

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)

MLEEYRKHVAERAAEGIAPKPLDANQMAALVELLKNPPAGEEEFLLDLLTNRVPPGVDEA
AYVKAGFLAAIAKGEAKSPLLTPEKAIELLGTMQGGYNIHPLIDALDDAKLAPIAAKALS
HTLLMFDNFYDVEEKAKAGNEYAKQVMQSWADAEWFLNRPALAEKLTVTVFVKTGETNTD
DLSPAPDAWSRPDIPLHALAMLKNAREGIEPDQPGVVGPIKQIEALQQKGFPPLAYVGDVV
GTGSSRSKATNSVLWFMGDDIPHVPNKRGGGLCLGGKIAPIFFNTMEDAGALPIEVDVSN
LNMGDVIDVYPYKGEVRNHETGELLATFELKTDVLIDEVRAGGRIPLIIGRGLTTKAREA
LGLPHSDVFRQAKDVAESDRGFSLAQKMVGRACGVKGIRPGAYCEPKMTSVGSQD TTGPM
TRDELKDLACLGF SADLVMQSFCHTAAYPKPVDVNTHTLPDFIMNRGGVSLRPGDGVIIH
SWLNRMLLPD TVTGGDSHTRFPIGISFPAGSGLVAF AAATGV MPLDMPESVLVRFKGKM
QPGITLRDLVHAIPLYAIKQGLLTVEKKGKKNIFSGRILEIEGLPDLKVEQAFELTDASA
ERSAAGCTIKLNKEPIIEYLNSNIVLLKWMIAEGYGDRRTLERRIQGMEKWLANPELLEA
DADAEYAAVIDIDLADIKEPILCAPNDPDDARPLSAVQGEKIDEVFIGSCMTNIGHFRAA
GKLLDAHKGQLPTRLWWAPPTRMDAAQLTEEGYYSVFGKSGARIEIPGCSLCMGNQARVA
DGATVVSTSTRNFPNRLGTGANVFLASAELA AVALIGKLPTPEEYQTYVAQVDKTAVDT
YRYLNFNQLSQYTEKADGVIFQTAV

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

MIKLSEKGVFLASNNEIIAEEHFTGEIKKEEAKKGTIAWSILSSHNTSGNMDKLKIKFDS
LASHDITFVGIVQTAKASGMERFPLPYVLTNCHNSLCAVGGTINGDDHVFGLSAAQRYGG
IFVPPHIAVIHQYMMREMMAGGGKMILGSDSHTRYGALGTMAVGEGGGELVKQLLNDTWDI
DYPGVVAVHLTGKPAPYVGPQDVALAIGAVFKNGYVKNKVMFVGPVGSALSTDFRNSV
DVMTTETTCLSSVWQTDEEVHNWLALHGRGQDYCQLNPQPMAYYDGCISVDLSAIKPMIA

LPFHPSNVYEIDTLNQNLTDILREIEIESERVAHGKAKLSLLDKVENGR LKVQQGIIAGC
SGGNYENVIAAANALRGQSCGNDTFS LAVYPSSQPVFMDLAKKGVVADLIGAGAIIRTAF
CGPCFGAGDTPINNGLSIRHTRNFPNREGSKPANGQMSAVALMDARSIAATAANGGYLT
SASELDCWDNVPEYAFDVTPYKNRVYQGFVKGATQQPLIYGPNIKDWPELGALTDNIVLK
VCSKILDEVTTTDELIPSGETSSYRSNPIGLAEFTLSRRDPGYVSRSKATAELENQRLAG
NVSELTEVFARIKQIAGQEHDPLQTEIGSMVYAVKPGDGSAREQAASCQRVIGGLANIA
EEYATKRYRSNVINWGMLPLQMAEVPTFEVGDYIYIPGIKAALDNP GTTTFKGYVIHEDAP
VTEITLYMESLTAEEREIIKAGSLINFNKNRQM

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

MSSTLREASKDTLQAKDKTYHYYS LPLAAKSLGDITRLPKSLKV LLENLLRWQDGNSVTE
EDIHALAGWLKNAHADREIAYRPARVLMQDFTGVPVVDLAAMREAVKRLGGDTAKVNPL
SPVDLVIDHSVTVD RFGDDEAFEENVRL EMERNHERYVFLKWGKQAFSRFSVVPPTGIC
HQVNLEYLGKAVWSELQDGEWIAYPDTLVGTDSHTTMINGLGLV LGWGVGGIEAEAAMLGQ
PVSM LIPDVVGFKLTGKLREGITATDLVLTVTQMLRKHG VVGKFVEFYGDGLDSLPLADR
ATIANMSPEYGATCGFFPIDAVTLDYMR LSGRSEDQVELVEKYAKAQGMWRNPGDEPIFT
STLELDMNDVEASLAGPKRPQDRVALPDV PKAFAASNELEVNATHKDRQPV DYVMNGHQY
QLPDGAVVIAAITSCTNTSNPSVLMAAGLLAKKAVTLGLKRQPWVKASLAPGSKVVSDYL
AKAKLTPYLDELGFNLVGYGCTTCIGNSGPLDP IETAIKKS DLTVGAVLSGNRNFEGRI
HPLVKTNWLAS PPLVVAYALAGNMNINLASEPIGHDRKGD PVYLKDIWPSAQEIARAVEQ
VSTEMFRKEYAEVFEGTA EWKGINVTRSDTYGWQEDSTYIRLSPFFDEM QATPAPVEDIH
GARILAMLGDSVTTDHISPAGSIKPDSPAGRYLQGRGVERKDFNSYGSRRGNHEVMMRGT
FANIRIRNEMVPGVEGGMTRHLPDSDVVSIYDAAMRYKQEQTPLAVIAGKEYGSGSSRDW
AAKGPRLLGIRVVIAESFERIHRSNLIGMGILP LEFPQGVTRKTLGLTGEEKIDIGDLQN
LQPGATVPVTLTRADGSQEVVPCR CRIDTATELTYYQNDGILHYVIRNMLK

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

MLSARSAIKRPIVRGLATVSNLTRDSKVNQN LLEDHSFINYKQNVETLDIVRKRLNRPFT
YAEKILYGHLD DDPHGQDIQRGVSYLLKRPDRVACQDATAQMAILQFMSAGLPQVAKPVTV
HCDHLIQAQVGGEKDLKRAIDLNKEVYDFLASATAKYNMGFWKPGSGIIHQIVLENYAFP
GALIIGTDSHTPNAGGLGQLAIGVGGADAVDVMAGR PWELKAPKILGVKLTGKMNGWTSP
KDIILKLAGITTVKGGTGKIVEYFGDGVDTFSATGMGTICNMGA EIGATTSVFPFNKSMI
EYLEATGRGKIADFAKLYHKDLLSADKDAEYDEVVEIDLNTLEPYINGPFTPDLATPVSK
MKEVAVANNWPLDVRVGLIGSCTNSSYEDMSRSASIVKDAAAHGLKSKTIFTVTPGSEQI
RATIERDGGQLET FKEFGGIVLANACGPCIGQWDRRDIKKGD KNTIVSSYNRNFTSRNDGN
PQTHAFVASPELVTAFAIAGDLRFNPLTDK LKDKDGNEFMLKPPHGDGLPQRGYDAGENT
YQAPPADRSTVEVKVSPTS DRLQLLKPFKPWDGKDAKDMPILIKAVGKTTTDHISMAGPW
LKYRGHLENISNNYMIGAINAENKKANCVKNVYTGEYKGV PDTARDYRDQGIKWVIGDE
NFGEGSSREHAAL EPRFLGGFAITKSFARIHETNLKKQGLLPLNFKNPADYDKINPDDR
IDILGLAELAPGKPV TMRVHPKNGKPWDVLTHTFNDEQIEWFKYGSALN KIKADEKK

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

MNSLLRLSHLAGPAHYRALHSSSSIWSKVAISKFEPKSYLPYEKLSQTVKIVKDRLKRPL
TLSEKILYGHLDPKTQDIERGVSYLRLRPDRVAMQDATAQMAMLQFISSGLPKTAVPST
IHCDHLIEAQKGGGAQDLARAKDLNKEVFNFATAGSKYGVGFWKPGSGIIHQIILENYAF
PGLLLIGTDSHTPNNGGGLGGLCIGVGGADAVDVMADIPWELKCPKVIGIKLTGKLNGWTS
AKDVILKVADILTVKGGTGAIVEYFGPGVDSISATGMGTICNMGAIEGATTSVFPYNESM
YKYLEATGRKEIAEEARKYKDLLTADDGANYDQIIINLDTLTPHVNGPFTPDLASSIDK
LGENAKKNGWPLDVKVSLIGSCTNSSYEDMTRAASIAKQALDKGLKAKTIFTITPGSEQV
RATIERDGLSKIFADFGGMVLNACGPCIGQWDRQDVKKGEKNTIVTSYNNRFTGRNDAN
PATHGFVTSPDITTAMASGRLDNFNPLTDELTAADGSKFKLQAPTGLDLPPKGYDPGEDT
FQAPSGSGQVDVSPSSDRLQLLSPFDKWDGKDLEDMMKILIKVTGKCTTDHISAAGPWLYK
RGHLDNISNNLFLTAINADNGEMNKVKNQVTGEYGAVPATARKYKADGVRWVAIGDENYG
EGSSREHAALPRHLGGRAIIVKSFARIHETNLKKQGMLPLTFANPADYDKIDPSDNVSI
VGLSSFAPGKPLTAIFKKTNGSKVEVTLNHTFNEQQIEWFKAGSALNRMKEVFAKSK

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

MAFNNLIRNLAIGDNVYKYFDLNGLNLDARYNELPISIKYLLEAAVRHCDEFHVLKKDVET
ILDWKN SQRNQAEIPFKPARVILQDFTGVPVVDLAAMRDAVQNMGADPAKINPVCPVDL
VIDHSVQVDHYGNLEALAKNQSIEFERNRERFNFLKWGSKAFDNLLIVPPGSGIVHQVNL
EYLARTVFVGKDGVLYPDSVVGTDSTTMDGSGVLGWGVGGIEAEAVMLGQPISMVIPE
VIGYELVGTLSDTVTSTDLVLTITKNLRDLGVVGKFVEFFGTGVASLSIADRATIANMCP
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
VRATIARDGIIDVLEKFGGTVLANACGPCIGQWDRKDKVMGEKNTIVTSYNRNFTGRNDA
NPATHCFTVTSPEMATALAIAGRLDFNPMTDEL TGTGDKTFKLKEPHGEELPSKGFDPGED
TYQAPPAKADDIKVNVDPKSDRLQLLEPF EKWDGKDYIDLMLVIKIKGKCTTDHISAAGP
WLKYRGHLDNISNNMFIGATNAENNEMNKVK NQKTGSFDAVPAVARDYKANKIKWCAVGE
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 AVRNCNDFHVL E
KDVQSILGWTPSLKQETSDVEVSFKPARVILQDFTGVP AVVDFAAMRDAVRELGGNPEKI
NPICPADLVIDHSVQVDFVRSSDALTKNESLEFQRNKERFTFLKWGARAFDNMLIVPPGS
GIVHQVNLEYLARVVFESDSSADGSKILYPDSVVGTD SHTTMINGLGVLGWGVGGIEAEA
VMLGQSSISMLLPEVIGYRLEGKLGPLATSTD LVLTTITKHLRQLGVVGKFVEFYGPGVAEL
SIADRATISNMCPEYGATVG YFPIDENTLSYMRQTNRSEKKIDIIRKYLKATRQLRDYSL
VDQDPQYTESVTLDLSTVVTSVSGPKRPHDRVSVSSMCEDFK SCLISPVGFKGFAIPPSA
LAASGEFQWDDGKSYKIGHGSVVIAAITSCTNTSNPSVMLGAGLLAKNAVQKGLSILPYI
KTSLSPGSGVVTTYLRESGVIPYLEQLGFDIVGYGCMTCIGNSGPLDENNVNTIEKNGLV
CCGVLSGNRNFEGRIHPNTRANYLASPLLVIAYA IAGRVDIDFEIEPLGVDSNGKEVFLR
DIWPTRSEIQEVEHKHVIPAMFQEVYSKIQLGSRDWQTLEVSDSKLYPWSEISTYIKLPP
FFEGMTRALPKLKGIEKARCLLLLGD SVTTDHISPAGSIARKSPAARYLSERGLTPRDFN
SYGSRRGNDAVMARGTFANIRLVNKLASKTGPSTLHVPSGEEMDIFDAAERYASEGTPLV
LVVGKDYGSGSSRDWAAKGPFLLGKAVIAESYERIHRSNLVGMGIPLQLFLPGQSADTL
KLSGREVYNIVLPEGELKPGQRIQVDADGNVFETT LRFDTEVDITYYKNGGILNYMIRKM
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
GQSISMMLPEVIGYKLEGKLSPLVTSTD LVLTTITKHLRQLGVVGKFVEFYGPGVAELSIA
DRATISNMCPEYGATVG YFPIDENTLGYMKQTNRSEKKIDIIRQYLKATQQLRNYADAAQ
DPKFTQSITL DLSTVVTSVSGPKRPHDRVSVSDMPEDFKSCLSSPVGFKGFAIAPEAQSA
FGEFQWDDGKTYKLHHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVEKGLSILPYIKTS
LSPGSGVVTTYLKESGVIPYLEKL GFDIVGYGCMTCIGNSGPLEENVNTIEKNGLVCAG
VLSGNRNFEGRIHPNTRANYLASPLLVIAYA IAGRVDIDFEKEPLGVDANGKNVFLQDIW

PTRSEIQEVENKHVIPAMFQEVYSKIELGSQDWQTLQVSEGKLFWSWSADSTYIKRPPFFE
GMTRDLPKLQSIQKARCLLFLGDSVTTDHISPAGSIARTSPAARFLSERNITPRDFNSYG
SRRGNDAIMSRGTFANIRLVNKLVEKTGPRTVHIPSQEELDIFDAAERYREEGTPLVLVV
GKDYGSGSSRDWAAKGPFLLGVKAVIAESYERIHRSNLVGMGIPLQLPQGSAETLNL
GREVYNIALPESGLKPGQKIQVEADGTVFETILRFDTEVDITYYKNGGILNYMIRKMLS

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

MAARLMNAQAQVCRLGKHVASEATVVRQFHASCYTASKVALSKFSDVYLPYEKLNKRLE
VVRGRLNRPLTLSEKVLVSHLDDPANQDIVRGTSYLRLRPDRVAMQDATAQMALLQFISS
GLKKVAVPSTVHCDHLIEAQIGGPKDLARAKDLNKEVYDFLASTCAKYGLGFWKPGSGII
HQIILENYAFPGLLMIGTDSHTPNGGGLGGLCIGVGGADAVDVMADIPWELKCPKVIGVN
LTGKISGWTSPKDVILKVADILTVKGGTGAIIEYHGKGVDSISCTGMATICNMGAIEGAT
TSLFPFNQRMADYLYKSTGRAGIASEAQKYQAKILSADKNCEYDELIEINLDTLEPHVNGP
FTPDLGHPISKLGENSEKNGYPMDIRVGLIGSCTNSSYEDMGRCAKSIKAMSHGLKSKI
PFNVTPGSEQIRATIERDGISEVFDKFGGTVLANACGPCIGQWDRKDVKKGDKNITVTSY
NRNFTGRNDANPATHCFVTSPELVTALSIAGRLDFNPLTDELTDGADGKKFKLKAPFGDEL
PAKGFDPGQDITYTAPPPSGENVKVAVDPKSTRLLQLEPFDKWNGQDLTDLTVLIKVKGKC
TTDHISAAGPWLKYRGHLDNISNNMFIGATNYENNEMNNIKNQNRNGSWGVPDVARDYKA
NGIKWVAVGDENYGESSREHAALPRHLGGRAIVKSFARIHETNLKKQGLLPLTFANP
ADYDKIQPTSKISLLNLKSLAPGKPVDAEIKNGDKVERIKLNHTLNDLQIGWFKAGSALN
RMKELAQ

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

MKNPFAHLAEPLDAAQPGKRFFNLNKLEDSRYGRLPFSIRVLLEAAVRNCDEFLVKKNDI
ENILNWNVMQHKNIEVPFKPARVILQDFTGVPVVDFAAMRDAVKKLGGNPEKINPVCPA
DLVIDHSIQVDFNRRADSLQKNQDLEFERNKERFEFLKWGSQAFCNMRIIPPGSGIIHQV
NLEYLARVVFDDQGCYYPDSLVTGDSHTTMIDGLGVLGWGVGGIEAEAVMLGQPISMVLP
QVIGYKLMGKPHPLVTSTDIVLTITKHLRQVGVVGKFVEFFGPGVAQLSIADRATIANMC
PEYGATAAFFPVDEVSIAYLLQTGREEDKVKHQKYLQAVGMFRDFNDTSQDPDFTQVVE
LDLKTVPCCSGPKRPQDKVAVSEMKKDFESCLGAKQGFKGFQVAPDRHNDRKTFLYSNS
EFTLAHGSVVIAITCTNTSNPSVMLGAGLLAKKAVEAGLSVKPYIKTSLSPGSGVVTY
YLRESGVMPYLSQLGFDVVGYGCMTCIGNSGPLPEPVVEAITQGDLVAVGVLSGNRNFE
RVHPNTRANYLASPLVIAYAIAGTVRIDFEKEPLGVNAQGRQVFLKDIWPTRDEIQAVE
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
HRMKKYLSKTGRDIDANLAEEFKDHLVPDPGCQYDQVIEINLNLKPHINGPFTPDLAHP
VADVGTVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGS
EQIRATIERDGYAQILRDVGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYNRNFTGRN
DANPETHAFVTSPEIVTALAIAGTLKFNPETDFLTGKDGGKFKLEAPDADELPRSDFDPG
QDTYQHPPKDSSGQRVDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAA
GPWLKFRGHLDNISNNLLIGAINIENGKANSVRNAVQTQFEGVPVDTARYYKKHGIRWVVI
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
PEYGATAAFFPVDEVSTITYLVQTGRDEEKLKYLKYLQAVGMFRDFNDPSQDPDFTQVVE
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
HRMKKYLSKTGREIDANLADEFKDHLVPDPGCHYDQLIEINLSELKPHINGPFTPDLAHP

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)

MSAKAVSELSGKEVLYKYFESTGIVSAPHAFHVKAGDKFSDVAAKYEWLAQDNKGVKIPD
QLIKRRGKLGVLKIGSPKELEAWFGKTANSYVKVGQTEGRLHTFIVEPFCAHTENEEMYI
AIYSERCRDVIMFYEQGGVDIGDVEEKARSVHVPVQLDDNAMSISERELGVLLGPCSDKD
DIRKFVRSLEYEAYKALHFTYLEINPFVLTNGKIHILDLAAKLDETASFLCSDKWSGRNAS
ARIAPTLEFPAPFGRDLTSEEQYISDMDAKTGASLKLTLNRKGRVWTMVAGGGASVVFT
DTVCDLGGSELANYGEYSGDPSEAQTYEYAKTILSVMTEGAPRPDGKVLIIIGGSIANFT
NVAKTFGGIVRAFETFIDKLKEHNVSIYVRRGGPNYQEGLRRVKDAATKLEIPIYVFGPE
THMTAIVGAALGLKPMPTVPTAPQTTGQFLLSPERN TAGTERPPASPAPNTSTIEHPLAK
RHPLHQSLFENDTKAIIWGQQHKAIQGMLDFDFVCCRHSVSVASTYPFTGDNKQKYYFG
QKEILIPAYKSMAKAFASHPDATVMVTFASMRSVFETVLEALQFTQIKVIAIIAEGVPEN
QTRKLLKIAEDKGVTLIGPATVGGIKPGCFKIGNTGGMMDNILASKLYRPGSVAYVSRSG
GMSNELNNIISQNTNGVYEGIAIGGDRYPGSTYTDHVMRYQHDDRVMIVLLGEVGGIEE
YRIVELLKEKKITKPLIAWCIGTCADHITSEVQFGHAGASANGQGETAACKNTALRTAGA
LVPDSFDDLGNKIRQTYEELLRLIIVPQPEVPPPAVPMDYAWARELGLIRKPASFMSTI
CDERGEELNYAGVPITKVLESMDGIGGVLGLLWVQKRLPPHANKFIEICLMLTADHGPAV
SGAHNTIVCARAGKDLISLTSGLLTIGDRFGGALDGAARQFSEAFDQGWSPNQFVGEMR
KRGTHIMGIGHRVKSINNPDKRVEILKRFALNKKEFAQETPLLDYALEVEKITTAKKPNL
ILNVDGAIIIFVDILRNSGMFTTAEAEQVIEIGALNGMFVLGRSIGFIGHYLDQSRLKQ
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
DTVCDLGGASELANANYGEYSGDPSESQTYEYAKTLLSVMTEGTTPRPDGKVLIIIGGSIANFT
NVAKTFGGIVRAFETFVSKLKEHKVTIFVRRGGPNYQEGLRRIKDAATKLELPIHVFGPE
THMTAIVGAALGVKPMPTVPTAPQTTGQFLLSPERN TGGTERAPPSPAANATPTEHPLTT
AQQNKLSFRGLFEDDTKAIIWGQQAKAIQGMLDFDYVCCRSSPSVSVASTYPFTGDNKQK
YYFGQKEILIPAYKSMAKAFATHPDASIMVTFASMRSVFETVLEALEFPQIKVIAIIAEG
VPENQTRKLLKIAHDRGVTLVGPATVGGIKPGCFKIGNTGGMMDNILASKLYRPGSVAYV
SRSGGMSNELNNIISQNTNGVYEGIAIGGDRYPGSTYTDHVIRYQNDDRVMIVLLGEVG
GVEEYKIVDLLKQKVKTKPLVAWCIGTCADHITSEVQFGHAGASANALGETAACKNAALR
ASGALVPESFDDLGNKIRQTYDELVSQQIIVPQPEVPPPAVPMDYAWARELGLIRKPASF
MTSICDERGEELNYAGVPITKVLESMDGIGGVLGLLWVQKRLPPHANKFIEICLMLTADH
GPAVSGAHNTIVCARAGKDLISLTSGLLTIGDRFGGALDGAARQFSEAFDQGWSANQFV

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
QLIKRRGKLGLIGVKNFEQVKQWIGERLNKDQKIGNAVGKLRFIIEPFVPHDAEEMY
VCIYSHRAADTILFYHQGGVDIGDVDAKAVKLDVPVNSSLADVKSKLLKEVKDAGTKE
RIAKFVSALYTTYVDLYFTYLEINPLVVTADNLYILDAAKLDSTADFICRPKWGEIDYP
PPFGRDAYPEEAYIADLDAKSGASLKLTLNRNGRIWTMVAGGGASVIYSDTICDLGGAS
ELANYGEYSGAPSEQQTYEYAKTILNLTSSPKHPDGKVLITGGGIANFTNVAATFQGII
TALREFQPKLVEHNVSIFVRRAGPNYQEGLRKM RDFGSTLGIPLHVFGPETHMTAICGMA
LGKRPIPQTASVEFSTANFLLPGGQQAQADLKAASDASEALGSGSALSPTAAKPIKLPII
SADEADSAGISGAQRNGSSSLNRKFFSNTTKAIVWGMQQRAVQSM LDFDFICRRDEPSVVA
MVYPFTGDHKQKYYWGHKEILIPVYKKMSDAIHKHKEVDVMVNFASMR SAYESTLEVLEF
PQIRTV AIIAEGIPENMTRKLIIEADKKGV AIGPATVGGVKPGCFKIGNTGGMLDNILH
SKLYRPGSVAYVSRSGGMSNELNNISKATDGVIEGIAIGGDRYPGSTFMDHILRYQADP
ETKLIVLLGEVGGTEEYDVCAALKDGRITKPLVAWCIGTCASMFTSEVQFGHAGSCANS
RETATAKNKGLRDAGAYVPDSFDTLGELIHHVYGELVKTGRVVPKEEVPPTVPM DYSWA
RELGLIRKPASFMTSICDERGQELIYAGMPISEVL SKDVGIGGVISLLWFQRCLPSYVCK
FFEMCLMVTADHGPVSGAHNTIVCARAGKDLVSSVVSGLLTIGDRFGGALDGSARQFSE
AYDTNLHPMEFVNKMRKEGKLILGIGHRVKSINNP DVRVKIIKEFVLENFPACPLLKYAL
EVEKITTNKKPNLILNVDGVIATAFVDMLRNSGSFTSEE AQEYINVGAINSLFVLGRSIG
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 KDG VYILDAAKV DATADYICKVKWGDIEFPP
PFGREAYPEEAYIADLDAKSGASLKL TLLNPKGRIWTMVAGGGASVVYSDTICDLGGVNE
LANYGEYSGAPSEQQTYDYAKTILSLMTREKHPEGKILIIGGSIANFTNVAATFKGIVRA
IRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFGTETHMTAIVGMALG
HRPIPNQPPTAAHTANFLLNASGSTSTPAPSRTASFSESRADEVAPAKKAKPAMPQGKSA
TLFSRHTKAIVWGMQTRAVQGMLDFDYVCSRDEPSVAAMVYPFTGDHKQKFYWGHKEILI
PVFKNMADAMKKHPEVDVLINFASLRSAYDSTMETMNYAQIRTI AIIAEGIPEALTRKLI
KKADQKGV TIIGPATVGGIKPGCFKIGNTGGMLDNILASKLYRPGSVAYVSRSGGMSNEL
NNIISRTTDGVYEGVAIGGDRYPGSTFMDHVLRYQDTPGVKMIVVLGEIGGTEEYKICRG
IKEGRLTKPVVCWCIGTCATMFSSEVQFGHAGACANQASETAVAKNQALKEAGVFVPRSF
DELGEIISVYEDLVAKGAIVPAQEVPPPTVPM DYSWARELGLIRKPASFMTSICDERGQ

ELIYAGMPITEVFKEEMGIGGV LGLLWFQRR LPKYSCQFIEMCLMVTADHGPAVSGAHNT
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
QLIKRRGKLGLVGVNLTLDGVKSWLKPRLGQEATVGKATGFLKNFLIEPFVPHSQAE EFY
VCIYATREGDYVLFHHEGGVDVGDVDAKAQKLLVGVDEKLN PEDIKKHLLVHAPEDKKEI
LASFISGLFNFYEDLYFTYLEINPLVVT KDGVYVLDLAAKV DATADYICKVKWGDIEFPP
PFGREAYPEEAYIADLDAKSGASLKL TLLNPKGRIWTM VAGGGASVVYS DTICDLGGVNE
LANYGEYSGAPSEQQTYDYAKTILSLMTREKHPDGKILIIGGSIANFTNVAATFKGIVRA
IRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFGTETHMTAIVGMALG
HRPIPNQPPTAAHTANFLLNASGSTSTPAPSRTASFSESRADEVAPAKKAKPAMPQDSVP
SPRSLQGKSTTLFSRHTKAIVWGMQTRAVQGMLDFDYVCSRDEPSVAAMVYPFTGDHKQK
FYWGHKEILIPVFKNMADAMRKHPEVDVLINFASLRSAYDSTMETMNYAQIRTIAIIAEG
IPEALTRKLIKKADQKGV 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
LFHAFRRDShPMaVMCGITGALAAFYHDSLDVNNPRHREIAAFRLLSKMPTMAAMCYKYS
IGQPFVYPRNDLSYAGNFLNMMFSTPCEPYEVNPILERAMDRILILHADHEQNASTSTVR
TAGSSGANPFACIAAGIASLWGPAHGGANEAAALKMLEEISSVKHIPEFVRRAKDKNDSFR
LMGFGHRVYKNYDPRATVMRETcheVLkelGtKDDLLEVAMELENIALNDPYFIEKKLYP
NVDFYSGIILKAMGIPSSMFTVIFAMARTVGWIAHWSEMHSdGMKIARPRQLYTGyEKRD
FKSDIKR

>sce:YCR005C K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT2; citrate (Si)-synthase
CIT2 (A)
MTVPYLNsnRnVAsYLQsnSSQeKtLkERfSEiYPIHAQDVRQFVKEHGKtKISDVLLEQ
VYGGMRGIPGSVWEGSVLDPEDGIRFRGRtiADIQKDLpkAKGSSQPLPEALFWLLTGE
VPTQAQVENLSADLMsrSElPSHVvQLLDnLPKDLHPMAQFSIAVTALESESKfAKAYAQ
GISKQDYWSYTFEDSLDLLGKLpVIAAKiYRNVfKdGKMGEVDPNADYAKNLVNLIGSKD
EDFVDLMRLYLtiHSDHEGGNVSAHTSHLVGSALSSPYLSLASGLNGLAGPLHGRANQEV
LEWLFALKEEVNDdYSKDTIEKYLWDTLNSGRVIPGYGHAVLRKTDPRYMAQRKFAMDHF
PDYELFKLVSSiYEVAPGVlTEHGKtKNPWPnVDAHSGVLLQYYGLKESSfYTVLFGVSR
AFGILAQLITDRAIGASIERPKSYSTEkyKELVKNIESKL

>sce:YNR001C K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT1, LYS6; citrate
(Si)-synthase CIT1 (A)
MSAILSTTSKsFLSRGSTRQCQNMqKAlFALLNARHySSASEQTLKerFAEIIPAKAEEI
KKfKKEHGKtVIGEvLLEqAYGGMRGIKGLVWEGSVLDPEEGIRFRGRtiPEiQRELpKA
EGSTEPLPEALFWLLTGEIPTDAQVKALSADLAARSEIPEHVIQLLDSLpKDLHPMAQF
SIAVTALESESKfAKAYAqGVSKKEYWSYTFEDSLDLLGKLpVIASkYRNVfKdGKiTS
TDPNADYgKNLAQLLGYENKDFIDLMRLYLtiHSDHEGGNVSAHTThLVGSALSSPYLSL
AAGLNGLAGPLHGRANQEVLEWLFKLREEVKGdYSKETIEKYLWDTLNAGRvVPGYGHAV
LRKTDPRYTAQREFALKHfPDYELFKLVSTiYEVAPGVlTKHGKtKNPWPnVDSHSGVLL
QYYGLTEASfYTVLFGVArAIGVLPQLIIDRAVGAPIERPKSFSTEkyKELVKKIESKN

>sce:YPR001W K01647 citrate synthase [EC:2.3.3.1] | (RefSeq) CIT3; citrate (Si)-synthase
CIT3 (A)
MVQRLLPGAHICRRSFNssAIKSSAlTLKEAlENVIPKKRDAVKKLKACyGSTfVGPIT
ISSVLGGMRGNQSMFWQGTSLDPEHGikfQGLTIEECQNRLPNTGIDGDNFLPESMLWLL
MTGGVPTfQQAASFRkELAIRGRKLPHYTEKVLSSLPKDMHPMTQLAIGLASMnKGSLFA
TNYQKGLIGKMEFWKDTLEDsLNLIASLPLLTGRIYSNITNEGHPLGQYSEEVDWCTNIC

SLLGMTNGTNSSNTCNLTSSQSLDFINLMRLYTGIHVDHEGGNVSAHTTHLVGSALSDPY
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
FYTVLFGVSRALGCLSQLIWARGMGLPLERPCKSHSTDGLIKLALAAKK

>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
FFLLTSGSMPTKKEAQEVTNEWLKRGSVPRYCLRMIDSMDKRVHPMAQLCAASACLNPQS
QFVEAYTKGARRADYWKYSYEDSMNLIAMLPTVAAAIYSNVFRDGEKSREVNYEEDWSGN
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)
MALLTAAAWFLGTKNPPCLVLAARHASASSTNLKDVLRLNLIPEQARIKTFRKKHGKTVV
GQITVDDMMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQKLLPKAKGGKEPLPEGLF
WLLVTGQMPTEEQVSWLSQEWVKRAALPSHVVTMLDNFPTKLHPMSQLSAAITVLNNESEN
FARAYAQGMNRTKYWELTYEDCMDLLAKLPCVAAKIYRNLYREDRNIKAIDSRLDWSHNF
TNMLGYTDPQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAALNGLAGPL
HGLANQEVLVWLTQLQKEVGEDASDEKLKNYIWNTLNHSGRVVPGYGHAVLRKTDPRYSCQ
REFALKHLPKDPMFKLVGQLYKIVPDILLEQGKAKNPWPNVDAHSGVLLQYYGMREMNNYY
TVLFGVSRALGVLSQLIWSRALGFPLERPCKSMSTDALMKFVNSESG

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

ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE

>eco:b0115 K00627 pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) aceF; pyruvate dehydrogenase, E2 subunit (A)
MAIEIKVPDIGADEVEITEILVKVGDKVEAEQSLITVEGDKASMEVPSPQAGIVKEIKVS
VGDKTQTGALIMIFDSADGAADAAPAAQAEKKEAAPAAAPAAAAAKDVNVPDIGSDEVEV
TEILVKVGDKVEAEQSLITVEGDKASMEVPAPFAGTVKEIKVNVGDKVSTGSLIMVFEVA
GEAGAAAPAAKQEAAPAAAPAPAAGVKEVNVPDIGGDEVEVTEVMVKVGDKVAAEQSLIT
VEGDKASMEVPAPFAGVVKELKVNVDGDKVKTGSLIMIFEVEGAAPAAAPAKQEAAPAPA
AKAEAPAAAPAAKAEGKSEFAENDAYVHATPLIRRLAREFGVNLAKVKGTGRKGRILRED
VQAYVKEAIKRAEAAPATGGGIPGMLPWPKVDFSKFGEIEEVELGRIQKISGANLSRNW
VMIPHVTHFDKTDITELEAFRKQQNEEAARKKLDVKITPVVFIMKAVAAALEQMFRNSS
LSEDGQRLTLKKYINIGVAVDTPNGLVVPVKDVNKKGIIELSRELMTISKKARDGKLTA
GEMQGGCFTISSIGGLGTTTFAPIVNAPEVAILGVSKSAMEPVWNGKEFVPRMLPLISLS
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
QLSPGEVIAEIEDKAQMDFEFQEDGYLAKILVPEGTKDIPVNKPIAVYVEDKADVPAFK
DFKLEDSGSDSKTSTKAQPAEPQAEKKQEAPAEETKTSAPAEKKSDVAAPQGRIFASPLA
KTIALEKGISLKDVHGTGPRGRITKADIESYLEKSSKQSSQTSGAAAATPAAATSSTTAG
SAPSPSSTASYEDVPISMRSIIGERLLQSTQGIPSYIVSSKISISKLLKLRQSLNATAN
DKYKLSINDLLVKAITVAAKRVDPANAYWLPNENVIRKFKNVDVSVAVATPTGLLTPIVK
NCEAKGLSQISNEIKELVKRARINKLAPEEFQGGTICISNMGMNNAVNMFTSIINPPQST
ILAIATVERVAVEDAAAENGFSFDNQVTITGTFDHRTIDGAKGAEFMKELKTVIENPLEM
LL

>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
GLGSVDISVAVATPTGLITPIVENSILGLVLAISSKVKELSGLARESKLKPQQFQGGST
ISNLGMFGSVTNFTAIINPPQCAILTIGGTRSEVVSDGQLETQKLMGVNLCFDGRAISE
ECAKRFLHFSESLSDPELLIAEPLSPELDFFDSRL

>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
FSIKQVRLYSSGNLPKHNRVALPALSPTELMELGTVVSWQKKEGDQLSEGDLLCEIETDKAT
MGFETPEEGYLAKILIQEGSKDVPKLLCIIVDNEADVAAFKDFKDDGASSGGSAPAAE
KAPEPAKPAASSQPSPPAQMYQAPSVPKSAPIPHSSSGRVASPFACKLAAENGLDLSGV
SGSGPGGRILASDLSQAPAKGATSTTTQAVSGQDYTDIPLSNMRKTIKRLTESKSTIPH
YYLTSEIQLDITLLQVREKLNGLLAKGTSGQATKISINDFIIKASALACQRVPEANSYWMD
SFIRENHVVDVSVAVSTPAGLITPIIFNAHAKGLATIASEIVELAQRAREGKLQPHEFQG
GTFTVSNLGMFGSVSDFTAINPPQSCILAIGGASDKLVPDEAEGYKKIKTMKVTLSCDH
RTVDGAVGAVWLRHFKEFLEKPHTMLL

>dme:Dmel_CG5261 K00627 pyruvate dehydrogenase E2 component
(dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12] | (RefSeq) muc; midline
uncoordinated, isoform C (A)

MLRSLATTRNELGALRSVLLRSNNATYVRRSTGNVVRALSSQLINSRKLQSIRSKLNTS
QSPVTWSYNFARAYANLPEHIRVPLPALSPTELMERGSIVSWEKKEGDKLNEGDLLCEIETD
KATMGFETPEEGFLAKILIQGGTKDVPVQQLLCIIVPDQGSVAAFANFKDDGAAAAAPAA
AAPAPAPAAAAAPPPPPPPAAAAAPAAAAPAAAGQKAAAKPAAAAAPAKAPRAA
GARYEDIPVTNMRAVIAKRLLLESKTQLPHYVTVQCQVDKLLKFRAKVNKKYEKQGARVS
VNDFIIKAVAIASLKVPEANSWMDTVIRKYDDVDVSVAVSTDKGLITPIVFNADRKGVL
EISKDVKALAAKARDNKLQPHEFQGGTISVSNLGMFGVNVQFAAVINPPQSCILAIGTTTK
QLVADPDSLKGFKENVMLTVTLSDHRVVDGAVAAARWLQHFRDYMEDPSNMVL

>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
SSSGGTVPNRLLRQLLGSPSRRSYSLPPHQKVPLPSLPTMQAGTIARWEKKEGEKISE
GDLIAEVETDKATVGFESLEECYMAKILVPEGTRDVPVGSIIICITVEKPQDIEAFKNYTL
DLAAAAAPQAAPAAAPAPAAAPAPSASAPGSSYPHTMQIVLPALSPMTMTGTVQRWEKK
VGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGAPLCIIVEKQEDIA
AFADYRPTEVTSCLKPQAAPPAPPPVAAVPPTPQPVAPTPSAAPAGPKGRVFSPLAKKLA
AEKGIDLTQVKGTGPEGRIKKDIDSFVPSKAAPAAAAAAMAPPGPRVAPAPAGVFTDIPI
SNIRRVIAQRLMQSKQTIPHYLSVDVNMGEVLLVRKELNKMLEGKGKISVNDFIIKASA
LACKLVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNHAIKGLETIASDVVSLA
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
LDSSAAPTQQAAPAPTPAATASPPTPSAQAPGSSYPHMQVLLPALSPMTMTMGTVQRWEK
KVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGTPLCIIVEKEADI
SAFADYRPTTEVTDLKPQVPPPTPPPVAAPPTPQPLAPTPSAPCPATPAGPKGRV FVSPL
AKKLAVEKGIDLTQVKGTGPDGRITKKDIDSFVPSKVAPAPAAVVPPTGPGMAPVPTGVF
TDIPISNIRRVIAQRLMQSKQTIPHYYSIDVNMGEVLLVRKELNKILEGRSKISVNDFI
IKASALACLKVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNAHIKGVETIAND
VVSLATKAREGKLQPHEFQGGTFTISNLGMFGIKNFSAIINPPQACILAIGASEDKLVPA
DNEKGFDVASMMSVTLSCDHRVVDGAVGAQWLAEFRKYLEKPITMLL

SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE

>eco:b0727 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) sucB; dihydrolipoyltranssuccinylase (A)
MSSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAV
LEDEGTTVTSRQILGRLREGNSAGKETSASEEKASTPAQRQQASLEEQNNDALSPAIRR
LLAEHNLDASAIKGTGVGGRLTREDVEKHLAKAPAKESAPAAAAPAAQPALAARSEKRVP
MTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFYVK
AVVEALKRYPEVNASIDGDDVVYHNYFDVSMVSTPRGLVTPVLRDVDTLGMADIEKKIK
ELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNG
QVEILPMMYLALSYDHRLLIDGRESVGFLVTIKELLEDPTRLLLDV

>sce:YDR148C K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) KGD2; dihydrolipoyl transsuccinylase (A)
MLSRATRATAAKSLVKSKVARNVMAASFVKRHASTSLFKQANKVESLGSYLSGKKISVA
ANPFSITSNRFKSTSIEVPPMAESLTEGSLKEYTKNVGDFIKEDELLATIETDKIDIEVN
SPVSGTVTKLNFKPEDTVTVGEELAQVEPGAEPAGSGESKPEPTEQAEPSQGVAARENS
SEETASKKEAAPKKEAAPKKEVTEPKKADQPKKTVSKAQEPPVASNSFTFPRTETRVKM
NRMRLRIAERLKESQNTAASLTTFNEVDMMSALMEMRKLYKDEIIKKTGTFKFGFMGLFSKA
CTLAAKDIPAVNGAIEGDQIVYRDYTDISVAVATPKGLVTPVVRNAESLSVLDIENEIVR
LSHKARDGKLTLEDMTGGTFTISNGGVFGSLYGTPIINSPQTAVLGLHGVKERPVTVNGQ
IVSRPMMYLALTYDHRLLDGREAVTFLKTVKELIEDPRKMLLW

>cel:CELE_W02F12.5 K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61] | (RefSeq) dlt-1; Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (A)
MLGRRASVHRFLSRAARQSVTAASSAQPSLQAKTSLLEPLVQNVRITSSANFHMSAVRM
SDVITVEGPFAESISEGDIRWLKQKGDHVNEDLVAEIETDKTSVEVPAPQAGTIVEFL
VEDGAKVTAKQKLYKLQPGAGGGSSSAPAKEEPSAPAKEESKPAPAKEDSKPAVTAAAP
PKPVSGDIPKSAPPVARPPSTPSSSTPVGAVPVTRVVVPKGVDP SHAITGARDEV RVKAN
RMRMRIAQRLKDAQNTYAMLTTFNEIDMSSLIEMRKTYQKDFVAKHGVKLGMMSPFVRAA
AYALQESPVVNAVLDENEIVYRHFVDISVAVATPKGLVVPVLRNVESMNYAQIELELANL
GVKARDGKLAVEDMEGGTFTISNGGVFGSMFGTPIINPPQSAILGMHGVFDRVVPVNGKP
EIRPIMQIALTYDHRLLIDGREAVTFLKKIKTAVEDPRIMFMNL

>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
RVKMNRMLKIAARLKDAQNTCAMLTTFNEVDMSYAMD FRKQNLDAFTKKYGIKFGFMSI
FAKASAYALQDQPVVNAVIDGTDIVYRDYVDISVAVATPRGLVVPVIRNVEGMNYADIEI
ALAGLADKARRDAITVEDMDGGTFTISNGGVFGSLMGTP IINPPQSAILGMHGIFERPIA
VKGEVKIRPMMYIALTYDHRIIDGREAVLFLRKIKAAVENPAIIVAGL

>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)
MLSRSRCVSRAFSRSLSAFQKGNCPLGRRSLPGVSLCRGPGYPDNRMVINS GSVFRVRF
FQTTAVCKNDVITVQTPAFAESVTEGDVRWEKAVGDVAEDEVVCEIETDKTSVQVPSPA
NGIIEALLVPDGGKVEGGTPLFTLRKTGAAPAKAKPAETPAPAHKAEPAAAPPPPAAP
VLTQMPPVPSPSQPPSSKPVSAIKPTAAPPLAEAGAAKGLRSEHREKMNRMRQRIAQRLK
EAQNTCAMLTTFNEVDMSNIQEMRARHKDAFLKKHNLKLGFM SAFVKASAFALQE QPVVN
AVIDDATKEVVYRDYIDISVAVATPRGLVVPVIRNVETMNYADIERTINELGEKARKNEL
AIEDMDGGTFTISNGGVFGSLFGTP IINPPQSAILGMHAIFDRPVAVGGKVEVRPMMYVA
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)
MLSRSRCVSRAFSRSLSAFQKGNCPLGRRSLPGVSLCQGP GYPNSRKVVINNSVFSVRFF
RTTAVCKDDLVTVKTPAFAESVTEGDVRWEKAVGDTVAEDEVVCEIETDKTSVQVPSPAN
GVIEALLVPDGGKVEGGTPLFTLRKTGAAPAKAKPAEAPAAAAPKAEPTAAAVPPPAPI
PTQMPPVPSPSQPPSGKPVSAVKPTVAPPLAEPGAGKGLRSEHREKMNRMRQRIAQRLKE
AQNTCAMLTTFNEIDMSNIQEMRARHKEAFLKKHNLKLGFM SAFVKASAFALQE QPVVNA
VIDDTTKEVVYRDYIDISVAVATPRGLVVPVIRNVEAMNFADIERTITELGEKARKNELA
IEDMDGGTFTISNGGVFGSLFGTP IINPPQSAILGMHGIFDRPVAIGGKVEVRPMMYVAL
TYDHRLIDGREAVTFLRKIKAAVEDPRVLLLDL

DIHYDROLIPOYL DEHYDROGENASE

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

MSTEIKTQVVVLGAGPAGYSAAFRCADLGLETVIVERYNTLGGVCLNVGCIPSKALLHVA
KVIEEAKALAEHGIVFGPKTDIDKIRTWKEKVINQLTGGLAGMAKGRKVKVNVNGLGKFT
GANTLEVEGENGKTVINFDNAIIAAGSRPIQLPFIPHEDPRIWDSTDALELKEVPERLLV
MGGGIIGLEMGTVYHALGSQIDVVMFDDQVIPAADKDVKVFTKRISKKNLMLLETKVTA
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
ASMDGEVAKATQKFLKKQGLDFKLSTKVISA KRNDKNNVVEIVVEDTKTNKQENLEAEVL
LVAVGRRPYIAGLGAEKIGLEV D KRGRLVIDDQFNSKFPHIKVVGDTVFGPMLAHKAE
GIAAVEMLKTGHGHVNNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRA
KTNQDTEGFVKILIDSKTERILGAHIIGPNAGEMIAEAGLALEYGASAEDVARVCHAHPT
LSEAFKEANMAAYDKAIHC

>cel:CELE_LLC1.3 K00382 dihydrolipoyl dehydrogenase [EC:1.8.1.4] | (RefSeq) dld-1; Dihydrolipoyl dehydrogenase, mitochondrial (A)

MSLSRTTQLPFAKRQFFQVLARNYSNTQDADLVVIGGGPGGYVAAIKAAQLGMKTVCVEK
NATLGGTCLNVGCIPSKALLNNSHYLHMAQHDFARGIDCTASLNLPKMMEAKSNSVKQL
TGGIKQLFKANKVGHVEGFATIVGPNTVQAKKNDG SVETINARNILIASGSEVTPFPGIT
IDEKQIVSSTGALSLGQVPKMMVIGAGVIGLELGSVWQRLGAEVTAVEFLGHVGGMGID
GEVSKNFQRSLTKQGFKLLNTKVMGASQNGSTITVEVEGAKDGKKQTLECDTLLVSVGR
RPYTEGLGLSNVQIDLDNRGRVPVNERFQTKVPSIFAIGDVIEGPMLAHKAEDEGILC
VEGIAGGPVHIDYNCVPSVVYTHPEVAWVGKAEELKQEGVAYKIGKFPFVANSRAKTNNDQ
EGFVKVLADKQTD RMLGVHIIGPNAGEMIAEATLAMEYGASAEDVARVCHPHPTLSEAFR
EANLAAYCGKAINNV

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

MQFTLRHVVS AVAKTPLRTNAAILGALNARCYSSTHEADIVVIGSGPGGYVAAIKAAQMG

MKTVSVEKEATLGGTCLNVGCIPSKALLNNSHYHMAHSGDLEKRGISCGSVSLDLEKLM
GQKSNVAVKALTGGIAMLFKKNKVTQLTGFGTIVNPNEVEVKKSDGSTETVTKNLIATG
SEVTPFPGIEIDEEVIVSSTGALKLAKVPKHLVVIGAGVIGLELGSVWSRLGAEVTAIEF
MDTIGGVGIDNEVSKTFQKVLTQQLKFKLGTKVTAASRSGDNVTVSVENAKSGEKEEIQ
CDALLVSVGRRPYTEGLGLEAVGIVKDDRGRIPVNATFQTVVPNIYAIGDCIHGPMLAHK
AEDEGLITIEGINGGHVHIDYNCVPSVYTHPEVAWVGKSEEQLKQEGVAYKVGKFPFLA
NSRAKTNNDDTDFVVKVLADQATDKILGTHIIGPGAGELINEAVLAMEYGAAAEDVARVCH
AHPTCSEALREANVAAAFGKPINF

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

MQSWSRVYRSLAKKGHFNRISHGLQGVSSVPLRTYADQPIEADVTVIGSGPGGYVAAIKS
AQLGFKTVICIEKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEIPEVRLNL
EKMMEQKHSVAVKALTGGIAHLFKQNKVVHVNGFGKITGKNQVTATKADGSTQVIDTKNIL
VATGSEVTPFPGITIDEDTIVSSTGALSLLKKVPEKLVVIGAGVIGVELGSVWQRLGADVT
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
AQLGFKTVICIEKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEIEMSEVRLNL
DKMMEQKSTAVKALTGGIAHLFKQNKVVHVNGYGKITGKNQVTATKADGGTQVIDTKNIL
IATGSEVTPFPGITIDEDTIVSSTGALSLLKKVPEKMMVVIGAGVIGVELGSVWQRLGADVT
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
DLGLLSEEKASAIRQAADEVLAGQHDDFPLAIWQTGSGTQSNMNMNEVLANRASELLGG
VRGMERKVHPNDDVNKSQSSNDVFPTAMHVAALLALRKQLIPQLKTLTQTLNEKSRAFAD
IVKIGRTHLQDATPLTLGQEISGWVAMLEHNLKHIEYSLPHVAELALGGTAVGTGLNTHP
EYARRVADELAVITCAPFVTAPNKFALATCDALVQAHGALKGLAASLMKIANDVRWLAS
GPRCGIGEISIPENEPGSSIMPGKVNPTQCEALTMLCCQVMGNDVAINMGGASGNFELNV
FRPMVIHNFLQSVRLLADGMESFNKHCAVGIEPNRERINQLLNESLMLVTALNTHIGYDK
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
YLSIGGPAAVLAQGSIKSLECEVEPELGMEAIWKIEVEDFPFILVDDKGNDFQIQIL
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)
MSNKPFIIYQAPFPMGKDNTEYYLLTSDYVSVADFDGETILKVEPEALTLLAQAFHDASF
MLRPAHQKQVAAILHDPEASENDKYVALQFLRNSEIAAKGVLPTCQDTGTAIIVGKKGQR
VWTGGGDEETLSKGVYNTYIEDNLRYSQNAALDMYKEVNTGTNLPAQIDLYAVDGDYEYKF
LCVAKGGGSANKTYLYQETKALLTPGKLKNFLVEKMRTLGTACPPYHIAFVIGGTS AET
NLKTVKLASAHHYDELPTEGNEHGQAFRDVQLEQELLEEAQKLGLGAQFGGKYFAHDIRV

IRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIEKLEHNPGQYIPQELRQAGEGEAVK
VDLNRPMKEILAQLSQYPVSTRSLTGTIIVGRDIAHAKLKEIDAGKELPQYIKDHPIY
YAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAKGNRSQQVTDACHKHGGF
YLGSI GGPAAVLAQQSIKHLECVAYPEL GMEAIWKIEVEDFP AFILVDDKGN DFFQQIVN
KQCANCTK

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

MLRFTNCSCKTFVKSSYKLNIRRMNSSFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIG
GARERMPLPLVHAFGVLKKSAIVNESLGGLDPKISKAIQQADEVASGKLDDHFPLVVF
QTGSGTQSNMNANEVISNRAIEILGGKIGSKQVHPNNHCNQSQSSNDTFPTVMHIAASLQ
IQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLTLGQEFSGYVQQVENGIQRV
AHSLKTL SFLAQGGTAVGTGLNTPGFDVKIAEQISKETGLKFQTAPNKF EALAAHDAIV
ECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELM LPENEPGSSIMPGKVNPTQNEALTQ
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)

MSAVSMLQGEMLARGGAVIARGASLATARNFSRTTVPM AKIRKERDTFGELEV PADKYYG
AQTARSQMNFKIGGPEERMPIPIVHAFGILKKAALVNTEFGLDKKLADAISQAADEVVD
GKLDEHFPLVTWQTGSGTQSNMNVNEVISNRAIEILGGELGSKKPVHPNDHVNMSQSSND
TFPTAMHIAVGREVNSRLLPALKKLRTALHNKAEEFKDIKIGRTH TQDAVPLTLGQEFS
AYVTQLDNSIARVESTLPRLYQLAAGGTAVGTGLNTRKGFAEKVAATVSELTGLPFVTAP
NKFEALAAHDALVEVHGALNTVAVSFMKIGNDIRFLGSGPRCGLGELSLPENEPGSSIMP
GKVNPTQCEAITMVA AQVMGNQVAVSVGGSNGHFELNVFKPLIVRNVLQSTRLLADSAVS
FTDHCVDGIVANKDNI AKIMRESLMLVTALNPHIGYDNAAKIAKTAHKNGTTLVQEAVKL
GILTEEQFAQWVKPENMLGPK

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

MVLPLLQRSTLRGVQQMTKPWAAIGSLRLASQEFRVESDTFGELKVPADKYYGAQTMRSQ
INFPIGGATERMPKPVVQAMGILKKA AEVNKEFGLDSKVSE AISKAAADDVISGKLYDDH
FPLVIWQTGSGTQSNMNVNEVISNRAIELLGGKLGSKTPVHPNDHVNKSQSSNDTFPTAI
HISVALELNNNLKPAIKTLHDALRAKSEEFKDIKIGRTH TMDAVPLTLGQEFSGYAQQ L
AYAQERIDACLPRVYELALGGTAVGTGLNTRKGFAEKCAAKIAELTSLPFVTAPNKF EAL
AARDAMVEVHGV LNTIAVSLMKIANDIRFLGSGPRCGLGELSLPENEPGSSIMPGKVNPT
QCESLTMLS AQVMGNQVAVTIGGSNGHFELNVFKPLIVSNVLR SIRLLSDGSRTFTANCV
NGIQANRENI AKIMNESLMLVTALNPHIGYDKAAKIAKTAHKNGTTLKEEAINLGYLTEQ
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 RSLMKFPIGGVEER
MPRPLIKALGIVKKSAAETNKIHCLEEHLCDAISKACDDVISGKLYDEEHFPLVIWQDGS
GEHTNMNVNEVICNRAIEILGGQMGSKEPVDPNEHV NMAQSSHDTFSTAVRIAVAMQLQE
TLYPSLRTFIDLLGKKSNDWMDLIKIGRTHLMDAVPLSLGQEFSGYQQQLVNGRTRLDC A
MCRLYQLPMGGTSVGTKVDTKAEYSAQCIKRIAELTFLPFVESPNFFESISACDCLVELH
GELNTIAASVMKIANDIRFLGSGPRCGFGELHLPENEPGSSIMPGKVNPTQCEAMSMICA
QVMGNHVAVSMGGSSGHFQLNTFMPMIAS NVLRSITLLGDGMKSFC TNCLEGIEPNRSKI
GSIVKESLMLVTALSPHIGYERSAAIAKAAHHNGTTLEQEAILDGIQREDFREWVQPSKM
LGPE

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

MYRALRLLARSRRLLRVPSAGAAVS 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
KVPNDKYYGAQTVRSTMNFKIGGVTERMPTPVIKAFGILKRAAAEVNQDYGLDPKIANAI
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
CMNLNGDYISDALAAQVGGIGIAPGANIGDECALFEATHGTAPKYAGQDKVNPGSIIILSA
EMMLRHMGWTEAADLIVKGMEGAINAKTVTYDFERLMDGAKLLKCSEFGDAIENM

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

MSMLSRRLFSTSRLLAFSKIKVKQPVELDGDDEMTRIWDKIKKKLILPYLDVDLKYYDL
SVESRDATSDKITQDAAEAIKKYGVGIKCATITPDEARVKEFNLHKMWKSPNGTIRNILG
GTVFREPIVIPRIPLVPRWEKPIIIGRHAHGDQYKATDTLIPGPSLELVYKPSDPTTA
QPQTLKVYDYKGSVAMAMYNNTDESIEGFAHSSFKLAIDKKLNLFLSTKNTILKKYDGRF
KDIFQEVYEAQYKSKFEQLGIHYEHLIDDMVAQMIKSKGGFIMALKNYDGDVQSDIVAQ
GFGSLGLMTSILVTPDGKTFESEAAHGTVTRHYRKYQKGEETSTNSIASIFAWSRGLLKR
GELDNTPALCKFANILESATLNTVQQDGIMTKDLALACGNERSAYVTTEEFDAVEKRL
QKEIKSIE

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

MTKIKVANPIVEMDGEQTRIIWHLIRDKLVLPYLDVDLKYYDLSVEYRDQTNDQVTVDS
ATATLKYGVAVKCATITPDEARVEEFHLKKMWKSPNGTIRNILGGTVFREPIIIPRIPL
VPQWEKPIIIGRHAFGDQYKATDVIVPEEGELRLVYKSKSGTHDVLKVFDPYEHGGVAM
MMYNNTTDSIEGFAKASFELAIERKLPLYSTTKNTILKKYDGKFKDVFEAMYARSYKEKFE
SLGIWYEHRLIDDMVAQMLKSKGGYIIMKNYDGDVESDIVAQGFGSLGLMTSVLITPDG
KTFESEAAHGTVTRHFRQHQQGKETSTNSIASIFAWTRGIIQRGKLDNTPDVVKFGQILE
SATVNTVQEDGIMTKDLALILGKSERSAYVTTEEFIDAVESRLKKEFEAAAL

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

MSKIKVVHPIVEMDGEQTRVIWKLIEKLILPYLDVDLKYYDLSIQERDRTNDQVTKDS
SYATLKYGVAVKCATITPDEARMKEFNLKEMWKSPNGTIRNILGGTVFREPIIIPKIPRL
VPHWEKPIIIGRHAFGDQYRATDIKIKKAGKLRLQFSSDDGKENIDLKVYEFPKSGGIAM
AMFNTNDSIKGFAKASFELALKRKLPLFFTTKNTILKNYDNQFKQIFDNLFDKEYKEKFKQ
ALKITYEHRLIDDMVAQMLKSKGGFIAMKNYDGDVQSDIVAQGFGSLGLMTSILITPDG

KTFESEAAHGTVTRHFRKHQRGEETSTNSIASIFAWTRAIQRGKLDNTDDVIKFGNLL
KATLDTVQVGGMKTKDALMLGKTNRSSYVTTEEFIDEVAKRLQNMMLSSNEDKKGMCKL

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

MLNRTIAKRTLATAAQAERTLPKKYGGRTVTLPDGDVGKEITDSVRTIFEAEENIPIDW
ETINIKQTDHKEGVYEAVESLKRNIKGLKGLWHTPADQTHGSLNVALRKQLDIYANVAL
FKSLKGVKTRIPDIDLIVIRENTEGEFSGLEHESVPGVVESLKVMTRPKTERIARFAFDF
AKKYNRKSVTAVHKANIMKLGDGLFRNIITEIGQKEYPDIDVSSIIVDNASMQAVAKPHQ
FDVLVTPSMYGTILGNIGAALIGGPGLVAGANFGRDYAVFEPGSRHVGLDIKGQNVANPT
AMILSSTLMLNHLGLNEYATRISKAVHETIAEGKHTTRDIGSSSTTDFTEIINKLSTM

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

MLRNTFFRNTSRRFLATVKQPSIGRYTGKPNPSTGKYTVSFIEGDGIGPEISKSVKKIFS
AANVPIEWESCDVSPIFVNGLTTPDAVQSITKNLVALKGPLATPIGKGHRSLNLTLRK
TFGLFANVRPAKSIEGFKTTYENVDLVLIRENTEGEYSGLIEHIVCPGVVQSILITRDAS
ERVIRYAFEYARAIGRPRVIVVHKSTIQLADGLFVNVAKELSKEYPDLTLETIDNSV
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
CHAPVNFEEVQVSSSLDGDMDAAMLAIERNGVAIKGNIETKHDDPQFNSRNVELRTKLD
LYANILHCVTIPTVPTRHSGIDIVLIRENTEGEYSGLEHEAVPGIVESIKIVTREKIERI
SRMAFEYAKANGRKKVTAVHKANIQKLGDGLFLKVVRDMSEDYKDIKFEAMIVDNASMQL
VSKPQQFDVMVMPNLYGNIISNIACGLVGGPGLVSGMNLGDKYAVFETGTRNTGTSLAGK
DIANPTAFIRASVDMLRYLGCHYHANIISDALWKALVEQRIHTADIGGNNASDVINATL
QNIKVLMDENPKH

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

MLSRLTSRNVLLARNVATAATQERQKIKVDNPVVDLDGDEMTRIHWKEIKNKLILPYLDL
DIKYYDLGLEVRDETNDQVTIDAHAILEHSGIKCATITPDEARIKEFNLKKMWLSPNG
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
LQGLNMRLRRSLDLFANVVHIKTLDGIKTRHKGKQLDFVIVREQTEGEYSSLEHELVPGLV
ECLKISTRRTKAERIAKFAFDYATKTGRKKVTAVHKANIMKLGDGLFLRTCEGVAKQYPKI
QFESMIIDNTCMQLVSKPEQFDVMVMPNLYGNIIDNLAAGLVGGAGVVPQGQSVGRDFVIF
EPGSRHSFQEAMGRSIANPTAMILCAANMLNHLHLDAWGNSLRQAVADVKEGKVRTRDL
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
AKAEYPDIEFNAMIVDNASMQLVSRPQQFDVMLMPNLYGNIISNIACGLVGGPGLVSGMN
IGEDYAVFETGTRNTGTTLAGKDLANPTAFIRAAMDMLRFLGLQSHADMISDSLFRTLVD
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
RQNGRKVVTAVHKANIMRQSDGLFLSICREQAALYPDIKFKEAYLDTVCLNMVQDPSQYD
VLVMPNLYGDILSDLCAGLVGGLGVTPSGNIGKGAAVFESVHGTAPDIAGQDKANPTALL
LSAVMMLRYMNLQPQHAARIEKAVFDAIADGRAKTGDLGGTGTCSSTADVCAVVKDLE

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

GLAHRATLDKNSALETFANNLEAVCIETMEAGFLTDLAICVKGGNASAVTRTDYLNTE
FLDKLAENLAKKQAH

>dme:Dmel_CG3483 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq)
CG3483; uncharacterized protein (A)
MNTLRKLNSLPPFRSVGGAYRLFAGKDQKKDSAGQKTRQPEKPPQDKQKSKGASGKAKSA
GSTDSAKKTTKVTLINGEGVGRELMDAVQEVCAPKAPIEWDVHDEFKAKDSDDVSPEVL
KSLRANKVGIKGPVDSRHWQRQIRKQFAQFAYVSLCSHIEGLDSPYGDFFDVIIRDQMEG
DYSGIEHLVVPVGMQTIKVSTTAGAARIAEFVFNAYVKNKRKRITVAHKANIMRMTDGNF
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
PEQMAQKIKAGPVVDVLGDEMTRIWDISIQLILPFLDIELHTYDLGIENRDKTEDQVT
IDCAEAIKKYNVGIKCATITPDEKRVEEFNLKMMWKSPNGTIRNILGGTVFREAIICKNV
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
IQFEEKYLDTVCLNMVQNPQKYDVLVMPNLYGDILSDMCAGLVGGLGLTPSGNMGLNGAL
FESVHGTAPDIAGKDLANPTALLLSAVMMLRHMELENTYADKIERAAFETIKEGKYLTGDL
GGRACSEFTNEICAKL

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

MSGNWFKWTALHGRPRTVGLNTNGRILRLDDAVVRFRQPFYESWRRRRRLEDIEKREIP
VRQQVPRIRHNRCPGAKENPCRKMPSVLPKGGEVLVPSRIQPPRNSMGFSVIRLFGSSTN
DGGSGEPPENREGKLIKFTVGSRIAKPKTGKIEISKKGPLGFETTKLPVQESLPQSDYLS
GLSKKSPDKDTPDTSTTQASDRSGKEGNEEKIKDDIPRSFSEYIIHWDSESKNPSGIQS
QQPERCESAGNPPSGGKPPPTKPPTGPSTPSGPSNPSRPPSRKDNNPFSGMGSEPPKKPPL
GSKPPSKLPPRSTSPKKPPTGSTPPQKPTKSSKPPNKPAPGPGKKSASKPPTASKPPVKS
PAGGQQGQGGAGGKSGKASGEPRVITLMPGDGIGPEISMAVIKILEAAKTPLIFEPVDVT
PVLNSQGMTSVPEQVIESMNRTKVGLKGPLMTPVGTGFRSLNLTLRQLFNLYANIRPCRS
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)

MSRKIQGGSVVEMQGDDEMTRIIEWELIKEKLILPYVELDLHSYDLGIENRDATNDQVTKDA
AEAIIKYNVGVKCATITPDEKRVEEFKLKQMWKSPNGTIRNILGGTVFREAIICKNIPRL
VTGWVKPIIIGRHAYGDQYRATDFVVPGPQKVEITYTPKDGTTQKVITYMVHDFEEGGGVAM
GMYNQDKSIEDFAHSSSQMALSKGWPLYLSTKNTILKKYDGRFKDIFQEIYDKKYKSQFE
AQKICYEHRLIDDMVAQAMKSEGGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLICPDG
KTVEAEAAHGTVTRHYRMYQKGQETSTNPIASIFAWSRGLAHRKLDNNTLSFFAKALE
DVCIIETIEAGFMTKDLAACIKGLPNVQRSDYLNTFEFMDKLGENLKAKLAQAKL

>mmu:15929 K00030 isocitrate dehydrogenase (NAD+) [EC:1.1.1.41] | (RefSeq) Idh3g;
isocitrate dehydrogenase 3 (NAD+), gamma (A)
MALKVAIAAGGAAKAMLKPTLLCRPWEVLAAHVAPRRSISQQTIPPSAKYGGRHTVTMI
PGDGIGPELMLHVKS VFRHACVPVDFEEVHVSSNADEEDIRNAIMAIRNRVALKGNIET
NHNLPSSHKSRNNILRTSLDLYANVIHCKSLPGVVTRHKDIDILIVRENTEGEYSSLEHE
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
YANVRPCVSIEGYKTPYTDVNIVTIRENTEGEYSGIEHVIVDGVVQSIKLITEEASKRIA
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
GIGPELMVHVKKIFRSNCVPVDFEEVWVTSTSNEEEINNALMAIRNRNRVALKGNIATNHN
LPARYKSHNTKFRTILDLYASVVHFKTFPGVMTRHKDIDILVVRENTEGEYTNLEHESVK
GVVESLKIVTKTKSVRIADYAFKLAQKMGRKKVTVVHKANIMKLG DGLFLQCKDVAAHY
PQITLESMIIDNTTMQLVSKPQQFDVMVMPNLYGNIINSICTGLVGGSGIVPGANYGDSY
AIFEMGSKEIGKDLAHRNIANPVAMLLTSCIMLDYLDLQPYATHIRSAVMASLQNKAVCT
PDIGGGQGNTASTVEYILHMHMKEQTSGCHPNFFLQFT

>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
SGGFVWACKNYDGDVQSDILAQQFGSLGLMTSVLVCPDGKTIEAEAAHGTVTRHYREHQB
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)
MSKKISGGSVVEMQGDDEMTRIIWELIKEKLIFPYVELDLHSYDLGIENRDATNDQVTKDA
AEAIKHNHVGKCATITPDEKRVVEEFKLKQMMWKSPNGTIRNILGGTVFREAIICKNIPRL
VSGWVKPIIIGRHAYGDQYRATDFVVPGPVKVEITYTPSDGTQKVTVLVHNFEEGGGVAM
GMYNQDKSIEDFAHSSSQMALSKGWPLYLSTKNILKKYDGRFKDIFQEIDKQYKSQFE
AQKIWYEHRLIDDMVAQAMKSEGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLVCPDG
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)
MAGYLRVVRSLCRASGSRPWAPAALTAPTSQEPRRHAYADKRIKVAKPVVEMDGDDEMTR
IIWQFIKEKLILPHVDIQLKYFDLGLPNRDQTDDQVTIDSALATQKYSVAVKCATITPDE
ARVEEFKLKMMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGWTKPITIGRHAHGDQYK
ATDFVADRAAGTFKMFVFTPKDGSGVKEWEVYNFPAGGVGMGMYNNTDESISGFAHSCFQYAI
QKKWPLYMSTKNILKAYDGRFKDIFQEIFDKHYKTDFDKNKIWYEHRLIDDMVAQVLKS
SGGFVWACKNYDGDVQSDILAQQFGSLGLMTSVLVCPDGKTIEAEAAHGTVTRHYREHQB
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
QDPSQFQDVLVMPNLYGDILSDLCAGLIGGLGVTPSGNIGANGVAIFESVHGTAPDIAGKD
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
YKGELASYDMRLRRKLDLFANVVHVKSPLPGYMTRHNNLDLVIIREQTEGEYSSLEHESAR
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 VFRHACVPVDFEEVHVSSNADEEDIRNAIMAIRRNRVALKGNIET
NHNLP PSHKSRNNILRTSLDLYANVIHCKSLPGVVTRHKDIDILIVRENTGEYSSLEHE
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
WAPLVMGRDPQQKVAATRTEIGTDVNYGEITRQLIASLQKKS NFSLQLSSEVRALKRND
DNTWTVTVADLKNGT AQNIRAKFVFIGAGGAALKLLQESGIPEAKDYAGFPVGGQFLVSE
NPDVVNHHLAKVYGKASVGAPPMSPHIDTRVLDGKRVLFGPFATFSTKFLKNGSLWDL
MSSTTTSNVMPMMHVGLDNFDLVKYLVSQVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQ
RVQIIKRDAEKGGVLRRLGTEVVSDQQGTIAALLGASPGASTAAPIMLNLEKVFGRVSS
PQWQATLKAIVPSYGRKLNGDVAATERELQYTSEVLGLNYDKPQAADSTPKPQLKPQPVQ
KEVADIAL

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

dehydrogenase (A)

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSG
EDATPALEGADVVLISAGVARKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNP
VNTTVAIAAEVLKAGVYDKNKLFVTTLDIIRSNTFVAELKGKQPGEVEVPVIGGHSGV
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
VTVIGGHSGETIIPITDKSLVFQLDKQYEHFIHRVQFGGDEIVKAKQGAGSATLSMAFA
GAKFAEEVLR SFHNEKPETESLSAFVYLPGLKNGKKAQQLVGDNSIEYFSLPIVLRNGSV
VSIDTSVLEKLSPREEQLVNTAVKELRKNIEKGKSFILDSSKL

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

dehydrogenase MDH1 (A)

MLSRVAKRAFSSTVANPYKVTVLGAGGGIGQPLSLLLKLNHKVTDLRLYDLKGAKGVATD
LSHIPTNSVVKGFTPEEPDGLNNALKD TDMVLIPAGVPRKPGMTRDDLFAINASIVRDLA
AATAESAPNAAILVISNPVNSTVPIVAQVLKNKG VYNPKKLFGVTTLDSIRAARFISEVE
NTDPTQERVNVIGGHSGITIIP LISQTNHKLMSDDKRHELIHRIQFGGDEVVKAKNGAGS
ATLSMAHAGAKFANAVLSGFKGERDVIEPSFVDSPLFKSEGIEFFASPVTLGPDGIEKIH

PIGELSSEEEEMLQCKETLKKNIEKGVNFVASK

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

MPHSVTPSIEQDSLKIAILGAAGGIGQSLSLLLKAQLQYQLKESNRSVTHIHLALYDVNQ
EAINGVTADLSHIDTPISVSSHSPAGGIENCLHNASIVVIPAGVPRKPGMTRDDLFNVNA
GIISQLGDSIAECCDLSKVFLVISNPVNSLVPVMVSNILKNHPQSRNSGIERRIMGVTK
LDIVRASTFLREINIESGLTPRVNSMPDVPVIGGHSGETIIPLFSQSNFLSRLNEDQLKY
LIHRVQYGGDEVVKAKNGKGSATLSMAHAGYKCVVQFVSLLLGNIEQIHGTYVPLKDAN
NFPIAPGADQLLPLVDGADYFAIPLTITTKGVSYVDYDIVNRMNDMERNQMLPICVSQLK
KNIDKGLEFVASRSASS

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

MSLPAKTLVQAAANSGLRAVSVRHSSQAPKVALLGAAGGIGQPLGLLLKQDPLVAHLALY
DVVNTPGVAADLSHIDSNAKVTAHTGPKELYAAVENADVIVIPAGVPRKPGMTRDDLFNT
NAGIVRDLAAVIAKASPKALIAITNPVNSTVPIASEVLKKAGVYDPKRVFGVTTLDVVR
SQAFVSELKGHDAKSTVVPVVGGHAGITIIPLLSQVKPSTKFSEEEISKLTPIQDAGTE
VVNAKAGAGSATLSMALAGARFANALVRGIKGEKNVQCAYVASDAVKGVEYFSTPVELGP
NGVEKILGVGKVSAYEQKLIDASVPELNKNIAKGVAFAVKGN

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

MSAPLRVLVTGAAGQIGYSIVIRIADGTVFGKEQPVELVLLDVPQCSNILEGVVFELQDC
ALPTLFSVVAVTDEKSAFTGIDYAFVLVGAMPRREGMERKDLLAANVKIFKSQGKALAEYA
KPTTKVIVVGNPANTNAFIAAKYAAGKIPAKNFSAMTRLDHNRALAQLALKTGTTIGNVK
NVIIWGNHSGTQFPDVTHATVNKNGTETDAYAAVGDN AFLQGPF IATVQKRGGVII EK RK
LSSAMSAAKAACDHIHDWHFGTKAGQFVSMAPSDGSYGIPQGLIFSPVTIEGGEWKIV
QGLSFDDFAKGKIAATTKELEEERDDALKACDDANI

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

MAEPIRVVVTGAAGQIAYSLLYMIARGEVFGKDQPIVLHLLDIPPMVGVLEGVVMELADC
ALPLLVEVPTTDPVAGFKDVSA AFLVGAMPRKEG MERKDLLSANVKIFRTQGGALDKFA
KKDVKVLVGNPANTNALVCSSYAPSIPRENFSAMTRLDQNRATSQIAAKLGVPISAVKN
IIIWGNHSSTQYPDAGQAKVTANGTVKSVVD AINDNGYLQGSFVETVQKRGA AVIAARKM
SSAMSAAKAACDHMHDDWWNGTAPGQFVSMGVFSDGSYDSPKDVIFSFPVEIKNKQWKIVS
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
KVATAISNASPRAHLAFITNPVNMIHPAAAEVLMAHGTFDSRRLFGITTLDVVRSKKFIG
DSMNISPDDVNIPVIGGHAGITILPLISQCQPIYRCDLQEIQNLTHRIQEAGTEVVNAKA
GKGSATLSMAYAGATFVNSLLRGIAGQDGLIECAFVASKLTDAPFFASPLELGKDGKRY
IPLPQMSDYEKEALEKLLPILRQNADEGVNFAKMILSGQSHSPIAALP

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

MFLASRLLSHVGNLPPKVQQLGYINRGLKVAVVGSVGGIGQPLSLLLKHNPIQISTLSLYD
IKNTTGVGVDLSHINTRASVCPFEGKNGLLKKAMDKADIVVIPAGLPRKPGMKREDLVDVN
ASVACEVAFAASEVCPGAMLAFITNPINVIVPIVATILKAKGTYPNRLFGVTTLDVVRA
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

KKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCLTRLDHNRAKSQIALKLGVTADDVKN
VIIWGNHSSTQYPDVNHAKVKLQGKEVGVEALKDDSWLKGEFITTQQRGAAVIKARKL
SSAMSAAKAIADHIRDIWFGTPEGEFVSMGVISDGNSYGVPPDLLYSFPVVIKNKTKWKFV
EGLPINDFSREKMDLTAKELTEEKETAFAFEFLSSA

>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
ALPLLKDVIATDKEDVAFKDLVDAILVGSMRREGMERKDLLKANVKIFKSQGAALDKYA
KKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCLTRLDHNRAKAQIALKLGVTANDVKN
VIIWGNHSSTQYPDVNHAKVKLQGKEVGVEALKDDSWLKGEFVTTVQQRGAAVIKARKL
SSAMSAAKAICDHVRDIWFGTPEGEFVSMGVISDGNSYGVPPDLLYSFPVVIKNKTKWKFV
EGLPINDFSREKMDLTAKELTEEKESAFEFLSSA

>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

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
ADLDPSFHDLTADFQETFNVGSSFASGKETMKLGELLEALKQTYCGPIGAEYMHITSTEE
KRWIQQRIESGRATFNSEEKKRFLSELTAEEGLERYLGAKFPGAKRFSLEGGDALIPMLK
EMIRHAGNSGTREVVLGMAHRGRLNVLVNLGKKPQDLFDEFAGKHKEHLGTGDVKYHMG
FSSDFQTDGGLVHLALAFNPSHLEIVSPVVIGSVRARLDRLDEPSSNKVLPITIHGDAAV
TGQGVVQETLNMSKARGYEVGGTVRIVINNQVGFTTSNPLDARSTPYCTDIGKMVQAPIF
HVNADDPEAVAFVTRLALDFRNTFKRDVFIDLVCYRRHGHNEADEPSATQPLMYQKIKKH
PTPRKIYADKLEQEKVATLEDATMVNLYRDALDAGDCVVAEWRPMMNHSFTWSPYLNHE
WDEEYPNKVEMKRLQELAKRISTVPEAVEMQSRVAKIYGDRQAMAAGEKLFDWGGAENLA
YATLVDEGIPVRLSGEDSGRGTFFHRHAVIHNSNGSTYTPLQHIHNGQGAFRVWDSVLS
EEAVLAFEYGYATAEPRTLTIWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLLPH
GYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRGMRRPLVVMSPKS
LLRHPLAVSSLEELANGTFLPAIGEIDELDPKGVKRVVMCSGKVYYDLLEQRRKNNQHDV
AIVRIEQLYPFPHKAMQEVLLQQFAHVKDFVWCQEEPLNQGAWYCSQHHEFREVIPFGASLR
YAGRPASASPAVGYSVHQKQQQDLVNDALNVE

>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)
MHRASLICRLASPSRINAIRNASSGKSHISASTLVQHRNQSVAAAVKHEPFLNGSSSIYI
EQMYEAWLQDPSSVHTSWDAYFRNVEAGAGPGQAFQAPPATAYAGALGVSPAAAQVTTSS
APATRLDTNASVQSISDHLKIQLLIRSYQTRGHNIADLDPLGINSADLDDTIPPELELSF
YGLGERDLDRFLLPPTTFISEKKSLTLREILQRLKDIYCTSTGVEYMHNNLEQQDWIR
RRFEAPRVTELSHDQKKVLFKRLIRSTKFEEFLAKKWPSEKRFGLGCEVLIPAMKQVID
SSSTLGVDSFVIGMPHRGRLNVLANVCRQPLATILSQFSTLEPADEGSGDVKYHLGVCIE
RLNRQSQKNVKIAVVANPSHLEAVDPVVMGKVRAEAFYAGDEKCDRTMAILLHGDAAFAG
QGVVLETFNLDLPSYTTTHGAIHVVNNQIGFTTDPRSSRSPYCTDVGRVVGCPIFHVN
VDDPEAVMHVCNVAADWRKTFKKDVIVDLVCYRRHGHNELDEPMFTQPLMYQRIKQTKTA
LEKYQEKILNEGVANEQYVKEELTKYGSILEDAYENAQKVITYVRNRDWLDSPWDDFFKKR
DPLKLPSTGIEQENIEQIIGKFSQYPEGFNLHRGLERTLKGRQQMLKDNSLDWACGEALA
FGSLLKEGIHVRLSGQDVQRGTFSHRHHVLHDQKVDQKIYNPLNDLSEGQGEYTVCNSSL
SEYAVLGFELGYSMVDPNSLVIWEAQFGDFSNTAQCIIDQFISSGQSKWIRQSGLVMLLP
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)
MHRAHTAFSLALSPMAHKNFATWLLKSSSSQQMAKVTA AAAVRTYNSAAAE PFANGSTAS
YVEEMYNALWRDPTSVHTSWDAYFRSNSYVSPPNLAPVQANTLPLTAFNFGGAVAGAAPD
SKTIDDHLAVQAIIRSYQIRGHNIAHLDPLEINTPELPGNSSTKSIYANFSFGEQDMDRQ
FKLPSTTFIGGDEASLPLKEILNRLENVYCNIKIGVEFMFINSLEQCNWIRKRFETPGVLN
FSPEEKRLILARLTRATGFEAFLAKKYSSEKRFGLGCEIMIPALKEIIDVSTELGVESV
IMGMPHRGRLNTLANVCRKPLNQIFTQFAGLEAADDGSGDVKYHLGTYIERLNRVTNKN
RLAVVANPSHLEAVDPVVQGKTRAEQFYRGDQEGKKVMSILIHGDAAF CGQGVVYETMHL
SDLPDYTTHTGTHVANNQIGFTTDPFRFSRSPYCTDVARVVNAPIFHVNADDPEAVMHV
CKVAAEWRAFTHKDCVIDLVGYRRNGHNEIDEPMTQPLMYQKIRKHKNCCLDYADKLIA
EGVTAAEEVKSVAAKYENICEEAFALAKTETHVKYKDWLDSPWSGFFEGKDPLKVAPTGV
KEETLIHIGNRFSSPPNAAEFVIHKGLLRVLAARKAMVDEK VADWALGEAMAFGSLLKE
GIHVRLSGQDVERGTFSHRHHVLHHQLVDKATYNSLQHMYPDQAPYSVSNSSLSEYAVLG
FEHGYSMTNPNALVLWEAQFGDFSNTAQSIIDQFISSGQSKWVRQSGLVMLLPHGMGEGMG
PEHSSCRVERFLQMSSDDPDYFPPESEDFGVRQLHDINWIVANCSTPANYYHILRRQIAL
PFRKPLILCTPKSLLRHPEAKSPFSEMSEGSEFQRIIPDNGPAGQNPSNVKKVFCSGRV
YYDLTKTRREKQLEGEIAIVRVEQISPFDFLVKEQANLYKNAELVWAQEEHKNQGSWTY
VQPRFLTALNHSRDVSQSDEQSSSTNTTTTDDHTNHESD TDSDSKSKPWLSRMFAAPNSS
TGGDPKDPATLGDFNAAKHFDLKNVRHDFNRPAGIAAAPGARIAKTGRKISYVGRACG
ASTATGSKAQHIRELNALLNDAIST

>dme:Dmel_CG33791 K00164 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2] | (RefSeq) CG33791; uncharacterized protein, isoform C (A)
MNQCRLRLSARIRSLTLGLRGTDQHVLRARQALRTIQTTSQRRGVHDLDSFANGCSAAYI
EGLYNKWKRNPSSVDESWNELFSSNDWSSPKRSPLQVSHSRKYRRPPVERIAVKARSGER
TASGGASAAPAAPPSDWKNIDHHVIQAIIRAYQSRGHLAADLDPLGIVGPKKRTSVDGT
QRHAAREVLRQHFSYIFNDLNTVFKLPSSTMIGGDQEFSLKEILDRLERIYCGHIGVEY
MQITSLTKTNWLRDRFEKPGGLDLTKEEKKLILERLTRSTGFENFLAKKFSSEKRFGLG
CDIMIPAIKEVVDRATDHGVESILIGMAHRGRLNVLANICRKPISDILSQFHGLQATDSG
SGDVKYHLGVFQERLNRQTNRMVRI TVVANPSHLEHVN PVLLGKARAEMFQRGDT CGSTV
MPIIIHGDAFSGQGVVYESMHLSDLPNYTTYGTI HIVSNNQVGFTTDP RFSRSSRYCTD
VAKVVNAPILHVNADDPEACIQCARIAIDYRTRFKKDVVIDIVGYRRNGHNEADEPMFTQ
PLMYQRIKKLKPCLQLYADKLIKEGVVTDSEFKAMVSSYEKICEDAWAKSKTIKTIKYSS
WIDSPWPGFFEGDRDLKLCPTGISTDTLKTIGNMFSTPPPPEHKFETHKGILRILAQRTQ
MVQDKVADWSLGEAFAGSLLKEGIHVRLSGQDVERGTFSHRHHVLHHQSEDKV VYNSLD
HLYPDQAPYSVSNSSLSECAVLGFEHGYSMASPNALVMWEGQFGDFCNTAQCIIDTFIAS
GETKWVRQSGVVMLLPHSMEGMGPEHSSGRIERFLQMSDDDPDVYPDTCDADFVARQLMN
VNWIVTNLSTPANLFHCLRRQVKMGFRKPLINFSPKSLLRHPLARSPFKDFNECSCFQRI
IPDKGPAGKQPCDCVQKLVFCSGKVYYDLVKERDDHEQVETVALVRVEQLCPFPYDLISQQ
LELYPKAELLWAQEEHKNMGAWSYVQPRFDTALLKNENESRCVSYHGRPPSASPATGNKV
QHYNEYKALITSIFGELTPENKKRIEDRIKKQAKAKADAQSKPSTKPPAAPPKGGSSPP
PGPAPRKPLISLPSRPPRGGKQRSGSAPAPNLVDEDSAARNREP DASAYDGASPSAWKRS
GSAPAPSVVPRASASRSPSRKSPSPSHDGISPSTRQESLSKKKSGSAPAPTPTSRGPFR
TAPSNTTEFIKRRPAKDYGSRNETQSTPGESELDPTKPQP

>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 KLG FYGLHES
DLDKVFHLP TTTTFIGGQEPALPLREIIRLEMAYCQHIGVEFMFINDLEQCQWIRQKFET
PGIMQFTNEEKRTLRLVRSTRFEEFLQRKWSSEKRFGLGCEVLIPALKTIIDMSSAN
GVDYVIMGMPHRGRLNVLANVIRKELEQIFCQFDSKLEAADEGSGDMKYHLGMYHRRINR
VTDRNITLSLVANPSHLEAADPVVMGKTAEQFYCGDTEGKKVMSILLHGDAAFAGQGIV
YETFHLSDLPSYTTHTGTVHVVVNNQIGFTTDP RMARSSPYPTDVARVVNAPIFHVNSDDP
EAVMYVCKVAAEWRNTFHKDVVDLV CYRRNGHNEMDEPMFTQPLMYKQIRKQKPV LQKY
AELLVSQGVVNQPEYEEEEISKYDKICEEAFTRSKDEKILHIKHWLDSPWPGFFTL DGQPR
SMTCPSTGLEEDVLFHIGKVASSVPVENFTIHGGLSRILKTRRELVTNRTVDWALAEYMA
FGSLLKEGIHVRLSGQDVERGTFSHRHHVLHDQNVDKRTCIPMNLHWP NQAPYTV CNSSL
SEYGV LGFELGFAMASPNALVLWEAQFGDFNNMAQCIIDQFICPGQAKWVRQNGIVLLLP
HGMEGMGPEHSSARPERFLQMCNDDPDVLPDLQEENFDINQLYDCNWIVVNCSTPGNFFH
VLRRQILLPFRKPLIVFTPKSLLRHPEARTSFDEMLPGTHFQRVIPENGPA AQDPHKV KR

LLFCTGKVVYDLTRERKARNMEEVAITRIEQLSPFPFDLLLKEAQKYPNAELAWCQEEH
KNQGYDYVKPRLRTTIDRAKPVWYAGRDPAAAPATGNKKTHLTELRFLDTAFDLDAFK
KFS

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

MSQLRLLPFRLGPRATKLLATRAIPVFSGCRRSSGPPTTIPRSRSGVSSSYVEEMYFAWL
ENPQSVHKSWSDSFFQRASKEASVGPAQPQLPAVLQESRTSVSSCTKTSKLVEDHLAVQSL
IRAYQIRGHHVAQLDPLGILDADLDSFVPSDLITTIDKLAFYDLQEADLDKEFRLPTTTF
IGGPENTLSLREIIRRESTYCQHIGLEFMFINDVEQCQWIRQKFETPGVMQFSVEEKRT
LLARLVRSRMRFEDFLARKWSSEKRFGLGCEVMIPALKTIIDKSSEMGIENVILGMPHRG
RLNVLANVIRKDLEQIFCQFDPKLEAADEGSGDVKYHLGMYHERINRVNITLSLVAN
PSHLEAVDPVVQGKTKAEQFYRGDAQGRKVMISILVHGDAAFAGQGVVYETFHLSDLPSYT
TNGTVHVVVNNQIGFTTDPRMARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEW
RNTFNKDVVVDLVCYRRRGHNEMDEPMFTQPLMYKQIHKQVPVLKKYADKLIAEGTVTLQ
EFEEEEIAKYDRICEEAYGRSKDKKILHIKHWLDSPWPGFFNVDGEPKSMTCPTTGIPEEM
LTHIGSVASSVPLEDFKIHTGLSRILRGRADMTKKRTVDWALAEYMAFGSLLKEGIHVRL
SGQDVERGTFSHRHHVLHDQEVDRRTCVPNMHLWPDQAPYTVCNSSLSEYGVVLFELGYA
MASPNALVLWEAQFGDFHNTAQCIIDQFISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSA
RPERFLQMSNDDSDAYPVFTEDFEVSQLYDCNWIVVNCSTPASVFHVLRRQILLPFRKPL
IVFTPKSLLRHPDAKSSFDQMVSGTSFQRLIPEDGPAAHSPEQVQRLIFCTGKVVYDLVK
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
PGIMQFTNEEKRTLLARLVSTRFEEFLQRKWSSEKRFGLGCEVLIPALKTIIDKSEN
GVDYVIMGMPHRGRLNVLANVIRKELEQIFCQFDSKLEAADEGSGDVKYHLGMYHRRINR
VTDRNITLSLVANPSHLEAADPVVMGKTKAEQFYCGDTEGKKVMSILLHGDAAFAGQGIV
YETFHLSDLPSYTTHTGTVHVVVNNQIGFTTDPRMARSSPYPTDVARVVNAPIFHVNSDDP
EAVMYVCKVAAEWSTFHKDVVVDLVCYRRRGHNEMDEPMFTQPLMYKQIRKQKPVVLQKY
AELLVSQGVVNQPEYEEEEISKYDKICEEAFARSKDEKILHIKHWLDSPWPGFFTLDGQPR
SMSCPSTGLTEDILTHIGNVASSVPVENFTIHGGLSRILKTRGEMVKNRTVDWALAEYMA
FGSLLKEGIHIRLSGQDVERGTFSHRHHVLHDQNVDKRTCIPNMHLWPNQAPYTVCNSSL
SEYGVVLFELGFAMASPNALVLWEAQFGDFHNTAQCIIDQFICPGQAKWVRQNGIVLLL
HMEGMGPEHSSARPERFLQMCNDDPDVLPDLKEANFDINQLYDCNWVVVNCSTPGNFFH
VLRRQILLPFRKPLIIFTPKSLLRHPEARSSFDEMLPGTHFQRVIPEDGPAAQNPENVKR

LLFCTGKVYYDLTRERKARDMVGQVAITRIEQLSPFPDLLLKEVQKYPNAELAWCQEEH
KNQGYDYVKPRLRTTISRAKPVWYAGRDPAAAPATGNKKTHLTELRLLDTAFDLDVFK
NFS

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

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
GDVAVFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFNFEGGCYAKTIKLSKEAEPEI
YNAIRRDALLENVTVREDGTIDFDDGSKTENTRVSYPIYHIDNIVKPVSKAGHATKVIFL
TADAFGVLPVPSRLTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQ
YAEVLVKRMQAAGAQAAYLVNTGWNGTGKRISIKDTRAIDAILNGSLDNAETFTLPMFNL
AIPTELPGVDTKILDPRNTYASPEQWQEKAETLAKLFDNFDKYTDTPAGAALVAAGPKL

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

MSPSKMNATVGSTSEVEQKIRQELALSDEVTTIRRNAPAAVLYEDGLKENKTVISSSGAL
IAYSGVKTGRSPKDKRIVEEPTSKDEIWWGPVNKPCSERTWSINRERAADYLRTRDHIYI
VDAFAGWDPKYRIKVRVVCARAYHALFMTNMLIRPTEEEELAHFGEPDFTVWNAGQFPANL
HTQDMSSKSTIEINFKAMEMIILGTEYAGEMKKGIFTVMFYLMPVHHNVLT LHSSANQGI
QNGDVTLLFFGLSGTGKTTLSADPHRLIGDDEHCWSDHGVFNIEGGCYAKCINLSAEKEP
EIFDAIKFGSVLENIYDEKSHVVDYDDSSITENTRCAYPIDYIPSAKIPCLADSHPKNI
ILLTCDASGVLPPVSKLTPEQVMYHFISGYTSKMAGTEQGVTEPEPTFSSCFGQPFLALH
PIRYATMLATKMSQHKANAYLINTGWTGSSYVSGGKRCPLKYTRAILDSIHGGLANETY
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
KTWMVTKNKYDTVTHTKEGVPEIMGHWLAPEDLATELDSRFP GCMAGRIMYVIPFSMGPV
GGPLSKIGIQLTDSNYVVL SMRIMTRVNNDVWDALGNQDFVRCIHSVGLPRPVKQRVINH
WPCNPERVLI AHRPPEREIWSFGSGYGGNSLLGKKCFALRIASNIAKDEGWMAEHMLIMG
VTRPCGREHFIAAAFPSACGKTNLAMLEPTLP GWKVRVCGDDIAWMKFGEDGRLYAINPE
AGFFGVAPGTSNKTNPMAVATFQKNSIFTNVAETANGEYFWEGLEDEIADKNVDITTWLG
EKWHIGEPGVA AHPNSRFAAPANQCPIIHPDWESPQGVPIEAIIFGGRRPQGVPLIYETN
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
TNAMAMESCRANTIFTNVAETADGEYFWEGLEKELKEAKGYTDEQLKHLEITNWLGGERWH
IGDEGKAAHPNSRFTAPAKQCPNIHPDWEAPQGVPIDAIVFGGRRPEGVPLVFESFSWEH
GILVGALVKSETTAAAEFTGKNVMHDPAMMRPFMGYNYGKYLEHWIKLGKAPHKAPKIFH
VNWFRETDKHKFLWPGFGDNIRVLDWILRRVAGGEEIEIAIETAIGYVPKRGTINLDGLPR
IDWNDLMSIPKDYWVEDVDESRLFDTQVGSDDLPPQIRDELDKLEKRVHAL

>dme:Dmel_CG10924 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] |
(RefSeq) Pepck2; phosphoenolpyruvate carboxykinase 2, isoform B (A)
MLKKGTTIPLPKYENCWLARTNPADVARVEGKTFISTDSKEQTPVPTEKATPGMLGNWIA
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)
MPELIEQSKIISGNVCGLPQLHKLRQDNCGLYSHIRGIPISYGNVDLLTTGVRAFVEEGI
ALCQPDQVHICDGSEQUENKVLISLLEAGTIVPLPKYDNCWLARTNPADVARVESRTFIC
TERREETIPTVEGVKGTGLGNWISPSDMDAAVQQRFPGCMKGRTMYVVPFSMGPVGSPLS
KIGIELTDSAYVVASMRIMTRMGAAVLRQLAKKEEFVRALHSVGAANGQVEQPSWPCDP
ERTIILHKPAENLIVSYGSGYGGNSLLGKKCFALRIGSTIAKQEGWLAEHMLILGITDPK
GEKKYITAAFPACGKTNLAMLNPSLANYSKVECVGDDIAWMKFDSQGVLRRAINPENGFFG
VAPGTSMETNPIAMNTVFNKTIFTNASTSDGGVFWEGMESSLAPNVQITDWLGKPWTKD
SGKPAHPNSRFCTPAAQCPIIDEAWEDPAGVPISAMLFGGRRPAGVPLIYEARDWTHGV
FIGAAMRSEATAAAEHKGVIMHDPFAMRPFPGYNFGDYVAHWLSMEKRGQVPKIFHVNW
FRKSAEGKFMWPGYGENSRVLEWILRRVNGESCYVDSAIGHIPAEGALNLDGMKDKVDVK
EIFSLPKEFWSQEVKDIRTYFESQVGADLPASIYQQDELSSRVDNL

>mmu:18534 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq)
Pck1, PEPCK, PEPCK-C, Pck-1; phosphoenolpyruvate carboxykinase 1, cytosolic (A)
MPPQLHNGLDFS AKVIQGS LDSL PQA VRKFVEGNAQLCQPEYIHICDGSEEEYGQLLAHM
QEEGVIRKLKKYDNCWLALTDPRDVARIESKTVIITQEQRDTVPIPKTGLSQLGRWMSEE
DFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLAKIGIELTDSPLYVVASMRIMTRMGISV
LEALGDGEFIKCLHSVGCPLPLKKPLVNNWACNPELTIAHL PDRREIISFGSGYGGNSL
LGKKCFALRIASRLAKEEGWLAEHMLILGITNPEGKKKYLA AAFPSACGKTNLAMMNPSL
PGWKVECVGDDIAWMKFDAQGNLR AINPENGFFGVAPGTSVKTNPN AIKTIQKNTIFTNV
AETSDGGVYWE GIDEPLAPGVTITSWKNKEWRPQDAEP CAHPNSRFCTPASQCPIIDPAW
ESPEGVPIEGII FGGRRPEGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPF
AMRPFFGYNFGKYLAHWLSMAHRPAAKLPKIFHVNWFRKDKDGKFLWPGFGENSRVLEWM
FGRIEGEDSAKLTPIGYIPKENALNLKGLGGVNVEELFGISKEFW EKEVEEIDRYLEDQV
NTDLPYEIERELRALKQRISQM

>mmu:74551 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq)
Pck2, 1810010O14Rik, 9130022B02Rik, PEPCK-M; phosphoenolpyruvate carboxykinase 2
(mitochondrial) (A)
MAAMYLPGLRLSRHGLRPWCWSPCRSIQTLHVLSGDMSQLPAGVRDFVARSAHLCQPEGI
HICDGTEAENTAILALLEEQGLIRKLPKYKNCWLARTDPKDVARVESKTVIVTPSQRDTV
PLLAGGARGQLGNWMS PDEFQRAVDERFPGCMQGRIMYVLPFSMGPVGSPLSRIGVQLTD
SAYVVASMRIMTRLGTPVLQALGDGDFIKCLHSVGGQPLTGHGDPVGQWPCNPEKTLIGHV
PDQREIVSFGSGYGGNSLLGKKCFALRIASRLARDEGWLAEHMLILGITNPAGKKRYVAA
AFPSACGKTNLAMMRPALPGWKVECVGDDIAWMRFDSEGQLRAINPENGFFGVAPGTSAA
TNPNAMATIQSNTLFTNVAETSDGGVYWE GIDQPLPPGVTITSWLGKPWKPGDKEPCAHP
NSRFCVPARQCPIMDPAWEAPEGVPIDAIIFGGRRPKGVPLVYEAFNWRHGVFVGSAMRS
ESTAAAEHKGKTI MHDPFAMRPFFGYNFGRYLEHWLSMEGQKGARLPRIFHVNWFRRDEA
GRFLWPGFGENARVLDWICRRLEGEDSAQETPIGLVPKEGALDLSGLSAVDTSQLFSIPK
DFWEQEV RDIRGYLTEQVNQDLPKEVLAELEALEGRVQKM

>hsa:5105 K01596 phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32] | (RefSeq) PCK1,
PCKDC, PEPCK-C, PEPCK1, PEPCKC; phosphoenolpyruvate carboxykinase 1 (A)
MPPQLQNGLNLSAKVVQGS LDSL PQA VREFLENN AELCQPDHIHICDGSEEEENGRLLGQM
EEEGILRRLKKYDNCWLALTDPRDVARIESKTVIVTQEQRDTVPIPKTGLSQLGRWMSEE
DFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGIELTDSPLYVVASMRIMTRMGTPV
LEAVGDGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTIAHL PDRREIISFGSGYGGNSL
LGKKCFALRMASRLAKEEGWLAEHMLILGITNPEGEKKYLA AAFPSACGKTNLAMMNPSL
PGWKVECVGDDIAWMKFDAQGHLRAINPENGFFGVAPGTSVKTNPN AIKTIQKNTIFTNV
AETSDGGVYWE GIDEPLASGVTITSWKNKEWSSEDGEPCAHPNSRFCTPASQCPIIDAAW
ESPEGVPIEGII FGGRRPAGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPF
AMRPFFGYNFGKYLAHWLSMAQH PAAKLPKIFHVNWFRKDKGKFLWPGFGENSRVLEWM
FNRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFSISKEFW EKEVEDIEKYLEDQV

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
SAYVVASMRIMTRLGTPVLQALGDGDFVKCLHSVGQPLTGQGEPVSQWPCNPEKTLIGHV
PDQREIISFGSGYGGNSLLGKKCFALRIASRLARDEGWLAEHMLILGITSPAGKKRYVAA
AFPSACGKTNLAMMRPALPGWKVECVGDDIAWMRFDSEGRLRAINPENGFFGVAPGTSAT
TNPNAMATIQSNTIFTNVAETSDGGVYWEGIDQPLPPGVTVTSWLGKPWKPGDKEPCAHP
NSRFCAPARQCPIMDPAWEAPEGVPIDAIIFGGRRPKGVPLVYEAFNWRHGVFVGSAMRS
ESTAAAEHKGKIIMHDPFAMRPFFGYNFGHYLEHWLSMEGRKGAQLPRIFHVNWFRRDEA
GHFLWPGFGENARVLDWICRRLEGEDSARETPIGLVPKEGALDLSGLRAIDTTQLFSLPK
DFWEQEVDRDIRSYLTEQVNQDLPKEVLAELEALERRVHKM

PYRUVATE CARBOXYLASE

>sce:YBR218C K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PYC2; pyruvate carboxylase 2 (A)

MSSSKKLAGLRDNFSLLGEKNKILVANRGEIPRIFRSAHEL SMRTIAIYSHEDRLSMHR
LKADEAYVIGEEGQYTPVGAYLAMDEIIEIAKKHKVDFIHPGYGFLSENSEFADKVVKAG
ITWIGPPAEVIDSVGDKVSARHLAARANVPTVPGTPGPIETVQEALDFVNEYGYPVIIKA
AFGGGGRGMRVVREGDDVADAFQRATSEARTAFGNGTCFVERFLDKPKHIEVQLLADNHG
NVVHLFERDCSVQRRHQKVVEVAPAKTLPREVRDAILTDAVKLAKVCGYRNAGTAEFLVD
NQNRHYFIEINPRIQVEHTITEEITGIDIVSAQIQIAAGATLTQLGLLQDKITTRGFSIQ
CRITTEDPSKNFQPD TGRLEVYRSAGGNGVRLDGGNAYAGATISPHYDSMLVKCSCSGST
YEIVRRKMIRALIEFRIRGVKTNIPFLLTLLTNPVFIEGTYWTTFIDDPQLFQMVSSQN
RAQKLLHYLADLAVNGSSIKGQIGLPKLKSNPSVPHLHDAQGNVINVTKSAPPSGWRQVL
LEKGPSEFAKQVRQFNGTLLMDTTWRDAHQSLLATRVTRTHDLATIAPTTAHALAGAFAL
CWGGATFDVAMRFLHEDPWERLRKLRSLVPNIPFQMLLRGANGVAYSSLPDNAIDHFVKQ
AKDNGVDIFRVFDALNDLEQLKVG VNAVKKAGGVVEATVCYSGDMLQPGKKYNLDYYLEV
VEKIVQMGTHILGIKDMAGTMKPAAAKLLIGSLRTRYPDLPPIHVHSHDSAGTAVASMTAC
ALAGADVVDVAINSM SGLTSQPSINALLASLEGNIDTGINVEHVRELDAYWAEMRLLYSC
FEADLKGPDPPEVYQHEIPGGQLTNLLFQAQQLGLGEQWAETKRAYREANYLLGDIVKVTP
TSKVVGDLAQFMVSNKLTSDDIRRLANSLDFPDSVMDFFEGLIGQPYGGFPEPLRSDVLR
NKRRKLT CRPGLELEPFDLEKIREDLQNRFGDIDECDVASYNMYPRVYEDFQKIRETYGD
LSVLPTKNFLAPAEPDEEIEVTIEQGKTLIIKLQAVGDLNKKTGQREVYFELNGELRKIR
VADKSQNIQSVAKPKADVHDTHQIGAPMAGVIIEVKVHKGSLVKKGESIAVLSAMKMEMV
VSSPADGQVKDVFIKDGESVDASDLLVLEEETLPPSQKK

>sce:YGL062W K01958 pyruvate carboxylase [EC:6.4.1.1] | (RefSeq) PYC1; pyruvate carboxylase 1 (A)

MSQRKFAGLRDNFNLLGEKNKILVANRGEIPRIFRTAHEL SMQTVAIYSHEDRLSTHKQ
KADEAYVIGEVGQYTPVGAYLAIDEIISIAQKHQVDFIHPGYGFLSENSEFADKVVKAGI
TWIGPPAEVIDSVGDKVSARNLAAKANVPTVPGTPGPIETVEEALDFVNEYGYPVIIKAA
FGGGGGRGMRVVREGDDVADAFQRATSEARTAFGNGTCFVERFLDKPKHIEVQLLADNHGN
VVHLFERDCSVQRRHQKVVEVAPAKTLPREVRDAILTDAVKLAKECGYRNAGTAEFLVDN
QNRHYFIEINPRIQVEHTITEEITGIDIVAAQIQIAAGASLPQLGLFQDKITTRGFAIQC
RITTEDPAKNFQPD TGRIEVYRSAGGNGVRLDGGNAYAGTIISPHYDSMLVKCSCSGSTY
EIVRRKMIRALIEFRIRGVKTNIPFLLTLLTNPVFIEGTYWTTFIDDPQLFQMVSSQNR
AQKLLHYLADLAVNGSSIKGQIGLPKLKSNPSVPHLHDAQGNVINVTKSAPPSGWRQVLL
EKGP AEFARQVRQFNGTLLMDTTWRDAHQSLLATRVTRTHDLATIAPTTAHALAGRFALEC
WGGATFDVAMRFLHEDPWERLRKLRSLVPNIPFQMLLRGANGVAYSSLPDNAIDHFVKQA
KDNGVDIFRVFDALNDLEQLKVGVDVAVKKAGGVVEATVCFSGDMLQPGKKYNLDYYLEIA
EKIVQMGTHILGIKDMAGTMKPAAAKLLIGSLRAKYPDLPPIHVHSHDSAGTAVASMTACA
LAGADVVDVAINSM SGLTSQPSINALLASLEGNIDTGINVEHVRELDAYWAEMRLLYSCF
EADLKGPDPPEVYQHEIPGGQLTNLLFQAQQLGLGEQWAETKRAYREANYLLGDIVKVTP

SKVVGDLAQFMVSNKLTSDDVRRRLANS�DFPDSVMDFFEGLIGQPYGGFPEPFRSDVLRN
KRRKLTCTPGLLEPFDELEKIREDLQNRFGDVDECDVASYNMYPRVYEDFQKMRETYGDL
SVLPTRSFLSPLETDEEIEVVIEQGKTLIIKLQAVGDLNKKTGEREVYFDLNGEMRKIRV
ADRSQKVETVTKSKADMHDPLHIGAPMAGVIVEVKVHKGSLIKKGQPVAVLSAMKMEMII
SSPSDGQVKEVFDVSDGENVDSSDLLVLLEDQVPVETKA

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

MRFSRIPPIFANVVRQTHYRNYANGVIKPREFNKVMVANRGEIAIRVFRALTELNKTSA
IYAEQDKNSMHRLEKADAYLVGKGLPPVAAYLTIDQIETALKHNIDAIHPGYGFLSERS
DFAAACQNAGIVFIGPSPDVMARMGDKVAARQAAIEAGVQVVPGTGPITTADAEVEFAK
QYGTPIILKAAYGGGGGRGIRRVDKLEEVEEAFRRSYSEAQAAGDGSFVEKFVERPRHI
EVQLLDGHHGNIVHLYERDCSVQRRHQKVVEIAPAPALPEGVREKILADALRLARHVG
YQ NAGTVEFLVDQKGNYYFIEVNARLQVEHTVTEEITGVDLVQAQIRIAEGKSLDDLKLSQE
TIQTTGSAIQCRVTTEDPAKGFQPD SGRIEVRSGEGMGIRLDSASAFAGSVISPHYDSL
MVKVIASARNHPNAAAKMIRALKKFRIRGVKTNIPFLLNVLRQPSFLDASVDTYFIDEHP
ELFQFKPSQNRAQKLLNYLGEVKVNGPTTPLATDLKPAVVSPPIPYIPAGAKPPTGLRDV
LVQRGPTFAKEVRSRPGCMITDTTFRDAHQSLLATRVRTYDMAAISPFVAQSFNGLFSL
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)

MFIPAAQSAYRTLRTQPRVRLNAIFKNGYSSKVEYKPIRSVLVANRGEIAIRVFRAC
TE LGIKSVAVYSEQDKMHMHRQKADESIVGKGLPPVEAYLNIPELIRVCKENDVDAVHPGY
GFLSERSDFAQVIDAGLRFIGPSPEVVQKMGDKVAARVAAIEAGVPIVPGTDGPVTTKE
EALFCKKHGLPVIFKAAYGGGGGRGMRVVVRKMEDVEESFQRASSEAKAAFGNGAMFIEKF
IERPRHIEVQLLDGKAGNVVHLYERDCSVQRRHQKVVEIAPAPRLPIEIRDKMTEAAVRL
ARHVG YENAGTVEFLCDESGNFYFIEVNARLQVEHTVTEEITGIDLVSQIRVAEGMTLP
ELGYTQDKIVPRGYAIQCRVTTEDPANDFQPN TGRLEVFRSGEGMGIRLDSASAYAGAI
SPYYDSLLVKVISHASDLQSSASKMNRALREFRIRGVKTNIPFLLNVLENQKFLHGVLD
TYFIDEHPQLFKFKPSLNRAQKLLNYMGEVLVNGPQTPLATTLKPAVSPHVPEVPLDLS
P EAIEREERGEAKVTEPPKGLREVLVCEGPEAFAKEVRNRKELLLMDTTFRDAHQSLLAT
R VRSHDLLKISPYVTHKFNNLYSLENWGGATFDVALRFLHECPWERLEEMRKRIPNIPFQM

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
FIDENPELFQLRPAQNRAQKLLHYLG HVMVNGPTTPIPVNVSPSPVDPAPVVPVIGPPPA
GFRDILLREGPEGFARAVRNHQGLLLMDTTFRDAHQSLLATRVRTHDLKKIAPYVAHNFN
KLFSMENWGGATFDVAMRFLYEC PWRRQLQELRELIPNIPFQMLLRGANAVGYTNYPDNV
FKFCEVAKENGMDVFRVFD SLNYLPNMLLGMEAAGSAGGVVEAAISYTG DVADPSRTKYS
LEYMGLAEELVRAGTHILCIKDMAGLLKPAACTMLVSSLRDRFPDLPLHIH THDTSGAG
VAAMLACAQAGADVVDVAVD SMSGMTSQPSMGALVACTKGTPLDTEVPLERVFDYSEYWE
GARGLYAAFDCTATMKSGNSDVYENEIPGGQYT NLHFQAHSMGLGSKFKEVKKAYVEANQ
MLGDLIKVTPSSKIVGDLAQFMVQNGLSRAEAE AQAEELSFP RSVVEFLQGYIGIPHGGF
PEPFRSKVLKDLPRIEGRPGASLPPLNLKELEKDLIDRHGEEVTPEDVLSAAMPD VFAQ
FKDFTATFGPLDSL NTRLFLQGPKIAEEFEVELERGKTLHIKALAVSDLN RAGQRQVFFE
LNGQLRSILVKDTQAMKEMHFHPKALKDVKGQIGAPMPGKV IDIKVAAGDKVAKGQPLCV
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
LFSMENWGGATFDVAMRFLYECPWRLQELRELIPNIPFQMLLRGANAVGYTNYPDNVVF
KFCEVAKENGMDVFRVFDSLNYLPNMLLGMEAAGSAGGVVEAAISYTGADVADPSRTKYSL
QYYMGLAEELVRAGTHILCIKDMAGLLKPTACTMLVSSLRDRFPDLPLHIHHTDTSGAGV
AAMLACAQAGADVVDVAADSMGMSQPSMGALVACTRGTPLDTEVPMERVFDYSEYWEG
ARGLYAAFDCATMKSGNSDVYENEIPGGQYTNLHFQAHSMGLGSKFKEVKKAYVEANQM
LGDLIKVTPSSKIVGDLAQFMVQNGLSRAEAEAEELSFPERSVVEFLQGYIGVPHGGFP
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)

MSEKFPNDVDPIETRDWLQAIESVIREEGVERAQYLIDQLLAEARKGGVNVAAGTGISNY
INTIPVEEQPEYPGNLELERRIRSAIRWNAIMTVLRASKKDLELGGHMASFQSSATIYDV
CFNHFFRARNEDQGGDLVYFQGHISPGVYARAFLEGRLTQEQLDNFRQEVHGNGLSSYPH
PKLMPEFWQFPTVSMGLGPIGAIYQAKFLKYLEHRGLKDTSKQTVYAFLGDGEMDEPESK
GAITATREKLDNLVFINCNLQRLDGPVTGNGKIINELEGIFEGAGWNVIKVMWGSRW
ELLRKDTSGKLIQLMNETVDGDYQTFKSKDGAYVREHFFGKYPETAALVADWTDEQIWA
NRGGHDPKKIYAFAKKAQETKGKATVILAHTIKGYGMGDAAEGKNIAHQVKMNMMDGVRH
IRDRFNVPVSDADIEKLPYITFPEGSEEHTYLHAQRQKLHGYPSPRQPNFTEKLELPSLQ
DFGALLEEQSKEISTTIAFVRALNVMKNSIKDRLVPIADEARTFGMEGLFRQIGIYS
PNGQQYTPQDREQVAYYKEDEKGQILQEGINELGAGCSWLAAATSYSTNNLPMIPFYIYY
SMFGFQIRIGDLCWAAGDQQARGFLIGGTSGRTTLNGEGLQHEDGHSHIQSLTIPNCISYD
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
LIGEEVAQYNGAYKVSGLLDRFGERRVVDTPITEYGFGLAVGAALKGLKPIVEFMSFN
FSMQAIDHVVNSAAKTHYMSGGTQKCQMVFRGPNGAAVGVGAQHSQDFSPWYGSIPGLKV
LVPYSAEDARGLLKAAIRDPNPVVFLENELLYGESFEISEEALSPEFTLPYKAKIEREGT
DISIVTYTRNVQFSLEAAEILQKKYGVSAEVLNRSIRPLDTEAIKTVKKTNHLITVES
TFPSFGVGAEIVAQVMESEAFDYLDAPIQRVGTGADVPTPYAKELEDFAFPDTPTIVKAVK
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)
MLAASFQRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTTDDKKAPEDIEGSDTVQIELPES
SFESYMLEPPDLSYETSKATLLQMYKDMVIIRMEMACDALYKAKKIRGFCHLSVGQEAI
AVGIENAITKLDSIITSYRCHGFTFMRGASVKAVLAELMGRRAGVSYGKGSMHLYAPGF
YGGNGIVGAQVPLGAGLAFHQYKNEDACSFTLYGDGASNQGQVFESFNMAKLWNLPVVF
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
ISKGLWKKHGDKRVDTPITEMGFAGIAVGAFAGLRPICFMTFNFMSMQAIDQIINSAA
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
EGDAVITAYRCHGWTWLLGATVTEVLAELTGRVAGNVHKGKGSMMHYTKNFYGGNGIVGA
QQPLGAGVALAMKYREQKNVCVTLYGDGAANQGQLFEATNMAKLWDLPLVFCENNGFGM
GTTAERSSASTEYYTRGDYVPGIWVDGMDILAVREATKWAKEYCDSGKGPLMMEMATYRY
HGHMSDPGTSYRTREEIQEVRKTRDPITGFKDRIITSSLATEEELKAIDKEVRKEVDEA
LKIATSDGVLPPEALYADIYHNTPAQEIRGATIDETIVQPFKTSADVLKSIGRA

>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
SCNTDYYTRGDALPGIWVDGMDVLAVRSATEFAINYVNTHGPLVMETNTYRYSGHMSDP
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
LAHSYRKDNGVSVVLYGDGAANQGQIFESFNMAKLWCLPCIFVCENNHYGMGTHVKRASA
MTEFYMRGQYIPGLWVDGNQVLAVRSATQFAVDHALKHGPIVLEMSTYRYVGHMSDPGT
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)
MLRTRLIQAASSAQRAFSTSQKALAAKQMTVRDALNSALDDELARDDRVLGEEVAQYD
GAYKVSRLWKKYGDKRVIDTPITEMGFAGIAVGAAMAGLRPVCFMTWNFSMQAIDHII
NSAAKTFYMSAGAVNPVIFRGPNGAASGVAAQHSQCFAAWYAHCPGLKVLSPYDAEDAR
GLLKSAIRDPPDPVVFLNELVYGTAFFVADNVADKDFLVPIGKAKVMRPGKDITLVAHSK
AVETSLAAAEALAKKGIEAEVINLRSIRPLDTATIFASVRKTHHLTVENGWPQHGVGAE
ICARIMEDQTFELDAPVWRCAGVDVPMPLYAKTLEAHALPRVQDLVEATLKVLGGKVGKA
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)
MRKMLAAVSRVLGSAQKPASRVLVASRNFANDATFEIKKCDLHRLEEGPPVTTVLTRD
GLKYYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFTRGLPVRAILAEALTGRRGCAKKGKGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPCIFICENNRYGMGTSVERAAAST
DYYKRGDFIPGLRVDGMDILCVREATKFAAAYCRSGKGPILMELQTYRYHGHSMSPDGV
YRTREEIQEVRSKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVRGANQWIKFKSVS

>mmu:18598 K00161 pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1] | (RefSeq) Pdha2, Pdha2; pyruvate dehydrogenase E1 alpha 2 (A)
MRKMLTAVLSHVFSGMVQKPALRGLLSSLKFSNDATCDIKKCDLYRLEEGPPTSTVLTRA
EALKYYRTMQVIRRMELKADQLYKQKFIRGFCHLCDGQEACCVGLEAGINPTDHSVITSYR
AHGFCYTRGLSVKSILAEALTGRKGGCAKKGKGGSMHMYGKNFYGGNGIVGAQVPLGAGVAF
ACKYLKNGQVCLALYGDGAANQGQVFEAYNMSALWKLPCVFICENNLYGMGTSNERSAAS
TDYHKKGFIPGLRVNGMDILCVREATKFAADHCRSGKGPIVMELQTYRYHGHSMSPDGI
SYRSREEVHNVRSKSDPIMLLRERIISNNLSNIEELKEIDADVKEVEDAAQFATTDPEP
AVEDIANLYHQDPPFEVRGAHKWLKYKSHS

>mmu:68263 K00162 pyruvate dehydrogenase E1 component subunit beta [EC:1.2.4.1] | (RefSeq) Pdhb, 2610103L06Rik; pyruvate dehydrogenase (lipoamide) beta (A)
MAVVAGLVRGPLRQASGLLKRRFHRSAAPVQLTVREAINQGMDEELERDEKVFLLGEEV
AQYDGAYKVSRLWKKYGDKRVIDTPISEMGFAGIAVGAAMAGLRPICFMTFNFMSQAI
DQVINSAAKTYYSAGLQPVPIVFRGPNGASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVMLENELMYGVAFELPAEAQSKDFLIPIGKAKIERQGTHITVV
AHSRPVGHCLEAAVLSKEGIECEVINLRTIRPMDIEAIEASVMKTNHLTVVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVPMPLYAKVLEDNSVPQVKDIIFAVKKTLLNI

>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
CKYKGNDEICLTLYGDGAANQGQIAEAFNMAALWKLPCVFICENNLYGMGTSTERAAASPDY
YKRGNFIPGLKVDGMDVLCVREATKFAANYCRSGKGPILMELQTYRYHGHSMSPDGVSYR
TREEIQEVRSKRDPPIILQDRMVNSKLATVEELKEIGAEVRKEIDDAQFATTDPEPHLE
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
DQVINSAAKTYTMSGGLQPVPVIFRGPNGASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVVLENELMYGVPPFEFPPEAQSKDFLIPIGKAKIERQGTHITVV
SHSRPVGHCLEAAAVLSKEGVECEVINMRTIRPMDMETIEASVMKTNHLVTVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVPMPLYAKILEDNSIPQVKDIIFAIKKTLNI

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
QAMNDFSAAATGRQYQPFEEYGHPPQAERVIIILMGSAIGTCEEVVDLLTRGEKVGVLKVR
YRPFSAKHLLQALPGSVRSVAVLDRTKEPGAQAEPLYLDVMTALAEAFNNGERETLPRVI
GGRYGLSSKEFGPDCVLAVFAELNAAKPKARFTVGIYDDVTNLSLPLPENTLPNSAKLEA
LFYGLGSDGSVSATKNNIKIIGNSTPWYAQGYFVYDSKKAGGLTVSHLRVSEQPIRSAYL
ISQADFGVCHQLQFIDKYQMAERLKPGGIFLLNTPYSADEVWSRLPQEVQAVLNQKKARF
YVINAAKIARECGLAARINTVMQMAFFHLTQILPGDSALAELQGAIKSYSSKGGQDLVER
NWQALALARESVEEVPLQPVNPHSANRPPVVS DAAPDFVKT VTAAMLGLGDALPV SALP
PDGTWPMGTTRWEKRNIAEEIPIWKEELCTQCNHCVAACPHSAIRAKVVPPEAMENAPAS
LHSLDVKS RDMRGQKYVLQVAPEDCTGCNLCVEVCPAKDRQNPEIKAINMMSRLEHV EEE
KINYDFFLNLPEIDRSKLERIDIRTSQLITPLFEYSGACSGCGETPYIKLLTQLYGDRML
IANATGCSSYGGNLPSTPYTTDANGRGPAWANS LFEDNAEFGLGFRLTV DQHRVRVLR L
LDQFADKIPAELLTALKSDATPEVRREQVAALRQQ LNDVAEAHELLRDADALVEKSIWLI
GGDGWAYDIGFGGLDHVLSLTENVN ILVLDTQCYSNTGGQASKATPLGAVTKFGEHGKRK
ARKDLGVSM MYGHVYVAQISLGAQLNQTVKAIQEA EAYPGPSLIAYSPCEEHGYDLAL
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
GSDGLNMNGKNGLACITPISALNQPGKKIVIRPLPGLPVIRDLVVDMGQFYAQYEKIKPY
LLNNGQNPPAREHLQMPEQREKLDGLYECILCACSTSCPSFWWNPDKFIGPAGLLAAYR
FLIDSRDTETDSRLDGLSDAFSVFRCHSIMNCVSVCPKGLNPTRAIGHIKSMMLLQRNA

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

MINPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLFAFAQ
SFIGRVFLFLMIVLPLWCGLHRMHAMHDLKIHPAGKWVIFYGLAAILT 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
DSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGCPWSRRPDGSVNVRRFGGM
KIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGT
LVQIRANAVVMATGGAGRVYRYNTNGGIVTGDGMGMALSHGVPLRDMFVQYHPTGLPGS
GILMTEGCRGEGGILVNKNKYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWHEWR
KGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEIPVRPTAHYTMG
GIETDQNCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQATERAATAGN
GNEAAIEAQAAGVEQRLKDLVNQDGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKL
AELQERFKRVITDTSVFNTDLLYTIELGHGLNVAECMAHSAMARKESRGAHQRLDEGC
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
AAFGLAEAGYKTACLSKLPTRSHTVAAQGGINAALGNMHPDDWKSHMYDTVKGSDWLGD
QDAIHYMTREAPKSVIELEHYGMPFSRTEDGRIYQRAFGGQSKDFGKGGQAYRTCAVADR

TGHAMLHTLYGQALKNNTHFFIEYFAMDLLTHNGEVVGVIAYNQEDGTIHRFRAHKT VIA
TGGYGRAYFSCTSAHTCTGDGNAMVSRAGFPLEDFVQFHPSGIYGSGLITEGARGE
GFLNSEGERFMERYAPTAKDLASRDVVSRAITMEIRAGRGVGKNKDHILLQLSHLPPEV
LKERLPGISETAAVFAGVDVTQEPIPVLPVHYNMGGIPTKWTGEALTIDEETGEDKVIP
GLMACGEAACVSVHGANRLGANSLLDLVVFGRAVANTIADTLQPGLPHKPLASNIGHESI
ANLDKVRNARGSLKTSQIRLNMQRTMQKDVSFRTQDTLDEGVRNITEVDKTFEDVHVSD
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
GYALIGFTAVLGTYYLLTL

>sce:YKL148C K00234 succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1]
| (RefSeq) SDH1; succinate dehydrogenase flavoprotein subunit SDH1 (A)
MLSLKKSALSKLTLLRNTRTFTSSALVRQTQGSVNGSASRSADGKYHIIDHEYDCVVIGA
GGAGLRAAFGLAEAGYKTACISKLFPTRSHTVAAQGGINAALGNMHKDNWKWHMYDTVKG
SDWLGDQDSIHYMTREAPKSIIELEHYGVFPFSRTENGKIYQRAFGGQTKEYGKGAQAYRT
CAVADRTGHALLHTLYGQALRHDTHFFIEYFALDLLTHNGEVVGVIAYNQEDGTIHRFRA
HKTIIATGGYGRAYFSCTSAHTCTGDGNAMVSRAGFPLQDLEFVQFHPSGIYGSGLITE
GARGEGLVNSEGERFMERYAPTAKDLACRDVVSRAITMEIREGRGVGKKKDHMYLQLS
HLPPEVLKERLPGISETAAIFAGVDVTKEPIIPTVHYNMGGIPTKWNGEALTIDEETG
EDKVIPGLMACGEAACVSVHGANRLGANSLLDLVVFGRAVAHTVADTLQPGLPHKPLPSD
LGKESIANLDKLRNANGSRSTAEIRMNMKQTMQKDVSFRTQSSLDEGVRNITAVEKTFD
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
WIVERGLSLAVLPLIAVPLVTTGPISTFTDTFLSLVLLGHCHIGFQSCIIDYISERVYGK
VHHYAMYLLSLGSFLSFVGIYKLESQEAGLIASLKSLLW\$DNKPVEKKRQ

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

MKATIQRVTSVFGVPRASVFPRI\$TPFILHNYISNGRMDLFSKEFHNGRV\$SKSDLWSSN
KEEELLVSQRKKRPI\$PHLTVYEPMSWYLSSLHRISGVLLALGFYAFTITLGVTTIMGM
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\$VVGAGGAGLRAAMG
LAEGGLKTAVITKLFPT\$RSHTVAAQGGINAALGNMNP\$DNWRWHFYDTVKGSDWLGDQDAI
HYMTRE\$AERAVIELENYGMPFSRTTDGKIYQRAFGGQ\$SNDFGRGGQAHRTCCVADRTGHS
LLHTLYGASLQYNCNYFVEYFALDLIMENGVCVGV\$IAMDLEDGTIHRFR\$SKNTVLATGGY
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\$VVGAGGAGLRAAMGLSEGGMK
TAVITKLFPT\$RSHTVAAQGGVNAALGNMNP\$DNWRWHFYDTVKGSDWLGDQDAIHYMTRE\$A
ERAIIELENYGMPFSRTTDGKIYQRAFGGQ\$SNDFGRGGQAHRTCCVADRTGHSLLHTLYG
ASLQYDCNYFVEYFALDLIMDKGKCIGVVALDIETGQIHRFRAKNTVLATGGYGRAYFSC
T\$AHTCTGDGTALTARAGIRNSDMEFVQFHPTGIYGVGCLITEGSRGEGGYLVNSQGERF
MERYAPNAKDLASRDVVS\$RAMTMEINEGRGVGPNKDHIYLLQLHHLPAEQLQQR\$LPGISET
AQIFAGVDV\$TKEPIPIPTVHYNMGGVPTNYKGQVLDFTP\$EGGDKVIPGLYAAGECA\$AHS
VHGANRLGANSLLDLVIFGRSCALTILNENKPGDSIPEL\$PVNCEEKSCDNLNGLLH\$SKGD
ISSIELRQKMQMTMQKHA\$AVFRRGDLLKEGV\$DKMSSYKEQQNLKACADSGKVWNS\$ELVE
TLELQ\$NLLINANQTIVAAENRTESRG\$AHARDDFQERIDEYDYSNP\$LEGQQKPPDQHW\$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
ILPASYFIHGPMVMDAVLTVALTLHHWGIHGVVYDYARPYVIGEAAAKAAHVGVYLITGL
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
EKQMHQSVAERDRLDGLYECILCACCTSCPSYWWNADKYLGPAVLMQAYRWVIDSRDDY
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 VTA VFKY
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
EKPYMQTYEVDLRECGPMVLDALIKIKNEMDPTLTFRRSCREGICGSCAMNIGGTNTLAC
ISKIDINTSKSLKVYPLPHMYVVRDLVPDMNNFYEQYRNIQPWLQRKNEAGEKKGKAQYL
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 MYGMPFSRKPDGKIYQRPFGGQTL DYGKGGVARRACACADR
TGHALIHTLYGQTLKHSDSCHYFVDYFVLDLIMSQGACVGCLAWKLD DGT FHRFLAKNTV
VAAGGCGRVYFSTTAGHTCTGDGN AWVSRQELPLMDMEFVQFHPTGIY GAGCLITEGVRG
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
KKEPKKDAKDKKKDEEGKSAK

>dme:Dmel_CG6666 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit
| (RefSeq) SdhC; succinate dehydrogenase, subunit C, isoform B (A)
MYALSSSLIRSPALRQGLQMAAASRPVSMKVVSVAETQKDESFFEKNERLGRELSPHLTI
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
AAKPGGAAPAGAAKPGGAAAAAAGSAKPGGASTGKPASGNAPATPPPPPPPPPAKSAPPV
KAKKPRLKTFEIYRWKPGDQPQTQTYEVDLEQCGAMVLDALIKIKNEMDPTLTFRSCRE
GICGSCAMNINGTNTLACVSSIDQNESKCCRIYPLPHLYVVRDLVPDMSQFYDQYRSIQP
WLQRKDLKREAGTAQYLQSVDDRLVLDGLYECILCACCQTSCPSYWWNSNKYLGPVLMQ
AYRWVIDSRDEATEQRDLFLKDPWKLYRCHSIMNCTNTCPKHLNPARAIQLKQLLVGLK
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
YDTVKGSDWLGDQDAIHYMTREAPKAVIELENYGMPFSRTQDGKIYQRAFGGQSLKFGKG
GQAHRCCAVADRTGHSLLHTLYGQSLSYDCNYFVEYFALDLIFEDGECRGV LALNLEDGT
LHRFRAKNTVIATGGYGRAFFSCTSAHTCTGDGTAMVARQGLPSQDLEFVQFHPTGIYGA
GCLITEGCRGEGGYLINGNGERFMERYAPVAKDLASRDVVSRSMTIEIMEGRGAGPEKDH
VYLQLHHLPPKQLAERLPGISETAMIFAGVDVTREPIPVLPVHYNMGGVPTNYRGQVIT
IDKDGDVIVPGLYAAGEAASSSVHGANRLGANSLLDLVVFGRACAKTIAELNKP GAPAP
TLKENAGEASVANLDKLRHANGQITTADLRLKMQKTMQHHA AVFRDGPILQDGVNKMKEI
YKQFKDIKVDRSLIWNSDLVETLELQNLLANAQMTIVSAEARKESRGAHAREDFKVRED
EYDFSKPLDGQKQKPMQDQHWKHTLSWVCNDNGDITLDYRNVIDTTLDNEVSTVPPAIRS
Y

>mmu:66052 K00236 succinate dehydrogenase (ubiquinone) cytochrome b560 subunit | (RefSeq) Sdhc, 0610010E03Rik; succinate dehydrogenase complex, subunit C, integral membrane protein (A)
MAAFLLRHVSRHCLRAHLNAQLCIRNAAPLGTTAKEEMERFWKKNTSSNRPLSPHLTIYK
WSLPMALSVCHRGSGIALSGGVSLFGLSALLPGNFESYLMFVKS LCLGPTLIYSAKFVL
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
WHFYDTVKGSDWLGDQDAIHYMTEQAPASVVELENYGMPFSRTEDGKIYQRAFGGQSLKF
GKGGQAHRCCCVADRTGHSLLHTLYGRSLRYDTSYFVEYFALDLLMENGE CRGVIALCIE
DGSIHRIKNTVIATGGYGRTYFSCTSAHTSTGDGTAMVTRAGLPCQDLEFVQFHPTGI
YGAGCLITEGCRGEGGILINSQGERFMERYAPVAKDLASRDVVSRSMTLEIREGRGCGPE
KDHVYLQLHHLPP EQLATRLPGISETAMIFAGVDVTKEPIPVLPVHYNMGGIPTNYKGQ
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 KIYPLPHMYVIKDLVPDLSNFYAQYKSIEPYLKKKDESQEGKQQYLQSIEDRE
KLDGLYECILCACCSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDDFTEERLAKLQDPF
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
GKGGQAHRCCCVA DRTGHSLLHTLYGRSLRYDTSYFVEYFALDLLMENGE CRGVIALCIE
DGSIHRIKANTV VATTGGYGRTYFSCTSAHTSTGDGTAMITRAGLPCQDLEFVQFHPTGI
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)

MAAVVALSLRRRLPATTLGACLQASRGAQTAAATAPRIKKFAIYRWDPDKAGDKPHMQT
YEVDLNKCGPMVLDALIKIKNEVDSTLTFRRSCREGICGSCAMNINGGNTLACTRRIDTN
LNKVS KIYPLPHMYVIKDLVPDLSNFYAQYKSIEPYLKKKDESQEGKQQYLQSIEREKL
DGLYECILCACCSTSCPSYWWNGDKYLGPAVLMQAYRWMIDSRDDFTEERLAKLQDPFSL
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
VFPLMYHTWNGIRHLMWDLGKGLKIPQLYQSGVVVLVTLVLSMGLAAM

>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
QKAAKAGLLALSALTFAGLCYFNYHDTV GICKAVAMLWKL

SUCCINYL- CoA SYNTHETASE

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

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGV
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)

MSILIDKNTKVICQGFTGSQGFHSEQAIA YGTKMVGGVTPGKGGTTHLGLPVFNTVREA
VAATGATASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMI
GPNC PGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGG
DPIPGSNFIDILEMFEKDPQTEAIVMIGEIGGSAEEEEAAAYIKEHVTKPVVGYIAGVTAP
KGKRMGHAGAIAGGKGTADEKFAALEAAGVKTVRSLADIGEALKTVLK

>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
AFEAAKKLNTNKLVIKAQALTGGRGKGHFDTGYKSGVHMIESPQQAEDVAKEMLNHNLIT
KQTGIAGKPVSAVYIVKRVDTKHEAYLSILMDRQTKKPMIIASSQGGMNIEEVAERTPDA
IKKFSIETSKGLSPQMAKDVAKSLGFSPDAQDEAAKAVSNLYKIFMERDATQVEINPLSE
IEHDP THKIMCTDAKFGFDDNASFRQEKIYSWRDLSQEDPDEVKAKKYDLNFVKLKGNIG
CLVNGAGLAMATMDVIKLNGGDPANFLDCGGGATPETIKQGFELILSNKNVDAIFVNIFG
GIVRCDYVALGLVEAARELEV RVPIVARLQG 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)

MLRSTVSKASLKICRHFHRESIPYDKTIKNLLLPKDTKVIFQGFTGKQGT FHASISQEYG
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
EEEEAAAYLKEHNSGANRKPVVSFIAGVTAPPGRRMGHAGAIISGGKGTAAADKINALREAG
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)
MLRAAGNLSKSMMSQRRFLNLQEFQSKEILEKHGCSVQNFWASNRKEAEEKWMSFGDH
EYVVKAILAGGRGKGKFINGTKGIGGVFITKEKDAALEAIDEMIGKRLVTKQTTSEGV
VDKVMIAEGVDIKRETYLAVLMDRESNGPVVVASPDGGMDIEAVAETPERIFKTPIDIQ
MGMTGQSLKIAKDLQFEGKLIGVAAQEIKRLYDLFIAVDATQVEINPLVETADGRVFCV
DAKMNFDDSAAYRQKEIFAYETFEEDHPREVDHAFNLNYIGMDGNIACLVNGAGLAMAT
MDLIKLHGGEPAFLDVGGAVTEDAVFNAVRIITSDPRVKCVLINIFGGIVNCATIANGV
VSAVNKIGLNVPMVVRLEGTVDAKQIMKKSGLKILTANNLDEAAKAVSSLPK

>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
NVVVTDSAPKLGVMQKALLG

>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
KKCEEVMVCKRLFTRREYYFSITLDRNTNGPIVIASSQGGVNIEEVAATNPDAIVKMPID
VNVGITKELAHEIAVKMGFSKDCEQQASEIIEKLYQMFKGSDATLVEINPMAEDVNGDVY
CMDCKLLLDLSNAEFRQAKLFDLKDKKQEDELEIRAAAAANLNYIRLDGTIGCMVNGAGLAM
ATMDIIKLHGGEPAFLDVGGGATVEQVTEAFKIITADKDKVSAILVNIFGGIMRCDVIA
QGIIQAARELDLKIPIVVRLQGTVEDAKALIATSQLRILPCDNLDEAAKMVVKLSNIVD
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
LIVCITEGVPPQHDMVKVKHALISQSKSRLVGPNCPIIAPEQCKIGIMPGHIHKRGKIGV
VSRSGTLTYEAVHQTTEVGLGQTLGCVGIGGDPFNGTDFIDCLEVFLKDPETKGIILIGEI
GGVAEEKAADYLTEYNSGIKAKPVVSFIAGVSAPPGRRMGHAGAIISGGKGGANDKIAAL
EKAGVIVTRSPAKMGHELFKEMKRLELV

>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)
MSLNRRGSKMLLRALTPQILRRGKADYGKTVCNLKINKATKVLVQGFTGKQATFHSEESIK
YGTNIVGGVNPCKGGTEHLGKPVFKSVAEAVEKAKPDATVIFIPPPSAAEGICAAIESEI
GLIVAITEGIPQADMVRISQMLNCQEKSRLLGPNCPIISPDQCKIGIMPGDIHKRGVVG
IVSRSGTLTYESVHQTNNVGLGQALCVGLGGDPFNGTSFIDALKVFLSDKEIKGIVMIGE
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
ECPEYVVKAILAGGRGKGTDFDNGFKGGVHITTNKSEVLSLTQQMIGNRLITKQTPKSGI
LVNKVMVARSINITRETYLCILLDREHNGPVLIASPAGGMDIEAVAEETPEKIKTVPLDI
GKPIPESTLLEVAKFLEFKGDSVKRCAEEIQKLYTLFKAVDVAVQIEINPLAETDKGEVIS
VDAKLNFDNAQFRQKDIFSMVDTEESDPREVEAAKYNLNYVAMDGNIGCLVNGAGLAM
ATMDIIKLNGGEPANFLDVGGGVREDQVAKAFEILTADPKVKGILVNVFGGIVNCATIAN
GIVAASKKLQNLVPLVVRLEGTVNVQAREILKNSGLPIQTASDLDDAAHKAVAALN

>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
AADLAVHLAQIVKLAREMKMDVNFEPDAQKGKGDCKKDQKQPDSSKGGKKSEKKDDKKSD
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
MELLQEAGVSVPKGFVAKSSDEAYAIKKLGSKDVVIKAQVLAGGRGKGTFTSGLKGGVK
IVFSPEEAKAVSSQMIGQKLITKQTGEKGRICNQVLVCERKYPRREYYFAITMERSFQGP
VLIGSAQGGVNIEDVAAENPEAIVKEPIDIVEGIKKEQAVTLAQKMGFSPSNIVDSAAENM
IKLYNLFLKYDATMVEINPMVEDSDGKVLCDAMKINFDNSNSAYRQKKIFDLQDWSQEDER
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
VAASSPELIFKEQIDIFEGIKDSQAQRMAENLGFLGSLKNQAADQITKLYHLFLKIDATQ
VEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSENEPIEENEAARYDLKYIGL
DGNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKEAQVYEAFLKLLTSDPKVEAIL
VNIFGGIVNCAIIANGITKACRELELKVPLVVRLEGTNVQEAQNILKSSGLPITSVDLE
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)

MTATVAAAATATMVSSSSGLAAARLLSRTFLQNGIRHGSYTASRKHIYIDKNTKIIC
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
AASNPELIFKEQIDIFEGIKDSQAQRMAENLGFGVPLKSQAADQITKLYNLFLKIDATQV
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
PPPFAAAAINEAIEAEIPLVVCITEGIPQQDMVRVKHKLLRQEKTRLIGPNCPGVINPGE
CKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTQVGLGQSLCVGIGGDPFNGTDFIDCL
EIFLNDSTATEGIIIGEIGGNAEENAAEFLKQHNSGPNKPVVSFIAGLTAPPGRRMGHA
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
IVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQVLVCERKYPRREYYFAITMERSFQGP
VLIGSSHGGVNIEDVAAESPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENM
VKLYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQKKIFDLQDWTQEDER
DKDAAKANLNYIGLDGNIGCLVNGAGLAMATMDIIKLHGGTPANFLDVGGGATVHQVTEA
FKLITSDKKVLAILVNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKALI
ADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLPI