

Table S6. Fasta sequences of the pyruvate to acetate formation pathways I, II and IV, commonly found in Bacteria according to MetaCyc (<https://metacyc.org/META/NEW-IMAGE?object=Super-Pathways&detail-level=3>).

1. Acetate formation pathway I.

>sp|P94692|POR_DESAF Pyruvate synthase OS=Desulfovibrio africanus GN=por PE=1 SV=1

MGKKMMTTDGNTATAHVAYAMSEVAAIYPITPSSTMGEEADDWAAQGRKNIFGQTLTIRE
MQSEAGAAGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVVTARAAHA
LSIFGDHQDIYAARQTGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEI
QKIEVLDYADMASLVNQKALAEFRAKSMNPEHPHVRGTAQNPDIFYQGREAAANPYYLKVP
GIVAEYMQKVASLTGRSYKLFVDYVGPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLI
KVRLYRPFVSEAFFAALPASAKVITVLDRTKEPGAPGDPLYLDVCSAFVERGEAMPKILA
GRYGLGSKEFSPAMVKSVDNMSGAKKNHFTVGIEDDVTGTSLPVDNAFADTTPKGTIQC
QFWGLGADGTVGANKQAIKIIGDNTDLFAQGYFSYDSKSKSGGITISHLRFGEKPIQSTYL
VNRADYVACHNPAYVGIYDILEGIKDGFTVLNSPWSSELEDMDKHLPSGIKRTIANKKLL
FYNI DAVKIATDVGLGGRINMIMQTAFKLAGVLPFEKAVDLLKKS IHKAYGKKGEKIVK
MNTDAVDQAVTSLQEFKYPDSWKDAPAETKAEPMTNEFFKNVVKPILTQQGDKLPVSAFE
ADGRFPLGTSQFEKRGVA INVPQWVPENCIQCNQCAFVCPHSAILPVLAKKEELVGPAN
FTALEAKGKELKGYKFRIQINTLDCMCGCNCADICPPKEKALVMQPLDTQRDAQVPNLEY
AARI PVKSEVLPRDSLKGSQFQEPLEMFSGACSGCGETPYVRVITQLFGERMFIANATGC
SSIWGASAPSMFYKTNRLGQGPWAGNSLFEDAAEYGFGMNMSMFARRTHLADLAAKALES
DASGDVKEALQGWLAGKNDPIKSKEYGDKLKLKLLAGQKDGLLQIAAMSDLYTKKSVWIF
GGDGWAYDIGYGGDLHVLASGEDVNVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRT
GKKDLARMVMTYGYVYVATVSMGYSKQQFLKVLKEAESFPGPSLVIAYATCINQGLRKG
GKSQDVMNTAVKSGYWPLFRYDPRLAAQGNPFQLDSKAPDGSVEEFLMAQNRFAVLDRS
FPEDAKRLRAQVAHELDVRFKELEHMAATNIFESFAPAGGKADGSVDFGEGAEFCTRDDT
PMMARPDSGEACDQNRAGTSEQQGDLSKRTTK

>sp|Q51804|PORA_PYRFU Pyruvate synthase subunit PorA OS=Pyrococcus
furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) GN=porA PE=1
SV=2

MPIRKVMKANEAAAWAAKLAKPKVIAAFPITPSTLIPEKISEFVANGELDAEFIKVESEH
SAISACVGAAGVVRTFTATASQGLALMHEILFIAAGMRLPIVMAIGNRALSAPINIWND
WQDTISQRDTGWMQFYAENNOEALDLILIAKVAEDERVLLPAMVGFDAFILTHTVEPVE
IPDQEVVDEFLGEYEPKHAYIDPARPITQGLAFPAHYMESRYTVWEAMERAKKVIDEAF
AEFEKKFGRKYQKIEEYKTEDADIIFVTMGS LAGTLKEWIDKKREEGYKVGAAKITVYRP
FPVEEIRELAKKAKVLAFLKKNITIGLYGAVFTDASAALINESEKPLMVDFIVGLGGRDV
TFNQLDEALEIAEKALKEGKVENPINWIGLRWELVK

>sp|P80521|PORA_METBF Pyruvate synthase subunit PorA OS=Methanosarcina
barkeri (strain Fusaro / DSM 804) GN=porA PE=1 SV=2

MIDPAYRKKMVVVEGSYAVAHSAKVC RPNVISAYPITPQTHIVEHLSQFMADGEIPNCEY
VNVEAEFS AISALIGASAVGARTYSATTSQGLLLMHEALFNTSGMRLPVVMTVANRAVSA
PINIWNHDQDAIAQRDTGWMQLYVEDVQEACDTPQLYKIAEDNEIMVPGMVCMDGFILS
HVYEPVVLLEQDLTDNLFPPFQPEDILDPEDPKTFGAFASPDTYEEFRYLHEQAMQKALP
KIEATAKEFEVEYGRYHGGLIDGYMLDDAEIVVMAMGSILGTVKDVVDKYRAKGEKIGVL
KVRSEFRPFKEQICKAVKNAHAVVLDKNISIGTNEGALFTETKSCLYNSKVRVPVIGYT
IGHGGRDIPVESIAKVIEETTKVAKSGITIESQFMDLKEELL

>sp|P80900|PORA_METTM Pyruvate synthase subunit PorA
OS=Methanothermobacter marburgensis (strain DSM 2133 / 14651 / NBRC
100331 / OCM 82 / Marburg) GN=porA PE=1 SV=2

MVLKVISANQAVAEAAKLAKPKVIPVYPITPQTSISEYLAKYVADGELDAEYIRVESEHS
AMSACVGASGAGVRVFTATSSQGLALMHEIVYAAAGLRNP IVMANANRALSAPLSIWNDQ
QDSIAERDSGWMQIYAESQGEALDSVLLSYRVEDRDLVLLPSMVCLDGFILTHTVEPVDI
PSQDEVDTFLPEFQPAVLDPEPMSLGTFTDPNYYMEARYEVERAMERSRKVIAKACQE
FSEMFRREYGFVEDYRCEDAEIIILVAMGSVCSTLREVIDDMRDEGKPVGLLKVRIHRPFP
AEEIKKAVSNAHKIAVLDKNITFSVGGALHTELKALLPDKEVYGFIVGLGGRDITPEHIM

EIVRK TENPERTVSWIGLKEESQ

>sp|O05651|PORA_THEME Pyruvate synthase subunit PorA OS=Thermotoga
maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=porA PE=1
SV=2

MERVVERVAVTGAEAVANAMRQIEPDVVAAYPITPQTPIVEYFARFVADGVVRTEMIPVE
SEHSAMSAVVGAAAAGARAMTATSANGLALMHEIVYIAASYRLPIVMPVNNRALS GPINI
HCDHSDAMAERDSGWIQLFAETNQEAYDFTILAVRLAEHEDVRLPVMVNL DGFILSHGVE
PVEFY PDELVKKFV GELKPMY PLLDTEHPVTWG PLDLYDY FEFHQRQIEAMENVKVF
EIAKEFEETFGRKYWFVEPYRMEDA EHV MVALGSTNSTIKYV VDELREEGYKVGSLKIWM
FRFPFKEQLQELLNGRKS VVVLDRAVSFGAEAPLYEAVKSALYEVAARPMLGSYVYGLGG
RDIKPEHIRKAFEDAINGNLI ADEQRYLGLRE

>sp|P80522|PORB_METBF Pyruvate synthase subunit PorB OS=Methanosarcina
barkeri (strain Fusaro / DSM 804) GN=porB PE=1 SV=3

MSKTAPKTYITSGHSGCAGCCDAFAAKFTLMGAGPNTIVINPTGCLEVMSTPFPYSSWQV
PWIHSLFENAGAVASGVEAALKALGKKDDVKVVSIGGDGSTM DIGLGALS GAFERGHDF
YVCM DNEAYMNTGVQRSSGTPFDASTTTTTPAGKVSFGNPRPKKNMPA IMAAHGSPYVATT
SIGFPRDMIRKVKKATEIVGPTYIHAQAPCPTGWGFDT SKTLEIAKLAVETCLWPMYEME
NGEITQVRKVNPRPVEEYLRAQKRFKHLFTMEGGEEI KKIQA IADWNIKHFE LQ

>sp|P80901|PORB_METTM Pyruvate synthase subunit PorB
OS=Methanothermobacter marburgensis (strain DSM 2133 / 14651 / NBRC
100331 / OCM 82 / Marburg) GN=porB PE=1 SV=2

MKIPEEEFLAPGHRGCAGCGATVGVRLALKVLGKNTVAVSSTGCLEVITTPYPETAWEIP
WIHVAFENAAVASGVERALRARGRGEVNVVAFAGDGGTADIGLQSLSGAMERGHNI IYI
CYDNEAYMNTGIQRSASTPYGASTTTS PHGKESFGEDRPKKNMPL IMAAHGVPYVATASI
SYPEDFMEKVRKARDIEGPAYIHLHQ PCTTGWGFDP SKTVELGR LAVETG SWILYEIEDG
DFRVTYRPVQRKPV E EYLNAQKRFRHL TEEQKAKIQEYVDSVCQELRI

>sp|Q51805|PORB_PYRFU Pyruvate synthase subunit PorB OS=Pyrococcus
furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) GN=porB PE=1
SV=3

MAVRKPPITTREYWAPGHAACAGCGCATALRLATKALSEAMEEKY GDNFAFAIAHATGCM
EVSVAVFPYTAWKAPWIHVAFENAAVASGIEAAWKKLGRKGKILAIGDGGTADIGLQA
LSGMLERWHNVLYL MYDNEAYMNTGIQRS SSTPYGAWTTTSP PGKYSVGEDKPKKVALI
AAAHQIPYVATASIGNPLDFVRKIKKAGKIDGPAFVQV LCTCPTGWRSPLEKGV E IARLA
IETGIWPLFEIENGDIWNIKI QPPGGGAKVYKEGNRVVRIEFKKPI E EYLKLQGRFKHLF
KRPEAIEELRNQVKAMWKVLGVEAILRPEE

>sp|Q56317|PORB_THEME Pyruvate synthase subunit PorB OS=Thermotoga
maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=porB PE=1
SV=3

MPVNIKQLAQEFDKKEIGITQGHRLCPGCGAPITVKFVMMIARHLGYEPVVGLATGCLEV
STSIYPYTAWSVPIYIHN AFENVAATMSGVETAYKALKNKGKI PEDKKYAFIAFGDGGTY
DIGLQSLSGMLERGHKVLVLYDNEGYMNTGNQRS GSTPPGSDTTTAPV GKKLP GKVQLK
KNIVEIVAAHENVYAATASLSEPMDFFAKVEKALNFDGPSFLAVFSPCVRFWRVND DKT
EISKLAVETKYWPLYEVERGVYRVTRKPRQFKPV E EFLKAQGRFRKLLSRPDAKEIVDEL
QEYVDRRWERLLTLEEVTKDKPIR

>sp|P80902|PORC_METTM Pyruvate synthase subunit PorC
OS=Methanothermobacter marburgensis (strain DSM 2133 / 14651 / NBRC
100331 / OCM 82 / Marburg) GN=porC PE=1 SV=2

MIEIRFHGRGGQGA VTA AEILAKAAFEDGKYSQAF PFFGVERRGAPVMAFTRINDEPIRR
RYQVYNPDYVVVLD EGLVDVDFV SGLKEDGVLLNTAGTFTSENAKIHTIDATGIALEN
LGRPIVNTVMLGAFAGVTGLV SIDSLIKI IKETFPGKIGDKNAEAARIAYEKMKHSG

>sp|P80523|PORC_METBF Pyruvate synthase subunit PorC OS=Methanosarcina
barkeri (strain Fusaro / DSM 804) GN=porC PE=1 SV=2

MKEIRIHGRGGQGSVTA AEMLSVA AFEDGKFSQAFPAFGVERRGAPVQAFTRINNNPIRL
RSQVYTPDYVIVQDATLLETVDVASGVKDDGIIIVNTTENPESLKLNTKARVMTVDATKV
AMDIIIGVPIVNTVLLGAFAGATGEINVESIQHAIRARFSGKVGEKNANAIQKAYKLIRGE
EA

>sp|Q51799|PORC_PYRFU Pyruvate/ketoisovalerate oxidoreductases common subunit gamma OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) GN=porG PE=1 SV=1

MIEVRFHGRGGQGAVTAANILAEAAFLEGGKYVQAFPPFFGVERRGAPVTAFTTRIDNKPIRI
KTQIYEPDVVVVLDPSLLDAVDVDTAGLKDEGIVIVNTEKSKEEVLEKLLKKKPKKLAIVDA
TTIALEILGLPITNTAILGAVAKATGLVKIESIEEAIKDTFSGELGEKNARAAREAYEKT
EVFEL

>sp|O05650|PORC_THEMA Pyruvate synthase subunit PorC OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=porC PE=1 SV=4

MPVAKKYFEIRWHGRAGQGAKSASQMLAEAALEAGKYVQAFPEYGAERTGAPMRAFNRI
DEYIRVRSVENPDVVVIDETLLSPAIVEGLSEDGILLVNTVKDFEFVRKKTGFNGKIC
VVDATDIALQEIKRGIPNTPMLGALVRVTGIVPLEAIEKRIEKMFGKKFPQEVIDANKRA
LRRGYEEVKCSE

>sp|P84820|PORC_THELN Pyruvate/ketoisovalerate oxidoreductases common subunit gamma OS=Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C) GN=porG PE=1 SV=2

MIEIRFHGRGGQGAVTAANILAEAAFLEGGKYVQAFPPFFGVERRGAPVTAFTTRIDDKPIRI
KTQIYEPDVVVVLDPSLLDVTVDVDTAGLKDEGIVIVNTEKTKKEEVLEKLLKKKPAKLALVDA
TTIALEILGLPITNTSILGAVAKATGIVKIESVEEAIKDTFSGELGKKNAKAAREAFEKT
VVYEL

>sp|P84819|PORC_PYREN Pyruvate/ketoisovalerate oxidoreductases common subunit gamma (Fragment) OS=Pyrococcus endeavori GN=porG PE=1 SV=1

MIEIRFHGRGGQGAV

>sp|P0A9M8|PTA_ECOLI Phosphate acetyltransferase OS=Escherichia coli (strain K12) GN=pta PE=1 SV=2

MSRIIMLIPTGTSVGLTSVSLGVIRAMERKGVRLSVFKPIAQPRGGDAPDQTTTIVRAN
SSTTTAAEPLKMSYVEGLLSSNQKDVLMEEIVANYHANTKDAEVVLEGLVPTRKHQFAQ
SLNYEIAKTLNAEIVFVMSQGTDTPEQLKERIELTRNSFGGAKNTNITGVIVNKLNAPVD
EQGRTRPDLSEIFDDSSKAKVNNVDPKQLQESSPLPVLGAVPWSFDLIATRAIDMARHLN
ATIINEGDINTRRVKSVTFCARSI PHMLEHFRAAGSLLVTSADRDPDLVAACLAAMNGVEI
GALLLTGGYEMDARISKLCERAFATGLPVFVMTNTWQTSLSLQSFNLEVPVDDHERIEK
VQEVYANYINADWIESLTATSESRRLSPPAFRYQLTELARKAGKRIVLPEGDEPRTVKA
AAICAERGIATCVLLGNPAEINRVAASQGVLEAGIEIVDPEVVRESYVGRVLELRKNGK
MTETVAREQLEDNVVLGTLMLLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSV
FFMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAAAFGIEPRVAMLSYSTGTSGAGS
DVEKVVREATRLAQEKRPDLMDGFLQYDAVMADVAKSKAPNSPVAGRATVFIFPDLNTG
NTTYKAVQRSADLISIGPMLQGMKRPVNDLSRGALVDDIVYTIALTAIQSAQQQ

>sp|P38503|PTAS_METTE Phosphate acetyltransferase OS=Methanosarcina thermophila GN=pta PE=1 SV=3

MVTFLEKISERAKKLNKTIALPETEDIRTLQAAKILERGIADIVLVGNEADIKALAGDL
DLSKAKIVDPKTYEKKDEYINAFYELRKHKGITLENAAEIMSDYVYFVMMAKLGEVDGV
VSGAAHSSDTLRPAVQIVKTAKGAALASAFFIISVPDCEYGS DGTFLFADSGMVEMPSV
EDVANIAVISAKTFELLVQDVPKVAMLSYSTKGSASKLATEATIASTKLAQELAPDIAID
GELQVDAAIIVPKVAASKAPGSPVAGKANVFIFPDLNCGNIAYKIAQRLAKAEAYGPITQG
LAKPINDLSRGCSDEDIVGAVAITCVQAAAQDK

>sp|P39646|PTAS_BACSU Phosphate acetyltransferase OS=Bacillus subtilis (strain 168) GN=pta PE=1 SV=3

MADLFSTVQEKVAGKDVKIVFPEGLDERILEAVSKLAGNKVLNPIVIGNENEIQAKAKEL
NLTLGGVKIYDPHTYEGMEDLVQAFVERRKKGATEEQARKALLDENYFGTMLVYKGLADG
LVSGAAHSTADTVRPAQLIKTKEGVKKTSGVFIMARGEQYVFADCAINIAPDSQDLAE
IAIESANTAKMFDIEPRVAMLSFSTKGSAKSDETEKVADAVKIAKEKAPELTDGEFQFD
AAFVPSVAEKKAPDSEIKGDANVVFVPSLEAGNIGYKIAQRLGNFEAVGPILQGLNMPVN
DLSRGCNAEDVYNLALITAAQAL

>sp|Q8ZND6|PTA_SALTY Phosphate acetyltransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=pta PE=1 SV=1

MSRIIMLIPTGTSVGLTSVSLGVIRAMERKGVRLSVFKPIAQPRAGGDAPDQTTTIVRAN
STLPAAEPLKMSHVESLLSSNQKDVLMEEIIANYHANTKDAEVVLEGLVPTRKHQFAQS

LNVEIAKTLNAEIVFVMSQGTDTPEQLNERIELTRSSFSGGAKNTNITGVI INKLNAPVDE
QGRTRPDLSEIFDDSSKAQVIKIDPAKLQESSPLPVLGAVPWSFDLIATRAIDMARHLNA
TI INEGDIKTRRVKSVTFCARSI PHMLEHFRAGSLLVTSADRPDVLVAACLAAMNGVEIG
ALLLTGGYEMDARI SKLCERAFATGLPVFMVNTNTWQTSLSLQSFNLEVPVDDHERIEKV
QEYVANYVNAEWIESLTATSESRRLSPPAFRYQLTELARKAGKRVVLPEGDEPRTVKAA
AICAERGIATCVLLGNPDEINRVAASQGVELGAGIEIVDPEVVRESYVARLVELRKSJGM
TEPVAREQLEDNVVLGTLMLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSVF
FMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAIAFGIEPRVAMLSYSTGTSGAGSD
VEKVREATRLAQEKRPDLMDGPLQYDAAVMADVAKSKAPNSPVAGRATVFI FPDNLNTGN
TTYKAVQRSADLISIGPMLQGMKPVNDLSRGALVDDIVYTIALTAIQASQQQQ
>sp|P99092|PTAS_STAAN Phosphate acetyltransferase OS=Staphylococcus
aureus (strain N315) GN=pta PE=1 SV=1
MADLLNVLKDGLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
DLDISNIELINPATSELKAEVLVQSFVERRKKGKATEEQAEQLLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTVPRALQIIKTKPGVSRTSGIFFMIKGDQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGSKSDVTKVQEAVKLAQQKAEKLEAII DGE
FQFDDAIVPGVAEKKAPGAKLQGDANVVFVPSLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSIEDVYNLSIITAAQALQ
>sp|Q6GJ80|PTAS_STAAR Phosphate acetyltransferase OS=Staphylococcus
aureus (strain MRSA252) GN=pta PE=1 SV=1
MADLLNVLKDGLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
NLDISNIELINPATSELKAEVLVQSFVERRKKGKTEEQAEQLLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTVPRALQIIKTKPGVSRTSGIFFMIKGDQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGSKSDVTKVQEAVKLAQQKAEKLEAII DGE
FQFDDAIVPGVAEKKAPGAKLQGDANVVFVPSLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSIEDVYNLSFITAAQALQ
>sp|Q9X0L4|PTAS_THEMEA Phosphate acetyltransferase OS=Thermotoga maritima
(strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=pta PE=1 SV=1
MFLEKLVEMARGKGGKLAVAANDDHVIEAVYRAWREVRCEPVLFGPEEEITRIIEELVP
EWKNPQIIDCPPEEAGRLAVEAVSKGECDFLMKGGIKTGDLMKIYLDERYGLRTGKTMAM
VSVMEIPDFPRPLIISDPGMLISPTLEQKVDMIEHCVRVANVMGLET PKVAVVGAIEVVN
PKMPITMEAAILSKMNQRGQIKGCIVDGPFDLNVVSEEAAKKGGIQSPVAGKADILILP
DIEAANILYKALVFLAKAKSASTILGGKVPVVLTSRADSEETKFYSIALSAVFA
>sp|P9WHP1|PTA_MYCTU Phosphate acetyltransferase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=pta PE=1 SV=1
MADSSAIYLAAPESQTGKSTIALGLLHRLTAMVAKVGVFRPITRLSAERDYILELLLAHT
SAGLPYERCVGVTYQQLHADRDDAIAEIVDSYHAMADECDVAVVVGSDYTDVTSPTELSV
NGRIAVNLGAPVLLTVRAKDRTPDQVASVVEVCLAELDTQRAHTAAVVANRCELSAIPAV
TDALRRFTPPSYVPEEPLLSAPTVAELTQAVNGAVVSGDVALREREVMGVLAAGMTADH
VLERLTDGMAVITPGDRSDVVLAVASAHAAEGFPSSLSCIVLNGGFQLHPAIAALVSGRLR
RLPVIAATALGTYDTASAAASARGLVTATSQRKIDTALELMDRHVDVAGLLAQLTIPIPTV
TTPQMFTYRLLQQARSDLMRIVLPEGDDDRILKSAGRLLQRGIVDLTILGDEAKVRLRAA
ELGVDLDGATVIEPCASELHDQFADQYAQLRKAKGITVEHAREIMNDATYFGTMLVHNC
ADGMVSGAAHTTAHTVPRPALEI IKTVPGISTVSSIIFLMCLPDRVLAYGDCAIIPNPTVEQ
LADIAICSAARTAAQFGIEPRVAMLSYSTGDSGKGADVDKVRATELVRAREPQLPVEGPI
QYDAAVEPSVAATKLRDSPVAGRATVLI FPDNLNTGNNTYKAVQRSAGAIAIGPVLQGLRK
PVNDLSRGALVDDIVNTVAITAIQAQGVHE
>sp|Q9I5A5|PTA_PSEAE Phosphate acetyltransferase OS=Pseudomonas
aeruginosa (strain ATCC 15692 / PA01 / 1C / PRS 101 / LMG 12228) GN=pta
PE=1 SV=1
MHTFFIAPTGFVGLTSLISLGLLRALERAGLVGFFKPIAQLHPGDLGPERSSSELVARTH
GLDTPKPLPLAQVERMLGDGQLELLEEIISLYQRAAADKDVVIVEGMVPTRHASYAARV
NFHLAKSLDAEVLVLSAPENETLTELTDRIEIQQLFGGPRDPKVLGVILNKVRGEADAA
NAEDGVADFARRLTEHSPLLRDDFRILGICIPWQDELNAARTRDIADLLSARVINAGDYEQ
RRVQKIVLCARAVPNTVQLLKPGLVVTGDRDDIILAASLAAMNGVPLAGLLCSDFPP
DPRIMELCRGALQGGPLVLSVATGSYDTATNLNRMNKEIPVDDRERAERVTEFVAGHIDF
EWLQRCGTRELRLSPPAFRYQVVQRAQKAGKRIVLPEGSEPRTVQAAAICQARGIARC
VLLAKPEEVQAVAQAQGVIVLPEGLEIIDPDLVRQRYVEPMVELRKGKGLNAPMAEQQLED

SVVLATMMLALDEVDGLVSGAIHTTASTIRPALQLIKTAPGYNLVSSVFFMLLPDQVLVY
GDCAVNPDPSASDLAEI AVQSAASAQAFGIPARVAMISYSTGDSGSGVDVVKVREATRLA
REQRPDLLIDGPLQYDAAAIASVGRQKAPNSPVAGQATVFI FPDLNTGNTTYKAVQRSAD
CVSVGPMLOGLRKPVNDL SRGALVEDIVYTIALTAIQADAQAPA

>sp|P0A6A3|ACKA_ECOLI Acetate kinase OS=Escherichia coli (strain K12)
GN=ackA PE=1 SV=1

MSSKLVLVNLCGSSSLKFALIDAVNGEEYLSGLAECFHLPEARIKWKMDGNKQEAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDAASFA
PLHNPAHLIGIEEALKSFPQLKDKNVAVFDATAFHQTMPEESYLYALPYNLYKEHGIRRYG
AHGTSHFYVTQEAAKMLNKPVEELNIITCHLGNNGSVSAIRNGKCVDTSMGLTPLEGLVM
GTRSGDIDPAIIFHLHDTLGMVDAINKLLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIGAYTALMDGRLDAVVFTGGIGENAAMVRELSLGLKLVLFGEVDHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA

>sp|P38502|ACKA_METTE Acetate kinase OS=Methanosarcina thermophila
GN=ackA PE=1 SV=1

MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTH
KDALEEVVKALTDDEFGVIKDMGEINAVGHRVHVHGGEKFTTSALYDEGVEKAIKDCFELA
PLHNPPNMMGISACAEIMPPTMVI VFDATAFHQTMPPYAYMYALPYDLYEKHGVRKYGFH
GTSHKYVAERAALMLGKPAEETKIITCHLGNSSITAVEGGKSVETSMGFTPLEGLAMGT
RCGSIDPAIVPFLMEKEGLTTREIDTLMNKSGVLGVSGLSNDFRDLDEAASKGNRKAEL
ALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKKN
IRGQEI D I STPAKVRVFIPTNEELAIARETKEIVETEVLKRSSIPV

>sp|P37877|ACKA_BACSU Acetate kinase OS=Bacillus subtilis (strain 168)
GN=ackA PE=1 SV=1

MSKIIAINAGSSSLKQFLFEMPSETVLT KGLVERIGIADSVFTISVNGEKNTEVTDIPDH
AVAVKMLLNKLT EFGI IKDLNEIDGIGHRVVHGGEKFSDSVLLTDETIKEIEDISELAPL
HNPANIVGIKAFKEVLPNPAVAVFDATAFHQTMPEQSYLYSLPYEYKFKGIRKYGFHGT
SHKYVTERAAELLGRPLKDLRLISCHLGN GASIAAVEGGKSIDTSMGFTPLAGVAMGTRS
GNIDPALIPYIMEKTGQTADDEV LNTLNKKSGLLGISGFSDDL RDIVEATKEGNERAETAL
EVFASRIHKYIGSYAARMSGVD A I I FTAGIGENSVEVRERVL RGLFEMGVYWDPALNNVR
GEEAFISYPHSPVKVMIIPTDEEVMIARDVVRLAK

>sp|A0QQK1|ACKA_MYCS2 Acetate kinase OS=Mycobacterium smegmatis (strain
ATCC 700084 / mc(2)155) GN=ackA PE=1 SV=1

MTVLVNSGSSSLKYAVVRPASGEFLADGIIIEIGSGAVPDHDAALRAAFDELAAGLHL
EDLDLKA VGH RMVHGKTFYKPSVVDDELIAKARELSPLAPLHNPPAIK GIEVARKLLPD
LPHIAVFDATAFFHDL PASTY AIDRELAETWHIKRYGFHGT SHEYVSQQA AIFLDRPLE
SLNQIVLHLNGASASAVAGGKAVD TSMGLTPMEGLVMGTRSGDIDPGVIMYLWRTAGMS
VDDIESMLNRRSGVLGLGGASDFRKLRELIESGDEHAKLAYDVYIHR LRKYIGAYMAVLG
RTDVISFTAGVGENVPPVRRDALAGLGLGIEIDDALNSAKSDEPRLISTPDSRVTVLVV
PTNEELAIARACVGVV

>sp|P63411|ACKA_SALTY Acetate kinase OS=Salmonella typhimurium (strain
LT2 / SGSC1412 / ATCC 700720) GN=ackA PE=1 SV=1

MSSKLVLVNLCGSSSLKFALIDAVNGDEYLSGLAECFHLPEARIKWKMDGSKQEAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDSASFA
PLHNPAHLIGIAEALKSFPQLKDKNVAVFDATAFHQTMPEESYLYALPYSLYKEHGVRRYG
AHGTSHFYVTQEAAKMLNKPVEELNIITCHLGNNGSVSAIRNGKCVDTSMGLTPLEGLVM
GTRSGDIDPAIIFHLHDTLGMVSDQINKMLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIGSYTALMDGRLDAVVFTGGIGENAAMVRELSLGLKLVLFGEVDHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA

>sp|Q9WYB1|ACKA_THEMA Acetate kinase OS=Thermotoga maritima (strain ATCC
43589 / MSB8 / DSM 3109 / JCM 10099) GN=ackA PE=1 SV=1

MRVLVINSGSSSIKYQLIEME GEEKVLCKGIAERIGIEGSRLVHRV GDEKHVIERELPDHE
EALKLI LNTLVDEKLGVIKDLKEIDAVGHRVHVHGGERFKESVLVDEEVLKAIEEVSPLAP
LHN PANLMGIKAAMKLLPGV PNVAVFDATAFHQTIPQKAYLYAIPYEYKIRRYGFHGT
TSHRYVSKRAAEILGKKLEELKIITCHIGNGASVA AVKYGKCVDTSMGFTPLEGLVMGTR
SGDLDP A I PFFIMEKEGISPQEMYDILNKKSGVYGLSKGFSSDMRDIEEAALKGDEWCKL
VLEIYDYRIAKYIGAYAAAMNGVD A I VFTAGVGENSPITREDVCSYLEFLGVKLDKQKNE
ETIRGKEGIISTPDSRVKVLVPTNEELMIARDTKEIVEKIGR

>sp|A0QLU8|ACKA_MYCA1 Acetate kinase OS=Mycobacterium avium (strain 104)
GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPESGVAASTGIVERIGEESSVPPDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALLGI
EVARRLLPGIAHVAVFDTGFFHDLPPAAATYAIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSVVS
YLCHTAGMGVDDVESMLNHRSGVVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHTDVISFTAGIGENDAAVRRDAVSGMEELGIVLDERRNLPGAKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG

>sp|B2HPZ3|ACKA_MYCMM Acetate kinase OS=Mycobacterium marinum (strain
ATCC BAA-535 / M) GN=ackA PE=1 SV=1
MSASRPNRVVLVNSGSSSLKFQLVEPDSGMSRATGNIERIGEESSVPPDHDAALRRVFE
ILAEDDIDLQSCGLVAVGHRVVHGGKDFYEPTLLNDAVIGKLELSPLAPLHNPPAVLCI
RVARALLPDVPHIAVFDTAFFHQLPPAAATYAIDRELADVWKIRRYGFHGTSHRYVVSQQA
AEFLGKPIGDLNQIVLHLGNGASASAVAGRPVETSMGLTPLEGLVMGTRSGDLDPGVIG
YLWRTAKLGVDEIESMLNHRSGMLGLAGERDFRRLRAMIDDGDPAAELAYDVFIHRLRKY
VGAYLAVLGHTDVVSFTAGIGEHDAVRRDLAGMAELGISLDERRNACPSGGARRISAD
DSPVTVLVIPTNEELAIARHCCSVLVAV

>sp|Q73T33|ACKA_MYCPA Acetate kinase OS=Mycobacterium paratuberculosis
(strain ATCC BAA-968 / K-10) GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPEFGVAASTGIVERIGEESSVPPDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALQGI
EVARRLLPDIAHVAVFDTGFFHDLPPAAATYAIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSIVS
YLCHTAGMGVDDVESMLNHRSGVVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHTDVISFTAGIGENDAAVRRDAVSGMEELGIVLDERRNLAGGKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG

>sp|P75245|ACKA_MYCPN Acetate kinase OS=Mycoplasma pneumoniae (strain
ATCC 29342 / M129) GN=ackA PE=1 SV=1
MNDNKILVNVNAGSSSIKFQLFDYHKKVLAKALCERIFVDGFFKLEFNEQKVEEKVAFPDH
HAAVTHFLNLTLLKHKHIQELSDIILVGHRRVQGANFYKDSVIVDAEALAKIKEFIKLAPL
HNKPEADVIEIFFKEVPSAKNVAVFDTTFHTTIPQENYLYAVPRSWEQKHLVRRYGFHGT
SYKFINNYLEKHLNKQNLNLIVCHLNGASVCAIKNGKSFNTSMGFTPLEGLIMGTRSGD
LDPAIIGYVAEQENMSASDVVNALNKKSGMLALTGASDMRDVFAKPQENAVAIKMYVNRV
ADYIAKYNQLEGNIDGLVFTGGIGENASDCVELFINAVKSLGFATDLKLFVKYGDSCVV
STPQSKYKIYRVRTNEELMIVEDSIRLTQK

>sp|P9WQH1|ACKA_MYCTU Acetate kinase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=ackA PE=1 SV=1
MSSTVLVINSGSSSLKFQLVEPVAGMSRAAGIVERIGERSPPVADHAQALHRAFKMLAED
GIDLQTCGLVAVGHRVVHGGTEFHQPTLLDDTVIGKLEELSALAPLHNPPAVLGIVARR
LLANVAHVAVFDTAFFHDLPPAAATYAIDRDVADRWHIRRYGFHGTSHQYVSERAAFLG
RPLDGLNQIVLHLGNGASASAIARGRPVETSMGLTPLEGLVMGTRSGDLDPGVISYLWRT
ARMGVEDIESMLNHRSGMLGLAGERDFRRLRLVIETGDRSAQLAYEVFIHRLRKYLGAYL
AVLGHTDVVSFTAGIGENDAAVRRDALAGLQGLGIALDQDRNLGPGHGARRISSDDSPIA
VLVPTNEELAIARDCLRVLGGRRRA

>sp|Q99TF2|ACKA_STAAN Acetate kinase OS=Staphylococcus aureus (strain
N315) GN=ackA PE=1 SV=1
MSKLILAINAGSSSLKFQLIRMPEEELVTKGLIERIGLKDSIFTIEVNGEKVKTQDIKD
HVEAVDIMLDAFKAHNIINDINDIDGTGHRVVHGGKFPESVAITDEVEKEIEELSELAP
LHNPANLMGIRAFRKLNPNI PHVAIFDTAFHQTMPEKAYLYSLPYHYYKDYGIRKYGFHG
TSHKFVSQRAAEMLDKPIEDLRIISCHINGASIAAIDGGKSIDTSMGFTPLAGVTMGT
SGNIDPALIPFIMEKTGKTAEQVLEILNKESGLLGLSGTSSDLRDLSEEAESEKARSQMA
LDVVFASKIHKYIGSYAARMHGVDVIVFTAGIGENSVEIRAKVLEGLEFMGVYWDPKKNEN
LLRGKEGFINYPHSPVKVVVVIPTDEESMIARDVMTFGGLK

2. Acetate formation pathway II.

>sp|P08559|ODPA_HUMAN Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3
MRKMLAAVSRVLSGASQKPASRVLVASRNFANDATFEIKKCDLHRLEEGPPVTTVLTRED
GLKYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFTRGLSVREILAEALTGRKGGCAKGGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPCIFICENNRYGMGTSVERAAAST
DYYKRGDFIPGLRVDGMDILCVREATRFAAAYCRSGKGPILMELQTYRYHGHSMSPDGV
YRTREEIQEVRKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVRGANQWIKFKSVS

>sp|P35486|ODPA_MOUSE Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=PDHA1 PE=1 SV=1
MRKMLAAVSRVLAGSAQKPASRVLVASRNFANDATFEIKKCDLHRLEEGPPVTTVLTRED
GLKYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFTRGLPVRAILAEALTGRRGCAKGGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPCIFICENNRYGMGTSVERAAAST
DYYKRGDFIPGLRVDGMDILCVREATKFAAAYCRSGKGPILMELQTYRYHGHSMSPDGV
YRTREEIQEVRKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVRGANQWIKFKSVS

>sp|P11177|ODPB_HUMAN Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3
MAAVSGLVRRPLREVSGLLKRFRHWTAPAALQVTVRDAINQGMDEELERDEKVFLLGEEV
AQYDGAYKVSRLWKKYGDKRIIDTPISEMFGAGIAVGAAMAGLRPICEFMTFNFMSQAI
DQVINSAAKTYMSSGGLQVPVIVFRGPNASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVLENELMYGVPFEPPEAQSKDFLIPIGKAKIERQGTHTTVV
SHSRPVGHCLEAAAVLSKEGVECEVINMRTIRPMDMETIEASVMKTNHLVTVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVMPYAKILEDNSIPQVKDIIFAIKKTLNI

>sp|P0AFG8|ODP1_ECOLI Pyruvate dehydrogenase E1 component OS=Escherichia coli (strain K12) GN=aceE PE=1 SV=2
MSERFPNDVDPIETRDWLQAIESVIREEGVERAQYLIDQLLAEARKGGVNVAAGTGISNY
INTIPVEEQPEYPGNLELERRIRSAIRWNAIMTVLRASKKDLELGGHMASFQSSATIYDV
CFNHFFRARNEQDGGDLVYFQGHISPGVYARAFLEGRLTQEQLDNFRQEVHGNGLSSYPH
PKLMPEFWQFPVSMGLGPIGAIYQAKFLKYLEHRGLKDTSKQTVYAFLGDGEMDEPESK
GAIITATREKLDNLVFINCNLQRLDGPVTGNGKINELEGI FEGAGWNVIKVMWGSRW
ELLRKDTSGKLIQLMNETVDGDYQTFKSKDGAYVREHFFGKYPETAALVADWTDEQI
NRGGHDPKKIYAAFKAQETK GKATVILAHTIKGYGMGDAEAGKNIAHQVKKMMDGVRH
IRDRFNVPVSDADIEKLPYITFPEGSEEHTYLHAQRQKLHGYP SRQPNFTEKLELPSLQ
DFGALLEEQSKEISTTIAFVRALNVMLKNKSIKDRLVPIIADEARTFGMEGLFRQIGIYS
PNGQQYTPQDREQVAYYKEDEKQILQEGINELGAGCSWLAATSYSTNNLPMIPFYIYY
SMFGFQRIGDLCWAAGDQQARGFLIGGTSGR TTLNGEGLQHEDGHSHIQSLTIPNCISYD
PAYAYEVAVIMHDGLERMYGEKQENVYIITLNNYHMPAMPEGAEEGIRKGIYKLETI
EGSKGKVQLLGSILRHVREAAEILAKDYGVGSDVYSVTSFTELARDGQDCERWNMLHP
LETPRVPYIAQVMNDAPAVASTDYMKLFAEQVRTYVPADDYRVLGTDGFGRSDSRENLRH
HFEVDASYVVVAALGELAKRGEIDKKVVADAIKFNIDADKVNPRLA

>sp|P29803|ODPAT_HUMAN Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial OS=Homo sapiens GN=PDHA2 PE=1 SV=1
MLAAFISRVLRRVAQKSARRVLVASRNSSNDATFEIKKCDLYLLEEGPPVTTVLTAEGL
KYRMMMLTVRRMELKADQLYKQKFIIRGFCHLCDGQEACCVGLEAGINPSDHVITSYRAHG
VCYTRGLSVRSILAELTGRRGCAKGGGSMHMYTKNFYGGNGIVGAQGPLGAGIALACK
YKGNDEICLTLYGDGAANQGQIAEAFNMAALWKLPCVFCENNLYGMGTSTERRAAASPDY
YKRGNFIPGLKVDGMDVLCVREATKFAAAYCRSGKGPILMELQTYRYHGHSMSPDGVSYR
TREEIQEVRKSDPIIILQDRMVNSKLATVEELKEIGAEVRKEIDDAQFATTDPEPHLE
ELGHHIYSSDSSFEVRGANPWIKFKSVS

>sp|P16387|ODPA_YEAST Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PDA1 PE=1 SV=2
MLAASFKRQPSQLVRGLGAVLRTPTRIGHVRTMATLKTDDKKAPEDIEGSDTVQIPELPS
SFESYMLEPPDLSYETSKATLLQMYKDMVIIRMEMACDALYKAKKIRGFCHLSVGQEAI
AVGIENAITKLSIITSYRCHGFTFMRGASVKAVLAELMGRRAGVSYGKGGSMHLYAPGF

YGGNGIVGAQVPLGAGLAFAHQYKNEDACSFTLYGDGASNQGQVFESFNMAKLWNLPVVF
CCENNKYGMGTAASRSSAMTEYFKRGQYIPLKVNMDILAVYQASKFAKDWCLSGKGPL
VLEYETYRYGGHSMSPDPTTYRTRDEIQHMRSKNDPIAGLKMHLIDLGIATEAEVKAYDK
SARKYVDEQVELADAAPPPEAKLSILFEDVYVKGTTETPTLRGRIPEDTWFKKQGFASRD
>sp|Q8H1Y0|ODPA2_ARATH Pyruvate dehydrogenase E1 component subunit alpha-
2, mitochondrial OS=Arabidopsis thaliana GN=IAR4 PE=1 SV=2
MALSRSSRSNTFLKPAITALPSSIRRHVSTDSSPITITAVPFTSHLCESPSRSVETSS
EEILAFFRDMARMRRMEIAADSLYKAKLIRGFCHLYDQGEALAVGMEAAITKKDAIITSY
RDHCTFIGRGGKLVDAFSELMGRKTGCSHGKGGSMHFYKKDASFYGGHGIVGAQIPLGCG
LAFQAQYKNDKDEAVTFALYGDGAANQGQLFEALNISALWDLPAILVCENNHYGMGTATWRS
AKSPAYFKRGDYVPLKVDGMDALAVKQACKFAKEHALKNGPIILEMDTYRYHGHSMSPD
GSTYRTRDEISGVRQVRDPIERVKLLTHDIATEKELKDMKEIRKEVDDAVAQAKESP
IPDASELFTNMYVKDCGVESFGADRKELKVTLP
>sp|P35487|ODPAT_MOUSE Pyruvate dehydrogenase E1 component subunit alpha,
testis-specific form, mitochondrial OS=Mus musculus GN=Pdha2 PE=1 SV=1
MRKMLTAVLSHVFSGMVQKPALRGLLSSLKFSNDATCDIKKCDLYRLEEGPPTSTVLTRA
EALKYYRTMQVIRRMELKADQLYKQKFIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
AHGFCYTRGLSVKSILAEELTGRKGGCAKGGKGGSMHMYGKNFYGGNGIVGAQVPLGAGVAF
ACKYLKNGQVCLALYGDGAANQGQVFEAYNMSALWKLPCVIFCENNLYGMGTSNERSAAS
TDYHKKGFIIPLRVNMDILCVREATKFAADHCRSGKGPVIMELQTYRYHGHSMSPDGI
SYRSREEVHNVRKSDPIMLLRERIISNNLSNIEELKEIDADVKEVEDAAQFATTDPEP
AVEDIANLYHQDPPFEVIRGAGHKLKYSHS
>sp|P26284|ODPA_RAT Pyruvate dehydrogenase E1 component subunit alpha,
somatic form, mitochondrial OS=Rattus norvegicus GN=Pdha1 PE=1 SV=2
MRKMLAAVSRVLAGAAQKSPASRVLVASRNFANDATFEIKKCDLHRLEEGPPVTTVLTRED
GLKYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRA
HGFTFNRGHAVRAILAEELTGRKGGCAKGGKGGSMHMYAKNFYGGNGIVGAQVPLGAGIALA
CKYNGKDEVCLTLYGDGAANQGQIFEAYNMAALWKLPCIFCENNRYGMGTSVERAAAST
DYKRGDFIPGLRVDGMDILCVREATKFAAAYCRSGKGPVIMELQTYRYHGHSMSPDGV
YRTREEIQEVRSKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPP
LEELGYHIYSSDPPFEVIRGANQWIKFKSVS
>sp|Q38799|ODPB1_ARATH Pyruvate dehydrogenase E1 component subunit beta-
1, mitochondrial OS=Arabidopsis thaliana GN=PDH2 PE=1 SV=2
MLGILRQRAIDGASTLRTRFALVSARSYAAGAKEMTVRDALNSAIDEEMSADPKVFMG
EEVGQYQAYKITKGLLEKYGPVRYDTPITEAGFTGIGVGAAYAGLKPVVEFMTFNFMS
QAIDHIINSAAKSNYSAGQINVPVFRGPNAAAGVGAQHSQCYAAWYASVPGLKVLAP
YSAEDARGLLKAIRDPDPVVFLENELLYGESFPISEEALDSSFCLPIGKAKIEREGKDV
TIVTFSKMVGFKALAAEKLAEEGISAIEVINLRSIRPLDRATINASVRKTSRLVTVVEEGFP
QHGVC AEICASVVEESFSYLDAPVERIAGADVMPYAAANLERLALPQIEDIVRASKRACY
RSK
>sp|Q9D051|ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Mus musculus GN=Pdha3 PE=1 SV=1
MAVVAGLVGRPLRQASGLLKRFRHRSAPAAVQLTVREAINQGMDEELERDEKVFLLGEEV
AQYDQAYKVSRLWKKYGDKRIIDTPISEMFGAGIAGVGAAMAGLRPICEFMTFNFMSQAI
DQVINSAAKTYMSAGLQVPIVFRGPNASAGVAAQHSQCYAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNNPVVMLENELMYGVAFELPAEAQSKDFLIPIGKAKIERQGTHTV
AHSRPVGHCCLEAAAVLSKEGIECEVINLRITRPMIEAIEASVMKTNHLVTVVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVMPYAKVLEDNSVPQVKDIIFAVKKTLNI
>sp|P32473|ODPB_YEAST Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
GN=PDB1 PE=1 SV=2
MFSRLPTSLARNVARRAPTSFVRPSAAAAALRFSSTKTMTVREALNSAMAEELDRDDDDV
LIGEEVAQYNGAYKVSGLLDRFGERRVVDTPITEYGFGLAVGAALKGLKPIVEFMSFN
FSMQAIDHVVNSAAKTHYMSGGTQKQCMVFRGPNAAAGVGAQHSQDFSPWYGSIPGLKV
LVPYSAEDARGLLKAIRDPNPVVFLENELLYGESFPISEEALSPEFTLPYKAKIEREGT
DISIVTYTRNVQFSLEAAEILQKKYGVSAIEVINLRSIRPLDTEAIIKTVKKTNHLITVES
TFPSFGVGAIEVAQVMESEAFDYLDAPVIRVTVGADVPTPYAKELEDFAFPDTPTIVKAVK
EVLISIE

>sp|Q8NNF6|ODP1_CORGL Pyruvate dehydrogenase E1 component
OS=Corynebacterium glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 /
LMG 3730 / NCIMB 10025) GN=aceE PE=1 SV=1
MADQAKLGGKPSDDSNFAMIRDGVASYLNDSPEETNEWMDSLDGLLQESSPERARYLML
RLLERASAKRVSLPMTSTDYVNTIPTSMPEFPFGDEEMEKRYRRWIRWNAAIMVHRAQR
PGIGVGGHISTYAGAAPLYEVGFNFHFRGKDHPPGGDQIFFQGHASPGMYARAFMEGRLS
EDDLDFRQEVRSREQGGIPSYPHPHGMKDFWEFPTVSMGLGPMDAIYQARFNRYLENRGI
KDTSDQHVAFLGDGEMDEPESRGLIQQAALNNLDNLTFVNCNLQRLDGPVVRGNTKIIQ
ELESFVRGAGWSVIKVVWGREWDELLEKQDQALVEIMNNTSDGDYQTFKANDGAYVREH
FFGRDPRTAKLVENMTDEEIKWKLPRGGHDYRKVYAAAYKRALETKDRPTVILAHTIKGYGL
GHNFEGRNATHQMKKLTLDLKLFRDKQGIPTDEQLEKDPYLPYYHPGEDAPEIKYMK
ERRAALGGYLPERRNEYDPIQVPLDKLRSVRKGSQKQIATTMATVRTFKELMRDKGLA
DRLVPIIPDEARTFGLDSWFPTLKIYNPHGQNYVPVDHDLMLSYREAPQILHEGINEA
GSVASFIAAGTSYATHGKAMIPLYIFYSMFGFQRTGDSIWAADQMARGFLLGATAGRTT
LTGEGQLQHMDDHSPVLASTNEGVEYDPSFAYEIAHLVHRGIDRMYGPGKGEDVIYYITI
YNEPTPQPAEPEGLDVEGLHKGIIYLSRGEETGHEANILASGVMQWALKAASILEADYG
VRANIYSATSWVNLARDGAARNKAQLRNPGADAGEAFVTTQLKQTSQPYVAVSDFSTDLP
NQIREWVPGDYTVLGDGFGFSDFTRPAARRFFNIDAESIVVAVLNSLAREGKIDVSVAAQ
AAEKFKLDDPTS SVSDPNAPEE

>sp|P0AFG9|ODP1_EC057 Pyruvate dehydrogenase E1 component OS=Escherichia
coli O157:H7 GN=aceE PE=1 SV=2
MSERFPNDVDPIETRDWLQAIESVIREEGVERAQYLIDQLLAEARKGGVNVAAGTGISNY
INTIPVEEQPEYPGNLELERRIRSAIRWNAIMTVLRASKKDLELGGHMASFQSSATIYDV
CFNHFFRARNEDQDGGDLVYFQGHISPGVYARAFLEGRLTQEQLDNFRQEVHGNGLSSYPH
PKLMPEFWQFPTVSMGLGPIGAIYQAKFLKYLEHRGLKDTSKQTVYAFVLDGEMDEPESK
GAIITATREKLDNLVFINCNLQRLDGPVTGNGKIINELEGI FEGAGWNVIKVMWGSRW
ELLRKDTSGKLIQLMNETVDGDYQTFKSKDGAYVREHFFGKYPETAALVADWTDEQIWA
NRGGHDPKKIYAAFKAQETK GKATVILAHTIKGYGMGDAEAGKNIAHQVKKMMDGVRH
IRDRFNVPVSDADIEKLPYITFPEGSEEHTYLHAQRQKLHGYP SRQPNFTEKLELPSLQ
DFGALLEEQSKEISTTIAFVRALNVMKNSIKDRLVPIIADEARTFGMEGLFRQIGIYS
PNGQQYTPQDREQVAYYKEDEKQILQEGINELGAGCSWLAATSYSTNNLPMIPFYIYY
SMFGFQRIGDLCAAGDQARGFLIGGTSGRTTLNQEGQLHEDGHSHIQSLTIPNCISYD
PAYAYEVAVIMHDGLERMYGEKQENVYIITLNNYHMPAMPEGAEEGIRKGIYKLETI
EGSKGKVQLLGSISLRHVREAAEILAKDYGVGSDVYSVTSFTELARDGQDCERWNMLHP
LETPRVPYIAQVMNDAPAVASTDYMKLFAEQVRTYVPADDYRVLTGDFGFRSDSRENLRH
HFEVDASYVVVAALGELAKRGEIDKKVVADAIKFNIDADKVNPRLA

>sp|P9WIS9|ODP1_MYCTU Pyruvate dehydrogenase E1 component
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aceE PE=1
SV=2
MTTDFARHDLAQNNSASEPDRVRVIREGVASYLPDIDPEETSEWLESFDTLLQRCGPSR
ARYLMLRLLERAGEQRVAIPALTSTDYVNTIPTLEPWFPGDEDVERRYRAWIRWNAAIM
VHRAQRPGVGVGGHISTYASSAALYEVGFNFHFRGKSHPPGGDQVFIQGHASPGIYARAF
LEGRLTAEQLDGFQRQEHSHVGGGLPSYPHPRMLMPDFWEFPTVSMGLGPLNAIYQARFNHY
LHDRGIKDTSDQHVVCFVLDGEMDEPESRGLAHVGALEGLDNLTFVINCNLQRLDGPVVRG
NGKIQELESFVRGAGWNVIKVVWGREWDALLHADRDGALVNLMTTPDGDYQTYKANDG
GYVRDHFGRDPRTKALVENMSDQDIWNLKRGGHDYRKVYAAAYRAAVDHKGQPTVILAKT
IKGYALGKHFEGRNATHQMKKLTLEDLKEFRDTQRI PVSDAQLEENPYLPYYHPGLNAP
EIRYMLDRRALGGFVPERRTKSKALTLPGRDIYAPLKKGSGHQEVATTMATVRTFKEVL
RDKQIGPRIVPIIPDEARTFGMDSWFP SLKIYNRNGQLYTAVDADLMLAYKESEVGQILH
EGINEAGSVGSFIAAGTSYATHNEPMIPIYIFYSMFGFQRTGDSFWAADQMARGFVLGA
TAGRTTTLTGEGLQHADGHSLLLAATNPVAVYDPAFAYEIAIYVESGLARMCGENPIF
FYITVYNEPYVQPEPENFDPEGVLRGIYRYHAATEQRTNKAQILASGVAMPAALRAAQM
LAAEWDVAADVSVTSWGELNRDGVAIETEKLRHPDRPAGVPYVTRALENARGPVIASD
WMRAVPEQIRPWVPGTYLTLGTDGFGFSDFTRPAARRYFNTDAESQVVAVLEALAGDGEID
PSVPVAAAARQYRIDDVAAAPEQTTPDGPGA

>sp|Q06437|ODPAT_RAT Pyruvate dehydrogenase E1 component subunit alpha,
testis-specific form, mitochondrial OS=Rattus norvegicus GN=Pdha2 PE=1
SV=1

MRKMLATVLSQVFSGMVQKPALRGLLSSSLKFSNDATCDIKKCDLYLLEQGPPTSTVLTRE
EALKYYRNMQVIRRMELKADQLYKQKFIRGFCHLCDGQEACNVGLEAGINPTDHIITSYR
AHGLCYTRGLSVKSI LAELTGRKGGCAKGGKSMHMYAKNFYGGNGIVGAQVPLGAGVAL
ACKYLKNGQICLALYGDGAANQGOVFEAYNMSALWKLPCVFCENNRGMGTAIERSAAS
TDYHKKGFVPIGLRVNGMDILSVREATKFAADHCRSGKGPVIMELQTYRYHGHSMSPGI
SYRTREEVQNVRSKSDPIMLLRERMISNNLSSVEELKEIDADVKEVEEAAQFATTDPEP
PLEDLANYLYHQNPPEFVRGAHKWLKFKSVS

>sp|P21881|ODPA_BACSU Pyruvate dehydrogenase E1 component subunit alpha
OS=Bacillus subtilis (strain 168) GN=pdhA PE=1 SV=3

MAAKTKKAIIVDSKKQFDAIKKQFETQILNEKGEVVNEAAMPDLTDDQLKELMRRMVFTR
VLDQRSISLNRQGRGLGFYAPTAGQEASQIATHFALEKEDFVLPGYRDVPQLIWHGLPLYQ
AFLFSRGHFRGNQMPDDVNALSPQIIIGAQYIQTAGVALGLKRGKKAVAITYTGDGGAS
QGDYFEGINFAGAYKAPAI FVVQNNRYAISTPVEKQSAAEITIAQKAVAAGIVGVQVDGMD
PLAVYAATAEARERAINGEGPTLIETLTFRYGPHTMAGDDPTKYRTKEIENEWEQKDPLV
RFRAFLENKGLWSEEEEEAKVIEDAKEEIKQAIIKKAADAEPKQKVTDLMKIMYEKMPHNLEE
QFEIYTQKESK

>sp|P21874|ODPB_GEOSE Pyruvate dehydrogenase E1 component subunit beta
OS=Geobacillus stearothermophilus GN=pdhB PE=1 SV=2

MAQMTMVQAITDALRIELKNDPNVLIFGEDVGVNNGVFRATEGLQAEFGEDRVFDTPLAE
SGIGGLAIGLALQGFRPVPEIQFFGFVYEVMSICGQMARIRYRTGGRYHMPITIRSPFG
GGVHTPELHSDSLEGLVAQQPGLKVVIPSTPYDAKGLLISAIRDNDPVIFLEHLKLYRSF
RQEVPEGEYTIPIGKADIKREGKDITIIAYGAMVHESLKAEELEKEGISAEEVDLRTVQ
PLDIETIIGSVEKTGRAIVVQEAQRQAGIAANVVAEINERAILSLEAPVLRVAAPDTVYP
FAQAESVWLPNFKDVIETAKKVMNF

>sp|P49432|ODPB_RAT Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Rattus norvegicus GN=Pdhb PE=1 SV=2

MAAVAGLVGRPLRQASGLLKRFRHSAPAAVQLTVREAINQGMDEELERDEKVFLLGEEV
AQYDYGAYKVSRLWKKYGDKRIIDTPISEMFGAGIAGVGAAMAGLRPICEFMTFNFSMQAI
DQVINSAAKTYMSAGLQFPVPIVFRGPNASAGVAAQHSQCFAAWYGHCPGLKVVSPWNS
EDAKGLIKSAIRDNDPNVMLENELMYGVAFELPTEAQSKDFLIPIGKAKIERQGTHITVV
AHSRPVGHCCLEAAAVLSKEGIECEVINLRITRPMIDIEAIEASVMKTNHLVTVEGGWPQFG
VGAEICARIMEGPAFNFLDAPAVRVTGADVMPYAKILEDNSIPQVKDIIFAIKKTLNI

>sp|A0R0B0|ODP1_MYCS2 Pyruvate dehydrogenase E1 component
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=aceE PE=1
SV=1

MTTEFVRQDLAQNSSSTAAEPDRVRVIREGVASYLPDIDTEETAEWLESFDELLERSGPAR
ARYLMLRLLERAGEQ RVAIPALTSTDYVNTIPTLEPWFPGDEDVERRYRAWIRWNAAIM
VHRAQRPGVGVGGHISTYASSATLYEVGFNHFRRGKSHPGGGDHVFIQGHASPGIYARAF
LEGRLTDDQLDGFQRQEHSHSGGGLPSYPHPRMLPDEFWEFPTVSMGLGPMNAIYQARFNHY
LHDRGIKDTSDQHVVAFGLDGMDEPESRGLIQVAANEALDNLTFVINCNLQRLDGPVRG
NGKIQELESFFRAGAGWNVIKVVWGREWDVLLHADRDGALVNLNMPDGDYQTYKANDG
AYVRDHFGRDPRTKALVADMSDQEIWNLKRGGHDYRKVYAAARAAMEHKGQPTVILAKT
IKGYTLGQHFEGRNATHQMKKLALEDLKNFRDVTVPVSDAQLEEDPYLPPYYPGPEAP
EIRYLLERRRALGGFVPSRRTKSKPLALPGSDTYKALKKSGSQAVATTMATVTRTFKELL
RDKNIGPRIVPIIPDEARTFGMDSWFP SLKIYNRNGQLYTSVDSELMLAYKESEVQIILH
EGINEAGSTSSFTAVGTSYSTHDEPMIPIYIFYSMFGFQRTGDGLWAAADQMARGFVLGA
TAGRTTLTGEGLQHADGHSLLLASTNPAAVTYDPAFAYEIAHIESGLQRMYGEDPENVF
FYLTIYNEPYQQPAEPENLDVEALLKGLYLRYPAPEKRAKSAQILASGVAMPEALRAADL
LASDWDVAADVSVTSWGELNREGVAIEKHRLRHPDEPAGTPHVTSALADAAGPVIAVSD
WMRAVPEQIRPVWPGTYVTLGTDGFGFS DTRPAARRYFN TDAESVVVAVLQGLARDGEID
ASVAAQAAEQYRIDDDVSAAGVSYADTGSA

>sp|Q4MTG0|ODPA_BACCE Pyruvate dehydrogenase E1 component subunit alpha
OS=Bacillus cereus GN=pdhA PE=1 SV=3

MGTKTKKTLFNVDEQMKAI AQAQFETLQILNEKGEVVNEAAMP ELSDDQLKELMRRMVYTR
VLDQRSISLNRQGRGLGFYAPTAGQEASQLASHFALEAEDFILPGYRDVPQLVWHGLPLYQ
AFLFSRGHFMGNQMPENVNALAPQIIIGAQIQTAGVALGMKLRGKKSVAITYTGDGGAS
QGDYFEGMNFAGAFKAPAI FVVQNNRYAISTPVEKQSAAKTVAQKAVAAGIYGIQVDGMD
PLAVYAATAFARERAVNGEGPTLIETLTFRYGPHTMAGDDPTRYRTKDIENEWEQKDPIV

RFRAFLENKGLWSQEVEEKVIEEAKEDIKQAIKADQAPKQKVTDLMEIMYEKMPYNLAE
QYEIYKEKESK

>sp|P26267|ODPA_ASCSU Pyruvate dehydrogenase E1 component subunit alpha
type I, mitochondrial OS=Ascaris suum PE=1 SV=1

MIFVVFANIFKVPVSPVMAISVRLASTEATFQTKPFKHLKLDSGPDINVHVTKEDAVHY
YTQMLTIRRMESAAGNLYKEKKVRFCHLYSGQEACAVGTKAAMDAGDAAVTAYRCHGWT
YLSGSSVAKVLCELTGRITGNVYKGGSMHMYGENFYGGNGIVGAQQPLGTGIAFAMKYR
KEKNVCITMFGDGTNQGQLFESMNAKLWDLPLVLYVCENNGYGMGTAAARSSASTDYIT
RGDYVPGIIVWDGMDVLAVRQAVRWAKEWCNAGKGPLMIEMATYRYSGHSMSPGTSYRTR
EEVQEVKTRDPITGFKDKIVTAGLVTEDEIKEIDKQVRKEIDA AVKQAHTDKESPVELM
LTDIYYNTPAQYVRCTTDEVLQKYLTSEEAVKALAK

>sp|P21873|ODPA_GEOSE Pyruvate dehydrogenase E1 component subunit alpha
OS=Geobacillus stearothermophilus GN=pdhA PE=1 SV=2

MGVKTFFQFPFAEQLEKVAEQFPTFQILNEEGEVVNEEAMPELSDEQLKELMRRMVYTRIL
DQRSISLNRQRLGFYAPTAGQEASQIASHFALEKEDFILPGYRDVPQIIWHGLPLYQAF
LFSRHFHGNQIPEGVNVLPPQIIIGAQYIQAAGVALGLKMRGKKAVAITYTGDGGTSQG
DFYEGINFAGAFKAPAI FVVQNNRFAISTPVEKQTVAKTLAQKAVAAGIPGIQVDGMDPL
AVYAAVKAARERAINGEGPTLIETLCFRYGPHTMSGDDPTRYRSKELENEWAKKDPLVRF
RKFLKGLWSEEEENNVI EQAKEEIKEAIKKADETPKQKVTDLISIMFEELPFNLKEQY
EIYKEKESK

>sp|Q54C70|ODPA_DICDI Pyruvate dehydrogenase E1 component subunit alpha,
mitochondrial OS=Dictyostelium discoideum GN=pdhA PE=1 SV=1

MLSNFLKVNKALGHIRTFASKSGEIKHNFKKADTYLCDGSPSDSTVTNKDELISFFTEMS
RFRRLTVCDGLYKKKLIRGFCHLYTGQEA VCAGLESATKDDHIIITAYRDHTYMLSRGA
TPEEIFAELLMKETGCSKGGKGGSMHMFTKNFYGGNGIVGAQCPLGAGIAFAQKYNKTGNV
CLAMYGDGAANQGQLFEAFNMA SLWKLPVIFICENNKYGMGTSQKRSTAGHDFYTRGHYV
AGLKVDGMDVFAVKEAGKYAAEWC RAGNGPIIILEMDTYRYVGHSMSPGITYRTREEVNH
VRQTRDPIENIRQIILDNKIATEDQLAAIEETVRDEMEKASEKAIAAPLPQARELFTNVY
LQEVVVRGVEFVNSFKP

>sp|P29804|ODPA_PIG Pyruvate dehydrogenase E1 component subunit alpha,
somatic form, mitochondrial (Fragment) OS=Sus scrofa GN=PDHA1 PE=1 SV=1

GKMLAAVSRVLSGVAQKPASRVLVASRTFANDATFEIKKCDLHRLEEGPPVTTVLTREDD
LKYYRMMQTVRRMELKADQLYKQKIIRGFCHLCDGQEACCVGLEAGINPTDHLITAYRAH
GFTFTRGLSVREILAE LTGRRGCGKGGKGGSMHMYAKNFYGGNGIVGAQVPLGAGIALAC
KYNGKDEVCLTLYGDGAANQGQIF EAYNMAALWKLPCV FICENNR YGMGTSVERAAA STD
YYKRGDFIPGLRVDGMDILCVREATRFAAAYCRSGKGPILMELQTYRYHGHSMSPGVS Y
RTREEIQEVRSKSDPIMLLKDRMVNSNLASVEELKEIDVEVRKEIEDAAQFATADPEPPL
EELGYHIYCNPPFEVVRGANQWIKFKSIS

>sp|Q10489|ODPA_SCHPO Pyruvate dehydrogenase E1 component subunit alpha,
mitochondrial OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843)
GN=pdal PE=1 SV=1

MFRTCTKIGTVPKVLVNQKGLIDGLRRVTTDATTSRANPAHVPEEHDKPFVVKLDDSVFE
GYKIDVPSTEIEVTKGELLGLYEKMVTIRRELELACDALYKAKKIRGFCHLSIGQEAVAAG
IEGAI TLDDSIITSYRCHGFAYTRGLSIRSIIIGELMGRQCGASKGKGGSMHIFAKNFYGG
NGIVGAQIPLGAGIGFAQKYLEKPTTTFFALYGDGASNQQAFAEFNMAKLWGLPVI FACE
NNKYGMGTS AERSSAMTEFYKRGQYIPGLLVNGMDVLAVLQASKFAKKYTVENSQPLLME
FVTYRYGGHSMSPGTTYSREEVQKVRAARDPIEGLKKHIMEWGVANANELKNIKRI R
GMVDEEVRIAEE SPFPDPIEESLFS DVYVAGTEPAYARGRNSLEYHQYK

>sp|P52903|ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha,
mitochondrial OS=Solanum tuberosum PE=1 SV=1

MALSTSRRAINHMKPLSAAVCATRRLLSSDSTATITVETSLPFTSHNIDPPSRSVETSPKE
LMTFFKDMTEMRRMEIAADSLYKAKLIRGFCHLYDGOEAVAVGMEAAITKKDCIITAYRD
HCIFLGRGGTLVEAFAELMGRDGC SRGKGGSMHFYKKE SGFYGGH GIVGAQVPLGIGLA
FAQKYKEDYVTFAMYGDGAANQGQLFEALNMAALWDLPAI LVCENNH YGMGTAEWRAAK
SPAYYKRGDYVPLRVDGMDVFAVKQACTFAKQHALKNGPIIILEMDTYRYHGHSMSPG S
TYRTRDEISGVRQERDPVERIRSLILAHNIATEAELKDIEKENRKVVDEAIAKAKES PMP
DPSELFTNVYVKGFGVEAYGADRKELRATLP

>sp|Q820A6|ODPA_STAAN Pyruvate dehydrogenase E1 component subunit alpha
OS=Staphylococcus aureus (strain N315) GN=pdhA PE=1 SV=1
MAPKLQAQFDVAVKVLNNDTQSKFEMVQILDENGNVVDLVPDLTDEQLVELMERMVWTRI
LDQRSISLNRQGRGLGFYAPTAGQEASQLASQYALEKEDYILPGYRDVPQIIWHGLPLTEA
FLFSRGRHFKGNQFPEGVNALSPQIIIGAQYIQAAGVAFALKKRGKNAVAITYTGDGSSQ
GDFYEGINFAAAYKAPAI FVIQNNNYAISTPRSKQTAAETLAQKAI AVGIPGIQVDGMDA
LAVYQATKEARDRAVAGEGPTLIETMTYRYGPHTMAGDDPTRYRTSDEDAEWKDKDPLVR
FRKFLENKGLWNEDKENEVIERAKADIKAAIKEADNTEKQTVTSLMEIMYEDMPQNLAEQ
YEIYKEKESK

>sp|O44451|ODPB_CAEEEL Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Caenorhabditis elegans GN=pdhb-1 PE=1 SV=2
MALRKCGNLFVARLAGTSTRAASTMTVRDALNQAAMDEEIKRDDRFLMGEEVAQYDGAYK
ISKGLWKKHGDKRVDTPITEMGFAGI AVGA AFAGLRPICEFMTFNFSMQAIDQIINSAA
KTTYMSAGRVPVPIVFRGPNGAAAGVAAQHSQDFSAWYAHCPGLKVVCPYSAEDAKGLLK
AAIRDNDNPVFLENEILYQGSFPVGDEVLSDDFVVPPIGKAKIERAGDHVTIVSYSRGVEF
SLEAAKQLEAIGVSAEVINLRSRPFDFESIRQSVHKTTHLLVSVETGWPFAGIGSEIAAQ
VMESDVFQDLDAPLLRTGVDVMPYQTLEAAALPTAEHVVKAVKKS LNIA

>sp|P11966|ODPB_BOVIN Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Bos taurus GN=PDHB PE=1 SV=2
MAVVAVLVRKPLEQVSGLLRRRFRHTAPAALQVTVREAINQGMDEELERDEKVFLLGEEV
AQYDGAYKVSRLGWKKYGDKRIIDTPISEMFGAGI AVGA AMAGLRPICEFMTFNFSMQAI
DQVINSAAKTYMSGGLQSVPIVFRGPNGASAGVAAQHSQCFAAWYGHCPGLKVVSPWSS
EDAKGLIKSAIRDNDNPVFLENEILYQGSFPVGDEVLSDDFVVPPIGKAKIERAGDHVTIV
AHSRVPVGHCCLEAATVLSKEGIECEVINLRITRPMDIETIEGSMKTNHLVTVEGGWPFQF
VGAEICARIMEGPAFNFLDAPAVRVTGADVMPYAKIILEDNSVPPQVKDIIFAIKKTLNI

>sp|Q86HX0|ODPB_DICDI Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Dictyostelium discoideum GN=pdhB PE=1 SV=1
MLSSILKKIQPSLLVNFRIITRITYATKEVTVRDALNSALDEELARDEKVFIMGEEVAQYN
GAYKITKGLFDKYGGDRIIDTPIEAGFAGIGVGAAMAGTRPIIEFMTFNFSMQAIDHII
NSSAKTHYMSGGKVFNPVWRGPNGPPTAVGAQHSQCFAAWYGSVPGLKVVAPWSAADHR
GLLKS AIRDDNPVYLESELLNYKFDLSDQEQDKEYLVPIGKAKVEREGKDVTVGFGR
IVSNCMEAAEILAKEGISAEVINLRITRIPIDAETIVNSLKKTNKLVTVEEGWASGIGAE
ISALMMEHAFDYLDAPIERICGADVMPYASNLENAAMVQTNIVNAAKRVTQRNK

>sp|P99063|ODPB_STAAN Pyruvate dehydrogenase E1 component subunit beta
OS=Staphylococcus aureus (strain N315) GN=pdhB PE=1 SV=1
MAQMTMVQAINDAKTELKNDQDVLIFGEDVGVNGGVFRVTEGLQKEFGEDRVFDTPLAE
SGIGGLAMGLAVEGFRPVMEVQFLGFVFEVFDIAIAGQIARTFRFRSGGKTAPVTIRSPFG
GGVHTPELHADNLEGILAQSPGLKVVIPSGPYDAKGLLISSIRSNPVPVYLEHMKLYRSF
REEVPEEYTIIDIGKANVKEGNDISIIITYGAMVQESMKAAEELEKDGYSVEVIDLRTVQ
PIDVDTIVASVEKTGRAVVVQEAQRQAGVGA AVVAELSERAILSLEAPIGRVAAADTIYP
FTQAENVWLPNKNDIIEKAKETLEF

>sp|P26269|ODPB_ASCSU Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial OS=Ascaris suum PE=1 SV=1
MAVNGCMRLLRNGLTSACALEQSVRRLASGTLNVTVRDALNAALDEEIKRDDRFLIGEE
VAQYDGAYKISKGLWKKYGDGRIWDTPIEMAIAGLSVGAAMNGLRPICEFMSMNFMSMQG
IDHIINSAAKAHYMSAGRFBVPIVFRGANGAAVGAQHSQDFTAWFMHCPGVKVVVPYD
CEDARGLLKA AVRDDNPVICLENEILYGMKFPVSPEAQSPDFVLPFGQAKIQRPK DITI
VSLSIGVDVSLHAADELAKSGIDCEVINLRVCRPLDFQTVKDSVIKTKHLVTVESGWPN
CVGAEISARVTESDAFGYLDGPILRVTVGVDVMPYAPLETAALPQPADVVKMVKKCLNV
Q

>sp|P35488|ODPB_ACHLA Pyruvate dehydrogenase E1 component subunit beta
OS=Acholeplasma laidlawii GN=pdhB PE=1 SV=1
MAIITLLEAINQAIQAMEKDESIVVFEGEDAGFEGGVFRVTAGLQKKYGETRVFDTPIAE
SAIVGSAVGMANGKPIAEIQDFGFI FPGYTDLVTHAARMNRNRSGQFTVPMVLRPLPHG
GGIRALEHHSEALEVLFSGIPGLKVVTPSTPYDAKGLLLAAINDPDPVVFLEPKRIYRAG
KQEVPAEMYEIPIGKAKVVKQGTDMTVVAVGSI VREVEKAVKLVEAEGISVEIIDLRTIS
PIDEETILNSVKKTKGFMVVTEAVKSYGPAEELITMVNEKAFFHLEAAPVRFTGFDITVP
LARGEHYHFPQPEKIAAYIRKLAKARP

>sp|P86222|ODPB_MESAU Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (Fragments) OS=Mesocricetus auratus GN=PDHB PE=1 SV=1
EAINQGMDEELERDEKVFLLGEEVAQYDGAYKVSRTYYMSAGLQPVPIVFRGPN GASAGV
AAQHSQCFAAWYGHCPGLKVVSPWNSEDAKGLIKSAIRDDNPVVMLENELMYGVAFELPT
EAQSKDFLIPIGKEGIECEVINLRTIRPMDIEAIEASVMKTNHLVTVEGGWPQFGVGAEI
CARIMEGPAFNFLDAPAVRVGTGADVMPYAK

>sp|P0A0A3|ODPB_STAAU Pyruvate dehydrogenase E1 component subunit beta
OS=Staphylococcus aureus GN=pdhB PE=1 SV=1
MAQMTMVQAINDALKTELKNDQDVLIFGEDVGVNGGVFRVTEGLQKEFGEDRVFDTPLAE
SGIGGLAMGLAVEGFRPVMEVQFLGFVFEVFDIAIAGQIARTRFRSGGKTAPVTIRSPFG
GGVHTPELHADNLEGILAQSPGLKVVIPSGPYDAKGLLISSIRSNP VVYLEHMKLYRSF
REEVPEEETIDIGKANVKKEGNDISIIITYGAMVQESMKAAEELEKDGYSVEVIDLRTVQ
PIDVDTIVASVEKTGRAVVVQEAQRQAGVGA AVVAELSERAILSLEAPIGRVAAAADTIYP
FTQAENVWLPNKNDIIEKAKETLEF

>sp|P49823|ODPA_CANFA Pyruvate dehydrogenase E1 component subunit alpha,
somatic form (Fragment) OS=Canis familiaris GN=PDHA1 PE=1 SV=1
XXDATFEIKKXDL

>sp|P81419|ODPB_SOLTU Pyruvate dehydrogenase E1 component subunit beta,
mitochondrial (Fragment) OS=Solanum tuberosum PE=1 SV=1
ISAVKEMTVRDALNSA

>sp|P10515|ODP2_HUMAN Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial OS=Homo
sapiens GN=DLAT PE=1 SV=3

MWRVCARRAQN VAPWAGLEARWTALQEVPGT PRVTSRSGPAPARRNSVTTGYGGV RALCG
WTPSSGATPRNRLLLQLLGS PGRYSLPPHQK VPLPSLSPTMQAGTIARWEKKEGDKIN
EGDLIAEVETDKATVGFESLEECYMAKILVAEGTRDVP IGAIIICITVGKPEDIEAFKNYT
LDSSAAPT PQAAPAPT PAATAS PPTPSAQAPGSSYP PHMQVLLPALSPTMTMGTVQRWEK
KVGEK LSEGDL LAE IETDKATIGFEVQEEGYLAKILVPEGTRDVPLGTPLCIIVEKEADI
SAFADYRPT EVDLTKPQVPPPTPPPVA AVPPTPQPLAPTSPAPCPATPAGPKGRV FVSPL
AKKLAVEK GIDLTQVKGTGPDGRITKKDIDSFVPSKVAPAPA AVVPPTGPGMAPVPTGVF
TDIPI SNIRRVIAQRLMQSKQTIPHYLSIDVNMGEVLLVRKELNKILEGRSKISVNDFI
IKASALACLK VPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNAHIKGVETIAND
VVSLATKAREGKLQ PHEFQGGTFTISNLGMFGIKNFSAI INPPQACILAIGASEDKLVPA
DNEKGF DVASMMSVTLSCDHRVVDGAVGAQWLAEFRKYLEKPITMLL

>sp|P06959|ODP2_ECOLI Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Escherichia coli (strain
K12) GN=aceF PE=1 SV=3

MAIEIKVPDIGADEVEITEILVKVGD KVEAEQSLITVEGDKASMEVPSQAGIVKEIKVS
VGDKTQTGALIMIFDSADGAADAAPAQAEEKKEAAPAAA PAAAAKDVNVPDIGSDEVEV
TEILVKVGD KVEAEQSLITVEGDKASMEVPAPFAGTVKEIKVNVGDKVSTGSLIMVFEVA
GEAGAAAPAAKQEAAPAAAPAPAAGVKEVNVPD IGGDEVEVTEVMVKVGDKVA AEQSLIT
VEGDKASMEVPAPFAGVVKELKVNVDKVKTGSLIMI FEVEGAAPAAAPAKQEAAPAPA
AKAEAPAAAPAAKAEGKSEFAENDAYVHATPLIRRLAREFGVNLAKVKGTGRKGRILRED
VQAYVKEAIKRAEAAPAATGGGIPGMLPWPVKVDFSKFGEIEEVELGRIQKISGANLSRNW
VMIPHVTHFDKTDITELAEFRKQNEEA AKRKL DVKITPVVFIMKAVAAALEQMPRFNSS
LSEDGQRLTLKKYINIGVAVDTPNGLVVPVFKDVNKKGI IELSRELMTISKKARDGKLT
GEMQGGCFTISSIGGLGTHFAPIVNAPEVA I LGVSKSAMEPVWNGKEFVPRMLLPISLS
FDHRVIDGADGARFITIINNTLSDIRRLVM

>sp|P12695|ODP2_YEAST Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial
OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LAT1 PE=1
SV=1

MSAFVRVVPRI SRSSVLTRSLRLQLRCYASYPEHTIIGMPALSPTMTQGNLAAWTKKEGD
QLSPGEVIAE IETDKAQMDFEFQEDGYLAKILVPEGTDI PVNKPIAVYVEDKADVPAFK
DFKLEDSGSDSKTSTKAQPAEPQAEKKQEAPAEETKTSAP EAKKSDVAAPQGRIFASPLA
KTIALEKGISLKD VHG TGPRGRITKADIESYLEKSSKQSSQTSGAAAATPAAATSSTTAG
SAPSPSSTASYEDVPISTMRSIIGERLLQSTQGI PSYIVSSKISISKLLKLRQSLNATAN
DKYKLSINDLLVKAITVA AKRVPDANAYWLPNENVIRKFKNVDVSVAVATPTGLLTPIVK

NCEAKGLSQISNEIKELVKRARINKLAPPEEFQGGTICISNMGMNNAVNMFTSIINPPQST
ILAIATVERVAVEDAAAENGFSFDNQVTITGTFDHRTIDGAKGAEFMKELKTVIENPLEM
LL

>sp|Q8NNJ2|ODP2_CORGL Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Corynebacterium glutamicum
(strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025)
GN=aceF PE=1 SV=1

MAFSVEMPELGESVTEGTITQWLKSVGDTVEVDEPLLEVSTDKVDTEIPSPVAGVILEIK
AEEDDTVDVGGVIAIIGDADETPANEAPADEAPAPAEPEEPVKEEPKKEAAPEAPAATGA
ATDVEMPELGESVTEGTITQWLKAVGDTVEVDEPLLEVSTDKVDTEIPSPVAGTIVEILA
DEDDTVDVGAVIARIGDANAAAAAPAEAAAAPAEPEEPVKEEPKKEAAPEAPAATGAATDV
EMPELGESVTEGTITQWLKAVGDTVEVDEPLLEVSTDKVDTEIPSPVAGTIVEILADEDD
TVDVGAVIARIGDANAAAAAPAEAAAAPAEPEEPVKEEPKKEEPKKEEPKKEAAATPAAAS
ATVSASGDVNPYVTPPLVRKLAEKHGVDLNTVTGTGIGGRIRKQDVLAAANGEAAPAEAAA
PVSAWSTKSVDPEKAKLRGTTQKVNRIREITAMKTVEALQISAQLTQLHEVDMTRVAELR
KKNKPAFIEKHGVLNLTYPFFVKAVVEALVSHPNVNASFNAKTKEMTYHSSVNLIAVDT
PAGLLTPVIHDAQDLSIPEIAKAIVDLADRSRNNKLPNDLSGGTFTITNIGSEGALSDT
PILVPPQAGILGTGAIVKRPVITEDGIDSIAIRQMVFLLPTYDHQVVDGADAGRFLTTI
KDRLETANFEGDLQL

>sp|P10802|ODP2_AZОВI Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Azotobacter vinelandii
PE=1 SV=3

MSEIIRVPDIDGGDEVIPELLVKTGDLIEVEQGLVVLESASAKASMEVPSPKAGVVKSVSVKL
GDKLKEGDALIELEPAAGAAAAAPAEAAVPAAPTQAVDEAEAPSPGASATPAPAAAASQEV
RVPDIGSAGKARVIEVLVKAGDQVQAEQSLIVLESKASMEIPSPASGVVESVAIQLNAE
VGTGDLILTLRTTGAQAQPTAPAAAAAASPAPAPLAPAAAAGPQEVKVPDIGSAGKARVIE
VLVKAGDQVQAEQSLIVLESKASMEIPSPAAGVVESVAVQLNAEVGTGDQILTLRVAGA
APSGPRARGSPGQAAAAPGAAPAPAPVGPAPSRNGAKVHAGPAVRQLAREFGVELAAINST
GPRGRILKEDVQAYVKAMMQKAKEAPAAGAASGAGIPPIPPVDFAKYGEIEEVPMTRLMQ
IGATNLHRSWLNVPVHTQFESADITELEAFRVAQKAVAEKAGVCLTVLPLLLKACAYLLK
ELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLVFVIRNVDQKSLQLAAEAAELAEK
ARSKKLGADAMQACFTISSLGHIGGTAFTPIVNAPEVAIILGVSKASMQPVWDGKAFQPR
LMLPLSLSYDHRVINGAAAARFTKRLGDLADIRAILL

>sp|Q8BMF4|ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial OS=Mus
musculus GN=Dlat PE=1 SV=2

MWRVCARRARSVPRDGFRRARWAALKEGPGAPCGSPRIGPAAVRCGSGIPRYGVRSLCGW
SSSGTVPNRLLRQLLGGSPRRSYSLPPHQKVPLPSLSPTMQAGTIARWEKKEGEKISE
GDLIAEVETDKATVGFESLEECYMAKILVPEGTRDVPVGSIIICITVEKPDIEAFKNYTL
DLAAAAAPQAAPAAAPAPAAAPAPSASAPGSSYPHMQIVLPALSPTMTMGTVQRWEKK
VGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPVPLGAPLCIIVEKQEDIA
AFADYRPTVETSLKQQAAPPAPPPVAAPVPTPQPVAPTSAAPAGPKGRVFPVSPPLAKKLA
AEKIDLTQVKGTPGEGRIIKKDIDSFVPSKAAPAAAAAMAPPGRVAPAPAGVFTDPIPI
SNIRRVIAQRLMQSKQTI PHYYSVDVNMGEVLLVRKELNKMLEGKGISVNDFIKASA
LACLKVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNHAIKGLLETIASDVVSLA
SKAREGKLQPHFQGGTFTISNLGMFGIKNFSAINPPQACILAIGASEDKLIPADNEKG
FDVASVMSVTLSCDHRVVDGAVGAQWLAEFKKYLEKPIITMLL

>sp|P9WIS7|ODP2_MYCTU Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=dlat PE=1 SV=1

MAFSVQMPALGESVTEGTVTRWLKQEGDTVELDEPLVEVSTDKVDTEIPSPAAGVLTKII
AQEDDTVEVGGELAVIGDAKDAGEAAAPAEKVPAAQPEKPAPEPPPQPTSGAPAGGD
AKPVLMPPELGESVTEGTVIRWLKIGDSVQVDEPLVEVSTDKVDTEIPSPVAGVLVSISA
DEDATVPVGGELARIGVAADIGAAPAPKAPKVPPEPAPTPKAEPAPSPPAAPAGAAEG
APYVTPPLVRKLAENNIDLAVGTGTGVGGRIRKQDVLAAAEQKKRAKAPAPAAQAAAAAPA
PKAPPAPALAHLRGTTQKASRIRQITANKTRESLQATAQLTQTHEVDMTKIVGLRARA
KAAFAEREGVNLTFLPFFAKAVIDALKIHPNINASYNEDTKEITYYDAEHLGFAVDTEQG
LLSPVIHDAGDLSLAGLARAIAADIAARARSGNLKPDELSGGTFTITNIGSQGALFDTPII

VPPQAAMLGTGAIVKRPRVVVDASGNESIGVRSVCYLPLTYDHLRIDGADAGRFLTTIKH
RLEEGAFEADLGL

>sp|P11961|ODP2_GEOSE Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Geobacillus
stearothermophilus GN=pdhC PE=1 SV=3

MAFEFKLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCEVQNDKAVVEIPSPVKGVLEIL
VPEGTVATVGQTLITLDAPGYENMTFKGQEQEEAKKEEKTETVSKEEKVDAVAPNAPAAE
AEAGPNRRVIAMPSVRKYAREKGVDIRLVQGTGKNRVLKEDIDAFLLAGGAKPAPAAAEE
KAAPAAAKPATTEGEFPEKREKMSGIRRAIAKAMVHSHKHTAPHVTLMDADVTKLVAHRK
KFKAIAAEKGIKLTFLPYVVKALVSALREYPVLNTSIDDETEEIIQKHYYNIGIAADTDR
GLLVPVIKHADRKPIFALAQEINELA EKARDGKLTPEGEMKGASCTITNIGSAGGQWFTPV
INHPEVAILGIGRIAEKPIVRDGEIVAAPMLALSLSFDHRMIDGATAQKALNHIKRLLS
PELLLMEA

>sp|P08461|ODP2_RAT Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus
norvegicus GN=Dlat PE=1 SV=3

MWRVCARRVQSAVPRAGFRARWATLKGPRTPAAVRCGSGIPSYGVRSLCGWSYGSATVP
RNRILQQLLGSPPRSYSLLPPHQVPLPSLSPTMQAGTIARWEKKEGEKISEGDLIAEVE
TDKATVGFESLEECYMAKILVPEGTRDVPVGSIIICITVEKPDIEAFKNYTLDSATAATQ
AAPAPAAAPAAAPAAAPSASAPGSSYPVHMQIVLPALSPTMTMGTVQRWEKKVGEKLSEGD
LLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPVPLGTPLCIIVEKQEDIAAFADYRPT
VTSLKPQAPPPVPPVAAVPPIPQPLAPTSAAPAGPKGRVFSPLAKKLAEEKGIDLTO
VKGTGPEGRIIKKDIDSFVPTKAAPAAAAAPPGRVAPTAPAGVFIDIPISNIRRVIAQR
LMQSKQTIPIHYLLSVDVNMGEVLLVRKELNKMLEGKGISVNDFIKASALACLKVPEAN
SSWMDTVIRQNHVVVSVAVSTPAGLITPIVFNHAIKGLLETIASDVVSLASKAREGKLQP
HEFQGGTFTISNLGMFGIKNFSAIINPPQACILAI GASEDKLIPADNEKGFVDVASVMSVT
LSCDHRVVDGAVGAQWLAEFKKYLEKPVMTML

>sp|P21883|ODP2_BACSU Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Bacillus subtilis (strain
168) GN=pdhC PE=1 SV=2

MAFEFKLPDIGEGIHEGEIVKWFVKPNDEVEDDVLAEVQNDKAVVEIPSPVKGVLELK
VEEGTVATVGQTIITFDAPGYEDLQFKGSDESDDAKTEAQVQSTAEAGQDVAKEEQAEQEP
AKATGAGQQDQAEVDPNKRVIAMPSVRKYAREKGVDIRKVTGSGNNGRVVVEDIDSFVNG
GAQEAAPQETAAPQETAAPAAAPAPEGEFPEKREKMSGIRKAIKAMVNSKHTAPHVTL
MDEVDTVNLVAHRKQFKQVAADQGIKLTYPVVKALTSALKKFPVLNTSIDDKTDEVIQ
KHYFNIGIAADTEKGLLVVKNADRKSVEISDEINGLATKAREGKLAPAEMKGASCTI
TNIGSAGGQWFTPVINHPEVAILGIGRIAEKAIVRDGEIVAAPVLALSLSFDHRMIDGAT
AQNALNHIKRLLLNDPQLILMEA

>sp|P20285|ODP2_NEUCR Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial OS=Neurospora
crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC
987) GN=mrp-3 PE=1 SV=2

MIVPVLSRQALRHASVARVALPSLTRWYASYPHTVVKMPALSPTMTSGGIGAWQKKPGD
KIEPGEVLVEIETDKAQMDFEFQEEGVLA KILKDSGEKDVAVGNPIAILVEEGTDVNAFK
DFTLKDAGGETSPAVPKDEPKNESTASAPTPAPTAPPEPENTSFTGRFQTALEREPNALP
AAKRLAREKIDLRNVKSGSGPGKITEEDVKKALASAPAAGAAAAAYTDVPI SGMRKTIA
ARLKESVTENPHFFVSTNLSVSKLLKLRQALNSSADGRYKLSVNDFLIKAMGIASKRVPT
VNSSWRDGVIRQFETVDVSVAVATP NGLITPIVKGVEGKGLSISA AVKELAKKARDGKL
KPEEYQGGISISNMGMNPAVQSFTAI INPPQAAILAVGAPQKVAVPVENEDGTTGVS
WD EQIIVTASFHKKVVDGAVGAEWIRELKKVIENPLELLL

>sp|P27747|ACOC_CUPNH Dihydrolipoyllysine-residue acetyltransferase
component of acetoin cleaving system OS=Cupriavidus necator (strain ATCC
17699 / H16 / DSM 428 / Stanier 337) GN=acoC PE=1 SV=3

MATEISPTIIPVMPKWLMSMKEGTVNAWLVDGEITEITVGLPILDVETDKIANAVEAPDA
GTLRRKVAQAGDVLVVKALLGV LAPAEVSDAQIDDYVAAAYETPADDAGEEDAAAAAYQFAD
VDGIRVRYARKGGGAETVLFIHGFGDDL NWNLFNLDPLADAYTVVALDLP GHGQSSPRLA
GTTLAQMAGFVARFMDETGIEAAHVVGHSMMGGVAAQLAVDAPQRVLSVALVSPVGF
GD VNSGYTEGFVSAQSRRELKPVVELL FADAGLVS RQMLDDLRLRYKRLDGVTEAL
TALGQGL

FGGGRQSEQPGQRLANSKRVLVVWGGQDQIIIPAAHAEAAAPPGATVKVFADAGHMSQMEK
ANDFNALLKHLGG

>sp|P35489|ODP2_ACHLA Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Acholeplasma laidlawii
GN=pdhC PE=1 SV=1

MYEFKFADIGEGIHGTVLQWNFKVGDVKVEGETLVIVETDKVNAELPSPVDGTIVSLGA
KEGEEIHVQGIIVTIDDGTGTPAAAAPAPAQVSAPTPAPAAAAPQVAAPAASGDIYDFKFAD
IGEGIHGTVLQWNFKVGDVKVEGETLVVVETDKVNAELPSPVDGTILKLGKAEGEVIHV
GETVVLIGQNGATLEQAQAPKAEAPVSEPKKAGVVGIEVSDDIIGGSEEVHVVATTGK
VLASPVARKLASDLGVDIATIKSGEQGRVMKDDVQNSKAPAEAQAPVQQTQAPAQAAAS
VAPSFAAAGKPKQGDVEVVKITRLRKAVSNAMTRSKSIIIPETVLMDEINVDALVNFREAK
GLAESKGIKLTMAFIKAVLIALKEFPFNASFNHDTDEVYIKKFINLGMVAVDTPDGLI
VPIKNADRLSVFELASQVRSIADDTIARKISMDQQTGGTFTITNFGSAGIAFGTPVINY
PELAILGIGKIDRKPWVVGNEIKIAHTLPLSLAVDHRIIDGADGGRFLMRVKELLTNPTL
LLLS

>sp|Q19749|ODP2_CAEEEL Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial
OS=Caenorhabditis elegans GN=F23B12.5 PE=1 SV=1

MSKFPVPLRTIGGLRPSTTAAISAANIGFTQSSRALSTGAAAKSSGLVQVARQYPNAAA
FSIKQVRLYSSGNLPHNRVALPALSPMELGTVVSWQKKEGDQLSEGDLCEIETDKAT
MGFETPEEGYLAKILIQEGSKDVPKIGLLCIIVDNEADVAAFKDFKDDGASSGGSAPAAE
KAPEPAKPAASSQPSPPAQMYQAPSVPKSAPIPHSSSGRVSASPFKAKLAAENGLDLSGV
SGSGPGGRILASDLSQAPAKGATSTTTQAVSGQDYTDIPLSNMRKTIKRLTESKSTIPH
YYLTSEIQLDLTLQVREKLNGLLAKGTSGQATKISINDFIKASALACQRVPEANSYWM
SFIRENHVVDVSVAVSTPAGLITPIIFNAHAKGLATIASEIVELAQRRAREGKLPHEFQ
GTFTVSNLGMFGSVSDFTAIINPPQSCILAIGGASDKLVPDEAEGYKKIKTKMKTLS
CDHRTVDGAVGAVWLRHFKEFLEKPHMTML

>sp|P36413|ODP2_DICDI Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial
OS=Dictyostelium discoideum GN=pdhC PE=1 SV=2

MLRAINQNSAKVVKSLKQQLVVLEATNVVAYTGTGSFTTTTKTFNNTQTKPKIFTSSNVLS
FSSPSSSNVFEILNKRYSYSSKGEITMPALSPSMTEGNIVQWKKKEGDQIKAGDVIAEV
ETDKATMDFQYEDGNGYLAKILIEGTGKIEINKPIAIIIVSKKEDIESAVKNYKPPSQAS
STPVQEEAPKPKQEAQPKKSTKTYPAHKVVGMPALSPSMETGGIASWTKKEGDQIKAGDAI
AEVETDKATMDFQYEDGNGYLAKILVPGGTSGIQINQPVCIIVKNKEDCDKFADYSVEEQ
SSSSSSSSQESTPSSSSSSSSQESTPSQSSSQQTTRKSGERIFATPAARFEASSKGYDL
SAINGTGPNNRILKADVLEFVFPQKQEVAAQQQQQQTSTTTTKKPTTPTSSGEFTDIPHS
NIRKVTAAARLTESKQTIPIHYLLTMECRVDKLLKLRSELNAMNTVKISVNDFIVKASAA
ALRDNPVVNSTWTDQFIRRYHNIDINAVVNTPQGLFTPIVRGVDKGLNSISTSVKQLAE
KAQNGKLPHEFESGFTTISNLGMLGIKQFAAVINPPQAAILAVGTTETRVVLSNKPDS
PYETATILSVTLSCDHRVIDGAVGAEWLKSFKDYVENPIKLIL

>sp|P65636|ODP2_STAAN Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex OS=Staphylococcus aureus
(strain N315) GN=pdhC PE=1 SV=1

MAFEFRLPDIGEGIHGIVKWFVKAGDTIEEDDVLAEVQNDKSVVEIPSPVSGTVEEVM
VEEGTVAVVGDVIVKIDAPDAEDMQFKGHDDSSSKEEPAKEEAPAEQAPVATQTEEVDE
NRTVKAMPSVRKYAREKGVNIKAVSGSGKNGRITKEDVDAYLNGGAPTASNESASAATSE
EVAETPAAPAASVLEGDFPETTEKIIPAMRRRAIAKAMVNSKHTAPHVTLMDVIDVQAL
WDHKKKFKEIAAEQGTKLTLFLPYVVKALVSALKKYPALNTSFNEEAGEIVHKHYWNIG
IAADTDRGLLVVVKHADRKSIFQISDEINELAVKARDGKLTADEMKGATCTISNIGSAG
GQWFTPVINHPEVAIIGIGRIAQKPIVKDGEIVAAPVLALSLSFDHRQIDGATGQNA
MNHKRLLNPELLEMEG

>sp|P86197|ODP2_MESAU Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex, mitochondrial (Fragments)
OS=Mesocricetus auratus GN=DLAT PE=1 SV=1

VPLPSLSPMQAGTIARDVPLGAPLCIIIVEKGRVFSPLAKGIDLTQVKGTGPEGDIDSF
VPSKVPEANSSWMDTVIRQNHVVDVSVAVSTPAGLITPIVFNHAIKGLLETIASDVVSLAS
KEGKLPHEFQGGTFTISNLGMFGIKNFSAINPPQACILAIGASEDKLIPADNEKGFV

ASVMSVTLSCDHRVVDGAVGAQWLAEFKKYLEKPITMLL
>sp|P11180|ODP2_BOVIN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Bos taurus GN=DLAT PE=1 SV=1
VETDKATVGF
>sp|P81421|ODP2_SOLTU 78 kDa dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Solanum tuberosum PE=1 SV=1
ISAEAPLYAEVGMPLSPTMT
>sp|P81420|ODP3_SOLTU 55 kDa dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (Fragment) OS=Solanum tuberosum PE=1 SV=1
SSADSLPXHGAGXMP
>sp|P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2
MQSWSRVYCSLAKRGHFNRISHGLQGLSAVPLRTYADQPIDADVTVIGSGPGGYVAAIKA
AQLGFKTVCIKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEMSEVRLNL
DKMMEQKSTAVKALTGGIAHLFKQNKVVHVNGYGKITGKNQVTATKADGGTQVIDTKNIL
IATGSEVTPFPGITIDEDTIVSSTGALSLLKVKPEKMMVIGAGVIGVELGSVWQRLGADVT
AVEFLGHVGGVGDMEISKNFQRILQKQGFKFLNLTGATKKS DGKIDVSI EAASGGK
AEVITCDVLLVCIGRRPFTKNLGLLEELGIELDPRGRIPVNTRFQTKIPNIYAIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEYKVGK
FPFAANSRAKTNADTDGMVKILGQKSTDRVLGAHILGPGGAGEMVNEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAASFGKSINF
>sp|Q9M5K2|DLDH2_ARATH Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1
MAMASLARRKAYFLTRNINSPTDAFRFSFSLTRGFASSGSDNDVVIIGGGPGGYVAAI
KAAQLGLKTTICIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHV FANHGKVKVSSVEVD
LPAMLAQKDTAVKNLTRGVEGLFKKNKNVYVKGYGKFLSPSEVSVDTIDGENVVVKGKHI
IVATGSDVKSLPGITIDEKKIVSSTGALSLEIIPKKLIVIGAGYIGLEMGSVWGRLGSEV
TVVEFAADIVPAMDGEIRKQFQRSLEKQKMKFMLKTKVVGVDSSGDGVKLIVEPAEGGEQ
TTLEADVVLVSAGRTPFTSGLDLEKIGVETDKGGRILVNERFSTNVSGVYAIGDVIPGPM
LAHKAEDG VACVEFIAGKHGHVDYDKVPGVVYTYPEVASVGKTEEQLKKEGVSYNVVKF
PFMANSRAKAIDTAEGMVKILADKETDKILGVHIMSPNAGELIHEAVLAINYDASSEDIA
RVCHAHPTMSEAIKEAAMATYDKPIHM
>sp|P0A9P0|DLDH_ECOLI Dihydrolipoyl dehydrogenase OS=Escherichia coli (strain K12) GN=lpdA PE=1 SV=2
MSTEIKTQVVVLGAGPAGYSAAFRCADLGLLETVIVERYNTLGGVCLNVGCIPSKALLHVA
KVIEEAKALAEHGIVFGEPKTDIDKIRTWKEKVINQLTGGLAGMAKGRKVKVNVNGLGKFT
GANTLEVEGENGKTVINFDNAIIAAGSRPIQLPFI PHEDPRIWDSTDALELKEVPERLLV
MGGGIIGLEMGTVYHALGSQIDVEMFDQVI PAADKDIVKVF TKRISKKFNLMLETKVTA
VEAKEDGIYVTMEGKKAPAE PQRYDAVLVAIGRVPNGKNLDAGKAGVEVDDRGFIRVDKQ
LRTNVPHIFAIGDIVGQPM LAHKGVHEGHVAAEVIAGKKHYFDPKVI PSIAYTEPEVAWV
GLTEKEAKEKGISYETATFPWAASGRAIASDCADGMTKLI FDKESHRVIGGAI VGTNGGE
LLGEIGLAIEMGCD AEDIALTIHAHPTLHESVGLAAEVFE GSITDLPNPKAKKK
>sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1
MTHYDVVVLGAGPGGYVAAIRAAQLGLSTAI VE PKYWGVC LNVGCIPSKALLRNAELVH
IFTKDAKAFGISGEVTFDYGIAYDRSRKVAEGRVAGVHFLMKKNKITEIHGYGTFADANT
LLVDLNDGGTESVTFDNAI IATGSSTRLVPGTSLSANVVTYEEQILSRELPKSII IAGAG
AIGMEFGYVLKNYGVDVTFIVEFLPRALPNEDADVSKEIEKQFKKLGVTILTATKVESIAD
GGSQVTVTVTKDVAQELKAEKVLQAIGFAPNVEGYGLDKAGVALTDRKAI GVDVDMRTN
VGHIYAIGDVNGLLQLAHVAEAQGVVAAETIAGAETLTLGDHRMLPRATFCQPNVASFGL
TEQQARNEG YDVVAKFPFTANAKAHGVGDPSGFVKLVADAKHGELLGGHLVGHDAEELL
PELTLAQRWDLTASELARNVHTHPTMSEALQECFHGLVGHMINF
>sp|P09624|DLDH_YEAST Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=LPD1 PE=1 SV=1

MLRIRSLNKNKRAFSSSTVVRTLTINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGK
LGGTCLNVGCIPSKALLNNSHLFHQMHTEAQKRGIDVNGDIKINVANFQKAKDDAVKQLT
GGIELLFKKNKVITYYKNGNSFEDETKIRVTPVDGLEGTVKEDHILDVKNIIVATGSEVTP
FPGIEIDEEKIVSSTGALSLEKPKRLTIIGGGIIGLEMGSVYSRLGSKVTVVEFQFQIG
ASMDGEVAKATQKFLKKQGLDFKLSTKVISAKRNDKKNVVEIVVEDTKTNKQENLEAEVL
LVAVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDVTFGPMLAHKAEVE
GIAAVEMLKTGHGHVNYNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRA
KTNQDTEGFVKILIDSKTERILGAHIIGPNAGEMIAEAGLALLEYGASAEEDVARVCHAHPT
LSEAFKEANMAAYDKAIHC

>sp|Q9M5K3|DLDH1_ARATH Dihydrolipoyl dehydrogenase 1, mitochondrial
OS=Arabidopsis thaliana GN=LPD1 PE=1 SV=2

MAMASLARRKAYFLTRNLSNSPTDALRFSFSLSRGFASSGSDENDVVIIGGGPGGYVAAI
KASQLGLKTTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHSFANHGIKVSSVEVD
LPAMLAQKDNVKNLTRGIEGLFKKNKVITYYKGYGKFI SPNEVSVETIDGGNTIVKKGHI
IVATGSDVKSPLGITIDEKKIVSSTGALSLEVPKKLIVIGAGYIGLEMGSVWGRLGSEV
TVVEFAGDIVPSMDGEIRKQFQRSLEKQKMKFMLKTKVVSVDSSSDGVKLTVEPAEGGEQ
SILEADVVLVSAGRTPFTSGLDLEKIGVETDKAGRILVNDRFLSNVPGVYAIIGDVIIPGPM
LAHKAEEEDGVACVEFIAGKHGHVDYDKVPGVVYTHPEVASVGKTEEQLKKEGVSYRVGKF
PFMANSRAKAIIDNAEGLVKILADKETDKILGVHIMAPNAGELIHEAVLAINYDASSEIDIA
RVCHAHPTMSEALKEAAMATYDKPIHI

>sp|Q8NTE1|DLDH_CORGL Dihydrolipoyl dehydrogenase OS=Corynebacterium
glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB
10025) GN=lpd PE=1 SV=1

MTEHYDVVVLGAGPGGYVSAIRAAQLGKKVAVIEKQYWGGVCLNVGCIPSKSLIKNAEVA
HTFTHEKKTFFINGEVTFNEDAHKRSRGVSDKIVGGVHYLMKKNKIIIEIHGLGNFKDAK
TLEVTDGKDAGKTITFDDCI IATGSVVNTLRGVDFSENVVSFEEQILNPVAPKMMVIVGA
GAIGMEFAYVLGNYGVDVTVIEFMDRVLPNEDAESKVIKAYKKMGVKKLLPGHATTAVR
DNGDFVEVDYQKKGSDKTETLTVDVMVSVGFRPRVEGFLENTGVKLTERRGAEIDDDYM
RTNVDGIYAIIGDVTAKLQLAHVAEAQGI VAAETIAGAETQTLGDYMMMPRATFCNPQVSS
FGYTEEQAKEKWPDRKIVASFPFSANGKAVGLAETDGFKIVADADEFGELLGAHLVGN
ASELINELVLAQNWDLTTEEISRSVHIHPTLSEAVKEAAHGIGSHMINF

>sp|O08749|DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus
musculus GN=Dld PE=1 SV=2

MQSWSRVYRSLAKKGFHNRISHGLQGVSSVPLRITYADQPIEADVTVIGSGPGGYVAAIKS
AQLGFKTVCIKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEIPEVRLNL
EKMMEQKHSVAVKALTGGIAHLFKQNKVVHVNGFGKITGKNQVTATKADGSTQVIDTKNIL
VATGSEVTPFFGITIDEDTIVSSTGALSLEKVPKLVVIGAGVIGVELGVS VWQRLGADVT
AVEFLGHVGGIGIDMEISKNFQRILQRQGFKFLNKTGATKKS DGKIDVSVEAASGGK
AEVITCDVLLVCIGRRPFTQNLGLEELGIELDPKGRI PVNRRFQTKIPNIYAIIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEFKIGK
FPFAANSRAKTNADTDGMVKILGHKSTDRVLGAHILGPGAGEMVNEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAAAFGKPINF

>sp|P11959|DLDH1_GEOSE Dihydrolipoyl dehydrogenase OS=Geobacillus
stearothermophilus GN=pdhD PE=1 SV=2

MVVGDFAIETETLVVVGAGPGGYVAAIRAAQLGQKVTIVEKGNLGGVCLNVGCIPSKALIS
ASHRYEQAKHSEEMGIKAENVTIDFAKVQEWKASVVKLTGGVEGLLKGKVEIVKGEAY
FVDANTVRVNGDSAQTYTFKNAI IATGSRPIELPNFKFSNRILDSTGALNLGEVPSLV
VIGGGYIGIELGTAYANFGTKVTILEGAGEILSGFEKQMAAI IKRRLKKGVEVVTNALA
KGAEBEREDGVTVTYEANGETKTIDADYVLVTVGRRPNTDELGLEQIGIKMTNRGLIEVDQ
QCRTSVPNIFAIGDIVPGPALAHKASYESGKVAEAIAGHPSAVDYVAI PAVVFSDEPCAS
VGYFEQQAKDEGIDVIAAKFPFAANGRALANDTDGFLKLVVRKEDGVII GAQIIGPNAS
DMIAELGLAIEAGMTAEDIALTIHAHPTLGEIAMEAAEVALGTPIHIITK

>sp|P09063|DLDH1_PSEPU Dihydrolipoyl dehydrogenase OS=Pseudomonas putida
GN=lpdV PE=1 SV=1

MQQTITQTTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAE
QFHQASRFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKGHVKVHVHWAK
VLDGKQVEVDGQRIQCEHLLLATGSSSVLELPLPLGGPVISSTEALAPKALPQHLVVVGG
GYIGLELGIAYRKLGAQVSVVEARERILPTYDSELTAPVAESLKKLGIALLHGHVVEGYE

NGCLLANDGKGGQLRLEADRVLVAVGRRPRTKGFNLECLDLKMNGAAIAIDERQCOTSMHN
VWAIGDVAGEPMLAHRAMAQGEVVAEIIAGKARRFEPAAIAAVCFDPEVVVVVGKTPEQA
SQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNLHILGWQAVGVAVSELSTAFQA
SLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHALHI

>sp|P18925|DLDH_AZOVI Dihydrolipoyl dehydrogenase OS=Azotobacter
vinelandii PE=1 SV=1

MSQKFDVIVIGAGPGGYVAAIKSAQLGLKTALIEKYKKEGKTALGGTCLNVGCIPSKAL
LDSSYKFHEAHESFKLHGISTGEVAIDVPTMIARKDQIVRNLTGGVASLIKANGVTLFEG
HGKLLAGKKVEVTAADGSSQVLDTENVILASGSKPVEIPPAPVDQDVIVDSTGALDFQNV
PGKLGIVIGAGVIGLELGSVWARLGAEVTVLEAMDKFLPAVDEQVAKEAQKILTKQGLKIL
LGARVTGTEVKNQVTVKVFVDAEGEKSAQFDKLI VAVGRRPVTTDLAADSGVTLDERGF
IYVDDYCATSVPGVYAIAGDVVRGAMLAHKASEEGVVVAERIAGHKAQMNYDLIPAVIYTH
PEIAGVGKTEQALKAEGVAINVGVFPFAASGRAMAANDTAGFVKVIADAKTDRVLGVHVI
GPSAAELVQQGAIAMEFGTSAEDLGMVFAHPALSEALHEAALAVSGHAIHVANRKK

>sp|P49819|DLDH_CANFA Dihydrolipoyl dehydrogenase, mitochondrial OS=Canis
familiaris GN=DL D PE=1 SV=1

MQSWSRVYCSLAKRGHFSRISHGLQAVSAVPLRITYADQPIDADVTVIGSGPGGYVAAIKA
AQLGFKTVCEKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEMSEVRLNL
EKMMEQKSTAVKALTGGIAHLFKQNKVVHVNGYGKITGKNQVTAKKADGSTQVIDTKNIL
IATGSEVTPFPGITIDEDTIVSSTGALSLLKVPKMMVIGAGVIGVELGSVWQRLGADVT
AVEFLGHVGGVIGIDMEISKNFQRI LQKQGFKFLN TKVTGATKKS DGKIDVSI EGASGGK
AEVITCDVLLVCIGRRPFTQNLGLEELGIELDPRGRI PVNTRFQTKIPNIYAIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVPIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEYKVGK
FPFAANSRAKTNADTDGMVKILGQKSTDRVLGAHILGPGGAGEMVNEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAASFGKSINF

>sp|Q04829|DLDH_HALVD Dihydrolipoyl dehydrogenase OS=Haloferax volcanii
(strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM
B-1768 / DS2) GN=lpdA PE=1 SV=3

MVVGDIATGTELLVIGAGPGGYVAAIRAAQNGIDTTLVEKDAYGGTCLNYGCIPSKALIT
GANLAHEAGNAEEMGIHADPVVDMSQLRDWKSQVVDQLTGGVEKLCKANGVNLVEGTARF
KDENAVRIAHHGGEGQGETIEFEHCIIATGSRVQIPGFDFGDEPVWSSRDALEADTVPE
RLVVVGGGYIGMELSTTFALGADVTVVEMLDDILPGYESDVARVVRKRAEELGIDMHLG
EGASGWREDDGIMVTTETEDGEENEYRADKVLVAVGRSPVTD TMDIENAGLEADDRGFL
SVDDRRRTDVEHIYAVGDVVEDTPMLAHVASKEGIVAAEHVAGEPVAFDSQAVPAAVFTD
PEIGTVGMTEADAEAGFTPVVGMFPFRASGRALTTNHADGFVRVVADEESGFVLGAQIV
GPEASELIAELAFAIEMGATLEDVASTIHTHPTLAEAVMEAAENALGQAIHTLNR

>sp|P31023|DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial OS=Pisum
sativum GN=LPD PE=1 SV=2

MAMANLARRKGYSLLSSETLRYSFSLRSRAFASGSDENDVVIIGGGPGGYVAAIKAAQLG
FKTTCIEKRGALGGTCLNVGCIPSKALLHSSHYHMAHGKDFASRGIEMSEVRLNL
QKDKAVSNLTRGIEGLFKKNKVTYVKGKGFVSPSEISVDTIEGENTVVKGKHII IATGS
DVKSLPGVTIDEKKIVSSTGALALSEIPKLLVIGAGYIGLEMGSVWGRI GSEVTVVEFA
SEIVPTMDAEIRKQFORSLEKQGMKFKLTKVVGVDTSGDGVKLTVEPSAGGEQTIIEAD
VVLVSAGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAI GDVIPGPMLAHKAE
EDGVACVEYLAGKVGHVVDYDKVPGVVYTNPEVASVGKTEEQVKETGVEYRVGKFPFMANS
RAKAIDNAEGLVKIIAEKETDKILGVHIMAPNAGELIHEAAIALQYDASSEDIARVCHAH
PTMSEAIKEAAMATYDKPIHI

>sp|P09623|DLDH_PIG Dihydrolipoyl dehydrogenase, mitochondrial OS=Sus
scrofa GN=DL D PE=1 SV=1

MQSWSRVYCTLAKRGHFNRIAHGLQGVSAVPLRITYADQPIDADVTVIGSGPGGYVAAIKA
AQLGFKTVCEKNETLGGTCLNVGCIPSKALLNNSHYHMAHGKDFASRGIEMSEVRLNL
EKMMEQKSNVAVKALTGGIAHLFKQNKVVVRVNGYGKITGKNQVTATKADGSTEVINTKNIL
IATGSEVTPFPGITIDEDTVSSTGALSLLKVPKMMVIGAGVIGVELGSVWQRLGADVT
AVELLGHVGGIGIDMEVSKNFQRI LQKQGFKFLN TKVIGATKKS DGNIDVSI EAASGGK
AEVITCDVLLVCIGRRPFTQNLGLEELGIELDPRGRI PVNTRFQTKIPNIYAIGDVVAGP
MLAHKAEDEGIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEYKVGK
FPFAANSRAKTNADTDGMVKILGQKSTDRVLGAHIIGPGGAGEMINEAALALEYGASCEDI
ARVCHAHPTLSEAFREANLAASFGKAINF

>sp|Q9I1L9|DLDH1_PSEAE Dihydrolipoyl dehydrogenase OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=lpdV PE=1 SV=1

MSQILKTSLLIVGGGPGGYVAAIRAGQLGIPTVLVEGAALGGTCLNVGCIPSKALIHAAE
EYLKARHYASRSALGIQVQAPSIDIARTVEWKDAIVDRLTSGVAALLKKGVDVVQGWAR
ILDGKSVAVELAGGGSQRICEHLLLAAGSQSVELPILPLGGKVISSTEALAPGSLPKRL
VVVGGGYIGLELGTAYRKLGVAVVEAQPRILPGYDEELTKPVAQALRRLGVELYLGH
LLGPSENGVRVRDVGAGEEREIAADQVLVAVGRKPRSEGWNLESGLDMNGRAVKVDDQCR
TSMRNVWAIGDLAGEPMLAHRAMAQGEMVAELIAGKRRQFAPVAIPAVCFTDPEVVVAGL
SPEQAKDAGLDCLVASFPFAANGRAMTLEANEGFVRVVARRDNLVVGWQAVGKAVSELS
TAFQAQSLQEMGARLEDIAGTIHAHPTLGEAVQEAALRALGHALHI

>sp|P31046|DLDH3_PSEPU Dihydrolipoyl dehydrogenase 3 OS=Pseudomonas putida GN=lpd3 PE=1 SV=1

MKSYDVVIIGGGPGGYNAAIRAGQLGLTVACVEGRSTLGGTCLNVGCMPSKALLHASELY
EAASGDEFALHGLIEVKPTLNLAQMMKQKDESVTGLTKGIEYLFRKNKVDWIKGWGRLDGV
GKVVVKAEDGSETALQAKDIVIATGSEPTPLPGVTIDNQRIIDSTGALSPLQVPKHLVVI
GAGVIGLELGSVWRRLLGSQVTVIEYLDRICTGDTTETAKTLQKALAKQGMVFKLGSKVTO
ATASADGVSLSVLEPAAGGTAESLQADYVLAIGRRPYTKGLNLESVGLTDRKGMALQRT
PPTSVPGVWVIGDVTSGPMLAHKAEDEAVACIERIAGKPHEVNYNLIIPGVIYTRPELATV
GKTEEQLKAEGRAYKVGKFPFTANSRAKINHETEGFAKVIADAETDEVLGVHLVGPVSE
MIGFCVAMEFSASAEDIALTCHPHPTRSEALRQAAMNVDGMAMQI

>sp|P31052|DLDH2_PSEPU Dihydrolipoyl dehydrogenase OS=Pseudomonas putida GN=lpdG PE=1 SV=4

MTQKFDVVVIGAGPGGYVAAIKAAQLGLKTACIEKYTDAEGKLALGGTCLNVGCIPSKAL
LDSSWKYKEAKESFNHVGISTGEVKMDVAMVGRKAGIVKNLTGGVATLTKANGVTSIQG
HGKLLAGKKVEVTKADGTTEVIEAENVILASGSRPIDIPPAPVDQNVIVDSTGALEFQAV
PKRLGVIGAGVIGLELGSVWARLGAEVTVLEALDTFLMAADTAVSKEAQKTLTKQGLDIK
LGARVTGSKVNGNEVEVYTNAEQEKITFDKLIIVAVGRRPVTTDLAADSGVTIDERGY
IFVDDYCATSVPGVYVYIGDVVRGMLLAHKASEEGIMVVERIKGHKAQMNYDLIPSVIYTH
PEIAWVGKTEQALKAEGVEVNVGTFPFAASGRAMAANDTGGFVKVIADAKTDRVLGVHVI
GPSAAELVQQGAIAMEFGTSAEDLGMVVFSSHPTLSEALHEAALAVNGGAIHVANRKKR

>sp|Q811C4|DLDH_MESAU Dihydrolipoyl dehydrogenase, mitochondrial (Fragment) OS=Mesocricetus auratus GN=DLD PE=1 SV=1

FNRSXSPGLQGVSSVPLRTYADQPIDADVTVIGSGPGGYVAAIKAAQLGFKTVKIEKNETL
GGTCLNVGCIPSKALLNNSHYHHLAAGKDFASRGIELSEVRLNLEKMMEQKSSAVKALTG
GIAHLFKQNKVVHVNFGNITGKNQVTATKADGSSQVIGTKNLIATGSEVTPFPGITID
EDTIVSSTGALSLLKKVPEKLVVIGAGVIGVELGSVWQRLGAEVTAVEFLGHVGGIGIDME
ISKKFQRILOKQGFKFLNPKVPGATKRSIDGKIDVSVEAAPGGKAEVPCDVLVLCIGRR
PFTQNLGLEELGIELDPRGRIPVNTFRQTKIPNIYVAGVAGPMLAHKAEDEGICVEG
MAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGIEYKVGKFPFAANSRAKTNADTD
GMVKILGQKSTDRVLGAHILGPGAGEMVNEAALALEYGASCEDIARVCHAHPTLSEAFR

>sp|P14218|DLDH_PSEFL Dihydrolipoyl dehydrogenase OS=Pseudomonas fluorescens GN=lpd PE=1 SV=3

MSQKFDVVVIGAGPGGYVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPSKAL
LDSSYKYHEAKEAFKVHVGIEAKGVTIDVPAMVARKANIVKNLTGGIATLTKANGVTSFEG
HGKLLANKQVEVTGLDGKTQVLEAENVIIASGSRPVEIPPAPLSDDIIVDSTGALEFQAV
PKKLVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEALKVLTQQLNIR
LGARVTASEVKKKQVTFTFDANGEQKETFDKLIVAVGRRPVTTDLAADSGVTLDERGF
IYVDDHCKTSVPGVFAIGDVVRGAMLAHKASEEGVMVAERIAHGKAQMNYDLIPSVIYTH
PEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTGLVKVIADAKTDRVLGVHVI
GPSAAELVQQGAIAMEFGTSAEDLGMVVFSSHPTLSEALHEAALAVNGHAIHIANRKKR

>sp|Q6P6R2|DLDH_RAT Dihydrolipoyl dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Dld PE=1 SV=1

MQSWSRVYCSLAKKGHFNRLSHGLQGASSVPLRTYSDQPIDADVTVIGSGPGGYVAAIKA
AQLGFKTVKIEKNETLGGTCLNVGCIPSKALLNNSHYHHLAAGKDFASRGIEIPEVRLNL
EKMMEQKRSVAVKALTGGIAHLFKQNKVVHVNFGKITGKNQVTATTADGSTQVIGTKNIL
IATGSEVTPFPGITIDEDTIVSSTGALSLLKKVPEKLVVIGAGVIGVELGSVWQRLGADV
TAVEFLGHVGGIGIDMEISKNFQRILOKQGFKFLNPKVPGATKRSIDGKIDVSVEAASGGK

AEVITCDVLLVCIGRRPFTQNLGLEELGIELDPKGRI PVNTRFQTKIPNIFAIGDVVAGP
MLAHKAEDGEIICVEGMAGGAVHIDYNCVPSVIYTHPEVAWVGKSEEQLKEEGVEFKVGK
FPFAANSRAKTNADTDGMVKILGHKSTDRILGAHILGPGAGEMVNEAALALEYGASCEDV
ARVCHAHPTLSEAFREANLAASFGKPINF
>sp|P99084|DLDH_STAAN Dihydrolipoyl dehydrogenase OS=Staphylococcus
aureus (strain N315) GN=pdhD PE=1 SV=1
MVGDFPIETDTIVIGAGPGGYVAAIRAAQLGQKVTIVEKGNLGGVCLNVGCIPSKALLH
ASHRFVEAQHSENGLVIAESVSLNFQKVQEFKSSVVNKL TGGVEGLLKGKVNIVKGEAY
FVDNNSLRVMDEKSAQTYNFKNAIIATGSRPIEIPNFKFGKRVIDSTGALNLQEVPGKLV
VVG GYIGSELGTAFANFGSEVTILEGAKDILGGFEKQMTQPVKKGMKEKGV EIVTEAMA
KSAEETDNGVKVTYEAKGEEKTIEADYVLVTVGRRPNTDELGLEELGVKFA DRGLLEVDK
QSRTSISNIYAIGDIVPGLPLAHKASYEAKVAAEAIDGQAAEVDYIGMPAVCFTEPELAT
VGYSEAQAKEEGLAIKASKFPYAANGRALSLDDTNGFVKLITL KEDDTLIGAQVVG TGAS
DIISELGLAIEAGMNAEDIALTIHAHPTLGEMTMEAAEKAIGYPIHTM
>sp|P72740|DLDH_SYNY3 Dihydrolipoyl dehydrogenase OS=Synechocystis sp.
(strain PCC 6803 / Kazusa) GN=lpdA PE=1 SV=3
MSQDFDYDLV IIGAGVGGHGAALHAVKCGLKTAIIEAKDMGGTCVNRGCIPSKALLAASG
RVREMSDQDHLQQLGIQINGVTF TREAIAAHANDLVSKIQS DLTNSLRLKVD TIRGWGK
VSGPQEVTVIGDNETRILKAKEIMLCPGSVFPVPPGIEIDHKTVFTSDEAVKLETLPQWI
AII GSGYIGLEFSDVYTALGCEVTMIEALPDLMPGFDPEIAKIAERVLIKSRDIETYTG V
FATKIKAGSPVEIELTDAKTKEVIDTLEVDACL VATGRIPATKNL GLETVGVETDRR GFI
EVNDQM QVIKDGKVPVPHLWAVGDATGKMMLAHAASGQGVVAVENICGRKTEVDYRAIPAA
AFTHPEISYVGLTEAQAKELGEKEGFVVSTAKTYFKGNSKALAEKETDGI AKVVYRQDTG
ELLAGAHIIGI HASDLIQEAAQAIADRKSVRELA FHVHAHPTLSEVLDEAYKRAV
>sp|P85207|DLDH_THESS Dihydrolipoyl dehydrogenase OS=Thermus scotoductus
(strain ATCC 700910 / SA-01) GN=lpd PE=1 SV=2
MKTYDLIVIGTGP GGYPAAIRGAQLGLKVLAVEAAEVGGVCLNVGCIPKALLHAAETVH
HLKGAEGFGLKAKPELDLKKLGAWRDGVVKKLTGGVAGLLKGNKVELLRGFARFKGPREI
EVNGETYGAQSFIIATGSEPMPLKGFPPGEDVWDSTRALRVEEGIPKRLLVIGGGAVGLE
LGQIYHRLGSEVTLIEYMPEILPAGDRETAALLRKALEKEGLKVRTGT KAVGYEKKQDGL
HVLLEAAQGGSQEEIVVDKILVAVGRRPRTEGLGLEKAGVKVDERGFIQV NARMETSAPG
VYAIGDVARPPLLAHKAMKEGLVAAENAAGKNALFDFQVPSV VYTGP EWAGVGLTEEEAR
KAGYNVKVGKFPFSASGRALTLGGAEGLIKVVGDAETDLLLGVFVVGPPQAGELIAEATLA
LEMGATVSDLGLTIHPHPTLSEGLMEAAEALHKQAIHILNR
>sp|P90597|DLDH_TRYCR Dihydrolipoyl dehydrogenase OS=Trypanosoma cruzi
GN=LPD PE=1 SV=1
MFRRCVAVKLNPDV VVIGGGPGGYVASIKAAQLGMKTACVEKRGALGGTCLNVGCIPSKA
LLHATHVYHDAHANFARYGLMGGEVMTMSAKMQQOKERAVKGLTGGVEYLFKKNKVTTY
KGEGSFETAHSIRVNGLDGKQEMFETKKTIIATGSEPT ELPFLPFDEKVVLSSTGALALP
RVPKTMVVIGGGVIGLELGSVWARLGAKVTVVEFAPRCAPT LDEDVTNALV GALAKNEKM
KFMTSTKVVGGTNNGDSVSLEVEGKNGKRETVTCEALLV SVGRRPFTGGLGLDKIN VAKN
ERGFVKIGDHFETSIPDVYAIGDVVDKGPMLAHKAEDGEVACAEILAGKPGHVNYGVI PA
VIYTMPEVASVGKSEELKKEGVAYKVGKFPFNANSRAKAVSTEDGFVKVLVDKATDRIL
GVHIVCTTAGELIGEACLAMEYGASSEDVGR TCHAHPTMSEALKEACMALVAKTINF
>sp|P80503|DLDH_SOLTU Dihydrolipoyl dehydrogenase (Fragment) OS=Solanum
tuberosum PE=1 SV=1
ASGSDENDVVVIGGGPGGYVAAIKAAQLGLKTTXIEKRGT
>sp|P80647|DLDH_HYMDI Dihydrolipoyl dehydrogenase (Fragment)
OS=Hymenolepis diminuta PE=1 SV=1
LSSGEKDLVVIGSGPGGYVAAIKAAQLGMLTVCIEKYPTFGGTCLNVGCIPSK
>sp|P84545|DLDH_POPEU Dihydrolipoyl dehydrogenase (Fragment) OS=Populus
euphratica PE=1 SV=1
VGKFPLLANSR
>sp|P0A9M8|PTA_ECOLI Phosphate acetyltransferase OS=Escherichia coli
(strain K12) GN=pta PE=1 SV=2
MSRIIMLIPTGTSVGLTSVSLGVIRAMERKGVRLSVFKPIAQPR TGGDAPDQTTTIVRAN
SSTTTAAEPLKMSYVEGLLSSNQKDVLMEEIVANYHANTKDAEVVLVEGLVPTRKHQFAQ
SLNYEIAKTLNAEIVFVMSQGTDTPEQLKERIELTRNSFGGAKNTNITGVIVNKL NAPVD

EQGRTRPDLSEIFDDSSKAKVNNVDPKALQESSPLPVLGAVPWSFDLIATRAIDMARHLN
ATI INEGDINTRRVKSVTFCARSIPHMLEHFRAGSLLVTSADRPDVLVAACLAAMNGVEI
GALLLTGGYEMDARISKLCERAFATGLPVFMVNTNTWQTSLSLQSFNLEVPVDDHERIEK
VQEVVANYINADWIESLTATSESRRLSPPAFRYQLTELARKAGKRIVLPEGDEPRTVKA
AAICAERGIATCVLLGNPAEINRVAASQGVELGAGIEIVDPEVVRESYVGRVLELRKNKG
MTETVAREQLEDNVVLGTLMLLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSV
FFMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAAAFGIEPRVAMLSYSTGTSGAGS
DVEKVVREATRLAQEKRPDLMDGPLQYDAAVMADVAKSKAPNSPVAGRATVFI FPDLNTG
NTTYKAVQRSADLISIGPMLQGMKRPVNDLSRGALVDDIVYTIALTAIQSAQQQ
>sp|P38503|PTAS_METTE Phosphate acetyltransferase OS=Methanosarcina
thermophila GN=pta PE=1 SV=3
MVTFLEKISERAKKLNKTIALPETEDIRTLQAAAKILERGIADIVLVGNEADIKALAGDL
DLSKAKIVDPKTYEKKDEYINAFYELRKHKGITLENAAEIMSDYVYFAVMMAKLGEVDGV
VSGAAHSSDTLRPAVQIVKTAKGAALASAFFIISVPDCEYGS DGTFLFADSGMVEMPSV
EDVANIAVISAKTFELLVQDVPKVAMLSYSTKGS AKSKL TEATI ASTKLAQELAPDIAID
GELQVDAAI VPKVAASKAPGSPVAGKANVFIFPDLNCGNIA YKIAQRLAKAEAYGPITQG
LAKPINDLSRGCSDEDIVGAVAITCVQAAAQDK
>sp|P39646|PTAS_BACSU Phosphate acetyltransferase OS=Bacillus subtilis
(strain 168) GN=pta PE=1 SV=3
MADLFSTVQEKVAGKDVKIVFPEGLDERILEAVSKLAGNKVLNPIVIGNENEIQAKAKEL
NLTLGGVKIYDPHTYEGMEDLVQAFVERRK GKATEEQARKALLDENYFGTMLVYKGLADG
LVSGAAHSTADTVR PALQIIKTKEGVKKTSGVFIMARGEEQYVFADCAINIAPDSQDLAE
IAIESANTAKMFDIEPRVAMLSFSTKGS AKSDETEKVADAVKIAKEKAPELTLDGEFQFD
AAFVPSVAEKKAPDSEIKGDANVFVFP SLEAGNIGYKIAQRLGNFEAVGPILQGLNMPVN
DLSRGCAEDVYNLALITAAQAL
>sp|Q8ZND6|PTA_SALTY Phosphate acetyltransferase OS=Salmonella
typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=pta PE=1 SV=1
MSRIIMLIPTGTSVGLTSVSLGVIRAMERKGVRLSVFKPIAQPRAGGDAPDQTTTIVRAN
STLPAAEPLKMSHVESLLSSNQKDVLMEEIIANYHANTKDAEVLVLEGLVPTRKHQFAQS
LNYEIAKTLNAEIVFVMSQGTDTPEQLNERIELTRSSFGGAKNTNITGVI INKLNAPVDE
QGRTRPDLSEIFDDSSKAQVIKIDPAKLQESSPLPVLGAVPWSFDLIATRAIDMARHLNA
TI INEGDIKTRRVKSVTFCARSIPHMLEHFRAGSLLVTSADRPDVLVAACLAAMNGVEIG
ALLLTGGYEMDARISKLCERAFATGLPVFMVNTNTWQTSLSLQSFNLEVPVDDHERIEKV
QEYVANYVNAEWIESLTATSESRRLSPPAFRYQLTELARKAGKRIVLPEGDEPRTVKA
AICAERGIATCVLLGNPDEINRVAASQGVELGAGIEIVDPEVVRESYVARLVLELRKSKGM
TEPVAREQLEDNVVLGTLMLLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSV
FMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAAAFGIEPRVAMLSYSTGTSGAGSD
VEKVVREATRLAQEKRPDLMDGPLQYDAAVMADVAKSKAPNSPVAGRATVFI FPDLNTGN
TTYKAVQRSADLISIGPMLQGMKRPVNDLSRGALVDDIVYTIALTAIQSAQQQ
>sp|P99092|PTAS_STAAN Phosphate acetyltransferase OS=Staphylococcus
aureus (strain N315) GN=pta PE=1 SV=1
MADLLNVLKDKLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
DLDISNIELINPATSELKAEVLVQSFVERRK GKATEEQAEQLLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTV R PALQIIKT KPGVSRTSGIFFMIKGDEQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGS AKSDDVTKVQEA VKLAQQKAEEEKLEAIDIGE
FQFDAAI VPGVAEKKAPGAKLQGDANVFVFP SLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSIEDVYNLSIITAAQALQ
>sp|Q6GJ80|PTAS_STAAR Phosphate acetyltransferase OS=Staphylococcus
aureus (strain MRSA252) GN=pta PE=1 SV=1
MADLLNVLKDKLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
NLDISNIELINPATSELKAEVLVQSFVERRK GKATEEQAEQLLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTV R PALQIIKT KPGVSRTSGIFFMIKGDEQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGS AKSDDVTKVQEA VKLAQQKAEEEKLEAIDIGE
FQFDAAI VPGVAEKKAPGAKLQGDANVFVFP SLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSIEDVYNLSFITAAQALQ
>sp|Q9X0L4|PTAS_THEMEA Phosphate acetyltransferase OS=Thermotoga maritima
(strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=pta PE=1 SV=1
MFLEKLVEMARGKGGKLA VAAANDDHVIEAVYRAWRERVCEPVLFGPEEEITRIIEELVP

EWKNPQIIDCPPEEAGRLAVEAVSKGECDFLMKGIKTGDLMKIYLDERYGLRTGKTMAM
VSVMEIPDFPRPLIISDPGMLISPTLEQKVDMIEHCVRVANVMGLETPKVAVVGAIEVVN
PKMPITMEEAAILSKMNQRGQIKGCIVDGPFDLNVVSEEAAKKGIQSPVAGKADILILP
DIEAANILYKALVFLAKAKSASTILGGKVPVVLTSRADSEETKFYSIALSAVFA
>sp|P9WHP1|PTA_MYCTU Phosphate acetyltransferase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=pta PE=1 SV=1
MADSSAIYLAAPESQTGKSTIALGLLHRLTAMVAKVGVFRPITRLSAERDYILELLLAHT
SAGLPYERCVGVTYQQLHADRDDAIAEIVDSYHAMADECDAVVVVGSYTDVTSPTELSV
NGRIAVNLGAPVLLTVRAKDRTPDQVASVVEVCLAELDTQRAHTAAVVANRCELSAIPAV
TDALRRFTPPSYVPEEPLLSAPTVAELTQAVNGAVVSGDVALREREVMGVLAAGMTADH
VLERLTDGMAVITPGDRSDVVLAVASAHAAEGFPSSLSCIVLNGGFQLHPAIAALVSGRLR
RLPVIATALGTYDTASAAAARGLVLTATSQRKIDTALELMDRHVDVAGLLAQLTIPIPTV
TTPQMFTYRLLQQARSDLMRIVLPEGDDDRILKSAGRLLQRGIVDLTILGDEAKVRLRAA
ELGVDLDGATVIEPCASELHDQFADQYAQLRKAKGITVEHAREIMNDATYFGTMLVHNCH
ADGMVSGAAHTTAHTVRPALEI IKTVPGISTVSSIIFLMCLPDRVLAYGDCAIIPNPTVEQ
LADIAICSAARTAAQFGIEPRVAMLSYSTGDSGKGADVDKVRATELVREARPEQLPVEGPI
QYDAAVEPSVAATKLRDSPVAGRATVLIFFDLNTGNNTYKAVQRSAGAIAIGPVLQGLRK
PVNDLSRGALVDDIVNTVAITAIQAQGVHE
>sp|Q9I5A5|PTA_PSEAE Phosphate acetyltransferase OS=Pseudomonas
aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=pta
PE=1 SV=1
MHTFFIAPTGFVGLTSSISLGLLRALERAGLKVGFFKPIAQLHPGDLGPERSSELVARTH
GLDTPKPLPLAQVERMLGDGQDLELEEIIISLYQRAAADKDVVIVEGMVPTRHASYAARV
NFHLAKSLDAEIVILVSAPENETLTELTDRIEIQQLFGGPRDPKVLGVILNKVRGEADAA
NAEDGVADFARRLTEHSPLLRDDFRLIGCIPWQDELNAARTRDIADLLSARVINAGDYEQ
RRVQKIVLCARAVPNTVQLLKPGLVVTGDRDDIILAASLAAMNGVPLAGLLLCSDFP
DPRIMELCRGALQGGLPVLSVATGSYDTATNLNRMNKEIPVDDRERAERVTEFVAGHIDF
EWLQKRCGTPRELRLSPPAFRYQVVQRAQKAGKRIVLPEGSEPRTVQAAAICQARGIARC
VLLAKPEEVQAVAQAQGIIVLPEGLEIIDPDLVRQRYVEPMVELRKGGKGLNAPMAEQQLED
SVVLATMMLALDEVDGLVSGAIHTTASTIRPALQLIKTAPGYNLVSSVFFMLLPDQVLVY
GCAVNPDPASDLAEIAVQSAASAQAFGIPARVAMISYSTGDSGSGVDVDKVRATRLA
REQRPDLLIDGPLQYDAAAIAVGRQKAPNSPVAGQATVFIFFDLNTGNNTYKAVQRSAD
CVSVGPMQLQGLRKPVNDLSRGALVEDIVYTIALTAIQADAQAPA
>sp|P0A6A3|ACKA_ECOLI Acetate kinase OS=Escherichia coli (strain K12)
GN=ackA PE=1 SV=1
MSSKLVLVNLCGSSSLKFAIIDAVNGEEYLSGLAECFHLPEARIKWKMDGNKQEAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVIDESVIQGIKDAASFA
PLHNPAHLIGIEEALKSFPQLKDKNVAVFDTAFHQTMPEESYLYALPYNLYKEHGIRRYG
AHGTSHFYVTQEAAMLNKPVEELNIITCHLGNSSVSAIRNGKCVDTSMGLTPLEGLVM
GTRSGDIDPAIIFHLHDTLGMVDINKLLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIIGAYTALMDGRLDVAVFTGGIGENAMVRELSLGLKGLVGLGFVDDHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA
>sp|P38502|ACKA_METTE Acetate kinase OS=Methanosarcina thermophila
GN=ackA PE=1 SV=1
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTH
KDALEEVVKALTDDEFGVIKDMGEINAVGHRVHVGGEKFTTSALYDEGVEKAIKDCFELA
PLHNPPNMMGISACAEIMPPTMVIVFDTAHQTMPPYAYMYALPYDLYEKHGVRKYGFH
GTSHKYVAERAALMLGKPAEETKIITCHLGNSSITAVEGGKSVETSMGFTPLEGLAMGT
RCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGLVSVGLSNDFRDLDEAASKGNRKAEL
ALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNK
IRGQEIDISTPDAKVRVFIPTNEELAIARETKEIVETEVLKLRSSIPV
>sp|P37877|ACKA_BACSU Acetate kinase OS=Bacillus subtilis (strain 168)
GN=ackA PE=1 SV=1
MSKIIAINAGSSSLKFQLFEMPSETVLTGLKGLVERIGIADSVFTISVNGEKNTEVTDIPDH
AVAVKMLLNKLTTEFGI IKDLNEIDGIGHRVHVGGEKFSDSVLLTDETIKEIEDISELAPL
HNPANIVGIKAFKEVLPNVPAAVAVFDTAHQTMPEQSYLYSLPYEYEEKFGIRKYGFHGT
SHKYVTERAAELLGRPLKDLRLISCHLGNASIAAVEGGKSIDTSMGFTPLAGVAMGTRS
GNIDPALIPYIMEKTGQTADEVLNTLNKKSGLLGISGFSDDLDRDIVEATKEGNERAETAL

EVFASRIHKYIGSYAARMSGVDIIFTAGIGENSVEVRERVLRLGLEFMGVYWDPALNNVR
GEEAFISYPHSPVKVMIIPDDEEVMIAARDVVRLAK
>sp|A0QQK1|ACKA_MYCS2 Acetate kinase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=ackA PE=1 SV=1
MTVLVNSGSSSLKYAVVRPASGEFLADGIIIEEIGSGAVPDHDAALRAAFDELAAGLHL
EDLDLKAUGHMVGKTFYKPSVVDDELIAKARELSPLAPLHNPPAIKIEVARKLLPD
LPHIAVFDTAFFHDLPPASTYAIIDRELAETWHIKRYGFHGTSHHEYVSQAAIFLDRPLE
SLNQIVLHLGNGASASAVAGGKAVDTSMGLTPMEGLVMGTRSGDIDPGVIMYLWRTAGMS
VDDIESMLNRRSGVLGLGGASDFRKLRELIESGDEHAKLAYDVYIHRLRKYIGAYMAVLG
RTDVISFTAGVGENVPPVRRDALAGLGGGLGIEIDDALNSAKSDEPRLISTPDSRVTVLVV
PTNEELAIARACVGVV
>sp|P63411|ACKA_SALTY Acetate kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=ackA PE=1 SV=1
MSSKLVLVNCGSSSLKFAIIDAVNGDEYLSGLAECFHLPEARIKWKMDGSKQEAAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDSASFA
PLHNPAHLIGIAEALKSFPQLKDKNVAVFDTAHFQTMPEESYLYALPYSLYKEHGVRRYG
AHGTSHFYVTQEAAMKLNKPVVEELNIITCHLNGGSSVSAIRNGKCVDTSMGLTPLEGLVM
GTRSGDIDPAIIFHLHDTLGMVDQINKMLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIGSYTALMDGRLDAVVFTGGIGENAAMVRELSLGLKLVGFVDFHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA
>sp|Q9WYB1|ACKA_THEME Acetate kinase OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=ackA PE=1 SV=1
MRVLVINSGSSSIKYQLIEMEKEKVLCKGIAERIGIEGSRLVHRVGDKEKHVIERELPDHE
EALKLILNLTLDVDEKLGVIKDLKEIDAVGHRVHGGERFKESVLVDEEVLKAIIEEVSPLAP
LHNPANLMGIKAAKLLPGVNVAVFDTAHFQTIPOKAYLYAIPYEEYKYKIRRYGFHG
TSHRYVSKRAAEILGKKLEELKIITCHINGASVAAVKYGKCVDTSMGFTPLEGLVMGTR
SGDLDPAPFFIMEKEGISPQEMYDILNKSGVYGLSKGFSSDMRDIEEAALKGDEWCKL
VLEIYDYRIAKYIGAYAAAMNGVDIVFTAGVGENSPITREDVCSYLEFLGVKLDKQKNE
ETIRGKEGIISTPDSRVKVLVPTNEELMIARDTKEIVEKIGR
>sp|A0QLU8|ACKA_MYCA1 Acetate kinase OS=Mycobacterium avium (strain 104) GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPESGVAASTGIVERIGEESSVPPDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALLGI
EVARRLLPGIAHVAVFDTGFFHDLPPAAATYAIIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFLDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSVVS
YLCHTAGMGVDDVESMLNHRSGVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHDTDVISFTAGIGENDAAVRRDAVSGMEELGIVLDERRNLPGAKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG
>sp|B2HPZ3|ACKA_MYCMM Acetate kinase OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=ackA PE=1 SV=1
MSASRPNRVVLVNSGSSSLKFQLVEPDSGMSRATGNIERIGEESSVPPDHDAALRRVFE
ILAEDDIDLQSCGLVAVGHRVHGGKDFYEPTLLNDAVIGKLEDELSPLAPLHNPPAVLCI
RVARALLPDVPHIAVFDTAFFHQLPPAAATYAIIDRELADRWQIRRYGFHGTSHRYVSEQA
AEFLGKPIGDLNQIVLHLGNGASASAVAGRPVETSMGLTPLEGLVMGTRSGDLDPGVIG
YLWRTAKLGVDEIESMLNHRSGMLGLAGERDFRRLRAMIDDGDPAELAYDVFIHRLRKY
VGAYLAVLGHDTDVVSFTAGIGEHDAAVRRDTLAGMAELGISLDERRNACPSGGARRISAD
DSPVTVLVIPTNEELAIARHCCSVLVAV
>sp|Q73T33|ACKA_MYCPA Acetate kinase OS=Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10) GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPEFGVAASTGIVERIGEESSVPPDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALQGI
EVARRLLPDIAHVAVFDTGFFHDLPPAAATYAIIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFLDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSIVS
YLCHTAGMGVDDVESMLNHRSGVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHDTDVISFTAGIGENDAAVRRDAVSGMEELGIVLDERRNLAGGKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG
>sp|P75245|ACKA_MYCPN Acetate kinase OS=Mycoplasma pneumoniae (strain ATCC 29342 / M129) GN=ackA PE=1 SV=1

MNDNKILVVNAGSSSIKFLQFDYHKKVLAKALCERIFVDGFFKLEFNEQKVEEKVAFPDH
 HAAVTHFLNLTLLKHKIIQELSDIILVGHVQVQGANVYFKDSVIVDAEALAKIKEFIKLAPL
 HNKPEADVIEIFFKEVPSAKNVAVFDTTFFHTTIPQENYLYAVPRSWEQKHLVRRYGFHGT
 SYKFNNYLEKHLNKQNLNLIVCHLGNASVCAIKNGKSFNTSMGFTPLEGLIMGTRSGD
 LDPAIIGYVAEQENMSASDVVNALNKKSGMLALTGASDMRDVFAKPQENAVAIKMYVNRV
 ADYIAKYLNLQLEGNIDGLVFTGGIGENASDCVELFINAVKSLGFATDLKLFVVKYGDSCVV
 STPQSKYKIYRVRTNEELMIVEDSIRLTQK
 >sp|P9WQH1|ACKA_MYCTU Acetate kinase OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) GN=ackA PE=1 SV=1
 MSSTVLVINSGSSSLKFQLVEPVAGMSRAAGIVERIGERSSPVADHAQALHRAFKMLAED
 GIDLQTCGLVAVGHRVVHGGTEFHQPTLLDDTVIGKLEELSALAPLHNPPAVLGKIVARR
 LLANVAHVAVFDTAFFHDLPPAAATYAIARDVDADRWHIRRYGFHGTSHQYVSERAAFLG
 RPLDGLNQIVLHLGNASASAIARGRPVETSMLGTPLEGLVMGTRSGDLDPGVISYLRWT
 ARMGVEDIESMLNHRSGMLGLAGERDFRRLRLVIETGDRSAQLAYEVFIHRLRKYL GAYL
 AVLGHTDVVSFTAGIGENDAAVRRDALAGLQGLGIALDQDRNLGPGHGARRISSDDSPIA
 VLVVPTNEELAIARDCLRVLGGRRRA
 >sp|Q99TF2|ACKA_STAAN Acetate kinase OS=Staphylococcus aureus (strain
 N315) GN=ackA PE=1 SV=1
 MSKLILAINAGSSSLKFQLIRMPPEELVTKGLIERIGLKDSIFTIEVNGEKVKTVQDIKD
 HVEAVDIMLDAFKAHNIINDINDIDGTGHRVVHGGTEKFPESVAITDEVEKEIEELSELAP
 LHNPANLMGIRAFRKLNPNI PHVAIFDTAFHQTMPEKAYLYSLPYHYKDYGIRKYGFHG
 TSHKFVSQRAAEMLDKPIEDLRIISCHINGASIAAIDGGKSIDTSMGFTPLAGVTMGT
 SGNIDPALIPFIMEKTGKTAEQVLEILNKESGLLGLSGTSSDLRDLSEEAESGKARSQMA
 LDVFASKIHKYIGSYAARMHGVDVIVFTAGIGENSVEIRAKVLEGLEFMGVYWDPKKNEN
 LLRGKEGFINYHSPVKVVIPTDEESMIARDVMTFGGLK

3. Acetate formation pathway IV.

>sp|P09373|PFLB_ECOLI Formate acetyltransferase 1 OS=Escherichia coli
 (strain K12) GN=pflB PE=1 SV=2
 MSELNEKLATAWEGFTKGDWQNEVNRDFIQKNYTPYEGDESFLAGATEATTTLWDKVME
 GVKLENRTHAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMI
 GSCKAYNRELDPMIKKIFTEYRKTNNQGVFDVYTPDILRCRKSGLTGLPDAYGRGRIIG
 DYRRVALYGIDYLMKDKLAQFTSLQADLENGVNLEQTI RLREEIAEQHRALGQMKEMAAK
 YGYDISGPATNAQEAIQWTFYFGYLA AVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQ
 EAQEMVDHLVMKLRMVRFLRTPPEYDELFSGDPIWATESIGGMGLDGRTLVTKNSFRFLNT
 LYTMGSPPEPNMILWSEKLPNFKKFAAKVSI DTSSLQYENDDLMRPDFNDDYAIACC
 VSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLMQVGPKEPIKGDVLNYDEV MERM
 DHFMDWLAKQYITALNI IHYMHDKYSYEASLMALHDRDVIRTMACGIAGLSVAADSLSAI
 KYAKVKPIRDEDGLAIDFEIEGEYPPQFGNNDPRVDDLAVDLVERFMKKIQKLHTYRDAIP
 TQSVLTITSNVYVGKKTGNTPDGRRAGAPFGPGANPMHGRDQKGAVASLTSVAKLPFAYA
 KDGISYTFISIVPNALGKDDEVRKTNLAGLMDGYFHHEASIEGGQHLNVNVMNREMLLDAM
 ENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTFTQSM
 >sp|P42632|TDCE_ECOLI PFL-like enzyme TdcE OS=Escherichia coli (strain
 K12) GN=tdcE PE=1 SV=2
 MKVDIDTSDKLYADAWLGFKGTDWKNEINVRDFIQHNYTPYEGDESFLAEATPATELWE
 KVMEGIRIENATHAPVDFDTNIATTTITAHDAGYINQPLEKIVGLQTDAPLKRALHPFGGI
 NMIKSSFHAYGREMDSEFEYLFDTLRKTHNQGVFDVYSPDMLRCRKSGLTGLPDGYGRG
 RIIGDYRRVALYGISYLVRERELQFADLQSRLEKGEDLEATIRLREELAEHRHALLQIQE
 MAAKYGFDISRPAQNAQEAQWLYFAYLA AVKSQNGGAMSLGRTASFLDIYIERDFKAGV
 LNEQQAQELIDHFIMKIRMVRFLRTPPEFDSLFSGDPIWATEVIGGMGLDGRTLVTKNSFR
 YLHTLHTMGPAPEPNLTILWSEELPIAFKKYAAQVSI VTSSLQYENDDLMRTDFNSDDYA
 IACCVSPMIVGKQMQFFGARANLAKTLLYAINGGVDEKLMQVGPKEPIKGDVLNYDEV MERM
 MDSLDFHMDWLAVQYI SALNI IHYMHDKYSYEASLMALHDRDVYRTMACGIAGLSVATDS
 LSAIKYARVKPIRDENGLAVDFEIDGEYPPQYGNNDERVDSIACDLVERFMKKIKALPTYR
 NAVPTQSILTITSNVYVGKKTGNTPDGRRAGTFFAPGANPMHGRDRKGAVASLTSVAKLP
 FTYAKDGISYTFISIVPAALGKEDPVRKTNLVGLLDGYFHHEADVEGGQHLNVNVMNREML

LDAIEHPEKYPNLTIRVSGYAVRFNALTREQQQDVISRTFTQAL

>sp|Q5HJF4|PFLB_STAAC Formate acetyltransferase OS=Staphylococcus aureus (strain COL) GN=pflB PE=1 SV=1

MLETNKNHATAWQGFKNGRWRNRHVDVREFIQLNYTLYEGNDSFLAGPTEATSKLWEQVMQ
LSKEERERGGMWDMDTKVASTITSHDAGYLDKDLETIVGVQTEKPFKRSMQPFGGIRMAK
AACEAYGYELDEETEKIFTDYRKTHNQGVFDAYSREMLNCRKAGVITGLPDAYGRGRIIG
DYRRVALYGVDFLMEEKMHDFNTMSTEMSEDVIRLREELSEQYRALKELKELGQKYGFDL
SRPAENFKEAVQWLYLAYLAAIKEQNGAAMSLGRTSTFLDIYAERDLKAGVITESEVQEI
IDHFIMKLRIKVFARTPDYNELEFSGDPTWVTESIGGVGIDGRPLVTKNSFRFLHSLDNLG
PAPEPNLTVLWSVRLPDNFKTYCAKMSIKTSSIQYENDDIMRESYGDDYGIACCVSAMTI
GKQMQFFGARANLAKTLLYAINGGKDEKSGAQVGNPFEGINSEVLEYDEVFKKFDQMMDW
LAGVYINSLNVIHYMHDKYSYERIEMALHDTEIVRTMATGIAGLSVAADSLSAIKYAQVK
PIRNEEGLVVDVEIEGDFPKYGNNDDRVDIAVDLVERFMTKLRSHKTYRDSEHTMSVLT
ITSNVVYGKKTGNTPDGRKAGEPFAPGANPMHGRDQK GALSSLSSVAKIPYDCKDGISN
TFSIVPKSLGKEPEDQNRNLTSM LDGYAMQCGHHLNINVFNRETLIDAMEHPEEYPQLTI
RVSGYAVNFIKLTREQQQLDVISRTFHESM

>sp|Q7A7X6|PFLB_STAAN Formate acetyltransferase OS=Staphylococcus aureus (strain N315) GN=pflB PE=1 SV=1

MLETNKNHATAWQGFKNGRWRNRHVDVREFIQLNYTLYEGNDSFLAGPTEATSKLWEQVMQ
LSKEERERGGMWDMDTKVASTITSHDAGYLDKDLETIVGVQTEKPFKRSMQPFGGIRMAK
AACEAYGYELDEETEKIFTDYRKTHNQGVFDAYSREMLNCRKAGVITGLPDAYGRGRIIG
DYRRVALYGVDFLMEEKMHDFNTMSTEMSEDVIRLREELSEQYRALKELKELGQKYGFDL
SRPAENFKEAVQWLYLAYLAAIKEQNGAAMSLGRTSTFLDIYAERDLKAGVITESEVQEI
IDHFIMKLRIKVFARTPDYNELEFSGDPTWVTESIGGVGIDGRPLVTKNSFRFLHSLDNLG
PAPEPNLTVLWSVRLPDNFKTYCAKMSIKTSSIQYENDDIMRESYGDDYGIACCVSAMTI
GKQMQFFGARANLAKTLLYAINGGKDEKSGAQVGNPFEGINSEVLEYDEVFKKFDQMMDW
LAGVYINSLNVIHYMHDKYSYERIEMALHDTEIVRTMATGIAGLSVAADSLSAIKYAQVK
PIRNEEGLVVDVEIEGDFPKYGNNDDRVDIAVDLVERFMTKLRSHKTYRDSEHTMSVLT
ITSNVVYGKKTGNTPDGRKAGEPFAPGANPMHGRDQK GALSSLSSVAKIPYDCKDGISN
TFSIVPKSLGKEPEDQNRNLTSM LDGYAMQCGHHLNINVFNRETLIDAMEHPEEYPQLTI
RVSGYAVNFIKLTREQQQLDVISRTFHESM

>sp|P0A9M8|PTA_ECOLI Phosphate acetyltransferase OS=Escherichia coli (strain K12) GN=pta PE=1 SV=2

MSRIIMLIPTGTSVGLT SVSLGVIRAMERKGVRLSVFKPIAQPR TGGDAPDQTTTIVRAN
SSTTTAAEPLKMSYVEGLLSSNQKDVLMEEIVANYHANTKDAEVVLEGLVPTRKHQFAQ
SLNYEIAKTLNAEIVFVMSQGTDTPEQLKERIELTRNSFGGAKNTNITGVIVNKL NAPVD
EQGRTRPDLSEIFDDSSKAKVNNVDP AKLQESSPLPVLGAVPWSFDLIATRAIDMARHLN
ATIINEGDINTRRVKSVTF CARSIPHMLEHFRA GLLVTSADRPDV LVAACLAAMNGVEI
GALLLTGGYEMDARISKLCERAFATGLPVFVMVNTNTWQTSLSLQSFNLEVPVDDHERIEK
VQEVVANYINADWIESLTAT SERSRRLSPPAFRYQLTELARKAGKRIVLPEGDEPRTVKA
AAICAERGIATCVLLGNPAEINRVAASQGVELGAGIEIVDPEVVRESYVGR LVELRKNKG
MTETVAREQLEDNVVLGTLMLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSV
FFMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAAAFGIEPRVAMLSYSTGTSGAGS
DVEKVVREATRLAQEKRPDL MIDGPLQYDAVMADVAKSKAPNSPVAGRATVFI FPDLNTG
NTTYKAVQRSADLISIGPMLQGM RKPVN DLSRGALVDDIVYTIALTAIQSAQQQ

>sp|P38503|PTAS_METTE Phosphate acetyltransferase OS=Methanosarcina thermophila GN=pta PE=1 SV=3

MVTFLEKISERAKKLNKTIALPETEDIRTLQAAKILERGIADIVLVGNEADIKALAGDL
DLSKAKIVDPKTYEKKDEYINAFYELRKHKGITLENAAEIMSDYVYFAVMMAKLGEVDGV
VSGAAHSSSDTLRPAVQIVKTAKGAALASAFFIISVPDCEYGS DGTFLFADSGMVEMPSV
EDVANIAVISAKTFELLVQDVPKVAMLSYSTKGS AKSKLTEATI ASTKLAQELAPDIAID
GELQVDAAIIVPKVAASKAPGSPVAGKANVFIFPDLNCGNIAYKIAQRLAKAEAYGPITQG
LAKPINDLSRGCSEDIVGAVAITCVQAAAQDK

>sp|P39646|PTAS_BACSU Phosphate acetyltransferase OS=Bacillus subtilis (strain 168) GN=pta PE=1 SV=3

MADLFSTVQEKVAGKDVKIVFPEGLDERILEAVSKLAGNKVLNPIVIGNENEIQAKAKEL
NLTLGGVKIYDPHTYEGMEDLVQAFVERRK GKATEEQARKALLDENYFGTMLVYKGLADG
LVSGAAHSTADTVR PALQIIKTKEGVKKTSGVFIMARGE EQYVFADCAINIAPDSQDLAE

IAIESANTAKMFDIEPRVAMLSFSTKGSAKSDETEKVVADAVKIAKEKAPELTLDGEFQFD
AAFVPSVAEKKAPDSEIKGDANVVFVPSLEAGNIGYKIAQRLGNFEAVGPILQGLNMPVN
DLSRGCNAEDVYNLALITAAQAL

>sp|Q8ZND6|PTA_SALTY Phosphate acetyltransferase OS=Salmonella
typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=pta PE=1 SV=1
MSRIIMLIPTGTSVGLTSSVSLGVIRAMERKGVRLSVFKPIAQPRAGGDAPDQTTTIVRAN
STLPAAEPLKMSHVESLLSSNQKDVLMEEIIANYHANTKDAEVVLEGLVPTRKHQFAQS
LNYEIAKTLNAEIVFVMSQGTDTPEQLNERIELTRSSFSGGAKNTNITGVIINKLNAPVDE
QGRTRPDLSEIFDSSKAQVIKIDPAKLQESSPLPVLGAVPWSFDLIATRAIDMARHLNA
TIINEGDIKTRRVKSVTFCARSIPHMLEHFRAGSLLVTSADRPDVLVAACLAAMNGVEIG
ALLLTGGYEMDARI SKLCERAFATGLPVFMVNTNTWQTSLSLQSFNLEVPVDDHERIEKV
QEYVANYVNAEWIESLTATSESRRLSPPAFRYQLTELARKAGKRVVLEPGEPRTVKAA
AICAERGIATCVLLGNPDEINRVAASQGVELGAGIEIVDPEVVRESYVARLVELRKSJGK
TEPVAREQLEDNVVLGTLMLQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSVF
FMLLPEQVYVYGDCAINPDPTAEQLAEIAIQSADSAIAFGIEPRVAMLSYSTGTSGAGSD
VEKVREATRLAQEKRPDLMDGPLYDAAVMADVAKSKAPNSPVAGRATVFIIPDLNTGN
TTYKAVQRSADLISIGPMLQGMKPVNDLSRGALVDDIVYTIALTAIQASQQQQ

>sp|P99092|PTAS_STAAN Phosphate acetyltransferase OS=Staphylococcus
aureus (strain N315) GN=pta PE=1 SV=1
MADLLNVLKDKLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
DLDISNIELINPATSELKAEVQSFVERRKGKATEEQAEQLLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTVPRALQIIKTKPGVSRTSGIFFMIKGDQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGSAKSDDVTKVQEAVKLAQQKAEKLEAII DGE
FQFDAAIVPGVAEKKAPGAKLQGDANVVFVPSLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSDVYNLSIITAAQALQ

>sp|Q6GJ80|PTAS_STAAR Phosphate acetyltransferase OS=Staphylococcus
aureus (strain MRSA252) GN=pta PE=1 SV=1
MADLLNVLKDKLSGKNVKIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKL
NLDISNIELINPATSELKAEVQSFVERRKGKTTEEQAQELLNNVNYFGTMLVYAGKADG
LVSGAAHSTGDTVPRALQIIKTKPGVSRTSGIFFMIKGDQYIFGDCAINPELDSQGLAE
IAVESAKSALSFGMDPKVAMLSFSTKGSAKSDDVTKVQEAVKLAQQKAEKLEAII DGE
FQFDAAIVPGVAEKKAPGAKLQGDANVVFVPSLEAGNIGYKIAQRLGGYDAVGPVLQGLN
SPVNDLSRGCSDVYNLSFITAAQALQ

>sp|Q9X0L4|PTAS_THEMEA Phosphate acetyltransferase OS=Thermotoga maritima
(strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=pta PE=1 SV=1
MFLEKLVEMARGKGGKLAFAAANDDHVIEAVYRAWRERVCEPVLFGPEEEITRIIEELVP
EWKNPQIIDCPPEEAGRLAVEAVSKGECDFLMKGIKTGDLMKIYLDERYGLRTGKTMAM
VSVMEIPDFRPLIISDPGMLISPTLEQKVDMIEHCVRVANVMGLETPKVAVVGAIEVVN
PKMPITMEAAILSKMNQRGQIKGCIVDGPFDLNVVSEEAAKKGIQSPVAGKADILILP
DIEAANILYKALVFLAKAKSASTILGGKVPVVLTSRADSEETKFYSIALSAVFA

>sp|P9WHP1|PTA_MYCTU Phosphate acetyltransferase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=pta PE=1 SV=1
MADSSAIYLAAPESQTKSTIALGLLHRLTAMVAKVGVFRPITRLSAERDYILELLLAHT
SAGLPYERCVGVTYQQLHADRDDAIAEIVDSYHAMADECDVAVVVGSDYTDVTSPTELSV
NGRIAVNLGAPVLLTVRAKDRTPDQVASVVEVCLAELDTQRAHTAAVVANRCELSAIPAV
TDALRRFTPPSYVPEEPLLSAPTVAELTQAVNGAVVSGDVALRERREVMGVLAAGMTADH
VLERLTDGMAVITPGDRSDVVLAVASAHAAEGFPLSCLVNLGGFQLHPAIAALVSGRLR
RLPVIATALGTYDTASAAAARGLVATSSQRKIDTALELMDRHVDVAGLLAQLTIPIPTV
TTPQMFTYRLLQARSIDLMRIVLPEGDDDRILKSAGRLLQRGIVDLTILGDEAKVRLRAA
ELGVDLDGATVIEPCASELHDQFADQYAQLRKAKGITVEHAREIMNDATYFGTMLVHNC
ADGMVSGAAHTTAHTVRPALEIIKTVPGISTVSSIFLMCLPDRVLAYGDCAIIPNPTVEQ
LADIAICSARTAAQFGIEPRVAMLSYSTGDSGKADVDKVRATELVRAAREPQLPVEGPI
QYDAAVEPSVAATKLRDSPVAGRATVLIIPDLNTGNNTYKAVQRSAGAIAIGPVLQGLRK
PVNDLSRGALVDDIVNTVAITAIQAQGVHE

>sp|Q9I5A5|PTA_PSEAE Phosphate acetyltransferase OS=Pseudomonas
aeruginosa (strain ATCC 15692 / PA01 / 1C / PRS 101 / LMG 12228) GN=pta
PE=1 SV=1
MHTFFIAPTGFVGLTSSISLGLLRALERAGLVKGVFFKPIAQLHPGDLGPERSSSELVARTH

GLDTPKPLPLAQVERMLGDGQDELLEEEIISLYQRAAADKDVVIVEGMVPTRHASYAARV
NFHLAKSLDAEVILVSAPENETLTELTDRIEIQQLFGGPRDPKVLGVILNKVREGADAA
NAEDGVADFARRLTEHSPLLRDFRLIGCIPWQDELNAARTRDIADLLSARVINAGDYEQ
RRVQKIVLCARAVPNTVQLLKPGVLVVTGDRDDIILAASLAAMNGVPLAGLLCSDFPP
DPRIMELCRGALQGGLPVLVSVATGSYDTATNLNRMNKEIPVDDRERAERVTEFVAGHIDF
EWLKQRCGTPRELRLSPPAFRYQVVQRAQKAGKRIVLPEGSEPRTVQAAAICQARGIARC
VLLAKPEEVQAVAQAQGVILPEGLEIIDPDLVRQRYVEPMVELRKGKGLNAPMAEQQLED
SVVLATMMLALDEVDGLVSGAIHTTASTIRPALQLIKTAPGYNLVSSVFFMLLPDQVLVY
GDCAVNPDPSASDLAEIAVQSAASAQAFGIPARVAMISYSTGDSGSGVDVVKVREATRLA
REQRPDLLIDGPLQYDAAAIASVGRQKAPNSPVAGQATVFIIPDLNTGNTTYKAVQRSAD
CVSVGPMLQGLRKPVNDLSRGALVEDIVYTIALTAIQADAQAPA
>sp|P0A6A3|ACKA_ECOLI Acetate kinase OS=Escherichia coli (strain K12)
GN=ackA PE=1 SV=1
MSSKLVLVNCGSSSLKFAIIDAVNGEEYLSGLAECFHLPEARIKWKMDGNKQEAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDAASFA
PLHNPAHLIGIEEALKSFPQLKDKNVAVFDTAFHQTMPEESYLYALPYNLYKEHGIRRYG
AHGTSHFYVTQEAAMKLNKPVVEELNIITCHLGNNGSVSAIRNGKCVDTSMGLTGLEGLVM
GTRSGDIDPAIIFHLHDTLGMVDAINKLLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIGAYTALMDGRLDAVVFTGGIGENAAMVRELSLGLKLVGFVVDHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA
>sp|P38502|ACKA_METTE Acetate kinase OS=Methanosarcina thermophila
GN=ackA PE=1 SV=1
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTH
KDALEEVKALTDDEFGVIKDMGEINAVGHRVHVHGGEKFTTSALYDEGVEKAIKDCFELA
PLHNPPNMMGISACAEIMPGTPMVIVFDTAFHQTMPPYAYMYALPYDLYEKHGVRKYGFH
GTSHKYVAERAALMLGKPAEETKIITCHLGNNGSSITAVEGGKSVETSMGFTPLEGLAMGT
RCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLGVSGLSNDFRDLDEAASKGNRKAEL
ALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNK
IRGQEIDISTPDAKVRVFIPTNEELAIARETKEIVETEVLKLRSSIPV
>sp|P37877|ACKA_BACSU Acetate kinase OS=Bacillus subtilis (strain 168)
GN=ackA PE=1 SV=1
MSKIIAINAGSSSLKQFLFEMPSETVLTGLVERIGIADSVFTISVNGEKNTEVTDIPDH
AVAVKMLLNKLTEFGI IKDLNEIDGIGHRVVHGGEKFSDSVLLTDETIKEIEDISELAPL
HNPANIVGIKAFKEVLPNVPAAVAVFDTAFHQTMPEQSYLYSLPYEYKFGIRKYGFHGT
SHKYVTERAAELLGRPLKDLRLISCHLGNNGASIAAVEGGKSIDTSMGFTPLAGVAMGTRS
GNIDPALIPYIMEKTGQTADEVLNTLNKKSGLLGISGFSSDLRDIVEATKEGNERAETAL
EVFASRIHKYIGSYAARMSGVDIIFTAGIGENSVEVRERVLRLGLEFMGVYWDPALNNVR
GEEAFISYPHSPVKVMIIPTEDEEVMIAARDVVRLAK
>sp|A0QQK1|ACKA_MYCS2 Acetate kinase OS=Mycobacterium smegmatis (strain
ATCC 700084 / mc(2)155) GN=ackA PE=1 SV=1
MTVLVNSGSSSLKYAVVRPASGEFLADGIIIEIGS GAVPDHDAALRAAFDELAAGLHL
EDLDLKA VGHMRVHGKTFYKPSVVDDELIAKARELSPLAPLHNPPAIKGI EVARKLLPD
LPHIAVFDTAFFHDL PASTY AIDRELAETWHIKRYGFHGT SHEYVSQAAIFLDRPLE
SLNQIVLHLNGASASAVAGGKAVDTSMGLTPMEGLVMGTRSGDIDPGVIMYLWRTAGMS
VDDIESMLNRRSGVLGLGGASDFRKLRELIESGDEHAKLAYDVYIHRLRKYIGAYMAVLG
RTDVISFTAGVGENVPPVRRDALAGLGLGIEIDDALNSAKSDEPRLISTPDSRVTVLVV
PTNEELAIARACVGVV
>sp|P63411|ACKA_SALTY Acetate kinase OS=Salmonella typhimurium (strain
LT2 / SGSC1412 / ATCC 700720) GN=ackA PE=1 SV=1
MSSKLVLVNCGSSSLKFAIIDAVNGDEYLSGLAECFHLPEARIKWKMDGSKQEAALGAG
AAHSEALNFIVNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDSASFA
PLHNPAHLIGIAEALKSFPQLKDKNVAVFDTAFHQTMPEESYLYALPYSLYKEHGVRRYG
AHGTSHFYVTQEAAMKLNKPVVEELNIITCHLGNNGSVSAIRNGKCVDTSMGLTGLEGLVM
GTRSGDIDPAIIFHLHDTLGMVDAQINKMLTKESGLLGLTEVTSDCRYVEDNYATKEDAK
RAMDVYCHRLAKYIGSYTALMDGRLDAVVFTGGIGENAAMVRELSLGLKLVGFVVDHER
NLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA
>sp|Q9WYB1|ACKA_THEMA Acetate kinase OS=Thermotoga maritima (strain ATCC
43589 / MSB8 / DSM 3109 / JCM 10099) GN=ackA PE=1 SV=1

MRVLVINSGSSSIKYQLIEMEGEKVLCKGIAERIGIEGSRLVHRVGDEKHVIERELPDHE
EALKLIINTLVDEKLGVIKDLKEIDAVGHRVHVHGGERFKESVLVDEEVLKAIEEVSPLAP
LHNPANLMGIKAAMKLLPGVFNVAVFDTAHFQTIPOKAYLYAIPYEYKEYKIRRYGFHG
TSHRYVSKRAAEILGKKLEELKIITCHIGNGASVAAVKYGKCVDTSMGFTPLEGLVMGTR
SGDLDP AIPFFIMEKEGISPQEMYDILNKKSGVYGLSKGFSSDMRDIEEAALKGDEWCKL
VLEIYDYRIAKYIGAYAAAMNGVDAIVFTAGVGENSPITREDVCSYLEFLGVKLDKQKNE
ETIRGKEGIIISTPDSRVKVLVPTNEELMIARDTKEIVEKIGR
>sp|A0QLU8|ACKA_MYCA1 Acetate kinase OS=Mycobacterium avium (strain 104)
GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPESGVAASTGIVERIGEESPPVDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVHVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALLGI
EVARRLLPGIAHVAVFDTGFFHDLPPAAATYAIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFLDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSVVS
YLCHTAGMGVDDVESMLNHRSGVVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHTDVISFTAGIGENDAARRDAVSGMEELGIVLDERNLPGAKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG
>sp|B2HPZ3|ACKA_MYCMM Acetate kinase OS=Mycobacterium marinum (strain
ATCC BAA-535 / M) GN=ackA PE=1 SV=1
MSASRPNRVVLVINSGSSSLKFQLVEPDSGMSRATGNIERIGEESPPVDHDAALRRVFE
ILAEDDIDLQSCGLVAVGHRVHVHGGKDFYEPTLLNDAVIGKLELSPLAPLHNPPAVLCI
RVARALLPDVPHIAVFDTAFFHQLPAAATYAIDRELADVWKIRRYGFHGTSHRYVSEQA
AEFLGKPIGDLNQIVLHLGNGASASAVAGRPVETSMGLTPLEGLVMGTRSGDLDPGVIG
YLWRTAKLGVDEIESMLNHRSGMLGLAGERDFRRLRAMIDDGDPAAELAYDVFIHRLRKY
VGAYLAVLGHTDVVSFTAGIGEHDAAVRRDTLAGMAELGISLDERRNACPSGGARRISAD
DSPVTVLVIPTNEELAIARHCCSVLVAV
>sp|Q73T33|ACKA_MYCPA Acetate kinase OS=Mycobacterium paratuberculosis
(strain ATCC BAA-968 / K-10) GN=ackA PE=1 SV=1
MDGSDGARRVLVINSGSSSLKFQLVDPEFGVAASTGIVERIGEESPPVDHDAALRRAFD
MLAGDGVLDNTAGLVAVGHRVHVHGGNTFYRPTVLDDAVIARLHELSELAPLHNPPALQGI
EVARRLLPDIAHVAVFDTGFFHDLPPAAATYAIDRELADRWQIRRYGFHGTSHRYVSEQA
AAFLDRPLRGLKQIVLHLGNGCSASAIAGTRPLDTSMLTPLEGLVMGTRSGDIDPSIVS
YLCHTAGMGVDDVESMLNHRSGVVGLSGVRDFRRLRELIESGDGAAQLAYSVFTHRLRKY
IGAYLAVLGHTDVISFTAGIGENDAARRDAVSGMEELGIVLDERRNLAGGKGARQISAD
DSPITVLVPTNEELAIARDCVRVLGG
>sp|P75245|ACKA_MYCPN Acetate kinase OS=Mycoplasma pneumoniae (strain
ATCC 29342 / M129) GN=ackA PE=1 SV=1
MNDNKILVFNAGSSSIKQFLFDYHKKVLAKALCERIFVDGFFKLEFNEQKVEEKVAFPDH
HAAVTHFLNLTLLKHKHIQELSDIILVGHVQVQGANVYFKDSVIVDAEALAKIKEFIKLAPL
HNKPEADVIEIFFKEVPSAKNVAVFDTTFTHTTIPOENYLYAVPRSWEQKHLVRRYGFHGT
SYKFINNYLEKHLNKQNLNLIIVCHLNGASVCAIKNGKSFNTSMGFTPLEGLIMGTRSGD
LDP AIIIGYVAEQENMSASDVVNALNKKSGMLALTGASDMRDVFAKPQENAVAIKMYVNRV
ADYIAKYNQLEGNIDGLVFTGGIGENASDCVELFINAVKSLGFATDLKLFVKYGDSCVV
STPQSKYKIYRVRTNEELMIVEDSIRLTQK
>sp|P9WQH1|ACKA_MYCTU Acetate kinase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=ackA PE=1 SV=1
MSSTVLVINSGSSSLKFQLVEPVAGMSRAAGIVERIGERSPPVADHAQALHRAFKMLAED
GIDLQTCGLVAVGHRVHVHGGTEFHQPTLLDDTVIGKLEELSALAPLHNPPAVLGIVARR
LLANVAHVAVFDTAFFHDLPPAAATYAIDRDVADRWHIRRYGFHGTSHQYVSERAAFLG
RPLDGLNQIVLHLGNGASASAIARGRPVETSMGLTPLEGLVMGTRSGDLDPGVISYLWRT
ARMGVEDIESMLNHRSGMLGLAGERDFRRLRLVIETGDRSAQLAYEVFIHRLRKYLGAYL
AVLGHTDVVSFTAGIGENDAARRDALAGLQGLGIALDQDRNLGPGHGARRISSDDSPIA
VLVPTNEELAIARDCVRVLGG
>sp|Q99TF2|ACKA_STAAN Acetate kinase OS=Staphylococcus aureus (strain
N315) GN=ackA PE=1 SV=1
MSKLILAINAGSSSLKFQLIRMP EEEELVTKGLIERIGLKDSIFTIEVNGEKVKTQDIK
HVEAVDIMLDAFKAHNIINDINDIDGTGHRVHVHGGKFPESVAITDEVEKEIEELSELAP
LHNPANLMGIRAFRKLNPNI PHVAIFDTAFHQTMP EKAYLYSLPYHYKDYGIRKYGFHG
TSHKFVSQRAAEMLDKPIEDLRIISCHIGNGASIAAIDGGKSIDTSMGFTPLAGVTMGTR

SGNIDPALIPFIMEKTGKTAEQVLEILNKESGLLGLSGTSSDLRDLSEEAESGKARSQMA
LDVFASKIHKYIGSYAARMHGVDVIVFTAGIGENSVEIRAKVLEGLEFMGVYWDPKKNEN
LLRGKEGFINYPHSPVKVVVIPTDEESMIARDVMTFGGLK