

Pyruvate dehydrogenase related:

>PDH E1 alpha, Contig15930 (complete) 409 aa

MRRTCAALRPASRFGAEGRAARVLVISRRGYAEEASAFSGAKAEDLGNGK
YRFQVETPYAAHKCDGPEQVCETTKDELLAMFKQMVRIRRTETETADKLYK
QKEIRGFLHLYNGQEAFLVGMEEAALTLEDHIIITAYRDHGHLLTRGGTPKQ
VLAELMGRADGCSKKGKGSMMYSKEGNFYGGNGIVGAQVPLGAGIAFSQ
KYLKTGRVSVSMFGDGAANQGQLFEAYNMAALWKLPAIFMCENNKYGMGT
SIERSSASTEYYKRGDYLPGIKIDGMDALAVKQGMLYAADWARNKGPIMV
EAETRYRYGGHSMSPGTSYRTREEINRMRSTRDPIEKIRYKMLDNNIATK
EEIKAVEAEVKADEVDEALKEALQAPFLPIEATYQHVLLGEEALGAVRAVE
LSKSYVHKH

>PDH E1 beta, Contig19193 (complete) 372 aa

MRRALSSVSRVASTSSAPLLGSAALRSRAVAALATAVEPKKISVREALRE
AIDEEMERDSRVVMLGEEVAQYQAYKVS KGLMEKFGRERVVDTPITEAG
FAGIGVGAAMSGLVPIVEFMTMNFSLQAIDHIVNSAAKLRYSGGMYNVP
IVFRGPNPRAVGAQHSQCFGAWYSSVPGLKVVAPWNCNDAKGLLKA
RDPNPVVFLSEIGYNETYELSPEAQSKDYVLDIGKAHIEKEGSDITVLT
FSRMVGVAAEAQAQAAEKGISVEVVNLRSLRPLDLDTIVNSIKKTNRVFT
VEEGWPQCGIGSEIIALANEHCDFLDAPPERITGADVPMPTWPLEDEA
MVQTONIVNAIERVCYRNTTNO

>PDH E2, Contig7200 (complete) 509 aa

MKRGVSRSSRVARGVKGTSATAQCLRATAVAQRSASTLSSTSRRSASPLF
SGPVARSTATVQQFGVRSYATLPAHEVLGLPALSPTMTQGNLAKWLKKEG
DKIQPGDLIASIETDKATVDWEATEAGYLAKILIEGSKDVTVVGKPAVVT
VEEEEDVAKFKDFSPEGGDAAPAAAPKEEAPAAKAAAPAAPEQPKAAAPA
APKAAAPAAQAPAGGRVFAASPLARKVAQEQGVDAAVHGTGSNNRIRAD
VLDYAAKGPAPVPAATSVP TPAPGGLFTDIPNTQIRKVIAARLTESKQTV
PHYLLSIECRMDKLLKVRQELNAKGEKAYKLSVNDFIKAAALALQKKPT
CNSAWFGDYIRRYHNVDINAVSTDEGLFTPIVQDADKKGLATIANVTKD
LANKAKEKKLQPHFQGGTFTISNLGMFGVKQFAAVINPPQSCILAVGGT
EKKVVPNEDKETSAAQPYATAHVMTVTLSCDHRVVDGAVGAEWLKTFFKEL
VEDPVKMLL

>PDH E3, 507 aa, Contig588 (and 23476 and 11795) (complete)

MRRGLIQASRSASVPTSASGVFASRAFPRTFIASRGFATAAEQDDVIVIGG
GPGGYVAAIKAGQLGLKVTCVEKRGKLGTTCLNVGCIPSKALLHASHIYE
DTKKYFPDGHVFDNVKLDLGGAMMSKEKAVNGLTSGIEFLFKNNVYK
KGFVKVSGANEVTVDLAEGGEKKLSAKNIIIVATGSDVIGLPFLPIDEQV
VSSTGALALKEVPKMMVIGGGIIGLEMGSVWRRLGTEVTVVEFTDNLG
GAADGEVAKFKRILAKQGMKFKMGTKVTGAKVEPSSITLITEPRDGGKT
EEVACDVVLCVSGRRPYLDGLGLENVGKLDNRGRVAVDDHFRSNVPSIY
AIGDCIPGMLAHKAEEDGIAAVEIIAGGHGHVDYNNVPSVYVTHPEVAW
VGQTEEQQLKAQGIQYKVGKFPFKANSRARTNDDDEGFVKYLADAKTDKVL
GVHMIGAMVGMIAEPTLLMAYGGSSEDEVARTCHAHTLSEAVKEAAMAT
YDKAIHF

>pyruvate carboxylase Contig23294 (and 27416,12686,4892,10179) (internal gaps likely), 1222 aa, 5F4

MLRFARRSGQHAVGQLATASLPSTIIAHASPALACGSSLVQTTWRRHY
ASASSPTKPTKSKLPYRPIHKLLVANRGEIAIRVMRAGTELGIRTVGIYS
HQDEKSLHRQKADESIEVGGKMSPEAYLSIPEMVRVAKEVEADAIHPGY
GFLSESGDFAQALALDNNIRFIGPAPEVVRSMGDKVFARQMAIASGVQVV
PGTDAPVSTVEEAELFCNKFGFPVILKAAFGGGGRGMRVVHAREELHDAF
ERATSEAKSAFNGSMFIERFVPKPAPHRGSPGRQDWSGGALARTGLLR
PEETTRRWSRSPRLPSSPMLHQAETVLRRLRQAGHVCRIRKRPAGTVEFLV
DEQGRHYFIEVNARLQVEHTVTEEITGVLDLVQSQIRIAEGLTLQDLNLQ
DKIHVNGAAIQCRVTTEDPYHNFRPDVGRIDVFRGTGEGMGIRLDGGNSYS
GATISPYDSSLVKARNHEEAACKLQALNEFRIRGVKNNIPFLQNVLSH
PKFLAGGVNTSFIDTIPELFQFHETQNRASKILNFLANVHVNGSLTPLGT
SNKPANITPQAPDVPHTDPPQGWRSIFLEKGPNEFAKAVRAHKTLTLLTDT
TMRDAHQSLLATRVRTKDLLTIAPATAHLMAPLYSLEMWGGATFDVALRF

LRECPWERLQRLREAVPNIPFQMLLRGANAVGYTNYPDNVVHRFCREAKT
NGIDVFRVFDLSLNYFPNMELGIDAVGNAGGIVEAAICYTGDVTRGLTEKD
YKYNLDYYVDFAEKLVKRRIHVLCIKDMAGLLTPQAARLLIGTLREKFPE
VPIHVHTHTDTSAGVAAMVACAEAGADVDDAAIDSMGMSQPSMGALVA
SLKGTPHDGTGLKMDQLYPINNYWEQARTLYAPFECTTTMKAGSSDVYEHE
IPGGQYTNLHFQAYSLSGLAHQWPSIKKAYAQANRLLGDIVKVTSSKVVG
DLAQFMVQNNLDEESLLEKAEELNFPSSVVEYFEGFLIGQPPGGFPEPLRT
KVLKGRPSTNGRAGESLPLDFHKLKRELIEKHGKYHISELDVLSAAQYP
KVFDEYMDFKRLYGNVSSLPTRNYLTGPEVGEIEKADIEPGKSLHIMLKA
VGAPNADHKREMFELNGQPRSVFVEDKKATAKEGAGHAGSSKSRERADP
SNKKLVGAPMPGSIVGVKVKDQGEVKKGQPLLVLSAMKMETVVAAPADGK
VKRIIAKQGDSTAGDLLVEME

>putative pyruvate dehydrogenase phosphatase Contig3418 (and 931, 6270,E80POFO01EX230) (mostly complete, but with internal gap), 795 aa, 8C7

MLRLRQLASRSGPARGATSHVLKTTSGGYAFASPWASSPLFSTSAATATD
KRVDPKSRVVIIGGGVIGTSAFHLAKLGTVDVLLLEQGTLCGCTTWHAA
GLIGQLRANETETKLSRYGIQLYADLEKETGQGTGWKQCGGVTVARTQER
MTHIKRTL SRMRAFGIEGHLVSPMWAKQVGRLAGVNVPLHTCEHFYISTK
PIDGVDSYLPVLRDPDGYIYFREWSGGIIMGGFEPVAKPCFADGVPNDFQ
FQLFDEDWDHFSILMNSALERCPALETAEVRQLLNGPESFTPDNQYILGE
APEVRNFFVAAGFNSSGIASAAGAGKALSEWLIQGYPTMDLWSVDIRRFK
KYHANDNFQKQRMETLGLHYQIPWPKYELQSGRPLRVSPLYERLAARGA
QFGSKMGWERPNYFLPSSVSPSSIKYTFDRPAWL PYVGEHKA TRDEVAL
FDQTSFAKFVVKGRHVESFMQRLCANDVAVPVGRVVYTPMLNPRGGYETD
CTVTRVSEDSYFVVSSTAQATRDYDWSRNIQEDEEVSIVDVSPQYSTLS
LMGPKSRELLSRVIADRDL SNEAFPFGTSQEVPLGITQVRASRITYVGEL
GWELYVPIESTLLVYDLLHAKANEGTRIGLRDAGYYAIDGLRLEKGYRAW
GSDITPDDTPLEAGLGFVLDLKNETKNFLGKDVLLRQKKEGLEKRLAVFV
IDNDQEVYPHGGEPIFRDQVCGYLTSAVYGH TVGRSVGLGYVRKLANTA
TKEDRLVTPDWVKAGRYEVEVASKRVPASVSLQPPFPDPKNERVRM

>pyruvate dehydrogenase phosphatase catalytic subunit 2 Contig27417 (complete), 707 aa, C53

MLRVAGVGCARGHCLTNDLHLHHPSSTTASALSRSFVPHSTLPASAPA
KKATTQSAPVATAAALPTSSSSTSPSSTATASPSTLLASHSHSPRAIPTL
NSLFVLRNARPIAVSGVGRGPMAFGVAARRRMSASTGPNPNELQFPHTS
TPATSSIFKKLSRPLFIGGVGIA SFAASYGYFEYQKKRKYATSASPILD
ALTPSVSPDLVEQVTRKINANAQAF TVAPGNCHITEFHTNTIASNSPIED
RHNQLLHDPQIYDGSLSFGMYDGHGWAASEFVKNELDFVFKLELGILKIK
QEKFIDSIVKEKELRDRIVDLAKDPASPQLYEDLKGIIAKQSQLDEAHR
EQLLTPLDALFNPERNISQCLQLAFLRADS YFLYEALLDPEKLRDGFSGA
CVLLSYFLNDHIYVANAGDCRAVLGRKRDSSGDPIKGADTRRVWEAIELS
HDHG TENLEERKRLIEAHPNEDDIVLDERVKGSLQPTRGIGDGLFKDPNF
NDALARKLENWHPPYT TAMPEVISHKITPADQFVVLATDGLFDFFTSQEV
VDMVGHYLEHMQRDPKDDSHNSVQPPSELKLLQENASSYLIGKVLNK
AGYGKTP EVRMNF CITLPKEAKRGFFDDTTVTVIFLGP HITSGAVQDEHG
QEDTEAGTSGGSEPVLAKPAVMERVEGLIEQK VREDQESGMMWKAHQH
FAGGRSG

>pyruvate dehydrogenase kinase NOT DETECTED Contig2871 (and 5370) 441 aa

MMNRMRTTVASTSSHVHIPSSISSAASSSPVSWQRTMDDMIHRYANLK
QTPVSVKNMIVFGKDANMNTLLRSHAFRLRYELPIRLAHIAKEITALPEEL
LEVEPVQKVLNWRYSFSEVIESPVPNVADMELKTEDEQCASLHQFQDML
DHIKDRHSGVVTMAEGVLELKNRLGREMIDTSVQFFLDRLYMNRI SIRM
LITQHLELFKQAQTNNNLCAITSGASGRKIAEDAVDDARYLCSNNYSVCP
SVQIIVPPKLG TETSAGAP TLPYVPSHLYHMLFETIKNSLRAVVEVHGAN
AQSEDDLPPVRVVLVKGTEDLTIKISDMGGGIPHADVPKLFYFYTTAAP
PTKDTLDSLNEGAAPMAGLGYGLPISRLYARYFGGDLKVIPMEGYGTDAY
IHLKAAGETREVLPEYSPSTYLSQANLREWLNVDNCAFQL

Anaerobic pyruvate metabolism:

>pyruvate:ferredoxin oxidoreductase Contig16068 (11768,E80POFO01A6MEI) (likely complete), 1243

aa, 17B

MNRLFARHTRPIVAQRTFFPLSSAGTLRALSTPRWTAGPLRRLHGAVPMDG
NTAAAHVAYGLSDIHAIYPITPSSQMGELADKWSAEGRLNAFGNTPRVIE
MQSEMGAAGTLHGAAVGGALVSTFTASQGLLLMIPNLYRVAGELMPAVFH
VTARAI SQGLS IYGDHSDVMAVKQTGVAMLASASPOEAMDALVAHLSS
IRSSVPFVHFFDFGFRSHEINTVEPIKYEDMRKLLDEEALEQFRRRGMNP
ETPNLRGLIDGPEHYFQOVEAANTILDGVL PVVEGYLDEVHKL TGRKYGL
FDYHGHPEPRHVIVACGSSVSTVEEAVNHRNAQGERVGLIKVRLWRPFSI
KHLVDALPKSVEKVAVIDRVRDYLASGGPLFQEVCTSLMMGGRRDVLVN
GRYGLGSKDFTPGMALAIFDNLKQDQPLHNFVVGIKDDVTHKSLTVTEEP
DTLPAGTKQSFIFWGIGGDGTVGANEEAIKLIVENSNSAHKSGGVTVSHL
RFGEKPINSTYQVQONADLI AVHTTPYLKFKFPSLLGPLKEGGTVILNSPWN
DVAHLDRMLPDFVKRRIARRKARLINVDATAIAHEAGLRGRINMVMQAAF
FKASEVLPDVARAELRRVIDAQYARKGRDVLERNYAALDQGLARTVEVA
YPDAAEACRDDVDADYIVDPADAPEQLRKVLRPTQRQRMEGDSL PVSAFD
PRGAMPSGTSKYEKRGIAPAVAQWNTNPDCTCTQCNLCSALCPHAAIRPFLF
TQEEAGSAPEGWEGRKAVGKAGKSYQYRVQVSPYDCTGCDVCVKACPTQS
LAQVPFVDALDRGQARLWDFAAERLPIRSEVYPKESLKG SQFAKPCLEFS
GACAGCGETPVVKKLLTQLFGDELYIANATGCSIVWGGMFPWSAYTTNERG
HGPAWGHSLFEDAAEYGF GIRHAVRYRREALRCAVQRDLTAGAYAAEHPV
LAELLRRWDAAYDDRTQSPSLAAKVREYLERLPAPAAAARGPLRELHAER
HMLARKTQWIIGGDGWAYDIGFGGLDHLV LASGEKVNVLVLDNEVYANTGG
QASKATPRASQVKFANAGKTTAKKDLGAMMMQYGNVYVASICLEANPDHA
VQALAEAEAFDGP SLVIAIYAPCIAHGKAGISTEVEEAKRAIKAGYHILY
RYNPSLVEQGMNPLSLDSSPPDDQLLQFLRGENRYEALRQOHP ELTDEKQ
RLLRD VADRYRHYALLKEQLEPKDDGEEEEEEKADEAKEEATA

>acetyl-coa acetylase/transferase Contig19900 (complete), 472 aa, 1253

MKRLQOMSARTTVVSAASAGRASAFGRRSYQGRPQMLSADDAVKVIKTGD
RVFVHVSAAAPQALIHAMTRRAPELRDVEVCHMHI EGDASYADKKYEGSF
KNNNFFVVGKNVRKGVQEGRLDYTPVFLSEIPLLFRRGILPLDVALITVSP
PDQHGFC SLGTSVDASLAAVQCAKT VIAQVNPMPRTHGDGFVHESAI SF
MVDGPAPLIEHKRGKVTETIGKIGKNVAQLVEDGATLQMGIGVIPDAVLA
ELTHHKKLGIHTEMFSDGIIDLVERGVITGENKVIAPRTITVGFCLGTR
LYDFVHENPAVQFRAIEWVNNPILIKENPKMTAINSAVEVDLSGQICADS
IGSKLYSGVGGQDMFMRGAALSHGGKPIIALPSTTSRGESKIVPRLKRG
GVVTTTRAHVHVWVTEWGA VNLFGKPVKERMKALISIAHPLHRPWLEKEVE
RGFWFDVDENSPKIPESAHVDE

>ferredoxin Contig18230 (complete), 171 aa, 17F3

MMKRTTTLVTGRRFAGLQSPVVPFAWAGRQATSSSASTLRSARLYSADA
DSKKT VHVTFIDKDGTEIPLEAPVGKSVLELAHDNKIDLEGACEASLACS
TCHVILDKEYDYDKLPAPVEEEDMLDLAFGLTETSRLGCQIIISPELEGI
RLKLPATRNMMVDGYKPPHH

>HydF (from g4978t1) (likely complete), 485 aa, 22E0

MTKRAGTVCGIPPKHAASWSRAYAGQPLLRTNIGIFGAMNSGKSTLMNLI
SQQETSIVDSKPGTTADTKVALMEMHDLGPVKLFDTPGIDE EGLLGEKKR
RKAFDVLKECNAAVVVVPFNPASLKAARDV IQEASAKQKKGDDSAQMRV
MVVFNVFGQQTAEIRKATNTILDAAEKSLTPDGTNLQITSIALDLNSPEA
MGRVVKFVTTNTKPHSSNVSLPSALQLGPDSVVFLNIPMDAETPSGRLL
RPQALVQEELLROYASTFCYRMDLKKARSPIEEERREEEQRFRSSVDALK
SQNKLLKITDSQAMDVVHKWTMEPGTAAPSDQGGQSSQETVPLTTF SVM
MINYMSGRLSAFVEGKRFETLKHGDKVLICEACNHDR IQDDIGTVQIP
AKLRQRFGEGTIGVDHAFGREYQTKILNDYQLVIHCGGCMLDQOKMAARL
SDIEGSGVPITNYGLLLSYLAAKQGLSRVLRPWGL

TCA enzymes:

>citrate synthase Contig19816 (complete) 476 aa, 1456

MRRATVIATKSAASPAAVAVQARALAQSORLYATASLKDKFSEIVPKEQA
RVKCLKTEHGDLPLGQVTL SMAYGGMRGIKGLVTETSLLDPEEGIRFRGY

SIPECQAKLPKAKDGKQPLPEALLWLLLTSEIPTTEEQTQNLVHEISERSK
KFPAHVSHILKLNLPMTMHPMTQFTIGVNALQTESQFAKAYLEGVNKAKYW
EYAYEDMLNLI SFLPRTAAEIYRNVYHGGKLI PSDPKLDMGADYAHQLGF
ENKEFVDLMRLYLVLVHSDHEGGNVAHTTHLVGSALSDPYLSFSAGLNGL
AGPLHGLANQEVLRFLILKLRKFGGREVTDEELKKALWDLNLSGQVPIPGF
GHAFLRKTDPFRFTAQAEFASEYLPNDPLVKLVKQLYAVVPPVLTQOGKTK
NPWPNVDAHSGVLLQYYGLKEENYYTVLFGVSRALGVLP SLVLDRALGLP
IERPKSVTTEWLEKEAKKHAAPKH

>aconitase Contig17472 (complete) 788 aa, 7F4

MQSLKRATIVTPCTRALPSSVRSALGERNYAALSRLPSTTLPEYKMKSK
LSDVRKRLDRPLTLAEKILYSHLDDTKQEVVRGKTYLKLRPDRVAMQDAT
AQMAYLQFMTAGLPKVAVPTTIHCDHLIEAHVGGAQDLKNAKDINREYD
FLASSNKYIGIFWKP GSGIIHQIVLENYAFPGGLMIGTDSHTPNAGGLG
MVAIGVGGADAVDMADIPWELKAPKILGVKLTGALSGWTAPKDVILKLA
GILTVKGGTGYIVEYFGPGLDSISCTGMATICNMGAEIGATTSLFPFNHR
MSAYLKATSRADIASAAESFKDHLVADPGCEDLQNKLYDEVIEINLSELE
PHVNGPFTPDLATPLSKFAEAVKKNWPEKLAQGLIGSCTNSSYEDMSRS
ASIVQQAIDHGKAKSGFIITPGSEQIRATIARDGIINTFEKVGGTVLAN
ACGPCIGQWRDDIKKGDKNSIITSYNRNFTGRNDANPQTHAFVSSPELV
TAMSIAGDLTFNPLTDSLTDGADGKQFKLKS PYGDEL PARGFDAGEDTYQP
PAADGSKVTVVVDPSQRLQLPKFDEWNGSDAIENMPVLIKAKGKCTTD
HISMAGPWLKVRGHIDNISNMFIGAINAENKANCVQNQLTGEFGAVPD
VARAYKAGVPWIVIGDENYEGESSREHAAIEPRYLGGKAVVVRSFARIH
ETNLKQKQILPLTFANPADYDRISGNDRITIVGLKDLAPGKPVTLRVTPK
EGKPFDDVANQTLNEGQIAWWKAGSALNLMGKQORASAQ

>aconitate hydratase Contig806 (and 26672,5046) (incomplete, due to some internal gaps
largely derived from genome), 717 aa, 234A

MRANRACTTFFGPARLPMTVCP SHHISPLRCLNIFHSRECANAPKADLS
SPPPQGANRLFGT SRGVLRPAAMSRWELED PATSADIQRGKTYLKLKPD
RVAMQDASAQMALLQFISGLTSTAVPASTHCDHLIEAETGAAQDLESAK
VTNKEVF EFLSSASQKYIGIFWKP GSGIIHQIVLENYAFPGAMMIGTDSH
TPNAGGLIAIGVGGADAVDMAGMAWELEQRAPNVLGKLTGKLRGWASP
KDVILKLAGKLTVRGGTGSII EYFGPGVETLSCTGMATICNMGAEV GATT
SVFPLTESMLSYLAATGRKDIADTITAAKEIRGHLRADEGCHYDEVIEIN
LDELEPYINGPFTPDLATPLSQFADAVKKNQWPEKISAGLIGSCTNSSYE
DMSRAAAIARQASEKGTAKQSVFTVTPGSEQIRATI ERDGMQALRDIGG
LVLANACGPCIGQWKRSDAKGEKNSILTSFNRF SARNDGNPNTHNFLAS
PELVTAMSLAGSLTFNPTTDYLTDAQGNKYKLS PDAVDGYDQATATLPA
AGFDAGRSQDTYLAPPPADQASLEVAVSPTS DRLQLLEPFAPWPKGEKD
IRDAAVLIKVQKCTTDHISAAGPWLKYKGHLENIANNTLIGAVNADTGK
VNAVVSQLTGKEGTVPDVAREYQKAGVPWVVVAGKNYEGESAREHAALQP
PLPRRTGHHLPELCAHP

>isocitrate dehydrogenase NAD+ Contig22692 (complete) 379 aa, 1EB8

MRAASHLRLRSLPARLGSPLSHASSAPLVSRRLYADKPVENKTVTLIPGD
GIGEEISEAVVQIFAAAKVPVSWETVKVSTTTAKEGSLSSLLGGDVLESV
KTTRLALKGPLATPIGKGHMSLNLALRKQFNLYANVRPARSIPGVKTPYD
NVNIVVIRENTEGEYSIEHQVVPVCQS IKLITREASRRVAQYAFQYAE
THKKDKVTAVHKASIMNLS DGLFLKSCREVACAYPFVEYEEISVDKVCMQ
LVMAPEKFQVLVLPNLYGDIASDL CAGLVGGLGLTPSGNIGADSAIFESV
HGTAPDIAGQNKANPTALLLSAVMMLRHMGLYTHANRIERAAAYDVLREGK
VLTGDLGGSATTTQFTDAICKRVANDHEA

>isocitrate dehydrogenase, NAD+ Contig8357 (complete) 385 aa, 1D28

MRRTSAVALSRTSTSAACNARTLSVGSQRMLATSTGTEAPPASLSTGVRR
GLALGSEIPVTLIPGDGIGKEIADSVVGVFGALRVPIKWEVFERVGDITQ
NFDLLTSLARNQLCLKGQLKTDYEDSEHFKNNNLVLRKSLNLYANIVPIK
SLPGITTRHSGIDMVVFRENTEAEYSGFQEVTSGVVQSLKVVTRAACIR
IAEAAFGYAAAAGRKRVAIHKANIQKMSDGLFLESVREVAKKYPTVEFK
EMIIDNTCMQLVQNPQFDVLTVPNLYGNLIINVGSLVGGPGLVAGANY
GLHGEAVFEPGARHVAADIQGANVANPTGMLLSGVMLLRHVGLNEQAGRL
EKAIHDILLRGKVLTKDVGGFATTKFTKAVINHL

>isocitrate dehydrogenase, NADP+ Contig11724 (and 13189, 26192, E9BS9UA01CI7L8) (complete) 449 aa, 14F2

MRRQAINVAKRSTPTTWALAQRHLGATAVALTHSQVRLAHKKIDVKNPVV
ELDGDDEMTRIIWKRIKEELILPFLNIDLKYYDLGIEYRDQTNQVKTIEAA
EAIKQYNVGIKCATITPDENRVAEFKLLKMMWKS PNGTIRNII LGGTVFREP
IICKNVPRLLVPGWSQSIVIGRHAHGQYKATDLVVPKAGTYDLVFTPADG
SPKEVHQVYDFKTPGVIMGYNTDESIEGFAHSCFQYALAKNWPLYLSTK
NTILKQYDGRFKDIFQAIYDKDYKSQFEANKQWYEHRLIDDMVAFALKTS
GGFVWACKNYDGDVQSDIVAQGFGLSLGLMTSLLMCPDGKTVETEAAHGTV
TRHYRMWQKQOPTSTNPIASIFAWTKGLEHRAKLDNNTALAKFATALEEA
CVETVESGKMTKDLALCVHGSKMTNKDWLTTDDFLAAIRDTFQSKVEKF

>2-oxoglutarate dehydrogenase, E1 subunit Contig813 (and 9386) (complete) 826 aa, 1F33

MLSSRARAGLLSRGPLAFTGMGRAGFAGSRVASSSLTGGASSRWYSLTTA
SRQAAASPTSSSAVPLSRLSETFADGTSGAYVEDMYQAWKRDANSVHASW
GLLLPFRRRRSRPRRGLHRSPHPSRCHRRRSPAGGVSEEDLSRRVSDSMR
LLLLLVRAYQVRGHTLAKLDPLTGGPLSSFVPELLPSTYGF TDADMDRPI
HLGGESVISGFLSHGSATVTLREILVRLKQTYCSTIGVEYMHIPDRHECN
WIRERVETPEPFSFSPEQKFHLLDRLTWATL FERFLAMKYQNTKRFGLDG
CETLIPGMKTMIDTAADLGVESVVI GMPHRGRLNVLANVVRKPLDALLHE
FDLEGKNDHSDDLGLGTGDV KYHLGTSYDRPTASGKKVHLSLVANPSHLE
AVNPVVEGKARAKQOYMGDTERTRVMPVLLHGDAAFASQGVVYETLDLGI
WKNFTTGGTIHIVVNNQVGF T TALRGSRTNTASSYPTDVAKTVNAPIFHV
NGDDPEAVVHTLKLAAEYRQAFKKDVVIDIICYRRAGHNEGDEPRYTQPO
MYRMIEKHQSTLDLYRAKLKAEGVDDARIKQMEDFVNEEHNAKAFQASST
HVPNKADWFSSYWKGFKSAHQYSSIRPTAIPDAVISKIGATVSSSLPEGMK
LHPNLEKLIKRRKLMFESGKNIDWGTAEQALGSLALEGNLIRLTGQDVE
RGTFSHRHAVLHDRETGETYQPLRHIDPAQAPV FVHNSLSEYAVLGYEL
GFSLENPNSLVLWEAQGFDFANGAQVIVDQF ISSGEQKWQRQSGLVMLLP
HRYHGQKPDHLEAVNPVVEGKARAKQ

>2-oxoglutarate dehydrogenase E1 Contig20262 (and Contig25463,26471) (incomplete inner portion), 903 aa, 20C2

MLRVGARGTRTQGS SFLSSSRFTGV TAAAAARFCPAARSQTLGLVGRYSS
STTTTAVEGGKLTQEEVDNQNKHANVLR LRVNAYRTYGHF DAALDPLGRRQ
RGAPEGVLDAAARYGLGNEEVQLRGLFFGLDKEKASVSEIVDALKKTYCSS
VGVEFTHVENPEEQTWLARRFEAAMGR TATGATAQNALPAEDKKRILXLL
QTSEEFDHFLHTKFRAVKRYGLEGCESMMACMDTIFSKAAESSFDEAVIA
MPHRGRLNFLTGILRYPASKIFAKVSGFNDFPTVEGAVRPGTGDVLSHIA
QSVLDLEYQGNLHVSLIHNPSHLEAANPVAQGVRAKQDLGKGRKQALCI
VVHGDAAMSAQGVVPELTLTSQLPEYAVG GSMHV VVNNQIGFTTECHKGR
SSWYCTDVLRSVHAPAIHVNADDPEAVVIATRLAMDYLTTFRKDIIIVDLH
GYRRHGHNELDEPSFTQPLMYDSIRVRPTIAKLYGEKLI TMGGKWQKMTA
PQDMTKPVDTGYAE EELVKVGVASINPQGKT VHSRLQNF FCKPRQAKLES
KTGLDWATAESLAIGSLLEKYNVRLSGQDVGRGTF SHRHV ALTDQKTNE
RVIPLNLMSSDQKLVADSPLEMAVMGF EYGYSMEDPSTLVLWEAQFG
DFHNGAQI I IDQFLNSGEDKWWRSAL TLLLPHGYDGAGPEHSSCRIERF
LQLCDGDRLNPGDISNLVPMQVINPTTPANYFHALRRQMKRSFRKPMVV
VGPKTLRLRHPQAVSDLAEMAPGTSFQPVIADTTVSPAQVKRVVMCSGKVY
YDLVKHRETKKIDDVAIIRVEELSPFPYRALADELDKYRNADSYRWAQEE
PQNAGMWDYVAPRFSRLSAPVKLVSRPASAAPAVGLGSIHAQQQKAILDG
AFA

>2-oxoisovalerate dehydrogenase beta subunit Contig5667 (complete), 392 aa, 1A30

MKKRISASIGSSATAHRLVGGSVSGASPARSLLQPSARAFHVSPAHAAT
AHGGSSSTHQQPQGEGEVARMNFFTAVNNALDIALGADPKAVIFGEDVA
FGGVFRCTINLREKYGNRSRVFNTPLSEQGIAGFAIGMAAVGATPIAEMQF
ADYIFPAFDQLVNEAAKYRYRSGGQFDVAGLTVRTPCGAVGHGGHYHSQS
PEAYFCHTPGLKVMPSTPKEAKG LLLSSIRD PNPVIFLEPKILYRSAVE
DVPLGDYELPLGKARIVKEGSDVTVVGWGSQLHVLT DACGLAEKEGISCE
LIDLRTLAPWDVDTVEASVKKTGRLVVSHEAPKTGGFAGEICSTIQERCF
LHLESPIRRICGYDTPFPLVFEK FYVPDKLKNLEAIRSTVHF

>2-oxoglutarate dehydrogenase E2 subunit Contig8827 (complete), 451 aa, 1D73

MMKRTASMGRRPLFSACLVVQSNRGAAATLSGLRGVCSSSSHNGTGRIVA
SLTSHSRSLNVLPKRFYATAEVKTQAVPPMGDSITEGELKNWSKGVGEH
VAVDDLVAVIETDKVAVEIRAKEAGVIKEHFAEEGSTVSVGAPLFAYEAG
AEAPKKAEPVKEEPAKKTEQAPKPEAAAPKAEAPKTAAPAAATEGKAAP
KAEASKAPAPKTASPVAGGERKVKVTRMRERIAQRLKDAQNTYAMLTTFQ
EADMFNLIINMREDFKEEFQKKHGVKLGFM SAFVKASAAALKEIPAVNAVY
DGSNREIIYRDYVDISVAVATPRGLVVPVLRDCDHL SFADVEKRLSELSV
KARKDEITLEEMAGGTFITISNGGVYGS LMGTP IINPPQSAILGMHAINKR
PVVVNDQVVIRPIMYLALTYDHRLIDGKEAVTFLRHIKHSIEDPRRLLE
L

>dihydrolipoamide dehydrogenase Contig588 (and 23476 and 11795) (complete) 507 aa, 1240

MRRGLIQASRS AVPTSASGVFASRAFPRTFIASRGFATAAEQDDVIVIGG
GPGGYVAAIKAGQLGLKVTCVEKRGKLGGTCLNVGCIPSKALLHASHIYE
DTKKYFPDGHIVFDNVKLDLGAMMSKEKAVNGLTSGIEFLFKNNVYV
KGFVKVSGANEVTVDLAEGGEKKLSAKNIIIVATGSDVIGLPFLPIDEQRV
VSSTGALALKEVPKMMVIGGGIIGLEMGSVWRR LGTEVTVVEFTDNL CG
GAADGEVAKEFKRILAKQGMKFKMGTKVTGAKVEPSSITLITEPRDGGKT
EEVACDVVLC SVGRRPYLDGLGLENVGVKLDNRGRVAVDDHFRSNVPSIY
AIGDCIPGPMLAHKAEEDGIAAVEIIAGGHGHVDYNNVPSV VYTHPEVAW
VGQTEEQ LKAQGIQYKVGKFPFKANSRARTNDDDEGFVKYLADAKTDKVL
GVHMIGAMV GEMIAEPTLLMAYGGSSE DVARTCHAHTLSEAVKEAMAT
YDKAIHF

>succinyl-coa ligase, alpha Contig9628 (and 22544) (complete), 330 aa, 2652

MRSNRASLLR TCATTSAPS FATRRLYAAASKPRVLINKDTKVICQGFTGK
QGTFFHSKQAI EYGTGMVGGVSPGKGGSKHLDLPVFNSVKEAKENTGADAT
VIYVPPPF AAAAAIIEAIDAEIPLAVCITEGIPQ QDMVRVKKRLMAPGCKT
RLIGPNCPGIIKPGECKIGIMPGHIHTPGKIGIVSRSGTLTYEAVGQTTA
VGLGQSTCVGIGGDPFNGTNFVDVLK LFAEDPQTEGIILIGEIGGSDEEA
AAQWIKDNALVSKKPVV SFIAGLTAPPGRRMGHAGAIISGGKGTATSKIQ
ALQDAGVTISESPAKLGSTMLAAMRAAGKA

>succinyl coa ligase, beta subunit GDP Contig2792 (complete) 464 aa, 1C83

MRKTCRIGTAARATSGRVAATSARSFSSRTLSCGASGFLQSRTSVASSKL
IRRAAPINSTQVRFLNLQEFSSKGLMDQYGVRTQKWKLATTP EEALAAAK
ELKKNPECKELVVKAQILAGGRGKGVFDNGFKGGVHL CNTPEEAAQLTKQ
MLGHKLTTKQTGPEGTLVSKVMIAQSIDLKRETYFAILMDRAFSGPVMVA
SPQGGMDIEQVAEETPD LIFKEAIDINOGIKPEQTRRLAIAMGF DDEKKI
ADAQKQ MAGLYELFLKTDATQVEINPFAETPEGEVYCVDAKINFDDNASF
RQKAVFDMGDDSETDQREVEAAKYGLNYIGMDGNIGCMVNGAGLAMATMD
IIKLYK GSPANFLDVGGGANEQQVTQAFKILTDDHQVKAILVNI FGGIMK
CDVIAQGIINA AKEVKLNIPLVVRLEGTNVTIGKDLLEKSGLP IITANDL
DEAAQKAVASIGHH

>succinyl-coa ligase beta subunit, ADP Contig20053 (and E80POFO01EK8OZ, 2228) (complete), 462 aa, 101D

MWRRGARSVGMAGGMGRSLPARSALLQSNTATTLTSTSAQTGAARRWLN I
HEYQSQELMRKEGIRVPKGVAAASPEEAYKIAQQMQGGDADVIVKAQVL
AGGRGVGHFDSGLKGGVHTCTSP EEVKDVASKMLGHHIFTKQTGPEGKPC
NVVYLAERL FIRRETYFAILMDRAYNGPVIIGSSKGGSDIETLSAEHPDA
IFKIPIDIAEGVTPEKLELVADKLG FQSTKVKEQTKELVSKLYDLFIK KD
CTLAEINPLVEDHQQIVALDAKLRFDDNAEFRQKEIFALRDESQEDPRE
VAASKFDLNYIQ L NGNIGCLVNGAGLAMATMDIIK LKGGNPANFLDVGGG
ATEKQVTEAFRIFSSDKSVKAVMVNIFGGIMRCDIIAMGILNAVKVLNIK
VPLVVRLLGTNMKEAKDLLENSGARIIFASDLDEAAEKAVKVARIVDMAQ
EAQLNVSFELPL

>SdhA Contig11902 (complete) 648 aa, C05

MRLSRFSRS SALKSSFAGSAGIRTAPSSGLFRRNYAVVS NATPQAGESQ
TLTSSYDVVDHTYDCVVVGAGGAGLRAALGLTEKGYKTACISKLPTRSH
TVAAQGGINAALGNADNDDWRWHAYDTVKGS DWLGDQDAIH YMCREAPAS
VIELEHYGMPFSRTEEGKIYQRAF GGQSYNFGKGGQAHRC CAVADRTGHA
LLHTLYGQAVRHNCTFFIEYFALDLIMENGE CRGVVALCLEDGKIHRFRS
HQTVLATGGYGRTYLSATS AHTCTGDGNGMAVRAGLPCQDLEFVQFHPTG

IYGAGCLITEGSRGEGGILRNSDGERFMERYAPTAKDLASRDVVSRSITL
EIRAGRGVGGKHKHDVLLDLSHIPADILAERLPGISETAKIFAGVDVTKEP
IPILPTVHYNMGGVPTNYHGEVVTKKGDNPDCVVPGLMAAGEAACVSVHG
ANRLGANSLLDIVVFGRAVANVEETLKKDTPHKPLPKNAGLEAIHNLDK
LRFANGKYRTAEVRDKMQRMQNNAAVVRTGETLQEGVKLIDEVYDMFKE
VKTVDRLSVWNTDLVETLELQNLSSQAVLTMHSAEARKESRGAHAREDFP
DRDDANWTKHTLSWMDMESGKVKLDYRPVHDKPLNDEMPYVPPVKRVY

>SdhB Contig16868 (complete) 294 aa, 86F

MRRITARSVTTPLFTSKTASLAGSARPLFGIVSAADKVVPKDGLVTVEVY
RWSADEKEKPYIQSYKLDVNNCAPMVLDALEFRKNEQDPTLSFRRSCREG
ICGSCAMNIDGTNTLAELCPVAESVTNGKIKIYPLPHLAVVRDLVPLSN
FYEQHKSIQPYLQVDDHAALGSSKTEQLQTRDRKKLGLYECILCACCS
TSCPSYWWAGNENKYLGPAILLQAYRWIADSRDQHTNQRLRALAKEDMKV
YACHTIMNCTKVCCKGLNPAALAVAKVKKATLELDVQKQKQALAH

>SdhC Contig5019 (and 2707) (complete) 172 aa, 21E

MLRQATARTAPLFAVRGTVTGLQVLSRSPVALATRTLATLPSDASTEAKP
NRPLSPHVSIIYRFPLPALTSITNRATGGALTAGIYTAGALALFGAHDLPV
YIDAFKAAVPLLIVYPTKLLVSPFVYHTLAGIRHLYWDYTAKGLTLPEVY
TSSYALMGATALLTLGLTFYSI

>SdhD Contig22329 (complete) 157 aa, 1705

MRRATALFSARAAPSAAGASRGAARRLYATSTESSVLDTVLPATGAGKHR
LYHYTSIGLVTLIPIALVAPSSVVLVVDLALGFLLPPIHAHIGMAHIVEDY
VPKAGRTAAGWGLMLATGIAVAGLLKLNVTGSGLTSSVKTLWRKEPLTTT
QKESSTA

>fumarase Contig5809 (and 4472) (complete) 588 aa, 5AF

MRRLOPLLSSTAIAARSPACFAAAGPGRLIGLRALATAAPAKKSTPPAFE
FEPLFQADPFSATPYRKLFGPESGLIRTEKVAGREILHVEDEAIERLTFE
AMRDISHLLRPGHLEQLNSILKDPPEASDNDRFVALELLKNANIASGMIL
PSCQDTGTAIVMAKKGQYVWTSGDDEAAISKGIYQTYTQTNLRYSQMAPI
DMYKEVNTGTNLPAQIDIIYASEGNAYKFFHIAKGGGSANKTYLYQOTKAL
LNPDSLKMFVNENIRSLGTAACPPYHLAIVIGGTAESTLKTVKLASTKY
LDTLPTEGNKHGRAFRDLELEKILELAQKTSIGAQFGGKYFCHDVRVIR
LPRHGASCPVGIGVSCSADRQAVGKITPEGVFLEKLETNPAKYLPEITED
KLSDTVVNIDLKPMSEIQATLSKYPIKTRLSLSGTLVWARDIAHAKLKE
RLDNGOQLPQYVKDHIYYAGPAKTPEGYASGSFGPTTAGRMDSYVDMFM
KNGGSLITLAKGNRSKQVTEACKKYGGFYLGSI GGPAARLAQDCIRKVEV
LEYPELGMEAVWRIEVEDFPFVIVDDKGEDFFKNLSH

>malate dehydrogenase Contig10193 (complete) 454 aa, 63B

MRRGLSTVRSATVFGKQACLASSTLRVDRRAYATSPEDAALAEQIEKVL
DLVKKQGNLSEKLTVRKLTRELQTVPEIDRALSSVGD SAVKYMAELEKP
GAGPLSAVPPVRVTVTGAAGAIGYAMLFRIASGEMLGKHQPVILQLELE
PAMKALEGVIMELKDCAFPLLHGVTASSDVNKAFFEGADFAMLVGAKPRTK
GMERGDLLKENANIFSVQKALNKVANRDTLRVCVVGPNANTNALIASAN
APNIHPRRFTAMTRLDHNRGIAQLADKCLKCKVTDIERFAIWGNHSATQYP
DISHTQINGKWKDLVDEKWKDTFIPDVQORGAIIAARGSSAASAAN
AAIEHMRDWVKGVTNGQWTSMGVWTGNGKVG DYGTSPDIYYSFPVVCADGE
YTIVQNVVPDKFSAERMOKTNDDELVSEKNGV GELAKRTTDP AALLKEQYK
GGKQ

>cytosolic type malate dehydrogenase Contig26422 (and E80POFO01EQ035) (complete), 379 bases, 2029

MSADSNATTRRAVSRMSRIAAHMGVGSQTGFEEAATSASRVVSQOPPVTV
LVTGAAGQIAYSIVFLVAQGRLLGEETPIKLHLLDLPOFVGALQGLAMEL
EDCAFPLLRGVVCTGDLKEAFKGVDAVLLVGSFPRQAGMERNDLLAKNAA
IFKEQGRALDQYASKNVKCVVGNPANTNALIAQACAPSIPKENFTALTR
LDQNRAGFLAKKLVSPGQIHNAIIWGNHSSQFPDVS HGOVSI DGRTV
SLKEAVGGTEWVEKEFIPGVQORGA AVIKARQKSSAASAANAVVGHVHDW
LVGTPQGEWVSMGVYSDGSYGIPPGVIYSFPLTCSRGNWAI VQGLPVDA
ARKRMQATYDELHSEKETAFSFLGLDKKH