; malate dehydrogenase 1 (A)
MSEPIRVLVTGAAGQIAYSLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMEQLDC
ALPLLKDVIATDKEDVAFKDLVDAILVGSMPPREGMERKDLLKANVKIFKSQGAALDKYA
KKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCLTRLDHNRKAAQIALKLGVTANDVKN
VIIWGNHSSTQYPDVNHAKVKLQGKEVGVEALKDDSWLKGEFVTTVQQRGAAVIKARKL
SSAMSAAKAICDHVRDIWFGTPEGEFVSMGVISDGNSYGVPPDLLYSFPVVIKNKTKWKFV
EGLPINDFSREKMDLTAKELTEEEKESAFEFLSSA

>hsa:4191 K00026 malate dehydrogenase [EC:1.1.1.37] | (RefSeq) MDH2, DEE51, EIEE51,
M-MDH, MDH, MGC:3559, MOR1; malate dehydrogenase 2 (A)
MLSALARPASAALRRSFSTSAQNNAKVAVLGASGGIGQPLSLLLKNSPLVSRLTYDIAH
TPGVAADLSHIETKAAVKGYLGPEQLPDCLKGCDVVIPAGVPRKPGMTRDDLFNTNATI
VATLTAACAQHCPEAMICVIANPVNSTIPITAEVFKKHGVYNPNKIFGVTTLDIVRANTF
VAELKGLDPARVNPVIGGHAGKTIPLISQCTPKVDFPQDQLTALTGRIQEAGTEVVKA
KAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGIE
KNLGIGKVSSFEKMSDAIPELKASIKKGEDFVKTLK

OXOACID DEHYDROGENASE ACETYLTRANSFERASE

>cel:CELE_C30H6.7 K00627 pyruvate dehydrogenase E2 component
(dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) dlat-2; 2-oxoacid
dehydrogenase acyltransferase catalytic domain-containing protein (A)
MLAGSQALRHLSTAAQNQGACGPAVKLLLIQYGLENRKIDGTGPKNKNILKGDVMKIVEA
EKLKPVAAHHAHAPKETHIENKSIEKKSDIFGANNRSLRHHQDIPLSNIRATIAKRLTASK
QQIPHEYQGVDVRIDDILALRQKLKSGTAVSLNDFIIKAAALALRSVPTVNVVRWTPEGI
GLGSVDISVAVATPTGLITPIVENSILGVLAISSKVKELSGLARESCLKPQQFQGSFT
ISNLGMFGSVTNFTAIINPPQCAILTIGGTRSEVVSDGQLETQKLMGVNLCFDGRAISE
ECAKRFLHFSESLSDPELLIAEPLSPELDFDFSRL

>cel:CELE_F23B12.5 K00627 pyruvate dehydrogenase E2 component
(dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) dlat-1;
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex,
mitochondrial (A)
MSKFPVPLRTIGGLRPSTTAAISAANIGFTQSSRALSTGAAAKSSGLVGQVARQYPNAAA
FSIKQVRLYSSGNLPHNRVALPALSPMTMELGTVVSWQKKEGDQLSEGDLLCEIETDKAT
MGFETPEEGYLAKILIQEGSKDVPKLLCIIVDNEADVAAFDFKDDGASSGGSAPAAE
KAPEPAKPAASSQPSPPAQMYQAPSVPKSAIPHSSSGRVASPFACKLAAENGLDLSGV
SGSGPGGRILASDLSQAPAKGATSTTTQAVSGQDYTDIPLSNMRKTIKRLTESKSTIPH
YYLTSEIQLDTLLQVREKLNGLLAKGTSGQATKISINDFIIKASALACQRVPEANSYWMD
SFIRENHVVDVSVAVSTPAGLITPIIFNAHAKGLATIASEIVELAQRAREGKLQPHEFQG
GTFTVSNLGMFGSVSDFTAIINPPQSCILAIGGASDKLVPDEAEGYKKIKTMKVTLSCDH
RTVDGAVGAVWLRHFKEFLEKPHTMLL

OXOGLUTARATE DEHYDROGENASE

>eco:b0726 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
sucA; subunit of E1(0) component of 2-oxoglutarate dehydrogenase (A)
MQNSALKAWLDSSYLSGANQSWIEQLYEDFLTDPDSVDANWRSTFQQLPGTGVKPDQFHS
QTREYFRRLAKDASRYSSSTISDPDTNVKQVKVLQLINAYRFRGHQHANLDPLGLWQQDKV
ADLDPSFHDLTEADFQETFNVGSSFASGKETMKLGELLEALKQTYCGPIGAEYMHITSTEE
KRWIQQRIESGRATFNSEEKKRFLSELTAEEGLERYLGAKFPGAKRFSLEGGDALIPMLK
EMIRHAGNSGTREVVLGMAHRGRLNVLVNLGKKPQDLFDEFAGKHKEHLGTGDVKYHMG
FSSDFQTDGGLVHLALAFNPSHLEIVSPVVIGSVRARLDRLDEPSSNKVLPITIHGDAAV
TGQGVVQETLNMSKARGYEVGGTVRIVINNQVGFTTSNPLDARSTPYCTDIGKMVQAPIF
HVNADDPEAVAFVTRLALDFRNTFKRDVFIDLVCYRRHGHNEADEPSATQPLMYQKIKKH
PTPRKIYADKLEQEKVATLEDATMVNLYRDALDAGDCVVAEWRPMMNHSFTWSPYLNHE
WDEEYPNKVEMKRLQELAKRISTVPEAVEMQSRVAKIYGDRQAMAAGEKLFDWGGAENLA
YATLVDEGIPVRLSGEDSGRGTFFHRHAVIHNQSNGSTYTPLQHIHNGQGAFRVWDSVLS
EEAVLAFEYGYATAEPRTLTIWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLLPH
GYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRRPLVVMSPKS
LLRHPLAVSSLEELANGTFLPAIGEIDELDPKGVKRVVMCSGKVYYDLLEQRRKNNQHDV
AIVRIEQLYPFPHKAMQEVLLQQFAHVKDFVWCQEEPLNQGAWYCSQHHEFREVIPFGASLR
YAGRPASASPAVGYSVHQQKQQLVNDALNVE

>sce:YIL125W K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
KGD1, OGD1; alpha-ketoglutarate dehydrogenase KGD1 (A)
MLRFVSSQTCRYSSRGLLKTSLKNASTVKIVGRGLATTGTDNFLSTSNATYIDEMYQAW
QKDPSSVHVSWDAYFKNMSNPkipATKAFQAPPSISNFPQGTEAAPLGtAMTGsvDENVS
IHLKVQLLCRAYQVRGHLKAHIDPLGISFGSNKNNPVPPELTLDYYGFSKHDLdKEINLG
PGILPRFARDGKSKMSLKEIVDHLEKLYCSSYGVQYTHIPSKQKCDWLRERIEIPEPYQY
TVDQKRQILDRLTWATSFESFLSTKFPNDKRFGLGLESVVPGIKTLVDRSVELGVEDIV
LGMAHRGRLNVLSNVVRKPNEsIFSEfKGSSARDDIEGSGDVkYHLGMNYQRPTTSGKYV
NLSLVANPSHLESQDPVVLGRTRALLHAKNDLKEKTKALGVLLHGDAAFAGQGvVYETMG
FLTLPEYSTGGTIHVITNNQIGFTTDPRFARSTPYPSDLAKAIDAPIFHVnANDVEAVTF
IFNLAAEWRHKFHTDAIDVVGWRKHGHNETDQPSFTQPLMYKKIAKQKSVIDVYTEKLI
SEGTFskKDIDEHKKWVWNLfEDAFekAKDYVPSQREWLTAawEGfKSPkelATEILPHE
PTNVPESTLkELGKVLSSWPEGfEVHKNLKRILKNRGKSIETGEGIDWATGEALAFGTLV
LDGQNVrvSGEDVERGTFSQRHAVLHDQQSEAIYTPLSTLNNEKADFTIANSSLSEYgVM
GFEYGYSLTSPDYLVMWEAQFGDFANTAQVIIDQFIAGGEQKWkQRSGLVLSLPHGYDGGQ
GPEHSSGRlerFLQLANEDPRYFPSEEKLQRQHQCnFQVVYPTTPANLFHILRRQqHRQ
FRKPLALFFSKQLLRHPLARSSLSEfTEGGfQWIIEDIEHGKSIGtKEETKRLVLLSGQV
YtALHkRRESLGDKTTAFLKIEQLHPFPFAQLRDSLNSYPNLEEIVWCQEEPLNMGSWAY
TEPRLHTTLKETDKYKDFKVRYCGRNPSGAVAAGSKSLHLAEEDAFLKDVfQQS

>cel:CELE_T22B11.5 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] |
(RefSeq) ogdh-1; 2-oxoglutarate dehydrogenase, mitochondrial (A)
MHRASLICRLASPSRINAIRNASSGKSHISASTLVQHRNQSVAABKHEPFLNGSSSIYI
EQMYEAWLQDPSSVHTSWDAYFRNVEAGAGPGQAFQAPPATAYAGALGVSPAAAQVTTSS
APATRLDTNASVQSISDHLKIQLLIRSYQTRGHNIADLDPLGINSADLDDTIPPELELSF
YGLGERDLDRFLLPPTTFISEKKSLTLREILQRLKDIYCTSTGVEYMHNNLEQQDWIR
RRFEAPRVTELSHDQKKVLFKRLIRSTKFEEFLAKKWPSEKRFGLGCEVLIPAMKQVID
SSSTLGVDSFVIGMPHRGRLNVLANVCRQPLATILSQFSTLEPADEGSGDVKYHLGVCIE
RLNRQSQKNVKIAVVANPSHLEAVDPVVMGKVRAEAFYAGDEKCDRTMAILLHGDAAFAG
QGVVLETFNLDLPSYTTTHGAIHVVNNQIGFTTDPRSSRSPYCTDVGRVVGCPHFVN
VDDPEAVMHVCNVAADWRKTFKKDVIVDLVCYRRHGHNELDEPMFTQPLMYQRIKQTKTA
LEKYQEKILNEGVANEQYVKEELTKYGSILEDAYENAQKVTVVRNRDWLDSPWDDFFKKR
DPLKLPSTGIEQENIEQIIGKFSQYPEGFNLHRGLERTLKGRQQMLKDNSLDWACGEALA
FGSLLKEGIHVRLSGQDVQRGTFSHRHHVLHDQKVDQKIYNPLNDLSEGQGEYTVCNSSL
SEYAVLGFELGYSMVDPNSLVIWEAQFGDFSNTAQCIIDQFISSGQSKWIRQSGVLMLLP
HGYEGMGPEHSSARPERFLQMCNEDDEIDLEKIAFEGTFEAQLHDTNWIVANCTTPANI
YHLLRRQVTMPFRKPAVVFSPKSLLRHPMARSPVEDFQSGSNFQRVIPETGAPSQNPPDV
KRVVFCTGKVYYDMVAARKHVKGENDVALVRVEQLSPFPYDLVQQEQRKYQGAEILWAQE
EHKNMGAWSFVQPRINSLLSIDGRATKYAGRLPSSSPATGNKFTHMQEQKEMMSKVFVGP
KSKLEGFKA

>dme:Dmel_CG11661 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] |
(RefSeq) Ogdh; oxoglutarate dehydrogenase, isoform I (A)
MHRAHTAFSLALSPMAHKNFATWLLKSSSSQQMAKVTAATAAAVRTYNSAAAEFPFANGSTAS
YVEEMYNALWRDPTSVHTSWDAYFRSNSYVSPPNLAPVQANTLPLTAFNFGGAVAGAAPD
SKTIDDHLAVQAIIRSYQIRGHNIAHLDPLEINTPELPGNSSTKSIYANFSFGEQDMDRQ
FKLPSTTFIGGDEASLPLKEILNRLENVYCNIKIGVEFMFINSLEQCNWIRKRFETPGVLN
FSPEEKRLILARLTRATGFEAFLAKKYSSEKRFGLGCEIMIPALKEIIDVSTELGVESV
IMGMPHRGRLNTLANVCRKPLNQIFTQFAGLEAADDGSGDVKYHLGTYIERLNRVTNKN
RLAVVANPSHLEAVDPVVQGKTRAEQFYRGDQEGKKVMSILIHGDAAFCGQGVVYETMHL
SDLPDYTTHTGTHVANNQIGFTTDPFRFSRSPYCTDVARVVNAPIFHVNADDPEAVMHV
CKVAAEWRAFTHKDCVIDLVGYRRNGHNEIDEPMTQPLMYQKIRKHKNCCLDYADKLIA
EGVTAAEEVKSVAAKYENICEEAFALAKTETHVKYKDWLDSPWSGFFEGKDPLKVAPTGV
KEETLIHIGNRFSSPPNAAEFVIHKGLLRVLAARKAMVDEKQVADWALGEAMAFGSLLKE
GIHVRLSGQDVERGTFSHRHHVLHHQLVDKATYNSLQHMYPDQAPYSVSNSSLSEYAVLG
FEHGYSMTNPALVLWEAQFGDFSNTAQSIIDQFISSGQSKWVRQSGVLMMLPHGMMEGMG
PEHSSCRVERFLQMSSDDPDYFPPESEDFGVRQLHDINWIVANCSTPANYHILRRQIAL
PFRKPLILCTPKSLLRHPEAKSPFSEMSEGSEFQRIIPDNGPAGQNPSNVKKVFCSGRV
YYDLTKTRREKQLEGEIAIVRVEQISPFDFLVKEQANLYKNAELVWAQEEHKNQGSWTY
VQPRFLTALNHSRDVSQSDEQSSSTNTTTTDDHTNHESDTSDSKSKPWLSRMFAAPNSS
TGGDPKDPATLGGDFNAAKHFDLKNVRHDFNRPAGIAAAPGARIAKTGRKISYVGRACG
ASTATGSKAQHIRELNALLNDAIST

>dme:Dmel_CG33791 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq) CG33791; uncharacterized protein, isoform C (A)
MNQCRLRSLARIRSLTLGLRGTDQHVLRARQALRTIQTTSQRRGVHDLDSFANGCSAAYI
EGLYNKWKRNPSSVDESWNELFSSNDWSSPKRSPLQVSHSRKYRRPPVERIAVKARSGER
TASGGASAAPAAPPSDWKNIDDHHVIQAIIRAYQSRGHLAADLDPLGIVGPKKRTSVDGT
QRHAAREVLRQHFSYIFNDLNTVFKLPSSTMIGGDQEFSLKEILDRLERIYCGHIGVEY
MQITSLTKTNWLRDRFEKPGGLDLTKEEKKLILERLTRSTGFENFLAKKFSSEKRFGLG
CDIMIPAIKEVVDRATDHGVESILIGMAHRGRLNVLANICRKPISDILSQFHGLQATDSG
SGDVKYHLGVFQERLNRQTNRMVRI TVVANPSHLEHVN PVLLGKARAEMFQRGDT CGSTV
MPIIIHGDA SFSGQGVVYESMHLSDLPNYTTYGTI HIVSNNQVGFTTDPRFSRSSRYCTD
VAKVVNAPILHVNADDPEACIQCARIAIDYRTRFKKDVVIDIVGYRRNGHNEADEPMFTQ
PLMYQRIKKLKPCQLYADKLIKEGVVTDSEFKAMVSSYEKICEDAWAKSKTIKTIKYSS
WIDSPWPGFFEGDRDLKLCPTGISTDTLKTIGNMFSTPPPPEHKFETHKGILRILAQRTQ
MVQDKVADWSLGEAFAGSLLKEGIHVRLSGQDVERGTFSHRHHVLHHQSEDKV VYNSLD
HLYPDQAPYSVSNSSLSECAVLGFEHGYSMASPNALVMWEGQFGDFCNTAQCIIDTFIAS
GETKWVRQSGVVMLLPHSMEGMGPEHSSGRIERFLQMSDDDPDVYPDTCDADFVARQLMN
VNWIVTNLSTPANLFHCLRRQVKMGFRKPLINFSPKSLLRHPLARSPFKDFNECSCFQRI
IPDKGPAGKQPCDCVQKLVFCSGKVYYDLVKERDDHEQVETVALVRVEQLCPFPYDLISQQ
LELYPKAELLWAQEEHKNMGAWSYVQPRFDTALLKNENESRCVSYHGRPPSASPATGNKV
QHYNEYKALITSIFGELTPENKKRIEDRIKKQAKAKADAQSKPSTKPPAAPPKGGSSPP
PGPAPRKPLISLPSRPPRGGKQRSGSAPAPNLVDEDSAARNREPDA SAYDGASPSAWKRS
GSAPAPSVVPRASASRSPSRKSPSPSHDGISPSTRQESLSKKKSGSAPAPTPTSRGPFR
TAPSNTTEFIKRRPAKDYGSRNETQSTPGESELDPTKQP

>mmu:18293 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
Ogdh, 2210403E04Rik, 2210412K19Rik, E1o, OGDH-E1, d1401, mKIAA4192; oxoglutarate
(alpha-ketoglutarate) dehydrogenase (lipoamide) (A)
MFHLRTCAAKLRPLTASQTVKTF SQNKPAAIRTFQQIRCY SAPVAAEPFLSGTSSNYVEE
MYCAWLENPKSVHKSWDIFFRNTNAGAPPGTAYQSPLSLSRSSLATMAHAQSLVEAQPNV
DKLVEDHLAVQSLIRAYQIRGHHVAQLDPLGILDADLDSSVPADIISSTD KLGFYGLHES
DLDKVFHLP TTTTFIGGQEPALPLREIIRLEMAYCQHIGVEFMFINDLEQCQWIRQKFET
PGIMQFTNEEKRTLRLVRSTRFEEFLQRKWSSEKRFGLGCEVLIPALKTIIDMSSAN
GVDYVIMGMPHRGRLNVLANVIRKELEQIFCQFDSKLEAADEGSGDMKYHLGMYHRRINR
VTDRNITLSLVANPSHLEAADPVVMGKTAEQFYCGDTEGKKVMSILLHGDAAFAGQGIV
YETFHLSDLPSYTTHTGTVHVVVNNQIGFTTDPRMARSSPYPTDVARVVNAPIFHVNSDDP
EAVMYVCKVAAEWRNTFHKDVVDLV CYRRNGHNEMDEPMFTQPLMYKQIRKQKPV LQKY
AELLVSQGVVNQPEYEEEEEISKYDKICEEAFTRSKDEKILHIKHWLDSPWPGFFTLDGQPR
SMTCPSTGLEEDVLFHIGKVASSVPVENFTIHGGLSRILKTRRELVTNRTVDWALAEYMA
FGSLLKEGIHVRLSGQDVERGTFSHRHHVLHDQNVDKRTCIPMNLHWPNQAPYTV CNSSL
SEYGV LGFELGFAMASPNALVLWEAQFGDFNNMAQCIIDQFICPGQAKWVRQNGIVLLLP
HMEGMGPEHSSARPERFLQMCNDDPDVLPDLQEENFDINQLYDCNWIVVNCSTPGNFFH
VLRRQILLPFRKPLIVFTPKSLLRHPEARTSFDEMLPGTHFQRVIPENGPA AQDPHKVKR

LLFCTGKVYYDLTRERKARNMEEVAITRIEQLSPFPDLLLLKEAQKYPNAELAWCQEEH
KNQGYDYVKPRLRTTIDRAKPVWYAGRDPAAAPATGNKKTHLTELRFLDTAFDLDAFK
KFS

>mmu:239017 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
Ogdhl; oxoglutarate dehydrogenase-like (A)

MSQLRLLPFRLGPRATKLLATRAIPVFSGCRRSSGPPTTIPRSRSGVSSSYVEEMYFAWL
ENPQSVHKSWDSFFQRASKEASVGPAQPQLPAVLQESRTSVSSCTKTSKLVEDHLAVQSL
IRAYQIRGHHVAQLDPLGILDADLDSFVPSDLITTIDKLAFYDLQEADLDKEFRLPTTTF
IGGPENTLSLREIIRRESTYCQHIGLEFMFINDVEQCQWIRQKFETPGVMQFSVEEKRT
LLARLVRSMRFEDFLARKWSSEKRFGLGCEVMIPALKTIIDKSSEMGIENVILGMPHRG
RLNVLANVIRKDLEQIFCQFDPKLEAADEGSGDVKYHLGMYHERINRVNITLSLVAN
PSHLEAVDPVVQGKTKAEQFYRGDAQGRKVMISILVHGDAAFAGQGVVYETFHLSDLPSYT
TNGTVHVVVNNQIGFTTDPMARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEW
RNTFNKDVVVDLVCYRRRGHNEMDEPMFTQPLMYKQIHKQVPVLKKYADKLIAEGTVTLQ
EFEEEEIAKYDRICEEAYGRSKDKKILHIKHWLDSPWPGFFNVDGEPKSMTCPTTGIPEEM
LTHIGSVASSVPLEDFKIHTGLSRILRGRADMTKKRTVDWALAEYMAFGSLLKEGIHVRL
SGQDVERGTFSHRHHVLHDQEVDRRTCVPNMHLWPDQAPYTVCNSSLSEYGVLGFEFGYA
MASPNALVLWEAQFGDFHNTAQCIIDQFISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSA
RPERFLQMSNDDSDAYPVFTEDFEVSQLYDCNWIVVNCSTPASVFHVLRRQILLPFRKPL
IVFTPKSLLRHPDAKSSFDQMVSGTSFQRLIPEDGPAAHSPEQVQRLIFCTGKVYYDLVK
ERSSQGLEQQVAITRLEQISFPFDLIMREAKEYSGAELVWCQEEHKNMGYYDYISPRFM
TLLGHSRPIWYVGRDPAAAPATGNKNAHLVSLRRFLDTAFNLKAFEGKTF

>hsa:4967 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
OGDH, AKGDH, E1k, E1o, KGD1, OGDH, OGDH-E1, OGDH2, OGDHD; oxoglutarate
dehydrogenase (A)

MFHLRTCAAKLRPLTASQTVKTFSQNRPAARTFQQIRCYSAAPVAAEPFLSGTSSNYVEE
MYCAWLENPKSVHKSWDIFFRNTNAGAPPGTAYQSPLPLSRGSLAAVAHAQSLVEAQPNV
DKLVEDHLAVQSLIRAYQIRGHHVAQLDPLGILDADLDSVPADIISSTDKLGFYGLDES
DLDKVFHLPPTTTFIGGQESALPLREIIRLEMAYCQHIGVEFMFINDLEQCQWIRQKFET
PGIMQFTNEEKRTLARLVRSTRFEEFLQRKWSSEKRFGLGCEVLIPALKTIIDKSEN
GVDYVIMGMPHRGRLNVLANVIRKELEQIFCQFDSKLEAADEGSGDVKYHLGMYHRRINR
VTDRNITLSLVANPSHLEAADPVVMGKTKAEQFYCGDTEGKKVMSILLHGDAAFAGQGIV
YETFHLSDLPSYTTHTGTVHVVVNNQIGFTTDPMARSSPYPTDVARVVNAPIFHVNSDDP
EAVMYVCKVAAEWSTFHKDVVVDLVCYRRRGHNEMDEPMFTQPLMYKQIRKQKPVVLQKY
AELLVSQGVVNQPEYEEEEISKYDKICEEAFARSKDEKILHIKHWLDSPWPGFFTLDGQPR
SMSCPSTGLTEDILTHIGNVASSVPVENFTIHGGLSRILKTRGEMVKNRTVDWALAEYMA
FGSLLKEGIHRLSGQDVERGTFSHRHHVLHDQNVDKRTCIPNMHLWPNQAPYTVCNSSL
SEYGVLGFEFGFAMASPNALVLWEAQFGDFHNTAQCIIDQFICPGQAKWVRQNGIVLLL
HGMEGMGPEHSSARPERFLQMCNDDPDVLPDLKEANFDINQLYDCNWVVVNCSTPGNFFH
VLRRQILLPFRKPLIIFTPKSLLRHPEARSSFDEMLPGTHFQRVIPEDGPAAQNPENVKR

LLFCTGKVYYDLTRERKARDMVGQVAITRIEQLSPFPDLLLKEVQKYPNAELAWCQEEH
KNQGYDYVKPRLRTTISRAKPVWYAGRDPAAAPATGNKKTHLTELRLLDTAFDLDVFK
NFS

>hsa:55753 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq)
OGDHL, YOBELN; oxoglutarate dehydrogenase L (A)
MSQLRLLPSRLGVQAARLLAAHDVPVFGWRSRSSGPPATFPSSKGGGGSSYMEEMYFAWL
ENPQSVHKSWSDSFFREASEEAFSGSAQPRPPSVVHESRSASVSSRTKTSKLVEDHLAVQSL
IRAYQIRGHHVAQLDPLGILDADLDSFVPSDLITTIDKLAFYDLQEADLDKEFQLPTTTF
IGGSENTLSLREIIRRELENTYCQHIGLEFMFINDVEQCQWIRQKFETPGVMQFSSEEKRT
LLARLVRSRMRFEDFLARKWSSEKRFGLGCEVMIPALKTIIDKSSEMGIENVILGMPHRG
RLNVLANVIRKDLEQIFCQFDPKLEAADEGSGDVKYHLGMYHERINRVNITLSLVAN
PSHLEAVDPVVQGKTKAEQFYRGDAQGKKVMSILVHGDAAFAGQGQVYETFHLSDLPSYT
TNGTVHVVVNNQIGFTTDPRMARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEW
RNTFNKDVVVDLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYADKLIAEGTVTLQ
EFEETIAKYDRICEEAYGRSKDKKILHIKHWLDSPWPGFFNVDGEPKSMTCPATGIPEDM
LTHIGSVASSVPLEDFKIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
SGQDVERGTFSHRHHVLHDQEVDRTCVPMNHLWPDQAPYTVCNSSLSEYGVLGFEFGYA
MASPNALVLWEAQFGDFHNTAQCIIDQFISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSA
RPERFLQMSNDDSDAYPAFTKDFEVSQLYDCNWIVVNCSTPANYFHVLRQILLPFRKPL
IIFTPKSLLRHPEAKSSFDQMVSGTSFQRVIPEDGAAARAPEQVQRLIFCTGKVYYDLVK
ERSSQDLEEKVAITRLEQISFPFDLIKQEAEKYPGAELAWCQEEHKNMGYYDYISPRFM
TILRRARPIWYVGRDPAAAPATGNRNTHLVSLKKFLDTAFNLQAFEGKTF

OXOGLUTARATE DEHYDROGENASE SUCCINYLTRANSFERASE

>eco:b0727 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) sucB; dihydrolipoyltranssuccinylase (A)
MSSVDILVPDLPE SVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAV
LEDEGTTVTSRQILGRLREGNSAGKETS AKSEEKASTPAQRQQASLEE QNNDALSPAIRR
LLAEHNL DASA IKG TGVGGRLTREDVEKHLAKAPAKESAPAAAAPAAQPALAAARSEKRVP
MTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFYVK
AVVEALKRYPEVNASIDGDDVVYHNYFDVSM AVSTPRGLVTPVLRD VDTLGMADIEKKIK
ELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNG
QVEILPMMYLALS YDHR LIDGRESVGFLVTIKELLEDPTRLLLDV

>sce:YDR148C K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) KGD2; dihydrolipoyl transsuccinylase (A)
MLSRATR TAAAKSLV KSKVARNVMAASFVKRHASTSLFKQANKVESL GSIYLSGKKISVA
ANPFSITSNRFKSTSIEVPPMAESLTEGSLKEYTKNVGDFIKEDELLATIETDKIDIEVN
SPVSGTVTKLNF KPEDTVTVGEELAQVEPGAEPAGSGESKPEPTEQAEPSQGVAAARENS
SEETASKKEAAPKKEAAPKKEVTEPKKADQPKKTVSKAQEPVASNSFTFPFRTETRVKM
NRMRLRIAERLKESQNTAASLTTFNEVDM S ALMEMRKLYKDEI I KKTG TKFGFMGLFSKA
CTLAAKDIPAVNGAIEGDQIVYRDYTDISVAVATPKGLVTPVVRNAESLSVLDIENEIVR
LSHKARDGKLTLEDMTGGTFTISNGGVFGSLYGTPIINSPQTAVLGLHGVKERPVTVNGQ
IVSRPMMYLALTYDHRLLD GREAVTFLKTVKELIEDPRKMLLW

>cel:CELE_W02F12.5 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) dlst-1; Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (A)
MLGRRAVSVHRFLSRAARQSVTAASSAQPSLQAKTSLLEPLVQNVRITSSANFHMSAVRM
SDVITVEGP AFAESISEGDIRWLKQKGDHVNEDELVAEIETDKTSVEVPAPQAGTIVEFL
VEDGAKVTAKQKLYKLQPGAGGGSSSAPAKEE PKSAPAKEESKPAPAKEDSKPAVTAAAP
PKPVSGDIPKSAPPVARPPSTPSSSTPVGAVPVTRVVVPKGVDP SHAITGARDEV RVKAN
RMRMR I AQRLKDAQNTYAMLTTFNEIDMSSLIEMRKTYQKDFVAKHG VKLGMMSPFVR AA
AYALQESP VVNAVLDENEIVYRHFVDISVAVATPKGLVVPVLRNVESMNYAQIELELANL
GVKARDGKLAVEDMEGGTFTISNGGVFGSMFGTPIINPPQSAILGMHGVFDRVVPVNGKP
EIRPIMQIALTYDHR LIDGREAVTFLKKIKTAVEDPRIMFMNL

>dme:Dmel_CG5214 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) CG5214; uncharacterized protein (A)
MTGIISIVTRRLPQTLGMRALRSNEVKRCIRQYSRLVACAAQQQQLLRQDGSNRCQEATR
LLTWQGIHTTSSLWSEQTVNVPPFADSI AEGDIKFTCKVGDSFAADEAVMEIETDKTTVA

VPAPFSGTLTDILVKDGD TVKPGQALFKIKPGAAPAKAAAPAAAPAPAAPKAAPAPAAAP
KPAPPPPAAGAPKPPPPPPPKAAPRPPPPAPVAALKPAVAQVKVPPADGSRQILGTRSEQ
RVKMNRMLRKIAARLKDAQNTCAMLTTFNEVDMSYAMDFRKQNLD AFTKKYGIKFGFMSI
FAKASAYALQDQPVVNAVIDGTDIVYRDYVDISVAVATPRGLVVPVIRNVEGMNYADIEI
ALAGLADKARRDAITVEDMDGGTFTISNGGVFGSLMGTP IINPPQSAILGMHGIFERPIA
VKGEVKIRPMMYIALTYDHRIIDGREAVLFLRKIKAAVENPAIIVAGL

PHOSPHOENOLPYRUVATE CARBOXYKINASE

>eco:b3403 K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49] | (RefSeq) pck;
phosphoenolpyruvate carboxykinase (ATP) (A)

MRVNNGLTPQELEAYGISDVHDIVYNPSYDLLYQEELDPSLTGYERGVLTNLGAVAVDTG
IFTGRSPKDKYIVRDDTTRDTFWWADKKGKGNNDNKPLSPETWQHLKGLVTRQLSGKRLFV
VDAFCGANPDTRL SVRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQW
KEQGLNSEN FVAFNLTERMQLIGGTWYGGEMKKGMFSMMNYLLPLKGIASMHCSANVGEK
GDVAVFFGLSGTGKTTLS DPKRRLIGDDEHGWDDDG VFNFEGGCYAKTIKLSKEAEPEI
YNAIRRDALLENVT VREDGTIDFDDGSKTENTRVSYPIYHIDNIVKPVSKAGHATKVIFL
TADAFGVLPVPSRLTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQ
YAEVLVKRMQAAGAQAAYLVNTGWNGTGKRISIKDTRAIDAILNGSLDNAETFTLPMFNL
AIPTELPGVDTKILDPRNTYASPEQWQEKAETLAKLFDNFDKYTDTPAGAALVAAGPKL

>sce:YKR097W K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49] | (RefSeq)
PCK1, JPM2, PPC1; phosphoenolpyruvate carboxykinase PCK1 (A)

MSPSKMNATVGSTSEVEQKIRQELALSDEVTTIRRNAPAAVLYEDGLKENKTVISSSGAL
IAYSGVKTGRSPKDKRIVEEPTSKDEIWWGPVNKPCSERTWSINRERAADYLRTRDHIYI
VDAFAGWDPKYRIKVRVVCARAYHALFMTNMLIRPTEEE LAHFGE PDFTVWNAGQFPANL
HTQDMSSKSTIEINFKAMEMIILGTEYAGEMKKGIFTVMFYLMPVHHNVLT LHSSANQGI
QNGDVTLLFFGLSGTGKTTLSADPHRL LIGDDEHCWSDHG VFNIEGGCYAKCINLSAEKEP
EIFDAIKFGSVLENIYDEKSHVVDYDDSSITENTRCAYPIDYIPSAKIPCLADSHPKNI
ILLTCDASGVLPPVSKLTPEQVMYHFISGYTSKMAGTEQGVTEPEPTFSSCFGQPFLALH
PIRYATMLATKMSQHKANAYLINTGWTGSSYVSGGKRCPLKYTRAILDSIHDGSLANETY
ETLPIFNLQVPTKVNGVPAELLNPAKNWSQGESKYRGAVTNLANL FVQNFKIYQDRATPD
VLAAGPQFE

>cel:CELE_R11A5.4 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] |
(RefSeq) pck-2; phosphoenolpyruvate carboxykinase (GTP) (A)

MSVDPNLLTPYKNTGAANASLRQISED AFYVNEVVMKRLGHVPILKGDFHLLPAKVQRF
IAEKAELMRPRGIFICDGSQHEADELIDKLIERGMLSKLEAYENNYICRTDPKDVAVES
KTWMVTKNKYDTVTHTKEGV EPIMGHWLAPEDLATELDSRFP GCMAGRIMYVIPFSMGPV
GGPLSKIGIQLTDSNYVVL SMRIMTRVNNDVWDALGNQDFVRCIHSVGLPRPVKQRVINH
WPCNPERVLI AHRPPEREIWSFGSGYGGNSLLGKKCFALRIASNIAKDEGWMAEHMLIMG
VTRPCGREHFIAAAFPSACGKTNLAMLEPTLP GWKVRVCGDDIAWMKFGEDGRLYAINPE
AGFFGVAPGTSNKTNPMAVATFQKNSIFTNVAETANGEYFWEGLEDEIADKNVDITTWLG
EKWHIGEPGVA AHPNSRFAAPANQCPIIHPDWESPQGVPIEAIIFGRRRPQGVPLIYETN
SWEHGVFTG SCLKSEATAAAEFTGKTVMHDPMAMRPFMGYNFGKYLQHWLDLKTDSRKMP
KIYHVNWFRKDSNNKFLWPGFGDNIRVIDWIIRRLDGEQEIGVETPIGTVP AKGSINLEG
LGEVNWDELMSVPADYWKQDAQEIRKFLDEQVGEDLPEPVRAEMDAQEKRVTQL

>cel:CELE_W05G11.6 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] |
(RefSeq) pck-1; phosphoenolpyruvate carboxykinase (GTP) (A)
MANECRSLRNMETDGFQVVTEVTHKLNHIPIFKGDFASLSPKVQRFVAEKAELMNPAGI
YICDGSQKEYDDIVDKLVERGVLTPLKAYENNYLCRTDPRDVARVESKTWMVTKDKYDSV
CHTPDGVPRPIMGQWMSEEQFGVELDSRFPGCMAGRPMYVVPYSMGPIGGPLSKNGIELTD
SPYVVLCMRTMTRMGTKVLEALGDNDFVRCIHSVGLPRPVKQKVINHWPCNPEKVMIAHR
PKEREIWSFGSGYGGNSILGKKCFALRIACNIGRDEGWLAEHMLIMGVTNPEGEEKFIAA
AFPSACGKTNLAMLTPVPGWKVRVVGDDIAWMKFGADGRLYAINPEAGFFGVAPGTSHK
TNAMAMESCRANTIFTNVAETADGEYFWEGLEKELKEAKGYTDEQLKHLEITNWLGERWH
IGDEGKAAHPNSRFTAPAKQCPNIHPDWEAPQGVPIDAIVFGGRRPEGVPLVFESFSWEH
GILVGALVKSETTAAAEFTGKNVMHDPAMMRPFMGYNYGKYLEHWIKLGKAPHKAPKIFH
VNWFRETDKHKFLWPGFGDNIRVLDWILRRVAGGEEIEIAIETAIGYVPKRGTINLDGLPR
IDWNDLMSIPKDYWVEDVDESRLFDTQVGSDDLPPQIRDELDKLEKRVHAL

>dme:Dmel_CG10924 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] |
(RefSeq) Pepck2; phosphoenolpyruvate carboxykinase 2, isoform B (A)
MLKKGTIIPKYENCWLARTNPADVARVEGKTFISTDSKEQTPVPTEKATPGMLGNWIA
EKDMQAAIKERFPGCMKGRTMYVIPFSMGPVGSPLSKIGIEITDSPYVVESMKIMTRAGN
PVLNYLQSGDGQFVKCLHSVGTPKSGVQAMPSWPCDPERTIVLHKPAENEIVSYGSGYGG
NSLLGKKCLALRIGSTIAKREGWLAEHMLILGITNPQGKKIYIAAAFPSACGKTNLAMMT
PTLPGYKVECVGDDIAWMKFDNKGVLRAINPENGFFGVAPGTSRATNPIAMDTIFRNSVF
TNVASTSDGGVYWEKMEKDQLKGVTVTDWLGLKWSQESGKPAHPNSRFCTPASQCPIID
PAWEDSEGVPISAILFGGRRPSGVPLVYEARDWKHGVFIGAAMRSEATAAAEFKGVIMH
DPFAMRPFPGYNFGDYLGHWLSMEQRGQVPKIFHVNWFRKSSEGKFLWPGFGENSRVLDW
IFRRVEGEQCFCEDSPIGRPLPSKNSLNLDLENIDLDQLFDLPKDFWEQEVAAIERYFEEQ
VGHHLPGAVAEELRELKARVADM

>dme:Dmel_CG17725 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] |
(RefSeq) Pepck1; phosphoenolpyruvate carboxykinase 1 (A)
MPELIEQSKIISGNVCGLPQLHKLRQDNCGLYSHIRGIPIISYGNVDLLTTGVRAFVEEGI
ALCQPDQVHICDGSEQUENKVLISLLEAGTIVPLPKYDNCWLARTNPADVARVESRTFIC
TERREETIPTVEGVKGTGLGNWISPSDMDAAVQQRFPGCMKGRTMYVVPFSMGPVGSPLS
KIGIELTDSAYVVASMRIMTRMGAAVLRQLAKKEEFVRALHSVGAPANGQVEQPSWPCDP
ERTIILHKPAENLIVSYGSGYGGNSLLGKKCFALRIGSTIAKQEGWLAEHMLILGITDPK
GEKKYITAAFPACGKTNLAMLNPSLANYSKVECVGDDIAWMKFDSQGVLRRAINPENGFFG
VAPGTSMETNPIAMNTVFNKTIFTNASTSDGGVFWEGMESSLAPNVQITDWLGKPWTKD
SGKPAHPNSRFCTPAAQCPIIDEAWEDPAGVPISAMLFGGRRPAGVPLIYEARDWTHGV
FIGAAMRSEATAAAEHKGVIMHDPFAMRPFPGYNFGDYVAHWLSMEKRGQVPKIFHVNW
FRKSAEGKFMWPGYGENSRVLEWILRRVNGESCYVDSAIGHIPAEGALNLDGMKDKVDVK
EIFSLPKEFWSQEVKDIRTYFESQVGADLPASIIYQQLDELSSRVDNL

>mmu:18534 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq)
Pck1, PEPCK, PEPCK-C, Pck-1; phosphoenolpyruvate carboxykinase 1, cytosolic (A)
MPPQLHNGLDFSAKVIQGSLSLDPQAVRKFEVGNALCQPEYIHICDGSEEEYGQLLAHM
QEEGVIRKLKKYDNCWLALTDPRDVARIESTVITQEQRDTVPIPKTGLSQLGRWMSEE
DFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLAKIGIELTDSFYVVASMRIMTRMGISV
LEALGDGEFIKCLHSVGCPLPLKKPLVNNWACNPELTIAHLPDRREIISFGSGYGGNSL
LGKKCFALRIASRLAKEEGWLAEHMLILGITNPEGKKKYLAAPFSACGKTNLAMMNPSL
PGWKVECVGDDIAWMKFDAQGNLRINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNV
AETSDGGVYWEGIDEPLAPGVTITSWKNKEWRPQDAEPCAHNPSRFCTPASQCPIIDPAW
ESPEGVPIEGIIIFGGRRPEGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPF
AMRPFFGYNFGKYLAHWLSMAHRPAAKLPKIFHVNWFRKDKDGKFLWPGFGENSRVLEWM
FGRIEGEDSAKLTPIGYIPKENALNLKGLGGVNVEELFGISKEFWKEVEEIDRYLEDQV
NTDLPYEIERELRALKQRISQM

>mmu:74551 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq)
Pck2, 1810010O14Rik, 9130022B02Rik, PEPCK-M; phosphoenolpyruvate carboxykinase 2
(mitochondrial) (A)
MAAMYLPGLRLSRHGLRPWCWSPCRSIQTLHVLSGDMSQLPAGVRDFVARSAHLCQPEGI
HICDGTEAENTAILALLEEQGLIRKLPKYKNCWLARTDPKDVARVESKTIVITPSQRDTV
PLLAGGARGQLGNWMSPEDEFQRAVDERFPGCMQGRIMYVLPFSMGPVGSPLSRIGVQLTD
SAYVVASMRIMTRLGTPVLQALGDGDFIKCLHSVGGQPLTGHGDPVGQWPCNPEKTLIGHV
PDQREIVSFGSGYGGNSLLGKKCFALRIASRLARDEGWLAEHMLILGITNPAGKKRYVAA
AFPSACGKTNLAMMRPALPGWKVECVGDDIAWMRFDSEGQLRAINPENGFFGVAPGTSAA
TNPNAMATIQSNTLFTNVAETSDGGVYWEGIDQPLPPGVTITSWLGKPWKPGDKEPCAHN
NSRFCVPARQCPIMDPAWEAPEGVPIDAIIFGGRRPKGVPLVYEAFNWRHGVFVGSAMRS
ESTAAAEHKGKTIIMHDPFAMRPFFGYNFGRYLEHWLSMEGQKGARLPRIFHVNWFRRDEA
GRFLWPGFGENARVLDWICRRLEGEDSAQETPIGLVPKEGALDLSGLSAVDTSQLFSIPK
DFWEQEVDRDIRGYLTEQVNQDLPKEVLAELEALEGRVQKM

>hsa:5105 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq) PCK1,
PCKDC, PEPCK-C, PEPCK1, PEPCKC; phosphoenolpyruvate carboxykinase 1 (A)
MPPQLQNGLNLSAKVVQGSLSLDPQAVREFLENNAELCQPDHIHICDGSEEEENGRLLGQM
EEEGILRRLKKYDNCWLALTDPRDVARIESTVIVTQEQRDTVPIPKTGLSQLGRWMSEE
DFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGIELTDSFYVVASMRIMTRMGTPV
LEAVGDGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTIAHLPDRREIISFGSGYGGNSL
LGKKCFALRMASRLAKEEGWLAEHMLILGITNPEGEKKYLAAPFSACGKTNLAMMNPSL
PGWKVECVGDDIAWMKFDAQGHLRAINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNV
AETSDGGVYWEGIDEPLASGVTITSWKNKEWSSEDGEPCAHNPSRFCTPASQCPIIDAAW
ESPEGVPIEGIIIFGGRRPAGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPF
AMRPFFGYNFGKYLAHWLSMAQHAPAAKLPKIFHVNWFRKDKGKFLWPGFGENSRVLEWM
FNRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFSSISKEFWKEVEDIEKYLEDQV

NADLPCEIEREILALKQRISQM

>hsa:5106 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq) PCK2, PEPCK, PEPCK-M, PEPCK2; phosphoenolpyruvate carboxykinase 2, mitochondrial (A)
MAALYRPGLRLNWHGLSPLGWPSQRSIQTLRVLSGDLGQLPTGIRDFVEHSARLCQPEGI
HICDGTEAENTATLTLEQQGLIRKLPKYNNCWLARTDPKDVARVESKTVIVTPSQRDTV
PLPPGGARGQLGNWMSPADFQRAVDERFPGCMQGRMTMYVLPFSMGPVGSPLSRIGVQLTD
SAYVVASMRIMTRLGTPVLQALGDGDFVKCLHSGVGGQPLTGQGEPVSQWPCNPEKTLIGHV
PDQREIISFGSGYGGNSLLGKKCFALRIASRLARDEGWLAEHMLILGITSPAGKKRYVAA
AFPSACGKTNLAMMRPALPGWKVECVGDDIAWMRFDSEGRLRAINPENGFFGVAPGTSAT
TNPNAMATIQSNTIFTNVAETSDGGVYWEGIDQPLPPGVTVTSWLGKPWKPGDKEPCAHP
NSRFCAPARQCPIMDPAWEAPEGVPIIDAIIFGGRRPKGVPLVYEAFNWRHGVFVGSAMRS
ESTAAAEHKGKIIMHDPFAMRPFFGYNFGHYLEHWLSMEGRKGAQLPRIFHVNWFRRDEA
GHFLWPGFGENARVLDWICRRLEGEDSARETPIGLVPKEGALDLSGLRAIDTTQLFSLPK
DFWEQEVDRDIRSYLTEQVNQDLPKEVLAELEALERRVHKM

PYRUVATE CARBOXYLASE

>sce:YBR218C K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PYC2; pyruvate carboxylase 2 (A)
MSSSKLAGLRDNFSLLGEKNKILVANRGEIPRIFRSAHEL SMRTIAIYSHEDRLSMHR
LKADEAYVIGEEGQYTPVGAYLAMDEIIEIAKKHKVDFIHPGYGFLSENSEFADKVVKAG
ITWIGPPAEVIDSVGDKVSARHLAARANVPTVPGTPGPIETVQEALDFVNEYGYPVIIKA
AFGGGGRGMRVVREGDDVADAFQRTSEARTAFGNGTCFVERFLDKPKHIEVQLLADNHG
NVVHLFERDCSVQRRHQKVVEVAPAKTLPREVRDAILTDAVKLAKVCGYRNAGTAEFLVD
NQNRHYFIEINPRIQVEHTITEEITGIDIVSAQIQIAAGATLTQLGLLQDKITTRGFSIQ
CRITTEDPSKNFQPD TGRLEVYRSAGGNGVRLDGGNAYAGATISPHYDSMLVKCSCSGST
YEIVRRKMIRALIEFRIRGVKTNIPFLLTLLTNPVFIEGTYWTTFIDDPQLFQMVSSQN
RAQKLLHYLADLAVNGSSIKGQIGLPKLKSNPSVPHLHDAQGNVINVTKSAPPSGWRQVL
LEKGPSEFAKQVRQFNGTLLMDTTWRDAHQSLLATRVTRTHDLATIAPTTAHALAGAFAL
CWGGATFDVAMRFLHEDPWERLRKLRSLVPNIPFQMLLRGANGVAYSSLPD NAIDHFVKQ
AKDNGVDIFRVFDALNDLEQLKVG VNAVKKAGGVVEATVCYSGDMLQPGKKYNLDYYLEV
VEKIVQMGTHILGIKDMAGTMKPAAAKLLIGSLRTRYPDLP IHVHSHDSAGTAVASMTAC
ALAGADVVDVAINSM SGLTSQPSINALLASLEGNIDTGINVEHVRELDAYWAEMRLLYSC
FEADLKGPDP EVYQHEIPGGQLTNLLFQAQQLGLGEQWAETKRAYREANYLLGDIVKVTP
TSKVVGDLAQFMVSNKLTSDDIRRLANSLDFPDSVMDFFEGLIGQPYGGFPEPLRSDVLR
NKRRKLT CRPGLELEPFDLEKIREDLQNRFGDIDECDVASYNMYPRVYEDFQKIRETYGD
LSVLPTKNFLAPAEPDEEIEVTIEQGKTLIIKLQAVGDLNKKTGQREVYFELNGELRKIR
VADKSQNIQSVAKPKADVHDTHQIGAPMAGVII EVKVHKGSLVKKGESIAVLSAMKMEMV
VSSPADGQVKDVF IKDGESVDASDLLVLEEETLPPSQKK

>sce:YGL062W K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PYC1; pyruvate carboxylase 1 (A)
MSQRKFAGLRDNFNLLGEKNKILVANRGEIPRIFRTAHEL SMQTVAIYSHEDRLSTHKQ
KADEAYVIGEVGQYTPVGAYLAIDEIISIAQKHQVDFIHPGYGFLSENSEFADKVVKAGI
TWIGPPAEVIDSVGDKVSARNLAAKANVPTVPGTPGPIETVEEALDFVNEYGYPVIIKAA
FGGGGGRGMRVVREGDDVADAFQRTSEARTAFGNGTCFVERFLDKPKHIEVQLLADNHGN
VVHLFERDCSVQRRHQKVVEVAPAKTLPREVRDAILTDAVKLAKECGYRNAGTAEFLVDN
QNRHYFIEINPRIQVEHTITEEITGIDIVAAQIQIAAGASLPQLGLFQDKITTRGFAIQC
RITTEDPAKNFQPD TGRIEVYRSAGGNGVRLDGGNAYAGTIISPHYDSMLVKCSCSGSTY
EIVRRKMIRALIEFRIRGVKTNIPFLLTLLTNPVFIEGTYWTTFIDDPQLFQMVSSQNR
AQKLLHYLADLAVNGSSIKGQIGLPKLKSNPSVPHLHDAQGNVINVTKSAPPSGWRQVLL
EKGPAEFARQVRQFNGTLLMDTTWRDAHQSLLATRVTRTHDLATIAPTTAHALAGRFALEC
WGGATFDVAMRFLHEDPWERLRKLRSLVPNIPFQMLLRGANGVAYSSLPD NAIDHFVKQA
KDNGVDIFRVFDALNDLEQLKVGVD AVKKAGGVVEATVCFSGDMLQPGKKYNLDYYLEIA
EKIVQMGTHILGIKDMAGTMKPAAAKLLIGSLRAKYPDLPIHVHTHDSAGTAVASMTACA
LAGADVVDVAINSM SGLTSQPSINALLASLEGNIDTGINVEHVRELDAYWAEMRLLYSCF
EADLKGPDP EVYQHEIPGGQLTNLLFQAQQLGLGEQWAETKRAYREANYLLGDIVKVTP

SKVVGDLAQFMVSNKLTSDDVRRRLANS�DFPDSVMDFFEGLIGQPYGGFPEPFRSDVLRN
KRRKLTCTPGLELEPFDELEKIREDLQNRFGDVDECDVASYNMYPRVYEDFQKMRETYGDL
SVLPTRSFLSPLETDEEIEVVIEQGKTLIIKLQAVGDLNKKTGEREVYFDLNGEMRKIRV
ADRSQKVETVTKSKADMHDPLHIGAPMAGVIVEVKVHKGSLIKKGQPVAVLSAMKMEMII
SSPSDGQVKEVFDVSDGENVDSSDLLVLEDQVPVETKA

>cel:CELE_D2023.2 K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) pyc-1; Pyruvate
carboxylase 1 (A)

MRFSRIPPIFANVVRQTHYRNYANGVIKPREFNKVMVANRGEIAIRVFRALTELNKTSA
IYAEQDKNSMHRLKADEAYLVGKGLPPVAAYLTIDQIIETALKHNIDAIHPGYGFLSERS
DFAAACQNAGIVFIGPSPDVMARMGDKVAARQAAIEAGVQVVPGTPGPITTADAEVEFAK
QYGTPIILKAAYGGGGGRGIRRVDKLEEVEEAFRRSYSEAQAAGDGSFVEKFVERPRHI
EVQLLDGHHGNIVHLYERDCSVQRRHQKVVEIAPAPALPEGVREKILADALRLARHVG
YQ NAGTVEFLVDQKGNYYFIEVNARLQVEHTVTEEITGVDLVQAQIRIAEGKSLDDLKLSQE
TIQTTGSAIQCRVTTEDPAKGFQPD SGRIEVRSGEGMGIRLDSASAFAGSVISPHYDSL
MVKVIASARNHPNAAAKMIRALKKFRIRGVKTNIPFLLNVLRQPSFLDASVDTYFIDEHP
ELFQFKPSQNRAQKLLNYLGEVKVNGPTTPLATDLKPAVVSPPIPIYIPAGAKPPTGLRDV
LVQRGPTFEFAKEVRSRPGCMITDTTFRDAHQSLLATRVRTYDMAAISPFVAQSFNGLFSL
ENWGGATFDVSMRFLHECPWERLQTLRKLPNIPFQCLLRGANAMGYSNYPDNVIYKFCE
LAVKNGMDVFRVFDLSNLYPNLLVGMEAVGKAGGVVEAAIAYTGDVTDKSRDKYDLKYLL
NLADQLVKAQAHILSIKDMAGVLKPEAAKLLIGALRDKFPDIPIHVHHTDTSAGAGVAAML
ECAKAGADVDAAVDSMSGMTSQPSMGAIVASLQGTKHDTGLSLDDISKYSAYWESTRQL
YAPFECATTMKS GNADVYKHEIPGGQYTNLQFQAFSLGLGPQFDEVKRM YREANLVLGDI
IKVTPSSKIVGDLAQFMVQNNLTRETLDVDRADDLSFPKSVVDFMQGNVGQPPYGFPEPLR
TKVLRGKPKVDGRPGENAKPVDLDAVKVELEEKHGRTLSEEDVMSYSMFPTVFDEFETFR
QQYGPVDKLPTRLFLTGLEIAEEVDVEIESGKTLAIQLLAEGKLNKRGEREVFFDLNGQM
RSIFVVDKEASKEIVTRPRALPGVRGHIGAPMPGDVLELKIKEGDKVTKKQPLFVLSAMK
MEMVIDSPIAGTVKAIHAPQGTKCSAGDLVVEVEP

>dme:Dmel_CG1516 K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PCB; pyruvate
carboxylase, isoform M (A)

MFIPAAQSAYRTLRTKTPRVRLNAIFKNGYSSKVEYKPIRSVLVANRGEIAIRVFRAC
TE LGIKSVAVYSEQDKMHMHRQKADESYIVGKGLPPVEAYLNIPELIRVCKENDVDAVHPGY
GFLSERSDFAQAVIDAGLRFIGPSPEVVQKMGDKVAARVAAIEAGVPIVPGTDGPVTTKE
EALFCKKHGLPVIFKAAYGGGGGRGMRVVVRKMEDVEESFQRASSEAKAAFGNGAMFIEKF
IERPRHIEVQLLDGKAGNVVHLYERDCSVQRRHQKVVEIAPAPRLPIEIRDKMTEAAVRL
ARHVG YENAGTVEFLCDESGNFYFIEVNARLQVEHTVTEEITGIDLVSQIRVAEGMTLP
ELGYTQDKIVPRGYAIQCRVTTEDPANDFQPN TGRLEVFRSGEGMGIRLDSASAYAGAI
SPYYDSLLVKVISHASDLQSSASKMNRALREFRIRGVKTNIPFLLNVLENQKFLHGVLD
TYFIDEHPQLFKFKPSLNRAQKLLNYMGEVLVNGPQTPLATTLKPAVSPHVPEVPLDLS
P EAIEREERGEAKVTEPPKGLREVLVCEGPEAFAKEVRNRKELLLMDTTFRDAHQSLLAT
R VRSHDLLKISPYVTHKFNNLYSLENWGGATFDVALRFLHECPWERLEEMRKRIPIPFQM

LLRGANAVGYTSYPDNVVYKFCELA VQTGM DIFRVFDSLNYLPNLILGMEAAGKAGGVVE
AAISYTG DVSDPKRTKYDLKY YTNLADELVKAGTHVLCIKDMAGLLKPESARLLITAIRD
KHPDIPIHIH THDTSGAGVASMLACANAGADVVDVAVD SMSGMTSQPSMGAVVASLQGTP
LDTNLDLRTVSEYSAYWEQTRTLYAPFECTTTMRSGNADVYLNEIPGGQYT NLQFQAFSL
GLGDFFEDVKKAYREANLLLGDIIK VTPSSKVVGDLAQFMVQNDLTADQVLERAEELSFP
KSVVEYLQGSIGIPHGGFPEPLRSRVLKDMPRIEGRPGAELKDLD FDKLKKELQESHTCV
TNRDVMSAALYPQVTNDFLNFREKYGPVDKLDTRIFLTGPKVGEEFDVPLERGKTL SVKA
LAVSADLKPNGIREVFFELNGQLRAVHILDKEAVKEIHVHPKANKSNKSEVGAPMPGTVI
DIRVKVGDKVEKGQPLVLSAMKMEMVVSPLAGVVKLEIANGTKLEGEDLIMIIE

>mmu:18563 K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) Pcx, Pc, Pcb; pyruvate carboxylase (A)

MMLKFQTVRGGLRLLGVRRSSAPVASPNVRRLEYKPIKKVMVANRGEIAIRVFRACTEL
GIRTVAVYSEQDTGQMHQRKAD EAYLIGRGLAPVQAYLHIPDIIKVAKENGVD AVHPGYG
FLSERADFAQACQDAGVRFIGPSPEVVRKMGDKVEARAIAIAAGVPVVP GTDSPISSLHE
AHEFSNTYGFPIIFKAAYGGGGRGMRVVHSYEELEENYTRAYSEALAAF GNGALFVEKFI
EKPRHIEVQILGDQYGNILHLYERDCSIQRRHQKVVEIAPATHLDPQLRSRLTSDSVKLA
KQVGYENAGTVEFLVDKHGKH YFIEVNSRLQVEHTVTEEITDVDLVHAQIHVSEGRSLPD
LGLRQENIRINGCAIQCRVTTEDPARSFQPD TGRIEVFRSGEGMGIRLDNASAFQGAVIS
PHYDSSLVKVIAHGKDHPTAATKMSRALAEFRVRGVKTNIPFLQNVLNNQQFLAGTVDTQ
FIDENPELFQLRPAQNRAQKLLHYLGHVMVNGPTTPIPVNVSPSPVDP AVPVVPIGPPPA
GFRDILLREGPEGFARAVRNHQGLLLMDTTFRDAHQSLLATRVRTHDLKKIAPYVAHNFN
KLFSMENWGGATFDVAMRFLYECPWRRQLQELRELIPNIPFQMLLRGANAVGYTNYPDNV
FKFCEVAKENGMDVFRVFD SLNYLPNMLLGMEAAGSAGGVVEAAISYTG DVADPSRTKYS
LEYMGLAEELVRAGTHILCIKDMAGLLKPAACTMLVSSLRDRFPDLPLHIH THDTSGAG
VAAMLACAQAGADVVDVAVD SMSGMTSQPSMGALVACTKGTPLDTEVPLERVFDYSEYWE
GARGLYAAFDCTATMKSGNSDVYENEIPGGQYT NLHFQAHSMGLGSKFKEVKKAYVEANQ
MLGDLIKVTPSSKIVGDLAQFMVQNGLSRAEAE AQAEELSFP RSVVEFLQGYIGIPHGGF
PEPFRSKVLKDLPRIEGRPGASLPPLNLKELEKDLIDRHGEEVTPEDVLSAAMPDVFAQ
FKDFTATFGPLDSL NTRLFLQGPKIAEEFEVELERGKTLHIKALAVSDLN RAGQRQVFFE
LNGQLRSILVKDTQAMKEMHFHPKALKDVKGQIGAPMPGKVIDIKVAAGDKVAKGQPLCV
LSAMKMETVVTSPMEGTIRKVHVTKDMTLEGDDLILEIE

>hsa:5091 K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PC, PCB; pyruvate carboxylase (A)

MLKFRTVHGGRLLLGIRRTSTAPAASPNVRRLEYKPIKKVMVANRGEIAIRVFRACTELG
IRTVAIYSEQDTGQMHQRKAD EAYLIGRGLAPVQAYLHIPDIIKVAKENNVDAVHPGYGF
LSERADFAQACQDAGVRFIGPSPEVVRKMGDKVEARAIAIAAGVPVVP GTDAPITSLHEA
HEFSNTYGFPIIFKAAYGGGGRGMRVVHSYEELEENYTRAYSEALAAF GNGALFVEKFIE
KPRHIEVQILGDQYGNILHLYERDCSIQRRHQKVVEIAPAAHLDPQLRTRLTSDSVKLAK
QVGYENAGTVEFLVDRHGKH YFIEVNSRLQVEHTVTEEITDVDLVHAQIHVAEGRSLPD
LGLRQENIRINGCAIQCRVTTEDPARSFQPD TGRIEVFRSGEGMGIRLDNASAFQGAVIS

HYDSLLVKVIAHGKDHPTAATKMSRALAEFRVRGVKTNIAFLQNVLNNQQFLAGTVDTQF
IDENPELFQLRPAQNRAQKLLHYLGHVMVNGPTTPIPVKASPSPTDPVVPVPIGPPAG
FRDILLREGPEGFARAVRNHPGLLLMDTTFRDAHQSLLATRVRTHDLKKIAPYVAHNFSK
LFSMENWGGATFDVAMRFLYECPWRRLLQELRELIPNIPFQMLLRGANAVGYTNYPDNVVF
KFCEVAKENGMDVFRVFDSLNYLPNMLLGMEAAGSAGGVVEAAISYTGADVADPSRTKYSL
QYYMGLAEELVRAGTHILCIKDMAGLLKPTACTMLVSSLRDRFPDLPLHIHHTDTSGAGV
AAMLACAQAGADVVDVAADSMGMSQPSMGALVACTRGTPLDTEVPMERVFDYSEYWEG
ARGLYAAFDCATMKSGNSDVYENEIPGGQYTNLHFQAHSMGLGSKFKEVKKAYVEANQM
LGDLIKVTPSSKIVGDLAQFMVQNGLSRAEAEQAEELSFPRSVVEFLQGYIGVPHGGFP
EPFRSKVLKDLPRVEGRPGASLPPLDLQALEKELVDRHGEEVTPEDVLSAAMYPDVFAHF
KDFTATFGPLDSLNTLRLFLQGPKIAEEFEVELERGKTLHIKALAVSDLNRAGQRQVFFEL
NGQLRSILVKDTQAMKEMHFHPKALKDVKGQIGAPMPGKVIDIKVVAGAKVAKGQPLCVL
SAMKMETVVTSPMEGTVRKVHVTKDMTLEGDDLILEIE

PYRUVATE DEHYDROGENASE

>eco:b0114 K00163 pyruvate dehydrogenase E1 component [EC:1.2.4.1] | (RefSeq) aceE;
pyruvate dehydrogenase E1 component (A)

MSERFPNDVDPIETRDWLQAIESVIREEGVERAQYLIDQLLAEARKGGVNVAAGTGISNY
INTIPVEEQPEYPGNLELERRIRSAIRWNAIMTVLRASKKDLELGGHMASFQSSATIYDV
CFNHFFRARNEQDGGDLVYFQGHISPGVYARAFLEGRLTQEQLDNFRQEVHGNGLSSYPH
PKLMPEFWQFPTVSMGLGPIGAIYQAKFLKYLEHRGLKDTSKQTVYAFLGDGEMDEPESK
GAITIATREKLDNLVFINCNLQRLDGPVTGNGKIINELEGIFEGAGWNVIKVMWGSRW
ELLRKDTSGKLIQLMNETVDGDYQTFKSKDGAYVREHFFGKYPETAALVADWTDEQIWAL
NRGGHDPKKIYA AFKKAQETKGKATVILAHTIKGYGMGDAAEGKNIAHQVKMNMMDGVRH
IRDRFNVPVSDADIEKLPIYITFPEGSEEHTYLHAQRQKLHGYPSPRQPNFTEKLELPSLQ
DFGALLEEQSKEISTTIAFVRALNVMKNSIKDRLPVPIADEARTFGMEGLFRQIGIYS
PNGQQYTPQDREQVAYYKEDEKGQILQEGINELGAGCSWLAAATSYSTNNLPMIPFYIYY
SMFGFQRIGDLCWAAGDQQARGFLIGGTSGRTTLNGEGLQHEDGHSHIQSLTIPNCISYD
PAYAYEVAVIMHDGLERMYGEKQENVYYYITTLNENYHMPAMPEGAEEGIRKGIYKLETI
EGSKGKVQLLGSGLRHRVREAAEILAKDYGVSVDVSVTSFTELARDGQDCERWNMLHP
LETPRVPYIAQVMNDAPAVASTDYMKLFAEQVRTYVPADDYRVLGTDGFGGRSDSRENLRH
HFEVDASYVVVAALGELAKRGEIDKKVVADAIKFNIDADKVNPRLA

>sce:YBR221C K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1] |
(RefSeq) PDB1; pyruvate dehydrogenase (acetyl-transferring) subunit E1 beta (A)
MFSRLPTSLARNVARRAPTSFVRPSAAAAALRFSSTKTMTVREALNSAMAEELDRDDVDF
LIGEEVAQYNGAYKVSKGLLDRFGERRVVDTPITEYGFTGLAVGAALKGLKPIVEFMSFN
FSMQAIDHVVNSAAKTHYMSGGTQKCQMVFRGPNGAAVGVGAQHSQDFSPWYGSIPGLKV
LVPYSAEDARGLLKAAIRDPNPVVFLENELLYGESFEISEEALSPEFTLPYKAKIEREGT
DISIVTYTRNVQFSLEAAEILQKKYGVSAEVLNRSIRPLDTEAIKTVKKTNHLITVES
TFPSFGVGAEIVAQVMESEAFDYLDAPIQRVTGADVPTPYAKELEDFAFPDTPTIVKAVK
EVLSIE

>sce:YER178W K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] |
(RefSeq) PDA1; pyruvate dehydrogenase (acetyl-transferring) subunit E1 alpha (A)
MLAASFKRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTTDDKKAPEDIEGSDTVQIELPES
SFESYMLEPPDLSYETSKATLLQMYKDMVIIRMEMACDALYKAKKIRGFCHLSVGQEAI
AVGIENAITKLDSIITSYRCHGFTFMRGASVKAVLAELMGRRAGVSYGKGGSMLHYAPGF
YGGNGIVGAQVPLGAGLAFAHQYKNEDACSFTLYGDGASNQGQVFESFNMAKLWNLPVVF
CCENNKYGMGTAASRSSAMTEYFKRGQYIPGLKVNGMDILAVYQASKFAKDWCLSGKGPL
VLEYETYRYGGHSMSPGTTYRTRDEIQHMRSKNDPIAGLKMHLIDLGIATEAEVKAYDK
SARKYVDEQVELADAAPPPEAKLSILFEDVYVKGTTETPTLRGRIPEDTWDFKKQGFASRD

>cel:CELE_C04C3.3 K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1]
| (RefSeq) pdhb-1; Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (A)
MALRKCGNLFVARLAGTSTRAASTMTVRDALNQAMDEEIKRDDRFLMGEEVAQYDGAYK
ISKGLWKKHGDKRVDTPITEMGFAGIAVGAFAGLRPICEFMTFNFSMQAIDQIINSAA
KTYYSMSAGRPVPIVFRGPNGAAAGVAAQHSQDFSAWYAHCPGLKVVCYPYSAEDAKGLLK
AAIRDDNPVVFLENEILYGQSFPVGDEVLSDDFVVPKAKIERAGDHVTIVSYSRGVEF
SLEAAKQLEAIGVSAEVINLRSLRPFDFESIRQSVHKTHHLVSVETGWPFAGIGSEIAAQ
VMESDVFQQLDAPLLRVTGVDVPMPTQTLEAAALPTAEHVVKAVKKSLNIA

>cel:CELE_T05H10.6 K00161 pyruvate dehydrogenase E1 component subunit alpha
[EC:1.2.4.1] | (RefSeq) pdha-1; Pyruvate dehydrogenase E1 component subunit alpha (A)
MTKFLSLVHLERIWSTAMSLFARQLQSLTASGIRTQQVRLASTEVSFHTKPKLHKLDNG
PNTSVTLNREDALKYYRDMQVIRRMESAAGNLYKEKKIRGFCHLYSGQEACAVGMKAAMT
EGDAVITAYRCHGWTWLLGATVTEVLAELTGRVAGNVHKGKGGSMHMYTKNFYGGNGIVGA
QQPLGAGVALAMKYREQKNVCVTLYGDGAANQGQLFEATNMAKLWDLPLVFCENNNGFGM
GTTAERSSASTEYYTRGDYVPGIWVDGMDILAVREATKWAKEYCDSGKGPLMMEMATYRY
HGHMSMDPGTSYRTREEIQEVRKTRDPITGFKDRIITSSLATEEELKAIDKEVRKEVDEA
LKIATSDGVLPPPEALYADIYHNTPAQEIRGATIDETIVQPFKTSADVLKSIGRA

>dme:Dmel_CG7010 K00161 pyruvate dehydrogenase E1 component subunit alpha
[EC:1.2.4.1] | (RefSeq) Pdha; pyruvate dehydrogenase E1 alpha subunit, isoform A (A)
MLRTLRSRVSELPIIVKQLQKNAAQAGVSKTNNYATEATVQVNRPFKLHRLDEGPATEVKL
TKDQALKYYTQMQTIRRETAAGNLYKEKIIRGFCHLYSGQEACAVGMKAAMRDVDNIIS
AYRVHGWTYLMGVSPSGVLAELTGVQGGCARGKGGSMHMYAPNFYGGNGIVGAQVPLGAG
VGLACKYKGNNGMCLALYGDGAANQGQVFEAYNMAYLWKLPVIFVCENNNYGMGTSSERA
SCNTDYYTRGDALPGIWVDGMDVLAVRSATEFAINYVNTHGPLVMETNTYRYSGHMSMDP
GTSYRTREEIQEVRQKRDPITSFKELCIELGLITTDEVKAIDLKVRKEVDEATAFAKSDA
ELGVSHLWTDVYSNNLEPKLRGTIAYDIDHIQERKGVNH

>dme:Dmel_CG7024 K00161 pyruvate dehydrogenase E1 component subunit alpha
[EC:1.2.4.1] | (RefSeq) CG7024; uncharacterized protein (A)
MMKFSCVRVAMRCSGAHSILERNMLCRIIGRHKCSCLTLENTFKCYDLENGPTMDVELSR
EDALTYTQMLELRRFETVAGNYYKERKIRGFCHLYNGQEAVAVGMKQRLRSCDSVITAY
RCHAWTYLMGVSLYEIMAELFGVRTGCSRGKGGSMHMYSDKFYGGNGIVGAQVPLGAGIG
LAHSYRKDNGVSVVLYGDGAANQGQIFESFNMAKLWCLPCIFVCENNNHYGMGTHVKRASA
MTEFYMRGQYIPGLWVDGNQVLAVRSATQFAVDHALKHGPIVLEMSTYRYVGHMSMDPGT
SYRSREEVQSTREKRDPIITSFRSQIALLCLADEEELKALDDKTRKQVDSICKKATTDREV
ELDELHTDIYAKNVDGKIRGVSGFHLEHIKLAEVCFGKPKKTPASEINDVPVGAEIDVAK
AKERKAKQDAKKAKEAKEPKGGDKKGADAKQPKGEGDDGDKPKPAAQPPTKAPPAPKK

>dme:Dmel_CG11876 K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1] | (RefSeq) Pdhb; pyruvate dehydrogenase E1 beta subunit, isoform D (A)
MLRTRLIQAASSAQRAFSTSQKALAAKQMTVRDALNSALDDELARDDR VFILGEEVAQYD
GAYKVSRLWKKYGDKRVIDTPITEMGFAGIAVGAAMAGLRPVCFMTWNFSMQAIDHII
NSAAKTFYMSAGAVNPVIFRGPNGAASGVAAQHSQCFAAWYAHCPGLKVLSPYDAEDAR
GLLKSAIRD PDPVVFLNELVYGTAFPVADNVADKDFLVPIGKAKVMRPGKDITLVAHSK
AVETSLAAAE LAKKGIEAEVINLRSIRPLDTATIFASVRKTHHLTVENGWPQHGVGAE
ICARIMEDQTF FELDAPVWRCAGVDVPMPYAKTLEAHALPRVQDLVEATLKVLGGKVGKA
AAANK

>mmu:18597 K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] | (RefSeq) Pdha1, Pdha-1; pyruvate dehydrogenase E1 alpha 1 (A)
MRKMLAAVSRVLGSAQKPASRVLVASRN FANDATFEIKKCDLHRLEEGPPVTTVLTRED
GLKYYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFTRGLPVRAILAE LTGRRGGA KKGKGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPCIFICENNRYGMGTSVERAAAST
DYYKRGDFIPGLRVDGMDILCVREATKFAAAYCRSGKGPILMELQTYRYHGHSMSPDGV S
YRTREEIQEVRSKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVRGANQWIKFKSVS

>mmu:18598 K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] | (RefSeq) Pdha2, Pdha1; pyruvate dehydrogenase E1 alpha 2 (A)
MRKMLTAVLSHVFSGMVQKPALRGLLSSLKFSNDATCDIKKCDLYRLEEGPPTSTVLTRA
EALKYYRTMQVIRRMELKADQLYKQKFIRGFCHLCDGQEACCVGLEAGINPTDHSVITSYR
AHGFCYTRGLSVKSILAE LTGRKGGCAKKGKGGSMHMYGKNFYGGNGIVGAQVPLGAGVAF
ACKYLKNGQVCLALYGDGAANQGQVFEAYNMSALWKLPCVFICENNLYGMGTSNERSAAS
TDYHKKGFIPGLRVNGMDILCVREATKFAADHCRSGKGPIVMELQTYRYHGHSMSPDGI
SYRSREEVHNVRSKSDPIMLLRERIISNNLSNIEELKEIDADVKKEVEDAAQFATTDPEP
AVEDIANYLYHQDPPFEVRGAHKWLKYKSHS

>mmu:68263 K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1] | (RefSeq) Pdhb, 2610103L06Rik; pyruvate dehydrogenase (lipoamide) beta (A)
MAVVAGLVRGPLRQASGLLKRRFHR SAPAAVQLTVREAINQGMDEELERDEKVFLLGEEV
AQYDGAYKVSRLWKKYGDKRIIDTPISEMGFAGIAVGAAMAGLRPICFMTFNFMSQAI
DQVINSAAKTYYSAGLQPVPIVFRGPNGASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVMLENELMYGVAFELPAEAQSKDFLIPIGKAKIERQGTHITVV
AHSRPVGHCLEAAAVLSKEGIECEVINLRTIRPMDIEAIEASVMKTNHLTVEGGW PQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVPMPYAKVLEDNSVPQVKDIIFAVKKT LNI

>hsa:5160 K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] | (RefSeq) PDHA1, E1alpha, PDHA, PDHAD, PDHCE1A, PHE1A; pyruvate dehydrogenase E1 subunit alpha 1 (A)

MRKMLAAVSRVLSGASQKPASRVLVASRNFANDATFEIKKCDLHRLEEGPPVTTVLTR
EDGLKYYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFTRGLSVREILAEALTGRKGGCAKGKGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTYGDGAANQGQIFEAYNMAALWKLPCIFICENNRYGMGTsverAAAST
DYYKRGDFIPGLRVDGMDILCVREATRFAAAYCRSGKGPILMELQTYRYHGHSMSPDGV
SYRTREEIQEVRSKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVRGANQWIKFKSVS

>hsa:5161 K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] | (RefSeq) PDHA2, PDHAL, SPGF70; pyruvate dehydrogenase E1 subunit alpha 2 (A)

MLAAFISRVLRRVAQKSARRVLVASRNSSNDATFEIKKCDLYLLEEGPPVTTVLTRA
EGLKYYRMMLTVRRMELKADQLYKQKFIRGFCHLCDGQEACCVGLEAGINPSDHVITSYRA
HGVCYTRGLSVRSILAEALTGRRGGCAKGKGGSMHMYTKNFYGGNGIVGAQGPLGAGIALA
CKYKGNDEICLTLYGDGAANQGQIAEAFNMAALWKLPCVFICENNLYGMGTSTERAAAS
PDY YKRGNFIPGLKVDGMDVLCVREATKFAANYCRSGKGPILMELQTYRYHGHSMSPD
GVSYRTREEIQEVRSKRDPPIILQDRMVNSKLATVEELKEIGA
EVRKEIDDAQFATTDPEPHLE ELGHHIYSSDSSFEVRGANPWIKFKSVS

>hsa:5162 K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1] | (RefSeq) PDHB, E1beta, PDHBD, PDHE1-B, PDHE1B, PHE1B; pyruvate dehydrogenase E1 subunit beta (A)

MAAVSGLVRRPLREVSGLLKRRFHWTAALQVTVRDAINQGMDEELERDEKVFLLGEEV
AQYDGAYKVSRLWKKYGDKRIIDTPISEMGFAGIAVGAAMAGLRPICEFMTFNFSMQAI
DQVINSAAKTYTMSGGLQPVPVIFRGPNASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVLENELMYGVPFEFPPEAQSKDFLIPIGKAKIERQGTHITVV
SHSRPVGHCLEAAAVLSKEGVECEVINMRTIRPMDMETIEASVMKTNHLVTVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVPMPLYAKILEDNSIPQVKDIIFAIKKTLNI

PYRUVATE DEHYDROGENASE ACETYLTRANSFERASE

>eco:b0115 K00627 pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) aceF; pyruvate dehydrogenase, E2 subunit (A)
MAIEIKVPDIGADEVEITEILVKVGDKVEAEQSLITVEGDKASMEVPSPQAGIVKEIKVS
VGDKTQTGALIMIFDSADGAADAAPAQAEKKEAAPAAAPAAAAAKDVNVPDIGSDEVEV
TEILVKVGDKVEAEQSLITVEGDKASMEVPAPFAGTVKEIKVNVGDKVSTGSLIMVFEVA
GEAGAAAPAAKQEAAPAAAPAPAAGVKEVNVPDIGGDEVEVTEVMVKVGDKVAAEQSLIT
VEGDKASMEVPAPFAGVVKELKVNVDGDKVKTGSLIMIFEVEGAAPAAAPAKQEAAPAPA
AKAEAPAAAPAAKAEKGSEFAENDAYVHATPLIRRLAREFGVNLAKVKGTGRKGRILRED
VQAYVKEAIKRAEAAPATGGGIPGMLPWPVKVDFSKFGEIEEVELGRIQKISGANLSRNW
VMIPHVTHFDKTDITELEAFRKQQNEEAARKLDVKITPVVFIMKAVAAALEQMFRFNSS
LSEDGQRLTLKKYINIGVAVDTPNGLVVPVFKVDVNKKGIIELSRELMTISKKARDGKLT
GEMQGGCFTISSIGGLGTTTHFAPIVNAPEVAILGVSKSAMEPVWNGKEFVPRMLPLISLS
FDHRVIDGADGARFITIINNTLSDIRRLVM

>sce:YNL071W K00627 pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) LAT1, ODP2, PDA2; dihydrolipoyllysine-residue acetyltransferase (A)
MSAFVRVVPRISSVLTRSLRLQLRCYASYPEHTIIGMPALSPTMTQGNLAAWTKKEGD
QLSPGEVIAEIETDKAQMDFEFQEDGYLAKILVPEGTKDIPVNKPIAVYVEDKADVPFAK
DFKLEDGSDSKTSTKAQPAEPQAEKKQEAPAEETKTSAPAEAKSDVAAPQGRIFASPLA
KTIALEKGISLKDVHGTGPRGRITKADIESYLEKSSKQSSQTSAAAAATPAAATSSTTAG
SAPSPSSTASYEDVPISTMRSIIGERLLQSTQGIPSYIVSSKISISKLLKLRQSLNATAN
DKYKLSINDLLVKAITVAAKRVPDANAYWLPNENVIRKFKNVDVSVAVATPTGLLTPIVK
NCEAKGLSQISNEIKELVKRARINKLAPEEFQGGTICISNMGMNNAVNMFTSIINPPQST
ILAIATVERVAVEDAAAENGFSFDNQVTITGTFDHRTIDGAKGAEFMKELKTVIENPLEM
LL

>dme:Dmel_CG5261 K00627 pyruvate dehydrogenase E2 component
(dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) muc; midline
uncoordinated, isoform C (A)
MLRSLATTRNELGALRSVLLRSNNATYVRRSTGNVVVRALSSQLINSRKLQSIKSLNNTS
QSPVTWSYNFARAYANLPEHIRVPLPALSPMTERGSIVSWEKKEGDKLNEGDLLCEIETD
KATMGFETPEEGFLAKILIQGGTKDVPVGQLLCIIVPDQGSVAAFANFKDDGAAAAAPAP
AAPAPAPAAAAAPPPPPPPAAAPAAAAAPPPAPAAAPAAAGQKAAAKPAAAAAPAKAPRAA
GARYEDIPVTNMRAVIAKRLLSKTQLPHYVYTVQCQVDKLLKFRKVNKKYEKQGARVS
VNDFIIKAVAIASLKVPEANSAWMDTVIRKYDDVDVSVAVSTDKGLITPIVFNADRKGVL
EISKDVKALAAKARDNKLQPHFEFQGGTISVSNLGMFGVNVQFAAVINPPQSCILAIGTTTK
QLVADPDSLKGFKEVNMLTVTLSDHRVVDGAVAAARWLQHFRDYMEDPSNMVL

PYRUVATE- FERREDOXIN FLAVODOXIN OXIDOREDUCTASE

>eco:b1378 K03737 pyruvate-ferredoxin/flavodoxin oxidoreductase [EC:1.2.7.1 1.2.7.-] |
(RefSeq) ydbK; putative pyruvate-flavodoxin oxidoreductase (A)
MITIDGNGAVASVAFRTSEVIAIYPITPSSTMAEQADAWAGNGLKNVWGDTPRVVEMQSE
AGAIATVHGALQTGALSTSFTSSQGLLLMIPTLYKLAGELTPFVLHVAARTVATHALSIF
GDHSDVMAVRQTGCAMLCAANVQEAQDFALISQIATLKSRVPFIHFFDGFRTSHEINKIV
PLADDTILDMPQVEIDAHRRARALNPEHPVIRGTSANPDYFQSREATNPWYNAVYDHVE
QAMNDFSAAATGRQYQPFYYGHPQAERVIIILMGSAIGTCEEVVDLLTRGEKVGVLKVRL
YRPFSAKHLLQALPGSVRSVAVLDRTKEPGAQAEPLYLDVMTALAEAFNNGERETLPRVI
GGRYGLSSKEFGPDCVLAVFAELNAAKPKARFTVGIYDDVTNLSLPLPENTLPNSAKLEA
LFYGLGSDGSVSATKNNIKIIGNSTPWYAQGYFVYDSKKAGGLTVSHLRVSEQPIRSAYL
ISQADFGVCHQLQFIDKYQMAERLKPGGIFLLNTPYSADEVWSRLPQEVQAVLNQKKARF
YVINAAKIARECGLAARINTVMQMAFFHLTQILPGDSALAELQGAIKSYSSKGQDLVER
NWQALALARESVEEVPLQPVNPHSANRPPVVS DAAPDFVKT VTAAMLGLGDALPVSALP
PDGTWPMGTTRWEKRNIAEEIPIWKEELCTQCNHCVAACPHSAIRAKVVPPEAMENAPAS
LHSLDVKS RDMRGQKYVLQVAPEDCTGCNLCVEVCPAKDRQNPEIKAINMMSRLEHV EEE
KINYDFFLNLPEIDRSKLERIDIRTSQLITPLFEYSGACSGCGETPYIKLLTQLYGDRML
IANATGCSSIYGGNLPSTPYTTDANGRGPAWANS LFEDNAEFGLGFRLTVDQHRVRVLRL
LDQFADKIPAELLTALKSDATPEVRREQVAALRQQ LNDVAEAHELLRDADALVEKSIWLI
GGDGWAYDIGFGGLDHVLSLTENVNILLVDTQCYSNTGGQASKATPLGAVTKFGEHGKRK
ARKDLGVSM MYGHVYVAQISLGAQLNQTVKAIQEAEAYPGPSLIAYSPCEEHGYDLAL
SHDQMRQLTATGFWPLYRFDPRRADEGKLPLALDSRPPSEAPEETLLHEQRFRR LNSQQP
EVAEQLWKDAAADLQKRYDFLAQMAGKAEKSNTD

SUCCINATE DEHYDROGENASE

>eco:b0721 K00241 succinate dehydrogenase cytochrome b subunit | (RefSeq) sdhC;

succinate:quinone oxidoreductase, membrane protein SdhC (A)

MIRNVKKQRPVNLDLQTIRFPITAIASILHRVSGVITFVAVGILLWLLGTSLSSPEGFEQ
ASAIMGSFFVKFIMWGILTALAYHVVGIRHMMMDFGYLEETFEAGKRSAKISFVITVVL
SLLAGVLVW

>eco:b0722 K00242 succinate dehydrogenase membrane anchor subunit | (RefSeq) sdhD;

succinate:quinone oxidoreductase, membrane protein SdhD (A)

MVSNASALGRNGVHDFILVRATAIVLTLYIIMVGFFATSGELTYEVWIGFFASAFTKVF
TLLALFSILIHAWIGMWQVLTDYVKPLALRLMLQLVIVVALVYVIYGFVVVWGW

>eco:b0723 K00239 succinate dehydrogenase flavoprotein subunit [EC:1.3.5.1] | (RefSeq)

sdhA; succinate:quinone oxidoreductase, FAD binding protein (A)

MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT
HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILEEHMGLPFSRLDDGRIYQRPFG
GQSKNFGGEQAARTAAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGAVVGC
TALCIETGEVVYFKARATVLATGGAGRIYQSTTNAHINTGDGVGMAIRAGVPVQDMEMWQ
FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVARSIMIEIREG
RGCDGPWGPFAKLKLDHLGKEVLESRLPGILELSRTFAHVDPVKEPIPIPTCHYMMGGI
PTKVTGQALTVNEKGEDVVVPGLFAVGEIACVSVHGANRLGGNSLLDLVVFGRAGLHLQ
ESIAEQGALRDASESDVEASLDRLNRWNNNRNGEDPVAIRKALQECMQHNFSVFREGDAM
AKGLEQLKVIRERLKNARLDDTSSEFNTQRVECLELDNLMETAYATAVSANFRTESRGAH
SRFDFPDRDDENWLCHSLYLPESMSMTRRSVNMEPKLRPAFPKIRTY

>eco:b0724 K00240 succinate dehydrogenase iron-sulfur subunit [EC:1.3.5.1] | (RefSeq) sdhB;

succinate:quinone oxidoreductase, iron-sulfur cluster binding protein (A)

MRLEFSIYRYNPVDVDDAPRMQDYTLEADEGRDMMLLDALIQLKEKDPSLSFRRSCREGVC
GSDGLNMNGKNGLACITPISALNQPGKKIVIRPLPGLPVIRDLVVDMGQFYAQYEKIPY
LLNNGQNPPAREHLQMPEQREKLDGLYECILCACSTSCPSFWWNPDKFIGPAGLLAAYR
FLIDSRDTETDSRLDGLSDAFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMMLQRNA

>eco:b4151 K00247 succinate dehydrogenase subunit D | (RefSeq) frdD; fumarate reductase
membrane protein FrdD (A)

MINPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFAQ
SFIGRVFLFLMIVLPLWCGLHRMHAMHDLKIHVPAGKWVIFYGLAAILT VVTLIGVVTI

>eco:b4152 K00246 succinate dehydrogenase subunit C | (RefSeq) frdC; fumarate reductase membrane protein FrdC (A)

MTTKRKPYVRPMTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGF
VDFLQNPVIVIIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVA
TIVILFVALYW

>eco:b4153 K00245 succinate dehydrogenase iron-sulfur subunit [EC:1.3.5.1] | (RefSeq) frdB;
fumarate reductase iron-sulfur protein (A)

MAEMKNLKIEVVRYNPEVDTAPHSAFYEVYPDATTSLLDALGYIKDNLAPDLSYRWSCRM
AICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVDMTHFIESLEAIKPY
IIGNSRTADQGNTNIQTPAQMAKYHQFSGCINCGLCYAACQPQFGLNPEFIGPAAITLAHRY
NEDSRDHGKKERMAQLNSQNGVWSCFTVGYCSEVCPKHVDPAAAIQQGKVESSKDFLIAT
LKPR

>eco:b4154 K00244 succinate dehydrogenase flavoprotein subunit [EC:1.3.5.1] | (RefSeq) frdA;
fumarate reductase flavoprotein subunit (A)

MQTFQADLAIVGAGGAGLRRAAIAAAQANPNKIALISKVYPMRSHTVAAEGGSAAVAQDH
DSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGCPWSRRPDGSVNVRFRFGGM
KIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGT
LVQIRANAVVMATGGAGRVYRYNTNGGIVTGDGMGMALSHGVPLRDMFVQYHPTGLPGS
GILMTEGCRGEGGILVNKNKYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWHEWR
KGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEIPVRPTAHYTMG
GIETDQNCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQATERAATAGN
GNEAAIEAQAAGVEQRLKDLVNQDGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKL
AELQERFKRVKITDTSVFNTDLLYTIELGHGLNVAECMAHSAMARKESRGAHQRLDEGC
TERDDVNFLKHTLAFRDADGTTTRLEYSVDKITTLPKRVYGGEDAADKAEAAANKKEKA
NG

>sce:YDR178W K00237 succinate dehydrogenase (ubiquinone) membrane anchor subunit |
(RefSeq) SDH4, ACN18; succinate dehydrogenase membrane anchor subunit SDH4 (A)

MMLPRSMKFMTGRRIFHTATVRAFQSTAKKSLTIPFLPVLPQKPGGVRGTPNDAYVPPPE
NKLEGSYHWYMEKIFALSVVPLATTAMLTGPLSTAADSFFSVMLLGYCYMEFNCSITDY
ISERVYGVWHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSSEKDNSQKIEAK
K

>sce:YJL045W K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1]
| (RefSeq) SDH9; succinate dehydrogenase SDH1b (A)

MLSLKKGITKSYILQRTFTSSSVVRQIGEVKSESKPPAKYHIIDHEYDCVVVGAGGAGLR
AAFGLAEEAGYKTACLSKLPTRSHTVAAQGGINAALGNMHPDDWKSHMYDTVKGSDWLGD
QDAIHYMTREAPKSVIELEHYGMPFSRTEDGRIYQRAFGGQSKDFGKGGQAYRTCAVADR

TGHAMLHTLYGQALKNNTHFFIEYFAMDLLTHNGEVVGVIAYNQEDGTIHRFRAHKT VIA
TGGYGRAYFSCTSAHTCTGDGNAMVSRAGFPLEDFVQFHPSGIYSGCLITEGARGE
GFLNSEGERFMERYAPTAKDLASRDVVSRAITMEIRAGRGVGNKDHILLQLSHLPPEV
LKERLPGISETAAVFAGVDVTQEPIVLPVTVHYNMGGIPTKWTGEALTIDEETGEDKVIP
GLMACGEAACVSVHGANRLGANSLLDLVVFGRAVANTIADTLQPGLPHKPLASNIGHESI
ANLDKVRNARGSLKTSQIRLNMQRTMQKDVSVFRTQDTLDEGVRNITEVDKTFEDVHVSD
KSMIWNSDLVETLELQNLLTCATQTAVSASKRKESRGAHAREDYAKRDDVNWRKHTLSWQ
KGTSTPVKIKYRNVIAHTLDENECAPVPPAVRSY

>sce:YKL141W K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit |
(RefSeq) SDH3, CYB3, YKL4; succinate dehydrogenase cytochrome b subunit SDH3 (A)
MSAMMVKLGLNKSALLLKPSAFSRAAALSSSRLLFNTARTNFLSTSPLKNVASEMNTKA
AIAEEQILNKQRAKRPISPHLTIYQPQLTWYSSLHRISLVLMLGLGFYLFITLFGVSGLL
GLGLTTEKVSNNWYHQFSKITEWSIKGSFAYLFAIHYGGAIRHLIWD TAKELTLKGVYRT
GYALIGFTAVLGTYLTL

>sce:YKL148C K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1]
| (RefSeq) SDH1; succinate dehydrogenase flavoprotein subunit SDH1 (A)
MLSLKKSALSKLTLLRNTRTFTSSALVRQTQGSVNGSASRSADGKYHIIDHEYDCVVIGA
GGAGLRAAFGLAEAGYKTACISKLFPTRSHTVAAQGGINAALGNMHKDNWKWHMYDTVKG
SDWLGDQDSIHYMTREAPKSIIELEHYGVFPSRTENGKIYQRAFGGQTKEYGKGAQAYRT
CAVADRTGHALLHTLYGQALRHDTHFFIEYFALDLLTHNGEVVGVIAYNQEDGTIHRFRA
HKTIIATGGYGRAYFSCTSAHTCTGDGNAMVSRAGFPLQDLEFVQFHPSGIYSGCLITE
GARGEGLVNSEGERFMERYAPTAKDLACRDVVSRAITMEIREGRGVGKKKDHMYLQLS
HLPPEVLKERLPGISETAAIFAGVDVTKEPIIPTVHYNMGGIPTKWNGEALTIDEETG
EDKVIPGLMACGEAACVSVHGANRLGANSLLDLVVFGRAVAHTVADTLQPGLPHKPLPSD
LGKESIANLDKLRNANGSRSTAEIRMNMKQTMQKDVSVFRTQSSLDEGVRNITAVEKTFD
DVKTTDRSMIWNSDLVETLELQNLLTCASQTAVSAANRKESRGAHAREDYPNRDDEHWMK
HTLSWQKDVAAPVTLKYRRVIDHTLDEKECPSVPPTVRAY

>sce:YLL041C K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1] |
(RefSeq) SDH2, ACN17; succinate dehydrogenase iron-sulfur protein subunit SDH2 (A)
MLNVLLRRKAFCLVTKKGMATATTAAATHPTRLKTFKVYRWNPDEPSAKPHLQSYQVDLN
DCGPMVLDALLKIKDEQDSTLTFRSCREGICGSCAMNIGGRNTLACICKIDQNESKQLK
IYPLPHMFIVKDLVPDLTNFYQQYKSIQPYLQRSSF PKDGT EVLQSIEDRKLDGLYECI
LCACCSTSCPSYWWNQEQYLGPVLMQAYRWLIDSRDQATKTRKAMLNNSMSLYRCHTIM
NCTRTCPKGLNPGLAIAEIKKSLAFA

>sce:YLR164W K00237 succinate dehydrogenase (ubiquinone) membrane anchor subunit |
(RefSeq) SHH4; protein SHH4 (A)

MSSTKFLKPLCRIRAFHTSIARSFTIPFLPKIPQKPGGVSGTANDSSYMPPE\$RAQGSYH
WIVERGLSLAVLPLIAVPLVTTGPSTFTDTFLSLVLLGHCHIGFQSCIIDYISERVYGK
VHHYAMYLLSLGSFSLFVGIIKLESQEAGLIASLKSLLW\$DNKPVEKKRQ

>sce:YMR118C K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit |
(RefSeq) SHH3; protein SHH3 (A)

MKATIQRVTSVFGVPRASVFPRI\$TPFILHNYISNGRMDLFSKEFHNGRV\$KSDLWSSN
KEEELLVSQRKKRPI\$PHLTVYEPMSWYLLSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWD\$MGYELN\$RGVIKTGS
IVLAGTLVLGTYLLAQ

>cel:CELE_C03G5.1 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit
[EC:1.3.5.1] | (RefSeq) sdha-1; Succinate dehydrogenase [ubiquinone] flavoprotein subunit,
mitochondrial (A)

MLRAASNGLRNTVAARSVSL\$AANHSDAKRSDIAQYKVVDHAYDAV\$VGAGGAGLRAAMG
LAEGGLKTAVITKLFPT\$RSHTVAAQGGINAALGNMNP\$DNWRWHFYDTVKGSDWLGDQDAI
HYMTRE\$AERAVIELENYGMPFSRTTDGKIYQRAFGGQ\$SNDFGRGGQAHRTCCVADRTGHS
LLHTLYGASLQYNCNYFVEYFALDLIMENGVCVGV\$IAMDLEDGTIHRFR\$KNTVLATGGY
GRAFFSCT\$AHTCTGDGTALTARAGINNSDMEFVQFHPTGIY\$GAGCLITEGSRGEGGYLV
NSAGERFMERYAPNAKDLASRDVVSRSMTVEIMEGRGV\$GPDKDHIYLLQLHHLPAEQLQQR
LPGISETAMIFAGVDV\$TKEPIPIPTVHYNMGGVPTNYKGQVLNYTPKKGDEVVPGLYAA
GECGAH\$SVHGANRLGANSLLDLVIFGRACAIDILKNTSAGVGVPEL\$PKNAGEASVANIDK
LRHNKGDIS\$TAE\$RLTMQKSMQNHA\$AVFRRGDILKEGVKVL\$SKLYKDQAHLNVADKGLVW
NSDLIETLELQ\$NLLINATQTIVAAENREESRG\$AHARDDFPDRLDEL\$DYSKPLEGQTKKEL
KDHWRKHSIIRSNIETGEVSLDYRPVIDTTLDKSETDWVPPK\$VRSY

>cel:CELE_C34B2.7 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit
[EC:1.3.5.1] | (RefSeq) sdha-2; Succinate dehydrogenase [ubiquinone] flavoprotein subunit,
mitochondrial (A)

MLNVVKSINRAKTPVRTYMKKQVSATTNFDVVDHTF\$DAV\$VGAGGAGLRAAMGLSEGGMK
TAVITKLFPT\$RSHTVAAQGGVNAALGNMNP\$DNWRWHFYDTVKGSDWLGDQDAIHYMTRE\$A
ERAIIELENYGMPFSRTTDGKIYQRAFGGQ\$SNDFGRGGQAHRTCCVADRTGHSLLHTLYG
ASLQYDCNYFVEYFALDLIMDKGKCIGVVALDIETGQIHRFRAKNTVLATGGYGRAYFSC
T\$AHTCTGDGTALTARAGIRNSDMEFVQFHPTGIYGVGCLITEGSRGEGGYLVNSQGERF
MERYAPNAKDLASRDVVS\$RAMTMEINEGRGVGP\$NPKDHIYLLQLHHLPAEQLQQR\$LPGISET
AQIFAGVDV\$TKEPIPIPTVHYNMGGVPTNYKGQVLDF\$TPEG\$DKVIPGLYAAGECA\$AHS
VHGANRLGANSLLDLVIFGRSCALTILNENKPGDSIPEL\$PVNCEEKSCDNLNGLLH\$SKGD
ISSIELRQKMQMTMQKHA\$AVFRRGDLLKEGV\$DKMSSYKEQQNLKACADSGKVWNS\$ELVE
TLELQ\$NLLINANQTIVAAENRTESRG\$AHARDDFQERIDEYDYSNP\$LEGQ\$KPKPFDQHW\$RK
HSIIGIDTKTGAVDLTYRPVIDKTLDKSETDWVPPK\$VRSY

>cel:CELE_F33A8.5 K00237 succinate dehydrogenase (ubiquinone) membrane anchor subunit | (RefSeq) sdhd-1; Putative succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial (A)

MAASLRHMAHFQKALLVARSA PRISTIVRATSTLNDGASKVPDHSMHFKLERLWAVGMLP
ILPASYFIHGPMVMDAVLTVALTLHIHWGIHGVVYDYARPYVIGEAAAKAAHVGVYLITGL
LLGALLHFNTNDVGITKAFELVFSL

>cel:CELE_F42A8.2 K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1] | (RefSeq) sdhb-1; Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (A)

MLARSARLLHSAELAANAIRAASGAPATAAAAEASFPSTDDVAAKTKKTGNRIKTFEIYR
FNPEAPGAKPTVQKFDVDLDQCGTMILDALIKIKNEVDPTLTFRRSCREGICGSCAMNIG
GQNTLACICKIDSDTSKSTKIYPLPHMFVVKDLVPDMNLFYAQYASIQPWIKKTPLTLG
EKQMHQSVAERDRDLGLYECILCACCTSCPSYWWNADKYLGPAVLMQAYRWVIDSRDDY
ATERLHRMHDSFSAFKCHTIMNCTKTCPKHLNPAKAIGEIKSLTGFTSKPAAEPSAF

>cel:CELE_T07C4.7 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit | (RefSeq) mev-1; Succinate dehydrogenase cytochrome b560 subunit, mitochondrial (A)

MINIPTAILCRLGARSSISRSFGTSIVTKSEAKTPIQKFGWEYLLKQRSKNRPIAPHLTV
YQPQLTWMLSGFHRISGCV MAGTLLVGGIGFAVL PFDFTAFVDFIRSWNLPCA VTAVFKY
IIAFPIIFHTLNGIRFLGFDLAKGVNNVGQIYKSGYLVSGLSAILALAIVFNSCQNKSNK
TA

>dme:Dmel_CG3283 K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1] | (RefSeq) SdhB; succinate dehydrogenase, subunit B (iron-sulfur) (A)

MLATEARQILSRVGS LVARNQMR AISNGTAQLEQQAQPK EAQEPQIKKFEIYRWNP DNAG
EKP YMQTYEVDLRECGPMVLDALIKIKNEMDPTLTFRRSCREGICGSCAMNIGGTNTLAC
ISKIDINTSKSLKVYPLPHMYVVRDLVPDMNNFYEQYRNIPWLQRKNEAGEKKGKAQYL
QSVEDRSKLDGLYECILCACCTSCPSYWWNAEKYLGPAVLMQAYRWIIDS RDENSAERL
NKLKDPFSVYRCHTIMNCTRTCPKGLNPGRAIAEIKLLSGLASKPAPKLETAALHK

>dme:Dmel_CG5718 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1] | (RefSeq) SdhA; succinate dehydrogenase, subunit A (flavoprotein)-like (A)

MNRLFLKRAGQH VTRSL LGPN GSRL LQVSCVRDASCKDEYSLIDHKFDAIVIGAGGAGMR
AGFGLAEKGFQTAIISKLFPTRSHTVAAQGGVNAA LSNDKDDWKYHFYDTVKGSDWLGD
QNAIHYMCREAERAVCELD MYGMPFSRKPDGKIYQRPFGGQTLDYGKGGVARRACACADR
TGHALIHTLYGQTLKHSDSCHYFVDYFVLDLIMSQGACVGCLAWK LDDGTFHRFLAKNTV
VAAGGCGRVYFSTTAGHTCTGDGNAWVSRQELPLMDMEFVQFHPTGIYGAGCLITEGVRG
EGGFFLNCKGERFMERYAPKAKDLASRDVVARAMTMEVLAGNGCGPLKDHVHLQLHHIDA

KIIKQRLPGIMVTARIFAKVDVTKEPVPVLPTVHYNMGGIPTDYKGRVVTIDENGKEQVV
KGLYSCGETSCASVHGANRLGANSLLDLIFGRVCALDIAANNC PGDKPPQVEDKATEKS
LDNFKRLRCADGCIPTAVLRMELQRTMTKHA AVFREGKLLKEGLLKVAELCEQFKDIKT
DRTMVWNSNLVETLELQNMLANAVHIITAMENR KESRGSHARED FKTRVDELDYGAPLAG
QKKKPFEEHWRKHTMTFALGNKG CASIKYRPVVDTTLDSSVAIIPPAPRTY

>dme:Dmel_CG6629 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit
| (RefSeq) SdhCL; succinate dehydrogenase, subunit C-like (A)

MNTCRSLARGLNICSPQLRHLLAQKPFNSARLLATKAPKDHKASGPTTIGPSGDILVPPV
TLKVIPFRMPDLPYDDRNMLLGRQLSPHLSIYKIQLTSTLSAFLRISGFVLAVFVWFVG
ISGLCLQGDMEGFIKKVEKCDCHGMVTMAKVMVTMPFAYHTVAGTRHLIWYLNKFLTIPE
IYATGYVAVALTIALSAFLAVKVGEKVKEEVVDLT KTKKGQKAKKEAPKDAKKDAPKDT
KKEPKKDAKD KKKDEEGKSAK

>dme:Dmel_CG6666 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit
| (RefSeq) SdhC; succinate dehydrogenase, subunit C, isoform B (A)

MYALSSSLIRSPALRQGLQMAAASRPVSMKVVSVAETQKDESF FEKNERLGRELSPHLTI
YQPQLTSMLSICHRGTGLALGVGVWGLGLGALISSHDISHYVTMVEGLQLSGATLTALKF
IIAYPAGYHTANGIRHLLWDTGRFLKIKEVYSTGYAMVATSFVLSAILALL

>dme:Dmel_CG7349 K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit
[EC:1.3.5.1] | (RefSeq) SdhBL; succinate dehydrogenase, subunit B (iron-sulfur)-like, isoform C
(A)

MNLLRRQPRLLNKRSTWLFRNYVLANRDVSEPVSRPAAPMSTLSIPGPALAAATPVSAVS
LVPRCTHSSLQGGGQGAGGRGLRGSATGSSAAGGIATKRQYSGGAAPAGAAKPGGAAPAG
AAKPGGAAPAGAAKPGGAAAAAAGSAKPGGASTGKPASGNAPATPPPPPPPPAKSAPPV
KAKKPRLKTFEIYRWKPGDQPQTQTYEVDLEQCGAMVLDALIKIKNEMDPTLTFRSCRE
GICGSCAMNINGTNTLACVSSIDQNESKCCRIYPLPHLYVVRDLVPDMSQFYDQYRSIQP
WLQRKDLKREAGTAQYLQSVDDRLVLDGLYECILCACCQTSCPSYWWNSNKYLGPVLMQ
AYRWVIDSRDEATEQRDLFLKDPWKLYRCHSIMNCTNTCPKHLNPARAIIQLKQLLVGLK
KKGKPQLKTDALFAGKA

>dme:Dmel_CG10219 K00237 succinate dehydrogenase (ubiquinone) membrane anchor
subunit | (RefSeq) SdhD; succinate dehydrogenase, subunit D (A)

MSLSLLL RGAVRCNAANLVKSARITPLKSYSTLVANVQRKAVVQPLAVAKIVAPVVREIS
VSAPRMASAGSSHTLLWTVERIVSAGLLAVIPA AFIAPSQVLDALMAISVVIHTHWGVEA
MVVDYMRPSVVG NVLPKVAHIALIISVATLGGLFYFIQNDVGLANGIKRFWAIKGKDAE
KA

>dme:Dmel_CG17246 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1] | (RefSeq) SdhA; succinate dehydrogenase, subunit A (flavoprotein), isoform A (A)
MSGIMRVPSILAKNAVASMQRAAAVGVQRSYHITHGRQQASAANPDKISKQYPVVDHAYD
AIVVGAGGAGLRAAFGLVAEGFRTAVITKLFPTRSHTIAAQGGINAALGNMEEDDWKWHM
YDTVKGSDWLGDQDAIHMYMTREAPKAVIELENYGMPFSRTQDGKIYQRAFGGQSLKFGKG
GQAHRCCAVADRTGHSLLHTLYGQSLSYDCNYFVEYFALDLIFEDGECRGV LALNLEDGT
LHRFRAKNTVIATGGYGRAFFSCTSAHTCTGDGTAMVARQGLPSQDLEFVQFHPTGIYGA
GCLITEGCRGEGGYLINGNGERFMERYAPVAKDLASRDVVSRSMTIEIMEGRGAGPEKDH
VYLQLHHLPPKQLAERLPGISETAMIFAGVDVTREPIVLPVTVHYNMGGVPTNYRGQVIT
IDKDGDVIVPGLYAAGEAASSSVHGANRLGANSLLDLVVFGRACAKTIAELNKP GAPAP
TLKENAGEASVANLDKLRHANGQITTADLRLKMQKTMQHHA AVFRDGPILQDGVNKMKEI
YKQFKDIKVDRSLIWNSDLVETLELQNLLANAQMTIVSAEARKESRGAHAREDFKVRED
EYDFSKPLDGQKKPMDQHWRKHTLSWVCNDNGDITLDYRNVIDTTLDNEVSTVPPAIRS
Y

>mmu:66052 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit | (RefSeq) Sdhc, 0610010E03Rik; succinate dehydrogenase complex, subunit C, integral membrane protein (A)
MAAFLLRHVSRHCLRAHLNAQLCIRNAAPLGTTAKEEMERFWKKNTSSNRPLSPHLTIYK
WSLPMALSVCHRGSGIALSGGVSLFGLSALLPGNFESYLMFVKSLCLGPTLIYSAKFVL
VFPLMYHSLNGIRHLLWDLGKGLAIPQVWLSGVAVVVLAVLSSGGLAAL

>mmu:66925 K00237 succinate dehydrogenase (ubiquinone) membrane anchor subunit | (RefSeq) Sdhd, 3110001M13Rik, AVLL5809, CII-4, PRO19626, QPs3, cybS; succinate dehydrogenase complex, subunit D, integral membrane protein (A)
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVSVLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALT FAGLCYFNYHDVGICRAVAMLWKL

>mmu:66945 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1] | (RefSeq) Sdha, 1500032O14Rik, 2310034D06Rik, 4921513A11, FP, SDH2, SDHF; succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (A)
MAGVGAVSRLLRGRRALTGA WPGTLQKQTCGFHFSVGENKKASAKVSDAISTQYPVVDH
EFDVAVVGAGGAGLRAAFGLSEAGFNTACLTKLFPTRSHTVAAQGGINAALGNMEEDNWR
WHFYDTVKGSDWLGDQDAIHMYMTEQAPASVVELENYGMPFSRTEDGKIYQRAFGGQSLKF
GKGGQAHRCCCVADRTGHSLLHTLYGRSLRYDTSYFVEYFALDLLMENGE CRGVIALCIE
DGSIHRIKNTVIATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGI
YGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPE
KDHVYLQLHHLPP EQLATRLPGISETAMIFAGVDVTKEPIVLPVTVHYNMGGIPTNYKGQ
VLKHVNGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIAESCRPGDK
VPSIKANAGEESVMNLDKLRFADGSIRTSELRLNMQKSMQNHA AVFRVGSVLQEGCEKIS

QLYGDLKHLKTFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVR
VDEYDYSKPIQGQQKKPFGEHWRKHTLSYVDIKTGKVTLEYRVIDKTLNEADCATVPPA
IRSY

>mmu:67680 K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1] |
(RefSeq) Sdhb, 0710008N11Rik; succinate dehydrogenase complex, subunit B, iron sulfur (lp)
(A)

MAATVGVSLKRGFPAAVLGRVGLQFQACRGAQTAAAAAPRIKKFAIYRWDPDKTGDKPRM
QTYEVDLNKCGPMVLDALIKIKNEVDSTLTFRRSCREGICGSCAMNINGGNTLACTRRID
TDLSKVS KIYPLPHMYVIKDLVPDLSNFYAQYKSI EPYLKKKDESQEGKQQYLQSIEDRE
KLDGLYECILCACCSTSCPSYWWNGDKYLGPVLMQAYRWMIDSRDDFTEERLAKLQDPF
SVYRCHTIMNCTQTCPKGLNPGKAIAEIKKMMATYKEKRALA

>hsa:6389 K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1] |
(RefSeq) SDHA, CMD1GG, FP, MC2DN1, NDAXOA, PGL5, PPGL5, SDH1, SDH2, SDHF;
succinate dehydrogenase complex flavoprotein subunit A (A)

MSGVRGLSRLLSARRLALAKAWPTVLQTGTRGFHFTVDGNKRASAKVSDSISAQYPVVDH
EFDVVVGAGGAGLRAAFGLSEAGFNTACVTKLFPTRSHTVAAQGGINAALGNMEEDNWR
WHFYDTVKGSDWLGDQDAIHYMTEQAPAAVVELENYGMPFSRTEDGKIYQRAFGGQSLKF
GKGGQAHRCCC VADRTGHSLLHTLYGRSLRYDTSYFVEYFALDLLMENGE CRGVIALCIE
DGSIHRIKANTV VATTGGYGRTYFSC TSAHTSTGDGTAMITRAGLPCQDLEFVQFHPTGI
YGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPE
KDHVYLQLHHPPEQLATRLPGISETAMIFAGVDVTKEPIPVLP TVHYNMGGIPTNYKGQ
VLRHVNGQDQIVPGLYACGEAACASVHGANRLGANSLLDLVVFGRACALSIEESCRPGDK
VPIKPNAGEESVMNLDKLRFADGSIRTSELRLSMQKSMQNHA AVFRVGSVLQEGCGKIS
KLYGDLKHLKTFDRGMVWNTDLVETLELQNLMLCALQTIYGAEARKESRGAHAREDYKVR
IDEYDYSKPIQGQQKKPFEEHWRKHTLSYVDVGTGKVTLEYRVIDKTLNEADCATVPPA
IRSY

>hsa:6390 K00235 succinate dehydrogenase (ubiquinone) iron-sulfur subunit [EC:1.3.5.1] |
(RefSeq) SDHB, CWS2, IP, MC2DN4, PGL4, PPGL4, SDH, SDH1, SDH2, SDHIP; succinate
dehydrogenase complex iron sulfur subunit B (A)

MAAVVALSLRRRLPATT LGGACLQASRGAQTAAATAPRIKKFAIYRWDPDKAGDKPHMQT
YEVDLNKCGPMVLDALIKIKNEVDSTLTFRRSCREGICGSCAMNINGGNTLACTRRIDTN
LNKVS KIYPLPHMYVIKDLVPDLSNFYAQYKSI EPYLKKKDESQEGKQQYLQSI EEREKL
DGLYECILCACCSTSCPSYWWNGDKYLGPVLMQAYRWMIDSRDDFTEERLAKLQDPFSL
YRCHTIMNCTRTCPKGLNPGKAIAEIKKMMATYKEKKASV

>hsa:6391 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit | (RefSeq)
SDHC, CYB560, CYBL, PGL3, PPGL3, QPS1, SDH3; succinate dehydrogenase complex
subunit C (A)

MAALLLRHVGRHCLRAHFSPQLCIRNAVPLGTTAKEEMERFWNKNIGSNRPLSPHITIYS
WSLPMAMSICHRGTGIALSAGVSLFGMSALLLPGNFESYLELVKSLCLGPALIHAKFAL
VFPLMYHTWNGIRHLMWDLGKGLKIPQLYQSGVVVLVLTVLSSMGLAAM

>hsa:6392 K00237 succinate dehydrogenase (ubiquinone) membrane anchor subunit |
(RefSeq) SDHD, CBT1, CII-4, CWS3, MC2DN3, PGL, PGL1, PPGL1, QPs3, SDH4, cybS;
succinate dehydrogenase complex subunit D (A)

MAVLWRLSAVCGALGGRALLLRTPVVRPAHISAFLLQDRPIPEWCGVQHIHLSPSHHSGSK
AASLHWTSERVSVLLLGLLPAAYLNPCSAMDYSLAAALTLHGHWGLGQVVTDYVHGDAL
QKAAKAGLLALSALTFAGLCYFNYHDVGICKAVAMLWKL

SUCCINYL- CoA SYNTHETASE

>eco:b0728 K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5] | (RefSeq) sucC;
succinyl-CoA synthetase subunit beta (A)

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEAAASKIGAGPWVVKCQVHAGGRGKAGGV
KVVNSKEDIRAFENWL GKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRR
VVFMASTEGGVEIEKVAEETPHLIHKVALDPLTGMPYQGRELAFKLGLEGKLVQQFTKI
FMGLATIFLERDLALIEINPLVITKQGD LICLDGKL GADGNALFRQPD LREMRDQSQEDP
REAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGE PANFLDVGGGATKERVTE
AFKIILSDDKVKAVLVNIFGGIVRCDLIADGIIGAVA EVGVNVPVVRLEGNNAELGAKK
LADSGLNIIAAKGLTDAAQQVVA AVEGK

>eco:b0729 K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5] | (RefSeq) sucD;
succinyl-CoA synthetase subunit alpha (A)

MSILIDKNTKVICQGFTGSQGFHSEQAIAYGTKMVGGVTPGKGGTTHLGLPVFNTVREA
VAATGATASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMI
GPNC PGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGG
DPIPGSNFIDILEMFEKDPQTEAIVMIGEIGGSAEEEEAAAYIKEHVTKPVVGYIAGVTAP
KGKRMGHAGAIAGGKGTAD EKF AALEAAGVKTVRSLADIGEALKTVLK

>sce:YGR244C K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
LSC2; succinate--CoA ligase (GDP-forming) subunit beta (A)

MYSRKSLSLISKCGQLSRLNAQAALQARRHLSIHEYRSAQLLREYGIGTPEGFP AFTPEE
AFEA AKKLNTNKLVIKAQALTGGRGKGHFDTGYKSGVHMIESPQQAEDVAK EMLNHNLIT
KQTGIAGKPVSAVYIVKRVDTKHEAYLSILMDRQTKKPMIIASSQGGMNIEEVAERTPDA
IKKFSIETSKGLSPQMAKDVAKSLGFSPDAQDEAAKAVSNLYKIFMERDATQVEINPLSE
IEHDP THKIMCTDAKFGFDDNASFRQEKIYSWRDLSQEDPDEVKAKKYDLNFVKLKGNIG
CLVNGAGLAMATMDVIKLNGGDPANFLDCGGGATPETIKQGFELILSNKNVDAIFVNIFG
GIVRCDYVALGLVEAARELEVRVPIVARLQG TKVEEGRDIINKSGVKIYSFDELDPAAKK
VVELTQN

>sce:YOR142W K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
LSC1; succinate--CoA ligase (GDP-forming) subunit alpha (A)

MLRSTVSKASLKICRHFHRESIPYDKTIKNLLL PKDTKVIFQGFTGKQGTFHASISQEYG
TNVVG GTNPKKAGQTHLGQPVFASVKDAIKETGATASAIFVPPPIAAAAIKESIEAEIPL
AVCITEGIPQHDMLYIAEMLQTQDKTRLVGPNCPGIINPATKVRIGIQPPKIFQAGKIGI
ISRSGTLTYEAVQQTTKTDLGQSLVIGMGGDAFP GTDFIDALKLFLEDETTEGIIMLGEI
GGKAEIEAAQFLKEYNFSRSKPMPVASFIAGTVAGQMKGVRMGHSGAIVEGSGTDAESKK
QALRDVGVA VVESPGYLGQALLDQFAKFK

>cel:CELE_C05G5.4 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) suc1-1; Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial (A)
MLSQQIANNARTLQKGAARFYNSTYNNLKINKDTKVIVQGFTGKQGTFFHGKQMLEYNTKV
VGGVNANKAGTEHLGLPVFKNVSEARNKTGADASVIYVPASAAGSAIEEAMDAEIPLVVC
ITEGIPQHDMVRVKSRLKQNKTRLVGPNCPGIISADQCKIGIMPGHIHKRGCIGIVSRS
GTLTYEAVHQTTQVGFGQTLCVGIGGDPFNGTNFIDCLNVFLEDPETKGIILIGEIGGSA
EEEEAAAYLKEHNSGANRKPVVSFIAGVTAPPGRRMGHAGAIISGGKGTAADKINALREAG
VVVTDSPAKLGTSMATAFLGKI

>cel:CELE_C50F7.4 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) sucg-1; Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial (A)
MLRAAGNLSKSMMSQRRFLNLQEFQSKEILEKHGCSVQNFFVASNRKEAEEKWMSFGDH
EYVVKAILAGGRGKGKFINGTKGIGGVFITKEKDAALEAIDEMIGKRLVTKQTTSEGV
VDKVMIAEGVDIKRETYLAVLMDRESNGPVVVASPDGGMDIEAVAETPERIFKTPIDIQ
MGMTEGQSLKIAKDLQFEGKLIGVAAQEIKRLYDLFIAVDATQVEINPLVETADGRVFCV
DAKMNFDDSAAYRQKEIFAYETFEEDHPREVDHAFNLNYIGMDGNIACLVNGAGLAMAT
MDLIKHLHGEPANFLDVGGAVTEDAVFNAVRIITSDPRVKCVLINIFGGIVNCATIANGV
VSAVNKIGLNVPMVVRLEGTNVDAAKQIMKKSGLKILTANNLDEAAKAVSSLPK

>cel:CELE_F23H11.3 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) suc2-2; Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial (A)
MASTLASAARAATRAAVTRSVYNDTRNNLMINKSTKVIVQGFTGRQGTFFHSKQMLEYNTN
LVGGVSPNKAGQTHLGLPVFGSVAEAKDRTGADATVIYVPAAGAARAIHEAMDAEIGLIV
AITEGIPQQDMVRVKNRLLKQNKSRLLGPNCPGIISGDCKIGIMPGHIHKKGCIGIVSR
SGTLTYEAVHQTTTVGLGQTRCIGIGGDPFNGTNFIDCLEVFLEDEQTKGIILIGEIGGQ
AEEQAAEFLKSRNSGNAKPVVSFIAGVTAPPGRRMGHAGAIAGGKGTAGDKIEALRNA
NVVVTDSPAKLGVAMQKALLG

>cel:CELE_F47B10.1 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) suca-1; Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial (A)
MIGRISQPLLNTSQKFMAPAARTLMLHEHHGMKILQNYEIKVPPFGVAQDAETAFSEAKR
IGGKDYVVKAQVLGGRGKGRFSSGLQGGVQIVFTPDEVKQKAGMMIGANLITKQTDHRG
KKCEEVMVCKRFLFTRREYYFSITLDRNTNGPIVIASSQGGVNIEEVAATNPDAIVKMPID
VNVGITKELAHEIAVKMGFSKDCEQQASEIIEKLYQMFKGSDATLVEINPMAEDVNGDVY
CMDCKLLLDLSNAEFRQAKLFDLKDQKQDELEIRAAAAANLNYIRLDGTIGCMVNGAGLAM
ATMDIIKLHGEPANFLDVGGGATVEQVTEAFKIITADKDKVSAILVNIFGGIMRCDVIA
QGIIQAARELDLKIPIVVRLQGTVKVEDAKALIATSQLRILPCDNLDEAAKMVVKLSNIVD
LARATNVVDVKFELSI

>dme:Dmel_CG1065 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) Scsalpha1; Succinyl-coenzyme A synthetase alpha subunit 1, isoform B (A)
MAASMRALLKVRDGFVAGVRCNSQYNKTRGNLKLNGDSRVICQGFTGKQGTFFHSQQALEY
GTKLVGGISPKKGGTQHLGLPVFASVAEAKKATDPHATVIYVPPPGAAAAIIEALEAEIP
LIVCITEGVPQHDMVKVKHALISQSKSRLVGPNCPIIAPEQCKIGIMPGHIHKRGKIGV
VSRSGTLTYEAVHQTTEVGLGQTLGCVGIGGDPFNGTDFIDCLEVFLKDPETKGIILIGEI
GGVAEEKAADYLTEYNSGIKAKPVVSFIAGVSAPPGRRMGHAGAIISGGKGGANDKIAAL
EKAGVIVTRSPAKMGHELFEKEMKRLELV

>dme:Dmel_CG6255 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) Scsalpha2; Succinyl-coenzyme A synthetase alpha subunit 2 (A)
MSLNRGSKMLLRALTPQILRRGKADYGKTVCNLKINKATKVLVQGFTGKQATFHSEESIK
YGTNIVGGVNPCKGGTEHLGKPVFKSVAEAVEKAKPDATVIFIPPPSAAEGICAAIESEI
GLIVAITEGIPQADMVRISQMLNCQEKSRLLGPNCPIISPDQCKIGIMPGDIHKRGVVG
IVSRSGTLTYESVHQTNTNVLGQALCVGLGGDPFNGTSFIDALKVFLSDKEIKGIVMIGE
IGGSAEEEEAADFLKEKNTGCEAKPVVGFIAGQTAPPGRRMGHAGAIISGGKGAADKVAAL
LEKAGVRMTANPCHLGSTLLEEMIRLKLVPKPNKKKAQAGKK

>dme:Dmel_CG10622 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) ScsbetaG; Succinyl-coenzyme A synthetase beta subunit, GDP-forming, isoform C (A)
MSFLLKAVTTARHIVHKVPVRNLNLEFQSKDLLQKYGVAIQQFKVLNNSKADAEVVKTF
ECPEYVVKAILAGGRGKGTDFDNGFKGGVHITTNKSEVLSTQQMIGNRLITKQTPKSGI
LVNKVMVARSINITRETYLCILLDREHNGPVLIASPAGGMDIEAVAEETPEKIKTVPLDI
GKPIPESTLLEVAKFLEFKGDSVKRCAEEIQKLYTLFKAVDVAVQIEINPLAETDKGEVIS
VDAKLNFDNAQFRQKDIFSMVDTEEESDPREVEAAKYNLNYVAMDGNIGCLVNGAGLAM
ATMDIIKLNGGEPANFLDVGGGVREDQVAKAFEILTADPKVKGILVNVFGGIVNCATIAN
GIVAASKKLQNLVPLVVRLEGNTNVNQAREILKNSGLPIQTASDLDDAAHKAVAALN

>dme:Dmel_CG11963 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] |
(RefSeq) ScsbetaA; Succinyl-coenzyme A synthetase beta subunit, ADP-forming, isoform B (A)
MASFLARTGGPLIETVRPAAIKKILGLAPIAVQQLRNLVQEHVSYSLLNEAKIPTPRFA
VAKNGKEANDIATKLKTDNLVLKAQVLGGRGKGTFFKNGLKGGVRVYDPQTAEELSSKM
IDQLLVTKQTGAAGRICKKVMVAERKFPRREFYFAVMMERAFNGPVLIASKEGGVDIEEV
AASSPDAILYEPIDIGTGLTSEQAEKIVKKVGLGGDGEDTHVQMLLNLYDLFVKKDALLV
EINPYAEDAMSGFFALDAKLRFDDNAEFRQKELFALRDWTQEDPKEVEAAKYNLNYIALD
GTIGCMVNGAGLAMATMDIIKLYGGEPANFLDVGGGATAEAVKAAFKIITSDPKVLCILV
NIFGGIMRCDVIAEGIISATKDLNLMVPPVRLQGTVKEARELIRTSGLKILARDDLDK
AADLAVHLAQIVKLAREMKMDVNFIPDAQKGKGDCKKDQKQPDSSKGGKKSEKKDDKKSD
CTKKEEKKKEKKDICEKKGKK

>mmu:20916 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SucLa2, 4930547K18Rik, A-SCS, SCS-betaA; succinate-Coenzyme A ligase, ADP-forming, beta subunit (A)

MAASMFYGRQLAAAALRSHRPQTTLRAAAQVLGNSGLFNKHGLQVQQQQQRTLSLHEYLS
MELLQEAGVSVPKGFVAKSSDEAYAIKKLGSKDVIKAQVLAGGRGKGTFTSGLKGGVK
IVFSPEEAKAVSSQMIGQKLITKQTGEKGRICNQVLVCERKYPRREYYFAITMERSFQGP
VLIGSAQGGVNIEDVAAENPEAIVKEPIDIVEGIKKEQAVTLAQKMGFSPNIVDSAAENM
IKLYNLFLKYDATMVEINPMVEDSDGKVLCDAMKINFDSSNSAYRQKKIFDLQDWSQEDER
DKEANADINYIGLDGSIGCLVNGAGLAMATMDIILKHGGTPANFLDVGGGATVQQVTEA
FKLITSDKKVQAILVNIFGGIMRCDVIAQGIVMAVKDLEIRIPVVVRLQGTRVDDAKALI
ADSGLKILACDDLDEAAKMVVKLSEIVTLAKEAHVDVKFQLPI

>mmu:20917 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SucI2, D6Wsu120e, G-SCS, GTPSCS, SCS-betaG; succinate-Coenzyme A ligase, GDP-forming, beta subunit (A)

MASPVAIAAQAGKLLRERALLAVRSQAGHLTPRRWLNQLQEYQSKKLMSEHGVRVQRF
FVANTAKEALEAAKRLNAKEIVLKAQILAGGRGKGVFNNSGLKGGVHLTKDPKVVGELAQQ
MIGYNLATKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSHNGPVIVGSPQGGVDIEE
VAASSPELIFKEQIDIFEGIKDSQAQRMAENLGFGLSKLNQAADQITKLYHLFLKIDATQ
VEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSENEPIEENEAARYDLKYIGL
DGNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKEAQVYEAFLKLLTSDPKVEAIL
VNIFGGIVNCAIANGITKACRELELKVPLVVRLEGTNVQEAQNILKSSGLPITSVDLE
DAAKKAVASVAKK

>mmu:56451 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SucI1, 1500000I01Rik, SucLa1; succinate-CoA ligase, GDP-forming, alpha subunit (A)

MTATVAAAATATMVSSSSGLAAARLLSRTFLQNGIRHGSYASRKHIYIDKNTKIIC
QGFTGKQGTFFHSQQALEYGTLVGGTTPGKGGQKHLGLPVFNTVKEAKEKTGATASVIYV
PPPFAAAAINEAIDAEIPLVVCITEGIPQQDMVRVKHRLTRQGTTRLIGPNCPGVINPGE
CKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTQVGLGQSLCIGIGGDPFNGTDFIDCL
EVFLNDPATEGIILIGEIGHAEENAAFLKEHNSGPKAKPVVSFIAGITAPPGRRMGHA
GAIAGGKGGAKEKISALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>hsa:8801 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SUCLG2, G-SCS, GBETA, GTPSCS; succinate-CoA ligase GDP-forming subunit beta (A)

MASPVAQAQAGKLLRALALRPRFLAAGSQAVQLTSRRWLNQLQEYQSKKLMSDNGVRVQRFF
VADTANEALEAAKRLNAKEIVLKAQILAGGRGKGVFNNSGLKGGVHLTKDPNVVGQLAKQM
IGYNLATKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSCNGPVLVGSPQGGVDIEEV
AASNPELIFKEQIDIFEGIKDSQAQRMAENLGFVGPLKSQAADQITKLYNLFLKIDATQV
EVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSENEPIEENAAKYDLKYIGLD
GNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKEAQVYQAFKLLTADPKVEAILV

NIFGGIVNCAIIANGITKACRELELKVPLVVRLEGNTNVQEAQKILNNSGLPITSAIDLED
AAKKAVASVAKK

>hsa:8802 K01899 succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SUCLG1, GALPHA, MTDPS9, SUCLA1; succinate-CoA ligase GDP/ADP-forming subunit alpha
(A)

MTATLAAAADIATMVSGSSGLAAARLLSRSFLLPQNGIRHCSYTASRQHLYVDKNTKIIC
QGFTGKQGTFHSSQQALEYGTKLVGGTTPGKGGQTHLGLPVFNTVKEAKEQTGATASVIYV
PPPFAAAAINEAIEAEIPLVVCITEGIPQQDMVRVKHKLLRQEKTRLIGNCPGVINPGE
CKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTQVGLGQSLCVGIGGDPFNGTDFIDCL
EIFLNDSTATEGIIIGEIGGNAEENAAEFLKQHNSGPNSKPVVSFIAGLTAPPGRRMGHA
GAIIAGGKGGAKEKISALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>hsa:8803 K01900 succinyl-CoA synthetase beta subunit [EC:6.2.1.4 6.2.1.5] | (RefSeq)
SUCLA2, A-BETA, A-SCS, LINC00444, MTDPS5, SCS-betaA; succinate-CoA ligase
ADP-forming subunit beta (A)

MAASMFYGRLVAVATLRNHRPRTAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMS
MELLQEAGVSVPKGYVAKSPDEAYAIKKLGSKDVVIKAQVLAGGRGKGTTFESGLKGGVK
IVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQLVCERKYPRREYYFAITMERSFQGP
VLIGSSHGGVNIEDVAAESPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENM
VKLYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQKKIFDLQDWTQEDER
DKDAAKANLNYIGLDGNIGCLVNGAGLAMATMDIIKLHGGTPANFLDVGGGATVHQVTEA
FKLITSDKKVLAILVNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKALI
ADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLPI